GENE NAME	GAM SEQ-ID	PRECUR SEQ-ID	ORGANISM	CHR	CHROMOSOME OFFSET	SOURCE REF-ID	SOURCE OFFSET	SRC	GAM ACC
GAM25	206	156	hsa			EST72223		1	C
GAM28	260	141	hsa	12	54105760	AW001829	19	3	B
GAM29	380	81	hsa	22		AW952936	350	3	C
GAM30	346	125	hsa					3	C
GAM31	250	118	hsa	12	57935221	12	57935221	7	A
GAM32	384	187	hsa	19		AI880781	287	3	C
GAM33	317	77	hsa	14		BI767711	362	3	C
GAM34	314	59	hsa	19		BE314459	527	3	C
GAM35	247	101	hsa	9		BF672917	612	3	C
GAM36	351	149	hsa					3	C
GAM37	266	197	hsa					3	C
GAM38	271	89	hsa	16		AI745004	261	3	C
GAM39	386	27	hsa	3		AL709699	260	3	C
GAM40	396	126	hsa	10	72533165	AI656172	179	3	B
GAM41	215	13	hsa	5	66039675	AA680311	248	3	C
GAM42	224	190	hsa	13		BF082911	61	3	C
GAM43	234	95	hsa					3	C
GAM44	287	188	hsa	11	48222381	THC1430784	123	1	A
GAM45	324	25	hsa	9	35395141	BF109609	211	3	C
GAM46	364	41	hsa	16		BE092454	326	3	C
GAM47	269	113	hsa	4	149681013	NT_016606	1573	3	A
GAM49	338	184	hsa	16		BM016609	244	3	C
GAM50	368	150	hsa	1		BE741747	201	3	C
GAM51	201	49	hsa	7	70576684	BE327494	266	3	C
GAM52	373	39	hsa	6	2480402	AI085403	227	3	C
GAM53	359	136	hsa	17		AW439339	148	3	C
GAM54	275	167	hsa					3	C
GAM55	387	5	hsa	16	69071145	THC1550782	595	1	B
GAM56	315	23	hsa	5	167913324	BE538084	123	3	C
GAM57	329	157	hsa					3	C
GAM58	306	185	hsa	6	47201318	BG402766	198	3	C
GAM59	377	30	hsa	11		BG913775	3	3	C
GAM60	381	80	hsa					3	C
GAM61	293	63	hsa	16		BG990766	155	3	C
GAM62	220	194	hsa	16		AI277769	262	3	C
GAM63	348	155	hsa	3	2	THC1428940	1	4	A
GAM64	239	85	hsa					3	C
GAM65	272	33	hsa	14	72936952	AV726476	310	3	B
GAM66	238	62	hsa	10	82042170	THC1596213	310	1	B
GAM67	282	37	hsa	17	38369449	THC1561873	1228	1	B
GAM68	251	128	hsa	19		AI032366	85	3	C
GAM69	258	96	hsa					3	B
GAM70	358	158	hsa	17	38540894	BQ024160	59	3	C
GAM71	257	163	hsa	12	56709260	AI052780	361	3	C
GAM72	342	198	hsa					3	C
GAM73	264	18	hsa	14		BF185120	311	3	C
GAM74	254	87	hsa	18	60841960	BG258808	428	3	C

GAM75 210 177 hsa 3 BI223210 258 3 C
GAM76 292 129 hsa 17 AW157423 268 3 C
GAM77 390 123 hsa 21 BI488926 566 3 C
GAM78 277 119 hsa 3 C
GAM79 352 200 hsa 3 C
GAM80 362 116 hsa 19 AI880781 148 3 C
GAM81 256 192 hsa 3 BE082837 27 3 C
GAM82 333 64 hsa 17 5198759 AL712226 135 3 C
GAM83 287 172 hsa 11 48222374 THC1430784 116 1 A
GAM84 204 98 hsa 19 BG391958 169 3 C
GAM85 227 182 hsa 3 C
GAM86 382 56 hsa 2 BG778757 623 3 C
GAM87 366 120 hsa 1 BE879870 694 3 C
GAM88 310 178 hsa 13 26570785 BM923673 254 3 B
GAM89 235 106 hsa 19 BF984706 533 3 C
GAM90 374 131 hsa 3 C
GAM91 336 130 hsa 1 50784242 AI832222 224 3 C
GAM92 308 60 hsa 3 C
GAM93 397 14 hsa 21 32921767 AI741382 297 3 C
GAM94 332 2 hsa 3 B
GAM95 273 104 hsa 19 23786019 BE733663 52 3 C
GAM96 394 121 hsa 17 60893521 THC1500459 169 1 A
GAM97 274 175 hsa 1 AU137216 23 3 C
GAM98 344 61 hsa 12 BF058105 504 3 C
GAM99 320 135 hsa 10 15 THC1481711 14 4 A
GAM100 243 91 hsa 7 56 THC1436384 55 4 A
GAM101 302 43 hsa 4 T58800 267 3 C
GAM102 349 15 hsa 3 C
GAM103 276 132 hsa 2 BI545524 251 3 C
GAM104 355 137 hsa 193 3 B
GAM105 318 138 hsa 3 C
GAM106 231 173 hsa 20 13445376 THC1578040 51 1 B
GAM107 341 79 hsa 3 C
GAM108 298 171 hsa 18 BE253206 211 3 C
GAM109 290 90 hsa 3 C
GAM110 375 115 hsa 19 6152245 BF205383 165 3 C
GAM111 311 3 hsa 6 BG682690 23 3 C
GAM112 263 195 hsa X 47490563 NT_011568 160 3 B
GAM113 233 74 hsa 3 C
GAM114 288 75 hsa 2 BF902557 96 3 C
GAM115 229 103 hsa 17 80233984 AA464277 317 3 C
GAM116 301 100 hsa mir-24 3 A
GAM117 216 151 hsa 16 4744406 BG469029 308 3 C
GAM117 267 151 hsa 16 4745341 BG469029 308 3 C
GAM118 363 160 hsa 3 C
GAM119 391 4 hsa 4 AI438930 407 3 C
GAM120 285 191 hsa 3 130315489 AI799504 301 3 C
GAM121 309 69 hsa 5 AI609093 274 3 C
GAM122 337 34 hsa 2 242201799 AU130704 312 3 C
GAM123 212 166 hsa 3 C

GAM124	323	108	hsa	14		BG770878	36	3	C
GAM125	330	44	hsa	6	6134811	AI073816	502	3	C
GAM126	312	148	hsa					3	C
GAM127	321	53	hsa	18		AI276053	372	3	C
GAM128	316	168	hsa	2		AW809287	140	3	C
GAM129	213	181	hsa	10		AA448642	243	3	C
GAM130	331	127	hsa	10		AI921837	212	3	B
GAM131	313	170	hsa					3	C
GAM132	369	114	hsa	5		BE546515	686	3	C
GAM133	211	88	hsa	3	148414074	THC1469923	114	1	B
GAM134	339	45	hsa					3	C
GAM135	248	142	hsa	15	88359935	AI636409	192	3	C
GAM136	279	159	hsa	1		BG434786	684	3	C
GAM137	202	76	hsa	17		BI260726	421	3	C
GAM138	222	179	hsa					3	C
GAM139	327	31	hsa	11	93064885	THC1496079	33	1	B
GAM140	295	51	hsa	16		BF204163	680	3	C
GAM141	357	94	hsa	2		BM702658	557	3	C
GAM142	219	92	hsa	1	70918040	NT_004464	698	3	A
GAM143	325	21	hsa	8		BE566431	653	3	C
GAM144	361	143	hsa	22	29007723	THC1576209	25	1	A
GAM145	335	82	hsa	20		BE867626	364	3	C
GAM146	370	20	hsa	12		BF570034	556	3	C
GAM147	298	196	hsa	18		BI596604	374	3	C
GAM148	280	65	hsa	5		AA903584	493	3	B
GAM149	237	146	hsa					3	C
GAM150	261	6	hsa	8		BE220844	33	3	C
GAM151	205	71	hsa					3	C
GAM152	378	52	hsa					3	C
GAM153	244	186	hsa					3	C
GAM154	228	176	hsa	7		BF312261	709	3	C
GAM155	207	26	hsa	19		AA741519	377	3	C
GAM156	262	54	hsa	1		AA174034	220	3	C
GAM157	225	193	hsa	10		AW771403	166	3	C
GAM158	383	47	hsa	1	112174058	AA343041	234	3	C
GAM159	230	109	hsa	9	125133292	AI084962	302	3	B
GAM160	343	174	hsa	3	150162171	AI681978	355	3	C
GAM161	304	24	hsa	1	3119977	BG029926	290	3	C
GAM162	376	58	hsa	17	76562126	AA625731	2	3	C
GAM163	249	84	hsa					3	C
GAM164	322	66	hsa	4		BG741187	198	3	C
GAM165	270	134	hsa					3	C
GAM166	232	161	hsa					3	C
GAM167	236	140	hsa					3	C
GAM168	217	97	hsa	19	48046908	H55888	242	3	C
GAM169	365	55	hsa	3		AA742544	433	3	C
GAM170	283	72	hsa					3	C
GAM171	392	17	hsa	2	242532302	AI963043	283	3	C
GAM172	253	86	hsa	1	195192414	BQ004992	384	3	C
GAM173	208	124	hsa					3	C

GAM174	252	16	hsa				3	C		
GAM175	265	28	hsa	X	557	THC1505396	556	4	B	
GAM176	345	73	hsa	2		AW471133	539	3	C	
GAM177	385	133	hsa				3	C		
GAM178	223	32	hsa	3		BG179277	124	3	C	
GAM179	300	19	hsa	15	33981297	NT_010194	190	3	B	
GAM180	214	107	hsa	11	128815436	THC1481692	812	1	B	
GAM181	395	35	hsa	7		BG675379	336	3	C	
GAM182	307	144	hsa	16	1427020	AI391577	237	3	C	
GAM183	240	7	hsa	17		BF746880	54	3	C	
GAM184	284	50	hsa	19		AW809289	419	3	C	
GAM185	372	78	hsa	12		BM823709	240	3	C	
GAM186	353	57	hsa	6		BE620228	580	3	C	
GAM187	294	83	hsa	17	48266940	AW085088	143	3	C	
GAM188	286	12	hsa	14		AI582402	196	3	C	
GAM189	246	9	hsa	4	95450006	NT_016354	52	3	B	
GAM190	289	99	hsa	3	151667587	NT_005612	265	3	A	
GAM191	389	165	hsa				3	C		
GAM192	393	70	hsa	2	208634246	AA620888	236	3	C	
GAM193	268	139	hsa	7	362	THC1461695	361	4	A	
GAM194	350	40	hsa	13	49043012	AI968206	296	3	C	
GAM195	334	122	hsa	4	39124959	BI496955	181	3	B	
GAM196	209	67	hsa	17		AI791435	425	3	C	
GAM281	278	164	hsa			128		3	B	
GAM391	326	199	hsa			114		3	C	
GAM633	340	68	hsa	12		BE560202	207	3	C	
GAM895	379	93	hsa	11	93949146	11	93949146	7	A	
GAM1032	303	169	hsa	8	141427181	8	141427181	6	A	
GAM1338	360	36	hsa			132		3	C	
GAM2033	305	117	hsa			175		3	C	
GAM2071	371	102	hsa			181		3	B	
GAM2608	245	153	hsa	X	131249166	X	131249166	6	A	
GAM3027	242	8	hsa			76		3	A	
GAM3229	221	46	hsa			99		3	C	
GAM3298	259	111	hsa	X	131248914	X	131248914	6	A	
GAM3418	291	147	hsa			mir-24		3	A	
GAM3431	356	105	hsa	12	6952115	12	6952115	6	A	
GAM3499	226	38	hsa			64		3	A	
GAM3770	241	29	hsa			mir-24		3	C	
GAM3770	281	29	hsa			mir-24		3	C	
GAM5227	299	162	hsa	1	200067225	THC1482185	355	1	B	
GAM5346	319	152	hsa			209		3	B	
GAM5385	218	22	hsa	3	35621433	3	35621433	6	A	
GAM7052	296	10	hsa	7		283		3	C	
GAM7080	399	183	hsa			50		3	C	
GAM7553	354	48	hsa	7	26917454	7	26917454	6	A	
GAM7776	246	110	hsa			176		3	C	
GAM7809	398	180	hsa			195		3	A	
GAM7933	203	145	hsa	7	3260217	7	3260217	7	A	
GAM7957	297	42	hsa			133		3	C	

GAM8145	328	112	hsa	184	3	C
GAM8297	367	154	hsa	157	3	B
GAM8358	255	189	hsa	166	3	C
GAM8554	388	1	hsa	198	3	B
GAM8678	347	11	hsa	138	3	C

GENE NAME	PRECUR	PRECURSOR-SEQUENCE SEQ-ID (5`_TO_3`)	FOLDED-PRECURSOR	SRC ACC	GAM
GAM25	156	GAGGCAGGAGAATTGCTTGA ACCCAGGAAGTGGAGGCTTC AGTGAGCTGAGAACACGCCA CTGCACTCCAGTCCTGGGCA ACAGAGCAAGACTCTGTCTC	G AA GAA-- AG GCTT A - AGAA GAGGCAG AG TTGCTT CCCAGGA TGGAG CAGTG GC TG CTCTGTC TC AACGAG GGGTCCT ACCTC GTCAC CG AC - AG ACAAC G- AC-- - C ----	1	C
GAM28	141	GGGTTATCTGCAACTGAGAG GGGCTGGTTAAGGCGTCCCC AAGTTGGAAGGGCGCTTTGC TTCTGTTTTCTGGATGCAGA GTCCT	TTA A - G CT T -- AAGTT GGG TCTGCA CT GAGAG GG GGT AAGGCGTCC CC TCC AGACGT GG CTTTT TC TCG TTTCGCGGG GG TG- A T G T- - AA -----	3	B
GAM29	81	TGGTGGTGGCAGACTTTGGG CTGTCACGGCTCATAATGGA AGAGAGGAAAAGGGCCCCCA TGGAGAAGGCCACCCCCA	T AGA ---- G--- ACGG ATAATGGAA TGG GGTGGC CTTT GGGCT TC CTC ACC CCACCG GAGG CCCGG AG GAG C GAA TACC GAAA GA-- ---------	3	C
GAM30	125	TGAGGCGAGAGAATCGCTTG AACTGGGAGGCAGAAGTTGC AGTGAGCCAAGATCGTATCA TTGCACTCCAGCCTGGGCCA CAGAGCGAGACTCTGTCTCA	G AA GAAC G-- AGA T GCCAAGATCGTA TGAGGC AGAG TCGCTT TGG AGGC AGT GCAGTGA ACTCTG TCTC AGCGAG ACC TCCG TCA CGTTACT - AG AC-- GGG ACC - ----------	3	C
GAM31	118	GGCTGTGGCTGGATTCAAGT AATCCAGGATAGGCTGTTTC CATCTGTGAGGCCTATTCTT GATTACTTGTTTCTGGAGGC AGCT	GG TG TT C GTTTCCATCTGTGA GGCTGTGGCTGGATTCAAGT TCGACG G CT GTTCATTAG TCTTATCCGG GA GT TT T ----------	7	A
GAM32	187	TGCATCTTCATCTTGGTCAC CACGCCAGAGAGGATCCGCC CTCGAATGGACACATTACCA GTGAAGGGGCA	AT CT CACCACG GA- ATCCGC TGC CTTCAT TGGT CCA GAGG ACG GAAGTG ACCA GGT CTCC GG -- TTACACA AAG ------	3	C
GAM33	77	CACAACACTGCCATGCAACA CCTTCAGAGTCGTTGGAGTC AAGTTGCAGGATCAGCAGGT TGTG	A CA---- AC-- AGTCG CACAAC CTGC TGCAAC CTTCAG GTGTTG GACG ACGTTG GAGGTT - ACTAGG AACT -----	3	C
GAM34	59	CCTGGGCCTGCCCACTCCCA CGCCCTTCACCAATGCCGTC CAGCTGCTGCTGACGCTGAA GCTGGTGAGCCTGGCCAGTG AAGTCCAGG	CTGCC C- C CCT AT ----- C TGCT CCTGGGC CACT CCA GC TCACCA GC CGTC AGC GGACCTG GTGA GGT CG AGTGGT CG GCAG TCG AA--- CC C --- -- AAGTC - ----	3	C
GAM35	101	TGGTGAGGAATGTATCATCT TTTTGTCTCATATTACAAAT GGGCCAATACGGACTTGCCA	TG GAA CA- T CTCATATT TGG AG TGTAT TCT TTTGT ACC TC GCATA GGG AAACA	3	C

GT AG- ACC T --------
GAM36 149 GAAGTGGTAAAGCCTGGGGC TG AA T -- T AGTTG 3 C
TTCAGTGAAGTTGTCCTGCA GAAG GT AGCC GGGGCTT CAG GA
AGGCTTCTGGCTACATCTTC CTTC CA TCGG CTTCGGA GTC CT
TA -- T AC - -----
GAM37 197 GGCGCTATATATGGATCCAA AT G CAA - A ATCATGACA 3 C
TGGCAAGATCATCATGACAG GGCGCT ATAT GATC TG GCA GATC
ATCTGCGCGCGATCGATATC TCGCGA TATA CTAG GC CGT CTAG
AGCGCT C- G C-- G - ---------
GAM38 89 GCTGGGCCTGTTGGTCAGGC ---- T T CAG T - T CACTG 3 C
ATGGAGGAGCTGTGTGGTCA GCTG GGCC GT GGT GCA GGAG GAGCTG GTGGT
CTGGCCACTGGCTCTCTTCT TGAC TCGG CG CCA CGT CTTC CTCGGT CACCG
GCACCACCGCCGGCTCTGAC AGTC C - CCA - T - -----
AGT
GAM39 27 GTATGCACAGACAGAGTTGG G AGAG A-------- ACATAT GGCCTGGAGA 3 C
GACATGGGACATATCTTCAG GTAT CACAGAC TTGGG CATGGG CTTCAG
GGCCTGGAGACTGAAGCCAC CATA GTGTTTG GACCC GTATCC GAAGTC
CTATGACGCAGCCACCCAGG - AG-- ACCGACGCA ACC--- ----------
AGTTTGTGATAC
GAM40 126 GGTACAGTTGGTGGCTATCA - T TG A AA - T - AATT 3 B
AATTAGGACTCAGTAATTAC GGTA CAGT GG GCT TCA TTAG GAC CA GT
TTGTGTCACTGAGTGAAAGC CCGT GTTA TC CGA AGT AGTC CTG GT CA
TGCTCATTGCTGCC C C GT A G- A T T ----
GAM41 13 GGCTAAATTTATTTTCTTGT AAATTTATT TT CCTAGCA TTC- TATTCTTT 3 C
GTCTGCCTAGCAAGATAATT GGCT TTC GTGTCTG AGATAAT TC
TCTCTATTCTTTGACAGTAT CCGA AAG CACGGAC TCTGTTA AG
TGTCTCAGGCACCTGAATCA ATCCAGACT TC ------- TGAC --------
GACCTAAGCC
GAM42 190 GTAGTCTCCACTGGAGAAGT CTCCA ATTGA A GCC 3 C
TAATTGATGAGTAGTAGCCT GTAGT CTGGAGAAGTTA TGAGT GTA
ACAACTCAGGCTCTAGCTTC CATCA GACCTCTTCGAT ACTCA CAT
TCCAGGAACACTAC CAAG- CTCGG A ---
GAM43 95 ACTTTAAGAACTCGAATATA AG C ATA- TTAAATTAAC AG AAAGTAACAA 3 C
GGTCTTTTAAATTAACCAGT ACTTTA AACT GA TAGGTCTT CAGTC AC
CAGACAAAGTAACAAGTAGG TGAAAT TTGG CT GTTCGGAA GTCAG TG
ACTGAAACGAACAAGGCTTG GG C AAGA CAAGCAAA-- GA ----------
AGAATCCGGTTGGTAAAGT
GAM44 188 GAAAAGGTGGTGTCATGTTT - TG G ATGT AATCTTA 1 A
TGGGGAGAATCTTACTTCTC GAAAAG G GT TC TTTGGGGAG
AAATGGAAATTGCACTTTTT TTTTTC C TA AG AAACTCTTC
A GT A GT-- -------
GAM45 25 ACAAGTCTTGGGAAGTCCAT AG A CATCT TCT AAA 3 C
CTGACTCTCTGAAACAGTTT ACA TCTTGGGA GTC GAC CTG
GTCTCTGACCTCCCAGGAAG TGT AGGACCCT CAG CTG GAC
TGT GA C TCT-- TTT ---
GAM46 41 TTTGGGTGGATGCTGCTCTC TG TG A - - --- C CATCT 3 C
GAATAAGTCGGACATCTTCT TT GG G TGCTGC TCT CGAATA AGT GGA
ACTCTTTGTTCGAAGGTGCG AA TC C GCGGCG GGA GCTTGT TCA TCT
GCGCTGCTTGAA GT GT - T A TTC - -----
GAM47 113 GCCTACTGACTTAATAAATT T- AA-- AA C AA CTG AGC TCC 3 A

TCAGAGGCAGAAGAGAAGCT GCC ACTGACTT TA TTT AGAGGCAG GAGAAG CAG TCAG

GCAGAGCTCAGTCCTTGACA TGG TGACTGGA GT GAA TCTTCGTC CTCTTT GTC AGTT

CTGAACTTTCTCACTGCTTC TT GAAG GG - A- CAA AC- ---
TAAGGGTGGAAGAGGTCAGT
TTGGT

GAM49 184 ATGCGTGACGCCATCCCGCA - - A CG TCATC T A CGAAGCC 3 C
GCTCATCCAGCTGGACCAGG ATGCGT G ACGCC TCC CAGC CAGC GG CCAGG
CGAAGCCCCTGGCCGCTGTG TGCGCA C TGTGG AGG GTCG GTCG CC GGTCC
CTGAAGGAGGTGTGCGACGC G G - AA T---- - - -------
GT

GAM50 150 ATGTGGTCAGTGGGTTGCAT G A GGG - A T T--- GACTCAGA 3 C
CTTCGGGGAGCTGCTGACTC AT TGGTC GT TTG C TCT CGGGGAGC GCT
AGAAGCCTCTGTTCCCCGGG TA ACTAG TA GAC G AGG GCCCCTTG CGA
AAGTCAGAAATCGATCAGAT G C AA- T A - TCTC --------

GAM51 49 TGTGGGGTGCCCCCGATGGG TGCCCCC A TCCCATCTCC 3 C
AGGCTGTCCCATCTCCCAGT TGTGGGG GATGGG GGCTG
CCCCATCTCTTTTTCCCCAC ACACCCC CTACCC CTGAC
A TTTTTCT - ----------

GAM52 39 TGTCCCGTTCATCAATTTCT GTTCA A T -- ----- GG A TGC 3 C
CCTCTGCAGGGTGAGCTGTG TGTCCC TC ATT CTCCT CTG CAG TG GCTGTGG
GTGCCCGCAGCCAAACTGGG ACAGGG AG TGA GGGGA GAC GTC AC CGACGCC
TTCCAGTTAGGGGCAGTAGA GTTG- A C TT CTTGG AA - ---
GTTGGGGACA

GAM53 136 TCTGCAATGGCTGCCAGGCG G- - GGA A CCT- C CATCCC 3 C
GATCACTCCTCCACTGGAGC TCTGCAAT GCTGCCAG GC TC CT CCA TGGAGC
CATCCCGCTCCATGGCCAAA AGACGTTA TGACGGTT CG AG GA GGT ACCTCG
GCGAGAGCATTGGCAGTGAA AG A AG- C AACC - ------
TTGCAGA

GAM54 167 GGAGTGGAGGGGGCTGCCCA GT ------ CCCTC TACA 3 C
CCCTCGCTGTACACAGCTGG GGA GGAGGGGGCT GCCCA GCTG
GCCCAGATGGCCCCTTCTGA CCT TCTTCCCCGG CGGGT CGAC
TCC AG TAGACC ----- ----

GAM55 5 ACTGGAAATCACTGCCATTT ATCAC TCC - A--------- AGTTTTG 1 B
CCAGGAGATCACCTATCCTA ACTGGAA TGCCATT AGGAGATC ACCT TCCT
GTTTTGAGGAATAGTCATTG TGATCTT ACGGTAA TCCTTTGG TGGA AGGA
AGGTGGGTTTCCTTAATGGC CTCT- T-- G GTTACTGATA -------
ATCTCTTCTAGT

GAM56 23 GCTTCATTCATGGCTGTGTT TT- T---- TT TAACTAAAGTAAATTTTT 3 C
TGAGATAACTAAAGTAAATT GCTTCA CATGGC GTG TGAGA
TTTTTTCAGGTATTTGGTGT TGAGGT GTACTG TAT ACTTT
CATGTTTTGGAGT TTT TGGTT GG ----------

GAM57 157 GCTTGGGTGACAGAGTGAAA T -- C G -- CC A AAATAAATAAATAA 3 C
GCCCCATCTCTAAATAAATA GC TGGG TGA AGA TGAA AG CC TCTCT
AATAAAGAGAGGTCCTGATT TG ACCC ACT TTT ACTT TC GG AGAGA
CAGTTTATCAATCCCATGT T TA A G AG CT - ----------

GAM58 185 GCAATTCAACTTTGAGTTAT ------- C G CTTTTA T- TGTAT 3 C
CTTTTAAATATGTCTTGTAT GCAAT TCAA TTT AGTTAT AATATG CT
AGTTCATATTCATGGCTGAA CGTTA AGTT AAA TCGGTA TTATAC GA

ACTTGACCACACTATTGC TCACACC C G C----- TT -----

GAM59 30 CGACCTCGGGTCCACGTGTC AC C A- T TACTCGCC AGCCT 3 C

CCGGTACTCGCCGGCCGGAG CG CT GGGTCC CG GTCCCGG GGCCGG

CCTCCGGCTTCCCGGGGCCG GC GA TCCAGG GC CGGGGCC TCGGCC

GGGGACCTTAGCG -- T GG - CT------ -----

GAM60 80 TGCGTGTCCTAACTGGTTGG T--- A T G AAAACT ATCAC 3 C

AAAAACTGTGATCACCACTT TGCG GTCCT AC G TTGGA GTG

CAAGTGTAGGGACTCCTCGC ACGC CAGGG TG T AACTT CAC

A TCCT A - G ------ -----

GAM61 63 CTGGCAGCGCTTCAAGTCAT G CTTCAA T G C A C GATCTCAGG 3 C

GGTCCCCATCATGCAGGATC CTG CAGCG G CAT GT CCCATC TG AG

TCAGGCTCCACGATGGGCAC GAC GTCGT C GTA CA GGGTAG AC TC

AATGCCATTCTGCTGGCAG G CTTAC- - A C C C ---------

GAM62 194 CCTCGGCCGACTTTCCCAGG CCGA TC CA - - A- T AGTGTGCAG 3 C

CAGTGCAGGCTAGCCCAGTC CCTCGG CTT CCAGG GTG CAG GCT GCCCAG CCAGG

CAGGAGTGTGCAGCCTGGCT GGGGTC GAA GGTCT CAC GTC CGA TGGGTT GGTCC

TGGGTCGAGCTCTGTCACAT AAC- TA A- T T GC C ---------

CTGGATAAGCAACTGGGG

GAM63 155 GTGAGAAAGCACTGGGGTCC AGA ACT --- T G AGATG GCCATA 4 A

AGATGGGGAGAAGATGTTCT GTG AAGC GG GG CCAGAT GGGAGA TTCT

GCCATAAGAAAATCTCCTGG CAC TTCG CC CC GGTCTG TCCTCT AAGA

TCTGGTCCGTGCCTTGGCTT GA- GTT GTG T G AA--- ------

AGCAC

GAM64 85 GTGGCTCGGCTCAGCTGCCT CT T CT TG CC CCTA- CCTGT 3 C

GGGTTGTGGCCGCCCTAGCA GTGGCTCGG CAGC GC GGGTTG G GC GCAT

TCCTGTATGCCCACAGCTAC CACCGGGCC GTCG CG CCTAAT C CG CGTA

TGTAATCCCCGCTGCTGCTC TC T CC GT AT ACACC -----

CGGGCCAC

GAM65 33 TCTGCTGCTTCAACAACAGT TTCAACAAC G G C T CAGT 3 B

GACTTGCTCTCCAATGGTAT TCTGCTGC AGT ACTT CTCT CAATGG ATC

CCAGTGATTCGTTGAAGAGG AGACGATG TCG TGGA GAGA GTTGCT TAG

AGGTGCTCTGTAGCAGA TC------- - G A - ----

GAM66 62 AGTTTTGCACCTGAGACAGA A TCACTC TC- CCTA 1 B

TAGCCTCACTCGCCTCACCC AGTTTTGCACCTGAGACAGAT GCC GCC AC

TAGTCCTGGTGGCATTTGTC TTAAAACGTGGACTCTGTTTA CGG TGG TG

TCAGGTGCAAAATT - ------ TCC ----

GAM67 37 GGATGGGCTTGTGGTTAGCA T CT - G GG CA CTGCTTCA 1 B

GTTTTTGCCAGGATCATAGG GGA GGG TGT GGTTAGCA TTTTTGCCA AT TAGG

CTGCTTCACTTAGAGTAGTG CCT TCT ACA CCAGTCGT AGAAACGGT TG ATTC

GCAAAGATGCTGACCTACAT - T- T - GA AG --------

TCTTCC

GAM68 128 GGTCAGACAGGGGGACAGGG AGAC GG GGCAGA - A- GCTT 3 C

CAGAGCTAGCATAACTCAGG GGTC AGG GACAG GCTA GCATA CTCAG

CTTTTGGGGATGTGCATGGC CCGG TCC TTGTC CGGT CGTGT GGGTT

AGCTGTTTTCCTTTGGGGCC GGTT TT GA---- A AG ----

GAM69 96 TAACAACGAGGCCAGGAGGG AG C TTTTTACACAGA AGTGAG 3 B

ATTTTTACACAGACCCGAGT TAACAACG GC AGGAGGGA CCCG

GAGTGGGGGGACAATATTTT GTTGTTGT TG TCCTCCCT GGGT

CCCTCCTAGTTGTGTTGTTG GT A TTTATAACAGGG ------

GAM70 158 CAGAGTATATGGGGGCCTCT AT--- GC TGC-- C-- GCTGGGA 3 C
GCCACCCCCCAGGCTGGGAC CAGAGT ATGGGG CTC CAC CCCCAG
TGGGGCCTGTGACCTTGAGA GTCTTA TACTCC GAG GTG GGGGTC
ACCTCATCTCACATTCTG CACTC AA TTCCA TCC -------

GAM71 163 GCAGTTGTCAAATACCAGGA AG AAATA AGG CG AACTCCTC 3 C
GGGCATCAGCCGCAAACTCC GC TTGTC CCAGG GCATCAGC CA
TCTGAGCTGGTGTACCTGGA CG GACGG GGTCC TGTGGTCG GT
CAGGGCAGGGGC GG GACA- A-- A- --------

GAM72 198 TCGAACTCCTGACCTCGTGA A- C A C GCC C CCTC 3 C
TCTGCCCGCCTTGGCCTCCC TCGA CTC TG CCT GTGATCT CGC TTGG
AAAGTGCTGGGATTACAGGC GGCT GAG AC GGA CATTAGG GTG AACC
ATGAGCCTCGG CC T - - GTC A ----

GAM73 18 GGGAAATTTGCCTTTACCAC AA TA- AC AAGA T TG TTGAA 3 C
TGAAGATTATGACATGTTTG GGG ATTTGCCTT CC TG TTA GACA T
AAGTGTGTTTTGAGAGCAAG TCC TAGGCGGGA GG AC AGT TTGT G
GGAACAGGGCGGATACCT A- CAA GA GAG- T GT -----

GAM74 87 CAGGATAATAATATGGGGTC TAATA GG T TC CACCTTTT 3 C
TTGTCCTTCACCTTTTAAGT CAGGATAA TG GTCT G CTT
TCAGGCAACAGTTTGTCCTG GTCCTGTT AC CGGA C GAA
TG--- AA - TT --------

GAM75 177 GTCCTTTCTCTGGAGAGGCT TTCTCT---- TG CTCA ACGCTA 3 C
TGTGGGGCCTCAGGACGCTA GTCCT GGAGAGGCTTG GGGC GG
CCCACTGCTCTCCGGGCCTC CAGGG CCTCTCCGGGC CTCG CC
TCCTGCCGCCTCTGGGAC TCTCCGCCGT CT TCAC ------

GAM76 129 CTGTGCACCTCGTGGTAAAA G -- TAA--- CTT - C -- G TCATAT 3 C
CTCTTTGGGGTTCGCCAGCT CTGT CA CCTCGTGG AACT TGGG GTTCG CA GCT TAGC

GTAGCTCATATTTCATGTTG GACG GT GGAGCACC TTGA ACCC CAAGC GT TGG GTTG

GGGTCATGCCGAACACCCAT G CA TTGATG AGT A C AC G ------
GAAGTTGTAGTTCCACGAGG TTCAT
ACTGGGCAG

GAM77 123 ATCTGTAACTTAAATTGGGC - AAT - AATCA TG TTATCT 3 C
CAATCAGAATGGTTATCTTT ATCT GTAACTTA TG GGCC GAA G
GTTCAGGTCACATGAGTTGC TAGA CGTTGAGT AC CTGG CTT T
AAGAT A --- A A---- GT ------

GAM78 119 GGTTAGAGAAACTCATCAGA --- ACTCATCAGA TT ATCACTTCAC 3 C
AGAAAGTTTCAATCACTTCA GGTT AGAGAA AGAAAGT CA
CTGTTATTTTCTGCAATTCT CCGA TCTCTT TCTTTTA GT
TATTCTCTTATAGCC TAT ATTCTTAACG TT ----------

GAM79 200 TCCATGCGTATATCGGACGT A TATA GA TCATA T T GTGC 3 C
GGTCTCATACGCGTTGCTGC TCC TGCG TCG CGTGGTC CGCGT GC GCA
AGTGCTGTTGCACGCGGACA AGG ATGC AGC GTACCAG GCGCA CG TGT
TGACCATGCACGACGTAGGA - ---- AC TACAG - T ----

GAM80 116 GCCCACTGTGACGATGTCAC - TGT G ACCG- GACG AAG 3 C
CGATCTGGACGTCCCTGAAG GC CCAC GAC ATGTC ATCTG TCCCTG
CAGGGGGACAGGTGTACAGA CG GGTG TTG TACAG TGGAC GGGGAC

CATGTTCTTGTGGCGC C TTC - ACATG AG-- ---

GAM81 192 CCACCATTAAGCAGTTCATG TAA TT - - TCGCTACC 3 C
GACATCTTCTCGCTACCGGA CCACCAT GCAG CA TGGA CATCTTC
GATGCTCTGCTGTCCTGTGT GGTGGTG TGTC GT GTCT GTAGAGG
GGTGG --- CT C C --------

GAM82 64 CACATGTGATTGCATTACCT G GC- ATG - A ACTGA 3 C
TATGTGTATTAGAGACTGAC CACATGT ATT ATTACCTT TGTA TT GAG
TTAAGCTGCAACAAGGTGAT GTGTATA TGG TAGTGGAA ACGT GA TTC
AAAGGTGATATGTG G AAA CA- C A -----

GAM83 172 AAAGGATGAAAAGGTGGTGT ----- - TG G ATGT AATCTTA 1 A
CATGTTTTGGGGAGAATCTT AAAGGAT GAAAAG G GT TC TTTGGGGAG
ACTTCTCAAATGGAAATTGC TTTCCTA TTTTTC C TA AG AAACTCTTC
ACTTTTTGCTGAATCCTTT AGTCG A GT A GT-- -------

GAM84 98 GACTCCACCTTCTCCCTGGA TCCAC C CCAGCCC - CCT TGACCCT 3 C
CCAGCCCGGTGGCACCCTGG GAC CTTCTCC TGGA GGTGG CAC GGATC
ATCTGACCCTGATCCGTGCC CTG GAAGAGG ACCT CCGCC GTG CCTAG
CGCCTCCAGGAGAAGTTGTC TT--- - ------- C --- -------

GAM85 182 CCCAGGGCATGAAGATCACA - - ATCACA G TTC TTTT 3 C
ATGGGCCTGGTTCAGATTTT CCCAGG GC ATGAAG ATGG CCTGG AGA
TCTCCAGGGCCGTGGCAGCT GGGTCT CG TACTTT TGCC GGACC TCT
TTCATGGCATCTGGG A G CGACGG G --- ----

GAM86 56 GTGTAATGTGGTTCTAGTGT AATGT GT C - TT--- TC CTCG 3 C
CGCTGCGTGTTCATCCTCTC GTGT G TCTAGTGT GC TGCGTG CA CT
GAGCTTGTCTGTCACGTAGG CACG C AGATCACA TG ATGCAC GT GA
TCACACTAGACTCTGGGCAC GGT-- TC C G TGTCT TC ----

GAM87 120 GCTCCGCGTGAATGGGGCTG CGCG AT G A CGGC 3 C
GATCTTATGCCGGCGTACAA GCTC TGA GGGGCT GATCTT TGC
GATTAGGCCTCTCAAAAGAG CGAG ACT CTCCGG TTAGAA ATG
C AAA- -- A C ----

GAM88 178 TCTTAAGTCACATGGCTTCT ACA C - ACCTTTAA 3 B
GTCTTGGAAATTTTACCTTT TCTTAAGTC TGG TTCTGTCTTGGA AATTTT
AAAAGATTATTTAAGACAGG AGGGTTCGG ACC AGGACAGAATTT TTAGAA
AACCAGGAGGCTTGGGA AGG A A --------

GAM89 106 GGAACAAGGTGTTAACAGGC A TT CC - T A AAATCCCA 3 C
CTGGGAATCTAGAAAATCCC GGA CAAGGTG AACAGG TGG GAA CT GA
ATCAGCTTCACCATTTTGTT TCT GTTTTAC TTGTTT ACC CTT GA CT
TTCATTTTGTCT - TT T- A C - --------

GAM90 131 CCTTCCCTTCCACAGAGTTT - - - A A CC GTA 3 C
AGTTTCCTCATTTGTAAAAT CCTTCCCT TC CAC AG GTTT GTTT TCATTT
GAAGACAAACCTCGTGAGAG GGAAGGGA AG GTG TC CAAA CAGA AGTAAA
AGGGAAGG G A C - - -- ---

GAM91 130 CTGCGGAGCCCGCGTCGCAG C A C - A- GGA GGAAGA - - TC 3 C
CAGCCCGGACAGGAAGATTG CTG GG GC CGC GTCGCAGC GCCC CA TTGGTCTG GA
TGTGGG
GTCTGGATGTGGGTCCGGTC GGC CC CG GCG CAGCGTTG CGGG GT GACCGGGC CT
ACATTC

TTACAGTCGCGGGCCAGGAT - A C A GA A-- AG---- G G --
GAGGGCAGGTTGCGACAGCG CGGT
CGCACCCGG

```
                ----
GAM92   60   CAGTGTCCCATTGTCATCTA     CCC---------      - A C    CTAATA           3  C
             CTCAGTCTCTAATAGGGCTA CAGTGT          ATTGTCAT CT CT AGTCT
             AGGAGCATGATAGTATCTAT GTCACG          TGATAGTA GA GA TCGGG
             TTATAAGCACTG           AATATTTATCTA      C G A    ------
GAM93   14   TGTGCATTTTCAGCAACTTG      TT    A- T  AAG  AATTTTCCTG              3  C
             CCAAGTATAATTTTCCTGAT TGTGCAT  TCAGCA  CT GCC   TAT
             AAAGGCTGGGCTGCTGATAT ATATGTA  AGTCGT  GG CGG   ATA
             GTATA               T-     CG T   AA-  ----------
GAM94   2    TCCAGTTTTATCCTGACTGA     TTTTATCCT     TCTTTTCTGTT  CTTT     T   -    3  B
             TTCTTTTCTGTTGTCCTTTG TCCAG       GACTGAT        GTC   GTTTTCTT CTCCT CTTCT
             TTTTCTTTCTCCTCTTCTAG AGGTC       CTGACTG        CAG   CAAGAGAG GAGGG GGGGG
             ATCTCTAAATGATCTTTGGG    ---------     ----------  ----      T   T
             GGTGGGAGTGAGAGAACGAC --    TCTAAAT
             GTCAGTCCTGGA         AGATC
                          TCTAG
                         TT    -------
GAM95   104  GGAGCCCTTGATGTCCTGCA  A  -   - ---     AAA -    ---  ATGT          3  C
             AATGAAGGAGGAGGATGTCC GG GCC CTTGA TG   TCCTGC   TG AAGGAG   GAGG
             TTAAGTTCCTTGCAGCAGGA CC CGG GGATT AC   AGGACG   AC TTCCTT   TTCC
             ACCCACTTAGGTGGCACC    A  T    C CCA     --- G     GAA   ----
GAM96   121  CCGAGGTCGTGCCACTGCAG  G ----        --- AG      GCCA   AGCA    C  TCTA  1   A
             TCCACCTGGCCAACACAGCA CC AG   GTCGTGCCAC   TGC  TCCACCTG    ACAC    GGCCT TC

             GGCCTCTCTCTAAAATAATA GG TC   CAGTATGGTG   ACG  GGGTGGAC    TGTG    CCGGA AG

             ATTATTATTATTGTTATTCT   G  AAGA        TCT   --      AAGA   A---    C  TTCT
             TGACAGGCCAGTGTAGAACA A-        TATT
             GGTGGGGCATCTGTGGTATG   AATAATAAT
             ACAGAACTGGG          TTGTTATTA
                          TA       ----
GAM97   175  GAGATGGGTTTCACCATGTT   A    TTCAC    TT     CT   CTCGA              3  C
             GGTCAGGCTGGTCTCGAACT GAG TGGGT    CATG  GGTCAGG  GGT
             CCTGACCTCATGATCCGCCC CTC ACCCG    GTAC  CCAGTCC  TCA
             ACCTC              C    CCTA-   T-     --  -----
GAM98   61   CAGCTTCTCCTTCCGGGACA  GC   C     GA  ---  T    TGTTCCTCGTCCAT          3  C
             GCTCCACCTGTTCCTCGTCC CA  TTCT CTTCCGG  CA   GC CCACC
             ATGGTGGTGTCGATGGGCCG GT  AGGA GAAGGCC  GT   TG GGTGG
             GAAGTAGGACATG        AC   T     GG  AGC  T    ----------
GAM99   135  CCTTCAAAAAGTTTGTAGCC    AAAAAG    G  A  G   G    TAA----  AAG  -  GAT  4  A
             TATCGGGGTGGAGAGATAAG CCTTC     TTTGTA CCT TCG GGTG AGAGA     GCC   TAT CCA
             CCAAGTATCCAGATAACCAT GGGAG     AAACAT GGA AGT TCAT TCTTT     CGG   ATA GGT
             GGCATAAGGCAGAATATTTT    GGG---    -  G  A   G    TATAAGA  A--   C   ---
             CTGTACTATGAGAGGTACAA AACCA
             AGGGGAGGG

                          -----
GAM100  91   ATCAACACAATAATTGAAAT   AAC-   T   G    TTTT   C    - A -----    - AG  4  A
             ATTTTCAAGCTGATTACACC ATC    ACAA AATT AAATA    CAAG TGATT AC CC    GCAGCC CG  G
```

GCAGCCCGAGGCTAGCCTGG TAG TGTT TTAG TTTAT GTTC ACTAA TG GG CGTTGG GC C

TTGCTAAGGGTGAGCTCCGC ATAT T - TAC- T A A GGGAT C CT
GGTTGCTAGGGGGAGTAAAT A GGTTGCTAA
CATCTTGCATTATTTGATTT CT GCCT
TTGTTATAGAT GA TGGG
G ---------

GAM101 43 GAGGCTGTCTTCACGCTGAC GT - C CC GA - TGTTTGTG 3 C
CCAGACCTGGGGGGTGTTTG GAGGCT CTT CA GCTGA CA CCTG GGGGG
TGTCCTTACAGGATGTTCAG TTTCGG GAA GT TGACT GT GGAC TTCCT
TTTGCAAGGAGGCTTT AG C T T- A- A --------

GAM102 15 GTGCCATCAGTCAGGTACCA CCA G AGG ---- A AC CGACT 3 C
CTTAAAGGATGTACAGGCGA GTG TCA TC TACCA CTTAA GGATGT AGG
CTTCTAGATATCTGTTGAGA CAC AGT GG ATGGT GAGTT TCTATA TCT
GCCTGGTAAGGGGTGAAACA AA- G GA- CCGA G GA -----
C

GAM103 132 TCTGGTGTGGAGACTTCGTG G GGAGA GT--- C AAAGGAAGAAGAAG 3 C
GTGGTGCTAAGAAAAGGAAG TCT GTGT CTTC GGTGGTG TAAGA
AAGAAGTCTTACACCACTCC AGA CACG GAAG TCACCAC ATTCT
CAAGAAGAATAAGCACAAGA A AATAA AACCC - ----------

GAM104 137 TCGGAGACCCCACCAAGTTT CCCC CA ACA- A TCTT 3 B
GCCACATTTGTTTTCAACGT TCGGAGA AC AGTTTGCC TTTGTTTTCA CG
CTTTGATGAAAACAAGGACG AGCCTCT TG TTAAGCGG GAACAAAAGT GT
GGCGAATTGAGTTCTCCGA ---- AG GCAG A ----

GAM105 138 TGGCTGTGGTGTCTGGGTGT - T TGTGGCCT T CTGC 3 C
GGCCTGGGGCTCCCTCTGCA TGGCTGTGG TGTC GGG GGGGC CCCT
GGGGCCCCCCTCGGCAGCCA ACCGACACC ACGG TCC CCCCG GGGA
CAGCCA G C -------- - ----

GAM106 173 TGGGGCCTTGGTAATATAGG ------- G AAA C CAA G- TTGA 1 B
AAACCTTCTTGCCAATATAG TGGGGCCT TG TAATATAGG CCTT TTGC TATAG AATATG
GAATATGTTGACATATTAGC GTCTCGGA AC ATTATATTC GGAA AACG ATATC TTATAC
TATAGCAAAAGGCTTATATT GTAAGCC G --- - --- GA ----
AGCACCGAATGAGGCTCTG

GAM107 79 GCACTCTGTGTCCAGACTTT A --- TC T- AAA-- ATTT AGACTA 3 C
AACTAAAGGCGGATTTCCCG GC CTCT GTG CAGACTT AACT GGCGG CCCG
AGACTACGGGTGTGCTGTTA TG GAGA CAC GTCTGGG TTGG TTGTC GGGC
GAAGGGTTCTGGGTCTGTGC - AAT GT TC GAAGA GTGT ------
ACTAAAGAGGT

GAM108 171 GTCCTTGAACTTGGAACCTG GA- TGGAA- GACAAT G GTTTGGAA 3 C
ACAATGTTGGTGTTGTCGTG GTCCTT ACT CCT GTTGGT TTGTCGT
TTTGGAAATGATAAACTAAT CAGGAG TGA GGA TAATCA AATAGTA
TAAGGAAGGAGATATAGTGA AAG TATAGA AGGAAT - --------
AGAGGAC

GAM109 90 CCTGCCCCTCTGCCTGTGCT C--- C -- C - T - TTCCCGGT 3 C
CCTGGCAGTGTGGCTTCCCG CCTGC CCTCTGC TGT GCT CTG GCAG GTG GC
GTGCTCACCTGCACAGCAGT GGGCG GGAGACG ACA TGA GAC CGTC CAC CG
TAACAGCAGAGGCCGAGCGG AGCC - AT C A - T --------

G
GAM110 115 GGCAGCGAGTCCTCAGGGCG A G CTCAG C CACCAGTCT 3 C
CCCGGGAGCCACCAGTCTGC GGC GC AGTC GG GCCCGGGAGC
TCTCGGGCTCTACTCAGACT CCG CG TCAG TC CGGGCTCTCG
AGCGCC - A ACTCA T ---------
GAM111 3 TCAGCCTTGGTCATCTGCGA T CA T GA C - ------ AA AGGAC 3 C
TGGAGCGCTTTCTCAGAACT TCAGCCT GGT TC GC TGGAG GCT TTCT CAG CTGT
GTAGGACATAGAACTGTGCA AGTTGGA CCA AG CG ACCTT CGA AAGG GTC GATA
CAGGAACAGCTTCCAGAGCC - AA C AG - C ACACGT AA -----
GAAAACCAGGTTGA
GAM112 195 CAGTAAACATAAGTTCCTCA ACATA C - AGA T - G TAGAAC 3 B
GGAGAGTTTGATGTGTGTCA CAGTAA AGTTC TCA GG GTT GAT GTGTGTCAGGT CT
GGTGCTTAGAACAGGGCCTG GTCATT TCGAG AGT CC CGA CTA TATATAGTCCG GA
ATATATAATCAGCCCATGAT A---- T A --- - A G ------
GAGCTATTACTG
GAM113 74 GTTAGTTCAGTACTTATTAG CA- - ATTA- ------ G TAAC 3 C
CTGCAGGAGCTAACGTTCAT GTTAGTT GTA CTT GCT GCA GAGC
GCAAGAACAGCAACAGGGGA CAATCAG CAT GGG CGA CGT CTTG
TACAGCGACTAAC CGA A GACAA CAAGAA A ----
GAM114 75 AGTGATGGTCAGTATTTCTT G- TC--- A ACAA 3 C
TGAAATTCTACAAGGAACTT AGTGAT GTCAGTATT TTTGAA TTCT
CAGGCACATGGTGCTGATGA TTATTG TAGTCGTGG GGACTT AAGG
GTTATT AG TACAC C ----
GAM115 103 GCCTGACCGAGGCGAACGCG AC CGAAC G- CAA GAAGC CAAGGAA 3 C
TGGACAAAGTGAAGCTGATC GCCTG CGAGG GC TGGA AGT TGAT
AAGGAAATCAAGAACTACAT CGGAC GCTCC CG ACCT TCA ACTA
CCAAGGCATCAACCTCGTCC CT AACTA GA ACA AGA-- -------
AGGC
GAM116 100 CTCTAACAAGGTGCAGAGCT AACA ATTG TGAT TTT 3 A
TAGCTGATTGGTGAACAGTG CTCT AGGTGCAGAGCTTAGCTG GTGAACAG TGG
ATTGGTTTCCGCTTTGTTCA GAGA TCCACGTCTTGAATCGGT CACTTGTT GCC
CAGTGGCTAAGTTCTGCACC AG-- GA-- TC-- ---
TGAAGAG
GAM117 151 GGCTAAGTGCCAGCTCCTCT AAGT C CCCT AG TCAA 3 C
TTGCCCTCAAGGTGCTCAAG GGCT GCCAGCT CTCTTTG CA GTGC
CATGATGCCCGAGGAGAAGC CCGG TGGTCGA GAGGAGC GT TACG
TGGTTGAGGCC AGT- A CC-- AG ----
GAM118 160 ATTCAGCGGCAGTGGTGCTT GG G CCCGAATCT AATGC 3 C
TCCCGAATCTCAGAATGCCT ATTCAGC CAGTGGT CTTT CAG
GTTAAAAGATCACTGAAGTT TAGGTTG GTCACTA GAAA GTC
GGAT AA - ATT------ -----
GAM119 4 GTAATGGCATAAGAATACTG CATAA TAC -- C T AAGCCC 3 C
ACTTATTCTCGTTTAGAAAG GTAATGG GAA TGACT TATTCT GTT AGA
CCCTCTGGCAGAATACAAGT CATTGCC CTT ACTGA ATAAGA CGG TCT
CATTTCAATTTCCGTTAC TTTAA T-- AC - - ------
GAM120 191 GGCTCTCGGCCTTGGCAACG TCT AA- C GTCAT TACTG 3 C
GCCGTCGTCATGGTTACTGG GGC CGGCCTTGGC CGGC GTC GGT
CCCCTAGGCGCCGATGGCCG CCG GCCGGAGCCG GCCG CGG CCG
AGGCCGCGCC C-- GTA - ATCC- -----
GAM121 69 GGCTTGGCCATGGCGGCTGG T- --- T TG GATAA TTTCT 3 C

TGCTGATAACCATTTCTTGG GGCT GGCCATGGC GGC GG CT CCA
CAGAAGTGCCCGCCAAAGCT CTGA CCGGTGTCG CCG CC GA GGT
GTGGCCCTAGTC TC AAA C GT AGAC- -----
GAM122 34 GGTCCACATTCACTTTCCCG CACA TTTC T - AG - ACC 3 C
TGGAAGGTTCAGGAAGCGAC GGTC TTCAC CCG GGAAGG TTC GA AGCGAC
ACCGTTGTTATCAGGGGCCC CCGG AGGTG GGC CCTTCC GGG CT TTGTTG
TTCCTCGGATGTGGAGAAGG AAG- TA-- T C GA A ---
CC
GAM123 166 AGGGTTTTAAACACTAATCA TTTTAA A TCACAAAC - TTGA CAA CAACAA 3 C
CAAACTGGAATGACTTGACT AGGG AC CTAA TGGAA TGAC CTT AAGG
TCAAAAGGCAACAACCTTAA TCCC TG GATT ACCTT ACTG GAA TTCC
AGGGCCGTCATTTCCATTAG TTA--- - -------- T CCGG A-- ------
GTATTCCCT
GAM124 108 GGAGGCGGGGCAGACGGGCT GG AGACGG A A C C ACG 3 C
GCAAGAGGGAGCCGGCCCGA GGA CGGGGC GCTGCA G GGGAGC GG CCG
CGCGGACCGCTTCCCTGCAG CCT GCCCCG TGACGT C CCTTCG CC GGC
TGCCCCGAGTCC GA ------ - - - A ---
GAM125 44 GTCCATATTACCCTTCAGCA --- TTC--- C G CCCAA 3 C
CCTGAGTCCCAAGCTGAGGT GTCC ATATTACCC AG ACCT AGT
CTCAACATGGGTGATGTGAA CAGG TGTAGTGGG TC TGGA TCG
GGAC AAG TACAAC - G -----
GAM126 148 TGTACGGCAGTTCAGTAGTT AC CAG CAAAT-- TT TCAG 3 C
ATCAAATCAGTTGGTCTCAG TGT GG TTCAGTAGTTAT CAG GGTC
GACCCCTGTGTACTCATAAT ACA CC GAGTTATTAATA GTC CCAG
TATTGAGACCCAAACA AA CA- CTCATGT C- ----
GAM127 53 CAATGTGCAACTGACATCTG T-- - ACA T G AT CT AATATACA 3 C
CTAGTGATGATCTGGTAATA CAATG GCAA CTG TC GCTA TG GAT GGT
TACAACCTGTCCAGTAGCCG GTTAT TGTT GAC AG CGAT AC CTG CCA
AACAGTTTGTTTTTATTG TTT T A-- C G -- T- --------
GAM128 168 GACGAATCCTTAGTACTGTG - TTAGT - AAA AGACAGAAATATAAACCA 3 C
GAAAAGAGCAGACAGAAATA GACGAAT CC ACTGTG GA GAGC
TAAACCAGCTTCTCTCACAG CTGCTTA GG TGACAC CT TTCG
TGGAATTCGTC A ----- T C-- ----------
GAM129 181 CAGGGAGGCTGCATGGGGCC GCATGGGG G - G ACTCAG 3 C
AGCGCTAGGTGGCTGACTCA CAGGGAGGCT CCAGC CTA GGT GCTG
GCAGCAGCCATGGGGCTGGA GTCCCTTCGA GGTCG GGT CCG CGAC
AGAAGCTTCCCTG AGAA---- G A A ------
GAM130 127 TTTTGAGACAGAGTCTCACT CA C A - CAG GACGG 3 B
CTGTTGCCCAGACTGGACGG TTTTGAGA GAGT TC CTCT GTTGCC ACTG
CAGTGGCAACAAGAGCGAAA AAAACTCT CTCA AG GAGA CAACGG TGAC
CTCCATCTCAAAA AC A C A --- -----
GAM131 170 CGAGTGTGCCTCGGCAGGAG C- CG GA CTTC ACAGA AGCCCC 3 C
GGCTTGACTTTCTTCGGCAC CGAGTGTG CT GCAG GGGCTTGACTTT GGC GCT
AGAGCTAGCCCCAGTGCGGT GTTCATAC GA CGTC TCCGGGCTGAGG CTG TGA
CAACAGGAGTCGGGCCTCTC AA AT TC ACAA GCG-- ------
TGCTAAGAACATACTTG
GAM132 114 GCTTGCTCATGATGTACGCG ACGCGCAG AAG CTACTAC 3 C
CAGTCCAAAGGCATCTACTA GCTTGCTCATGATGT TCCA GCAT
CGTGCAGTGGAGGATGACAT CGAACGGGTGCTACA AGGT CGTG
CGTGGGCAAGC GTAGG--- GA- -------

GAM133 88 ACTGCAGGTCGTATAAACGT A ---------- CG- AA CCC TG 1 B
GATAAATGAATGCTACCCTG ACTGC GGTCG TATAAA TGATA TGAATGCTA TGC GCTC
CTGGCTCTCCGAGAGAGTGT TGACG CCGGC GTATTT ACTAT ATTTATGAT ATG TGAG

AATTAGTATTTATATCAAAA - TTTTAAACAAA AAA -- TA- --
TTTATGAAACAAATTTTCGG CGA
CCGCAGT TC
AG

GAM134 45 GCCCAGGCTTGGAGTTGCGG - T TTGC T - CAGTTTCAC C A TCC 3 C
GTGGCGTTGACCTTCAGTTT GCCC AGGC TGGAG GGGTGGCG TGA CCTT GTG AA GCC

CACGTGCAAAGCCTCCGGCC CGGG TCCG GCCTT TTTACCGC ACT GGGA CAC TT CGG

TTCACAGGGTTCACCGCCAT C T C--- C T --------- - C ---
TTCTTCCGTGCCTCGGGC
GAM135 142 GTTTGAGTTCAAAGATGGAG AG AAAGA- GA AG T A - GGAAGGGG 3 C
CGAGGGTGGATATGGTGGGA GTTTG TTC TG GCG GG GGAT TG GTG
AGGGGCACACGGGTTCTCAC CGGAC AAG AC CGC CT CTTG GC CAC
GCAACAACGGAGGAAGGCAG GG GAGGCA AA A- - G A --------
GC
GAM136 159 GAGAAGGGAGGCTGCAGTGA A GG AG-- A- A AT ---- CATT 3 C
GCCAAGATCGTGCCATTGCA GAGA GGGA CTGC TG GCC AG C GTGC
TTCAAGGCCTGGGTGACAAG CTCT CCTT GACG AC TGG TC G TACG
AAGCAGAATTCCATCTC A AA AAGA AG G CG AACT ----
GAM137 76 GATGTCAGTCCCAAGGACCA CCCA---- - TA CCAT 3 C
GTAGCTGCCATCAGTTTGGA GATGTCAGT AGGA CCAG GCTG
TTCTGAAAACTAACTGGCAT CTACGGTCA TCTT GGTT TGAC
C ATCAAAAG A -- ----
GAM138 179 CTGGCCAGGGTGGTGGCTAA G GGTGG A- GTAA- CACT 3 C
CGCCTGTAATCCCAGCACTT CTGGCCA GGT CTA CGCCT TCCCAG
TGGGAGGCCGAGGCGGGTGG GACTGGT TCA GGT GCGGA AGGGTT
ATCAACTGTGGTCAG G ACTA- GG GCCGG ----
GAM139 31 ATTGTGATTTCCTTCGTTGG - TT C CAG-- A T--- CCTAATCCT 1 B
AGCTGTGAGCAGCAGCACAT ATTGTGAT TTCCTTCG GGAG TGTGAG CAGC CA TGGC

TGGCCCTAATCCTGCCACCT TAATATTA AAGGAAGC TTTT ACATTC GTTG GT ACCG
TTGGTTGAAATTCTTACATT C -- - TTAAA - TTCC ---------
TTCGAAGGAACATTATAAT

GAM140 51 AGGGTCTTTCCAACTGTTCT CC G GGT G GACC 3 C
GGTCAGTGAGGACCCTGACT AGGGTCTTT AACT TTCT CAGT AG
GCAAGGAGGAGTTCTGGAGA TCCCAGAGG TTGA GAGG GTCA TC
CCCT TC G AAC G ----
GAM141 94 CATTGACTCAGCACACCAGG CACAC TGTCACAGCTT- TTTT 3 C
TATGTCACAGCTTGTGCTTT CATTGACTCAG CAGGTA GTGC
TGCACCTAATACCCTTTTAC GTAACTGGGTC GTTCAT CACG
TTGCTACTGGGTCAATG ATC-- TTTCCCATAATC ----

GAM142 92 GCTCAAACTTCCCAAAAAAT CA- C A A - AAAATAAAACCAGA 3 A
TCACCTTTGGGCTTAAAATA GCT AACTT CCAAA AATTC CCTTT GGGCTT
AAACCAGAAAGCCCAAAAGG CGA TTGAA GGTTT TTAAG GGAAA CCCGAA
AGAATTCTTTGGAAAGTTAC ACA A C A A ----------
AAGC
GAM143 21 GGAAGCCATGAAGCAGTCTT G --- TC-- GTGAATGG 3 C
CTTGCCGTGAATGGGGTAAA GGAA CCATGAA GCAGTCT TTGCC
TATGGACTGCGCATTCATGG CCTT GGTACTT CGTCAGG AATGG
GTTCC G ACG TATA --------
GAM144 143 GTGATCCACACGCTGGCCCA G ACA-- T C AG GACA GCGA 1 A
GGAGTTCGACATTTACCGCG GT ATCC CGC GGC CAGG TTC TTTACC
AGGTGGGCGGAGAGCCTGTG TA TAGG GTG CCG GTCC GAG GGGTGG
CCTGTGACGAGGGATGAT G GAGCA T T GA GC-- ----
GAM145 82 GGCCCAGGGATCGGCAGGGC G - G- - GCT GA AGCT 3 C
TGCTGGCAGAGGAATCCCAG GGCCCAG GA TC GCAGG GCT GGCA GGAATCCC
CTGGGGTTCCCATGCCCCAG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG
GCTCCTGCAGGACTTGCTGG G C GA T ACC AC ----
GCC
GAM146 20 GCCATCACGCCACAGTTTCC - CAGTTT GCCATCCACAG 3 C
CGGAGGGGCCATCCACAGTC GCCATCAC GCCA CCCGGAGGG
TTCTGGGTGGCAGTGATGGC CGGTAGTG CGGT GGGTCTTCT
A ------ ----------
GAM147 196 GTCCTTGAACTTGGAACCTG GA- TGGAA- GACAAT G GTTTGGGA 3 C
ACAATGTTGGTGTTGTCGTG GTCCTT ACT CCT GTTGGT TTGTCGT
TTTGGGAATGATAAACTAAT CAGGAG TGA GGA TAATCA AATAGTA
TAAGGAAGGAGATATAGTGA AAG TATAGA AGGAAT - --------
AGAGGAC
GAM148 65 GTCAGAGTCTTCTCATCTGT ---- A G - CC C GGATTT 3 B
GCCAGCACCCTTCATGGATT GTCAG AGTCTTCTC TCT TGCC AGCA CTT AT
TGTAAAGTTTGTTCGGCAAG CAGTT TCGGGAGAG AGA ACGG TTGT GAA TG
AAGAGAGGGCTGTTCTTGAC CTTG A - C TT A ------
GAM149 146 TTAGGATAACATTGCTGTCG AA TCGG T AA TAACG 3 C
GAGGTCACGCAAGCTAACGG TTAGGAT CATTGCTG AGG CACGC GC
CAAGTGTGTCTATCAGTAGT GGTCCTG GTGATGAC TCT GTGTG CG
GGTCCTGG -- TA-- - AA -----
GAM150 6 CTGGAAATGTATTCCATTTC AAATG TTTCA AA- G A AGCCACAAAACCAA 3 C
AAGAAAGTACGACTATCAGC CTGG TATTCCA AGA GTAC ACT TCAGC
AGCCACAAAACCAAGCTGAC GACT GTAAGGT TCT CGTG TGA AGTCG
AGTGTGCAACTCTCATTGGA CCAAA TAC-- CAA - C ----------
ATGAAACCTCAG
GAM151 71 CTGCAGCCCTTGTACCTCAA A-- GTA T AA A - --- A T CTCT 3 C
AGCGATCCCACAATGTCCAC CTGC GCCCTT CC CA GCG TC CC AC ATG CCA
TCTTGGTTATAGTACTGGTG GACG TGGGGA GG GT TGC AG GG TG TAT GGT
ACGTGGTGCGGCAAGGGGTA ACA AC- C GG - T TCA A T ----
CAGCAG
GAM152 52 AAAGTCTTGTGATTTCCTCT TTGT T T ------ A CCTGCCAA 3 C
CATCTTTTAGAGATTCCTGC AAAGTC GA TTCCTC CATCTTT TAGAG TT
CAAAAATTCTACCAAGCAGA TTTCAG CT GAGGAG GTAGAGA ATCTT AA
GATGGAGGAGCTCGACTTT ---- C - CGAACC A --------
GAM153 186 GACAAGAAATGCCCCTTCAC GAAA---- CC - - AA- GT T TTC CGGA 3 C

TGGTAATGTGTCCATTCGAG GACAA TGC CTTCA CT GGT T G CCA GAGGG
GGCGGATCCTCTCTGGCGTG CTGTT ACG GAAGT GA CCA G C GGT CTCCT
GTGACCAAGATGAAGATGCA ACCAGGAG TA A A GTG TG - CT- ----
GAGGACCATTGTC
GAM154 176 GTCTTGCTAGGCCAGGTCTT AG A TCT G GT ACCGG 3 C
CCAGGTGGTTACCGGGGTCA GTCTTGCT GCC GG TCCA GTG T
CATGGATTTCTGGGCGGAGC TAGAGCGA CGG TC AGGT CAC G
GAGAT GG G TTT A TG -----
GAM155 26 GGGTCAAGCTGAAAAGGCAA T - T - CAA- - AC TGAG 3 C
GGTTTCTTCAACTGGCTTGA GGG CAA GC GAA AAGG GGTTT CTTCA TGGCT
GAGCTATGAGGTAGGCTGTT CCC GTT CG TTT TTCC TCGGA GGAGT ATCGA
TCCTTCTTTCGCTTTGTCCC T T C C TTTG T -- ----
GAM156 54 GCCAAGGAAACAGGATGCTG -- AC A TGA C - G- GGACATGT 3 C
ATAGTCTCCAGCAGGGCCTG GCCA AGGAA AGG TGC TAGT TCCA GCA GGCCT
GACATGTGGGCTGGTGTGTG CGGT TCCTT TTC ACG GTCA AGGT TGT TCGGG
GAACTGCTGCAACTTTCTTC GG CT A TC- - G GG --------
CTGGTGGC
GAM157 193 GGGTCGGCAGGAAGTTGCGG AGTT A- CCC - T C GCC 3 C
CTGATGAGCAGCTCCCGGAG GGGTCGGCAGGA GCGGCTGATGAGC GCT GGAGC GG GGGG
GGG
CGGTGGGGCGGGGCCTCCTC TTTAGTCGTCCT TGCTGACTACTCG TGA CCTTG CC CTTC CCT

TTCTCCAGTTCCAGTACGCT CC-- CA --- A T T ---
CATCAGTCGTCCTCCTGCTG
ATTT
GAM158 47 TAGGGGAGGGAAGAGAACTA GA ---- A A C ACAAA 3 C
AGATGATACTAACAAATGCT TAGGGGAGG AG AGAACTA G TGATA TA
ATCACTGGTTTTGTGGCTGC ATTCCCTCC TC TTTTGGT C ACTAT GT
CTCCCTTA G- GGTG - - C -----
GAM159 109 TCTCCTCCATGTGTCTTGGC ATGTG G A ---- GTG TGTCG 3 B
AGGCACTCATTTCTGTGGCT TCTCCTCC TCTTGGCAG C CT CATTTCT GC
GTCGGCAGAGGGAATGTTCT AGAGGAGG GGAACCGTC G GG GTAAGGG CG
GGAGCTGCCAAGGAGGGAGG GA--- - A TCTT AGA -----
AGA
GAM160 174 TGTGGTACTTCAGGAACTCT ACT A----- TTT A ACATCA TACAT 3 C
TTTTCAAACTCACATCACAG TGTGGT TCAGGA CTCTT CAA CTC CAG
TACATCTGGAGATTGTCTAA ACACCA AGTCCT GAGAA GTT GAG GTC
GAGGCAGCCTCCTGACACCA C-- CCGACG TCT A ------ -----
CA
GAM161 24 GGAGGATCGCTTGAGCCCAG GA GA-- AGGA - GT C AGATGGCAC 3 C
GAGGCGGAGGTTGCAGTGAG GGAG TCGCTT GCCC GGC GGAG TGCAGTGAG TG
CTGAGATGGCACCACTTATT CCTC AGCGAG CGGG CCG CCTC ACGTTATTC AC
GCACTCCAGCCCGGGCGACA AG ACAG C--- A -- - ---------
GAGCGAGACTCC
GAM162 58 GACGAACCTTGGCCGCAGTC A-- TG TT GA CGCAA 3 C
CTTGCGAACTGTTCGCAAAA GACG ACCT GCCGCAGTCC GC ACTGTT
CAGTGCGGGCTGCGGTGGGT CTGC TGGG TGGCGTCGGG CG TGACAA
CAGCGTC GAC -- -- -- -----
GAM163 84 TTGTGGTCCATGGCGAGCCC - C- C A C --- AT - --- GCTC 3 C
AGGCCTCAGACAATGGCTGT TTGTGGT CCATGG GAG CC GGC TCAG ACA G GCTGTG GTGTT

GGTGTTGCTCAGACATGCAC GACACCA GGTACC CTC GG CCG AGTT TGT C CGACAC TACAG

ACAGCTCTCTGTACCTTGAG C AC T A - CCA CT T ACG ----
CCAGGTCTCCACCATGGCAC A
CACAG

-

GAM164 66 TGTTTGTGCCGTCTTTGGTC TG TCTT AG ATTG--- ATCATG 3 C
TGGGAGGAGTCGGATTGGCA TGTT TGCCG TGGTCTGGGAGG TCGG GCAGTT
GTTATCATGGGCTGTAAAGT ACAG GTGGT ACTAGGCCCTTC GGTC TGTCGG
GGCTGGTGCTTCCCGGATCA GT T--- GT GGTGAAA ------
TTGGTGTGGACA
GAM165 134 GCCGTCTCCCCTGCTCCCGG TCT CTC T C C CCCCTGACC 3 C
TGCTCTGCGAGATCTCCCCT GCCG CCCCTG CCGG GCT TG GAGATCT
GACCAGATCTCCACAGCCCG CGGT GGGGGC GGCC CGA AC CTCTAGA
GACCCGGGGGCTGGC C-- CCA - C - ---------
GAM166 161 GAGATGGTGCCTTGGACACC GAT ACACCCT C CTCGTT AA CGAG 3 C
CTTGCCTGGAACTCGTTAGC GA GGTGCCTTGG TG CTGGAA AGC CTG
AACTGCGAGCAGAAGCTTTC CT TCGCGGAACT AC GACCTT TCG GAC
CAGTCACACATCAAGGCGCT AGT ACAC--- T ------ AA ----
TGATC
GAM167 140 TTTCTGTCAAGAAGCAGTTT AAGAAG G A CTT 3 C
GAAGAATTAACCCTTGGTGA TTTCTGTC CAGTTT AAGAATT ACC
ATTTTTGAAACTGGACAGAG AGAGACAG GTCAAA TTTTTAA TGG
A ------ G G ---
GAM168 97 AGATGTTATGTAAAAGTTTG TGT--- AA GAGG - TATCTGACACTCTGT 3 C
AGGTTGAGATGACATATCTG AGA TATGTA AGTTT TTGAGA TGACA
ACACTCTGTTGTTACTCTCA TCT GTACAT TCGAA GACTCT ATTGT
GAAGCTACTACATGTGAAAT TAAAGT CA ---- C ----------
TCT
GAM169 55 GGCTAGTGTAATACTCCACA T -- CA AGAAGTAGACACCCCAAA 3 C
GAGAAGTAGACACCCCAAAC GGC AGTGTAATA CTC CAG
TGGAGAGCATGTTGCATTTG CCG TTACGTTGT GAG GTC
CC T AC AG ----------
GAM170 72 GTGGGGTGAAGGGTCATTAA GAA CA AG AC A CATAA C CCCTT 3 C
GGGCACGCAGTAGCCATAAT GTGGGGT GGGT TTA GGC GCAGT GC TG CACA
GCCACACCCTTTGTGCCAGC CACCCCA TCCA GGT TCG CGTCA CG AC GTGT
CACTGCGCTTCTGGAAACCT --- AA CT -- C ----- C -----
ACCCCAC
GAM171 17 CAGGTGTTCCGGGCCCCTTC TTCC CTT- GGG AAGT 3 C
ACCTGGGGCTCAAGTGAGAG CAGGTG GGGCCC CACCTG CTC
CAGGTGTTCTGGGCCCCTTC GTCCAC CCCGGG GTGGAC GAG
ACCTG TTC- TCTT GA- ----
GAM172 86 AAAAAGACATTGGACTAAAT ACATTG GC AT TAGAAGAT 3 C
GCTAATATATGGAATAGAAG AAAAAG GACTAAAT TAATAT GGAA
ATTTCCCAATGTTAATTTAG TTTTTC TTGATTTA ATTGTA CCTT
TTAACAACTTTTT AACAA- -- AC --------
GAM173 124 TGTCCAGTTCCCATTTTGGT TC ---- CCTCATAA AAACAGCTTAACA 3 C
CCTCATAATCAAAACAGCTT TGTCCAGT CCATT TTGGT TCA
AACATGACAGTCATCACCAG ATAGGTTA GGTGA GACCA AGT

TAATAGTGGCATTGGATA C- TAAT CTACTGAC ----------
GAM174 16 TCCCGTGGAGGCTCGCGCCG GT G G - A- --- GGGA 3 C
ACGGCGGCGGGGACGAGACT TCCC GGAG CTC CG CCG CGGCGG CG
GCCGAGCGGACGGAGGCTCC AGGG CCTC GAG GC GGC GCCGTC GC
GGGA -- G - A GA AGA ----
GAM175 28 TGAACCAGCTTCTCAGCTCT ACC - A A T TGA TG TTCA GT A TAT 4 B
ACTGTGTTTGACCCTGTGTT TGA AGC TTCTC GCTCT CTG GTT CCC TG AG T GGGGAAT

CAAGGTTAGGGGAATTATAG ACT TCG AAGAG CGGGG GAC TAA GGG GC TC G CCCTTTG

TTTCCCAGGTCTCCATCGTG --- G A A - TG- GT TACC TG A ---
GGGGTAATCAGAGGGGCAGA A
GAAGGCTTCA

-
GAM176 73 CTCTTCATCAGTACACCACT ATCAGTA C TG -- C AATGATAA 3 C
GTGAGCCGACTGAAATGATA CTCTTC CACCA TG AGC CGA TGA
ATCACTTGAAGCTATCATTG GAGAGG GTGGT AC TCG GTT ACT
GTGGGAGAG ------- T TA AA C --------
GAM177 133 CTTCCTGGGCCATTGTGGCT - CA- C C CTGGT 3 C
GGAGGTGCTGGTGCTGGTCA CTTCCTGG GC TTGTGG TGGAGGTG TGGTG
CCATCATCTTCATCTACGAG GAAGGGCC CG AGCATC ACTTCTAC ACCAC
AAGCGCCGGGAAG G AAG T T -----
GAM178 32 GGACGAGGAGATGAACCGCA AGGAGA A CA AGA T A TCG 3 C
TGCATGAGAGCATGAAGCTA GGACG TGAACCGC TG TG GCA GA GCTAT
TTCGATAGCATCTGCAACAA CCTGC ACTTGGTG AC AC CGT CT CGATA
CAAGTGGTTCACAGACACGT ACAGAC A A- AA- - A ---
CC
GAM179 19 CTCTTTGAGATGACTGGTAT T G T TG A AAT AG G AG C A CT CTAA 3 B
TGAATGGAGCAGTCTTTGAA C CTTT AGA GAC GT TTG GGAGC TCTTT AA G ACCA CC TC

AGGCACCAACCCTTCCTAAC G GAAA TCT CTG TA AAC TCTCG AGAAA TT C TGGT GG AG

TGATGGTGGTCTCTTGAAAG T G T TT - CT- G- G CT - - T- ----
AGGCTCTTCCAAATTTGTCT CT
TCTGAAAGTG

--
GAM180 107 GACCGCCTCTTCCTTGTGTC --------- T -- CC- T- T --- 1 B
TCCTCTGATCATCTCCCATG GACCGC CTCTTCCT GTGT CT TCTGA CATCTCCCA GAGA

AGATCAACCAGAAGAGCCCT CTGGTG GAGAAGGA TACG GA GGACT GTAGAGGGT CTTT

TTCTGGGAGATGTCTCAGGC TTGAAGTTT C TC CTC CT - CCC
TCAGCTGCATCAGGAAGAGT - AACCAGAA
TTGAAGTTGTGGTC TC
AG
G --------
GAM181 35 GTTGTTATTGGTGCAGGAGT TG-- TG AG AATAGG A GGTT 3 C
AATAGGTGTAGAACTGGGTT GTTGTTAT G C GAGT TGT GAACTG

CAGTTTGGCAAAGACTTGGT CGACAGTG C G TTCA ACG TTTGAC
GCAGATGTGACAGC TAGA GT G- GAA--- G ----
GAM182 144 CGGCTGCCCAGGCCCTGCCT CCCA CT TT G- TCTC 3 C
TGGCATGTGTGTCTCCAGAG CGGCTG GGCC GCC GGCATGT TG
CGTGCCCGGCCAGGCCATCC GCCGAC CCGG CGG CCGTGCG AC
CAGCCG CCTA AC C- AG ----
GAM183 7 TTTGTGAAGATGATTGGGAA AT GG TCAAAT T GCTG---- CTTTAA 3 C
ATCAAATAAGTAAAAACGCT TTTGTGAAG GATTG AAA AAG AAAAAC GGTCAAAA
GGGTCAAAACTTTAAAAATT GAACATTTC CTGAC TTT TTC TTTTTG TCGGTTTT

TTGGCTACTTTAAGGTTTTT GT TT CCGT-- - GAATTTCA ------
CTTTGCCTTTTTCAGTCTGC AAA
TTTACAAG

GAM184 50 TTCAAAACCAGAAGCAGTCG CA C AGACAT A CTAGCA 3 C
AGACATAGGACAACCTAGCA TTCAAAAC GAAG AGTCG AGG CAAC
GTTGGCCTTATAAGTGGCTC AAGTTTTG TTTC TCGGT TCC GTTG
TTTGTTTTGAA -- - GAATAT G ------
GAM185 78 TTTCTTCAGTTCCAACAAAA --- ----- AAA C CATCTGATA 3 C
GGTCTGTCATCTGATAACAA TTTCTTCAGT TCCA AC AGGT TGT
ACCTATGGTTAACTTGGATA AAGGAAGTCG AGGT TG TCCA ACA
AGCTGAAGGAA AAT TCAAT GTA A ---------
GAM186 57 TAGCATTGGGTGCCAATTTC G G ATTT G GGAATGGTG 3 C
GTGGTGTGGAATGGTGACAA TAGCATT GGT CCA CGTG TGT
CATGCGTGGAGCCAAGTGCT ATCGTGA CCG GGT GTAC ACA
A A A GC-- A ---------
GAM187 83 AGCTTCAAAAGCACAACTAC AAAA-- AC CT- -- CAA 3 C
ACACTTTGCCCAAGGTCTGA AGCTTC GCACA TACACA TT GCC
TTCTGTGTATCTGTGCATCT TCGAGG CGTGT ATGTGT AG TGG
GAGGAGCT AGTCTA CT CTT TC ---
GAM188 12 AATTCCTGCCAGAATGCGCA C AAT - CAG AT GCC G GTGCCA 3 C
CAGAACATAAGTCAGCCAAG AATTCCTG CAG GC GCA AAC AAGTCA AAGTGT TC
TGTGTCGTGCCAGGGATACT TTAGGGAT GTC CG CGT TTG TTCAGT TTCATA GG
TTGACTTTGGTTTGCTGCTG C GT- T --- GT --- G ------
CTGCTAGGGATT
GAM189 9 GAAGTTCCAGGCTGTAGTGC GT- T CT A- A ACGT 3 B
ACTATGATGATCGTACGTAT GAA TCCAGGCTG AGTGCA ATG TG TCGT
GAACAGCCATTGCACTCCAG CTT GGGTCCGAC TCACGT TAC AC AGTA
CCTGGGCAATTC AAC C -- CG A ----
GAM190 99 TTATTTAGTAAACATTCTTT AG A TC CTA TACAGATG ATGT 3 A
GAGTCTACACTATGTACAGA TTATTT TA ACATTCTTTGAG TACA TG TGCTGCT
TGTGCTGCTATGTAGTAGCA AATGAA GT TGTAAGGAACTC GTGT AC ACGATGA
AAGATTCAGGATGTGCCCTC CT C CC AGG TTAGAA-- ----
AAGGAATGTCTGTCAAGTAA
GAM191 165 GAGGGTACTGTAGAATCTTT - AG T TTATTATCTC A TAAAAAAT 3 C
ATTATCTCAACAATCTAAAA GAG GGTACTGT AA CT AACA TC
AATGATGTTTATTTCCTTAG TTC CCGTGATA TT GA TTGT AG
TTAGATAGTGCCACTT A GA - TTCCTTTAT- - --------
GAM192 70 TTTTTTCTAAATGGGAAAAG AAAT-- A AATA T- TTCATTCT 3 C

GGTTAATAAGGGCTTATGTT TTTTTTCT GGGAA AGGGTT AGGGC TATG
CATTCTTGTATTGCTCTCTA AAAGAAGA TCCTT TTTCAA TCTCG ATGT
AACTTTGTTCCTTGTCACAG CACTGT G ATC- TT --------
AAGAAA
GAM193 139 GCTGGATATTGCTAAGAATT - G AGAA AG CG AGA CCATACTA 4 A
CAGGTAGTCTCGGGATCTCC GCTGGAT ATT CTA TTCAGGT TCT GGATCTCC GTCT
AGAGTCTCCATACTAGGACA TGATCTG TAA GGT AGGTCCA AGA TCTAGAGG CAGG
GGAGATCTTCAGAACCTGGA A A AAGG -- CT A-- --------
GGAATGGAAATAGTCTAGT
GAM194 40 CACATATTCATACAAATGAC CA T --- T AA AGA TCCT 3 C
TTAGTAATCTAATATGAGAA CA TATTCA ACAAATG ACT AGT TCTAATATG AGTGG
GTGGTCCTTCACTTATATTA GT GTAAGT TGTTTAT TGG TCA GGATTATAT TCACT
GGAACTTGGTAAATATTTGT AA - AAA T A- --- ----
TGAATGAATG
GAM195 122 AAGCCTTGTTTTTTCCCAGA -- TTT AG-- A-- G GC- GACCTG 3 B
GCAACCATGTTTTAGCATAA AAGCCT TGTTT CCC AGC ACCAT TTTTA ATAATGGGAT
TGGGATGACCTGGTGTCCCA TTCGGA ACGAG GGG TCG TGGTG GAAAT TATTACCCTG

TTATAAATAAAGGGTGGTAT TG TAT AAGA GTA G AAA ------
GGCTAGAAGGGTATGAGCAG GT
TAGGCTT

--
GAM196 67 GCGGAGGTGGGGGTCTGGCT T - G TG- CA GT - AGT- -- AATAT 3 C
TCAGGGTCTCAGTCCTTCCC GCGGAGG GG GG TC GCTT GG CT C CCTTCCCT TTAG
TTTAGAATATCTGAGAGGGG CGTCTCC CC CT AG CGAA CC GA G GGAAGGGG AGTC
AAGGTCAGGAAGGTCCAAGC - A G TTG -- TG A GACT AG -----
GTTGAGTCACCCCTCTGC
GAM281 164 GAGGTGGGAGGATTGCTTGT TG G GA C GG A CTA - CTTGATT 3 B
TCCCCGGAGGTTGAAGCTAC GAGG G AG TTGCTTGTT CCC AGGTTG AG CAGTGA GC

AGTGAGCCTTGATTGTGTCA CTCT C TC AATGGACAA GGG TCCGAC TC GTCACT TG
CTGCACTCCAGCCTGGGCAA GT - AG C -- C AC- G -------
CAGGTAAGACTCTGTCTC
GAM391 199 AGGAGCAGACTTTTCTCTTG GG C TTTCTCT TCA A--- A - --- GG 3 C
TCACTTTGGAAGGAGAGGAT A AG AGACT TG CTTTGG AGG GA GGAT TGTGA CTGCC
TGTGAGGCTGCCCCTTTAAA T TC TTTGG AC GAAACC TCC CT CCTA ACACT GACGG
TAGCATTCCCGTAGGAGGCA A- - TTTTT-- TAC GTCA A G CCT A-
GATCACATCCATCCGTCACC - TTAAATAGCATTCCCGT
TACTGCCAAAGCATCATTTT CCT
TGGTTTCTAT GGA
A ----------
GAM633 68 GGTATTTCCCAAGTCTCTGG TCC A CT- TG GGTTG C - ------ 3 C
GTGGTTGGAAGGCTGTGGCT GGTATT CA GT C GGT GAAGG TGTGGCTGGT CTCAGT TG

GGTCTCAGTTGGGTTACTCA CCATAG GT CA G TCG TTTCT ATACCGACCA GAGTCG AC

ATGCCCAGGAGGGGCTGAGC TA- A CTT GT ----- - C GGGAGG
ACCAGCCATATCTTTGCTTG TACTCAAT
GTTCACATGATGATACC GGT

```
                    CCG
                     --------
GAM895  93   CCTGTAGACCACCTTATTCT   T--    CCTTA    T- TA----    ------ -   TGAA  7  A
        TTTCTTATGGGTATGTGGCA CCTG  AGACCA   TTCTTT  CT    TGGGTA    TG TGGCA
        TGAATGCCATCATTTATTTA GGAC  TCTGGT   AAGAAG  GA    ACCCAT    AC ACCGT
        CCCAGCTGCCAGTTGAAGAA   CTT    TTTAC    TT  CCGTCG    TTATTT  T   ----
        CATTTTGGTCTTTCCAGG
GAM1032 169  GCTAGTCACTGGGGCAAAGA  TAGT     CAAAG    AAACACTT   C        CA    6  A
        TGACTAAAACACTTTTCCTG GC   CACTGGGG   ATGACTA     TTCCTG CCTCGAGGAGCT  CAGT

        CCCTCGAGGAGCTCACAGTC CG   GTGGCTCC   TACTGGT     AGGGAC GGAGTTCCTCGA  GTCA

        TAGTATGTCTCATCCCCTAC  TT--     ACTCA    --------    A        A-
        TAGACTGAAGCTCCTTGAGG     TGTCTCATCCCC
        ACAGGGATGGTCATACTCAC CTAGTA
        CTCGGTGTTGC       GATCAT
                          ------------
GAM1338 36   GGAGAATGGCATGAACCCGG   AATG  A-  AA-    AGG   CT    A  AGAGATCAC     3  C
        GAGGTGGAGCTTGCAGTGAG GGAG   GC  TG   CCCGGG   TGGAG  TGCAGTG GC
        CAGAGATCACGCCACTGCAC CCTC   CG  AC   GGGTCC   ACCTC  ACGTCAC CG
        TCCAGCCTGGGCAACAGAGC   AGAG  AG  AAC    G--    --     - ---------
        GAGACTCC
GAM2033 117  GAAGAAGAAGAATGGGTTTG    ----  A        TGAGA   CCAATATTAAC         3  C
        GTGAGAGGGTTCCAATATTA GAAGA   AGA GAATGGGTTTGG    GGGTT
        ACAACCCAACTTCAAGCTCA CTTCT   TCT CTTACTCGAACT    CCCAA
        TTCCTCTAACCTCTTC       CCAA  C        TCAA-   ----------
GAM2071 102  GCTTGAACCCAGGAGGTGGA   GA--    AGG   GT    A  TGAGATCCT          3  B
        GGTTGCAGTGAGCTGAGATC GCTT   ACCCAGG   TGGAG  TGCAGTG GC
        CTGCCACTGCACTCCAGTCT CGAG   TGGGTCT   ACCTC  ACGTCAC CG
        GGGTGACAGAGC          ACAG    G--    --     - ---------
GAM2608 153  CTTTTGAGCTGCTTCTTATA      C   TCT   A  T  CT      --  T   C   T    TA  6  A
        ATGTGTCTCTTGTGTTAAGG CTTTTGAG TGCT   TATA TG GT  CTTGTGTTA  AGG GCAT TAG GCAGT

        TGCATCTAGTGCAGTTAGTG GAAAATTT ACGA   ATAT AT CG  GGACACGGT  TCC CGTA ATC
CGTCA
        AAGCAGCTTAGAATCTACTG      T   C--   A  C  TC      CT   C   A   C    TC
        CCCTAAATGCCCCTTCTGGC   GAAGCAGCTTAGA
        ACAGGCTGCCTAATATACAG GT
        CATTTTAAAAG       TA
                          -------------
GAM3027 8    TCTCTTACACAGGCTGACCG       - GGC       TCC     ---   TCTGT       3  A
        ATTTCTCCTGGTGTTCAGAG TCTCTTACA CA   TGACCGATTTC   TGGTGTT   CAGAG
        TCTGTTTTTGTCTAGCACCA GGGGGATGT GT   ATTGGCTAAAG   ACCACGA   GTTTT
        TTTGAAATCGGTTATGATGT       A ---       TTT     TCT    -----
        AGGGGG
GAM3229 46   TGAGGTGGGAGAATTGCTTG    TG   AA TG  GA--   ----  -   A  T   GAGCTGAG 3  C
        AACCCAGGAGGCAGAGGTTG TGAGG  GGAG  T  CTT   ACCCA   GGAG GCAG GGT GCAGT

        CAGTGAGCTGAGATTGCACC ACTCT  TCTC  A  GAG   TGGGT   CCTC CGTC CCA CGTTA
        ACTGCACTCCAGCCTGGGTA    GT   AG GT   ACAA    CCGA   A   A  -   --------
```

ACAGAGTGAGACTCTTGTCT
CA

GAM3298 111 TTGGGTCCTAGTAGTACCAA G- T T CA- G GT- TTGGCAT 6 A
AGTGCTCATAGTGCAGGTAG TTG GTCC AG AGTAC AAGTGCTCATA TGCAG AGTT
TTTTGGCATGACTCTACTGT AAC TAGG TC TCATG TTCACGGGTAT ATGTC TCAG
AGTATGGGCACTTCCAGTAC AA T - ACC G ATC -------
TCTTGGATAACAA
GAM3418 147 TGGGTTCCTGGCATGCTGAT -- - C GTGACTTAAGATTA 3 A
TTGTGACTTAAGATTAAAAT TGG GTTCCTGGCA TG TGATTT
CACATTGCCAGGGATTACCA ACC TAGGGACCGT AC ACTAAA
AT T - ----------
GAM3431 105 GGGCGGGGGCCCTCGTCTTA CT - A T T GGTTGGGA 6 A
CCCAGCAGTGTTTGGGTGCG GGGCGGGGGCC CGTC TTACCC GCAGTGTT GGG GC

GTTGGGAGTCTCTAATACTG CCTGTCCCCGG GTAG AATGGG CGTCATAA CTC TG
CCGGGTAATGATGGAGGCCC AG T C T - --------
CTGTCC
GAM3499 38 GCTTGTAACTTTCCAAAGAA T T T TCTGGTTTTATTTT 3 A
TTCTCCTTTTGGGCTTTCTG GCTTG AACTTTCCAAAGAATTC CCTTT GGGCTT
GTTTTATTTTAAGCCCAAAG CGAGT TTGAAGGGTTTTTTAAG GGAAA CCCGAA
GTGAATTTTTTGGGAAGTTT - T - ----------
GAGC
GAM3770 29 GCATGTGCTCCTGCGGCGTG - C ----- G GTA GGAAAAC TGTT 3 C
GGGGTTTGTAGACTTGGAAA GCA TGTG TCCTGC GGC TGGGGGTTT GACTT CC
ACCCTGTTGGCAGAAAGTTA CGT ACAC AGGACG CCG ACCCTCGAG TTGAA GG
AGAGCTCCCAGGCCTGAAGG G - GAAGT G AA- AGAC--- ----
CAGGACACAGTGC
GAM5227 162 GTTGCCTTTGCTCCAGATCT T C- CTAG - A TG-- CCA GT 1 B
AGGTGAGATCAGATGGAATG GTTGCCTT GCTC AGAT GTG AGATCAG TGGAA GAGGCT TCTG

GAGGCTCCATCTGGTCTTCA TAACGGAA CGAG TCTA TAC TCTAGTC ACTTT CTCTGA GGAC

GGAAGTCTCAAGTTTTCACT - AC AAA- A - TGAA A-- --
GATCTACATAAAATCTCAGA CTT
GCAAGGCAAT

GAM5346 152 TTGTGGATATTGAAGTTTGA ------ C GTTG-- TAGATGCAC 3 B
AGCCTGTTGTTCATCTATAG TTGTGGA TATTGAAGTTTGAAG CT TTCATCTA
ATGCACTGGATGGGATTGGA AACACCT ATGACTTTAGACTTC GA GGGTAGGT
AGTCTTCAGATTTCAGTAGG TTTGGG T AGGTTA ---------
GTTTTCCACAA
GAM5385 22 CAGTGGGAAGGGGGGCCGAT A ATA AC G- AGTAG 6 A
ACACTGTACGAGAGTGAGTA CAGTGGG AGGGGGGCCG CACTGT GAGA TG
GCAGGTCTCACAGTGAACCG GTCATCC TTTCTCTGGC GTGACA CTCT AC
GTCTCTTTCCCTACTG C CAA -- GG -----
GAM7052 10 GGTGCACGCATGTAATCCCA G GCA - A A --- T GGCAGGGGAA 3 C
GCTACTCAGGAGGCTGAGGC GGT CAC TGTAATC CC GCT CTCAGG AGGC GA

AGGGGAATCGCCTGAACCTG CCA GTG GCGTTGG GG CGG GGGTCC TCCG CT
GGAGGCGGAGGTTGCGGTGA - --- A - A AAG - ----------
CC

GAM7080 183 CCATTTTTTTTGTAGGTCAGA T A - A --- AAAC TTTTT CTCTTCC 3 C
AGTGGTTGCAAACTGGATTT CCA TTTTTTGT GG TC GAAG TGGTTGC TGGA AGA TGT
TTAGACTCTTCCTGTTGGGG GGT AAGAAACA CC AG CTTC ACCGGCG ACCT TCT ACA
GTCTCGGACATTTGCTCTTT C - G A TTA AC-- TT--- CGTTT--
TCCACAGCGGCCAATTCTTC G GGTC
AGAGCCACAAAGAACTGG T GG
G CT
G ----

GAM7553 48 AACTGGTCGGTGATTTAGGT TC TT T C TCCACCTTTC 6 A
AGTTTCCTGTTGTTGGGATC AACTGG GGTGAT AGGTAGT TC TGTTGTTGGGA
CACCTTTCTCTCGACAGCAC TTGACT TCATTA TCCGTCA AG ACGACAGCTCT
GACACTGCCTTCATTACTTC -- CT C C ----------
AGTT

GAM7776 110 GAGGCAGGAGAATCGCTTGA G AATC GAA--- AGGC - T GA AAGAT 3 C
ACCCAGGAGGCGGAGGTTGT GAGGCAG AG GCTT CCCAGG GGAG GT GTGGT GCG

GGTGAGCGAAGATCGTGCCA CTCTGTC TC CGAG GGGTCC CCTC CG TACCG TGC
TTGCACTCCAGCCTGGGCAA - AAAA AACAAC GA-- A T -- -----
CAAGAGCAAAACTCTGTCTC

GAM7809 180 GTACCACCTTGTCGGGTAGC CCT GT A A A T AATCT 3 A
TTATCAGACTGATGTTGACT GTACCA TGTCGG AGCTTATC GACTG TGTTG CTGT G
GTTGAATCTCATGGCAACAC TATGGT ACAGTC TCGGGTAG CTGAC ACAAC GGTA C
CAGTCGATGGGCTGTCTGAC TTT TG - C - - -----
ATTTTGGTAT

GAM7933 145 GGCTTCCTCACCACCTTGTG CC-- CC - CAC CC- ACCACA 7 A
CACTGCTGCTCCCACACCAC GGCTT TCA ACC TTGTG TGCTGCT CAC
AGTGACTAGCAGCACATAAT TCGAA AGT TGG AATAC ACGACGA GTG
GGTTTGAATTAAAGCT ATTA T- T --- TCA ------

GAM7957 42 GGAGTCTCCCTCTGTCGCCC TC CCT TC --- T -- TG ATCT 3 C
AGGCTGGAGTGCAGTGGTGT GGAG TC CTG GCCC AGGC GGAG TGCAGTGG TG
GATCTCGGTTCACTGCAACC CCTC AG GAC TGGG TCCG TCTC ACGTCACT GC
TCTGCCTCCCGGGTTCCAGT TT T-- CT CCC - CA TG ----
GATTCTCC

GAM8145 112 GGACCAGACTATTGTGACAT - GA TT CAT -- A G--- TATTCAAT 3 C
GGAGAATGTAGAGGAATTAT GGA CCA CTA GTGA GGAGA ATGT GA GAAT
TCAATGTTCAGGATCAACAT CCT GGT GAT CACT CCTCT TACA CT CTTG
GATCTCCTCACTCTAGGATG A AG CT --- AG A AGGA --------
GATCC

GAM8297 154 AGGCAACATGCTGTTGTTAA ACA - A GCA ATTGG TTGT 3 B
GGGCACTTGGGCCATTGGTG AGGCA TGCTGTT GTT AGG CTTGGGCC TGTT
TTTTGTGACAGCTGGGCTCA TCCGT GCGACGA CAA TCT GGACTCGG ACAG
GGCATCTCAACAAGCAGCGG GTG A C AC- GTCG- ----
TGTGCCT

GAM8358 189 CCCAAGCCCTTGACCTCCTT CCC ACCTCCTTTT AA G TG TG GATTCCT 3 C
TTCCTTATCTGAAATGTTGC CCCAAG TTG CCTTATCTGA T T C T
TGTGATTCCTGTGGTGAGAT GGGTTC GAC GGAGTAGACT A A G G
CAGATGAGGCAGCACTTGGG AC- ---------- -- G GT GT -------

```
GAM8554 1    GTTTTGACCACTTCCACCTA    -    CCA     AATT---     CATTA          3  B
        TGAAAATTATCTGAACATTA GTTTTG ACCACTT  CCTATGAA     ATCTGAA
        TTCAGATTTAAGAGTTCATG CAAGAC TGGTGGA  GGGTACTT     TAGACTT
        GGAGCAGGTGGTACAGAAC     A     CGA     GAGAATT     -----
GAM8678 11   GTGAGATGTGTTCCAGGAAG   AG    CC    C-  ----------    CCCAT       3  C
        TCGTCTTGAGCACCCATTGC GTG  ATGTGTT  AGGAAGT  GTCT       TGAGCA
        TCAGAGTTTATATTGGACTT CAC  TACACGA  TCTTTCG  CAGG       ACTCGT
        GCTTTCTAGCACATACCAC   CA    --     TT   TTATATTTGAG    -----
```

GENE NAME	GAM SEQ-ID	GENE_SEQUENCE (5`_TO_3`)	PRECUR SEQ-ID	SOURCE REF-ID	SRC ACC	GAM	
GAM25	206	AATTGCTTGAACCCAGGAAGTG	156	EST72223	1	C	
GAM28	260	CTTTGCTTCTGTTTTCTGGATGCA	141	AW001829	3	B	
GAM29	380	GTGGTGGCAGACTTTGGGCTGTCA	81	AW952936	3	C	
GAM30	346	ATTGCACTCCAGCCTGGGCCACAG	125		3	C	
GAM31	250	TCAAGTAATCCAGGATAGGCTG	118	12	7	A	
GAM32	384	TCGAATGGACACATTACCAGTGAA	187	AI880781	3	C	
GAM33	317	AGTCAAGTTGCAGGATCAGCAGGT	77	BI767711	3	C	
GAM34	314	TGACGCTGAAGCTGGTGAGCCTGG	59	BE314459	3	C	
GAM35	247	TGAGGAATGTATCATCTTTTTGTC	101	BF672917	3	C	
GAM36	351	CTGCAAGGCTTCTGGCTACATCTT	149		3	C	
GAM37	266	TATATGGATCCAATGGCAAGATCA	197		3	C	
GAM38	271	AGGCATGGAGGAGCTGTGTGGTCA	89	AI745004	3	C	
GAM39	386	AAGCCACCTATGACGCAGCCACCC	27	AL709699	3	C	
GAM40	396	TGTGTCACTGAGTGAAAGCTGC	126	AI656172	3	B	
GAM41	215	TGTCTCAGGCACCTGAATCAGACC	13	AA680311	3	C	
GAM42	224	CAACTCAGGCTCTAGCTTCTCCAG	190	BF082911	3	C	
GAM43	234	TGAAACGAACAAGGCTTGAGAATC	95		3	C	
GAM44	287	AAGGTGGTGTCATGTTTTGGGG	188	THC1430784	1	A	
GAM45	324	TTTGTCTCTGACCTCCCAGGAAGT	25	BF109609	3	C	
GAM46	364	TGGGTGGATGCTGCTCTCGAATAA	41	BE092454	3	C	
GAM47	269	AGGCAGAAGAGAAGCTGCAGAG	113	NT_016606	3	A	
GAM49	338	GCCGCTGTGCTGAAGGAGGTGTGC	184	BM016609	3	C	
GAM50	368	CCCCGGGAAGTCAGAAATCGATCA	150	BE741747	3	C	
GAM51	201	TCCCCATCTCTTTTTCCCCACA	49	BE327494	3	C	
GAM52	373	GTTCCAGTTAGGGGCAGTAGAGTT	39	AI085403	3	C	
GAM53	359	GAGCATTGGCAGTGAATTGCAGA	136	AW439339	3	C	
GAM54	275	CTGGGCCCAGATGGCCCCTTCTGA	167		3	C	
GAM55	387	CTGCCATTTCCAGGAGATCACC	5	THC1550782	1	B	
GAM56	315	AGGTATTTGGTGTCATGTTTTGGA	23	BE538084	3	C	
GAM57	329	AGAGGTCCTGATTCAGTTTATCAA	157		3	C	
GAM58	306	TGAGTTATCTTTTAAATATGTCTT	185	BG402766	3	C	
GAM59	377	TCCCGGGGCCGGGGGACCTTAGCG	30	BG913775	3	C	
GAM60	381	CTTCAAGTGTAGGGACTCCTCGCA	80		3	C	
GAM61	293	CACGATGGGCACAATGCCATTCTG	63	BG990766	3	C	
GAM62	220	TGGCTTGGGTCGAGCTCTGTCACA	194	AI277769	3	C	
GAM63	348	GGTCCAGATGGGGAGAAGATGT	155	THC1428940	4	A	
GAM64	239	CAGCTGCCTGGGTTGTGGCCGCCC	85		3	C	
GAM65	272	ACAGTGACTTGCTCTCCAATGG	33	AV726476	3	B	
GAM66	238	TTTGCACCTGAGACAGATAGCC	62	THC1596213	1	B	
GAM67	282	TGGCAAAGATGCTGACCTACAT	37	THC1561873	1	B	
GAM68	251	TGTGCATGGCAGCTGTTTTCCTTT	128	AI032366	3	C	
GAM69	258	TCCCTCCTAGTTGTGTTGTTG	96		3	B	
GAM70	358	GGGCCTGTGACCTTGAGAACCTCA	158	BQ024160	3	C	
GAM71	257	TACCTGGACAGGGCAGGGGC	163	AI052780	3	C	
GAM72	342	AAAGTGCTGGGATTACAGGCATGA	198		3	C	
GAM73	264	TGAGAGCAAGGGAACAGGGCGGAT	18	BF185120	3	C	
GAM74	254	TTCAGGCAACAGTTTGTCCTG	87	BG258808	3	C	

GAM75 210 CACTGCTCTCCGGGCCTCTCCTGC 177 BI223210 3 C
GAM76 292 TGGGGTCATGCCGAACACCCATGA 129 AW157423 3 C
GAM77 390 TTCAGGTCACATGAGTTGCAAGAT 123 BI488926 3 C
GAM78 277 TCTGCAATTCTTATTCTCTTATAG 119 3 C
GAM79 352 TTGCACGCGGACATGACCATGCAC 200 3 C
GAM80 362 GGGGACAGGTGTACAGACATGTTC 116 AI880781 3 C
GAM81 256 AGATGCTCTGCTGTCCTGTGTGGT 192 BE082837 3 C
GAM82 333 AAGCTGCAACAAGGTGATAAAGGT 64 AL712226 3 C
GAM83 287 AAGGTGGTGTCATGTTTTGGGG 172 THC1430784 1 A
GAM84 204 TCCCTGGACCAGCCCGGTGGCACC 98 BG391958 3 C
GAM85 227 GGGCATGAAGATCACAATGGGCCT 182 3 C
GAM86 382 TGTCACGTAGGTCACACTAGACTC 56 BG778757 3 C
GAM87 366 CAAGATTAGGCCTCTCAAAAGAGC 120 BE879870 3 C
GAM88 310 ATGGCTTCTGTCTTGGAAATTT 178 BM923673 3 B
GAM89 235 CTTCACCATTTTGTTTTCATTTTG 106 BF984706 3 C
GAM90 374 TCCACAGAGTTTAGTTTCCTCATT 131 3 C
GAM91 336 TCGCAGCAGCCCGGACAGGAAGAT 130 AI832222 3 C
GAM92 308 AAGGAGCATGATAGTATCTATTTA 60 3 C
GAM93 397 AAGGCTGGGCTGCTGATATGTATA 14 AI741382 3 C
GAM94 332 TTGTTTTCTTTCTCCTCTTCTA 2 3 B
GAM95 273 TTCCTTGCAGCAGGAACCCACTTA 104 BE733663 3 C
GAM96 394 TCTGTGGTATGACAGAACTGGG 121 THC1500459 1 A
GAM97 274 GATGGGTTTCACCATGTTGGTCAG 175 AU137216 3 C
GAM98 344 TGGTGTCGATGGGCCGGAAGTAGG 61 BF058105 3 C
GAM99 320 TGGAGAGATAAGCCAAGTATCC 135 THC1481711 4 A
GAM100 243 TGAAATATTTTCAAGCTGATTA 91 THC1436384 4 A
GAM101 302 TACAGGATGTTCAGTTTGCAAGGA 43 T58800 3 C
GAM102 349 TCTGTTGAGAGCCTGGTAAGGGGT 15 3 C
GAM103 276 TACACCACTCCCAAGAAGAATAAG 132 BI545524 3 C
GAM104 355 TGAAAACAAGGACGGGCGAATT 137 3 B
GAM105 318 GCTGTGGTGTCTGGGTGTGGCCTG 138 3 C
GAM106 231 ATTAGCTATAGCAAAAGGCTTA 173 THC1578040 1 B
GAM107 341 GTGTGCTGTTAGAAGGGTTCTGGG 79 3 C
GAM108 298 TGGAACCTGACAATGTTGGTGTTG 171 BE253206 3 C
GAM109 290 CACCTGCACAGCAGTTAACAGCAG 90 3 C
GAM110 375 TCTCGGGCTCTACTCAGACTAGCG 115 BF205383 3 C
GAM111 311 GAACTGTGCACAGGAACAGCTTCC 3 BG682690 3 C
GAM112 263 TGATATATAATCAGCCCATGAT 195 NT_011568 3 B
GAM113 233 CAGTACTTATTAGCTGCAGGAGCT 74 3 C
GAM114 288 ACTTCAGGCACATGGTGCTGATGA 75 BF902557 3 C
GAM115 229 AAGAACTACATCCAAGGCATCAAC 103 AA464277 3 C
GAM116 301 TTCACAGTGGCTAAGTTCTGCA 100 mir-24 3 A
GAM117 216 TGCCCGAGGAGAAGCTGGTTGAGG 151 BG469029 3 C
GAM117 267 ATGCCCGAGGAGAAGCTGGTTGAG 151 BG469029 3 C
GAM118 363 TTAAAAGATCACTGAAGTTGGAT 160 3 C
GAM119 391 TGGCAGAATACAAGTCATTTCAAT 4 AI438930 3 C
GAM120 285 TCTCGGCCTTGGCAACGGCCGTCG 191 AI799504 3 C
GAM121 309 AAGTGCCCGCCAAAGCTGTGGCCC 69 AI609093 3 C
GAM122 337 TTATCAGGGGCCCTTCCTCGGATG 34 AU130704 3 C
GAM123 212 TTAAAGGGCCGTCATTTCCATTAG 166 3 C

GAM124	323	GACCGCTTCCCTGCAGTGCCCCGA	108	BG770878	3	C
GAM125	330	TATTACCCTTCAGCACCTGAGTCC	44	AI073816	3	C
GAM126	312	CCTGTGTACTCATAATTATTGAGA	148		3	C
GAM127	321	TGTCCAGTAGCCGAACAGTTTGTT	53	AI276053	3	C
GAM128	316	TCACAGTGGAATTCGTC	168	AW809287	3	C
GAM129	213	GGGCTGGAAGAAGCTTCCCTG	181	AA448642	3	C
GAM130	331	GGCAACAAGAGCGAAACTCCAT	127	AI921837	3	B
GAM131	313	GGTCAACAGGAGTCGGGCCTCTCT	170		3	C
GAM132	369	CTCATGATGTACGCGCAGTCCAAA	114	BE546515	3	C
GAM133	211	TGAATGCTACCCTGCTGGCTCT	88	THC1469923	1	B
GAM134	339	CACAGGGTTCACCGCCATTTCTTC	45		3	C
GAM135	248	CGGGTTCTCACGCAACAACGGAGG	142	AI636409	3	C
GAM136	279	CTGCAGTGAGCCAAGATCGTGCCA	159	BG434786	3	C
GAM137	202	TTTGGATTCTGAAAACTAACTGGC	76	BI260726	3	C
GAM138	222	GCCAGGGTGGTGGCTAACGCCTGT	179		3	C
GAM139	327	TGGAGCTGTGAGCAGCAGCACA	31	THC1496079	1	B
GAM140	295	TGCAAGGAGGAGTTCTGGAGACCC	51	BF204163	3	C
GAM141	357	ACCAGGTATGTCACAGCTTGTGCT	94	BM702658	3	C
GAM142	219	CAAAAAATTCACCTTTGGGCTT	92	NT_004464	3	A
GAM143	325	TGGACTGCGCATTCATGGGTTCC	21	BE566431	3	C
GAM144	361	CTGTGCCTGTGACGAGGGATGA	143	THC1576209	1	A
GAM145	335	TTCCCATGCCCCAGGCTCCTGCAG	82	BE867626	3	C
GAM146	370	TTCTGGGTGGCAGTGATGGC	20	BF570034	3	C
GAM147	298	TGGAACCTGACAATGTTGGTGTTG	196	BI596604	3	C
GAM148	280	TGTTCGGCAAGAAGAGAGGGCT	65	AA903584	3	B
GAM149	237	AAGTGTGTCTATCAGTAGTGGTCC	146		3	C
GAM150	261	TGACAGTGTGCAACTCTCATTGGA	6	BE220844	3	C
GAM151	205	ATAGTACTGGTGACGTGGTGCGGC	71		3	C
GAM152	378	ATTCTACCAAGCAGAGATGGAGGA	52		3	C
GAM153	244	TGGCGTGGTGACCAAGATGAAGAT	186		3	C
GAM154	228	TCACATGGATTTCTGGGCGGAGCG	176	BF312261	3	C
GAM155	207	TGAGGTAGGCTGTTTCCTTCTTTC	26	AA741519	3	C
GAM156	262	TGATAGTCTCCAGCAGGGCCTGGA	54	AA174034	3	C
GAM157	225	TCTCCAGTTCCAGTACGCTCATCA	193	AW771403	3	C
GAM158	383	TCACTGGTTTTGTGGCTGCCTCCC	47	AA343041	3	C
GAM159	230	GGGAATGTTCTGGAGCTGCCAAGG	109	AI084962	3	B
GAM160	343	TACTTCAGGAACTCTTTTTCAAAC	174	AI681978	3	C
GAM161	304	TTATTGCACTCCAGCCCGGGCGAC	24	BG029926	3	C
GAM162	376	TGGCCGCAGTCCTTGCGAACTGTT	58	AA625731	3	C
GAM163	249	CATGCACACAGCTCTCTGTACCTT	84		3	C
GAM164	322	TGTAAAGTGGCTGGTGCTTCCCGG	66	BG741187	3	C
GAM165	270	TCCCGGTGCTCTGCGAGATCTCCC	134		3	C
GAM166	232	TTTCCAGTCACACATCAAGGCGCT	161		3	C
GAM167	236	TGAATTTTTGAAACTGGACAGAGA	140		3	C
GAM168	217	TCAGAAGCTACTACATGTGAAATT	97	H55888	3	C
GAM169	365	GGAGAGCATGTTGCATTTGCC	55	AA742544	3	C
GAM170	283	CCACTGCGCTTCTGGAAACCTACC	72		3	C
GAM171	392	GAGCAGGTGTTCTGGGCCCCTTCA	17	AI963043	3	C
GAM172	253	CCAATGTTAATTTAGTTAACAACT	86	BQ004992	3	C
GAM173	208	TCACCAGTAATAGTGGCATTGGAT	124		3	C

GAM174	252	TGCCGAGCGGACGGAGGCTCCGGG	16		3	C	
GAM175	265	GACCCTGTGTTCAAGGTTAGGG	28	THC1505396	4	B	
GAM176	345	TACACCACTGTGAGCCGACTGAAA	73	AW471133	3	C	
GAM177	385	CATTGTGGCTGGAGGTGCTGGTGC	133		3	C	
GAM178	223	TCTGCAACAACAAGTGGTTCACAG	32	BG179277	3	C	
GAM179	300	TGGTCTCTTGAAAGAGGCTCTT	19	NT_010194	3	B	
GAM180	214	TTTCTGGGAGATGTCTCAGGCT	107	THC1481692	1	B	
GAM181	395	TTTGGCAAAGACTTGGTGCAGATG	35	BG675379	3	C	
GAM182	307	AGGCCCTGCCTTGGCATGTGTGTC	144	AI391577	3	C	
GAM183	240	TAAGTAAAAACGCTGGGTCAAAAC	7	BF746880	3	C	
GAM184	284	TTATAAGTGGCTCTTTGTTTTGAA	50	AW809289	3	C	
GAM185	372	TCTTCAGTTCCAACAAAAGGTCTG	78	BM823709	3	C	
GAM186	353	TGGGTGCCAATTTCGTGGTGTGGA	57	BE620228	3	C	
GAM187	294	AAGCACAACTACACACTTTGCCCA	83	AW085088	3	C	
GAM188	286	TACTTTGACTTTGGTTTGCTGCTG	12	AI582402	3	C	
GAM189	246	CATTGCACTCCAGCCTGGGCAA	9	NT_016354	3	B	
GAM190	289	GTAGCAAAGATTCAGGATGTGC	99	NT_005612	3	A	
GAM191	389	TGTAGAATCTTTATTATCTCAACA	165		3	C	
GAM192	393	TATTGCTCTCTAAACTTTGTTCCT	70	AA620888	3	C	
GAM193	268	TATTGCTAAGAATTCAGGTAGT	139	THC1461695	4	A	
GAM194	350	CAAATGACTTAGTAATCTAATATG	40	AI968206	3	C	
GAM195	334	AACCATGTTTTAGCATAATGGG	122	BI496955	3	B	
GAM196	209	GGGGAAGGTCAGGAAGGTCCAAGC	67	AI791435	3	C	
GAM281	278	CACTGCACTCCAGCCTGGGCAA	164	128	3	B	
GAM391	326	CAGATCACATCCATCCGTCACC	199	114	3	C	
GAM633	340	CTGAGCACCAGCCATATCTTTGCT	68	BE560202	3	C	
GAM895	379	AGCTGCCAGTTGAAGAACATTT	93	11	7	A	
GAM1032	303	CTAGACTGAAGCTCCTTGAGGA	169	8	6	A	
GAM1338	360	ACTGCACTCCAGCCTGGGCAAC	36	132	3	C	
GAM2033	305	TCAAGCTCATTCCTCTAACCTC	117	175	3	C	
GAM2071	371	ACTGCACTCCAGTCTGGGTGAC	102	181	3	B	
GAM2608	245	TAAGGTGCATCTAGTGCAGTTA	153	X	6	A	
GAM3027	242	TAGCACCATTTGAAATCGGTTA	8	76	3	A	
GAM3229	221	TGAGGTGGGAGAATTGCTTGAA	46	99	3	C	
GAM3298	259	AAAGTGCTCATAGTGCAGGTAG	111	X	6	A	
GAM3418	291	ATCACATTGCCAGGGATTACCA	147	mir-24	3	A	
GAM3431	356	TAATACTGCCGGGTAATGATGG	105	12	6	A	
GAM3499	226	AAAGAATTCTCCTTTTGGGCTT	38	64	3	A	
GAM3770	241	CGGCGTGGGGGTTTGTAGACTT	29	mir-24	3	C	
GAM3770	281	AAGTTAAGAGCTCCCAGGCCTG	29	mir-24	3	C	
GAM5227	299	GAGATCAGATGGAATGGAGGCT	162	THC1482185	1	B	
GAM5346	319	GAAGTTTGAAGCCTGTTGTTCA	152	209	3	B	
GAM5385	218	TCACAGTGAACCGGTCTCTTTC	22	3	6	A	
GAM7052	296	CATGTAATCCCAGCTACTCAGG	10	283	3	C	
GAM7080	399	TTTCCACAGCGGCCAATTCTTC	183	50	3	C	
GAM7553	354	TAGGTAGTTTCCTGTTGTTGGG	48	7	6	A	
GAM7776	246	CATTGCACTCCAGCCTGGGCAA	110	176	3	C	
GAM7809	398	TAGCTTATCAGACTGATGTTGA	180	195	3	A	
GAM7933	203	TAGCAGCACATAATGGTTTGAA	145	7	7	A	
GAM7957	297	TCACTGCAACCTCTGCCTCCCG	42	133	3	C	

GAM8145	328	ACATGATCTCCTCACTCTAGGA	112	184	3	C
GAM8297	367	GCTGTTGTTAAGGGCACTTGGG	154	157	3	B
GAM8358	255	GATGAGGCAGCACTTGGG	189	166	3	C
GAM8554	388	TTCATGGGAGCAGGTGGTACAG	1	198	3	B
GAM8678	347	GTGTTCCAGGAAGTCGTCTTGA	11	138	3	C

```
GENE NAME GAM    TARGET  #BS TARGET TARGET      UTR UTR    TAR-BINDING- BINDING-SITE-DRAW
   SRC GAM BS  TAR
      SEQ-ID          SEQ-ID REF-ID        OFFSET SITE-SEQ    (UPPER:GAM;LOWER:TARGET)         ACC
ACC ACC
========= ======= ======= === ====== =========== === ====== ===========
============================== === === === ===
GAM25   206   A1BG   1  10249 NP_570602.2  3 1445  ACCTCTACCTCC   TG         A         1  C  c  c
                                TGGGTTCAAGTG AAT  CTTGAACCCAGGA GTG
                                ATTCTCGT    TTA  GAACTTGGGTCCT CAT
                                         GT          C
GAM25   206   ACADSB 1  2370  NP_001600.1  3 370   GCCTTGACCTCC   TG T      A         1  C  c  c
                                TGGGTTCCGGTG AAT  CT GAACCCAGGA GT
                                ATTCTCAT    TTA  GG CTTGGGTCCT CA
                                         GT  C        C
GAM25   206   ADAMTS4 2  7708  NP_005090.1  3 878   ACCTTCGCCACC      T      AA         1  C  c  c
                                TGGGTTCCAGCA AATTGCT GAACCCAGG  GTG
                                ATTCTCCT    TTAACGA CTTGGGTCC  CGC
                                           C       AC
GAM25   206   ADAMTS4 2  12986 NP_005090.1  3 718   TCCTCCGCCTCC   TG      A  A        1  C  c
c
                                CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTCAT    TTA  GAACTTGGG CCT CGC
                                         GT       C  C
GAM25   206   AHR    1  13044 NP_001612.1  3 1681  ACCTCTACCTCC   TG         A         1  C  c  c
                                TGGGTTCAAGTG AAT  CTTGAACCCAGGA GTG
                                ATTCTCTT    TTA  GAACTTGGGTCCT CAT
                                         GT          C
GAM25   206   AP1S3  1  16221 XP_291023.1  3 1066  ACCTGGACCTCC A-----      A     A      1  C  c  c
                                TGGGCTCAAGCA      ATTGCTTGA CCCAGGA GT
                                ATCCTCTC          TAACGAACT GGGTCCT CA
                                        CTCTCC       C      C
GAM25   206   APAF1  2  8675  NP_001151.1  3 677   ATCGCTGCCTCC             ---        1  C  b  b
                                TGGGTTCAAGCA AATTGCTTGAACCCAGGA   AGTG
                                ATTCTCCT    TTAACGAACTTGGGTCCT   TCGC
                                            CCG
GAM25   206   APAF1  2  8675  NP_037361.1  3 677   ATCGCTGCCTCC             ---        1  C  b  b
                                TGGGTTCAAGCA AATTGCTTGAACCCAGGA   AGTG
                                ATTCTCCT    TTAACGAACTTGGGTCCT   TCGC
                                            CCG
GAM25   206   APAF1  2  9041  NP_001151.1  3 976   GCCTCAGACTCC A-----           A      1  C  c  b
                                TGGGTTCAAGCA      ATTGCTTGAACCCAGGA GT
                                ATCCTCCT          TAACGAACTTGGGTCCT CA
                                        TCCTCC             -
GAM25   206   APAF1  2  9041  NP_037361.1  3 976   GCCTCAGACTCC A-----           A      1  C  c  b
                                TGGGTTCAAGCA      ATTGCTTGAACCCAGGA GT
                                ATCCTCCT          TAACGAACTTGGGTCCT CA
                                        TCCTCC             -
GAM25   206   APM1   1  10422 NP_004788.1  3 860   GCCTCCTTCTCC       A      AGT        1  C  c  c
                                TGGGTCCAAGCA AATTGCTTG ACCCAGGA
                                ATTATTGT    TTAACGAAC TGGGTCCT
```

C CTT
GAM25 206 APOBEC3 1 11252 NP_660341.2 3 400 AACTCTGCCTAC C--- A-- 1 C c c
F CAGGTTCAAGCG AATTGCTTGAACC AGG AGT
ATTCTCCT TTAGCGAACTTGG TCC TCA
ACCA GTC
GAM25 206 AQP6 1 6016 NP_001643.1 3 662 ACCTCTACCTCC G A 1 C c c
TGGGTTCAAGGG AATT CTTGAACCCAGGA GTG
ATTCTCCT TTAG GAACTTGGGTCCT CAT
G C
GAM25 206 AQP6 1 6016 NP_445738.1 3 1828 ACCTCTACCTCC G A 1 C c c
TGGGTTCAAGGG AATT CTTGAACCCAGGA GTG
ATTCTCCT TTAG GAACTTGGGTCCT CAT
G C
GAM25 206 ARCN1 1 17729 NP_001646.2 3 454 ACCTCCGCCTCC AA----- A 1 C c c
TGGGTTCAAGCA TTGCTTGAACCCAGGA GTG
AGTCTCCT AACGAACTTGGGTCCT CGC
TCCTCTG C
GAM25 206 ARHF 1 8788 NP_061907.1 3 1140 AGCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCTT TTAGCGAACTTGGGTCCT CAC
C
GAM25 206 ARHGAP1 1 13340 NP_004299.1 3 1178 ACCTCCGCCTTC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCTT CGC
C
GAM25 206 ARPP-19 1 15452 NP_006619.1 3 3539 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
GTTCTCCT TTGACGAACTTGGGTCCT
CCG
GAM25 206 ART5 1 5997 NP_443750.2 3 131 ATGGGGACTTCC AA------ AA 1 C c c
TGGGACAAGCAA TTGCTTG CCCAGGAAGT
GGAAAGTA AACGAAC GGGTCCTTCA
ATGAAAGG A-
GAM25 206 ASB16 1 7753 NP_543139.4 3 191 ACTTCTACCACC C AA 1 C c c
TAGGTTCAAGCG AATTGCTTGAACC AGG GTG
ATTCTTGT TTAGCGAACTTGG TCC CAT
A AC
GAM25 206 ASE-1 1 17464 NP_036231.1 3 791 ACCTCCGCCTCC CTT A 1 C c c
TGGGTTCCAACG AATTG GAACCCAGGA GTG
ATTCTCCT TTAGC CTTGGGTCCT CGC
AAC C
GAM25 206 ATF7IP2 1 17594 NP_079273.1 3 577 ACCTCCATCTCC AC A - 1 C c c
CTGGCTCAAGCA AATTGCTTGA CCAGG AG TG
ATTCTCCT TTAACGAACT GGTCC TC AC
C- C T
GAM25 206 ATP1B2 1 9693 NP_001669.1 3 871 ACTTCCGCATCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCC TTAGCGAACTTGG CCT CGC
AC A
GAM25 206 ATP6V1A 1 12374 NP_001681.2 3 724 GCCTTCGCCTCC TG A A 1 C c
c

CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C

GAM25 206 ATP8B2 1 4561 XP_290875.1 3 1064 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 B3GALT3 1 20124 NP_003772.1 3 1184 GCCCCCTGTTCC T GT 1 C c c

TGGGTTTATGCA AATTGC TGAACCCAGGAA
GTTTTCTT TTGACG ATTTGGGTCCTT
T GT

GAM25 206 B4GALT5 1 15509 NP_004767.1 3 1674 GTCTCGAACTCC A----- AC A 1 C c
c
TGGACTCAAGCA ATTGCTTGA CCAGGA GT
ATCCGCCC TAACGAACT GGTCCT CA
CCCGCC CA -

GAM25 206 BAG5 1 14301 NP_004864.1 3 1918 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C

GAM25 206 BHD 2 11559 NP_659434.2 3 960 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 BHD 2 19921 NP_659434.2 3 1242 GTCTTGAACTCC A----- C A 1 C c c
TGAGTTCAAGCA ATTGCTTGAAC CAGGA GT
GTCCTCCT TGACGAACTTG GTCCT CA
TCCTCC A -

GAM25 206 BNIP2 1 20177 NP_004321.1 3 506 AAATACATTTCC G --- 1 C c c
TGGGTAACTTAG AATT CTTGA ACCCAGGAAGTG
GAAATTAA TTAA GGATT TGGGTCCTTTAC
A CAA

GAM25 206 BRIP1 1 11243 NP_114432.1 3 256 AACCTTCACCTC TG CA A 1 C c c
CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT A- C

GAM25 206 BTN3A1 1 17690 NP_008979.2 3 1103 ACCTCCACCTCC C A 1 C b b
TGGGTTCAAACA AATTG TTGAACCCAGGA GTG
ATTCTCCT TTAAC AACTTGGGTCCT CAC
A C

GAM25 206 C14orf5 1 16501 XP_058620.2 3 159 TTTAAATCTTCC G A- T 1 C c c
3 TGGGTCCCAAGG AATT CTTG ACCCAGGAAG
AATTAGAA TTAA GAAC TGGGTCCTTC
G CC T

GAM25 206 C1orf24 1 14976 NP_443198.1 3 1510 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCAGGAG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GGACTTGGGTCCT CGC
GA C

GAM25 206 C1orf34 1 4034 XP_027172.1 3 2218 GTCTTGAACTCC A----- AA A 1 C c c

TGGGCCCAAGCA ATTGCTTG CCCAGGA GT
ATCTTCCC TAACGAAC GGGTCCT CA
CCCTTC CC -

GAM25 206 C3F 1 12542 NP_005759.2 3 272 ACCTCCACCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTTTCCT TTA GAACTTGGGTCCT CAC
GT C

GAM25 206 C4orf9 1 4561 XP_035572.1 3 402 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 C6orf16 1 5162 NP_849145.1 3 690 CCTTCCAACTCC A----- G A 1 C c c
5 TGGGTTCAAGGG ATT CTTGAACCCAGGA GT
ATCGTCTT TAG GAACTTGGGTCCT CA
TTCTGC G -

GAM25 206 C6orf5 1 11730 NP_056339.2 3 1476 ACCTGCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTTCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 206 C7 1 17349 NP_000578.1 3 679 ACCTCCGCCTCC G A 1 C c c
TGGGTTGAAGCG AATTGCTT AACCCAGGA GTG
ATTCTTGT TTAGCGAA TTGGGTCCT CGC
G C

GAM25 206 C9orf9 1 5324 NP_061829.2 3 904 AACCTCCACCTC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
A- C

GAM25 206 CALN1 1 5444 NP_113656.1 3 1883 TGCAAAACTTCC AA ---- - 1 C c c
TGGAGTTCAGCC TTGCT TGAAC CCAGGAAGT
CAGCAAGG AACGA ACTTG GGTCCTTCA
GG CCCG A

GAM25 206 CAMLG 2 15900 NP_001736.1 3 839 CCTCCACCTTCC G C T 1 C c c
TGGTTCAAGGGA AATT CTTGAACC AGGAAG
TTCTCCTG TTAG GAACTTGG TCCTTC
G - C

GAM25 206 CAMLG 2 17054 NP_001736.1 3 839 ACCTCCACCTTC G C T 1 C c c
CTGGTTCAAGGG AATT CTTGAACC AGGAAG
ATTCTCCT TTAG GAACTTGG TCCTTC
G - C

GAM25 206 CCL22 1 11778 NP_002981.2 3 1323 ACCTCGACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GT
ATTCTCCC TTAGCGAACTTGGGTCCT CA
C

GAM25 206 CD209 1 18420 NP_066978.1 3 1638 ACTTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 206 CD34 1 18308 NP_001764.1 3 1261 CCTGCCGACTCC T G A 1 C c c
TGGGTTGAGCTG AAT GCTT AACCCAGGA GT
TTGCCTCA TTG CGAG TTGGGTCCT CA

T - -

GAM25 206 CDC2L2 1 9240 NP_296370.1 5 66 ACCTCCACCTCC A 1 C b b
TGGGTTCAGGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGGACTTGGGTCCT CAC
C

GAM25 206 CDCP1 2 14151 NP_073753.3 3 1820 ACCTCTGCCTCC A AGT 1 C c c

TGGGCTCAAGCA AATTGCTTGA CCCAGGA
ATTCTCCC TTAACGAACT GGGTCCT
C CCG

GAM25 206 CDCP1 2 19953 NP_073753.3 3 1954 GTCTCAACCTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C C

GAM25 206 CDH1 1 2489 NP_004351.1 3 962 GTCTTAAACTCC A----- AC A 1 C c c
TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTTCT TAACGAACT GGTCCT CA
TCTTCC CC -

GAM25 206 CDH17 1 3901 NP_004054.2 3 238 ACCTCCGCCTCC CT A 1 C c c
TGGGTTCACATG AATTG TGAACCCAGGA GTG
ATTCTCCT TTAGT ACTTGGGTCCT CGC
AC C

GAM25 206 CHSY1 1 14947 NP_055733.2 3 687 ACCTCCACTTCC CA 1 C b b
CTGGTTCAAGCA AATTGCTTGAACC GGAAGTG
ATTCCCCT TTAACGAACTTGG CCTTCAC
TC

GAM25 206 CIAS1 1 2330 NP_004886.2 5 337 GCCTCCACCTCC C A A 1 C c c
CGGGTTCAATCA AATTG TTGAACCC GGA GTG
ATTCTCCT TTAAC AACTTGGG CCT CAC
T C C

GAM25 206 CIP29 1 12541 NP_115740.3 3 211 ACCTCTGTCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCC TTAACGAACTTGGG CCT
C CTG

GAM25 206 CKAP2 1 6323 NP_060674.2 3 775 ACTTCACTTGAT CCC----- - 1 C c c
AGTTTTTAAGCA AATTGCTTGAA AG GAAGT
ATTAGAAT TTAACGAATTT TC CTTCA
TTGATAGT A

GAM25 206 CLECSF1 1 18038 NP_072092.2 3 1018 ACCTCCGCCCCC AA 1 C b b

2 TGGGTTCAAGCA AATTGCTTGAACCCAGG GTG
ATTCTCCT TTAACGAACTTGGGTCC CGC
CC

GAM25 206 CNP 1 16430 NP_149124.1 3 609 GCCTCGAACTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C -

GAM25 206 COG3 1 12970 NP_113619.1 3 1341 CAGGTCACTTCC CT CCC 1 C c
c

TTTTCACTCAGT AATTG TGAA AGGAAGTG

TTAAATTG TTGAC ACTT TCCTTCAC
TC T--

GAM25 206 COLEC12 1 583 NP_110408.2 3 152 ACCCCCACATCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CAC
GT C A

GAM25 206 COX15 1 907 NP_510870.1 3 709 ACCTCCACTTCC CA 1 C b b
CAGGTTCAAGCG AATTGCTTGAACC GGAAGTG
ATTCTCAT TTAGCGAACTTGG CCTTCAC
AC

GAM25 206 CPA4 1 11559 NP_057436.1 3 653 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 cPLA2de 1 7513 NP_828848.1 3 2172 TCCTCAACTTCC A----- TG A 1 C c c
lta TGGGCTCAAGTG AT CTTGA CCCAGGAAGT
ATCCTTCC TA GAACT GGGTCCTTCA
CCTTCC GT C

GAM25 206 cPLA2de 1 7513 XP_208820.2 3 1265 TCCTCAACTTCC A----- TG A 1 C c c
lta TGGGCTCAAGTG AT CTTGA CCCAGGAAGT
ATCCTTCC TA GAACT GGGTCCTTCA
CCTTCC GT C

GAM25 206 CPSF2 2 4882 XP_029311.2 3 2095 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 CPSF2 2 7665 XP_029311.2 3 1268 ACCTCTTCCTCC TG --- T 1 C c c
AGGGTTCAAGTG AAT CTTGAACCC AGGAAG
ATTCTCCC TTA GAACTTGGG TCCTTC
GT ACC T

GAM25 206 CRB3 1 16619 NP_777378.1 5 61 GTCTCGGACTCC A----- AC A 1 C c c
TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCTT TAACGAACT GGTCCT CA
TTCTCC CC -

GAM25 206 CRTAP 1 18797 NP_006362.1 3 315 ACCTCCGCCTCT A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTGCT TTAACGAACTTGGGTTCT CGC
C

GAM25 206 CSNK2A2 1 19142 NP_001887.1 5 49 ACCTCCACCTCC CA A 1 C c c
CTGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
TC C

GAM25 206 CTEN 1 9806 NP_116254.3 3 815 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTATCCT TTAACGAACTTGG CCT CAC
AC C

GAM25 206 CXCL16 1 3618 NP_071342.1 3 388 ACCCCCATCTCC CA AG 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA TG
ATTCTCCT TTAGCGAACTTGG CCT AC
AC CT

GAM25 206 CYCS 1 18428 NP_061820.1 3 2668 ACCTCCGCCTTC CA T 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGAAG
ATTCTCCT TTAGCGAACTTGG CCTTC
A- C

GAM25 206 CYorf15 1 7001 NP_115965.1 5 76 TAGGTTACTTTT CCC 1 C c c
B TCTCTTTAAGCA AATTGCTTGAA AGGAAGTG
ATTATTCC TTAACGAATTT TTTTTCAT
CTC

GAM25 206 CYP1A2 1 1202 NP_000752.1 3 835 ACCTCCGCCTCC CCA A 1 C c c
CATGTTCAAGCG AATTGCTTGAAC GGA GTG
ATTCTCCT TTAGCGAACTTG CCT CGC
TAC C

GAM25 206 CYP2B6 1 6624 NP_000758.1 3 751 ACCTCCACATCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CAC
GT A

GAM25 206 CYP51A1 1 17115 NP_000777.1 3 932 TCCTCTGCCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCTG TTAACGAACTTGGG CCT
C CCG

GAM25 206 CYP8B1 1 10741 NP_004382.1 3 600 ACCTCTGCCTCC AGT 1 C c c
TGGGTTTAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAATTTGGGTCCT
CCG

GAM25 206 DBR1 1 19169 NP_057300.1 3 134 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
AC C

GAM25 206 DENR 1 3444 NP_003668.2 3 614 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C

GAM25 206 DENR 1 3444 XP_113714.2 3 537 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C

GAM25 206 DKFZP43 1 5045 NP_113664.1 3 2149 ACTGCCGCCTCC A A 1 C c c
4B044 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCAT TTAACGAACTTGGG CCT CGC
C C

GAM25 206 DKFZp43 1 3728 NP_060068.1 3 909 GCCTCCGCCTCC A A 1 C b b
4C0923 TGGGCTCAAGCA AATTGCTTGA CCCAGGA GTG
ATTCTCCC TTAACGAACT GGGTCCT CGC
C C

GAM25 206 DKFZP43 1 10108 NP_056410.2 3 858 ACCTCTGCTTCC TG C T 1 C c c
4D146 TAGGTTCAAGTG AAT CTTGAACC AGGAAG
ATTCTCCT TTA GAACTTGG TCCTTC
GT A G

GAM25 206 DKFZp43 1 17183 NP_060082.1 5 820 ACCTCCGCCTCC A A 1 C c c
4E2220 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 DKFZP43 1 14934 NP_110444.1 3 2460 ACCTCCGACTCC A 1 C b b
4F0318 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GT
ATTCTTCT TTAACGAACTTGGGTCCT CA
-
GAM25 206 DKFZp54 1 10247 NP_064546.1 3 306 ACCTCCACCTCC TG A 1 C c c
7H025 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTTGT TTA GAACTTGGGTCCT CAC
GT C
GAM25 206 DKFZP56 1 2610 NP_056274.1 3 570 ACCTCTGCCTGC A A T 1 C c c
4J0863 CGGGTTCAAGCA AATTGCTTGAACCC GG AG
GTTCTCCT TTGACGAACTTGGG CC TC
- G C
GAM25 206 DKFZP56 1 6069 NP_115496.1 3 274 ACCTCCACCTCC A A 1 C c c
4O0523 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C
GAM25 206 DKFZP56 1 3248 NP_056226.1 3 760 GCCTTGAATTCC AA GT 1 C c c
6I1024 TGGGCCCAAGCA AATTGCTTG CCCAGGAA
ATTCTCCC TTAACGAAC GGGTCCTT
CC AA
GAM25 206 DKFZp66 1 19212 NP_808881.1 3 1014 ACCTCCGCCCCC AA 1 C c c
7B1218 TGGGTTTAAGCG AATTGCTTGAACCCAGG GTG
ATTCTCCT TTAGCGAATTTGGGTCC CGC
CC
GAM25 206 DKFZp66 1 19169 XP_117353.1 3 344 ACCTCCGCCTCC CA A 1 C c c
7E0512 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
AC C
GAM25 206 DKFZp76 1 13045 NP_775734.1 3 2813 ACCTCCACCTCC TG A A 1 C c
c
1B107 CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCATGT TTA GAACTTGGG CCT CAC
GT C C
GAM25 206 DKFZp76 1 16380 NP_061181.1 3 935 AACTCTGCCTCC A AGT 1 C c c

1H039 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 DKFZp76 1 17889 NP_115656.1 5 1510 ACGTCCACCTCT C A 1 C c c
1J139 TGAGTTCAAGCG AATTGCTTGAAC CAGGA GTG
ATTCTCCT TTAGCGAACTTG GTTCT CAC
A C
GAM25 206 DKFZp76 1 18358 XP_172976.2 3 1946 AACCTCCACCTC A A A 1 C c c
2H185 CCGGGTCAAGCA AATTGCTTGA CCC GGA GTG
ATTCTCCT TTAACGAACT GGG CCT CAC
- C C

GAM25 206 DSCR6 1 13892 NP_061835.1 3 594 ACCTCCACTTCT TG 1 C b b
TGGGTTCAAGTG AAT CTTGAACCCAGGAAGTG
ATTCTCCT TTA GAACTTGGGTTCTTCAC
GT
GAM25 206 DUSP18 1 17445 NP_689724.2 3 836 GTCTCAAACTCC A----- AC A 1 C c c
TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCAC TAACGAACT GGTCCT CA
CACTCC CC -
GAM25 206 EEF2K 1 1130 NP_037434.1 3 393 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C
GAM25 206 EHD2 1 7811 NP_055416.2 3 954 ACCTCCACCTCC TG G A 1 C c c
TGGGTTGAAGTG AAT CTT AACCCAGGA GTG
ATTCTCGT TTA GAA TTGGGTCCT CAC
GT G C
GAM25 206 ELP3 1 4705 NP_060561.3 3 949 TCCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCC TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 ET(B)R-LP-2 1 3185 NP_004758.2 3 561 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 EVC 1 6657 NP_055371.1 3 2273 ATCTCCATCTCC A AG 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA TG
ATTTTCCT TTAGCGAACTTGGG CCT AC
C CT
GAM25 206 EVC 1 6657 NP_714928.1 3 2273 ATCTCCATCTCC A AG 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA TG
ATTTTCCT TTAGCGAACTTGGG CCT AC
C CT
GAM25 206 EVI5 2 19191 NP_005656.2 3 2264 ACTTCCACTTCC A 1 C b b
CGGGTTCAAGCG AATTGCTTGAACCC GGAAGTG
ATTCTCCT TTAGCGAACTTGGG CCTTCAC
C
GAM25 206 EVI5 2 19835 NP_005656.2 3 564 ACTTCCGCTTCC CA 1 C b b
CAGGTTCAAGCA AATTGCTTGAACC GGAAGTG
ATTTTCCT TTAACGAACTTGG CCTTCGC
AC
GAM25 206 F2RL3 1 18613 NP_003941.1 3 3054 AGCTCGGCCTCC GC A 1 C c c
TGGGTTCAAATG AATT TTGAACCCAGGA GT
ATTCTCCT TTAG AACTTGGGTCCT CG
TA C
GAM25 206 F3 1 14357 NP_001984.1 3 474 CCCTCCGTCTCT AG AG 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GA TG
ATTGTCTG TTAACGAACTTGGG CT GC
CT CT
GAM25 206 FAT3 1 421 XP_061871.5 3 1407 ATCTCCACCTCC A 1 C b b

TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 FCAR 2 17765 NP_001991.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579803.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579805.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579806.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579807.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579808.1 3 323 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579811.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 17765 NP_579812.1 3 199 CATTGAACCTCT TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTTGT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 FCAR 2 19049 NP_579813.1 3 291 ACCTTCGCCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
AC C

GAM25 206 FCRH1 1 17141 NP_443170.1 3 968 GTCTCAAACTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATGTATTG TAACGAACT GGGTCCT CA
GTTATG C -

GAM25 206 FER1L4 1 4561 XP_300246.1 3 270 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 FER1L4 1 4561 XP_300246.1 3 419 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC

C

GAM25 2062 FLJ1023 1 7686 NP_060503.1 3 843 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGAG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GA C C

GAM25 2068 FLJ1029 1 6660 NP_060520.2 3 234 ACCTCCGTCTCC AG 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA TG
ATTCTCCT TTAGCGAACTTGGGTCCT GC
CT

GAM25 2060 FLJ1052 1 18266 NP_060594.2 3 1530 GTCTTGGACTCC A----- AC A 1 C c c
TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCC TAACGAACT GGTCCT CA
CCCTCC CC -

GAM25 2063 FLJ1071 1 6272 NP_060659.1 3 408 ATCTCCGCCTCC GC A 1 C c c
TGGGTTCAAATG AATT TTGAACCCAGGA GTG
ATTCTCCT TTAG AACTTGGGTCCT CGC
TA C

GAM25 2067 FLJ1084 1 14648 NP_060712.2 3 539 CCTCGAACTCTT A----- - A 1 C c c
GGGCTTCAAGCA ATTGCTTGAA CCCAGGA GT
ATCCTCCT TAACGAACTT GGGTTCT CA
TCCTCC C -

GAM25 2061 FLJ1087 1 12436 NP_060720.1 5 24 GAAGACGCTTCC G TG 1 C c c
TGGGTTTGAGGA AATT CT AACCCAGGAAGTG
GTTCAGTG TTGA GA TTGGGTCCTTCGC
G GT

GAM25 2062 FLJ1092 1 14510 NP_060743.1 3 2099 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCGGGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GGGCTTGGGTCCT CGC
GT C

GAM25 2066 FLJ1093 1 2724 NP_060749.2 3 1429 AGCTCCGCCTCC TG T A 1 C c c
TGGGTTCACGTG AAT C TGAACCCAGGA GTG
ATTCTCAT TTA G ACTTGGGTCCT CGC
GT C C

GAM25 2063 FLJ1119 1 17071 NP_060826.1 3 645 GTCTCAAACTCC A----- AA A 1 C c c
TGGGCACAAGCA ATTGCTTG CCCAGGA GT
ATCCACCT TAACGAAC GGGTCCT CA
TCCACC AC -

GAM25 2060 FLJ1171 1 6789 NP_079122.1 3 1059 GCCTTGAATTCC A GT 1 C c c
TGGGCTCGAGCG AATTGCTTGA CCCAGGAA
GTTCTCCT TTGGCGAGCT GGGTCCTT
C AA

GAM25 2060 FLJ1180 1 11881 NP_079250.1 3 1290 GCCTCAACCTTC A----- A 1 C c c
TGGGTTCAAGCG ATTGCTTGAACCCAGGA GT
ATCCTCCC TAGCGAACTTGGGTCTT CA
CCCTCC C

GAM25 2067 FLJ1268 1 7950 NP_079193.2 3 260 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCGT TTA GAACTTGGG CCT CGC
GT C C

GAM25 2063 FLJ1290 1 5568 NP_073590.1 3 1606 ACCTCCGCCTCC G A 1 C c c
TGGGTTCAAGGG AATT CTTGAACCCAGGA GTG
ATTCTCCT TTAG GAACTTGGGTCCT CGC
G C

GAM25 2063 FLJ1297 1 5363 NP_079184.1 3 343 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C

GAM25 2065 FLJ1297 1 1128 NP_079085.2 3 107 ACCTCCTCCTCT AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTTCT
CCT

GAM25 2064 FLJ1311 1 19143 NP_078817.1 3 659 GCCTCCGCTTCC 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGAAGTG
ATTCTCCT TTAGCGAACTTGGGTCCTTCGC

GAM25 2068 FLJ1318 1 8655 NP_071346.1 3 462 ACCACTGCTTCC TG T 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGAAG
ATTCTCAT TTA GAACTTGGGTCCTTC
GT G

GAM25 2066 FLJ1410 1 2043 NP_079343.1 3 374 TCTCTTCCTTTG ---- CC T 1 C c c
TCATTTCAAGCA AATTGCTTGA AC AGGAAG
ATTTTCAT TTAACGAACT TG TCCTTC
TTAC TT T

GAM25 2062 FLJ1444 1 12170 NP_116174.1 3 2284 ACTTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCCCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 2065 FLJ2004 1 3234 NP_060108.1 3 180 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAGGCA AATTGCTTGAACCCAGGA
ATTCTCCC TTAACGGACTTGGGTCCT
CCG

GAM25 2065 FLJ2024 1 4882 NP_060193.1 3 2347 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 2064 FLJ2034 1 6297 NP_060246.1 3 753 ACCTCCGCCTCT C A 1 C c c
TGGGTTCAACCG AATTG TTGAACCCAGGA GTG
ATTCTCCT TTAGC AACTTGGGTTCT CGC
C C

GAM25 2067 FLJ2050 1 14232 NP_060319.1 3 2379 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTATCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 2061 FLJ2067 1 9310 NP_060394.1 3 1587 ATCTCCGCCTCC A CA A 1 C c c
CAGGCTCAAGCA AATTGCTTGA CC GGA GTG
ATTCTCCT TTAACGAACT GG CCT CGC
C AC C

GAM25 2062 FLJ2130 1 11560 NP_075052.1 3 1076 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG

ATTCTTCT TTAACGAACTTGGGTCCT CGC
C

GAM25 2069 FLJ22521 7859 NP_079065.1 3 193 GAAACCACCACC CA AA 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GG GTG
ATTATCCT TTAACGAACTTGG CC CAC
AC AC

GAM25 2061 FLJ22531 1207 NP_078926.2 5 390 ACCTCCACCTCC TG CA A 1 C c c
CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCAT TTA GAACTTGG CCT CAC
GT AC C

GAM25 2064 FLJ22791 15478 NP_071357.1 3 304 ACTTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTTAT TTAGCGAACTTGG CCT CAC
AC C

GAM25 2064 FLJ23021 12540 NP_079212.1 3 378 ACCTCTGCCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG

GAM25 2060 FLJ23041 18555 NP_079450.1 3 283 TTCTGGAACTTC A G 1 C b b
TGGGCTCAAGCA AATTGCTTGA CCCAG AAGT
ATTTTCCT TTAACGAACT GGGTC TTCA
C -

GAM25 2066 FLJ23551 4537 NP_079156.1 3 772 ACTTGCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCA TTAGCGAACTTGGG CCT CGC
C C

GAM25 2067 FLJ30501 9488 NP_694555.1 5 116 ATCTCCATCTCC A AG 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA TG
ATTCTCCT TTAGCGAACTTGGG CCT AC
C CT

GAM25 2062 FLJ30531 5994 NP_653325.1 3 239 GCCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 2069 FLJ31131 6914 NP_775928.1 3 446 CCTCCTGCTTCC T 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGAAG
ATTCTCCT TTAGCGAACTTGGGTCCTTC
G

GAM25 2066 FLJ31161 13479 NP_694567.1 3 1188 ACCTCCACCTCC C A A 1 C c c
CGGATTCAAGCA AATTGCTTGAA CC GGA GTG
ATTCTTCT TTAACGAACTT GG CCT CAC
A C C

GAM25 2064 FLJ31381 13568 NP_689685.1 3 975 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCCTCT TTAGCGAACTTGGGTCCT CGC
C

GAM25 2066 FLJ32092 4882 NP_776156.1 3 1161 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 2066 FLJ3209 2 5363 NP_776156.1 3 1465 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C

GAM25 2060 FLJ3213 1 19156 NP_689671.2 3 1488 ACCTCCGCCTCC A 1 C c c
TGGGTTCGGGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGGGCTTGGGTCCT CGC
C

GAM25 2065 FLJ3365 1 17105 NP_775912.1 3 374 ACTTCCACCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CAC
C

GAM25 2064 FLJ3381 1 17298 NP_775781.1 3 923 ACCTCCATCTCC A AG 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA TG
ATTCTCCT TTAACGAACTTGGG CCT AC
C CT

GAM25 2067 FLJ3481 1 4161 NP_689516.1 3 255 GCTTCAACTTCC A----- A 1 C c c
TGGGCTCAAGTA ATTGCTTGA CCCAGGAAGT
ATCCTCCC TAATGAACT GGGTCCTTCA
CCCTCC C

GAM25 2067 FLJ3548 1 19925 NP_776181.1 3 714 GTCTCAAGCTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCTGCTT TAACGAACT GGGTCCT CG
TTCGTC C -

GAM25 2061 FLJ3572 1 16439 NP_775955.1 3 955 TTCTGTGCTTCC TT C T 1 C c c
TGGTTTTGCAAT AATTGC GAACC AGGAAG
TGGATTGA TTAACG TTTGG TCCTTC
T- - G

GAM25 2065 FLJ3704 1 14054 NP_787085.1 3 810 ACCTCCACTTCC A----- CA 1 C c c
CAGGTTCAAGCG ATTGCTTGAACC GGAAGTG
ATCCTCCT TAGCGAACTTGG CCTTCAC
TCCTCC AC

GAM25 2063 FLJ3743 1 13505 NP_848612.1 3 246 ACCTCCACCTCC A A 1 C b b
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAC
C C

GAM25 2069 FLJ3814 2 5834 XP_091919.5 3 307 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTTCT TTA GAACTTGGG CCT CGC
GT C C

GAM25 2069 FLJ3814 2 14301 XP_091919.5 3 1480 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C

GAM25 2061 FLJ3828 2 761 NP_689814.1 3 158 ACCTCTGTCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CTG

GAM25 2061 FLJ3828 2 13396 NP_689814.1 3 2014 ACCTCTGCCTTC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA

ATTGTCCT TTAACGAACTTGGGTCTT
CCG

GAM25 206 FLJ3879 1 7709 NP_848615.1 3 1210 ACTTCCGACTCC CA------ 1 C c c
2 CAGGTTCAAGCG AATTGCTTGAACC GGAAGT
ATTCTCCT TTAGCGAACTTGG CCTTCA
ACCCTCAG

GAM25 206 FLJ3881 1 16529 NP_665872.1 3 400 GTCTCAAACTCC A----- AC A 1 C c c
9 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCC TAACGAACT GGTCCT CA
CCCTCC CC -

GAM25 206 FLJ3959 1 14114 NP_776164.1 3 675 GCCTCCATCCTC AA 1 C c c
9 TGGGTTCAAGCA AATTGCTTGAACCCAGG GTG
ATTCTCCT TTAACGAACTTGGGTCT TAC
CC

GAM25 206 FNBP1 1 4631 XP_052666.3 3 1060 ACCTCCACCTCC T A 1 C b b
TGGGTTCCAGCG AATTGCT GAACCCAGGA GTG
ATTCTCCT TTAGCGA CTTGGGTCCT CAC
C C

GAM25 206 FUT1 1 5787 NP_000139.1 3 661 ACTTCCGCCTCC C A 1 C c c
TGTGTTCAAGCG AATTGCTTGAAC CAGGA GTG
ATTCTCCT TTAGCGAACTTG GTCCT CGC
T C

GAM25 206 G6PC 1 5991 NP_000142.1 3 1477 AACCTCTTCCTC C-- T 1 C c c
CTGGTTCAAGCG AATTGCTTGAACC AGGAAG
ATTCTCAT TTAGCGAACTTGG TCCTTC
TCC T

GAM25 206 GGCX 1 15130 NP_000812.2 3 591 TAAAGTGGCTCT GAA A 1 C c c
TGGGGAAAAGCA AATTGCTT CCCAGGA GT
ATTTAATG TTAACGAA GGGTTCT CG
AAG -

GAM25 206 GM2A 1 17079 NP_000396.1 3 809 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CGC
C

GAM25 206 GNA15 1 9918 NP_002059.1 5 36 AGCCGGGCTTCC AA-- --- 1 C c c
TGGGTGTTTCAG TTGCTTGA ACCCAGGAAGT
GCAAGGAA AACGGACT TGGGTCCTTCG
AAGG TTG

GAM25 206 GNG4 1 4561 NP_004476.1 3 656 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 GOLGA3 1 2365 NP_005886.2 3 649 AGCTCCGCCATC AA 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGG GTG
ATTCTCCT TTAGCGAACTTGGGTCT CGC
AC

GAM25 206 GPP34R 1 6905 NP_060648.2 3 1050 GTCTTGAATTCC A GT 1 C c c
TGGGCTCAAGCA AATTGCTTGA CCCAGGAA
ATTCTTCC TTAACGAACT GGGTCCTT
C AA

GAM25 206 GPR48 1 15965 NP_060960.1 3 579 AGAACTATAAAT CCAG 1 C c c
TTTGTTTAAGCA AATTGCTTGAAC GAAGT
ATTTATAA TTAACGAATTTG TTTTA

GAM25 206 GPR56 1 7949 NP_005673.2 5 73 ACCTCCACCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCAT TTA GAACTTGGG CCT CAC
GT C C
GAM25 206 GPR66 1 7428 NP_006047.2 3 578 ACCTCCGCCTCC A A 1 C c c
GGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
G C
GAM25 206 GPR81 1 12540 NP_115943.1 3 423 ACCTCTGCCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 GRAF 1 3444 NP_055886.1 3 2849 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C
GAM25 206 GRWD 1 18015 NP_113673.2 3 421 ACCTCCGCCTCC TG G A 1 C c c
TGGGTTAAAGTG AAT CTT AACCCAGGA GTG
ATTCTCTC TTA GAA TTGGGTCCT CGC
GT A C
GAM25 206 GSDM 2 13018 NP_835465.1 3 344 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
GTTCTCCT TTGACGAACTTGG CCT CGC
AC C
GAM25 206 GSDM 2 19169 XP_209009.1 3 342 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
AC C
GAM25 206 GTF2E1 1 4882 NP_005504.1 3 354 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 GTF2IRD 1 5571 NP_115579.3 3 191 ACTTCCAGCTCC C A 1 C c c
2 TGGGTTCGAACG AATTG TTGAACCCAGGA GT
ATTCTCCT TTAGC AGCTTGGGTCCT CG
A -
GAM25 206 GTF2IRD 1 5571 NP_775808.1 3 191 ACTTCCAGCTCC C A 1 C c c
2 TGGGTTCGAACG AATTG TTGAACCCAGGA GT
ATTCTCCT TTAGC AGCTTGGGTCCT CG
A -
GAM25 206 GTPBG3 1 13666 NP_116009.1 3 679 ACCTCCACCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CAC
GT C C

GAM25 206 H63 1 2380 NP_612432.2 3 513 ACCTCCGCCTCC A 1 C b b
TGGGTTCAGGCA AATTGCTTGAACCCAGGA GTG
ATTTTCCT TTAACGGACTTGGGTCCT CGC
C
GAM25 206 H63 1 2380 NP_816929.1 3 513 ACCTCCGCCTCC A 1 C b b
TGGGTTCAGGCA AATTGCTTGAACCCAGGA GTG
ATTTTCCT TTAACGGACTTGGGTCCT CGC
C
GAM25 206 HAVCR2 1 14385 NP_116171.2 3 545 AGCTCCGCCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 HE9 1 6046 NP_741997.1 3 258 ACCTCCGCCTCC CCA A 1 C c c
CGAGTTCAAGCG AATTGCTTGAAC GGA GTG
ATTCTCCT TTAGCGAACTTG CCT CGC
AGC C
GAM25 206 HIF3A 1 10710 NP_690009.1 3 140 GTCTTGAACTCC A----- C A 1 C c c
TGAGTTCAAGCG ATTGCTTGAAC CAGGA GT
ATCCACCT TAGCGAACTTG GTCCT CA
TCCACC A -
GAM25 206 HRH4 1 5567 NP_067637.2 3 1465 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTTGT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 HSD3B7 1 18589 NP_079469.2 3 258 CCCTCAACCTCC A----- A 1 C c c
TGGGTTCAAGCA ATTGCTTGAACCCAGGA GT
ATCCTCCT TAACGAACTTGGGTCCT CA
TCCTCC C
GAM25 206 HSPC065 2 2552 NP_054876.2 3 2341 ACCTCCTCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCT
GAM25 206 HSPC065 2 17865 NP_054876.2 3 2174 ACCTCCACCTCT - AA 1 C c c
GGGATTCAAGCA AATTGCTTGAA CCCAGG GTG
ATTCTCCC TTAACGAACTT GGGTCT CAC
A C-
GAM25 206 HTR1D 1 9485 NP_000855.1 3 338 ACCTCCGCATCC TG A A 1 C c c
CGGGTTCAAGAG AAT CTTGAACCC GGA GTG
ATTCTGCC TTA GAACTTGGG CCT CGC
GA C A
GAM25 206 HYAL4 1 4683 NP_036401.1 5 131 GCCACTGCCTCC TG --- 1 C c c
TGGGTTCAGGTG AAT CTTGAACCCAGGA AGTG
ATTCTCCT TTA GGACTTGGGTCCT TCAC
GT CCG
GAM25 206 IGF1 1 4732 NP_000609.1 3 5396 ACCTCCACCTCC A 1 C b b
TGGGTTTAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAATTTGGGTCCT CAC
C
GAM25 206 IL11 1 13505 NP_000632.1 3 748 ACCTCCACCTCC A A 1 C b b
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG

ATTCTCCT TTAACGAACTTGGG CCT CAC
C C
GAM25 206 IL19 1 6724 NP_037503.2 5 39 GTCTTCAACTCC ACC A 1 C c c
TGACCTCAAGCA AATTGCTTGA CAGGA GT
ATTGTCCT TTAACGAACT GTCCT CA
CCA -
GAM25 206 IL28RA 1 13666 NP_734464.1 3 2316 ACCTCCACCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CAC
GT C C
GAM25 206 IL28RA 1 13666 NP_775087.1 3 2316 ACCTCCACCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CAC
GT C C
GAM25 206 IL28RA 1 13666 NP_775088.1 3 3013 ACCTCCACCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CAC
GT C C
GAM25 206 INHBE 1 17098 NP_113667.1 3 711 ACCTCCGTCTCC TG AG 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA TG
ATTCTTCT TTA GAACTTGGGTCCT GC
GT CT
GAM25 206 ITGAX 1 5590 NP_000878.1 3 444 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGTA AATTGCTTGAACCC GGA GTG
ATTCTGCT TTAATGAACTTGGG CCT CGC
C C
GAM25 206 JAK3 1 9292 NP_000206.1 3 452 ACCTCTGCTTCC CA T 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGAAG
ATTCTCCT TTAGCGAACTTGG CCTTC
AC G
GAM25 206 KCNJ11 1 612 NP_000516.2 5 101 ACCTCCGCCTCT AG A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GA GTG
ATTCTCCT TTAGCGAACTTGGG CT CGC
CT C
GAM25 206 KIAA006 1 6721 NP_055691.1 3 675 AACCTCCACCTC C A 1 C b b
3 CTGGTTCAAGCG AATTGCTTGAACC AGGA GTG
ATTCTCAG TTAGCGAACTTGG TCCT CAC
- C
GAM25 206 KIAA008 1 1183 NP_055584.1 3 2238 ACCTCTGCCACC CCA AA 1 C c
c
7 CATGTTCAAGCG AATTGCTTGAAC GG GTG
ATTCTCCT TTAGCGAACTTG CC CAC
TA- --
GAM25 206 KIAA039 1 4805 NP_055487.1 3 3134 ACCTCTGCCTCC AGT 1 C c c
1 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCAT TTAACGAACTTGGGTCCT
CCG
GAM25 206 KIAA045 1 6069 XP_027862.1 3 3752 ACCTCCACCTCC A A 1 C c c
9 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC

```
                                                C  C
GAM25   206   KIAA047 1  11244  NP_055679.1  3  1279  ACCTCCGTCTCC          CA  AG        1  C  c  c
        5                          CAGGTTCAAGCG AATTGCTTGAACC  GGA  TG
                                   ATTCTCTT    TTAGCGAACTTGG  CCT  GC
                                                 AC   CT
GAM25   206   KIAA049 1  10283  XP_031397.1  3  2850  ACCTCCGTCTCC          CA  AG        1  C  c  c
        5                          CAGGTTCAAGCG AATTGCTTGAACC  GGA  TG
                                   ATTCTTCT    TTAGCGAACTTGG  CCT  GC
                                                 AC   CT
GAM25   206   KIAA051 2  13505  NP_055547.1  3  3722  ACCTCCACCTCC           A   A        1  C  b  b
        3                          CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
                                   ATTCTCCT    TTAACGAACTTGGG CCT CAC
                                                 C   C
GAM25   206   KIAA051 2  14774  NP_055547.1  5  138   GCCTCCACCTCC   TG     CA  A        1  C  c
b
        3                          CCGGTTCAAGTG AAT  CTTGAACC  GGA GTG
                                   ATTCTCCT    TTA  GAACTTGG  CCT CAC
                                             GT      CC  C
GAM25   206   KIAA055 1  13127  XP_085507.1  3  2654  ACCTCCACCTCC   TG     CA  A        1  C  c
c
        7                          CAGGTTCAAGTG AAT  CTTGAACC  GGA GTG
                                   ATTCTCCT    TTA  GAACTTGG  CCT CAC
                                             GT      AC  C
GAM25   206   KIAA056 1  14373  XP_038150.2  3  369   ACCTCCGCCTCC          CCA  A        1  C  c  c
        1                          CAAGTTCAAGCG AATTGCTTGAAC   GGA GTG
                                   ATTGTCCT    TTAGCGAACTTG   CCT CGC
                                                 AAC   C
GAM25   206   KIAA060 1  16135  NP_055509.1  5  117   ACCTCCACCTCC          CA  A        1  C  c  c
        5                          CAGGTTCAAGCA AATTGCTTGAACC  GGA GTG
                                   ATTCTCCT    TTAACGAACTTGG  CCT CAC
                                                 AC   C
GAM25   206   KIAA065 1  1046   XP_113962.1  3  1827  GTCTTGAACTCC A-----           A      1  C  c  c
        0                          TGGGTTCAAGCA      ATTGCTTGAACCCAGGA GT
                                   GTCTTCCT          TGACGAACTTGGGTCCT CA
                                           TCCTTC             -
GAM25   206   KIAA066 1  887    NP_055642.1  5  9     ACCTCCGCCTCC    G       A  A        1  C  c  c
        3                          CGGGTTCAAGAA AATT CTTGAACCC GGA GTG
                                   GTTTCCCT    TTGA GAACTTGGG CCT CGC
                                             A       C  C
GAM25   206   KIAA068 1  9165   NP_055667.1  3  67    GGGCTCACCTCC          CA  A        1  C  c  c
        2                          CTGGTTCAAGCG AATTGCTTGAACC  GGA GTG
                                   ATTGTCCC    TTAGCGAACTTGG  CCT CAC
                                                 TC   C
GAM25   206   KIAA082 1  8283   NP_056143.1  3  2545  GTCTCAAACTCC A-----       A     A      1  C  c  c
        8                          TGGGCTCAAGCA      ATTGCTTGA CCCAGGA GT
                                   ATCCTCCT          TAACGAACT GGGTCCT CA
                                           TCCTCC        C      -
GAM25   206   KIAA083 1  9780   NP_055739.1  3  1966  ACCACCATCTCC            AG        1  C  b  b
```

1 TGGGTTCAGGCG AATTGCTTGAACCCAGGA TG
ATTCTTCC TTAGCGGACTTGGGTCCT AC
CT

GAM25 2069 KIAA0881 18023 NP_056192.1 3 784 ACCTCCGCCTCC C A 1 C c c
TGGGTTCAAACA AATTG TTGAACCCAGGA GTG
ATTCTGTC TTAAC AACTTGGGTCCT CGC
A C

GAM25 2064 KIAA0921 13300 NP_055712.1 3 1775 GCCTCCAACTCT AA----- A 1 C c c
TGGGTTCAAGCA TTGCTTGAACCCAGGA GT
ACCCTGCC AACGAACTTGGGTTCT CA
CCGTCCC -

GAM25 2065 KIAA0931 7586 XP_052620.6 3 1262 ACCTGCACCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCA TTAACGAACTTGGGTCCT CAC
C

GAM25 2062 KIAA0961 8363 XP_290942.1 3 1572 ACCTCCACATCC TG CA A 1 C c c

CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT AC A

GAM25 2062 KIAA1001 18510 XP_290584.1 3 363 ACCTCCAGCTCC TG A 1 C c c
TGGGTTCAGGTG AAT CTTGAACCCAGGA GT
ATTCTCCT TTA GGACTTGGGTCCT CG
GT -

GAM25 2060 KIAA1041 19942 XP_051091.3 3 2504 ACCTCTGCTTCC A T 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGAAG
GTTTCCTG TTGACGAACTTGGG CCTTC
C G

GAM25 2061 KIAA1041 16595 NP_055762.1 3 1016 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CGC
C C

GAM25 2060 KIAA1171 17183 XP_045907.2 3 1293 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 2065 KIAA1181 7542 NP_065761.1 3 202 GCCTGTGTCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CTG

GAM25 2068 KIAA1193 9534 NP_065765.1 3 3757 ACCTCCACTTCT CA 1 C b b
CAGGTTCAAGCA AATTGCTTGAACC GGAAGTG
ATTCTCCT TTAACGAACTTGG TCTTCAC
AC

GAM25 2068 KIAA1193 14842 NP_065765.1 3 766 CACTGTAACCTC AAGT 1 C c b
TGGGTTCAAGCA AATTGCTTGAACCCAGG
ATTCTTCT TTAACGAACTTGGGTCT
CCAA

GAM25 2068 KIAA1193 17079 NP_065765.1 3 469 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG

ATTCTCCT TTAACGAACTTGGGTCCT CGC
C

GAM25 2067 KIAA1251 17183 XP_031577.2 3 3614 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 2068 KIAA1261 11503 XP_291055.1 3 946 GCCACTGCCTCC TG CA --- 1 C c c
CAGGTTCAAGTG AAT CTTGAACC GGA AGTG
ATTCTCCT TTA GAACTTGG CCT TCAC
GT AC CCG

GAM25 2063 KIAA1271 16475 XP_300760.1 5 427 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCATCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 2065 KIAA1461 11959 XP_027396.4 3 618 TCTTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 2063 KIAA1491 6658 XP_034415.1 3 3014 AGCTCCCCTTCC CA T 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGAAG
ATTCTCCT TTAACGAACTTGG CCTTC
AC C

GAM25 2060 KIAA1531 2247 XP_042661.5 3 1225 ACTACCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCGCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 2061 KIAA1571 13505 XP_027744.1 3 930 ACCTCCACCTCC A A 1 C b b
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAC
C C

GAM25 2065 KIAA1611 16197 NP_066002.1 3 1735 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCCCCT TTAGCGAACTTGG CCT CAC
AC C

GAM25 2061 KIAA1672 613 XP_037809.1 3 1919 GTCTCGAACTTC A G 1 C b b
TGGGCTCAAGCA AATTGCTTGA CCCAG AAGT
ATTGTCCC TTAACGAACT GGGTC TTCA
C -

GAM25 2061 KIAA1672 6719 XP_037809.1 3 4141 GCCTCCAACTCC A----- A A 1 C c b
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCTC TAACGAACT GGGTCCT CA
CTCTCC C -

GAM25 2067 KIAA1731 1130 NP_219494.1 3 1475 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 2064 KIAA1781 16595 NP_115820.1 3 390 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CGC

C C
GAM25 2067 KIAA1821 16595 XP_290834.1 3 1354 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CGC
C C
GAM25 2066 KIAA1831 4984 XP_114087.2 3 1726 ACCCCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 2061 KIAA1971 9625 XP_058720.4 3 610 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCTG TTAACGAACTTGG CCT CAC
AC C
GAM25 2067 KIAA1981 3377 XP_113870.1 5 250 ATCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCTT TTAGCGAACTTGG CCT CGC
AC C
GAM25 2068 KIAA2022 3481 XP_059415.2 3 939 GTCTTGAACTCC A----- AC A 1 C c c
TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCTC TAACGAACT GGTCCT CA
CTCTCC CC -
GAM25 2068 KIAA2022 4224 XP_059415.2 3 1243 GTCTCAAACTCC A----- A 1 C c c
TGGGTTCAAGCA ATTGCTTGAACCCAGGA GT
ATCCTCCC TAACGAACTTGGGTCCT CA
CCCTCC -
GAM25 206 KLK7 1 2523 NP_005037.1 3 582 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCGT TTA GAACTTGGGTCCT CGC
GT C
GAM25 206 KLK7 1 2523 NP_644806.1 3 582 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCGT TTA GAACTTGGGTCCT CGC
GT C
GAM25 206 KSR 1 9413 XP_290793.1 5 1196 GCCTCTGCCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 LAMP3 1 3444 NP_055213.1 3 613 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C
GAM25 206 LIPT1 1 6069 NP_057013.1 5 144 ACCTCCACCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C
GAM25 206 LIPT1 1 6069 NP_660198.1 5 144 ACCTCCACCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C
GAM25 206 LIPT1 1 6069 NP_660199.1 5 144 ACCTCCACCTCC A A 1 C c c

CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C

GAM25 206 LNIR 1 14735 NP_112178.1 3 881 GCCTTGAACTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C -

GAM25 206 LNK 2 6553 NP_005466.1 3 1731 ACCTCCACCTTC C T 1 C b b
CTGGTTCAAGCG AATTGCTTGAACC AGGAAG
ATTCTGCC TTAGCGAACTTGG TCCTTC
- C

GAM25 206 LNK 2 19673 NP_005466.1 3 1731 CCTCCACCTTCC C T 1 C b b
TGGTTCAAGCGA AATTGCTTGAACC AGGAAG
TTCTGCCT TTAGCGAACTTGG TCCTTC
- C

GAM25 206 LOC1128 1 19177 NP_612422.2 3 450 GATCTCGCCTCC A 1 C b b
17 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C

GAM25 206 LOC1134 2 4156 NP_612437.2 3 900 ACTTCTGCCTCC AGT 1 C c b
44 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 LOC1134 2 7668 NP_612437.2 3 1225 ACCTCCACCTCT A 1 C b b
44 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTTCT CAC
C

GAM25 206 LOC1150 1 5447 NP_612451.1 5 44 GTCTTGAACTCC A----- AC A 1 C c c
98 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCT TAACGAACT GGTCCT CA
TCCTCC CC -

GAM25 206 LOC1152 1 19046 XP_055499.2 5 1803 ACCTCCGCCTCC C A 1 C c c
19 TGGGTTCAAACA AATTG TTGAACCCAGGA GTG
ATTCTCCT TTAAC AACTTGGGTCCT CGC
A C

GAM25 206 LOC1156 1 6718 NP_663299.1 3 704 ACCTTTGCCTCC CC A T 1 C c c
48 CTAGTTCAAGCG AATTGCTTGAAC AGG AG
ATTTTCCT TTAGCGAACTTG TCC TC
A- C C

GAM25 206 LOC1184 1 1129 XP_060981.3 3 267 GCCTCCGCCTCC TG A 1 C c c
90 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
GTTCTCCT TTG GAACTTGGGTCCT CGC
GT C

GAM25 206 LOC1205 1 5254 XP_058475.1 3 727 ACCTCCGTCTCC TG AG 1 C c c
26 TGGGTTCAAGTG AAT CTTGAACCCAGGA TG
ATTCTCCA TTA GAACTTGGGTCCT GC
GT CT

GAM25 206 LOC1250 1 13505 XP_058889.3 3 455 ACCTCCACCTCC A A 1 C b b
61 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAC

C C

GAM25 206 LOC1266 1 5257 XP_060121.4 3 243 ACATCTGACTCC A 1 C b b
69 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GT
GTTCTTCC TTGACGAACTTGGGTCCT CA
-

GAM25 206 LOC1322 1 7296 XP_059583.1 5 131 GCCTCCGCTTCC A 1 C b b
41 GGGGTTCAAGCG AATTGCTTGAACCC GGAAGTG
ATTCTCCT TTAGCGAACTTGGG CCTTCGC
G

GAM25 206 LOC1352 1 19636 XP_072402.4 3 1162 GCCTCAAACTCC A----- A A 1 C c c
93 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C -

GAM25 206 LOC1357 1 11364 NP_612639.1 3 87 ACCTCCGCCTCC A 1 C b b
63 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCA TTAGCGAACTTGGGTCCT CGC
C

GAM25 206 LOC1444 1 6245 XP_096611.2 3 257 ACCTCCACCTCT CA A 1 C c c
81 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCAT TTAACGAACTTGG TCT CAC
AC C

GAM25 206 LOC1448 1 2317 XP_096698.1 3 406 AGGGACACCTCC A A 1 C b b
71 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
GTTCTCCT TTGACGAACTTGGG CCT CAC
C C

GAM25 206 LOC1452 1 1754 XP_085072.1 5 685 ACCTCCACCCGC A AA- 1 C c c
68 CGGGTTCAAGCG AATTGCTTGAACCC GG GTG
ATTCTCCT TTAGCGAACTTGGG CC CAC
- GCC

GAM25 206 LOC1458 1 2677 XP_085242.1 3 987 GCTTCACCATCC A------ A A- 1 C c c
00 TGGGTCAAGCAG ATTGCTTGA CCCAGGA GTG
TGTTCCTT TGACGAACT GGGTCCT CAC
TTCCTTG - AC

GAM25 206 LOC1458 1 634 XP_096873.1 5 108 ACCTTGACGTCC CA A 1 C c c
13 CAGGTTCAAGCG AATTGCTTGAACC GGA GT
ATTCTCTC TTAGCGAACTTGG CCT CA
AC G

GAM25 206 LOC1461 1 4315 NP_778229.1 5 240 ACCTCCGCCTCC C A 1 C c c
77 TGGGTTCAAACG AATTG TTGAACCCAGGA GTG
ATTCTCCT TTAGC AACTTGGGTCCT CGC
A C

GAM25 206 LOC1462 2 6069 XP_085387.1 3 3258 ACCTCCACCTCC A A 1 C c c
29 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C

GAM25 206 LOC1462 2 11151 XP_085387.1 3 4082 AGCCCTGCCTCC AGT 1 C c c
29 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTGTA TTAACGAACTTGGGTCCT

CCG

GAM25 206 LOC1463 1 15193 XP_085430.1 5 436 TCCTCCGACTCC C A 1 C b b
46 CTGGTTCAAGCG AATTGCTTGAACC AGG AGT
ATTGTCCT TTAGCGAACTTGG TCC TCA
- C

GAM25 206 LOC1464 1 11432 XP_096998.2 5 585 GCCTCCAACTCT C GA 1 C c c
29 CTGGTTCAAGCG AATTGCTTGAACC AG AGT
ATTCTCCT TTAGCGAACTTGG TC TCA
- TC

GAM25 206 LOC1467 1 14301 XP_085588.1 5 938 ACCTCCACCTCC CA A 1 C c c
84 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C

GAM25 206 LOC1468 1 4887 XP_085603.1 5 19 ACCTCCGCATCC A A 1 C c c
20 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C A

GAM25 206 LOC1468 1 14231 NP_660316.1 3 1216 AACTCCGCCTCC TG A 1 C c c

94 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTTCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 206 LOC1469 1 18521 XP_085634.2 3 710 ACCTCCGCCTCC A 1 C b b
09 TGGGTTCAAGTA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAATGAACTTGGGTCCT CGC
C

GAM25 206 LOC1471 1 1828 XP_085722.2 3 300 AGCTCCGCCTCC CCA A 1 C c c

66 CGAGTTCAAGCA AATTGCTTGAAC GGA GTG
ATTCTCCT TTAACGAACTTG CCT CGC
AGC C

GAM25 206 LOC1478 2 13127 XP_085903.1 3 329 ACCTCCACCTCC TG CA A 1 C c
b
17 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT AC C

GAM25 206 LOC1478 2 20074 XP_085903.1 3 493 ATCTCTGCTTCC A T 1 C b b
17 CGGGTTCAAGCA AATTGCTTGAACCC GGAAG
ATTCTTCT TTAACGAACTTGGG CCTTC
C G

GAM25 206 LOC1478 1 4882 XP_085924.2 3 194 ACCTCTGCCTCC AGT 1 C c c
41 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 LOC1481 1 6069 NP_653293.1 3 2572 ACCTCCACCTCC A A 1 C c c
37 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C

GAM25 206 LOC1481 1 4479 XP_086087.1 5 673 ACCTCCACCTCC A 1 C b b
89 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG

ATTCTTAT TTAGCGAACTTGGGTCCT CAC
C
GAM25 206 LOC1482 1 16166 XP_086095.1 3 1225 CTCGCTGTGTCC CA --- 1 C c c
03 CAGGTTCAAGCA AATTGCTTGAACC GGA AGTG
GTTCTCCT TTGACGAACTTGG CCT TCGC
AC GTG
GAM25 206 LOC1487 2 11549 XP_086281.1 5 192 AACTCAAGCTCC ACC A 1 C c c
09 TGAACTCAAGCA AATTGCTTGA CAGGA GT
ATTCTCCT TTAACGAACT GTCCT CG
CAA -
GAM25 206 LOC1487 2 18101 XP_086281.1 3 445 ACCTCCGCCTCC TG A A 1 C c c
09 TGGGTCCAAGTG AAT CTTG ACCCAGGA GTG
ATTCTCCT TTA GAAC TGGGTCCT CGC
GT C C
GAM25 206 LOC1491 1 16301 XP_097598.1 5 3365 ACCTCCGCCTCC A 1 C b b
49 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
GTTCTCTT TTGACGAACTTGGGTCCT CGC
C
GAM25 206 LOC1494 1 3185 XP_086546.1 3 611 ACCTCCGCCTCC A 1 C b b
66 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 LOC1494 1 18212 XP_086536.1 3 124 AACTCCGCCTCC A A 1 C c c
78 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCGT TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 LOC1495 1 14533 XP_097661.1 3 3148 ACTTCCACCTCC A----- A A 1 C c c
06 CGGGTTCAAGCG ATTGCTTGAACCC GGA GTG
ATCCTGCC TAGCGAACTTGGG CCT CAC
CCGTCC C C
GAM25 206 LOC1500 1 9448 XP_097797.1 5 641 AACCTTCGCCTC TG ---- T 1 C c c
54 TGGGTTCAAGTG AAT CTTGAACCCAG GAAG
ATTCTCCT TTA GAACTTGGGTC CTTC
GT TCCG C
GAM25 206 LOC1503 1 17183 XP_086907.1 3 527 ACCTCCGCCTCC A A 1 C c c
97 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 LOC1505 1 19636 XP_097917.1 3 199 GCCTCAAACTCC A----- A A 1 C c c
87 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C -
GAM25 206 LOC1508 1 7130 XP_097963.1 3 316 ACATCATATACT GAACCC 1 C c
c
86 TCCTCAGAAGCA AATTGCTT AGGAAGTG
ATTGCAAC TTAACGAA TCCTTCAT
GAC---

GAM25 206 LOC1512 1 9269 XP_098021.1 5 142 CTATTTGCTTCC G C- T 1 C c c
01 TGGTATTGGAGC AATTGCTT AA CCAGGAAG
AGTTCAGT TTGACGAG TT GGTCCTTC
G AT G
GAM25 206 LOC1514 2 4882 XP_098063.1 5 787 ACCTCTGCCTCC AGT 1 C c c
75 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 LOC1514 2 14301 XP_098063.1 5 148 ACCTCCACCTCC CA A 1 C c c
75 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 LOC1516 1 17818 NP_612144.1 3 939 ACCTCCACTTCC A 1 C b b
36 CGGGTTCAAGCG AATTGCTTGAACCC GGAAGTG
ATTCTCCT TTAGCGAACTTGGG CCTTCAC
C
GAM25 206 LOC1524 1 11559 XP_098231.1 3 572 ACCTCTGCCTCC AGT 1 C c c
45 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC1526 1 3060 XP_011108.2 3 757 AACCTCTGCCTC A AGT 1 C c c
20 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
- CCG
GAM25 206 LOC1526 1 4383 XP_087500.1 5 14 GTCTCCACCTCC A A 1 C c c
67 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C
GAM25 206 LOC1527 1 12540 XP_098257.1 5 164 ACCTCTGCCTCC A AGT 1 C c c
19 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 LOC1530 1 16720 XP_098307.1 3 853 ACCTCCGCCTCC A 1 C b b
77 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTGTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 LOC1536 1 14611 XP_098412.1 5 337 GCCTCGACTTCC A----- T A 1 C c c
84 TGGGATCCAGCG ATTGCT GA CCCAGGAAGT
ATCCTCCC TAGCGA CT GGGTCCTTCA
CCCTCC C A
GAM25 206 LOC1542 1 16702 XP_098505.1 5 165 ACCTCCACCTCC CA A 1 C c c
82 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTTCT TTAACGAACTTGG CCT CAC
AC C
GAM25 206 LOC1548 1 14064 XP_098618.3 5 2882 ACCTCTGTCTCC A AGT 1 C c c
22 TGGGCTCAAGCA AATTGCTTGA CCCAGGA
ATTCTTCT TTAACGAACT GGGTCCT
C CTG

GAM25 206 LOC1548 3 11691 XP_098626.1 3 351 ACCTCCATCTCC TGA AG 1 C c b
77 TGGGTCCCAGCG AATTGCT ACCCAGGA TG
ATTCTCCT TTAGCGA TGGGTCCT AC
CCC CT
GAM25 206 LOC1548 3 13046 XP_098626.1 3 3589 ACCTCTACCTCC A 1 C b b
77 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAT
C
GAM25 206 LOC1548 3 13635 XP_098626.1 3 1031 GCTTTGACTTCC A----- A 1 C c b
77 TGGGCTCAAGCA ATTGCTTGA CCCAGGAAGT
ATCCTCCC TAACGAACT GGGTCCTTCA
CCCTCC C
GAM25 206 LOC1580 1 684 XP_088442.1 5 3628 ATCTCCGCCTCC CCA A 1 C c c
14 CCAGTTCAAGCG AATTGCTTGAAC GGA GTG
ATTCTCCT TTAGCGAACTTG CCT CGC
ACC C
GAM25 206 LOC1583 1 19625 XP_098919.1 5 420 ACCTTGGCCTCC CCA A 1 C c c
10 CGTGTTCAAGCG AATTGCTTGAAC GGA GT
ATTCTCCT TTAGCGAACTTG CCT CG
TGC C
GAM25 206 LOC1584 2 15086 XP_098955.1 3 1264 GTAATCACCTAC C GAA 1 C c b
76 TGGATTCAAGCA AATTGCTTGAA CCAG GTG
ATTCTCCT TTAACGAACTT GGTC CAC
A ATC
GAM25 206 LOC1584 2 18466 XP_098955.1 3 941 ACCTCCGCCCCC AA 1 C b b
76 TGGGTTCAAGCG AATTGCTTGAACCCAGG GTG
ATTCTCCT TTAGCGAACTTGGGTCC CGC
CC
GAM25 206 LOC1588 1 11559 XP_099000.1 5 23 ACCTCTGCCTCC AGT 1 C c c
65 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC1611 1 12540 XP_101622.1 3 1196 ACCTCTGCCTCC A AGT 1 C c c
45 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 LOC1632 2 1888 NP_775802.1 3 3406 ACCTCTGCCTTC CA T 1 C c b
27 CAGGTTCAAGCA AATTGCTTGAACC GGAAG
ATTATCCT TTAACGAACTTGG CCTTC
A- C
GAM25 206 LOC1632 2 15025 NP_775802.1 3 1716 ACCTCCACCTCC T A 1 C b b
27 TGGGTTCACGCA AATTGC TGAACCCAGGA GTG
ATTCTCCT TTAACG ACTTGGGTCCT CAC
C C
GAM25 206 LOC1640 1 8030 XP_089356.1 3 874 ACCTCCGCCTCC CA A 1 C c c
91 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG

ATTTTCCT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 LOC1696 1 17790 XP_095809.4 3 1168 ATCTCCGCCTCC TG A A 1 C c c
11 CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C
GAM25 206 LOC1962 1 5567 XP_113683.1 3 858 ACCTCTGCCTCC AGT 1 C c c
64 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTTGT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 LOC1969 1 2677 XP_113795.1 3 986 GCTTCACCATCC A------ A A- 1 C c c
88 TGGGTCAAGCAG ATTGCTTGA CCCAGGA GTG
TGTTCCTT TGACGAACT GGGTCCT CAC
TTCCTTG - AC
GAM25 206 LOC1999 1 9410 XP_114052.1 3 1273 ACCTCCGCCTAC TG GAA 1 C c c
06 TGGGTTCAAGTG AAT CTTGAACCCAG GTG
ATTCTCTT TTA GAACTTGGGTC CGC
GT ATC
GAM25 206 LOC2001 1 5567 XP_117200.1 5 572 ACCTCTGCCTCC AGT 1 C c c
69 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTTGT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 LOC2008 1 13127 XP_117289.1 3 697 ACCTCCACCTCC TG CA A 1 C c c
60 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT AC C
GAM25 206 LOC2008 1 3030 NP_789785.1 3 984 CTTCAGCCTTCC CA T 1 C c c
95 CAGGTTCAAGCA AATTGCTTGAACC GGAAG
ATTCTCCT TTAACGAACTTGG CCTTC
AC C
GAM25 206 LOC2024 1 12745 XP_114493.1 5 2089 ACCTCCACCTCC G TG A 1 C c c
60 TGGGTTTGAGGA AATT CT AACCCAGGA GTG
ATTGTCCT TTAA GA TTGGGTCCT CAC
G GT C
GAM25 206 LOC2035 1 18584 XP_114719.1 3 2942 ACCTCCGCCTCC A A 1 C c c
47 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
GTTCTCCT TTGACGAACTTGGG CCT CGC
C C
GAM25 206 LOC2192 1 4935 XP_166599.2 3 1088 GTCTCCAACTCC A----- A A 1 C c c
93 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C -
GAM25 206 LOC2200 1 2821 NP_660352.1 3 431 ACCTCCGCCTGC GAA 1 C c c
74 TGGGTTCAAGCG AATTGCTTGAACCCAG GTG
ATTCTCCT TTAGCGAACTTGGGTC CGC
GTC

GAM25 206 LOC2210 1 1598 XP_169026.1 3 602 ACGTCCACCTCC A 1 C b b
91 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C
GAM25 206 LOC2220 1 1130 XP_168371.1 3 2574 ACCTCCGCCTCC TG A 1 C c c
31 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C
GAM25 206 LOC2221 1 12545 XP_212100.1 5 123 ACCTCCACCTCC A 1 C b b
59 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTTTCTT TTAGCGAACTTGGGTCCT CAC
C
GAM25 206 LOC2222 1 13949 XP_168473.1 5 495 ACCTCAGCCTCC A A 1 C b b
24 TGGGCTCAAGCA AATTGCTTGA CCCAGGA GT
ATTCTCAT TTAACGAACT GGGTCCT CG
C C
GAM25 206 LOC2529 1 13976 XP_170858.2 3 328 GCCTCAACCTCC TG A 1 C c c
83 TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTCCC TTA GAACTTGGGTCCT CA
GT C
GAM25 206 LOC2551 1 2252 XP_172941.1 3 661 TCCTCCACCTCC CA A 1 C c c
77 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCTT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 LOC2554 1 15698 XP_173150.1 3 498 TAACTATGACTT AC GG 1 C c c
58 TGGTCTTAAGCA AATTGCTTGA CCA AAGT
ATTTTCTT TTAACGAATT GGT TTCA
CT --
GAM25 206 LOC2566 1 16894 XP_172864.1 3 908 ACCTCCGCCTCC A----- A A 1 C c c
14 CGGGTTCAAGCA ATTGCTTGAACCC GGA GTG
ATCCTCCC TAACGAACTTGGG CCT CGC
CCCTCC C C
GAM25 206 LOC2829 1 17558 XP_208473.1 3 669 GTCTTGAACTCC A----- A A 1 C c c
97 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCAGCCC TAACGAACT GGGTCCT CA
CCCGAC C -
GAM25 206 LOC2830 1 10453 XP_210859.1 3 1873 ACTTCCACCTCC G A 1 C b b
31 TGGGTTGAAGCA AATTGCTT AACCCAGGA GTG
ATTCTTCT TTAACGAA TTGGGTCCT CAC
G C
GAM25 206 LOC2830 1 18635 XP_210875.1 3 1436 GCCTCGACCTCC A----- A A 1 C c c
61 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCAC TAACGAACT GGGTCCT CA
CACTCC C C
GAM25 206 LOC2830 1 1684 XP_210885.1 5 1769 ACATCCACCTCC A 1 C b b
89 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CAC
C

GAM25 206 LOC2831 1 1051 XP_210895.1 3 886 GTCTCCAACTCC A----- AC A 1 C c c
19 TGGACTCAAGCA ATTGCTTGA CCAGGA GT
ATCTGCCC TAACGAACT GGTCCT CA
CCCGTC CA -
GAM25 206 LOC2832 1 14301 NP_787089.1 5 110 ACCTCCACCTCC CA A 1 C c c
41 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 LOC2833 1 14710 XP_210973.1 3 57 ACCTCCGCCTCC A 1 C b b
23 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCACCC TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 LOC2833 1 11355 XP_210981.1 3 1685 ACCTCCACTTCC A 1 C b b
35 CGGGTTCAAGCG AATTGCTTGAACCC GGAAGTG
ATTCTTCT TTAGCGAACTTGGG CCTTCAC
C
GAM25 206 LOC2834 1 10938 XP_211024.1 5 493 ACCTCCTGCTCC AGT 1 C c c
00 TGGGTTCGAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAGCTTGGGTCCT
CGT
GAM25 206 LOC2834 1 14301 XP_211049.1 5 176 ACCTCCACCTCC CA A 1 C c c
54 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 LOC2834 1 3816 XP_211062.1 3 724 ACCTCCACTTTC CA 1 C b b
87 CAGGTTCAAGCA AATTGCTTGAACC GGAAGTG
ATTCTCCT TTAACGAACTTGG CTTTCAC
AC
GAM25 206 LOC2835 1 4772 XP_211075.1 3 1868 AACTCCACCTCC G CA A 1 C c c
07 CAGGTTCAAGGA AATT CTTGAACC GGA GTG
ATTCCTGT TTAA GAACTTGG CCT CAC
G AC C
GAM25 206 LOC2835 1 13127 XP_211083.1 3 3327 ACCTCCACCTCC TG CA A 1 C c
c
34 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT AC C
GAM25 206 LOC2835 1 15674 XP_211110.1 3 972 GTCTTGAACTCC A----- AC A 1 C c c
51 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTTCC TAACGAACT GGTCCT CA
CCTTCC CC -
GAM25 206 LOC2835 2 16702 XP_211095.1 5 933 ACCTCCACCTCC CA A 1 C c c
75 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTTCT TTAACGAACTTGG CCT CAC
AC C
GAM25 206 LOC2835 2 17611 XP_211095.1 5 470 CCCTCAACCTCC A----- A A 1 C c c
75 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT

ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C C
GAM25 206 LOC2835 1 7310 XP_208741.1 3 1510 ACCTCCACCTCC G CA A 1 C c c
90 CAGGTTCAAGGG AATT CTTGAACC GGA GTG
ATTCTCCC TTAG GAACTTGG CCT CAC
G AC C
GAM25 206 LOC2836 1 15694 XP_211126.1 5 3937 ACCTCCGCCTCC CA A 1 C c c
24 CAGGTTCAAGTA AATTGCTTGAACC GGA GTG
ATTCTGCC TTAATGAACTTGG CCT CGC
AC C
GAM25 206 LOC2836 1 18297 XP_208764.1 3 275 GCCTCCGTCTCC CA AG 1 C c
c
41 CAGGTTCAAGCA AATTGCTTGAACC GGA TG
GTTCTCCT TTGACGAACTTGG CCT GC
AC CT
GAM25 206 LOC2836 1 14685 XP_211152.1 5 67 ACTTCCACCTCC TG CA A 1 C c c
72 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT AC C
GAM25 206 LOC2837 1 11559 XP_208835.1 3 347 ACCTCTGCCTCC AGT 1 C c c
67 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC2838 1 5363 XP_211236.1 5 1217 ACCTCCGCCTCC CA A 1 C c c
57 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 LOC2838 1 5363 NP_787095.1 3 1083 ACCTCCGCCTCC CA A 1 C c c
61 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 LOC2838 1 10892 XP_208875.1 3 1554 GCCTCCACCTCC A A 1 C c c
63 AGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
A C
GAM25 206 LOC2838 1 5497 XP_208899.1 5 337 ACCTCCACCTCT C AG A 1 C c c
89 CGGCTTCAAGCA AATTGCTTGAA CC GA GTG
ATTCTCCT TTAACGAACTT GG CT CAC
C CT C
GAM25 206 LOC2839 1 13152 XP_208909.1 5 2468 ACCTTCACCGCC CA AA 1 C c
c
28 CAGGTTCAAGCG AATTGCTTGAACC GG GTG
ATTCTCTT TTAGCGAACTTGG CC CAC
AC GC
GAM25 206 LOC2840 1 20163 XP_208958.2 3 1533 ACCTCCTCCTCC A AGT 1 C c
c
01 CGGGTTCAAGCA AATTGCTTGAACCC GGA

ATTCTCCC TTAACGAACTTGGG CCT
C CCT

GAM25 206 LOC2840 1 13339 XP_211298.1 3 64 ACTTCCGCCTCC A 1 C b b
16 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CGC
C

GAM25 206 LOC2840 1 12195 XP_208983.3 3 1066 GCCTCCGCCTCC CA A 1 C c c
23 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C

GAM25 206 LOC2840 1 11517 XP_211312.1 5 203 GAATGCCTTACC - - T 1 C c c
39 TGGGTTCTGGGC AATTGCTT GAACCCAGG AAG
AGTTCTTC TTGACGGG CTTGGGTCC TTC
T A C

GAM25 206 LOC2840 1 15667 XP_211309.1 3 733 GTCTTGAACTCC A----- A A 1 C c c
41 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C -

GAM25 206 LOC2840 1 15234 XP_211321.1 3 1031 ATCTCCACCTCC A 1 C b b
74 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTTTCTT TTAACGAACTTGGGTCCT CAC
C

GAM25 206 LOC2840 1 5191 XP_211324.1 3 192 CTCTGCTTCCCG -- A T 1 C c c
95 GGTTCACAAGCA AATTGCT TGAACCC GGAAG
ATTCTCAT TTAACGA ACTTGGG CCTTC
AC C G

GAM25 206 LOC2840 1 13505 XP_209008.3 3 246 ACCTCCACCTCC A A 1 C b b
98 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAC
C C

GAM25 206 LOC2841 4 5279 XP_211327.3 3 857 GCCTCCAACTCC A----- G A 1 C c b
02 TGGGTTCAAGGG ATT CTTGAACCCAGGA GT
ATCCTCCC TAG GAACTTGGGTCCT CA
CCCTCC G -

GAM25 206 LOC2841 4 18051 XP_211327.3 3 656 ACCTCCGCCTCC CA A 1 C c b
02 CTGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
TC C

GAM25 206 LOC2841 4 18323 XP_211327.3 5 93 ACCTCCACCTCC A 1 C b b
02 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CAC
C

GAM25 206 LOC2841 4 18496 XP_211327.3 3 204 GTCTAGAACTCC A----- A 1 C c b
02 TGGGTTCAAGTA ATTGCTTGAACCCAGGA GT
ATCCTCCC TAATGAACTTGGGTCCT CA
CCCTCC -

GAM25 206 LOC2841 1 7936 XP_209032.1 3 588 ACATCCAGCTCC T A 1 C c c
35 TGGGTTTCAGCA AATTGCT GAACCCAGGA GT
ATTCTCCT TTAACGA TTTGGGTCCT CG

C -

GAM25 206 LOC2841 1 5339 XP_211363.1 5 755 ACCCCCACCTCC A A 1 C c c
74 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCACCT TTAGCGAACTTGGG CCT CAC
C C

GAM25 206 LOC2841 2 4426 XP_209059.1 5 970 TTTTCCACCTTG -- AA 1 C c c
83 GGAGTTCAAGCG AATTGCTTGAA CCCAGG GTG
ATTTTCCC TTAGCGAACTT GGGTTC CAC
GA --

GAM25 206 LOC2841 2 19169 XP_209059.1 5 470 ACCTCCGCCTCC CA A 1 C c c
83 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
AC C

GAM25 206 LOC2841 1 7709 XP_209060.2 3 1210 ACTTCCGACTCC CA------ 1 C c c
86 CAGGTTCAAGCG AATTGCTTGAACC GGAAGT
ATTCTCCT TTAGCGAACTTGG CCTTCA
ACCCTCAG

GAM25 206 LOC2841 1 18296 XP_211377.1 5 112 ACCTCCGCCTCC CA A 1 C c c
91 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCC TTAACGAACTTGG CCT CGC
AC C

GAM25 206 LOC2842 1 5343 XP_211408.1 3 30 ACCTCCGCCTCC CA A 1 C c c
60 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTGCT TTAACGAACTTGG CCT CGC
AC C

GAM25 206 LOC2842 1 13505 XP_211412.1 5 1075 ACCTCCACCTCC A A 1 C b b
76 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAC
C C

GAM25 206 LOC2842 1 17183 XP_211419.1 3 1877 ACCTCCGCCTCC A A 1 C c c
86 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 206 LOC2843 1 12209 XP_302720.1 3 404 ACCTCCGCCCCC CA AA 1 C c
c
11 CAGGTTCAAGCG AATTGCTTGAACC GG GTG
ATTCTGCC TTAGCGAACTTGG CC CGC
AC CC

GAM25 206 LOC2843 1 13899 XP_209143.1 3 1081 GCCTCCACTTCC TG CA 1 C c
c
25 CAGGTTCAAGTG AAT CTTGAACC GGAAGTG
ATTCTCCT TTA GAACTTGG CCTTCAC
GT AC

GAM25 206 LOC2843 1 19019 XP_211435.1 3 578 ACCTCCACCTCC CA A 1 C c c
62 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCTT TTAACGAACTTGG CCT CAC
AC C

GAM25 206 LOC2843 1 8491 XP_209157.1 3 1268 AGCTCCGCCTCC T T A 1 C c c
76 TGGGTTCACGTC AAT GC TGAACCCAGGA GTG
ATTTTCCT TTA TG ACTTGGGTCCT CGC

C C C

GAM25 206 LOC2843 1 1125 XP_209163.1 3 432 ACCTCCGCCTCC TG A A 1 C c c
79 CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCCCCT TTA GAACTTGGG CCT CGC
GT C C

GAM25 206 LOC2844 1 1637 XP_209200.1 3 103 ACCACTGTCTCC A --- 1 C b b
21 CGGGTTCAAGCG AATTGCTTGAACCC GGA AGTG
ATTCTCCC TTAGCGAACTTGGG CCT TCAC
C CTG

GAM25 206 LOC2844 3 4108 XP_209198.1 3 525 GCCTCTGCCTCC - AGT 1 C c b
26 TGGGTTCCAAGC AATTGCTTG AACCCAGGA
GATTCTCC TTAGCGAAC TTGGGTCCT
C CCG

GAM25 206 LOC2844 3 4541 XP_209198.1 3 359 GCCTCCGCCTCC A 1 C b b
26 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTACC TTAACGAACTTGGGTCCT CGC
C

GAM25 206 LOC2844 3 10929 XP_209198.1 3 925 ACCTCCACCTCT CA A 1 C c b
26 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG TCT CAC
AC C

GAM25 206 LOC2844 1 4882 XP_209216.1 5 1164 ACCTCTGCCTCC AGT 1 C c c
54 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 LOC2845 1 18133 XP_211515.1 3 1351 ACCACTCTCTCC TG --- 1 C b b
51 TGGGTTCAAGTG AAT CTTGAACCCAGGA AGTG
ATTCTCCT TTA GAACTTGGGTCCT TCAC
GT CTC

GAM25 206 LOC2846 1 12373 XP_211561.1 5 553 GCCTCCGCCTCC TG A 1 C c c
28 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 206 LOC2846 1 10320 XP_211563.1 5 590 CTACCCGCTTCC C AAC 1 C c c
32 TGGAGCAAACAG AATTG TTG CCAGGAAGTG
TTGGGGGT TTGAC AAC GGTCCTTCGC
A GA-

GAM25 206 LOC2846 1 4131 XP_211573.1 5 33 ACCTCTGCCTCC AGT 1 C c c
46 TGGGTTTAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAATTTGGGTCCT
CCG

GAM25 206 LOC2846 1 3190 XP_209310.1 5 56 GTCTCAAACTCC A----- A 1 C c c
63 TGGGTTCAAGCA ATTGCTTGAACCCAGGA GT
GTCCTCCC TGACGAACTTGGGTCCT CA
CCCTCC -

GAM25 206 LOC2847 2 5347 XP_211602.1 3 109 ACCTTGGCCTCC C A 1 C c c
23 TAGGTTCAAGCA AATTGCTTGAACC AGGA GT
ATTCTCCT TTAACGAACTTGG TCCT CG
A C

GAM25 206 LOC2847 2 13127 XP_211602.1 3 520 ACCTCCACCTCC TG CA A 1 C c c
23 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTCCT TTA GAACTTGG CCT CAC
GT AC C
GAM25 206 LOC2848 1 12293 XP_209371.1 3 1265 ACCTCCACCTTC TG A T 1 C c c
05 CGGGTTCAAGTG AAT CTTGAACCC GGAAG
ATTCTCCT TTA GAACTTGGG CCTTC
GT - C
GAM25 206 LOC2848 1 15964 XP_209383.1 3 186 ACCTCTGCCTTC AGT 1 C c c
53 TGGGTTCGAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAGCTTGGGTCTT
CCG
GAM25 206 LOC2848 1 15861 XP_211668.2 3 667 ACCTCCACCTCC G CA A 1 C c c
56 CAGGTTCAAGGG AATT CTTGAACC GGA GTG
ATTCGTCT TTAG GAACTTGG CCT CAC
G AC C
GAM25 206 LOC2848 1 15861 XP_302835.1 3 156 ACCTCCACCTCC G CA A 1 C c c
56 CAGGTTCAAGGG AATT CTTGAACC GGA GTG
ATTCGTCT TTAG GAACTTGG CCT CAC
G AC C
GAM25 206 LOC2848 1 16384 XP_211672.1 3 118 ATCTCCACCTCC CA A 1 C c c
65 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CAC
AC C
GAM25 206 LOC2849 2 2551 XP_211696.1 5 705 ACCTCCACCTCC TG CA A 1 C c c
34 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTTCT TTA GAACTTGG CCT CAC
GT AC C
GAM25 206 LOC2849 2 11777 XP_211696.1 5 841 GTCTAGAACTTC A----- AC G 1 C c c
34 TGGTCTCAAGCA ATTGCTTGA CCAG AAGT
ATCTGCCC TAACGAACT GGTC TTCA
CCCGTC CT -
GAM25 206 LOC2849 1 3185 XP_211703.1 3 211 ACCTCCGCCTCC A 1 C b b
50 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 LOC2850 1 11586 XP_211731.2 3 686 ACCTCTGCTTCC T 1 C b b
02 TGGGTTCAAGCG AATTGCTTGAACCCAGGAAG
ATTCTCCT TTAGCGAACTTGGGTCCTTC
G
GAM25 206 LOC2850 1 13592 XP_209440.1 3 2430 ACCTCCAGCTCC A 1 C b b
26 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GT
ATTCTCAT TTAACGAACTTGGGTCCT CG
-

GAM25 206 LOC2850 1 20139 XP_211739.1 3 60 GTCTCAAACTCC A----- C A 1 C c c
33 TGGCTTCAAGCA ATTGCTTGAA CCAGGA GT
ATCCTTCC TAACGAACTT GGTCCT CA
CCTTCC C -
GAM25 206 LOC2850 1 12540 XP_209465.1 3 90 ACCTCTGCCTCC A AGT 1 C c c
88 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 LOC2851 1 14649 XP_211771.1 3 459 GTCTCAAACTCC A----- TG A 1 C c c
27 TGGGTTCAAGTG AT CTTGAACCCAGGA GT
ATCATTCC TA GAACTTGGGTCCT CA
CCTTAC GT -
GAM25 206 LOC2851 1 3517 XP_211777.1 5 378 GTCTCAAACTCC A----- AC A 1 C c c
36 TGGACTCAAGCA ATTGCTTGA CCAGGA GT
ATCTGCCC TAACGAACT GGTCCT CA
CCCGTC CA -
GAM25 206 LOC2852 1 2421 XP_209554.1 3 447 ACCTCTGCTTCC C T 1 C c c
99 TGGGTTCAAACA AATTG TTGAACCCAGGAAG
ATTCTCAT TTAAC AACTTGGGTCCTTC
A G
GAM25 206 LOC2853 1 9968 XP_211844.1 3 646 GTCTCAAACTCC A----- A A 1 C c c
34 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C -
GAM25 206 LOC2853 1 14925 XP_211853.1 5 31 GTCTGGAACTCC A----- A A 1 C c c
44 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C -
GAM25 206 LOC2853 1 1100 XP_211854.1 3 1058 GTCTCAAACTCC A----- A A 1 C c c
45 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCACCC TAACGAACT GGGTCCT CA
CCCACC C -
GAM25 206 LOC2853 2 2929 XP_209593.1 3 1256 GCCTCAAACTCC A----- A A 1 C c c
98 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C -
GAM25 206 LOC2853 2 17312 XP_209593.1 3 955 AGCTCTGCCTCC AGT 1 C c c
98 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCTT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 LOC2855 1 1520 XP_209643.1 3 59 ACCTCCACCTCC TG C A 1 C c c
10 TAGGTTCAAGTG AAT CTTGAACC AGGA GTG
ATTCTACT TTA GAACTTGG TCCT CAC
GT A C
GAM25 206 LOC2855 1 13006 NP_775933.1 3 134 CTAAGTAAACTT ACCCAG 1 C c
c
33 TGTTGTCAAGCA AATTGCTTGA GAAGT
ATTTGTCC TTAACGAACT TTTCA
GTTG--

GAM25 206 LOC2855 2 8906 XP_209671.1 3 315 ACTTCTGCCACC CA------ 1 C c c
89 CAGGTTCAAGCA AATTGCTTGAACC GGAAGT
ATTCTCCT TTAACGAACTTGG TCTTCA
ACCCACCG
GAM25 206 LOC2855 2 16135 XP_209671.1 3 769 ACCTCCACCTCC CA A 1 C c c
89 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CAC
AC C
GAM25 206 LOC2856 1 9340 XP_211959.1 5 897 GCCTCAAACTCC AA----- A 1 C c c
26 TGGGTTCAAGTA TTGCTTGAACCCAGGA GT
ACCCTCCC AATGAACTTGGGTCCT CA
CCCTCCC -
GAM25 206 LOC2856 1 4038 XP_211980.1 5 59 GTCTCCACCTCC ACC A 1 C c c
83 TGAGCTCAAGCA AATTGCTTGA CAGGA GTG
ATTCTCAT TTAACGAACT GTCCT CAC
CGA C
GAM25 206 LOC2856 1 12373 XP_209724.1 3 1137 GCCTCCGCCTCC TG A 1 C c c
89 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C
GAM25 206 LOC2857 2 13900 XP_209743.1 3 1543 GTCTCAAACTCC ACC A 1 C c
c
44 TGACCTCAAGCA AATTGCTTGA CAGGA GT
ATTTGCCC TTAACGAACT GTCCT CA
CCA -
GAM25 206 LOC2857 2 18188 XP_209743.1 3 1415 ACCTCCACCTAC A C GAA 1 C c
c
44 TAGGCTCAAGCA AATTGCTTGA CC AG GTG
ATTCTCGT TTAACGAACT GG TC CAC
C A ATC
GAM25 206 LOC2857 1 8007 XP_209750.1 3 421 ACTTCCGCCTCC C A A 1 C c c
60 CGGTTTCAAGCA AATTGCTTGAA CC GGA GTG
GTTCTCCA TTGACGAACTT GG CCT CGC
T C C
GAM25 206 LOC2857 1 15725 XP_212017.1 5 143 AAGCTTAGTGCT CT ---- 1 C c c
68 TGGGTTCAGACA AATTG TGAACCCAGG AAGT
GTTGTGGG TTGAC ACTTGGGTTC TTCG
AG GTGA
GAM25 206 LOC2858 1 6449 XP_212055.1 3 766 AACACCGCCTCC A A 1 C c c
12 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 LOC2858 1 7686 XP_212036.1 5 126 ACCTCCGCCTCC TG A A 1 C c c
13 CGGGTTCAAGAG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GA C C
GAM25 206 LOC2858 1 7527 XP_209777.1 5 1408 ACTTCCACTTCC TG CA 1 C c c
22 CAGGTTCAAGTG AAT CTTGAACC GGAAGTG
ATTCTCCT TTA GAACTTGG CCTTCAC

GT AC

GAM25 206 LOC2858 1 11310 XP_212034.1 5 645 ACATCCACCTCC A 1 C b b
43 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 LOC2858 1 4561 XP_209779.1 3 44 ACCTCCACCTCC A 1 C b b
53 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 LOC2858 1 9727 XP_209806.1 3 27 GTACATCTGCCG - AA- 1 C c c
96 TGGGTTCAAGCG AATTGCTTGAACCCA GG GTG
ATTCTCCT TTAGCGAACTTGGGT CC TAC
G GTC

GAM25 206 LOC2859 1 951 XP_212104.1 3 219 GTTTCAAACTCC A----- AC A 1 C c c
23 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCT TAACGAACT GGTCCT CA
TCCTCC CC -

GAM25 206 LOC2859 1 12786 XP_209818.1 5 193 GCCTCGACCTCC A----- A A 1 C c c

30 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C C

GAM25 206 LOC2859 1 20178 XP_212105.1 3 914 GCCTCCGCCTCC A A 1 C c c
72 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCAT TTAACGAACTTGGG CCT CGC
C C

GAM25 206 LOC2860 1 8978 XP_212133.1 5 2575 CCTTTTACTTCC C- CC 1 C c c
07 TGAATTCAATTC AATTG TTGAA CAGGAAGTG
AGTTTGAT TTGAC AACTT GTCCTTCAT
TT AA

GAM25 206 LOC2860 2 1126 XP_212163.1 3 499 ACCTCCGCCTCC A 1 C b b
78 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCTT TTAGCGAACTTGGGTCCT CGC
C

GAM25 206 LOC2860 2 11384 XP_212163.1 3 960 GTATTGAACTCC A----- AC A 1 C c b

78 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCC TAACGAACT GGTCCT CA
CCCTCC CC -

GAM25 206 LOC2860 1 6502 XP_212166.3 5 190 ACGTCCGCCTCC TG A 1 C c c
90 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTTCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 206 LOC2861 1 9054 XP_212175.1 5 546 CTACTACGTCAC GAAC A 1 C c c

08 TACCTGGAAGCA AATTGCTT CCAGG AGTG
ATTGCCTT TTAACGAA GGTCC TCAC
---- A

GAM25 206 LOC2862 3 2802 XP_212230.1 3 1505 ACCTCTGTCTTC CA T 1 C c c
08 CAGGTTCAAGCA AATTGCTTGAACC GGAAG

ATTCTGCC TTAACGAACTTGG CCTTC
A- T
GAM25 206 LOC2862 3 4183 XP_212230.1 3 1706 ACCTCTGCCTCT AGT 1 C c c
08 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTTCT TTAACGAACTTGGGTTCT
CCG
GAM25 206 LOC2862 3 16198 XP_212230.1 3 2332 ACCTTCACCTCC CA A 1 C c c
08 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 LOC2862 1 18265 XP_212228.1 5 602 GTCACCTCCTCT TG C--- A 1 C c c
15 CAGGTTCAAGTG AAT CTTGAACC AGGA GTG
ATTCTCCT TTA GAACTTGG TCCT CAC
GT ACTC C
GAM25 206 LOC2863 1 12540 XP_212278.1 3 461 ACCTCTGCCTCC A AGT 1 C c c
41 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 LOC2863 1 18747 XP_212298.1 3 80 ACCACTGCCTCC TG CA --- 1 C c c
81 CAGGTTCAAGAG AAT CTTGAACC GGA AGTG
ATTCTCCT TTA GAACTTGG CCT TCAC
GA AC CCG
GAM25 206 LOC2864 1 7029 XP_212310.1 5 549 ATCTCCACCTCC C A A 1 C c c
01 CGGATTCAAGCA AATTGCTTGAA CC GGA GTG
GTTTTCCT TTGACGAACTT GG CCT CAC
A C C
GAM25 206 LOC2864 1 18922 XP_210047.1 3 856 GCCCTGAACTCC A----- AC A 1 C c
c
35 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCC TAACGAACT GGTCCT CA
CCCTCC CC -
GAM25 206 LOC3385 1 9042 XP_294654.1 3 1222 ACCTCCAACTCC C A 1 C b b
62 CTGGTTCAAGCG AATTGCTTGAACC AGG AGT
ATTCTCCT TTAGCGAACTTGG TCC TCA
- C
GAM25 206 LOC3387 1 8986 XP_290570.1 3 935 CAATCCGCCTCC CA A 1 C c c
73 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCC TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 LOC3388 1 3313 XP_290597.1 3 929 CTATATACTTCC TGAACC 1 C c
c
41 TGTGAGTAGTAA AATTGCT CAGGAAGTG
TTTTAGTT TTAATGA GTCCTTCAT
TGAGT-
GAM25 206 LOC3388 1 7214 XP_294740.1 5 610 ACCTCCGCCTCC A 1 C b b
99 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCACCT TTAGCGAACTTGGGTCCT CGC

C

GAM25 206 LOC3389 2 9654 XP_294742.1 3 2092 ATCTCTGCCTTC TG A T 1 C c c
23 CGGGTTCAAGTG AAT CTTGAACCC GGAAG
ATTCTCGT TTA GAACTTGGG CCTTC
GT - C

GAM25 206 LOC3389 2 14301 XP_294742.1 3 485 ACCTCCACCTCC CA A 1 C c c
23 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C

GAM25 206 LOC3389 1 11559 XP_290663.1 3 347 ACCTCTGCCTCC AGT 1 C c c
91 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 LOC3389 1 11559 XP_290659.1 3 347 ACCTCTGCCTCC AGT 1 C c c
99 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 LOC3390 1 4804 XP_294802.2 3 944 ACCTCTGCCTCC G AGT 1 C c c
77 TGGGTTCAAGAA AATT CTTGAACCCAGGA
ATTCTCCT TTAA GAACTTGGGTCCT
A CCG

GAM25 206 LOC3390 1 7452 XP_290692.1 3 2011 GTCTCAAACTCC AC A 1 C b b
78 TGGCCTCAAGCA AATTGCTTGA CCAGGA GT
ATTCTCCC TTAACGAACT GGTCCT CA
CC -

GAM25 206 LOC3391 1 9303 XP_294825.1 5 497 ACCTGGGCCTCC A A 1 C c c
46 CGGGTTCAAGCA AATTGCTTGAACCC GGA GT
ATTCTGTC TTAACGAACTTGGG CCT CG
C C

GAM25 206 LOC3391 1 12883 XP_290742.1 3 722 ACCTCTGCCTCC AGT 1 C c c
78 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTTTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 LOC3392 1 13583 XP_294899.2 5 1365 GTTTCGAACTCT A----- A A 1 C c c
83 GGGGTTCAAGCA ATTGCTTGAACCC GGA GT
ATCTGCCC TAACGAACTTGGG TCT CA
CCCGTC G -

GAM25 206 LOC3394 1 14390 XP_290902.1 3 356 ACCTCCACCTCC TG A 1 C c c
48 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CAC
GT C

GAM25 206 LOC3394 2 5531 XP_290919.1 3 1435 ACCTCTGCCTCC C AGT 1 C c c
92 TTGGTTCAAGCA AATTGCTTGAACC AGGA
ATTCTCCT TTAACGAACTTGG TCCT
T CCG

GAM25 206 LOC3394 2 14483 XP_290919.1 3 1129 ACCTCTGCCTCC A AGT 1 C c
c
92 TGGGTGCAAGCA AATTGCTTG ACCCAGGA
ATTATCCT TTAACGAAC TGGGTCCT

```
                                                  G      CCG
GAM25   206     LOC3396 1   12194  XP_295016.1  5  1556  ACCTCCGCCTCC         CA  A        1  C  c  c
        22                                        CAGGTTCAAGCG AATTGCTTGAACC  GGA GTG
                                                  GTTCTCCT    TTGGCGAACTTGG  CCT CGC
                                                              AC  C
GAM25   206     LOC3396 1   5829   XP_290981.1  3  1643  AGCTCTGCCTCC            AGT       1  C  c  c
        59                                        TGGGTTCAAGCG AATTGCTTGAACCCAGGA
                                                  ATTCCCCT    TTAGCGAACTTGGGTCCT
                                                              CCG
GAM25   206     LOC3396 1   3727   XP_295035.1  5  882   GCCTCCGCTTCC                    1  C  b  b
        94                                        TGGGTTCAAGCA AATTGCTTGAACCCAGGAAGTG
                                                  ATTCTCCC    TTAACGAACTTGGGTCCTTCGC

GAM25   206     LOC3397 1   13056  XP_295038.1  3  1320  ACCTCCACCTCC            A        1  C  b  b
        11                                        TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
                                                  ATTCTGCT    TTAGCGAACTTGGGTCCT CAC
                                                              C
GAM25   206     LOC3398 2   1207   XP_295074.1  5  696   ACCTCCACCTCC   TG      CA  A        1  C  c  c
        13                                        CAGGTTCAAGTG AAT  CTTGAACC  GGA GTG
                                                  ATTCTCAT    TTA  GAACTTGG  CCT CAC
                                                              GT       AC  C
GAM25   206     LOC3398 2   13017  XP_295074.1  5  132   GCCTCCAACTCC A-----       A     A      1  C  c  c
        13                                        TGGGCTCAAGCA      ATTGCTTGA CCCAGGA GT
                                                  ATCCACCT          TAACGAACT GGGTCCT CA
                                                            TCCACC        C      -
GAM25   206     LOC3398 2   3980   XP_295079.1  5  40    CCTCCGCCTTCC   TG      C     T        1  C  c  c
        32                                        TGGTTCAAGTGA AAT  CTTGAACC AGGAAG
                                                  TTCTCCTG    TTA  GAACTTGG TCCTTC
                                                              GT       -     C
GAM25   206     LOC3398 2   7498   XP_295079.1  5  40    ACCTCCGCCTTC   TG      C     T        1  C  c  c
        32                                        CTGGTTCAAGTG AAT  CTTGAACC AGGAAG
                                                  ATTCTCCT    TTA  GAACTTGG TCCTTC
                                                              GT       -     C
GAM25   206     LOC3398 1   1624   XP_291031.1  3  609   ACCTCCGTTTCC   TG                  1  C  c  c
        33                                        TGGGTTCGAGTG AAT  CTTGAACCCAGGAAGTG
                                                  ATTCTCCT    TTA  GAGCTTGGGTCCTTTGC
                                                              GT
GAM25   206     LOC3398 1   1784   XP_291050.1  5  519   ACCTCCGCCTCC   TG      A  A        1  C  c  c
        72                                        CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                                  ATTCTCCA    TTA  GAACTTGGG CCT CGC
                                                              GT       C  C
GAM25   206     LOC3399 1   6629   XP_295103.1  3  34    ACCTCCACCTCC    G       A  A        1  C  c  c
        24                                        CGGGTTCAAGGG AATT CTTGAACCC GGA GTG
                                                  ATTCTGCC    TTAG GAACTTGGG CCT CAC
                                                              G       C  C
GAM25   206     LOC3400 1   1128   XP_295137.1  3  84    ACCTCCTCCTCT            AGT       1  C  c  c
        37                                        TGGGTTCAAGCG AATTGCTTGAACCCAGGA
                                                  ATTCTCCT    TTAGCGAACTTGGGTTCT
```

CCT

GAM25 206 LOC3401 1 18048 XP_291153.1 3 2189 ACCTCTGCCTCC C A T 1 C c c
38 CTGGTTCAAGCG AATTGCTTGAACC AGG AG
ATTCTTCT TTAGCGAACTTGG TCC TC
- C C

GAM25 206 LOC3401 1 5363 XP_291158.1 3 1489 ACCTCCGCCTCC CA A 1 C c c
56 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C

GAM25 206 LOC3402 1 2255 XP_291211.1 3 89 GCCTCCACCTCC CA A 1 C c c
49 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CAC
AC C

GAM25 206 LOC3402 1 4561 XP_295190.1 5 1046 ACCTCCACCTCC A 1 C b b
59 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 LOC3404 1 11179 XP_295240.1 3 222 ACCTCCGCCTTC A 1 C b b
14 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
GTTCTCGT TTGACGAACTTGGGTCTT CGC
C

GAM25 206 LOC3405 1 15544 XP_291331.1 3 435 ACCTCCGCTCCC A 1 C b b
47 TGGGTTCAAGCG AATTGCTTGAACCCAGG AGTG
ATTCTCCT TTAGCGAACTTGGGTCC TCGC
C

GAM25 206 LOC3429 1 12088 XP_292790.2 3 859 ACCTCTGTCTCC A AGT 1 C c c
26 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CTG

GAM25 206 LOC3466 1 16571 XP_294357.2 3 420 ACCTCCACCTCC A 1 C b b
53 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCA TTAACGAACTTGGGTCCT CAC
C

GAM25 206 LOC3478 1 3732 XP_302618.1 3 676 ACTTCTGCCTTC CA T 1 C c c
82 CAGGTTCAAGCG AATTGCTTGAACC GGAAG
ATTCTCCT TTAGCGAACTTGG CCTTC
A- C

GAM25 206 LOC3479 1 5342 XP_300565.1 5 237 ACCTCCGTCTCC CA AG 1 C c c
18 CAGGTTCAAGCG AATTGCTTGAACC GGA TG
ATTCTCCC TTAGCGAACTTGG CCT GC
AC CT

GAM25 206 LOC3480 1 19164 XP_300592.1 5 367 ACCTCGACCTCT TG A 1 C c c
24 TGGGTTCAAGTG AAT CTTGAACCCAGGA GT
ATTCTCCT TTA GAACTTGGGTTCT CA
GT C

GAM25 206 LOC3480 1 14669 XP_300615.1 5 102 ACCTCCAGCTCC G CA A 1 C c c
94 CAGGTTGAAGCA AATTGCTT AACC GGA GT
ATTCTCCT TTAACGAA TTGG CCT CG
G AC -

GAM25 206 LOC3481 1 11559 XP_300623.1 3 347 ACCTCTGCCTCC AGT 1 C c c
13 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC3481 1 5344 XP_300626.1 5 602 ACCTCCGCCTCC CA A 1 C c c
15 CAGGTTCAAGTA AATTGCTTGAACC GGA GTG
ATTCCTCT TTAATGAACTTGG CCT CGC
AC C
GAM25 206 LOC3481 1 11559 XP_300635.1 3 347 ACCTCTGCCTCC AGT 1 C c c
37 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC3481 1 11559 XP_300636.1 3 347 ACCTCTGCCTCC AGT 1 C c c
42 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC3482 1 8807 XP_300670.1 3 1579 ACCTCCACCTCC CA A 1 C c c
35 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
GTTCTCTG TTGACGAACTTGG CCT CAC
AC C
GAM25 206 LOC3483 1 4883 XP_300696.1 3 1808 CCAACCTCCTCC T AGT 1 C c c
26 TGGGTTCCAGCG AATTGCT GAACCCAGGA
ATTCTCCT TTAGCGA CTTGGGTCCT
C CCT
GAM25 206 LOC3483 2 2896 XP_302741.1 3 65 GTCTTGAACTCC A----- AC A 1 C c b
93 TGGACTCAAGCA ATTGCTTGA CCAGGA GT
ATCCCCCC TAACGAACT GGTCCT CA
CCCCCC CA -
GAM25 206 LOC3483 2 4259 XP_302741.1 3 1254 ACCTCCACTTCC C 1 C b b
93 TAGGTTCAAGCA AATTGCTTGAACC AGGAAGTG
ATTCTCCT TTAACGAACTTGG TCCTTCAC
A
GAM25 206 LOC3483 1 15782 XP_300729.1 3 1081 ACCACTGCCTCC CA --- 1 C c c
96 CAGGTTCAAGCG AATTGCTTGAACC GGA AGTG
ATTCTCCT TTAGCGAACTTGG CCT TCAC
AC CCG
GAM25 206 LOC3484 2 5531 XP_300730.1 3 676 ACCTCTGCCTCC C AGT 1 C c c
02 TTGGTTCAAGCA AATTGCTTGAACC AGGA
ATTCTCCT TTAACGAACTTGG TCCT
T CCG
GAM25 206 LOC3484 2 14483 XP_300730.1 3 370 ACCTCTGCCTCC A AGT 1 C c c
02 TGGGTGCAAGCA AATTGCTTG ACCCAGGA
ATTATCCT TTAACGAAC TGGGTCCT
G CCG
GAM25 206 LOC3484 1 15122 XP_302753.1 5 130 GCCTCCACTTCC A 1 C b b
28 TGGGCTCAAGCG AATTGCTTGA CCCAGGAAGTG
ATTCTCCT TTAGCGAACT GGGTCCTTCAC
C

GAM25 206 LOC3484 1 4883 XP_300738.1 3 1808 CCAACCTCCTCC T AGT 1 C c c
45 TGGGTTCCAGCG AATTGCT GAACCCAGGA
ATTCTCCT TTAGCGA CTTGGGTCCT
C CCT
GAM25 206 LOC3485 1 4935 XP_300762.1 3 1088 GTCTCCAACTCC A----- A A 1 C c c
03 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C -
GAM25 206 LOC3485 2 2896 XP_302818.1 3 65 GTCTTGAACTCC A----- AC A 1 C c b
32 TGGACTCAAGCA ATTGCTTGA CCAGGA GT
ATCCCCCC TAACGAACT GGTCCT CA
CCCCCC CA -
GAM25 206 LOC3485 2 4259 XP_302818.1 3 1254 ACCTCCACTTCC C 1 C b b
32 TAGGTTCAAGCA AATTGCTTGAACC AGGAAGTG
ATTCTCCT TTAACGAACTTGG TCCTTCAC
A
GAM25 206 LOC3485 1 12540 XP_300378.1 3 676 ACCTCTGCCTCC A AGT 1 C c c
67 CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 LOC3485 1 5363 XP_302833.1 3 360 ACCTCCGCCTCC CA A 1 C c c
83 CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 LOC3487 1 9567 XP_300843.1 3 631 GTTTTGAACTCC A----- AC A 1 C c c
90 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCACTC TAACGAACT GGTCCT CA
CTCACC CC -
GAM25 206 LOC3487 1 1441 XP_300845.1 3 1445 ACCTCTGCCTCC AGT 1 C c c
98 TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCAG TTAGCGAACTTGGGTCCT
CCG
GAM25 206 LOC3489 1 12770 XP_302929.1 3 351 CCTCCGCCTTCC C T 1 C c c
47 TGAGTTCAAGCG AATTGCTTGAAC CAGGAAG
ATTCTCCT TTAGCGAACTTG GTCCTTC
A C
GAM25 206 LOC3489 1 16135 XP_300434.1 3 654 ACCTCCACCTCC CA A 1 C c c
95 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CAC
AC C
GAM25 206 LOC3490 1 644 XP_300250.1 5 581 ACCTCTGCCTCC AGT 1 C c c
24 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCGT TTAACGAACTTGGGTCCT
CCG
GAM25 206 LOC3490 1 12101 XP_300932.1 3 225 ACCTCTGCCACC AAGT 1 C c c
75 TGGGTTCAAGCG AATTGCTTGAACCCAGG
ATTCTCCT TTAGCGAACTTGGGTCC

ACCG

GAM25 206 LOC3490 1 997 XP_302952.1 3 878 TGGTAAGACTTC GCT G 1 C c c
80 TGGGTTCATGAA AATT TGAACCCAG AAGT
GTTTCGGC TTGA ACTTGGGTC TTCA
AGT -

GAM25 206 LOC3491 2 4803 XP_300969.1 3 880 ACCTCCACCTCC A 1 C b b
70 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTTGT TTAACGAACTTGGGTCCT CAC
C

GAM25 206 LOC3491 2 14563 XP_300969.1 3 1418 GCCTCCACCTCC CA A 1 C c b

70 CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCGT TTAACGAACTTGG CCT CAC
AC C

GAM25 206 LOC3492 1 18801 XP_300998.1 5 138 GCCTCCGCCTTC A 1 C b b
61 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCTT CGC
C

GAM25 206 LOC3493 1 17187 XP_088528.1 5 495 ACCTCCGCCTCC TG A A 1 C c c

60 CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCTT TTA GAACTTGGG CCT CGC
GT C C

GAM25 206 LOC3494 1 18922 XP_301084.1 3 856 GCCCTGAACTCC A----- AC A 1 C c
c
30 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCC TAACGAACT GGTCCT CA
CCCTCC CC -

GAM25 206 LOC5119 1 5306 NP_057415.1 3 913 GTCTCAAACTCC A----- AC A 1 C c c

3 TGGACTCAAGCA ATTGCTTGA CCAGGA GT
ATCCTCCC TAACGAACT GGTCCT CA
CCCTCC CA -

GAM25 206 LOC5710 1 1130 NP_065114.2 3 635 ACCTCCGCCTCC TG A 1 C c c
7 TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 206 LOC9040 1 16076 XP_031517.1 5 1694 ACCTCTACCTCC A----- A 1 C c c
8 TGGGTTCAAGCA ATTGCTTGAACCCAGGA GTG
ATCCTCCT TAACGAACTTGGGTCCT CAT
TCCTCC C

GAM25 206 LOC9048 1 1125 XP_032059.1 3 1389 ACCTCCGCCTCC TG A A 1 C c c

5 CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCCCCT TTA GAACTTGGG CCT CGC
GT C C

GAM25 206 LOC9117 1 12009 XP_036612.1 5 258 GCCTCAACCTCC CA A 1 C c c
0 CAGGTTCAAGCG AATTGCTTGAACC GGA GT
ATTCTCCT TTAGCGAACTTGG CCT CA
AC C

GAM25 206 LOC9125 1 11626 XP_037135.1 5 2255 GCCTCCACCTCC CCCA A 1 C c c
0 CAGTTTCAAGCA AATTGCTTGAA GGA GTG
ATTCTCAT TTAACGAACTT CCT CAC
TGAC C
GAM25 206 LOC9166 1 10068 NP_612382.1 3 387 ACCCCCGCCTCC A 1 C b b
3 TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 LOC9313 1 17183 XP_049396.1 5 1282 ACCTCCGCCTCC A A 1 C c c
2 CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 LOST1 1 1474 NP_758955.1 3 313 CCCACAATTTCC AA- ---- 1 C c c
TGGGTTCCACCA TTGCTT GAACCCAGGAAGT
AGCAGCGA GACGAA CTTGGGTCCTTTA
AGC CCAC
GAM25 206 LTB4R 1 12498 NP_000743.1 5 351 GCCTCCACTTCC CT 1 C c c
TGGGTTCACATG AATTG TGAACCCAGGAAGTG
ATTCTCCT TTAGT ACTTGGGTCCTTCAC
AC
GAM25 206 LY75 1 13431 NP_002340.1 3 622 ATCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 LZTS1 1 9584 NP_066300.1 3 1493 GCCTCATACTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GTG
ATCCTCCT TAACGAACT GGGTCCT CAT
TCCTCC C -
GAM25 206 MAK 1 14390 NP_005897.1 3 692 ACCTCCACCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CAC
GT C
GAM25 206 MAPA 1 1130 NP_660299.1 3 854 ACCTCCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C
GAM25 206 MEFV 1 14301 NP_000234.1 3 559 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 MGC1081 1 12698 NP_085045.2 3 137 ACCTCTGCCTTC AGT 1 C c c
8 TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCTG TTAACGAACTTGGGTCTT
CCG
GAM25 206 MGC1138 1 9968 NP_116322.1 3 553 GTCTCAAACTCC A----- A A 1 C c c
6 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C -
GAM25 206 MGC1320 1 19279 NP_113653.1 3 177 ACCACCACTTCC 1 C b b

4 TGGGTTCAAGCG AATTGCTTGAACCCAGGAAGTG
ATTCTCCT TTAGCGAACTTGGGTCCTTCAC

GAM25 206 MGC1428 1 13910 NP_542391.1 3 500 GCCTTGACTTCC A----- TG A 1 C c c
9 TGGGCTCAAGTG AT CTTGA CCCAGGAAGT
ATCATCCC TA GAACT GGGTCCTTCA
CCCTAC GT C
GAM25 206 MGC1560 1 9022 NP_659474.1 5 338 GCCTCGACCTCC A CA A 1 C c c
6 CAGGCTCAAGCA AATTGCTTGA CC GGA GT
ATTCTCCT TTAACGAACT GG CCT CA
C AC C
GAM25 206 MGC1791 1 1373 NP_653222.2 3 44 ACCTCCACCTCC A---- - A 1 C c c
9 TGGGTTCAAGAC ATTG CTTGAACCCAGGA GTG
AATCCTCC TAAC GAACTTGGGTCCT CAC
CCTCC A C
GAM25 206 MGC1842 1 1785 XP_037797.2 3 1467 ACCTCCGCCTCC A----- A 1 C c c
TGGGTTCAAGCG ATTGCTTGAACCCAGGA GTG
ATCCTCCT TAGCGAACTTGGGTCCT CGC
TCCTCC C
GAM25 206 MGC2418 1 9950 NP_689565.1 5 262 ACATCCACCTCC TG CA A 1 C c c
0 CAGGTTCAAGTG AAT CTTGAACC GGA GTG
ATTCTTGT TTA GAACTTGG CCT CAC
GT AC C
GAM25 206 MGC2474 1 18706 NP_076420.1 3 1498 GTCTCAAACTCC C A 1 C b b
TCGGTTCAAGCA AATTGCTTGAACC AGGA GT
ATTCGCCC TTAACGAACTTGG TCCT CA
C -
GAM25 206 MGC2734 1 17971 XP_300964.1 5 1717 ACCTCCACCCCC CA AA 1 C c c
5 CAGGTTCAAGCA AATTGCTTGAACC GG GTG
GTTCTTCC TTGACGAACTTGG CC CAC
AC CC
GAM25 206 MGC3113 1 1235 NP_076940.1 3 903 GTCTCAAACTTC A G 1 C b b
TGGGCTCAAGCA AATTGCTTGA CCCAG AAGT
ATTCATCT TTAACGAACT GGGTC TTCA
C -
GAM25 206 MGC3363 1 16595 NP_689809.1 3 732 ACCTCCGCCTCC A A 1 C c c
7 CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CGC
C C
GAM25 206 MGC3516 1 6047 NP_689765.1 3 52 ACCTCCGCCTCC A 1 C b b
3 TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCTG TTAACGAACTTGGGTCCT CGC
C
GAM25 206 MGC3771 1 13827 NP_112232.1 5 796 ACCTCCGCCTCC A 1 C b b
TGGGTTCAGGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGGACTTGGGTCCT CGC

```
                                                    C
GAM25   206   MGC4057 1  7100  NP_689989.1  3 382   GCCTCGGCTTCC  TG   A          1 C c c
        9                          TGGGCTCAGGTG AAT  CTTGA CCCAGGAAGT
                                   ATTCTTCC    TTA  GGACT GGGTCCTTCG
                                               GT   C
GAM25   206   MGC5033 1  13976 NP_848604.1  3 328   GCCTCAACCTCC  TG       A       1 C c c

        7                          TGGGTTCAAGTG AAT  CTTGAACCCAGGA GT
                                   ATTCTCCC    TTA  GAACTTGGGTCCT CA
                                               GT        C
GAM25   206   MHC2TA 1  15607 NP_000237.1  3 487   ACCTCCGCCTCT          A       1 C b b
                                   TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
                                   ATTCTTCT    TTAGCGAACTTGGGTTCT CGC
                                               C
GAM25   206   MLANA  1  19169 NP_005502.1  3 659   ACCTCCGCCTCC        CA  A       1 C c c
                                   CAGGTTCAAGCA AATTGCTTGAACC  GGA GTG
                                   ATTCTCCT    TTAACGAACTTGG  CCT CGC
                                               AC  C
GAM25   206   moblak 1  17041 NP_570719.1  3 1045  TCCTCCACCTCC  TG       A       1 C c c
                                   TGGGTTCAAGTG AAT  CTTGAACCCAGGA GTG
                                   ATTCTCCT    TTA  GAACTTGGGTCCT CAC
                                               GT        C
GAM25   206   MOCS3  1  5363  NP_055299.1  3 627   ACCTCCGCCTCC        CA  A       1 C c c
                                   CAGGTTCAAGCG AATTGCTTGAACC  GGA GTG
                                   ATTCTCCT    TTAGCGAACTTGG  CCT CGC
                                               AC  C
GAM25   206   MPI    1  11116 NP_002426.1  3 481   TTACACCCTTGT      -----  CC  AA     1 C c c
                                   TCTGTCAAAGCA AATTGCTT    GAAC  AGG  GTG
                                   ATTAAAGA    TTAACGAA    CTTG  TCC  CAC
                                               ACTGT   T-  --
GAM25   206   MPL    1  12310 NP_005364.1  3 617   AACCTCCACCTC        A  A       1 C b b
                                   CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
                                   ATTCTTGT    TTAGCGAACTTGGG CCT CAC
                                               -  C
GAM25   206   MRPL44 1  400   NP_075066.1  3 307   ACCTCCACCTCA        CAG  A       1 C c c
                                   CAGGTTCAAGCG AATTGCTTGAACC   GA GTG
                                   ATTCTCGT    TTAGCGAACTTGG   CT CAC
                                               ACA  C
GAM25   206   MRPS27 1  8246  NP_055899.1  3 478   ACCTCCGACTCC        CA  A       1 C c c
                                   CAGGTTCAAGCA AATTGCTTGAACC  GGA GT
                                   ATTCTCCT    TTAACGAACTTGG  CCT CA
                                               AC  -
GAM25   206   MSTP028 1  9881  NP_114160.1  3 1955  ACTTGTGCCTCC          AGT       1 C c c
                                   TGGGTTCAAGCG AATTGCTTGAACCCAGGA
                                   ATTCTGCT    TTAGCGAACTTGGGTCCT
                                               CCG
GAM25   206   MtFMT  1  19169 NP_640335.1  3 191   ACCTCCGCCTCC        CA  A       1 C c c
                                   CAGGTTCAAGCA AATTGCTTGAACC  GGA GTG
                                   ATTCTCCT    TTAACGAACTTGG  CCT CGC
                                               AC  C
```

GAM25 206 MTH2 1 12362 NP_060753.1 3 899 GCCTCCGCCACC AA 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGG GTG
ATTCTCCT TTAACGAACTTGGGTCC CGC
AC
GAM25 206 MYLC2PL 1 2680 NP_612412.1 5 417 ACCTCTGCCTCA --- A T 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC AGG AG
ATTCTCCT TTAACGAACTTGGG TCC TC
CAC G T
GAM25 206 MYO5C 1 3499 NP_061198.1 3 676 ACCTCCGCTTCC C 1 C b b
TGGGTTCAAACA AATTG TTGAACCCAGGAAGTG
ATTCTCCT TTAAC AACTTGGGTCCTTCGC
A
GAM25 206 NDRG3 1 6322 NP_114402.1 3 1200 ACCTCTGCCCCC AAGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGG
ATTCTCCT TTAGCGAACTTGGGTCC
CCCG
GAM25 206 NDUFC2 1 18323 NP_004540.1 3 1288 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CAC
C
GAM25 206 NEK4 1 15238 NP_003148.1 3 739 ACAAATTTCATT CCCA 1 C c c
TCCATTTAAGCA AATTGCTTGAA GGAAGTG
ATTTGTAA TTAACGAATTT CCTTTAC
A---
GAM25 206 NF2 1 18419 NP_057502.1 5 528 ACCTCCGCCTCC C A A 1 C c c
CGGATTCAAGCA AATTGCTTGAA CC GGA GTG
ATTCTCCC TTAACGAACTT GG CCT CGC
A C C
GAM25 206 NFAT5 1 18076 NP_006590.1 3 4702 GCCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 NFAT5 1 18076 NP_619727.1 3 4702 GCCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 NFAT5 1 18076 NP_619728.2 3 4702 GCCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 NFAT5 1 18076 NP_775321.1 3 4702 GCCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C
GAM25 206 NUDT4 1 17183 NP_061967.2 3 1338 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 NUMA1 1 14301 NP_006176.1 5 167 ACCTCCACCTCC CA A 1 C c c

CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CAC
AC C

GAM25 206 NUP43 1 15705 NP_078923.2 3 653 ACCTCCACCTCC A A 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
GTTCTCCT TTGACGAACTTGGG CCT CAC
C C

GAM25 206 OPHN1 1 1657 NP_002538.1 3 777 TTTTTGACAGCT A----- ACC 1 C c c
TCCTGTCAAGCA ATTGCTTGA CAGGAAGT
ATCAAGAA TAACGAACT GTCCTTCG
AAGAAC ---

GAM25 206 OSBPL2 1 17183 NP_055650.1 3 1174 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 206 OSBPL2 1 17183 NP_653081.1 3 1174 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 206 PCDHA9 1 12010 NP_054724.1 3 1362 ACGTCTGCCTCC AGT 1 C c c

TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 PCDHB11 1 13873 NP_061754.1 3 240 CCCTCCGCCTCT AG A 1 C c c

CGGGTTCAAGCA AATTGCTTGAACCC GA GTG
ATTCTCCT TTAACGAACTTGGG CT CGC
CT C

GAM25 206 PCDHB9 1 5363 NP_061992.2 3 575 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCCT TTAGCGAACTTGG CCT CGC
AC C

GAM25 206 PDCL 1 6421 NP_005379.2 3 1909 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
GTTCTCCC TTGACGAACTTGGGTCCT CAC
C

GAM25 206 PDE6B 1 2250 NP_000274.1 3 245 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCGT TTAGCGAACTTGG CCT CAC
AC C

GAM25 206 PFAS 1 12883 NP_036525.1 3 722 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTTTCCT TTAACGAACTTGGGTCCT
CCG

GAM25 206 PHF6 1 19225 NP_115834.1 3 567 ATAGTTTGCAGT GAA G 1 C c c
TTCTGGGAAGCA AATTGCTT CCCAGGAA TG
ATTGAAAC TTAACGAA GGGTCTTT AC
--- G

GAM25 206 PKNOX1 1 4340 NP_004562.2 3 1869 ACCTCCACCTCT CC A 1 C c c

TATGTTCAAGCA AATTGCTTGAAC AGGA GTG
ATTCTCCT TTAACGAACTTG TTCT CAC
TA C

GAM25 206 PMCHL1 1 15693 NP_114093.1 3 574 ACCTCTGCCTCC A AGT 1 C c c

CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTTCCTG TTAACGAACTTGGG CCT
C CCG

GAM25 206 PMCHL2 1 14075 NP_114094.1 3 572 ACCTCTGCCTCC A AGT 1 C c c

CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCCCTG TTAACGAACTTGGG CCT
C CCG

GAM25 206 PPID 1 15356 NP_005029.1 3 295 TCCTCTGCCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG

GAM25 206 PPIL2 1 12323 NP_055152.1 3 440 GCCTCGACCTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCT TAACGAACT GGGTCCT CA
TCCTCC C C

GAM25 206 PRKWNK3 1 5566 NP_065973.1 3 690 ACCTCCCCCTCC AGT 1 C c c

TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCC

GAM25 206 PRO1787 1 4037 NP_061076.1 3 0 CCTTCACAAGGG A AG-- T 1 C c c
TCAAGCAATTGT AATTGCTTGA CCC GAAG
GCTTGGGT TTAACGAACT GGG CTTC
- AACA C

GAM25 206 PTGES 1 16132 NP_004869.1 3 575 GCCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCC TTAGCGAACTTGGG CCT CGC
C C

GAM25 206 PTGIS 1 11686 NP_000952.1 3 3316 ACCTCCACCTCC A----- A 1 C c c
TGGGTTTAAGCA ATTGCTTGAACCCAGGA GTG
ATGCTTCT TAACGAATTTGGGTCCT CAC
TCTTCG C

GAM25 206 PXK 1 18264 NP_060241.2 3 93 CTACCCTCTTCC GAA T 1 C c c
TGGGAAAGTAAT AATTGCTT CCCAGGAAG
TGCTGAGC TTAATGAA GGGTCCTTC
A-- T

GAM25 206 RAB33B 1 797 NP_112586.1 3 499 GCCTTGAGCTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CG
CCCTCC C -

GAM25 206 RAB39 2 4103 XP_084662.1 3 942 GTCTCCAACTCC ACCC A 1 C c c
TCGCCTCAAGCA AATTGCTTGA AGGA GT
ATTCGCCC TTAACGAACT TCCT CA
CCGC -

```
GAM25  206  RAB39  2  9341  XP_084662.1  3  801   ACCTCTGCTTCC  TG         T       1  C  c  c
                                TGGGTTCAGGTG AAT  CTTGAACCCAGGAAG
                                ATTGTCAG    TTA  GGACTTGGGTCCTTC
                                      GT          G
GAM25  206  RAI   1  14580 NP_006654.1  5  77    ACCTCCGCCTCC            A        1  C  b  b
                                TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
                                ATTCCTGT    TTAGCGAACTTGGGTCCT CGC
                                              C
GAM25  206  RASSF2 1  13814 NP_055552.1  3  3395  ACATCCGCCTCT  TG     A  A       1  C  c  c

                                GGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTCCT    TTA  GAACTTGGG TCT CGC
                                      GT       G  C
GAM25  206  RASSF2 1  13814 NP_739579.1  3  3621  ACATCCGCCTCT  TG     A  A       1  C  c  c

                                GGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTCCT    TTA  GAACTTGGG TCT CGC
                                      GT       G  C
GAM25  206  RASSF2 1  13814 NP_739580.1  3  3395  ACATCCGCCTCT  TG     A  A       1  C  c  c

                                GGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTCCT    TTA  GAACTTGGG TCT CGC
                                      GT       G  C
GAM25  206  RBBP9  1  1307  NP_006597.2  3  1905  ACCTGCACCTCC  TG     A  A       1  C  c  c
                                CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTCAT    TTA  GAACTTGGG CCT CAC
                                      GT       C  C
GAM25  206  RE2   1  3366  NP_722561.1  5  211   GATCTCGGCTCC            A        1  C  b  b
                                TGGGTTCAAGCA AATTGCTTGAACCCAGGA GT
                                ATTCTCCT    TTAACGAACTTGGGTCCT CG
                                              -
GAM25  206  RHD   2  10248 NP_057208.2  3  329   ACCTCTACCTCC AA-----        A     1  C  c  c
                                TGGGTTCAAGCA      TTGCTTGAACCCAGGA GTG
                                AATCTCCT         AACGAACTTGGGTCCT CAT
                                      TCCTCTA           C
GAM25  206  RHD   2  10248 NP_057309.2  3  418   ACCTCTACCTCC AA-----        A     1  C  c  c
                                TGGGTTCAAGCA      TTGCTTGAACCCAGGA GTG
                                AATCTCCT         AACGAACTTGGGTCCT CAT
                                      TCCTCTA           C
GAM25  206  RHD   2  19169 NP_057208.2  3  738   ACCTCCGCCTCC         CA  A       1  C  c  c
                                CAGGTTCAAGCA AATTGCTTGAACC  GGA GTG
                                ATTCTCCT    TTAACGAACTTGG  CCT CGC
                                        AC  C
GAM25  206  RHD   2  19169 NP_057309.2  3  827   ACCTCCGCCTCC         CA  A       1  C  c  c
                                CAGGTTCAAGCA AATTGCTTGAACC  GGA GTG
                                ATTCTCCT    TTAACGAACTTGG  CCT CGC
                                        AC  C
GAM25  206  RP2   1  9423  NP_008846.1  3  1814  ACATCCGCCTCC            A        1  C  b  b
                                TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
                                ATTCTCCT    TTAGCGAACTTGGGTCCT CGC
```

C
GAM25 206 SBLF 1 5568 NP_006864.2 3 1656 ACCTCCGCCTCC G A 1 C c c
TGGGTTCAAGGG AATT CTTGAACCCAGGA GTG
ATTCTCCT TTAG GAACTTGGGTCCT CGC
G C
GAM25 206 SCML2 1 18167 NP_006080.1 3 1360 AACCTCGCCTCC CA A 1 C c c
CTGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
TC C
GAM25 206 SCN3B 2 1161 NP_060870.1 3 1102 ACCTCTGCCTCT AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
ATTCTCAT TTAACGAACTTGGGTTCT
CCG
GAM25 206 SCN3B 2 6473 NP_060870.1 3 2197 ATCTTGAACTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCTGCCA TAACGAACT GGGTCCT CA
ACCGTC C -
GAM25 206 SDS-RS1 1 3444 NP_612441.1 5 139 ACCTCCGCCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT C C
GAM25 206 SEDL 2 13505 NP_055378.1 3 686 ACCTCCACCTCC A A 1 C b b
CGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAC
C C
GAM25 206 SEDL 2 18323 NP_055378.1 3 1048 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAACGAACTTGGGTCCT CAC
C
GAM25 206 SEPN1 1 19019 NP_065184.1 3 1605 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCTT TTAACGAACTTGG CCT CAC
AC C
GAM25 206 SERF1A 2 4475 NP_068802.1 3 458 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCA TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 SERF1A 2 13469 NP_068802.1 3 291 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
GTTCTCTT TTGACGAACTTGGGTCCT
CCG
GAM25 206 SERF1B 2 4475 NP_075267.1 3 458 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCA TTAGCGAACTTGGG CCT CGC
C C
GAM25 206 SERF1B 2 13469 NP_075267.1 3 291 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCA AATTGCTTGAACCCAGGA
GTTCTCTT TTGACGAACTTGGGTCCT
CCG

GAM25 206 SERPINB 2 5564 NP_004146.1 3 2407 ACCTCCTCCTCC C AGT 1 C c c

9 TGGATTCAAGCA AATTGCTTGAA CCAGGA
ATTCTCTT TTAACGAACTT GGTCCT
A CCT

GAM25 206 SERPINB 2 8945 NP_004146.1 3 2542 GTCTTGAACTCC A----- AC A 1 C c
c

9 TGGCCTCAAGCA ATTGCTTGA CCAGGA GT
ATCCGCCT TAACGAACT GGTCCT CA
TCCGCC CC -

GAM25 206 SH3BP4 1 5112 NP_055336.1 3 1405 CAGGACACTTCC TTGA C 1 C c
c

TGTGTGCCTGCA AATTGC AC CAGGAAGTG
GTTGTCAG TTGACG TG GTCCTTCAC
TCCG T

GAM25 206 SHOX 2 2929 NP_006874.1 3 364 GCCTCAAACTCC A----- A A 1 C c c
TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCTCCC TAACGAACT GGGTCCT CA
CCCTCC C -

GAM25 206 SHOX 2 6046 NP_006874.1 3 44 ACCTCCGCCTCC CCA A 1 C c c
CGAGTTCAAGCG AATTGCTTGAAC GGA GTG
ATTCTCCT TTAGCGAACTTG CCT CGC
AGC C

GAM25 206 SIGLEC1 1 17145 NP_443116.1 3 355 GTCTCGGACTCC A----- A A 1 C c c

1 TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCTGCCC TAACGAACT GGGTCCT CA
CCCGTC C -

GAM25 206 SIL 1 15610 NP_003026.1 3 409 ACCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTTTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 SIRPB1 1 14288 NP_006056.1 3 2089 ACCCCCGCCTCC TG A A 1 C c c

AGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCCT TTA GAACTTGGG CCT CGC
GT A C

GAM25 206 SLC12A8 1 2145 NP_078904.1 3 257 ACCTCTGCTTCC CCA T 1 C c c
CGAGTTCAAGCA AATTGCTTGAAC GGAAG
ATTCTCCT TTAACGAACTTG CCTTC
AGC G

GAM25 206 SLC15A1 1 9045 NP_005064.1 3 267 ACCTCCGCCTCC CA A 1 C c c
CAGGTTCAAGTA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAATGAACTTGG CCT CGC
AC C

GAM25 206 SLC16A4 1 9949 NP_004687.1 3 231 ATCTCCGCCTCC G A 1 C c c
TGGGTTCAAGGG AATT CTTGAACCCAGGA GTG
ATTCTCCT TTAG GAACTTGGGTCCT CGC
G C

GAM25 206 SLC24A1 1 4560 NP_004718.1 3 735 ACCTTCACCTCC CA A 1 C c c

CCGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CAC
CC C

GAM25 206 SLC2A10 1 8872 NP_110404.1 3 552 ACCTCCACTTCC 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGAAGTG
ATTCTCCT TTAGCGAACTTGGGTCCTTCAC

GAM25 206 SLC7A6 1 6848 NP_003974.1 5 170 ACCTCCGACTCC C A 1 C b b
CTGGTTCAAGCG AATTGCTTGAACC AGG AGT
ATTCTCCT TTAGCGAACTTGG TCC TCA
- C

GAM25 206 SNAP23 1 12860 NP_003816.2 3 722 ACCTCCGCCTCC CA A 1 C c c
CTGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
TC C

GAM25 206 SNAP23 1 12860 NP_570710.1 3 722 ACCTCCGCCTCC CA A 1 C c c
CTGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG CCT CGC
TC C

GAM25 206 SNARK 1 17183 NP_112214.1 3 650 ACCTCCGCCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CGC
C C

GAM25 206 SNX15 1 2251 NP_037438.2 3 318 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
GTTCTCCT TTGACGAACTTGG CCT CAC
AC C

GAM25 206 SNX15 1 2251 NP_680086.1 3 318 ACCTCCACCTCC CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
GTTCTCCT TTGACGAACTTGG CCT CAC
AC C

GAM25 206 SNX22 1 1855 NP_079074.1 3 567 ACCCCCGCTTCC A 1 C b b
CGGGTTCAAGCA AATTGCTTGAACCC GGAAGTG
ATTCTCCT TTAACGAACTTGGG CCTTCGC
C

GAM25 206 SNX27 1 5280 NP_112180.4 3 3157 CCCTCTGCCTCT AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTTCT
CCG

GAM25 206 SPCX 1 4224 NP_775260.1 5 49 GTCTCAAACTCC A----- A 1 C c c
TGGGTTCAAGCA ATTGCTTGAACCCAGGA GT
ATCCTCCC TAACGAACTTGGGTCCT CA
CCCTCC -

GAM25 206 SPOP 1 17186 NP_003554.1 5 178 ACCTTTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTTCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 SRL 1 5566 XP_064152.3 3 633 ACCTCCCCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT

```
                                                    CCC
GAM25  206  SS18   1  13018 NP_005628.1  3 1722  ACCTCCGCCTCC          CA  A         1  C  c  c
                                CAGGTTCAAGCA AATTGCTTGAACC  GGA GTG
                                GTTCTCCT    TTGACGAACTTGG  CCT CGC
                                             AC   C
GAM25  206  STOM   1  12669 NP_004090.3  3  544  ACCTCCGCCTCC   TG         A         1  C  c  c
                                TGGGTTCAAGAG AAT  CTTGAACCCAGGA GTG
                                ATTCTCCT    TTA  GAACTTGGGTCCT CGC
                                          GA          C
GAM25  206  SYT13  1  14302 NP_065877.1  3 1574  ACCTCCGCCTCC          CCA  A         1  C  c  c
                                CAAGTTCAAGCG AATTGCTTGAAC   GGA GTG
                                ATTCTCCT    TTAGCGAACTTG   CCT CGC
                                             AAC   C
GAM25  206  TAF11  1  11091 NP_005634.1  3  566  GTCGTGAACTCC A-----       C    A      1  C  c  c
                                TGGCTTCAAGCA      ATTGCTTGAA CCAGGA GT
                                GTCCTCCT          TGACGAACTT GGTCCT CA
                                        TCCTCC        C    -
GAM25  206  TAPBP  1  14128 NP_003181.3  3  277  ACCTCCGCCTCC             A         1  C  b  b
                                TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
                                ATTCTGTG    TTAACGAACTTGGGTCCT CGC
                                             C
GAM25  206  TAT    1  14386 NP_000344.1  3  827  ACCTCCACCTCC             A         1  C  b  b
                                TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
                                ATTCTCTT    TTAGCGAACTTGGGTCCT CAC
                                             C
GAM25  206  TCL6   1  17146 NP_036600.2  5  693  GCCTTCACCTCC   TG      A  A         1  C  c  c
                                CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTTCT    TTA  GAACTTGGG CCT CAC
                                          GT       C  C
GAM25  206  TCL6   1  17146 NP_055233.1  5  693  GCCTTCACCTCC   TG      A  A         1  C  c  c
                                CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTTCT    TTA  GAACTTGGG CCT CAC
                                          GT       C  C
GAM25  206  TCL6   1  17146 NP_065575.1  5  693  GCCTTCACCTCC   TG      A  A         1  C  c  c
                                CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTTCT    TTA  GAACTTGGG CCT CAC
                                          GT       C  C
GAM25  206  TCL6   1  17146 NP_065577.2  5  693  GCCTTCACCTCC   TG      A  A         1  C  c  c
                                CGGGTTCAAGTG AAT  CTTGAACCC GGA GTG
                                ATTCTTCT    TTA  GAACTTGGG CCT CAC
                                          GT       C  C
GAM25  206  TIM50L 1  20014 XP_053074.2  3  1454  TCCTCCGCCTCC A-----        A  A      1  C  c  c
                                CGGGTTCAAGCA      ATTGCTTGAACCC GGA GTG
                                ATGCTCCC          TAACGAACTTGGG CCT CGC
                                        CCCTCG          C  C
GAM25  206  TLR5   1  5535  NP_003259.2  5  144  ACCACTGCCTCC          ---  A       1  C  b  b
                                AGGGTTCAAGCG AATTGCTTGAACCC   AGG AGTG
                                ATTCTCTT    TTAGCGAACTTGGG   TCC TCAC
                                             ACC   G
GAM25  206  TMPRSS3 1  2655  NP_076927.1  3  293  GCCTCCGCTTCC          CA          1  C  b  b
```

CTGGTTCAAGCG AATTGCTTGAACC GGAAGTG
ATTCTCTT TTAGCGAACTTGG CCTTCGC
TC

GAM25 206 TMPRSS3 1 2655 NP_115777.1 3 293 GCCTCCGCTTCC CA 1 C b b
CTGGTTCAAGCG AATTGCTTGAACC GGAAGTG
ATTCTCTT TTAGCGAACTTGG CCTTCGC
TC

GAM25 206 TMPRSS3 1 2655 NP_115780.1 3 293 GCCTCCGCTTCC CA 1 C b b
CTGGTTCAAGCG AATTGCTTGAACC GGAAGTG
ATTCTCTT TTAGCGAACTTGG CCTTCGC
TC

GAM25 206 TNFRSF1 1 5563 NP_003833.3 3 2070 ACCTCCGCCTCC A 1 C b b
0B TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCGT TTAGCGAACTTGGGTCCT CGC
C

GAM25 206 TNFRSF1 1 5563 NP_671716.1 3 2070 ACCTCCGCCTCC A 1 C b b
0B TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCGT TTAGCGAACTTGGGTCCT CGC
C

GAM25 206 TNFRSF1 1 9317 NP_003830.1 3 551 GCCTCTAACTCC A----- A A 1 C c c
1A TGGGCTCAAGCA ATTGCTTGA CCCAGGA GT
ATCCAAGT TAACGAACT GGGTCCT CA
TGAACC C -

GAM25 206 TPH2 1 3185 NP_775489.1 3 1130 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C

GAM25 206 TRIM16 1 1828 NP_006461.2 3 297 AGCTCCGCCTCC CCA A 1 C c c
CGAGTTCAAGCA AATTGCTTGAAC GGA GTG
ATTCTCCT TTAACGAACTTG CCT CGC
AGC C

GAM25 206 TRIM5 1 4983 NP_149023.1 3 699 ACCTCCACCTCT CCCA A 1 C c c
CAGATTCAAGCA AATTGCTTGAA GGA GTG
ATTCTCCT TTAACGAACTT TCT CAC
AGAC C

GAM25 206 TRPM6 1 18834 NP_060132.3 3 1645 CAGCAAACCTCC GC TG A 1 C c
c
TGGGTTTGAAAA AATT T AACCCAGGA GT
ATTCCAAC TTAA A TTGGGTCCT CA
AA GT C

GAM25 206 TSPYL 1 6069 XP_166325.1 3 706 ACCTCCACCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C

GAM25 206 TU12B1- 1 1130 NP_057659.1 3 3230 ACCTCCGCCTCC TG A 1 C c c
TY TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
ATTCTCCT TTA GAACTTGGGTCCT CGC
GT C

GAM25 206 TUCAN 1 16692 NP_055774.1 3 2505 AACCTCTGCCTC C AGT 1 C c c

CTGGTTCAAGCG AATTGCTTGAACC AGGA
ATTATTGT TTAGCGAACTTGG TCCT
- CCG

GAM25 206 USP22 1 18783 XP_042698.2 3 2072 ACCTCCACCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
GTTCTCGT TTGACGAACTTGGGTCCT CAC
C

GAM25 206 VDU1 1 15118 NP_055832.2 3 326 GCCTCCACCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CAC
C

GAM25 206 VENTX2 1 7014 NP_055283.1 3 353 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCA AATTGCTTGAACCCAGGA GTG
ATTCTCCA TTAACGAACTTGGGTCCT CGC
C

GAM25 206 VPS33A 1 17693 NP_075067.2 3 280 ACCTCCACCTCC C A 1 C b b
TAGGTTCAAGCA AATTGCTTGAACC AGGA GTG
ATTCTCCT TTAACGAACTTGG TCCT CAC
A C

GAM25 206 WBSCR18 1 6069 NP_115693.2 3 880 ACCTCCACCTCC A A 1 C c c
CGGGTTCAAGCG AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAGCGAACTTGGG CCT CAC
C C

GAM25 206 WBSCR20 1 4882 NP_663620.1 5 439 ACCTCTGCCTCC AGT 1 C c c

B TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 WBSCR20 1 4882 NP_115534.2 5 532 ACCTCTGCCTCC AGT 1 C c c

C TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 WBSCR20 1 4882 NP_683738.1 5 532 ACCTCTGCCTCC AGT 1 C c c

C TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 WBSCR20 1 4882 NP_683881.1 5 640 ACCTCTGCCTCC AGT 1 C c c

C TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCTCCT TTAGCGAACTTGGGTCCT
CCG

GAM25 206 WBSCR23 1 9809 NP_079318.1 3 30 ACCTCCGCCTCT CA A 1 C c c
CAGGTTCAAGCA AATTGCTTGAACC GGA GTG
ATTCTCCT TTAACGAACTTGG TCT CGC
AC C

GAM25 206 WFDC8 1 11481 NP_852611.1 3 78 ACCTCTGCTTCC TG A T 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGAAG
ATTCTCCT TTA GAACTTGGG CCTTC

GT C G
GAM25 206 ZAP 1 12540 NP_064504.2 3 356 ACCTCTGCCTCC A AGT 1 C c c
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTCTCCT TTAACGAACTTGGG CCT
C CCG
GAM25 206 ZFP42 1 14670 NP_777560.1 3 691 ACCTCCACCTCC TG A A 1 C c c
CGGGTTCAAGTG AAT CTTGAACCC GGA GTG
ATTCTCTG TTA GAACTTGGG CCT CAC
GT C C
GAM25 206 ZFP64 1 667 NP_060667.1 3 199 ACGTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCAT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 ZFP64 1 667 NP_071371.2 3 199 ACGTCCGCCTCC CA A 1 C c c
CAGGTTCAAGCG AATTGCTTGAACC GGA GTG
ATTCTCAT TTAGCGAACTTGG CCT CGC
AC C
GAM25 206 ZMYND17 1 1129 NP_848546.1 3 267 GCCTCCGCCTCC TG A 1 C c c
TGGGTTCAAGTG AAT CTTGAACCCAGGA GTG
GTTCTCCT TTG GAACTTGGGTCCT CGC
GT C
GAM25 206 ZNF264 2 3185 NP_003408.1 3 3026 ACCTCCGCCTCC A 1 C b b
TGGGTTCAAGCG AATTGCTTGAACCCAGGA GTG
ATTCTCCT TTAGCGAACTTGGGTCCT CGC
C
GAM25 206 ZNF264 2 16732 NP_003408.1 3 2652 ACCTCTGCCTCC A AGT 1 C c b
CGGGTTCAAGCA AATTGCTTGAACCC GGA
ATTAACTG TTAACGAACTTGGG CCT
C CCG
GAM25 206 ZNF398 1 13567 NP_065832.1 5 303 ACCTCTGCCTCC C A T 1 C c c
CTGGTTCAAGCA AATTGCTTGAACC AGG AG
ATTCTCAT TTAACGAACTTGG TCC TC
- C C
GAM25 206 ZNF440 1 8954 NP_689570.1 3 1272 ACCTCTACCTCC A A 1 C c c
AGGGTTCAAGCA AATTGCTTGAACCC GGA GTG
ATTCTCCT TTAACGAACTTGGG CCT CAT
A C
GAM25 206 ZNF70 1 5829 NP_068735.1 3 1643 AGCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCCCCT TTAGCGAACTTGGGTCCT
CCG
GAM25 206 ZNF70 1 5829 NP_852101.1 3 1643 AGCTCTGCCTCC AGT 1 C c c
TGGGTTCAAGCG AATTGCTTGAACCCAGGA
ATTCCCCT TTAGCGAACTTGGGTCCT
CCG
GAM28 260 COG3 1 8233 NM_031431.2 3 TGCAGAATGAAA CTGGA 3 B c c
TAGAAGCAAAG CTTTGCTTCTGTTTT TGCA
GAAACGAAGATAAAG ACGT

TAAG-

GAM28 260 ESRRBL1 1 8766 NM_018010.2 3 TGCATTTCAATC TTTTCT 3 B c c
AGAAGCAAAG CTTTGCTTCTG GGATGCA
GAAACGAAGAC TTTACGT
TAAC--

GAM28 260 KRT6IRS 1 4708 NM_033448.1 3 TGCACCCAGAAG GC T A 3 B c c
CAGAGAAAAG CTTT TTCTGTTT CTGG TGCA
GAAA GAGACGAA GACC ACGT
A- - C

GAM28 260 TBL1X 1 12893 NM_005647.2 3 GCAAAAACAGAA C CTGGA A 3 B c c

GCAAA TTTGCTTCTGTTTT TGC
AAACGAAGACAAAA ACG
- ----- -

GAM29 380 KIAA022 1 11419 NM_014643.1 5 GACAGAAAGCTG GA- GGG A 3 C c
c
2 TGCCGCCAC GTGGTGGCA CTTT CTGTC
CACCGCCGT GAAA GACAG
GTC --- -

GAM29 380 LOC2547 1 8734 3 GACAGGCACATG GACTT G - A 3 C c c
78 CCACCAC GTGGTGGCA TG GC TGTC
CACCACCGT AC CG ACAG
----- A G -

GAM30 346 AHR 1 10227 NM_001621.2 3 CTGCCGCCCAAA CC CA 3 C c c
CTGGAGTGCAGT ATTGCACTCCAG TGGGC CAG
TGACGTGAGGTC ACCCG GTC
AA CC

GAM30 346 APAF1 1 8324 NM_013229.1 3 TTGTTGCCAGGC G C 3 C b b
TGGAGTGCAGT ATTGCACTCCAGCCTGG C ACAG
TGACGTGAGGTCGGACC G TGTT
- T

GAM30 346 APM1 1 11325 NM_004797.1 3 CTGTTGCCAGGC C G C 3 C c c
TAGAGTGCAGT ATTGCACTC AGCCTGG C ACAG
TGACGTGAG TCGGACC G TGTC
A - T

GAM30 346 APOL1 1 19014 NM_145343.1 3 CTGTCGCCAAGT CTG C 3 C c c
TGGAGTGCAAT ATTGCACTCCAGC GGC ACAG
TAACGTGAGGTTG CCG TGTC
AA- C

GAM30 346 ARCN1 1 19563 NM_001655.3 3 TGTAACCCAGGC C CC G 3 C c c
TGGAATGCAAT ATTGCA TCCAGCCTGGG ACA
TAACGT AGGTCGGACCC TGT
A AA -

GAM30 346 ARHF 1 11167 NM_019034.1 3 CTGTCACTCAGG C CC 3 C c c
CTAGAGTGCAGT ATTGCACTC AGCCTGGG ACAG
TGACGTGAG TCGGACTC TGTC
A AC

GAM30 346 ARHGAP1 1 13439 NM_014783.1 5 CTGTCGTCCAGG C 3 C b b
1A CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC ACAG
TGACGTGAGGTCGGACCTG TGTC

C

GAM30 346 ASB16 1 16342 NM_080863.4 3 GCTGTGGCCCAG C - 3 C b b
GCTGAAGTGCAG ATTGCACT CAGCCTGGGCCACAG
T TGACGTGA GTCGGACCCGGTGTC
A G

GAM30 346 BA108L7 1 15814 NM_030971.1 5 CCCAGGCTGGAG CCACAG 3 C c
c
.2 TGCGAT ATTGCACTCCAGCCTGGG
TAGCGTGAGGTCGGACCC

GAM30 346 BTN3A1 1 1769 NM_007048.2 3 CTGTTGCTAGGC G C 3 C b b
TGGAGTGCAGT ATTGCACTCCAGCCTGG C ACAG
TGACGTGAGGTCGGATC G TGTC
- T

GAM30 346 BY55 1 3163 NM_007053.1 5 CTGTCAACCAGG CA GCC 3 C c c
CCAGAGTGCAGT ATTGCACTC GCCTGG ACAG
TGACGTGAG CGGACC TGTC
AC AAC

GAM30 346 C22orf1 1 2557 NM_003678.2 3 CTGTTGTCCAGG C 3 C b b
9 CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC ACAG
TGACGTGAGGTCGGACCTG TGTC
T

GAM30 346 CDC14B 1 1166 NM_033332.1 3 TTGTTGTCCAGG C 3 C b b
CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC ACAG
TGACGTGAGGTCGGACCTG TGTT
T

GAM30 346 CDH1 1 8905 NM_004360.2 3 GGCCAGGCTGGA G ACAG 3 C c c
GTGCAGT ATTGCACTCCAGCCTGG CC
TGACGTGAGGTCGGACC GG
- ----

GAM30 346 CORO2B 1 9083 NM_006091.1 5 CTGTTGCCCAAG C C 3 C b b
CTGGAGTGCAGT ATTGCACTCCAGC TGGGC ACAG
TGACGTGAGGTCG ACCCG TGTC
A T

GAM30 346 CYP1A2 1 12133 NM_000761.2 3 CTGTTGCCAGGC G C 3 C b b
TGGAGTGCAGT ATTGCACTCCAGCCTGG C ACAG
TGACGTGAGGTCGGACC G TGTC
- T

GAM30 346 CYP2B6 1 19432 NM_000767.3 3 CTGTCTCCCAGG ATT CC 3 C c c
CTGGAGTGC GCACTCCAGCCTGGG ACAG
CGTGAGGTCGGACCC TGTC
--- TC

GAM30 346 DBR1 1 13182 NM_016216.1 3 TTGTCACCTAGA C CC 3 C c c
CTGGAGTGCAAT ATTGCACTCCAG CTGGG ACAG
TAACGTGAGGTC GATCC TGTT
A AC

GAM30 346 DCOHM 1 5214 NM_032151.2 3 CTGTCATGCAGA C GGCC 3 C c c
CTGGAGTGCAGT ATTGCACTCCAG CTG ACAG
TGACGTGAGGTC GAC TGTC
A GTAC

GAM30 346 DKFZP43 1 19580 XM_044196.4 5 CCCAGGCTGGAG CCACAG 3 C c c
4C212 TGCAAT ATTGCACTCCAGCCTGGG
TAACGTGAGGTCGGACCC

GAM30 346 DKFZp76 1 1969 XM_086327.6 3 CTGTTGCCAGGC C G C 3 C c c
1N1114 TGGAATGCAGT ATTGCA TCCAGCCTGG C ACAG
TGACGT AGGTCGGACC G TGTC
A - T
GAM30 346 DSC3 1 17152 NM_001941.2 3 CTGACGCACAGG G CA 3 C c c
CTGGAGTGCAGT ATTGCACTCCAGCCTG GC CAG
TGACGTGAGGTCGGAC CG GTC
A CA
GAM30 346 EVI5 1 12844 NM_005665.2 3 CTGCACTCAGGC CCA 3 C c c
TGGAGTGCAGT ATTGCACTCCAGCCTGGG CAG
TGACGTGAGGTCGGACTC GTC
AC-
GAM30 346 FEZ1 1 14745 NM_005103.3 3 GCCCAGGCTGGA CACAG 3 C c c
GTGCAAT ATTGCACTCCAGCCTGGGC
TAACGTGAGGTCGGACCCG

GAM30 346 FLJ1010 1 8594 NM_024718.1 3 TGTGGCCCAGGC G 3 C b b
1 TGGAGTGCAGT ATTGCACTCCAGCCTGGGCCACA
TGACGTGAGGTCGGACCCGGTGT
-
GAM30 346 FLJ1023 1 1399 NM_018033.1 3 CTGTCACCCAGG CC 3 C b b
2 CTGGAGTGCGAT ATTGCACTCCAGCCTGGG ACAG
TAGCGTGAGGTCGGACCC TGTC
AC
GAM30 346 FLJ1029 1 2525 3 CTGTGTTGCCCA C -- 3 C b b
7 GGCTAGAGTGCA ATTGCACTC AGCCTGGGC CACAG
GT TGACGTGAG TCGGACCCG GTGTC
A TT
GAM30 346 FLJ1307 1 17545 XM_117117.2 5 CTGTCGGCCAGG G - 3 C b b
2 CTGGAGTGCAGT ATTGCACTCCAGCCTGG CC ACAG
TGACGTGAGGTCGGACC GG TGTC
- C
GAM30 346 FLJ1345 1 4252 XM_038291.5 3 CTGTCGCCCAAG C C 3 C b b
6 CTGGAGTGCAGT ATTGCACTCCAGC TGGGC ACAG
TGACGTGAGGTCG ACCCG TGTC
A C
GAM30 346 FLJ1480 1 9230 NM_032842.1 3 CTGTCAACGCAG C GGCC- 3 C c c
3 ACTGGAGTGCAG ATTGCACTCCAG CTG ACAG
T TGACGTGAGGTC GAC TGTC
A GCAAC
GAM30 346 FLJ2014 1 1636 NM_017687.1 3 CTGTGTTGCCCA AT C -- 3 C c c
7 GGCTAGAGTGCA TGCACTC AGCCTGGGC CACAG
G ACGTGAG TCGGACCCG GTGTC
G- A TT
GAM30 346 FLJ2034 1 3352 NM_017776.1 3 CTGTCATCCAAA CC CC 3 C c c

4 CTGGAGTGCAGT ATTGCACTCCAG TGGG ACAG
TGACGTGAGGTC ACCT TGTC
AA AC

GAM30 346 FLJ2302 1 13913 NM_014150.1 3 CTGTCTCCCAGG C CC 3 C b b
4 CTAGAGTGCAAT ATTGCACTC AGCCTGGG ACAG
TAACGTGAG TCGGACCC TGTC
A TC

GAM30 346 FLJ3289 1 16385 NM_144667.1 3 CTGTTGTCCAGG AT C 3 C c c
4 CTGGAGTGCAG TGCACTCCAGCCTGGGC ACAG
ACGTGAGGTCGGACCTG TGTC
G- T

GAM30 346 FUT1 1 18831 NM_000148.1 3 CTGTAGCCCAGG CA C 3 C c c
CCAGAGTGCAGT ATTGCACTC GCCTGGGC ACAG
TGACGTGAG CGGACCCG TGTC
AC A

GAM30 346 GMPPB 1 4133 NM_021971.1 5 CTGTTGCCCAGG C 3 C b b
CTGGAGTGCGAT ATTGCACTCCAGCCTGGGC ACAG
TAGCGTGAGGTCGGACCCG TGTC
T

GAM30 346 GP5 1 17377 NM_004488.1 3 CTGTGGCCCAGG T 3 C b b
CTGGCGTGCAGT ATTGCAC CCAGCCTGGGCCACAG
TGACGTG GGTCGGACCCGGTGTC
C

GAM30 346 GPR81 1 10820 NM_032554.2 3 CTGTGTCCCAGG C 3 C b b
CTGGAGTGCAGT ATTGCACTCCAGCCTGGG CACAG
TGACGTGAGGTCGGACCC GTGTC
T

GAM30 346 IFNAR2 1 15858 NM_000874.2 3 CTGTCGCCCAAG A C C 3 C c c
CTGGAGCGCAAT ATTGC CTCCAGC TGGGC ACAG
TAACG GAGGTCG ACCCG TGTC
C A C

GAM30 346 IL22R 1 3063 3 CTGTGGCCCCTG C CAG T- 3 C c c
GACGGGTACAAT ATTG ACTC CC GGGCCACAG
TAAC TGGG GG CCCGGTGTC
A CA- TC

GAM30 346 JM11 1 19790 NM_033626.1 3 CTGTCACCAGGC AT GCC 3 C c c
TGGAGTGCAG TGCACTCCAGCCTGG ACAG
ACGTGAGGTCGGACC TGTC
G- AC-

GAM30 346 KIAA092 1 8885 NM_014897.1 3 TGTTGCCCAGGC C C G 3 C c c
4 TAGAGTGCAGT ATTGCACTC AGCCTGGGC ACA
TGACGTGAG TCGGACCCG TGT
A T -

GAM30 346 KIAA093 1 17048 XM_041191.4 3 CTCAGGCTGGAG CCACAG 3 C c
c
1 TGCAAT ATTGCACTCCAGCCTGGG
TAACGTGAGGTCGGACTC

GAM30 346 KIAA102 1 7839 3 CTGTCACCCAAG C CC 3 C c c
8 CTGGAGTGCAGT ATTGCACTCCAGC TGGG ACAG

TGACGTGAGGTCG ACCC TGTC
A AC

GAM30	346	KIAA120	1	11820	XM_027307.2	3	CTGTTGCCCAAG		C	C		3	C	b b
	9						TTGGAGTGCAAT ATTGCACTCCAGC TGGGC ACAG							

TAACGTGAGGTTG ACCCG TGTC
A T

GAM30	346	KIAA144	1	10360	NM_020834.1	3	CTGTCGCCCAGG		C	C		3	C	b b
	3						CTGTAGTGCAAT ATTGCACT CAGCCTGGGC ACAG							

TAACGTGA GTCGGACCCG TGTC
T C

GAM30	346	KIAA153	1	10234	XM_042661.5	3	CTGTCGCCAGGC		G C			3	C	b b
	0						TGGAGTGCAAT ATTGCACTCCAGCCTGG C ACAG							

TAACGTGAGGTCGGACC G TGTC
- C

GAM30	346	KIAA161	1	11333	NM_020951.1	3	CTGTCACCAGGC		A	GCC		3	C	c c
	5						CGGAGTGCAGT ATTGCACTCC GCCTGG ACAG							

TGACGTGAGG CGGACC TGTC
C AC-

GAM30	346	KIAA167	1	6380	XM_037809.3	3	CTGTTGGCCAGG		C	G -		3	C	b b
	1						CTGGAATGCAGT ATTGCA TCCAGCCTGG CCA CAG							

TGACGT AGGTCGGACC GGT GTC
A - T

GAM30	346	KIAA175	1	14311	XM_028810.4	3	CTGGTGTCCAGG		CA			3	C	b b
	5						CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC CAG							

TGACGTGAGGTCGGACCTG GTC
TG

GAM30	346	KIAA197	1	16931	XM_058720.5	3	CTGTCATCCAGG		C	CC		3	C	c c
	1						CTAGAGTGCAGT ATTGCACTC AGCCTGGG ACAG							

TGACGTGAG TCGGACCT TGTC
A AC

GAM30	346	KMO	1	4388	NM_003679.1	3	CTGTTGACCAGG		GCC			3	C	c c
							CTGGAGTGCAGT ATTGCACTCCAGCCTGG ACAG							

TGACGTGAGGTCGGACC TGTC
AGT

GAM30	346	LILRA3	1	6616	NM_006865.1	3	CTGTCACCAGGC		C	GCC		3	C	c c
							TGGAATGCAGT ATTGCA TCCAGCCTGG ACAG							

TGACGT AGGTCGGACC TGTC
A AC-

GAM30	346	LOC1126	1	17001	XM_053145.2	3	TGGTAACAGGCT		T	G-	CAG	3	C	c c
	87						GGGTGCAAT ATTGCAC CCAGCCTG GCCA							

TAACGTG GGTCGGAC TGGT
- AA ---

GAM30	346	LOC1127	1	18154		5	CTGTCGCCAGGC		C	G C		3	C	c c
	24						TGGAATGCAGT ATTGCA TCCAGCCTGG C ACAG							

TGACGT AGGTCGGACC G TGTC
A - C

GAM30	346	LOC1201	1	3066		3	CTGTCACCCAGG		C	CC		3	C	b b
	14						CTAGAGTGCAAT ATTGCACTC AGCCTGGG ACAG							

TAACGTGAG TCGGACCC TGTC

A AC

GAM30 346 LOC1266 1 2535 XM_060121.4 3 CTGTGTTGCCCA -- 3 C b b
69 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC CACAG
AT TAACGTGAGGTCGGACCCG GTGTC
TT

GAM30 346 LOC1308 1 9431 XM_065904.2 3 CTGTCGCCTAGG A C 3 C b b
13 CTGGAGTGCAA TTGCACTCCAGCCTGGGC ACAG
AACGTGAGGTCGGATCCG TGTC
- C

GAM30 346 LOC1313 1 19649 3 TGTCACTCAGGC CC G 3 C c c
08 TGGAGTGCAGT ATTGCACTCCAGCCTGGG ACA
TGACGTGAGGTCGGACTC TGT
AC -

GAM30 346 LOC1443 1 10860 XM_084813.4 5 CTGTCGCCCAGG C 3 C b b
17 CTGGAGTGCGAT ATTGCACTCCAGCCTGGGC ACAG
TAGCGTGAGGTCGGACCCG TGTC
C

GAM30 346 LOC1447 1 12238 XM_084964.1 5 CTGTTGCCCAGG C 3 C b b
76 CTGGAGTGCAAT ATTGCACTCCAGCCTGGGC ACAG
TAACGTGAGGTCGGACCCG TGTC
T

GAM30 346 LOC1457 1 18697 XM_085211.7 3 CTGTCACCAGGC C GCC 3 C c c
25 TGGAGTACAGT ATTG ACTCCAGCCTGG ACAG
TGAC TGAGGTCGGACC TGTC
A AC-

GAM30 346 LOC1468 1 2861 NM_145273.1 3 CTGCTGCCCAGG CA 3 C b b
94 CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC CAG
TGACGTGAGGTCGGACCCG GTC
TC

GAM30 346 LOC1476 1 10444 3 GCCCAGGCTAGA C CACAG 3 C c c
60 GTGCAAT ATTGCACTC AGCCTGGGC
TAACGTGAG TCGGACCCG
A -----

GAM30 346 LOC1478 1 1405 XM_085903.2 3 CTGTCGCCCAGG C 3 C b b
17 CTGGAGTGCAAT ATTGCACTCCAGCCTGGGC ACAG
TAACGTGAGGTCGGACCCG TGTC
C

GAM30 346 LOC1478 1 9060 XM_085924.6 3 TTGTTGTCCAGT C C 3 C c c
41 CTGGAGTGCAAT ATTGCACTCCAG CTGGGC ACAG
TAACGTGAGGTC GACCTG TGTT
T T

GAM30 346 LOC1481 1 4235 NM_144692.1 5 CTGTCACCCAGG ATT CC 3 C c c
37 CTGGAGTGC GCACTCCAGCCTGGG ACAG
CGTGAGGTCGGACCC TGTC
--- AC

GAM30 346 LOC1495 1 13189 XM_097661.4 3 GGCCAGGCTAGA C G ACAG 3 C c
c
06 GTGCAGT ATTGCACTC AGCCTGG CC
TGACGTGAG TCGGACC GG
A - ----

GAM30 346 LOC1495 1 14550 3 CTGCCACCCAAG C CCA 3 C c c
77 CTGGAGTGCAGT ATTGCACTCCAGC TGGG CAG
TGACGTGAGGTCG ACCC GTC
A ACC
GAM30 346 LOC1502 1 4075 XM_097870.1 3 CTGTCGCTCAGG C 3 C b b
25 CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC ACAG
TGACGTGAGGTCGGACTCG TGTC
C
GAM30 346 LOC1503 1 2564 XM_086907.1 3 CTGTCGTCCAGG C C 3 C c c
97 TTAGAGTGCAAT ATTGCACTC AGCCTGGGC ACAG
TAACGTGAG TTGGACCTG TGTC
A C
GAM30 346 LOC1504 1 7870 XM_086906.1 3 CTGTTGTCCAGG C C 3 C c c
07 CTAGAGTGCAGT ATTGCACTC AGCCTGGGC ACAG
TGACGTGAG TCGGACCTG TGTC
A T
GAM30 346 LOC1511 1 11539 3 GTTGTCCAGGCT C AG 3 C c c
95 GGAGTGCAGT ATTGCACTCCAGCCTGGGC AC
TGACGTGAGGTCGGACCTG TG
T --
GAM30 346 LOC1512 1 8212 XM_098021.1 3 CTGTCACCCAGG C CC 3 C c c
01 CTGGAGTCCAAT ATTG ACTCCAGCCTGGG ACAG
TAAC TGAGGTCGGACCC TGTC
C AC
GAM30 346 LOC1514 1 9643 XM_098063.1 5 CTGTGGCCCAGG 3 C b b
75 CTGGAGTGTAGT ATTGCACTCCAGCCTGGGCCACAG
TGATGTGAGGTCGGACCCGGTGTC

GAM30 346 LOC1522 1 13105 3 CTGTCACTCAGG CC 3 C b b
20 CTGGAGTGCAGT ATTGCACTCCAGCCTGGG ACAG
TGACGTGAGGTCGGACTC TGTC
AC
GAM30 346 LOC1522 1 8742 XM_098182.1 3 CTGTAGCCCAGG AT C 3 C c c
45 CTGGAGTGCA TGCACTCCAGCCTGGGC ACAG
ACGTGAGGTCGGACCCG TGTC
-- A
GAM30 346 LOC1528 1 3475 3 TGGCCTAGGCTG CAG 3 C c c
51 GAGTGCAGT ATTGCACTCCAGCCTGGGCCA
TGACGTGAGGTCGGATCCGGT

GAM30 346 LOC1539 1 18292 XM_087801.1 5 CTGTAGCCCAGT C C 3 C b b
10 CTGGAGTGCAGT ATTGCACTCCAG CTGGGC ACAG
TGACGTGAGGTC GACCCG TGTC
T A
GAM30 346 LOC1548 1 19686 XM_098626.4 3 CTGTCTCGCAGG CA - CC 3 C c c
77 CCAGAGTGCAGT ATTGCACTC GCCTG GG ACAG
TGACGTGAG CGGAC CT TGTC
AC G C-
GAM30 346 LOC1962 1 1093 XM_113683.2 3 CTGTCGCCAGGC G C 3 C b b
64 TGGAGTGCAGT ATTGCACTCCAGCCTGG C ACAG

TGACGTGAGGTCGGACC G TGTC
- C

GAM30	346	LOC1998 1	3354	XM_117153.2	5	CTGTGTCTCAGG	C	C	3	C	c	c
	99					CTGGAGTACAGT ATTG ACTCCAGCCTGGG CACAG						
						TGAC TGAGGTCGGACTC GTGTC						
						A T						
GAM30	346	LOC1999 1	4862	XM_114052.1	3	CTGTGTTGTCCA	--		3	C	b	b
	06					GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC CACAG						
					GT	TGACGTGAGGTCGGACCTG GTGTC						
						TT						
GAM30	346	LOC2003 1	737		3	CTGTCGCCCAGA	C C	C	3	C	c	c
	16					CTAGAGTGCAAT ATTGCACTC AG CTGGGC ACAG						
						TAACGTGAG TC GACCCG TGTC						
						A A C						
GAM30	346	LOC2012 1	10229	XM_113950.4	3	CTGTTGCCAGGC	CA	G C	3	C	c	c
	94					CAGAGTGCAGT ATTGCACTC GCCTGG C ACAG						
						TGACGTGAG CGGACC G TGTC						
						AC - T						
GAM30	346	LOC2032 1	10855		5	CTGTCACCCAGG	CC		3	C	b	b
	97					CTGGAGTGCAAT ATTGCACTCCAGCCTGGG ACAG						
						TAACGTGAGGTCGGACCC TGTC						
						AC						
GAM30	346	LOC2197 1	6006	XM_167596.2	5	CTGTCATCCAGG	CC		3	C	b	b
	31					CTGGAGTGCAGT ATTGCACTCCAGCCTGGG ACAG						
						TGACGTGAGGTCGGACCT TGTC						
						AC						
GAM30	346	LOC2200 1	18789	NM_145309.1	5	CTGTCACACAGG	GGCC		3	C	c	c
	74					CTGGAGTGCAGT ATTGCACTCCAGCCTG ACAG						
						TGACGTGAGGTCGGAC TGTC						
						ACAC						
GAM30	346	LOC2208 1	17037		3	CTGTGGCCCAGG AT A C			3	C	c	c
	46					CTGAGAGCAG TGC CTC AGCCTGGGCCACAG						
						ACG GAG TCGGACCCGGTGTC						
						G- A -						
GAM30	346	LOC2210 1	10230	XM_167640.4	5	CTGTCACCAGGC	GCC		3	C	b	b
	35					TGGAGTGCAGT ATTGCACTCCAGCCTGG ACAG						
						TGACGTGAGGTCGGACC TGTC						
						AC-						
GAM30	346	LOC2211 1	8153	XM_167867.3	3	GGCCACAGCTGC	----- -	ACAG	3	C	c	c
	22					TGCTGGAGTGCA ATTGCACTCCAGC CTG GGCC						
					AT	TAACGTGAGGTCG GAC CCGG						
						TCGTC A ----						
GAM30	346	LOC2212 1	11173		3	CTGTCACTCAGG	CC		3	C	b	b
	71					CTGGAGTGCAAT ATTGCACTCCAGCCTGGG ACAG						
						TAACGTGAGGTCGGACTC TGTC						
						AC						
GAM30	346	LOC2218 1	7134	XM_168226.1	5	CTGTCGCCAAGC	CA CTG C		3	C	c	c
	14					CAGAGTGCAGT ATTGCACTC GC GGC ACAG						
						TGACGTGAG CG CCG TGTC						

```
                                                AC  AA-   C
GAM30   346   LOC2219 1   5655   XM_165859.1  3       GTGACCCAGGCT      C         C  AG       3  C  c  c
        60                          GGAATGCAAT   ATTGCA TCCAGCCTGGG CAC
                                          TAACGT AGGTCGGACCC GTG
                                             A         A  --
GAM30   346   LOC2220 1   3096          5       CCCAGGCTGGAG              CCACAG       3  C  c  c
        70                          TGCAGT      ATTGCACTCCAGCCTGGG
                                          TGACGTGAGGTCGGACCC
                                                  ------
GAM30   346   LOC2540 1   6592          5       CTGTGTCGCCCA        C  C    --         3  C  c  c
        82                          AGCTAGAGTGCA ATTGCACTC AGC TGGGC  CACAG
                                    GT         TGACGTGAG TCG ACCCG  GTGTC
                                             A  A    CT
GAM30   346   LOC2543 1   5429          5       CTGCGGCCCGGG AT   A       -    A        3  C  c  c
        81                          GCTGGAGCGCAG   TGC CTCCAGCCT GGGCC CAG
                                          ACG GAGGTCGGG CCCGG GTC
                                          G-  C       G    C
GAM30   346   LOC2551 1   6253          5       GCTCAGGCTGGA              CACAG       3  C  c  c
        96                          GTGCAGT     ATTGCACTCCAGCCTGGGC
                                          TGACGTGAGGTCGGACTCG
                                                  -----
GAM30   346   LOC2562 1   19801         3       CTGTAACTCAGG              CC          3  C  b  b
        21                          CTGGAGTGCAGT ATTGCACTCCAGCCTGGG  ACAG
                                          TGACGTGAGGTCGGACTC  TGTC
                                                AA
GAM30   346   LOC2574 1   8329          3       CTGTCTTCCAGG              CC          3  C  b  b
        65                          CTGGAGTGCAGT ATTGCACTCCAGCCTGGG  ACAG
                                          TGACGTGAGGTCGGACCT  TGTC
                                                TC
GAM30   346   LOC5103 1   20151         5       CTGTCATCAGGC              GCC         3  C  c  c
        1                           TGGAGTGCAGT  ATTGCACTCCAGCCTGG   ACAG
                                          TGACGTGAGGTCGGACT   TGTC
                                                AC-
GAM30   346   LOC5133 1   4139   NM_016646.1  3       CTGTTACCCAGG              CC          3  C  b  b
        6                           CTGGAGTGCAAT ATTGCACTCCAGCCTGGG  ACAG
                                          TAACGTGAGGTCGGACCC  TGTC
                                                AT
GAM30   346   LOC9015 1   12504         3       TGTCCCAGGCTA        C      C  CAG      3  C  c  c
        5                           GAGTGCAGT    ATTGCACTC AGCCTGGG CA
                                          TGACGTGAG TCGGACCC GT
                                             A       T  ---
GAM30   346   LOC9166 1   3371   NM_138372.1  3       CTGTCGGCCAGG      C       G -        3  C  b  b
        1                           CTGGAATGCAAT ATTGCA TCCAGCCTGG CC ACAG
                                          TAACGT AGGTCGGACC GG TGTC
                                             A        - C
GAM30   346   LOC9214 1   14208  XM_043160.9  5       CTGCCGCCCAGG        C       CA         3  C  c  c
        8                           CTAGAGTGCAGT ATTGCACTC AGCCTGGGC  CAG
                                          TGACGTGAG TCGGACCCG  GTC
                                             A       CC
GAM30   346   LOC9230 1   16126         3       CCCGGGCTGGAG              CCACAG       3  C  c  c
```

3 TGCAAT ATTGCACTCCAGCCTGGG
TAACGTGAGGTCGGGCCC

GAM30 346 LOC9340 1 3385 NM_138403.1 5 CTGTCGCCCAGG A C 3 C b b
8 CTGGAGCGCAAT ATTGC CTCCAGCCTGGGC ACAG
TAACG GAGGTCGGACCCG TGTC
C C

GAM30 346 LTB4R 1 14766 NM_000752.1 5 CTGTCATTCAGG CC 3 C c c
CTGGAGTGCAGT ATTGCACTCCAGCCTGGG ACAG
TGACGTGAGGTCGGACTT TGTC
AC

GAM30 346 LY75 1 5206 NM_002349.1 3 CTGTTGCCCAGG C C 3 C b b
CTGGAGTACAAT ATTG ACTCCAGCCTGGGC ACAG
TAAC TGAGGTCGGACCCG TGTC
A T

GAM30 346 MAK 1 12945 NM_005906.2 3 TTGTGTCCAGGC C 3 C b b
TGGAGTGCAGT ATTGCACTCCAGCCTGGGC ACAG
TGACGTGAGGTCGGACCTG TGTT
-

GAM30 346 MGC1081 1 6357 NM_030568.2 3 CTGTCGCCCAGG C C 3 C b b
8 CTGGAGTACAAT ATTG ACTCCAGCCTGGGC ACAG
TAAC TGAGGTCGGACCCG TGTC
A C

GAM30 346 MGC5149 1 1092 XM_051200.4 3 CTGTCACCAGGC C GCC 3 C c c
TAGAGTGCAGT ATTGCACTC AGCCTGG ACAG
TGACGTGAG TCGGACC TGTC
A AC-

GAM30 346 MGC9912 1 12264 NM_080664.1 3 CTGTCGCCAGAC C G C 3 C c c
TGGAGTGCAGT ATTGCACTCCAG CTGG C ACAG
TGACGTGAGGTC GACC G TGTC
A - C

GAM30 346 MMPL1 1 4015 3 CTGTCCTCCAGG CC 3 C b b
CTGGAGTGCAAT ATTGCACTCCAGCCTGGG ACAG
TAACGTGAGGTCGGACCT TGTC
CC

GAM30 346 MPL 2 6226 NM_005373.1 3 CTGTCACCCAGG C CC 3 C b b
CTGCAGTGCAAT ATTGCACT CAGCCTGGG ACAG
TAACGTGA GTCGGACCC TGTC
C AC

GAM30 346 MPL 2 17342 NM_005373.1 3 CTGTTGCCAGAC C G C 3 C c b
TGGAGTGCAGT ATTGCACTCCAG CTGG C ACAG
TGACGTGAGGTC GACC G TGTC
A - T

GAM30 346 NCOA6IP 1 10449 NM_024831.5 3 GCCCAGGCTGGA CACAG 3 C c
c
GTGCAGT ATTGCACTCCAGCCTGGGC
TGACGTGAGGTCGGACCCG

GAM30 346 NOSIP 1 12237 NM_015953.2 5 TTGTTGCCTAGG C 3 C b b
CTGGAGTGCAAT ATTGCACTCCAGCCTGGGC ACAG

TAACGTGAGGTCGGATCCG TGTT
T
GAM30 346 NT5C2 1 13752 NM_012229.2 5 CTGCTGCCCAGG C CA 3 C c c
CTGGAGTACAGT ATTG ACTCCAGCCTGGGC CAG
TGAC TGAGGTCGGACCCG GTC
A TC
GAM30 346 PCDHA9 1 1499 NM_031857.1 3 CTGCCACCCAGG C CCA 3 C c c
CTGGAGTACAGT ATTG ACTCCAGCCTGGG CAG
TGAC TGAGGTCGGACCC GTC
A ACC
GAM30 346 PCDHB11 1 1970 NM_018931.2 3 CTGTCGCCCTGG T C 3 C b b
CTGGAGTGCAAT ATTGCACTCCAGCC GGGC ACAG
TAACGTGAGGTCGG CCCG TGTC
T C
GAM30 346 PDCL 1 13181 NM_005388.2 3 CTGTCACCCAGG C CC 3 C c c
CTGGAGTACAAT ATTG ACTCCAGCCTGGG ACAG
TAAC TGAGGTCGGACCC TGTC
A AC
GAM30 346 POLE3 1 11472 NM_017443.2 3 CTGTGGCCCAGG 3 C b b
CTGGAGTGCAGT ATTGCACTCCAGCCTGGGCCACAG
TGACGTGAGGTCGGACCCGGTGTC

GAM30 346 POU2AF1 1 1335 NM_006235.1 3 GCCCAGGCTGGA C CACAG 3 C c
c
GTACAAT ATTG ACTCCAGCCTGGGC
TAAC TGAGGTCGGACCCG
A -----
GAM30 346 PRO0365 1 7384 NM_014126.1 5 CTGTCGCCAGGC C G C 3 C c c
TGAAGTGCAGT ATTGCACT CAGCCTGG C ACAG
TGACGTGA GTCGGACC G TGTC
A - C
GAM30 346 PRX 1 6453 NM_020956.1 3 CTGTGGCCGTCA AT C GC -- 3 C c c
GTGGAATGCAG TGCA TCCA CTG GGCCACAG
ACGT AGGT GAC CCGGTGTC
G- A -- TG
GAM30 346 PSMD9 1 8316 NM_002813.3 3 TGTGGCCCACCA CCAGCC G 3 C c
c
GTGTAAT ATTGCACT TGGGCCACA
TAATGTGA ACCCGGTGT
CC---- -
GAM30 346 PTGIS 1 701 NM_000961.2 3 CTGCTGCCCAGG C CA 3 C c c
CTAGAGTGCAGT ATTGCACTC AGCCTGGGC CAG
TGACGTGAG TCGGACCCG GTC
A TC
GAM30 346 RAB14 1 14594 NM_016322.2 3 CTGCGGCTTGTT TC CT A 3 C c c
GAGGTGCAAT ATTGCAC CAGC GGGCC CAG
TAACGTG GTTG TTCGG GTC
GA -- C
GAM30 346 RAB33B 1 8204 NM_031296.1 3 CTGTCTCCAGGC CC 3 C b b
TGGAGTGCAGT ATTGCACTCCAGCCTGGG ACAG

TGACGTGAGGTCGGACCT TGTC
C-
GAM30 346 RAP140 1 7259 NM_015224.1 3 CTGTCGCCCAAG C C C 3 C c c
CTGGAGTACAGT ATTG ACTCCAGC TGGGC ACAG
TGAC TGAGGTCG ACCCG TGTC
A A C
GAM30 346 RNF8 1 9153 NM_003958.1 3 CTGTTGCCCAAG C C C 3 C c c
CTGGAGTACAGT ATTG ACTCCAGC TGGGC ACAG
TGAC TGAGGTCG ACCCG TGTC
A A T
GAM30 346 SCYA20 1 4575 3 CTGTGGCTTTTC G C CCT 3 C c c
TGGAATGGAAT ATT CA TCCAG GGGCCACAG
TAA GT AGGTC TTCGGTGTC
G A TT-
GAM30 346 SEDL 2 7862 NM_014563.1 3 CTGTTGTCCAGG C 3 C b b
CTGGAGTGCAAT ATTGCACTCCAGCCTGGGC ACAG
TAACGTGAGGTCGGACCTG TGTC
T
GAM30 346 SEDL 2 8461 NM_014563.1 3 CTGTTGTGCAGG G C 3 C c b
CTGGAGTGCAGT ATTGCACTCCAGCCTG GC ACAG
TGACGTGAGGTCGGAC TG TGTC
G T
GAM30 346 SERF1B 1 18696 NM_022978.1 3 CTGTCACCAGAC C GCC 3 C c c
TGGAGTGCAGT ATTGCACTCCAG CTGG ACAG
TGACGTGAGGTC GACC TGTC
A AC-
GAM30 346 SIL 1 14916 NM_003035.1 3 TTGTAGCCCAGG C 3 C b b
CTGGAGTGCAAT ATTGCACTCCAGCCTGGGC ACAG
TAACGTGAGGTCGGACCCG TGTT
A
GAM30 346 SLC15A1 1 18389 NM_005073.1 3 TTGTTGTCCAGG C 3 C b b
CTGGAGTGCAAT ATTGCACTCCAGCCTGGGC ACAG
TAACGTGAGGTCGGACCTG TGTT
T
GAM30 346 SNAP23 1 12976 NM_003825.2 3 GTCCAGGCTGGA CACAG 3 C c c

GTGCAAT ATTGCACTCCAGCCTGGGC
TAACGTGAGGTCGGACCTG

GAM30 346 TAL1 1 4348 NM_003189.1 3 CTGTCACTCAGG C CC 3 C c c
CTGGAGTACAGT ATTG ACTCCAGCCTGGG ACAG
TGAC TGAGGTCGGACTC TGTC
A AC
GAM30 346 TBXA2R 1 3670 NM_001060.2 3 CTGTGGCCCAGC C C 3 C b b
CTGGAGTACAGT ATTG ACTCCAG CTGGGCCACAG
TGAC TGAGGTC GACCCGGTGTC
A C
GAM30 346 TCL6 2 8729 NM_020553.2 5 CTGTCACTCAGG C CC 3 C c c
CTGGAATGCAGT ATTGCA TCCAGCCTGGG ACAG
TGACGT AGGTCGGACTC TGTC

A AC
GAM30 346 TCL6 2 16523 NM_020553.2 5 CTGTGCCAGGCC CA GC 3 C c c
AGAGTGCAGT ATTGCACTC GCCTGG CACAG
TGACGTGAG CGGACC GTGTC
AC --
GAM30 346 TDGF1 1 14244 NM_003212.1 3 CTGTCACCCAGG C CC 3 C c c
CTGGACTGCAAT ATTGCA TCCAGCCTGGG ACAG
TAACGT AGGTCGGACCC TGTC
C AC
GAM30 346 TNFAIP2 1 14761 NM_006291.2 3 CTGTGTTGCCCA -- 3 C b b
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC CACAG
GT TGACGTGAGGTCGGACCCG GTGTC
TT
GAM30 346 TNFRSF1 1 1494 NM_147187.1 5 CTGTCTCCCAGG CC 3 C b b
0B CTGGAGTGCAAT ATTGCACTCCAGCCTGGG ACAG
TAACGTGAGGTCGGACCC TGTC
TC
GAM30 346 TNFRSF1 1 4393 NM_003839.2 3 TGGCCCAGGCTA C CAG 3 C c c
1A GAGTGCAGT ATTGCACTC AGCCTGGGCCA
TGACGTGAG TCGGACCCGGT
A ---
GAM30 346 TOR1B 1 17084 NM_014506.1 3 GTCATCCAAGCT C CC AG 3 C c c
GGAGTGCAGT ATTGCACTCCAGC TGGG AC
TGACGTGAGGTCG ACCT TG
A AC --
GAM30 346 TUCAN 1 19251 NM_014959.1 3 CTGTCATCTAGG CC 3 C c c
CTGGAGTGCAGT ATTGCACTCCAGCCTGGG ACAG
TGACGTGAGGTCGGATCT TGTC
AC
GAM30 346 WHSC1 1 12757 NM_133332.1 3 CTGTTGGCCAGG G - 3 C b b
CTGGAGTGCAGT ATTGCACTCCAGCCTGG CCA CAG
TGACGTGAGGTCGGACC GGT GTC
- T
GAM30 346 YES1 1 3761 NM_005433.2 3 CTGCCGCCCAGG CA 3 C b b
CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC CAG
TGACGTGAGGTCGGACCCG GTC
CC
GAM31 250 1 12532 NP_444285.1 5 477 GGTTTGTTGTTT G T 7 A c c
GTTTGGATTACT TCAAGTAATCCAG ATAGGC
TGAAAACC AGTTCATTAGGTT TGTTTG
- T
GAM31 250 ACRC 1 8811 NP_443189.1 3 361 TTGGGATCTACC -- A - 7 A c c
TTGGGTCTTACT TCAAGTA ATCCAGG TAGG CT
TGAGTTCC AGTTCAT TGGGTTC ATCT GG
TC C A
GAM31 250 ASRGL1 1 8589 NP_079356.2 3 207 AATGCCCGTATT AG-- -- T 7 A c c
AGGAGGATTACT TCAAGTAATCC GATA GGC
TGAGCCCT AGTTCATTAGG TTAT CCG
AGGA GC T
GAM31 250 ATM 1 12329 NP_612150.1 3 372 ATGCCCAACCTA G TC--- C 7 A c c

TCCTGTTCTTTT TCAA TAA CAGGATAGG TG
AATTGAAA AGTT ATT GTCCTATCC AC
A TTCTT A

GAM31 250.4 BA526D8 1 10428 XP_046861.2 3 111 GTATAGTGGCCA C A T 7 A c c
TCTTTGGTTACT TCAAGTAATC AGGAT GGC
TGATATTG AGTTCATTGG TTCTA CCG
T - G

GAM31 250 BCL7B 2 12161 NP_001698.2 3 391 GAAGAGAGCGTG C- A G 7 A c c
CCTCAGGTTACT TCAAGTAATC AGG TA GCT
TGAACTTG AGTTCATTGG TCC GT CGA
AC - G

GAM31 250 BCL7B 2 18017 NP_619713.1 3 28 AAAGAGAGCGTG C- A G 7 A c c
CCTCAGGTTACT TCAAGTAATC AGG TA GCT
TGAACTTG AGTTCATTGG TCC GT CGA
AC - G

GAM31 250 C1orf22 1 17483 NP_079467.2 3 1903 CAAAATAGTTGA CCAGGA 7 A c c
AGCTTAATTACT TCAAGTAAT TAGGCT
TGACTTGC AGTTCATTA ATTCGA

GAM31 25008 C21orf1 1 1584 XP_114191.2 3 1482 TCTTTGAGACTA AATC G 7 A c c
TCCTGAACTTGA TCAAGT CAGGATAG CT
AATCCCAC AGTTCA GTCCTATC GA
A--- A

GAM31 250 C6orf33 1 8970 NP_588608.1 3 856 TTACCAGTGGAC AGGA --- 7 A c c
TACAGGATTACT TCAAGTAATCC TAG GCTG
TGAGAGTT AGTTCATTAGG ATC TGAC
AC-- AGG

GAM31 250 CCL15 1 13409 NP_004158.1 3 311 CGCGTCAGCGGA - G AG 7 A c c
TTATGGATTACT TCA AGTAATCCA GAT GCTG
ATGAGACC AGT TCATTAGGT TTA CGAC
A A GG

GAM31 250 CCL15 1 13409 NP_116740.1 3 263 CGCGTCAGCGGA - G AG 7 A c c
TTATGGATTACT TCA AGTAATCCA GAT GCTG
ATGAGACC AGT TCATTAGGT TTA CGAC
A A GG

GAM31 250 CD5L 1 1774 NP_005885.1 3 20 GCTCAGGATATA - GG- 7 A c c
TCCTGGTGTTGC TCAAGTAAT CCAGGATA CT
TTGACCTG AGTTCGTTG GGTCCTAT GG
T ATA

GAM31 250 CLIC6 1 15773 NP_444507.1 3 1406 TAACAGAAACTA AG - G-- 7 A c c
TCCTGGGATTAG TCA TAATCC AGGATAG CTG
GTGAAAAA AGT ATTAGG TCCTATC GAC
GG G AAA

GAM31 250 CNGA3 1 5811 NP_001289.1 3 765 AGACAGCCCCTA T CC -- 7 A c c
TCCTCCATTCTT TCAAG AAT AGGATA GGCTG
GAGTCAGG AGTTC TTA TCCTAT CCGAC
- CC CC

GAM31 250 CXCL5 1 1275 NP_002985.1 3 153 AGTTAGCTTTCT - ---- T-- 7 A c c
TCCTGGATTCCT TCAA GT AATCCAGGA AGGCTG

CACTTTGA AGTT CA TTAGGTCCT TTCGAT
T CTCC TCT

GAM31 250 DKFZP57 1 17529 NP_149350.1 5 286 TCCTATTCAGCA A -- AG 7 A c c
2C163 TCCTGGAACTTA TCA GTAA TCCAGGAT GCTG
TGTGGGAT GGT TATT AGGTCCTA CGAC
G CA --

GAM31 250 EGFL5 1 14518 XP_098838.1 5 2813 CAAGAGAAAAGC CCAG A 7 A c
c
CATCATATTACT TCAAGTAAT GAT GGCT
TGGGATCT GGTTCATTA CTA CCGA
TA-- -

GAM31 250 FLJ1029 1 2300 NP_060518.1 3 1098 GCCAAATGAGGC CA A 7 A c c
2 CTACTGATTACT TCAAGTAATC GG TAGGCT
TGAGGTGT AGTTCATTAG TC ATCCGG
-- -

GAM31 250 FLJ1078 1 8309 XP_291008.1 3 715 GGGTCCAGCTTA - TA- 7 A c c
5 TCCTGGGTGCTC TCA AG ATCCAGGATAGGCTG
TGTGATCA AGT TC TGGGTCCTATTCGAC
G TCG

GAM31 250 FLJ1443 1 15994 NP_115967.1 3 580 TTGATTTGCATA A - G T 7 A c c
7 TCCTGGGTGTAC TCA GTA ATCCAGGATA GC
TGAGCCAC AGT CAT TGGGTCCTAT CG
- G A T

GAM31 250 FLJ2595 1 586 XP_092154.2 3 332 TAACAACGTGTC - -- TA T 7 A c c
5 TCCTGGATTTTA TCAA GTA ATCCAGGA GGC
CTTTGAAG AGTT CAT TAGGTCCT CTG
T TT -- T

GAM31 250 FLJ3872 1 19912 NP_776166.1 3 1159 CCATGCTGAGCA A AA AG 7 A c
c
3 TCCTGGAGGACC TCA GT TCCAGGAT GCT
TGGAGAGC GGT CA AGGTCCTA CGA
C GG --

GAM31 250 FLJ3881 1 12225 NP_665872.1 3 474 GTACCCAGCCTA TA- C-- 7 A c c
9 TCTTTTTGATAC TCAAG ATC AGGATAGGCTG
TTTTGAAT AGTTT TAG TTCTATCCGAC
TCA TTT

GAM31 250 FUT9 1 6340 NP_006572.1 3 990 ATGATGAGCCTA AATCCAG 7 A c c
TCATTTGATTTG TCAAGT GATAGGCT
AGTTCTAT AGTTTA CTATCCGA
GTTTA--

GAM31 250 KBRAS2 1 703 NP_060065.2 3 670 GGAGGCCAAGGC CAG AG 7 A c
c
GGGTCGATTACT TCAAGTAATC GAT GCT
TGAGGTCA AGTTCATTAG CTG CGG
--- GG

GAM31 250 KCNJ10 1 10380 NP_002232.2 3 733 CACCCATATCTA A T CT 7 A c c
TCCTGGATTCTG TCA G AATCCAGGATAGG
AACTCTTC AGT C TTAGGTCCTATCT
- - AT

GAM31 250 KIAA001 1 2192 NP_055486.1 3 936 GCCCACTTGTCT A T T 7 A c c
0 TCCTGGATATTT TCAAGTA TCCAGGA AGGC
GGGGGTGA GGTTTAT AGGTCCT TCTG
- - T
GAM31 250 KIAA015 1 10689 NP_055545.1 3 583 ATCTGGAAGCCT AG---- T 7 A c c
2 TTCTGGATTAAT TCA TAATCCAGGA AGGCT
CCAGTGAT AGT ATTAGGTCTT TCCGA
GACCTA -
GAM31 250 KIAA045 1 5812 XP_027862.1 3 4310 GTTTAGCATCCT - C--- AG 7 A c c
9 TGCAGAATTACT TCAAGTAAT C AGGAT GCTG
TGAGAAGG AGTTCATTA G TCCTA CGAT
A ACGT --
GAM31 250 KIAA155 1 528 XP_054472.2 3 3061 TAAATTCAGTAT - G AG 7 A c c
9 GTTGGCATTACT TCAAGTAAT CCAG AT GCTG
TGGACCTG GGTTCATTA GGTT TA TGAC
C G --
GAM31 250 KIDINS2 1 13145 XP_291015.1 3 66 ATGACAGAATTG GT G- 7 A c c
20 TCCTGGATTTTG TCAA AATCCAGGATAG CTG
ACTCCATC AGTT TTAGGTCCTGTT GAC
-- AA
GAM31 250 LARP 1 7293 NP_056130.1 5 1445 CCAGCCTGCCTG A T A T 7 A c c
ACCTGGATTCTG TCA G AATCCAGG TAGGC
AGAACTGG AGT C TTAGGTCC GTCCG
- - A T
GAM31 250 LETM1 1 15302 NP_036450.1 3 1222 TCAGACAATGCC CCA T- T 7 A c c
TTCTCCATTACT TCAAGTAAT GGA AGGC
TGAAGCTT AGTTCATTA CCT TCCG
--- CT T
GAM31 250 LOC1389 1 11374 XP_071218.2 5 57 ACTGATGGCCTG T A------ 7 A c c
61 TCCTGGATGCCA CAAGT ATCCAGGATAGGCTG
GGCACTTG GTTCA TAGGTCCTGTCCGGT
- CGGACCG
GAM31 250 LOC1444 1 10309 XP_084860.1 5 695 TTTTGCAGCCTA AATC GG 7 A c
c
38 TATGACTTGAGA TCAAGT CA ATAGGCTG
TTGGAGCT AGTTCA GT TATCCGAC
---- A-
GAM31 250 LOC1450 1 5430 XP_085022.1 5 1259 ATATCAGCTATT TC TA- 7 A c c
98 TCCTGTCTTACT TCAAGTAA CAGGA GGCTG
TGAAAAGT AGTTCATT GTCCT TCGAC
CT TTA
GAM31 250 LOC1456 1 15718 XP_096829.1 3 586 AGTTTGAGACTA A AAT G 7 A c c
63 TCCTGGTCAACA TCA GT CCAGGATAG CT
TGATGAAA AGT CA GGTCCTATC GA
A ACT A
GAM31 250 LOC1456 1 2590 XP_096832.1 3 1003 CTCCAGGAGCCA AGTAA A 7 A c
c
78 TCCTGGAATTTC TCA TCCAGGAT GGCT

TGACCTTG AGT AGGTCCTA CCGA
CTTTA -
GAM31 250 LOC1469 1 5431 XP_097142.1 3 282 TAGCCCAGCCTA A A- C-- 7 A c c
58 TCCTAATGAACT TCA GTA TC AGGATAGGCTG
ACCTGATT AGT CAT AG TCCTATCCGAC
C CA TAA
GAM31 250 LOC1518 1 11456 XP_087329.1 3 489 AAATCAAGTCTA TCCAGG 7 A c
c
78 TGTAAGCTTACT TCAAGTAA ATAGGCT
TGAAA AGTTCATT TATCTGA
CGAATG
GAM31 250 LOC1576 1 11401 XP_088366.2 5 1886 AAGGAAGCAGCA TAA AG- 7 A c
c
93 TCCTGGACCCTT TCAAG TCCAGGAT GCT
GAGGCCCT AGTTC AGGTCCTA CGA
CC- CGA
GAM31 250 LOC2199 1 7818 XP_166197.1 3 342 CCAGTCACGTTC T -- TA-- 7 A c c
18 CTCAGGCTTACT TCAAGTAA CC AGGA GGCTG
TGATCTAT AGTTCATT GG TCCT CTGAC
C AC TGCA
GAM31 250 LOC2219 1 8106 XP_168344.1 3 849 AAGAAAGACTCT T G -- 7 A c c
81 ATTGTGGTTACT TCAAGTAA CCA GATAG G CT
TGAAAAAT AGTTCATT GGT TTATC C GA
- G T A
GAM31 250 LOC2829 1 19230 XP_212615.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
58 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG
GAM31 250 LOC2829 1 19230 XP_208472.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
89 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG
GAM31 250 LOC2831 1 7739 XP_208535.1 3 1007 GGCAGGCTGTGC AGG--- G 7 A c
c
70 AGGAGGGTTACT TCAAGTAATCC ATAG CTG
TGAGCCCA AGTTCATTGGG TGTC GAC
AGGACG G
GAM31 250 LOC2832 1 19000 XP_208593.1 5 3 GTGTCTGTGTCC C --- T 7 A c c
63 CTGATTACTTGA TCAAGTAATC AGG ATAGGC
GATTAGGG AGTTCATTAG TCC TGTCTG
- CTG T
GAM31 250 LOC2833 1 19230 XP_208611.1 5 66 GCAGTGTTTGTG CA G---- 7 A c c
09 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG
GAM31 250 LOC2834 1 19230 XP_208697.1 5 56 GCAGTGTTTGTG CA G---- 7 A c c
95 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG
GAM31 250 LOC2835 1 19620 XP_211082.1 3 576 GAAGCCAGCCTA AGTAAT -- 7 A c
c

38 TCACCTGGCTGG TCA CCAGG ATAGGCTG
GTGAGAAG AGT GGTCC TATCCGAC
GGGTC- AC

GAM31 250 LOC2835 1 19230 XP_208740.1 5 56 GCAGTGTTTGTG CA G---- 7 A c c
50 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2836 1 19230 XP_208767.1 5 11 GCAGTGTTTGTG CA G---- 7 A c c
40 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2839 1 20102 XP_211257.2 3 277 AGAGGCCAGGTT AG-- A- 7 A c c

14 GAGGGGATTACT TCAAGTAATCC GAT GGCT
TGAGCCCA AGTTCATTAGG TTG CCGG
GGAG GA

GAM31 250 LOC2840 1 14941 XP_211302.1 5 2202 AGCTGATGTTCT - --- -- 7 A c c
19 TTGGGTATTACT TCAAGTAAT CC AGGATA GGCT
TGAGTAGT AGTTCATTA GG TCTTGT TCGA
T GTT AG

GAM31 250 LOC2843 1 19230 XP_209151.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
24 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2843 1 19230 XP_209180.1 5 56 GCAGTGTTTGTG CA G---- 7 A c c
97 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2844 1 19230 XP_209215.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
53 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2844 1 2443 XP_209218.1 5 56 ACAGTGTTTGTG CA G---- 7 A c c
55 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2845 1 17707 XP_211521.1 3 6 TCTCATCACCTA A AA CT 7 A c c
70 TCCTGGAACTGA TCA GT TCCAGGATAGG
TGCAATTA AGT CA AGGTCCTATCC
- -- AC

GAM31 250 LOC2846 1 16822 XP_211591.1 3 202 TACCAGACCCTG A- A -- 7 A c c
73 TCCTGGATGCTG TC AGTA TCCAGGATAGG CTG
GGATACAA AG TCGT AGGTCCTGTCC GAC
GG - CA

GAM31 250 LOC2847 1 3831 XP_211598.1 3 946 AGATTGAGACCA A A A - 7 A c c
07 TCCTGGATAACA TCA GT ATCCAGGAT GG CT
TGGTGAAA GGT CA TAGGTCCTA CC GA
A A - A

GAM31 250 LOC2853 1 19230 XP_209571.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
33 TCCCTGATTACT TCAAGTAATC GGATA GCTG

TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2855 1 19230 XP_209642.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
04 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2857 1 6281 XP_209730.2 5 62 GCCGTGTTTGTG CA ------- T 7 A c c
09 TCCCTGATTACT TCAAGTAATC GGATA GGC
TGAGATTA AGTTCATTAG CCTGT CCG
TC GTTTGTG -

GAM31 250 LOC2857 1 12265 XP_211991.1 5 455 TGATGATTACAG CCAGGA 7 A c
c
17 TCTAGAGTTACT TCAAGTAAT TAGGCTG
TGAAATGG AGTTCATTG ATCTGAC
AG----

GAM31 250 LOC2857 1 13675 XP_212026.1 3 591 CCCCAGCCCAGA - AA A-- 7 A c c

97 TCCTGGAGGGCT TCAA GT TCCAGGAT GGCTG
TTGGGCTT GGTT CG AGGTCCTA CCGAC
T GG GAC

GAM31 250 LOC2858 1 19230 XP_209771.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
38 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2859 1 9426 XP_209861.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
82 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATCA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2860 1 9960 XP_212133.1 5 776 CAGGTAAGCCAT A A TA 7 A c c
07 TCCTGGATACCT TCA GTA TCCAGGA GGCT
GACCCTTG AGT CAT AGGTCCT CCGA
C - TA

GAM31 250 LOC2861 1 19230 XP_209929.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
82 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC2863 1 19230 XP_210030.1 5 65 GCAGTGTTTGTG CA G---- 7 A c c
83 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG

GAM31 250 LOC3387 1 15655 XP_294690.1 3 861 TAATTAAGTGTA - GGA G 7 A c c
39 ATATGGATTACT TCAA GTAATCCA TA GCT
TTGAAACT AGTT CATTAGGT AT TGA
T ATA G

GAM31 250 LOC3391 1 12276 XP_294842.1 3 533 ATGTGGCAGTTT AG- TA 7 A c c
87 CAAAGGATTACT TCAAGTAATCC GA GGCTG
TGATGCAA AGTTCATTAGG CT TTGAC
AAA --

GAM31 250 LOC3398 1 13170 XP_295070.1 3 642 GACTCCGTGCCT TC A- T 7 A c c

07 GGACCTGTTACT TCAAGTAA CAGG TAGGC
TGATTAGG AGTTCATT GTCC GTCCG
-- AG T
GAM31 250 LOC3401 1 2443 XP_291146.1 5 65 ACAGTGTTTGTG CA G---- 7 A c c
12 TCCCTGATTACT TCAAGTAATC GGATA GCTG
TGAGATTA AGTTCATTAG CCTGT TGAC
TC GTTTG
GAM31 250 LOC3401 1 14005 XP_291158.1 3 2592 TCATGATTACAG CCAGGA 7 A c
c
56 TCTAGAGTTACT TCAAGTAAT TAGGCTG
TGAAATGG AGTTCATTG ATCTGAC
AG----
GAM31 250 LOC3482 1 11369 XP_300667.1 3 109 TTAGTCAGGCTA AATC- G 7 A c
c
41 TCCTGACAAGAC TCAAGT CAGGATAG CTG
TTGACCTA AGTTCA GTCCTATC GAC
GAACA G
GAM31 250 LOC3485 1 16926 XP_300775.1 3 121 CACGGAAGCCTA - TA AG- 7 A c
c
26 TCAACGGATGCC TCA AG ATCC GATAGGCT
TGTGATTC AGT TC TAGG CTATCCGA
G CG CAA
GAM31 250 LOC3487 1 9248 XP_302883.1 5 363 TCCCTGTCCTCC G T- - T 7 A c c
68 TCCTGGATTGTT TCAA TAATCCAGGA AGG C
GAGGAAAA AGTT GTTAGGTCCT TCC G
- CC T T
GAM31 250 LOC3492 1 17529 XP_300996.1 5 795 TCCTATTCAGCA A -- AG 7 A c c
57 TCCTGGAACTTA TCA GTAA TCCAGGAT GCTG
TGTGGGAT GGT TATT AGGTCCTA CGAC
G CA --
GAM31 250 LOC3492 1 17529 XP_300995.1 3 562 TCCTATTCAGCA A -- AG 7 A c c
58 TCCTGGAACTTA TCA GTAA TCCAGGAT GCTG
TGTGGGAT GGT TATT AGGTCCTA CGAC
G CA --
GAM31 250 LOC3492 1 17529 XP_301000.1 5 795 TCCTATTCAGCA A -- AG 7 A c c
65 TCCTGGAACTTA TCA GTAA TCCAGGAT GCTG
TGTGGGAT GGT TATT AGGTCCTA CGAC
G CA --
GAM31 250 LOC3492 1 17529 XP_300999.1 3 562 TCCTATTCAGCA A -- AG 7 A c c
66 TCCTGGAACTTA TCA GTAA TCCAGGAT GCTG
TGTGGGAT GGT TATT AGGTCCTA CGAC
G CA --
GAM31 250 LOC3509 1 607 XP_301844.1 5 30 TGCCCCAGCCTA A A CA 7 A c c
05 TCTGATGGCATG TCA GT ATC GGATAGGCTG
GTCCCTGG GGT CG TAG TCTATCCGAC
A G --
GAM31 250 LOC3527 1 8832 XP_305938.1 5 18 AAAAACAGCCTA TA CAGG 7 A c
c
39 TGATAGTTTGAA TCAAG ATC ATAGGCTG
TCCCCCTC AGTTT TAG TATCCGAC

GA ----

GAM31 2509 LOC516 1 20004 NP_057067.1 3 516 AGTCTCAGCTTA GTAA- 7 A c c
TCCTGGAGGGAA TCAA TCCAGGATAGGCTG
TTGGGAAC GGTT AGGTCCTATTCGAC
AAGGG

GAM31 2500 LOC906 1 9139 XP_033352.1 3 937 TAAAGCTGGTTT C TA--- 7 A c c
TTCTTGATTACT TCAAGTAATC AGGA GGCT
TGAGAAGC AGTTCATTAG TCTT TCGA
T TTTGG

GAM31 2506 LOC915 1 16059 NP_710181.1 3 624 GGAGGCCGAGGC GATA--- 7 A c c
AGTTGGATTACT TCAAGTAATCCAG GGCT
TGAGGCCA AGTTCATTAGGTT CCGG
GACGGAG

GAM31 2507 LOC965 1 19996 XP_039922.1 3 975 CATGGCAGCCTA T----- - GGA 7 A c c
CATGGCATTACT CAAGTAAT CCA TAGGCTG
TGTGACCA GTTCATTA GGT ATCCGAC
ACCAGT C AC-

GAM31 250 LPIN2 1 8573 NP_055461.1 3 3118 ATGTTCAGCCTA ATC GG 7 A c c
TGATGAAGTATT TCAAGTA CA ATAGGCTG
TGATTATT AGTTTAT GT TATCCGAC
GAA AG

GAM31 250 LRRN4 1 8168 NP_002310.2 3 1772 TCCCGTAGCCCT A TA TA 7 A c c
TCCTGGATCTGG TC AG ATCCAGGA GGCTG
AGAGAGCA AG TC TAGGTCCT CCGAT
G -- TC

GAM31 250 MAP3K2 1 17136 NP_006600.2 3 902 TAAACAGTTTTG TC - 7 A c c
TTTTGTTTTACT TCAAGTAA CAGGATAGG CTG
TGAGGGGG AGTTCATT GTTTTGTTT GAC
TT T

GAM31 250 MCLC 1 17231 NP_055942.1 3 571 GTGCCCAGCCTA ATCCAGG 7 A c c
TATCTACTTGAG TCAAGTA ATAGGCTG
CCTGTGTG AGTTCAT TATCCGAC
CTA----

GAM31 250 MEF2B 1 16083 NP_005910.1 5 362 TCCTCAGCCTGA A AA-- - 7 A c c
TCCTGGAAGAGA TC AGT TCCAGGAT AGGCTG
CTCGGGGC GG TCA AGGTCCTA TCCGAC
C GAGA G

GAM31 250 MEGF11 1 10033 NP_115821.1 3 236 CAGCCCCAAATG A A ----- 7 A c c
CCCTGGATTATA TCA GTAATCCAGG TA GGCTG
TGATTTTT AGT TATTAGGTCC GT CCGAC
A C AAACC

GAM31 2505 MGC2466 1 755 NP_689521.1 3 941 TTGTAGACTTTC G AT- - 7 A c c
ACCTGGATTATT TCAA TAATCCAGG AGG CTG
GATATTCT AGTT ATTAGGTCC TTC GAT
- ACT A

GAM31 250 MGC2941 1 789 NP_077273.1 3 503 GTCCTCAGCCTA AA -- 7 A c c
TCCCCTGGAGCT TCAAGT TCCA GGATAGGCTG

TGGATACT GGTTCG AGGT CCTATCCGAC
-- CC

GAM31 250 MGC3392 1 18620 NP_689603.1 3 132 CCTGCCAGCCCT A TA 7 A c c

6 TTCTGGATTACT TCA GTAATCCAGGA GGCTG
GATAGAAA AGT CATTAGGTCTT CCGAC
- TC

GAM31 250 MGC3546 1 19738 NP_694976.1 3 738 GAAAACATCAGC CCAG A 7 A c c

8 CATTACATTACT TCAAGTAAT GAT GGCTG
TGGCTCTG GGTTCATTA TTA CCGAC
CA-- -

GAM31 250 MGC4504 1 8302 NP_077016.1 3 292 GCAGTGGCCCCA AA A- T 7 A c c

TCCTGGAACTTG TCAAGT TCCAGGAT GGC
ACCAGATT AGTTCA AGGTCCTA CCG
-- CC G

GAM31 250 MIDORI 1 1428 NP_065829.1 3 1866 CCCAGCCTGTAT - CA --- 7 A c c
ACCCAGATTACT TCAA GTAATC GG ATAGGCTG
TTGGTGAA GGTT CATTAG CC TGTCCGAC
T AC ATA

GAM31 250 PACE4 1 3372 NP_612196.1 3 559 TGGCTCAATCTA ATC GC 7 A c c
TCCTGTGCTTGA TCAAGTA CAGGATAG TG
TGCTAGAA AGTTCGT GTCCTATC AC
--- TA

GAM31 250 PACE4 1 3372 NP_612197.1 3 518 TGGCTCAATCTA ATC GC 7 A c c
TCCTGTGCTTGA TCAAGTA CAGGATAG TG
TGCTAGAA AGTTCGT GTCCTATC AC
--- TA

GAM31 250 PDE4B 1 17193 NP_002591.1 3 132 GGGCCACCTGGC ------- ATA 7 A c c
CTTTCAGTTACT TCAAGTAAT CCAGG GGCT
TGAGTTTG AGTTCATTG GGTCC CCGG
ACTTTCC A--

GAM31 250 PEG10 1 1451 NP_055883.1 3 2417 TTCCTTAGTGAG CCA TAG 7 A c c

CTCCACATTACT TCAAGTAAT GGA GCT
TGATGGTA AGTTCATTA CCT CGA
CA- ---

GAM31 250 PLCG1 1 760 NP_002651.1 3 128 TCGCAGCCTGAA A- --- A-- 7 A c c
GCCTGGATTCCA TCA GT AATCCAGG TAGGCTG
GCAGTGAA AGT CG TTAGGTCC GTCCGAC
GA ACC GAA

GAM31 250 PLOD 1 15113 NP_000293.1 3 675 TGGGTCACCCTG - TA C 7 A c c
TCCTGGATGCCT TCA AG ATCCAGGATAGG TG
CTGAAGAG AGT TC TAGGTCCTGTCC AC
C CG C

GAM31 250 RODH 1 14449 NP_003716.2 3 397 TATGTTGGTGTG ATCC T 7 A c c
TTTGTCCTTACT TCAAGTA AGGATAGGC
TGAAATGG AGTTCAT TCCTGTTTG
---- T

GAM31 250 SACS 1 14450 NP_055178.1 3 565 GTAGAGTATTTT CC AG---- 7 A c c
AATCCTATTACT TCAAGTAAT AGGAT GCT
TGACTAAG AGTTCATTA TCCTA TGA
-- ATTTTA
GAM31 250 SARA1 1 9126 NP_064535.1 3 239 TGCAGGTCAGTA AA -- 7 A c c
TCCTGGGACTTG TCAAGT TCCAGGATA GGCT
GAAGCTGG GGTTCA GGGTCCTAT CTGG
-- GA
GAM31 250 SFPQ 1 16010 NP_005057.1 3 729 TGGCCCTATGAT TCC CT 7 A c c
CTATCCTTTACT TCAAGTAA AGGATAGG
TGAAAGCT AGTTCATT TCCTATCT
--- AG
GAM31 250 Siat7c 1 11487 NP_694541.1 3 630 GACATCCTACAC --- GA C 7 A c c
TTCAGGATTACT TCAAGTAATCC AG TAGG TG
TGACTATC AGTTCATTAGG TC ATCC AC
ACT AC T
GAM31 250 SLC19A3 1 16645 NP_079519.1 3 348 AAACTCCAGCCA GTAA A 7 A c
c
TCCTGGAGTTGA TCAA TCCAGGAT GGCTG
TATTCACC AGTT AGGTCCTA CCGAC
G--- -
GAM31 250 SPINLW1 1 10499 NP_065131.1 3 1126 TTATCCAGCCTA A G---- 7 A c c
TCGTTGATGGAT TCAAGTA TCCA GATAGGCTG
ATTTGGTT GGTTTAT AGGT CTATCCGAC
- AGTTG
GAM31 250 SPINLW1 1 10499 NP_852479.1 3 1126 TTATCCAGCCTA A G---- 7 A c c
TCGTTGATGGAT TCAAGTA TCCA GATAGGCTG
ATTTGGTT GGTTTAT AGGT CTATCCGAC
- AGTTG
GAM31 250 SSX2IP 1 5546 NP_054740.1 3 385 GGCATTGGAAGT TCC A 7 A c c
TTAGCCTTTACT TCAAGTAA AGG TAGGCT
TGAATGTA AGTTCATT TCC ATTTGA
--- G
GAM31 250 THRA 1 5656 NP_003241.2 5 405 TGCTGGAGGGCA GTA- AG 7 A c c
TCCTGGATGGAA TCAA ATCCAGGAT GCT
TTGAAGTG AGTT TAGGTCCTA CGG
AAGG --
GAM31 250 TNK1 1 16242 NP_003976.1 3 434 GCAGGGCAGCCA AAGTA A 7 A c
c
TCCTGGATGATG TC ATCCAGGAT GGCTG
GAAGCCAC AG TAGGTCCTA CCGAC
GTAG- -
GAM31 250 TRIM8 1 7224 NP_112174.1 3 833 AGTTGGGTCCTT GT AT - 7 A c c
GCCTGGATTTTG TCAA AATCCAGG AGG CT
ACACAGCA AGTT TTAGGTCC TCC GG
-- GT T
GAM31 250 TXNL 1 18077 NP_004777.1 3 65 CAGATCTACAGC --- TAG 7 A c c
TCCTGGATAATT TCAAGTA ATCCAGGA GCTG
GCTTGATT AGTTCGT TAGGTCCT CGAC
TAA ---

GAM31 250 VTS5863 1 11083 NP_201572.1 3 1067 GATCTCAGACTA AG- C G 7 A c c
5 TCCTGATTAATC TCA TAATC AGGATAG CTG
TGGGGAAG GGT ATTAG TCCTATC GAC
CTA - A
GAM31 250 ZDHHC6 1 11341 NP_071939.1 3 50 ATCCTTTAAGTC CC A 7 A c c
TGCTTAATTACT TCAAGTAAT AGG TAGGCT
TGAAAATT AGTTCATTA TTC GTCTGA
A- -
GAM31 250 ZF 1 16486 NP_067035.1 3 1307 TAAATGGCCGTT - TA 7 A c c
TTTGGAATTACT TCAAGTAAT CCAGGA GGCTG
TGATAAGA AGTTCATTA GGTTTT CCGGT
A TG
GAM31 250 ZNF238 1 5764 NP_006343.2 3 1788 CTTGGAGCATTA CC - 7 A c c
TCTTTAGTTACT TCAAGTAAT AGGATAG GCT
TGAAGAGT AGTTCATTG TTCTATT CGA
AT A
GAM31 250 ZNF259 1 13366 NP_003895.1 3 203 CAAGTGTGAGCC TC G 7 A c c
TATTGTGTTACT TCAAGTAA CA GATAGGCT
TGACCTTA AGTTCATT GT TTATCCGA
-- G
GAM31 250 ZNF294 1 13175 NP_056380.1 3 1180 AGCATATCTAAT C ------ G 7 A c c
ATCTAGGTTACT TCAAGTAATC AG GATA GCT
TGAGAGAC AGTTCATTGG TC CTAT CGA
A TATAAT A
GAM31 250 ZNF294 1 13175 XP_047829.3 3 1180 AGCATATCTAAT C ------ G 7 A c c
ATCTAGGTTACT TCAAGTAATC AG GATA GCT
TGAGAGAC AGTTCATTGG TC CTAT CGA
A TATAAT A
GAM31 250 ZNF36 1 13144 XP_168302.1 3 2028 CTAAGCAGTTTC CCAG - 7 A c c
ATCAGCATTACT TCAAGTAAT GAT AGGCTG
TGGGAAAA GGTTCATTA CTA TTTGAC
CGA- C
GAM32 384 CUL3 1 7209 NM_003590.1 3 CTGGAATGTGTC G A TGAA 3 C c c
CATTGA TC AATGGACACATT CCAG
AG TTACCTGTGTAA GGTC
- - ----
GAM32 384 KIAA023 1 16243 NM_014747.1 3 TTCACTGCATGA - A C- 3 C c c
7 AGTTGTTCATTT TCGAATGGACA C TTA CAGTGAA
GG GGTTTACTTGT G AGT GTCACTT
T A AC
GAM32 384 KIAA051 1 11389 NM_014696.1 3 TTCACTGTTGAT TG C 3 C c c
4 GTGTTTGTTTGG TCGAA GACACATTA CAGTGAA
GGTTT TTGTGTAGT GTCACTT
GT T
GAM32 384 LOC1497 1 1549 3 TTTACTGGTAGT TC AC 3 C c c
34 GTCCTCATTC GAATGG ACATTACCAGTGAA
CTTACT TGTGATGGTCATTT
-- CC
GAM32 384 LOC1519 1 11716 XM_098144.1 3 TTTACTGGGCGG C ATTA 3 C c c

59 TTTCCATTTGA TCGAATGGA AC CCAGTGAA
AGTTTACCT TG GGTCATTT
T GCG-
GAM32 384 LOC9036 1 5001 5 TTCATGTACATG TC - CA 3 C c c
2 TGTCTATTC GAATGGACACAT TAC GTGAA
CTTATCTGTGTA ATG TACTT
-- C --
GAM32 384 PCDH11Y 1 14519 NM_032972.1 3 TTCATTGGTGAG T CACA- 3 C c c
GATTTCCTTTGA TCGAA GGA TTACCAGTGAA
AGTTT CCT AGTGGTTACTT
- TTAGG
GAM32 384 PCDHB3 1 4570 NM_018937.2 3 TTTACTGCTTTG G CATTAC 3 C c c
TCCATTGGA TC AATGGACA CAGTGAA
AG TTACCTGT GTCATTT
G TTC---
GAM32 384 POU4F2 1 19158 NM_004575.1 3 TTTACTGGTAGT T - C 3 C c c
GTTCTGATTTG CGAAT GGA ACATTACCAGTGAA
GTTTA TCT TGTGATGGTCATTT
- G -
GAM32 384 PRO2266 1 12617 3 TCATGGTTGTCC CATT G A 3 C c c
ATTTGA TCGAATGGACA ACCA TGA
AGTTTACCTGT TGGT ACT
---- - -
GAM32 384 SPP1 1 13484 NM_000582.1 3 TTTATTGGTTGA -- -- 3 C c c
ATGTGTATCTAT TCGAATGGA CACATT ACCAGTGAA
TTGA AGTTTATCT GTGTAA TGGTTATTT
AT GT
GAM32 384 TIMELES 1 11356 NM_003920.1 3 TTTATTGGTCTG T C TT 3 C c c
S TTCCTTTGG TCGAA GGA ACA ACCAGTGAA
GGTTT CCT TGT TGGTTATTT
- - C-
GAM33 317 KIAA094 1 14036 NM_014912.1 3 CTGACCTGCAAC A CAGGT 3 C c c
0 TTGACT AGTCAAGTTGCAGG TCAG
TCAGTTCAACGTCC AGTC
- -----
GAM33 317 LOC1336 1 18335 3 GCCACTGATCCT T CA 3 C b b
88 GCAACTTGCT AG CAAGTTGCAGGATCAG GGT
TC GTTCAACGTCCTAGTC CCG
- A-
GAM33 317 LOC1591 1 6634 5 ACCTGCTGGCCA A AG - A 3 C c c
99 TGCAAGCTGAC GTCA TTGCA GG TCAGCAGGT
CAGT AACGT CC GGTCGTCCA
- CG A -
GAM33 317 LOC2053 1 17537 5 ACCTGCTGACCC A TTG A 3 C c c
60 TGGCCTTGGC GTCAAG CAGG TCAGCAGGT
CGGTTC GTCC AGTCGTCCA
- CG- C

GAM34 314 DKFZP43 1 6705 NM_015621.1 3 CCAGGCCCTAAG AA GGTGA 3 C c c

4C171 CCAGCGTCA TGACGCTG GCT GCCTGG
ACTGCGAC CGA CGGACC
-- ATCC-

GAM34 314 FLJ1058 1 13120 3 CAGGCTCACTGC C AAGC G 3 C c c
3 AGCCTCA TGA GCTG TGGTGAGCCTG
ACT CGAC GTCACTCGGAC
C ---- -

GAM34 314 FLJ1258 1 11111 NM_022480.2 3 CCAGACCGCGGC - G AGC 3 C c c
7 CTTCAGTGTCA TGACGCTGAAG CTG TG CTGG
ACTGTGACTTC GGC GC GACC
C - CA-

GAM34 314 FLJ2184 1 6943 NM_024609.1 3 CCAAGCTCACCA A TGAA C 3 C c c
1 GCCCTGCGCCA TG CGC GCTGGTGAGC TGG
AC GCG CGACCACTCG ACC
C TCC- A

GAM34 314 FLJ2255 1 12516 NM_024928.2 3 CCAGGCTCTGAC C CTGGT 3 C c c

9 TTTCAGCATCA TGA GCTGAAG GAGCCTGG
ACT CGACTTT CTCGGACC
A CAGT-

GAM34 314 FLJ3176 1 6375 3 CCAGGCTTGCCC C AGCT TG 3 C c c
2 CTCAGCTCA TGA GCTGA GG AGCCTGG
ACT CGACT CC TCGGACC
- CC-- GT

GAM34 314 KIAA066 1 12553 3 CCAATGCTCACC G AA C- 3 C c c
2 AGCCCCAGAGTC TGAC CTG GCTGGTGAGC TGG
A ACTG GAC CGACCACTCG ACC
A CC TA

GAM34 314 LOC1443 1 5515 XM_084813.4 5 CCAAGCCCACCA TGA - A C 3 C c c
17 GCTTTCAGCG CGCTGAA GCTGGTG GC TGG
GCGACTT CGACCAC CG ACC
--- T C A

GAM34 314 LOC1481 1 2036 XM_086077.1 5 CCATCTTCCGGC A T CC 3 C c c
66 TCCAGCGTCA TGACGCTG AGCTGG GAG TGG
ACTGCGAC TCGGCC TTC ACC
C - T-

GAM34 314 LOC1491 1 2210 XM_097594.1 5 CCAGTCGCCCAG A - GC 3 C c c
34 CTCCAGTGTCA TGACGCTG AGCTGG TGA CTGG
ACTGTGAC TCGACC GCT GACC
C C --

GAM34 314 LOC1696 1 7929 XM_095809.4 3 CCAGGCTCACAC C GAA - 3 C b b
11 AGCAGCTCA TGA GCT GCTG GTGAGCCTGG
ACT CGA CGAC CACTCGGACC
- --- A

GAM34 314 NGFB 1 7978 NM_002506.1 5 CAAGCTCAGCTC T A GGT C G 3 C c c
AGCGTC GACGCTGA GCT GAGC TG
CTGCGACT CGA CTCG AC
- - --- A -

GAM34 314 RAD50 1 15035 NM_005732.2 3 CCAGGCTCACTC G AAGCT 3 C c c

ACAGAGTCA TGAC CTG GGTGAGCCTGG
ACTG GAC TCACTCGGACC
A AC---

GAM34 314 RNASE4 1 1775 NM_002937.2 3 CCAGGCTCTGTC C AGCTGGT 3 C c c

TCCTCAGCTCA TGA GCTGA GAGCCTGG
ACT CGACT CTCGGACC
- CCTCTGT

GAM35 247 LOC1445 1 14499 3 GACAAAAAAGAC - ATCATC 3 C c c
58 ATTCCCTCA TGAGG AATGT TTTTTGTC
ACTCC TTACA AAAAACAG
C GA----

GAM35 247 LOC1448 1 6700 XM_096698.4 3 GACAAAATTTAA TATCATCT 3 C c c

71 TTCATTCCTCA TGAGGAATG TTTTGTC
ACTCCTTAC AAAACAG
TTAATTT-

GAM35 247 LOC5165 1 17491 3 ACAAAAAGAAAT GTATCA C 3 C c c
2 TTCTCA TGAGGAAT TCTTTTTGT
ACTCTTTA AGAAAAACA
A----- -

GAM35 247 My015 1 12036 3 ACAAAAATTGAT G C-- -- C 3 C c c
ATAATACATTCA TGA GAATGTAT ATC TTTTTGT
TCA ACT CTTACATA TAG AAAAACA
A ATA TT -

GAM36 351 CIS4 1 11967 5 AGATGCAGCCTT TCTGGCTA T 3 C c c
GCAG CTGCAAGGCT CATCT
GACGTTCCGA GTAGA
C------- -

GAM36 351 FGF2 1 14146 NM_002006.2 3 AAGATGCAGGAG C GG- A--- 3 C c c
AGAGGAAGCCTT TGCAAGGCTTCT CT CATCTT
GCA ACGTTCCGAAGG GA GTAGAA
- AGA GGAC

GAM36 351 LOC1478 1 13329 NM_145276.1 3 ATGTAGGGAAGC C GG CTT 3 C c c

37 CTTCAG CTG AAGGCTTCT CTACAT
GAC TTCCGAAGG GATGTA
- -- ---

GAM36 351 LPHH1 1 8148 NM_012302.1 3 AGATGACTGAAC C T CTA T 3 C c c
CTTGCAG CTGCAAGG TTC GG CATCT
GACGTTCC AAG TC GTAGA
- - A-- -

GAM36 351 OSBPL10 1 19783 NM_017784.3 3 AAGATTTATGCC T - C 3 C b b
AGAGCCTTGCAG CTGCAAGGCT CTGGC TA ATCTT
GACGTTCCGA GACCG AT TAGAA
- T T

GAM36 351 RTN4IP1 1 14226 NM_032730.1 5 AAGTTGTCCAAA C C CT T 3 C c c
AGCCTTCAG CTG AAGGCTT TGG ACA CTT

GAC TTCCGAA ACC TGT GAA
- A -- T

GAM37 266 CLOCK 1 9594 NM_004898.2 3 TGACCTTATGCC TCCA -- A 3 C c c
ATTCCATATA TATATGGA ATGGCA AG TCA
ATATACCT TACCGT TC AGT
---- AT C

GAM37 266 HSC3 1 19698 NM_145174.1 3 TGATCTTGCCAT TATA TC- 3 C c c
TGCACTCCA TGGA CAATGGCAAGATCA
ACCT GTTACCGTTCTAGT
---- CAC

GAM37 266 LOC1510 1 12533 3 TGATCTTGCCAT TAT TC 3 C c c
05 TGCTCCAT ATGGA CAATGGCAAGATCA
TACCT GTTACCGTTCTAGT
--- C-

GAM37 266 STAU 1 602 NM_017454.1 3 TGATCTCCATGT CCA CA 3 C c c
AGTCCATATA TATATGGAT ATGG AGATCA
ATATACCTG TACC TCTAGT
ATG --

GAM38 271 CD34 1 10905 NM_001773.1 3 TGACCACGTGCT A A - TGT 3 C c c
ACCCCCATGCT GGCATGG GG AGC GTGGTCA
TCGTACC CC TCG CACCAGT
- C A TG-

GAM38 271 DKFZP43 1 15656 NM_014549.1 3 GCCCACCTCCTC CT T CA 3 C c c
4P211 CATGCCT AGGCATGGAGGAG GTG GGT
TCCGTACCTCCTC CAC CCG
-- - --

GAM38 271 FLJ2050 1 1188 NM_017849.1 3 TGACCACACAGC A CA GA A 3 C c c
7 CTACACCC GG TG GG GCTGTGTGGTCA
CC AC TC CGACACACCAGT
C -- A- -

GAM38 271 LOC1517 1 3460 XM_087279.6 5 GACCACAGCCAT A --- GCTG A 3 C c
c
20 CCCTCTCCATGC GGCATGGA GGA TGTGGTC
C CCGTACCT CCT ACACCAG
- CTC ACCG -

GAM38 271 LOC2548 1 19887 XM_173133.4 3 TGACCACACAGG TGGA A - 3 C c c
48 CACCTGCCT AGGCA GG GC TGTGTGGTCA
TCCGT CC CG ACACACCAGT
---- A G

GAM38 271 LOC2559 1 20152 XM_171083.2 5 GGCCCAGCTCCT T TGT A 3 C c c
75 CCTGCCT AGGCA GGAGGAGCTG GGTC
TCCGT CCTCCTCGAC CCGG
- --- -

GAM38 271 MAAT1 1 18969 3 CACAGCTCCTCC TGGTCA 3 C c c
ATGCCT AGGCATGGAGGAGCTGTG
TCCGTACCTCCTCGACAC

GAM38 271 MAP1B 1 6168 NM_005909.2 5 GACCACACAAAC A AGGAGC A 3 C c
c

CCAGCCT AGGC TGG TGTGTGGTC
TCCG ACC ACACACCAG
- CAA--- -
GAM38 271 MGC2168 1 6874 NM_144635.1 3 CCCACCCTCCCC A CT T TCA 3 C c
c
8 ATGCCT AGGCATGG GGAG GTG GG
TCCGTACC CCTC CAC CC
- C- - ---
GAM38 271 PCOLN3 1 14968 NM_002768.1 3 GACCACACCCCA GGA AGCT A 3 C c
c
ATGCCT AGGCAT GG GTGTGGTC
TCCGTA CC CACACCAG
AC- ---- -
GAM39 386 C20orf1 1 13958 XM_290955.1 3 GGTGGCTGGGCG A T ACG C 3 C c c
77 TGGTGGCT AGCCACC ATG CAGCCACC
TCGGTGG TGC GTCGGTGG
- - GG- -
GAM39 386 CHRNA10 1 3642 NM_020402.2 3 GGTGGCTGCTTT AC AT C C 3 C c
c
GCAGGGCTT AAGCC CT GA GCAGCCACC
TTCGG GA TT CGTCGGTGG
-- CG T -
GAM39 386 DHRS2 1 1429 NM_005794.1 3 GGGCGGCTGCGT A CTATG A 3 C c
c
AGCTGTGGTCC A GCCAC ACGCAGCC CCC
C TGGTG TGCGTCGG GGG
C TCGA- C
GAM39 386 FLJ2347 1 18143 NM_024640.1 3 GGTGGCTGCGTG A TATG C 3 C c c
6 TGGTGGCT AGCCACC ACGCAGCCACC
TCGGTGG TGCGTCGGTGG
- TG-- -
GAM39 386 KIAA192 1 17872 NM_153239.2 3 GGGTGGCTGCGT A ACCTAT 3 C c
c
4 CTGAAGGCT AGCC GACGCAGCCACCC
TCGG CTGCGTCGGTGGG
- AAGT--
GAM39 386 LOC5116 1 15881 NM_016210.1 5 GGTGGCTGTGCA AA AT A C 3 C c
c
1 GGTGGC GCCACCT G CGCAGCCACC
CGGTGGA C GTGTCGGTGG
-- -- - -
GAM39 386 LOC9104 1 18287 3 GGTGGCTGGGAG A ATGACG C 3 C c c
0 GTGGCT AGCCACCT CAGCCACC
TCGGTGGA GTCGGTGG
- GG---- -
GAM39 386 MGC1070 1 19440 NM_032658.1 5 GGGTGGCTGGGG A A GACG 3 C c
c
1 TAGGGGCT AGCC CCTAT CAGCCACCC

TCGG GGATG GTCGGTGGG
- - GG--
GAM39 386 MGC1133 1 15461 NM_030819.2 3 GGGTGAAGCCAG A A AC AGC 3 C c c
5 AGGTGGCT AGCCACCT TG GC CACCC
TCGGTGGA AC CG GTGGG
- G -- AA-
GAM39 386 RAD1 1 16511 NM_133377.1 3 GGTGGCCGGGTG TATG A-- C 3 C c c
TGGTGGCTT AAGCCACC ACGC GCCACC
TTCGGTGG TGTG CGGTGG
---- GGC -
GAM39 386 SNAPC4 1 8252 NM_003086.1 5 GGGTGGCCAGTT CTAT- GCA 3 C c c
TCCATGTGGCTT AAGCCAC GAC GCCACCC
TTCGGTG TTG CGGTGGG
TACCT AC-
GAM40 396 ABCA9 1 10551 NP_525022.2 5 114 TTCCTCCAGCTT G A G T 3 B c c
TCCTGAGAGAAA TGT TC CT AG GAAAGCTG
CAGGTCAA ACA AG GA TC CTTTCGAC
A A G -
GAM40 396 ABCA9 1 10551 NP_759018.1 5 114 TTCCTCCAGCTT G A G T 3 B c c
TCCTGAGAGAAA TGT TC CT AG GAAAGCTG
CAGGTCAA ACA AG GA TC CTTTCGAC
A A G -
GAM40 396 ACTG2 1 465 NP_001606.1 5 55 CCAGTCCCCAGC CA AA 3 B c c
TCACTCAGCCAC TGTGT CTGAGTGA GCTG
ACACACCA ACACA GACTCACT CGAC
CC --
GAM40 396 ADPRTL3 1 2591 NP_005476.1 3 276 TAAGGGCAGCTT TC GA 3 B c c
TTATAGGTTCCA TGTG ACT GTGAAAGCTGC
CATGTAAG ACAC TGG TATTTTCGACG
CT A-
GAM40 396 AK5 1 6701 NP_036225.2 3 1147 TAACTGCATCTT - C A C 3 B c c
CCACTCAGTCAC TGT GT ACTGAGTG AAG TGC
TACAAAAA ACA CA TGACTCAC TTC ACG
T C C T
GAM40 396 AK5 1 6701 NP_777283.1 3 1147 TAACTGCATCTT - C A C 3 B c c
CCACTCAGTCAC TGT GT ACTGAGTG AAG TGC
TACAAAAA ACA CA TGACTCAC TTC ACG
T C C T
GAM40 396 AMELX 1 5458 NP_001133.1 3 58 ACTTCAGATGCT GAG TG 3 B c c
TTCAGGAGTGAC TGTGTCACT TGAAAGC
ACAAGAAC ACACAGTGA ACTTTCG
GG- TA
GAM40 396 BIVM 1 10429 NP_060163.2 3 473 AATTTCTAGTTT T-- ---- C 3 B c c
TCACTCATGGTT GTGT CA TGAGTGAAAGCTG
AACACGCA CACA GT ACTCACTTTTGAT
ACG ATTG -

GAM40 396 C14orf4 1 7225 NP_079333.1 3 752 TATTTGGTACTT CAC C 3 B c c
5 TCACTTACTACA TGTGT TGAGTGAAAG TGC
CATCATTT ACACA ATTCACTTTC ATG
TC- -
GAM40 396 CASQ2 1 14756 NP_001223.1 3 393 AATTGACAGCTT AC -- 3 B c c
TCTAACTCACAG TGTGTC TGAGT GAAAGCTG
GCATAGAG ATACGG ACTCA CTTTCGAC
AC AT
GAM40 396 CDK11 1 2021 XP_166324.1 3 3883 TGATGAAGTAGA A AAG 3 B c c
TCATGCAGTGAC TGTGTCACTG GTGA CTGC
ATACAAAG ATACAGTGAC TACT GATG
G A--
GAM40 396 CGI-01 1 18067 NP_057019.2 3 588 ATTTGACAGCTT T TG T 3 B c c
TCCTTGGTGACC TG GTCAC AG GAAAGCTG
CAAACCTT AC CAGTG TC CTTTCGAC
C GT -
GAM40 396 CLCN6 1 2020 NP_001277.1 3 1211 AAGCGCACCCTG - A C- 3 B c c
TCGTTCAGTGAC TG TGTCACTGAGTGA AG TGC
GTCATTCT AC GCAGTGACTTGCT TC ACG
T G CC
GAM40 396 CLCN6 1 2020 NP_068503.1 3 1211 AAGCGCACCCTG - A C- 3 B c c
TCGTTCAGTGAC TG TGTCACTGAGTGA AG TGC
GTCATTCT AC GCAGTGACTTGCT TC ACG
T G CC
GAM40 396 CLCN6 1 2020 NP_068504.1 3 1211 AAGCGCACCCTG - A C- 3 B c c
TCGTTCAGTGAC TG TGTCACTGAGTGA AG TGC
GTCATTCT AC GCAGTGACTTGCT TC ACG
T G CC
GAM40 396 CLCN6 1 2020 NP_068505.1 3 1211 AAGCGCACCCTG - A C- 3 B c c
TCGTTCAGTGAC TG TGTCACTGAGTGA AG TGC
GTCATTCT AC GCAGTGACTTGCT TC ACG
T G CC
GAM40 396 CXCR4 1 7288 NP_003458.1 3 6 GTCTTCAAGTTT CA - G 3 B c c
TCACTCCAGCTA TGTGT CTG AGTGAAAGCT
CACAGATG ACACA GAC TCACTTTTGA
TC C A
GAM40 396 CYP19A1 1 20107 NP_000094.2 3 110 TCCTCACAGTGA T AAA 3 B c c
ACACTCAGTGGC TG GTCACTGAGTG GCTG
CCATGGCA AC CGGTGACTCAC TGAC
C AAG
GAM40 396 CYP19A1 1 20107 NP_112503.1 3 110 TCCTCACAGTGA T AAA 3 B c c
ACACTCAGTGGC TG GTCACTGAGTG GCTG
CCATGGCA AC CGGTGACTCAC TGAC
C AAG
GAM40 396 DKFZp54 1 18002 NP_061175.1 3 8 TTTCCCCCAGTT T G G 3 B c c
7G183 TTGGTCTGTGAC TGTGTCAC GA T AAAGCTG
ACATTTGG ACACAGTG CT G TTTTGAC
T - G

GAM40 396 DMD 1 16644 NP_004004.1 5 978 TACTCAGACTGT - A - 3 B c c
TACTCTGGTGAC TGTGTCACT GAGTGA AG CTG
ACAACCTG ACACAGTGG CTCATT TC GAC
T G A
GAM40 396 DMD 1 16644 NP_004011.1 5 978 TACTCAGACTGT - A - 3 B c c
TACTCTGGTGAC TGTGTCACT GAGTGA AG CTG
ACAACCTG ACACAGTGG CTCATT TC GAC
T G A
GAM40 396 DMD 1 16644 NP_004012.1 5 978 TACTCAGACTGT - A - 3 B c c
TACTCTGGTGAC TGTGTCACT GAGTGA AG CTG
ACAACCTG ACACAGTGG CTCATT TC GAC
T G A
GAM40 396 DMD 1 16644 NP_004013.1 5 978 TACTCAGACTGT - A - 3 B c c
TACTCTGGTGAC TGTGTCACT GAGTGA AG CTG
ACAACCTG ACACAGTGG CTCATT TC GAC
T G A
GAM40 396 DMD 1 16644 NP_004014.1 5 978 TACTCAGACTGT - A - 3 B c c
TACTCTGGTGAC TGTGTCACT GAGTGA AG CTG
ACAACCTG ACACAGTGG CTCATT TC GAC
T G A
GAM40 396 DPM2 1 18873 NP_003854.1 3 431 CCAAGGCAGCTT C-- T 3 B b b
TCCTTACCCTGA TGTGTCA TGAG GAAAGCTGC
CACAGCCC ACACAGT ATTC CTTTCGACG
CCC -
GAM40 396 DPM2 1 18873 NP_689903.1 3 1257 CCAAGGCAGCTT C-- T 3 B b b
TCCTTACCCTGA TGTGTCA TGAG GAAAGCTGC
CACAGCCC ACACAGT ATTC CTTTCGACG
CCC -
GAM40 396 DT1P1A1 1 3408 NP_477511.1 3 400 GCAGCAGCAGCA G AAA 3 B c c

0 GTACTCAGTGAT T TGTCACTGAGTG GCTGC
AGGGGGCT G ATAGTGACTCAT CGACG
G GA-
GAM40 396 ELF5 1 16375 NP_001413.1 5 106 CACGGTAATGTT GA ---- 3 B c c
GGACTCGGTGAC TGTGTCACTGAGT AA GCTG
ACACAGCA ACACAGTGGCTCA TT TGGC
GG GTAA
GAM40 396 EMP1 1 8730 NP_001414.1 3 286 TGGCCTCCAGCT TGAA 3 B c c
GTTCTTAGTGAC TGTGTCACTGAG AGCTG
ACACACTG ACACAGTGATTC TCGAC
TTG-
GAM40 396 EPO 1 3988 NP_000790.1 3 265 AGAGAGCAGCTT G A G- 3 B c c
TAAACTCAGGGA T TGTC CTGAGT AAAGCTGC
CAGAGCCA A ACAG GACTCA TTTCGACG
G G AA
GAM40 396 FAT3 1 4550 XP_061871.5 3 1980 TCTGTGCATTAT AC AGC 3 B c c
TCACTCAGACAT TGTGTC TGAGTGAA TGC
ATTTTTAG ATACAG ACTCACTT ACG
-- ATT
GAM40 396 FBXL7 1 13859 NP_036436.1 3 1084 CATCAGTTGCTT TGT- T 3 B c c

TTACTCAGTGTT TG CACTGAGTGAAAGC GC
TTCAAATA AC GTGACTCATTTTCG TG
TTTT T

GAM40 3960 FLJ1280 1 1742 NP_075054.1 3 842 ACCACAGAGCTT T TGA G 3 B c c
GCCCTCAGTGAC TG GTCACTGAG AAGCT
CAAATAAT AC CAGTGACTC TTCGA
- CCG G

GAM40 3965 FLJ1287 1 5414 NP_078820.1 3 963 CCGTCGCAGCTT T - TG - -- 3 B c c
TGACATCTTGGT TG GT CAC AG TG AAAGCTGC
GTACTCAT AC CA GTG TC AC TTTCGACG
T T GT T AG

GAM40 3964 FLJ1315 1 14841 NP_078874.1 3 1133 CCCCAGCAGCTT G A AGT 3 B c c
TCCCAGAGAGGC TGT TC CTG GAAAGCTGC
AGAGGGGC ACG AG GAC CTTTCGACG
G A C--

GAM40 3962 FLJ1408 1 6617 NP_079300.1 3 1941 GTGACTCAGTTG -- GAA 3 B c c
AAACTCAGTGTT TGTGT CACTGAGT AGCTG
GCATACAT ATACG GTGACTCA TTGAC
TT AAG

GAM40 3963 FLJ1475 1 17383 NP_115947.1 5 38 ATGTAGCTGATG CA A--- 3 B c c
TCACTCAGGAGC TGTGT CTGAGTGA AGCTGC
ACGAGCGA GCACG GACTCACT TCGATG
AG GTAG

GAM40 3963 FLJ2283 1 18402 NP_073748.1 3 1361 CAATTGCAGCTT CA A 3 B c c
TATTCAGAAATA TGTGT CTGAGTGAA GCTGC
TAAAAGTG ATATA GACTTATTT CGACG
AA -

GAM40 3966 FLJ2597 1 11913 NP_777603.1 5 295 ACTCCGCAGCTT G -- 3 B c c
TCGGCCTCGGTG TGT TCACTGAG TGAAAGCTGC
AGCGGGTG GCG AGTGGCTC GCTTTCGACG
- CG

GAM40 3960 FLJ3231 1 2295 NP_689549.1 3 151 ACCCCCAGCTTT -- TG T 3 B c c
TCTTGGTGTGAC TGTGTC AC AG GAAAGCTG
ACAAAGGT ACACAG TG TC TTTTCGAC
TG GT -

GAM40 3961 FLJ3877 2 10364 NP_775782.1 3 123 GTGCTCCAGCTT T-------- AGT 3 B c c
TCCAGTGACATG GTGTCACTG GAAAGCTG
TGACGGCG TACAGTGAC CTTTCGAC
GCGGCAGTG ---

GAM40 3961 FLJ3877 2 16753 NP_775782.1 3 123 GATGTGCTCCAG T----- AGT 3 B c c
CTTTCCAGTGAC GTGTCACTG GAAAGCTG
ATGTGACG TACAGTGAC CTTTCGAC
GCAGTG ---

GAM40 3969 FLJ3924 1 17581 NP_775935.1 3 454 TGTGGGCAGCTT AG GA 3 B c c
CTGAGTGGTGAC TGTGTCACTG T AAGCTGC
ACAGCAAG ACACAGTGGT G TTCGACG
GA TC

GAM40 396 FLJ4043 1 5127 NP_848596.1 3 806 ATAACTCAGCTT CA AG 3 B c c
4 TCAACAGCCATA TGTGT CTG TGAAAGCTG
CATCCAAA ACATA GAC ACTTTCGAC
CC A-
GAM40 396 IL1R1 1 6956 NP_000868.1 3 2334 AGGGCCTAGCTT CTG 3 B b b
TCATTTGACACA TGTGTCA AGTGAAAGCTG
CAGACTAC ACACAGT TTACTTTCGAT

GAM40 396 IRF4 1 18288 NP_002451.1 3 2585 AGAATTTAGTTT G A 3 B c c
GTACTCAGTGGA TGT TCACTGAGTG AAGCTG
CAGTGCTG ACA GGTGACTCAT TTTGAT
- G
GAM40 396 IRS3L 1 11000 XP_295210.1 3 1561 ACCCAGCACCCA --- AAA 3 B c c
AGGTTCAGTGAC TGTGTCACTGAG TG GCTG
ACAGGGTG ACACAGTGACTT AC CGAC
GGA CCA
GAM40 396 ITGA10 1 19590 NP_003628.1 3 56 CCCTGGCAGCTT -- A - T 3 B c c
TCTTCAAGAGAC TGT GTC CT GAG GAAAGCTGC
TTGCATAA ACG CAG GA CTT CTTTCGACG
TT A A -
GAM40 396 KAL1 1 4267 NP_000207.1 3 1867 GTTTTGCAGCTT C GA - 3 B c c
TGTACAAGTAAC TGTGT ACT GTG AAAGCTGC
ATAAATTG ATACA TGA CAT TTTCGACG
A A- G
GAM40 396 KCNAB2 1 13392 NP_003627.1 3 305 ACCACCCAGCTT TCA AGT 3 B c
c
TCTCCCAGCCAC TGTG CTG GAAAGCTG
AGCCAAGA ACAC GAC CTTTCGAC
C-- CCT
GAM40 396 KCNAB2 1 13392 NP_742128.1 3 305 ACCACCCAGCTT TCA AGT 3 B c
c
TCTCCCAGCCAC TGTG CTG GAAAGCTG
AGCCAAGA ACAC GAC CTTTCGAC
C-- CCT
GAM40 396 KIAA021 1 13419 NP_055550.1 3 294 TTGGGGCAGCTT C AGT 3 B c c
5 TCCGGTTATATA TGTGT ACTG GAAAGCTGC
ACACATTG ATATA TGGC CTTTCGACG
T ---
GAM40 396 KIAA023 1 7703 NP_056103.2 3 348 TCCAGCCCACTG G AAA---- 3 B c c
9 CCACTGGGTGAC TGTGTCACT AGTG GCTG
ACAGACTG ACACAGTGG TCAC CGAC
G CGTCACC
GAM40 396 KIAA032 1 1236 XP_034819.1 3 2448 GGGGAGCAGCTT T A --- 3 B c c
6 TTGGGGCTCAGA TG GTC CTGAGT GAAAGCTGC
GGCCAGTC AC CGG GACTCG TTTTCGACG
- A GGG
GAM40 396 KIAA053 1 6434 XP_049349.8 3 3556 CATGATACATCT - T C 3 B c c
4 TTTCTCAGTGAA TGTGT CACTGAG GAAAG TG
CATAAAAC ATACA GTGACTC TTTTC AC
A - T

GAM40 396 KIAA079 1 1060 XP_087353.4 3 396 AGCATGGTACTT GTCA C 3 B c c
4 TCACTCAGCTTA TGT CTGAGTGAAAG TGC
ACATGCAG ACA GACTCACTTTC ATG
ATTC -
GAM40 396 KIAA115 1 14430 XP_051093.2 3 3512 GGTTCTCAGCTT T A - T 3 B c c
7 TCCTTAAGCGAC TG GTC CT GAG GAAAGCTG
CCAGCAGC AC CAG GA TTC CTTTCGAC
C C A -
GAM40 396 KIAA146 1 4325 XP_051160.2 3 468 ACTACTCAGCTT TC--- T 3 B c c
3 TCTTTCAGTCAA TGTG ACTGAG GAAAGCTG
CCCATAAG ATAC TGACTT CTTTCGAC
CCAAC T
GAM40 396 KIAA172 1 4832 XP_114418.2 3 1283 GCTGCTCAGCTT G A GT 3 B c c
9 TCTCAGGGAAGC TGT TC CTGA GAAAGCTG
AACTCCAG ACG AG GACT CTTTCGAC
A G --
GAM40 396 KIAA193 1 19854 XP_087672.1 3 452 AAATACAGCCTG TG AA- 3 B c c
5 TCACTGTGTGAC TGTGTCAC AGTGA GCTG
ACAGATTG ACACAGTG TCACT CGAC
TG GTC
GAM40 396 KIAA200 1 9738 XP_291322.1 3 1233 GGCCTGCTGCTG - GAA T 3 B c c
1 TGCTTCAGTGAC TGTGTCACTGA GT AGC GC
ACAGTAAA ACACAGTGACT CG TCG CG
T TG- T
GAM40 396 KLF12 1 8149 NP_057369.1 3 139 TGTCAGCAGCTT T-- - - - 3 B c c
TTCATTCAGCTG GTGT CA CTGAGTGAAA GCTGC
AATGCTCT CGTA GT GACTTACTTT CGACG
TCT A C T
GAM40 396 KLHL3 1 3437 NP_059111.1 3 2629 TGAATGCAGCTT A G 3 B b b
TGCCAGTGGCAT TGTGTCACTG GT AAAGCTGC
ATCTGTCA ATACGGTGAC CG TTTCGACG
- -
GAM40 396 KLHL6 1 5266 NP_569713.1 3 3492 TATAAATAGCCA G AAA 3 B c c
ACACTCAGTGAA TGT TCACTGAGTG GCTG
CAAAATCC ACA AGTGACTCAC CGAT
- AAC
GAM40 396 LDB3 1 3058 XP_084376.6 3 316 AACAAGCAGCTT A GAGT 3 B c c
TCCCAAAGCGAT TGTGTC CT GAAAGCTGC
ACACTTGC ACATAG GA CTTTCGACG
C AACC
GAM40 396 Link-GE 1 576 NP_057423.1 3 1772 GCCCTGCAGCTT TG GA G 3 B c c
FII TAACAGAGTGAA TG TCACT GT AAAGCTGC
CCATGTGT AC AGTGA CA TTTCGACG
CA GA A
GAM40 396 LOC1160 1 16127 XP_057296.1 3 262 GGTTTGCAGTTT TC - 3 B c c
64 TCACTCAAGTTT TGTG ACT GAGTGAAAGCTGC
TGCATGAA ACGT TGA CTCACTTTTGACG
TT A
GAM40 396 LOC1306 1 14210 XP_059461.1 5 342 GCACAGCCTCTT T CA --- 3 B c c

12 TCACTCAGAAGC TG GT CTGAGTGAAA GCTG
TCAGGTCG AC CG GACTCACTTT CGAC
T AA CTC
GAM40 396 LOC1339 1 2660 XP_059674.1 5 227 TCTGTGCAGCTT T - AG 3 B c c
26 TCGAGCGGTAGA TG GTC ACTG TGAAAGCTGC
CTCACCCT AC CAG TGGC GCTTTCGACG
T A GA
GAM40 396 LOC1463 1 2307 XP_091306.2 5 13 ACCGTGCAGCTT ACTGA G 3 B c
c
33 TGGCCTGGGCAC TGTGTC GT AAAGCTGC
AGACCCTG ACACGG CG TTTCGACG
GTC-- G
GAM40 396 LOC1471 1 9200 XP_085714.2 3 554 TGAGATTGGCTT -- C - 3 B c c
23 TCACTGCACTGA TGTG TCA TG AGTGAAAGCTG
GCCACAAT ACAC AGT AC TCACTTTCGGT
CG C G
GAM40 396 LOC1492 1 3643 XP_086475.1 3 902 ACTCCAGTTCAT T -- 3 B c c
71 TCACTCAGTGGC TG GTCACTGAGTGAA AGCTG
TCATCCAC AC CGGTGACTCACTT TTGAC
T AC
GAM40 396 LOC1576 1 16783 XP_088346.6 5 281 TATTCCTGAGTT T G G 3 B c c
23 TTACTCTGTGAC TGTGTCAC GAGTGAAA CT
ACATTTAA ACACAGTG CTCATTTT GA
T - G
GAM40 396 LOC1576 1 545 XP_088366.2 5 954 AGTGTTATTTTC T-- CT 3 B c c
93 TTTCTCAGTGAC TGTGTCACTGAG GAAAG GC
ACATAACA ACACAGTGACTC CTTTT TG
TTT AT
GAM40 396 LOC1589 1 14337 XP_088728.1 3 1031 GTCTGGCCTCTT TCA CT 3 B c
c
69 TCACTCAGCACA TGTG CTGAGTGAAAG GC
ATTCTTTT ACAC GACTCACTTTC CG
--- TC
GAM40 396 LOC1620 1 8480 XP_091339.2 5 241 GTGTCCAGCAGC T----- TGAA 3 B c
c
83 TACCTCAGTGAC GTGTCACTGAG AGCTGC
ACCCAGAG CACAGTGACTC TCGACG
GAGACC CA--
GAM40 396 LOC1637 1 5127 XP_089112.3 3 806 ATAACTCAGCTT CA AG 3 B c c
42 TCAACAGCCATA TGTGT CTG TGAAAGCTG
CATCCAAA ACATA GAC ACTTTCGAC
CC A-
GAM40 396 LOC1973 1 8342 XP_113869.1 3 3531 CAGACTGCAGGC TG AAAG 3 B c
c
42 CCATTTGGTGAC TGTGTCAC AGTG CTGC
ACAGGACA ACACAGTG TTAC GACG
GT CCG-
GAM40 396 LOC1973 1 9461 XP_113872.2 3 317 CTGCAGAGCAAT GT AG--- 3 B c c
58 TCCATCAGTGAC TGTGTCACTGA GAA CTGC

GCAGGAGT ACGCAGTGACT CTT GACG
AC AACGA
GAM40 396 LOC2016 1 15732 XP_117315.1 3 281 ACCTCTGTAGCT GA GAA 3 B c c
17 CCAATGAGTGAC TGTGTCACT GT AGCTGC
ACATAGTA ACACAGTGA TA TCGATG
G- ACC
GAM40 396 LOC2532 1 12568 XP_171113.3 3 814 TATAAGAAGCTT - - G 3 B c c
28 TCATATTAGTGA TG TGTCACTGA GTGAAAGCT
TGTCATCT AC GTAGTGATT TACTTTCGA
T A A
GAM40 396 LOC2535 1 17582 NP_694854.1 3 414 ATTGGACAGCTT G C GA 3 B c c
59 TCACAAGTAACA T TGT ACT GTGAAAGCTG
GGATTAGG G ACA TGA CACTTTCGAC
G A A-
GAM40 396 LOC2563 1 7091 XP_170878.1 5 35 TTTCTCCCAGTT TG A- 3 B c c
72 TGGCACTGTGAC TGTGTCAC AGTG AAGCTG
ACAGTTCA ACACAGTG TCAC TTTGAC
-- GG
GAM40 396 LOC2838 1 13171 XP_211240.1 5 178 CCCGAGAAGCTT - TGA G 3 B c c
77 CCTCTCAGTGAC TGTG TCACTGAG AAGCT
CACAATAT ACAC AGTGACTC TTCGA
C TCC A
GAM40 396 LOC2838 1 16848 XP_211250.1 3 524 GGTGAGCGAGTT CT GC 3 B c c
94 TCACTCTGATGC TGTGTCA GAGTGAAA TGC
AACAGAAA ACGTAGT CTCACTTT GCG
-- GA
GAM40 396 LOC2839 1 16848 XP_211256.1 3 524 GGTGAGCGAGTT CT GC 3 B c c
09 TCACTCTGATGC TGTGTCA GAGTGAAA TGC
AACAGAAA ACGTAGT CTCACTTT GCG
-- GA
GAM40 396 LOC2841 1 9638 XP_211362.1 3 48 GGTGGCAGCTTG GA- A 3 B c c
73 TGCCAGAGTGAC TGTGTCACT GTG AAGCTGC
ACAGGCTT ACACAGTGA CGT TTCGACG
GAC G
GAM40 396 LOC2845 1 17120 XP_209272.1 3 310 TCTATTCAGCAA G AAA 3 B c c
73 ACACTCAGTGAG TGT TCACTGAGTG GCTG
ACAACCAT ACA AGTGACTCAC CGAC
G AAA
GAM40 396 LOC2848 1 1215 XP_211671.1 5 309 ACTCGGCAGCTT CTGA G- 3 B c c
57 TGAGCCCTGGCA TGTGTCA GT AAAGCTGC
CAGCTTCG ACACGGT CG TTTCGACG
CC-- AG
GAM40 396 LOC2851 1 16376 XP_211770.1 5 248 TACCTGCAGCTT CTG TG 3 B c c

22 TTCCTGCTTGAT TGTGTCA AG AAAGCTGC
ATAGCACA ATATAGT TC TTTCGACG
TCG CT

GAM40 396 LOC2853 1 10325 XP_211876.1 3 510 GTTACTTAGCAT GAGT - 3 B c c
97 TTCTTAGGTGAC TGTGTCACT GAAA GCTG
ACAACATT ACACAGTGG CTTT CGAT
ATT- A

GAM40 396 LOC2855 1 2315 XP_211943.1 3 191 ACAGAACAGCTT TG- C - 3 B c c
82 TCTGCTCATTGA TG TCA TGAGT GAAAGCTG
ACCCAGAG AC AGT ACTCG CTTTCGAC
CCA T T

GAM40 396 LOC2857 1 6307 XP_212006.1 3 501 GCAGTTCAGCAA --- - AA- 3 B c c
33 CTCTTAAGTGAC TGTGTCACT GAGT G AGCTGC
ACAGTTCA ACACAGTGA CTCA C TTGACG
ATT A GAC

GAM40 396 LOC3176 1 13035 NP_775498.1 5 72 CAGCTCAGCTGT T - A 3 B b b
71 CATCTCAGTGAC TG GTCACTGAG TGA AGCTG
CAGTTTTT AC CAGTGACTC ACT TCGAC
- T G

GAM40 396 LOC3389 1 9478 XP_294744.1 3 300 ATTTCACAGCTT TCA A 3 B c c
09 TCACATAGCACA TGTG CTG GTGAAAGCTG
GATAACTC ACAC GAT CACTTTCGAC
--- A

GAM40 396 LOC3396 1 5510 XP_293152.2 5 51 GGTGTTCACCTT G C C 3 B c c
04 TCACTCATGAGC TGT TCA TGAGTGAAAG TG
AATGTGCC ACG AGT ACTCACTTTC AC
- - C

GAM40 396 LOC3396 1 4299 XP_295035.1 3 996 GTTAAGTACCTT - GA C 3 B c c
94 GACTCAGGTGAC TGTGTCAC TGAGT AAG TGC
ACAGCAAT ACACAGTG ACTCA TTC ATG
G G- C

GAM40 396 LOC3445 1 18874 XP_297702.2 5 37 CCAGCTCATCTT T G ----- 3 B c c
43 TGATTCAGTGAC TG GTCACTGAGT AA AGCTG
CAACATAC AC CAGTGACTTA TT TCGAC
- G TCTAC

GAM40 396 LOC3454 1 14296 XP_298768.2 5 62 TTTGCCCAGCTT ACT GT 3 B c c
22 TCTGTCTGGGGC TGTGTC GA GAAAGCTG
GCACGGAG ACGCGG CT CTTTCGAC
GGT GT

GAM40 396 LOC3518 1 19662 XP_305245.1 5 16 GGAAATTAGCTT C - 3 B c c
87 TCAATTTAGTAT TGTGT ACTGAGT GAAAGCTG
ACGGAAAG GCATA TGATTTA CTTTCGAT
- A

GAM40 396 LOC9146 1 3304 XP_038589.1 3 470 TTCATGCATGCA T G A - 3 B c c
4 TTCATCCGTGAC TGTGTCAC GA TGAA GC TGC
ACATGAGT ACACAGTG CT ACTT CG ACG
C - A T

GAM40 396 LOC9259 1 5178 NP_775739.1 3 4246 TTTTAAATGTTT G - TG 3 B c c
7 TCACTCAGATGA TGT TCA CTGAGTGAAAGC
ACAATTTG ACA AGT GACTCACTTTTG

```
                                        -  A          TA
GAM40   396   MASP1   1   18072  NP_001870.3  3  484   TGGGTCTTAGCA         G G  A          3  B  c  c
                                    TTGATCAGTGAC TGTGTCACTGA T AA GCTG
                                    ACACCTCT    ACACAGTGACT A TT CGAT
                                              - G  A
GAM40   396   MGC2048 1   5846   NP_443081.1  3  103   GCGAGCAGCGTG  -        GAAA-          3  B  c
c
        1                           GAGCTCAGTGAC TG TGTCACTGAGT    GCTGC
                                    AGCAGCAG    AC ACAGTGACTCG    CGACG
                                          G         AGGTG
GAM40   396   MGC2187 1   11186  XP_291105.1  3  397   AGCCACCAGCTA        G T  --          3  B  c  c
        4                           TTTCCTGGTGAC TGTGTCACT AG GAA  AGCTG
                                    ACAAGCTC    ACACAGTGG TC CTT  TCGAC
                                          -  -  TA
GAM40   396   MGC2677 2   2280   NP_659447.1  3  1020  CCTTTTCTGCAG  T  A     AAA          3  B  c
c
        8                           TCACTCAGGGAC TG GTC CTGAGTG   GCTGC
                                    CCAGACTT    AC CAG GACTCAC   TGACG
                                          C  G      ---
GAM40   396   MGC2677 2   19180  NP_659447.1  3  1262  TGTTCCATGCAG  T  A     AAA          3  B  c
c
        8                           TCACTCAGGGAC TG GTC CTGAGTG   GCTGC
                                    CCAGTCTC    AC CAG GACTCAC   TGACG
                                          C  G      ---
GAM40   396   MGC3101 1   756    NP_076948.1  3  1333  GCCCAGCAGCTT   TC    T--          3  B  c  c
                                    TCTCTTTCAGTC TGTG  ACTGAG   GAAAGCTGC
                                    CCATAAGG    ATAC  TGACTT   CTTTCGACG
                                          CC     TCT
GAM40   396   MGC3932 1   3154   NP_671722.1  3  1228  TACAGTTAGCTG T----    -     A        3  B  c  c
        5                           TCACTCAGCTGA     GTGTCA CTGAGTGA AGCTG
                                    CACCATGA         CACAGT GACTCACT TCGAT
                                          AGTAC     C       G
GAM40   396   NGFB    1   19589  NP_002497.1  5  129   AGGGAGCAGCTT   -  CT  GT          3  B  c  c
                                    TCTATCCTGGCC TGTG TCA  GA  GAAAGCTGC
                                    ACACTGAG    ACAC GGT  CT  CTTTCGACG
                                          C   C-  AT
GAM40   396   NLI-IF  1   12146  NP_067021.1  3  449   CCCGCCCAGCTT     A  AGT          3  B  c  c
                                    TCCCAGGGGCAC TGTGTC CTG   GAAAGCTG
                                    AGCTCTAG    ACACGG GAC   CTTTCGAC
                                          G   C--
GAM40   396   NPHP4   1   19408  NP_055917.1  3  111   CTCTGCAGCCTT T---  T-    -    -     3  B  c  c
                                    TCACTTCAGTGC    GTG  CACTGA GTGAAAG CTGC
                                    CCACCTGG        CAC  GTGACT CACTTTC GACG
                                          GGTC  CC     T      C
GAM40   396   NR0B2   1   17061  NP_068804.1  3  153   AGGAACAGCTCT T-----  CA     -     3  B  c  c
                                    TCACTCAGCCAC      GTGT  CTGAGTGAA AGCTG
                                    ACCCCACA          CACA  GACTCACTT TCGAC
                                          ACACCC    CC       C
GAM40   396   NR3C2   1   13835  NP_000892.1  3  1837  TAATCATCAGGT  TG-        AG         3  B  c  c
                                    TTACTCAGTGAA TG   TCACTGAGTGAA  CTG
```

ATCATATT AC AGTGACTCATTT GAC
TAA G-
GAM40 396 P2RY2 1 15265 NP_002555.2 3 707 GCAGGGAAGCTT CA A G 3 B c c
TCACCAGCCACA TGTGT CTG GTGAAAGCT
CAAGGGTC ACACA GAC CACTTTCGA
CC - A
GAM40 396 P2RY2 1 15265 NP_788085.1 3 707 GCAGGGAAGCTT CA A G 3 B c c
TCACCAGCCACA TGTGT CTG GTGAAAGCT
CAAGGGTC ACACA GAC CACTTTCGA
CC - A
GAM40 396 P2RY2 1 15265 NP_788086.1 3 707 GCAGGGAAGCTT CA A G 3 B c c
TCACCAGCCACA TGTGT CTG GTGAAAGCT
CAAGGGTC ACACA GAC CACTTTCGA
CC - A
GAM40 396 PAX5 1 1514 NP_057953.1 5 264 AACGTTTAGTTT T GA 3 B c c
CAGCTCAGTGAT TG GTCACTGAGT AAGCTG
CAGCTACC AC TAGTGACTCG TTTGAT
- AC
GAM40 396 PPYR1 1 4618 NP_005963.1 3 306 GCAGGCAGGGTT - AG 3 B c c
CATTCTGGTGAC TGTGTCACT GAGTGAA CTGC
ACAGCAAC ACACAGTGG CTTACTT GACG
T GG
GAM40 396 PTGS1 1 11891 NP_000953.2 3 2410 TTTATGGCTGCT G GAA T 3 B c c
GGGCTGAGTGAC TGTGTCACT AGT AGC GC
ACAAGCAC ACACAGTGA TCG TCG CG
G GG- T
GAM40 396 PTGS1 1 11891 NP_542158.1 3 2410 TTTATGGCTGCT G GAA T 3 B c c
GGGCTGAGTGAC TGTGTCACT AGT AGC GC
ACAAGCAC ACACAGTGA TCG TCG CG
G GG- T
GAM40 396 RBM7 1 651 NP_057174.1 3 114 ACAGAGCAGCTT T - GA A 3 B c c
TACAAGTTGTCA TGTG CA CT GTGAA GCTGC
CATTTCTT ACAC GT GA CATTT CGACG
T T A- -
GAM40 396 RGS5 2 7379 NP_003608.1 3 110 CCACAGCAGCTT T------ G 3 B c c
TGCTCAGTGATA GTGTCACTGAGT AAAGCTGC
CCCACATG CATAGTGACTCG TTTCGACG
GTACACC -
GAM40 396 RGS5 2 12110 NP_003608.1 3 110 CCCACAGCAGCT T----- G 3 B c c
TTGCTCAGTGAT GTGTCACTGAGT AAAGCTGC
ACCCACAT CATAGTGACTCG TTTCGACG
TACACC -
GAM40 396 RNAH 1 4545 NP_006819.1 3 161 GGCTGCAGTATT - G A 3 B c c
GACTCCAGTGAC TGTGTCACTG AGT AA GCTGC
ATAAAGTT ATACAGTGAC TCA TT TGACG
C G A
GAM40 396 RPL15 1 14209 NP_002939.2 3 358 AACCTGCAGCTT - GAGTG 3 B c c

TATCGGAGTGAT TGT GTCACT AAAGCTGC
GGCAATGC ACG TAGTGA TTTCGACG
G GGCTA

GAM40 396 SCOTIN 1 13969 NP_057563.3 3 422 GTGGCGCAGCTT TGAGT 3 B c c

TCTGTGTGATGC TGTGTCAC GAAAGCTGC
AGATGTGT ACGTAGTG CTTTCGACG
TGT--

GAM40 396 SEC15L 1 870 NP_061926.2 3 31 CTCACATGGCTT T----- A 3 B c c
GCACTCAGTGAC GTGTCACTGAGTG AAGCTG
ACCAAATC CACAGTGACTCAC TTCGGT
CTAAAC G

GAM40 396 SFRP1 1 597 NP_003003.2 3 2333 CCATAGCAGCTT T CT TG 3 B c c
TGTCTCTGTCAC TGTG CA GAG AAAGCTGC
ATCAGCAA ACAC GT CTC TTTCGACG
T -- TG

GAM40 396 SFXN1 1 1452 NP_073591.2 3 691 GACTGGCAGCTT C--- - 3 B c c
TTATTTCAGTAT TGTGT ACTGAG TGAAAGCTGC
TAGCACAG ACACG TGACTT ATTTTCGACG
ATTA T

GAM40 396 SLC1A5 1 6435 NP_005619.1 5 339 AACTCCCAGCTT C- AG 3 B c c
TCGGACATCTGG TGTGTCA TG TGAAAGCTG
CACACGGG ACACGGT AC GCTTTCGAC
CT AG

GAM40 396 SLC9A6 1 8100 NP_006350.1 3 1630 TCGTGGCAGCTT CTG G 3 B c c

TGACTGTTGGCA TGTGTCA AGT AAAGCTGC
TAGCCATT ATACGGT TCA TTTCGACG
TG- G

GAM40 396 SMAP-1 1 11457 NP_061141.2 3 91 CGGAAGCAGCTT -- -- G 3 B c c
TGGCTGGTGGTG TGT GTCACTG AGT AAAGCTGC
GCTGGCAT ACG CGGTGGT TCG TTTCGACG
GT GG G

GAM40 396 SPAG4 1 7992 NP_003107.1 5 76 AGCGGCGGCTTT --- - G 3 B c c
AGCGTCAGTGAC TGT GTCACTGA GT AAAGCTGC
TAGGCAGC ACG CAGTGACT CG TTTCGGCG
GAT G A

GAM40 396 TLR5 1 9677 NP_003259.2 5 101 CCGCCCAGGCTG - GAA G 3 B c c
GACTGCAGTGAC TGTGTCACTG AGT AGCT
ACAATCTC ACACAGTGAC TCA TCGG
G GG- A

GAM40 396 TOMM70A 1 14026 NP_055635.1 3 212 GTCTTGCAGCTT GT T-- 3 B c c

TTATTCCCTGTG TGT CAC GAGTGAAAGCTGC
CAACAAAA ACA GTG CTTATTTTCGACG
AC TCC

GAM40 396 TRADD 1 9944 NP_003780.1 3 309 GCCCTTACAGTT G C G 3 B c c
TCACTCATGAAG TGT TCA TGAGTGAAA CTG
CACCTTGA ACG AGT ACTCACTTT GAC
A - -

GAM40 396 TRADD 1 9944 NP_700474.1 3 309 GCCCTTACAGTT G C G 3 B c c
TCACTCATGAAG TGT TCA TGAGTGAAA CTG
CACCTTGA ACG AGT ACTCACTTT GAC
A - -
GAM40 396 WHN 1 9862 NP_003584.2 3 711 TCTGTCCAGCTT GAGT- 3 B c c
TCCCCAGGGTGA TGTGTCACT GAAAGCTG
CATACAGA ATACAGTGG CTTTCGAC
GACCC
GAM40 396 YWHAG 1 19676 NP_036611.2 3 2739 ATCTTTAGCAGT G T G 3 B c c
TTCCTCAGTGAT T TGTCACTGAG GAAA CTGC
GGAATATC A GTAGTGACTC CTTT GACG
G - -
GAM40 396 ZNF408 1 14053 NP_079017.1 3 23 CACCTGCAGCTT CT-- TG 3 B c c
TGCCTTTTGCTG TGTGTCA GAG AAAGCTGC
ACACAGCT ACACAGT TTC TTTCGACG
CGTT CG
GAM41 215 AF3P21 1 6543 NM_016453.1 3 GGTCTGGGAGCT - C GAA 3 C c c
GTTCTGGGGCA TGTCTCAGG CA CT TCAGACC
ACGGGGTCT GT GA GGTCTGG
T C G--
GAM41 215 AP2A1 1 16866 NM_014203.2 3 GGTTTGGGGGAT T - GAA 3 C c c
GCCTGGGAC GTCTCAGGCA CCT TCAGACC
CAGGGTCCGT GGG GGTTTGG
- A ---
GAM41 215 CAPN1 1 3659 NM_005186.2 3 GGTTATGGGGGT A GAA - 3 C c c
GCCAGAGGCA TGTCTC GGCACCT TCA GACC
ACGGAG CCGTGGG GGT TTGG
A --- A
GAM41 215 CASQ1 1 4693 NM_001231.2 3 GGTCTATATGCT G A- C- 3 C c c
GGGTGCTGAGAC TGTCTCAG CACCTG AT AGACC
A ACAGAGTC GTGGGT TA TCTGG
- CG TA
GAM41 215 CCR5 1 8238 NM_000579.1 3 GGTCTGGTTTGC C AC -- 3 C c c
AGAGCTTGAACA TGT TCAGGC CTG AATCAGACC
ACA AGTTCG GAC TTGGTCTGG
- A- GT
GAM41 215 FLJ2281 1 2530 NM_024916.1 3 GGTTCCTGAGGG - GAA -- 3 C c c
4 GTGATTTGGGAC TGTCTCAGG CACCT TCAG ACC
A ACAGGGTTT GTGGG AGTC TGG
A G-- CT
GAM41 215 IL11 1 20064 NM_000641.2 3 GGTCTGAGCCTT T CCTGAA 3 C c c
GCCTGGGGC GTCTCAGGCA TCAGACC
CGGGGTCCGT AGTCTGG
- TCCG--
GAM41 215 LOC1439 1 15225 3 GGTCTGATTTTG T - CCT 3 C c c
15 CCCTGGGGC GTCTCAGG CA GAATCAGACC
CGGGGTCC GT TTTAGTCTGG
- C ---
GAM41 215 LOC1517 1 17948 XM_087279.6 5 GGTCTGGTTCAC AGGCACC 3 C c
c

20 CAATGGGGACA TGTCTC TGAATCAGACC
ACAGGG ACTTGGTCTGG
GTAACC-

GAM41 215 LOC1964 1 1265 NM_173542.1 3 GGTTTGGGAAGG C GAA 3 C c c
63 TCCTGGGGCA TGTCTCAGG ACCT TCAGACC
ACGGGGTCC TGGA GGTTTGG
- AG-

GAM41 215 LOC2002 1 14178 XM_114152.1 3 GGTCTAGAGGGG A GAA - 3 C c c
05 TCTGGGGCA TGTCTCAGGC CCT TC AGACC
ACGGGGTCTG GGG AG TCTGG
- --- A

GAM41 215 PITX3 1 8284 NM_005029.3 3 GGTCTGAAAGGG T GAA 3 C c c
GTGTTTGGGCA TGTC CAGGCACCT TCAGACC
ACGG GTTTGTGGG AGTCTGG
- GAA

GAM41 215 POLA2 1 16991 NM_002689.2 5 GGTCTGAGGTCT T CCT A- 3 C c c
TGCTTGGGCCA TG CTCAGGCA GA TCAGACC
AC GGGTTCGT CT AGTCTGG
C T-- GG

GAM41 215 SSH2 1 8354 XM_290798.1 3 GGTTTGGTTTCC CAC -- 3 C c c
AGACCTGAGGCA TGTCTCAGG CTG AATCAGACC
ACGGAGTCC GAC TTGGTTTGG
A-- CT

GAM41 215 TRIAD3 1 11583 NM_019011.3 3 GGTTTCTAGCGG T AATC 3 C c c
TGCCTGAGGCA TGTCTCAGGCACC G AGACC
ACGGAGTCCGTGG C TTTGG
- GATC

GAM42 224 CDR2 1 4901 XM_071866.2 3 CTGGAGAAGTAG C - T G 3 C b b
GCCTGGAGTT AACTC AGGC CTA CTTCTCCAG
TTGAG TCCG GAT GAAGAGGTC
- G - -

GAM42 224 CDT1 1 1061 NM_030928.2 3 CTGGAGAGGTGA C C TA 3 C c c
TCCTGAATTG CAA TCAGG TC GCTTCTCCAG
GTT AGTCC AG TGGAGAGGTC
A T --

GAM42 224 FMR2 1 17857 NM_002025.1 3 CTGGAGAACATG G TAGC 3 C c c
AGCTGAGTTG CAACTCAG CTC TTCTCCAG
GTTGAGTC GAG AAGAGGTC
- TAC-

GAM42 224 FUT1 1 10946 NM_000148.1 3 CTGGAAAAGCTG CAG C 3 C c c
GGGTAGTTG CAACT GCTCTAGCTT TCCAG
GTTGA TGGGGTCGAA AGGTC
--- A

GAM42 224 GADD45A 1 510 NM_001924.2 5 GGAGAGCGCCAG A A - AG 3 C c c
GGCCTGAGCTG CA CTCAGGCTCT GC TTCTCC
GT GAGTCCGGGA CG GAGAGG
C C C --

GAM42 224 HCGIV.9 1 5331 NM_018985.1 3 CTGGAAAAGTTG CA TC C 3 C c c
TGCCTGAGT ACTCAGGC TAGCTT TCCAG
TGAGTCCG GTTGAA AGGTC

```
                                        --      T-     A
GAM42   224   LOC1238 1  13097 XM_058742.3  5       CTGGAGGCCCAA       GCTCTA  TT          3  C  c
c
          72                          ACTGAGTTG   CAACTCAG     GC  CTCCAG
                                            GTTGAGTC     CG  GAGGTC
                                               AAACC-  --
GAM42   224   LOC1584 1  11756 NM_139246.2  3       CTGAGGGATAGA CAA        GCT   -       3  C  c
c
          27                          GCCTGAG       CTCAGGCTCTA   TCTC CAG
                                            GAGTCCGAGAT   AGGG GTC
                                            ---         ---    A
GAM42   224   LOC1972 1  3966  XM_113839.4  3       CTGGGAACCAGT  A      T  AGC   T        3  C  c  c

          01                          GCCTGAGTCA   C ACTCAGGC CT   TTC CCAG
                                            A TGAGTCCG GA   AAG GGTC
                                             C       T  CC-   -
GAM42   224   LOC2032 1  4902  XM_038391.6  3       CTGGAGAAGCTA  A  T     C             3  C  b  b
          02                          CAGCCTGGTCA  C AC CAGGCT TAGCTTCTCCAG
                                            A TG GTCCGA ATCGAAGAGGTC
                                             C  -     C
GAM42   224   LOC2568 1  18604          5       CTGGAGAACCGG C        CTAGC           3  C  c  c
          30                          CCTGGGTT     AACTCAGGCT    TTCTCCAG
                                            TTGGGTCCGG    AAGAGGTC
                                            -         CC---
GAM42   224   POFUT1  1  7440  NM_015352.1  3       CTGGAGGGACCA  A        AGC          3  C  c  c
                                      GAGTCTGAGCTG CA CTCAGGCTCT   TTCTCCAG
                                            GT GAGTCTGAGA   GGGAGGTC
                                             C        CCA
GAM42   224   SMARCD1 1  9206  NM_139071.1  3       CTGGAGAATAGC       -  CTAGC          3  C  c
c
                                      GCTGAGTTG   CAACTCAG GCT    TTCTCCAG
                                            GTTGAGTC CGA    AAGAGGTC
                                               G  T----
GAM43   234   MYLE    1  19493 NM_014015.2  3       GATTCTCGCTCC    C  ACA  CT          3  C  c  c
                                      TTCATTTCA   TGAAA GA   AGG  TGAGAATC
                                            ACTTT CT   TCC  GCTCTTAG
                                               A  ---  TC
GAM43   234   NRF     1  18272 NM_017544.1  3       TCTCACCTTGTT    C      CT    ATC      3  C  c  c
                                      CATTTCA     TGAAA GAACAAGG  TGAGA
                                            ACTTT CTTGTTCC  ACTCT
                                               A       --     ---
GAM44   287   ACE     1  2830  NP_690044.1  3  141  CGTGGGCCGCCA        T  TGT    -        1  A  c  c
                                      GATCTGCACCAC AAGGTGGTG CA   TTTGG GG
                                      CTTCGAGC    TTCCACCAC GT   AGACC CC
                                               -  CT-    G
GAM44   287   ANP32E  2  11390 NP_112182.1  3  316  CCCATAATTAAA     GT       ------       1  A  c  c
                                      ACATGATCACTT AAGGTG  GTCATGTTT     TGGG
                                      TTACACAG    TTTCAC  TAGTACAAA     ACCC
                                               --        ATTAAT
GAM44   287   ANP32E  2  16172 NP_112182.1  3  1737  GGAATCCCCAAA     G   ATG           1  A  c
c
```

AAGATAACATTT AAGGTG TGTC TTTTGGGG
TTCTTCTG TTTTAC ATAG AAAACCCC
A A--

GAM44 287 AP3M2 1 17766 NP_006794.1 3 841 TTCTAACCCAAA T TCA----- 1 A c c
ACAGTTCTACTC AAGG GGTG TGTTTTGGG
ACTTCCTT TTCC TCAC ACAAAACCC
T TCATCTTG

GAM44 2872 ARHGEF1 1 6308 NP_056128.1 3 2806 GTAATTTAACAT - TT- 1 A c c
CATGATTACCAC AAGGTGGTG TCATG TTGGG
CTTCGAAG TTCCACCAT AGTAC AATTT
T TAC

GAM44 287 ASPH 1 11418 NP_064549.1 3 496 CTCCCCAGGCTC T-- T- 1 A c c
ATGTGCCACCAC AAGGTGGTG CATG TTTGGGG
CTTCCCTC TTCCACCAC GTAC GGACCCC
CGT TC

GAM44 287 ASPH 1 11418 NP_115856.1 3 496 CTCCCCAGGCTC T-- T- 1 A c c
ATGTGCCACCAC AAGGTGGTG CATG TTTGGGG
CTTCCCTC TTCCACCAC GTAC GGACCCC
CGT TC

GAM44 287 ATP1B3 1 9521 NP_001670.1 3 96 TCCATTCTAGAA G - 1 A c c
TTATGAGACCAC AAGGTGGT TCATG TTTTGGGG
CTTGGAGA TTCCACCA AGTAT AAGATCTT
G T

GAM44 287 ATP2C1 1 9108 NP_055197.1 3 290 TTAAAAAGGCAA G T GG 1 A c c
AACCTGAACCAC AAGGTGGT TCA GTTTTG
CTTCTGCA TTCCACCA AGT CAAAAC
- C GG

GAM44 287 BACH2 1 13836 NP_068585.1 3 5262 TGAGCCATTCAA CA 1 A c c
GGCAAGCACCAC AAGGTGGTGT TGTTTTGGG
CTTTGCTA TTCCACCACG ACGGAACTT
A-

GAM44 287 BHC80 1 7380 NP_057705.2 5 176 AGTTTCCCCAAA ---- T- AT 1 A c c
ATTGGACTTCTC AAGGT GG GTC GTTTTGGGG
AGAACCTT TTCCA TC CAG TAAAACCCC
AGAC TT GT

GAM44 2874 C14orf2 1 831 NP_775878.1 3 1824 AATAGTTCTAAA -- GT- 1 A c c
ACATGCTAACCT AAGGT GGT CATGTTTTGGGG
GACCTTTT TTCCA CCA GTACAAAATCTT
GT ATC

GAM44 2879 C14orf3 1 10766 NP_777638.1 3 91 TTATTGCTTAAA TG G- 1 A c c
ACATGAAGACTG AAGG GT TCATGTTTTGGG
CTTTCTTT TTTC CA AGTACAAAATTC
GT GA

GAM44 2878 C14orf7 1 11042 XP_290629.1 3 357 ATACCCAACAGA TGGT -- 1 A c c
ACATGACTGTTT AAGG GTCATGTTTTG GGG
CTTTGAGG TTCT CAGTACAAGAC CCC
TTGT AA

GAM44 2875 C21orf5 1 15819 NP_060303.1 5 83 GACCTCCCTTGC - TTTT 1 A c c
CATGATAACCAC AAGGTGGT GTCATG GGGG
CTTCGCAG TTCCACCA TAGTAC TCCC

A CGT-
GAM44 287 C5orf4 2 2131 NP_115761.1 3 1200 CCACCTCCATGG G T -- 1 A c c
GACTGACACCAT AA GTGGTGTCA GTTT TGGGG
GTTCAAGC TT TACCACAGT CAGG ACCTC
G - GT
GAM44 287 C5orf4 2 16902 NP_057432.1 5 200 ACCATCTCCCAC - TTT 1 A c c
TGTGGCTACCAC AAGGTGGT GTCATG TGGGG
CTTCCCTT TTCCACCA CGGTGT ACCCT
T C--
GAM44 287 C5orf4 2 16902 NP_115761.1 3 306 ACCATCTCCCAC - TTT 1 A c c
TGTGGCTACCAC AAGGTGGT GTCATG TGGGG
CTTCCCTT TTCCACCA CGGTGT ACCCT
T C--
GAM44 287 CASP10 1 18232 NP_116756.1 3 103 GGAAACCTCCCT CA TTT 1 A c c
TTACAGCACCAC AAGGTGGTGT TGT GGGG
CTTGCGAT TTCCACCACG ACA TCCC
-- TT-
GAM44 287 CCKBR 1 6458 NP_000722.2 3 243 TGGCCCATAGAA - --- 1 A b b
ACATGACACTGA AAGGT GGTGTCATGTTT TGGG
CCTTGGAG TTCCA TCACAGTACAAA ACCC
G GAT
GAM44 287 CCKBR 1 6458 NP_795344.1 3 243 TGGCCCATAGAA - --- 1 A b b
ACATGACACTGA AAGGT GGTGTCATGTTT TGGG
CCTTGGAG TTCCA TCACAGTACAAA ACCC
G GAT
GAM44 287 COLQ 1 9718 NP_536803.1 3 286 TGAACACCCAAA TG TCA 1 A c c
ACGCCATTGCCT AAGG GTG TGTTTTGGG
TCCGCAGA TTCC TAC GCAAAACCC
GT C--
GAM44 287 COLQ 1 9718 NP_536804.1 3 34 TGAACACCCAAA TG TCA 1 A c c
ACGCCATTGCCT AAGG GTG TGTTTTGGG
TCCGCAGA TTCC TAC GCAAAACCC
GT C--
GAM44 287 CR1 1 10491 NP_000564.1 3 822 GTCCGCCTCCCG TGT 1 A c c
GGTTGACACCAT AAGGTGGTGTCA TTTGGGG
TTTCCTGC TTTTACCACAGT GGGCCCT
T--
GAM44 287 CX3CR1 1 10405 NP_001328.1 3 444 CCCCCAGACTTT G ---- 1 A c c
ACATGACACAGC AAGGT GTGTCATGT TTTGGGG
TTTATCAC TTTCG CACAGTACA AGACCCC
A TTTC
GAM44 287 CYLD 1 11043 NP_056062.1 5 260 ATCTTAATACAA G - --- 1 A c c
CATGGACACCAC AA GTGGTGTC ATGTT TTGGGG
GTTGCTGA TT CACCACAG TACAA AATTCT
G G CAT
GAM44 287 DHCR24 1 14070 NP_055577.1 3 142 CCCACCCTGACA CAT - TG 1 A c
c
GCCCAACACCAC AAGGTGGTGT GTT T GGG
CTTCCTCC TTCCACCACA CGA A CCC

```
                                                ACC   C GT
GAM44   287   DIRAS2 2   14097 NP_060064.2  3  71    CTCACTCCCCCA AA----    -    GT        1  A  c  c
                                AAATGACACCCA      GGTGG TGTCAT  TTTGGGG
                                CCGTCGTC          CCACC ACAGTA  AAACCCC
                                        CTGCTG    C     --
GAM44   287   DIRAS2 2   16186 NP_060064.2  3  71    CACTCCCCCAAA AA------   -    GT        1  A  c  c
                                ATGACACCCACC      GGTGG TGTCAT  TTTGGGG
                                GTCGTCAG          CCACC ACAGTA  AAACCCC
                                        GACTGCTG    C     --
GAM44   287   DKFZp54 1   2790  NP_115531.1  5  238   CACCTGCCCAAA     G   CAT--          1  A  c  c

        7I094                     ACCAAACGCAGC AAGGTG TGT    GTTTTGGG
                                ATCTTCCC    TTCTAC ACG    CAAAACCC
                                        G   CAAAC
GAM44   287   DKFZP56 1   1156  XP_166254.2  3  3186  CATCCTCAGCCC       TCAT  TTT         1  A  c
c
        4O0423                      CTCTGCCACCAC AAGGTGGTG   GT   GGGG
                                CTTAAATA    TTCCACCAC   CG   CCCC
                                        ----  TCT
GAM44   287   DKFZP58 1   12701 XP_291242.1  3  63    TCTACTTTTACA      GTCATGTT          1  A  c
c
        6F2423                      TCCCCAAACCAC AAGGTGGT      TTGGGG
                                CTTTGTCA    TTCCACCA      AACCCC
                                        --------
GAM44   287   DKFZp76 1   19365 NP_775734.1  3  2427  CTACAGTTCTGA    -         T         1  A  c  c
        1B107                       GCATGACACTAG AAGG TGGTGTCATGTTT GGG
                                CCTTCTCT    TTCC ATCACAGTACGAG CTT
                                        G         T
GAM44   287   E2F3   1   13295 NP_001940.1  3  1826  TGGGGTCAAGAC  - -     --     G     1  A  c  c
                                AGATGACACCAG AAG G TGGTGTCA  TGTTTTGG
                                CACTTTAA    TTC C ACCACAGT  ACAGAACT
                                        A G      AG      G
GAM44   287   EDG2   1   10299 NP_001392.2  3  976   ATATCACAACCC      GTCATG          1  A  c  c

                                AGAAGTAACCAC AAGGTGGT     TTTTGGG
                                CTTTAAAA    TTCCACCA     AAGACCC
                                        ATG---
GAM44   287   EDG2   1   10299 NP_476500.1  3  976   ATATCACAACCC      GTCATG          1  A  c  c

                                AGAAGTAACCAC AAGGTGGT     TTTTGGG
                                CTTTAAAA    TTCCACCA     AAGACCC
                                        ATG---
GAM44   287   FKBP2  1   11911 NP_004461.2  3  175   CTCAGCTCCAGC       TCA   T         1  A  c  c
                                ATACCCCACCAC AAGGTGGTG   TGT TTGGGG
                                CTTCTCCT    TTCCACCAC   ATA GACCTC
                                        CCC   C
GAM44   287   FKBP2  1   11911 NP_476433.1  3  175   CTCAGCTCCAGC       TCA   T         1  A  c  c
                                ATACCCCACCAC AAGGTGGTG   TGT TTGGGG
                                CTTCTCCT    TTCCACCAC   ATA GACCTC
                                        CCC   C
```

GAM44 287 FLJ1094 1 3221 NP_060750.1 3 919 GATGCTCAGACT TGT-- 1 A c c
5 CCCTGATACCAC AAGGTGGTGTCA TTTGGG
CTTTCCTG TTCCACCATAGT AGACTC
CCCTC
GAM44 287 FLJ1173 1 13471 NP_073593.1 3 319 GTCTCCCCCAAA G T--- 1 A c c
0 ACTGGCTGGCAC AAG TGGTGTCA GTTTTGGGG
CAGCTTCA TTC ACCACGGT CAAAACCCC
G CGGT
GAM44 287 FLJ1187 1 18221 NP_079393.1 3 1432 AGACCACTCAAA - - --- 1 A c c
1 ACATGCTTACAC AAG GT GGTGT CATGTTTTGGG
TAACACTT TTC CA TCACA GTACAAAACTC
A A TTC
GAM44 287 FLJ1242 1 7079 XP_098290.1 3 2103 TTTTTAAACAAA GG GG 1 A c c
5 ACATGACAACCT AAGGT TGTCATGTTTTG
TGGCTTTT TTCCA ACAGTACAAAAC
-- AA
GAM44 287 FLJ1252 1 17806 NP_079087.2 3 1844 TTTGTTTTTACT GTTT 1 A c c
9 CAATGACACCAT AAGGTGGTGTCAT TGGG
TTTTAGTT TTTTACCACAGTA ACTC

GAM44 287 FLJ1308 1 10552 NP_079229.1 3 56 CTCTGCAACAGA GG 1 A c c
9 ATATGACACCAT AAGGTGGTGTCATGTTTTG
CTTCCCAG TTCTACCACAGTATAAGAC
AA
GAM44 287 FLJ1384 1 19252 NP_079047.1 3 2176 TTCATTTCCAAA TGTC 1 A c c
8 ACATCCATCTTT AAGGTGG ATGTTTTGGGG
CTCCACTT TTCTACC TACAAAACCTT

GAM44 287 FLJ1472 1 14879 NP_116218.1 3 753 GCACCTTGTCCA ATG 1 A c c
1 AGGAGACACCAC AAGGTGGTGTC TTTTGGG
TTTCACCC TTTCACCACAG GGAACCT
A--
GAM44 287 FLJ2085 1 3537 NP_079419.1 5 425 CTCTTCCCCAAA CAT 1 A c c
6 ATCCAGCACCAC AAGGTGGTGT GTTTTGGGG
CTTGGTTA TTCCACCACG TAAAACCCC
ACC
GAM44 287 FLJ2115 1 485 NP_078878.1 3 626 TCTCAACACACA T ----- T 1 A c c
6 AAGTGCCACCAC AAGGTGGTG CA TGT TTGGGG
CTTCCCTG TTCCACCAC GT ACA AACTCT
C GAAAC C
GAM44 287 FLJ2351 1 11473 NP_079001.2 3 144 ATTTTGTTTAAA GT 1 A c c
8 ACATGATTATCT AAGGTG GTCATGTTTTGGG
TAATTCCT TTCTAT TAGTACAAAATTT
--
GAM44 287 FLJ2553 1 1034 NP_694966.2 3 2017 ATGACTTCCTCA T T 1 A b b
4 AACTGACACCAT AAGGTGGTGTCA GTTT GGGG
CTTAATTA TTCTACCACAGT CAAA CTCC
- -
GAM44 287 FLJ3053 1 1559 NP_653325.1 3 853 ACACCTAGGGAA T G --- 1 A c c
2 ACATGAGGCCCC AAGG GGT TCATGTTTT GGG

TTATGGGA TTCC CCG AGTACAAAG TCC
- G GGA

GAM44 287 FLJ3206 1 19969 NP_694578.1 3 604 CTTCCGGAACAT T---- 1 A c c
9 GTTCTTCACCAC AAGGTGGTG CATGTTTTGGGG
CTTTTGGA TTCCACCAC GTACAAGGCCTT
TTCTT

GAM44 287 FLJ3231 1 6992 NP_653310.1 3 378 TTCCCTCCACAA C G - 1 A c c
2 GAGATATACCAC AAGGTGGTGT AT TTTTG GGG
CTTTAAAA TTCCACCATA TA AGAAC CCT
- G A

GAM44 287 FLJ3404 1 5426 NP_775940.1 3 1821 AACAAACAACTC CAT T 1 A c c
7 CGGGCACACCAC AAGGTGGTGT GTTT GGGG
CTTTAAGA TTCCACCACA CGGG CCTC
--- -

GAM44 287 FLJ3963 1 7460 XP_290687.1 3 246 GCTGACCCCAAA - TGTCAT 1 A c c
9 ACCCTTCCACAC AAG GTGG GTTTTGGGG
TTTATTAG TTC CACC CAAAACCCC
A TTCC--

GAM44 287 FLJ4028 1 15256 NP_775953.1 3 503 CAGTCCCCAGGA - A 1 A c c
8 CAGGGTCACCAC AAGGTGGTG TC TGTTTTGGGG
CTTTCTCT TTCCACCAC GG ACAGGACCCC
T G

GAM44 287 FNBP4 1 13556 NP_056123.1 3 700 CCCTGTTCCAAA T TCA-- 1 A c c
ACAAAATTCACC AAGG GGTG TGTTTTGGGG
TCCTTTCT TTCC CCAC ACAAAACCTT
T TTAAA

GAM44 287 GAS8 1 6978 NP_001472.1 3 68 TAGGAACACTCG T TG 1 A c c
GGATGACACCCC AAGG GGTGTCA TTTTGGG
TTATCACA TTCC CCACAGT AGGGCTC
- --

GAM44 287 GATA2 1 2059 NP_116027.2 3 92 GCATTTCCCGAA A AT G 1 A c c
GGCCGACACCAC A GGTGGTGTC GTTTT GGG
TCCTGCCA C TCACCACAG CGGAA CCC
C C- G

GAM44 287 GPLD1 1 17577 NP_001494.2 3 736 TGTAACAAACCC G TTTT 1 A c c
CCATGACACACC AAGGTG TGTCATG GGGG
TTTATGTA TTCCAC ACAGTAC CCCC
- ----

GAM44 287 GPR68 1 4765 NP_003476.1 5 242 AGCCCTTGGTAG G T ---- 1 A c c
AGCTTGAACCAC AAGGTGGT TCA GTTTT GGGG
CTTCTATA TTCCACCA AGT CGAGA TCCC
- T TGGT

GAM44 287 GPR77 1 2326 NP_060955.1 5 40 AGGACTCCCAAA A ---- AT-- 1 A c c
ACCAGAGACACC AGGT GGTGTC GTTTTGGGG
AGGAGCCT TCCG CCACAG CAAAACCCT
- AGGA AGAC

GAM44 287 GW112 1 17202 NP_006409.2 5 251 CTCTGTTTCCCT A TTTT 1 A c c
GCCAGACACCAC AAGGTGGTGTC TG GGGG
CTTTCCCG TTCCACCACAG AC CCCT

- CGT-

GAM44 287 HAVCR1 1 1838 NP_036338.1 3 274 GTTTTCTCTCAA GTG T 1 A c c
ACATGAACACTT AAGGTG TCATGTTT GGGG
TAGAATTG TTTCAC AGTACAAA TCTC
A-- C

GAM44 287 HOXB7 1 14802 NP_004493.2 3 499 GGGAGCCCCAAA A TCAT 1 A c
c
ACCTACCACTCG A GGTGGTG GTTTTGGGG
CGTGTTCC G TCACCAT CAAAACCCC
C C---

GAM44 287 HPS3 1 10776 NP_115759.2 3 355 CTGTTGTTGGAG - G 1 A c c
ACATGACAATCA AAGGTGGT GTCATGTTTT GG
TTTTCATC TTTTACTA CAGTACAGAG TT
A G

GAM44 287 HSPC133 1 19037 NP_054887.1 3 324 CAGACCAGAAAT ---- G G 1 A c c
GACTCACACCAC AAGGTGGT GTCAT TTTTGG
CTTATAGC TTCCACCA CAGTA AAGACC
CACT - A

GAM44 287 HT001 1 2559 NP_054784.1 5 164 AGCTCTGGCCAA TCA G 1 A c c
AGCGCGTACCAC AAGGTGGTG TGTTTTGG
CTTTCATC TTCCACCAT GCGAAACC
GC- G

GAM44 287 ICK 1 4546 NP_055735.1 3 3801 AAGGTGTTTAAA GG T 1 A c c
ACATGTCAACCT AAGGT TG CATGTTTTGGG
TATGTAAG TTCCA AC GTACAAAATTT
-- T

GAM44 287 ICK 1 4546 NP_057597.2 3 3801 AAGGTGTTTAAA GG T 1 A c c
ACATGTCAACCT AAGGT TG CATGTTTTGGG
TATGTAAG TTCCA AC GTACAAAATTT
-- T

GAM44 287 IGF2R 1 11950 NP_000867.1 3 944 CTCTTCAGGTTC T--- 1 A c c
TCATGATACCAC AAGGTGGTGTCATG TTTGGGG
CTTTACTG TTCCACCATAGTAC GGACTTC
TCTT

GAM44 287 IL28RA 1 3043 NP_775088.1 3 181 GCTTCCAGCCCT G - TTT 1 A c c
ACATTGAACCAC AAGGTGGT TCA TGT GGGG
CTTCTTTC TTCCACCA AGT ACA TCCC
- T ---

GAM44 287 IMMP2L 1 2346 NP_115938.1 3 251 AATGCCCCCAAA GG T 1 A c c
ATATGCAGACCT AAGGT TG CATGTTTTGGGG
TTGGGAAT TTCCA AC GTATAAAACCCC
G- -

GAM44 287 INPP5E 1 17360 NP_063945.1 3 854 GCTGGAAGTTCA T TG 1 A c c
GGATGCCACCAC AAGGTGGTG CA TTTTGGG
CTTGAACA TTCCACCAC GT AGGACTT
C --

GAM44 287 ITK 1 1134 NP_005537.3 5 48 GAGGTGATGCCC T GT 1 A c c
AAGGTGCACCAC AAGGTGGTG CAT TTTGGG
CTTTCAAG TTCCACCAC GTG GAACCC
- --

GAM44 287 KIAA039 1 728 NP_055487.1 5 196 AGTAGCCCCAAA GG CATG 1 A c c
1 AGCAGAACCTTG AAGGT TGT TTTTGGGG
ATTTGTCT TTCCA ACG AAAACCCC
AG ----
GAM44 287 KIAA052 1 2007 XP_041964.5 3 242 CCTCCTCAGACA A AT- - 1 A c c
3 CTCAGACACCAC A GGTGGTGTC GT TTTGGGG
TCCAGGCT C TCACCACAG CA AGACTCC
C ACT C
GAM44 287 KIAA078 1 1640 XP_033113.1 3 764 GTGACCTTGAGA T- TG 1 A c c
9 TCCTGATACCAC AAGGTGGTGTCA GTTT GGG
CTTCAAGG TTCCACCATAGT TAGA TCC
CC GT
GAM44 287 KIAA098 1 12474 XP_037557.2 3 1952 CCAAAGTTAAGC -- ----- G 1 A c c
4 AAATGACACCAT AAGGTGGTGTCA TGT TTTGG
TTTCTTCC TTTTACCACAGT ACG AAACC
AA AATTG -
GAM44 287 KIAA133 1 12318 XP_048774.2 3 1597 CCTAATTTCAAA CA TT- 1 A c c
2 ACATCACCTTGC AAGGTGGTGT TG TTGGG
CACCCTGA TTCCACTACA AC AATCC
AA TTT
GAM44 287 KIAA168 1 12907 XP_290806.1 3 264 AAAACTAAAAAC CAT T G 1 A c c
4 CAAACACACCAC AAGGTGGTGT GTTT GG
CTTCCTTG TTCCACCACA CAAA CC
--- - A
GAM44 287 KIAA172 1 15787 NP_085148.1 3 589 CTGTGTGCCTCC ATG 1 A c c
0 GGAAGACACCAC AAGGTGGTGTC TTTTGGGG
CTTTCCCT TTCCACCACAG AAGGCCTC

GAM44 287 KIAA192 1 8388 XP_085210.1 5 2053 GGCACCCCAGTA A----- - T - 1 A c c
0 GCTGGCCACCAC AGGTGGTG TCA GTT TTGGGG
CTGCAGTT TCCACCAC GGT CGA GACCCC
TTGACG C - T
GAM44 287 KIAA194 1 8568 NP_803237.1 3 734 GAGAACCCAGAG A---- - - 1 A c c
6 CAATGACACCAG AGG TGGTGTCAT GTTTTGGG
TCTGGACT TCT ACCACAGTA CGAGACCC
TCAGG G A
GAM44 287 KPNA6 1 16094 NP_036448.1 3 2150 AAAATCCCACCC T-- TTT 1 A c c
ATGTTGTACCAC AAGGTGGTG CATG TGGGG
CTTGGTGA TTCCACCAT GTAC ACCCT
GTT CC-
GAM44 287 LARGE 1 14179 NP_004728.1 3 1162 ACCTGTCCAAGG - ATG 1 A c c
GTAGGCAACCAC AAGGTGGT GTC TTTTGGG
CTTCACCT TTCCACCA CGG GGAACCT
A ATG
GAM44 287 LARGE 1 14179 NP_598397.1 3 1162 ACCTGTCCAAGG - ATG 1 A c c
GTAGGCAACCAC AAGGTGGT GTC TTTTGGG
CTTCACCT TTCCACCA CGG GGAACCT
A ATG
GAM44 287 LAX 1 9263 NP_060243.1 3 548 CCAGCCTGGCCA T -- TG 1 A c c

ACATGACCCATC AAGGTGG GTCATGTT T GG
TTTACTAA TTCTACC CAGTACAA G CC
- CC GT

GAM44 287 LDOC1 1 2933 NP_036449.1 3 457 CACATCCCACCT - A TT- 1 A c c
ACAGACTACCAC AAGGTGGT GTC TGT TGGGG
CTTTCGAG TTCCACCA CAG ACA ACCCT
T - TCC

GAM44 287 LHFP 1 12839 NP_005771.1 3 79 GGAGAGGTCAAA - TC G 1 A c c
ACATCCACCTAC AAGGT GGTG ATGTTTTGG
CTTCAAAA TTCCA CCAC TACAAAACT
T C- G

GAM44 287 LIN7A 1 3012 NP_004655.1 5 50 AGCTTTCTTCTC TCAT TT 1 A c c
CACCACCACCAC AAGGTGGTG GT TGGGG
CTTCCTTC TTCCACCAC CA ACCTC
---- CC

GAM44 287 LOC1189 1 9092 NP_776152.1 3 176 TTTCCAGTAAAA G TG GG-- 1 A c
c
87 ACATGACCAGCT AAG TGG TCATGTTTT GG
TACAAAAA TTC ACC AGTACAAAA CC
G -- ATGA

GAM44 287 LOC1260 1 19476 XP_064903.7 3 766 TCTGGCCAACAA G -- G 1 A c c
17 ACATGAGCCACT AAGGTGGT TCATGTTT TGG
TTTCCCAG TTTCACCG AGTACAAA ACC
- CA G

GAM44 287 LOC1267 1 18542 NP_660300.1 3 307 AATCTTTTAAGA ---- - 1 A c c
31 TACTGACACCAA AAGGT GGTGTCA TGTTTTGGGG
ATGCCTTT TTCCG CCACAGT ATAGAATTTT
TAAA C

GAM44 287 LOC1307 1 10734 XP_059468.3 3 286 TCCAAATCAGAT ------- A T 1 A c c
52 TCCTCAAACCAC AAGGTGGT GTC TG TTTGGG
CTTTGAAA TTCCACCA TAG AC AAACCT
AACTCCT - T

GAM44 287 LOC1444 1 16849 XP_096608.1 3 546 GAGTTGCCCAAA TCAT 1 A c c
86 ACCATTACTTTT AAGGTGGTG GTTTTGGG
AAACGCTG TTTCATTAC CAAAACCC

GAM44 287 LOC1450 1 16596 XP_096714.1 3 1471 TCCTTGTTCAAA GTC 1 A c c
53 ACATTTAATCAT AAGGTGGT ATGTTTTGGG
CTTAAGCA TTCTACTA TACAAAACTT
ATT

GAM44 287 LOC1452 1 18659 XP_096730.1 3 1184 AAATGTATTTCC TCATGT 1 A c
c
16 AAATACCACCAC AAGGTGGTG TTTGGGG
CTTAAGGG TTCCACCAC AAACCTT
CAT---

GAM44 287 LOC1462 1 1810 XP_085374.2 3 799 GGATATGCTCCC CATG T 1 A c c

27 CATAAATACCAC AAGGTGGTGT TT TGGGG
CTTGCCAC TTCCACCATA AA ACCCC
---- T

GAM44 287 LOC1464 1 15013 XP_085461.6 3 171 TGGTGCCCCAAA A---- - CAT 1 A c c

43 ACTTCACAACCA AGGTGGT GT GTTTTGGGG
CCTAGACA TCCACCA CA CAAAACCCC
ACAGA A CTT

GAM44 287 LOC1467 1 16534 XP_097074.1 5 490 TCTCAGCACCAC CAT TT - 1 A c c

28 CTAACGCACCAC AAGGTGGTGT GTT GG GG
CTTGCCCT TTCCACCACG CAA CC CC
--- T- A

GAM44 287 LOC1468 1 17740 XP_096086.1 3 447 TGGGGTCAAGAC - - -- G 1 A c c

56 AGGTGACACCAG AAG G TGGTGTCA TGTTTTGG
CACTTTAA TTC C ACCACAGT ACAGAACT
A G GG G

GAM44 287 LOC1479 1 6702 XP_085974.1 3 1019 ATTATTGACCCA G GTTT 1 A c c

47 TAGTGACACCAG AAG TGGTGTCAT TGGG
TTTTGGGA TTT ACCACAGTG ACCC
G AT--

GAM44 287 LOC1484 1 18524 XP_086210.2 5 1200 ATTTTTCCCAAA -- T CA 1 A c c

90 ACAAAGCCCATG AAGGT GG GT TGTTTTGGGG
CCTTGCTC TTCCG CC CG ACAAAACCCT
TA - AA

GAM44 287 LOC1494 1 19107 NP_690048.1 5 134 CACTGCTTCAGA G A - 1 A c c

20 GACACGAACCAC AAGGTGGT TC TGTTT TGGGG
CTTGAGTG TTCCACCA AG ACAGA ACTTC
- C G

GAM44 287 LOC1512 1 1944 XP_087137.2 3 105 ATCCCAACACAA A----- CA ---- 1 A c c

42 AACAAACACCAC AGGTGGTGT TGTTTTG GGG
CTCCGATT TCCACCACA ACAAAAC CCC
TTAGCC A- ACAA

GAM44 287 LOC1516 1 12037 XP_087245.1 5 396 GGGTGTTGTCTG TCAT G 1 A c c

10 CAGAACCACCAC AAGGTGGTG GTTTTG GG
CTTGAAAG TTCCACCAC CAAGAC TC
---- G

GAM44 287 LOC1525 1 12979 XP_087483.3 3 566 TTGAGCTCAGGA G ATG- 1 A c c

19 GTTCGAGACCAC AAGGTGGT TC TTTTGGG
CTTGGGCC TTCCACCA AG AGGACTC
G CTTG

GAM44 287 LOC1530 1 16808 XP_098307.1 3 2756 TTATGGGCTTAA G- ATG 1 A c c

77 GAAGAAGACCAC AAGGTGGT TC TTTTGGG
CTTGTCTA TTCCACCA AG AGAATTC
GA A--

GAM44 287 LOC1575 1 3461 XP_098772.1 3 124 AGAGGCCCAGTA A----- T -- 1 A c c

31 GACATGCACCAC AGGTGGTG CATGTTT TGGG
CTGCTTGA TCCACCAC GTACAGA ACCC
AGTTCG - TG

GAM44 287 LOC1581 1 8554 XP_088492.2 3 12 GACCCTCAAACC GTCA --- 1 A c c
25 TACACCAACCAC AAGGTGGT TGT TTTGGGG
CTTAGATG TTCCACCA ACA AAACTCC
ACC- TCC
GAM44 287 LOC2027 1 9377 XP_117455.1 3 1328 ATCCTTAAATTT T T--- 1 A c c
81 TTATGACACCCT AAGG GGTGTCATG TTTGGGG
TTGTAATC TTTC CCACAGTAT AAATTCC
- TTTT
GAM44 287 LOC2196 1 690 XP_168585.2 5 1884 AGGCCTCAGTGA TC --- 1 A c c
12 GGCATCTACCAC AAGGTGGTG ATGTTT TGGGG
CTTCTACA TTCCACCAT TACGGA ACTCC
C- GTG
GAM44 287 LOC2197 1 5054 XP_167596.1 5 228 GCCTCAACCTGG G T ---- 1 A c c
31 ACCTGACACCAA AAG TGGTGTCA GTT TTGGGG
CTTCGCCG TTC ACCACAGT CAG AACTCC
A C GTCC
GAM44 287 LOC2199 1 15995 XP_167788.1 3 103 AGAAACAAACTC CAT T 1 A c c
14 CAGACGCACCAC AAGGTGGTGT GTTT GGGG
CTTAAGAG TTCCACCACG CAGA CCTC
--- -
GAM44 287 LOC2199 1 10767 XP_167790.1 3 279 AGAAATAATCCC CATGT 1 A c c
42 AAGTCACACCAC AAGGTGGTGT TTTGGGG
CTTCTATT TTCCACCACA GAACCCT
CT---
GAM44 287 LOC2829 1 2531 XP_210838.1 3 642 ACAAATGTTCAG TCAT 1 A c c
76 AATTCTCACCAC AAGGTGGTG GTTTTGGG
CTTCTGGT TTCCACCAC TAAGACTT
TCT-
GAM44 287 LOC2833 1 19120 XP_210969.1 3 118 AAGGAAACTCCA A----- CA 1 A c c
14 GGACAGCACCAC AGGTGGTGT TGTTTTGGGG
CTCCCCTA TCCACCACG ACAGGACCTC
ATCCCC --
GAM44 287 LOC2833 1 7249 XP_300560.1 3 1278 TCCTCTCTGCTC TCAT T 1 A c c
37 CAATACCACCAC AAGGTGGTG GT TTGGGG
CTTGTCCA TTCCACCAC CA AACCTC
---- T
GAM44 287 LOC2834 1 17012 XP_211053.1 3 427 CTATCCTCCAAA G- A- 1 A c c
84 ACAGAGGGAGCC AAGGTGGT TC TGTTTTGGGG
ATTTTATA TTTTACCG GG ACAAAACCTC
AG AG
GAM44 287 LOC2837 1 1502 XP_208835.1 3 788 GGCCGCCCCAAA G ATG 1 A c c
67 AGAGCCGCTTTG AAGGTGGT TC TTTTGGGG
ACCAGGCT TTTCGCCG AG AAAACCCC
- ---
GAM44 287 LOC2837 1 14021 XP_211196.1 5 258 AACTAACAACTC CAT T 1 A c c
76 CAGACGCACCAC AAGGTGGTGT GTTT GGGG
CTTTATGA TTCCACCACG CAGA CCTC

```
                                                  ---   -
GAM44   287   LOC2838 1  3222  XP_211218.1  5  7    TAAAACATGCTT   T     T  ---        1  A  c  c
          18                                  CAGAAGAACTGG AAGG GGTGTCA GTTT  TGGGG
                                              CACCCCTT    TTCC CCACGGT CAAG  ACTTC
                                                    -     -  AAG
GAM44   287   LOC2839 1  19383 XP_211254.1  5  124  CTCACATCCTTT     TG   G  TG        1  A  c  c
          06                                  GAAGATGACCAC AAGGTGG  TCAT TTT  GGG
                                              CTTGAAGA    TTCCACC  AGTA AAG  TCC
                                                    --  G  TT
GAM44   287   LOC2840 1  1826  XP_208982.1  3  221  GCTCAGAGACCT        A   TT         1  A  c  c
          31                                  GGCAGACACCAC AAGGTGGTGTC TGTT  GGG
                                              CTTAACCC    TTCCACCACAG ACGG  TCC
                                                    -   --
GAM44   287   LOC2844 1  17281 XP_211475.1  3  330  TCTGTGACTCCC       T-  GTTT        1  A  c  c
          62                                  AGTGTTCACCAC AAGGTGGTG  CAT   TGGGG
                                              CTTCCTGA    TTCCACCAC  GTG   ACCCT
                                                       TT  ----
GAM44   287   LOC2844 1  7971  XP_211474.1  3  161  TGCGCCCGGCAG      -  TG -        1  A  c  c
          73                                  TCTGGCGACCAC AAGGTGGT GTCA  TT TTGGG
                                              CTTGCGGG    TTCCACCA CGGT  GA GGCCC
                                                     G   CT  C
GAM44   287   LOC2845 1  13654 XP_211526.1  5  3    TGTTCTCTGCAT       TCATGTTTT        1  A  c
c
          78                                  CCCCTCACCACC AAGGTGGTG       GGGG
                                              TTCCTTTG    TTCCACCAC       CCCC
                                                       T--------
GAM44   287   LOC2846 1  1698  XP_209313.2  3  2332  CCTAAGAAATGC      GTCA     G       1  A  c
c
          71                                  CAGAACAACCAC AAGGTGGT   TGTTTTGG
                                              CTTATTTC    TTCCACCA   ACAAGACC
                                                       ----      G
GAM44   287   LOC2846 1  2205  XP_209316.1  3  79   CTCTTGCCCTCC       TC  TTTT        1  A  c  c
          84                                  CCATCCCACCAC AAGGTGGTG  ATG   GGG
                                              CTTGGAGC    TTCCACCAC  TAC   CCC
                                                       CC  CCCT
GAM44   287   LOC2847 1  19513 XP_211635.1  3  481  AAATATATCAAA     -  ---      G     1  A  c  c
          75                                  ACATGTAAACGC AAGGTGG TGT  CATGTTTTGG
                                              CCACCTTA    TTCCACC GCA  GTACAAAACT
                                                       C  AAT       A
GAM44   287   LOC2847 1  18378 XP_211639.1  3  265  ACGCGACCCAAA AA---   T   ---        1  A  c  c
          98                                  ACCAAATGACCC    GGTGG GTCAT  GTTTTGGG
                                              ACCACCAC        CCACC CAGTA  CAAAACCC
                                                     CACCA   -   AAC
GAM44   287   LOC2853 1  7404  XP_211856.1  5  1021 TCCAACCCCAAA    -  TCA          1  A  c  c
          51                                  ACACCACTGGCC AAGGT GGTG  TGTTTTGGGG
                                              TTCTTTCA    TTCCG TCAC  ACAAAACCCC
                                                       G   C--
```

GAM44 287 LOC2854 1 2002 XP_211885.1 3 1067 CCACTCCCCAAA A----- - T T 1 A c c
04 ACTGACCCCAAT AGGT GG GTCA GTTTTGGGG
CTCTGTGT TCTA CC CAGT CAAAACCCC
TGTGTC A C -
GAM44 287 LOC2854 1 5221 XP_211894.1 3 1577 ATACTCAATGAT G -- - 1 A c c
22 TGATGACACCAG AAG TGGTGTCAT GTT TTGGG
TTTTGGCT TTT ACCACAGTA TAG AACTC
G GT T
GAM44 287 LOC2854 1 18486 XP_211897.1 3 617 TTCAGAAGCCCT GTC 1 A b b
41 AAAACATACCAC AAGGTGGT ATGTTTTGGGG
CTTGGCTA TTCCACCA TACAAAATCCC

GAM44 287 LOC2855 1 3710 XP_211936.1 3 189 TTCAGCCCCAAA - TC- 1 A c c
48 ACATCTCTGCCT AAGGT GGTG ATGTTTTGGGG
GCCTTTAT TTCCG CCGT TACAAAACCCC
T CTC
GAM44 287 LOC2856 1 1605 XP_211958.1 3 435 ATGGCCAACAAA GTG -- 1 A c c
23 ACATGAAACACC AAGGTG TCATGTTTTG GG
TTGAACCC TTCCAC AGTACAAAAC CC
AA- AA
GAM44 287 LOC2857 1 16029 XP_209742.1 3 1382 CTGGGACTGTAA - - TG 1 A c c
47 ACATGACAGCCG AAG GTGG TGTCATGTTT GG
CACTTCAC TTC CGCC ACAGTACAAA TC
A G TG
GAM44 287 LOC2859 1 19964 XP_212103.1 3 2130 AGCCTCCTCACA G - T 1 A c c
46 ACATGACAGCTG AAG TGG TGTCATGTT TGGGG
GCTTAGTA TTC GTC ACAGTACAA ACTCC
G G C
GAM44 287 LOC2863 1 1540 XP_210021.1 5 27 GGCTTCCCCAAA G --- A 1 A c c
45 ATGGGCAACTTC AAG TGG TGTC TGTTTTGGGG
AGCTTAAG TTC ACT ACGG GTAAAACCCC
G TCA -
GAM44 287 LOC2864 1 17170 XP_212323.1 5 70 ACACTCCCCAAA T CATGT 1 A c
c
52 ACACCCCTTTCC AAGG GGTGT TTTGGGG
AGTTACAA TTCC CCACA AAACCCC
- -----
GAM44 287 LOC2864 1 14618 XP_208434.1 5 459 ATAGAAGACCAG - ATG G 1 A c c

84 AAAGGCGACCAC AAGGTGGT GTC TTTTGG
CTTGTGAA TTCCACCA CGG AAGACC
G A-- A
GAM44 287 LOC3385 1 10340 XP_294659.1 5 682 GCTGAAGAATAT ---- G- 1 A c c
88 GAGAGACACCAC AAGGTGGTGTC ATGTTTT GG
CTTTTAAA TTCCACCACAG TATAAGA TC
AGAG AG
GAM44 287 LOC3389 1 1502 XP_290663.1 3 788 GGCCGCCCCAAA G ATG 1 A c c

91 AGAGCCGCTTTG AAGGTGGT TC TTTTGGGG
ACCAGGCT TTTCGCCG AG AAAACCCC

```
                                                - ---
GAM44   287   LOC3389 1  1502  XP_290659.1  3  788   GGCCGCCCCAAA      G ATG          1  A  c  c

        99                                       AGAGCCGCTTTG AAGGTGGT TC  TTTTGGGG
                                                ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                                - ---
GAM44   287   LOC3391 1  7871  XP_294835.1  5  667   CAGCAGCTCCTC      T T TT         1  A  c  c
        61                                       CAGCTGCACCAC AAGGTGGTG CA GT  TGGGG
                                                CTTCAGCA    TTCCACCAC GT CG  ACCTC
                                                - - --
GAM44   287   LOC3391 1  5261  XP_290743.1  3  840   GGCTGTGTCCAC      --    TTT        1  A  c  c
        84                                       ATGAGCTACCAC AAGGTGGTG  TCATGT  GGG
                                                CTTGCGTT    TTCCACCAT  AGTACA  CCT
                                                  CG     ---
GAM44   287   LOC3394 1  19567 XP_290899.1  5  147   AGAGATTCTAAA     G T-           1  A  c  c
        37                                       ACATGTTCAGCA AAGGTG TG  CATGTTTTGGGG
                                                CTTTCTGG    TTTCAC AC  GTACAAAATCTT
                                                  G  TT
GAM44   287   LOC3404 1  2003  XP_295258.1  5  119   GCACTCCCCAAA      TGTC           1  A  c  c
        78                                       ACATCCCATTTT AAGGTGG   ATGTTTTGGGG
                                                GCAGGTGT    TTTTACC    TACAAAACCCC
                                                  C---
GAM44   287   LOC3417 1  11667 XP_296409.1  3  146   GAGTCCCAACCA A-  -   TCA     -      1  A  c  c

        44                                       CCGAAACACCAC   AGG TGGTG   TGTTTTGG GG
                                                CATCCTGT      TCC ACCAC   ACAAAGCC CC
                                                    TG  T    C--       A
GAM44   287   LOC3481 1  1502  XP_300623.1  3  788   GGCCGCCCCAAA      G ATG          1  A  c  c

        13                                       AGAGCCGCTTTG AAGGTGGT TC  TTTTGGGG
                                                ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                                - ---
GAM44   287   LOC3481 1  10142 XP_300635.1  3  789   GGCCGCCCCAAA      G ATG          1  A  c
c
        37                                       AGAGCCACTTTG AAGGTGGT TC  TTTTGGGG
                                                ACCAGGCT    TTTCACCG AG   AAAACCCC
                                                - ---
GAM44   287   LOC3481 1  1502  XP_300636.1  3  788   GGCCGCCCCAAA      G ATG          1  A  c  c

        42                                       AGAGCCGCTTTG AAGGTGGT TC  TTTTGGGG
                                                ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                                - ---
GAM44   287   LOC3481 1  18221 XP_300638.1  3  1406  AGACCACTCAAA  - -   ---        1  A  c  c
        44                                       ACATGCTTACAC AAG GT GGTGT  CATGTTTTGGG
                                                TAACACTT    TTC CA TCACA  GTACAAAACTC
                                                    A  A    TTC
GAM44   287   LOC3481 1  11592 XP_302676.1  5  655   GCTCAGTTCCAG      G A  -         1  A  c  c
        82                                       TAGCAGAACCAC AAGGTGGT TC TGTT TTGGGG
                                                CTTAGTTG    TTCCACCA AG ACGA GACCTT
                                                - -   T
```

GAM44 287 LOC3487 1 14195 XP_302883.1 3 222 CCATGGTCCCCC A----- T TT 1 A c c

68 AGCGTGCACCAC AGGTGGTG CATGT TGGGG
CTGGCCCG TCCACCAC GTGCG ACCCC
GCCCGG - --

GAM44 287 LOC3501 1 3208 XP_303867.1 5 81 TGAGCATTTAAA - GTG 1 A c c

32 ACATGAAAACAC AAG GTG TCATGTTTTGGG
TCTTGTTT TTC CAC AGTACAAAATTT
T AAA

GAM44 287 LOC3501 1 15430 XP_303825.1 5 110 CAAATAATAACA TC GG 1 A c c

47 AAGCATTACCAC AAGGTGGTG ATGTTTTG
CTTGTGTC TTCCACCAT TACGAAAC
-- AA

GAM44 287 LOC3510 1 8285 XP_304632.1 5 0 CCCCAAAACATC A--------- --- TC 1 A c c

42 ACCAGTCCCTAC AGG TGGTG ATGTTTTG
TACTTGCT TCC ACCAC TACAAAAC
TCGTTCATCA CTG --

GGG
CCC

GAM44 287 LOC5710 1 5002 NP_065114.2 3 1527 CCCTCCCCCAAA GTC -- 1 A c c

7 AGTTATAAAACC AAGGTGGT ATG TTTTGGGG
ATTTTATC TTTTACCA TAT AAAACCCC
AAA TG

GAM44 287 LOC9014 1 4641 XP_029430.1 3 766 AAGGAGAAACCT A TT 1 A c c

8 GGCAGATACCAC AAGGTGGTGTC TGTT GGG
CTTAACCA TTCCACCATAG ACGG TCC
- --

GAM44 287 LOC9297 1 14969 XP_048529.2 5 3132 CTCCAGTGTCCT G TT----- 1 A c c

3 CCATGACACCAG AAG TGGTGTCATG TTGGGG
CTTTCTCC TTC ACCACAGTAC GACCTC
G CTCCTGT

GAM44 287 LOC9334 1 17460 NP_612411.2 3 498 AGTCCCCACTCA - TT- 1 A c c

9 CGGTGACACCAC AAGGTGGTGTCAT GT TGGGG
CTTCCTGA TTCCACCACAGTG CA ACCCC
G CTC

GAM44 287 LSM10 1 918 NP_116270.1 3 142 AAGCTGGTGTCC A----- A TT 1 A c c
AACAGACACCAC AGGTGGTGTC TGT TGGG
CTGTCAAA TCCACCACAG ACA ACCT
AAACTG - --

GAM44 287 LTA 1 3286 NP_000586.2 5 133 CCTTGGTTCTCC A----- TTTT 1 A c c
CCATGACACCAC AGGTGGTGTCATG GGGG
CTGAACGT TCCACCACAGTAC CCCT
TGCAAG ----

GAM44 287 MECP2 1 689 NP_004983.1 3 7972 TGGGCTCCCAAA A--- T - -- 1 A c c
ACACCTGACAGC AGG GG TGTCA TGTTTTGGGG
CCCTCCCT TCC CC ACAGT ACAAAACCCT
TCCC - G CC

GAM44 287 MEIS1 1 12764 NP_002389.1 3 1074 TTGTCCCCATGC TCA T-- 1 A c c
AACAACCACCAC AAGGTGGTG TGTT TGGGG
CTTATACA TTCCACCAC ACAA ACCCC
CA- CGT
GAM44 287 MFAP2 1 2746 NP_002394.1 3 380 ACAGCCCCCGTG G - 1 A c c
GGCATGGACCAC AAGGTGGT TCATGTTT TGGGG
CTTTATTT TTCCACCA GGTACGGG GCCCC
- T
GAM44 287 MFAP2 1 2746 NP_059453.1 3 380 ACAGCCCCCGTG G - 1 A c c
GGCATGGACCAC AAGGTGGT TCATGTTT TGGGG
CTTTATTT TTCCACCA GGTACGGG GCCCC
- T
GAM44 287 MGC1064 1 5646 NP_116082.1 3 156 ACTCTTAACTCT GTCA - 1 A c c
6 ATAAACAACCAC AAGGTGGT TGTTT TGGGG
CTTTCACA TTCCACCA ACAAA ATCTC
---- T
GAM44 287 MGC1243 1 7109 NP_113615.1 3 191 TTTCTCCCCAAA - --- T 1 A c c
5 ACTGGTAATGCC AAGGT GGTGT CA GTTTTGGGG
AACCTTAT TTCCA CCGTA GT CAAAACCCC
A ATG -
GAM44 287 MGC1307 1 8673 NP_116078.2 3 1492 AGCCCCGATGAT C TT--- 1 A c c
1 TCGTAACACCAC AAGGTGGTGT ATG TTGGGG
CTTTCGCC TTCCACCACA TGC AGCCCC
A TTAGT
GAM44 287 MGC1751 1 16554 NP_689684.1 5 311 TTTCTCCCCAAA --- CATG 1 A c
c
5 AATACATCCTAG AAGGT GGTGT TTTTGGGG
CCTTAATG TTCCG CTACA AAAACCCC
ATC TA--
GAM44 287 MGC2306 1 2059 NP_002041.2 3 92 GCATTTCCCGAA A AT G 1 A c c
GGCCGACACCAC A GGTGGTGTC GTTTT GGG
TCCTGCCA C TCACCACAG CGGAA CCC
C C- G
GAM44 287 MGC3101 1 6021 NP_076948.1 3 561 AGCGGCCCCAAA TGTCAT 1 A c
c
ATTCCCACCTTG AAGGTGG GTTTTGGGG
ATTTCCAT TTCCACC TAAAACCCC
CT----
GAM44 287 MGC3321 1 9985 NP_722517.1 3 736 CCCACAACCAAA T GTCA G 1 A c
c
5 ACAACCCCTTTT AAGG GGT TGTTTTGG
AAAAGAGT TTCC CCA ACAAAACC
- ---- A
GAM44 287 MGC3397 1 19531 NP_699181.1 3 714 GTCCGCCCCAAA - TGTCAT 1 A c
c
4 ACCCGGCCTTGG AAGGT GG GTTTTGGGG
TCCCTGGC TTCCG CC CAAAACCCC
G ------
GAM44 287 MGC3544 1 1776 NP_694952.1 3 592 ACTGGGACCCCA A----- T T 1 A c c

0 GGCATGCACCAC AGGTGGTG CATGTTT GGGG
CTCACCAA TCCACCAC GTACGGA CCCC
AACCAC - -
GAM44 287 MOCS3 1 4326 NP_055299.1 3 857 GTTTACCAAAAT G A-- G 1 A c c
AAAGGAAACCAC AAGGTGGT TC TGTTTTGG
CTTTGTAG TTCCACCA AG ATAAAACC
A GAA A
GAM44 287 MRPL21 1 1724 NP_852616.1 5 199 CTAAAACATCCC --- ---- G 1 A c c
TGAGTTCACCAC AAGGTGGTG TCA TGTTTTGG
CTTGGCCA TTCCACCAC AGT ACAAAATC
TTG CCCT -
GAM44 287 MRPL30 1 8553 NP_660213.1 3 1016 AAGCTGACCAAA TG- G 1 A c c
ACATGGTCCCCA AAGGTGG TCATGTTTTGG
CCTTTTGG TTCCACC GGTACAAAACC
CCT A
GAM44 287 MYL9 1 1500 NP_006088.2 3 243 CTGACCCCTCCA GTCATG 1 A c c
AGGAAAGACCAC AAGGTGGT TTTTGGGG
CTTCTGGG TTCCACCA GGAACCTC
GAAA--
GAM44 287 MYL9 1 1500 NP_852667.1 3 243 CTGACCCCTCCA GTCATG 1 A c c
AGGAAAGACCAC AAGGTGGT TTTTGGGG
CTTCTGGG TTCCACCA GGAACCTC
GAAA--
GAM44 287 NCAM2 1 15637 NP_004531.1 3 1691 TACAGCAGGACA TG GG 1 A c
c
GAATATGACCAC AAGGTGG TCATGTTTTG
CTTCGTTT TTCCACC AGTATAAGAC
-- AG
GAM44 287 NEK6 1 1469 NP_055212.2 3 141 AGGTTCCCCAAA -- - ATG 1 A c c
AGGCTGCCCAGC AAGGT GGT GTC TTTTGGGG
CTTACAGC TTCCG CCG CGG AAAACCCC
AC T ---
GAM44 287 NFASC 1 8725 XP_046808.8 3 101 GACCTACCACGA TCAT - 1 A c c
AGCCACCACCAC AAGGTGGTG GTTTTG GG
CTTCAGTA TTCCACCAC CGAAGC CC
CAC- A
GAM44 287 NK4 1 19318 NP_004212.3 3 21 CTCAAAATGAGA ------ 1 A c c
TACTGACACCAC AAGGTGGTGTCA TGTTTTGGG
CTTTGCCC TTCCACCACAGT GTAAAACTC
CATAGA
GAM44 287 NP220 1 9969 NP_055312.2 5 256 TTGCCTCACATG ----- TTT 1 A c c
GTTCAACACCAC AAGGTGGTGT CATGT GGGG
CTTATACT TTCCACCACA GTACA CTCC
ACTTG ---
GAM44 287 NPTXR 1 3192 NP_055108.2 3 1979 AGATGCTTTCCA ----- TT 1 A c c
ACATGACACCTG AAGGT GGTGTCATGT TGGGG
AACATCTT TTCTA CCACAGTACA ACCTT
CAAGT --
GAM44 287 NPTXR 1 3192 NP_478058.1 3 1979 AGATGCTTTCCA ----- TT 1 A c c
ACATGACACCTG AAGGT GGTGTCATGT TGGGG

AACATCTT TTCTA CCACAGTACA ACCTT
CAAGT --
GAM44 287 P2RX5 1 4268 NP_002552.2 3 507 TACTCTCTCTCC ATGT 1 A c c
TAAAGACACCAC AAGGTGGTGTC TTTGGGG
CTTCCTGC TTCCACCACAG AAATCCT

GAM44 287 P2RX5 1 4268 NP_778255.1 3 507 TACTCTCTCTCC ATGT 1 A c c
TAAAGACACCAC AAGGTGGTGTC TTTGGGG
CTTCCTGC TTCCACCACAG AAATCCT

GAM44 287 PDE5A 1 19020 NP_246273.1 5 61 CACCCAAAGGCA GG ---- 1 A c c
ACATGACGGAAC AAGGT TGTCATGTT TTGGG
CTTGCCAA TTCCA GCAGTACAA AACCC
AG CGGA
GAM44 287 PELI2 1 7435 NP_067078.1 3 2160 ATATCCCCCAAA TG GT 1 A c c
ATGAAGTTACCT AAGGTGG TCAT TTTGGGG
TCCAAGTT TTCCATT AGTA AAACCCC
GA --
GAM44 287 PEPD 1 4327 NP_000276.1 3 202 TAATTACCCTTT A TTT 1 A c c
TGCAGGCACCAC AAGGTGGTGTC TGT GGGG
CTTTAATC TTCCACCACGG ACG TCCC
- TTT
GAM44 287 PILRB 1 5459 NP_038468.3 5 1258 CAGCAGCCCCTG CAT TTT 1 A c c
CGCCAACACCAC AAGGTGGTGT GT GGGG
CTTCTGCT TTCCACCACA CG CCCC
AC- CGT
GAM44 287 PILRB 1 5459 NP_778212.2 5 1320 CAGCAGCCCCTG CAT TTT 1 A c c
CGCCAACACCAC AAGGTGGTGT GT GGGG
CTTCTGCT TTCCACCACA CG CCCC
AC- CGT
GAM44 287 POGZ 1 11143 NP_055915.1 3 704 GGCTTTAAAAAT G --- 1 A c c
GCATGAAACCAC AAGGTGGT TCATGT TTTGGGG
CTTTAATT TTCCACCA AGTACG AAATTTC
A TAA
GAM44 287 POLR2D 1 4052 NP_004796.1 3 58 CCACATCCCCAG C T 1 A b b
GCATAACACCAC AAGGTGGTGT ATGTTT GGGG
CTTCCCAC TTCCACCACA TACGGA CCCC
A -
GAM44 287 POU2AF1 1 16639 NP_006226.1 5 143 TTCCCACAGCTT ---- T T 1 A c c
GCCCCACACCAC AAGGTGGTGT CA GTT TGGGG
CTTCACAC TTCCACCACA GT CGA ACCCT
CCCC T C
GAM44 287 PPP1R3A 1 20165 NP_002702.1 3 1407 TTCCTTCATAAA - -- --- 1 A c c
ACATGTAACACT AAGGT GGTGT CATGTTTTG GGG
GATCTTCA TTCTA TCACA GTACAAAAT TCC
G AT ACT
GAM44 287 PRDM2 1 12854 NP_056950.2 3 30 AAAGCCCCCAAA GG CA 1 A c c
ACAAAACAAACC AAGGT TGT TGTTTTGGGG

TTAATTGA TTCCA ACA ACAAAACCCC
A- AA
GAM44 287 PRKCN 1 19159 NP_005804.1 3 845 TATGCATGTTCT T TT 1 A c c
GACTGACACCAT AAGGTGGTGTCA GTT GGG
CTTGATGC TTCTACCACAGT CAG CTT
- T-
GAM44 287 PRO0461 1 19001 NP_112558.1 5 864 GCTCACTTCCAG G A - 1 A c c
TAGCAGAACCAC AAGGTGGT TC TGTT TTGGGG
CTTAGTTG TTCCACCA AG ACGA GACCTT
- - T
GAM44 287 PYCR1 2 7092 NP_008838.2 3 257 GCTCCCAAACCA --- T T 1 A c c
TGTCAGGACCAC AAGGTGGT G CATG TTTGGGG
CTTCCTCT TTCCACCA C GTAC AAACCCT
GGA T C
GAM44 287 PYCR1 2 17062 NP_008838.2 3 38 GCCTGACCACCA T TGTTT - 1 A c c

TCCTGCCACCAC AAGGTGGTG CA TGG GG
CTTCTCTT TTCCACCAC GT ACC CC
C CCT-- A
GAM44 287 Rab11-F 1 7165 NP_055719.1 3 774 TCTTTCCCCAAA --- GT G-- 1 A c c
IP2 AGTGATGATCTC AAGG TG GTCAT TTTTGGGG
AAGTCCTT TTCC AC TAGTA AAAACCCC
TGA TC GTG
GAM44 287 RAB39B 1 14419 NP_741995.1 3 1409 ACCCACCCCAAA A--- ---- GT 1 A c c

ATGACCTTGGCC AGGTGGT GTCAT TTTGGGG
ACCTGTCT TCCACCG CAGTA AAACCCC
TCTG GTTC --
GAM44 287 RAP1B 1 7459 NP_056461.1 3 604 CTTGTCTTTAAA TGG 1 A c c
ACATGATAGTCC AAGG TGTCATGTTTTGGGG
TTTCAGTA TTCC ATAGTACAAAATTTC
TG-
GAM44 287 RAP2A 1 12939 NP_066361.1 3 1925 TTATAATCCTCA G TT 1 A c c
ATTATGAACCAC AAGGTGGT TCATG TTGGGG
CTTGTTTA TTCCACCA AGTAT AACTCC
- T-
GAM44 287 RASGRP2 1 18244 NP_005816.2 5 32 CCTCTCCCCAAA TGTC 1 A c c

ATATTCCCATCT AAGGTGG ATGTTTTGGGG
TGTCCTAG TTCTACC TATAAAACCCC
CT--
GAM44 287 RASGRP2 1 18244 NP_722541.1 5 32 CCTCTCCCCAAA TGTC 1 A c c

ATATTCCCATCT AAGGTGG ATGTTTTGGGG
TGTCCTAG TTCTACC TATAAAACCCC
CT--
GAM44 287 RING1 1 11106 NP_002922.1 5 23 CCCTTTCCCTCT CAT TT 1 A c c
AACCCACACCAC AAGGTGGTGT GTT GGGG
CTTTCTAC TTCCACCACA CAA TCCC
CC- TC

GAM44 287 RNF39 1 5743 NP_079512.1 3 157 TTTCGCCCCAAA A-- -- G - 1 A c c
ATAATGAGACCT AGGT GGT TCAT GTTTTGGGG
CACCTGGT TCCA CCA AGTA TAAAACCCC
TGG CT G A
GAM44 287 RNF39 1 5743 NP_739575.1 3 157 TTTCGCCCCAAA A-- -- G - 1 A c c
ATAATGAGACCT AGGT GGT TCAT GTTTTGGGG
CACCTGGT TCCA CCA AGTA TAAAACCCC
TGG CT G A
GAM44 287 SALPR 1 1044 NP_057652.1 5 329 TTGTCCCCCAGA A ------ T 1 A c c
ACATGACCTAGA AGGT GG GTCATGTTTTGGGG
GGTACCTG TCCA TC CAGTACAAGACCCC
G TGGAGA -
GAM44 287 SCA1 1 17933 NP_000323.1 3 2587 TGGACTCAGAAA CATG-- 1 A c c
AACACACACCAC AAGGTGGTGT TTTTGGG
CTTTTGGC TTCCACCACA AAGACTC
CACAAA
GAM44 287 SCNN1A 1 16640 NP_001029.1 3 816 GTCTTCCCCAAA T--- T 1 A c c
ATTGATCACTCC AAGGTGG GTCA GTTTTGGGG
GCCTTCTC TTCCGCC TAGT TAAAACCCC
TCAC -
GAM44 287 SEMA4C 1 13121 NP_060259.2 5 351 GGACACCTCCTG CA TT 1 A c c
GCACAACACCAC AAGGTGGTGT TGTT GGGG
CTTCTTTG TTCCACCACA ACGG CTCC
AC TC
GAM44 287 SFRS2IP 1 13515 NP_004710.1 3 602 TTAGTGTTCAAA - GTG - 1 A c c
ACATTGAAACAC AAG GTG TCA TGTTTTGGG
TCTTCACC TTC CAC AGT ACAAAACTT
T AA- T
GAM44 287 SIAT6 1 8130 NP_006270.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777623.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777624.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777625.1 3 582 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777626.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777627.1 3 582 GCCCCCTCCAGC ----- TT 1 A c c

TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777628.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777629.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777630.1 3 582 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777631.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SIAT6 1 8130 NP_777632.1 3 1153 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC
GAM44 287 SLC30A7 1 7436 NP_598003.1 3 80 GTACGATCCAAA G T - - 1 A c c
ACATTGTACCCA AAG TGG GT CA TGTTTTGGG
GCTTTTTA TTC ACC CA GT ACAAAACCT
G - T T
GAM44 287 SNTG2 1 9285 NP_061841.1 3 136 GATACCAATAAA G T -- 1 A c c
ACATGTCACTAG AAG TGGTG CATGTTTTG GG
TTTCCAAA TTT ATCAC GTACAAAAT CC
G T AA
GAM44 287 SOX4 1 9249 NP_003098.1 3 469 GTCTCCCCCTTC TC TTT-- 1 A c c
CTGCATCACCAC AAGGTGGTG ATGT GGGG
CTTGGTTT TTCCACCAC TACG CCCC
-- TCCTT
GAM44 287 SOX7 1 4922 NP_113627.1 3 1542 CCTGCCCCCAAA TGTC 1 A c c
ATATTTTCATCT AAGGTGG ATGTTTTGGGG
TTCCCCCA TTCTACT TATAAAACCCC
TT--
GAM44 287 SPRR4 1 1276 NP_775103.1 3 187 CGTACCCTTCCC GTC TT 1 A c c
CACACATACCAC AAGGTGGT ATGT TGGGG
CTTGGCTT TTCCACCA TACA ACCCC
--- C-
GAM44 287 SRPR 1 14130 NP_003130.2 3 475 TCCCCAGGACCT A---- - ---- 1 A c c
GGATGACACCCG AGGTGG TGTCAT GTTTTGGGG
CCTCACTG TCCGCC ACAGTA CAGGACCCC
GTCAC C GGTC
GAM44 287 SSA1 1 18743 NP_003132.2 3 93 TTTTCCCCATGA G T- - 1 A c c
ACTCTGAACCAC AAGGTGGT TCA GTTT TGGGG
CTTTGTCT TTCCACCA AGT CAAG ACCCC

```
                                        - CT  T
GAM44  287  STAT1  1  15202 NP_644671.1  3 243  AATTTTCCCAAA   T    T          1 A c c
                                ACTGATACCCTT AAGG GGTGTCA GTTTTGGGG
                                TGAAAAAG    TTTC CCATAGT CAAAACCCT
                                        -    -
GAM44  287  STHM   1  1189  NP_006447.1  3 684  GTCCCATTAGAG      T-- G --       1 A c c
                                ATGTATCACCAC AAGGTGGTG  CAT TTT  TGGGG
                                CTTGTCAC    TTCCACCAC  GTA AGA  ACCCT
                                        TAT  G  TT
GAM44  287  SUPT4H1 1  16861 NP_003159.1  3 346  AAGTTCTGAAGG   -    - G       1 A c c
                                CCATGACACCTG AAGGT GGTGTCATG TTTT GGG
                                CCTTGCCT    TTCCG CCACAGTAC GGAA TCT
                                        T      C  G
GAM44  287  SVIL   1  2228  NP_003165.1  3 699  TATCTCCCCAAA    G - G         1 A c c
                                AATGTATAGTGC AAGGTG TGT CAT TTTTGGGG
                                CTTGTTTT    TTCCGT ATA GTA AAAACCCC
                                        G  T  -
GAM44  287  SVIL   1  2228  NP_068506.1  3 699  TATCTCCCCAAA    G - G         1 A c c
                                AATGTATAGTGC AAGGTG TGT CAT TTTTGGGG
                                CTTGTTTT    TTCCGT ATA GTA AAAACCCC
                                        G  T  -
GAM44  287  TARSH  1  14655 NP_079077.1  3 371  AGAATCCCCAAA    G T  G         1 A c c
                                AGTGTCATGCTT AAGGTG TG CAT TTTTGGGG
                                TTAAACAA    TTTCGT AC GTG AAAACCCC
                                        - T  -
GAM44  287  TCOF1  1  12765 NP_000347.1  3 347  AAAGGCCTCGGG      TCAT         1 A c c
                                ACTTCCCACCAC AAGGTGGTG  GTTTTGGGG
                                CTTGCTCC    TTCCACCAC  CAGGGCTCC
                                        CCTT
GAM44  287  TD-60  1  17170 NP_061185.1  3 360  ACACTCCCCAAA   T   CATGT         1 A c c
                                ACACCCCTTTCC AAGG GGTGT   TTTGGGG
                                AGTTACAA    TTCC CCACA    AAACCCC
                                        -    -----
GAM44  287  TNRC6  1  3142  NP_055309.1  3 154  GTTTTCCCCAAA  G  GTC          1 A c c
                                ACATATCAGTTT AAG TGGT  ATGTTTTGGGG
                                GAATACTT    TTT ACTA  TACAAAACCCC
                                        G   ---
GAM44  287  TNRC6  1  3142  NP_065898.1  3 154  GTTTTCCCCAAA  G  GTC          1 A c c
                                ACATATCAGTTT AAG TGGT  ATGTTTTGGGG
                                GAATACTT    TTT ACTA  TACAAAACCCC
                                        G   ---
GAM44  287  TP53I11 1  10684 NP_006025.1  3 582  TCCCCAACCCCA     TG A T         1 A c c
                                AATCAAGACCAC AAGGTGG  TC TG TTTGGGG
                                CTTTCTTC    TTCCACC  AG AC AAACCCC
                                        -- A  T
GAM44  287  TRIM37 1  19079 NP_056109.1  3 926  AATTAGCCCAAA   --  TCA         1 A c c
                                ACAGTTGCCAAA AAGGT  GGTG  TGTTTTGGG
                                CTTTGCCA    TTTCA  CCGT  ACAAAACCC
                                        AA   TG-
GAM44  287  TRIP-Br 2  1237  NP_055570.1  3 3611  TTAAAGCTTAAA      G   T-         1 A c c
```

2 TTTATGAACCAC AAGGTGGT TCATG TTTGGG
CTTTGTGG TTCCACCA AGTAT AAATTC
- TT

GAM44 287 TRIP-Br 2 18572 NP_055570.1 3 1511 TTTTACCCCAAA GG AT- 1 A c c
2 ACTCAGACAGGA AAGGT TGTC GTTTTGGGG
CTTTCTAT TTTCA ACAG CAAAACCCC
GG ACT

GAM44 287 TUBA3 1 7845 NP_006000.2 3 153 CTATGCTCTAAA GGTG 1 A c c
ACATGAATGCTT AAGGT TCATGTTTTGGGG
TGTTACAG TTTCG AGTACAAAATCTC
TA--

GAM44 287 TWISTNB 1 8569 XP_166508.1 3 2569 AATGTAAAAGAC ATGTTT 1 A c
c
CTCAGGCACCAC AAGGTGGTGTC TGGGG
CTTCGCAT TTCCACCACGG ACTCC

GAM44 287 UBE2V1 1 8971 NP_003340.1 3 772 ACCCAACACCTT T TT----- 1 A c c
CCATGACACTTC AAGG GGTGTCATG TTGGG
CTTGCTTT TTCC TCACAGTAC AACCC
T CTTCCAC

GAM44 287 UBE2V1 1 8971 NP_068823.1 3 772 ACCCAACACCTT T TT----- 1 A c c
CCATGACACTTC AAGG GGTGTCATG TTGGG
CTTGCTTT TTCC TCACAGTAC AACCC
T CTTCCAC

GAM44 287 UBE2V1 1 8971 NP_071887.1 3 772 ACCCAACACCTT T TT----- 1 A c c
CCATGACACTTC AAGG GGTGTCATG TTGGG
CTTGCTTT TTCC TCACAGTAC AACCC
T CTTCCAC

GAM44 287 UBN1 1 17578 NP_058632.1 3 592 TTTCTCCTCGGA - GG--- 1 A c c
ACATGACAATGA AAG GT TGTCATGTTTTGGGG
AGCTCTTT TTC CG ACAGTACAAGGCTCC
T AAGTA

GAM44 287 WBP3 1 1501 NP_783863.2 3 2772 TATTTCCCCAAA G T CA 1 A c c
ACAACCCAGCTT AAG TGG GT TGTTTTGGGG
CACCCCAT TTC ACC CA ACAAAACCCC
G - --

GAM44 287 YWHAG 1 15404 NP_036611.2 3 1556 TCCCGAGACGTG - ----- 1 A c c
TAATGACACCAC AAG GTGGTGTCAT GTTTTGGGG
ACTTGTTT TTC CACCACAGTA CAGAGCCCT
A ATGTG

GAM44 287 ZFYVE26 1 7546 XP_031077.1 3 1862 AACACCACCAAA G - A - 1 A c c
ACAGATACCCAT AA GTGG TGTC TGTTTTGG GG
GTTGAGGG TT TACC ATAG ACAAAACC CC
G C - A

GAM45 324 FLJ2517 1 9905 NM_144670.1 3 ACTTCCTGGGAG T CTC - 3 C c c
9 TGTTAACAA TTGT TGAC CTCCCAGGAAGT
AACA ATTG GAGGGTCCTTCA
- --- T

GAM45 324 LOC9135 1 7915 3 TTTTCTGGAGAA ACC - T 3 C c c
1 GACAGAGACAAA TTTGTCTCTG TC CCAGGAAG

AAACAGAGAC AG GGTCTTTT
AGA A -

GAM45 324 UNC13 1 4217 NM_006377.1 3 ACTTCCTGGGAG 3 C a a
GTCAGAGACAAA TTTGTCTCTGACCTCCCAGGAAGT
AAACAGAGACTGGAGGGTCCTTCA

GAM46 364 FLJ2318 1 5875 NM_024616.1 3 TATTCTTGAAGC - GC TC A 3 C c c
6 ACTCCACCCA TGGGTGGA TGCT TC GAATA
ACCCACCT ACGA AG CTTAT
C -- TT -

GAM47 269 ABCA6 1 8771 NP_758854.1 3 1282 CCTGGTTATGCA GA GA 3 A c c
GCTTCTCTTGTC AGGCA AGAGAAGCTGCA
TTCTTCAT TCTGT TCTCTTCGACGT
-- AT

GAM47 269 ABCB9 1 9595 NP_062570.1 3 818 GTTCATGAGATG GC GA 3 A c c
CATTCTCTTCTG AGGCAGAAGAGAA TGCA
TCTTTGGT TCTGTCTTCTCTT ACGT
-- AG

GAM47 269 ABCB9 1 9595 NP_062571.1 3 818 GTTCATGAGATG GC GA 3 A c c
CATTCTCTTCTG AGGCAGAAGAGAA TGCA
TCTTTGGT TCTGTCTTCTCTT ACGT
-- AG

GAM47 269 ABCD2 1 2296 NP_005155.1 5 22 TCTCCCTTTCTG AAGCT 3 A c c
CTTGCTCTTCTG AGGCAGAAGAG GCAGAG
TTTGCGGT TTTGTCTTCTC CGTCTT
GTT--

GAM47 269 ABHD4 1 14056 NP_071343.1 3 1045 TCAGTCTCTGCA A---- A- 3 A c c
GTTTCTCTACCT GGCAG AGAGAAGCTGCAGAG
GCCCCCAG CCGTC TCTCTTTGACGTCTC
GACCC CA

GAM47 269 ACINUS 1 5032 NP_055792.1 3 446 CCCTGCAGTTCC - ----- A 3 A c c
CAGTCTCTTCTG AGG CAGAAGAGA AGCTGCAG
TCCTGCAG TCC GTCTTCTCT TTGACGTC
T GACCC C

GAM47 269 ADAM10 1 9109 NP_001101.1 3 22 GACGCTACTGCA GAAGA A 3 A c
c
GCTTTTGCCTTG AGGCA GAAGCTGCAG
GTTCTTCC TCCGT TTTCGACGTC
----- A

GAM47 269 ADAMTS5 1 13500 NP_008969.1 3 506 AGTAGGTCTGCA C AA - 3 A c c
GCTATTTCAACT AGG AG GAGA AGCTGCAGA
TCCTTCCG TCC TC CTTT TCGACGTCT
T AA A

GAM47 269 ADMP 1 20029 NP_659472.1 3 138 TTCTCTATGCAC GAG C- -- 3 A c c
TCTTATATTCTG AGGCAGAA AAG TGCA GAG
CCTTTCTG TCCGTCTT TTC ACGT CTC
ATA TC AT

GAM47 269 AKR1B1 1 5813 NP_001619.1 3 351 CCTTTCAGCAAG A - - A 3 A c c
ACTTCTCTTTGC AGGCAGA GAGAAG CT GC GAG

CTCAAATA TCCGTTT CTCTTC GA CG CTT
- A A A

GAM47 269 ALKBH 1 8481 NP_006011.1 3 541 CAAATTCTTTGA CA CTG 3 A c c
TCTTCTCTTCCA AGG GAAGAGAAG CAGAG
CCTCTCTG TCC CTTCTCTTC GTTTC
AC TA-

GAM47 269 ALOX12B 1 9630 NP_001130.1 5 165 ACTCTGTGCCTG -- ---- 3 A b b
GCTTCTCTTGCC AGGCAG AAGAGAAGCT GCAGAG
TGCCTTGG TCCGTC TTCTCTTCGG TGTCTC
CG TCCG

GAM47 269 AMPH 1 18267 NP_001626.1 3 885 GCAGCTAAGCAG - AGA 3 A c c
TCTTCTCTTCTG AGGCAGAAGAGAAG CTGC
CCTTTATG TCCGTCTTCTCTTC GACG
T AAT

GAM47 269 AMPH 1 18267 NP_647477.1 3 885 GCAGCTAAGCAG - AGA 3 A c c
TCTTCTCTTCTG AGGCAGAAGAGAAG CTGC
CCTTTATG TCCGTCTTCTCTTC GACG
T AAT

GAM47 269 ANK2 1 17426 NP_001139.2 3 235 ACTCAATATGCA AAGA ---- 3 A c c
GCTTCCTGTTTC AGGCAG GAAGCTGCA GAG
AGTAGGGG TTTGTC CTTCGACGT CTC
---- ATAA

GAM47 269 ANK2 1 17426 NP_066187.1 3 235 ACTCAATATGCA AAGA ---- 3 A c c
GCTTCCTGTTTC AGGCAG GAAGCTGCA GAG
AGTAGGGG TTTGTC CTTCGACGT CTC
---- ATAA

GAM47 269 ANP32E 1 16499 NP_112182.1 5 160 GACTCCATTTGC C GCT 3 A c c
TATTCTCTTCTT AGG AGAAGAGAA GCAGA
TCTCCCCC TCT TCTTCTCTT CGTTT
T AT-

GAM47 269 AOC3 1 17921 NP_003725.1 3 524 CTCCTGTTCCTG C- CT A 3 A c c
CCTTCTCTTCTA AGG AGAAGAGAAG GCAG
TCCTGCAA TCC TCTTCTCTTC CGTC
TA -- C

GAM47 269 AP1GBP1 1 6227 NP_542118.1 3 1693 AGGCATTTGAGT -- G 3 A c c
TTGCCTCTTCTG AGGCAGAAGAG AAGCT CAGA
CTTTAATC TTCGTCTTCTC TTTGA GTTT
CG -

GAM47 269 AP1S1 1 5641 NP_476430.1 3 238 GCCAGCCAGGCA AGA AGA 3 A c
c
GCTTCTCTGCCT AGGCAGA GAAGCTGC
GGGAGGGG TCCGTCT CTTCGACG
--- GAC

GAM47 269 APLN 1 12239 NP_059109.2 3 409 AAGTCCTTTGTC GA CT 3 A c c
ACTTCTCTTGCC AGGCA AGAGAAG GCAGAG
TTAGTGTG TCCGT TCTCTTC TGTTTC
-- AC

GAM47 269 APM1 1 913 NP_004788.1 3 2283 TTTTCTGTATGT G C--- 3 A c c
CCTTCTGTTCTG AGGCAGAA AGAAG TGCAGAG
CCTTCCGC TCCGTCTT TCTTC ATGTCTT

G CTGT
GAM47 269 APOBEC3 1 19621 NP_055323.2 3 204 TCTTCCTGCAGA -- AAG A 3 A c c
C GGCTCCTTTCTG AGGCAGAA GAG CTGCAG
CCTCCATG TCCGTCTT CTC GACGTC
TC GGA C
GAM47 269 APOBEC3 1 18776 NP_660341.2 3 205 TCTTCCTGCAGA - AAG- A 3 A c c
F GGCCTCTTTCTG AGGCAGAA GAG CTGCAG
CCTCCATG TCCGTCTT CTC GACGTC
T CGGA C
GAM47 269 APP 1 4997 NP_000475.1 3 441 GGGAGTTCAGCT GA T A 3 A c c
GCTTCTCTTGCC AGGCA AGAGAAGC GC GAG
TAAGTATT TCCGT TCTCTTCG CG CTT
-- T A
GAM47 269 AR 1 7646 NP_000035.2 3 63 ATGCCCCCTTTC GAAG C 3 A c c
AGATGTCTTCTG AGGCAGAAGA CTG AGAG
CCTGTTAT TCCGTCTTCT GAC TTTC
GTA- -
GAM47 269 ARTN 1 2193 NP_003967.1 5 0 CTCTGAGCTTCT AGA G 3 A c c
CTGAGCCTTGTT AGGC AGAGAAGCT CAGAG
TGCTCATC TCCG TCTCTTCGA GTCTC
AG- -
GAM47 269 ASAH1 1 17659 NP_004306.2 3 88 CCGAACACTGCA - AGAGA A 3 A c c
GCTGTCTGACCT AGG CAGA AGCTGCAG
TCCAAAGA TCC GTCT TCGACGTC
A G---- A
GAM47 269 ASAH1 1 17659 NP_808592.1 3 88 CCGAACACTGCA - AGAGA A 3 A c c
GCTGTCTGACCT AGG CAGA AGCTGCAG
TCCAAAGA TCC GTCT TCGACGTC
A G---- A
GAM47 269 ASB1 1 18379 NP_057198.1 3 4346 CTGGCTCTGGGG AGA- G 3 A c c
CTACAGCTTCTG AGGCAGAAG AGCT CAGAG
CCTCCTCA TCCGTCTTC TCGG GTCTC
GACA G
GAM47 269 ATP1A3 1 12442 NP_689509.1 3 179 CCACTCTGGCTG A--- A-- - - 3 A c c
GCTTCTCTCCCC GGCAG AGAGAAGCT GC AGAG
TGCCCCAA CCGTC TCTCTTCGG CG TCTC
AACC CCC T G
GAM47 269 ATPIF1 1 6903 NP_835498.1 3 742 TTGTCCTTTGGC A CTG 3 A c c
CTTTCACTTCTG AGGCAGAAG GAAG CAGAG
CCTTCTGT TCCGTCTTC CTTT GTTTC
A CCG
GAM47 269 ATRN 1 1478 NP_647537.1 3 1596 CAGCCTCCCAGA A GCA-- 3 A c c
AGCTCTCTTCTG AGGCAGAAGAGA GCT GAG
CTTCAAAA TTCGTCTTCTCT CGA CTC
- AGACC

GAM47 269 AXL 1 5379 NP_001690.2 3 1456 CTTTAGGTTCTT GAGAA T 3 A c c
TGCTGCATTCTG AGGCAGAA GC GCAGAG
CCTCTCTA TCCGTCTT CG CGTTTC
A---- T
GAM47 269 AXL 1 5379 NP_068713.2 3 1456 CTTTAGGTTCTT GAGAA T 3 A c c
TGCTGCATTCTG AGGCAGAA GC GCAGAG
CCTCTCTA TCCGTCTT CG CGTTTC
A---- T
GAM47 269 BAALC 1 7066 NP_079088.1 3 1900 ATGTGCTTTGTG A-- TG 3 A c c
GCTTCTCTTTAC AGGC GAAGAGAAGC CAGAG
AGCTTTGT TTCG TTTCTCTTCG GTTTC
ACA GT
GAM47 269 BAZ2A 1 12314 NP_038477.1 5 80 TCTTGGGTTTCA AA C 3 A c c
GTGATTTTTCTG AGGCAGAAGAG GCTG AGA
CCTCGGCC TCCGTCTTTTT TGAC TTT
AG -
GAM47 269 BCL2L13 1 1370 NP_056182.1 3 1234 GGCTGCTCTGCA G AG G 3 A c
c
GATTCTAGTTTG AG CAGA AGAA CTGCAGAG
GCTTTCAG TC GTTT TCTT GACGTCTC
G GA A
GAM47 269 BIA2 2 11493 NP_056246.1 5 136 ACTGCGGCCACA AGAA- A 3 A c c
GCTTCTGCCTCA AGGCAGAAG GCTGCAG
GGTGCATC TCCGTCTTC CGGCGTC
GACAC A
GAM47 269 BIA2 2 18069 NP_056246.1 5 135 CGTGGACTGCGG AGAA- A 3 A c c
CCACAGCTTCTG AGGCAGAAG GCTGCAG
CCTCAGGT TCCGTCTTC CGGCGTC
GACAC A
GAM47 269 BIG1 1 7522 NP_006412.1 5 48 CTCTCCTTTCTC CA- CTGC 3 A c c
TCTTCTCTTCCT AGG GAAGAGAAG AGAG
TCCTCTCC TCC CTTCTCTTC TCTC
TTC ----
GAM47 269 BMP4 1 18502 NP_001193.1 5 378 CGCACTGCTGCA AGA A A 3 A c c
GCTTCCCTGAGC AGGC AG GAAGCTGCAG
CTTTCCAG TCCG TC CTTCGACGTC
AG- C G
GAM47 269 BMP4 1 18502 NP_570911.1 5 169 CGCACTGCTGCA AGA A A 3 A c c
GCTTCCCTGAGC AGGC AG GAAGCTGCAG
CTTTCCAG TCCG TC CTTCGACGTC
AG- C G
GAM47 269 BMP4 1 18502 NP_570912.1 5 158 CGCACTGCTGCA AGA A A 3 A c c
GCTTCCCTGAGC AGGC AG GAAGCTGCAG
CTTTCCAG TCCG TC CTTCGACGTC
AG- C G
GAM47 269 BMPR2 1 14836 NP_001195.2 5 243 GAAAGCTCTGCA A A A ------ 3 A c c
GCTAGGTCCTCT GGC GA GAGA AGCTGCAGAG
CATCAGCC CCG CT CTCT TCGACGTCTC
- A A CCTGGA
GAM47 269 BOCT 1 18592 NP_065105.2 5 7 CCAGCAGCTGCA A A--- A 3 A c c

GCTCGGCCTCTG AGGCAG AGAG AGCTGCAG
CTGCCTGC TCCGTC TCTC TCGACGTC
G CGGC G

GAM47 269 BOP1 1 13557 NP_056016.1 3 13 TCCGCCTCTTCA G A C C 3 A c c
CCTACTGTTCTG AGGCAGAA AG AG TG AGAG
CCTGCCTG TCCGTCTT TC TC AC TCTC
G A C T

GAM47 269 BRD2 1 2747 NP_005095.1 5 748 GTGGGTCTCTGC AA 3 A b b
GGCACTCTTCTG AGGCAGAAGAG GCTGCAGAG
CCTGGTGA TCCGTCTTCTC CGGCGTCTC
A-

GAM47 269 BTF3 1 14803 NP_001198.2 3 165 TTGGACACTGCA ------ A A 3 A c c
GCTCTTTTCAGT AGGCA GAAGAGA GCTGCAG
TTTTGCTT TTCGT CTTTTCT CGACGTC
TTTTGA - A

GAM47 269 BXDC1 1 577 XP_166303.1 3 1415 CTCCCAGGTTCA ------ G CA 3 A c c
AGCATTCTTCTG AGGCAGAAGA GAA CTG GAG
CCTCAGCC TCCGTCTTCT CTT GAC CTC
TACGAA G C-

GAM47 269 C11orf9 1 5599 NP_037411.1 3 855 GATGGTATTGCA AAGA A 3 A c c
GCTTCACTGCCT AGGCAG GAAGCTGCAG
GCGTTCCT TCCGTC CTTCGACGTT
A--- A

GAM47 269 C14orf1 1 9006 NP_060578.2 3 1306 AGAGAACCCTCA A C A 3 A c c
30 GCTTCTCTCTGC AGGCAGA GAGAAGCTG AG
CTCTGGAG TCCGTCT CTCTTCGAC TC
- - C

GAM47 269 C14orf1 1 3922 NP_064600.1 3 2377 AGCAAATCTGCA - ---- C 3 A c c
32 TCTTCTCTTATT AGG CAGA AGAGAAG TGCAGA
TCTGACCT TCC GTCT TCTCTTC ACGTCT
A TTAT T

GAM47 269 C14orf1 1 8260 NP_075601.1 3 1438 TGTCAGATTTGT AA T 3 A c c
37 GTCACTCTTCTG AGGCAGAAGAG GC GCAGA
CCTTCGTG TCCGTCTTCTC TG TGTTT
AC -

GAM47 269 C14orf5 1 529 XP_027244.1 5 938 AGCCACACCACA AGAAGC A 3 A c c

6 CCTGCACTTCTG AGGCAGAAG TGCAG
CCTCACTT TCCGTCTTC ACGTC
------ C

GAM47 269 C1orf34 1 6254 XP_027172.1 3 2008 TCAGAGGCCTCT C - A CT 3 A c c
GCTTCTCTCTTG AGG AG AAGAGA G GCAGAG
CTCCTAGA TCC TC TTCTCT C CGTCTC
- G - TT

GAM47 269 C1orf6 1 8781 NP_064516.1 3 95 TTACCCTCTGCA A A ----- 3 A c c
GCTTGTCCTCCC AGGC GAAG GA AGCTGCAGAG
TTCCGTCT TCTG CTTC CT TCGACGTCTC
C C CCTGT

GAM47 269 C1QR1 1 8931 NP_036204.1 3 3787 TTTCTCTTCTTA AA C-- 3 A c c
GCTTCTCCATTG AGGCAG GAGAAGCTG AGAG

TCTAAATC TCTGTT CTCTTCGAT TCTC
AC TCT

GAM47 269 C1QTNF6 1 621 NP_114116.2 3 192 GCCTATTTCTGC C A CT 3 A c c
TCCTCTCTTCTC AGG AGAAGAGA G GCAGAG
TCTTGGAC TCT TCTTCTCT C CGTCTT
C - CT

GAM47 269 10 C20orf1 1 4643 XP_086728.2 3 594 GCTTTTAGTCTC A CTGC 3 A c c
CCCTTCCTTCTG AGGCAGAAG GAAG AGA
CCTTGGGG TCCGTCTTC CTTC TCT
- CCC-

GAM47 269 50 C20orf1 1 12630 XP_037265.1 3 153 TCCGCTGGTGCA - AG GA 3 A c c
GCTTTCCTTTTT AGGCAGAA G AAGCTGCA
GCCTCTTT TCCGTTTT C TTCGACGT
T CT GG

GAM47 269 77 C20orf1 1 893 XP_290955.1 3 2575 GTGACTTTGCTT AG T- 3 A c c
GTTTACTTTCTG AGGCAGAAG AAGC GCAGAG
CCTCAGAT TCCGTCTTT TTTG CGTTTC
CA TT

GAM47 269 9 C20orf2 1 13011 NP_060817.1 3 857 CAGGATTCTGCA A----- G A 3 A c c
GCTCCTTTTGTG GGCA AAGAG AGCTGCAGAG
CCAAGCCC CCGT TTTTC TCGACGTCTT
CCCGAA G C

GAM47 269 C20orf9 1 4613 NP_057088.1 3 33 CCATGCCTCTTG GA GC- 3 A c c
AAGCTTTTTCTG AGGCAGAA GAAGCT AGAG
CCTCCTGA TCCGTCTT TTTCGA TCTC
-- AGT

GAM47 269 5 C21orf8 1 3085 NP_715634.1 5 592 TAGGTTTTTGGA - --- G 3 A c c
GCTTCTCTGCTT AGGCA GA AGAGAAGCT CAGAG
CATGTCTT TCTGT CT TCTCTTCGA GTTTT
A TCG G

GAM47 269 8 C21orf8 1 7197 NP_715635.1 3 141 TTAAGGTCTGCA C GA A 3 A c c
GCCTTAATTCTA AGG AGAA GA GCTGCAGA
CCTGCAAA TCC TCTT TT CGACGTCT
A AA C

GAM47 269 C5orf7 1 13501 NP_057688.1 3 150 AAACTCTCCAGC ----- A-- C 3 A c c
CACTCTCTTCTA AGGCA GAAGAGA GCTG AGAG
CGCTGCCT TCCGT CTTCTCT CGAC TCTC
CGCAT CAC C

GAM47 269 C6orf33 1 14931 NP_588608.1 3 3041 ACACATTTGCCT GA T- 3 A c c
GCTTCTCTCTTG AGGCA AGAGAAGC GCAGA
CCTAATTC TCCGT TCTCTTCG CGTTT
TC TC

GAM47 269 C6orf50 1 3566 XP_166460.1 3 412 GGTTTCTCTGCA - AG-- 3 A c c
GAAGCTCTCTTT AGGCAGAA GAGA CTGCAGAG
TTGCCTCC TCCGTTTT CTCT GACGTCTC
T CGAA

GAM47 269 C6orf67 1 10872 NP_060717.1 3 820 TGCTTGGCAGAC - -- A 3 A c c
CTTCATCTTCTG AGGCAGAAGA GAAG CTGC GAG
CCTCAACT TCCGTCTTCT CTTC GACG TTC
A CA G

GAM47 269 CA10 1 9177 NP_064563.1 3 96 GTCCCCCTTCTT C A TGC 3 A c c
GCTTCTCTCTCC AGG AGA GAGAAGC AGAG
TTCTTTCC TCC TCT CTCTTCG TCTT
- - T--
GAM47 269 CABC1 1 2169 NP_064632.1 5 395 GAGCCTCCACAG A - CA 3 A c c
ACTTCTCTTCAG AGGC GAAGAGAAG CTG GAG
CCTCCGCT TCCG CTTCTCTTC GAC CTC
A A AC
GAM47 269 CACNG4 1 9768 NP_055220.1 3 1199 GGACCGAGCTGG CA- G A 3 A c
c
GCTTCTCTTCCT AGG GAAGAGAAGCT CAG
CCCTACAG TCC CTTCTCTTCGG GTC
CTC - G
GAM47 269 CALN1 1 9427 NP_113656.1 3 2352 GTGGCTTTTCTG AAGC 3 A c c
CGAGTTCTTCTG AGGCAGAAGAG TGCAGAG
CCTCCTGC TCCGTCTTCTT GCGTCTT
GA--
GAM47 269 CAMKK2 1 10400 NP_006540.3 3 1993 AGCTTCTGCAGG GA -- 3 A c c
GCTTCTCTTGTT AGGCA AGAGAAGCT GCAGAG
TACACAGC TTTGT TCTCTTCGG CGTCTT
-- GA
GAM47 269 CAMKK2 1 10400 NP_705719.2 3 2091 AGCTTCTGCAGG GA -- 3 A c c
GCTTCTCTTGTT AGGCA AGAGAAGCT GCAGAG
TACACAGC TTTGT TCTCTTCGG CGTCTT
-- GA
GAM47 269 CAMKK2 1 10400 NP_705720.1 3 2091 AGCTTCTGCAGG GA -- 3 A c c
GCTTCTCTTGTT AGGCA AGAGAAGCT GCAGAG
TACACAGC TTTGT TCTCTTCGG CGTCTT
-- GA
GAM47 269 CAMKK2 1 10400 NP_757365.1 3 1993 AGCTTCTGCAGG GA -- 3 A c c
GCTTCTCTTGTT AGGCA AGAGAAGCT GCAGAG
TACACAGC TTTGT TCTCTTCGG CGTCTT
-- GA
GAM47 269 CAMKK2 1 10400 NP_757380.1 3 2092 AGCTTCTGCAGG GA -- 3 A c c
GCTTCTCTTGTT AGGCA AGAGAAGCT GCAGAG
TACACAGC TTTGT TCTCTTCGG CGTCTT
-- GA
GAM47 269 CAPG 1 15413 NP_001738.1 3 71 ACCTGCCTGCTT A- T- A 3 A c c
GCTTCTCTGGCT AGGCAG AGAGAAGC GCAG
GCCTGGTC TCCGTC TCTCTTCG CGTC
GG TT C
GAM47 269 CBLN1 1 10839 NP_004343.1 3 396 CTAGCCCCCTCT A AG TG 3 A c c
GGAATCCTTCTG AGGCAGAAG GA C CAGAG
CCTACTGA TCCGTCTTC CT G GTCTC
- AA --
GAM47 269 CCL2 1 10130 NP_002973.1 3 46 CAAGAATCTGCA CA GA---- 3 A c c
GCTAACTTATTT AGG GAAGA AGCTGCAGA
TCCCCTAG TCC CTTTT TCGACGTCT
C- ATTCAA

GAM47 269 CCND2 1 18032 NP_001750.1 3 3872 CTCTGTACTGGA G A ------ 3 A c c
GGCTCTGTTCTG AGGCAGAA AGA GCT GCAGAG
CCTCTTAT TCCGTCTT TCT CGG TGTCTC
G - AGGTCA
GAM47 269 CCNE1 1 11860 NP_001229.1 3 61 GCGCCTGCTCCA GCT--- A 3 A c c
CGTTCTCTTCTG AGGCAGAAGAGAA GCAG
TCTGTTGC TCTGTCTTCTCTT CGTC
GCACCT C
GAM47 269 CCNE1 1 11860 NP_476530.1 3 61 GCGCCTGCTCCA GCT--- A 3 A c c
CGTTCTCTTCTG AGGCAGAAGAGAA GCAG
TCTGTTGC TCTGTCTTCTCTT CGTC
GCACCT C
GAM47 269 CCR7 1 13600 NP_001829.1 3 17 CTTCTCCCCATA AA CA-- 3 A c c
GCGACTCTTCTG AGGCAGAAGAG GCTG GAG
CCTGGACT TCCGTCTTCTC CGAT CTC
AG ACCC
GAM47 269 CDC42EP 1 18102 NP_659494.2 5 138 GACTGGGCGGTG A- -- AG 3 A c
c
5 ATTCCGCTTCTG AGGCAGAAG GAA GCTGC AG
CCTGGGCT TCCGTCTTC CTT TGGCG TC
GC AG GG
GAM47 269 CDH1 1 6768 NP_004351.1 3 972 TCCTGGCCTCAA A AGC A- 3 A c c
GCAATCCTTCTG AGGCAGAAG GA TGC GAG
CCTTGGCC TCCGTCTTC CT ACG CTC
- A-- AA
GAM47 269 CGA 1 4642 NP_000726.1 3 156 GGATATACTGCA AAGA A 3 A c c
GCTTTACTGCCT AGGCAG GAAGCTGCAG
TCCTCCTT TCCGTC TTTCGACGTC
A--- A
GAM47 269 CGI-115 1 5086 NP_057136.1 3 371 CTCTTTGAAGTT A--- G 3 A c c
AATATTTTTCTG AGGCAGAAGAG AGCT CAGAG
CCTTCTAA TCCGTCTTTTT TTGA GTTTC
ATAA A
GAM47 269 CGI-30 1 4236 NP_057042.1 5 83 ATTCTCTCAGCG C AG A 3 A c c
GTCTCTCTTCTC AGG AGAAGAGA CTGC GAG
CTCAAGTT TCC TCTTCTCT GGCG CTC
- CT A
GAM47 269 CHKL 1 4091 NP_689466.1 3 3616 AGGGATCGACAG AA GCA- 3 A c c
GCACCTCTTCTG AGGCAGAAGAG GCT GA
CCTTTACT TCCGTCTTCTC CGG CT
CA ACAG
GAM47 269 CHRAC1 1 15944 NP_059140.1 3 1378 CTGTTCCTCTGT C A CT 3 A c c
TCCTCTCTTCTC AGG AGAAGAGA G GCAGAG
CTGCCCCC TCC TCTTCTCT C TGTCTC
- - CT
GAM47 269 CISH 1 1811 NP_037456.4 3 605 AACTCTGCCCTG A-- C --- --- 3 A c c
GCTTCTCTGGTT GG AGA AGAGAAGCT GCAGAG
CTTCCCTG CC TCT TCTCTTCGG CGTCTC

GTC T TGG TCC

GAM47 269 CISH 1 1811 NP_659508.1 3 605 AACTCTGCCCTG A-- C --- --- 3 A c c

GCTTCTCTGGTT GG AGA AGAGAAGCT GCAGAG

CTTCCCTG CC TCT TCTCTTCGG CGTCTC

GTC T TGG TCC

GAM47 269 CIT 1 9863 XP_045786.2 3 1519 AGCTAACTCGCG A A A 3 A c c

GCCTTATTTCTG AGGCAGAAG GA GCTGC GAG

CCTTTAAT TCCGTCTTT TT CGGCG CTC

A C -

GAM47 269 CLECSF1 1 11168 NP_072092.2 3 356 CGACTCACTGCA A A - A 3 A c c

2 GCTATCTCTCGC AGGC GA GAGA AGCTGCAG

CTCAGCCC TCCG CT CTCT TCGACGTC

- - A A

GAM47 269 CLECSF5 1 2913 NP_037384.1 3 145 GGGAAACTGAGC - -- G A 3 A c c

TTCTTTCTTCTG AG GCAGAAGA GAAGCT CAG

CACTGGGG TC CGTCTTCT CTTCGA GTC

A TT - A

GAM47 269 CLECSF9 1 8709 NP_055173.1 3 421 CTGACAAGTCTG -- CT 3 A c c

TCTTCTCTTCTT AGGC AGAAGAGAAG GCAGA

GGTTTCAT TTTG TCTTCTCTTC TGTCT

GT --

GAM47 269 CLIC6 1 2170 NP_444507.1 3 668 CACCCCCACTCT A AGCT 3 A c c

GCCTCATTTCTG AGGCAGAAG GA GCAGAG

CCTCCAGG TCCGTCTTT CT CGTCTC

A C---

GAM47 269 CLSTN2 1 15486 NP_071414.1 3 1180 GCAATCATTGCA A ----- A 3 A c c

GCTTCTTCTTTC GGCAGAAGA GAAGCTGCAG

TTCTGCTC TCGTCTTCT CTTCGACGTT

C TTCTT A

GAM47 269 CNNM4 1 14167 NP_064569.1 3 1525 TGAAACTCTGCA A AGAAG 3 A c

c

GGCCTTCCGCCT AGGC GAAG CTGCAGAG

GATTATTA TCCG CTTC GACGTCTC

C CG---

GAM47 269 COPA 1 5791 NP_004362.1 3 105 CTTCCCCCTGCA G ----- A A 3 A c c

GCTACTCTTCAG AG CAGA AGAG AGCTGCAG

ATCTGGCT TC GTCT TCTC TCGACGTC

G AGACT A C

GAM47 269 CPT1B 1 4091 NP_689453.1 3 230 AGGGATCGACAG AA GCA- 3 A c c

GCACCTCTTCTG AGGCAGAAGAG GCT GA

CCTTTACT TCCGTCTTCTC CGG CT

CA ACAG

GAM47 269 CRSP2 1 14259 NP_004220.2 3 1550 CCTTTCTTCTTT AG CT 3 A c c

GTCTTATTTCTG AGGCAGAAG AAG GCAGAG

CCTTCATC TCCGTCTTT TTC TGTTTC

A- --

GAM47 269 CSAD 1 12878 NP_057073.2 5 150 CCAGACTGTCTT ---- CT A 3 A c c

CAAATTCTTCTG AGGCAGAAGA GAAG GCAG

CCTAGCCT TCCGTCTTCT CTTC TGTC

TAAA -- A

GAM47 269 CUGBP1 1 7087 NP_006551.1 3 136 CCTGTCTCTTCA GA C 3 A c c
GCTTCTCTGATG AGGCA AGAGAAGCTG AGAG
CTTGAACT TTCGT TCTCTTCGAC TCTC
AG T

GAM47 269 CXCL3 1 16187 NP_002081.1 3 603 GTCCATTCTGCA CA -- 3 A c c
GCGTTTCTCTTT AGG GAAGAGAA GCTGCAGAG
CCCTTGGA TCC TTTCTCTT CGACGTCTT
C- TG

GAM47 269 CYP2C9 1 10215 NP_000762.2 3 58 GCAGTCCCTGCA CA A A 3 A c c
GCTCTCTTTCCT AGG GAAGAGA GCTGCAG
CTGGGGCA TCT TTTCTCT CGACGTC
CC - C

GAM47 269 CYP51A1 1 2685 NP_000777.1 5 254 GACCATCTGCCA A-- A --- - 3 A c c
GCTTCTCTCGTT GGC GA AGAGAAGCTG CAGA
CCGTCGAT CTG CT TCTCTTCGAC GTCT
TAG C TGC C

GAM47 269 CYP8B1 2 704 NP_004382.1 3 2024 TTGCTTTCTGTG AG C 3 A c c
TCTTGGTTTCTG AGGCAGAAG AAG TGCAGAG
CCTGCTGC TCCGTCTTT TTC GTGTCTT
GG T

GAM47 269 CYP8B1 2 3660 NP_004382.1 3 1642 TGTGATCTCTGC A ----- T 3 A c c
GTTTCTCTTCTA GGCA GAAGAGAAGC GCAGAG
CACTGCTG TCGT CTTCTCTTTG CGTCTC
G CACAT -

GAM47 269 DAAM2 1 3097 XP_166434.3 3 1670 CTACTCTCAGCT GA--- C 3 A c c
GCCTATCTTCTG AGGCAGAAGA AGCTG AGAG
CCTTTCAC TCCGTCTTCT TCGAC TCTC
ATCCG -

GAM47 269 DCTN1 1 5744 NP_004073.2 5 72 CTTCATTACTGC - CT A 3 A c c
CCTTCTCTTGCT AGGCAG AAGAGAAG GCAG
GCCTCCTG TCCGTC TTCTCTTC CGTC
G C- A

GAM47 269 DEC1 1 927 NP_059114.1 5 55 GAACACTCTGCG CAGA--- 3 A c c
GCTTCTCTGAGA AGG AGAGAAGCTGCAGAG
AACCCTAT TCC TCTCTTCGGCGTCTC
CAAAGAG

GAM47 269 DEFB123 1 13953 NP_697019.1 5 60 ATCGGACTTGCA --- - A 3 A c c
GCTTCATTTTGG AGGCAG AAGA GAAGCTGCAG
GCTGCCTT TCCGTC TTTT CTTCGACGTT
GGG A C

GAM47 269 DGCR7 1 5400 XP_295022.1 5 416 TGCAATGGCTCA CA- C A 3 A c c
GCTTCTCTTCCA AGG GAAGAGAAGCTG AG
ACCTGTCC TCC CTTCTCTTCGAC TC
AAC - G

GAM47 269 DJ473B4 1 7830 NP_062456.1 3 1032 TACATTTCTTTA - AA C 3 A c c
TAGCCTCTTCTG AGG CAGAAGAG GCTG AGAG
ATCTCTAA TCT GTCTTCTC CGAT TTTC
A -- A

GAM47 269 DKFZP43 1 18103 NP_115508.2 5 26 GTGCAGCCTCGT - GAA - 3 A c c

4A1315 GCAGCTCTTCTG AGGC AGAAGA GCTGCA GAG
GTCTCCGG TCTG TCTTCT CGACGT CTC
G --- G
GAM47 269 DKFZP43 1 1801 XP_046264.6 3 238 TAACAGTCTCTG A- TGC 3 A c c
4B172 CTTTGCCTTCTG AGGCAGAAG GAAGC AGAG
CCTGGTAG TCCGTCTTC TTTCG TCTC
CG ---
GAM47 269 DKFZp43 1 9333 NP_115635.1 5 158 CCGGGGTCGCCG A CA 3 A c c
4F054 GCTTCTCTCCTG AGGCAG AGAGAAGCTG GA
CCTCCGGT TCCGTC TCTCTTCGGC CT
C CG
GAM47 269 DKFZp43 1 16769 NP_115630.1 3 31 ACAGCCTCTGCA GA A --- 3 A c c
4F142 GGCCCTGCTCTT AGGCA AGAG AG CTGCAGAG
GCCTCTTA TCCGT TCTC TC GACGTCTC
-- G CCG
GAM47 269 DKFZP43 1 15842 NP_056307.1 3 57 GTCACTCTCCAC A C- C 3 A c c
4H132 CCTTCCCTTCTG AGGCAGAAG GAAG TG AGAG
CCTGCCCA TCCGTCTTC CTTC AC TCTC
C CC C
GAM47 269 DKFZP43 1 7685 NP_056409.1 5 2328 GGGGGCTCTGCA A A- A----- 3 A c
c
4O047 GCTGCCCAGCTC GGC GAAGAG AGCTGCAGAG
TTCCAGCT TCG CTTCTC TCGACGTCTC
- AC GACCCG
GAM47 269 DKFZp45 1 9563 NP_694967.1 5 79 CTCCTTCCTCTC - - CTGC 3 A c c
1A175 CTCTCTCTTCTT AGGCA GAAGAGA AG AGAG
GCTTAGCT TTCGT CTTCTCT TC TCTC
T C C---
GAM47 269 DKFZp54 1 18222 NP_115531.1 3 312 TGTGGCTCTGCA AG -- AA--- 3 A c
c
7I094 GCCCCTGCTCCT GCAGAA GAG GCTGCAGAG
TTCTGCGG CGTCTT CTC CGACGTCTC
GG TC GTCCC
GAM47 269 DKFZP56 1 16836 XP_294974.1 3 275 CTGCTCTGCAAC ----- C-- 3 A c c
4C196 CTTTCTCTTCTC AGGC AGAAGAGAAG TGCAGAG
ACGGGTCT TCTG TCTTCTCTTT ACGTCTC
GGCAC CCA
GAM47 269 DKFZP56 1 8181 NP_114431.2 3 1063 TTGTGCTCTGCA AGG--- -- 3 A c c

4D172 GCCTTTTTCTTC CAGAAGAGAA GCTGCAGAG
TGAAAGGC GTCTTCTTTT CGACGTCTC
CGGAAA TC
GAM47 269 DKFZP58 1 17013 NP_056348.2 3 79 GGTGGCCTTTGT A CT 3 A c c
6B1621 CACTTCCTTCTG AGGCAGAAG GAAG GCAGAG
CCTTCCAA TCCGTCTTC CTTC TGTTTC
- AC
GAM47 269 DKFZP58 1 7358 NP_056291.1 3 722 ATTTCTTTTGCA ------ A 3 A c c
6M1523 GCTTCCTATAAA AGGCAGA AG GAAGCTGCAGAG
GTTTGTCT TCTGTTT TC CTTCGACGTTTT
GAAATA -

GAM47 269 DKFZP76 1 4962 NP_113643.1 3 1402 CACTGTCAGATT --- - - A 3 A c c
1F241 TCCACTCTTCTG AGGCAGAAGA GAAG CTG CAG
CCTTTAGG TCCGTCTTCT CTTT GAC GTC
CAC A T A
GAM47 269 DKFZp76 3 6944 NP_689874.1 3 1537 GGTGCCTCTGCA AA GAAG- 3 A c
c
1G0122 GAGAGATCCCTG AGGCAG GA CTGCAGAG
CCTGGGAC TCCGTC CT GACGTCTC
C- AGAGA
GAM47 269 DKFZp76 3 8022 NP_689874.1 3 123 AACTCAAGCTCA AGA GCA 3 A c
c
1G0122 GCTTCTGCCTCC AGGCAGAAG AGCT GAG
TGTCTCCT TCCGTCTTC TCGA CTC
GAC A--
GAM47 269 DKFZp76 3 10800 NP_689874.1 3 123 GGAGGAACTCAA AGA GCA 3 A c
c
1G0122 GCTCAGCTTCTG AGGCAGAAG AGCT GAG
CCTCCTGT TCCGTCTTC TCGA CTC
GAC A--
GAM47 269 DKFZP76 1 20088 XP_295135.1 3 863 ACCTGCTCTGCA AGAAG-- A 3 A c
c
1M1511 GCTGCTATAAAT AGGC AG AGCTGCAGAG
AGCCTCCC TCCG TC TCGACGTCTC
ATAAATA G
GAM47 269 DKK2 1 17469 NP_055236.1 3 1418 CAAACCTCTGCA A-- -- - A 3 A c c
GCATCTGCTTTA GGCA GAAG AGA GCTGCAGAG
TTGCCAAA CCGT TTTC TCT CGACGTCTC
AAA TA G A
GAM47 269 DMRTB1 1 18599 NP_149056.1 3 515 GCAGGTTCTGCA AAGA A 3 A c
c
GCATCCTGCCTT AGGCAG GA GCTGCAGAG
GCTGCTCT TCCGTC CT CGACGTCTT
---- A
GAM47 269 DNMT3A 1 18807 NP_783329.1 3 359 TAGTTTTCTGCA AGAAG A 3 A c
c
GCTCTACCTGGC AGGC AGA GCTGCAGAG
CTGCTTAC TCCG TCT CGACGTCTT
GTCCA -
GAM47 269 DPYSL2 1 9773 NP_001377.1 3 744 CTTTGAGGATTC C G G 3 A c c
TCTTCTCTTTTA AGG AGAAGAGAA CT CAGAG
CCATTTTT TTC TCTTCTCTT GG GTTTC
- A A
GAM47 269 DRG2 1 8205 NP_001379.1 3 438 CAGCTCTTGCCA CAGA - - 3 A c c
GCTTCTCTGACA AGG AGAGAAGCTG CA GAG
CTTGGGTT TTC TCTCTTCGAC GT CTC
ACAG C T
GAM47 269 DTX2 1 15714 NP_065943.1 3 356 GGTTCTGGGTCA CAG --- 3 A c c
GCTTCTTTTACC AGG AAGAGAAGCTG CAGAG
TCAATTTT TCC TTTTCTTCGAC GTCTT
A-- TGG

GAM47 269 DTYMK 1 3722 NP_036277.1 3 150 GAGATCTGCAGG A----- A- - 3 A c c
CTGCCTCTTCTG GGCAGAAGAG AGC TGCAGA
CCCCGGAG CCGTCTTCTC TCG ACGTCT
GAGGCC CG G
GAM47 269 DULLARD 1 11968 NP_056158.2 5 330 CCCCTCTCTGCA A------- AA A 3 A c
c
GCCTCTCCTGCC GGCAG GAGA GCTGCAGAG
ACTCGGGG CCGTC CTCT CGACGTCTC
GGGGCTCA -- C
GAM47 269 DVL3 1 18567 NP_004414.2 3 199 ATTGGCTCTGCA AAG AA- 3 A c c
GCCCCCTAACCT AGGCAG AG GCTGCAGAG
GCCTCTGG TCCGTC TC CGACGTCTC
CAA CCC
GAM47 269 EFNB2 1 8500 NP_004084.1 3 541 CAGGGCTCTGCA --- AA AA 3 A c c
GCACCTCACCTG AGG CAG GAG GCTGCAGAG
AGACCTCC TCC GTC CTC CGACGTCTC
AGA CA CA
GAM47 269 EHF 1 7855 NP_036285.2 3 1746 ATCCCTTTTGCA G - 3 A c c
GCTTTTCTTTTT AG CAGAA GAGAAGCTGCAGAG
GGCTCTCT TC GTTTT CTTTTCGACGTTTT
G T
GAM47 269 EHF 1 7855 NP_758433.1 3 1746 ATCCCTTTTGCA G - 3 A c c
GCTTTTCTTTTT AG CAGAA GAGAAGCTGCAGAG
GGCTCTCT TC GTTTT CTTTTCGACGTTTT
G T
GAM47 269 EHHADH 1 11906 NP_001957.1 3 546 CCTCTTCTGGTC -- - C- 3 A c c
TTTCCTCTTCTG AGGCAGAAGAG AAG CTG AGAG
TTTATGGA TTTGTCTTCTC TTC GGT TCTC
CT T CT
GAM47 269 EI24 1 3180 NP_004870.2 3 260 GGTTTTTCTGCA A ---- -- 3 A c c
GCTATTTTCTAG GGCAGA AGAGA AGCTGCAGAG
CATTTGCC CCGTTT TCTTT TCGACGTCTT
- ACGA TA
GAM47 269 ELOVL2 1 11804 NP_060240.1 3 244 AGAACTGGTGCA C A GA 3 A c c
GCTTCTCTCTCC AGG AGA GAGAAGCTGCA
CTCCCTCC TCC TCT CTCTTCGACGT
C - GG
GAM47 269 EMR3 1 3525 NP_693634.1 3 779 ACTGCATCTGCA A- A 3 A b b
GCTCTCGCTCTG AGGCAGA GAGA GCTGCAGA
CCTCTTCC TCCGTCT CTCT CGACGTCT
CG -
GAM47 269 ENDOGLY 1 11245 NP_079032.1 3 396 TCTCTTGCTTCC C CT--- - 3 A c c
X1 TCTTCTCTTCTC AGG AGAAGAGAAG GCA GAG
CCTTATCG TCC TCTTCTCTTC CGT CTC
C TCCTT T
GAM47 269 ENO1 1 19121 NP_001419.1 5 91 TCGGTGTCTGCA C AA AA- 3 A c c
GCACCCTCCGCT AGG AG GAG GCTGCAGA
TCCTCTCC TCC TC CTC CGACGTCT

T GC CCA
GAM47 269 EPB49 1 9779 NP_001969.1 3 473 TCCTGCACTGCA C A A A 3 A c c
GCTTCCTGCTCC AGG AG AG GAAGCTGCAG
TCTGACTC TCC TC TC CTTCGACGTC
- G - A
GAM47 269 F11R 1 7420 NP_058642.1 3 522 ATCTCTGGGGCC A--- G 3 A c c
CACTCTCTTCTG AGGCAGAAGAGA GCT CAGAG
TCTTCCCA TCTGTCTTCTCT CGG GTCTC
CACC G
GAM47 269 F11R 1 7420 NP_653084.1 3 522 ATCTCTGGGGCC A--- G 3 A c c
CACTCTCTTCTG AGGCAGAAGAGA GCT CAGAG
TCTTCCCA TCTGTCTTCTCT CGG GTCTC
CACC G
GAM47 269 F11R 1 7420 NP_653085.1 3 522 ATCTCTGGGGCC A--- G 3 A c c
CACTCTCTTCTG AGGCAGAAGAGA GCT CAGAG
TCTTCCCA TCTGTCTTCTCT CGG GTCTC
CACC G
GAM47 269 F11R 1 7420 NP_653086.1 3 522 ATCTCTGGGGCC A--- G 3 A c c
CACTCTCTTCTG AGGCAGAAGAGA GCT CAGAG
TCTTCCCA TCTGTCTTCTCT CGG GTCTC
CACC G
GAM47 269 F11R 1 7420 NP_653087.1 3 522 ATCTCTGGGGCC A--- G 3 A c c
CACTCTCTTCTG AGGCAGAAGAGA GCT CAGAG
TCTTCCCA TCTGTCTTCTCT CGG GTCTC
CACC G
GAM47 269 FACL4 1 7050 NP_004449.1 3 373 AGGAAATTTGCA GAAGA 3 A c c
GCTTCCAATGCC AGGCA GAAGCTGCAGA
TCTTGTCT TCCGT CTTCGACGTTT
AAC--
GAM47 269 FACL4 1 7050 NP_075266.1 3 373 AGGAAATTTGCA GAAGA 3 A c c
GCTTCCAATGCC AGGCA GAAGCTGCAGA
TCTTGTCT TCCGT CTTCGACGTTT
AAC--
GAM47 269 FACL5 1 17702 NP_057318.1 5 89 GGGACACTCTGG AGAA G 3 A c c
GCCGGCCTTCTG AGGCAGAAG GCT CAGAG
CCTGCATG TCCGTCTTC CGG GTCTC
CGGC -
GAM47 269 FBXL2 1 11065 NP_036289.2 3 19 TCATTCTCTGCA AAGAGAA 3 A c c
GCAGCTGCCTGG AGGCAG GCTGCAGAG
GCCCAAGG TCCGTC CGACGTCTC
GA-----
GAM47 269 FGF23 1 15431 NP_065689.1 3 1905 AAATTTATCTCA AG G C 3 A c c
GCTTCTGTTAGC AGGC AA AGAAGCTG AGA
TTATCCTC TTCG TT TCTTCGAC TCT
A- G -
GAM47 269 FKSG44 1 14084 NP_114110.1 3 231 GGCTCCTCTGCA AAG AA 3 A c
c
GCCTGCCCTGCC AGGCAG AG GCTGCAGAG

TTCCCCCG TCCGTC TC CGACGTCTC
CCG --

GAM47	269 9	FLJ1125	1	1282	NP_060840.1	3	956	TGTTTATTTGCT CCTTCTCTTCAT AGGCA GAAGAGAAG GCAGA GCCTGTGG TCCGT CTTCTCTTC CGTTT A CT	-	CT		3	A	c	c
GAM47	269 0	FLJ1128	1	5027	NP_060849.2	3	320	CCTATCCAGAAT GCATCTCTTCTG AGGCAGAAGAGA TGCA CTTCCCAT TTCGTCTTCTCT ACGT --- AA	AGC	GA		3	A	c	c
GAM47	269 9	FLJ1153	1	16128	NP_079024.1	3	419	GGCAAATCTGCA GCCGCTCGCTTT AGG AGAA GAG GCTGCAGA CTCCTCTG TCC TCTT CTC CGACGTCT - TCG GC	C	---	AA	3	A	c	c
GAM47	269 5	FLJ1156	1	4833	NP_078933.2	3	41	TGTATACCCTTC TCTTCTCTTATC AGGCAGAAGA AAG AGAG TTCTGTCT TCTGTCTTCT TTC TCTC A TCT-	G	CTGC		3	A	c	c
GAM47	269 8	FLJ1160	1	4010	NP_078833.2	3	232	GACAGCTTCGCT CTTTCTCTTCCT AGGCAG AAGAGAAG GC AG GCCTTTCC TCCGTC TTCTCTTT CG TC C CT CT	-	CT AG		3	A	c	c
GAM47	269 1	FLJ1222	1	15788	XP_031342.1	3	642	AAGTCCTCGCTG CCCTCTCTTCTC AGG AGAAGAGA GC GC GAG ACCTGCTA TCC TCTTCTCT CG CG CTC AC CC T -	C-	A- T A		3	A	c	c
GAM47	269 0	FLJ1227	1	6928	XP_290704.1	3	180	GGTGGGCCTCTG CCTTCTCTTCTG AGGCAGAAGAGAAG GCAGAG TTTGGCCA TTTGTCTTCTCTTC CGTCTC --		CT		3	A	b	b
GAM47	269 5	FLJ1242	1	3483	XP_098290.1	3	1773	ACAAGTGATTTG CATTCTCTTCTT AGGC AGAAGAGAA TGCAGA CACGCTTT TTCG TCTTCTCTT ACGTTT CACT --	----	GC		3	A	c	c
GAM47	269 2	FLJ1255	1	3923	NP_073743.2	3	438	TACCCATTTTCA GCTTCTCTGCCT AGGCAGA GAAGCTG AGA CTCTTCTG TCCGTCT CTTCGAC TTT --- T	AGA	C		3	A	c	c
GAM47	269 4	FLJ1270	1	871	NP_079274.1	3	174	CTGACCTCTGCA A--- GCCTCTCTCATC GGCAGA AGAGA GCTGCAGAG TGCCAATT CCGTCT TCTCT CGACGTCTC TTAA AC C	--	A		3	A	c	c
GAM47	269 8	FLJ1278	1	2532	NP_071937.1	3	560	AAGCATCTGGGC CTTTCTCTTCCT AGG GAAGAGAA GCT CAGA CTTGGTCC TTC CTTCTCTT CGG GTCT TC TC -	CA	-- G		3	A	c	c
GAM47	269 4	FLJ1315	1	17478	NP_078874.1	3	263	CCTCTCCTCTCT TCCTCTCTTCTC AGG AGA GAGAAG AGAG TCTTCCTC TCC TCT CTCTTC TCTC	C A	CTGC		3	A	c	c

T - ----

GAM47 2694 FLJ1320 1 7166 NP_079037.2 3 2262 AAAATCTCTGCA C A --- 3 A c c
GTCAATTTTTAT AGG AGA GAGAA GCTGCAGAG
CTCCTCTG TCC TCT TTTTT TGACGTCTC
- A AAC

GAM47 2690 FLJ1371 1 18875 NP_079093.1 3 1150 CACAGCTCTGCA A-- AA--- 3 A c c
GCCTGGGCTCTG AGGCAG AGAG GCTGCAGAG
CCCTGCCT TCCGTC TCTC CGACGTCTC
CCG GGGTC

GAM47 2695 FLJ1385 2 5049 NP_075567.1 3 1097 GCTCCTCCCCTT A CTGC 3 A c c
CTTTCTCTTCCT AGGCAGAAG GAAG AGAG
TCTGCCTC TCCGTCTTC CTTC TCTT
- TCTT

GAM47 2695 FLJ1385 2 13447 NP_075567.1 3 1099 CTCCCCTTCTTT A CTGC 3 A c c
CTCTTCCTTCTG AGGCAGAAG GAAG AGAG
CCTCCCCC TCCGTCTTC CTTC TCTT
- TCTT

GAM47 2696 FLJ1414 1 888 NP_078985.1 3 771 GGACTACTCTGG AAG G 3 A c c
AGGGCTCTTCTG AGGCAGAAGAG CT CAGAG
CCTGGCAT TCCGTCTTCTC GA GTCTC
GG- G

GAM47 2692 FLJ1444 2 8273 NP_116174.1 3 372 TATCCTCTCCCA CA C C- 3 A c c
CTTTCTCTTCCC AGG GAAGAGAAG TG AGAG
TCTACTCA TCC CTTCTCTTT AC TCTC
-- C CC

GAM47 2692 FLJ1444 2 17024 NP_116174.1 3 473 CACCTGTCCTGT CA T A 3 A c c
GCTTCTCTTTCC AGG GAAGAGAAGC GCAG
TTACTTCT TCC TTTCTCTTCG TGTC
-- - C

GAM47 2691 FLJ1475 1 3661 NP_116223.1 3 1051 CCTTTCCCTCTG CA-- CT 3 A c c
TCTTCTCTTCAT AGG GAAGAGAAG GCAGAG
TACCTTTT TCC CTTCTCTTC TGTCTC
ATTA --

GAM47 2690 FLJ2006 1 14321 NP_060115.3 3 1942 AATGTGATTGCA A --- A 3 A c c
GCTTTTTGCCTT AGGC GAAG AGAAGCTGCAG
CAGCCTTT TCCG CTTC TTTTCGACGTT
A CGT A

GAM47 2692 FLJ2023 1 8193 NP_061881.2 3 1556 AAGCTCTCTGCA A- CA-- - - 3 A c c
GCTGTCTCATTC GG GAA GAGA AGCTGCAGAG
CTTCCCAA CC CTT CTCT TCGACGTCTC
AA CTTC A G

GAM47 2690 FLJ2040 2 4963 NP_060274.1 3 601 ACTGGGCCTGCA C A A A 3 A c c
GCTCCCTTCTCC AGG AGAAG GA GCTGCAG
TGGGACTT TCC TCTTC CT CGACGTC
- C - C

GAM47 2690 FLJ2040 2 12810 NP_060274.1 5 53 GCCGCCATTGCA --- G A 3 A c c
GCTTGTTTTCAC AGGCA GAAGA AAGCTGCAG
TTGCTTTT TTCGT CTTTT TTCGACGTT

TCA G A

GAM47 269 FLJ2048 1 7395 NP_060312.1 3 404 CTCCAGCCCTGC GA T A 3 A c c
9 GTTTCCATTCTG AGGCAGAA GAAGC GCAG
CCTTCTCA TCCGTCTT CTTTG CGTC
AC - C

GAM47 269 FLJ2075 1 19231 NP_060422.2 3 370 CCCTCTCCTGCT AGA T A 3 A c c
8 GCTGGACTTCTG AGGCAGAAG AGC GCAG
CCTTTGTT TCCGTCTTC TCG CGTC
AGG T C

GAM47 269 FLJ2081 1 11077 NP_060431.1 3 930 TTAGTCTCTGCA GA AA 3 A c c
3 GTCTCTTGTCTT AGGCA AGAG GCTGCAGAG
GAATTAAT TCTGT TCTC TGACGTCTC
-- --

GAM47 269 FLJ2088 1 636 NP_079475.1 3 242 CTTCCTCATCCT C TGCA- 3 A c c
6 GCTTCTCTTTTC AGG AGAAGAGAAGC GAG
CTCGCAGA TCC TTTTCTCTTCG CTC
- TCCTA

GAM47 269 FLJ2159 1 19872 NP_079099.1 3 2247 AATCCTACTTTC GA A C 3 A c c
6 AGCGTCATTCTG AGGCAGAA GA GCTG AGAG
CCTTTTGT TCCGTCTT CT CGAC TTTC
A- G -

GAM47 269 FLJ2217 1 12089 NP_079437.2 5 1138 GCAGAAGCTGCA GAAG A 3 A c c
5 GAGAATTTTCTG AGGCAGAAGA CTGCAG
CCTGACGA TCCGTCTTTT GACGTC
AAGA G

GAM47 269 FLJ2218 1 8410 XP_300713.1 5 21 ACCTCCTCTGCA A - A --- 3 A c c
4 GGCCCTTCCCTC AGGC GA AG GAAG CTGCAGAG
TCCGCCTG TCCG CT TC CTTC GACGTCTC
C C C CCG

GAM47 269 FLJ2230 1 889 NP_079112.1 3 374 GCCTTTATTCTG - GA CT 3 A c c
1 TCTTCTCTTGTC AGG CA AGAGAAG GCAGAG
CTATCTCA TCC GT TCTCTTC TGTCTT
T -- --

GAM47 269 FLJ2294 1 5374 NP_079421.2 3 16 CAGCACGTCGTG A AA - 3 A c c
4 TAGTCCTTTCTG AGGCAGAAG G GCTGCA GA
CCTCCAGG TCCGTCTTT C TGATGT CT
C -- G

GAM47 269 FLJ2351 1 12934 NP_078996.1 3 718 AACACCTCTGCA C- - AA 3 A c c
0 GTGCCTGCTTCT AGG AGAAG AG GCTGCAGAG
TACCTGGC TCC TCTTC TC TGACGTCTC
AT G CG

GAM47 269 FLJ3059 1 2004 NP_694556.1 5 285 CCTTCCCTGAGA C - - G A 3 A c c
4 CTGTCTCTTCTC AGG AGAAGAGA AG CT CAG
CTGTGAAA TCC TCTTCTCT TC GA GTC
- G A - C

GAM47 269 FLJ3068 1 8907 XP_166291.1 3 125 CATACATTTTTC C CTGC 3 A c c
1 TCTTCTCTTCTC AGG AGAAGAGAAG AGAG
CTGACGTC TCC TCTTCTCTTC TCTT

```
                                                  -       ----
GAM47   269   FLJ3105 1  18738  NP_689591.1  3  391   GTCCCCTCTGCA   CA  -  AAG          3  A  c
c
          2                          GGCTCATTCCTC AGG  GAA GAG   CTGCAGAG
                                     CTTGGTCT    TCC  CTT CTC   GACGTCTC
                                               TC   A   G--
GAM47   269   FLJ3112 1  12105  NP_653324.1  3  730   TAGATTGTTTCA    GA       C         3  A  c  c
          1                          GCTTCTCTTGTT AGGCA  AGAGAAGCTG AGA
                                     TCATTTTC    TTTGT  TCTCTTCGAC TTT
                                                --       -
GAM47   269   FLJ3161 1  3137   NP_689786.1  3  588   GTAACCTCTGCA     AAGAG---  -        3  A  c  c
          4                          GACTTAAGTGTC AGGCAG       AAG CTGCAGAG
                                     CCTGTCTG    TCTGTC       TTC GACGTCTC
                                                  CCTGTGAA   A
GAM47   269   FLJ3211 1  17063  NP_689534.1  3  226   CTTAAAATCTCG   C       C  C         3  A  c  c
          5                          TTTTCTCTTCTT AGG AGAAGAGAAG TG AGA
                                     CCTTCTTT    TCC TCTTCTCTTT GC TCT
                                               T       T  -
GAM47   269   FLJ3278 1  15892  NP_653224.1  3  314   GGTGTCTCTGCA    AGAA  A--          3  A  c
c
          4                          GCTGGCCTCCGG AGGC   GAG   AGCTGCAGAG
                                     AGCCTTCC    TCCG   CTC   TCGACGTCTC
                                                  AGGC   CGG
GAM47   269   FLJ3308 1  17824  NP_689713.1  3  442   CTTAACTTTTCT        AAGC          3  A  c  c
          4                          GTACCTCTTCTG AGGCAGAAGAG   TGCAGAG
                                     TTTTTGTA    TTTGTCTTCTC    ATGTCTT
                                                  C---
GAM47   269   FLJ3362 1  20089  XP_087304.2  5  31    GGAAACTCTGCA  GC   A  -          3  A  c  c
          0                          GCTTTGTCATCT AG  AGA GA GAAGCTGCAGAG
                                     AACTCTTC    TC  TCT CT TTTCGACGTCTC
                                               AA   A  G
GAM47   269   FLJ3364 1  460    NP_689900.1  3  1015  TTCCTTCACAGC        --    CA       3  A  c  c
          1                          TTTGCTTTTCTG AGGCAGAAGAG  AAGCTG  GAG
                                     CCTCTTCT    TCCGTCTTTTC  TTCGAC  TTC
                                                  GT     AC
GAM47   269   FLJ3620 1  17922  XP_208927.2  5  1510  GAGCCTCCAGTA    AGA       A-       3  A  c  c
          8                          GCTTCTCTGGGC AGGC   AGAGAAGCTGC  GAG
                                     CTGGCAGA    TCCG   TCTCTTCGATG  CTC
                                                  GG-         AC
GAM47   269   FLJ3688 1  2080   NP_849152.1  3  517   TTCACTTTGTTC          CT-         3  A  c  c
          8                          ATTTCTCTTCTG AGGCAGAAGAGAAG   GCAGAG
                                     TTTTCTGT    TTTGTCTTCTCTTT   TGTTTC
                                                  ACT
GAM47   269   FLJ3688 1  2080   XP_059053.7  3  517   TTCACTTTGTTC          CT-         3  A  c  c
          8                          ATTTCTCTTCTG AGGCAGAAGAGAAG   GCAGAG
                                     TTTTCTGT    TTTGTCTTCTCTTT   TGTTTC
                                                  ACT
GAM47   269   FLJ3773 1  890    NP_787087.1  3  320   CCCTTCCACCTC       AGAAGCT          3  A  c
c
```

5 TGTTGGTTTCTG AGGCAGAAG GCAGAG
CCTCCCTT TCCGTCTTT TGTCTC
GGT----

GAM47 269 FLJ3792 1 832 NP_689836.1 3 1095 ATCTGAATTCTT C A TG----- 3 A c c
7 GCTTCTCTCTCC AGG AGA GAGAAGC CAGA
TTTTCCTT TCC TCT CTCTTCG GTCT
- - TTCTTAA

GAM47 269 FLJ3835 1 7421 NP_689731.1 3 191 ACAACACAGCTG AGCT A 3 A c c
9 CCGTTTCTTCTG AGGCAGAAGAGA GCAG
CCTGCTTA TCCGTCTTCTTT CGTC
GC-- G

GAM47 269 FLJ3870 1 13655 NP_776193.1 3 835 GTGCCCTCGGCA A- AGA A 3 A c
c
5 GCTTCGGTCCAG AGGC GA GAAGCTGC GAG
CCTGCATC TCCG CT CTTCGACG CTC
AC GG- G

GAM47 269 FLJ9025 1 4053 NP_775962.1 3 94 CAGGGACTACTG AGAAGC - 3 A c
c
4 CACCCGCTTCTG AGGCAGAAG TGCAG AG
CCTTGTTT TCCGTCTTC ACGTC TC
GCCC-- A

GAM47 269 FLJ9058 1 4834 NP_776189.1 3 190 GTCACAGCCCCT C AA C A 3 A c c
3 CAGTCTCTTCTC AGG AGAAGAG GCTG AG
CTTCCCCT TCC TCTTCTC TGAC TC
- -- - C

GAM47 269 FOXP4 1 4743 NP_612466.1 3 907 GGCCTCTCTGCA C AA- A- 3 A c c
GTCCTCTCACCC AGG AG GAGA GCTGCAGAG
TCCCTCAG TCC TC CTCT TGACGTCTC
C CCA CC

GAM47 269 FRCP2 1 7324 NP_715637.1 3 687 CTAGCTGCACAG C - -- A 3 A c c
TTCTCTCTTCTC AGG AGAAGAGA AGCT GCAG
CTTGTCCT TCC TCTTCTCT TTGA CGTC
- C CA G

GAM47 269 FUT6 1 979 NP_000141.1 3 160 TCACCTGTTGCA AAGA A 3 A c c
GCTTCACCTGCC AGGCAG GAAGCTGCAG
TGGGGATT TCCGTC CTTCGACGTT
CA-- G

GAM47 269 GABBR1 1 9955 NP_001461.1 3 372 GCAACCCCTGCA A A A A 3 A c c
GCTCCTCTGCCT AGGCAGA G GA GCTGCAG
TTGTGCTC TCCGTCT C CT CGACGTC
- - - C

GAM47 269 GABBR1 1 9955 NP_068703.1 3 372 GCAACCCCTGCA A A A A 3 A c c
GCTCCTCTGCCT AGGCAGA G GA GCTGCAG
TTGTGCTC TCCGTCT C CT CGACGTC
- - - C

GAM47 269 GABBR1 1 9955 NP_068704.1 3 372 GCAACCCCTGCA A A A A 3 A c c
GCTCCTCTGCCT AGGCAGA G GA GCTGCAG
TTGTGCTC TCCGTCT C CT CGACGTC
- - - C

GAM47 269 GABBR1 1 9955 NP_068705.1 3 1369 GCAACCCCTGCA A A A A 3 A c c

GCTCCTCTGCCT AGGCAGA G GA GCTGCAG
TTGTGCTC TCCGTCT C CT CGACGTC
- - - C

GAM47 269 GAD1 1 10685 NP_000808.1 5 312 GCCTCTCCGAAT C - C-- C 3 A c c
CTCTCTCTTCTC AGG AGAAGAGA AG TG AGAG
CTGGCGCT TCC TCTTCTCT TC GC TCTC
- C TAA C

GAM47 269 GALNT10 1 8570 NP_060010.2 5 4 CACATTTCTTAG AGA C 3 A c c
CTTCTCTGAGCC AGGC AGAGAAGCTG AGAG
TCCATTTC TCCG TCTCTTCGAT TCTT
AG- -

GAM47 269 GALT 1 14804 NP_667342.1 3 661 TCCTGGGCACAT C--- AG 3 A c c
TCTTTTCTTCTG AGGCAGAAGAGAAG TGC AG
CTTCCCTT TTCGTCTTCTTTTC ACG TC
TTAC GG

GAM47 269 GALT 1 14804 NP_667343.1 3 172 TCCTGGGCACAT C--- AG 3 A c c
TCTTTTCTTCTG AGGCAGAAGAGAAG TGC AG
CTTCCCTT TTCGTCTTCTTTTC ACG TC
TTAC GG

GAM47 269 GAN 1 1594 NP_071324.1 3 797 AGGGTCTCCTGC GAGAA A 3 A c c
AGTGCCATTCTG AGGCAGAA GCTGCAG
CCTTCTCA TCCGTCTT TGACGTC
ACCG- C

GAM47 269 GATA2 1 3495 NP_116027.2 3 491 CAGCCTGCACCC G C--- A 3 A c c
TCTTCTCTTCTG AG CAGAAGAGAAG TGCAG
GCTTCCCT TC GTCTTCTCTTC ACGTC
G TCCC C

GAM47 269 GBP5 2 10024 NP_443174.1 5 103 GGAATGTCTGCA A-- --- A A 3 A c c
GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A

GAM47 269 GBP5 2 14365 NP_443174.1 5 207 CGAAGGTCTGCA A--- -- A A 3 A c c
GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AGCCAGCC CCG TC TC CTTCGACGTCT
CCGA AG C A

GAM47 269 GCN5L2 1 1805 NP_066564.1 3 156 CCCGATCCTGCA -- A A A 3 A c c
GCTCTTTCTGGA AGG CAGA GAGA GCTGCAG
CCTTCAGG TCC GTCT TTCT CGACGTC
AG - - C

GAM47 269 GDF1 1 13970 NP_001483.2 5 378 GAGCGCTTGGAA C GCA 3 A c c
GTTTCTCTTCTA AGG AGAAGAGAAGCT GAG
CCTGGGCA TCC TCTTCTCTTTGA TTC
A AGG

GAM47 269 GLTSCR1 1 18169 NP_056526.1 5 10 CTCCACTCTGCA C AA- AA 3 A c
c

GCCTCAAACTCC AGG AG GAG GCTGCAGAG
TGGGCTCC TCC TC CTC CGACGTCTC
- AAA --

GAM47 269 GMPR 1 9389 NP_006868.2 3 134 TGGAATGCTGTG A- T A 3 A c c
TCCTCTCTTCTG AGGCAGAAGAGA GC GCAG

TCTCCTGC TCTGTCTTCTCT TG TGTC
CC - G
GAM47 269 GNA15 1 1917 NP_002059.1 3 155 CCCGCTGCTGGC -- A-- - A 3 A c c
CGCTCTCTTCTC AGGCAGA AGAGA GCT GCAG
TGCCTCTC TCCGTCT TCTCT CGG CGTC
CT CGC T G
GAM47 269 GP1BA 1 19965 NP_000164.1 5 12 TCTGTGCCTTCG - ----- CT 3 A c c
GAGGTCTTTCTG AGGCAGAA GA GAAG GCAGA
CCTGCCTG TCCGTCTT CT CTTC TGTCT
T GGAGG CG
GAM47 269 GPR74 1 16837 NP_444264.1 5 7 CCTCTGCCCACC CT---- 3 A c c
TCTTCTCTTCTG AGGCAGAAGAGAAG GCAGAG
CTTCCATA TTCGTCTTCTCTTC CGTCTC
TCCACC
GAM47 269 GPR92 1 17507 NP_065133.1 3 779 CTCTCTCCTCTC C - CTGC 3 A c c
CTCTCTCTTCTC AGG AGAAGAGA AG AGAG
CTCTTCTC TCC TCTTCTCT TC TCTC
- C C---
GAM47 269 GSTM5 1 10604 NP_000842.2 3 124 TTCTTTCTACTC A----- CTGC 3 A c c
TCTTCTCTTCCC AGGC GAAGAGAAG AGAG
CAAGGCCT TCCG CTTCTCTTC TCTC
GAACCC ----
GAM47 269 HABP2 1 14769 NP_004123.1 3 201 CACAATATCACC GA GCA- 3 A c c
AGGCTTCTTCTG AGGCAGAAGA AGCT GA
CCTCCCTT TCCGTCTTCT TCGG CT
-- ACCA
GAM47 269 HDAC5 1 1806 NP_631944.1 3 562 ACCATCTCTGCA C A AAG- 3 A c c
GACCCCTCTCCT AGG AG AGAG CTGCAGAG
CCTCCTTC TCC TC TCTC GACGTCTC
- C CCCA
GAM47 269 HES2 1 4547 XP_290879.1 3 593 CACCTCCACTCC AGA GCA 3 A c c
TAGGCTTTTCTG AGGCAGA GAAGCT GAG
CCTAGAGC TCCGTCT TTTCGG CTC
--- ATC
GAM47 269 HEXA 1 13753 NP_000511.1 3 338 ACCTATAGCCTT GAGA T 3 A c c
TGTGCTGTTCTG AGGCAGAA AGC GCAGAG
CCTTGCCT TCCGTCTT TCG TGTTTC
G--- -
GAM47 269 HGS 1 10117 NP_004703.1 3 445 TTCAGGTCTCCA A -- --- C 3 A c c
GCTTCTCTGCTT GGC AGA AGAGAAGCTG AGA
CTCAGCTG TCG TCT TCTCTTCGAC TCT
G AC TCG C
GAM47 269 HIRIP3 1 12016 NP_003600.2 5 95 CGCGAGGATGCC CT GA 3 A c c
TTTTCTCTTCTG AGGCAGAAGAGAAG GCA
CCTTGCGA TCCGTCTTCTCTTT CGT
TC AG
GAM47 269 HLA-DOB 1 11289 NP_002111.1 3 29 GTCCTCACTGAA --- - G A 3 A c c

GCTTCTCTCTCT AGGC AGA AGAGAAGCT CAG
GGAGCCTG TCCG TCT TCTCTTCGA GTC
AGG C A A

GAM47 269 HOXA3 1 2711 NP_705896.1 5 69 GCGGCTGCTGCC AA--- T A 3 A c c
CTCCCTCTTCTG AGGCAGAAGAG GC GCAG
CCTCCCCT TCCGTCTTCTC CG CGTC
CCTCC T G

GAM47 269 HOXB8 1 1287 NP_076921.1 3 594 GCTTTCTCTCTG C - C 3 A c c
GCTTCTCTCTTT AGG AGA AGAGAAGCTG AGAG
TCCTCCTC TCC TTT TCTCTTCGGT TCTC
T C C

GAM47 269 HRH1 1 16395 NP_000852.1 3 579 CCTTCTCAGAAA -- ---- C 3 A c c
ACTTCTCTTCTG AGGC AGAAGAGAAG CTG AGAG
AGCCTCTT TCCG TCTTCTCTTC GAC TCTT
AG AAAA -

GAM47 269 HS2ST1 2 2206 NP_036394.1 3 4290 ATGCTCACTACT C A CTGC 3 A c
c

TTCTCTCTTCTC AGG AGA GAGAAG AGAG
TCTCCCTG TCC TCT CTCTTC TCTC
C - ----

GAM47 269 HS2ST1 2 10600 NP_036394.1 3 395 AGATGAGTCCAT AAGCT 3 A c c

TTGCCTCTTCTG AGGCAGAAGAG GCAGA
CCTTCACT TCCGTCTTCTC CGTTT

GAM47 269 HS3ST4 1 3789 XP_056254.4 3 90 TTGAATACCCCA AG GA A 3 A c c
GCTTCTGCAGCT GCA AG GAAGCTGCAGAG
TCACTTGC CGT TC CTTCGACGTCTT
-- -- A

GAM47 269 HSD3B7 1 17703 NP_079469.2 3 641 GTGGCCTGCCCC G A --- A 3 A c c

AGCTCTCTTCTG AG CAGAAGAGA GCT GCAG
GCTTTCTG TC GTCTTCTCT CGA CGTC
G - CCC C

GAM47 269 HTATIP 1 10365 NP_006379.1 3 387 CAAAAATTTCTG CAG TG 3 A c c
GCTTCTCTTACC AGG AAGAGAAGC CAGAG
CCTATTGC TCC TTCTCTTCG GTCTT
CCA --

GAM47 269 HYOU1 1 10294 NP_006380.1 3 527 CTCCCTCTGCGG ---- - - 3 A b b
GCTTCTCTTGCT AGGC AG AAGAGAAGCT GCAGAG
CTGAGCCT TCCG TC TTCTCTTCGG CGTCTC
AGTC G G

GAM47 269 HYPB 1 10651 NP_036403.1 3 215 GCTCCCTCTCAC AAGC- C 3 A c c
CACCCTCTTCTG AGGCAGAAGAG TG AGAG
CCTATGAG TCCGTCTTCTC AC TCTC
CCACC -

GAM47 269 IAN4L1 1 18040 NP_060854.2 3 548 TATTTGAGCTCC C ----- G 3 A c c
GGGTCTCTTCTA AGG AGAAGAGA AGCT CAGA
CCTGCATT TCC TCTTCTCT TCGA GTTT
A GGGCC -

GAM47 269 IBA2 1 6376 NP_113614.1 3 941 AAACCTGACTCT A A CT 3 A c c
GCTTCTCTCATT AGGCAGA GAGA G GCAGAG
TGTCTTCC TCTGTTT CTCT C CGTCTC
A - TT
GAM47 269 IL1RL1 1 1862 NP_003847.2 3 182 TGTTTGCTGGGA A ---- 3 A c c
GCTTCTCTGCTG AGGCAG AGAGAAGCT GCAGA
CTTAAATT TTCGTC TCTCTTCGA CGTTT
G GGGT
GAM47 269 IL1RL1 1 1862 NP_775661.1 3 559 TGTTTGCTGGGA A ---- 3 A c c
GCTTCTCTGCTG AGGCAG AGAGAAGCT GCAGA
CTTAAATT TTCGTC TCTCTTCGA CGTTT
G GGGT
GAM47 269 IRS3L 1 3181 XP_295210.1 3 245 CCTTTGCATGTT C --- - 3 A c c
CCATCTCTTCTC AGG AGAAGAGA AGC TGCAGAG
TTTCTCCC TTC TCTTCTCT TTG ACGTTTC
- ACC T
GAM47 269 ITGAD 1 15692 XP_113880.1 3 1097 GACCTCTTCACT CA A -- C 3 A c c
GCTTCTCTCCCC AGG GA GAGAAGC TG AGAG
TTCGAGAA TCC CT CTCTTCG AC TCTC
C- - TC T
GAM47 269 ITPR2 1 15620 NP_002214.1 5 155 GCGGCGGCTGCG AGA- A 3 A c c
GCTTCTCTGGGC AGGC AGAGAAGCTGCAG
GCCTGGGC TCCG TCTCTTCGGCGTC
CGGG G
GAM47 269 JMJ 2 14602 NP_004964.2 3 497 CTTTGCTTTGGC A----- - - --- 3 A c c
TGTCGTCTTCTG GGCAGAAGA GA AGCT GCAGA
CCGTGTGC CCGTCTTCT CT TCGG CGTTT
CGTGTG G G TTT

G
C

GAM47 269 JMJ 2 14768 NP_004964.2 3 1627 CCTCTTTTTGAC AGAA - 3 A c c
AGTAAACTTCTG AGGCAGAAG GCTG CAGAG
CCTATGGC TCCGTCTTC TGAC GTTTT
AAA- A
GAM47 269 JPHL1 2 511 XP_033366.1 5 148 CTACCCACCCTC C CTGC- 3 A c c
TTCTCTCTTCTC AGG AGAAGAGAAG AGAG
TTCTCCCT TCC TCTTCTCTTC TCTC
C TCTCT
GAM47 269 JPHL1 2 7827 XP_033366.1 5 150 CACCCTCTTCTC C CTGC- 3 A c c
TCTTCTCTTCTC AGG AGAAGAGAAG AGAG
CCTGCCCC TCC TCTTCTCTTC TCTC
C TCTCT
GAM47 269 K5B 1 19844 NP_775487.1 5 32 TGTCCGTCTGCA AAGAGA 3 A c c
GCTGCGTGACTG AGGCAG AGCTGCAGA
TCTGTCTC TCTGTC TCGACGTCT
AGTGCG
GAM47 269 KBF2 1 16939 NP_056958.1 3 1113 TTTCATTCAGCA GAAG A 3 A c c
GGGTATTTTCTG AGGCAGAAGA CTGC GAG

CCTTGTTG TCCGTCTTTT GACG CTT
ATGG A
GAM47 269 KCNJ10 1 13377 NP_002232.2 3 944 ACACTGTACCTG C ---- A 3 A c c
GCTTCTCTTCTT AGG AGAAGAGAAGCT GCAG
CCTTTCCT TCC TCTTCTCTTCGG TGTC
T TCCA A
GAM47 269 KCNN2 2 7656 NP_740721.1 5 210 CGAAGGTCTGCA A--- -- A A 3 A c c
GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AGCCAGCG CCG TC TC CTTCGACGTCT
GCGA AG C A
GAM47 269 KCNN2 2 17552 NP_740721.1 5 106 GAAAGGTCTGCA A-- --- A A 3 A c c
GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A
GAM47 269 KCNQ2 1 5313 NP_004509.2 3 2189 TTTCCTGGCCCA C - --- A 3 A c c
GCTTCTCCTTCT AGG AGAAG AGAAGCTG CAG
CCCTCTGC TCC TCTTC TCTTCGAC GTC
C C CCG C
GAM47 269 KHK 1 14640 NP_000212.1 3 232 TCCTCAGAGCCA ---- A - A-- 3 A c c
GCTTCTCCTCTC AGGCA GA GAGAAGCTG C GAG
AATGTCTG TCTGT CT CTCTTCGAC G CTC
AACT C C AGA
GAM47 269 KHK 1 14640 NP_006479.1 3 232 TCCTCAGAGCCA ---- A - A-- 3 A c c
GCTTCTCCTCTC AGGCA GA GAGAAGCTG C GAG
AATGTCTG TCTGT CT CTCTTCGAC G CTC
AACT C C AGA
GAM47 269 KIAA004 1 9372 NP_055471.1 3 2163 ATGCTTCTCTGA AAGCTG 3 A c
c
0 TTCCCTCTTCTG AGGCAGAAGAG CAGAG
CCTGCACC TCCGTCTTCTC GTCTC
CCTTA-
GAM47 269 KIAA012 1 11734 NP_055607.1 3 2402 AGCACCTCTGCA AGA AGAA 3 A c
c
5 GCCTGCTGGGCC AGGC AG GCTGCAGAG
TCAGGTTC TCCG TC CGACGTCTC
GG- GTC-
GAM47 269 KIAA014 1 19181 NP_055476.1 3 295 GCTTTGAAGTTT A TG---- 3 A c c
0 GCGTCTTTTCTG AGGCAGAAGAGA GC CAGAG
CCTCTTTC TCCGTCTTTTCT CG GTTTC
G TTTGAA
GAM47 269 KIAA015 1 15014 NP_055545.1 3 2274 GTAAGCCAAGCA AG AGA 3 A c
c
2 GCTTTGCTTCTG AGGCAGAAG AAGCTGC
CCTCTGTT TCCGTCTTC TTCGACG
GT AAC
GAM47 269 KIAA024 1 11188 NP_055549.1 3 3560 GTGAGGCTGGGA AG G- A 3 A c
c
7 GCTTCTCTTGGG AGGC AAGAGAAGCT CAG
CCTGCTGG TCCG TTCTCTTCGA GTC
GG GG G

GAM47 269 KIAA026 1 19568 XP_045954.2 3 2592 TTTATGCCTGCT AGA T A 3 A c c
5 GCTTCTCTGCCT AGGCAGA GAAGC GCAG
CTTTGAGG TCCGTCT CTTCG CGTC
--- T C
GAM47 269 KIAA034 1 9739 XP_047357.3 3 603 TTTCTCTCTGTG AA TG 3 A c c
2 GCGACTTTTCTG AGGCAGAAGAG GC CAGAG
CCTTCCCT TCCGTCTTTTC CG GTCTC
AG GT
GAM47 269 KIAA045 1 9509 XP_044546.3 3 1822 AGCTCCTCTGCA A A - 3 A b b
3 GCTTCCTCCTCA AGGC GA GAG AAGCTGCAGAG
GCCTCCCT TCCG CT CTC TTCGACGTCTC
A C C
GAM47 269 KIAA045 1 8206 NP_055654.1 3 749 CTTTTCTGCATA -- 3 A b b
5 GTTTTTCTTCTG AGGCAGAAGAGAAGCT GCAGAG
CTTACTTT TTCGTCTTCTTTTTGA CGTCTT
TA
GAM47 269 KIAA045 1 8206 XP_051785.3 3 749 CTTTTCTGCATA -- 3 A b b
5 GTTTTTCTTCTG AGGCAGAAGAGAAGCT GCAGAG
CTTACTTT TTCGTCTTCTTTTTGA CGTCTT
TA
GAM47 269 KIAA047 1 15061 NP_055672.1 3 4063 CACAGCTCTGCA CA G AA 3 A c
c
1 GCCTGTTTCCTA AGG GAA AG GCTGCAGAG
CAACCAGA TCC TTT TC CGACGTCTC
-- G --
GAM47 269 KIAA047 1 18719 XP_290898.1 5 79 TTCTGGGTTCAA AA - ---- 3 A c c
2 GTGATTCTTCTG AGGCAGAAGAG GCT G CAGAG
CCTCAGCC TCCGTCTTCTT TGA C GTCTT
AG A TTGG
GAM47 269 KIAA053 1 5472 XP_047659.6 3 1283 TGGCTCACTGCA AA --- A 3 A c c
2 GCTTAAGCTCAC AGGCAG GAG AAGCTGCAG
TGCCTGGG TCCGTC CTC TTCGACGTC
A- GAA A
GAM47 269 KIAA057 1 4468 XP_291018.1 3 4726 TCTATCTCTGCA - AG G 3 A c c
0 GTTCTGTCTGAC AGG CAGA AGAA CTGCAGAG
TTAGCTGA TTC GTCT TCTT GACGTCTC
A G- -
GAM47 269 KIAA060 1 19802 NP_055509.1 3 76 GGGGCTGCTGCA AGAAG A 3 A c
c
5 GCTTCTGGGGCC AGGC AGAAGCTGCAG
TCCACAGA TCCG TCTTCGACGTC
GGG-- G
GAM47 269 KIAA072 1 5642 NP_067680.2 3 1726 CCTCATTTCTCA CA ------- C 3 A c c
1 GCTTCTGCATTT AGG GAAG AGAAGCTG AGAG
CCTTCCCT TCC CTTC TCTTCGAC TCTT
-- CTTTACG -
GAM47 269 KIAA079 1 12202 NP_056093.1 3 384 TCTGATAGTGCC AA----- - 3 A c c
0 CTTGCTCTTCTG AGGCAGAAGAG GCTG CAGA
TCTGTCAT TCTGTCTTCTC TGAT GTCT

GTTCCCG A

GAM47 2695 KIAA0791 6957 NP_079286.1 3 1042 GGATACTTTGCA GA A 3 A c c
GCTTCCTATGTT AGGCA AG GAAGCTGCAGAG
TGAGTGAC TTTGT TC CTTCGACGTTTC
A- -

GAM47 2691 KIAA0841 11413 XP_049237.1 3 1020 GGGTTATATCTG A----- TG 3 A c c
GCTTCTCTCCAG AGGCAG AGAGAAGC CAGA
ACCTGCTT TTCGTC TCTCTTCG GTCT
CAGACC --

GAM47 2693 KIAA0841 5395 NP_055760.1 3 335 GTGCCTGAAGAA A CTGC 3 A c c
GTCTCTCTTCTC AGGCAGA GAGAAG AGAG
TCTGCTTC TTCGTCT CTCTTC TCTC
- ----

GAM47 2699 KIAA0881 4048 NP_056192.1 3 1374 ACAACCTCAGCA AA A 3 A c c
GCTTCTCCCTGT AGGCAG GAGAAGCTGC GAG
CTTCCTCT TCTGTC CTCTTCGACG CTC
C- A

GAM47 2699 KIAA0881 4048 NP_689470.1 3 581 ACAACCTCAGCA AA A 3 A c c
GCTTCTCCCTGT AGGCAG GAGAAGCTGC GAG
CTTCCTCT TCTGTC CTCTTCGACG CTC
C- A

GAM47 2696 KIAA1071 6169 XP_037523.6 3 1808 TTCTCTTCCGTT AGAA 3 A c c
TGCGGTTTTCTG AGGCAGAAG GCTGCAGA
CCTAATTG TCCGTCTTT TGGCGTTT

GAM47 2695 KIAA1141 14401 NP_065749.1 3 2773 TTAATCTCTGCA C A - 3 A c c
GTTTATTCTCTC AGG AGA GAG AAGCTGCAGAG
TTAAGGAA TTC TCT CTT TTTGACGTCTC
- - A

GAM47 2695 KIAA1151 17447 XP_030864.2 3 3869 AGCACCTCTGCA A AA--- 3 A c c
GCCTCTGCTCTG AGGCAG AGAG GCTGCAGAG
CTGCCTTG TCCGTC TCTC CGACGTCTC
G GTCTC

GAM47 2697 KIAA1151 715 XP_051093.2 3 1856 TCTTCATCTGCA CA A-- 3 A c c
GCACGTTTCTTC AGG GAAGAGA GCTGCAGA
CTCCTGCA TCC CTTCTTT CGACGTCT
TC GCA

GAM47 2698 KIAA1191 11270 NP_065765.1 3 775 CTCTGGGTTCAA AA - ---- 3 A c c
GCAATTCTTCTG AGGCAGAAGAG GCT G CAGAG
CCTCAGCC TCCGTCTTCTT CGA C GTCTC
AA A TTGG

GAM47 2697 KIAA1251 5577 XP_031577.2 5 158 GTGCGCTCTGCA GA- A A-- 3 A c c
GCATGTCGCTAC AGGCA AG GA GCTGCAGAG
ATGCCTGG TCCGT TC CT CGACGTCTC
ACA G GTA

GAM47 2694 KIAA1471 13050 NP_065907.1 3 1352 TCCCACACTGCA A- - A 3 A c c
GCTTTATCTTTA AGGC GAAGA GAAGCTGCAG
GGCTTATG TTCG TTTCT TTTCGACGTC
GA A A

GAM47 269 KIAA151 1 15469 XP_046581.5 3 1425 CTTTAGCTCCAT - G CA 3 A c c
1 AGTTCTCTTCTC AGGC AGAAGAGAA CTG GAG
GCCTCATA TCCG TCTTCTCTT GAT CTC
C - AC
GAM47 269 KIAA157 1 2423 NP_060681.1 3 1699 TTTTGCATTACT GA--- C-- 3 A c c
9 GTATGTCTTCTG AGGCAGAAGA AG TGCAGAG
CCTCCACA TCCGTCTTCT TC ACGTTTT
GTATG ATT
GAM47 269 KIAA159 1 16420 XP_048128.4 3 772 GTTCACTCTGCA A- ----- G 3 A c c
6 GTTCTCTTGCCT GGCAG AAGAGAA CTGCAGAG
ACTGCCAT CCGTC TTCTCTT GACGTCTC
TA ATCCG -
GAM47 269 KIAA169 1 8926 XP_166523.1 3 540 CATCTCTCTGCA A A AA- 3 A c c
1 GTGCCCTCCTCG AGGC GA GAG GCTGCAGAG
CCTGTGCA TCCG CT CTC TGACGTCTC
- C CCG
GAM47 269 KIAA173 2 11569 XP_290496.1 3 655 TAAGACCTTGGG A- G A 3 A c c
5 CTGCCTCTTCTG AGGCAGAAGAG AGCT CAG
TCTTAACT TCTGTCTTCTC TCGG GTT
CG - C
GAM47 269 KIAA173 2 15572 XP_290496.1 3 684 ACTGGTTCTGCA A---- - G 3 A c c
5 GCTTGTCCTTTT GGCAGAAG A AAGCTGCAGAG
GCCCACAT CCGTTTTC T TTCGACGTCTT
TACAC C G
GAM47 269 KIAA175 1 15393 NP_277047.1 3 84 TTTGGCTCTCTG A----- CT 3 A c c
0 CCTTCTCTTCAT AGGC GAAGAGAAG GCAGAG
GTTGGCCT TCCG CTTCTCTTC CGTCTC
GTTGTA --
GAM47 269 KIAA175 1 18714 NP_203755.1 3 2087 GGATCTCCCATA A CA- 3 A c c
4 GCTTCTCCTTTG AGGCAGA GAGAAGCTG GAG
CTTCCAGG TTCGTTT CTCTTCGAT CTC
C ACC
GAM47 269 KIAA182 1 8005 XP_290834.1 3 996 TCCTGGGCTCAA A AA A- 3 A c c
7 GCAGTCCTTCTG AGGCAGAAG G GCTGC GAG
CCTTAGCC TCCGTCTTC C TGACG CTC
- -- AA
GAM47 269 KIAA184 1 9906 NP_852149.1 3 932 CTGGGACCTGCA AGAGAA A 3 A c
c
7 GCTCTGCCTTTG AGGCAGA GCTGCAG
CTGGCTGG TCCGTCT CGACGTC
------ C
GAM47 269 KIAA185 2 9110 XP_049884.1 3 2620 CCCTCTGCAGGA A------- AA --- 3 A c c
4 GCTTCTCCTGCC GGCAG GAGAAGCT GCAGA
GCCAGCCA CCGTC CTCTTCGA CGTCT
ACCGACCG -- GGA

G
C

GAM47 269 KIAA185 2 16614 XP_049884.1 3 2620 AACCCCTCTGCA A---- AA --- 3 A c c

4 GGAGCTTCTCCT GGCAG GAGAAGCT GCAGAG
GCCGCCAG CCGTC CTCTTCGA CGTCTC
GACCG -- GGA

GAM47 269 KIAA190 1 1062 XP_056282.1 3 639 GAACCCCCTGCA ---- G A A 3 A c c
4 GCTCTCTTGTGG AGG CA AAGAGA GCTGCAG
ACCCCTGC TCC GT TTCTCT CGACGTC
CCAG G - C

GAM47 269 KIAA190 1 4011 XP_055834.1 5 624 GATCGGATTTGC CT 3 A b b
8 TTTTCTCTTCTG AGGCAGAAGAGAAG GCAGA
CCTCGGAT TCCGTCTTCTCTTT CGTTT
T-

GAM47 269 KIAA197 1 1151 XP_058800.3 5 730 CGAGCAACTGTC AA - A 3 A c c
7 AGCATTTTTCTG AGGCAGAAGAG GCTG CAG
CCTGCCTG TCCGTCTTTTT CGAC GTC
A- T A

GAM47 269 KIF12 1 13316 NP_612433.1 5 114 CCGGACTCTGCA - AA 3 A b b
GTTTCTCCTGCA AG GCAG GAGAAGCTGCAGAG
CTGTTTTC TC CGTC CTCTTTGACGTCTC
A --

GAM47 269 KIF5A 1 12319 NP_004975.1 3 220 AGCTGCTGCTAT ----- T A 3 A c c
GTCTCTCTTCTG AGGCAGAAGAGA AGC GCAG
TCTTATTC TCTGTCTTCTCT TCG CGTC
CTGTA T G

GAM47 269 KPNA4 1 18627 NP_002259.1 3 752 GTTTACTCTGCA GAA-- 3 A c c
GCCTGTGTTTTC AGGCAGAAGA GCTGCAGAG
TGTTTCCC TTTGTCTTTT CGACGTCTC
GTGTC

GAM47 269 KSP37 1 11509 NP_114156.1 3 159 TCTTGATCTGCA AGA 3 A c c
GCTTCTCTGAAG AGGC AGAGAAGCTGCAGA
TTTGGAAA TTTG TCTCTTCGACGTCT
AAG

GAM47 269 LENG8 1 5511 NP_443157.1 3 824 CACGTCATGTTG C - T - 3 A c c
CCTTCTCTTTTC AGG AGAAGAGAAG C GCA GA
TTTGTGTG TTC TTTTCTCTTC G TGT CT
- C T A

GAM47 269 LEP5 1 598 NP_848130.1 3 40 GACTTCCTCTTC G- CTGC 3 A c c
CTTCTGATTCTG AGGCAGAA AGAAG AGAG
CCTGAATA TCCGTCTT TCTTC TCTC
AG CT--

GAM47 269 LGI3 1 11001 NP_644807.1 3 284 CCCTACTCTGCA A A----- A 3 A c c
GCCTTTCCCATG GGCAGA GAGA GCTGCAGAG
CTCTGCCC CCGTCT CTTT CGACGTCTC
C CGTACC C

GAM47 269 LHX1 1 2371 NP_005559.2 5 395 TTAGGATCCAAA C A GCA 3 A c c
GCTTCTCTGCTC AGG AG AGAGAAGCT GA
CTTTTGTT TCC TC TCTCTTCGA CT
- G AAC

GAM47 269 LIF 1 3616 NP_002300.1 3 2597 GCCGGGAGCTGG CA G A 3 A c c
GTTTCTCTTCCC AGG GAAGAGAAGCT CAG
TTTTTATC TCC CTTCTCTTTGG GTC

```
                                                --          -  G
GAM47   269   LIPG   1  19350 NP_006024.1  3  990   CTGCTTTGGAGC          A--  G          3  A  c  c
                                  AAATCTCTTCTG AGGCAGAAGAGA  GCT CAGAG
                                  TTTAGAGA    TTTGTCTTCTCT  CGA GTTTC
                                                AAA  G
GAM47   269   LITAF  1  18731 NP_004853.1  3  697   TCCTGGGCTCAA        A A-  --- AG       3  A  c  c
                                  GCGATCCTTCTG AGGCAGAAG GA  GCT  GC  AG
                                  CCTTGGCC    TCCGTCTTC CT  CGA  CG  TC
                                                - AG  ACT  GG
GAM47   269   LNIR   1  9127  NP_112178.1  5  147   AAGAACTCTGCA      AAGA              3  A  b  b
                                  GCTTCCTGCCTT AGGCAG   GAAGCTGCAGAG
                                  CTGGGTCA    TCCGTC   CTTCGACGTCTC
                                                ----
GAM47   269   LOC1136 1  7603  XP_054492.1  3  888   CTTTCATCCTCT        AG-  CTGC          3  A  c
c
        12                        CTTACCCTTCTG AGGCAGAAG  AAG   AGAG
                                  CCTTCCAC    TCCGTCTTC  TTC   TCTC
                                                CCA  ----
GAM47   269   LOC1222 1  18448 XP_063046.4  3  505   TTGAAGGTGTCT        GAA   C           3  A  c  c

        82                        TGGCATCTTCTG AGGCAGAAGA  GCTG AGA
                                  CCTTTGCT    TCCGTCTTCT  CGGT TCT
                                                A--  -
GAM47   269   LOC1225 1  4360  NP_803235.1  3  2137  GGATTTGCCAGC          AA--  -          3  A  c  c
        53                        ATCCCTCTTCTG AGGCAGAAGAG   GCTG CAGA
                                  CTTCTCAG    TTCGTCTTCTC   CGAC GTTT
                                                CCTA  C
GAM47   269   LOC1247 1  9596  XP_064298.4  5  91    CCTCAGTCTGCA A-------  C       A          3  A  c  c
        51                        GCTCTTTTCTCC        GG AGAAGAGA GCTGCAGA
                                  ACCGCGCG           CC TCTTTTCT CGACGTCT
                                                GCGCGCCA  -       -
GAM47   269   LOC1249 2  8653  XP_058879.5  3  793   CAACTCTGCAGG A----   A-        --        3  A  c  c
        76                        GCTTCTCTCCCT     GGCAG  AGAGAAGCT  GCAGAG
                                  GCCACCAC         CCGTC  TCTCTTCGG  CGTCTC
                                                CACCA    CC        GA
GAM47   269   LOC1249 2  16219 XP_058879.5  3  793   CCCAACTCTGCA A--    A-        --        3  A  c  c
        76                        GGGCTTCTCTCC    GGCAG  AGAGAAGCT  GCAGAG
                                  CTGCCACC        CCGTC  TCTCTTCGG  CGTCTC
                                                CCA    CC        GA
GAM47   269   LOC1289 3  2506  XP_066252.3  5  723   GTGCATGGTCTG        AGA  T           3  A  c  c
        54                        TGCTGCCTTCTG AGGCAGAAG   AGC GCAGA
                                  CCTGGGTC    TCCGTCTTC   TCG TGTCT
                                                CG-  -
GAM47   269   LOC1289 3  8041  XP_066252.3  5  888   GTGCACGGCCTG        AGA  T   A       3  A  c
c
        54                        TGCTGCCTTCTG AGGCAGAAG   AGC GCAG
                                  CCTGGGCC    TCCGTCTTC   TCG TGTC
                                                CG-  -  C
GAM47   269   LOC1289 3  8782  XP_066252.3  5  806   GTGCATGGCCTG        AGA  T   A       3  A  c
c
```

54 TGCTGCCTTCTG AGGCAGAAG AGC GCAG
CCTGGCTC TCCGTCTTC TCG TGTC
CG- - C

GAM47 269 LOC1308 1 1990 NP_777559.2 3 76 TCTTCAGTGTCC A------ C 3 A c c
88 AAATCTCTTCTG AGGCAGAAGAGA GCTG AGA
TCTCCTTT TCTGTCTTCTCT TGAC TCT
AAACCTG T

GAM47 269 LOC1363 1 11849 XP_072455.2 3 654 CTCCCGTTGCAT AGA - - A 3 A c c

45 GTCTGGCTTCTG AGGCAGAAG AG C TGCAG
CCTGTGCT TCCGTCTTC TC G ACGTT
GG- T T G

GAM47 269 LOC1383 1 7694 NP_848564.1 3 1184 GCTGACTCTGCA - AA- A 3 A c c
07 GCTCCTCATGCT AGGC AG GAG AGCTGCAGAG
GGCCTATC TCCG TC CTC TCGACGTCTC
G GTA C

GAM47 269 LOC1434 1 5310 NP_783860.1 3 959 CACAGCTTTTGG AGA G 3 A c c
25 GCTTCTCTGGCC AGGC AGAGAAGCT CAGAG
TGAATGCC TCCG TCTCTTCGG GTTTT
G-- -

GAM47 269 LOC1436 1 16903 XP_096471.1 3 34 ACCGTGTCTGCA A AGAA 3 A c c

77 GCACGCTTCCGT AGGC GAAG GCTGCAGA
CTCCGCAT TCTG CTTC CGACGTCT
C GCA-

GAM47 269 LOC1444 1 7641 XP_096611.2 3 1928 CCTCTTTGCCCA A----- AA -- 3 A c c
81 GCTTCTCCCCTG GGCAG GAGAAGCT GCAGAG
CCCTATTC CCGTC CTCTTCGA CGTTTC
CTTATC CC CC

GAM47 269 LOC1447 1 17282 XP_084963.2 5 239 TCTCAGGTTCAA ------- G C 3 A c c
66 GCGATTTTTCTG AGGCAGAAGA GAA CTG AGA
CCTCAGCC TCCGTCTTTT CTT GAC TCT
TAGCGAA G -

GAM47 269 LOC1448 1 4355 NP_612483.1 3 20 CTCCTTAGCCAA A -- A 3 A c c
45 GCTTCTCTCTGT AGGCAGA GAGAAGCT GC GAG
CTTCCCTC TCTGTCT CTCTTCGA CG TTC
- AC A

GAM47 269 LOC1448 1 8101 XP_096696.1 5 231 GCTTATCTGTTG AG - 3 A c c
74 GCTTCTCTTGGC AGGC AAGAGAAGCTG CAGA
CTGTGGGA TCCG TTCTCTTCGGT GTCT
G- T

GAM47 269 LOC1451 2 3438 XP_085025.1 3 59 TCTCTCCTTCTC ---- CTGC 3 A c c
25 TCTTCTCTTCTT AGGCA GAAGAGAAG AGAG
CTTGCCTG TCCGT CTTCTCTTC TCTC
TCTT ----

GAM47 269 LOC1451 2 18124 XP_085025.1 3 51 GCTCTTCTCTCC C CTGC 3 A c c

25 TTCTCTCTTCTC AGG AGAAGAGAAG AGAG
TTCTTCTT TTC TCTTCTCTTC TCTC
T ----

GAM47 269 LOC1456 1 11711 XP_096832.1 5 96 TAACTCTGTGAG A----- AA- - 3 A c c
78 TATGCTCTTCTG GGCAGAAGAG GCT GCAGAG
CCCAAAAA CCGTCTTCTC TGA TGTCTC
AAAAAC GTA G
GAM47 269 LOC1458 1 11784 XP_085243.1 5 130 TGAAGGTCTGCA A-- AG- -- 3 A c c
14 GCTTCGTTCTTA GGC AAGA GAAGCTGCAGA
AAGCCAGC CCG TTCT CTTCGACGTCT
CGA AAA TG
GAM47 269 LOC1467 1 2465 XP_097085.5 3 313 CCTCTGTCTGCA AAGAGA 3 A c
c
56 GCTGCTGCTGCC AGGCAG AGCTGCAGA
TGGACCTA TCCGTC TCGACGTCT
GTCG--
GAM47 269 LOC1475 1 7233 XP_097243.1 3 948 ATTGCTGTAGCA G --- A 3 A c c
15 GATTCTGTTCTG AGGCAGAA AGAA GCTGCAG
CCTGCTGC TCCGTCTT TCTT CGATGTC
G AGA G
GAM47 269 LOC1484 1 16652 XP_086210.2 3 133 ACCCTTGGTCTT AGAA C 3 A c
c
90 GGCACCCTTCTG AGGCAGAAG GCTG AGA
CCTTATAC TCCGTCTTC CGGT TCT
CCA- -
GAM47 269 LOC1487 1 14757 XP_097514.1 3 1067 ATTTGCCCACCA --- A ----- 3 A c c
60 GCTTCTCCTCTG AGGC AGA GAGAAGCT GCAGA
GAGCCTGA TCCG TCT CTCTTCGA CGTTT
AGG C CCACC
GAM47 269 LOC1489 1 17867 XP_086385.2 5 723 CTGCTTTCTTTG C- CT 3 A c c
87 CTTTCTCTTCTC AGG AGAAGAGAAG GCAGAG
ACCTTTGG TCC TCTTCTCTTT CGTTTC
AC --
GAM47 269 LOC1490 1 18240 XP_097580.2 3 415 TCCAGCTCTGCA C AG AA 3 A c
c
86 GCAGTTGTCTCC AGG AGA AG GCTGCAGAG
TAATGTGA TCC TCT TT CGACGTCTC
- G- GA
GAM47 269 LOC1491 1 4614 XP_097605.1 3 28 TAGTACCTGGCA A A- - A 3 A c c
82 GCTTCTCCCTTA AGGC GA GAGAAGCTGC AG
GCCTGGAA TCCG TT CTCTTCGACG TC
A CC G C
GAM47 269 LOC1498 1 967 XP_097747.1 5 913 CAAGTTCGACCA GA CA- 3 A c c
37 GCTTCTTTGTGC AGGCA AGAGAAGCTG GAG
CTCTTTTC TCCGT TTTCTTCGAC CTT
G- CAG
GAM47 269 LOC1501 1 2818 XP_097824.1 5 876 AGGTGTATGCAG AAG- GA 3 A c
c
66 GGCCCTCTTCTG AGGCAGAAGAG CTGCA
CCTTAGCG TCCGTCTTCTC GACGT
CCGG AT
GAM47 269 LOC1509 2 17336 XP_097971.1 3 651 TCAAGCTCTGCA ---- - A 3 A c b

33 GTTTCCTGTCTG AGG CAGA AG GAAGCTGCAGAG
GCACCCTG TCC GTCT TC CTTTGACGTCTC
CACG G -
GAM47 269 LOC1509 2 19544 XP_097971.1 3 847 CCTTCTTTACCT GAGA G 3 A b
b
33 CTGAGCTTTCTG AGGCAGAA AGCT CAGAG
CCTTCTGA TCCGTCTT TCGA GTCTC
---- -
GAM47 269 LOC1509 1 6510 XP_097977.2 3 1186 CCAAAGTGCCAG - - GA 3 A c c
46 CCTTCTCTTCTG AGGCAGAAGAGAAG CTG CA
CCTTACCT TCCGTCTTCTCTTC GAC GT
C C GA
GAM47 269 LOC1515 1 17844 XP_098072.2 3 214 TGGGTCTCTGCA AA AA- - 3 A c c
12 GGCCTGCTCACC AGGCAG GAG GC TGCAGAG
TGCCTCCA TCCGTC CTC CG ACGTCTC
CA GTC G
GAM47 269 LOC1533 1 15715 XP_087657.1 3 934 TGAAGATCTGCA C A 3 A c c
64 GCTATTCTTTTA AGG AGAAGAG AGCTGCAGA
CTTAACAT TTC TTTTCTT TCGACGTCT
A A
GAM47 269 LOC1534 1 11271 XP_098373.1 3 319 CTTTATCTGTCA A------ AA - 3 A c c
42 GCTTCTCCCTGC GGCAG GAGAAGCTG CAGA
CACTTCAC CCGTC CTCTTCGAC GTCT
CACTTCA C- T
GAM47 269 LOC1548 2 6200 XP_098618.3 5 1128 ACTTTGCCTGCA CA - A 3 A c c
22 GCTTCTGCTTTC AGG GAAG AGAAGCTGCAG
CTGAAATT TCC TTTC TCTTCGACGTC
-- G C
GAM47 269 LOC1548 2 14022 XP_098618.3 5 2892 TCCTGGGCTCAA AA --- AG 3 A c
c
22 GCAATTCTTCTG AGGCAGAAGAG GCT GC AG
CCTCAGCC TCCGTCTTCTT CGA CG TC
AA ACT GG
GAM47 269 LOC1549 1 18568 XP_088109.3 5 116 ACAGCCTCTGCA GA A --- 3 A c c
90 GGCCCTGCTCTT AGGCA AGAG AG CTGCAGAG
GCCTCCCA TCCGT TCTC TC GACGTCTC
-- G CCG
GAM47 269 LOC1550 1 7762 XP_088117.1 3 1301 CTGGTGTCTTCA A----- A C 3 A c c
06 GCTTCTCTGCTG GGCAG AGAGAAGCTG AGA
CCATGTTC CCGTC TCTCTTCGAC TCT
CTTGTA G T
GAM47 269 LOC1550 1 11849 XP_098647.1 5 421 CTCCCGTTGCAT AGA - - A 3 A c c
32 GTCTGGCTTCTG AGGCAGAAG AG C TGCAG
CCTGTGCT TCCGTCTTC TC G ACGTT
GG- T T G
GAM47 269 LOC1550 1 5512 XP_098651.1 5 1186 CTTCTGGTTTTG - TG--- 3 A c c
36 TTTCTTGTTCTG AGGCAGAA GAGAAGC CAGAG
CCTGACTG TCCGTCTT TTCTTTG GTCTT

G TTTTG

GAM47 269 LOC1573 1 19137 XP_098754.5 5 1579 TGCTCTTCTGCA A----- A - A 3 A c c

81 GCCTCATCTCTG GGCAGA GA GA GCTGCAGAG
CCATTCTT CCGTCT CT CT CGACGTCTT
TTCTTA - A C

GAM47 269 LOC1574 1 2791 XP_098756.1 5 701 TCATTTCTGCCA - AGAA - 3 A c c

21 GCTTCTTATGGT AGG C GAGAAGCTG CAGAG
CCTGAGGC TCC G TTCTTCGAC GTCTT
T GTA- C

GAM47 269 LOC1577 1 15243 XP_088391.4 3 309 AGCTCCGTCGGT C -- - A 3 A c c

84 CTTTCTCTTCTC AGG AGAAGAGAA GCTG C GAG
TTTTAAGA TTC TCTTCTCTT TGGC G CTC
- TC T C

GAM47 269 LOC1585 1 8854 XP_088594.1 5 297 TCCACTTCTGCA C AGAA 3 A c c

27 GCAAGCTTCTTC AGG AGAAG GCTGCAGAG
CTGGACAT TCC TCTTC CGACGTCTT
T GAA-

GAM47 269 LOC1585 1 13743 XP_088606.1 5 2260 AAAAAGATCTCT A CT-- 3 A c c

63 GCCTCTCTTCTC AGGCAGA GAGAAG GCAGAG
TCTGCCTC TCCGTCT CTCTTC CGTCTC
- TCTC

GAM47 269 LOC1589 1 4356 XP_088736.1 5 42 CCTTCTTCTGCA AAG- A 3 A c c

97 GCTCCTGGTGCT AGGCAG AG AGCTGCAGAG
GCTTGTGT TTCGTC TC TCGACGTCTT
GTGG C

GAM47 269 LOC1664 1 18985 XP_093876.5 5 1 GCTTTTGCGTCA AGAA T 3 A c c

49 GGCTTCTGCCTG AGGCAGAAG GC GCAGAG
AGCTCGGT TCCGTCTTC TG CGTTTT
GGAC -

GAM47 269 LOC1964 1 7300 XP_116917.2 3 383 GAAGAGTCTGCA C G A 3 A c c

15 GCATTTGTTCTC AGG AGAA AGA GCTGCAGA
CTGGCTCC TCC TCTT TTT CGACGTCT
- G A

GAM47 269 LOC1969 1 16202 XP_113796.1 3 163 CCTCCCCGCAGC CA -- A-- 3 A c c

96 TCTTCTCTTCCC AGG GAAGAGA AGCTGC GAG
TCTATGAG TCC CTTCTCT TCGACG CTC
-- TC CCC

GAM47 269 LOC1973 1 7381 XP_117029.1 5 8 CCTACTTTCCTC GAGA TGC 3 A c
c

79 TCCTGCTTTCTG AGGCAGAA AGC AGAG
CCTGTGAC TCCGTCTT TCG TCTC
---- TCC

GAM47 269 LOC2000 1 8828 XP_114089.3 3 908 GCGCACTGCAGT GAGA-- A 3 A c
c

08 TAATGAATTCTG AGGCAGAA AGCTGCAG
CCTTCAAC TCCGTCTT TTGACGTC
AAGTAA A

GAM47 269 LOC2006 2 2866 XP_117256.1 5 865 CATAATGCCTTT GAAG G 3 A c c
09 GAGATTCTTCTG AGGCAGAAGA CT CAGAG
CTTGTATC TTCGTCTTCT GA GTTTC
TA-- -
GAM47 269 LOC2006 2 14180 XP_117256.1 5 2551 TGTGAGTCTTCC A C- 3 A c c
09 AGCTTTCTTCTG AGGCAGAAGAGA GCTG AGA
CTTTTTCA TTCGTCTTCTTT CGAC TCT
- CT
GAM47 269 LOC2019 1 16641 XP_117345.1 5 740 TACCTCAACACA A CA-- 3 A c c
52 GTTGCTTTTCTG AGGCAGAAGAG AGCTG GAG
CCTTGTCT TCCGTCTTTTC TTGAC CTC
G ACAA
GAM47 269 LOC2021 1 18733 XP_117365.1 3 203 TCAGTCTGGTCT A TG-- 3 A c c
34 GTTACTTTTCTG AGGCAGAAGAG AGC CAGA
CCTAGAGG TCCGTCTTTTC TTG GTCT
A TCTG
GAM47 269 LOC2199 1 7987 XP_167788.1 5 106 CAAAGGTCTGCA A-- --- A A 3 A c c
14 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A
GAM47 269 LOC2209 1 10560 XP_167629.1 3 424 CCACAATCTGCA AA GAA 3 A c
c
80 GCCATCAACTGC AGGCAG GA GCTGCAGA
CTCTGCTG TCCGTC CT CGACGTCT
AA AC-
GAM47 269 LOC2215 1 15414 XP_166477.2 5 25 TTCCTGACTGCA A-- ---- A A 3 A c c
09 GCTCTCTTCATT GGCAGA AGAGA GCTGCAG
CTGCCAAC CCGTCT TCTCT CGACGTC
CAA TACT - A
GAM47 269 LOC2216 1 7560 XP_168131.1 5 1108 TAACTCTTTTGC A----- CT 3 A c c
63 CCTTCTCTTCTG GGCAGAAGAGAAG GCAGAG
CCAGTGAA CCGTCTTCTCTTC CGTTTT
AAGTGA C-
GAM47 269 LOC2216 1 493 XP_168089.1 3 649 CCCTGATCTCTA AGAA C 3 A c c
83 GCTTCTCAGCCT AGGC GAGAAGCTG AGA
CCAGAACT TCCG CTCTTCGAT TCT
A--- C
GAM47 269 LOC2218 1 9970 XP_166513.1 3 439 CATTCCCTCAGT - T A 3 A c c
89 GCTTCTCTTCTG AGG CAGAAGAGAAGC GC GAG
ACCTGCAT TCC GTCTTCTCTTCG TG CTC
A - A
GAM47 269 LOC2219 1 5808 XP_166553.1 5 192 AGCCCCTCTGCA AG AGA- 3 A c
c
29 GCTCACCCTTGG AGGC AAG AGCTGCAGAG
CTTGTTTT TTCG TTC TCGACGTCTC
G- CCAC
GAM47 269 LOC2219 1 14006 XP_168342.1 3 1515 GCAAACTCTGCA C-- A AG- 3 A c
c
64 GGTGTCTTTCTT AGG AGA GAGA CTGCAGAG

```
                                ATCCTAGT    TCC   TCT TTCT   GACGTCTC
                                        TAT   -   GTG
GAM47   269   LOC2532 2  6102  XP_173010.1  3  854   AAGGCTCATCAG       A - -  CA       3  A  c  c
        21                     TCTATCCTTCTG AGGCAGAAG GA AG CTG  GAG
                               CCTCCATA    TCCGTCTTC CT TC GAC  CTC
                                       - A T   TA
GAM47   269   LOC2532 2  18027 XP_173010.1  3  1446  CTCACACACTCT       A   CTGC         3  A  c
c
        21                     TTTTCCCTTCTG AGGCAGAAG GAAG   AGAG
                               CCTTCACC    TCCGTCTTC CTTT   TCTC
                                       C   T---
GAM47   269   LOC2542 1  6802  XP_173221.1  3  2457  TCTACATCTGCA    A  AGAG             3  A  c
c
        66                     GCTTGAGGTTAG AGGC GA   AAGCTGCAGA
                               CCTCATAT    TCCG TT   TTCGACGTCT
                                       A  GGAG
GAM47   269   LOC2559 2  2592  XP_171083.2  5  2113  ACAGCCTCTGCA    GA   A ---         3  A  c  c
        75                     GGGCCTGCTCTT AGGCA  AGAG AG   CTGCAGAG
                               GCCTCCCA    TCCGT  TCTC TC   GACGTCTC
                                       --   G  CGG
GAM47   269   LOC2559 2  11873 XP_171083.2  5  3316  TCACCCTCTGCA     A  AGAA -         3  A  c
c
        75                     GGCCCAGCTCCT AGGCAG AG   GC TGCAGAG
                               GCCTCCAA    TCCGTC TC    CG ACGTCTC
                                       C  GACC  G
GAM47   269   LOC2572 1  17331 XP_173125.1  5  200   AGAAGGTCTGCA A---  -- A  A          3  A  c  c
        39                     GCTTCACTCCTG    GGC  AG AG GAAGCTGCAGA
                               AGCCAGCG        CCG  TC TC CTTCGACGTCT
                                       GCGA   AG  C  A
GAM47   269   LOC2573 1  12197 XP_173138.1  3  776   AGCCTCTCTGCA   C      AA           3  A  c  c
        58                     GCCCCTCTTTTC AGG AGAAGAG  GCTGCAGAG
                               CTTCAATC    TCC TTTTCTC  CGACGTCTC
                                       -      CC
GAM47   269   LOC2828 1  6358  XP_212581.1  5  908   CTCCTTGCAAAT        ---  GC    A      3  A  c  c
        90                     TCCTTTCTTCTG AGGCAGAAGA   GAA  TGCAG
                               CCTCTGTT    TCCGTCTTCT   CTT  ACGTT
                                       TTC   AA    C
GAM47   269   LOC2829 1  6358  XP_212629.1  5  908   CTCCTTGCAAAT        ---  GC    A      3  A  c  c
        27                     TCCTTTCTTCTG AGGCAGAAGA   GAA  TGCAG
                               CCTCTGTT    TCCGTCTTCT   CTT  ACGTT
                                       TTC   AA    C
GAM47   269   LOC2830 1  1447  XP_210868.1  3  1434  CATCTTAGCCTG        A   -- A        3  A  c  c
        49                     GCTCCTCTTCTG AGGCAGAAGAG AGCT  GC GAG
                               TCTCTAGG    TCTGTCTTCTC TCGG  CG TTC
                                       C   TC  A
GAM47   269   LOC2831 1  3946  XP_210910.1  3  612   CAGCTTCTCCTG     AA       CAGA        3  A  c
c
        68                     CCTCTTCTTCTG AGGCAG  GAGAAGCTG
                               CAATCCTC    TCCGTC  CTCTTCGAC
                                       --       ----
```

GAM47 269 LOC2831 1 17013 XP_210929.1 5 85 GGTGGCCTTTGT A CT 3 A c c
99 CACTTCCTTCTG AGGCAGAAG GAAG GCAGAG
CCTTCCAA TCCGTCTTC CTTC TGTTTC
- AC
GAM47 269 LOC2833 1 11579 XP_208657.1 3 501 CAGTGCTCTGCA CA A AAG- 3 A c
c
91 GAAGCCTCTCCC AGG GA GAG CTGCAGAG
CCTCACAG TCC CT CTC GACGTCTC
CC - CGAA
GAM47 269 LOC2834 1 20097 XP_211037.1 5 1806 CAGGTGCCTCTG C-- AA TG 3 A c
c
42 TGGTCTCTTCTC AGG AGAAGAG GC CAGAG
ATCCTCAC TCC TCTTCTC TG GTCTC
TAC -- GT
GAM47 269 LOC2834 1 1821 XP_211051.1 3 555 TCCTGGCCTCAA A A- GCA 3 A c
c
68 GTGATCCTTCTG AGGCAGAAG GA GCT GAG
CCTCAGTC TCCGTCTTC CT TGA CTC
- AG A--
GAM47 269 LOC2834 1 1898 XP_208091.1 3 84 TGAGCCATCTCA AA-- C 3 A c c
93 GCTTCTCAACCT AGGCAG GAGAAGCTG AGA
TGCCTGTT TCCGTT CTCTTCGAC TCT
CCAA -
GAM47 269 LOC2835 1 8927 XP_211081.1 3 1451 TCCAAGTCTGCA AGA ------ 3 A c c
26 GCCTCCCATTCT AGGC AGAGAA GCTGCAGA
CTAGGCCT TCCG TCTCTT CGACGTCT
GA- ACCCTC
GAM47 269 LOC2835 1 15864 XP_211095.1 3 767 TTATTTTTGCTG AG - T 3 A c c
75 TCTTCTCTTGGC AGGC AAGAGAAG C GCAGAG
TTATTTTT TTCG TTCTCTTC G CGTTTT
G- T T
GAM47 269 LOC2835 1 7987 XP_211119.1 5 113 CAAAGGTCTGCA A-- --- A A 3 A c c
82 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A
GAM47 269 LOC2836 1 19410 XP_211144.1 3 1514 CTTGGAATTTGG AAG G 3 A c
c
55 GATCCTCTTCTG AGGCAGAAGAG CT CAGA
TCTCTTGA TCTGTCTTCTC GG GTTT
CTA -
GAM47 269 LOC2836 1 19850 XP_211167.1 3 5219 ATGTACTTTTCT AGAAGC 3 A c
c
90 GCATAATTTCTG AGGCAGAAG TGCAGAG
CCTTCTGT TCCGTCTTT ACGTCTT
AAT---
GAM47 269 LOC2837 1 16095 XP_211170.3 3 2952 TCAACTGCAACA C--- A 3 A c c
01 TTTTCTTTTCTG AGGCAGAAGAGAAG TGCAG
CCTATCTT TCCGTCTTTTCTTT ACGTC
TACA A
GAM47 269 LOC2837 1 1631 XP_211183.3 3 424 CAACTGGCAAAA --- - A 3 A c c

28 GCTTCTTTTCTG AGGCAGAAGAGAAGCT GC AG
CCTATCTT TCCGTCTTTTCTTCGA CG TC
AAA G A

GAM47 269 LOC2837 1 10019 XP_208837.1 3 661 CTGTAGGCCTGG - A G A 3 A c c
77 AGCTCTCTTCTG AGGC AGAAGAGA GCT CAG
GCCTGGTA TCCG TCTTCTCT CGA GTC
G - G C

GAM47 269 LOC2838 1 3242 XP_208867.3 3 480 GCACAGTCTGCA CAGA A 3 A c
c
43 GCTTCCTGAGTC AGG AG GAAGCTGCAGA
CTGTTCTG TCC TC CTTCGACGTCT
TGAG -

GAM47 269 LOC2838 1 3242 XP_208126.1 5 2069 GCACAGTCTGCA CAGA A 3 A c
c
46 GCTTCCTGAGTC AGG AG GAAGCTGCAGA
CTGTTCTG TCC TC CTTCGACGTCT
TGAG -

GAM47 269 LOC2838 1 15767 XP_211229.1 3 875 CTTGGCACTCAA A AA A- 3 A c c
51 GCAGTCCTTCTG AGGCAGAAG G GCTGC GAG
CCTCAGCC TCCGTCTTC C TGACG CTC
- -- AA

GAM47 269 LOC2838 1 652 XP_211237.1 5 277 TCCTCCGCTGCA C A ----- A 3 A c c
62 GCTTTCCATCTC AGG AGA GAGA AGCTGCAG
ATCTCCTT TCC TCT CTCT TCGACGTC
- A ACCTT G

GAM47 269 LOC2839 1 18771 XP_211259.2 5 886 TTTTTCTCTGCA GA ------- 3 A c c
11 GATAGTTGCTTC AGGCA AGAGAAGC TGCAGAG
TCTTGCTT TTCGT TCTCTTCG ACGTCTC
-- TTGATAG

GAM47 269 LOC2839 1 10020 XP_211275.2 3 521 CATCGTGCATCA A - C-- - 3 A c c
63 CTCTCCCTTCTG AGGCAGAAG GA AG TGCA GA
CCTCCTTC TCCGTCTTC CT TC ACGT CT
C C ACT G

GAM47 269 LOC2839 1 8565 XP_208940.2 3 544 CACTGCTGGTGC - ---- - A 3 A c c
80 CCTTCTCTTCTG AGG CAGAAGAGAAG CT GCAG
ACCTGCTG TCC GTCTTCTCTTC GG CGTC
A CCGT T A

GAM47 269 LOC2840 1 13640 XP_210779.1 5 4 CCTTCTTCTGCC AAG- T 3 A c c
77 GCTTCTGGTGCT AGGCAG AGAAGC GCAGAG
GCTTGTGT TTCGTC TCTTCG CGTCTT
GTGG C

GAM47 269 LOC2840 1 15510 XP_211322.1 5 675 CCGTTGAATGCA A - GA 3 A c c
80 AGCTCTCTTCTG AGGCAGAAGAGA GCT GCA
CCTTCTCA TCCGTCTTCTCT CGA CGT
- A AA

GAM47 269 LOC2840 1 15774 XP_211324.1 3 879 GAGCTCACTGCA G A -- A 3 A c c
95 GCTTCAATCTCC AG CAG AGA GAAGCTGCAG
TGGCTCAA TC GTC TCT CTTCGACGTC
G C AA A

GAM47 269 LOC2841 1 13676 XP_211361.1 3 956 TCACTCTCTGCA GAGA G 3 A c
c

```
          72                          GGTTTTTGCCTA AGGCAGAA   A CTGCAGAG
                                     CACTTTGA    TCCGTTTT   T GACGTCTC
                                                 ---- G
GAM47     269   LOC2842 1  14057  XP_211385.1  3  1165  CCTCTCCCTGCA    GA - ---      A     3  A  c  c

          19                          GCTTTCACTGCT AGGCA  AG AG   AAGCTGCAG
                                     CTTGCCTA    TCCGT  TC TC   TTCGACGTC
                                                 TC  G  ACT       C
GAM47     269   LOC2842 1  705    XP_211388.1  3  1425  TCCAGCTCTGCA    AAGAGAA          3  A  c
c
          33                          GTGTGGCTGCTT AGGCAG      GCTGCAGAG
                                     CTTGATTC    TTCGTC      TGACGTCTC
                                                 GGTG---
GAM47     269   LOC2842 1  3763   XP_211399.1  3  77    GTGGATCCTTAG    --      - CA       3  A  c  c
          44                          TTTTCTCTTCAC AGGCA  GAAGAGAAG CTG  GA
                                     TGCCTGCC    TCCGT  CTTCTCTTT GAT  CT
                                                 CA       T  TC
GAM47     269   LOC2842 1  8411   XP_211410.1  5  643   CTTGATCGTGTG       -  T  -       3  A  c  c
          59                          TTTCATTTTCTG AGGCAGAAGA GAAGC GCA GA
                                     CCTCTTTG    TCCGTCTTTT CTTTG TGT CT
                                                 A    -  G
GAM47     269   LOC2842 1  11107  XP_211411.1  5  1226  TCTCACTCTGCA    A  A  AG-          3  A  c  c

          67                          GGGATCCTCCTG AGGCAG AG GA   CTGCAGAG
                                     CCTCTCCT    TCCGTC TC CT   GACGTCTC
                                                 C  -  AGG
GAM47     269   LOC2843 1  1174   XP_211454.1  3  1928  ATGATTCTGAGC       AGAA--  G        3  A  c
c
          95                          ACATGGTTTCTG AGGCAGAAG     GCT CAGAG
                                     CCTCCAGC    TCCGTCTTT     CGA GTCTT
                                                 GGTACA   -
GAM47     269   LOC2844 1  12213  XP_210787.1  5  6     TCATCCTCGTTG      AGA     GCA        3  A  c
c
          33                          GCTTCTCTGCCT AGGCAGA   GAAGCT   GAG
                                     TCCCCCAC    TCCGTCT   CTTCGG   CTC
                                                 ---      TTG
GAM47     269   LOC2844 1  18092  XP_209212.1  3  827   TTCACTTTGCAG A-----       AA-        3  A  c  c
          45                          CCTCCTCTTCTG     GGCAGAAGAG   GCTGCAGAG
                                     TCACCAAC         CTGTCTTCTC   CGACGTTTC
                                                 CAACCA         CTC
GAM47     269   LOC2844 2  6952   XP_211470.1  5  167   CTCCTCTCGTCC   C       CT- -       3  A  c  c
          56                          TCTTCTCTTTTC AGG AGAAGAGAAG   GC AGAG
                                     CTCATTCT    TCC TTTTCTCTTC   TG TCTC
                                                 -        TCC  C
GAM47     269   LOC2844 2  18111  XP_211470.1  5  1809  AGTACCTCTTGA       GA   GC         3  A  c
c
          56                          GTTAATTTTCTG AGGCAGAAGA  AGCT  AGAG
                                     CCTCCAGT    TCCGTCTTTT  TTGA  TCTC
                                                 AA    GT
GAM47     269   LOC2844 1  3315   XP_211474.1  3  3399  CAACACTCCCCA       AG A    CA        3  A  c
c
```

73 GCCTTGCTTCTG AGGCAGAAG A GCTG GAG
CCTAACCC TCCGTCTTC T CGAC CTC
GT C CC

GAM47 269 LOC2844 1 598 XP_211488.1 3 40 GACTTCCTCTTC G- CTGC 3 A c c
91 CTTCTGATTCTG AGGCAGAA AGAAG AGAG
CCTGAATA TCCGTCTT TCTTC TCTC
AG CT--

GAM47 269 LOC2844 1 1464 XP_209237.1 5 94 CGAAGGTCTGCA A-- --- A A 3 A c c
99 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A

GAM47 269 LOC2845 1 6672 XP_208220.1 3 889 TTCGCTTGAACA --- AA CA- 3 A c c
59 GCTTCTCCTGAG AGG CAG GAGAAGCTG GAG
TCCTCCTT TCC GTC CTCTTCGAC TTC
TGA -- AAG

GAM47 269 LOC2846 1 9093 XP_211553.1 3 734 CATGGGCTCTAA A GC 3 A c c
15 GCTGCTCTTCTG AGGCAGAAGAG AGCT AGAG
TCTGTCTG TCTGTCTTCTC TCGA TCTC
G A-

GAM47 269 LOC2846 1 8169 XP_211588.1 3 346 TTCTGCCTGGTG AG ----- 3 A c c
88 GTCTTTCTTCTG AGGCAGAAGAGA CT GCAGAG
CCTGCTAT TCCGTCTTCTTT GG CGTCTT
CT TGGTC

GAM47 269 LOC2847 1 18028 XP_211634.1 3 175 ATCTGTCACTCA GA ----- 3 A c c
58 GCTTCTCTGTGT AGGCA AGAGAAGCTG CAGA
CTCTGGTT TCTGT TCTCTTCGAC GTCT
G- TCACT

GAM47 269 LOC2848 1 11298 XP_211654.1 5 1434 CACACTCCTATC A----- AGAAGC 3 A
c c
36 TCTGCACTTCTG GGCAGAAG TGCAGAG
CCCTCCAT CCGTCTTC ACGTCTC
TACCTC ------

GAM47 269 LOC2848 1 4964 XP_211667.1 3 522 CATCATGCATCA A - C-- - 3 A c c
51 CTCTCCCTTCTG AGGCAGAAG GA AG TGCA GA
CCTCCTTC TCCGTCTTC CT TC ACGT CT
C C ACT A

GAM47 269 LOC2848 1 5108 XP_209386.1 3 189 ATTTTTGTTTTG A- T-- 3 A c c
58 TTCACTCTTCTG AGGCAGAAGAG AGC GCAGAG
CCTTCAGT TCCGTCTTCTC TTG TGTTTT
AC TTT

GAM47 269 LOC2849 1 1266 XP_211700.1 5 1438 CACCTCTCTGCA A-------- C A A 3 A c
c
39 GCTCCTTCTCCA GG AGAAG GA GCTGCAGAG
ATCTCATG CC TCTTC CT CGACGTCTC
GTACTCTAA - - -

GAM47 269 LOC2849 1 7359 XP_211713.1 5 2622 GAGGACCTTTTG AGA C 3 A c c

74 GCTTCTCTGGAG AGGC AGAGAAGCTG AGAG
CCTGCAAG TCCG TCTCTTCGGT TTTC
AGG -

GAM47 269 LOC2850 1 9504 XP_211731.2 3 1183 CTCTCTGCTACA G AA --- 3 A c c
02 GCTTCTTGGCTG AG CAG GAGAAGCT GCAGAG
GCTCTGAA TC GTC TTCTTCGA CGTCTC
G GG CAT
GAM47 269 LOC2851 1 18888 XP_211770.1 5 245 CTTTTACCTGCA AA A 3 A c c
22 GCTTTTCCTGCT AGGCAG GAGAAGCTGCAG
TGATATAG TTCGTC CTTTTCGACGTC
-- C
GAM47 269 LOC2853 1 16710 XP_209569.1 3 95 TTACCCTCTGCA A A ----- 3 A c c
29 GCTTGTCATCCC AGGC GAAG GA AGCTGCAGAG
TTCCGTCT TCTG CTTC CT TCGACGTCTC
C C ACTGT
GAM47 269 LOC2853 1 671 XP_209573.1 5 1045 AACACTACTTTA --- A C - 3 A c c
38 GCTTCTCTCCTG AGGC AG AGAGAAGCTG AG AG
AAGCCTTA TCCG TC TCTCTTCGAT TC TC
AAG C T A
GAM47 269 LOC2853 1 19888 XP_211861.3 3 75 AAGAGCTCTGCA AA AG 3 A c c
69 GGCTTTCCACTG AGGCAG GAGA CTGCAGAG
CCTGTATT TCCGTC CTTT GACGTCTC
AC CG
GAM47 269 LOC2854 1 7301 XP_211884.1 5 48 CTGGGCTCAGAC AGA CA- 3 A c c
02 GGCTGGCTTCTG AGGCAGAAG AGCTG GAG
CCTACCCG TCCGTCTTC TCGGC CTC
GG- AGA
GAM47 269 LOC2855 1 14586 XP_211927.1 5 51 ATTTTCTTCTGT A-- --- T 3 A c c
26 GCTTCTCTCTAT GGCAGA AGAGAAGC GCAGAG
CTGCTCTG TCGTCT TCTCTTCG TGTCTT
GTC ATC -
GAM47 269 LOC2855 1 1609 XP_209655.2 3 186 GTGACCTCTGCA A A AA 3 A c c
44 GTACTCCTTAGC AGGC GA GAG GCTGCAGAG
CTGCGTTT TCCG TT CTC TGACGTCTC
A C A-
GAM47 269 LOC2856 1 7695 XP_209700.3 3 199 TTCCAACTTCCT AA C A 3 A c c
47 CAGTCTTTTCTG AGGCAGAAGAG GCTG AG
CCTCAACT TCCGTCTTTTC TGAC TC
-- - C
GAM47 269 LOC2856 2 18509 XP_211975.1 3 301 GGGCACTCTGCA AGAGA G 3 A c
c
54 GGTTCTGCCTTT AGGCAGA A CTGCAGAG
GAGTCCTC TCCGTCT T GACGTCTC
----- G
GAM47 269 LOC2856 2 19966 XP_211975.1 3 300 GTCTGGGGCACT AGAGA G 3 A c
c
54 CTGCAGGTTCTG AGGCAGA A CTGCAGAG
CCTTTGAG TCCGTCT T GACGTCTC
----- G
GAM47 269 LOC2856 1 13387 XP_209709.2 3 2678 GTGCTGCCATCA A ---- A 3 A c c
71 GTTTCACTTCTG AGGCAGAAG GAAGCT GCAG
CCTTGGAA TCCGTCTTC CTTTGA CGTC

A CTAC G

GAM47 269 LOC2856 1 5657 XP_211979.1 5 195 AGGCATTTGCAG -- - AG 3 A c c
82 GGTCCTCTTCTG AGGC AGAAGAG A CTGCAGA
GGCCTGAC TCCG TCTTCTC T GACGTTT
GG C GG

GAM47 269 LOC2857 1 13540 XP_211990.1 5 273 ATTTGCAGCCTA C ----- 3 A c c
19 ACTTCTCTTTTC AGG AGAAGAGAA GCTGCAGA
CTTTTAAA TCC TTTTCTCTT CGACGTTT
- CAATC

GAM47 269 LOC2857 1 3336 XP_209751.1 3 514 GGAAGGTCTGCA A--- -- A A 3 A c c
56 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AGCCAGCG CCG TC TC CTTCGACGTCT
GCGA AG C A

GAM47 269 LOC2858 1 17058 XP_212027.1 5 450 GGTGCTCCCGCA - -- A- A- 3 A c c
05 GCTTCGCCTCCT AGGC AGA AG GAAGCTGC GAG
CTCGTCTT TCTG TCT TC CTTCGACG CTC
C CC CG CC

GAM47 269 LOC2858 1 17839 XP_209777.1 5 374 TGTGCATTTTTG A CT 3 A c c
22 CCCTTCTTTCTG AGGCAGA GAGAAG GCAGAG
CCTCTCAG TCCGTCT TTCTTC CGTTTT
- C-

GAM47 269 LOC2859 1 1135 XP_209812.1 3 645 TTGTCTCTTCAC GAA - C 3 A c c
08 GCCCATCTTCTG AGGCAGAAGA GC TG AGAG
CCTCATAG TCCGTCTTCT CG AC TCTC
ACC C T

GAM47 269 LOC2859 1 6593 XP_209811.1 3 651 TCTCGGGCTCAA AA --- A- 3 A c c
09 GCCATTTTTCTG AGGCAGAAGAG GCT GC GAG
CCTCAGCT TCCGTCTTTTT CGA CG CTC
AC ACT GG

GAM47 269 LOC2859 1 15820 XP_209802.1 3 1246 GGGCCCTCTGCA A A A ------- 3 A c
c
15 GCCCAGCCTTTC GGC GAAG GAA GCTGCAGAG
CTTCCGTC CTG CTTC CTT CGACGTCTC
- C - TCCGACC

GAM47 269 LOC2859 1 8682 NP_777609.1 3 453 GGATATTCTGCA AGAA 3 A c c
31 GCGCTTCTGTCT AGGCAGAAG GCTGCAGAG
TTTTCTTG TCTGTCTTC CGACGTCTT
G---

GAM47 269 LOC2859 1 1535 XP_212090.1 5 307 AGCCAGTCTCAC GAGA CA 3 A c
c
51 CAGTTGATTCTG AGGCAGAA AGCTG GAG
CCTTAATC TCCGTCTT TTGAC CTC
AG-- CA

GAM47 269 LOC2860 2 3734 XP_212133.1 5 227 CGAAGGTCTGCA A--- -- A A 3 A c c
07 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AGCCAGGG CCG TC TC CTTCGACGTCT
GGGA AG C A

GAM47 269 LOC2860 2 17618 XP_212133.1 5 123 TGAAGGTCTGCA A-- --- A A 3 A c c
07 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT

CGA AAG C A

GAM47 269 LOC2860 1 3883 XP_209868.1 5 1261 TCTTTGCACATC - A C--- 3 A c c
30 CTGCTCTTTCTG AGGCAGAA GAG AG TGCAGAG
CCTGAAAA TCCGTCTT CTC TC ACGTTTC
T G CTAC

GAM47 269 LOC2860 1 18519 XP_212140.3 5 17 TATTTCTCTGCA A-- A--- A - 3 A c c
41 GCGTTCCTTCCC GGC GAAG GAA GCTGCAGAG
TGGCCCGG CCG CTTC CTT CGACGTCTC
GGC GTCC - G

GAM47 269 LOC2860 1 7355 XP_212163.1 5 694 CTTCCCTCTGGC A- - TG 3 A c c
78 TCTCCACTTCTG AGGCAGAAG GA AGC CAGAG
CCTCCCTC TCCGTCTTC CT TCG GTCTC
AC C --

GAM47 269 LOC2861 1 18003 XP_212204.1 3 802 AAGAAGGTGCCT T- GA 3 A c c
54 GCTTCTCTTTTG AGGCAGAAGAGAAGC GCA
CCTTCTAC TCCGTTTTCTCTTCG CGT
TC GG

GAM47 269 LOC2862 1 12697 XP_212230.1 3 863 TGTGCCTTTCCA AAG-- C 3 A c c
08 GCTTCTAGAGGC AGGCAG AGAAGCTG AGAG
TGCCTGCG TCCGTC TCTTCGAC TTTC
GGAGA C

GAM47 269 LOC2862 1 4829 XP_212232.1 3 2451 GCAGTCCTCAGA AGA GCA 3 A c
c
17 GCTTCTCTGCCT AGGCAGA GAAGCT GAG
ATGGAGTA TCCGTCT CTTCGA CTC
--- GA-

GAM47 269 LOC2863 1 14402 XP_212273.1 3 1028 GCTCTGCCTGCA AGAGA A 3 A c
c
32 GCTGGGCCTCTG AGGCAGA AGCTGCAG
CCTCATCC TCCGTCT TCGACGTC
CCGGG C

GAM47 269 LOC2863 1 14402 XP_212271.1 3 1028 GCTCTGCCTGCA AGAGA A 3 A c
c
33 GCTGGGCCTCTG AGGCAGA AGCTGCAG
CCTCATCC TCCGTCT TCGACGTC
CCGGG C

GAM47 269 LOC2863 1 13526 NP_789789.1 3 1444 TCTCAGTCTACC ------ - C 3 A c c
99 TCCTCTTTTCTG AGGCAGAAGAGA AG CTG AGA
CCTCTGAA TCCGTCTTTTCT TC GAC TCT
CCTCCA T -

GAM47 269 LOC2864 1 15266 XP_301085.1 5 0 TGTCTGTGTCTC A C 3 A c c
34 CTCTTCTGTCTC AGGCAGAAGAG AG TGCAGA
TTAGAAGG TCTGTCTTCTC TC GTGTCT
C T

GAM47 269 LOC3388 1 1464 XP_290588.1 5 171 CGAAGGTCTGCA A-- --- A A 3 A c c
17 GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A

GAM47 269 LOC3390 1 3242 XP_290675.1 5 51 GCACAGTCTGCA CAGA A 3 A c c

```
         56                    GCTTCCTGAGTC AGG   AG GAAGCTGCAGA
                               CTGTTCTG    TCC   TC CTTCGACGTCT
                                     TGAG  -
GAM47    269  LOC3391 1  1464  XP_294837.1  5  206   CGAAGGTCTGCA A--  --- A  A          3  A  c  c
         66                    GCTTCACTCCTG   GGC  AG AG GAAGCTGCAGA
                               AAGCCAGC      CCG  TC TC CTTCGACGTCT
                                  CGA  AAG  C  A
GAM47    269  LOC3391 1  784   XP_290743.1  3  1121  TACACTCTTTCA     A  A  GC--       3  A  c  c
         84                    GGCCTCTTTCTG AGGCAGA GAGA GCT   AGAG
                               CCTTTTGT    TCCGTCT TTCT CGG   TCTC
                                     -   C  ACTT
GAM47    269  LOC3392 1  15710 XP_290271.2  3  693   CAATCAGATGCA   A  -  -   GA      3  A  c  c
         12                    GCTTTCTCCTTC AGGC GAAG AGAA GCTGCA
                               GTCTGGTC    TCTG CTTC TCTT CGACGT
                                     -   C  T    AG
GAM47    269  LOC3392 1  9358  XP_294901.1  5  4210  CTTTTTCCTTTC      --  CTGC       3  A  c  c
         90                    TTCATTTTTCTG AGGCAGAAGA  GAAG   AGAG
                               CCTGGAAT    TCCGTCTTTT  CTTC   TTTC
                                        TA  ----
GAM47    269  LOC3392 1  14984 XP_294903.1  3  72    AGGCATTCTGCA   A  AGAGA          3  A  c
c
         98                    GCTGGGATCAGC AGGC GA    AGCTGCAGAG
                               CTCAGCTT    TCCG CT    TCGACGTCTT
                                     A  AGGG-
GAM47    269  LOC3393 1  5262  XP_290857.1  5  44    GTCCTCACTACT       GAAGC        3  A  c  c
         89                    CTGTGTCTTCTG AGGCAGAAGA    TGCAGAG
                               CTTTTAGG    TTCGTCTTCT    GTGTCTC
                                     -----
GAM47    269  LOC3394 1  11819 XP_294944.1  5  2146  AAGGTCTCTGCA     AGA  G          3  A  c
c
         17                    GGTTTATCTGCC AGGCAGA   GAA CTGCAGAG
                               TGGAGCGA    TCCGTCT   TTT GACGTCTC
                                     A--  G
GAM47    269  LOC3394 1  6001  XP_294950.1  5  57    TCGGCCTCTGCA     AGAGAA-         3  A  c
c
         35                    GTCCCAACGTCT AGGCAGA     GCTGCAGAG
                               GCCTCACA    TCCGTCT     TGACGTCTC
                                     GCAACCC
GAM47    269  LOC3394 1  18568 XP_294951.1  5  116   ACAGCCTCTGCA    GA  A ---       3  A  c  c
         40                    GGCCCTGCTCTT AGGCA  AGAG AG   CTGCAGAG
                               GCCTCCCA    TCCGT  TCTC TC   GACGTCTC
                                     --   G  CCG
GAM47    269  LOC3397 1  11933 XP_295048.1  3  1161  GGGATGCTGCCT     AGAGA  T         3  A  c
 c
         38                    CTGCTGCTTCTG AGGCAGA    AGC GCAGAG
                               CCTTCTTT    TCCGTCT    TCG CGTCTC
                                     -----  T
GAM47    269  LOC3397 1  7421  XP_290339.1  3  191   ACAACACAGCTG       AGCT  A       3  A  c  c

         40                    CCGTTTCTTCTG AGGCAGAAGAGA   GCAG
```

CCTGCTTA TCCGTCTTCTTT CGTC
GC-- G
GAM47 269 LOC3399 1 11593 XP_295115.1 5 398 CCAGCCCTCAGA GA- - C A 3 A c c
75 CTGGATCTTCTG AGGCAGAAGA AG CTG AG
CCTCCAAA TCCGTCTTCT TC GAC TC
AGG A - C
GAM47 269 LOC3399 1 11593 XP_295115.1 5 895 CCAGCCCTCAGA GA- - C A 3 A c c
75 CTGGATCTTCTG AGGCAGAAGA AG CTG AG
CCTCCAAA TCCGTCTTCT TC GAC TC
AGG A - C
GAM47 269 LOC3400 1 18520 XP_291113.2 3 2766 TGGGGCTCTGCA AGA ------ 3 A c c
12 GTTCCTGCATCT AGGC AGAGA AGCTGCAGAG
CTAAGCTT TTCG TCTCT TTGACGTCTC
AA- ACGTCC
GAM47 269 LOC3400 2 13577 XP_291120.2 5 4 ACTCGCCCTCCA AAG C A 3 A c c
24 GCTTCTGCCCTG AGGCAG AGAAGCTG AG
CCTGCTGT TCCGTC TCTTCGAC TC
CCG C C
GAM47 269 LOC3400 2 15024 XP_291120.2 3 470 GCTCTTCTTCAT AAGC- C 3 A c c
24 TATGCTCTTCTG AGGCAGAAGAG TG AGAG
CCTGGGGC TCCGTCTTCTC AC TCTT
GTATT T
GAM47 269 LOC3400 1 4588 XP_295149.1 3 119 TCTGGAGCTGCA G A- A A 3 A c c
73 GCTTCCTCCCTG AG CAG AG GAAGCTGCAG
GCTGTGGG TC GTC TC CTTCGACGTC
G CC - G
GAM47 269 LOC3401 1 3367 XP_295167.1 3 1024 TTTTTCCGCAGC - GA- A 3 A c c
50 TGCATCTTTCTG AGGCAGAA GA AGCTGC GAG
CCTGGACT TCCGTCTT CT TCGACG CTT
T ACG C
GAM47 269 LOC3402 2 1256 XP_291214.1 3 1308 GTGGCCTCTGCA AAGAGAAG 3 A c c
90 GGAGCAAAACTG AGGCAG CTGCAGAG
CCTCAAGT TCCGTC GACGTCTC
AAAACGAG
GAM47 269 LOC3402 2 11873 XP_291214.1 3 1026 TCACCCTCTGCA A AGAA - 3 A c c
90 GGCCCAGCTCCT AGGCAG AG GC TGCAGAG
GCCTCCAA TCCGTC TC CG ACGTCTC
C GACC G
GAM47 269 LOC3403 1 2631 XP_290401.1 3 1242 GGGCCCTCTGCA A A A ------- 3 A c c
18 GCCCATCCTTTC GGC GAAG GAA GCTGCAGAG
CTTCCGTC CTG CTTC CTT CGACGTCTC
- C - TCCTACC

GAM47 269 LOC3403 1 18568 XP_295213.2 5 116 ACAGCCTCTGCA GA A --- 3 A c c
46 GGCCCTGCTCTT AGGCA AGAG AG CTGCAGAG
GCCTCCCA TCCGT TCTC TC GACGTCTC
-- G CCG
GAM47 269 LOC3403 1 2445 NP_848659.1 3 686 AGCCCCTCTGCA A----- - A AG 3 A c
c
71 GATCTCCTCTGG GGC AGA GAGA CTGCAGAG
CCACTGCA CCG TCT CTCT GACGTCTC
ACGTCA G C A-
GAM47 269 LOC3403 1 2445 XP_291255.2 3 686 AGCCCCTCTGCA A----- - A AG 3 A c c
71 GATCTCCTCTGG GGC AGA GAGA CTGCAGAG
CCACTGCA CCG TCT CTCT GACGTCTC
ACGTCA G C A-
GAM47 269 LOC3426 1 1726 XP_297028.1 5 1359 CAGAGTGCTGCA GAGA A 3 A c
c
63 GCTGTTTCTGTC AGGCAGAA AGCTGCAG
TCGAACGG TCTGTCTT TCGACGTC
TG-- G
GAM47 269 LOC3438 1 19955 XP_297948.1 5 730 ACCCCTCGCAGC A --- A 3 A b b
95 TGCTTCCTTCTG AGGCAGAAG GA AGCTGC GAG
CCTGGGAT TCCGTCTTC CT TCGACG CTC
- TCG -
GAM47 269 LOC3442 1 12043 XP_297483.2 5 98 CCCTAATCTGCA AGAGAA 3 A c
c
56 GCCCCGCCTTTG AGGCAGA GCTGCAGA
CCTACTCC TCCGTTT CGACGTCT
CCGCCC
GAM47 269 LOC3451 2 15447 XP_298603.1 5 119 CCCGCTCTGCAG A----- AGAA - 3 A c
c
90 GCCGCCCTTCTG GGCAGAAG GC TGCAGAG
CCAGCTGG CCGTCTTC CG ACGTCTC
GGTCGA CCGC G
GAM47 269 LOC3451 2 17998 XP_298603.1 5 119 CCCCGCTCTGCA A---- AGAA - 3 A c
c
90 GGCCGCCCTTCT GGCAGAAG GC TGCAGAG
GCCAGCTG CCGTCTTC CG ACGTCTC
GTCGA CCGC G
GAM47 269 LOC3476 1 6358 XP_300206.1 5 908 CTCCTTGCAAAT --- GC A 3 A c c
44 TCCTTTCTTCTG AGGCAGAAGA GAA TGCAG
CCTCTGTT TCCGTCTTCT CTT ACGTT
TTC AA C
GAM47 269 LOC3479 1 19514 XP_300570.1 3 85 CCTTCCTCACCG AGAAG A-- 3 A c
c
24 CAGATGTTTCTG AGGCAGAAG CTGC GAG
CCTCTTAA TCCGTCTTT GACG CTC
GTA-- CCA
GAM47 269 LOC3480 1 13822 XP_300595.1 3 1244 TTATTCAGTAGG AG-- A 3 A c c
35 AACTCTCTTCTG AGGCAGAAGAGA CTGC GAG
CCTGGTTT TCCGTCTTCTCT GATG CTT

CAAG A

GAM47 269 LOC3480 1 16095 XP_302653.1 3 2949 TCAACTGCAACA C--- A 3 A c c
75 TTTTCTTTTCTG AGGCAGAAGAGAAG TGCAG
CCTATCTT TCCGTCTTTTCTTT ACGTC
TACA A

GAM47 269 LOC3482 2 670 XP_300686.1 3 157 GTCCCTCTGTTT C--- CT- 3 A c c
58 CCTTCTCTTCTC AGG AGAAGAGAAG GCAGAG
TTTCCTCC TCC TCTTCTCTTC TGTCTC
TTTC CTT

GAM47 269 LOC3482 2 4358 XP_300686.1 3 159 TCTGTTTCCTTC C--- CT- 3 A c c
58 TCTTCTCTTTCC AGG AGAAGAGAAG GCAGA
TCCCTCTC TCC TCTTCTCTTC TGTCT
TTTC CTT

GAM47 269 LOC3482 1 3316 XP_302704.1 3 4 CCAGGCTGCAGC AAG--- A 3 A c c
61 TTCTGTGGGACT AGGCAG AGAAGCTGCAG
GCCTTAAG TCCGTC TCTTCGACGTC
AGGGTG G

GAM47 269 LOC3483 1 19986 XP_302735.1 5 285 AGTCTGGCTCCG G AA ---- 3 A c c

73 GTCACTCTTCTG AG CAGAAGAG GCTG CAGA
GCTTAGGT TC GTCTTCTC TGGC GTCT
G AC CTCG

GAM47 269 LOC3484 1 15244 XP_301160.1 5 36 GACCGCTCTGCA A AA--- 3 A c c
22 GTACCAGCTCCT AGGCAGA GAG GCTGCAGAG
CTGTCTCC TCTGTCT CTC TGACGTCTC
C GACCA

GAM47 269 LOC3484 1 18772 XP_302755.1 3 400 GCCCCCTCTGCA A---- - AG 3 A c c

27 GGCTCTCTGTCT GGCAGA AGAGA CTGCAGAG
GCCCTGGG CCGTCT TCTCT GACGTCTC
GGGTC G CG

GAM47 269 LOC3484 1 18568 XP_302758.1 5 657 ACAGCCTCTGCA GA A --- 3 A c c
50 GGCCCTGCTCTT AGGCA AGAG AG CTGCAGAG
GCCTCCCA TCCGT TCTC TC GACGTCTC
-- G CCG

GAM47 269 LOC3485 2 3438 XP_302814.1 3 34 TCTCTCCTTCTC ---- CTGC 3 A c c
28 TCTTCTCTTCTT AGGCA GAAGAGAAG AGAG
CTTGCCTG TCCGT CTTCTCTTC TCTC
TCTT ----

GAM47 269 LOC3485 2 18124 XP_302814.1 3 26 GCTCTTCTCTCC C CTGC 3 A c c

28 TTCTCTCTTCTC AGG AGAAGAGAAG AGAG
TTCTTCTT TTC TCTTCTCTTC TCTC
T ----

GAM47 269 LOC3485 1 967 XP_209362.1 3 1193 CAAGTTCGACCA GA CA- 3 A c c
52 GCTTCTTTGTGC AGGCA AGAGAAGCTG GAG
CTCTTTTC TCCGT TTTCTTCGAC CTT
G- CAG

GAM47 269 LOC3487 1 6335 XP_300845.1 3 333 TCCTGGGCTCAA A A- --- AG 3 A c c

```
        98                      GCGATCCTTCTG AGGCAGAAG GA  GCT   GC  AG
                                CCTCAGCC    TCCGTCTTC CT  CGA   CG  TC
                                          - AG   ACT  GG
GAM47   269   LOC3490 1  15010 XP_302948.1  5  231   CTGCTCCTCTGA A-------    AA      G       3  A  c
c
        62                      GCTTCTCCTGCT       GGCAG  GAGAAGCT CAGAG
                                CCTCTCTG           TCGTC  CTCTTCGA GTCTC
                                        GTCTCTCC    --       -
GAM47   269   LOC3493 1  18092 XP_301042.1  3  852   TTCACTTTGCAG A-----        AA-         3  A  c  c
        39                      CCTCCTCTTCTG     GGCAGAAGAG   GCTGCAGAG
                                TCACCAAC         CTGTCTTCTC   CGACGTTTC
                                        CAACCA         CTC
GAM47   269   LOC3506 1  15197 XP_304260.1  3  532   CGGTCTGGAGCC       ---  A  G        3  A  c  c
        29                      TCTGGGCTTCTG AGGCAGAAG   AGA GCT CAGA
                                CCTACAGA    TCCGTCTTC   TCT CGA GTCT
                                          GGG   C   G
GAM47   269   LOC3522 1  6201  XP_305527.1  5  83    TGGACTCTCAGC       G  AA--   C        3  A  c  c
        58                      CTTGCTGTTCTG AGGCAGAA AG    GCTG AGAG
                                CCTGGAGA    TCCGTCTT TC    CGAC TCTC
                                          G  GTTC   -
GAM47   269   LOC3522 2  3237  XP_305558.1  5  87    AGAGCTGTTCTG           CT          3  A  c  c
        87                      TCTTCTCTTCTG AGGCAGAAGAGAAG  GCAGAG
                                TCTCTTCT    TCTGTCTTCTCTTC  TGTCTT
                                            --
GAM47   269   LOC3522 2  16371 XP_305558.1  5  90    CTGTCTTCTCTT           CT   A       3  A  c  c
        87                      CTGTCTCTTCTC AGGCAGAAGAGAAG  GCAG
                                TTTCATCT    TCTGTCTTCTCTTC  TGTC
                                            --   -
GAM47   269   LOC5133 1  16030 NP_057731.1  3  1043  CCTCTCCTGGCA   C  A--       ----      3  A  c  c
        7                       GCTTCTCAGGTC AGG AGA   GAGAAGCTGC    AGAG
                                TCCCTAAT    TCC TCT   CTCTTCGACG    TCTC
                                          C   GGA        GTCC
GAM47   269   LOC5618 1  19514 NP_062457.2  3  85    CCTTCCTCACCG        AGAAG   A--        3  A  c
c
        1                       CAGATGTTTCTG AGGCAGAAG    CTGC   GAG
                                CCTCTTAA    TCCGTCTTT    GACG   CTC
                                          GTA--    CCA
GAM47   269   LOC9013 1  17943 XP_029323.1  5  772   CTTCACTGTGCA    AGAAG-       G        3  A  c
c
        3                       GCTTCTGGGGTG AGGC     AGAAGCTGCA AG
                                GCCTGGGC    TCCG     TCTTCGACGT TC
                                          GTGGGG         G
GAM47   269   LOC9040 1  3764  XP_031517.1  5  351   ACATCCCTCTGT    CA       CT          3  A  c  c
        8                       TCTTCTCTTCCT AGG  GAAGAGAAG  GCAGAG
                                CCTTCAGC    TCC  CTTCTCTTC  TGTCTC
                                          TC        T-
GAM47   269   LOC9084 1  18600 XP_034427.2  3  1307  GTTTCACCTGCA      AGA       A        3  A  c  c

        1                       GCTTTCAGTCTG AGGCAGA   GAAGCTGCAG
                                CTTTGTCT    TTCGTCT   TTTCGACGTC
```

GAC C

GAM47 269 LOC9105 1 3924 NP_612377.1 3 963 TCCTGGGCTTAA ------ G A 3 A c c
6 ATGACTCTTCTG AGGCAGAAGAG AAGCT CAG
CCTCAGCC TCCGTCTTCTC TTCGG GTC
AGTAAA - C

GAM47 269 LOC9109 1 1470 XP_035977.1 3 425 GCGCAATCTGAA CTG 3 A c c
7 ACTTCTCTTCTG AGGCAGAAGAGAAG CAGA
TTTTCTTT TTTGTCTTCTCTTC GTCT
AAA

GAM47 269 LOC9120 1 6400 XP_036935.1 5 416 TGCAATGGCTCA A- G C A 3 A c c
8 GGTTCTCTTCCA AGGC GAAGAGAA CTG AG
GCCTGTCC TCCG CTTCTCTT GAC TC
AC G - G

GAM47 269 LOC9149 1 6539 XP_038788.1 5 2467 ACATGTACTGCA A-- A 3 A c c
6 GCTTCTTGTCTC AGGCAGA GAGAAGCTGCAG
TGTTTTGG TTTGTCT TTCTTCGACGTC
CTG A

GAM47 269 LOC9163 1 6540 XP_039721.2 5 383 GAGTGAGCTCTG A----- AA T 3 A c c
2 CTGCCTCTTCTG GGCAGAAGAG GC GCAGAG
CTGCCCGC TCGTCTTCTC CG CGTCTC
CGCCCG -- T

GAM47 269 LOC9214 1 18532 XP_043160.1 5 607 TCCTGAGCTCTG AAGCTG 3 A c c
8 ATTCCTCTTCTG AGGCAGAAGAG CAGAG
TCTGGCTG TCTGTCTTCTC GTCTC
CTTA--

GAM47 269 LOC9265 1 3316 XP_046434.3 3 4 CCAGGCTGCAGC AAG--- A 3 A c c
9 TTCTGTGGGACT AGGCAG AGAAGCTGCAG
GCCTTAAG TCCGTC TCTTCGACGTC
AGGGTG G

GAM47 269 LOC9580 1 16795 XP_047816.5 3 191 CTGTACTCTGCA AAGAGAA 3 A c c
3 GCCTGCCTTCCT AGGCAG GCTGCAGAG
AGAGTTGG TCCGTC CGACGTCTC

GAM47 269 LRP11 1 15632 NP_116221.2 3 95 TGGATATTTACA GA C 3 A c c
GCTTCTTTTGTT AGGCAGAAGA AGCTG AGA
TTTAATTG TTTGTTTTCT TCGAC TTT
-- A

GAM47 269 LUZP1 1 13539 NP_361013.1 3 196 AAAGGAAATCTG CA CT 3 A c c
TCTTCTCTTCCC AGG GAAGAGAAG GCAGA
TTGGTTTG TCC CTTCTCTTC TGTCT
-- --

GAM47 269 MAFG 2 670 NP_002350.1 3 93 GTCCCTCTGTTT C--- CT- 3 A c c
CCTTCTCTTCTC AGG AGAAGAGAAG GCAGAG
TTTCCTCC TCC TCTTCTCTTC TGTCTC
TTTC CTT

GAM47 269 MAFG 2 4358 NP_002350.1 3 95 TCTGTTTCCTTC C--- CT- 3 A c c
TCTTCTCTTTCC AGG AGAAGAGAAG GCAGA

TCCCTCTC TCC TCTTCTCTTC TGTCT
TTTC CTT

GAM47 269 MBD4 1 6697 NP_003916.1 3 25 CTTAACTCTGCA A A ----- 3 A c c
GCTTTCAAGCTC GGCAGA GAG AAGCTGCAGAG
ATCTGTTA TTGTCT CTC TTCGACGTCTC
A A GAACT

GAM47 269 MCF2L 1 2630 NP_079255.2 3 180 TCTGCATAGTTT C - -- 3 A c c
CTTTCTCTTCCT AGG AGA AGAGAAGCT GCAGA
TCATAGAT TCC TCT TTTCTTTGA CGTCT
T C TA

GAM47 269 MCOLN2 1 4917 NP_694991.1 3 84 ATGATCTCTGCA CAG- -- 3 A c c
GCATTTTTCTTG AGG AAGAGAA GCTGCAGAG
GAACCTCT TCC TTCTTTT CGACGTCTC
AAGG TA

GAM47 269 MDGA1 1 10254 NP_705691.1 3 3796 ACAGTGTCTGCA A-- C --- A 3 A c c

GCTGCTGCCCTT GG AGAAG AG AGCTGCAGA
CTCCCAGG CC TCTTC TC TCGACGTCT
GGA C CCG G

GAM47 269 MFRP 1 9575 NP_113621.1 3 307 TCTGCTTTTTCA AA---- ------ 3 A c c
GCTTCTCCATCG AGGCAG GAGAAGCT GCAGA
CCTGCCTT TCCGTC CTCTTCGA CGTCT
CGCTAC CTTTTT

GAM47 269 MGA 1 4593 XP_031689.3 3 82 CCTTTCTCTGCA AG A - 3 A c c
GGCATCTGTTTG AGGCAGA AGA GC TGCAGAG
TTTGTGTC TTTGTTT TCT CG ACGTCTC
G- A G

GAM47 269 MGC1110 1 16794 NP_115701.2 3 817 GACATTCTCATG AGAA G - 3 A c c
2 AGTAACCTTCTG AGGCAGAAG GCT CA GAG
CCTTCACT TCCGTCTTC TGA GT CTC
CAA- - A

GAM47 269 MGC1276 1 16318 NP_116112.1 3 739 GGACTCCTCTTC C - CTGC 3 A c c
0 CTCTCTCTTCTC AGG AGAAGAGA AG AGAG
CTACTCTG TCC TCTTCTCT TC TCTC
- C CT--

GAM47 269 MGC1428 1 20024 NP_542391.1 3 175 CTGCTATCTGCA GAAG A 3 A c c
9 GCTCCTAGGTGC AGGCA AG AGCTGCAGA
TTTCCTCA TTCGT TC TCGACGTCT
GGA- C

GAM47 269 MGC1437 1 12840 NP_116284.1 3 109 CACCATTTCTCT GAGA GC- 3 A c c
6 CCAGGCTTTCTG AGGCAGAA AGCT AGAG
CCTCCGAG TCCGTCTT TCGG TCTC
---- ACC

GAM47 269 MGC1542 1 12226 NP_116139.1 3 73 CTCTCTTGCACG A--- C-- - - - 3 A c c
9 CTCTCTCTTCTC GG AGAAGAGA AGC TGCA GAG
TCCCAGGC CC TCTTCTCT TCG ACGT CTC

```
                                        CGGA CTC      C  C   T
GAM47   269   MGC2201 1  3989  XP_035307.1  3 4390  TTCTCTGACCCA       AGAA  ---        3  A  c
c
        4                          GCGTTGCTTCTG AGGCAGAAG   GCTG  CAGAG
                                   CCTCTCAT   TCCGTCTTC   CGAC  GTCTC
                                              GTTG   CCA
GAM47   269   MGC2474 1  7232  NP_076420.1  3 724   TTGGGCTCTCAG A-----       AA   --     3  A  c  c

                                   CAGCCTCTTCTG     GGCAGAAGAG  GCTGC  AGAG
                                   CCAGCACC         CCGTCTTCTC  CGACG  TCTC
                                            CCACGA       --   AC
GAM47   269   MGC3321 1  19827 NP_722517.1  3 1654  GTCTGCTCTGCA     AA-----   G         3  A  c
c
        5                          GGTTCTTCATAC AGGCAG      GAGAA CTGCAGAG
                                   AGCTGCCT    TCCGTC      TTCTT GACGTCTC
                                               GACATAC    G
GAM47   269   MGC3472 1  1406  NP_689746.1  5 89    CAGGGTCCTGCA  G   -- G      A      3  A  c  c
        8                          GCTTGTCCTTTC AG CAGAA  GA AAGCTGCAG
                                   TGGCTGGA    TC GTCTT  CT TTCGACGTC
                                            G    TC  G       C
GAM47   269   MGC3480 1  8668  NP_694959.1  3 56    CCCAGCCTGTCA       AA  --   A      3  A  c  c
        0                          AGTCCTCTTCTG AGGCAGAAGAG  GCT  GCAG
                                   CCTCAGCT    TCCGTCTTCTC  TGA  TGTC
                                               C-   AC   C
GAM47   269   MGC4057 2  7455  NP_689989.1  3 968   TCTCGGGTTCAA       AA  --- A-      3  A  c  c
        9                          GTGACTCTTCTG AGGCAGAAGAG  GCT   GC  GAG
                                   CCTCAGCC    TCCGTCTTCTC  TGA   TG  CTC
                                               AG   ACT  GG
GAM47   269   MGC4057 2  9195  NP_689989.1  3 1640  TGCCTGGGTGCA   - A-       GA      3  A  c
c
        9                          GCTTCTCTAGCT AGGC AG  AGAGAAGCTGCA
                                   GGCCTTGC    TCCG TC  TCTCTTCGACGT
                                            G  GA          GG
GAM47   269   MGC4210 1  1753  NP_699192.1  5 816   CTCCCACCCTCT A-----       AA  G      3  A  c
c
        5                          GAGCCTCTTCTG     GGCAGAAGAG  GCT CAGAG
                                   CTCCTGCA         TCGTCTTCTC  CGA GTCTC
                                            ACGTCC       --   -
GAM47   269   MGC4504 1  2337  NP_077016.1  3 176   TGCCAGCCTGCA     AA   A     A      3  A  c  c

                                   GCTCTCCTGCTT AGGCAG  GAGA GCTGCAG
                                   GACACTGA    TTCGTC  CTCT CGACGTC
                                            --   -      C
GAM47   269   MI-ER1  1  10996 NP_065999.1  3 3038  TCCATTCACTCT A-----         GCT       3  A  c  c
                                   GTTTCTCTTCTG     GGCAGAAGAGAA  GCAGAG
                                   CTGGATTA         TCGTCTTCTCTT  TGTCTC
                                            ATTAGG         ---
GAM47   269   MIDORI  1  16823 NP_065829.1  3 1260  GGTAGGTCTGCA  C  A  AGA            3  A  c
c
                                   GCTAGCCTACTC AGG AG AG   AGCTGCAGA
```

CCTTTGGA TCC TC TC TCGACGTCT
C A CGA
GAM47 269 MINPP1 1 3843 NP_004888.2 3 421 ATTGTTCTGCAG C-- - 3 A c c
TTCTCTCTTCTT AGG AGAAGAGA AGCTGCAGAG
TTCCTCAG TCC TCTTCTCT TTGACGTCTT
TTT C
GAM47 269 MN1 1 16715 NP_002421.2 3 733 CTTCCACTTGAG C - G A 3 A c c
TTCTCTCTTCTC AGG AGAAGAGA AGCT CAG
CTGCTGGA TCC TCTTCTCT TTGA GTT
- C - C
GAM47 269 MOCS1 1 18692 NP_005933.1 3 380 TCTCATTTTGGG C - G 3 A c c
TTTTCTCTTCTC AGG AGAAGAGAAG CT CAGAG
CTGCTTTC TCC TCTTCTCTTT GG GTTTT
- T -
GAM47 269 MOCS1 1 18692 NP_005934.2 3 1148 TCTCATTTTGGG C - G 3 A c c
TTTTCTCTTCTC AGG AGAAGAGAAG CT CAGAG
CTGCTTTC TCC TCTTCTCTTT GG GTTTT
- T -
GAM47 269 MOCS1 1 18692 NP_620306.1 3 380 TCTCATTTTGGG C - G 3 A c c
TTTTCTCTTCTC AGG AGAAGAGAAG CT CAGAG
CTGCTTTC TCC TCTTCTCTTT GG GTTTT
- T -
GAM47 269 MOXD1 1 5314 NP_056344.1 3 183 AGACATCAATCA C G CA- 3 A c c
GGTTCTCTTCTC AGG AGAAGAGAA CTG GA
TTTCTTAG TTC TCTTCTCTT GAC CT
- G TAA
GAM47 269 MRF2 1 16396 XP_084482.2 3 1276 GCAGTCCTGATA AGA - A 3 A c c
GCTTCTCTAGCC AGGC AGAGAAGCTG CAG
TCGGTCTT TCCG TCTCTTCGAT GTC
A-- A C
GAM47 269 MRPL10 1 9128 NP_660298.2 3 817 TTACTCTCAGGG - ---- GC-- 3 A c c
GCTTCTCTGTCA AGG CAGA AGAGAAGCT AGAG
TCTGACTT TTC GTCT TCTCTTCGG TCTC
A ACTG GGAC
GAM47 269 MRPL10 1 9128 NP_683685.1 3 817 TTACTCTCAGGG - ---- GC-- 3 A c c
GCTTCTCTGTCA AGG CAGA AGAGAAGCT AGAG
TCTGACTT TTC GTCT TCTCTTCGG TCTC
A ACTG GGAC
GAM47 269 MTA3 1 1271 XP_038567.5 3 2477 ACAGGCTCTGCA G A--- - - 3 A c c
GGCTATCTCCCC AG CAGA GAGA AGC TGCAGAG
CTCTGGCT TC GTCT CTCT TCG ACGTCTC
G CCCC A G
GAM47 269 NAP1L2 1 9926 NP_068798.1 5 81 CAGCTCTCTGCA AG A ----- - 3 A c c
GTCTCCGGCTCT GCAG AGAGA AG CTGCAGAG
CTCCTGCA CGTC TCTCT TC GACGTCTC
A- C CGGCC T
GAM47 269 NAP1L4 1 10186 NP_005960.1 3 320 GCACCCTCTGCA GAA AA 3 A c
c
GCCTTGGTGCCT AGGCA GAG GCTGCAGAG
GTAGCTCT TCCGT TTC CGACGTCTC

GG- --
GAM47 269 NBL1 1 10001 NP_005371.1 3 1057 GCTCTCTCTAGC GAGA-- C 3 A c c

TCCCCAATTCTG AGGCAGAA AGCTG AGAG
CCTGCCTC TCCGTCTT TCGAT TCTC
AACCCC C
GAM47 269 NDRG1 1 3602 NP_006087.1 3 782 TGAAGGCTTTAG AGAAGCT 3 A c c

TTCTGCTTTCTG AGGCAGAAG GCAGAG
CCTCTCCT TCCGTCTTT CGTCTT

GAM47 269 NDUFA6 1 13883 NP_002481.1 3 125 CAATTTTCTGCA A A 3 A c c
GCCTCTTTTTGC AGGCAGA GAGA GCTGCAGAG
CTGAGCAA TCCGTTT TTCT CGACGTCTT
- C
GAM47 269 NFATC4 1 11848 NP_004545.2 3 136 CCTCTTTCCCCA AG C---- 3 A c c
GCTTCTGTCTGT AGGCAGA AGAAGCTG AGAG
CTCACTGT TCTGTCT TCTTCGAC TCTC
G- CCCTT
GAM47 269 NIPSNAP 2 2560 NP_003625.1 3 14 CTCGCCTCTGCA AAGAGAA 3 A c c
1 GTGTGCTGCCTA AGGCAG GCTGCAGAG
CACCTCCA TCCGTC TGACGTCTC
GTG----
GAM47 269 NIPSNAP 2 15009 NP_003625.1 3 1070 GAACCCTTGGGT GAG A- 3 A c c
1 AGCTTGATTCTG AGGCAGAA AAGCTGC GAG
CCTACCAT TCCGTCTT TTCGATG TTC
AG- GG
GAM47 269 NLGN4 1 11053 NP_065793.1 5 380 TATCTCTCTGCA AGA A-- - 3 A c c
GGCTCGCCTCTG AGGC AGAG AGC TGCAGAG
GGCTTTGT TTCG TCTC TCG ACGTCTC
GG- CGC G
GAM47 269 NLGN4 1 11053 NP_851849.1 5 346 TATCTCTCTGCA AGA A-- - 3 A c c
GGCTCGCCTCTG AGGC AGAG AGC TGCAGAG
GGCTTTGT TTCG TCTC TCG ACGTCTC
GG- CGC G
GAM47 269 NOL3 1 4812 NP_003937.1 3 589 TTTAATTGTCTG G- A TG 3 A c c
GCTTCTCTCTGG AG CAGA GAGAAGC CAGA
ACTGGGAG TC GTCT CTCTTCG GTCT
AG - --
GAM47 269 NOTCH2 1 4571 NP_077719.2 3 2698 TTTCTTTCTTTG A CTG 3 A c c
ACTCCTCTTCTG AGGCAGAAGAG AG CAGAG
CCTGCCTT TCCGTCTTCTC TC GTTTC
C A--
GAM47 269 NPHP4 1 5716 NP_055917.1 3 108 CGCCTCTCTGCA A- -- A -- 3 A c c
GCCTTTCACTTC GGCA GAAG GAA GCTGCAGAG
AGTGCCCA CCGT CTTC CTT CGACGTCTC
AC GA A TC
GAM47 269 NR2F6 1 3179 NP_005225.2 3 119 CCCAGGACTCTG CAGA TG 3 A c c

GCTTCTCTCCTC AGG AGAGAAGC CAGAG
AGACTTCT TCC TCTCTTCG GTCTC
---- --

GAM47 269 OSBPL3 1 13242 NP_663163.1 3 775 ACTGTGGCGGCG A AGA 3 A c c

GCTCCTCTTCTG AGGCAGAAGAG AGCTGC
CCTGTGTA TCCGTCTTCTC TCGGCG
C GCG

GAM47 269 OSBPL3 1 13242 NP_663164.1 3 775 ACTGTGGCGGCG A AGA 3 A c c

GCTCCTCTTCTG AGGCAGAAGAG AGCTGC
CCTGTGTA TCCGTCTTCTC TCGGCG
C GCG

GAM47 269 OTOP3 1 1725 XP_292588.2 5 503 GCTCTTCGGCAG AGA- --- 3 A c c
CTGCACCTTCTG AGGCAGAAG AGCTGC AGAG
CCTCAACA TCCGTCTTC TCGACG TCTC
CACG GCT

GAM47 269 PAH 1 1332 NP_000268.1 5 349 GACACCCTTTGT C A C 3 A c c
AACTCTCTTCTC AGG AGAAGAGA G TGCAGAG
CTCCCTAG TCC TCTTCTCT C ATGTTTC
- - A

GAM47 269 PANK4 1 18928 NP_060686.1 3 33 CGCTGCAGCTGC A----- A 3 A c c
CGGACTCTTCTG AGGCAGAAGAG AGCTGCAG
CTTGTCAC TTCGTCTTCTC TCGACGTC
AGGCCG G

GAM47 269 PAPOLB 1 2967 NP_064529.2 3 1022 TTTGCCTCCCTC A CTGC 3 A c c

TCTTCTCTTTGC AGGCAGA GAGAAG AGAG
CTGTATGC TCCGTTT CTCTTC TCTC
- ----

GAM47 269 PAX2 1 5547 NP_000269.1 3 1640 TCTCTCCTCTCC ----- T C 3 A c c
GCTTCTCTCCCC AGGCAGA AGAGAAGC G AGAG
CTCTGTCT TCTGTCT TCTCTTCG C TCTC
CCCCC - C

GAM47 269 PAX2 1 5547 NP_003978.1 3 1640 TCTCTCCTCTCC ----- T C 3 A c c
GCTTCTCTCCCC AGGCAGA AGAGAAGC G AGAG
CTCTGTCT TCTGTCT TCTCTTCG C TCTC
CCCCC - C

GAM47 269 PAX2 1 5547 NP_003979.1 3 1640 TCTCTCCTCTCC ----- T C 3 A c c
GCTTCTCTCCCC AGGCAGA AGAGAAGC G AGAG
CTCTGTCT TCTGTCT TCTCTTCG C TCTC
CCCCC - C

GAM47 269 PAX2 1 5547 NP_003980.1 3 1576 TCTCTCCTCTCC ----- T C 3 A c c
GCTTCTCTCCCC AGGCAGA AGAGAAGC G AGAG
CTCTGTCT TCTGTCT TCTCTTCG C TCTC
CCCCC - C

GAM47 269 PAX2 1 5547 NP_003981.1 3 1576 TCTCTCCTCTCC ----- T C 3 A c c
GCTTCTCTCCCC AGGCAGA AGAGAAGC G AGAG
CTCTGTCT TCTGTCT TCTCTTCG C TCTC
CCCCC - C

GAM47 269 PBX1 2 8409 NP_002576.1 3 148 CAATAAGAGTCT C CTGC 3 A c c
CCTTCTCTTCTC AGG AGAAGAGAAG AGA
TTCTTTGG TTC TCTTCTCTTC TCT
- C---
GAM47 269 PBX1 2 18068 NP_002576.1 3 149 AGAGTCTCCTTC C CTGC 3 A c c
TCTTCTCTTCTT AGG AGAAGAGAAG AGA
TGGGATGC TTC TCTTCTCTTC TCT
- C---
GAM47 269 PCDH7 1 7631 NP_115833.1 3 138 ACAAAGCTTTGC AGAA T- 3 A c c
CTGCCACTTCTG AGGCAGAAG GC GCAGAG
CCTCCAGA TCCGTCTTC CG CGTTTC
AC-- TC
GAM47 269 PDE4B 1 19366 NP_002591.1 5 536 TGAGAAAACTCT AGAA C 3 A c c
TTGGTGCTTCTG AGGCAGAAG GCTG AGAG
CCTTTAGT TCCGTCTTC TGGT TCTC
G--- T
GAM47 269 PDE4DIP 1 18790 NP_055459.1 3 890 TTTGCTTGAACA --- AA CA- 3 A c c
GCTTCTCCTGAG AGG CAG GAGAAGCTG GAG
TCCTCCTT TCC GTC CTCTTCGAC TTC
TGA -- AAG
GAM47 269 PDZK3 1 13259 NP_055837.2 3 41 AATCATTTTCTC C G C 3 A c c
AGTTCTCTTCTT AGG AGAAGAGAA CTG AGAG
TCTTTAGC TCT TCTTCTCTT GAC TCTT
T - -
GAM47 269 PDZK3 1 13259 NP_835260.1 3 41 AATCATTTTCTC C G C 3 A c c
AGTTCTCTTCTT AGG AGAAGAGAA CTG AGAG
TCTTTAGC TCT TCTTCTCTT GAC TCTT
T - -
GAM47 269 PEA15 1 5427 NP_003759.1 3 1834 TTGCCCCTATCT AA TGC 3 A c c
TGTGCTCTTCTG AGGCAGAAGAG GC AGA
TCTGCAGT TCTGTCTTCTC TG TCT
G- T--
GAM47 269 PEX1 1 19226 NP_000457.1 3 406 TTATGCTTAGCA AA A 3 A c c
GCTTCTTCACTG AGGCAG GAGAAGCTGC GAG
TTTTGAAA TTTGTC TTCTTCGACG TTC
AC A
GAM47 269 PFKFB3 1 12032 NP_004557.1 3 55 TCCATTTCTGCA - G AG 3 A c c
GCTTAGCTTGTG AGG CA AAG AAGCTGCAGAG
TCCTGCCC TCC GT TTC TTCGACGTCTT
T G GA
GAM47 269 PFKFB4 1 14338 NP_004558.1 3 1038 TTCTCTGGTGTT --- G TG 3 A c c
TGTTGACTTCTG AGGCAGAAG A AAGC CAGAG
CCTGTGGG TCCGTCTTC T TTTG GTCTC
AGT G TG
GAM47 269 PFTK1 1 10701 NP_036527.1 3 2380 TCCCTCTGCTTC A----- CT-- 3 A c c
TTTTCTCTTCTG GGCAGAAGAGAAG GCAGAG
CCCTCCTT CCGTCTTCTCTTT CGTCTC
TTCCTC TCTT
GAM47 269 PHGDHL1 1 14585 NP_808882.1 3 556 GAGGACTCTGCA C AGAA 3 A c
c

GTACCTTCTCCT AGG AGAAG GCTGCAGAG
ACATCTAG TCC TCTTC TGACGTCTC
- CA--

GAM47 269 PIGB 1 10347 NP_004846.3 5 211 CGCGCTACTGCA A A A 3 A c c
GCTTTCTTCCGC AGGC GAAGAGA GCTGCAG
CTTAGGAA TCCG CTTCTTT CGACGTC
C - A

GAM47 269 PIP5K2C 1 10143 NP_079055.2 3 1107 GATTTGTTTTTC - AGCT 3 A c c
TGTTCTCTTCTG AGG CAGAAGAGA GCAGAG
TCCTGTCT TCC GTCTTCTCT TGTCTT
T ----

GAM47 269 PLAG1 1 9631 NP_002646.1 3 5264 AATAGTACTGCA AGAA A 3 A c c
GCTTCTTGTGGC AGGC GAGAAGCTGCAG
CTACAGTG TCCG TTCTTCGACGTC
GTG- A

GAM47 269 PLD1 1 5891 NP_002653.1 3 205 AGCAAGACTTTA A GC C 3 A c c
TAATTCCTTCTG AGGCAGAAG GAA TG AGAG
CCTAACTT TCCGTCTTC CTT AT TTTC
- A- A

GAM47 269 POFUT1 1 18732 NP_056167.1 3 1795 TCCCAGGCTCAA A A- GCA 3 A c c
GCGATCCTTCTG AGGCAGAAG GA GCT GAG
CCTCAGCC TCCGTCTTC CT CGA CTC
- AG A--

GAM47 269 POM121 1 2631 NP_742017.1 3 1245 GGGCCCTCTGCA A A A ------- 3 A c c
GCCCATCCTTTC GGC GAAG GAA GCTGCAGAG
CTTCCGTC CTG CTTC CTT CGACGTCTC
- C - TCCTACC

GAM47 269 POU4F2 1 12824 NP_004566.1 3 68 CGCTCTTTTCTC -- CTGC- 3 A c c
TCCTCTCTTCTG AGGCAGAAGAGA AG AGAG
CCTCTTTT TCCGTCTTCTCT TC TCTC
CC TCTTT

GAM47 269 PPIL2 1 15498 NP_680480.1 3 295 CATCCCTCTGCA AA - A-- 3 A c c
GCCTGTCATCCC AGGCAG GA GA GCTGCAGAG
TGTCTGTG TCTGTC CT CT CGACGTCTC
C- A GTC

GAM47 269 PPIL2 1 15498 NP_680481.1 3 132 CATCCCTCTGCA AA - A-- 3 A c c
GCCTGTCATCCC AGGCAG GA GA GCTGCAGAG
TGTCTGTG TCTGTC CT CT CGACGTCTC
C- A GTC

GAM47 269 PPP1R3B 1 1614 NP_078883.1 3 819 GGGACACTTTCA - C 3 A b b
GCTTCTACTTTT AGGCAGAAG AGAAGCTG AGAG
GCCTTCTA TCCGTTTTC TCTTCGAC TTTC
A -

GAM47 269 PREB 1 9801 NP_037520.1 3 274 ATACTCCCTGCC AGCT A 3 A c c
TCCTTTCTTCTG AGGCAGAAGAGA GCAG
CCTACCAG TCCGTCTTCTTT CGTC
CCTC C

GAM47 269 PRICKLE 1 17660 XP_093799.2 3 3437 CTTCCTTCTGCA A AA 3 A c c

2 GCAGCTTTCTGC AGGCAGA GAG GCTGCAGAG
TTCTTGGG TTCGTCT TTC CGACGTCTT
- GA

GAM47 269 PRKACA 1 2912 NP_002721.1 3 293 CTCAGCCCTCCC AGAA CA 3 A c c

AGCCCACTTCTG AGGCAGAAG GCTG GAG
CCTGTTTT TCCGTCTTC CGAC CTC
ACC- C-

GAM47 269 PRKACG 1 8827 NP_002723.2 3 241 TGGTCCCTCTGT C --- T 3 A c c
GCTTCTCTCTTT AGG AGA AGAGAAGC GCAGAG
CTCCTCCC TCC TCT TCTCTTCG TGTCTC
- TTC -

GAM47 269 PRKAR1A 1 15538 NP_002725.1 3 124 ACTGGCATCGCA - A A 3 A c c
GCTTCCTGTCTG AGGCAGA AG GAAGCTGC GA
TTTATATA TTTGTCT TC CTTCGACG CT
G - -

GAM47 269 PRO2435 1 19591 NP_060997.1 5 878 ATCCACTTTGCA CAGA--- 3 A c c

GCTTCTTTGAGA AGG AGAGAAGCTGCAGAG
TTACCTAT TCC TTTCTTCGACGTTTC
ATTAGAG

GAM47 269 PRSS21 1 19855 NP_006790.1 3 67 AAGTCAGGCCCT G --- A- 3 A c c
GGTTCTCTTCTG AGGCAGAAGAGAA CT GC GA
TCTTGTTT TCTGTCTTCTCTT GG CG CT
- TCC GA

GAM47 269 PRSS21 1 19855 NP_659205.1 3 67 AAGTCAGGCCCT G --- A- 3 A c c
GGTTCTCTTCTG AGGCAGAAGAGAA CT GC GA
TCTTGTTT TCTGTCTTCTCTT GG CG CT
- TCC GA

GAM47 269 PRSS21 1 19855 NP_659206.1 3 67 AAGTCAGGCCCT G --- A- 3 A c c
GGTTCTCTTCTG AGGCAGAAGAGAA CT GC GA
TCTTGTTT TCTGTCTTCTCTT GG CG CT
- TCC GA

GAM47 269 PSCD4 1 7145 NP_037517.1 3 322 CAGAATGCTGCA C C A 3 A c c
ACTTCTCTTCTC AGG AGAAGAGAAG TGCAG
TCTGGACT TCT TCTTCTCTTC ACGTC
C A G

GAM47 269 PSEN1 1 10827 NP_000012.1 3 140 TGGACTTTTGCA A-- A 3 A c c
GCTTCCTTCCAA AGGC GAAG GAAGCTGCAGAG
GTCTTCCT TCTG CTTC CTTCGACGTTTT
AAC -

GAM47 269 PSEN1 1 10827 NP_015557.1 3 140 TGGACTTTTGCA A-- A 3 A c c
GCTTCCTTCCAA AGGC GAAG GAAGCTGCAGAG
GTCTTCCT TCTG CTTC CTTCGACGTTTT
AAC -

GAM47 269 PTCRA 1 10565 NP_612153.1 5 44 CTCAGGTCTGCA AAGAGA 3 A c c

GCTGGGTCCTGC AGGCAG AGCTGCAGA
CTCCTTCC TCCGTC TCGACGTCT
CTGGG-

GAM47 269 PTHLH 1 2062 NP_002811.1 3 69 CTGGGTTTTGGA A A G 3 A c c
GCCTCCCTTCTG AGGCAGAAG GA GCT CAGAG
CCTTGGCT TCCGTCTTC CT CGA GTTTT
C C G
GAM47 269 PTP4A3 2 12368 NP_009010.2 5 290 GCCTTCTCTGCA A------- A AA 3 A c c
GTCCCTTCTGCC GGCAGAAG G GCTGCAGAG
CTGCCGGG CCGTCTTC C TGACGTCTC
GGGCCGTC C --
GAM47 269 PTP4A3 2 12368 NP_116000.1 5 290 GCCTTCTCTGCA A------- A AA 3 A c c
GTCCCTTCTGCC GGCAGAAG G GCTGCAGAG
CTGCCGGG CCGTCTTC C TGACGTCTC
GGGCCGTC C --
GAM47 269 PTP4A3 2 16927 NP_009010.2 5 290 CAGCCTTCTCTG A----- A AA 3 A c c
CAGTCCCTTCTG GGCAGAAG G GCTGCAGAG
CCCTGCCG CCGTCTTC C TGACGTCTC
GCCGTC C --
GAM47 269 PTP4A3 2 16927 NP_116000.1 5 290 CAGCCTTCTCTG A----- A AA 3 A c c
CAGTCCCTTCTG GGCAGAAG G GCTGCAGAG
CCCTGCCG CCGTCTTC C TGACGTCTC
GCCGTC C --
GAM47 269 PVR 1 12007 NP_006496.2 3 1208 CCAGCATCTGCA A------ A AA 3 A c c
GCCACTTTCTGC GGCAGA GAG GCTGCAGA
CAGCATCT CCGTCT TTC CGACGTCT
TCTACGA - AC
GAM47 269 PXN 1 11342 NP_002850.1 3 1240 GCTTCTATGGGG - G GA 3 A c c
CTCTCTCTTCTG AGGCAGAAGAGA AGCT CA
CCTTCTCA TCCGTCTTCTCT TCGG GT
C G AT
GAM47 269 RA-GEF- 1 16978 NP_057424.1 3 2439 ACATACCCTGCA G AA A A 3 A c
c
2 GCTCTCAGCTGG AG CAG GAGA GCTGCAG
CTGCAGTA TC GTC CTCT CGACGTC
G GA - C
GAM47 269 RANBP3 1 1057 NP_015560.1 3 140 ACTCATTGCACA A C-- -- 3 A c c
TCTTCTCTTCAG AGGC GAAGAGAAG TGCA GAG
TTTAGAGA TTTG CTTCTCTTC ACGT CTC
A TAC TA
GAM47 269 RBM8A 1 6484 NP_005096.1 3 377 TCTTGGGCTCAA A A- --- A- 3 A c c
GCCATCCTTCTG AGGCAGAAG GA GCT GC GAG
CCTCACTG TCCGTCTTC CT CGA CG TTC
- AC ACT GG
GAM47 269 RERE 1 12774 NP_036234.2 3 1889 CATTTTTCTCTC A- GC C 3 A c c
ATTCCATTTCTG AGGCAGAAG GAA TG AGAG
CCTTAACT TCCGTCTTT CTT AC TCTC
AC -- -
GAM47 269 REST 1 13891 NP_005603.2 5 173 GCACCCTCTGCA AGAA AA-- 3 A c
c
GCCCCACTCCTG AGGC GAG GCTGCAGAG

GGCCTTCT TCCG CTC CGACGTCTC
GGTC ACCC
GAM47 269 RET 1 12696 NP_000314.1 3 84 TGGGAAGTCTCA G AA C 3 A c c
GCAGCTCTTCTG AG CAGAAGAG GCTG AGA
GCTGTGTT TC GTCTTCTC CGAC TCT
G GA -
GAM47 269 RET 1 12696 NP_065681.1 3 2831 TGGGAAGTCTCA G AA C 3 A c c
GCAGCTCTTCTG AG CAGAAGAG GCTG AGA
GCTGTGTT TC GTCTTCTC CGAC TCT
G GA -
GAM47 269 RET 1 12696 NP_066124.1 3 1316 TGGGAAGTCTCA G AA C 3 A c c
GCAGCTCTTCTG AG CAGAAGAG GCTG AGA
GCTGTGTT TC GTCTTCTC CGAC TCT
G GA -
GAM47 269 SCRG1 1 18361 NP_009212.1 5 300 CCTTCCAGCACC A - CTGC 3 A c
c
TCCTCTCTTCTC GGCAGAAG AGAAG AGAG
CTTTTGCC CCGTTTTC TCTTC TCTC
- C ----
GAM47 269 SDC1 2 6892 NP_002988.3 3 192 TCCACTCTGCTT -- A CT 3 A c c
CTCTGACTTCTG AGGCAGAAG AGA G GCAGAG
CCTGGAGA TCCGTCTTC TCT C CGTCTC
AG - TT
GAM47 269 SDC1 2 8422 NP_002988.3 3 192 GAGCTCCACTCT -- A CT 3 A c c
GCTTCTCTGACT AGGCAGAAG AGA G GCAGAG
TCTGCCTG TCCGTCTTC TCT C CGTCTC
AG - TT
GAM47 269 SDS3 1 5572 XP_045014.1 3 198 TTCCAACTTTGT AA - 3 A c c
CAGTCTTTTCTG AGGCAGAAGAG GCTG CAGAG
CCTCAACT TCCGTCTTTTC TGAC GTTTC
-- T
GAM47 269 SEC15B 1 6612 XP_039570.3 3 1692 GTCCTCTCTGCA A A ---- 3 A c c
GTTTTATTCCCT AGGC GAAG GAA GCTGCAGAG
TTAGTCTT TCTG TTTC CTT TGACGTCTC
A C ATTT
GAM47 269 SEC61A1 1 13837 NP_037468.1 3 670 TGGCTCTTCTAG G A- C- 3 A c c
CTGACTCTTCTG AG CAGAAGAG AGCTG AGAG
GTTGGGCT TT GTCTTCTC TCGAT TCTC
G AG CT
GAM47 269 SEMA7A 1 17524 NP_003603.1 3 521 CTGTCCTCTGCA -- A A- 3 A b b
GCTCCCTCTCTG AGG CAGA GAG AGCTGCAGAG
GTCCTGGG TCC GTCT CTC TCGACGTCTC
TG - CC
GAM47 269 SFRP2 1 14061 XP_050625.1 3 137 TCAGCCTGGGCA AAGA AG 3 A c
c
GCTTCCCCCTGC AGGCAG GAAGCTGC AG
CTTTTGCA TCCGTC CTTCGACG TC
CCC- GG
GAM47 269 SFXN1 1 7501 NP_073591.2 3 38 GAAACCTCTGCA A------- GA A 3 A c c
GCTCATTCTGCC GGCAGAA GA GCTGCAGAG

ACTGCAAA CCGTCTT CT CGACGTCTC
AAACGTCA A- -
GAM47 269 SH3BP2 1 12033 NP_003014.2 3 1593 GCCACCTCTGCA A - --- 3 A c c
GGGGTTTCCTCT AGGC GAAGAG AAGCT GCAGAG
TCAGCCTG TCCG CTTCTC TTTGG CGTCTC
A C GGA
GAM47 269 SH3GLB2 1 19409 NP_064530.1 3 609 TTTTATCTGGTG - TG 3 A c c
TTTTTACTTCTG AGGCAGAAG AGAAGC CAGA
CCTGCGTT TCCGTCTTC TTTTTG GTCT
A TG
GAM47 269 SHFM3 1 18245 NP_071322.1 3 66 AGCTACTCAGGG GA - GCA 3 A c
c
ACTTCTCTTGCC AGGCA AGAGAAG CT GAG
TGGAGGGT TCCGT TCTCTTC GG CTC
-- A GA-
GAM47 269 SKP1A 1 7175 NP_008861.2 5 56 TTCGTCTTCGGT C A C 3 A c c
TTTTCTCTTCCT AGG AGA GAGAAGCTG AGA
TCGCTAAC TCC TCT CTTTTTGGC TCT
T - T
GAM47 269 SKP1A 1 7175 NP_733779.1 5 56 TTCGTCTTCGGT C A C 3 A c c
TTTTCTCTTCCT AGG AGA GAGAAGCTG AGA
TCGCTAAC TCC TCT CTTTTTGGC TCT
T - T
GAM47 269 SLC9A8 2 1205 XP_030524.2 3 2226 TCGATCTCCTCT A----- AA G 3 A c c
GAGCCTCTTCTG GGCAGAAGAG GCT CAGAG
CCCCCTGT CCGTCTTCTC CGA GTCTC
TGTCCC -- -
GAM47 269 SLC9A8 2 9672 XP_030524.2 3 481 GATGCCTCTGCA - GAGAA 3 A c c
GCCACAATTCTG AGG CAGAA GCTGCAGAG
ACCTAAGT TCC GTCTT CGACGTCTC
A AACAC
GAM47 269 SMOC1 1 5573 NP_071420.1 3 1331 ACTGATCTTGGG GA- GC 3 A c c
TTTCCTATTCTG AGGCAGAA GAAGCT AGA
CCTCCCCT TCCGTCTT CTTTGG TCT
ATC GT
GAM47 269 SOD3 1 3673 NP_003093.1 3 73 CTCTGCCTTTGA A----- A ----- 3 A c c
GCTTCTCCTCTG GGCAGA GAGAAGCT GCAGA
CTCCAACA TCGTCT CTCTTCGA CGTCT
ACAACC C GTTTC
G
C
GAM47 269 SPARC 1 10553 NP_003109.1 3 336 ACACACATTGCA C --- A 3 A c c
GCTTCAACTTTT AGG AGAAGA GAAGCTGCAG
CTCTTTAG TTC TCTTTT CTTCGACGTT
- CAA A
GAM47 269 SPOCK 1 11060 NP_004589.1 3 432 CAGTGTCTAAGT - G TGC- 3 A c c

GCTTCTCTTGTG AGG CA AAGAGAAGC AGA
TCCTGTAG TCC GT TTCTCTTCG TCT
T G TGAA

GAM47 269 SPRR4 1 18654 NP_775103.1 3 416 CCCCTGCTCTGG A G 3 A c c
GCTTCTCTCCTG AGGCAG AGAGAAGCT CAGAG
TTTTCCCC TTTGTC TCTCTTCGG GTCTC
C -

GAM47 269 SQSTM1 1 18350 NP_003891.1 3 41 CCTCTTCTGCGT AA - 3 A c c
GCCCCTCTTCTG AGGCAGAAGAG GC TGCAGAG
TCTCATAG TCTGTCTTCTC CG GCGTCTT
CC T

GAM47 269 STAT3 1 19871 NP_003141.2 3 399 CCTGGTGCCTGC A A A 3 A c c
GGCATCCTTCTG AGGCAGAAG GA GCTGCAG
CCTGTTTC TCCGTCTTC CT CGGCGTC
- A C

GAM47 269 STAT3 1 19871 NP_644805.1 3 399 CCTGGTGCCTGC A A A 3 A c c
GGCATCCTTCTG AGGCAGAAG GA GCTGCAG
CCTGTTTC TCCGTCTTC CT CGGCGTC
- A C

GAM47 269 STK16 1 5128 NP_003682.1 3 140 CTCAGTCCTGCA C A 3 A c c
TCTTTTCTTCTG AGGCAGAAGAGAAG TGCAG
CTTTCTTC TTCGTCTTCTTTTC ACGTC
T C

GAM47 269 STX6 1 15081 NP_005810.1 3 379 ATCTTTGGCAGC A----- -- - 3 A c c
TCTTTTCTTCTG GGCAGAAGAGA AGCTGC AGAG
CTCAGACC TCGTCTTCTTT TCGACG TTTC
CCAGAC TC G

GAM47 269 SULT1B1 1 12908 NP_055280.2 5 193 TACTCTACAGCA AAGA --- 3 A c c

GCTTCACTGCCT AGGCAG GAAGCTGC AGAG
GAAAATGA TCCGTC CTTCGACG TCTC
A--- ACA

GAM47 269 SUV39H1 1 11187 NP_003164.1 3 362 TATTTGTTTTTG AGA C 3 A c c
CACCTGCTTCTG AGGCAGAAG AG TGCAGAG
CCTGGAGA TCCGTCTTC TC ACGTTTT
G-- C

GAM47 269 SYT2 1 3462 NP_796376.2 3 500 GTGTCTTTGAGC CA- -- G 3 A c c
ATTTCTCTTCAT AGG GAAGAGAA GCT CAGAG
TCCTGGAA TCC CTTCTCTT CGA GTTTC
TTA TA -

GAM47 269 SYT6 1 7804 XP_086135.1 5 28 GGAGACTCTGCA C AA GA- - 3 A c c
GGCTCCATCCCT AGG AG GA AGC TGCAGAG
CCTTATTC TCC TC CT TCG ACGTCTC
- C- ACC G

GAM47 269 SYTL2 1 13084 NP_115755.2 3 578 ACTGAAACTACT AA TG - 3 A c c
GGTGTTTTTCTG AGGCAGAAGAG GC CAG AG
CCTTGAGA TCCGTCTTTTT TG GTC TC
G- -- A

GAM47 269 SYTL2 1 13084 NP_116561.1 3 578 ACTGAAACTACT AA TG - 3 A c c
GGTGTTTTTCTG AGGCAGAAGAG GC CAG AG

CCTTGAGA TCCGTCTTTTT TG GTC TC
G- -- A
GAM47 269 TAF9L 1 18397 NP_057059.2 3 276 TTCTGTTTTTGA AAG ----- 3 A c c
GACACTTTTCTG AGGCAGAAGAG CT GCAGAG
CCTTCTAT TCCGTCTTTTC GA TGTCTT
ACA GTTTT
GAM47 269 TBX15 2 4394 NP_689593.1 3 231 CGCAACTCAGTG AA TG A 3 A c c
GCCATTCTTCTG AGGCAGAAGAG GC C GAG
CCTTCCCA TCCGTCTTCTT CG G CTC
AC GT A
GAM47 269 TBX15 2 5309 NP_689593.1 3 587 TTCTCCCCTGCA A A A 3 A c c
GCTTCCTCTGCT AGGCAGA G GAAGCTGCAG
TCTGGAAT TTCGTCT C CTTCGACGTC
- - C
GAM47 269 TBX19 1 14889 NP_005140.1 3 244 ATTTTCTCTGCA A------ GA - 3 A c c
GCTTATTCTTGC GGCA AGAG AAGCTGCAGAG
CATGCTTA CCGT TCTT TTCGACGTCTC
ATTCGTA -- A
GAM47 269 TCFL4 1 9522 NP_037515.2 3 1012 CCTAGTTCTCCA A GC C 3 A c c
AATTCACTTCTG AGGCAGAAG GAA TG AGAG
CCTTCCTC TCCGTCTTC CTT AC TCTT
A AA C
GAM47 269 TCFL4 1 9522 NP_733752.1 3 1012 CCTAGTTCTCCA A GC C 3 A c c
AATTCACTTCTG AGGCAGAAG GAA TG AGAG
CCTTCCTC TCCGTCTTC CTT AC TCTT
A AA C
GAM47 269 TCFL4 1 9522 NP_733753.1 3 1012 CCTAGTTCTCCA A GC C 3 A c c
AATTCACTTCTG AGGCAGAAG GAA TG AGAG
CCTTCCTC TCCGTCTTC CTT AC TCTT
A AA C
GAM47 269 TCL1B 1 19739 NP_004909.1 3 99 GATCTTCATGTA A C - 3 A c c
CCTGCTCTTCTG AGGCAGAAGAG AG TGCA GAG
TTTGCACA TTTGTCTTCTC TC ATGT CTT
G C A
GAM47 269 TFDP2 1 17242 NP_006277.1 3 418 CGTGTTTCTGAC -- TG 3 A c c
GTTTCTCTTCCT AGGCA GAAGAGAAGC CAGAG
TGCCTGGA TCCGT CTTCTCTTTG GTCTT
TC CA
GAM47 269 TGFBR3 1 17248 NP_003234.1 3 537 CCTTTGTCTGGA - AA TG- 3 A c c
TGCACTCTTCTG AGG CAGAAGAG GC CAGA
ACCTTGCT TCC GTCTTCTC CG GTCT
A A- TAG
GAM47 269 TIMM22 1 19351 NP_037469.1 3 164 GGGAGCTGCCTG --- A- -- A 3 A c c
GCTTCTCTGCCT AGGC AG AGAGAAGCT GCAG
CCAGCCTT TCCG TC TCTCTTCGG CGTC
ACC CG TC G
GAM47 269 TIMP3 1 11578 NP_000353.1 3 2907 TTCCTCCTTTGG A G 3 A b b
GCATCTCTTCTG AGGCAGAAGAGA GCT CAGAG
CCTCCCAA TCCGTCTTCTCT CGG GTTTC

A -
GAM47 269 TM6SF2 1 6832 NP_075378.1 3 2034 AGGTCGGTTTGG GAG G 3 A c c
GTTTGAATTCTG AGGCAGAA AAGCT CAGA
CCTCTTCT TCCGTCTT TTTGG GTTT
AAG -
GAM47 269 TMEM2 1 15379 NP_037522.1 3 743 ACCATTTTTGCA A A -- 3 A c c
GCTTTAATCCTT AGGC GA GA GAAGCTGCAGAG
AGCCTCTT TCCG TT CT TTTCGACGTTTT
A C AA
GAM47 269 TMEPAI 1 3022 NP_064567.2 3 1416 CAGAATTCTTCA CA C C 3 A c c
CCTTCTCTTCCC AGG GAAGAGAAG TG AGAG
CTTTCCAT TCC CTTCTCTTC AC TCTT
C- C T
GAM47 269 TMIE 1 7061 NP_671729.1 3 964 AGCTTCTTTGCA A---- C - 3 A c c
GCTTCCTCTTCT GG AGAAGAG AAGCTGCAGAG
ACCATTTC CC TCTTCTC TTCGACGTTTC
CTTTA A C
GAM47 269 TNFAIP2 1 12369 NP_006282.2 3 133 TCCTGTGCTCTG AGA TG 3 A c c
ATGCTACTTCTG AGGCAGAAG AGC CAGAG
CCTAGCCC TCCGTCTTC TCG GTCTC
A-- TA
GAM47 269 TP53BPL 1 19807 NP_005793.1 3 506 TTAATCTGCACA A----- G -- 3 A c c
GTTTATCTTCTG GGCAGAAGA AAGCT GCAGA
CCAAAATA CCGTCTTCT TTTGA CGTCT
ATAAAA A CA
GAM47 269 TPCN2 1 19148 NP_620714.1 3 336 CTGTCCCCTGCA GAAGA A 3 A c c
GCTTCCGTGGTG AGGCA GAAGCTGCAG
CCTTTGCT TCCGT CTTCGACGTC
GGTGC C
GAM47 269 TRIM29 1 9558 NP_036233.2 3 141 CTGCCCTCTGCA AGA- AA 3 A c c
GCCCTCTGCCAG AGGC AGAG GCTGCAGAG
CCTCTTGG TCCG TCTC CGACGTCTC
ACCG C-
GAM47 269 TRIP-Br 1 4744 NP_055570.1 3 1292 TTGTCTTCTGCA CA A 3 A c c
2 GCTTCCTTTCCC AGG GAAG GAAGCTGCAGAG
TAGAGCTT TCC TTTC CTTCGACGTCTT
C- -
GAM47 269 TRIP13 1 1424 NP_004228.1 3 7 AAGAAGCTTGCA - AGAG A 3 A c c
GCTTACATCTGT AGG CAGA AAGCTGCAG
CCTGGGCT TCC GTCT TTCGACGTT
T ACA- C
GAM47 269 TTC7 1 14260 XP_031626.4 3 148 AACGCCTCTGCA C - A----- 3 A c c
GCTGCAGCCCTC AGG AGAA GAG AGCTGCAGAG
GTTCTCTT TTC TCTT CTC TCGACGTCTC
- G CCGACG
GAM47 269 TUBB5 1 15573 NP_006078.2 3 674 CCTCTGACCCCA A-- ---- A ---- 3 A c c
GCTTCTCTCTGA GG CAGA GAGAAGCTG CAGA

TTCCCACA CC GTCT CTCTTCGAC GTCT
ACA CTTA - CCCA

G
C

GAM47 269 TXL-2 1 14725 NP_835231.1 3 615 TACCTCTTACTT ---- C C 3 A c c
CAAATTCTTCTG AGGCAGAAGA GAAG TG AGAG
CCTCCCTC TCCGTCTTCT CTTC AT TCTC
TAAA - -
GAM47 269 U1SNRNP 1 19714 NP_008951.1 5 61 CTGTCGCCTGCA AA A A 3 A c
c
BP GCTGCTCGCCTG AGGCAG GAG AGCTGCAG
TCTCCGTC TCTGTC CTC TCGACGTC
CG G C
GAM47 269 U1SNRNP 1 19714 NP_073208.1 5 61 CTGTCGCCTGCA AA A A 3 A c
c
BP GCTGCTCGCCTG AGGCAG GAG AGCTGCAG
TCTCCGTC TCTGTC CTC TCGACGTC
CG G C
GAM47 269 U1SNRNP 1 19714 NP_851030.1 5 61 CTGTCGCCTGCA AA A A 3 A c
c
BP GCTGCTCGCCTG AGGCAG GAG AGCTGCAG
TCTCCGTC TCTGTC CTC TCGACGTC
CG G C
GAM47 269 U1SNRNP 1 19714 NP_851034.1 5 61 CTGTCGCCTGCA AA A A 3 A c
c
BP GCTGCTCGCCTG AGGCAG GAG AGCTGCAG
TCTCCGTC TCTGTC CTC TCGACGTC
CG G C
GAM47 269 ULK2 1 2470 NP_055498.2 3 1080 AGGAAAATGGGC GA AGA 3 A c c
AGCTGTCTTCTG AGGCAGAAGA AGCTGC
CCTAATGT TCCGTCTTCT TCGACG
G- GGT
GAM47 269 USP4 1 10548 NP_003354.1 3 89 TGACACTCTGCA G--- A - 3 A c c
GACTGCTAGTGT AGGCAGAA AG AG CTGCAGAG
TCTGTCTA TCTGTCTT TC TC GACGTCTC
GTGA G A
GAM47 269 VANGL2 2 2781 XP_049695.4 3 2926 TCAGTCCGTCTG A- ---- CT 3 A c c
TCTTCTCTTTCC GGCAGA AGAGAAG GCAGA
TCTGCCCT CCGTCT TCTCTTC TGTCT
TC CCTT --
GAM47 269 VANGL2 2 20059 XP_049695.4 3 1814 GTCTGTCTCTTT C CT 3 A c c
TCTTCTCTTCAA AGG AGAAGAGAAG GCAGA
AAACTTTG TTC TCTTCTTTTC TGTCT
- TC
GAM47 269 VEGFB 1 1771 NP_003368.1 3 204 TGGGCCTCTCAG A----- AAG- C 3 A c
c
AGGGCTCTTCTG GGCAGAAGAG CTG AGAG
CCATCCCT CCGTCTTCTC GAC TCTC

TCCCTA GGGA -

GAM47 269 VIPR1 1 10605 NP_004615.2 3 346 CTCTGCCCCCTG A----- A- T---- 3 A c c

CTGGCTCTTCTG GGCAGAAGAG AGC GCAGA

CCCAATTG CCGTCTTCTC TCG CGTCT

GTTAAC GG TCCCC

G

C

GAM47 269 VPS28 1 1076 NP_057292.1 3 123 TCACTGTCTGCA GA GA--- 3 A c c

GCTGCCTGTCTG AGGCA AGA AGCTGCAGA

GTGTCTGT TCTGT TCT TCGACGTCT

GG GTCCG

GAM47 269 VPS4A 1 15139 NP_037377.1 3 261 CTGGATGCTCAT A A CA 3 A c c

CAGCTCCTTCTG AGGCAGAAG GA GCTG GAG

CCTCCCCC TCCGTCTTC CT CGAC CTC

- - TA

GAM47 269 WBSCR1 1 9970 NP_071496.1 3 439 CATTCCCTCAGT - T A 3 A c c

GCTTCTCTTCTG AGG CAGAAGAGAAGC GC GAG

ACCTGCAT TCC GTCTTCTCTTCG TG CTC

A - A

GAM47 269 WBSCR1 1 9970 NP_114381.1 3 439 CATTCCCTCAGT - T A 3 A c c

GCTTCTCTTCTG AGG CAGAAGAGAAGC GC GAG

ACCTGCAT TCC GTCTTCTCTTCG TG CTC

A - A

GAM47 269 WDR22 1 1630 XP_031102.1 3 2036 CACTCAGTGTGT CA - -- 3 A c c

GTTTCTCTTCCC AGG GAAGAGAAGC TGCA GAG

CTTCTTAG TCC CTTCTCTTTG GTGT CTC

C- T GA

GAM47 269 WFDC13 1 15789 NP_742002.1 5 20 TTTGCCCTCTTT C CTGC 3 A c c

CCTTCTCTTCTC AGG AGAAGAGAAG AGAG

CTCACAGC TCC TCTTCTCTTC TCTC

- CTT-

GAM47 269 XPC 1 3193 NP_004619.2 3 304 ACTTTGCTAGGA AAG ---- 3 A c c

GATACTCTTCTG AGGCAGAAGAG CT GCAGAG

CCTCCTAG TCCGTCTTCTC GA CGTTTC

ATA GGAT

GAM47 269 ZAP 1 2097 NP_064504.2 5 0 CTTTTAGTTTCT C C 3 A c c

CTTCTTTCTAAA AGG AGAAGAGAAGCTG AGAG

GAAGGCTC TCT TCTTCTCTTTGAT TTTC

T -

GAM47 269 ZAP 1 2097 NP_078901.3 5 0 CTTTTAGTTTCT C C 3 A c c

CTTCTTTCTAAA AGG AGAAGAGAAGCTG AGAG

GAAGGCTC TCT TCTTCTCTTTGAT TTTC

T -

GAM47 269 ZDHHC5 1 17547 XP_290511.1 5 981 TGTGTTTCTTAA A CTGC 3 A c c

TCTTCCCTTCTG AGGCAGAAG GAAG AGAG

CCTTGTTC TCCGTCTTC CTTC TCTT

C TAAT

GAM47 269 ZDHHC6 1 7010 NP_071939.1 3 365 TCTGCATGTGGT C ----- - 3 A c c

ACTTCTCTTTTC AGG AGAAGAGAAG C TGCAGA

CCTCAGTT TCC TTTTCTCTTC G ACGTCT

C ATGGT T

GAM47 269 ZFP1 1 2444 NP_710155.1 5 108 GGAGGCTGCGCC --- AA T A 3 A c c

CCTCCAGTTCTG AGGCAGAA GAG GC GCAG

CCTTCATA TCCGTCTT CTC CG CGTC

GAC CC - G

GAM47 269 ZFP29 1 6538 NP_060364.1 3 259 GGGTTTGTCTGT AGA CT 3 A c c

CCCTGACTTCTG AGGCAGAAG AG GCAGA

CCTCTGAG TCCGTCTTC TC TGTCT

AG- CC

GAM47 269 ZFP95 1 10540 NP_055384.1 3 382 AGTAAGCTTTAT AGAGA 3 A c c

TTGTAGCTTCTG AGGCAGA AGCTGCAGA

CCTTGTTT TCCGTCT TCGATGTTT

GAM47 269 ZFP95 1 10540 NP_659570.1 3 382 AGTAAGCTTTAT AGAGA 3 A c c

TTGTAGCTTCTG AGGCAGA AGCTGCAGA

CCTTGTTT TCCGTCT TCGATGTTT

GAM47 269 ZHX2 1 3967 NP_055758.1 3 938 GCTTTGGTTTTC ----- C ----- 3 A c c

ATTTCTCTTCTT AGGCA GAAGAGAAG TG CAGA

CACTGCCT TCCGT CTTCTCTTT AC GTTT

CACTT - TTTTG

G

C

GAM47 269 ZNF137 1 18802 NP_003429.1 3 1242 GATTCTGCTAAA C-- - --- 3 A c c

GCTTCTCTGTCT AGG AGA AGAGAAGCT GCAGAG

TTCCCTGT TCC TCT TCTCTTCGA CGTCTT

CTT G AAT

GAM47 269 ZNF142 1 4359 NP_005072.1 3 321 TTACCCACTCCA CA C CA 3 A c c

TCTTCTCTTTCC AGG GAAGAGAAG TG GAG

TTCTTACT TCC TTTCTCTTC AC CTC

-- T --

GAM47 269 ZNF336 1 11735 NP_071927.1 3 136 ATGGCCTCTGCA A ------ G 3 A c c

GATTTTCCTGAA GGCAGAA GAGAA CTGCAGAG

CTTCTGCT TCGTCTT CTTTT GACGTCTC

- CAAGTC A

GAM47 269 ZNF431 1 4664 XP_086098.2 3 1544 TTCTGGTTTCAA AA - ---- 3 A c c

GCAACTCTTCTG AGGCAGAAGAG GCT G CAGAG

CCTCAGCA TCCGTCTTCTC CGA C GTCTT

AA A TTTG

GAM47 269 ZNF441 1 10390 NP_689568.1 5 21 ACGTCTGTGGCA AGAA TG 3 A c

c

GCTTCTGTCTCG AGGCAGAAG GC CAGA

CTGGGACC TCTGTCTTC CG GTCT

GA-- GT

GAM47 269 ZNF75A 1 15281 NP_694573.1 3 175 ACTTGCTCTGCA AG ----- A-- 3 A c c
GCCACTCAGTAG GCAGAAGA GA GCTGCAGAG
TCTTCTGT TGTCTTCT CT CGACGTCTC
-- GATGA CAC
GAM47 269 ZNF80 2 3538 NP_009067.1 5 146 CAAACGTCTGCA A-- --- A A 3 A c c
GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AAGCCAGC CCG TC TC CTTCGACGTCT
CGA AAG C A
GAM47 269 ZNF80 2 7656 NP_009067.1 5 257 CGAAGGTCTGCA A--- -- A A 3 A c c
GCTTCACTCCTG GGC AG AG GAAGCTGCAGA
AGCCAGCG CCG TC TC CTTCGACGTCT
GCGA AG C A
GAM49 338 FGF18 1 6988 NM_003862.1 5 GCGCCTCCTGCA TGA GC 3 C c c
CAGCGGC GCCGCTGTGC AGGAGGTGT
CGGCGACACG TCCTCCGCG
--- --
GAM49 338 FLJ1385 1 19352 NM_023079.2 3 CACACCTCTCCA G CTGAA C 3 C c
c
5 CAGGGC GCC CTGTG GGAGGTGTG
CGG GACAC TCTCCACAC
- C---- -
GAM49 338 FRAT1 1 9462 NM_005479.1 3 CACACAGCCTAG C GA AG C 3 C c c
CACAGCAGC GC GCTGTGCT AGG GTGTG
CG CGACACGA TCC CACAC
A -- GA -
GAM49 338 KIAA008 1 7226 NM_014769.1 3 GCACACCGTTGA C G GGA 3 C c c
7 GCACAGCAGC GC GCTGTGCT AA GGTGTGC
CG CGACACGA TT CCACACG
A G G--
GAM49 338 KIAA167 1 16549 XM_046570.3 3 GCACACCTCCCC CG GCTGAA 3 C c
c
9 AACAGAAGC GC CTGT GGAGGTGTGC
CG GACA CCTCCACACG
AA ACC---
GAM49 338 NINJ2 1 18923 NM_016533.3 5 GCACACCTCCCC C GTG AA 3 C c c
CAGAGGCTGC GC GCT CTG GGAGGTGTGC
CG CGG GAC CCTCCACACG
T A-- CC
GAM49 338 S100B 1 5375 NM_006272.1 3 CGTGCCTCCAGC - GAA TG C 3 C c c
ACATGCGGC GCCGC TGTGCT GGAGG TG
CGGCG ACACGA CCTCC GC
T --- GT -
GAM49 338 SEMA4B 1 17188 XM_044533.9 3 ACACTGCCCAGC G AA A GC 3 C c
c
ACAGGGGC GCC CTGTGCTG GG GGTGT
CGG GACACGAC CC TCACA
G -- G --
GAM49 338 TNFRSF6 1 17121 3 GCACCTTCTCAG C T A GC 3 C c c
B CCAGCAGC GC GCTG GCTGA GGAGGTGT
CG CGAC CGACT CTTCCACG

A - - --

GAM50 368 LOC8502 1 11482 NM_053040.1 5 GATCGAGGACTT G AGAAA A 3 C c c

8 CCGGGG CCCCGG AAGTC TCGATC

GGGGCC TTCAG AGCTAG

- G---- -

GAM51 201 ABCD4 1 1712 NM_020323.1 3 TGTGGAGGAGGA TC CT - 3 C c c

AGATGGG CCCATCT TTTTCC CCACA

GGGTAGA AGGAGG GGTGT

-- -- A

GAM51 201 ACAD8 1 1175 NM_014384.1 3 TGTGGGAAGGGG T - C C 3 C c c

AAATGGAGG CC CCAT TCTTTTTCCC ACA

GG GGTA AGGGGAAGGG TGT

- A A -

GAM51 201 ANP32A 1 9401 NM_006305.2 3 TGTGGGAACGAG A T TTC 3 C c c

AGGGGA TCCCC TCTC TT CCCACA

AGGGG AGAG AA GGGTGT

- C ---

GAM51 201 AP4S1 1 13777 NM_007077.2 5 TGCGGGAAAGAG A - CA 3 C c c

GGAGGGGGA TCCCC TCTCTTTTTCCC CA

AGGGG AGGGAGAAAGGG GT

G C --

GAM51 201 AQP6 1 17661 NM_053286.1 5 TGTGGGGATCAC T C TTTT- 3 C c c

TGAGATGAGG CC CATCTC TCCCCACA

GG GTAGAG AGGGGTGT

- A TCACT

GAM51 201 ATP1A2 1 15415 NM_000702.1 3 TGTGGGGATGGT C T TTT 3 C c c

GATGGAGA TC CCATC CT TCCCCACA

AG GGTAG GG AGGGGTGT

A T T--

GAM51 201 BMP1 1 4998 NM_006128.1 3 GTGGGGAGCCGA TCTTT A 3 C c c

TGGGGA TCCCCATC TTCCCCAC

AGGGGTAG GAGGGGTG

CC--- -

GAM51 201 C14orf1 1 19752 NM_007176.1 3 TGTGGGGTGGGC CT TTT 3 C c c

AGTGGGGA TCCCCAT CTT CCCCACA

AGGGGTG GGG GGGGTGT

AC T--

GAM51 201 C20orf8 1 2115 XM_097736.3 3 TGTGGGCAGAAG T TC 3 C b b

2 GATGGGGA TCCCCATC CTTTT CCCACA

AGGGGTAG GAAGA GGGTGT

- C-

GAM51 201 CCR5 1 15737 NM_000579.1 3 TGTGGCCTGGGA T TCC 3 C c c

GAGCTGGGGA TCCCCA CTCTTTT CCACA

AGGGGT GAGAGGG GGTGT

C TCC

GAM51 201 CENTD2 1 11402 NM_139181.1 3 TGTGGGGCTGGA TC TT 3 C c c

GAGATGGG CCCATCTCTTT CCCCACA

GGGTAGAGAGG GGGGTGT

-- TC

GAM51 201 CRHR2 1 3504 NM_001883.1 3 GTGGGGCAGGAG TC TTT A 3 C c c

ATGGG CCCATCTCTT CCCCAC
GGGTAGAGGA GGGGTG
-- C-- -

GAM51 201 CYP4F2 1 7657 NM_001082.3 3 TGTGGGGAGGTG C - TT 3 C c c
GGACTGAGGA TCC CA TCTC TTTCCCCACA
AGG GT AGGG GGAGGGGTGT
A C T-

GAM51 201 DKFZp43 1 2188 NM_017600.1 3 TGTGGGGAGACA C CTT 3 C c c
4M0331 GGTGGAGA TC CCATCT TTTCCCCACA
AG GGTGGA AGAGGGGTGT
A C--

GAM51 201 DKFZp76 1 17559 NM_032289.1 3 TGTGGGCCCAGG C TTTC 3 C c c

1B0514 AGATGGAGA TC CCATCTCTT CCCACA
AG GGTAGAGGA GGGTGT
A CCC-

GAM51 201 DRPLA 1 17538 NM_001940.2 3 TGTGGTGTGCAG TTTTCC 3 C c c
AGGTGGGGA TCCCCATCTCT CCACA
AGGGGTGGAGA GGTGT
CGTGT-

GAM51 201 FLJ1045 1 8966 NM_018095.2 3 TGTGGGGAGGGG C A TTT 3 C c c
0 AGGAGA TC CC TCTCT TCCCCACA
AG GG AGGGG AGGGGTGT
A - ---

GAM51 201 FLJ1369 1 8310 NM_024807.1 3 TGTGGGGAGAGT CA ---- 3 C c c
3 GGAAGAGGCAGG TCCC TCTCTTT TTCCCCACA
GA AGGG GGAGAAG GAGGGGTGT
AC GTGA

GAM51 201 FLJ1394 1 4113 3 TGTGGGGAAGAA T - C 3 C c c
0 AAGATAGGGG CCCC ATCT TTTTTCCCCACA
GGGG TAGA AAGAAGGGGTGT
- A A

GAM51 201 FLJ1414 1 14366 NM_024709.1 3 GGGGCTGAGAGA T- ACA 3 C c c
6 GATGGGGG TCCCCATCTCTTTT CCCC
GGGGGTAGAGAGAG GGGG
TC ---

GAM51 201 FLJ2050 1 13954 NM_017850.1 3 TGTGGACCTAAA TTCC 3 C c c
8 GAGGTGGGGA TCCCCATCTCTTT CCACA
AGGGGTGGAGAAA GGTGT
TCCA

GAM51 201 FLJ2519 1 11138 NM_144985.1 3 TGTGGGGAAAGT CC CTCT 3 C c c

3 ATGTAGA TC CAT TTTTCCCCACA
AG GTA GAAAGGGGTGT
AT T---

GAM51 201 GABARAP 1 11020 NM_031412.1 3 TGTGGGGTGGGA T TTT 3 C c c

L1 GTGGGGA TCCCCA CTCTT CCCCACA

AGGGGT GAGGG GGGGTGT
- T--

GAM51 201 GNB2 1 818 NM_005273.2 3 TGTGGAGATAAG ATC TT C 3 C c c
AAGGGGA TCCCC TCTT TC CCACA
AGGGG AGAA AG GGTGT
A-- T- A

GAM51 201 HEMK 1 12563 NM_016173.1 3 TGTGGGAAAAGC TCT TC 3 C c c
CCTGGGGG TCCCCA CTTTT CCCACA
GGGGGT GAAAA GGGTGT
CCC --

GAM51 201 HIVEP2 1 1152 NM_006734.2 3 TGTGGAAGGGGG A-- TCC 3 C c c
AAAAGGGGA TCCCC TCTCTTTT CCACA
AGGGG AGGGGGAA GGTGT
AAA ---

GAM51 201 HN1L 1 14161 NM_144570.1 3 TGTGGGGATGAA T C TTTT 3 C c c
ATGGGG CCCCAT TC TCCCCACA
GGGGTA AG AGGGGTGT
- A T---

GAM51 201 HNRPK 1 19122 NM_031262.1 3 TGTGAAGAACTA CTTT CC 3 C c c
AGGTGGGGA TCCCCATCT TTC CACA
AGGGGTGGA AAG GTGT
ATC- AA

GAM51 201 HOXD4 1 16160 NM_014621.2 3 GTGGGGAGAAAG TC TCT A 3 C c c

TGGG CCCA CTTTTTCCCCAC
GGGT GAAAGAGGGGTG
-- --- -

GAM51 201 HPIP 1 13420 NM_020524.2 3 TGTGAAGGGGGA - TTTT -- 3 C c c
GATGGGAGA TC CCCATCTCT CCC CACA
AG GGGTAGAGG GGG GTGT
A ---- AA

GAM51 201 ITGAM 1 2813 NM_000632.2 3 TGTGGGTGAAGA TC A TC 3 C c c
GAGAGGG CCC TCTCTTTT CCCACA
GGG AGAGAGAA GGGTGT
-- - GT

GAM51 201 JRKL 1 8555 NM_003772.2 3 TGTGGGTTGCAA AT TTTC 3 C c c
GAGGGGGA TCCCC CTCTT CCCACA
AGGGG GAGAA GGGTGT
-- CGTT

GAM51 201 KIAA001 1 10549 NM_014671.1 3 TGTGGATGTGAG TTTTTCC 3 C c c

0 GTGGGGA TCCCCATCTC CCACA
AGGGGTGGAG GGTGT
TGTA---

GAM51 201 KIAA042 1 20045 NM_014772.1 3 GGGAGAAAGAAA C CACA 3 C c c
7 TGGGGA TCCCCAT TCTTTTTCCC
AGGGGTA AGAAAGAGGG
A ----

GAM51 201 KIAA044 1 15553 NM_014675.1 3 GTGGGAAAGAGG AT C A 3 C c c
5 AGGGGGA TCCCC CTCTTTTT CCCAC

AGGGG GAGGAGAA GGGTG
-- A -

GAM51	201	KIAA077 1	17868		5	TGCGGGAGGAAG	TCT	- CA	3	C	c	c
	5			TGGGGA	TCCCCA	CTTTTTCCC CA						
				AGGGGT	GAAGGAGGG GT							
				---	C --							
GAM51	201	KIAA137 1	15843	XM_028413.6	3	TGCAGGGAGGAG	C	CA	3	C	c	c
	4			GAAATGGGGG	TCCCCAT	TCTTTTTCCC CA						
				GGGGGTA	AGGAGGAGGG GT							
				A	AC							
GAM51	201	KIAA150 1	16249		3	TGGGTGAATGAT	TCTTT -	CA	3	C	c	c
	0			GGGGA	TCCCCATC	TTC CCCA						
				AGGGGTAG	AAG GGGT							
				T----	T --							
GAM51	201	KIAA157 1	4415	XM_031545.5	3	TGTGTTTGACAG	T	TCCC	3	C	c	c
	3			AGATGGGGA	TCCCCATCTCT	TT CACA						
				AGGGGTAGAGA	AG GTGT							
				C	TTT-							
GAM51	201	KIAA164 1	819		5	TGTGGGAAGGGT	--- T	TTTC	3	C	c	c
	9			TGCCAGGGA	TCCC	CA CTCTT	CCCACA					
				AGGG	GT GGGAA	GGGTGT						
				ACC T	----							
GAM51	201	LOC1315 1	4254		3	TGCGGGGAGATT	A TT-	A	3	C	c	c
	83			TGAGAGGGGA	TCCCC	TCTC TTTCCCC CA						
				AGGGG	AGAG AGAGGGG GT							
				-	TTT C							
GAM51	201	LOC1459 1	16078		3	TGTAAGAAAAAG	- T-	CCC	3	C	c	c
	51			TTGAGTGGGGA	TCCCCA	TC CTTTTTC	ACA					
				AGGGGT	AG GAAAAAG	TGT						
				G	TT AA-							
GAM51	201	LOC1459 1	14131	XM_085289.4	3	TGCAGGGGGAGG	A	TT CA	3	C	c	c
	90			GAGAGGGGA	TCCCC	TCTCTTT CCC CA						
				AGGGG	AGAGGGA GGG GT							
				-	GG AC							
GAM51	201	LOC1461 1	13023		3	TGTGGGGAAGGT T	CT TTT		3	C	c	c
	08			ATGGGG	CCCCAT	CT TCCCCACA						
				GGGGTA	GA AGGGGTGT							
				-	TG ---							
GAM51	201	LOC1472 1	12528	XM_085742.2	5	TGTGGAAAAGAA	A --	CC	3	C	c	c
	29			TGGAGAGGGGA	TCCCC	TCTCT TTTT	CCACA					
				AGGGG	AGAGG AGAA	GGTGT						
				-	TA AA							
GAM51	201	LOC1493 1	4322	XM_097631.1	5	TGTAAGACAGGA	T -	CCC	3	C	c	c
	86			GGATGGGGA	TCCCCATC	CTTTT TC	ACA					
				AGGGGTAG	GAGGA AG	TGT						
				-	C AA-							
GAM51	201	LOC1510 1	16461		3	TGTGGGGTGGGG	A-	TT	3	C	c	c
	40			GGAGCGGGGA	TCCCC	TCTCTTT	CCCCACA					
				AGGGG	AGGGGGG	GGGGTGT						

CG T-

GAM51 201 LOC1514 1 5376 XM_098060.1 5 TGTGGTCTCAAG TTTCC 3 C c c
38 AGATGGGGG TCCCCATCTCTT CCACA
GGGGGGTAGAGAA GGTGT
CTCT-

GAM51 201 LOC1584 1 10627 XM_098936.1 5 TGTGAGAAGCAG C T CC 3 C c c
02 AGATAGGGA TCCC ATCTCT TTTC CACA
AGGG TAGAGA GAAG GTGT
A C A-

GAM51 201 LOC1624 1 4357 3 TGTGGGGAGGTG C CTT 3 C c c
61 GGTGGAGA TC CCATCT TTTCCCCACA
AG GGTGGG GGAGGGGTGT
A T--

GAM51 201 LOC2002 1 14994 XM_114157.1 3 TGTGAGGGAGAG A TTTT - 3 C c c
20 ACGGGGA TCCCC TCTC TCCC CACA
AGGGG AGAG AGGG GTGT
C ---- A

GAM51 201 LOC2204 1 7875 5 TGTGGGGAAAAG -- 3 C b b
31 GAAAGATGGGGG TCCCCATC TCTTTTTCCCCACA
GGGGGTAG AGGAAAAGGGGTGT
AA

GAM51 201 LOC2551 1 6202 XM_172929.2 5 TGTAGAGGGAGG T CC- 3 C c c
89 AGCGATGGGGA TCCCCATC CTTTTTCC ACA
AGGGGTAG GAGGAGGG TGT
C AGA

GAM51 201 LOC2556 1 16025 3 TGCGGGGAGAAG - A CTT A 3 C c c
50 ACGGAGGA TCC CC TCT TTTCCCC CA
AGG GG AGA AGAGGGG GT
A C --- C

GAM51 201 LOC2561 1 5147 5 GTGGATGAAGGA T TTCC A 3 C c c
58 TGGGGA TCCCCATC CTTT CCAC
AGGGGTAG GAAG GGTG
- TA-- -

GAM51 201 LOC2565 1 410 NM_174937.1 3 TGTGGGGAAGCA CA T T 3 C c c
36 GGAACGGGA TCCC TC CT TTTCCCCACA
AGGG AG GA GAAGGGGTGT
CA - C

GAM51 201 LOC2567 1 18655 5 TGTGGGAAACTG A TT C 3 C c c
33 AGAGGGGA TCCCC TCTC TTTCCC ACA
AGGGG AGAG AAAGGG TGT
- TC -

GAM51 201 LOC9113 1 2831 3 GTGGGGAGAAAG CATC A 3 C c c
3 AGGGA TCCC TCTTTTTCCCCAC
AGGG AGAAAGAGGGGTG
---- -

GAM51 201 LOC9135 1 9849 3 TGTGGGAAAAAG TCC T C 3 C c c
1 AGCTGG CCA CTCTTTTTCCC ACA
GGT GAGAAAAAGGG TGT
--- C -

GAM51 201 LTA 1 19202 NM_000595.2 3 TGGAGGATGGAG A TT - CA 3 C c c

AGAGGGGA TCCCC TCTCTT TCC CCA
AGGGG AGAGAG AGG GGT
- GT A --

GAM51 201 MGC1071 1 17807 NM_024325.3 3 TGTGGGGAGAAT CCA CT 3 C c c

5 GGACAAGGA TCC TCT TTTTCCCCACA
AGG AGG AAGAGGGGTGT
AAC T-

GAM51 201 MGC1098 1 13552 NM_030576.2 3 TGGGGGAGGAGA TT CA 3 C c c

6 TGGGGA TCCCCATCTCT TTCCCCA
AGGGGTAGAGG AGGGGGT
-- --

GAM51 201 MGC1587 1 6309 NM_032920.1 3 TGTAAGAAGAAG C CCC 3 C c c

3 AGATGAGGA TCC CATCTCTTTTTC ACA
AGG GTAGAGAAGAAG TGT
A AA-

GAM51 201 MGC1614 1 15996 NM_032763.1 5 TGTGGGGAGGGA C CTC 3 C c c

2 AAATGAGGA TCC CAT TTTTTCCCCACA
AGG GTA AGGGAGGGGTGT
A AA-

GAM51 201 MGC5356 1 5507 NM_024059.2 5 GTGGGGGTGGAG C TTT A 3 C c c

ATGAGGA TCC CATCTCT TCCCCAC
AGG GTAGAGG GGGGGTG
A T-- -

GAM51 201 MJD 1 19294 NM_030660.1 3 TGTGTCAAAGAG C TTCCC 3 C c c

ATGAGGA TCC CATCTCTTT CACA
AGG GTAGAGAAA GTGT
A CT---

GAM51 201 OTOF 1 6635 NM_004802.1 3 TGTGAGAAGCAG A - T CC 3 C c c

CAGAGGGGA TCCCC TCT CT TTTC CACA
AGGGG AGA GA GAAG GTGT
- C C A-

GAM51 201 PAG 1 8895 NM_018440.2 3 TGCGGGTGAAGG TT - CA 3 C c c

GATGGGGA TCCCCATCTCTTT CCC CA
AGGGGTAGGGAAG GGG GT
T- C --

GAM51 201 PATE 1 11458 NM_138294.1 3 TGTGGCCTGAAG TTCC 3 C c c

GGATGGGGA TCCCCATCTCTTT CCACA
AGGGGTAGGGAAG GGTGT
TCC-

GAM51 201 PP1057 1 461 NM_031285.1 5 TGTGGGGGTGGG C T TT 3 C c c

AGTGGAGA TC CCA CTCTT TCCCCACA
AG GGT GAGGG GGGGGTGT
A - T-

GAM51 201 PPP1R12 1 7244 NM_032105.1 3 GGAGGAATGAGA T - ACA 3 C c c

B GGTGGGGA TCCCCATCTCTT TTCC CC
AGGGGTGGAGAG AAGG GG

T A ---

GAM51 201 PRO0659 1 4863 NM_014138.1 3 TGTGGGAAAGGA C CT TTC 3 C c c

ATGTGGA TCC CAT CTTT CCCACA

AGG GTA GAAA GGGTGT

T AG ---

GAM51 201 PTPRN2 1 19987 NM_130842.1 3 TGTGGGGCCCCA A TTTT 3 C c c

GAGAGGGGA TCCCC TCTCT CCCCACA

AGGGG AGAGA GGGGTGT

- CCCC

GAM51 201 RGL 1 20166 NM_015149.2 3 GTGGGGAAAGAG T TT A 3 C c c

ATGGGG CCCCATCTCTT TCCCCAC

GGGGTAGAGAA AGGGGTG

- -- -

GAM51 201 RoXaN 1 16809 NM_017590.4 3 TGTGAAGGCAGA - TTTT C- 3 C c c

GTATGGGGA TCCCCAT CTCT CC CACA

AGGGGTA GAGA GG GTGT

T C--- AA

GAM51 201 SCYD1 1 18728 3 TGTGGGAAGGGG T C- C 3 C c c

AGATAAGGG CCC ATCTCTTTTTCCC ACA

GGG TAGAGGGGAAGGG TGT

- AA -

GAM51 201 SLC2A1 1 17243 NM_006516.1 3 TGAGGGAGGAGA A TTT - CA 3 C c c

GGGGA TCCCC TCTCT TCCC CA

AGGGG AGAGG AGGG GT

- --- A --

GAM51 201 STOML1 1 17548 NM_004809.2 3 TGCGGGGATTGG --- A 3 C c c

AGAGGGATGGGG TCCCCATCTCTTTT TCCCC CA

A AGGGGTAGGGAGAG AGGGG GT

GTT C

GAM51 201 TUSP 1 12909 NM_020245.2 3 TGTGGGGAGGAG CC - 3 C c c

AGAGATGCAGA TC CATCTCTTTT TCCCCACA

AG GTAGAGAGAG AGGGGTGT

AC G

GAM51 201 UBE2I 1 17025 NM_003345.1 5 TGTGAGGAGGGC C TTT C 3 C c c

GTGGGGA TCCCCAT TCT TCC CACA

AGGGGTG GGG AGG GTGT

C --- A

GAM52 373 GJA5 1 15528 NM_005266.3 3 AACTCTACCACC G TA GCA 3 C c c

TGGGCTGGAA TTCCAGT GGG GTAGAGTT

AAGGTCG TCC CATCTCAA

- GG AC-

GAM52 373 PTPNS1 1 15053 NM_080792.1 3 AACCCTACTGGG A GG- A 3 C c c

ATCAAACTGGAA GTTCCAGTT GG CAGTAG GTT

T TAAGGTCAA CT GTCATC CAA

A AGG C

GAM53 359 C20orf3 1 14770 NM_024893.1 3 TCTGCAGCCTGC GA TGAA 3 C c c

9 CAGTGC GCATTGGCAG TTGCAGA

CGTGACCGTC GACGTCT

```
                                        --       C---
GAM53   359   FLJ1068 1  20126          3       TCTGCATAATGT   CA        ----       3  C  c  c
        7                              TCACTGCCAAAC GAG  TTGGCAGTGAAT   TGCAGA
                                       TC        CTC  AACCGTCACTTG   ACGTCT
                                         A-         TAAT
GAM53   359   FOSB   1  7846  NM_006732.1  3       TCTGACTGTCCC        T  ATTG        3  C  c  c
                                       TGCCAATGCTC  GAGCATTGGCAG GA   CAGA
                                            CTCGTAACCGTC CT   GTCT
                                                  C  GTCA
GAM53   359   HBP17  1  15114 NM_005130.1  5       CTGCAATTCACT GA  T  C       A      3  C  c  c
                                       CCCACTGC      GCA TGG AGTGAATTGCAG
                                            CGT ACC TCACTTAACGTC
                                       --  C  C         -
GAM53   359   LDHA   1  6401  NM_005566.1  3       TCTGACGCACCA G         AAT -       3  C  c  c
                                       CTGCCAATGCT   AGCATTGGCAGTG   TG CAGA
                                            TCGTAACCGTCAC   GC GTCT
                                       -          CAC  A
GAM53   359   LOC1252 1  6730          3       TCTGAAGAACTG GA        GAA  G        3  C  c  c
        68                             CCAATGC       GCATTGGCAGT   TT CAGA
                                            CGTAACCGTCA   AA GTCT
                                       --         AG-  -
GAM53   359   TTTY11  1  10980 NM_031929.1  3       TCTGCAAAACAG G       A  GAA          3  C  c  c
                                       CCAATGCT     AGCATTGGC GT   TTGCAGA
                                            TCGTAACCG CA   AACGTCT
                                       -       A  A--
GAM54   275   AKAP13  1  18908 NM_007200.2  3       TCAGAAGGGGCC  T    CAGA            3  C  c  c

                                       ACGGCCTCC    C GGGCC    TGGCCCCTTCTGA
                                            C TCCGG    ACCGGGGAAGACT
                                            C    C---
GAM54   275   ATP2A3  1  11692 NM_174957.1  3       TCAGAAGGGGCC                    3  C  a  a
                                       ATCTGGGCCCAG CTGGGCCCAGATGGCCCCTTCTGA
                                            GACCCGGGTCTACCGGGGAAGACT

GAM54   275   BN51T   1  16770          3       CAGAAGGGGCCC C    C  AT       A      3  C  c  c
                                       ACTGAGCCCA   TGGGC CAG  GGCCCCTTCTG
                                            ACCCG GTC  CCGGGGAAGAC
                                       -    A  AC         -
GAM54   275   DKFZP72 1  15727 XM_045308.6  3       TCAGAAGGCACC       AGA---  CC         3  C  c
c
        7G051                             AGCACCAGGGCC CTGGGCCC     TGG  CCTTCTGA
                                       CAG         GACCCGGG     ACC  GGAAGACT
                                              ACCACG   AC
GAM54   275   FCGRT   1  3505  NM_004107.1  3       CAGAAGGGGTTC         TG       A      3  C  b  b
                                       TGGGCCTAG   CTGGGCCCAGA  GCCCCTTCTG
                                            GATCCGGGTCT  TGGGGAAGAC
                                              --        -
GAM54   275   FLJ2042 1  6197  NM_017814.1  3       TCAGAACTGTCT        AT--  CCC         3  C  c  c
        2                              CTCCTGGGCCCA CTGGGCCCAG    GGC   TTCTGA
                                       G          GACCCGGGTC    CTG   AAGACT
```

CTCT TC-

GAM54 275 KIAA045 1 1094 NM_014638.1 5 CAGGCAGGGACC AT C - A 3 C c c
0 TCCTGGGCCCAG CTGGGCCCAG GG CCCT TCTG
GACCCGGGTC CC GGGA GGAC
CT A C -

GAM54 275 LOC1452 1 19216 XM_096740.1 3 CAGAATAGCTGG ATGGCCCC A 3 C
c c
31 GCCCAG CTGGGCCCAG TTCTG
GACCCGGGTC AAGAC
GAT----- -

GAM54 275 LOC1500 1 6667 XM_097795.1 3 TCAGAAGGGTGC - CAGA - 3 C b b
05 CAGGCCACAG CTG GGCC TGGC CCCTTCTGA
GAC CCGG ACCG GGGAAGACT
A ---- T

GAM54 275 LOC1525 1 738 5 TCAGAAGGAGGG - AGA -- 3 C c c
80 CTGGGTGCCCAG CTGGGC CC TGGCCC CTTCTGA
GACCCG GG GTCGGG GAAGACT
T --- AG

GAM54 275 LOC2539 1 16736 3 TCAGAAGGGTGG CT G G C 3 C c c
55 TGTGGGCCC GGGCCCA AT GCCC TTCTGA
CCCGGGT TG TGGG AAGACT
-- G G -

GAM54 275 MATN1 1 18773 NM_002379.2 5 TCAGTTGGGGGC C CC A T- 3 C c c
CACCTGACCCA TGGG CAG TGGCCCCT CTGA
ACCC GTC ACCGGGGG GACT
- A- C TT

GAM54 275 NDUFV3 1 18615 NM_021075.2 5 TCAGAAGGAGCG CAGATG C 3 C c
c
TGGCCCAG CTGGGCC GC CCTTCTGA
GACCCGG CG GGAAGACT
TG---- A

GAM54 275 OS4 1 19362 NM_005730.2 3 TCAGAAGGCTGT C- CC 3 C c c
CTGGCACCCAG CTGGG CCAGATGGCC TTCTGA
GACCC GGTCTGTCGG AAGACT
AC --

GAM54 275 PAX8 1 1852 NM_013992.1 5 TCAGAAGGAGGA AGATGG--- - 3 C c c
GAGACACCGGGC CTGGGCCC CC CCTTCTGA
CCAG GACCCGGG GG GGAAGACT
CCACAGAGA A

GAM54 275 PDZD2 1 16711 5 TCGGAAGACCCC C AT CCC 3 C c c
TGGGCCCA TGGGCCCAG GG CTTCTGA
ACCCGGGTC CC GAAGGCT
- C- A--

GAM54 275 PI4KII 1 4231 NM_018425.2 3 TCAGAAGGAAAT ATGGCC 3 C c c
TGGGTCCAG CTGGGCCCAG CCTTCTGA
GACCTGGGTT GGAAGACT
AAA---

GAM54 275 RCD-8 1 7302 NM_014329.2 3 TCAGAAGGTTTA ATGGCC 3 C c c
GCTGGGCCCAG CTGGGCCCAG CCTTCTGA
GACCCGGGTC GGAAGACT

GATTT-
GAM54 275 RGS11 1 3919 NM_003834.1 3 CAGAAGGAATGG GATGGCC A 3 C c c
GTCCAG CTGGGCCCA CCTTCTG
GACCTGGGT GGAAGAC
AA----- -
GAM54 275 XAP135 1 4269 5 CAAAAGGAGGCG GATG - C A 3 C c c
AATGGGCTCAG CTGGGCCCA GCC CCTT TG
GACTCGGGT CGG GGAA AC
AAG- A A -
GAM54 275 ZDHHC3 1 16992 NM_016598.1 3 TCAGAAGGGACC G CAGAT C 3 C c c
TTGGCACAG CTG GCC GG CCCTTCTGA
GAC CGG CC GGGAAGACT
A TT--- A
GAM55 387 ABLIM1 1 18812 NP_002304.2 3 2163 TCTCTCTGTGCC TC AT 1 B c c
CTCCTGCAATGG CTGCCATT CAGGAG CAC
CAGCCTTG GACGGTAA GTCCTC GTG
C- CC
GAM55 387 ABLIM1 1 18812 NP_006710.2 3 2163 TCTCTCTGTGCC TC AT 1 B c c
CTCCTGCAATGG CTGCCATT CAGGAG CAC
CAGCCTTG GACGGTAA GTCCTC GTG
C- CC
GAM55 387 ABLIM1 1 18812 NP_006711.2 3 2163 TCTCTCTGTGCC TC AT 1 B c c
CTCCTGCAATGG CTGCCATT CAGGAG CAC
CAGCCTTG GACGGTAA GTCCTC GTG
C- CC
GAM55 387 ACVR2 1 11850 NP_001607.1 3 122 GAGTAGGATGTC GC- CA 1 B c c
TCTTGGAAATGT CT CATTTCCAGGAGAT CC
TAAGAAAG GA GTAAAGGTTCTCTG GG
ATT TA
GAM55 387 AP2B1 1 7416 NP_001273.1 3 708 GGAACGGTGATC C-- -- C 1 B c c
TTCTTGAATGAT CTG CATT TC AGGAGATCACC
GTTTCAGT GAC GTAG AG TCTTCTAGTGG
TTT TA T
GAM55 387 APOARGC 1 6057 NP_077818.1 3 229 GTAGGAGTGCTA - - - AT 1 B c c
CCATGGAAATGG CTG CCATTTCCA GG AG CAC
ACAGAGTT GAC GGTAAAGGT CC TC GTG
A A A --
GAM55 387 APOARGC 1 6057 NP_663779.1 3 229 GTAGGAGTGCTA - - - AT 1 B c c
CCATGGAAATGG CTG CCATTTCCA GG AG CAC
ACAGAGTT GAC GGTAAAGGT CC TC GTG
A A A --
GAM55 387 BCAS1 1 6939 NP_003648.1 3 311 GTTCGGGTTAAG C GGAGA 1 B c c
TGATGAAAATGG CTGCCATTT CA TCAC
CAGTGGTG GACGGTAAA GT AGTG
A -----
GAM55 387 BOP 1 18720 XP_097915.2 3 2657 CAGATTGTGAGC AT A 1 B c c

TCCTGGAGGGCA CTGCC TTCCAGGAG TCAC
GGAGCTGT GACGG GAGGTCCTC AGTG
-- G

GAM55 387 BRD2 1 3080 NP_005095.1 3 241 TGGGGAGTGATC CCATT 1 B c c
TCTTGGACACAG CTG TCCAGGAGATCAC
AGCCCCCA GAC AGGTTCTCTAGTG
AC---

GAM55 387 C1orf21 1 3784 NP_110433.1 3 608 CTGTGATGTGAC -- A 1 B b b
TCCTGGAAGTGA CTGC CATTTCCAGGAG TCAC
CGTAGGAG GATG GTGAAGGTCCTC AGTG
CA -

GAM55 387 C21orf4 1 3897 NP_061817.1 5 7 GCGCGGGCGATT T AGG A 1 B c c
5 TGTAGGTAATGG CTGCCATT CC AGATC CC
CAGGCGTT GACGGTAA GG TTTAG GG
T ATG C

GAM55 387 C6orf14 1 15036 NP_065141.2 5 461 CACCTGGGAATT C - A A 1 B c c
9 CGCTGGAAATGC CTGC ATTTCCAG GAG TC CC
AGGCTCAA GACG TAAAGGTC CTT AG GG
- G A -

GAM55 387 CAV2 1 3984 NP_001224.1 3 485 AATATACAATGA C GA C 1 B c c
TCCTGGAAATTG CTGC ATTTCCAGGA TCA
CAGTAACA GACG TAAAGGTCCT AGT
T -- A

GAM55 387 CBFA2T2 1 4255 NP_005084.1 3 864 GAGTGGATCATC C ---- 1 B b b
TCTTGGAAATGC CTGC ATTTCCAGGAGAT CAC
AGAACTTC GACG TAAAGGTTCTCTA GTG
- CTAG

GAM55 387 CBFA2T2 1 4255 NP_787060.1 3 864 GAGTGGATCATC C ---- 1 B b b
TCTTGGAAATGC CTGC ATTTCCAGGAGAT CAC
AGAACTTC GACG TAAAGGTTCTCTA GTG
- CTAG

GAM55 387 CGI-01 1 19545 NP_057019.2 3 418 ATAGGAGTGATC C CAG- 1 B c c
TCAAGTGAGATA CTGC ATTTC GAGATCAC
GCAGAGCA GACG TAGAG CTCTAGTG
A TGAA

GAM55 387 CPT1C 1 13296 NP_689572.1 5 15 GTGACGGTGATC ATT AG 1 B c c
TCGGGGTGGGCA CTGCC TCC GAGATCACC
GGACTCCA GACGG GGG CTCTAGTGG
GT- G-

GAM55 387 CREG 1 7517 NP_003842.1 3 202 TGTTATTGGATT --- AC 1 B c c
TCCTGGAAGATG CTGCCAT TTCCAGGAGATC
TGGTAGCT GATGGTG AAGGTCCTTTAG
TAG GT

GAM55 387 CRMP1 1 16155 NP_001304.1 3 590 GAGATCCGTGAA T AG A 1 B c c
TTCTCGGAATGG CTGCCATT CC GAG TCAC
CAGGGGAA GACGGTAA GG CTT AGTG
- CT A

GAM55 387 CUL3 1 7104 NP_003581.1 3 3312 TCCAAGGTTGCT AGG- ATC 1 B c c

AGCAGGAAATGG CTGCCATTTCC AG ACC

CAGAGCCA GACGGTAAAGG TC TGG
ACGA GT-
GAM55 387 DCTN4 1 4858 NP_057305.1 3 305 GGGATGGGTGTT C----- A T 1 B c c
CCTTGGAAATGG TGCCATTTCCAGG GA CACC
CATTGTAT ACGGTAAAGGTTC CT GTGG
TATGTT - T
GAM55 387 DKFZp76 1 2906 NP_115663.1 3 852 ACAAGGTGGGTC G ATT- - 1 B c c
1O17121 TCCTGGGTAAGG CT CC TCCAGGAGATC ACC
GAAGCAAG GA GG GGGTCCTCTGG TGG
A GAAT G
GAM55 387 DNCL2A 1 3470 NP_054902.1 5 45 GGCTACCGGATC A A- AC 1 B c c
GGTCGGAAATGG CTGCCATTTCC GG GATC
CAGAGGTG GACGGTAAAGG CT CTAG
- GG GC
GAM55 387 DNCL2A 1 3470 NP_808853.1 5 45 GGCTACCGGATC A A- AC 1 B c c
GGTCGGAAATGG CTGCCATTTCC GG GATC
CAGAGGTG GACGGTAAAGG CT CTAG
- GG GC
GAM55 387 DPF3 1 7186 NP_036206.1 3 1438 ATTCAGGTGATC - C - 1 B c c
TCTGTGGAGGTA CTG C ATTTCCA GGAGATCACC
GTCAGGGA GAC G TGGAGGT TCTCTAGTGG
T A G
GAM55 387 EDG3 1 10947 NP_005217.1 3 915 GCAGGGGTCTGC G --- G A 1 B c c
TTCAGGAAATGG CT CCATTTCC AG AGATC CC
AAGCTGTC GA GGTAAAGG TC TCTGG GG
A ACT G -
GAM55 387 EPHB6 1 4191 NP_004436.1 5 549 CTTCTTTGTTGT T C G C 1 B c c
GTCCTCGAATGG CTGCCATT C AGGA AT AC
CAGAAAAA GACGGTAA G TCCT TG TG
- C G T
GAM55 387 EPN2 1 13330 NP_055779.1 3 1289 AAGATGGGGATA GGAG A 1 B c
c
ATGTGGAAATGG CTGCCATTTCCA ATC CC
CAGTTGTC GACGGTAAAGGT TAG GG
GTAA G
GAM55 387 EPN2 1 13330 NP_683723.1 3 1289 AAGATGGGGATA GGAG A 1 B c
c
ATGTGGAAATGG CTGCCATTTCCA ATC CC
CAGTTGTC GACGGTAAAGGT TAG GG
GTAA G
GAM55 387 FBXO25 1 11736 NP_036305.1 5 46 GGACTGGAGATC G TT A 1 B c c
TCCTGGATGGAG CT CCA TCCAGGAGATC CC
TTGGATTA GA GGT AGGTCCTCTAG GG
- -- A
GAM55 387 FLJ1277 1 14361 NP_115550.2 3 118 TGCTGGGTGATC CA --- A 1 B c c
0 TCTAGGACCCAG CTGC TT TCC GGAGATCACC
GAGCAGAG GACG GA AGG TCTCTAGTGG
AG CCC A
GAM55 387 FLJ2007 1 9927 NP_060123.2 5 310 AGACAGGTTGTC C C 1 B c c

	1				TTTTGGAAATGC CTGC ATTTCCAGGAGAT ACC AGGTTTAA GACG TAAAGGTTTTCTG TGG - T									
GAM55	387 6	FLJ2115 1	9244	NP_078878.1	5 151	TGCTGGTGAAGC GC TCCTGGAAGTGA CT CATTTCCAGGAG TCACC TGGAAGGA GG GTGAAGGTCCTC AGTGG TA GA		A-		1	B	c	c
GAM55	387 6	FLJ2173 1	4353	NP_079198.1	5 426	AGGGCTGGGGTC -- --- TCCTGGATACAA CTGC CATT TCCAGGAGATC CC TGGAGCAG GACG GTAA AGGTCCTCTGG GG AG CAT -		A		1	B	c	c
GAM55	387 1	FLJ2546 1	16876	NP_659403.1	3 306	TGCAATGGGATC G --- GCCTGGAAAGCC CT CCA TTTCCAGG GATC CC TGGAGTCC GA GGT AAAGGTCC CTAG GG - CCG G -		A A		1	B	c	c
GAM55	387 0	FLJ3211 1	9463	XP_294323.1	5 128	ATCTGAATGTGT -- TTCTGGAAATGG CTG CCATTTCCAGGAG CAC ACCAGCAT GAC GGTAAAGGTCTTT GTG CA --		AT		1	B	c	c
GAM55	387 4	FLJ3293 1	16951	NP_653223.1	5 37	TCAGCGGGCATC A- TCCTGGAGACAG CTGCC TTTCCAGGAGAT CC GCAGACAT GACGG AGAGGTCCTCTA GG AC CG		CA		1	B	c	c
GAM55	387 6	FLJ3597 1	16319	NP_775910.1	3 1128	TAGACCATGATC CAT - TCCTTGGAAGCA CTGC TTCCA GGAGATCA GGGACAGT GACG AAGGT CCTCTAGT --- T A		C		1	B	c	c
GAM55	387 7	FLJ3926 1	14964	NP_775821.1	3 89	GCCTAGGTGAAG G A ACCTGGAAAAGG CT CC TTTCCAGG TCACC AAGGGTTA GA GG AAAGGTCC AGTGG A A AGA		AGA		1	B	c	c
GAM55	387 4	FLJ3965 1	8343	NP_787110.1	3 984	GAATATGTGATG CACTGGAAATGG CTGCCATTTCCAG ATCAC CAGAGGCT GACGGTAAAGGTC TAGTG ACG		GAG		1	B	b	b
GAM55	387 1	FLJ4020 1	3723	NP_689820.1	3 21	CCAATGTAGATC CAT - TCCTGTGAAGCA CTGC TTC CAGGAGATC GAACCAAC GACG AAG GTCCTCTAG --- T AT		AC		1	B	c	c
GAM55	387 L1	GABARAP 1	12594	NP_113600.1	3 7	GATGAGAGTGTC TG TATGGGAAATGG C CCATTTCC AGA CAC TGGTTGGA G GGTAAAGG TCT GTG GT GTA -		AGG T		1	B	c	c
GAM55	387 14	GENX-34 1	5371	NP_003934.1	3 424	CTTTAGGTGATC TTTAAACTATGG CTGCCAT GGAGATCACC TAGTAAAA GATGGTA TTTCTAGTGG TCAAA		TTCCA		1	B	c	c
GAM55	387	HAT1 1	7198	NP_003633.1	5 20	CGGGTGATCGTA		- GA--		1	B	c	c

GCTCGGAAATGG CTGCCATTTCC AG GATCACC
CGGGATTT GGCGGTAAAGG TC CTAGTGG
C GATG

GAM55 387 IPT 1 10622 NP_060116.1 3 226 TGTGGCTGATGT -- AG- - 1 B c c
GTCTGGAAATGA CTGC CATTTCCAGG ATCA CC
TGTAGTTC GATG GTAAAGGTCT TAGT GG
TA GTG C

GAM55 387 JAG1 1 10391 NP_000205.1 3 1031 AGGCAGGTGATC CA C G 1 B c c
TGCTGCAGAGCA CTGC TTT CAG AGATCACC
GTAAGGGA GACG AGA GTC TCTAGTGG
-- C G

GAM55 387 KIAA008 1 16156 NP_055956.1 3 1299 ATTCCAGGTGTT T A A T 1 B c c
9 CCCTGGAAAGGT C GCC TTTCCAGG GA CACC
CAAGTGAG A TGG AAAGGTCC CT GTGG
C - - T

GAM55 387 KIAA046 1 3457 NP_055666.1 3 3021 CCCCTGGGTTTC - TCA 1 B c c
9 TCTTGGAAATGG CTG CCATTTCCAGGAGA CC
TCAGTTTC GAC GGTAAAGGTTCTCT GG
T TTG

GAM55 387 KIAA104 1 1089 XP_048592.1 3 3776 AATGGCGAGATC G T AC 1 B c c
5 TCCTGGAGTGGG CT CCATT CCAGGAGATC
GGATATTC GG GGTGA GGTCCTCTAG
G - AG

GAM55 387 KIAA190 1 15699 XP_055834.1 3 318 TGGTAGGTGATC CAT AG 1 B c c

8 TCAGGAATTGCA CTGC TTCC GAGATCACC
GGGGAAAG GACG AAGG CTCTAGTGG
TT- A-

GAM55 387 KIAA193 1 3380 XP_057107.3 3 255 ATGCAGGTGGTC CA- 1 B c c
7 TCCTGGGAAAGT CTGC TTTCCAGGAGATCACC
GTAGAGGA GATG AAGGGTCCTCTGGTGG
TGA

GAM55 387 KRT6A 1 5931 NP_005545.1 5 30 AGCTCTCTCATC - -- CAC 1 B c c
TCCTGGAACCAT CTG CCAT TTCCAGGAGAT
GGCCAGCA GAC GGTA AAGGTCCTCTA
C CC CTC

GAM55 387 KRT6E 1 16583 NP_775109.1 5 22 AGCCCTCTCATC - -- CAC 1 B c c
TCCTGGAACCAT CTG CCAT TTCCAGGAGAT
GGCCAGCA GAC GGTA AAGGTCCTCTA
C CC CTC

GAM55 387 LOC1209 1 8330 XP_058518.3 5 64 TGGAGATAGCGC A ---- A 1 B c c
35 TCCTGGAGAGGG CTGCC TTTCCAGGAG ATC CC
CAGAGTAG GACGG AGAGGTCCTC TAG GG
G GCGA A

GAM55 387 LOC1318 1 2874 XP_067585.6 5 752 TTTCAAGGGAGC C T A A 1 B c c
73 TCCTGGAGTTGA CTG CA TTCCAGGAG TC CC
CAGTAGCA GAC GT GAGGTCCTC AG GG
A T G -

GAM55 387 LOC1392 1 716 XP_208439.1 3 1711 GGACCAGATGAG CAGG AC 1 B c
c

```
          01                          GATCTGAAATGG CTGCCATTTC  AGATC
                                     CAGCCTTT   GACGGTAAAG  TCTAG
                                                ----   GA
GAM55   387   LOC1442 1  2814  XP_084770.5  3  269  AGCGGTGGTCAG TG      GGA--          1  B  c
c
          02                          ACGTGGAAATGG C  CCATTTCCA   GATCACC
                                     TGGGGAGA   G  GGTAAAGGT   CTGGTGG
                                           GT       GCAGA
GAM55   387   LOC1444 1  11985 XP_096608.1  3  646  GGAAAAAGATCA        A  -  AC       1  B  c  c
          86                          TTCGGGAAATGG CTGCCATTTCC GGA GATC
                                     CGGTGGCT   GGCGGTAAAGG CTT CTAG
                                           G  A   AA
GAM55   387   LOC1464 1  6929  XP_096998.2  5  440  AGATGAGGAGGC        CA   AT A        1  B  c
c
          29                          CTCCAGAAATGG CTGCCATTTC  GGAG  C CC
                                     CAGAATTC   GACGGTAAAG  CCTC  G GG
                                           A-   CG A
GAM55   387   LOC1514 1  14420 XP_087208.1  3  140  GGGGGTACTGAT   C      G    C       1  B  c  c

          51                          CTTTGGAAATGT CTG CATTTCCAG AGATCA
                                     CAGTCCTG   GAC GTAAAGGTT TCTAGT
                                           T      -    C
GAM55   387   LOC1515 1  3403  NP_612491.1  5  603  GAGCTGGGGTGT  - A       AT       1  B  c  c
          34                          TCCTGGAAGAGG CTG CC TTTCCAGGAG  CACC
                                     TCGGGGAG   GGC GG GAAGGTCCTT  GTGG
                                           T  A       --
GAM55   387   LOC1524 1  11108 XP_098225.1  3  838  ACATAGGCTATA    -       GATCA       1  B  c
c
          26                          TCCTGGAAGTGG CTGCC ATTTCCAGGA   CC
                                     GCAGGGGA   GACGG TGAAGGTCCT   GG
                                           G       ATATC
GAM55   387   LOC1540 1  13591 XP_087842.1  3  31   TGCAGATGGGGT   C      G    A       1  B  c  c
          62                          CTTTGGAAATGT CTG CATTTCCAG AGATC CC
                                     TAGTCACC   GAT GTAAAGGTT TCTGG GG
                                           T      -    -
GAM55   387   LOC2006 1  14431 XP_117256.1  5  3257  ATTCTGGTGATC       C---  G         1  B  c  c
          09                          TACTGCACAGGA CTGCCATTT   CAG AGATCACC
                                     TGGTAGCC   GATGGTAGG   GTC TCTAGTGG
                                           ACAC  A
GAM55   387   LOC2042 1  5396  XP_115290.2  3  522  AGCGGTGGTCAG TG      GGA--          1  B  c
c
          75                          ACATGGAAATGG C  CCATTTCCA   GATCACC
                                     TGGGGAGA   G  GGTAAAGGT   CTGGTGG
                                           GT       ACAGA
GAM55   387   LOC2542 1  10172 XP_170654.1  3  276  CATGGCAGTCAT    A      --  CA       1  B  c  c
          63                          TCCTGGAAGGGG CTGCC TTTCCAGGA  GAT  CC
                                     CAGGACCT   GACGG GAAGGTCCT  CTG  GG
                                           G       TA  AC
GAM55   387   LOC2553 1  16456 XP_172920.1  5  178  TCTTGGTTTGGT       C  A   C       1  B  c  c
          28                          CCCTAGAAATGG CTGCCATTTC AGG GATCA
```

CAGCCTGC GACGGTAAAG TCC CTGGT
A - T

GAM55 387 LOC2829 1 12044 XP_210834.1 3 1128 GGGAGGAGAATG A G - A 1 B c c

63 TCCTGGAAGGGC CTGCC TTTCCAGGA AT C CC
AGGACTCT GACGG GAAGGTCCT TA G GG
- G A A

GAM55 387 LOC2831 1 1899 XP_210911.1 3 851 TAAAATATGTAA CC C 1 B c c

40 TCTCTTAAATGG CTGCCATTT AGGAGAT AC
CAGTAAGA GACGGTAAA TTCTCTA TG
-- A

GAM55 387 LOC2840 1 2281 XP_208958.2 3 1976 GCATGGCTGAGC A--- A - 1 B c c

01 TCCTGGAGACGA CTGCC TTTCCAGGAG TCA CC
GGGCGGGC GGCGG AGAGGTCCTC AGT GG
GAGC G C

GAM55 387 LOC2842 1 7062 XP_211415.1 5 514 CGCCAGTGAGCC A A- 1 B b b

81 TCCTGGAAGGGC CTGCC TTTCCAGGAG TCAC
AGCAAGTT GACGG GAAGGTCCTC AGTG
- CG

GAM55 387 LOC2848 1 9719 XP_211683.1 5 575 GCTGAATGGACT C - A C 1 B c c

91 CCGTGAAAATGG CTGCCATTT CA GGAG TCA
CAGACACG GACGGTAAA GT CCTC GGT
A G A A

GAM55 387 LOC2849 1 2906 XP_209414.1 3 1164 ACAAGGTGGGTC G ATT- - 1 B c c

25 TCCTGGGTAAGG CT CC TCCAGGAGATC ACC
GAAGCAAG GA GG GGGTCCTCTGG TGG
A GAAT G

GAM55 387 LOC2849 1 2110 XP_211695.1 5 369 GAGGGTGGAGCC C- A-- 1 B c c

33 TCCTGGAAGTGA CTG CATTTCCAGGAG TCACC
CCAGAGCC GAC GTGAAGGTCCTC GGTGG
CA CGA

GAM55 387 LOC2851 1 17470 XP_211798.1 5 521 ACGTGGATGAGC G T A - 1 B c c

74 TCCTGGACATGG CT CCAT TCCAGGAG TCA CC
AGAGTGAC GA GGTA AGGTCCTC AGT GG
- C G A

GAM55 387 LOC2854 1 6402 XP_211898.1 5 63 CTTCGGATGAAT CA A - - 1 B c c

31 CCCTGGAAAGCA CTGC TTTCCAGG GAT CA CC
GAGAGGCA GACG AAAGGTCC CTA GT GG
-- - A A

GAM55 387 LOC2856 1 4959 XP_209676.1 5 2165 GTCTGTTTTCTT C -- TC 1 B c c

02 ACCTGCAAATGG CTGCCATTT CAGG AGA AC
CAGGTACT GACGGTAAA GTCC TCT TG
C AT TT

GAM55 387 LOC2864 1 11434 XP_210471.1 5 525 ATTGGATGAGCT - AGG A - 1 B c c

18 GCAGGAAAATGG CTGCCATTT CC AG TCA CC
CAGGCAGG GACGGTAAA GG TC AGT GG
A ACG G A

GAM55 387 LOC2865 1 8042 XP_212336.1 3 1298 AAAATGGGGATC CA CC A 1 B c c

27 TCCTCCAAAGAG CTGC TTT AGGAGATC CC
CAGATTTC GACG AAA TCCTCTAG GG
AG CC G
GAM55 387 LOC3481 1 13521 XP_302656.1 5 341 AGGTGATGGTTA G T G---- 1 B c c
09 TCCTGGAACTGG CT CCA TTCCAGGA ATCACC
AGATTA GA GGT AAGGTCCT TAGTGG
- C ATTGG
GAM55 387 LOC3484 1 15633 XP_290909.1 3 84 CTCATGGTGGTC T TT 1 B c c
54 TCCTGGGCTTGG C GCCA TCCAGGAGATCACC
TCACTGTC A TGGT GGGTCCTCTGGTGG
C TC
GAM55 387 LOC3489 1 6953 XP_302915.1 3 99 TCCAAGGATGAA C GA - 1 B c c
11 TCCTGGAAATTG CTGC ATTTCCAGGA TCA CC
CAGTTAGC GACG TAAAGGTCCT AGT GG
T A- A
GAM55 387 LOC3489 1 1743 XP_300883.1 3 1696 CAACAAGTTGGC TC A C 1 B c c
38 TCTTGAGAATGG CTGCCATT CAGGAG TCA
CAGTAAAC GACGGTAA GTTCTC GGT
GA - T
GAM55 387 LOC3492 1 1579 XP_300988.1 3 1546 GTGGAGTGTTCT G A - T 1 B c c
36 ACTGGGAAATGG CT CCATTTCC GG AGA CAC
AGTTATGA GA GGTAAAGG TC TCT GTG
- G A T
GAM55 387 LOC3493 1 5396 XP_301067.1 3 485 AGCGGTGGTCAG TG GGA-- 1 B c
c
95 ACATGGAAATGG C CCATTTCCA GATCACC
TGGGGAGA G GGTAAAGGT CTGGTGG
GT ACAGA
GAM55 387 LOC9052 1 17696 NP_835223.1 3 649 GAGTGGGAGATC T - A 1 B c c
9 ATCTTGGAATGG CTGCCATT CCAGGA GATC CC
CAGTGGCC GACGGTAA GGTTCT CTAG GG
- A A
GAM55 387 LOC9166 1 19784 NP_612381.1 3 951 TGGCAGGTGGTC CATT 1 B c c
1 TCCTGGGTAGCA CTGC TCCAGGAGATCACC
GGATCTGG GACG GGGTCCTCTGGTGG
AT--
GAM55 387 MAP3K8 1 10457 NP_005195.2 3 56 ACAGCATTGATC T - C 1 B c c
TCCTGGAGGCTG C GCCA TTTCCAGGAGATCA
GTTCTGCT C TGGT GGAGGTCCTCTAGT
T C T
GAM55 387 MAWBP 1 14451 NP_071412.1 3 1339 TTTAAGGTGATC TCCAG 1 B c
c
TCATTGATGGTA CTGCCATT GAGATCACC
GTTCTCAG GATGGTAG CTCTAGTGG
TTA--
GAM55 387 MBD2 1 12364 NP_003918.1 3 296 CCAGGTGCAATC C--- -- G -- 1 B c c
TACTGGAAATGT TGC CATTTCCAG AGAT CACC
AGCACTTA ACG GTAAAGGTC TCTA GTGG

```
                                        ATTC  AT      A   AC
GAM55   387   MBD2   1  12364 NP_056647.1  3 831   CCAGGTGCAATC C---  --      G   --     1 B c c
                                        TACTGGAAATGT   TGC  CATTTCCAG AGAT  CACC
                                        AGCACTTA       ACG  GTAAAGGTC TCTA  GTGG
                                        ATTC  AT       A   AC
GAM55   387   MCC    1  2297  NP_002378.1  3 575   TAAGAGGTGATC   CC      G          1 B c c
                                        TCTGGGAGTTAT CTG  ATTTCCAG AGATCACC
                                        AGGTCATG    GAT  TGAGGGTC TCTAGTGG
                                          AT      -
GAM55   387   MCSP   1  11169 NP_109588.2  3 200   AGGGAGGCCTCC   G      ---   AT A      1 B c c

                                        ATCTGGAAATGG CT CCATTTCCA   GGAG  C CC
                                        GAGGATGA    GA GGTAAAGGT   CCTC  G GG
                                          G       CTA   CG A
GAM55   387   MGAT4B 1  15568 NP_463459.1  5 377   AGTGAGGTGGGC   -- T      AT        1 B c c

                                        TCCTGGAACTGC CTGC  CA TTCCAGGAG  CACC
                                        AGCAGCCA    GACG  GT AAGGTCCTC  GTGG
                                          AC  C       GG
GAM55   387   MGC1438 1  18289 NP_291022.1  5 946   GGCCAGGTGTTC    AT--      T        1 B c c

        6                               TCCTGGGGCGGG CTGCC   TTCCAGGAGA CACC
                                        GGCAGGCA    GACGG   GGGGTCCTCT GTGG
                                          GGGC        T
GAM55   387   MGC2316 1  19091 NP_689948.1  3 768   TGACTAGTGATC C------       AG        1 B c
c
        6                               TCAGGAGATGGC      TGCCATTTCC  GAGATCAC
                                        ACTGTCCT        ACGGTAGAGG  CTCTAGTG
                                          TCCTGTC       A-
GAM55   387   NaGLT1 1  14714 NP_699200.1  5 272   GTGGTGGTGGTC  TG  A-  -          1 B c c
                                        TCCTGGCAGAGC C  CC  TTT CCAGGAGATCACC
                                        GGTGGGAC    G  GG  AGA GGTCCTCTGGTGG
                                          GT  CG  C
GAM55   387   NAT8   1  12162 NP_003951.2  5 10    CCAGACGGTATC   -  ----      C      1 B c c
                                        TCCTGGATGCCA CTGC CATT   TCCAGGAGAT ACC
                                        GTGAGCGG    GGCG GTGA    AGGTCCTCTA TGG
                                          A   CCGT      -
GAM55   387   NKX2-8 1  10500 NP_055175.2  3 4     CCGCCCTGGTCT  TG  T        C        1 B c c
                                        CCTGGAACTGGT C  CCA TTCCAGGAGATCA
                                        GGGCCGCA    G  GGT AAGGTCCTCTGGT
                                          GT  C         C
GAM55   387   NPM1   1  5396  NP_002511.1  3 270   AGCGGTGGTCAG  TG      GGA--         1 B c c

                                        ACATGGAAATGG C  CCATTTCCA    GATCACC
                                        TGGGGAGA    G  GGTAAAGGT    CTGGTGG
                                          GT       ACAGA
GAM55   387   PART1  1  6436  NP_057674.1  3 182   GGACAGGTGATC    CA    AGG          1 B c c

                                        TGGGGAAAACGC CTGC  TTTCC   AGATCACC
                                        AGCTACAC    GACG  AAAGG   TCTAGTGG
```

CA GG-
GAM55 387 PKNOX1 1 6249 NP_004562.2 3 1283 TTGTGGCTGGTC C TTT - 1 B c c

TCCTGGTGTCAG CTG CA CCAGGAGATCA CC
TGTTCTCT GAC GT GGTCCTCTGGT GG
T --- C
GAM55 387 PSMA1 1 4352 NP_683877.1 5 303 TAGGTGACTGTC ---- --- 1 B b b
TCCTGGAAATGT CTGC CATTTCCAGGAGA TCACC
TATGCAGC GACG GTAAAGGTCCTCT AGTGG
TATT GTC
GAM55 387 PTER 1 8150 NP_109589.2 3 941 AAAGGTCAGATC C G -- 1 B c c
TATTGGAAATGA CTG CATTTCCAG AGATC ACC
CAGCCCGA GAC GTAAAGGTT TCTAG TGG
A A AC
GAM55 387 RAI15 1 9537 XP_039548.2 3 578 CCTGAGGCTGTC GC CA 1 B c c
TCCTGGGAATGC CT CATTTCCAGGAGAT CC
TGGACCAG GG GTAAGGGTCCTCTG GG
TC TC
GAM55 387 RASSF2 1 6459 NP_055552.1 3 2721 GAGGGAAGGTGA CC AG 1 B c
c

TGACTTAAATGG CTGCCATTT AGG ATCACC
CAGGGGGT GACGGTAAA TTC TAGTGG
-- AG
GAM55 387 RASSF2 1 6459 NP_739579.1 3 2947 GAGGGAAGGTGA CC AG 1 B c
c

TGACTTAAATGG CTGCCATTT AGG ATCACC
CAGGGGGT GACGGTAAA TTC TAGTGG
-- AG
GAM55 387 RASSF2 1 6459 NP_739580.1 3 2721 GAGGGAAGGTGA CC AG 1 B c
c

TGACTTAAATGG CTGCCATTT AGG ATCACC
CAGGGGGT GACGGTAAA TTC TAGTGG
-- AG
GAM55 387 RPL17 1 14681 NP_000976.1 5 270 CTCTAGGTGATC T C GG 1 B c c
TGTGAAAATGGT C GCCATTT CA AGATCACC
TCGCTATT C TGGTAAA GT TCTAGTGG
T A G-
GAM55 387 SEC22L3 1 5454 NP_004197.1 3 628 TAAATGAGGTGG CA A 1 B c c
CTTCAGAAATGG CTGCCATTTC GGAG TCACC
CAGAATAA GACGGTAAAG CTTC GGTGG
A- -
GAM55 387 SLC25A1 1 15569 NP_036272.2 5 79 GGGATTGGGCTC T- TCA 1 B c c

0 TCCTGGGCCATG CTGCCAT TCCAGGAGA CC
GCAGCCGA GACGGTA GGGTCCTCT GG
CC CG-
GAM55 387 SYNE2 1 19149 NP_055995.2 3 270 TAGTTTAGGGAT C G A 1 B c c
CTCTGGAAATGT CTG CATTTCCAG AGATC CC
CAGTTTCC GAC GTAAAGGTC TCTAG GG
T - -

GAM55 387 TA-PP2C 1 2661 NP_644812.1 3 746 TAAGGCCTGATC A A C 1 B c c
TCCAGGAGGGGT CTGCC TTTCC GGAGATCA
AGGGGAGA GATGG GGAGG CCTCTAGT
- A C
GAM55 387 TRIM10 1 7339 NP_006769.1 3 13 TTCTCCCTGAGC CA A C 1 B c c
TCCTGGAAGGAG CTGC TTTCCAGGAG TCA
CAGTTACC GACG GAAGGTCCTC AGT
AG G C
GAM55 387 TXNRD2 1 14503 NP_665690.1 5 211 GGGACTATGATC - TT C 1 B c c
TCCTGGTGGTCG CTGCC AT CCAGGAGATCA
GCGGGGGA GGCGG TG GGTCCTCTAGT
C GT A
GAM55 387 VEZATIN 2 14500 NP_060069.2 3 1737 AAATTAGTAGTT C A C 1 B c c
ACCTGTAAATGG CTGCCATTT CAGG GAT AC
CAGATCTT GACGGTAAA GTCC TTG TG
T A A
GAM55 387 VEZATIN 2 18752 NP_060069.2 3 107 CTTAGGGATGGT C---- - G - 1 B c c
TCCTGGAAGTGG TG CCATTTCCAGGA ATCA CC
ACACATTT AC GGTGAAGGTCCT TGGT GG
TTTAC A - A
GAM55 387 VMP1 1 8550 NP_112200.2 5 100 AAGAGTTACTGA CAGG C 1 B c c
TCTATGAAATGG CTGCCATTTC AGATCA
CAGAGAAT GACGGTAAAG TCTAGT
TA-- C
GAM55 387 ZNF41 1 10401 NP_009061.1 3 303 GACCTCTTGAGC C A C 1 B c c
TCCTGGAAATAG CTGC ATTTCCAGGAG TCA
TAGAATTA GATG TAAAGGTCCTC AGT
A G T
GAM55 387 ZNF41 1 10401 NP_700359.1 3 303 GACCTCTTGAGC C A C 1 B c c
TCCTGGAAATAG CTGC ATTTCCAGGAG TCA
TAGAATTA GATG TAAAGGTCCTC AGT
A G T
GAM56 315 EFEMP1 1 10550 NM_004105.2 3 CCAAAATGAACC A G GT A 3 C c c
AGATACC GGTATTTGGT TCAT TTTGG
CCATAGACCA AGTA AAACC
- - -- -
GAM57 329 LOC2531 1 14514 5 TTGAGTCTGACC AT TTTA 3 C c c
50 CAGGACCTCT AGAGGTCCTG TCAG TCAA
TCTCCAGGAC AGTC AGTT
CC TG--
GAM58 306 MYH10 1 6588 XM_290747.2 5 AAGACTGTGAAA - AA T 3 C c c
AATGATAACTCA TGAGTTATC TTTT ATA GTCTT
ACTCAATAG AAAA TGT CAGAA
T AG -
GAM58 306 NFAT5 1 12511 NM_138714.2 3 AAGACCATAGGT C- A- - 3 C c c
TAGAAAAATAAC TGAGTTAT TTTTAA TATG TCTT
TCA ACTCAATA AAGATT ATAC AGAA
AA GG C
GAM59 377 ARTN 1 13442 NM_057091.1 5 CGCTCCCAGCCC CCG ACCTT 3 C c
c

CACCCCGGGA TCCCGGGG GGGG AGCG
AGGGCCCC CCCC TCGC
A-- GACCC

GAM59 377 CENTA1 1 7819 NM_006869.1 5 CGCTCCCGGCCC TC GA TT- 3 C c c

CGGCCCCGG CCGGGGCCGGGG CC AGCG
GGCCCCGGCCCC GG TCGC
-- -- CCC

GAM59 377 HYPH 1 11217 5 CGCCTCGCCCGA - G CCTTA 3 C c c

GCCCCGGGA TCCCGGGGC CGGG GA GCG
AGGGCCCCG GCCC CT CGC
A G C----

GAM59 377 KCNT1 1 13367 XM_029962.2 3 CGCCCACCCCCG C ACCTTA 3 C c c

GCTCCAGGA TCC GGGGCCGGGGG GCG
AGG CCTCGGCCCCC CGC
A ACC---

GAM59 377 KIAA113 1 19640 XM_031104.5 5 CGCCCCCGCCCC C GACCTTA 3 C c c

0 GGCCCCGAGA TC CGGGGCCGGGG GCG
AG GCCCCGGCCCC CGC
A GCCCC--

GAM59 377 LOC1484 1 16524 5 CGCCCGAGCCCC T C AC A- 3 C c c

79 CAGCCCCGGG CCCGGGGC GGGGG CTT GCG
GGGCCCCG CCCCC GAG CGC
- A -- CC

GAM59 377 LOC2209 1 18057 3 CGCCGTCCGCCC C- - CTTA 3 C c c

32 CAGCCCCGGGG TCCCGGGGC GGG GGAC GCG
GGGGCCCCG CCC CCTG CGC
AC G C---

GAM59 377 LOC2215 1 12315 5 CTAAGTCGGCTC GGGAC CG 3 C c c

83 CGGGA TCCCGGGGCCGG CTTAG
AGGGCCTCGGCT GAATC
----- --

GAM59 377 MGC2964 1 10131 NM_144586.1 5 CGCTTGCCCTCT CCTT- 3 C c c

3 CCCGGCCCCGGG TCCCGGGGCCGGGGGA AGCG
A AGGGCCCCGGCCCTCT TCGC
CCCGT

GAM59 377 PITX1 1 20144 NM_002653.3 5 CGCCCAGCCCCG C GAC TA 3 C c c

GCCCCTGGA TCC GGGGCCGGGG CT GCG
AGG CCCCGGCCCC GA CGC
T --- CC

GAM59 377 TBX6 1 19956 NM_004608.2 5 GCCAAGGTGTGT - GGGGG A G 3 C c c

CCCGGGA TCCCGGGGC C ACCTT GC
AGGGCCCTG G TGGAA CG
T ----- C -

GAM59 377 YAP1 1 7221 NM_006106.2 5 CGCAGCCCCCCG C AC TA 3 C c c

GCCCTGAGA TC CGGGGCCGGGGG CT GCG
AG GTCCCGGCCCCC GA CGC

A C- --
GAM60 381 AP1G2 1 8669 NM_080545.1 5 GCGAGGAGGCCT TGT GA A 3 C c c
CTTGAAG CTTCAAG AGG CTCCTCGC
GAAGTTC TCC GAGGAGCG
--- G- -
GAM60 381 BARD1 1 16824 NM_000465.1 5 TGCGAGGAGCCT AA T A 3 C c c
TTCATCCGAAG CTTC GTG AGGG CTCCTCGCA
GAAG TAC TTCC GAGGAGCGT
CC T -
GAM60 381 HGC6.2 1 19650 NM_014356.1 5 GCGAGGAGTCCC AAGTGTA A 3 C c
c
CGGGGAG CTTC GGGACTCCTCGC
GAGG CCCTGAGGAGCG
GGC---- -
GAM61 293 DPYSL4 1 9939 NM_006426.1 3 CAGAGGCCTGTG CA AT AT 3 C c c
CCCATCG CGATGGGCACA GCC TCTG
GCTACCCGTGT CGG AGAC
-- C- --
GAM61 293 LOC1972 1 7360 3 CAGAAGTGCATG C A A CA 3 C c c
85 GCCCATCGT ACGATGGGC CA TGC TTCTG
TGCTACCCG GT ACG AAGAC
- - - TG
GAM61 293 LOC2574 1 15784 5 CAGAACGGGCAG ACAA A- 3 C b b
58 CCCATCGTG CACGATGGGC TGCC TTCTG
GTGCTACCCG ACGG AAGAC
---- GC
GAM62 220 GBL 1 11551 NM_022372.2 3 ATGTGACAGAGC - 3 C b b
TCGACCCAAGCC TGGCTTGGGTCGAGCTCTGTCACA
A ACCGAACCCAGCTCGAGACAGTGT
A
GAM62 220 LOC1443 1 4572 XM_084850.1 3 TGACAGAGACCT GAGC CA 3 C c c
95 AAGCCA TGGCTTGGGTC TCTGTCA
ACCGAATCCAG AGACAGT
---- --
GAM62 220 ZNF141 1 15865 NM_003441.1 3 TGTGACAAAACC -- CGAGCTC 3 C c
c
TTTAAGCCA TGGCTT GGGT TGTCACA
ACCGAA TCCA ACAGTGT
TT AA-----
GAM63 348 ABCA13 1 16335 NP_689914.2 3 6 CACACACATCAC - G AA 4 A c c
TTGCCCATCTGG GGT CCAGATGGG AG GATGT
CACTAAAG TCA GGTCTACCC TT CTACA
C G CA
GAM63 348 ABL1 1 820 NP_005148.1 3 1346 GCCTGCCATCTT TC AT-- 4 A c c
CTCCCCGAGGCT GG CAG GGGGAGAAGATG
GCCCCAGG CC GTC CCCCTCTTCTAC
CC GGAG
GAM63 348 ABL1 1 820 NP_009297.1 3 1346 GCCTGCCATCTT TC AT-- 4 A c c
CTCCCCGAGGCT GG CAG GGGGAGAAGATG

GCCCCAGG CC GTC CCCCTCTTCTAC
CC GGAG
GAM63 348 ACP1 1 6377 NP_004291.1 3 659 GTCAGCCCATTG C G AA 4 A c c
GCTCCCATCTGA GGT CAGATGGG AG GATG
ACCACTTT CCA GTCTACCC TC TTAC
A - GG
GAM63 348 ACP1 1 6377 NP_009030.1 3 659 GTCAGCCCATTG C G AA 4 A c c
GCTCCCATCTGA GGT CAGATGGG AG GATG
ACCACTTT CCA GTCTACCC TC TTAC
A - GG
GAM63 348 ACP1 1 6377 NP_808222.1 3 952 GTCAGCCCATTG C G AA 4 A c c
GCTCCCATCTGA GGT CAGATGGG AG GATG
ACCACTTT CCA GTCTACCC TC TTAC
A - GG
GAM63 348 AD031 1 7594 NP_114410.1 3 461 GATAACCCCTTT T ATG 4 A c c
CTCCCCTTTGGA GGTCCAGA GGGGAGAAG
CCATCTGC CCAGGTTT CCCCTCTTT
- CCC
GAM63 348 ADAM10 1 10402 NP_001101.1 5 393 CCCCTTCAGCTT A TG A 4 A c c
CTCCCTCCGGAT GGTCC GA GGGAGAAG TG
CGATGTGC CTAGG CT CCCTCTTC AC
C -- G
GAM63 348 ADAM33 1 15499 NP_079496.1 3 537 CCACCCTGTCTT T- GA - 4 A c c
CTCCCCTAGGTG GG CCA T GGGGAGAAGATG
GTTCCTGA CC GGT A CCCCTCTTCTGT
TT GG T
GAM63 348 ADAM33 1 15499 NP_694882.1 3 537 CCACCCTGTCTT T- GA - 4 A c c
CTCCCCTAGGTG GG CCA T GGGGAGAAGATG
GTTCCTGA CC GGT A CCCCTCTTCTGT
TT GG T
GAM63 348 AGPAT1 1 3844 NP_006402.1 3 46 CTCCTCCCATCT TCC- GA 4 A c c
GTCCCCATCTTC GG AGATGGGGA AGATG
CTCCCCAC CC TCTACCCCT TCTAC
TCCT G-
GAM63 348 AGPAT1 1 3844 NP_116130.2 3 46 CTCCTCCCATCT TCC- GA 4 A c c
GTCCCCATCTTC GG AGATGGGGA AGATG
CTCCCCAC CC TCTACCCCT TCTAC
TCCT G-
GAM63 348 AIP1 1 1560 NP_036433.2 3 1784 CAATTAGTCTTT GAT - G 4 A c c
CTCCCCTGGACT GGTCCA GGGGAGAA GAT
AGAAATCC TCAGGT CCCCTCTT CTG
--- T A
GAM63 348 ALDH9A1 1 19851 NP_000687.2 3 319 ATAATACATCTT T GGGA 4 A c
c
CCACACATTTGG GG CCAGATG GAAGATGT
CCCACTGA CC GGTTTAC CTTCTACA
C ACAC
GAM63 348 ALKBH 1 14952 NP_006011.1 3 507 TAGTCTCATCTT - A T ---- 4 A c c
CTTAACTCCCTC GGT CC GA GGG GAGAAGATG
AGGCATCA CTA GG CT CCC TTCTTCTAC

C A - TCAA

GAM63 348 ALOX12B 1 14007 NP_001130.1 3 40 CCCGTCTCTCCT TC - ---- 4 A c c
CTCCCCATTCTG GG CAGA TGGGGAGA AGATG
TGCCCTAC CC GTCT ACCCCTCT TCTGC
GT T CCTC

GAM63 348 ALS2CR2 1 968 NP_061041.2 3 386 CAAGTACATCTT T TG---- 4 A c c
CTCCCAGATTCT GG CCAGA GGGAGAAGATGT
CTGGCCTT CC GGTCT CCCTCTTCTACA
- CTTAGA

GAM63 348 AMFR 1 1001 NP_001135.3 3 756 TCAGCATTTCCT -- A 4 A c c
TGTCCCGTCTGG GGTCCAGATGGG GAG AGATGT
ACCTGGGG CCAGGTCTGCCC TTC TTTACG
TG C

GAM63 348 AMFR 1 1001 NP_620408.1 3 1372 TCAGCATTTCCT -- A 4 A c c
TGTCCCGTCTGG GGTCCAGATGGG GAG AGATGT
ACCTGGGG CCAGGTCTGCCC TTC TTTACG
TG C

GAM63 348 AP1B1 1 9898 NP_001118.2 3 87 GCAGCACATCTT AGA--- - 4 A c c
CCTCCTCGCAGG GGTCC TGGGGAG AAGATGT
AGGGACCA CCAGG GCTCCTC TTCTACA
GAGGAC C

GAM63 348 AP1B1 1 9898 NP_663782.1 3 87 GCAGCACATCTT AGA--- - 4 A c c
CCTCCTCGCAGG GGTCC TGGGGAG AAGATGT
AGGGACCA CCAGG GCTCCTC TTCTACA
GAGGAC C

GAM63 348 AP1GBP1 1 4092 NP_542118.1 5 12 TTTCGCCATCTT GATGG 4 A c c

CTCCATGGACCA GGTCCA GGAGAAGATG
CTATATAC CCAGGT CCTCTTCTAC
A----

GAM63 348 APOL4 1 9016 NP_085146.2 5 250 AAAATCTTTGTC - G ---- G 4 A c c
GTCTGCATCTGG GGT CCAGATG GGA GAAGAT
AACCAAAA CCA GGTCTAC TCT TTTCTA
A G GCTG A

GAM63 348 APOL4 1 9016 NP_663694.1 5 250 AAAATCTTTGTC - G ---- G 4 A c c
GTCTGCATCTGG GGT CCAGATG GGA GAAGAT
AACCAAAA CCA GGTCTAC TCT TTTCTA
A G GCTG A

GAM63 348 ASH2L 1 4049 NP_004665.1 3 188 TTTCACCATTTT CA-- -- 4 A c c
CTCCCCACTTCC GGTC GA TGGGGAGAAGATG
AGTGACTG TCAG CT ACCCCTCTTTTAC
TGAC TC

GAM63 348 ATP12A 1 6304 NP_001667.2 3 73 CTTGTTCATCTT --- GG 4 A c c
CTGACCGTTTGC GGTCCAG ATGG AGAAGATG
TGGGCTAT TCGGGTC TGCC TCTTCTAC
GTT AG

GAM63 348 AUTL2 1 914 NP_443168.2 3 45 CTTGAAGGTCTG - G - G 4 A c c
TCTTCCATCTGG GGT CCAGATGGG AGA AGAT
CACCATAA CCA GGTCTACCT TCT TCTG
C - G G

GAM63 348 AUTL2 1 914 NP_840054.1 3 45 CTTGAAGGTCTG - G - G 4 A c c
TCTTCCATCTGG GGT CCAGATGGG AGA AGAT
CACCATAA CCA GGTCTACCT TCT TCTG
C - G G
GAM63 348 AUTL2 1 914 NP_840055.1 3 45 CTTGAAGGTCTG - G - G 4 A c c
TCTTCCATCTGG GGT CCAGATGGG AGA AGAT
CACCATAA CCA GGTCTACCT TCT TCTG
C - G G
GAM63 348 BAPX1 1 17409 NP_001180.1 3 699 TCTCCACATCTT TC-- T A 4 A c c
CCTTCTCTGAAG GG CAGA GGGG GAAGATGT
TCCAGGTA CC GTCT CTTC CTTCTACA
TGAA - -
GAM63 348 BAT8 2 16535 NP_006700.2 3 118 CTGCCATCTTCT CCAGAT 4 A c c
CTCCCCACCACC GGT GGGGAGAAGATG
CTTTCACA CCA CCTCTCTTCTAC
CCACC-
GAM63 348 BAT8 2 16535 NP_079532.4 3 118 CTGCCATCTTCT CCAGAT 4 A c c
CTCCCCACCACC GGT GGGGAGAAGATG
CTTTCACA CCA CCTCTCTTCTAC
CCACC-
GAM63 348 BAT8 2 17987 NP_006700.2 3 118 TGCTGCCATCTT CCAGAT 4 A c c
CTCTCCCCACCA GGT GGGGAGAAGATG
CCCTTTCA CCA CCTCTCTTCTAC
CCACC-
GAM63 348 BAT8 2 17987 NP_079532.4 3 118 TGCTGCCATCTT CCAGAT 4 A c c
CTCTCCCCACCA GGT GGGGAGAAGATG
CCCTTTCA CCA CCTCTCTTCTAC
CCACC-
GAM63 348 BAZ2A 1 2148 NP_038477.1 3 711 TCCCTGTCTTCT CC-- -- 4 A c c
GTCCCCATCTTC GGT AGATGGGGA GAAGATG
CTGCCGAT CCG TCTACCCCT CTTCTGT
TCCT GT
GAM63 348 BLAME 1 10762 NP_064510.1 3 230 CTCTCCCATCTT GT - GG 4 A c c
CTCATATCCTGG G CCAG ATG GAGAAGATG
CTCTTCTC C GGTC TAT CTCTTCTAC
TC C A-
GAM63 348 BMF 1 13024 NP_277038.1 3 2023 ACATACGTTGTT T- - 4 A c c
CTCCCCTCTCTG GGTCCAGA GGGGAGAA GATGT
GATCAAGG CTAGGTCT CCCCTCTT TTGCA
CT G
GAM63 348 BMP1 2 10746 NP_001190.1 3 164 TGGTGCTCTCTT TC A TG 4 A c c
CTCCCCACTGTG GG CAG TGGGGAGAAGA
CCCGTCCG CC GTC ACCCCTCTTCT
GT - CT
GAM63 348 BMP1 2 10746 NP_006119.1 3 251 TGGTGCTCTCTT TC A TG 4 A c c
CTCCCCACTGTG GG CAG TGGGGAGAAGA
CCCGTCCG CC GTC ACCCCTCTTCT
GT - CT
GAM63 348 BMP1 2 16512 NP_006122.1 3 326 GCTCCCCATCTT C A 4 A c c
CTCCTTACTGCA GGT CAG TGGGGAGAAGATG

TCTCAGCC CTA GTC ATTCCTCTTCTAC
C -

GAM63 348 BRD2 1 2992 NP_005095.1 3 543 GGTTTCAGTCAT T A G 4 A c c
CTCCCCATTTGG GG CCAGATGGGGAGA GAT
TCCCCTGG CC GGTTTACCCCTCT CTG
T A A

GAM63 348 C10orf5 1 19283 NP_848931.1 3 2830 TCACCCATCTTT -- - 4 A c c
GTTCCCATCTGA GGTCC AGATGGGGA GAAGATG
GGACTCAG TCAGG TCTACCCTT TTTCTAC
AG G

GAM63 348 C14orf1 1 8879 NP_009107.1 3 68 CTTGGCCATCTT TCC ----- 4 A c c
CTTCCTTCGTCG GG AGATG GGGAGAAGATG
TCTCTCCT CC TCTGC CCTTCTTCTAC
TC- TGCTT

GAM63 348 C14orf1 1 9576 NP_060440.1 3 966 TTTTCTTATCTT C TGG- 4 A c c
02 CTCCGAGCTCTA GGTC AGA GGAGAAGATG
GACTGGCT TCAG TCT CCTCTTCTAT
A CGAG

GAM63 348 C14orf1 1 8516 NP_064600.1 3 2381 AATCTGCATCTT C TG- 4 A c c
32 CTCTTATTTCTG GGTC AGA GGGAGAAGATGT
ACCTTTTT CCAG TCT TTCTCTTCTACG
- TTA

GAM63 348 C16orf7 1 5690 NP_004904.1 3 143 GGAACCCTTTTT - A TG 4 A c c
CTCCCCGCTGTG GGTC CAG TGGGGAGAAGA
GCCTCTGC CCGG GTC GCCCCTCTTTT
T - TC

GAM63 348 C1orf21 1 13283 NP_110433.1 3 6229 CGTCTTGCTTTG TC ----- - 4 A c c
TGCCCCATCTGT GG CAGATGGGG AG AAGATG
GCCTGGAT CC GTCTACCCC TC TTCTGC
GT GTGTT G

GAM63 348 C1orf24 1 17211 NP_443198.1 3 1249 AAAACACATCTT -- GA GG 4 A c c
CTTAACGGATGG GGT CCA TG GAGAAGATGT
TGACCTAT CCA GGT GC TTCTTCTACA
GT AG AA

GAM63 348 C1orf6 1 1257 NP_064516.1 3 117 CCCTTCCGTCTT TCCA - 4 A c c
CTCCCTCATCCT GG GATG GGGAGAAGATG
TTCCAAAC CC CTAC CCCTCTTCTGC
TTTC T

GAM63 348 C1QR1 1 7246 NP_036204.1 3 354 CCTGAATATCTT CC- A -- 4 A c c
CTCTGCTCACTT GGT AG TGGG GAGAAGATGT
CCACCATC CCA TC ACTC CTCTTCTATA
CCT - GT

GAM63 348 C2 1 540 NP_000054.2 3 71 CCCCTCCATCTT T GAT- - 4 A c c
CTACCTCTGAAT GG CCA GGGG AGAAGATG
GGCCACCC CC GGT CTCC TCTTCTAC
- AAGT A

GAM63 348 C20orf1 1 13238 NP_076424.1 3 74 GCTATACATCTT CCA T GA 4 A c c
16 CATCCCTCCCCA GGT GA GGG GAAGATGT
CCATCCTG CCA CT CCC CTTCTACA
CCC - TA

GAM63 348 C20orf1 1 1272 NP_653229.1 5 37 GAGCCGCGTCTT CC ATG 4 A c c
40 CTCCCGGCTCCG GGT AG GGGAGAAGATGT
CCACCAGC CCG TC CCCTCTTCTGCG
CC GG-
GAM63 348 C20orf1 1 15267 NP_291020.1 3 1112 TTAGGCCACCTT AT- A 4 A c c
69 CTCCCTTTCCTG GGTCCAG GGGGAGAAG TG
GACCCCAG CCAGGTC TCCCTCTTC AC
CTT C
GAM63 348 C20orf9 1 15768 NP_079234.1 3 663 GAAACACATCTT AT A-- 4 A c c
8 CAGCCTCCTCCT GGTCCAG GGGG GAAGATGT
GGGCCAGC CCGGGTC CCTC CTTCTACA
CT CGA
GAM63 348 C21orf9 1 20078 NP_660162.1 3 926 CTGGGCGCAGAC T GA A- 4 A c c
3 TTCACCTTCTGG GGTCCAGA GGG GAAG TGT
ACCTTCTC CCAGGTCT TCC CTTC ACG
- A- AG
GAM63 348 C22orf5 1 4323 NP_036396.1 3 1068 GGCCTGGTGTTC T - G G 4 A c c
TACCCCATCTGG GG CCAGATGGGG AGAA AT
CCCCTGGC CC GGTCTACCCC TCTT TG
- A G G
GAM63 348 C3 1 3699 NP_000055.1 5 6 CTCCTCCCCATC TC TG A 4 A c c
CTCTCCCTCTGT GG CAGA GGGAGA GATG
CCCTCTGT CC GTCT CCCTCT CTAC
CT -- C
GAM63 348 C3F 1 15076 NP_005759.2 3 556 ATTGCCTTATCT CC A 4 A c c
CTCCCCATCTAG GGT AGATGGGGAGA GATG
CCAGGAAT CCG TCTACCCCTCT CTAT
A- -
GAM63 348 C6orf13 1 7531 NP_659466.1 5 482 CTTCCCCATCTT T T-- 4 A c c
6 CTCCTCTATTCT GG CCAGA GGGGAGAAGATG
GGTCTCCC TC GGTCT CTCCTCTTCTAC
T TAT
GAM63 348 C6orf67 1 5174 NP_060717.1 3 832 GACCTTCATCTT C-- A - 4 A c c
CTGCCTCAACTG GGT CAG TGGGG AGAAGATG
TAAACCAC CCA GTC ACTCC TCTTCTAC
AAT A G
GAM63 348 CAB2 1 12488 NP_219487.2 3 514 TTCACGGCGATT AG GA 4 A c c
CTCCCCATGGGA GGTCC ATGGGGAGAA TGT
TCTTGAGG CTAGG TACCCCTCTT GCG
G- A-
GAM63 348 CACNG6 1 11907 NP_114103.2 3 85 CCAAGATCTTTT TCC -- G 4 A c c
TGCCCCATCTCC GG AGATGGGG AGAAGAT
TAGAGAAA CC TCTACCCC TTTTCTA
--- GT G
GAM63 348 CACNG6 1 11907 NP_665813.1 3 85 CCAAGATCTTTT TCC -- G 4 A c c
TGCCCCATCTCC GG AGATGGGG AGAAGAT
TAGAGAAA CC TCTACCCC TTTTCTA
--- GT G
GAM63 348 CACNG6 1 11907 NP_665814.1 3 85 CCAAGATCTTTT TCC -- G 4 A c c
TGCCCCATCTCC GG AGATGGGG AGAAGAT

TAGAGAAA CC TCTACCCC TTTTCTA
--- GT G

GAM63 348 CAMKK1 1 5691 NP_115670.1 3 1552 GGGTCCACGTTT ----- A 4 A c c
CTCCCCGGCTCC GGTCCAGA TGGGGAGA GATGT
TCTGGGCT TCGGGTCT GCCCCTCT TTGCA
CCTCG -

GAM63 348 CAMKK1 1 5691 NP_757343.1 3 1552 GGGTCCACGTTT ----- A 4 A c c
CTCCCCGGCTCC GGTCCAGA TGGGGAGA GATGT
TCTGGGCT TCGGGTCT GCCCCTCT TTGCA
CCTCG -

GAM63 348 CAMKK2 1 14352 NP_006540.3 3 2036 ACAATGCCATTT - AGA- A 4 A c
c
CTCCCCACCACG GGT CC TGGGGAGA GATG
GAACCTTC CCA GG ACCCCTCT TTAC
A CACC -

GAM63 348 CAMKK2 1 14352 NP_705719.2 3 2134 ACAATGCCATTT - AGA- A 4 A c
c
CTCCCCACCACG GGT CC TGGGGAGA GATG
GAACCTTC CCA GG ACCCCTCT TTAC
A CACC -

GAM63 348 CAMKK2 1 14352 NP_705720.1 3 2134 ACAATGCCATTT - AGA- A 4 A c
c
CTCCCCACCACG GGT CC TGGGGAGA GATG
GAACCTTC CCA GG ACCCCTCT TTAC
A CACC -

GAM63 348 CAMKK2 1 14352 NP_757365.1 3 2036 ACAATGCCATTT - AGA- A 4 A c
c
CTCCCCACCACG GGT CC TGGGGAGA GATG
GAACCTTC CCA GG ACCCCTCT TTAC
A CACC -

GAM63 348 CAMKK2 1 14352 NP_757380.1 3 2135 ACAATGCCATTT - AGA- A 4 A c
c
CTCCCCACCACG GGT CC TGGGGAGA GATG
GAACCTTC CCA GG ACCCCTCT TTAC
A CACC -

GAM63 348 CAP350 1 19295 NP_055625.2 3 2165 TTTCTACATCTT GGA 4 A c c
CATTATTTGGAC GGTCCAGATGG GAAGATGT
CTAAAACC CCAGGTTTATT CTTCTACA
A--

GAM63 348 CBFA2T2 1 9720 NP_005084.1 3 972 TGTGGGCATCTT GA G 4 A c c
CTGCCCATGGGC GGTCCA TGGG AGAAGATGT
TCCATTTG TCGGGT ACCC TCTTCTACG
-- G

GAM63 348 CBFA2T2 1 9720 NP_787060.1 3 972 TGTGGGCATCTT GA G 4 A c c
CTGCCCATGGGC GGTCCA TGGG AGAAGATGT
TCCATTTG TCGGGT ACCC TCTTCTACG
-- G

GAM63 348 CBX7 1 8537 NP_783640.1 3 1232 ATTCTGCATCCC CCA AA 4 A c c
CTCCCCATCCAA GGT GATGGGGAG GATGT
CCTAAATG CCA CTACCCCTC CTACG

AC- CC
GAM63 348 CCNH 1 13215 NP_001230.1 5 193 GGTTCTCGTCTG T GAGA- 4 A c c

CAGACCCTCTGG GGTCCAGA GGG AGATG
ACCTGGTC CCAGGTCT CCC TCTGC
- AGACG
GAM63 348 CCR7 1 19038 NP_001829.1 3 8 CACCACCACCTT CAG A 4 A c c
CTCCCCATAGCG GGTC ATGGGGAGAAG TG
ACTCTTCT TCAG TACCCCTCTTC AC
CGA C
GAM63 348 CD2AP 1 12070 NP_036252.1 5 21 GGACGTCGGCTT - AGA --- 4 A c c
CTCCCCGCGGGA GG TCC TGGGGAGAA GATGT
GCCCCCAG CC AGG GCCCCTCTT CTGCA
G GC- CGG
GAM63 348 CD37 1 19108 NP_001765.1 3 209 CCACAGCTTCCT -- --- A 4 A c c
GTCCCCATCTGT GGTC CAGATGGGGA GAAG TGT
CGGCCTAC CCGG GTCTACCCCT CTTC ACA
CT GTC G
GAM63 348 CD8B1 1 13025 NP_004922.1 3 605 TCACTTCATCTT CC ---- 4 A c c
CTCAGCTCCCAT GGT AGATGGG GAGAAGATG
TTCTACTC TCA TTTACCC CTCTTCTAC
TC TCGA
GAM63 348 CD8B1 1 13025 NP_742097.1 3 555 TCACTTCATCTT CC ---- 4 A c c
CTCAGCTCCCAT GGT AGATGGG GAGAAGATG
TTCTACTC TCA TTTACCC CTCTTCTAC
TC TCGA
GAM63 348 CDC42 1 5028 NP_001782.1 3 585 TTAGAAAACATG - GA G 4 A c c
TTCCCCATCTGG GGT CCAGATGGGGA A ATGT
TGCTCTTA TCG GGTCTACCCCT T TACA
T -- G
GAM63 348 CECR1 2 8125 NP_059120.2 3 267 TTTCAGAGTCTT C T- G 4 A c c
CTCCTCTCTCTG GGTC AGA GGGGAGAAGAT
ATCTCTGT CTAG TCT CTCCTCTTCTG
- CT A
GAM63 348 CECR1 2 8125 NP_803124.1 3 267 TTTCAGAGTCTT C T- G 4 A c c
CTCCTCTCTCTG GGTC AGA GGGGAGAAGAT
ATCTCTGT CTAG TCT CTCCTCTTCTG
- CT A
GAM63 348 CECR1 2 8928 NP_059120.2 3 1120 CATCAGAACGCA AGAA 4 A c c
TCCCTCATCTGG GGTCCAGATGGGG GATGT
ACTCCAGC TCAGGTCTACTCC CTACG

GAM63 348 CECR1 2 8928 NP_803124.1 3 1120 CATCAGAACGCA AGAA 4 A c c
TCCCTCATCTGG GGTCCAGATGGGG GATGT
ACTCCAGC TCAGGTCTACTCC CTACG

GAM63 348 CELSR2 1 2706 NP_001399.1 3 1299 CCAGGCCATCAT TCC A A 4 A c
c

CTCCCCACCTCT GG AG TGGGGAGA GATG
CCTCCCCT CC TC ACCCCTCT CTAC

TC- C A

GAM63 348 CENPB 1 16636 NP_001801.1 3 237 GAATCCTCTTTC T -- TG 4 A c c
CTCCCCATTTGG GG CCAGATGGGGAG AAGA
CCCTGGGC CC GGTTTACCCCTC TTCT
C CT CC

GAM63 348 CHC1 1 16629 NP_001260.1 5 11 TGGTCGCTTCTT GATG T 4 A c c
CTCCTTGGATTT GGTCCA GGGAGAAGA GT
GTTAAGGA TTAGGT TCCTCTTCT CG
---- T

GAM63 348 CHD4 1 6002 NP_001264.1 3 83 TTGTCCCAGCTT AGAT A 4 A c c
CTCCCCTGGGGG GGTCC GGGGAGAAG TG
CCTGAGAG CCGGG CCCCTCTTC AC
GGT- G

GAM63 348 CHRNB2 1 14758 NP_000739.1 3 137 GATCCATCCTTT -- - - 4 A c c
TGCTTCATCTGG GG TCCAGATGGGG AGAAG ATG
AGTCCCTC CC AGGTCTACTTC TTTTC TAC
TG G C

GAM63 348 CHST1 1 19217 NP_003645.1 3 476 GGTGTCCATCCT CCA A 4 A c c
TTCCCCATCCCT GGT GATGGGGAGA GATG
GCCTCCTG CCG CTACCCCTTT CTAC
TCC C

GAM63 348 CKLFSF3 1 19997 NP_653202.1 3 251 ATCCCACTCCTT TC -- AT 4 A c c
CTCCCCATTTCT GG CAGA TGGGGAGAAG GT
GTCCCACA CC GTCT ACCCCTCTTC CA
CT TT CT

GAM63 348 CKLFSF5 1 10840 NP_612469.1 5 103 GCTCCTGTCTGT CCA - 4 A c c
TTCCCCATCCTG GGT GATGGGGAGA AGATG
CCAGATTT CCG CTACCCCTTT TCTGT
TC- G

GAM63 348 CKMT1 1 12177 NP_066270.1 3 18 CACCAAGCATTA CCA AA 4 A c c
CTCCCCATCGCC GGT GATGGGGAG GATGT
AGCTGATG CCG CTACCCCTC TTACG
--- A-

GAM63 348 CLCN6 1 1912 NP_001277.1 3 1233 GACGTCATTCTT T A- - - 4 A c c
CTCCAGGCTGGC GG CCAG TGG GGAGAA GATGT
CCGCCCCC CC GGTC ACC CTTCTT CTGCA
C GG T A

GAM63 348 CLCN6 1 1912 NP_068503.1 3 1233 GACGTCATTCTT T A- - - 4 A c c
CTCCAGGCTGGC GG CCAG TGG GGAGAA GATGT
CCGCCCCC CC GGTC ACC CTTCTT CTGCA
C GG T A

GAM63 348 CLCN6 1 1912 NP_068504.1 3 1233 GACGTCATTCTT T A- - - 4 A c c
CTCCAGGCTGGC GG CCAG TGG GGAGAA GATGT
CCGCCCCC CC GGTC ACC CTTCTT CTGCA
C GG T A

GAM63 348 CLCN6 1 1912 NP_068505.1 3 1233 GACGTCATTCTT T A- - - 4 A c c
CTCCAGGCTGGC GG CCAG TGG GGAGAA GATGT
CCGCCCCC CC GGTC ACC CTTCTT CTGCA
C GG T A

GAM63 348 CLDN15 1 13079 NP_055158.1 3 238 ATCCCTCATCTT --- -- 4 A c c

CTGACCCTGGGT GGTCCAGA TGGGG AGAAGATG
TCTGGGCT TCGGGTCT GTCCC TCTTCTAC
TGG AG

GAM63 348 CLL-1 1 1380 NP_612210.1 3 404 AGGGTGGCATGG - - AAG 4 A c c
CTCCCCATCTCG GG TCC AGATGGGGAG ATGT
GGTCCATC CC GGG TCTACCCCTC TACG
T C GG-

GAM63 348 COL1A2 1 5175 NP_000080.1 3 726 CATTTTCATCTT T- GATG 4 A c c
CTTCCATGGTTC GG CCA GGGAGAAGATG
CACAGAAG CC GGT CCTTCTTCTAC
TT A---

GAM63 348 COL9A2 1 13362 NP_001843.1 3 462 TCCTGATCCCAT T - A-- G 4 A c c
CTCACTCTCTGG GGTCCAGA GGG GAGA GAT
ACCTACCA CCAGGTCT CTC CTCT CTA
- A ACC G

GAM63 348 CPA5 1 5792 NP_525124.2 3 48 GGCTCCATCCTT - --- - 4 A c c
CTCCCCAAGGTC GGTC CAGA TGGGGAGAAG ATG
TGTGGCTC TCGG GTCT ACCCCTCTTC TAC
T GGA C

GAM63 348 cPLA2de 1 10856 NP_828848.1 3 1338 CCTCCTCATCTT TCC A 4 A c c
lta CTTCCTGCTCCT GG AG TGGGGAGAAGATG
CCACCTCC CC TC GTCCTTCTTCTAC
TCC -

GAM63 348 cPLA2de 1 10856 XP_208820.2 3 432 CCTCCTCATCTT TCC A 4 A c c
lta CTTCCTGCTCCT GG AG TGGGGAGAAGATG
CCACCTCC CC TC GTCCTTCTTCTAC
TCC -

GAM63 348 CPLX2 1 6535 NP_006641.1 5 262 TTGTCACATCTT CAGA --- A 4 A c c
CCCAAGCCAGGC GGTC TGG GG GAAGATGT
CAGCCAGG CCGG ACC CC CTTCTACA
---- GAA -

GAM63 348 CUL3 1 7916 NP_003581.1 3 588 CTTACTCATCTT CAG -- 4 A c c
CTAGCCTTATGA GGTC ATGGGG AGAAGATG
CCAGGAAC CCAG TATTCC TCTTCTAC
--- GA

GAM63 348 CXCL12 1 785 NP_000600.1 3 1253 TAACCTCATCTT ---- - 4 A c c
CTTCACCATTTG GGT CCAGATGG GGAGAAGATG
GCAATGCC CCG GGTTTACC CTTCTTCTAC
TAAC A

GAM63 348 CYP27B1 1 18862 NP_000776.1 3 104 GGTATACATCTT C ------- A 4 A c c
CCCCTAATGCCT GGTC AGAT GGGG GAAGATGT
ATCTGACC CCAG TCTA TCCC CTTCTACA
- TCCGTAA -

GAM63 348 D21S205 1 6022 NP_003674.1 3 911 TGCCCGCATCTT - AG - 4 A c c
6E CTGTTCCATGGG GGT CC ATGGGG AGAAGATGT
TGCCCAGC CCG GG TACCTT TCTTCTACG
T G- G

GAM63 348 DAG1 1 15198 NP_004384.1 3 1840 CCCTTGCGCCTT AGA - A 4 A c c
CTCCCACAGGGC GGTCC TG GGGAGAAG TGT
CCAGCCCC CCGGG AC CCCTCTTC GCG

--- A C

GAM63 348 DAZAP2 1 757 NP_055579.1 3 605 TTCCTCGCACTT CCA - A 4 A c c
CTCCCCACTCGT GGT GA TGGGGAGAAG TGT
CATCTTTT CTA CT ACCCCTCTTC ACG
CTG C -

GAM63 348 DDX11 1 5910 NP_004390.2 3 822 TGCGCCTGTCTT C TG 4 A c c
CTCCCTCTGACC GGTC AGA GGGAGAAGATG
CCAGAGAA CCAG TCT CCCTCTTCTGT
- --

GAM63 348 DDX11 1 5910 NP_085911.1 3 823 TGCGCCTGTCTT C TG 4 A c c
CTCCCTCTGACC GGTC AGA GGGAGAAGATG
CCAGAGAA CCAG TCT CCCTCTTCTGT
- --

GAM63 348 DDX11 1 5910 NP_085913.1 3 2963 TGCGCCTGTCTT C TG 4 A c c
CTCCCTCTGACC GGTC AGA GGGAGAAGATG
CCAGAGAA CCAG TCT CCCTCTTCTGT
- --

GAM63 348 DDX34 1 1581 NP_055496.1 3 590 AGCGACTGTCTC T --- - A 4 A c c
CGAACCTTCTGG GGTCCAGA GG GGAGA AG TGT
ACCTGCCC CCAGGTCT CC CCTCT TC GCG
T AAG G A

GAM63 348 DEFB127 1 11155 NP_620713.1 3 89 GATATACATCTT T- T 4 A c c
CTTCCTTTTGGT GG CCAGA GGGGAGAAGATGT
TTCTTGAT CT GGTTT TCCTTCTTCTACA
TT -

GAM63 348 DGCR6 1 4437 NP_005666.2 3 52 AGAGTTCATCTT T T G- 4 A c c
CTTGACCTTTGG GG CCAGA GG GAGAAGATG
CCACTGCC CC GGTTT CC TTCTTCTAC
- - AG

GAM63 348 DGCR6L 1 4437 NP_150282.1 3 52 AGAGTTCATCTT T T G- 4 A c c
CTTGACCTTTGG GG CCAGA GG GAGAAGATG
CCACTGCC CC GGTTT CC TTCTTCTAC
- - AG

GAM63 348 DISPB 1 17539 NP_277045.1 3 550 GCTGGGACCTCT TC A A T 4 A c c
CTCCCCAACTGC GG CAG TGGGGAGA GA GT
CCTGCTCT CC GTC ACCCCTCT CT CA
C- A - C

GAM63 348 DKFZP43 1 9123 XP_114297.2 3 1094 ATACTATATTTT CCAGA 4 A c c

4D193 CTCCCCAATACC GGT TGGGGAGAAGATGT
ACCAACGA CCA ACCCCTCTTTTATA
CCATA

GAM63 348 DKFZP43 1 15958 NP_056458.1 3 561 TAACTGCATCTT - AT --- 4 A c c
4F122 CTCTGACCCCTG GGT CCAG GGG GAGAAGATGT
GTACCAGA CCA GGTC CCC CTCTTCTACG
T -- AGT

GAM63 348 DKFZp43 1 18569 NP_115630.1 3 1562 CTGGCCCATCTT T GA- - 4 A c c

4F142 CTGCCTCACAGT GG CCA TGGGG AGAAGATG
GGCCACTC CC GGT ACTCC TCTTCTAC

```
                                        -  GAC    G
GAM63   348   DKFZp43 1  15511 XP_064865.3  3  27   TGAAGGGAACAT  T      GGAG          4  A  c
c
        4H055                      CTTACCATCTGG GG CCAGATGG   AAGATGT
                                  CCATTCAC    CC GGTCTACC   TTCTACA
                                        -       A---
GAM63   348   DKFZp43 1  18924 XP_088463.5  5  347  GCGTCTTCTCTT    CA  T              4  A  c  c
        4M1411                     CTCCAGGCCTAT GGTC  GA GGGGAGAAGATGT
                                  GGTCCTGC    CCGG  CT CTTCTCTTCTGCG
                                        AC  -
GAM63   348   DKFZP43 1  12595 XP_041116.1  3  2281  CTCATGGCAGTT         AG  GA        4  A  c
c
        4P0111                     GGCTCCATCTGG GGTCCAGATGGGG  AA  TGT
                                  ACCTCCCA    CCAGGTCTACCTC  TT  ACG
                                        GG  G-
GAM63   348   DKFZP56 1  2440  XP_300857.1  3  128   ATTTATACACTT   C   TG      A        4  A  c  c
        4J0123                     CTCCCATTTTGT GGT CAGA  GGGAGAAG TGT
                                  ATCAGGTG    CTA GTTT  CCCTCTTC ACA
                                        T   TA      -
GAM63   348   DKFZP56 1  20108 NP_056278.1  3  114   ACACCATTGCTG   -        AA--        4  A  c  c
        6K1924                     TTCCCCATCTGG GGT CCAGATGGGGAG   GATG
                                  TACTAATG    TCA GGTCTACCCCTT   TTAC
                                        T         GTCG
GAM63   348   DKFZp66 1  19396 XP_290795.1  5  415   AAGTTCATGTCT        GG--  AG        4  A  c  c

        7M2411                     CATGTTATCTGG GGTCCAGATG   GAGA  ATG
                                  ACCTTGA     CCAGGTCTAT   CTCT  TAC
                                        TGTA   G-
GAM63   348   DKFZp76 1  8017  NP_775734.1  3  1310  TTCTCACATCTT  T   AT  GG-          4  A  c  c

        1B107                      CTAAACCCTGGT GG CCAG  GG   AGAAGATGT
                                  CCATTCTC    CC GGTC  CC   TCTTCTACA
                                        T   --  AAA
GAM63   348   DKFZp76 1  2815  NP_690877.1  5  131   CGCCCCACGCTT    A  TG      A        4  A  c  c
        1L1417                     CTCCCGCTCCGG GGTCC GA  GGGAGAAG TGT
                                  GCCCCGCA    CCGGG CT  CCCTCTTC GCA
                                        C  CG       -
GAM63   348   DPCR1  1  6228  NP_543146.1  3  898   GTTACCCATCTT  TC  ATGG            4  A  c  c

                                  CTCTACTGTCCC GG  CAG   GGAGAAGATG
                                  CATTCTCT    CC  GTC   TCTCTTCTAC
                                        CT   A---
GAM63   348   DPF3   1  1393  NP_036206.1  3  2372  CTGCAACATTTT  TCCA     G          4  A  c  c
                                  ATCCCCATCATT GG   GATGGGGA AAGATGT
                                  CCAAAATG    CC   CTACCCCT TTTTACA
                                        TTA-       A
GAM63   348   DVL3   1  19305 NP_004414.2  3  1253  CCTGACACCCTT   ---  AT-      A-     4  A  c  c
                                  CTCCCCTTCCTG GGT  CCAG  GGGGAGAAG  TGT
                                  GTAGACCT    CCA  GGTC  CCCCTCTTC  ACA
                                        GAT   CTT       CC
```

GAM63 348 DYRK1A 1 9660 NP_567824.1 3 397 CCTCGACATCTT -- AT - 4 A c c
CCTCCTCTACTG GGT CCAG GGGGAG AAGATGT
GTAACCAA CCA GGTC CTCCTC TTCTACA
AT AT C
GAM63 348 DYRK1A 1 9660 NP_569121.1 3 356 CCTCGACATCTT -- AT - 4 A c c
CCTCCTCTACTG GGT CCAG GGGGAG AAGATGT
GTAACCAA CCA GGTC CTCCTC TTCTACA
AT AT C
GAM63 348 DYRK1A 1 9660 NP_569122.1 3 306 CCTCGACATCTT -- AT - 4 A c c
CCTCCTCTACTG GGT CCAG GGGGAG AAGATGT
GTAACCAA CCA GGTC CTCCTC TTCTACA
AT AT C
GAM63 348 DYRK1B 1 3553 NP_004705.1 3 56 GAAGCCATACCC -- - AAG 4 A c c
TCCCCCATCTGG GGT CCAGATGGGG AG ATG
GGGCCCTG CCG GGTCTACCCC TC TAC
GG C CCA
GAM63 348 DYRK1B 1 3553 NP_006474.1 3 56 GAAGCCATACCC -- - AAG 4 A c c
TCCCCCATCTGG GGT CCAGATGGGG AG ATG
GGGCCCTG CCG GGTCTACCCC TC TAC
GG C CCA
GAM63 348 DYRK1B 1 3553 NP_006475.1 3 56 GAAGCCATACCC -- - AAG 4 A c c
TCCCCCATCTGG GGT CCAGATGGGG AG ATG
GGGCCCTG CCG GGTCTACCCC TC TAC
GG C CCA
GAM63 348 EAT2 1 4918 NP_444512.1 3 616 ATGTGCACCCTT A- -- A- 4 A c c
CTCCCTCCAGCC GGTCCAG TGG GGAGAAG TGT
TGGGCTAC TCGGGTC ACC CCTCTTC ACG
CG TC CC
GAM63 348 EFS 1 1802 NP_005855.1 3 174 CAGAGGTGTCTT CC AT TG 4 A c c
CTCCCCCTAACC GGT AG GGGGAGAAGA T
TACAGCTT CCA TC CCCCTCTTCT G
A- -- GT
GAM63 348 EFS 1 1802 NP_115835.1 3 174 CAGAGGTGTCTT CC AT TG 4 A c c
CTCCCCCTAACC GGT AG GGGGAGAAGA T
TACAGCTT CCA TC CCCCTCTTCT G
A- -- GT
GAM63 348 EGR3 1 4416 NP_004421.2 3 1601 CAGTCTCACCTT CC A- A 4 A c c
CTCCCCACCCTA GGT AG TGGGGAGAAG TG
CCTCACCT CCA TC ACCCCTCTTC AC
-- CC C
GAM63 348 ENO2 1 13106 NP_001966.1 3 780 CTCTATACATCT T- - A-- A 4 A c c
CTCCCCAACCCT GG CC AG TGGGGAGA GATGT
AGGTTCCC CC GG TC ACCCCTCT CTACA
TT A CCA -
GAM63 348 ERAL1 1 5170 NP_005693.1 3 478 CACCCCATCCCT G--- - - A- 4 A c c
CTCCCCAGTCTT GTCCA GA TGGGGAGA GATG
GGATACTA TAGGT CT ACCCCTCT CTAC
ATCA T G CC
GAM63 348 ERBB3 1 12198 NP_001973.1 3 83 GGGTACCGTCTT TCCA 4 A c c
CTCCCTATTCCC GG GATGGGGAGAAGATG

TCTCTCTC CC TTATCCCTCTTCTGC
C---
GAM63 348 ESPL1 1 2372 NP_036423.1 5 860 CTGGGCTTCTTT AGA - T 4 A c c
CTCCCCAGAGGG GGTCC TGGGGAGAA GA GT
CCCTCTGC CCGGG ACCCCTCTT CT CG
AG- T T
GAM63 348 F11R 1 15037 NP_058642.1 3 1742 ATTGCTTTCTTC - TG 4 A c c
CTCCCCATTTGG GGTCCAGATGGGGAG AAGA
ACCCTTCT CCAGGTTTACCCCTC TTCT
C TT
GAM63 348 F11R 1 15037 NP_653085.1 3 1742 ATTGCTTTCTTC - TG 4 A c c
CTCCCCATTTGG GGTCCAGATGGGGAG AAGA
ACCCTTCT CCAGGTTTACCCCTC TTCT
C TT
GAM63 348 F11R 1 15037 NP_653086.1 3 1744 ATTGCTTTCTTC - TG 4 A c c
CTCCCCATTTGG GGTCCAGATGGGGAG AAGA
ACCCTTCT CCAGGTTTACCCCTC TTCT
C TT
GAM63 348 F11R 1 15037 NP_653087.1 3 1744 ATTGCTTTCTTC - TG 4 A c c
CTCCCCATTTGG GGTCCAGATGGGGAG AAGA
ACCCTTCT CCAGGTTTACCCCTC TTCT
C TT
GAM63 348 FAM3A 1 11015 NP_068578.1 3 318 CACGCCATCTCC -- C GA- 4 A c c
ATCCCCATCTTG GG TC AGATGGGGA AGATG
AGTCCTGG CC AG TCTACCCCT TCTAC
TG T ACC
GAM63 348 FBXW8 1 15570 NP_036306.1 3 2323 CTCTCATAGTCT GG-- AG 4 A c c
TAATGCGTCTGG GGTCCAGATG GAGA ATG
ACCACTGG CCAGGTCTGC TTCT TAC
GTAA GA
GAM63 348 FBXW8 1 15570 NP_699179.2 3 2323 CTCTCATAGTCT GG-- AG 4 A c c
TAATGCGTCTGG GGTCCAGATG GAGA ATG
ACCACTGG CCAGGTCTGC TTCT TAC
GTAA GA
GAM63 348 FLJ0000 2 3839 XP_088525.2 3 2227 TGGAGCCATCTT A- G--- 4 A c c
1 CTCCATAGCATT GGTCC GATG GGAGAAGATG
ACGGACTT TCAGG TTAC CCTCTTCTAC
CA GATA
GAM63 348 FLJ0000 2 9347 XP_088525.2 3 1538 AAGCGGCCACTT - AT A 4 A c c
1 CTCCCTCCCTGA GGTC CAG GGGGAGAAG TG
GACCCGAG CCAG GTC TCCCTCTTC AC
A CC -
GAM63 348 FLJ0002 1 16819 NP_203745.1 3 864 GCCTGGCCTCTT TCC T T 4 A c c
4 CTCCCCTCTCTT GG AGA GGGGAGAAGA GT
CCCAGCAG CC TCT CCCCTCTTCT CG
TTC - C
GAM63 348 FLJ0002 1 16819 XP_033361.2 3 864 GCCTGGCCTCTT TCC T T 4 A c c

4 CTCCCCTCTCTT GG AGA GGGGAGAAGA GT
CCCAGCAG CC TCT CCCCTCTTCT CG
TTC - C

GAM63 3483 FLJ0010 1 7642 XP_036104.5 3 1287 CTCCTCAGCTTC -- - A 4 A c c
CTCCCCATCTGG GGT CCAGATGGGGAG AAG TG
GTGCCCCA CCG GGTCTACCCCTC TTC AC
TG C G

GAM63 3480 FLJ1090 1 16238 NP_060734.1 3 840 GGTCTCCATCTT - ATG- GG 4 A c c
CTTTCACTCCTG GGTC CAG G AGAAGATG
TGGCCCTG CCGG GTC C TCTTCTAC
T CTCA TT

GAM63 3482 FLJ1092 1 16820 NP_060743.1 3 134 CCAGGCCAACTT G -- --- A 4 A c c
CTCCCCGCTGTC GTCC AGAT GGGGAGAAG TG
TGAGGACA CAGG TCTG CCCCTCTTC AC
A AG TCG A

GAM63 3481 FLJ1115 1 11328 NP_060810.1 3 1057 TTACCGCATCTT C --- GG 4 A c c
CTCAGCAGCTTC GGTC AGA TG GAGAAGATGT
TGACCACT CCAG TCT AC CTCTTCTACG
- TCG GA

GAM63 3480 FLJ1266 1 6133 NP_079428.1 3 483 ATGAACCTCTGC A- T 4 A c c
TTCTTCATCTGG GGTCCAGATGGGGAG AGA GT
ATCACACT CTAGGTCTACTTCTT TCT CA
CG C

GAM63 3484 FLJ1320 1 3368 NP_079037.2 3 1073 AGCCGTCATTCT TCC A AG 4 A c c
CTCCCCACTCCA GG AG TGGGGAGA ATG
CGCTCCCC CC TC ACCCCTCT TAC
--- - CT

GAM63 3485 FLJ1321 2 5332 NP_079280.1 3 77 GACCAGCATGTT CAGA G 4 A c c
CTCCCCAAAGAC GGTC TGGGGAGAA ATGT
CAAGATAT CCAG ACCCCTCTT TACG
AA-- G

GAM63 3485 FLJ1321 2 18857 NP_079280.1 3 167 GACCAGCATGTT CAGA G 4 A c c
CTCCCCAAAGAC GGTC TGGGGAGAA ATGT
CAGAATAT CCAG ACCCCTCTT TACG
AA-- G

GAM63 3489 FLJ1363 1 19873 NP_078981.1 3 404 CTGTTCACGTCT GA A 4 A c c
CTCCCCAGTGGG GGTCCA TGGGGAGA GATGT
CTCCTAAG TCGGGT ACCCCTCT CTGCA
G- -

GAM63 3487 FLJ1400 1 11969 NP_078975.1 3 338 TTGTGTCATCTT CAG GG 4 A c c
CTTACCATGATC GGTC ATGG AGAAGATG
AAAGGCGA CTAG TACC TCTTCTAC
--- AT

GAM63 3480 FLJ1405 1 19808 NP_079145.1 5 46 TGTCCACTCCTG --- G A A 4 A c c
CCCTCAGTCTGG GGTCCAGAT GGG AG AG TG
ACCTGCCC CCAGGTCTG CCC TC TC AC

ACT G C -

GAM63 3487 FLJ2048 1 14156 NP_060311.1 3 603 AGTCAACATCTT A GGA 4 A c c
CATCATTGGGCT GGTCCAG TGG GAAGATGT
TTCTTTAA TCGGGTT ACT CTTCTACA
- A--

GAM63 3489 FLJ2061 1 9038 NP_060374.1 3 811 TCCCCTCATCTT TCC A - 4 A c c
CTCCACTACTAT GG AG TGG GGAGAAGATG
CCACATGA CC TC ATC CCTCTTCTAC
TA- - A

GAM63 3485 FLJ2082 1 1853 NP_060432.1 3 1 TCAAAGCATCTC C-- A A 4 A c c
CCCCATCTGCAT GGT CAGATGGGG GA GATGT
ACCCAGCA CCA GTCTACCCC CT CTACG
TAC - -

GAM63 3487 FLJ2197 1 19347 NP_115589.2 3 1057 ACCCACTCTCTT C AT TG 4 A c c
CTCCCCCTGACC GGTC AG GGGGAGAAGA
CCCGCTCC CCAG TC CCCCTCTTCT
- -- CT

GAM63 3480 FLJ2216 1 4897 NP_078861.1 3 764 TAACTGCATCTT CCA T 4 A c c
CTCCCCTTGCCA GGT GA GGGGAGAAGATGT
CCCCATGG CCA TT CCCCTCTTCTACG
CCG -

GAM63 3489 FLJ2216 1 9940 NP_076990.1 3 126 CCTGCGCTCCTT C- A AT 4 A c c
CTCCCCGCTGCA GGT CAG TGGGGAGAAG GT
ACCCGGGC CCA GTC GCCCCTCTTC CG
AC - CT

GAM63 3489 FLJ2232 1 2748 NP_078932.2 3 86 TGAGGACATCAG T - AGAA 4 A c c
GGCCACCTCTGG GGTCCAGA GG GG GATGT
ACCCCTTG CCAGGTCT CC CC CTACA
- A GGGA

GAM63 3488 FLJ2267 1 5171 NP_078812.2 3 390 ATCTCCCAACTT T A 4 A b b
CTCCCTTTTGGA GGTCCAGA GGGGAGAAG TG
CCCTGCCG CCAGGTTT TCCCTCTTC AC
- A

GAM63 3480 FLJ2342 1 20060 NP_079337.1 5 307 GGCCCACCTCTT T ATGG T 4 A c c
CTCCAAGCTGGC GG CCAG GGAGAAGA GT
CTTCTGTT CC GGTC CCTCTTCT CA
- GAA- C

GAM63 3487 FLJ3031 1 19586 NP_742148.1 3 1078 ACCCTCACACCG T - AAGA 4 A c c
CTGCTCCTCTGG GGTCCAGA GGGG AG TGT
ACCTCTGT CCAGGTCT CCTC TC ACA
- G GCC-

GAM63 3483 FLJ3047 1 18935 NP_653305.1 3 261 GCCCTGCCTCTT A -- T 4 A c c
CTCCCTCTATTG GGTCC GAT GGGGAGAAGA GT
GGACTGGT TCAGG TTA TCCCTCTTCT CG
G TC C

GAM63 3481 FLJ3113 1 15810 NP_689748.1 5 328 GTGACGGTCTTT T - G 4 A c c
ATTCCCATCTGG GG CCAGATGGGGA GAAGAT

CTTCTGCA TC GGTCTACCCTT TTTCTG
- A G

GAM63 3483 FLJ3171 1 19852 NP_689788.1 3 830 TCTTGTCATCTT C T - 4 A c c
CTCATCCTCTGC GGT CAGA GGG GAGAAGATG
GCCAAGAA CCG GTCT CCT CTCTTCTAC
C - A

GAM63 3489 FLJ3181 1 18693 NP_689742.2 5 86 GACGGTGGTCTT - AT G 4 A c c
CTCCCTGCTTGG GGT CCAG GGGGAGAAGAT
CACCCTGC CCA GGTT TCCCTCTTCTG
C CG G

GAM63 3481 FLJ3182 1 855 NP_694574.1 5 149 AACATCTTTACT ---- A 4 A c c
CTTATTGTCTGG GGTCCAGAT GGGG GAAGATGT
ACCTTCAA CCAGGTCTG TCTC TTTCTACA
TTAT A

GAM63 3485 FLJ3206 1 15838 NP_694577.1 3 1498 ACTCTTTATCTT T AT - 4 A c c
CTCATCTTACTG GG CCAG GGG GAGAAGATG
GCCTGGTC CC GGTC TCT CTCTTCTAT
- AT A

GAM63 3489 FLJ3206 1 10747 NP_694578.1 3 523 AAAGAGCATCTT C A - 4 A b b
CTCTCCCACTGC GGT CAG TGGG GAGAAGATGT
ACCCCTTC CCA GTC ACCC CTCTTCTACG
C - T

GAM63 3484 FLJ3278 1 7437 NP_653224.1 3 508 CTGTGACAGCTT T ----- A 4 A c c
CTCCCTGGAGCC GG CCAGA TGGGGAGAAG TGT
TCTGGCCA CC GGTCT GTCCCTCTTC ACA
- CCGAG G

GAM63 3480 FLJ3361 1 17301 NP_775968.1 3 87 AAGCTCTGTCTT TC-- TG 4 A c c
CTCCCTCTGCCC GG CAGA GGGAGAAGATG
TCCAACAG CC GTCT CCCTCTTCTGT
TCCC --

GAM63 3481 FLJ3364 1 15987 NP_689900.1 3 596 TCTAGATATCTT C -- T - 4 A c c
CTCCACCCTCCT GGT CA GA GG GGAGAAGATGT
TGCACCAG CCA GT CT CC CCTCTTCTATA
C TC C A

GAM63 3487 FLJ3381 1 19519 NP_689561.1 3 303 CTACCTTCACTT TC -- A 4 A c c
CTCCCCAGCTCT GG CAGA TGGGGAGAAG TG
GCCCTCTG CC GTCT ACCCCTCTTC AC
C- CG -

GAM63 3480 FLJ3522 1 7479 NP_775898.2 3 1023 CACTGGCATCTT ATG 4 A c c
CTTTTAACTTGG GGTCCAG GGGAGAAGATGT
GCCATCTG CCGGGTT TTTTCTTCTACG
CAA

GAM63 3483 FLJ3528 1 19021 NP_689915.1 3 879 CTTTGTCTCCTC TC -- - -- 4 A c c
TTCCCCATCTAT GG CA GATGGGGA GA AGATG
GTCCCTTT CC GT CTACCCCT CT TCTGT
CT AT T CC

GAM63 3483 FLJ3561 1 6698 NP_775924.1 3 738 ACCAGGTTTCTT CCAG TG 4 A c c
CTCCCCATACCA GGT ATGGGGAGAAGA
CGTTGTGC CCA TACCCCTCTTCT

```
                                        ----          TT
GAM63   348   FLJ3747 1   7911   NP_848652.1  3  924   AGCCCACAGCTT   C-  ATG      A        4  A  c  c
        8                            CTCCCAGCCTGA GGT  CAG   GGGAGAAG TGT
                                     AACCAACA    CCA  GTC   CCCTCTTC ACA
                                           AA   CGA       G
GAM63   348   FLJ3862 1   3281   NP_689480.2  3  1642  TCCCCATCTCTT   C   T    GA          4  A  c  c
        8                            CTCCTTTGTACC GGT CAGA GGGGA  AGATG
                                     TGTCAACA    CCA GTTT CCTCT  TCTAC
                                           T   -    TC
GAM63   348   FLJ3879 1   2686   NP_848615.1  3  1777  AGGGCGTCTCAT   - AGA      --        4  A  c  c
        2                            CTCCCCACAGGC GGT CC   TGGGGAGA  AGATGT
                                     ATCTGCTG    CTA GG   ACCCCTCT  TCTGCG
                                           C  AC-       AC
GAM63   348   FLJ3924 1   16239  NP_775935.1  3  1338  GGGTACATCACT       T  --  AA        4  A  c  c
        9                            CAGCCTTTCTGG GGTCCAGA GGG  GAG  GATGT
                                     ACCCAATT    CCAGGTCT TCC  CTC  CTACA
                                           T  GA  A-
GAM63   348   FMO4   1   13036  NP_002013.1  3  209   CCAATGCATCTT   CC A    -           4  A  c  c
                                     CTACCCTGCTAC GGT  AG TGGGG AGAAGATGT
                                     CTCAGTGA    CCA  TC GTCCC TCTTCTACG
                                           -- -    A
GAM63   348   FREQ   1   12692  NP_055101.2  3  982   CGCATCCTTGTT   T AGAT     ----        4  A  c  c
                                     CTCCCCTGGGTC GG CC    GGGGAGAA    GATGT
                                     CGTAACAT    CC GG    CCCCTCTT    CTACG
                                           T  GT--       GTTC
GAM63   348   FTL    1   15882  NP_000137.2  5  110   CGGGACCATCTT   TCC     G-          4  A  c  c
                                     CTCGGCCATCTC GG   AGATGG  GAGAAGATG
                                     CTGCTTCT    CC   TCTACC  CTCTTCTAC
                                           ---     GG
GAM63   348   FYCO1  1   19663  NP_078789.1  3  1830  CTCAATCATCTT    CAGATG             4  A  c
c
                                     CTCCTGGCCAAG GGTC     GGGAGAAGATG
                                     GCTCTGAC    CCGG     TCCTCTTCTAC
                                           ------
GAM63   348   GAB2   1   7245   NP_036428.1  3  3444  CAGAGTTCTTCC          --    TG      4  A  c  c
                                     TTCCCCATCTGG GGTCCAGATGGGGA  GAAGA
                                     GCCTTCAT    CCGGGTCTACCCCT  CTTCT
                                                 TC    TG
GAM63   348   GAB2   1   7245   NP_536739.1  3  3444  CAGAGTTCTTCC          --    TG      4  A  c  c
                                     TTCCCCATCTGG GGTCCAGATGGGGA  GAAGA
                                     GCCTTCAT    CCGGGTCTACCCCT  CTTCT
                                                 TC    TG
GAM63   348   GABBR1 1   19441  NP_001461.1  3  1083  CACAATCATCTT   TC  ATG-            4  A  c
c
                                     CTCCCAAGACTG GG  CAG   GGGAGAAGATG
                                     CTCCCTTT    CC  GTC   CCCTCTTCTAC
                                           TC   AGAA
GAM63   348   GABBR1 1   19441  NP_068703.1  3  1083  CACAATCATCTT   TC  ATG-            4  A  c
c
                                     CTCCCAAGACTG GG  CAG   GGGAGAAGATG
```

CTCCCTTT CC GTC CCCTCTTCTAC
TC AGAA
GAM63 348 GABBR1 1 19441 NP_068704.1 3 1083 CACAATCATCTT TC ATG- 4 A c c
CTCCCAAGACTG GG CAG GGGAGAAGATG
CTCCCTTT CC GTC CCCTCTTCTAC
TC AGAA
GAM63 348 GABBR1 1 19441 NP_068705.1 3 2080 CACAATCATCTT TC ATG- 4 A c c
CTCCCAAGACTG GG CAG GGGAGAAGATG
CTCCCTTT CC GTC CCCTCTTCTAC
TC AGAA
GAM63 348 GATA4 1 980 NP_002043.1 3 634 AGCTGGCAACTT - AGAT A 4 A c c
CTCCCCCAGGTG GGT CC GGGGAGAAG TGT
CCTTCCCC CCG GG CCCCTCTTC ACG
T AC-- A
GAM63 348 GBF1 2 2843 NP_004184.1 5 104 GGCTCCTTCTCT C- G TG 4 A c c
TCTCCCATCTGC GGT CAGATGGG AGAAGA
TACCAGAG CCA GTCTACCC TCTTCT
TC - CT
GAM63 348 GBF1 2 12139 NP_004184.1 5 104 GCTCCTTCTCTT C- G TG 4 A c c
CTCCCATCTGCT GGT CAGATGGG AGAAGA
ACCAGAGC CCA GTCTACCC TCTTCT
TC - CT
GAM63 348 GENX-34 1 3554 NP_003934.1 3 928 CTCCCACTTCTT CCA- T T 4 A c c
14 CTCCCCTCCCCC GGT GA GGGGAGAAGA GT
ACCGCATC CCA CT CCCCTCTTCT CA
CCCC - T
GAM63 348 GGTLA1 1 9172 NP_004112.1 5 256 TCTGTGCATCTT TC ----- 4 A c c
CTTGTCCATTCA GG CAGATGGG GAGAAGATGT
TCTGCCCA CC GTCTACTT TTCTTCTACG
C- ACCTG
GAM63 348 GPR56 1 11435 NP_005673.2 3 833 GGCTAGGTCCCT G A- G 4 A c c
CTGTCCATCTGG GGTCCAGATGGG AGA GAT
GCCTTTGT CCGGGTCTACCT TCT CTG
G CC G
GAM63 348 GRID1 1 15134 XP_043613.8 3 538 CAGGGACCTCTT AGATG T 4 A c c
CTCCCAGAGGAT GGTCC GGGAGAAGA GT
CCTGGAGC CTAGG CCCTCTTCT CA
AGA-- C
GAM63 348 GRM6 1 4232 NP_000834.1 5 61 CCCGAGCGCCTT AGA A 4 A c c
CTCCCCAGGACC GGTCC TGGGGAGAAG TGT
CCGGTGTC CCAGG ACCCCTCTTC GCG
--- C
GAM63 348 GYS1 1 14495 NP_002094.2 3 739 TCCTGTCTTTCT T -- - 4 A c c
GGCCCTTTCTGG GGTCCAGA GGGG AGAA GATG
ACCAGATC CCAGGTCT TCCC TCTT CTGT
T GG T
GAM63 348 HDAC7A 1 13926 NP_056216.1 3 267 CGAGAACAGATT GAT---- GA 4 A c c

CTCCCCTCCAGT GGTCCA GGGGAGAA TGT
ATGGGCCC CCGGGT CCCCTCTT ACA
ATGACCT AG

GAM63 348 HDAC7A 1 13926 NP_057680.2 3 267 CGAGAACAGATT GAT---- GA 4 A c c

CTCCCCTCCAGT GGTCCA GGGGAGAA TGT
ATGGGCCC CCGGGT CCCCTCTT ACA
ATGACCT AG

GAM63 348 HEMK 1 13927 NP_057257.1 3 4226 AGACAGCCTCTT AGAT T 4 A c c

CTCCTCTGGGGC GGTCC GGGGAGAAGA GT
CTCAAGAA CCGGG CTCCTCTTCT CG
GT-- C

GAM63 348 HH114 1 14866 NP_115888.1 5 149 GCTGAGCATCTT CCAGATG 4 A c c

CTCCCAGGAGTA GGT GGGAGAAGATGT
CCAGAAAC CCA CCCTCTTCTACG
TGAGGA-

GAM63 348 HIF3A 1 11103 NP_690007.1 3 27 TGGCCGGCTCCT TC A TG 4 A c c

CTCCCCATCTGC GG CAGATGGGGAGA GA
CTTCTCCT CC GTCTACCCCTCT CT
-- C CG

GAM63 348 HIVEP3 1 11510 NP_078779.1 3 102 TCCCACTTCCTC TC A---- A 4 A c c

AGCCCCATCTGT GG CAGATGGGG GAAG TG
CCCTCCAT CC GTCTACCCC CTTC AC
CT GACTC -

GAM63 348 HNRPDL 1 17189 NP_005454.1 3 590 AGGCTTCATCTT - -- 4 A c c

CTCCCTGTAACT GGTC CAG ATGGGGAGAAGATG
GAGATTTC TTAG GTC TGTCCCTCTTCTAC
A AA

GAM63 348 HNRPDL 1 17189 NP_112740.1 3 485 AGGCTTCATCTT - -- 4 A c c

CTCCCTGTAACT GGTC CAG ATGGGGAGAAGATG
GAGATTTC TTAG GTC TGTCCCTCTTCTAC
A AA

GAM63 348 HOXA4 1 3176 NP_002132.2 3 96 CCTCATCCACCC AA--- 4 A b b

CTCCCCATCTGG GGTCCAGATGGGGAG GATG
ACCATAAT CCAGGTCTACCCCTC CTAC
CCCAC

GAM63 348 HPS6 1 15251 NP_079023.1 5 711 GTGGCCCACGTT - G GA 4 A c c

CTACTCATCTGG GG TCCAGATGGG AGAA TG
AGCCCAGG CC AGGTCTACTC TCTT AC
G A GC

GAM63 348 HSN44A4 1 15821 NP_056187.1 3 5 TAGCAACATCTT C- - GG 4 A c c
A CTCCGAGTCCTG GGT CAG AT GGAGAAGATGT
CAGCCAGC CCG GTC TG CCTCTTCTACA
AC C AG

GAM63 348 HSPC065 1 4438 NP_054876.2 3 639 CTTTACATCCTT C --- - 4 A c c

CTCCCTAACATC GGTC AGATG GGGAGAAG ATGT
TAGACTAT TCAG TCTAC CCCTCTTC TACA
A AAT C

GAM63 348 IAN4L1 1 4785 NP_060854.2 3 16 TCTTTCATTACA TGGG GA 4 A c c
TTTAATCTCTGG GGTCCAGA GA AGATGT
ACCCTGGA CCAGGTCT CT TTTACA
---- AA
GAM63 348 IDH3G 1 7580 NP_777358.1 3 78 TGGCCCCATCTT - AT- -- 4 A c c
CTGGCCCTTAGC GGT CCAG GGGG AGAAGATG
TGGTGCCA CCG GGTC TCCC TCTTCTAC
T GAT GG
GAM63 348 IGSF9 1 2016 NP_065840.1 5 143 ACATCCCTTGGC ------ AA 4 A c c
CCCTCCATCTGG GGTCCAGATGGGG AG GATGT
GCTCCTGT TCGGGTCTACCTC TC CTACA
CCCGGT C-
GAM63 348 IL17B 1 5717 NP_055258.1 3 14 CACCTGCATCTT T A GG 4 A c c
CTGATCACCTGG GG CCAG TGG AGAAGATGT
CCCAGAAG CC GGTC ACT TCTTCTACG
C C AG
GAM63 348 IL2RG 1 3947 NP_000197.1 3 218 CATGTTTTTCTT T -- TG 4 A c c
CTCCCTCAGTCT GG CCAGAT GGGGAGAAGA
GGCCCTTC CC GGTCTG TCCCTCTTCT
C AC TT
GAM63 348 ILF3 1 6170 NP_036350.2 3 53 CTTCTGCACTTA CA-- - A 4 A c c
CTCCCCATCAGA GGTC GATGGGGAG AAG TGT
AGATCGAG CTAG CTACCCCTC TTC ACG
AAGA A -
GAM63 348 IRF2 1 17355 NP_002190.1 5 5 CTCCTTGTTTTG G GG - 4 A c c
CTTTCGATCTGG GGTCCAGAT G AG AAGATG
ACTGTTCT TCAGGTCTA C TC TTTTGT
G TT G
GAM63 348 ISL2 1 3035 NP_665804.1 3 330 CGCCCCACCTGT C GA- A 4 A c c
GTCCCCATCTCG GGTC AGATGGGGA AG TG
GCCGGCCC CCGG TCTACCCCT TC AC
C GTG C
GAM63 348 ITIH1 1 18461 NP_002206.1 3 13 CCCCGACATCTT T T G- 4 A b b
CTGGCCCTCTGG GG CCAGA GGG AGAAGATGT
CCAGCACG CC GGTCT CCC TCTTCTACA
- - GG
GAM63 348 ITPKB 1 14689 NP_002212.1 3 2245 GCCACTCGCTTC T -- A AT- 4 A c c
CCTGCCATCTGG GG CCAGATGG GG GAAG GT
CCCTTCCC CC GGTCTACC CC CTTC CA
C GT - GCT
GAM63 348 JTB 1 4192 NP_006685.1 3 139 TTTCCCCATCTT CA T 4 A c c
CTTCTTTCAGAT GGTC GA GGGGAGAAGATG
CATTAATG CTAG CT TTCTTCTTCTAC
A- -
GAM63 348 K5B 1 9971 NP_775487.1 5 63 TGCCATGTCTCT AG- - 4 A c c
CTCCCCATGCCG GGTCC ATGGGGAGA AGATGT
GGCCC CCGGG TACCCCTCT TCTGTA
CCG C
GAM63 348 KCNA6 1 14965 NP_002226.1 3 729 CTACATTTAGTT TC - --- 4 A c c
CTCCCCACTCTG GG CAGA TGGGGAGAA GATGT

ATCCCCTG CC GTCT ACCCCTCTT TTACA
TA C GAT

GAM63 348 KCNJ1 1 16832 NP_722450.1 5 215 TACTGTGCCTTC - - ATG 4 A c c
ATCCCCATCCTG GGTCCAG ATGGGGA GAAG
GGCCCTGA CCGGGTC TACCCCT CTTC
C A CGT

GAM63 348 KCNJ1 1 16832 NP_722451.1 5 348 TACTGTGCCTTC - - ATG 4 A c c
ATCCCCATCCTG GGTCCAG ATGGGGA GAAG
GGCCCTGA CCGGGTC TACCCCT CTTC
C A CGT

GAM63 348 KCNT1 1 10138 XP_029962.2 3 2747 GAGCCACGTCTT - A T - 4 A c c
CTCCACCTCGGA GG TCC GA GG GGAGAAGATGT
GCCCCACG CC AGG CT CC CCTCTTCTGCA
G - - A

GAM63 348 KIAA006 1 17332 NP_055691.1 3 1739 GCGTTATATCTT T A GG 4 A c c
3 CTCAGCAACTGG GG CCAG TG GAGAAGATGT
CCGCAGTC CC GGTC AC CTCTTCTATA
- A GA

GAM63 348 KIAA021 1 3254 XP_040265.4 5 19 AGCATTACACTT - GATG A 4 A c c
7 CTCCCAGTGGAG GG TCCA GGGAGAAG TGT
CCCATGAC CC AGGT CCCTCTTC ACA
G GA-- -

GAM63 348 KIAA022 1 16188 XP_027236.1 3 3437 GAAGTAAATCTT TC ----- G 4 A c c
7 CTCCCTACCCCG GG CAGATGGGG AGAAGAT
TCTGCCAG CC GTCTGCCCC TCTTCTA
-- ATCCC A

GAM63 348 KIAA023 1 10118 XP_291106.1 3 2628 AATCAGCGGCTC CC A A 4 A c c
2 CTCCCCATCTCA GGT AGATGGGGAG AG TGT
CCCCCAGC CCA TCTACCCCTC TC GCG
C- C G

GAM63 348 KIAA025 1 16597 XP_034905.1 3 3252 TACAGACATCTT TCCA - ---- 4 A c c
6 CCTCCTCCCTCA GG GATG GGGA GAAGATGT
TCCCTTCC CC CTAC CCCT CTTCTACA
TTCC T CCTC

GAM63 348 KIAA025 1 15208 NP_055600.1 3 1379 GTTTCTGTCTTT GAT - 4 A c c
8 CTCCCCTGGGCT GGTCCA GGGGAGAA GATG
CCTGTCTC TCGGGT CCCCTCTT CTGT
--- T

GAM63 348 KIAA029 1 14490 NP_055514.1 3 1285 AGACCTCAGCTT C TG A 4 A c c
6 CTCCCTCTGAAC GGT CAGA GGGAGAAG TG
TTCAAGTC TCA GTCT CCCTCTTC AC
A -- G

GAM63 348 KIAA041 1 15657 XP_166527.2 3 52 GGTGCCAGCCTT G - GA A- 4 A c c
5 CTCCCCAGTGAG G TC CA TGGGGAGAAG TG
AACAGTTT C AG GT ACCCCTCTTC AC
A A G- CG

GAM63 348 KIAA042 1 15166 NP_055587.1 3 305 CCCGCCTCTCCC CA A-- T 4 A c c
7 CTCCCCATCAGA GGTC GATGGGGAG AGA GT

CCCATCCC CCAG CTACCCCTC TCT CG
A- CCC C

GAM63 348 KIAA045 1 12861 NP_055453.1 5 1859 CCTGCCGTCTAT TC GA - 4 A c c
0 CCACCCATCTGT GG CAGATGGG GA AGATG
TCCTCGTC CC GTCTACCC CT TCTGC
TT AC A

GAM63 348 KIAA047 1 3805 XP_290898.1 5 171 TAGAGACGGGGT T - AGA 4 A c c
2 CTCCCCATATTG GG CCAG ATGGGGAGA TGT
GCCAGGCT CC GGTT TACCCCTCT GCA
- A GGG

GAM63 348 KIAA047 1 19144 NP_055679.1 3 2500 TCATTTCATTTT TC- G 4 A c c
5 ATTCCCATCTGT GG CAGATGGGGA AAGATG
TTTCAAAC CT GTCTACCCTT TTTTAC
TTT A

GAM63 348 KIAA054 1 6128 XP_032278.3 3 1739 TGATGCCATCTT TCCA - 4 A c c
5 CTCCCCCATCCC GG GATGGGG AGAAGATG
CTTCTCTG CC CTACCCC TCTTCTAC
C--- C

GAM63 348 KIAA059 1 13331 XP_085127.6 5 1198 CTCTGCCATCTT A---- T 4 A c c
9 CTCTCCTTCCCA GGTCC GA GGGGAGAAGATG
AAGGATCT CTAGG CT CCTCTCTTCTAC
AAACC T

GAM63 348 KIAA066 1 16391 NP_055594.1 5 18 CGCGGCCATTTC C AGA 4 A c c
9 AGCCCCATCTTG GGTC AGATGGGG AGATG
GCCCAGCG CCGG TCTACCCC TTTAC
T GAC

GAM63 348 KIAA067 1 11139 NP_055858.1 3 783 GCCTCCCAACTT CAGA A 4 A c c
6 CTCCCCAGGCCA GGTC TGGGGAGAAG TG
AGTATGGG CCGG ACCCCTCTTC AC
---- A

GAM63 348 KIAA071 1 12253 NP_055686.1 3 379 TGCAGCTGTCTT - A-- 4 A c c
0 CTCCTCAGTGCT GGT CCAG TGGGGAGAAGATG
GGCGCTCT TCG GGTC ACTCCTCTTCTGT
C GTG

GAM63 348 KIAA076 1 16026 XP_027105.2 3 1909 GGCCACACCTCT AGA - A 4 A c c
7 CTCCCCAGGGCC GGTCC TGGGGAGA AG TGT
CGGCAGTG CCGGG ACCCCTCT TC ACA
--- C C

GAM63 348 KIAA077 1 13455 NP_055505.1 3 2843 GTTTATTATCTT CAGATGG 4 A c c
3 CTCCACGACCTC GGTC GGAGAAGATG
ACCTATAC CCAG CCTCTTCTAT
CA-----

GAM63 348 KIAA082 1 11299 XP_027906.5 3 370 AGAGAATATATT C G 4 A c c
5 TTTCCCATCTGT GGT CAGATGGGGAGAA ATGT
ATTGTTCT TTA GTCTACCCTTTTT TATA
T A

GAM63 348 KIAA088 1 1863 NP_056192.1 3 1378 CCTCAGCAGCTT TCC A 4 A c c
9 CTCCCTGTCTTC GG AGATGGGGAGAAG TGT
CTCTCCTC CC TCTGTCCCTCTTC ACG
T-- G
GAM63 348 KIAA088 1 1863 NP_689470.1 3 585 CCTCAGCAGCTT TCC A 4 A c c
9 CTCCCTGTCTTC GG AGATGGGGAGAAG TGT
CTCTCCTC CC TCTGTCCCTCTTC ACG
T-- G
GAM63 348 KIAA111 1 6397 XP_171233.1 3 1065 GACTCACATCTT GAT A 4 A c c
1 CACTCCTGGGCC GGTCCA GGGG GAAGATGT
TTTGCACT CCGGGT CCTC CTTCTACA
--- A
GAM63 348 KIAA111 1 17435 NP_055746.1 3 136 ACACCCCCACAT T GA 4 A c c
5 TCTCTCCTCTGG GGTCCAGA GGGGAGAA TG
ACCCCCAG CCAGGTCT CCTCTCTT AC
- AC
GAM63 348 KIAA119 1 19022 NP_065765.1 3 1606 TGGGAACATCTT C- GGGA- 4 A c
c
8 CAATGACATCTG GGT CAGATG GAAGATGT
CAACCATT CCA GTCTAC CTTCTACA
AC AGTAA
GAM63 348 KIAA120 1 12583 XP_049683.4 3 533 TTTCTGCACTTT CC A A 4 A c c
3 CGCCCCATCTAC GGT AGATGGGG GAAG TGT
CAGTCTTT CCA TCTACCCC CTTT ACG
-- G C
GAM63 348 KIAA121 1 6250 XP_172801.1 3 963 TTGAAACATCTT AGAT ------ 4 A c c
0 CCCTGTGTCCCT GGTCC GGGGA GAAGATGT
GGGGGCCC CCGGG TCCCT CTTCTACA
GG-- GTGTCC
GAM63 348 KIAA131 1 5129 NP_065820.1 3 33 CCATGGAATCTT C ---- G 4 A c c
8 CTCCTGTGATAT GGTC AGATG GGGAGAAGAT
CTGACTCG TCAG TCTAT TCCTCTTCTA
- AGTG A
GAM63 348 KIAA139 1 5415 XP_032054.2 3 1484 AGAATGCCTCTT AGA - T 4 A c c
6 CTCCTCCAAAGG GGTCC TGG GGAGAAGA GT
ATCACAAC CTAGG ACC CCTCTTCT CG
AA- T C
GAM63 348 KIAA141 1 2332 XP_098762.3 3 76 GAAACATTCCTT A --- -- 4 A b b
6 CTCCCGGACAGC GGTCCAG TG GGGAGAAG ATGT
TGGACCCA CCAGGTC AC CCCTCTTC TACA
G AGG CT
GAM63 348 KIAA149 1 18298 XP_034415.1 3 156 CTGTGAGATCTT TC -- - G 4 A c c
3 CTCCACCTAGTC GG CAGAT GG GGAGAAGAT
TGCCCTAA CC GTCTG CC CCTCTTCTA
C- AT A G
GAM63 348 KIAA151 1 2587 XP_046581.5 3 1327 GCTAAACGTTTG TC -- A 4 A c c
1 TTCCCCATCTCT GG CAGA TGGGGAG AGATGT
GTGCCTCC CC GTCT ACCCCTT TTTGCA
GT CT G
GAM63 348 KIAA153 1 8145 XP_042661.5 3 670 ACCGAACATCTT T A ----- 4 A c c

0 CTCGTGGGCTTA GG CCAG TGGG GAGAAGATGT
CTGGCCAT CC GGTC ATTC CTCTTCTACA
- - GGGTG

GAM63 348 KIAA165 1 15785 XP_038022.1 3 5219 TGCCTGGCTCTT ATGG TG 4 A c c
6 CTCCACTGGACC GGTCCAG GGAGAAGA
AGGGAGCT CCAGGTC CCTCTTCT
A--- CG

GAM63 348 KIAA167 1 8923 XP_290462.1 3 1900 ATAATGCATCTT CC- AT 4 A c c
4 CTTCCCTCCTTC GGT AG GGGGAGAAGATGT
TACTGTAC TCA TC CCCTTCTTCTACG
TCT CT

GAM63 348 KIAA175 1 6431 XP_036115.3 3 51 GGCCCAGATCTT AGA - G 4 A c c
3 CTCACCTAGGAC GGTCC TGGG GAGAAGAT
TTTTTAAA TCAGG ATCC CTCTTCTA
--- A G

GAM63 348 KIAA180 1 17427 NP_115810.1 3 928 TGCGCATTCCTT GATG -- 4 A c c
5 CTCCCTGGACTT GGTCCA GGGAGAAG ATGT
TACCTTAC TCAGGT CCCTCTTC TACG
---- CT

GAM63 348 KIAA192 1 17296 XP_085210.1 5 2989 ACACTGCATATG T GAAG 4 A c c
0 GTCCCCATCTGG GG CCAGATGGGGA ATGT
CCTGAGAG CC GGTCTACCCCT TACG
- GGTA

GAM63 348 KIAA202 1 16952 XP_290463.1 3 100 CAAAAGCTTCTT C AT--- T 4 A c c
0 CTCCCCCAGTGC GGTC AG GGGGAGAAGA GT
TGATCTTG CTAG TC CCCCTCTTCT CG
- GTGAC T

GAM63 348 KIF3C 1 10471 NP_002245.2 3 422 AACCTCCATCTT G--- -- A - 4 A c c
CTCCCACACTGA GTC CAG TG GGGAGAAGATG
TGGCGAGC CGG GTC AC CCCTCTTCTAC
CGAG TA - A

GAM63 348 KIRREL 1 6373 NP_060710.1 3 855 CACAAGCCTCCT TC - A T 4 A c c
CTCCCCAGTCTG GG CAGA TGGGGAGA GA GT
CCCCACTT CC GTCT ACCCCTCT CT CG
CC G C C

GAM63 348 KLF2 1 446 NP_057354.1 3 282 AAGTGGCATCTT GT AGA - 4 A c c
CTCTCCCACCGG G CC TGGG GAGAAGATGT
GTCTACAC C GG ACCC CTCTTCTACG
TG CC- T

GAM63 348 KPNA1 1 8053 NP_002255.1 3 1144 AATAACCATCTT CAG GG 4 A c c
CTCAACATGACC GGTC ATG GAGAAGATG
TGCTTAAC CCAG TAC CTCTTCTAC
--- AA

GAM63 348 KPNB2 1 10216 NP_002261.2 3 220 GTTGGGAAACGT - GGGAG 4 A c c
TTTAACATCTGG GG TCCAGATG AAGATGT
AGCCTTTG CC AGGTCTAC TTTTGCA
G AA---

GAM63 348 KPNB2 1 10216 NP_694858.1 3 220 GTTGGGAAACGT - GGGAG 4 A c c
TTTAACATCTGG GG TCCAGATG AAGATGT
AGCCTTTG CC AGGTCTAC TTTTGCA
G AA---
GAM63 3485 KRTAP1-1 20046 NP_114163.1 3 77 TGTTCATCCCTT T - A- A- 4 A c c
GACCACCTCTGG GGTCCAGA GG GG GA GATG
ACCACTAA CCAGGTCT CC CC TT CTAC
- A AG CC
GAM63 3481 KRTAP3-1 6804 NP_114164.1 3 63 CCCAATGTCCTC GG- A 4 A c c
TGCACCATCTGG GGTCCAGATGG AGA GATGT
GCTTCAGC TCGGGTCTACC TCT CTGTA
ACG C
GAM63 348 LACE1 1 5643 NP_660358.2 3 123 TTAATTATGCAC T GA A 4 A c c
TTTGTCCTCTGG GGTCCAGA GGG GAAG TGT
ACCATTTT CCAGGTCT CCT TTTC ACG
- G- -
GAM63 348 LAMB1 1 12728 NP_002282.1 5 285 GGCGGGCGTCTT TC T --- 4 A c c
CTCCACTCCTCT GG CAGA GG GGAGAAGATGT
GCCGCGTC CC GTCT CC CCTCTTCTGCG
-- - TCA
GAM63 348 LCHN 1 447 XP_098615.2 3 4196 CCCTCCTGTCTT CCAG 4 A c c
CTCCCCGTACCT GGT ATGGGGAGAAGATG
TGTAGTTA CCA TGCCCCTCTTCTGT

GAM63 348 LEREPO4 1 12248 NP_060941.1 3 258 TCCCTACATCTT T T--- 4 A c c
CTCTTCTGACTT GG CCAGA GGGGAGAAGATGT
TGGCTACA TC GGTTT CTTCTCTTCTACA
- CAGT
GAM63 34876 LOC1124 1 13020 NP_660282.1 5 149 GCTATTTCCATC AG AA 4 A c c
CTCCCCATAGGG GGTCC ATGGGGAG GATG
GCTCTCTC TCGGG TACCCCTC CTAC
GA --
GAM63 34840 LOC1128 1 3419 NP_542397.1 3 883 AGACTTTCATTA AA 4 A c c
TTTCTCATCTGG GGTCCAGATGGGGAG GATG
ATTACCAG TTAGGTCTACTCTTT TTAC
A-
GAM63 34809 LOC1187 1 10613 XP_058338.2 3 1147 CTTCTTGGTCTT TG G 4 A c c
CTCCTTCTGGGC GGTCCAGA GGGAGAAGAT
CTCATGGC CCGGGTCT TCCTCTTCTG
-- G
GAM63 348 LOC1203 1 15763 XP_071712.3 5 355 TTGCACCATCTT AGA GGG 4 A c c
76 CTGCAGGACTGT GGTCC TG AGAAGATG
ATTTTGAG TCAGG AC TCTTCTAC
--- G--
GAM63 34858 LOC1222 1 14397 NP_660291.1 5 7 GAGAACATCCTT GG---- A - - 4 A c c
CTCCCTCAGCTG TCCAG TG GGGAGAAG ATGT
GAGGGAGC AGGTC AC CCCTCTTC TACA
CGAGGG G T C

GAM63 348 LOC1233 1 1872 XP_063609.1 3 229 GTGCCACATCTT TCC A A 4 A c c
46 CCCTCCACTCCC GG AG TGGGG GAAGATGT
CTGCTTAA CC TC ACCTC CTTCTACA
CC- - C
GAM63 348 LOC1242 1 3920 NP_653205.2 5 68 AAGGGACGTCTT CA - --- 4 A c c
45 CTCCACGCCGCT GGTC GA TGG GGAGAAGATGT
CCGACTCC TCAG CT GCC CCTCTTCTGCA
C- C GCA
GAM63 348 LOC1300 1 8538 XP_072228.2 3 3747 GAGCACGTATTT CC- T - 4 A c c
74 CTCCCCTCTAGT GGT AGA GGGGAGAAG ATGT
ACCTCTGC CCA TCT CCCCTCTTT TGCA
TGA - A
GAM63 348 LOC1306 1 11552 XP_065813.2 3 340 CCCGACCATCTT --- ATG-- 4 A c c
44 CTCCTATTTCCT GGT CCAG GGGAGAAGATG
GGGGAGCC CCG GGTC TCCTCTTCTAC
AGG CTTTA
GAM63 348 LOC1309 1 2189 XP_059481.2 5 21 TGCTGCCATCTT T GA- G 4 A c c
16 CTCCGCGCTATG GG CCA TG GGAGAAGATG
GCTGCGTT TC GGT GC CCTCTTCTAC
- ATC G
GAM63 348 LOC1322 1 19785 XP_072302.1 5 670 TGCATTCTACTG G - -- A - 4 A c c
35 TCACCCATCTGG G TCCAGATGGG GA G AGA TGT
AGCAGCTT C AGGTCTACCC CT C TCT ACG
G A GT A T
GAM63 348 LOC1329 2 3612 NP_660307.1 3 30 ACATTCCTTCCT G ATG 4 A c c
48 TCTCCCATCTGG GGTCCAGATGGG AGAAG
ATTCCTAA TTAGGTCTACCC TCTTC
- CTT
GAM63 348 LOC1329 2 7690 NP_660307.1 3 30 CATTCCTTCCTT G ATG 4 A c c
48 CTCCCATCTGGA GGTCCAGATGGG AGAAG
TTCCTAAG TTAGGTCTACCC TCTTC
- CTT
GAM63 348 LOC1392 2 1459 XP_208439.1 3 2326 CTCTGCTGTCAG GT AA 4 A c c
01 CTTCCCATCTGG G CCAGATGGGGAG GATG
CTCAGCAT C GGTCTACCCTTC CTGT
TC GA
GAM63 348 LOC1392 2 11945 XP_208439.1 3 2187 TTTCCTTATCTT - GAT 4 A c c
01 CTCCCCCATGGC GGT CCA GGGGAGAAGATG
ATCCTAAA CTA GGT CCCCTCTTCTAT
C AC-
GAM63 348 LOC1444 1 10729 NP_612482.1 5 39 CCGTCTCATCTT C G 4 A b b
67 CTCTCATCTGAT GGTC AGATGGG AGAAGATG
CACTTCAT CTAG TCTACTC TCTTCTAC
- -
GAM63 348 LOC1446 1 19348 XP_096648.1 3 1286 GGTCCTGCACTT GA-- A 4 A c c
67 CTCCCCAGAGGT GGTCCA TGGGGAGAAG TGT
GGGCCCTC CCGGGT ACCCCTCTTC ACG

GGAG -

GAM63 348 LOC1447 1 10034 XP_096669.1 3 1 TGGACACCTTCG T--- - A 4 A c c
05 TCTCCATCTGGT GG CCAGATGGGGA GAAG TGT
GGTCCAGC CC GGTCTACCTCT CTTC ACA
TGGT G C

GAM63 348 LOC1465 1 2282 NP_631909.1 3 284 GGGCTACAGATG T G AGA- 4 A c
c
62 TCTGCTCTCTGG GGTCCAGA GGG AGA TGT
ACCCCACG CCAGGTCT CTC TCT ACA
- G GTAG

GAM63 348 LOC1471 1 2993 XP_085714.2 5 1252 GAACCACATCTT AGATGG 4 A c
c
23 CTTCAGGGATCG GGTCC GGAGAAGATGT
ATATGGAG CTAGG CTTCTTCTACA
GA----

GAM63 348 LOC1480 1 4395 XP_097380.1 3 47 CCAGCCCATCTT C - TG- 4 A c c
56 CTCCCGCTTCTT GGT CA GA GGGAGAAGATG
GCGCTCCT TCG GT CT CCCTCTTCTAC
C T TCG

GAM63 348 LOC1494 1 3852 XP_086546.1 3 8 CAGGGACCACTT T- TG A 4 A c c
66 CTCCCTCTGGCT GG CCAGA GGGAGAAG TG
CCCATCTT CC GGTCT CCCTCTTC AC
TC -- -

GAM63 348 LOC1494 1 8470 XP_086536.1 5 706 CCCGGGAGCATC T - AGAA 4 A c
c
78 ACCGCTTTCTGG GGTCCAGA GG GG GATGT
ACCTGTCC CCAGGTCT TC CC CTACG
T G A---

GAM63 348 LOC1500 1 15062 XP_097793.1 5 387 ACATCTCATCTT GA -- 4 A c c
35 CTGTCCTCAGAT GGTCCA TGGGGA GAAGATG
GGATTTAC TTAGGT ACTCCT CTTCTAC
AG GT

GAM63 348 LOC1500 1 10173 XP_097797.1 5 66 TACTCACATCTT CCAGA -- 4 A c c
54 CATTCTCTAACC GGT TGGGGA GAAGATGT
ACTCTATT CCA ATCTCT CTTCTACA
----- TA

GAM63 348 LOC1503 1 18710 XP_086905.1 3 180 ATCACTGACAGC TG AAGA 4 A c
c
83 AGCTCCTTCTGG GGTCCAGA GGGAG TGT
ACCCAGTC CCAGGTCT TCCTC ACA
-- GACG

GAM63 348 LOC1514 1 8600 XP_098063.1 3 664 ACCTGGCATCTT GG -- ---- - 4 A c c
75 CTGCCCTGTTCA TCC AGATG GGG AGAAGATGT
TCTACGGA AGG TCTAC CCC TCTTCTACG
-- CA TTGT G

GAM63 348 LOC1516 1 8648 XP_098096.5 5 564 CGTGTATATTTT C GAT 4 A c c
23 CTCCCCCAATGA GGT CA GGGGAGAAGATGT
ATCAATTG CTA GT CCCCTCTTTTATA
A AAC

GAM63 348 LOC1537 1 14953 XP_098419.1 5 109 GACATCAAAGCA TGGG AA 4 A c c
11 TCAGCTCTCTGG GGTCCAGA GAG GATGT
ACCTGGGA CCAGGTCT CTC CTACG
---- GA
GAM63 348 LOC1538 1 16220 XP_087796.1 5 264 TACTCCACCTTC GGA- A 4 A c c
94 GGTGCCATCTGG GGTCCAGATGG GAAG TG
ACTCCCAC TCAGGTCTACC CTTC AC
GTGG C
GAM63 348 LOC1572 1 8648 XP_098741.2 3 221 CGTGTATATTTT C GAT 4 A c c
78 CTCCCCCAATGA GGT CA GGGGAGAAGATGT
ATCAATTG CTA GT CCCCTCTTTTATA
A AAC
GAM63 348 LOC1579 1 3446 XP_098845.1 5 249 CTGTCATTTTGC G --- AG 4 A c c
31 CATTTCATCTGG G TCCAGATGG GG AAGATG
AGCTTTCA C AGGTCTACT CC TTTTAC
G TTA G-
GAM63 348 LOC1585 1 1153 XP_088606.1 5 1937 ACATTCTCATTT GGG ----- 4 A c c
63 CTAAACATCTGG GGTCCAGATG AGAA GATGT
ATCTGGGT CTAGGTCTAC TCTT TTACA
AAA TACTC
GAM63 348 LOC1587 1 17046 XP_088648.1 5 721 ATAAATTATCTT - A ---- 4 A c c
09 CTCTCTTTGTAT GGT CC GAT GGGGAGAAGATG
TGGGAACC CCA GG TTA TCTCTCTTCTAT
A G TGTT
GAM63 348 LOC1591 1 6485 XP_099028.1 5 955 CTGCAACATCTT CAGA - 4 A c c
21 CTCCTCCAGGAA GGTC TGG GGAGAAGATGT
GGCTTCCT TCGG ACC CCTCTTCTACA
AAGG T
GAM63 348 LOC1599 1 5201 XP_089960.6 5 261 TGGAAACATCTT CAGA 4 A c c
63 CTTCCTGAGACC GGTC TGGGGAGAAGATGT
TCGTTGAA CCAG GTCCTTCTTCTACA
A---
GAM63 348 LOC1608 1 4898 XP_090522.2 5 884 TGCCAACATCTT T A GG - 4 A c c
24 CATCACAGTTGG GG CCAG TG GA GAAGATGT
CTGTTAGG TC GGTT AC CT CTTCTACA
- G A- A
GAM63 348 LOC1964 1 19172 XP_113722.2 5 99 TTAGTGCATCTT AGATGG 4 A c c
46 CTCCAAGAAGGG GGTCC GGAGAAGATGT
CCGTTCAT CCGGG CCTCTTCTACG
AAGAA-
GAM63 348 LOC1969 1 405 XP_113796.1 3 1566 TCTCTTCATGCT TCCA AG 4 A c c
96 CTCCCCATCCCA GG GATGGGGAGA ATG
GTTTTTAG CC CTACCCCTCT TAC
---- CG
GAM63 348 LOC1998 1 19093 XP_114028.1 5 5 CCACGTCAACTT C ATG A 4 A c c
13 CTCCCACCTGAC GGTC AG GGGAGAAG TG

CACAAAGG CCAG TC CCCTCTTC AC
- CA- A

GAM63 348 LOC2000 1 19405 XP_117174.2 5 831 CCTCTACATCTT -- GG- A 4 A c c
10 CACCAAGATCTC GGTCC AGAT GG GAAGATGT
GGGATCCT CTAGG TCTA CC CTTCTACA
GC GAA A

GAM63 348 LOC2007 1 7136 XP_114286.1 3 86 TACTCTCATCTT TCC-- AT 4 A c c
34 CTCCCCCGCTCC GG AG GGGGAGAAGATG
CTTCCACT CC TC CCCCTCTTCTAC
TTCCC GC

GAM63 348 LOC2199 1 13636 XP_166197.1 3 87 CCTTCCCAGTTT CCAGA A 4 A c
c
18 CTCCCCAACCTC GGT TGGGGAGAAG TG
CCCTTTTC CCA ACCCCTCTTT AC
----- G

GAM63 348 LOC2200 1 13636 XP_167848.1 3 87 CCTTCCCAGTTT CCAGA A 4 A c
c
71 CTCCCCAACCTC GGT TGGGGAGAAG TG
CCCTTTTC CCA ACCCCTCTTT AC
----- G

GAM63 348 LOC2210 1 560 NP_660356.1 5 98 GTCCGTTGTCTT -- G- 4 A c c
02 CTCCAGCATCCT GGTCCA GATG GGAGAAGATG
TGGGCCCA CCGGGT CTAC CCTCTTCTGT
TC GA

GAM63 348 LOC2214 1 2939 XP_168136.1 3 1826 GGAAGCCCATTC T --- AA 4 A c c
95 CTCCCCATCAGT GG CCA GATGGGGAG GATG
TGGCCTCT CC GGT CTACCCCTC TTAC
- TGA C-

GAM63 348 LOC2216 1 11468 XP_168131.1 3 51 AAAGCATTCATT G---- - -- 4 A c c
63 CTCCCCATTTGT GTC CAGATGGGGAGAA GATGT
GACATTTG CAG GTTTACCCCTCTT TTACG
GTTTA T AC

GAM63 348 LOC2220 1 11030 XP_168371.1 3 1992 CCTGACCATCTT AGAT 4 A c c
31 CTCCTCCCAGGG GGTCC GGGGAGAAGATG
CCACAGCT CCGGG CTCCTCTTCTAC
ACC-

GAM63 348 LOC2220 2 11430 XP_166594.2 5 463 CCCAGACATCAC TG GG AA 4 A c
c
57 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA

GAM63 348 LOC2220 2 12029 XP_166594.2 3 1861 GCTTTGCATCTT ATGG- 4 A c c
57 CTCCAGGCCCTG GGTCCAG GGAGAAGATGT
GACTTCCT TCAGGTC CCTCTTCTACG
CCGGA

GAM63 348 LOC2226 1 14980 XP_167095.3 3 776 CTCATCTCTCTT A- T A 4 A c c
74 CTCCAGGACTCC GGTCC GA GGGGAGA GATG
TGCACTGA TCAGG CT CTTCTCT CTAC

AC - -

GAM63 348 LOC2545 1 19218 XP_172931.2 3 473 GGACCCCATAAT GT G AG 4 A c c

59 CTGCCCATCTGG G CCAGATGGG AGA ATG

GACTTGGC C GGTCTACCC TCT TAC

AG G AA

GAM63 348 LOC2557 1 1120 XP_171089.2 3 79 AATTCTCATCTT TCC T 4 A c c

43 CTCTCCTCTTCT GG AGA GGGGAGAAGATG

CCCTTTTA CC TCT CCTCTCTTCTAC

TCT -

GAM63 348 LOC2559 1 17165 XP_171083.2 5 583 CCCAAACATCAC TG GG AA 4 A c c

75 CTTTCATTCTGG GGTCCAGA G AG GATGT

ACCTACCA CCAGGTCT C TC CTACA

TA TT CA

GAM63 348 LOC2561 1 11964 XP_172187.1 3 435 CTCCTCCCTCTT - TGG TG 4 A c c

06 CTCCTCTGTGGC GGTC CAGA GGAGAAGA

CTGGGAGA CCGG GTCT CCTCTTCT

T --- CC

GAM63 348 LOC2829 1 12554 XP_212622.1 3 775 CTCGTCTCTCTT A- T A 4 A c c

59 CTCCAGGACTCC GGTCC GA GGGGAGA GATG

TGCACTGA TCAGG CT CTTCTCT CTGC

AC - -

GAM63 348 LOC2829 1 9105 XP_208460.1 3 191 CCCAACGTGATT TC -- G- 4 A c c

66 CTCCCCAGCTCT GG CAGA TGGGGAGAA ATGT

GAGTCTCT CT GTCT ACCCCTCTT TGCA

GA CG AG

GAM63 348 LOC2830 1 2411 XP_210887.2 5 1230 TCTGAATGTTTG -- - A - 4 A c c

99 TCCCCCATCTAG GG TCC AGATGGGG GA AGATGT

GATTCCAG CC AGG TCTACCCC CT TTTGTA

TT A - G

GAM63 348 LOC2831 1 13317 XP_208530.1 3 765 CTCTCTGGTCTT ATG G 4 A c c

58 CTCCCAGGCTGG GGTCCAG GGGAGAAGAT

ATCTGGGC CTAGGTC CCCTCTTCTG

GGA G

GAM63 348 LOC2831 1 1528 XP_210903.1 3 199 GCGCTGCATTTT TCC- T 4 A c c

77 CTCCCCTCTCCC GG AGA GGGGAGAAGATGT

TCCCTCCT CC TCT CCCCTCTTTTACG

TCCC -

GAM63 348 LOC2832 1 12802 NP_777600.1 3 657 TTAGCCACACTT AGAT A 4 A c c

32 CTCCCTTCAGGG GGTCC GGGGAGAAG TGT

GCTTCGGA TCGGG TCCCTCTTC ACA

GACT -

GAM63 348 LOC2832 1 8648 XP_210947.2 5 828 CGTGTATATTTT C GAT 4 A c c

43 CTCCCCCAATGA GGT CA GGGGAGAAGATGT

ATCAATTG CTA GT CCCCTCTTTTATA

A AAC

GAM63 348 LOC2833 1 13636 XP_208617.1 3 328 CCTTCCCAGTTT CCAGA A 4 A c c

24 CTCCCCAACCTC GGT TGGGGAGAAG TG
CCCTTTTC CCA ACCCCTCTTT AC
----- G
GAM63 348 LOC2833 1 10668 XP_208618.1 3 377 CGTGTATATTTT CAGAT 4 A c c

25 CTCCCCCAATGA GGTC GGGGAGAAGATGT
CTCAATTG TCAG CCCCTCTTTTATA
TAAC-
GAM63 348 LOC2833 1 3471 XP_211003.1 5 102 GGGAAACAACTT AGA A 4 A c c
64 CTCCCCAGGGGC GGTCC TGGGGAGAAG TGT
CCCTGGGA CCGGG ACCCCTCTTC ACA
G-- A
GAM63 348 LOC2833 1 10231 XP_211009.1 5 66 CCACGGCATCCC TCC AA 4 A c
c
89 CTCCCCATCTCC GG AGATGGGGAG GATGT
CCTTTGTC CC TCTACCCCTC CTACG
CC- CC
GAM63 348 LOC2835 1 12549 XP_211075.1 5 609 TCCCTGTCTTCT TCC -- 4 A c c
07 CTCCCCATTTTG GG AGATGGGGAGA AGATG
TCCTTTGC CC TTTACCCCTCT TCTGT
TGT CT
GAM63 348 LOC2835 1 12227 XP_210264.2 3 728 CTGTGCCGTCTT - TG 4 A c c
14 CTCCTGCTCTGG GGT CCAGA GGGAGAAGATG
AATCAAAG CTA GGTCT TCCTCTTCTGC
A CG
GAM63 348 LOC2837 1 10969 XP_208804.3 3 552 GTTTCTCATCTT TC A 4 A c c
06 CTCTCTACTGCC GG CAG TGGGGAGAAGATG
TCTGAGTT CC GTC ATCTCTCTTCTAC
-- -
GAM63 348 LOC2838 1 6589 XP_211243.1 3 55 AGCTGTCACCTT CC A 4 A c c
68 CTCCCTGTCTCA GGT AGATGGGGAGAAG TG
GCTGAGGG TCG TCTGTCCCTCTTC AC
AC C
GAM63 348 LOC2839 1 11030 XP_211259.2 3 301 CCTGACCATCTT AGAT 4 A c c
11 CTCCTCCCAGGG GGTCC GGGGAGAAGATG
CCACAGCT CCGGG CTCCTCTTCTAC
ACC-
GAM63 348 LOC2839 1 2373 XP_211273.1 5 4 ACCGACGTGTTT CAGAT - 4 A c c
50 CTCCCCGACCGT GGTC GGGGAGAAG ATGT
GGCTTTGC CCAG CCCCTCTTT TGCA
----- G
GAM63 348 LOC2840 1 15991 XP_211321.1 3 1363 AGGAGACATTGT GT A A 4 A c
c
74 CTCCCCAGTTGG G CCAG TGGGGAGA GATGT
TTCTGTCC C GGTT ACCCCTCT TTACA
TT G G
GAM63 348 LOC2841 1 12578 XP_211345.1 3 200 AGCCACATCCTC --- AA 4 A b b
34 CAGTCCATCTGG GGTCCAGATGG GGAG GATGT
ACTAGCAA TCAGGTCTACC CCTC CTACA
TGA --

GAM63 348 LOC2841 1 15364 XP_209032.1 3 1247 ACCACACATGGT T- A AG 4 A c c
35 CTCCCCACCTGG GG CCAG TGGGGAGA ATGT
TTTCAGCT CT GGTC ACCCCTCT TACA
TT C GG
GAM63 348 LOC2841 1 2686 XP_209060.2 3 1777 AGGGCGTCTCAT - AGA -- 4 A c c
86 CTCCCCACAGGC GGT CC TGGGGAGA AGATGT
ATCTGCTG CTA GG ACCCCTCT TCTGCG
C AC- AC
GAM63 348 LOC2841 1 11712 XP_211366.2 3 920 CTCCCCACCTGC ---- - A A 4 A c c
87 TACCCCATCTGC GGTCCA GATGGGG AG AG TG
TTGGGCCC CCGGGT CTACCCC TC TC AC
TCGT A G C
GAM63 348 LOC2843 1 16203 XP_209177.1 5 58 CCTCAACCTCTT CCAGA T 4 A c c
82 CTCCCCACAACC GGT TGGGGAGAAGA GT
CCAACCCC CCA ACCCCTCTTCT CA
AC--- C
GAM63 348 LOC2843 2 2616 XP_210786.1 5 51 CACCACTATCTC - A 4 A c c
94 TGTTCCATCTGG GGTCCAGATGGGG AGA GATG
GCTTATAT TCGGGTCTACCTT TCT CTAT
G -
GAM63 348 LOC2843 2 10139 XP_210786.1 3 585 CCCTTCCCATTT CC ------ A 4 A c c
94 CTCCCCACTTTC GGT AGA TGGGGAGA GATG
ATCTACCT CCA TCT ACCCCTCT TTAC
-- ACTTTC -
GAM63 348 LOC2844 1 8896 XP_211470.1 5 49 TCTCTTCGTCTT TC -- T 4 A c c
56 CTCCTCTTCCTT GG CA GA GGGGAGAAGATG
GTCCCCTC CC GT CT CTCCTCTTCTGC
CT TC T
GAM63 348 LOC2845 1 18870 XP_209277.2 5 1079 TACAAGCATCTT GATGG 4 A c c
85 CTCTGGCGTGGA GGTCCA GGAGAAGATGT
TCCGCTGC CTAGGT TCTCTTCTACG
GCGG-
GAM63 348 LOC2846 1 4694 XP_211591.1 3 246 GGTGCCCATCTT - C AT 4 A c c
73 CTCTCTCCTAGA GG TC AG GGGGAGAAGATG
GCCCATAC CC AG TC TCTCTCTTCTAC
G A C-
GAM63 348 LOC2846 1 13363 XP_209318.1 3 375 CTGGGACATCTT A -- A 4 A c c
78 CCCTTGGATCAG GGTCC GAT GGGG GAAGATGT
GATCCTTC CTAGG CTA TTCC CTTCTACA
A GG -
GAM63 348 LOC2847 1 11430 XP_294994.1 5 585 CCCAGACATCAC TG GG AA 4 A c c
01 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA
GAM63 348 LOC2848 1 14432 XP_211658.1 3 111 GCTCAGGCGCTT T ATG A 4 A c c

37 CTCCCACCTTGG GG CCAG GGGAGAAG TGT
CCTCCTGA CC GGTT CCCTCTTC GCG
- CCA -

GAM63 348 LOC2848 1 17073 XP_211683.1 5 252 CGAAAGCATCTT A-- -- 4 A c c
91 CTCCTTCCGTTC GGTCC GATGG GGAGAAGATGT
ACGGATTT TTAGG TTGCC CCTCTTCTACG
CAC TT

GAM63 348 LOC2849 1 12266 XP_211689.1 3 1049 GGGTGAGTCTGT T -- G 4 A c c
27 TTTCCTCTCTGG GGTCCAGA GGGGAGA AGAT
ACCTCAGT CCAGGTCT CTCCTTT TCTG
- TG A

GAM63 348 LOC2850 1 5397 XP_211742.1 3 1057 GATGAAGTTTTC TC - G 4 A c c
43 ATCCCCATCTGC GG CAGATGGGGA GAAGAT
CTGTTAAT CC GTCTACCCCT CTTTTG
-- A A

GAM63 348 LOC2850 1 1894 XP_211744.1 3 1217 TTTTCACATCTT G ---- - - 4 A c c
45 CATTCACTGGGA GTCCAGA TGG GGA GAAGATGT
TTCTGGAC CAGGTCT GTC CTT CTTCTACA
- TAGG A A

GAM63 348 LOC2851 1 7658 XP_211800.1 3 1289 TGGGTCTCAGTT ---- G 4 A c c
82 TTCCCCATCTGG GGTCCAGATGGGGAGA AGAT
ACCCTTGC CCAGGTCTACCCCTTT TCTG
TGAC G

GAM63 348 LOC2853 1 1257 XP_209569.1 3 117 CCCTTCCGTCTT TCCA - 4 A c c
29 CTCCCTCATCCT GG GATG GGGAGAAGATG
TTCCAAAC CC CTAC CCCTCTTCTGC
TTTC T

GAM63 348 LOC2853 1 18813 XP_211847.1 5 378 TGTTAGCCTTTT CAGA T 4 A c c

37 CTCCCCAGACTT GGTC TGGGGAGAAGA GT
GTTGGCAT TCAG ACCCCTCTTTT CG
---- C

GAM63 348 LOC2853 1 10101 XP_211870.1 5 1247 TAAATAGCCTCT G - A T 4 A c c
63 CTCCCCATTTAG G TCC AGATGGGGAGA GA GT
GAGCAGCC C AGG TTTACCCCTCT CT CG
G A - C

GAM63 348 LOC2854 1 8648 XP_211886.3 5 953 CGTGTATATTTT C GAT 4 A c c
08 CTCCCCCAATGA GGT CA GGGGAGAAGATGT
ATCAATTG CTA GT CCCCTCTTTTATA
A AAC

GAM63 348 LOC2855 1 1035 XP_211941.1 5 1210 GAATGAATATGT TC - AG 4 A c c
77 TTCCCCATCTTG GG CA GATGGGGAGA ATGT
TGCCCTTT CC GT CTACCCCTTT TATA
GT T G-

GAM63 348 LOC2856 1 15209 XP_209691.1 3 430 TTTCAACATCTT GG A---- -- 4 A c c
34 CTCCAGCCAGTT TCCAG TGG GGAGAAGATGT
TACTGGAA AGGTC ACC CCTCTTCTACA
A- ATTTG GA

GAM63 348 LOC2856 1 11929 XP_209723.1 5 411 GTCACCATCCTC - ---- - A 4 A c c
90 ATCCCCATCTTC GGT CCA GATGGGGA GA GATG

ATGGAACC CCA GGT CTACCCCT CT CTAC
A ACTT A C

GAM63 348 LOC2857 1 12512 XP_211994.1 3 1347 TTGCTTCATCTT - - GG 4 A c c
14 CTGGCTGTTGTG GGT CCA GATGG AGAAGATG
GCACTGAC TCA GGT TTGTC TCTTCTAC
C G GG

GAM63 348 LOC2857 1 1407 XP_211998.1 5 957 GAGAGAGCCACT T AG A 4 A c c
26 TAACCTCTCTGG GGTCCAGA GGGG AAG TG
ACCTTGTT CCAGGTCT CTCC TTC AC
- AA -

GAM63 348 LOC2857 1 18138 XP_209742.1 5 1483 TCCCGGGCACTT C A A 4 A c c

47 CTCCCCACCTCG GGTC AG TGGGGAGAAG TGT
GCCCCGCG CCGG TC ACCCCTCTTC ACG
C C -

GAM63 348 LOC2857 2 11218 XP_209755.1 3 912 TTATTGCTTCTT TC G T 4 A c c
69 CTCCCATCTGCC GG CAGATGGG AGAAGA GT
CGTTGACA CC GTCTACCC TCTTCT CG
C- - T

GAM63 348 LOC2857 2 20180 XP_209755.1 3 912 TTTATTGCTTCT TC G T 4 A c c
69 TCTCCCATCTGC GG CAGATGGG AGAAGA GT
CCGTTGAC CC GTCTACCC TCTTCT CG
C- - T

GAM63 348 LOC2857 1 13902 XP_212015.1 3 917 TTCTGCTCATCT TCC A 4 A c c
71 CTCCCCATTTCT GG AGATGGGGAGA GATG
TTCTTCCC CT TTTACCCCTCT CTAC
TTC -

GAM63 348 LOC2858 1 15227 XP_209784.1 5 752 AAAATCCACCTG G G - A 4 A c c
31 TCTCCCATCTGG G TCCAGATGGG AGA AG TG
GGCTCTTT C GGGTCTACCC TCT TC AC
G - G C

GAM63 348 LOC2858 1 15227 XP_212577.1 5 752 AAAATCCACCTG G G - A 4 A c c
31 TCTCCCATCTGG G TCCAGATGGG AGA AG TG
GGCTCTTT C GGGTCTACCC TCT TC AC
G - G C

GAM63 348 LOC2858 1 15227 XP_212625.1 5 752 AAAATCCACCTG G G - A 4 A c c
31 TCTCCCATCTGG G TCCAGATGGG AGA AG TG
GGCTCTTT C GGGTCTACCC TCT TC AC
G - G C

GAM63 348 LOC2859 1 8743 XP_209812.1 3 656 CACGCCCATCTT T G- - 4 A c c
08 CTGCCTCATAGT GG CCA ATGGGG AGAAGATG
GGTCACTC CT GGT TACTCC TCTTCTAC
- GA G

GAM63 348 LOC2860 1 17819 XP_212134.1 3 543 CCTCATCATCTT C- ATGG 4 A c
c
08 CTCCAACTGACA GGT CAG GGAGAAGATG
CCTAGTTA CCA GTC CCTCTTCTAC
CA AA--

GAM63 348 LOC2860 1 12513 XP_209868.1 5 175 GCTATCCCATCT G AGA 4 A c c

30 GCCCCCATCTGG G TCCAGATGGGG AGATG
AGCTCGGC C AGGTCTACCCC TCTAC
G CG-
GAM63 348 LOC2860 1 11886 XP_209867.2 5 73 CCGGGGCGTCTT AGA- --- 4 A c c
32 CTCCTACGCAGG GGTCC TG GGGAGAAGATGT
AAGGGCCA CCGGG AC TCCTCTTCTGCG
AAGG GCA
GAM63 348 LOC2860 1 12513 XP_209873.1 5 175 GCTATCCCATCT G AGA 4 A c c

39 GCCCCCATCTGG G TCCAGATGGGG AGATG
AGCTCGGC C AGGTCTACCCC TCTAC
G CG-
GAM63 348 LOC2860 1 14796 XP_212156.1 3 1610 CCATCCTCTCCC T--- ----- A 4 A c c
59 ACTTCCATCTGG GG CCAGATGG GGAGA GATG
CGTCCCAT CC GGTCTACC CCTCT CTAC
CTGC TTCAC C
GAM63 348 LOC2861 1 8298 XP_212205.1 3 809 TTCCCACATCTT TC T --- 4 A c c
41 CCTGTCTTCTTC GG CAGA GGGGA GAAGATGT
TGAGCCTT CC GTCT CTTCT CTTCTACA
GA T GTC
GAM63 348 LOC2861 1 10366 XP_209922.1 3 1040 GAGAGCCATCTT T AT -- 4 A b b
63 CTTACCCCCTGG GG CCAG GGGG AGAAGATG
CCACATGG CC GGTC CCCC TCTTCTAC
- -- AT
GAM63 348 LOC2861 1 7887 XP_212227.1 5 102 TTTCTAAGTCTT GATGG G 4 A c
c
99 CTCCTGGATCTA GGTCCA GGAGAAGAT
CATTTCCA CTAGGT CCTCTTCTG
----- A
GAM63 348 LOC2862 1 19160 XP_212228.1 3 551 TCTCCTTTTCTT -- T TG 4 A c c
15 CTCCTTTCTGCT GGTC CAGA GGGGAGAAGA
GACCAGAA CCAG GTCT TTCCTCTTCT
TC - TT
GAM63 348 LOC2862 1 593 XP_212236.1 3 611 CCAGGCTGTCTT G-- A--- 4 A c c
19 CTCCTCATCACA GTCC GATGGGGAGAAGATG
GGGACGAG CAGG CTACTCCTCTTCTGT
GAG GACA
GAM63 348 LOC2862 1 15764 XP_212233.1 5 1221 ACAGGGCATCTT AGATGG 4 A c
c
21 CTCCAGGGCCTC GGTCC GGAGAAGATGT
ATTCAGTC CCGGG CCTCTTCTACG
A-----
GAM63 348 LOC2862 1 16796 XP_209970.2 3 432 GGGCCACATCTT CC T - 4 A c c
56 CTGCCCCTTCTC GGT AGA GGGG AGAAGATGT
AGCCTCCC CCG TCT CCCC TCTTCTACA
AC T G
GAM63 348 LOC2864 1 17046 XP_301085.1 5 1082 ATAAATTATCTT - A ---- 4 A c c
34 CTCTCTTTGTAT GGT CC GAT GGGGAGAAGATG
TGGGAACC CCA GG TTA TCTCTCTTCTAT
A G TGTT

GAM63 348 LOC2865 1 10562 XP_210079.1 5 17 ACTGAGCTTCCT AGA A T 4 A c c
01 CTCCCCAGGACC GGTCC TGGGGAGA GA GT
CGCATGGG CCAGG ACCCCTCT CT CG
--- C T
GAM63 348 LOC2865 1 12106 XP_212343.1 5 1353 ACACTGCATATG T GAAG 4 A c
c
67 GTCCCCATCTGG GG CCAGATGGGGA ATGT
CCTCAGAG CC GGTCTACCCCT TACG
- GGTA
GAM63 348 LOC2865 1 12106 XP_212341.1 5 1353 ACACTGCATATG T GAAG 4 A c
c
72 GTCCCCATCTGG GG CCAGATGGGGA ATGT
CCTCAGAG CC GGTCTACCCCT TACG
- GGTA
GAM63 348 LOC3387 1 11430 XP_211595.2 5 402 CCCAGACATCAC TG GG AA 4 A c
c
09 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA
GAM63 348 LOC3387 1 16183 XP_290556.2 3 23 GGTTGACATCTT TGGGGA 4 A c
c
60 CATTTCTGGGCT GGTCCAGA GAAGATGT
ACTACTAT TCGGGTCT CTTCTACA
TTA---
GAM63 348 LOC3388 1 5910 XP_290587.2 3 627 TGCGCCTGTCTT C TG 4 A c c
12 CTCCCTCTGACC GGTC AGA GGGAGAAGATG
CCAGAGAA CCAG TCT CCCTCTTCTGT
- --
GAM63 348 LOC3388 1 3177 XP_294729.1 5 718 TTTCTAGCATCT G - --- A 4 A c c
42 CTCCCCACCCTC G TC CAGA TGGGGAGA GATGT
TGAGAGCT C AG GTCT ACCCCTCT CTACG
G A CCC -
GAM63 348 LOC3391 1 9390 XP_290742.1 3 469 CACCACCTCATT - G - T 4 A c c
78 GTTCTCATCTGG GGT CCAGATGGGGA AA GA GT
AACTGAAA TCA GGTCTACTCTT TT CT CA
A G A C
GAM63 348 LOC3392 1 12179 XP_290756.1 5 193 GGCTCGTCCCTC C AA-- 4 A c c
01 CTCCCCATCTCG GGTC AGATGGGGAG GATG
GCCCTGAG CCGG TCTACCCCTC CTGC
C CTCC
GAM63 348 LOC3392 2 4093 XP_290783.1 5 27 CCTCTCCGTCTT TCC- AT 4 A c c
38 CTCCCCTCCTTC GG AG GGGGAGAAGATG
TTCCCCAC CC TC CCCCTCTTCTGC
TTCT CT
GAM63 348 LOC3392 2 14379 XP_290784.1 5 0 CATCTTCTCTTC TCC T 4 A c c
38 CTCTTCCCCACC GG AGA GGGGAGAAGATG
GTCCTCTC CC TCT CTTCTCTTCTAC
CCT C
GAM63 348 LOC3392 1 14427 XP_294901.1 5 1175 TCATCCACTCAG TG AGA 4 A c
c

90 GTCTTCCTCTGG GGTCCAGA GGGAGA TG
ACCTGCAT CCAGGTCT CCTTCT AC
-- GG-
GAM63 348 LOC3393 1 15380 XP_294925.1 3 61 GGTACACGCTTT - AGA A 4 A c c
92 CTCCCCAGACGG GGT CC TGGGGAGAAG TGT
CACCCACT CCA GG ACCCCTCTTT GCA
C CAG C
GAM63 348 LOC3397 1 12879 XP_295061.1 5 215 CCCCACCATCTT CCAGA- - 4 A c
c
78 CTCCACCAACCC GGT TGG GGAGAAGATG
CAACCTCC CCA ACC CCTCTTCTAC
ACCCCA A
GAM63 348 LOC3398 1 14168 XP_295084.1 3 586 CCAACATAGTTT CC A -- 4 A c c
46 CACCCCATCTCT GGT AGATGGGG GAAG ATGT
ACT TCA TCTACCCC CTTT TACA
TC A GA
GAM63 348 LOC3398 1 17721 XP_291044.1 3 147 GTGCCACATCTT TCC T 4 A c c
62 CTCCCCCTTTAT GG AGA GGGGAGAAGATGT
CCCTACAA CC TTT CCCCTCTTCTACA
TA- C
GAM63 348 LOC3399 1 3281 XP_294630.1 5 1835 TCCCCATCTCTT C T GA 4 A c c
50 CTCCTTTGTACC GGT CAGA GGGGA AGATG
TGTCAACA CCA GTTT CCTCT TCTAC
T - TC
GAM63 348 LOC3399 1 7911 XP_291101.1 3 924 AGCCCACAGCTT C- ATG A 4 A c
c
83 CTCCCAGCCTGA GGT CAG GGGAGAAG TGT
AACCAACA CCA GTC CCCTCTTC ACA
AA CGA G
GAM63 348 LOC3401 1 11430 XP_291150.1 5 402 CCCAGACATCAC TG GG AA 4 A c
c
25 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA
GAM63 348 LOC3402 1 11430 XP_291203.1 5 402 CCCAGACATCAC TG GG AA 4 A c
c
27 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA
GAM63 348 LOC3402 1 11430 XP_291214.1 5 1069 CCCAGACATCAC TG GG AA 4 A c
c
90 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA
GAM63 348 LOC3403 1 14545 XP_295215.1 3 250 TCATCACATCTT G - AT-- --- 4 A c c
40 CTCTGGCCCTCG GTC CAG GGG GAGAAGATGT
ACTGAGAT TAG GTC CCC CTCTTCTACA
- A AGCT GGT
GAM63 348 LOC3403 1 16910 XP_295225.1 3 1073 GGGTGAAATCTT CAG G 4 A c
c

62 CTCCCCATGACT GGTC ATGGGGAGAAGAT
ATGTTTTC TCAG TACCCCTCTTCTA
--- A
GAM63 348 LOC3404 1 12513 XP_291274.1 5 175 GCTATCCCATCT G AGA 4 A c c

08 GCCCCCATCTGG G TCCAGATGGGG AGATG
AGCTCGGC C AGGTCTACCCC TCTAC
G CG-
GAM63 348 LOC3405 1 12693 XP_295268.1 3 65 CCACAGTTTTTC --- A 4 A c c
28 CCTGCCTTCTGG GGTCCAGA TGGGGAGAAG TGT
ACCCTCAG CCAGGTCT GTCCCTTTTT ACA
TCC G
GAM63 348 LOC3410 1 990 XP_295967.2 5 566 CATGCCTGTGTT AGAT G 4 A c c
36 CTCCCCCGGGGC GGTCC GGGGAGAA ATG
CACTTAGA CCGGG CCCCTCTT TGT
GC-- G
GAM63 348 LOC3421 1 752 XP_292413.1 5 2140 TCCACCATATTT C - - 4 A c c
95 CTCCCCACTCTG GGT CAGA TGGGGAGAAG ATG
TACCTTCT CCA GTCT ACCCCTCTTT TAC
T C A
GAM63 348 LOC3430 1 11315 XP_295309.1 3 503 TGAGCACGTCTT - ATGG 4 A c c

52 CTCCAACCTGGA GG TCCAG GGAGAAGATGT
GCCTGCCA CC AGGTC CCTCTTCTGCA
G CAA-
GAM63 348 LOC3431 1 15167 XP_295364.1 5 441 GTACAGCTTCTT T ----- T 4 A c c
27 CTCCTCACCCAG GG CCAGA TGGGGAGAAGA GT
TTTGGCCA CC GGTTT ACTCCTCTTCT CG
- GACCC T
GAM63 348 LOC3440 1 6198 XP_297346.1 5 235 TCATCACCCAGT T ------ 4 A c c
51 TTTTCCCTCTGG GGTCCAGA GGGGAGAA GATG
ACCCAGGA CCAGGTCT CCCTTTTT CTAC
- GACCCA
GAM63 348 LOC3478 1 16952 XP_166630.4 3 100 CAAAAGCTTCTT C AT--- T 4 A c c
04 CTCCCCCAGTGC GGTC AG GGGGAGAAGA GT
TGATCTTG CTAG TC CCCCTCTTCT CG
- GTGAC T
GAM63 348 LOC3480 1 19753 XP_300620.1 3 552 GTTTCTCATCTT CAGA 4 A c c
71 CTCTCTACGGCC GGTC TGGGGAGAAGATG
TCTGAGTT CCGG ATCTCTCTTCTAC
C---
GAM63 348 LOC3481 1 2347 XP_300640.1 3 131 CATGCACTCCTT CAGA AT 4 A c
c
46 CTCCCCAAGGCC GGTC TGGGGAGAAG GT
AGGGCAGA CCGG ACCCCTCTTC CA
A--- CT
GAM63 348 LOC3483 1 5103 XP_302739.1 5 111 CTCAGGAATCTT CAGA G 4 A c c

89 CTCCCCAGAGAC GGTC TGGGGAGAAGAT
TCCTAAGT TCAG ACCCCTCTTCTA

AG-- A
GAM63 348 LOC3484 1 6373 XP_300733.1 5 76 CACAAGCCTCCT TC - A T 4 A c c
16 CTCCCCAGTCTG GG CAGA TGGGGAGA GA GT
CCCCACTT CC GTCT ACCCCTCT CT CG
CC G C C
GAM63 348 LOC3484 1 14880 XP_300742.1 5 366 GGGCACCATCTT G ---- - 4 A c c
52 CTCATTCATCTC GTCC AGATGGG GAGAAGATG
CAAGGACG CAGG TCTACTT CTCTTCTAC
G AACC A
GAM63 348 LOC3484 1 14543 XP_300352.1 3 1396 TCTCCAACATCT C-- A A 4 A c c
88 CTCCCCACCTCA GGTC AG TGGGGAGA GATGT
TGATTGTC TTAG TC ACCCCTCT CTACA
TAC C -
GAM63 348 LOC3485 2 11430 XP_302806.1 5 464 CCCAGACATCAC TG GG AA 4 A c
c
08 CTTTCATTCTGG GGTCCAGA G AG GATGT
ACCTACCA CCAGGTCT C TC CTACA
TA TT CA
GAM63 348 LOC3485 2 12029 XP_302806.1 3 1868 GCTTTGCATCTT ATGG- 4 A c c

08 CTCCAGGCCCTG GGTCCAG GGAGAAGATGT
GACTTCCT TCAGGTC CCTCTTCTACG
CCGGA
GAM63 348 LOC3485 1 928 XP_302833.1 3 1421 TCCAGCTATCTT - A --- 4 A c c
83 CTCCTTTCCACT GGT CCAG TGG GGAGAAGATG
GGTGCCAG CCG GGTC ACC CCTCTTCTAT
T - TTT
GAM63 348 LOC3487 1 1681 XP_300810.1 3 2851 TTCTTCTACATC C -- AA 4 A c c
01 CTCCCCATTTCT GGT CAGA TGGGGAG GATGT
GTACTGAA TCA GTCT ACCCCTC CTACA
T TT --
GAM63 348 LOC3487 1 17525 XP_302884.1 5 640 TCAATTTATCTT AGA--- 4 A c c
80 CTCCCTGGAATT GGTCC TGGGGAGAAGATG
GGGACCAC CCAGG GTCCCTCTTCTAT
GTTAAG
GAM63 348 LOC3490 1 11232 XP_302952.1 3 1537 GGCATCTCACGT - AGA---- 4 A c
c
80 ACCCCCATCTGA GGTC CAGATGGGG AGATGT
GACCTCTT CCAG GTCTACCCC TCTACG
A CATGCAC
GAM63 348 LOC3491 1 18078 XP_302970.1 3 384 CTCCCCATGTTT -- C A - 4 A c c
61 CTCCCCACTAGA GGT C AG TGGGGAGAAG ATG
AGCCTCCG CCG G TC ACCCCTCTTT TAC
AA A - G
GAM63 348 LOC3492 1 9154 XP_303016.1 5 2063 ATACCACATCTT -- G-- - 4 A c c
77 CTCACTTATAGA GGT CCA ATGGG GAGAAGATGT
TGGTAGCT TCG GGT TATTC CTCTTCTACA
AT AGA A
GAM63 348 LOC3492 1 9154 XP_303021.1 5 2059 ATACCACATCTT -- G-- - 4 A c c
99 CTCACTTATAGA GGT CCA ATGGG GAGAAGATGT

TGGTAGCT TCG GGT TATTC CTCTTCTACA
AT AGA A
GAM63 348 LOC3493 1 18870 XP_301019.1 5 1079 TACAAGCATCTT GATGG 4 A c c
05 CTCTGGCGTGGA GGTCCA GGAGAAGATGT
TCCGCTGC CTAGGT TCTCTTCTACG
GCGG-
GAM63 348 LOC3493 1 10059 XP_303024.1 3 1048 GGAAATTGTCTT CCAGA 4 A c c
07 CTCCTCAGCCCG GGT TGGGGAGAAGATG
TTCGCTGG CCG ACTCCTCTTCTGT

GAM63 348 LOC3494 1 11964 XP_301075.1 3 435 CTCCTCCCTCTT - TGG TG 4 A c c
20 CTCCTCTGTGGC GGTC CAGA GGAGAAGA
CTGGGAGA CCGG GTCT CCTCTTCT
T --- CC
GAM63 348 LOC3494 1 17046 XP_301083.1 5 506 ATAAATTATCTT - A ---- 4 A c c
29 CTCTCTTTGTAT GGT CC GAT GGGGAGAAGATG
TGGGAACC CCA GG TTA TCTCTCTTCTAT
A G TGTT
GAM63 348 LOC3508 1 8471 XP_303256.1 5 322 TATCTACATCTT - TGGGGA 4 A c c
97 CACGGTCTCTGA GGTC CAGA GAAGATGT
GATCCTGA CTAG GTCT CTTCTACA
A CTGGCA
GAM63 348 LOC5123 1 6536 NP_057542.2 3 835 CCTTACGTGCTT GAT - 4 A b b
6 CTCCCCTGGACC GGTCCA GGGGAGAAG ATGT
TATGTGCA CCAGGT CCCCTCTTC TGCA
--- G
GAM63 348 LOC9057 1 12424 XP_032678.2 5 48 CCGCGGCGTCTT C A -- 4 A c c
6 CTCCACCCACCT GGT CAG TGGG GAGAAGATGT
GCGCTGGG TCG GTC ACCC CTCTTCTGCG
C C AC
GAM63 348 LOC9090 1 10295 XP_034809.1 3 4492 CCTTCTCAGTTT CCAGA A 4 A c c
6 CTCCCCAACCTC GGT TGGGGAGAAG TG
CCCTTTTC CCA ACCCCTCTTT AC
----- G
GAM63 348 LOC9139 2 11988 XP_038219.2 5 864 TGCCGACTTCTT T A--- T 4 A c c
7 CTCCCCAGAGCC GG CCAG TGGGGAGAAGA GT
TGGCTTTT TC GGTC ACCCCTCTTCT CA
- CGAG T
GAM63 348 LOC9139 2 12564 XP_038219.2 5 543 TGTTGACATTTT CCA T 4 A c c
7 CTCCCCTTCCTC GGT GA GGGGAGAAGATGT
ACTTACAG TCA CT CCCCTCTTTTACA
CTC T
GAM63 348 LOC9180 1 6003 XP_040819.1 3 10 AATTTCCAACTT CC- A 4 A c c
7 CTCCCTATCTTC GGT AGATGGGGAGAAG TG
AACTCTGC TCA TCTATCCCTCTTC AC

ACT A
GAM63 348 LOC9297 1 17973 XP_048529.2 5 1249 CATTCTCTCTCC ---- - TG 4 A c c
3 TTTTCCATCTGG GGTCCAGATGG GGAGA AGA
ACCACCCA CCAGGTCTACC CCTCT TCT
TTTT C TA
GAM63 348 LOC9325 1 18965 XP_050105.1 5 1183 GCTCCTGCACTT AGA-- A 4 A c
c
9 CTCCCCAGAGCG GGTCC TGGGGAGAAG TGT
GGACCCTC CCAGG ACCCCTCTTC ACG
GCGAG -
GAM63 348 LPXN 1 14409 NP_004802.1 3 386 TACTCATATCTT T GG 4 A c c
CTCTAATTTGGT GG CCAGAT GGAGAAGATGT
CCTGATAC CC GGTTTA TCTCTTCTATA
T A-
GAM63 348 MAGED4 1 11993 NP_803881.1 3 0 CCAGCTTCTTCT AT A 4 A c c
CCTGGATCCAGT GGTCCAG GGGGAGAAG TG
AGAGTTTC CTAGGTC CTCTTCTTC AC
-- G
GAM63 348 MAMDC1 1 11453 XP_090827.3 3 597 GCATTCATGTTT TCC A - 4 A c c
CTCCCCACCTTA GG AG TGGGGAGAAG ATG
TCCCCATC CC TC ACCCCTCTTT TAC
TAT C G
GAM63 348 MAP2K4 2 7023 NP_003001.1 3 1971 CTCTGCTGTCAA GT AA 4 A c c
CTTCCCATCTGG G CCAGATGGGGAG GATG
CTCAGCAT C GGTCTACCCTTC CTGT
TC AA
GAM63 348 MAP2K4 2 17579 NP_003001.1 3 1832 TTTCCCTATCTT - AGAT 4 A c c
CTCCCCCACGGT GGT CC GGGGAGAAGATG
ATCCTAAA CTA GG CCCCTCTTCTAT
T CAC-
GAM63 348 MARK2 1 4411 NP_004945.2 3 135 CTGCTGGCACTT T AT- A 4 A c c
CTCCCCTCCCTG GG CCAG GGGGAGAAG TGT
GCCCTTCT CC GGTC CCCCTCTTC ACG
C CCT -
GAM63 348 MARK2 1 4411 NP_059672.1 3 135 CTGCTGGCACTT T AT- A 4 A c c
CTCCCCTCCCTG GG CCAG GGGGAGAAG TGT
GCCCTTCT CC GGTC CCCCTCTTC ACG
C CCT -
GAM63 348 MCP 1 3578 NP_002380.3 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG
GAM63 348 MCP 1 3578 NP_722548.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG
GAM63 348 MCP 1 3578 NP_758860.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT

A GCG

GAM63 348 MCP 1 3578 NP_758861.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758862.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758863.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758864.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758865.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758866.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758867.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758868.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758869.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758870.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MCP 1 3578 NP_758871.1 5 53 GGGATTGTTGCG - GAA 4 A c c
TCCCATATCTGG GGTCCAGATG GGGA GATG
ACCCAGAA CCAGGTCTAT CCCT TTGT
A GCG

GAM63 348 MEP50 1 18671 NP_077007.1 3 841 GCCTGACATCTT T GAT G 4 A c c
CTGCCCTGGTCC GG CCA GGG AGAAGATGT
CCTTTCTC CC GGT CCC TCTTCTACA
T --- G

GAM63 348 MESDC2 1 20061 XP_051854.1 3 583 GAATGATATCTT C TG 4 A c c

CTCTTTCTTTGA GGT CAGA GGGAGAAGATGT
ACCATCTC CCA GTTT TTCTCTTCTATA
A CT
GAM63 348 MESP2 1 12071 XP_085261.1 3 11 CCTGGGCATCTT T GA GG 4 A c c

CTACTAATGGCC GG CCA TGG AGAAGATGT
TCGGCTTC CC GGT ATC TCTTCTACG
- A- A-
GAM63 348 MGA 1 11668 XP_031689.3 3 852 AAAATGCATTAT CAGA A 4 A c c
CTCCCCAGACCA GGTC TGGGGAGA GATGT
GAGACAGT CCAG ACCCCTCT TTACG
---- A
GAM63 348 MGAT5 1 13161 NP_002401.1 5 2054 CTGGCATATCTT --- A G 4 A c c
CTCTGTGCTGGT GGT CCAG TG GGAGAAGATGT
GCACCTAG CCA GGTC GT TCTCTTCTATA
CGT - G
GAM63 348 MGC1033 1 14880 XP_300761.1 5 366 GGGCACCATCTT G ---- - 4 A c c
4 CTCATTCATCTC GTCC AGATGGG GAGAAGATG
CAAGGACG CAGG TCTACTT CTCTTCTAC
G AACC A
GAM63 348 MGC1111 1 13254 NP_115686.2 3 1121 TCACGCTGGTTT AGA AT- 4 A c
c
5 CTCCCCAGGACC GGTCC TGGGGAGAAG GT
CATGAGCT CCAGG ACCCCTCTTT CG
--- GGT
GAM63 348 MGC1226 1 15149 NP_116085.1 5 380 ATACACATTCTT GA -- - 4 A c c
2 CTCCTAGCACAT GGTCCA TG GGGAGAAGA TGT
GGATCTTT CTAGGT AC TCCTCTTCT ACA
AC GA T
GAM63 348 MGC1483 1 19092 NP_542390.1 3 169 GCGTCCCATTTT T GAT 4 A c c

9 CTCCCCTGGCCT GG CCA GGGGAGAAGATG
CTTACTTG CC GGT CCCCTCTTTTAC
- ---
GAM63 348 MGC1604 1 13269 NP_612380.1 5 231 AAATGTCATCTT T A--- 4 A c c
4 CTCCCCAGACGC GG CCAG TGGGGAGAAGATG
TGGCTTGC TC GGTC ACCCCTCTTCTAC
- GCAG
GAM63 348 MGC1821 1 10002 NP_689665.1 3 244 TGTTGGCCATGT TCC A AG 4 A c
c
6 CTCCCCAACTCC GG AG TGGGGAGA ATG
ACAATATC CC TC ACCCCTCT TAC
--- A G-
GAM63 348 MGC2047 1 18986 NP_659490.1 5 109 AGCTTCCACCTG TC A A 4 A c
c
0 CTCCCCATCTGC GG CAGATGGGGAG AG TG
CCACCCAC CC GTCTACCCCTC TC AC
C- G C
GAM63 348 MGC2659 1 3683 NP_689851.1 5 398 CAGCTTCAGGTC GG AA G 4 A c
c

8 GCTACCATCTGG GGTCCAGATGG AG GAT
ACCTCTCG CCAGGTCTACC TC CTG
A- G- G
GAM63 348 MGC3047 1 2308 NP_115724.1 3 578 GCACCATCTGTT AGA -- 4 A c c
CTCCCCAGGGAC GGTCC TGGGGAGA AGATG
CTGCTGAC CCAGG ACCCCTCT TCTAC
G-- TG
GAM63 348 MGC3101 1 12469 NP_076948.1 3 1396 GCCAGGGTCTTC TCC - G 4 A c
c
CTCCCCATCTTT GG AGATGGGGAG AAGAT
CCATCCTT CC TCTACCCCTC TTCTG
TT- C G
GAM63 348 MGC3202 1 11644 NP_689479.1 3 44 CCACGGCATCTT CAGATG 4 A c
c
0 CTCCCGAGACCA GGTC GGGAGAAGATGT
CAAACACC CCAG CCCTCTTCTACG
AG----
GAM63 348 MGC3340 1 16203 NP_848620.1 5 58 CCTCAACCTCTT CCAGA T 4 A c
c
7 CTCCCCACAACC GGT TGGGGAGAAGA GT
CCAACCCC CCA ACCCCTCTTCT CA
AC--- C
GAM63 348 MGC3388 1 15982 NP_699161.1 5 168 CACCGGCCACTT C ----- A 4 A c c
4 CTCCCCCGTCCA GGTC AGAT GGGGAGAAG TG
TCTGACCA CCAG TCTA CCCCTCTTC AC
- CCTGC -
GAM63 348 MGC3483 1 10386 NP_689590.1 3 80 AGACACATGTTT CCAGA - 4 A c
c
7 CTCCCCAGCCTA GGT TGGGGAGAAG ATGT
AGTGTAGT CCG ACCCCTCTTT TACA
----- G
GAM63 348 MGC3533 1 17534 NP_689602.1 3 737 TGTGGATATCTT C-- G 4 A c c
8 CTCTCATCTTAT GGTC AGATGGG AGAAGATGT
GATTTGTC TTAG TCTACTC TCTTCTATA
TAT -
GAM63 348 MGC3951 1 7979 NP_776183.1 3 207 TTCCTACATCTT TCC A 4 A c c
8 CTCTTCACCTAT GG AG TGGGGAGAAGATGT
CCCTTGTA CC TC ACTTCTCTTCTACA
TA- C
GAM63 348 MGC4893 1 16796 NP_848631.1 3 432 GGGCCACATCTT CC T - 4 A c c
5 CTGCCCCTTCTC GGT AGA GGGG AGAAGATGT
AGCCTCCC CCG TCT CCCC TCTTCTACA
AC T G
GAM63 348 MGC5201 1 5201 NP_848593.1 5 228 TGGAAACATCTT CAGA 4 A c c
9 CTTCCTGAGACC GGTC TGGGGAGAAGATGT
TCGTTGAA CCAG GTCCTTCTTCTACA
A---
GAM63 348 MIDORI 1 8948 NP_065829.1 3 1833 ACTCCACATCTT TC G - - 4 A c c
CTGCCCCAGTGT GG CA A TGGGG AGAAGATGT

GTCCCCAC CC GT T ACCCC TCTTCTACA
CT G G G

GAM63 348 MKRN4 1 6983 NP_110384.1 5 176 CCTCGCCATCTT AGA-- 4 A c c
CTTCTCACAGCC GGTCC TGGGGAGAAGATG
GGACCGGA CCAGG ACTCTTCTTCTAC
CCGAC

GAM63 348 MME 1 9503 NP_009218.1 5 133 AGCCTCCAACTT A ------ A 4 A c c
CTCCCGAATCCC GGTCCAG TGGG GAGAAG TG
ACTGGATT TTAGGTC ACCC CTCTTC AC
- TAAGCC A

GAM63 348 MMP28 1 13641 NP_116568.1 3 334 CTCCATCATCTT CAGATG 4 A c c
CTTCCGAGATGA GGTC GGGAGAAGATG
CCGCTACT CCAG CCTTCTTCTAC
TAGAG-

GAM63 348 MRPS27 1 7135 NP_055899.1 3 859 TTCTGCCACATC T A A 4 A b b
TCGCCCTTCTGG GGTCCAGA GGGG GA GATGT
ACCTGCAC CCAGGTCT TCCC CT CTACA
- G -

GAM63 348 MS4A2 1 18155 NP_000130.1 3 2654 CAATGTCATCTT CAGATGG 4 A c c
CTCCATGAAGAC GGTC GGAGAAGATG
CACTGAAT CCAG CCTCTTCTAC
AAGTA--

GAM63 348 MTMR9 1 10289 NP_056273.2 3 2748 ATTCAGCATCTT G G -- 4 A c c
CTCTATTCATGT G TCCA ATGG GGAGAAGATGT
GGAGTGAA T AGGT TACT TCTCTTCTACG
G G TA

GAM63 348 MUC3B 1 12658 XP_168578.2 3 903 TCCTTGTATCTT TC T G 4 A c c
CTCCCCTTCTGA GG CAGA GGGGAGAAGAT
GCCTGTCC CC GTCT CCCCTCTTCTA
GA T T

GAM63 348 MYLC2PL 1 17797 NP_612412.1 5 310 CTCCAACGTCTT C GG 4 A c c
CTCCATGTTTGA GGTC AGAT GGAGAAGATGT
TCAGTCCC CTAG TTTG CCTCTTCTGCA
- TA

GAM63 348 NEK6 1 13237 NP_055212.2 3 643 CAGGAGCATCTT A- G---- 4 A c c
CTTGGCAGCCAG GGTCCAG TGG GAGAAGATGT
GCTGGGCC CCGGGTC ACC TTCTTCTACG
GG GACGG

GAM63 348 NFKBIE 1 16403 NP_004547.1 3 426 GGTGTCCATCTT A- G 4 A c c
CTTGCTGTTGAG GGTCC GATGG GAGAAGATG
GACCCTGA CCAGG TTGTC TTCTTCTAC
AG G

GAM63 348 NIN283 1 2207 NP_115644.1 3 581 TTTTGCTCTTTT - AT TG 4 A c c
CTCCCCTTGAGA GGTC CAG GGGGAGAAGA
CCCTAATA CCAG GTT CCCCTCTTTT
A -- CT

GAM63 348 NNAT 1 9458 NP_005377.1 3 824 CATTAGTTGTCT C A A 4 A c c

CTCCCCAGCTAG GGTC AG TGGGGAGA GATG
ATTGTAAG TTAG TC ACCCCTCT CTGT
A G -

GAM63 348 NR3C1 1 10686 NP_000167.1 3 1177 ACCCATTTTCAC C- --- 4 A c c
ATTCCCATCTGT GGT CAGATGGGGA GAAGATG
CACCAATT CCA GTCTACCCTT CTTTTAC
CT ACA

GAM63 348 NRXN1 1 8566 NP_620072.1 5 52 CGTCTGCATCTT TC--- A 4 A c c
CTTCTCAGCTGC GG CAG TGGGGAGAAGATGT
CTTTCCGC CC GTC ACTCTTCTTCTACG
TTTCC G

GAM63 348 NSE2 1 5906 NP_777571.1 3 114 TGCCACTGTCTG --- AGA 4 A c c
GGCCCCATCTGG GG TCCAGATGGGG AGATG
GATTCCTG CC GGGTCTACCCC TCTGT
TTA GGG

GAM63 348 NTN4 1 14085 NP_067052.1 3 160 TCTTATCTAATT T GA---- 4 A c c
TATCTCTTCTGG GGTCCAGA GGGGA AGATG
ACCCATGT CCAGGTCT TCTCT TCTAT
- ATTTAA

GAM63 348 NUP54 1 6251 NP_059122.2 3 57 GAAATGCATCTT CA G -- 4 A c c
CTTACTGCATCA GGTC GATG GG AGAAGATGT
GACCTTCC CCAG CTAC TC TCTTCTACG
A- G AT

GAM63 348 OAS3 1 6803 NP_006178.1 3 1904 CCTCCATCCCTG - - A A--- 4 A c c
TCCCCCATCTTG GGT CCA GATGGGG GA GATG
GTGCTGAA TCG GGT CTACCCC CT CTAC
T T - GTCC

GAM63 348 OGG1 1 19616 NP_002533.1 3 76 CCCCACTTCTCT CCA - T 4 A c c
CTCCCCATCCCC GGT GATGGGGAGA AGA GT
ACCCAGTC CCA CTACCCCTCT TCT CA
CCC C T

GAM63 348 OGG1 1 19616 NP_058212.1 3 383 CCCCACTTCTCT CCA - T 4 A c c
CTCCCCATCCCC GGT GATGGGGAGA AGA GT
ACCCAGTC CCA CTACCCCTCT TCT CA
CCC C T

GAM63 348 OPA3 1 16306 NP_079412.1 3 485 CAGTGGCCTTTT CCA T T 4 A c c
CTCCCCCTCACC GGT GA GGGGAGAAGA GT
TTCTAAGG CCA CT CCCCTCTTTT CG
--- C C

GAM63 348 OPTC 1 3539 NP_055174.1 5 87 AGTCCCATCTGA T- AG A- 4 A c c
CTCCCCATGAGG GG CC ATGGGGAG AGATG
CTCCTGGC CC GG TACCCCTC TCTAC
TC AG AG

GAM63 348 OSBPL7 1 16404 NP_060201.3 3 139 CTCCAGCATCTT T AT-- - 4 A c c
CTTCCCCTTCCC GG CCAG GGGGA GAAGATGT
TGGCCCTG CC GGTC CCCCT CTTCTACG
C CCTT T

GAM63 348 p100 1 16615 NP_055205.1 3 485 TGTTCACATCTT T TGGGGA 4 A c c
CGCTCTGGCCAG GG CCAGA GAAGATGT
CCCATTCT CC GGTCT CTTCTACA

```
                                        -    CG----
GAM63   348   P114-RH 1   14048 NP_056133.1  3  11    AGACGTCATCTT     AGATG              4  A  c  c
          O-GEF                          CTTCTAAAGGGC GGTCC     GGGAGAAGATG
                                       CGTGACTC    CCGGG    TCTTCTTCTAC
                                            AAA--
GAM63   348   P5-1    1   14464 NP_006665.1  3  177   CCACTTCCACCC       -----  A-   A     4  A  c  c
                                       CTTGGTATCTGG GGTCCAGAT    GGGG  GAAG TG
                                       ACCCACGT    CCAGGTCTA    CCCC  CTTC AC
                                              TGGTT   AC   -
GAM63   348   PACE4   1   10623 NP_002561.1  3  130   TGACAGCTTTAT  G   AGA      --- A       4  A  c  c

                                       CTCCCCAGGAGC G TCC   TGGGGAGA   AG TGT
                                       AGCATCTC    C AGG   ACCCCTCT   TC ACA
                                              G  ---      ATT  G
GAM63   348   PACE4   1   10623 NP_612192.1  3  130   TGACAGCTTTAT  G   AGA      --- A       4  A  c  c

                                       CTCCCCAGGAGC G TCC   TGGGGAGA   AG TGT
                                       AGCATCTC    C AGG   ACCCCTCT   TC ACA
                                              G  ---      ATT  G
GAM63   348   PAGE-5  1   8319  NP_569734.2  5  60    TTCCAACATCTT    C  A    -----          4  A  c  c
                                       CGTTCTTTCTCA GGTC AG TGGGGA    GAAGATGT
                                       CTGACCGA    CCAG TC ACTCTT    CTTCTACA
                                              - -     TCTTG
GAM63   348   PALM    1   5652  NP_002570.1  3  863   CCCCGGCCTCTT      AT- --      T       4  A  c  c
                                       CTCCATCCTGCT GGTCCAG   GG  GGAGAAGA GT
                                       TGGACCAG    CCAGGTT   CC  CCTCTTCT CG
                                              CGT  TA       C
GAM63   348   PAPOLB  1   5455  NP_064529.2  3  136   AGACAGCATCTT   T   GATGG              4  A  c
c
                                       CTCTATTGGCCT GG CCA    GGAGAAGATGT
                                       CTCAGGGA    CC GGT    TCTCTTCTACG
                                              -  TA---
GAM63   348   PCBP3   1   4999  NP_065389.1  5  136   TGACGCCTTCTG   TC       ---    A       4  A  c  c
                                       GGCCCCATCTGT GG  CAGATGGGG   AGAAG TGT
                                       CCTTCCTC    CC  GTCTACCCC   TCTTC GCA
                                              T-       GGG    C
GAM63   348   PCBP4   1   13884 NP_065151.1  3  6     GCGGCAGAAATT      AT-      GA--       4  A  c  c
                                       CTCCCCCTACTG GGTCCAG   GGGGAGAA    TGT
                                       GGCCAGCT    CCGGGTC   CCCCTCTT    ACG
                                              ATC       AAAG
GAM63   348   PCBP4   1   13884 NP_127501.1  3  6     GCGGCAGAAATT      AT-      GA--       4  A  c  c
                                       CTCCCCCTACTG GGTCCAG   GGGGAGAA    TGT
                                       GGCCAGCT    CCGGGTC   CCCCTCTT    ACG
                                              ATC       AAAG
GAM63   348   PCBP4   1   13884 NP_127502.1  3  6     GCGGCAGAAATT      AT-      GA--       4  A  c  c
                                       CTCCCCCTACTG GGTCCAG   GGGGAGAA    TGT
                                       GGCCAGCT    CCGGGTC   CCCCTCTT    ACG
                                              ATC       AAAG
GAM63   348   PCBP4   1   13884 NP_127503.1  3  6     GCGGCAGAAATT      AT-      GA--       4  A  c  c
                                       CTCCCCCTACTG GGTCCAG   GGGGAGAA    TGT
```

GGCCAGCT CCGGGTC CCCCTCTT ACG
ATC AAAG
GAM63 348 PCDH1 1 8176 NP_115796.2 3 614 ATGCCCACGCCT AGA A 4 A c c
AGTCCCATCTGG GGTCCAGATGGGG AG TGT
GCCCCCAT CCGGGTCTACCCT TC GCA
GA- C
GAM63 348 PCDH12 1 5173 NP_057664.1 5 685 CGTGGACAGCAG T AAGA 4 A c
c
CTTCCCATCTGG GG CCAGATGGGGAG TGT
CCTGTCCC CC GGTCTACCCTTC ACA
- GACG
GAM63 348 PDIP38 1 19488 NP_056399.1 3 97 CAGAACTCTTCT - A TG 4 A c c
CTCCCCATCATG GGTCCA GATGGGGAGA GA
GGCCACAG CCGGGT CTACCCCTCT CT
A - TC
GAM63 348 PDIP46 1 2149 NP_115687.2 3 572 GCCTCTTGTCCT T- GA A 4 A c c
CTCCCCAGTGGC GG CCA TGGGGAGA GATG
TCCAGGCC CC GGT ACCCCTCT CTGT
TC G- C
GAM63 348 PDIP46 1 2149 NP_835237.1 3 572 GCCTCTTGTCCT T- GA A 4 A c c
CTCCCCAGTGGC GG CCA TGGGGAGA GATG
TCCAGGCC CC GGT ACCCCTCT CTGT
TC G- C
GAM63 348 PDZGEF1 1 2782 NP_055062.1 3 164 ATGGGGCTTCTT TCC T T 4 A c
c
CTCCCCTTCTTC GG AGA GGGGAGAAGA GT
CTTTCCCC CC TCT CCCCTCTTCT CG
T-- T T
GAM63 348 PER1 1 10857 NP_002607.1 3 128 CTGCCCCAGCTT AG- -- A 4 A c c
CTCCCACCATAG GGTCC ATGG GGAGAAG TG
GGGGCCGG CCGGG TACC CCTCTTC AC
GGA AC G
GAM63 348 PFAS 1 9390 NP_036525.1 3 469 CACCACCTCATT - G - T 4 A c c
GTTCTCATCTGG GGT CCAGATGGGGA AA GA GT
AACTGAAA TCA GGTCTACTCTT TT CT CA
A G A C
GAM63 348 PFKL 1 975 NP_002617.2 3 334 GGCCCTCAGCGT - AGA 4 A c c
CTCCCCATGCTG GGTCCAG ATGGGGAGA TG
GGCTCACT TCGGGTC TACCCCTCT AC
G GCG
GAM63 348 PFN2 2 1957 NP_002619.1 3 24 GTGTAGCAGCCT CC AGA 4 A c c
CTCCCCATCTAC GGT AGATGGGGAGA TGT
CTAGCAAC CCA TCTACCCCTCT ACG
-- CCG
GAM63 348 PFN2 2 15687 NP_444252.1 3 346 TGTAAGCAGCCT CC AGA 4 A c c
CTCCCCATCTAC GGT AGATGGGGAGA TGT
CTAGCAAC CCA TCTACCCCTCT ACG
-- CCG
GAM63 348 PHKG2 1 7564 NP_000285.1 3 150 CCCGGTACCTCT T A A TG 4 A c c
CTCCCCACTGGC GG CCAG TGGGGAGA GA

CAGGACTC CC GGTC ACCCCTCT CT
- - - CC
GAM63 348 PIP5K2B 1 16136 NP_003550.1 3 1496 TTCCTGCATCTT CC AT - 4 A c c
CTCACCCCCTCA GGT AG GGG GAGAAGATGT
ACCAGGAA CCA TC CCC CTCTTCTACG
AC C- A
GAM63 348 PLEK 1 11928 NP_002655.1 3 555 TTTAGACATCTT C - G 4 A c c
CTACTTGCTCTT GGTC AGA TGGG AGAAGATGT
GGCCTTGA CCGG TCT GTTC TCTTCTACA
T C A
GAM63 348 PLP1 1 11746 NP_000524.2 3 761 TGTCAGCATCTT TCC T --- 4 A c c
CTCACTCCCTTC GG AGA GGG GAGAAGATGT
TCCTTGAT CC TCT CCC CTCTTCTACG
--- T TCA
GAM63 348 PNUTL1 1 3567 NP_002679.2 3 697 TCGAGGCCTCTT CCAGA T 4 A c
c
CTCCCCAGCACC GGT TGGGGAGAAGA GT
GCTGTGGT CCA ACCCCTCTTCT CG
CG--- C
GAM63 348 POF1B 1 8710 NP_079197.2 3 1041 AATTTTACATTT T GA A 4 A c c
CAACCCATCTGG GG CCAGATGGG GA GATGT
CTAAAGTT TC GGTCTACCC CT TTACA
- AA -
GAM63 348 PPM1B 1 1077 NP_002697.1 5 372 CCTAGACATCTT CC AT 4 A c c
CTCCCTCCCTTG GGT AG GGGGAGAAGATGT
CCTCAGAT CCG TC TCCCTCTTCTACA
T- CC
GAM63 348 PPM1B 1 1077 NP_808907.1 5 372 CCTAGACATCTT CC AT 4 A c c
CTCCCTCCCTTG GGT AG GGGGAGAAGATGT
CCTCAGAT CCG TC TCCCTCTTCTACA
T- CC
GAM63 348 PPT2 1 3705 NP_005146.3 5 101 CTGCTTTTTCCT T A A TG 4 A c c
CTCCCCACTGGC GG CCAG TGGGGAGA GA
CTAAATGG CC GGTC ACCCCTCT CT
- - C TT
GAM63 348 PPT2 1 3705 NP_620312.1 5 101 CTGCTTTTTCCT T A A TG 4 A c c
CTCCCCACTGGC GG CCAG TGGGGAGA GA
CTAAATGG CC GGTC ACCCCTCT CT
- - C TT
GAM63 348 PRLR 1 2391 NP_000940.1 5 52 TACTCACTCCTT T-- AT 4 A c c
CTCCCTCTTTCT GGTCCAGA GGGGAGAAG GT
GGATTTTA TTAGGTCT TCCCTCTTC CA
TTC CT
GAM63 348 PRO0159 1 17869 NP_054837.1 5 1636 TTGCACGTTCTT ---- - G - 4 A c c
CTCCCATCTTGG GG TCCA GATGGG AGAAGA TGT
AATATCCA CC AGGT CTACCC TCTTCT GCA
TATA T - T
GAM63 348 PRO0456 1 7771 NP_054846.1 5 315 AGACATTTTCAT CAGA-- --- 4 A c c
CTCCCCAAAAGG GGTC TGGGGAGA AGATGT
AGACCCCA CCAG ACCCCTCT TTTACA

AGGAAA ACT

GAM63 348 PROCR 1 20145 NP_006395.1 3 142 AGCTCCTTTCTT TC - TG 4 A c c
CTCCCACATCTG GG CAGATG GGGAGAAGA
CCCACTGA CC GTCTAC CCCTCTTCT
C- A TT

GAM63 348 PSG7 1 14910 NP_002774.1 3 45 CAATTCCATCTT - GATG 4 A c c
CTCCCATGGAAC GGT CCA GGGAGAAGATG
CTCAAAGA CCA GGT CCCTCTTCTAC
A A---

GAM63 348 PSMC3 1 16328 NP_002795.2 5 132 TGGTCCCATCTT TCC A G 4 A c c

CTGCCCGCTCCT GG AG TGGG AGAAGATG
CCAGGAAA CC TC GCCC TCTTCTAC
TCC - G

GAM63 348 PTDSS1 1 12178 NP_055569.1 3 802 ACACCACAGCTT - A- A 4 A c c
CTCCCCAGCTTG GGT CCAG TGGGGAGAAG TGT
GTGCCTTT CCG GGTT ACCCCTCTTC ACA
T CG G

GAM63 348 PTEN 1 6023 NP_000305.1 5 778 ATTATTCGTCTT CCA-- 4 A c c
CTCCCCATTCCG GGT GATGGGGAGAAGATG
CTGCCGCC CCG TTACCCCTCTTCTGC
TCGCC

GAM63 348 RAB1B 1 5292 NP_112243.1 3 152 CCCATCTCCTTC TC ---- A 4 A c c
TGGCCCATCTGC GG CAGATGGG GAG AGATG
CTGCTGCC CC GTCTACCC TTC TCTAC
-- GGTC C

GAM63 348 RABIF 1 10935 NP_002862.2 3 726 GAAGCAGATTTT -- AG G 4 A c c
AACCCCATCTGG GGT CCAGATGGGG AAGAT
CAGCCATT CCG GGTCTACCCC TTTTA
AC AA G

GAM63 348 RAI14 1 2934 NP_056392.1 3 562 ATTCCATGTTTT TC 4 A c c
CTTCCCATCTGC GG CAGATGGGGAGAAGATGT
CTTATATA CC GTCTACCCTTCTTTTGTA
--

GAM63 348 RDHL 2 5428 NP_005762.2 5 794 TTTAGATATTTA C-- A 4 A c c
CTCCCCATTTTA GGTC AGATGGGGAG AGATGT
TGATCCGG CTAG TTTACCCCTC TTTATA
TAT A

GAM63 348 RDHL 2 19957 NP_005762.2 5 526 CTCACCTATCTT CC ------ 4 A c c
CTCTCTTGCTCC GGT AGATGG GGAGAAGATG
ATCTACCA CCA TCTACC TCTCTTCTAT
-- TCGTTC

GAM63 348 REGL 1 7886 NP_006499.1 3 1425 CCATCTCTCTCC ------ A 4 A c c
ATATCAATCTGG GGTCCAGA TGGGGAGA GATG
ACCATCTC CCAGGTCT ACCTCTCT CTAC
AACTAT -

GAM63 348 RFX1 1 8417 NP_002909.2 3 616 GTGTCGCATCTT ATGG 4 A c c
CTCCAGCGCTGG GGTCCAG GGAGAAGATGT
GCCCTCCC CCGGGTC CCTCTTCTACG
GCGA

GAM63 348 RGL 1 13116 NP_055964.2 3 987 TGTCTGGAGTCT G A G 4 A c c
TTTGCCATCTGG GGTCCAGATGG GAGA GAT
ATCTTAGT CTAGGTCTACC TTTT CTG
G - A
GAM63 348 RGL3 1 15226 XP_290867.1 3 5 CACTCTGTCTGT G---- A- - 4 A c c
CTCCCCAAGCTG GTCCAG TGGGGAGA AGATG
GGCAGCCC CGGGTC ACCCCTCT TCTGT
CCCGA GA G
GAM63 348 RGNEF 1 18858 NP_071893.1 3 318 CACATTTTCTAC --- - 4 A c c
CCAATCATCTGG GGTCCAGATG GGG AGAAGATGT
ATTTCAAG TTAGGTCTAC CCC TCTTTTACA
TAA A
GAM63 348 RNF110 1 17598 NP_009075.1 3 496 CTCCCCGTTTCT C - 4 A c c
CTCCCCATCTTG GGTC AGATGGGGAGA AGATG
GCTGCTGT TCGG TCTACCCCTCT TTTGC
T C
GAM63 348 RNF3 1 6132 NP_006306.2 3 1360 TGTCATTGTCTT TC A- - 4 A c c
CTCCACCGGGCT GG CAG TGG GGAGAAGATG
GTTCCCAT CC GTC GCC CCTCTTCTGT
TT GG A
GAM63 348 RNTRE 1 17840 NP_055503.1 3 977 CTCACATGGCTT T AGA- -- 4 A c c
CTCCCCACGAAG GG CC TGGGGAGAAG ATGT
GTCCCAGG CC GG ACCCCTCTTC TACA
T AAGC GG
GAM63 348 RoXaN 1 18964 NP_060060.3 3 162 CCTGTCCATCTT CCAGA 4 A c c
CTCCCCACCACC GGT TGGGGAGAAGATG
GCCCCGGT CCG ACCCCTCTTCTAC
CCACC
GAM63 348 RPC2 1 3735 NP_060552.2 3 583 GAATGTCGTCTT GATG 4 A c c
CTCCTATGGACT GGTCCA GGGAGAAGATG
CAATTGCT TCAGGT TCCTCTTCTGC
A---
GAM63 348 RPS6KC1 1 8683 NP_036556.2 3 683 CAGCATCTTTCT TCC --- 4 A c c
TTCCCCATCTTT GG AGATGGGGA GAAGATGT
CTATTTTC TC TCTACCCCT TTTCTACG
TT- TTC
GAM63 348 RRAS2 1 15394 NP_036382.2 3 64 AGCCCTCATCTT TCC TG 4 A c c
CTCTTTCTCTCC GG AGA GGGAGAAGATG
TCAGTTTA CC TCT TTCTCTTCTAC
--- CT
GAM63 348 S100Z 1 12017 NP_570128.1 5 272 TAATAGTGTCTT -- -- TG 4 A c c
CTCCCCGGGTTT GGT CCAGAT GGGGAGAAGA T
GGTGGCCT CCG GGTTTG CCCCTCTTCT G
GT GG GT
GAM63 348 SAPAP3 1 14421 XP_035601.2 3 289 TGTCCCCACCTC - AG A A 4 A c c
CTCCCCATGGGC GGT CC ATGGGGAG AG TG
ACCATCTC CCA GG TACCCCTC TC AC
C G- C C
GAM63 348 SC65 1 5594 NP_006446.1 3 775 ATCCTGCCACTT T GG- A 4 A c c

CTATGTCTCTGG GGTCCAGA GG AGAAG TG
ACCACAGG CCAGGTCT CT TCTTC AC
- GTA -
GAM63 348 SCN8A 1 1580 NP_055006.1 3 542 AAAGCGCATCTT GATGG 4 A c c
CTCCACATGGGC GGTCCA GGAGAAGATGT
TTCACGTG TCGGGT CCTCTTCTACG
ACA--
GAM63 348 SDK2 1 16444 NP_061937.2 3 169 CACGCCTATCTT TC TG 4 A c c
CTCTCTCTGCTC GG CAGA GGGAGAAGATG
CTCCTTCC CC GTCT CTCTCTTCTAT
TC --
GAM63 348 SEC31B- 1 19442 NP_056305.1 3 310 GCAGGATATCTT AGAT 4 A c c
1 CTCCCCCAGGGA GGTCC GGGGAGAAGATGT
TCTTCTAT CTAGG CCCCTCTTCTATA
GAC-
GAM63 348 SELB 1 7377 NP_068756.1 3 298 AGTATCTTCCAC -- A---- G 4 A c c
TGCCCCATCTGT GGTC CAGATGGGG GAAGAT
TGGCCACC CCGG GTCTACCCC CTTCTA
TT GTCAC T
GAM63 348 SERPINB 1 8247 NP_002630.1 3 1274 GTGACATTCCTT TCC G -- 4 A c c
5 CTCCCATCTCTT GG AGATGGG AGAAG ATGT
CCTTGACA CC TCTACCC TCTTC TACA
TTC - CT
GAM63 348 SF3B3 1 10702 NP_036558.1 3 221 TTTGCTACACTT G---- - A A 4 A c c
CTCCCCACCTGG GT CCAG TGGGGAGAAG TGT
TACATGAT CA GGTC ACCCCTCTTC ACA
TAGTA T C -
GAM63 348 SHOX 1 10815 NP_000442.1 3 1775 AGAAACTATCTT CC -- 4 A c c
CTCCCAACATTT GGT AGATG GGGAGAAGATG
ACTAACAT TCA TTTAC CCCTCTTCTAT
-- AA
GAM63 348 SIAT1 1 17508 NP_003023.1 3 2603 TTTGATAGCCAT GAGA 4 A c c
CTATTCATCTGG GGTCCAGATGGG AGATG
ATCATGGG CTAGGTCTACTT TCTAC
A---
GAM63 348 SIAT1 1 17508 NP_775323.1 3 2603 TTTGATAGCCAT GAGA 4 A c c
CTATTCATCTGG GGTCCAGATGGG AGATG
ATCATGGG CTAGGTCTACTT TCTAC
A---
GAM63 348 SIAT1 1 17508 NP_775324.1 3 2603 TTTGATAGCCAT GAGA 4 A c c
CTATTCATCTGG GGTCCAGATGGG AGATG
ATCATGGG CTAGGTCTACTT TCTAC
A---
GAM63 348 SIAT8E 1 20017 NP_037437.2 5 135 GCCCGGGTCTTG T A - G 4 A c c
CTCCCCATTGGC GG CCAG TGGGGAG AAGAT
CGCCACCT CC GGTT ACCCCTC TTCTG
- - G G
GAM63 348 SIGLEC8 1 7604 NP_055257.1 3 264 CTGGCATCTCTT T AT GA 4 A c c
CTCCCTGGCCCC GG CCAG GGGGA AGATGT

AGCCATCC CC GGTC CCTCT TCTACG
- -- TC

GAM63 348 SLA 1 8297 NP_006739.1 3 168 AATTCGCATCTT CA - --- 4 A c c
CTCTATCCACAT GGTC GATG GG GAGAAGATGT
CATGACCA CCAG CTAC CC CTCTTCTACG
TA A TAT

GAM63 348 SLC16A2 1 12766 NP_006508.1 3 1984 CTGCTTCCATTT CC A A 4 A c c
CTCCCCACCTCA GGT AG TGGGGAGA GATG
CTCTCACC TCA TC ACCCCTCT TTAC
C- C -

GAM63 348 SLC21A3 1 7376 NP_066580.1 3 488 AGCCTACATCTT - - -- 4 A c c
CTTATTCTATTT GGT CC AGATGGG GAGAAGATGT
AGGAATCG CTA GG TTTATCT TTCTTCTACA
A A TA

GAM63 348 SLC21A3 1 7376 NP_602307.1 3 488 AGCCTACATCTT - - -- 4 A c c
CTTATTCTATTT GGT CC AGATGGG GAGAAGATGT
AGGAATCG CTA GG TTTATCT TTCTTCTACA
A A TA

GAM63 348 SLC24A3 1 3098 NP_065740.2 3 575 CTCTTGCATCTT ATG 4 A c c
CTTCCACTGGGC GGTCCAG GGGAGAAGATGT
TCTGGATT TCGGGTC CCTTCTTCTACG
A--

GAM63 348 SLC24A3 1 3098 XP_300245.1 3 575 CTCTTGCATCTT ATG 4 A c c
CTTCCACTGGGC GGTCCAG GGGAGAAGATGT
TCTGGATT TCGGGTC CCTTCTTCTACG
A--

GAM63 348 SLC25A1 1 1680 NP_055066.1 3 833 TATTCTCCTCAT - -- A TG 4 A c c
3 CTCCCCATCATT GGT CCA GATGGGGAGA GA
GGTACCCA CCA GGT CTACCCCTCT CT
T TA A CC

GAM63 348 SLC26A1 1 1293 NP_597996.1 5 2158 CCTGGATCATCT CCA- A 4 A c c
0 CTCCCCATCACT GGT GATGGGGAGA GATG
TGCCTTGG CCG CTACCCCTCT CTAC
TTCA -

GAM63 348 SLC39A4 1 9715 NP_060237.1 5 115 ACAGTCCCTCTT AGA TG 4 A c c
CTCCCCAGGACC GGTCC TGGGGAGAAGA
CCAGGGCC CCAGG ACCCCTCTTCT
--- CC

GAM63 348 SLC6A13 1 4114 NP_057699.2 5 4 AGATAATTCTTC AT- TG 4 A c c
TCCCCTGACTGG GGTCCAG GGGGAGAAGA
ACCTCTGG CCAGGTC CCCCTCTTCT
AGT TA

GAM63 348 SLC6A2 1 6372 NP_001034.1 3 6 TTGCAACACTGG T GG A- A 4 A c c
CTGGCCATCTGG GG CCAGATGG AG AG TGT
CCTGCCTG CC GGTCTACC TC TC ACA
- GG GG -

GAM63 348 SLC9A1 1 9899 NP_003038.2 3 288 AGATCCAGGCTT ATG- A- 4 A c c

CTCCCGGACCTG GGTCCAG GGGAGAAG TG
GACTAGGG TCAGGTC CCCTCTTC AC
CAGG GG

GAM63 348 SLC9A3R 1 10906 NP_004243.1 5 156 CCGTCCCGTCCC - A GAA 4 A c c

1 GTCCCCATCGGA GGT CC GATGGGGA GATG
ACCCCAAG CCA GG CTACCCCT CTGC
A - GCC

GAM63 348 SMARCD1 1 12120 NP_003067.2 3 1418 CAGCAGAATTTT TCC G 4 A c c

CTCCCCGTCTTC GG AGATGGGGAGAAGAT
CCCTTCCT CC TCTGCCCCTCTTTTA
CCT A

GAM63 348 SMARCD1 1 12120 NP_620710.1 3 1418 CAGCAGAATTTT TCC G 4 A c c

CTCCCCGTCTTC GG AGATGGGGAGAAGAT
CCCTTCCT CC TCTGCCCCTCTTTTA
CCT A

GAM63 348 SMCX 1 18708 NP_004178.1 3 379 CTCCTCCCTTCT T -- A TG 4 A c c
CTCCCCAGTTCT GG CCAGA TGGGGAGA GA
GGTCCTGG CC GGTCT ACCCCTCT CT
T TG - TC

GAM63 348 SNRK 1 17487 NP_060189.2 3 18 GTCATCTGCTGT T AGA---- 4 A c c
GGCCCCATCTGG GG CCAGATGGGG AGATG
CCGCTAGC CC GGTCTACCCC TCTAC
- GGTGTCG

GAM63 348 SNX7 1 16240 NP_057060.1 3 120 GAAAAATGTTTT --- GAG 4 A c c
GTACCCATCTGG GG TCCAGATGGG AAGATGT
AAAACCAA CC AGGTCTACCC TTTTGTA
AAA ATG

GAM63 348 SNX7 1 16240 NP_689424.1 3 120 GAAAAATGTTTT --- GAG 4 A c c
GTACCCATCTGG GG TCCAGATGGG AAGATGT
AAAACCAA CC AGGTCTACCC TTTTGTA
AAA ATG

GAM63 348 SOX9 1 14587 NP_000337.1 3 1603 TCTCTACATCTT G GATGG 4 A c c

CTCTTGGAGTGA G TCCA GGAGAAGATGT
GGGAGGCT T AGGT TCTCTTCTACA
G -----

GAM63 348 SSX1 1 2767 NP_005626.1 3 360 CTATCCTCATCT - GA A 4 A c c
CTCCCCAGATGT GGTC CA TGGGGAGA GATG
GACTACTG TCAG GT ACCCCTCT CTAC
T AG -

GAM63 348 SSX8 1 2767 NP_777621.1 3 481 CTATCCTCATCT - GA A 4 A c c
CTCCCCAGATGT GGTC CA TGGGGAGA GATG
GACTACTG TCAG GT ACCCCTCT CTAC
T AG -

GAM63 348 ST6GALN 1 1576 NP_038471.2 3 687 CTCGGGTCTGTC A-- G 4 A c c
AC6 CTCCCCGTCTGG GGTCCAGATGGGGAG AGAT
ACCCTCCC CCAGGTCTGCCCCTC TCTG

CTG G

GAM63 348 SULT4A1 1 12034 NP_795343.1 3 131 GAAGGACATCTT TCC GGA 4 A c c

CACCGTCTCCAT GG AGATGG GAAGATGT

GAATGAGA CC TCTGCC CTTCTACA

--- A--

GAM63 348 SYNGR1 1 8617 NP_004702.2 3 2559 CCAGGCATGATC ---- - AG 4 A c c

TTCCCCATCAGG GGTCCA GATGGGGA GA ATGT

CTGGGCTC TCGGGT CTACCCCT CT TACG

CGGA T AG

GAM63 348 TACC1 1 3381 NP_006274.1 3 4422 AGATGTCACTTT TC T A 4 A c c

CTCCCCCTCTGC GG CAGA GGGGAGAAG TG

CTTTTAGT CC GTCT CCCCTCTTT AC

-- C C

GAM63 348 TCEA3 1 9591 XP_114075.1 3 477 TTGAGTTCCTTC - ATG 4 A c c

TCTCCCATCTGG GGTCCAGATGGG GAGAAG

ATCTCCCA CTAGGTCTACCC CTCTTC

T CTT

GAM63 348 TCTA 2 8960 NP_071503.1 3 1168 GCAGCCTCATCA AA 4 A b b

TTTCCCATCTGG GGTCCAGATGGGGAG GATG

ACCTGGTA CCAGGTCTACCCTTT CTAC

A-

GAM63 348 TCTA 2 9236 NP_071503.1 3 1229 CACTAGCATCTT - CA T - 4 A c b

CTCTACCTTCAA GGT C GA GG GGAGAAGATGT

GAACCAGG CCA G CT CC TCTCTTCTACG

A AA T A

GAM63 348 TEM7 1 7488 NP_065138.2 3 2654 CAAATACATCCA CCAG AA 4 A c c

CTCCCCATGCCA GGT ATGGGGAG GATGT

CTGACATC CCG TACCCCTC CTACA

---- AC

GAM63 348 TGIF 1 14985 NP_003235.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_733796.2 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_775299.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_775300.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_775301.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_775302.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_775303.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 TGIF 1 14985 NP_777480.1 3 356 CTATAGCATCTT G G --- 4 A c c

CTCATTCCCATG G TCCA ATGGG GAGAAGATGT

TGGAACAG C AGGT TACCC CTCTTCTACG

A G TTA

GAM63 348 THPO 1 15986 NP_000451.1 5 7 TCTTCCTACCCA AGA A 4 A c c

TCTGCTCCCCAG GGTCC TGGGGAG AGATG

AGGGCTGC TCGGG ACCCCTC TCTAC

AG- G

GAM63 348 TIMM9 1 8618 NP_036592.1 5 185 TCCCACGTGTTC -- - G 4 A c c

TTTCCCATCTGG GGT CCAGATGGGGA GAA ATGT

CGGCCGCG CCG GGTCTACCCTT CTT TGCA

GC T G

GAM63 348 TIP-1 1 10187 NP_055419.1 3 82 CTTCCACACTCT T GA - 4 A c c

GTCCCCATCTGG GG CCAGATGGGGA AGA TGT

CTTCTGCT TC GGTCTACCCCT TCT ACA

- G- C

GAM63 348 TIX1 1 4786 NP_055850.1 3 1781 AAGTGTCATCTT TC AT- G 4 A c c

CTGCCCTCCCTG GG CAG GGG AGAAGATG

TCCCAATA CC GTC CCC TCTTCTAC

CT CCT G

GAM63 348 TMOD2 1 5911 NP_055363.1 3 81 AAACTCTTCTTC A - TG 4 A c c

TTCCCCATCAGG GGTCC GATGGGGA GAAGA

ACCATTTT CCAGG CTACCCCT CTTCT

A T TC

GAM63 348 TMSNB 1 6359 NP_068832.1 3 131 TTCGGATATCTT T ----- - 4 A c c

CTCACCTATGTT GG CCAG ATGGG GAGAAGATGT

CCCTGGCT TC GGTC TATCC CTCTTCTATA

- CCTTG A

GAM63 348 TNFRSF1 1 1812 NP_003833.3 3 1755 CCATCCTCTCCC - ----- A 4 A c c

0B ACTTCCATCTGG GGT CCAGATGG GGAGA GATG

CATCCCAC CTA GGTCTACC CCTCT CTAC

C TTCAC C

GAM63 348 TNFRSF1 1 1812 NP_671716.1 3 1755 CCATCCTCTCCC - ----- A 4 A c c

0B ACTTCCATCTGG GGT CCAGATGG GGAGA GATG

CATCCCAC CTA GGTCTACC CCTCT CTAC

C TTCAC C

GAM63 348 TNFRSF8 1 10652 NP_001234.1 3 1080 ACCCAGGCATCT TGG A 4 A c

c

GCTTTACTCTGG GGTCCAGA GGAG AGATGT

ACCATAGG CCAGGTCT TTTC TCTACG

CA- G

GAM63 348 TNFRSF8 1 10652 NP_694421.1 3 1080 ACCCAGGCATCT TGG A 4 A c c
GCTTTACTCTGG GGTCCAGA GGAG AGATGT
ACCATAGG CCAGGTCT TTTC TCTACG
CA- G
GAM63 348 TNRC4 1 4212 NP_009116.2 5 372 CCCCTCAGTCTC CCA A G 4 A c c
CTCCCCATCACC GGT GATGGGGAG AGAT
CTCCTCAG CCA CTACCCCTC TCTG
--- C A
GAM63 348 TOPBP1 1 19773 NP_008958.1 3 437 GATTTTTATCTT CC G 4 A c c
CTCACCATTTTA GGT AGATGG GAGAAGATG
CCTCTTTT CCA TTTACC CTCTTCTAT
T- A
GAM63 348 TOSO 1 18553 NP_005440.1 3 131 CATCACTTCCCA C A---- A 4 A c c
TGCCCCATCTCG GGTC AGATGGGG GAAG TG
ACTCCCAT TCAG TCTACCCC CTTC AC
C GTACC -
GAM63 348 TP53I11 2 945 NP_006025.1 5 1011 ACCACCCAGCTT AGA A 4 A c c
CTCCCTGAGGGC GGTCC TGGGGAGAAG TG
CCACCAGC CCGGG GTCCCTCTTC AC
A-- G
GAM63 348 TP53I11 2 2826 NP_006025.1 5 964 ACCGCCCAGCTT AGA A 4 A c c
CTCCCTGAGGGC GGTCC TGGGGAGAAG TG
CCACCAGC CCGGG GTCCCTCTTC AC
A-- G
GAM63 348 TPX1 1 10561 NP_003287.1 3 138 GCAATGCATCTT CAGAT 4 A c c
CTCCCCCAGATC GGTC GGGGAGAAGATGT
ATCACAGA CTAG CCCCTCTTCTACG
AC---
GAM63 348 2 TRIP-Br 1 14867 NP_055570.1 3 1445 ATTACGTCACAG -- AA-- 4 A c c
CTTCCCATCTGG GGT CCAGATGGGGAG GATGT
TTGCTTTC TCG GGTCTACCCTTC CTGCA
TT GACA
GAM63 348 TRPC6 1 20179 NP_004612.2 3 143 AACTTGGGCCAT - GG AA 4 A c c
CCTATCATCTGG GG TCCAGATGG AG GATG
AGCCCTAG CC AGGTCTACT TC CTAC
G A- --
GAM63 348 D U5-116K 1 4615 NP_004238.1 3 412 CCTCGTCTCCCC - - A-- 4 A c c
TGCCCCATCTGG GGT CCAGATGGGG AG AGATG
TGCTTACA TCG GGTCTACCCC TC TCTGC
T G CCC
GAM63 348 UBE2V1 1 17471 NP_071887.1 3 687 TCCCCATATCTT CCAGAT 4 A c c
CTCTCCCCCACC GGT GGGGAGAAGATGT
TTTATCGA CCA CCTCTCTTCTATA
CCC---
GAM63 348 UNC119 2 3155 NP_005139.1 3 488 CTAGCCCCATCC AG- AA 4 A c c
CTCCCCATGAGG GGTCC ATGGGGAG GATG
GGCCAAGA CCGGG TACCCCTC CTAC
GAG C-

GAM63 348 UNC119 2 3155 NP_473376.1 3 816 CTAGCCCCATCC AG- AA 4 A c c
CTCCCCATGAGG GGTCC ATGGGGAG GATG
GGCCAAGA CCGGG TACCCCTC CTAC
GAG C-
GAM63 348 UNC119 2 4264 NP_473376.1 3 58 CTGATCCCATTT G A- A 4 A c c
CTCCCCACCCTG G TCCAG TGGGGAGA GATG
GGGCTCTT C GGGTC ACCCCTCT TTAC
G CC -
GAM63 348 USP22 1 4050 XP_042698.2 3 2792 AATTTCTTTTAG T ---- TG 4 A c c
CTCCCCATCTGG GG CCAGATGGGGAG AAGA
CTGTGAAA TC GGTCTACCCCTC TTCT
- GATT TT
GAM63 348 UVRAG 1 11078 NP_003360.2 3 596 TCGCCCCATCTT GA G 4 A c c
CTCCGTGGATGG GGTCCA TG GGAGAAGATG
GCCATGCG CCGGGT GT CCTCTTCTAC
AG G
GAM63 348 VDR 2 637 NP_000367.1 3 940 GAGCCGCATCTT G-------- T GG 4 A c c
CTCCATCTGGCA G CCAGAT GGAGAAGATGT
GGGTGGGA C GGTCTA CCTCTTCTACG
AGGGTGGGA - --
GAM63 348 VDR 2 4294 NP_000367.1 3 940 GTGAGCCGCATC G------ T GG 4 A c c
TTCTCCATCTGG G CCAGAT GGAGAAGATGT
CAGGGTGG C GGTCTA CCTCTTCTACG
GGTGGGA - --
GAM63 348 VTS5863 1 9459 NP_201572.1 3 1019 TTGCCCCGTCTC C AGA 4 A c c
5 AACCCCATCTGA GGTC AGATGGGG AGATG
CTACCCCA TCAG TCTACCCC TCTGC
- AAC
GAM63 348 WBSCR17 1 3611 NP_071924.1 3 1423 TGATCATCTCCT CC- A -- 4 A c c
CACCCCATCTCC GGT AGATGGGG GA AGATG
CACCTTGT CCA TCTACCCC CT TCTAC
CCC A CC
GAM63 348 ZFP385 1 16862 NP_056296.1 3 6 ACCCATCCTCTT TC - TG 4 A c c
CTCCCCGTACTG GG CAG ATGGGGAGAAGA
CCTCAACC CC GTC TGCCCCTCTTCT
-- A CC
GAM63 348 zizimin 1 4665 NP_056111.1 3 69 CCTTCACATCTT A--- GGA- 4 A c c
1 CAACGCCATCAG GGTCC GATGG GAAGATGT
TGGGACTC TCAGG CTACC CTTCTACA
GTGA GCAA
GAM63 348 ZNF175 1 17154 NP_009078.1 3 84 AGAGAACATCTT T A GGG 4 A c c
CTCAGAATCAGG GG CC GAT GAGAAGATGT
TCTAATTA TC GG CTA CTCTTCTACA
T A AGA
GAM63 348 ZNF179 1 3345 NP_009079.1 3 897 AACACATCCTTT GAT -- 4 A c c
CTCCCCTGGGCT GGTCCA GGGGAGAA GATGT
TGTAAGAA TCGGGT CCCCTCTT CTACA
--- TC

GAM63 348 ZNF261 2 10852 NP_005087.1 3 1026 TGCCTACATCTT G- CC ----- 4 A c c
CTCTCTTCCCCA GT AGATGGGGA GAAGATGT
TCTTGCAT CG TCTACCCCT CTTCTACA
TA T- TCTCT
GAM63 348 ZNF261 2 12406 NP_005087.1 3 1027 ACATCTTCTCTC GG ------ ----- 4 A c c
TTCCCCATCTTG TCCA GATGGGGA GAAGAT
CATTGGAG AGGT CTACCCCT CTTCTA
G- TACGTT TCTCT

GT
CA

GAM63 348 ZNF272 1 9716 XP_030227.3 3 128 GAGAGGAAACAT T GGAG 4 A c c

CTTACCATCTGG GG CCAGATGG AAGATGT
TCATTCAT CT GGTCTACC TTCTACA
- A---
GAM63 348 ZNF323 1 13326 NP_112161.2 3 1089 TTCAAATCTTTC G - -- G 4 A c c
CTCCCCATTTGT G TC CAGATGGGGAG AAGAT
GAGCTGTG C AG GTTTACCCCTC TTCTA
G T CT A
GAM63 348 ZNF435 1 19017 NP_079507.1 3 128 TCAGTCATCATT TG GAG - 4 A c c

AAACTTCTCTGG GGTCCAGA GG AA GATG
ACCAAAAA CCAGGTCT TC TT CTAC
CT AAA A
GAM63 348 ZNF436 1 18528 NP_085137.1 3 486 CACACACATCTT AGA -- A 4 A c c
CCCTTCCAAAGG GGTCC TGG GG GAAGATGT
GCTTTTTC TCGGG ACC CC CTTCTACA
AA- TT -
GAM64 239 BAPX1 1 11199 NM_001189.2 3 GCGCACACCCAG CA T GC CC 3 C c
c

GCAGC GCTGCCTGGGT GTG CGC
CGACGGACCCA CAC GCG
-- - -- --
GAM64 239 DHFR 1 3874 NM_000791.2 5 GGGCGGCCACAA CA T CT 3 C c c
TTTCGCGC GC GC GGGTTGTGGCCGCCC
CG CG TTTAACACCGGCGGG
-- - C-
GAM64 239 FGFR2 1 6486 NM_023031.1 3 GGGCGGCCCGGC CA CTGG T 3 C c
c

AAGCAGC GCTGC GTTG GGCCGCCC
CGACG CGGC CCGGCGGG
-- AA-- -
GAM64 239 GFRA1 1 17656 NM_145793.1 5 GGGCGGCCAGAG CCTGG G 3 C c
c

CAGCACAGCTG CAGCTG GTT TGGCCGCCC
GTCGAC CGA ACCGGCGGG
ACGA- G
GAM64 239 KIAA116 1 12904 5 GGGCGGCCACAG C CCTGGG 3 C c c

```
          9                          ATTACACTG   CAG TG     TTGTGGCCGCCC
                                            GTC AC     GACACCGGCGGG
                                              - ATTA--
GAM64     239   KIAA139 1   13496  XM_032054.2  3       GGGCGGCCATTC CAG      GTT           3  C  c
c
          6                          GGGCAG       CTGCCTGG  GTGGCCGCCC
                                            GACGGGCT   TACCGGCGGG
                                           ---       ---
GAM64     239   KIAA150 1   10614  XM_029353.1  3       GGGCAGCCTGCA       GG  TGT  C        3  C  c
c
          9                          GGGCAGCTG   CAGCTGCCT  GT   GGC GCCC
                                            GTCGACGGG  CG   CCG CGGG
                                               A-  T--   A
GAM64     239   KIAA169 1   5765   XM_166523.1  3       GGCAGCCAGAGG       GGGT G   C  C      3  C  c
c
          1                          GCAGCTG     CAGCTGCCT    T TGGC GCC
                                            GTCGACGGG    A ACCG CGG
                                               ---- G    A   -
GAM64     239   LOC1446 1   10853  XM_096648.1  5       GTGCCACACCCA          T    C  CC      3  C  c  c
          67                         GGCAGCTG    CAGCTGCCTGGGT GTGGC GC
                                            GTCGACGGACCCA CACCG TG
                                                 -    - --
GAM64     239   LOC1973 1   15432  XM_113871.3  5       GGCAGCCACAGC       CTGGGT    C  C      3  C
c  c
          50                         AGCTG       CAGCTGC     TGTGGC GCC
                                            GTCGACG     ACACCG CGG
                                               ------      A   -
GAM64     239   LOC2205 1   11757           5       GGGCGGAGGAGA     G      GTGG          3  C  c  c
          49                         CCCAGGAAGCTG CAGCT CCTGGGTT    CCGCCC
                                            GTCGA GGACCCAG    GGCGGG
                                              A       AGGA
GAM64     239   LOC5446 1   9231            5       GGGCAACAAACC        G   G  GCC        3  C  c  c
          6                          AGGGCAGCTG   CAGCTGCCT GGTT TG   GCCC
                                            GTCGACGGG CCAA AC   CGGG
                                               A   - AA-
GAM64     239   MGC1111 1   4324   NM_032310.2  3       GGGCGGCTTGTC    T     TTGT          3  C  c  c

          5                          CCAGGCTGCTG  CAGC GCCTGGG    GGCCGCCC
                                            GTCG CGGACCC    TCGGCGGG
                                              T      TGT-
GAM64     239   MGC1842 1   8701   XM_037797.4  3       GGCAGCTGACGA       GG  GT  C  C      3  C  c
c
                                          GGCAGCTG    CAGCTGCCT  GTT  GGC GCC
                                            GTCGACGGA  CAG  TCG CGG
                                               G-   --   A   -
GAM64     239   NDRG4   1   19628  NM_020465.1  3       GGGCGCTCGGAC CA       GT  T  C        3  C  c
c
                                          CAGGCAGC      GCTGCCTGG  TG GGC GCCC
                                            CGACGGACC  GC TCG CGGG
                                           --        AG   -   -
```

GAM64 239 PDZD2 1 8880 5 GGCGGCCATCCA GC GTT C 3 C c c
GAAGCTG CAGCT CTGG GTGGCCGCC
GTCGA GACC TACCGGCGG
A- --- -
GAM64 239 RAD50 1 12678 NM_005732.2 5 GGGCGGCCGAGG G GGTTG 3 C c
c
CAGGAAGCTG CAGCT CCTG TGGCCGCCC
GTCGA GGAC GCCGGCGGG
A GGA--
GAM64 239 REPS2 1 7876 NM_004726.1 5 GCGGCCGCGCGG TGG T CC 3 C c
c
CAGCTG CAGCTGCC GT GTGGCCGC
GTCGACGG CG CGCCGGCG
--- - --
GAM65 272 ATF3 1 7146 NP_001665.1 3 92 TGAAGCCATTGG T-- TT 3 B c c
AGAGCTGTCTTC ACAG GAC GCTCTCCAATGG
CTGTGTAC TGTC CTG CGAGAGGTTACC
CTT T-
GAM65 272 ATF3 1 7146 NP_004015.2 3 423 TGAAGCCATTGG T-- TT 3 B c c
AGAGCTGTCTTC ACAG GAC GCTCTCCAATGG
CTGTGTAC TGTC CTG CGAGAGGTTACC
CTT T-
GAM65 272 BYSL 1 7672 NP_004044.2 3 314 TCTATGGCTATT CTCTC 3 B c c
GTGTCAGGTCAC ACAGTGACTTG CAATGG
TGTGGATA TGTCACTGGAC GTTATC
TGT--
GAM65 272 CA3 1 9592 NP_005172.1 3 62 ACCTACCATTGG C TG T- 3 B c c
AGAGCTTGGTTC A AG ACT GCTCTCCAATGG
CTTGCCTC G TC TGG CGAGAGGTTACC
T CT TT
GAM65 272 CBFA2T2 1 14682 NP_005084.1 3 588 CAGAGTCCACAG G C AA 3 B c
c
GAAAGAAGTCAC ACAGTGACTT CT TCC TGG
TGTTGCAA TGTCACTGAA GA AGG ACC
- A AC
GAM65 272 CBFA2T2 1 14682 NP_787060.1 3 588 CAGAGTCCACAG G C AA 3 B c
c
GAAAGAAGTCAC ACAGTGACTT CT TCC TGG
TGTTGCAA TGTCACTGAA GA AGG ACC
- A AC
GAM65 272 CD8A 1 11570 NP_001759.3 3 66 CTTCCTTTTGAG C T - T- 3 B c c
GGAGCAAGTCCT A AG GACTTGCTCTC CAA GG
TCCCTTTC C TC CTGAACGAGGG GTT CC
T - A TT
GAM65 272 CD8A 1 11570 NP_741969.1 3 66 CTTCCTTTTGAG C T - T- 3 B c c
GGAGCAAGTCCT A AG GACTTGCTCTC CAA GG
TCCCTTTC C TC CTGAACGAGGG GTT CC
T - A TT
GAM65 272 CES1 1 12659 NP_001257.3 3 155 AGAGGCCATGAA T CCA 3 B c c
GGAGCAAGTTTT ACAG GACTTGCTCT ATGG

GTATTTGT TGTT TTGAACGAGG TACC
- AAG

GAM65 272 CHGB 1 7161 NP_001810.1 3 27 TGCTGTCATTGG A TG - 3 B c c
AGCGGTGGGCAC ACAGTG CT CT CTCCAATGG
TGTTAAGA TGTCAC GG GG GAGGTTACT
- GT C

GAM65 272 CML66 1 10642 NP_116258.1 3 846 ATGTTCCATTGG A-- - C C-- 3 B c c
ACAAAGCAAATC CA GTGA TTGCT TCCAATGG
ACATGGCC GT CACT AACGA AGGTTACC
CCG A A AAC

GAM65 272 CSRP2BP 1 19687 NP_065397.1 3 55 ATGTGCTATTGG T C 3 B c c
AGAACAGGTCTT ACAG GACTTG TCTCCAATGG
TGTGGAGA TGTT CTGGAC AGAGGTTATC
T A

GAM65 272 CSRP2BP 1 19687 NP_808779.1 3 55 ATGTGCTATTGG T C 3 B c c
AGAACAGGTCTT ACAG GACTTG TCTCCAATGG
TGTGGAGA TGTT CTGGAC AGAGGTTATC
T A

GAM65 272 CX3CL1 1 17574 NP_002987.1 3 1624 TCTGGTCCATAG AC CA 3 B c c

AGAGCAAAACGC ACAGTG TTGCTCTC ATGG
TGTGCTGC TGTCGC AACGAGAG TACC
AA A-

GAM65 272 DBY 1 3439 NP_004651.2 3 2258 TGTAATCATTGA CTCTC 3 B c c
ACCTCGAGTCAC ACAGTGACTTG CAATGG
TGTAAAAG TGTCACTGAGC GTTACT
TCCAA

GAM65 272 EHD1 1 2264 NP_006786.2 3 1522 GCGCTGTCCTTG G TC T 3 B c c
CCGGGAAGTCAC ACAGTGACTT CTC CAA GG
TGTTGAAG TGTCACTGAA GGG GTT CC
- CC -

GAM65 272 ERN1 1 17882 NP_001424.1 3 557 TGTGCCCAGAGT -- - CAA 3 B c c
AGCCCAGGTCAC ACAGTGACTT GCT CTC TGG
TGTTAACT TGTCACTGGA CGA GAG ACC
CC T ---

GAM65 2724 FLJ0002 1 1895 NP_203745.1 5 300 AGTTGAGATTGG - AC- G 3 B c c
AGAGCAGCGCCG ACAG TG TTGCTCTCCAAT
TCTGTACT TGTC GC GACGAGAGGTTA
T CGC G

GAM65 2724 FLJ0002 1 1895 XP_033361.2 5 316 AGTTGAGATTGG - AC- G 3 B c c
AGAGCAGCGCCG ACAG TG TTGCTCTCCAAT
TCTGTACT TGTC GC GACGAGAGGTTA
T CGC G

GAM65 2720 FLJ2040 1 1121 NP_060274.1 3 399 GCTCACCATTGG A---- C C- 3 B c c
AGAATCAGCTCA CAGTGA TTG TCTCCAATGG
CTGCTCTC GTCACT GAC AGAGGTTACC
CTCTC C TA

GAM65 2724 FLJ2051 1 7512 NP_060326.1 5 126 CCAGCCCATTGG GC 3 B b b
AGAAAAGTTACT ACAGTGACTT TCTCCAATGG
GTTCAGTC TGTCATTGAA AGAGGTTACC

A-

GAM65 2724 FLJ30631 1 5870 NP_694559.1 3 219 TAATCTCATTGG GA G T 3 B c c
AGGAGGGAACTG ACAGT CTT C CTCCAATGG
TTTCCTGC TGTCA GGA G GAGGTTACT
AG - -

GAM65 2725 FLJ35151 1 13879 NP_689744.2 3 157 GAGACCTCCTGC TC AT- 3 B c c
CGGGCAGGTCAC ACAGTGACTTGCTC CA GG
TGTGCTGA TGTCACTGGACGGG GT CC
CC CCT

GAM65 272 GABRE 1 12964 NP_068819.1 5 496 CCCTGGCATTGG A- G 3 B b b
AGAGAAGCCCAC ACAGTG CTT CTCTCCAATG
TGTGGTCA TGTCAC GAA GAGAGGTTAC
CC -

GAM65 272 GABRE 1 12964 NP_068822.1 5 496 CCCTGGCATTGG A- G 3 B b b
AGAGAAGCCCAC ACAGTG CTT CTCTCCAATG
TGTGGTCA TGTCAC GAA GAGAGGTTAC
CC -

GAM65 272 GABRE 1 12964 NP_068830.1 5 1233 CCCTGGCATTGG A- G 3 B b b
AGAGAAGCCCAC ACAGTG CTT CTCTCCAATG
TGTGGTCA TGTCAC GAA GAGAGGTTAC
CC -

GAM65 272 GREB1 1 5081 NP_683701.1 3 773 CAGCCCGGGGAC A -- AAT 3 B c c
AGAGCAAGACAC ACAGTG CTTGCTC TCC GG
TGTCTCAA TGTCAC GAACGAG AGG CC
A AC GGC

GAM65 272 HBP1 1 19617 NP_036389.2 3 712 TTAATAGCATTG TGC T 3 B c c
GGATATAGTCAC ACAGTGACT TC CCAATG
TGTAATGG TGTCACTGA AG GGTTAC
TAT -

GAM65 272 HEMK 1 6305 NP_057257.1 3 1840 GTGCAGTGTTGG AC TG 3 B c c
AGAGTGACACTG ACAGTG T CTCTCCAATG
TCGGGGCA TGTCAC A GAGAGGTTGT
-- GT

GAM65 272 HNRPD 1 14479 NP_002129.2 3 283 CCCCAGTATTGT T C 3 B c c
AGAGCAAGTCTT ACAG GACTTGCTCT CAATG
GTGTTAAA TGTT CTGAACGAGA GTTAT
- T

GAM65 272 HNRPD 1 14479 NP_112737.1 3 283 CCCCAGTATTGT T C 3 B c c
AGAGCAAGTCTT ACAG GACTTGCTCT CAATG
GTGTTAAA TGTT CTGAACGAGA GTTAT
- T

GAM65 272 HNRPD 1 14479 NP_112738.1 3 283 CCCCAGTATTGT T C 3 B c c
AGAGCAAGTCTT ACAG GACTTGCTCT CAATG
GTGTTAAA TGTT CTGAACGAGA GTTAT
- T

GAM65 272 HS2ST1 1 19213 NP_036394.1 3 4389 CACATCTGTTGG C CTTG 3 B c c
AGAGATAATCAC A AGTGA CTCTCCAATGG
TCCTTTTC C TCACT GAGAGGTTGTC
C AATA

GAM65 272 HSPC056 1 8261 NP_054873.1 3 1003 CAAGACCATCAG - AC CA 3 B c c
AGAGCAAACCAC ACA GTG TTGCTCTC ATGG
ATGTTCTG TGT CAC AACGAGAG TACC
A CA AC
GAM65 272 ITGAV 1 15711 NP_002201.1 3 2050 ATCTTGTATTGG A GC-- 3 B c c
AGATTGAAAGAT ACAGTG CTT TCTCCAATG
GCTGTAAT TGTCGT GAA AGAGGTTAT
A AGTT
GAM65 272 KCNK7 1 19349 NP_005705.1 3 145 GTGCCAGTTGCC A----- C- - 3 B c c
AGGGCAAGTCAC CAGTGACTTGCTCT CAA TGG
TGCGCTGG GTCACTGAACGGGA GTT ACC
GGTCGC CC G
GAM65 272 KCNK7 1 19349 NP_258416.1 3 68 GTGCCAGTTGCC A----- C- - 3 B c c
AGGGCAAGTCAC CAGTGACTTGCTCT CAA TGG
TGCGCTGG GTCACTGAACGGGA GTT ACC
GGTCGC CC G
GAM65 272 KIAA035 1 594 XP_290667.1 3 395 CACAGAAGAATT CTC G 3 B c c
0 GGACCAGGTCAC ACAGTGACTTG TCCAAT
TGTACGTA TGTCACTGGAC AGGTTA
C-- A
GAM65 272 KIAA055 1 18362 XP_085507.1 3 1347 CCATTGCATTTG --- - TCTC- 3 B c c
7 TCACCTAGTCAC ACAGTGACT TG C CAATGG
TGTATATA TGTCACTGA AC G GTTACC
TCC T TTTAC
GAM65 272 KIAA056 1 13255 NP_055519.1 3 835 CTAAAGACATGT G TC A 3 B c c
2 GGAGGAAGTCAC ACAGTGACTT CTC CA TG
TGTTAAAT TGTCACTGAA GAG GT AC
G GT -
GAM65 272 KIAA063 1 14190 NP_056360.1 5 197 TGCAGCCCATGG A AC- A 3 B c c
2 AGAGCAACTACA AC GTG TTGCTCTCCA TGG
CGGTGCTG TG CAC AACGAGAGGT ACC
G ATC -
GAM65 272 KIAA080 1 15077 XP_291080.1 3 484 AGCATGCCTTGG A TG- T 3 B c c
4 AGAGAGCAGACA ACAGTG CT CTCTCCAA GG
CTGTGGGG TGTCAC GA GAGAGGTT CC
A CGA -
GAM65 272 KIAA134 1 4109 XP_047617.4 3 624 GTTCTTCATAGG GACT A 3 B c c
9 AGAGCAACTGTA ACAGT TGCTCTCC ATGG
GGTGATCA TGTCA ACGAGAGG TACT
---- A
GAM65 272 KIAA142 1 19203 XP_029703.1 3 3255 GTTTGACATTGG G T --- 3 B c c
3 AGATACGCTAGT ACAGT ACT GC TCTCCAATG
AACTGTGA TGTCA TGA CG AGAGGTTAC
A T CAT
GAM65 272 KIAA202 1 18104 XP_291326.1 3 4704 GTAAGGCATTGG G A GC 3 B c c
2 AGAAGGACAATG ACA TG CTT TCTCCAATG
TAAAAGAC TGT AC GGA AGAGGTTAC

A A --

GAM65 272 LNIR 1 18936 NP_112178.1 3 210 TCTCCCACCATG TCTCCA 3 B c c
CATGCAGGTCAC ACAGTGACTTGC ATGG
TGTGTGTG TGTCACTGGACG TACC
TACG--

GAM65 272 LOC1378 1 6165 XP_059923.2 3 177 TGCCAGGACTTG T CT ---- 3 B c c
29 GGAAGCAGTCAC ACAGTGACT GCT CCAA TGG
TGTGAAAT TGTCACTGA CGA GGTT ACC
- AG CAGG

GAM65 272 LOC1522 1 16959 XP_098182.1 3 658 GGGTTATATTGG A---- T- T 3 B c c
45 AGAGCCAGTCTT CAG GACT GCTCTCCAATG
CTGCGGTT GTC CTGA CGAGAGGTTAT
TTGGC TT C

GAM65 272 LOC1548 1 18739 XP_098626.1 3 2298 GGCAGGCAGAGG C A AA 3 B c
c
77 AGAGCAAGCTAC A AGTG CTTGCTCTCC TG
TTCTGGGA C TCAT GAACGAGAGG AC
T C AG

GAM65 272 LOC2209 1 20127 XP_166145.2 3 709 AACTCCAAATGG T - A- 3 B c c
63 AGAAGTAGTCAC ACAGTGACT GCT CTCCA TGG
TGTAGACT TGTCACTGA TGA GAGGT ACC
- A AA

GAM65 272 LOC2559 1 10361 NP_787050.1 3 215 GGCTGCCATTGG - TT T 3 B c c
67 AGGCTGTTATCT ACAG TGAC GC CTCCAATGG
GTGAAGAA TGTC ATTG CG GAGGTTACC
T T- -

GAM65 272 LOC2831 1 1913 XP_210922.1 3 1105 ATGGGCTCCTTG A CAAT 3 B c
c
54 AGAGCAAGCATT ACAGTG CTTGCTCTC GG
GTTTCCCA TGTTAC GAACGAGAG CC
- TT--

GAM65 272 LOC2831 1 19931 XP_208535.1 3 1087 AACCTGGGTGAT T ---- AAT 3 B c
c
70 AGAGCAAGTCTC ACAG GACTTGCTCT CC GG
TGTCTTTA TGTC CTGAACGAGA GG CC
T TAGT GT-

GAM65 272 LOC2836 1 18325 XP_208773.1 3 331 TCTGATTATTGG T GC- 3 B c c
64 AGACAGAAGTCC ACAG GACTT TCTCCAATGG
TGTCACTT TGTC CTGAA AGAGGTTATT
- GAC

GAM65 272 LOC2845 1 11631 XP_211518.1 3 64 CCAGTCCAAAGG T C AA 3 B c c
55 ACAGTGTGTCAC ACAGTGAC TGCT TCC TGG
TGTGAACT TGTCACTG GTGA AGG ACC
T C AA

GAM65 272 LOC2846 1 18217 XP_211569.1 3 1104 CAGCTCCATTGG A--- CT -- 3 B c c

47 AGGGGACACATC CAGTGA TG CTCTCCAATGG
ACTGGCTT GTCACT AC GGGAGGTTACC
TTCG AC AG

GAM65 272 LOC2852 1 5907 XP_209520.1 5 589 GGATATTATTGG --- C 3 B c c

16 AGACGGGGTTTC ACAGTGA CTTG TCTCCAATGG
ACTGTGTT TGTCACT GGGC AGAGGTTATT
TTG -
GAM65 272 LOC2858 1 12618 XP_212028.1 3 1295 GCTCTCTATTGG A--- G G-- 3 B c c

06 AGAGAGGAAGTG CAGT ACTT CTCTCCAATGG
ACTGGCCT GTCA TGAA GAGAGGTTATC
TCCG G GGA
GAM65 272 LOC2863 2 7390 XP_212293.1 5 1756 ACTCCCGTGGGG - - A 3 B c c
74 AAGCAGCGTCAC ACAGTGAC TTGCT CTCCA TGG
TGTGCCCT TGTCACTG GACGA GGGGT GCC
C A -
GAM65 272 LOC2863 2 19118 XP_212293.1 5 111 AAACAACACTGG GAC A 3 B c c

74 AGAGCAGAGGCT ACAGT TTGCTCTCCA TG
GTGGCTTG TGTCG GACGAGAGGT AC
GA- C
GAM65 272 LOC3395 1 11280 XP_290951.1 3 6 AGTTCACATTGG -- GC 3 B c c
56 AGAAAAGCCTTA ACAGTGA CTT TCTCCAATG
CTGTACTG TGTCATT GAA AGAGGTTAC
CC A-
GAM65 272 LOC3399 1 18421 XP_295105.1 3 1990 GTATGGGTGTGT TGC 3 B c c

29 TGGGGAAGTCAC ACAGTGACT TCTCCAATG
TGTGTTTC TGTCACTGA AGGGGTTGT

GAM65 272 LOC3490 1 13327 XP_302942.1 5 250 TGTAGCCCATGG TT CT A 3 B c
c
37 CCAGTCTGTCAC ACAGTGAC GCT CCA TGG
TGTGTCCT TGTCACTG TGA GGT ACC
TC CC -
GAM65 272 LOC9067 2 2098 XP_033352.1 3 709 CTCTTCCCTTGG TTGC T 3 B c c
0 AGAGTCACTGTT ACAGTGAC TCTCCAA GG
CACCTCAG TGTCACTG AGAGGTT CC
---- C
GAM65 272 LOC9067 2 18422 XP_033352.1 3 708 AAAACTCTTCCC TTGC T 3 B c c

0 TTGGAGAGTCAC ACAGTGAC TCTCCAA GG
TGTTCACC TGTCACTG AGAGGTT CC
---- C
GAM65 272 MAML1 1 4165 NP_055572.1 3 890 TGCCCATGGTGG - CA- 3 B c c
GAGCGTGGTCAC ACAGTGACT TGCTCTC ATGG
TGTGCAGT TGTCACTGG GCGAGGG TACC
T TGG
GAM65 272 MAPKAPK 1 16295 NP_004626.1 3 781 TTTTTCCACTTT TTGCTC -- 3 B c
c
3 GGAAAATGTCAC ACAGTGAC TCCAA TGG
TGTGACAA TGTCACTG AGGTT ACC
TAAA-- TC
GAM65 272 MCL1 1 13184 NP_068779.1 3 200 GCTCCCCATTGA GC TC- 3 B c c

TTGAAGAGTCAC ACAGTGACTT TC CAATGG
TGTCTGAA TGTCACTGAG AG GTTACC
A- TTA

GAM65 272 MGC1593 1 5372 NP_542392.2 3 995 CCCTGCCATTGG - TGCTC 3 B c c

7 AACTTGGATTAC ACAGTGA CT TCCAATGG
TGTGAACA TGTCATT GG AGGTTACC
A TTCA-

GAM65 272 MGC3360 1 13239 NP_689604.1 3 253 ATCTGCAGTGTT T T C 3 B c c

2 GAGGCCAGTCAC ACAGTGACT GC CTC AATG
TGTTGGAA TGTCACTGA CG GAG TTGT
C - -

GAM65 272 MGC3951 1 16267 NP_776183.1 3 684 CACCTCCATTGG A---- T -- 3 B c c

8 AGGGCAGGACTC CAG GA CTTGCTCTCCAATGG
TTGATTGT GTT CT GGACGGGAGGTTACC
TGTTA - CA

GAM65 272 MGC4248 1 12365 NP_115709.2 3 328 GGGAGGCCAAGG C T AA 3 B c c

TGAGCAAGTCAC A AGTGACTTGCTC CC TGG
TTGAGGTC G TCACTGAACGAG GG ACC
T T A-

GAM65 272 MGC955 1 19343 NP_077002.1 3 193 GAATAATCATTG GC C 3 B c c
AGACAGAGTCAC ACAGTGACTT TCTC AATGG
TGTCTTTC TGTCACTGAG AGAG TTACT
AC -

GAM65 272 NEURL 1 7940 NP_004201.2 3 1956 GCAGTGGGTGTG G ----- A 3 B c c
TGGGGAAGTCAC ACAGTGACTT CTC TCCA TG
TGTCCCAC TGTCACTGAA GGG GGGT AC
G TGTGT G

GAM65 272 PDE4C 1 1136 NP_000914.1 3 1219 CCTGGGGCTGAC A ----- AAT 3 B c c

AGAGCAAGACAC ACAGTG CTTGCTCT CC GG
TGTCTCAA TGTCAC GAACGAGA GG CC
A CAGTC GGT

GAM65 272 PIWIL2 1 15554 NP_060538.2 3 232 TGTTGCCTGTGT A C AT 3 B c c
AGAGCAAGTTAC AC GTGACTTGCTCT CA GG
GGTGGTAC TG CATTGAACGAGA GT CC
G T GT

GAM65 272 PLCG1 1 17197 NP_002651.1 3 38 CAGCCTCGTTGG GA -- 3 B c c
AGAGCAGCAGGT ACAGT CT TGCTCTCCAATGG
GCTGTGCG TGTCG GA ACGAGAGGTTGCT
TG CG

GAM65 272 PLXNA2 1 1002 NP_079455.1 3 557 GAGAGACATTGG GACTTG 3 B c c

AGAGAAAATGAC ACAGT CTCTCCAATG
TGTCTCCT TGTCA GAGAGGTTAC
GTAAAA

GAM65 272 RAD21 1 14920 NP_006256.1 5 136 AACTCCCAGCGG T- ---- AA 3 B c c
AGAGCAAGGTTT ACAG GA CTTGCTCTCC TGG
TCTTCTGT TGTC CT GAACGAGAGG ACC

TT TTTG CG

GAM65 272 RBM7 1 8355 NP_057174.1 3 634 AATCCCATTTGA C C- C 3 B c c
GGTATAAGTCAC A AGTGACTTG TCTC AATGG
TCAGGAAG A TCACTGAAT GGAG TTACC
C AT T

GAM65 272 SLA 1 16487 NP_006739.1 3 397 CAAGGTCATTGG TGACTTG 3 B c c

AGAGAACTTCTG ACAG CTCTCCAATGG
TATGGGCA TGTC GAGAGGTTACT
TTCAA--

GAM65 272 SYTL4 1 8344 NP_542775.1 3 872 TGCAGTCATTGG C T - TG 3 B c c
AGAGAGAGCTCC A AG GA CT CTCTCCAATGG
TCATTTCT A TC CT GA GAGAGGTTACT
C - C GA

GAM65 272 sytXIV 1 12988 NP_694994.1 3 703 CCTGATCCAAAG C CAA 3 B c c
AGACCAAGTCAC ACAGTGACTTG TCTC TGG
TGTACTGG TGTCACTGAAC AGAG ACC
C AA-

GAM65 272 SZF1 1 18762 NP_057173.1 3 381 AGTGTACCTTGG C ACTT T 3 B c c
AGAGCTATCCAC A AGTG GCTCTCCAA GG
TCAGGCCC A TCAC CGAGAGGTT CC
C CTAT -

GAM65 272 TBC1D5 1 11874 NP_055559.1 5 1299 CTTGTTCACTGG T C- A 3 B c c
ACCAGTAGTCAC ACAGTGACT GCT TCCA TGG
TGTTAAAT TGTCACTGA TGA AGGT ACT
- CC C

GAM65 272 TRPM7 1 14667 NP_060142.2 3 711 TTAAACATTGTT CTCTC- 3 B c c
TTATCAAGTCAC ACAGTGACTTG CAATG
TGTTAAGT TGTCACTGAAC GTTAC
TATTTT

GAM65 272 UBN1 1 2743 NP_058632.1 3 710 AAATGCCATTGG GA G C 3 B c c
ATAGAAGGGGAC ACAGT CTT CT TCCAATGG
TGTTCTTC TGTCA GGA GA AGGTTACC
GG A T

GAM65 272 VNN1 1 19406 NP_004657.1 3 1251 CTTCTGCACAGG C A AA 3 B c c
AGAGCAAGGCAC A AGTG CTTGCTCTCC TG
TTGCAGTA G TCAC GAACGAGAGG AC
T G AC

GAM65 272 VPS45A 1 2588 NP_009190.2 3 94 CAAAGGTGTTGG T ------ 3 B c c
AGAGCAGCTTTG ACAG GACT TGCTCTCCAATG
GGTTCTGT TGTC TTGG ACGAGAGGTTGT
- GTTTCG

GAM65 272 ZD52F10 1 1210 NP_201574.1 3 278 CTCCCTTTGGTG GC-- T T 3 B c c
ACCTGAAGTCAC ACAGTGACTT TC CCAA GG
TGTGACAG TGTCACTGAA AG GGTT CC
GTCC T T

GAM65 272 ZFD25 1 6103 NP_057304.1 3 1659 AATTTATATTGG A GC 3 B c c
AGAAAAGCACTG ACAGTG CTT TCTCCAATG
TAAATGTA TGTCAC GAA AGAGGTTAT
- A-

GAM65 272 ZNF177 1 16167 NP_003442.1 3 80 AACATATATTGG TGA G 3 B c c
AGAGAAGCCCTG ACAG CTT CTCTCCAATG
TTATGGTC TGTC GAA GAGAGGTTAT
CC- -
GAM65 272 ZNF192 1 1148 NP_006289.1 3 278 TAAAATAGCATT - TG CC 3 B c c
AGAGCAAGTTGC ACA G ACTTGCTCT AATG
TTGTCATG TGT C TGAACGAGA TTAC
T GT --
GAM65 272 ZNF211 1 11280 NP_006376.1 3 6 AGTTCACATTGG -- GC 3 B c c
AGAAAAGCCTTA ACAGTGA CTT TCTCCAATG
CTGTACTG TGTCATT GAA AGAGGTTAC
CC A-
GAM65 272 ZNF211 1 11280 XP_290823.1 3 6 AGTTCACATTGG -- GC 3 B c c
AGAAAAGCCTTA ACAGTGA CTT TCTCCAATG
CTGTACTG TGTCATT GAA AGAGGTTAC
CC A-
GAM65 272 ZNF397 1 2348 NP_115723.1 3 378 CAAGGACATTGG AC--- G-- 3 B c c
AGAGATAGAGTC AGTGACTT CTCTCCAATG
ACTATTAC TCACTGAG GAGAGGTTAC
CATTA ATA
GAM66 238 BOP 1 4943 XP_097915.2 3 2017 CACCCCACTGGC T----- C ATA 1 B c c
CTTCTCAGGTGC TTGCACCTGAGA AG GCC
AATCAGTA AACGTGGACTCT TC CGG
ATGACT - ---
GAM66 238 C12orf4 1 3404 NP_065107.1 3 369 AGAGGCTTGACT T----- - AT- 1 B c c
CGTCTCAGGTGC TTGCACCTGAGAC AG AGCC
AATCCTTA AACGTGGACTCTG TC TCGG
ATTCCT C AGT
GAM66 238 C5orf8 1 18156 NP_006807.1 3 247 TCCTGGGGCTGG A GA 1 B c c
TGTCTCAGGAGC TTTGC CCTGAGACA TAGCC
AGGGGTCT GGACG GGACTCTGT GTCGG
A G-
GAM66 238 C5R1 1 4433 NP_001727.1 3 790 CGAGGGAGGCTC ACC TA 1 B c c
TGTCTCAAAAGC TTTGC TGAGACAGA GCC
AAAGCAAA AAACG ACTCTGTCT CGG
AAA --
GAM66 238 CCND2 1 1190 NP_001750.1 3 2143 CAGGGCTGACTC G CA -- 1 B c c
CCTCTCAGGTGG TTT CACCTGAGA GA TAGCC
AAGGCAGG GAA GTGGACTCT CT GTCGG
G CC CA
GAM66 238 CRYZ 1 18125 NP_001880.2 3 210 TTTTATGCCATC CACC A 1 B c c
TGTCTCAAATCA TTTG TGAGACAGAT GC
AAGAGTCA AAAC ACTCTGTCTA CG
TAA- C
GAM66 238 DIAPH2 1 9802 NP_006720.1 3 2918 AAAATTTATGTC C GC 1 B c c
TGTCTCATGTGT TTTGCAC TGAGACAGATA
AAAAGACA AAATGTG ACTCTGTCTGT
T AT
GAM66 238 DKFZp43 1 7547 NP_115630.1 3 677 CCTTTTGGTGGC A C ATA 1 B c c

4F142 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC TGG
- C CGG

GAM66 238 DKFZp43 1 8684 NP_060076.1 3 1116 GTGGCCAAGCGA AGATA--- 1 B c c

4K1210 GGTCTCAGGTGC TTTGCACCTGAGAC GCC
AAAGCAAA AAACGTGGACTCTG CGG
GAGCGAAC

GAM66 238 FLJ3132 1 16215 NP_689600.1 3 633 ATGTATTGAGTG GA GC 1 B c c
2 TCTGTTAGGTGC TTTGCACCT GACAGATA
AAAGTATG AAACGTGGA TTGTCTGT
-- GA

GAM66 238 FLJ3293 1 16646 XP_061055.4 5 681 GAGCAGAGCCTT A TA 1 B c c
8 TGTCTCAGGAGC TTTGC CCTGAGACAGA GC
AAACCAGC AAACG GGACTCTGTTT CG
A C-

GAM66 238 FLJ3478 1 6166 NP_775922.1 3 1203 CCATTGCTTGTT - -- C - 1 B c c
0 TTTCTCAGGTTT TTTG C ACCTGAGA AGATA GC
GTCAAAGA AAAC G TGGACTCT TTTGT CG
T TT T T

GAM66 238 FLJ3730 1 5263 NP_775768.1 3 1198 GGTTGGTCTTGC - ATA- 1 B c c
6 TGTCTCAGGTGG TTTGC ACCTGAGACAG GCC
CAGAGGTG AGACG TGGACTCTGTC TGG
G GTTC

GAM66 238 FLJ4012 1 18889 NP_775870.1 3 732 TTCAGGTGTCCG -- A G 1 B c c
6 TTATTCAGGTGC TTTGCACCTGA GAC GATA CC
AAAGAAGA AAACGTGGACT TTG CTGT GG
TA C -

GAM66 238 H63 1 16055 NP_612432.2 3 1711 CAGGTTGTTCAC G A ---- 1 B c c
TTGCTGAGGTGC TTTGCACCT AG CA GATAGCC
AAAAATTC AAACGTGGA TC GT TTGTTGG
G - TCAC

GAM66 238 H63 1 16055 NP_816929.1 3 1711 CAGGTTGTTCAC G A ---- 1 B c c
TTGCTGAGGTGC TTTGCACCT AG CA GATAGCC
AAAAATTC AAACGTGGA TC GT TTGTTGG
G - TCAC

GAM66 238 IL16 1 16054 NP_004504.3 3 2091 ACAGAGGTTATC TT ------- A 1 B c c
TGTCCCAGGTTA TGC ACCTG GACAGATAGCC
TCTGGGCA ACG TGGAC CTGTCTATTGG
-- GGTCTAT C

GAM66 238 IL16 1 16054 NP_757366.1 3 2711 ACAGAGGTTATC TT ------- A 1 B c c
TGTCCCAGGTTA TGC ACCTG GACAGATAGCC
TCTGGGCA ACG TGGAC CTGTCTATTGG
-- GGTCTAT C

GAM66 238 INA 1 7210 NP_116116.1 3 280 CACAGTGATCGA A -- A 1 B c c
TGATTCAGGTGC TTTGCACCTGAG CA GAT GC
AGAGGAAG AGACGTGGACTT GT CTA TG
A AG G

GAM66 238 KCNK5 1 18276 NP_003731.1 3 728 AGCTGTGTTCCC T-- --- ----- 1 B c c
TGTCTCAGGTCA TTGC ACCTGAGACAG ATAGC

AGCAGTGG GACG TGGACTCTGTC TGTCG
GGT AAC CCTTG
GAM66 238 KIAA025 1 14205 NP_055953.1 3 1569 TGCTTGATAATC CA ----- 1 B c c
2 ACTCTCAGGTGT TTTGCACCTGAGA GAT AGC
AAAGCTCC AAATGTGGACTCT CTA TCG
CA ATAGT
GAM66 238 KIAA097 1 19828 NP_055732.1 3 263 TGAGGGCTACCT T----- AC- A 1 B c c
6 AGACTCAGGTGC TTGCACCTGAG AG TAGCC
AATTCCTT AACGTGGACTC TC ATCGG
TTCCTT AGA C
GAM66 238 KIAA112 1 7548 NP_061872.1 3 337 CAGTGGGTTATA CAC G 1 B c c
8 TGTCTCAGCCCA TTTG CTGAGACA ATAGCC
AGTCCTTG GAAC GACTCTGT TATTGG
CC- A
GAM66 238 KIAA132 1 7254 XP_051146.2 3 130 CATGTGCTGTAA A- AG 1 B c c
7 GTCCCTAGGTGC TTTGCACCTG GAC ATAGC
AAGCTTTT GAACGTGGAT CTG TGTCG
CC AA
GAM66 238 KIAA157 1 9184 XP_035299.1 5 120 AACCAATGCTCT - A TA 1 B c c
7 GCCTCAGGGTGC TTTGCACC TGAG CAGA GC
AAATGCCA AAACGTGG ACTC GTCT CG
G C --
GAM66 238 KIAA161 1 6857 XP_290769.2 3 104 GACACATAGTAA G CA A 1 B c c
8 TCTCTAAGGTGC TTTGCACCT AGA GAT GC
AAAACACA AAACGTGGA TCT CTA TG
A -- A
GAM66 238 KIAA187 1 15500 NP_149053.1 5 307 AGGAGGAGAGGC C ATAG- 1 B c
c
2 TGTCTCAGCTGC TTTGCA CTGAGACAG CC
AGAGGGGT AGACGT GACTCTGTC GG
C GGAGA
GAM66 238 LIF 1 4319 NP_002300.1 3 825 GGGGCAGGTTGC GAC A 1 B c c
TAAGTCAGGTGC TTTGCACCTGA AG TAGCC
AGAGGTTC AGACGTGGACT TC GTTGG
GAA -
GAM66 238 LOC1149 1 2099 XP_054936.4 3 1654 ATGGCATTTGTC - CT --- 1 B c c
71 TGTCTCTGTGTC TTTG CAC GAGACAGATA GCC
AAAGCACT AAAC GTG CTCTGTCTGT CGG
T T- TTA
GAM66 238 LOC1452 1 10362 XP_096740.1 3 1685 AAGGCTTCCTGT C AT--- 1 B c c
31 TGTCTCAGATGC TTTGCA CTGAGACAG AGCC
AGGAGCCA GGACGT GACTCTGTT TCGG
A GTCCT
GAM66 238 LOC1462 1 5104 XP_085374.2 3 337 ACCTGGGTCTGG A AGA - 1 B c c
27 GGTCTCAGGCGC TTTGC CCTGAGAC TAG CC
AAACTGGA AAACG GGACTCTG GTC GG
C GG- T
GAM66 238 LOC1464 1 9334 XP_085484.2 3 64 GGCGGCCTCTAT A G --- 1 B c c

81 GTGCTCAGGTGC TTTGCACCTGAG CA ATA GCC
AGACCTTC AGACGTGGACTC GT TAT CGG
- G CTC
GAM66 238 LOC1502 1 14049 XP_086827.2 5 378 CAATGGGCTCTG AG-- TA 1 B c c

12 TGGGGCAGGTGC TTTGCACCTG ACAGA GCC
AGAGGCCC AGACGTGGAC TGTCT CGG
GGGG --
GAM66 238 LOC1548 1 9864 XP_098623.1 5 192 AAATACGTTTTT - A T 1 B c c
60 GGCTGCGGGTGC TTTGCACCTG AG CAGA AGC
AAAGGGGA AAACGTGGGC TC GTTT TTG
G G -
GAM66 238 LOC1549 1 4166 XP_088109.3 3 574 CCTCTCGACGGC A C ATA 1 B c
c
90 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C ---
GAM66 238 LOC1647 1 13234 XP_104657.1 5 1811 CGGCCCAGCTGT AGA G 1 B c
c
14 GTGCACAGGTGC TTTGCACCTG CA ATAGC
AGGAGGAC GGACGTGGAC GT TGTCG
AC- G
GAM66 238 LOC2220 1 10021 XP_166594.2 3 2047 CCTCTCGGCGGC A C ATA 1 B c
c
57 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C CGG
GAM66 238 LOC2830 1 15529 XP_210867.1 5 1394 ATTGCGGCTTTC TG T T 1 B c c

48 TGTCTCTGGTGT TT CACC GAGACAGA AGCC
GAACAGGC AA GTGG CTCTGTCT TCGG
GT T T
GAM66 238 LOC2832 1 20167 XP_210939.1 5 370 CCAGGCTTTATC T------ - GA -- 1 B c c

16 TGTCAGGTGGCA TTGC ACCT GACAGAT AGCC
ATTCTCAC AACG TGGA CTGTCTA TCGG
CACTCTT G -- TT
GAM66 238 LOC2833 1 1999 XP_210973.1 5 197 CCGAGGCCAGCT - A ATA 1 B c c

23 GGCTGCAGGTGC TTTGCACCTG AG CAG GCC
AGGGCTAT GGACGTGGAC TC GTC CGG
G G GAC
GAM66 238 LOC2836 1 19902 XP_211148.1 5 394 TCTGATGCTTCT - C T 1 B c c
57 TTTGTCAGGTGC TTTGCACCTGA GA AGA AGC
AGAAGCAC AGACGTGGACT TT TCT TCG
G T -
GAM66 238 LOC2840 1 6336 XP_211322.1 3 423 TGGCAGGGTTCT G - TA--- 1 B c c
80 GTGCTCAGGTGG TTT CACCTGAG ACAGA GCC
GAAATCTG AAG GTGGACTC TGTCT CGG
G G TGGGA

GAM66 238 LOC2841 1 13823 XP_209024.1 3 3078 AAAGCTACTAAT C A--- 1 B c c
17 TGTCTCAGTGTA TTTGCAC TGAGACAG TAGC
AGTTTTAA GAATGTG ACTCTGTT ATCG
- AATC
GAM66 238 LOC2851 1 3059 XP_211777.1 5 479 TTTTAAGGTTGG GA C A 1 B c c
36 CTTCAGAGGTGC TTTGCACCT GA AG TAGCC
AAGTATAT GAACGTGGA CT TC GTTGG
GA - G
GAM66 238 LOC2853 1 11869 XP_211861.3 3 294 CTGCAAGCTCTG C -- TA 1 B c c
69 CCTCTCAGGTTC TTTG ACCTGAGA CAGA GC
AAGTGATT GAAC TGGACTCT GTCT CG
T CC --
GAM66 238 LOC2853 1 18757 XP_209588.1 3 534 CATGGCGTTCTC CC TA-- 1 B c c
87 TGTCTCACTGTA TTTGCA TGAGACAGA GCC
AACTAGTG AAATGT ACTCTGTCT CGG
C- CTTG
GAM66 238 LOC2860 1 16079 XP_212158.1 3 1031 TCTGAGGAAGAA G ATAG- 1 B c
c
58 CTGTCTGGGTGC TTTGCACCT AGACAG CC
AAAAGTCC AAACGTGGG TCTGTC GG
- AAGAA
GAM66 238 LOC2861 1 18656 XP_212202.1 5 746 TCGTGTTGTTAC G C A 1 B c c
49 TGTCTCAAGTGG TTT CAC TGAGACAG TAGC
AAGCGCCC GAA GTG ACTCTGTC ATTG
G A -
GAM66 238 LOC3394 1 10021 XP_294952.2 3 1772 CCTCTCGGCGGC A C ATA 1 B c
c
39 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C CGG
GAM66 238 LOC3401 1 10021 XP_295164.2 5 385 CCTCTCGGCGGC A C ATA 1 B c
c
28 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C CGG
GAM66 238 LOC3403 1 10021 XP_295213.2 3 1007 CCTCTCGGCGGC A C ATA 1 B c
c
46 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C CGG
GAM66 238 LOC3476 1 5082 XP_300226.1 3 1239 GCCCAGCTGGGC - A A- 1 B c c
48 TGCCTCAGGTGT TTTG CACCTGAG CAG TAGC
CAGGAAGG GGAC GTGGACTC GTC GTCG
T C GG
GAM66 238 LOC3483 1 866 XP_302717.1 3 88 GGTCTAATTCTC A-- C -- - 1 B c c
01 TCACCCAGGTGC TTTGCACCTG GA AGA TAG CC
AAATGACC AAACGTGGAC CT TCT ATC GG
CCA C TA T
GAM66 238 LOC3484 1 4166 XP_302758.1 3 574 CCTCTCGACGGC A C ATA 1 B c
c

50 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C ---
GAM66 238 LOC3485 1 10021 XP_302806.1 3 2054 CCTCTCGGCGGC A C ATA 1 B c
c
08 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C CGG
GAM66 238 LOC3485 1 6460 XP_302813.1 5 923 CTTAGAGTTGTC TG GAC 1 B c c

29 TAAGTTGGGTGC TTTGCACC A AGATAGC
AAATTTTC AAACGTGG T TCTGTTG
GT GAA
GAM66 238 LOC3488 1 4166 XP_300861.1 3 623 CCTCTCGACGGC A C ATA 1 B c
c
42 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C ---
GAM66 238 LOC3490 1 10021 XP_300933.1 5 265 CCTCTCGGCGGC A C ATA 1 B c
c
71 CTCTCCAGGTGC TTTGCACCTG GA AG GCC
AAAACTTC AAACGTGGAC CT TC CGG
- C CGG
GAM66 238 LOC3492 1 7680 XP_302588.1 5 0 GCTCCTGCTTCA GA AT 1 B c c
75 GGTGCAGAAACA TTTGCACCTGA CAG AGC
CAGCTATT AGACGTGGACT GTC TCG
TC C-
GAM66 238 LOC3492 1 7680 XP_302589.1 5 0 GCTCCTGCTTCA GA AT 1 B c c
97 GGTGCAGAAACA TTTGCACCTGA CAG AGC
CAGCTATT AGACGTGGACT GTC TCG
TC C-
GAM66 238 LOC3494 1 17974 XP_291356.1 5 28 GCTGCTGGTGTC TT ------ G 1 B c c
19 TGTCTCAGGGTA TGCACC TGAGACAGATA CC
CGGTGCAG ACGTGG ACTCTGTCTGT GG
G- CATGGG -
GAM66 238 LOC9052 1 19060 XP_032277.1 3 1067 TGTCTTGAGGTT AGACA 1 B c
c
0 GTCAGCAGGTGC TTTGCACCTG GATAGCC
AAGACACG GAACGTGGAC CTGTTGG
GA---
GAM66 238 LOC9259 1 14239 NP_775739.1 3 414 TTGGCAGGCTCA G C AT 1 B c c

7 CTTCTGAGGTGC TTTGCACCT AGA AG AGCC
AAAACATA AAACGTGGA TCT TC TCGG
G - AC
GAM66 238 MGC1666 1 3795 NP_775780.1 5 302 CCCAACTGCTGT T----- A 1 B c c
4 CTGCTCAGGTGT TTGCACCTGAG CAGATAGC
AGCCCGCG GATGTGGACTC GTCTGTCG
GCGCCC -
GAM66 238 MGC2025 1 8679 NP_443080.1 3 1707 TTGGCTGTCTGG - --- 1 B b b

5 CCTCTCAGGTGT TTTG CACCTGAGA CAGATAGCC
CAGGGCCA GGAC GTGGACTCT GTCTGTCGG
T CCG
GAM66 238 MGC4643 1 3909 NP_116104.1 3 401 GCCAAGCTAGTG - A- GA 1 B c c

GGCTTCAGGTGC TTTGCACCTGA G CA TAGC
AAGGGTAC GAACGTGGACT C GT ATCG
T GG G-
GAM66 238 PIGS 1 3985 NP_149975.1 3 504 TAGTTGGCTTTG T----- GA -- 1 B c c
TCTGTCAGGTGC TTGCACCT GACAGAT AGCC
AGTCTGGC GACGTGGA CTGTCTG TCGG
CGGTCT -- TT
GAM66 238 PRO1853 1 15239 NP_061077.1 3 186 TAGGGTTGTGAC T A -- 1 B c c
TGGCTTTGGTGC TTTGCACC GAG CAG ATAGCC
AAATGTGT AAACGTGG TTC GTC TGTTGG
T G AG
GAM66 238 RAD50 1 11752 NP_005723.2 3 1230 AAGGCATCTATC C AG --- 1 B c c
TGTGCTAGGTTA TTTG ACCTG ACAGATA GCC
AATGGTTG AAAT TGGAT TGTCTAT CGG
- CG CTA
GAM66 238 RAD50 1 11752 NP_597816.1 3 1230 AAGGCATCTATC C AG --- 1 B c c
TGTGCTAGGTTA TTTG ACCTG ACAGATA GCC
AATGGTTG AAAT TGGAT TGTCTAT CGG
- CG CTA
GAM66 238 RYR2 1 12550 NP_001026.1 3 672 AAACGGGTGGTG CA G A 1 B c c
TGTCTCAGGACA TTTG CCTGAGACA AT GCC
AAAGGAGG AAAC GGACTCTGT TG TGG
A- G G
GAM66 238 SETDB2 1 10049 NP_114121.1 5 336 TTTCAGCCTGTC T---- - C 1 B c c
TGTCTCAGGGTG TTGCACC TGAGACAGATAG
CAGCCTTA GACGTGG ACTCTGTCTGTC
ATTCC G C
GAM66 238 SLC19A1 1 3271 NP_003047.1 3 547 ATGTGGCTTCTC G CT T- 1 B c c
TGTCTCTGTGGA TTT CAC GAGACAGA AGCC
AAAGCCAT AAA GTG CTCTGTCT TCGG
G T- CT
GAM66 238 SMCY 1 10886 NP_004644.1 5 113 GTCCTCAGCGTT C A 1 B c c
TATCTCAGGTGC TTTGCACCTGAGA AGAT GC
GGAAGGTC AGGCGTGGACTCT TTTG CG
A -
GAM66 238 ST5 1 18268 NP_005409.2 3 341 TGTGCAGCTGAC CAC A 1 B c c
TGTCTCAGCCAA TTTG CTGAGACAG TAGC
ACCACTGA AAAC GACTCTGTC GTCG
C-- A
GAM66 238 ST5 1 18268 NP_631896.1 3 341 TGTGCAGCTGAC CAC A 1 B c c
TGTCTCAGCCAA TTTG CTGAGACAG TAGC
ACCACTGA AAAC GACTCTGTC GTCG
C-- A
GAM66 238 STAG2 1 11828 NP_006594.3 3 1099 GTTTTATCTATC CCT C 1 B c c
TGTCTTTGCAAG TTTGCA GAGACAGATAG

CAGTCTTC GAACGT TTCTGTCTATC
--- T

GAM66 238 STRN3 1 14812 NP_055389.1 3 134 GTGAAGGCTATC CA AGA 1 B c c

TGGGGCAGGCAC TTTG CCTG CAGATAGCC
AAATTGGT AAAC GGAC GTCTATCGG
AC GGG

GAM66 238 TYRP1 1 14058 NP_000541.1 3 584 CATATACTATTT C - C 1 B c c
AGTCTCAGGTTC TTTG ACCTGAGAC AGATAG
AAGGCTAC GAAC TGGACTCTG TTTATC
T A A

GAM66 238 UBAP1 1 14677 NP_057609.2 3 542 GGTTCTGCAATA G ------- TA 1 B c c
TCTCTGAGGTGC TTTGCACCT AGA CAGA GCC
AAAGAATG AAACGTGGA TCT GTCT TGG
G CTATAAC --

GAM66 238 XT3 1 9880 NP_064593.1 3 456 AGATGACCTATT TGA C 1 B c c
TGTCAGTGGTGC TTTGCACC GACAGATAG
AAAATTAA AAACGTGG CTGTTTATC
TGA C

GAM66 238 XT3 1 9880 NP_071800.1 3 456 AGATGACCTATT TGA C 1 B c c
TGTCAGTGGTGC TTTGCACC GACAGATAG
AAAATTAA AAACGTGG CTGTTTATC
TGA C

GAM66 238 ZNF313 1 8054 NP_061153.1 3 39 GTGCTTGCTATC C- C 1 B c c
TGTCTCATGTTA TTTG AC TGAGACAGATAGC
CAGAGCTT AGAC TG ACTCTGTCTATCG
AT T

GAM67 282 ALS2 1 12702 NP_065970.1 3 523 TCATGTGTGCAT T - CC 1 B c c
CATGTCTCTTTG TGGCAAAGA GC TGA TACAT
CCAAGGGA ACCGTTTCT TG ACT GTGTG
C T AC

GAM67 282 APC 1 10697 NP_000029.1 3 1415 CAGTGAAGTATA A CC- A 1 B c c
ATCAGCACTTTG TGGCAAAG TGCTGA TAC
CCATGCTC ACCGTTTC ACGACT ATG
- AAT A

GAM67 282 ARHGAP8 1 12147 NP_060171.2 5 315 CACCTGTGTAGG A A CT 1 B c c

TCTCACCTGTGC TGGCA AG TG GACCTACAT
CAGGTGTA ACCGT TC AC CTGGATGTG
G C T-

GAM67 282 ARNT2 1 19883 NP_055677.1 3 843 CACATGGGTAGG -- T A 1 B c c
TCAGTTCTTTGG TGG CAAAGA GCTGACCTAC
TCCAAGCC ACC GTTTCT TGACTGGATG
TG - G

GAM67 282 BRD8 1 5029 NP_006687.2 5 101 GAGAAGCTATGT - CCT 1 B c c
TTAGCATCTTCT TGGCA AAGATGCTGA ACAT
GTCATGAG ACTGT TTCTACGATT TGTA
C ---

GAM67 282 C14orf1 1 9342 NP_075601.1 3 1690 GATTTGTGAATA C CC-- 1 B c c
37 TCATCATCTTTG TGGCAAAGATG TGA TACA

CCAGACAA ACCGTTTCTAC ACT GTGT
T ATAA

GAM67 282 C20orf1 1 4739 NP_543011.1 3 672 CATTAAGGTAGG T---- - A 1 B c c
08 TCAGCGTCATTT GGCAAA GATGCTGACCTAC
GTCTCTGT CTGTTT CTGCGACTGGATG
TGTCT A G

GAM67 282 CDC25A 1 19913 NP_001780.1 5 37 AAGAGGTGTAGG - --- 1 B c c
TCGGCTTGGTTT TGGCA AAGAT GCTGACCTACAT
TCTGCTAC ATCGT TTTTG CGGCTGGATGTG
C GTT

GAM67 282 CDH12 1 4140 NP_004052.2 5 1066 TACTCTGCTGTA AT GA 1 B c c
GGAAAGCCTTTG TGGCAAAG GCT CCTACA
CCAATGCT ACCGTTTC CGA GGATGT
-- AA

GAM67 282 COE2 1 5083 XP_034639.1 3 1120 TGTTGGATGTGT ACC 1 B c c
ATAGTGTCTTTG TGGCAAAGATGCTG TACAT
CCATTTTA ACCGTTTCTGTGAT GTGTA
AT-

GAM67 282 COL4A2 1 1689 NP_001837.1 3 603 CACTGCGGTAGG - TGC A 1 B c c

TCATTCTTTTGC TGGCAAA GA TGACCTAC
CACATCCC ACCGTTT CT ACTGGATG
T T-- G

GAM67 282 CRTAC1 1 15719 NP_060528.1 5 195 CCCGTGGTGTGG T A T 1 B c c
CCAGCCTCTTTG TGGCAAAGA GCTG CC ACAT
CCGGACGC GCCGTTTCT CGAC GG TGTG
C C -

GAM67 282 CUL3 1 15180 NP_003581.1 3 3064 ATCAATTGTAGG CA - 1 B c c
TCATGTATTTTA TGG AAGATGC TGACCTACA
CTATATGT ATC TTTTATG ACTGGATGT
A- T

GAM67 282 CYP4F3 1 5739 NP_000887.1 3 717 AAGAATATGTTG C G CT 1 B c c
TGAGCATCTTTC TGG AAAGATGCT AC ACAT
CATGATAT ACC TTTCTACGA TG TGTA
- G T-

GAM67 282 E2F3 1 15738 NP_001940.1 3 2158 TCCAGCTTTGTG TGCT CC 1 B c c

TAATTCTCTTTG TGGCAAAGA GA TACAT
CCAGCTGC ACCGTTTCT CT ATGTG
---- TA

GAM67 282 FLJ2203 1 19766 NP_079350.1 3 546 TTTGTGAAGGTC ATG-- A 1 B c c
1 AGAGATGCTTTG TGGCAAAG CTGACCT CAT
CCAGTCTC ACCGTTTC GACTGGA GTG
GTAGA A

GAM67 282 FLJ2316 1 16056 NP_079331.2 3 433 GGCCACGATGTA A CT - 1 B b b
8 GGCTCCACTTTG TGGCAAAG TG GA CCTACAT
CCAACTTC ACCGTTTC AC CT GGATGTA
- -- C

GAM67 282 FLJ3206 1 5508 NP_694577.1 3 2697 TAGTCCTGTAGG C AT 1 B c c
5 TCAGCCTTTCTC TGG AAAG GCTGACCTACA

ACAAACTC ACT TTTC CGACTGGATGT
C --
GAM67 282 FLJ3476 1 6306 NP_848597.1 3 21 AGATGACTGAGG A C A A 1 B c c
6 ACATCGCCTTTG TGGCAAAG TG TG CCT CA
CCAAGGCC ACCGTTTC GC AC GGA GT
C T A -
GAM67 282 FLJ4020 1 9705 NP_689820.1 3 254 AGAGATGTATGG A CTGA - 1 B c c
1 GGATCACCTTTG TGGCAAAG TG CC TACAT
CCAGAGCT ACCGTTTC AC GG ATGTA
C TAGG T
GAM67 282 FZD4 1 2889 NP_036325.2 3 3206 GTATATTTGAGG A A A 1 B c c
ACAGCATCTTGC TGGCAA GATGCTG CCT CA
TAGAGAAA ATCGTT CTACGAC GGA GT
- A -
GAM67 282 HADHA 1 6337 NP_000173.2 3 392 CCAAACTCTGTG T----- CT 1 B c c
TCAGCATCTTTG GGCAAAGATGCTGAC ACA
CCCTTCTG CCGTTTCTACGACTG TGT
GTCTTC --
GAM67 282 KCNS2 1 16743 XP_043106.1 3 2809 TAAAAATATGAG G CTG A 1 B c c
GTGACATCTTTG TG CAAAGATG ACCT CAT
GCAACCAG AC GTTTCTAC TGGA GTA
G AG- -
GAM67 282 KIAA018 1 16445 XP_050495.4 3 1928 GACACTGGGAGG CA G A- 1 B c
c
2 TCAGCATGTTCC TGG AA ATGCTGACCT CA
ACAGGTGT ACC TT TACGACTGGA GT
-- G GG
GAM67 282 KIAA029 1 2259 XP_084529.6 3 1354 TGAACTGTGTAG T-- TGAC 1 B c c
8 TGCTCTTCTTTG TGGCAAAGA GC CTACAT
CCATTTGC ACCGTTTCT CG GATGTG
TCT T---
GAM67 282 KIAA036 1 19247 XP_036708.6 3 708 GAAAATGATTGT GC CCT 1 B c c
8 TTAGCATCTTTA TG AAAGATGCTGA ACA
CAGATGGA AC TTTCTACGATT TGT
A- ---
GAM67 282 KIAA051 1 16457 NP_055511.1 3 2892 ACAAATTTGGAG ATG G A 1 B c
c
4 GTGAGAGCTTTG TGGCAAAG CT ACCT CA
CCAGACCC ACCGTTTC GA TGGA GT
GA- G G
GAM67 282 KIAA077 1 19740 XP_166270.1 3 456 TTTTAGTGAAGG C A A 1 B c c
4 TCAGCAGTTTTC TGG AAAG TGCTGACCT CAT
TAACTTGT ATC TTTT ACGACTGGA GTG
- G A
GAM67 282 KIAA135 1 2094 XP_116034.2 3 24 AGCTGAGGACGA A A---- A 1 B c c
9 ACAGCATCTTAG TGGC AAGATGCTG CCT CA
CCAAGACC ACCG TTCTACGAC GGA GT

A AAGCA -

GAM67 282 KIAA144 1 15959 NP_065885.1 3 1694 AAAGGAAGTAGT AA- C A 1 B c c

3 TCAGCATCTATC TGGC AGATGCTGA CTAC

GCCAGCCA ACCG TCTACGACT GATG

CTA T A

GAM67 282 KIAA172 1 5509 XP_040280.2 3 3804 TGTCTTTGTAAG T--- - - C 1 B c c

4 TCAGCATGCTCT GGCAA AG ATGCTGAC TACA

TGCTTGAA TCGTT TC TACGACTG ATGT

AAGT C G A

GAM67 282 KIAA185 1 16006 XP_045184.1 5 525 AGAAAAGCTGGG AA CA 1 B c c

3 TCAGCATCTGGC TGGC AGATGCTGACCTA

CACCGAGC ACCG TCTACGACTGGGT

G- CG

GAM67 282 KIAA194 1 10647 NP_803237.1 3 309 CATACTGCTAAG AT C - 1 B c c

6 TCAGCTACTTTG TGGCAAAG GCTGAC TA CA

CCAAGAAA ACCGTTTC CGACTG AT GT

AT A C

GAM67 282 KPNA3 1 15262 NP_002258.1 3 29 ATTCAGTTGAGT C AC A 1 B c c

GCAGCATCTTTC TGG AAAGATGCTG CT CA

CCACATTC ACC TTTCTACGAC GA GT

C GT -

GAM67 282 LOC1334 1 5908 XP_059649.4 3 2586 GGAATCTCTGTA ATGC - 1 B c c

18 GGCTCACCTTTG TGGCAAAG TGA CCTACA

CCATTTCT ACCGTTTC ACT GGATGT

C--- C

GAM67 282 LOC1490 1 13860 XP_017261.1 3 114 CGCCTCCATGTT A CCT 1 B c c

50 TCAGCATCTATG TGGCA AGATGCTGA ACAT

TCATGGGC ACTGT TCTACGACT TGTA

A T--

GAM67 282 LOC1964 1 6306 XP_116915.2 3 21 AGATGACTGAGG A C A A 1 B c c

03 ACATCGCCTTTG TGGCAAAG TG TG CCT CA

CCAAGGCC ACCGTTTC GC AC GGA GT

C T A -

GAM67 282 LOC2210 1 9749 XP_167669.2 3 15 AGTCCTGTTGGT - TG T 1 B c c

42 TGGTCATCTTTG TGGCAAAGATG C ACC ACA

TCACTTCT ACTGTTTCTAC G TGG TGT

T GT T

GAM67 282 LOC2230 1 2240 XP_167336.2 3 432 TATCTGTGTAGG CA C 1 B c c

75 TCATATCTTCTC TGG AAGATG TGACCTACAT

TAGTAAAC ATC TTCTAT ACTGGATGTG

TC -

GAM67 282 LOC2538 1 5240 XP_173230.1 3 132 AACCCACTGTGG AA A 1 B c c

42 GCAGCATCTAAG TGGC AGATGCTG CCTACA

CCATGTCC ACCG TCTACGAC GGGTGT

AA -

GAM67 282 LOC2836 1 16123 XP_211150.1 3 657 AAACTCAGTGGA GAC A 1 B c c

58 TAAGCATCTTTG TGGCAAAGATGCT CTAC

TCATATTT ACTGTTTCTACGA GGTG
ATA A
GAM67 282 LOC2843 1 13410 XP_209160.1 3 315 GGCTTCTGATGG CA TA 1 B c c

55 TCAGCATCTTCC TGG AAGATGCTGACC CA
CCAACACT ACC TTCTACGACTGG GT
CC TA
GAM67 282 LOC2846 1 17988 XP_209318.1 5 84 TGCTGTAGGAGT CTGA--- 1 B c c

78 TGAACATCTTTG TGGCAAAGATG CCTACA
CCAGCTCC ACCGTTTCTAC GGATGT
AAGTTGA
GAM67 282 LOC2849 1 11370 XP_209429.2 3 802 ATTAAAATTTTG ATG CA 1 B c c
88 GGTCAGACTTTG TGGCAAAG CTGACCTA
CCATAATG ACCGTTTC GACTGGGT
A-- TT
GAM67 282 LOC2862 1 19868 XP_209946.1 3 168 TGCTCTGCTGGG AA- - 1 B c c
09 TCAGCATCTCCA TGGC AGATGCTGACCTA CA
GCCACCTG ACCG TCTACGACTGGGT GT
ACC C
GAM67 282 LOC2865 1 6979 XP_210107.1 3 19 GGATTTTGTAGG C GCT 1 B c c
62 TCCTGTTTTTCC TGG AAAGAT GACCTACA
CATCTGTG ACC TTTTTG CTGGATGT
C TC-
GAM67 282 LOC3396 1 15712 XP_295014.1 3 259 CTTGGTTGTAGG G GC--- 1 B c c

00 TCAACTCAATTT TG CAAAGAT TGACCTACA
TTGGTAGA AT GTTTTTA ACTGGATGT
G ACTCA
GAM67 282 LOC9309 1 1803 XP_049221.1 3 359 TGGACATGTAAT G C C- 1 B c c
7 GTCACATCTTTG T GCAAAGATG TGAC TACAT
TGGAGTGT G TGTTTCTAC ACTG ATGTA
G - TA
GAM67 282 MGC1071 1 13051 NP_077301.4 3 776 ACACATTGCAGG T- ---- T A 1 B c c

5 TCAGCTTCTTCC GGCA AAGA GCTGACCT CA
TCTGCCCA CCGT TTCT CGACTGGA GT
AC CTCC T C
GAM67 282 OPN1LW 1 11329 XP_301073.1 3 104 TAAAATAAATGT CTGACC 1 B c
c
AATTTATCTTTG TGGCAAAGATG TACAT
CCAAAACC ACCGTTTCTAT ATGTA
TTA---
GAM67 282 OSBPL3 1 1991 NP_663163.1 3 242 CCAGGGTATATG AT A T 1 B c c
TGGCAGCCTTTG TGGCAAAG GCTG CC ACAT
CCATATCA ACCGTTTC CGAC GG TGTA
-- - -
GAM67 282 OSBPL3 1 1991 NP_663164.1 3 242 CCAGGGTATATG AT A T 1 B c c
TGGCAGCCTTTG TGGCAAAG GCTG CC ACAT
CCATATCA ACCGTTTC CGAC GG TGTA

-- - -

GAM67 282 PPP1R10 1 14628 NP_002705.2 3 728 ACCGGTGGTGCT AT T TA 1 B c c

GGTCTGCCTTTG TGGCAAAG GC GACC CAT
CCAACTAT ACCGTTTC CG CTGG GTG
-- T TC

GAM67 282 RABIF 1 19664 NP_002862.2 3 820 TAGGATATGAGG ATG A 1 B c c

GTTAGGCCTTTG TGGCAAAG CTGACCT CAT
CCACATTA ACCGTTTC GATTGGG GTA
CG- A

GAM67 282 RNPC4 1 1626 NP_060577.2 3 581 CCTACTGTAGCC A C- 1 B c c

TCAGCATCTTGC TGGCAA GATGCTGA CTACA
TAGGAGGC ATCGTT CTACGACT GATGT
- CC

GAM67 282 SREBF1 1 9185 NP_004167.3 3 448 ACATAGTGTAGG T---- A - 1 B c c

TCAGCGTGCTTA GGC AAG ATGCTGACCTACAT
GCCTCCTG CCG TTC TGCGACTGGATGTG
GTCCT A G

GAM67 282 SYNPO2 1 12148 XP_050219.2 3 632 ACTTATTATGTA TG CC 1 B c c

TTAGGTTCTTTG TGGCAAAGA CTGA TACAT
CCAGATGT ACCGTTTCT GATT ATGTA
TG --

GAM67 282 SYT11 1 2632 NP_689493.2 3 2911 CTAGGAACTGCC ------- CA 1 B c c

TCAGTGTCTTTG TGGCAAAGATGCTGA CCTA
CCAGAAAA ACCGTTTCTGTGACT GGAT
CCGTCAA C-

GAM67 282 TAF4 1 9232 NP_003176.1 3 666 CTGAATGTGTGG GCAA - 1 B c c

TCAGCATCTGTA TG AGATGCTGACC TACAT
CAAATGCA AC TCTACGACTGG GTGTA
ATG- T

GAM67 282 TM4SF2 1 1003 NP_004606.2 3 673 TGTAGGCAGTTT T----- ------- A 1 B c c

AGTGCATCTTTG GGCAAAGATGC TG CCTA
CCTCTCAG CCGTTTCTACG AC GGAT
GACTCT TGATTTG -

CA
GT

GAM67 282 UBE2J1 1 4859 NP_057105.1 3 599 TGAGGAAATGAG C C A 1 B c c

ATCACATCTTTG TGGCAAAGATG TGA CT CAT
TCACTGGA ACTGTTTCTAC ACT GA GTA
- A -

GAM67 282 UPF3B 1 4390 NP_075386.1 3 668 CGTGTTTTGTCA C CCT 1 B c c

TCAGCATCTTTT TGG AAAGATGCTGA ACA
CTATTAAG ATC TTTCTACGACT TGT
T AC-

GAM67 282 UPF3B 1 4390 NP_542199.1 3 668 CGTGTTTTGTCA C CCT 1 B c c

TCAGCATCTTTT TGG AAAGATGCTGA ACA
CTATTAAG ATC TTTCTACGACT TGT
T AC-

GAM67 282 ZNF323 1 12107 NP_112161.2 3 926 TTTGGGGGTTGG ---- A T A 1 B c c
TCAGCAACTTTG TGGCA AAG TGCTGACC AC
AGTGCCAT ACCGT TTC ACGACTGG TG
GAGT A T G
GAM68 251 CDH13 1 8595 NM_001257.2 3 AAAGGTTTTAAC GCA T TT-- 3 C c c
CGCACATGCACA TGTGCATG GC GTT CCTTT
ACACGTAC CG CAA GGAAA
A-- C TTTT
GAM68 251 DNAJC5 1 15877 XM_028966.6 3 AAGGAACTGGCA G CTGTT T 3 C c
c
TGCACA TGTGCATG CAG TTCCTT
ACACGTAC GTC AAGGAA
G ----- -
GAM68 251 FENS-1 1 6852 3 AAAGGAAAGGGG A AG G 3 C c c
GTCACGCACA TGTGC TGGC CT TTTTCCTTT
ACACG ACTG GG GAAAGGAAA
C -- G
GAM68 251 GRLF1 1 486 NM_024342.1 3 AAGGGAGCCCCC CA GTTT T 3 C c c
ATGCACA TGTGCATGG GCT TCCTT
ACACGTACC CGA GGGAA
CC ---- -
GAM68 251 SORCS2 1 7018 NM_020777.1 3 AGGCCATCAGCT TTTT TT 3 C c c
GCCATGCACA TGTGCATGGCAGCTG CCT
ACACGTACCGTCGAC GGA
TACC --
GAM69 258 ABCB5 1 12174 XP_291215.1 3 171 CCAAATTACACT TT--- T 3 B c c
GAATCTAGGAGG TCCCTCCTAG GTGT GTT
GGAGTTG GGGGAGGATC CACA TAA
TAAGT T
GAM69 258 ADCY5 1 17269 XP_171048.2 5 470 GCACACAGACAG TT TG 3 B c c
TGCCCTAGGAGG TCCCTCCTAG G TTGTT
GAAACAG AGGGAGGATC C GACAG
C- GT
GAM69 258 ADCY8 1 16440 NP_001106.1 5 1340 CGAACTAGGAAA TTGT G 3 B c
c
GAGCCTAGGAGG TCCCTCCTAG GTT TT
GAGCCTC AGGGAGGATC CGA AA
---- G
GAM69 258 ADD2 1 12249 NP_001608.1 3 95 CCTGCAAGCACA - G T 3 B c c
GGGCTAAGGAGG TCCCTCCT AGTT TGT GTT
GATAGAG AGGGAGGA TCGG ACA CGA
A G -
GAM69 258 ADD2 1 12249 NP_059517.1 3 95 CCTGCAAGCACA - G T 3 B c c
GGGCTAAGGAGG TCCCTCCT AGTT TGT GTT
GATAGAG AGGGAGGA TCGG ACA CGA
A G -
GAM69 258 ADD2 1 12249 NP_059519.1 3 95 CCTGCAAGCACA - G T 3 B c c
GGGCTAAGGAGG TCCCTCCT AGTT TGT GTT
GATAGAG AGGGAGGA TCGG ACA CGA
A G -

GAM69 258 ADD2 1 12249 NP_059520.1 3 95 CCTGCAAGCACA - G T 3 B c c
GGGCTAAGGAGG TCCCTCCT AGTT TGT GTT
GATAGAG AGGGAGGA TCGG ACA CGA
A G -
GAM69 258 ADD2 1 12249 NP_059522.1 3 430 CCTGCAAGCACA - G T 3 B c c
GGGCTAAGGAGG TCCCTCCT AGTT TGT GTT
GATAGAG AGGGAGGA TCGG ACA CGA
A G -
GAM69 258 AQP6 1 5241 NP_445738.1 5 997 TCCTAACTACAC AG T T 3 B c c
ACAGGGAGGAGG TCCCTCCT TTGTGT GT
GAATTAT AGGGAGGA GACACA CA
GG - T
GAM69 258 C10orf5 1 12344 NP_848931.1 3 2652 CCTACCAACAAC CCTA T 3 B c c
ATACAGGGAAGA TCCCT GT GTGTTGTTG
GATACAG AGGGA CA TACAACAAC
---- -
GAM69 258 C1orf38 1 17232 NP_004839.1 3 1204 GGCTTCAAGAAC T ---- -- G 3 B c c
ACAACCTTAGGA CCC TCCTA GTTGTGTT TTG
CCTTGGG GGG AGGAT CAACACAA AAC
- TTCC TC G
GAM69 258 C1QTNF7 1 6301 NP_114117.1 3 1152 AGAGCAATGAAC AG G - 3 B c c
AGGAGAAGGAGG TCCCTCCT TT TGTT GTTG
GAGAGAG AGGGAGGA AG ACAA TAAC
AG G G
GAM69 258 CCNB1 1 4167 NP_114172.1 5 1 ACGAACAGGCCA A TG 3 B c c
ATAAGGAGGGAG TCCCTCCT GTTG TTGTT
CAGTGCG AGGGAGGA TAAC GACAA
A CG
GAM69 258 CNN1 1 462 NP_001290.2 5 64 GAGCTTCAAAAA AGT G 3 B c c
CATGTGAGGAGG TCCCTCCT TGTGTT TTG
GAAGAGT AGGGAGGA GTACAA AAC
GT- A
GAM69 258 COL11A2 1 1273 NP_542410.1 5 9 CAGAAGCGGCAG AGT T 3 B c c
CCACCGAGGAGG TCCCTCCT TG GTTGTTG
GAGCAGT AGGGAGGA AC CGACGGC
GCC -
GAM69 258 COL11A2 1 1273 NP_542411.1 5 9 CAGAAGCGGCAG AGT T 3 B c c
CCACCGAGGAGG TCCCTCCT TG GTTGTTG
GAGCAGT AGGGAGGA AC CGACGGC
GCC -
GAM69 258 COL11A2 1 1273 NP_542412.1 5 9 CAGAAGCGGCAG AGT T 3 B c c
CCACCGAGGAGG TCCCTCCT TG GTTGTTG
GAGCAGT AGGGAGGA AC CGACGGC
GCC -
GAM69 258 CTSE 1 11615 NP_001901.1 3 11 TGGCCCCAGCAG TTGTG 3 B c c
TCCCCTAGGAGG TCCCTCCTAG TTGTTG
GGCCTTG GGGGAGGATC GACGAC
CCCT-
GAM69 258 CYP21A2 1 4412 NP_000491.2 5 41 CAAAACAGTCTA A ---- 3 B b b

CACAGCAGGAGG TCCCTCCT GTTGTGT TGTT
GATGGCT AGGGAGGA CGACACA ACAA
- TCTG

GAM69 258 D13S106 1 16482 NP_005791.2 5 196 GGGTTGAACGTT C GT 3 B c c
E GCAACTAGGGTG TCC TCCTAGTTGT TGTT
GAGATCA AGG GGGATCAACG GCAA
T TT

GAM69 258 DKFZp54 1 12565 NP_061174.1 3 15 CTACCAGCAGCT TT - 3 B c c
7A023 ATCCCTAGGAGG TCCCTCCTAG GT GTTGTTG
GAGTCTC AGGGAGGATC TA CGACGAC
CC T

GAM69 258 DKFZp76 1 9816 NP_060892.1 5 1246 ATCAGCAACAAC C A - 3 B c c
1K1423 AGCGAGGATGGA TCC TCCT GTTGT GTTGTTG
AATGGAA AGG AGGA CGACA CAACGAC
T G A

GAM69 258 DMN 1 12222 NP_056101.4 5 63 CCGGGACAAGAC A --- G 3 B c c
CAGGGCAGGAGG TCCCTCCT GTT GT TTGTT
GAGCCGG AGGGAGGA CGG CA AACAG
- GAC G

GAM69 258 DMN 1 12222 NP_663780.1 5 63 CCGGGACAAGAC A --- G 3 B c c
CAGGGCAGGAGG TCCCTCCT GTT GT TTGTT
GAGCCGG AGGGAGGA CGG CA AACAG
- GAC G

GAM69 258 DOK4 1 2501 NP_060580.2 3 787 CTGCCCCAGGAA A G G 3 B c c
TAGGCCAGGAGG TCCCTCCT GTT TGTT TTG
GAAGGCC AGGGAGGA CGG ATAA GAC
C - G

GAM69 258 FGF18 1 14981 NP_003853.1 5 403 CAGCAGCAGCAG A T 3 B c c
CCGGCGAGGAGG TCCCTCCT GTTG GTTGTTG
GAGCAGC AGGGAGGA CGGC CGACGAC
G -

GAM69 258 FGF18 1 14981 NP_387498.1 5 403 CAGCAGCAGCAG A T 3 B c c
CCGGCGAGGAGG TCCCTCCT GTTG GTTGTTG
GAGCAGC AGGGAGGA CGGC CGACGAC
G -

GAM69 258 FLJ1042 1 6374 NP_060560.1 3 532 GCAGCTTGAGCT A - --- 3 B c c
0 ACAATCAGGAGG TCCCTCCT GTTGT GTT GTTG
GAAATTG AGGGAGGA TAACA CGA CGAC
C T GTT

GAM69 258 FLJ1318 2 5952 NP_079158.1 3 156 GAGGAAGACAAC A- 3 B b b
9 ACAACACAGGAG TCCCTCCT GTTGTGTTGTT
GGGATAA GGGGAGGA CAACACAACAG
CA

GAM69 258 FLJ1318 2 7088 NP_079158.1 3 156 AGACAACACAAC A- 3 B b b
9 ACAGGAGGGGAT TCCCTCCT GTTGTGTTGTT
AAGTACC GGGGAGGA CAACACAACAG
CA

GAM69 258 FLJ2136 1 15599 NP_079078.1 3 163 GGGAGGAGCATC G TG T 3 B c c

9 ATGAGTAGGAGG TCCCTCCTA T TG TGTT

GAGGCAG AGGGAGGAT A AC ACGA
G GT T

GAM69 2583 FLJ2284 1 1721 NP_079460.2 5 6 GGGCCAAACAAC - TA 3 B c c
ACGGCCGGGAGG TC CCTCC GTTGTGTTGTT
CGGCCGC GG GGAGG CGGCACAACAA
C GC

GAM69 2582 FLJ2346 1 10577 NP_079119.2 3 408 GACAATGATTTC C --- TG 3 B c c
ACAACTAGAGGG TCCCTC TAGTTGTG T TTG
AAGCAGT AGGGAG ATCAACAC A AAC
- TTT GT

GAM69 2584 FLJ3221 1 9977 NP_689686.1 5 164 ACAGGAAGAACA - TT G 3 B c c
CCTCTGAGGAGG TCCCTCCT AG GTGTT TT
GATTCCC AGGGAGGA TC CACAA AA
G TC G

GAM69 2585 FLJ3291 1 18785 NP_659451.1 5 347 TAAACCAACAAC CC- TT 3 B c c
ACCTAATTGGGG TCCCT TAG GTGTTGTTG
AAAGCAT AGGGG ATC CACAACAAC
TTA --

GAM69 2589 FLJ3598 1 8320 NP_689810.2 5 21 AACAGCGGTCCC AG --- 3 B c c
ACAGGCAGGAGG TCCCTCCT TTGTG TTGTTG
GATCTGG AGGGAGGA GACAC GGCGAC
CG CCT

GAM69 2581 FLJ9023 2 8670 NP_775852.1 3 454 AACAACAACAAC - C A G 3 B c c
AAAACAGCAGAG TCC CT CT GTT TGTTGTTG
GAATTGT AGG GA GA CAA ACAACAAC
A C - A

GAM69 2581 FLJ9023 2 14227 NP_775852.1 3 454 AATAACAACAAC - C A G 3 B c c
AACAAAACAGCA TCC CT CT GTT TGTTGTTG
GAGGAAT AGG GA GA CAA ACAACAAC
A C - A

GAM69 258 GABBR1 1 3948 NP_068705.1 3 773 TCGACCAACAAC - A - - 3 B c c
AACGAGGAGGAG TC CCTCCT GTTGT GTTG TTG
AAGTCCC AG GGAGGA CAACA CAAC AGC
A G A C

GAM69 258 GAS2L1 1 14222 NP_689423.1 3 185 CAAACCAACAAC T---- - 3 B c c
ACAGCTGGGGCG CCC TCCTAGTTGTGTTGTTG
GGCCCTG GGG GGGGTCGACACAACAAC
GTCCC C

GAM69 258 HAK 1 10217 NP_443179.1 5 169 AAAGAAGGCAAC CC - 3 B c c
ACAAATTGCAAG TCCCT TAGTT GTGTTGTT
GGAGAAG AGGGA GTTAA CACAACGG
AC A

GAM69 258 HAND1 1 12355 NP_004812.1 3 290 TGGCGGCAACAT AG -- 3 B c c
GCAAGAAGGAGG TCCCTCCT TTGT GTTGTTG
GACTGTC AGGGAGGA AACG CAACGGC
AG TA

GAM69 258 HNF4A 1 15282 NP_000448.3 3 1465 TCTGAAACTCAC T--- - - T- 3 B c c
ACAACTAGGAAG CC CT CCTAGTTGTGT GTT
TGGCTGA GG GA GGATCAACACA CAA
AGTC T A CT

GAM69 258 HNF4A 1 15282 NP_849180.1 3 1465 TCTGAAACTCAC T--- - - T- 3 B c c
ACAACTAGGAAG CC CT CCTAGTTGTGT GTT
TGGCTGA GG GA GGATCAACACA CAA
AGTC T A CT
GAM69 258 HOXB6 1 8188 NP_724778.1 3 790 GAAAGACAAGAT C - -- 3 B c c
GCAACTAGGAAG TC CT CCTAGTTGTGT TGTT
AGACACA AG GA GGATCAACGTA ACAG
A A GA
GAM69 258 HRD1 1 1224 NP_115807.1 3 578 ACTGGCAACCAC CCT T 3 B c c
ACAACTCAGGGA TCCCT AGTTGTGT GTTG
AAGGAAT AGGGA TCAACACA CAAC
C-- C
GAM69 258 HRD1 1 1224 NP_757385.1 3 578 ACTGGCAACCAC CCT T 3 B c c
ACAACTCAGGGA TCCCT AGTTGTGT GTTG
AAGGAAT AGGGA TCAACACA CAAC
C-- C
GAM69 258 IGF1 1 11594 NP_000609.1 3 6082 CGCTGCTAAACA A T T 3 B c c
CACTGCAGGAGG TCCCTCCT GT GTGT GTT
GACTCTG AGGGAGGA CG CACA CAA
- T -
GAM69 258 KCNA3 1 11200 NP_002223.2 5 35 GGGGCGGAGAGC AG G 3 B c c
GCGAGAAGGAGG TCCCTCCT TTGTGTT TT
GAGGAGG AGGGAGGA AGCGCGA AG
AG G
GAM69 258 KCNE2 1 9124 NP_751951.1 5 116 GCCCACACACTG A T T 3 B c c
CATAGCAGGAGG TCCCTCCT GTTGTGT GT
GAAGCAT AGGGAGGA CGATACG CA
- T C
GAM69 258 KIAA008 1 6751 NP_055865.1 3 1057 TTGGCCGACAAC AG 3 B c c
2 ACAGAGAGGAGG TCCCTCCT TTGTGTTGTTG
GGGAGCT GGGGAGGA GACACAACAGC
GA
GAM69 258 KIAA008 1 16667 XP_042841.3 5 12 CAGCACACAACC ------ T 3 B c c
4 TTGATTAGGAGG TCCCTCCTA GTTGTGT GTTG
GGCTGGG GGGGAGGAT CAACACA CGAC
TAGTTC -
GAM69 258 KIAA087 1 17704 NP_055755.1 3 1264 TCTCCAACCAGG AG G - 3 B c c
2 GCAGAAAGGAGG TCCCTCCT TTGT TTG TTG
GAGGATT AGGGAGGA GACG GAC AAC
AA G C
GAM69 258 KIAA101 1 7543 NP_055782.1 3 197 ACGTCGACTTCA A - TT 3 B c c
8 TCAGCCAGGAGG TCCCTCCT GTTG TG GTTG
GAGAGCT AGGGAGGA CGAC AC CAGC
C T TT
GAM69 258 KLK14 1 19306 NP_071329.1 5 102 TGAGAAAGCAAG AGT G 3 B c c
ACATCAAGGAGG TCCCTCCT TGT TTGTT
GACCTGT AGGGAGGA ACA AACGA
ACT G
GAM69 258 L3MBTL 1 3613 NP_115479.2 3 10 CCCAGCGTCACT T--- T 3 B c c
TCTGCTAGGAGG TCCCTCCTAGT GTG TGTTG

GACCCGT AGGGAGGATCG CAC GCGAC
TCTT T
GAM69 258 LOC1162 1 7565 NP_612472.1 5 67 GGTTCCCAGAAC - TT G 3 B c c
38 AGACCTAGGAGG TC CCTCCTAG GT TTGTT
CGGCCTC GG GGAGGATC CA GACAA
C -- -
GAM69 258 LOC1334 1 19039 XP_059655.2 3 892 AGGTGGAACTGG - GTGTT 3 B c
c
91 AAACTTAGGAGG TCCCTCCTA GTT GTT
GAAAGAC AGGGAGGAT CAA CAA
T AGGT-
GAM69 258 LOC1433 1 7544 XP_096411.1 5 593 ACTGCCGGCAGC A- G 3 B c c
08 AGGCAGAGGAGG TCCCTCCT GTT TGTTGTTG
GAGGGGG AGGGAGGA CGG ACGACGGC
GA -
GAM69 258 LOC1484 1 14446 XP_086210.2 3 301 CATCCAGACAGC A G 3 B c c
90 AAAGCAAGGAGG TCCCTCCT GTT TGTTGTT
GAGCGTG AGGGAGGA CGA ACGACAG
A A
GAM69 258 LOC1509 1 5653 XP_087049.1 3 2355 TCCCAGCCACAG AG T T 3 B c c
35 CCAGGCAGGAGG TCCCTCCT TTG GTTGT
GAGAAGC AGGGAGGA GAC CGACA
CG - C
GAM69 258 LOC1969 1 12012 XP_116971.3 5 197 GAAGAGACATCA GTT- T 3 B c c
93 CCCAGTAGGAGG TCCCTCCTA GTG TGTT
GAGTACG AGGGAGGAT CAC ACAG
GACC T
GAM69 258 LOC2011 1 5222 NP_777579.1 5 1014 GCGGGAGCCGCA AG- T 3 B c
c
75 CAGTCGAGGAGG TCCCTCCT TTGTGT GTT
GAGCGCG AGGGAGGA GACACG CGA
GCT C
GAM69 258 LOC2012 1 4960 NP_775818.1 3 272 TTGAAGGGGACA - G 3 B c c
92 CAGTCTAGGAGG TCCCTCCTAG TTGTGTT TT
GGGATAA GGGGAGGATC GACACAG GG
T G
GAM69 258 LOC2832 1 14650 XP_208061.3 3 272 ATGGCAATATAC AG TG - 3 B c c
59 ATGGAGAGGAGG TCCCTCCT T TGT TGTTG
GACTCTT AGGGAGGA G ACA ATAAC
GA GT T
GAM69 258 LOC2834 1 10763 XP_211062.1 3 3695 CCCTCTTAGCAC -- TT 3 B c c
87 AGGTCTAGGAGG TCCCTCCTAG TTGTGTTG
GAAAAAT AGGGAGGATC GACACGAT
TG TC
GAM69 258 LOC2837 1 7820 XP_211199.1 3 1555 CAACATTACAAA AG----- T 3 B c c
78 GGAAGGAGGAGG TCCCTCCT TTGTG TGTTG
GAAGAGA AGGGAGGA AACAT ACAAC

GGAAGGA T

GAM69 25888 LOC2838 2 4070 XP_211249.1 3 304 CCAACTTGCAAC ---- T 3 B c c
ACAAGACCCTAG TCCCTCCTAG TTGTGTTGT
GAGGGAG AGGGAGGATC AACACAACG
CCAG T

GAM69 25888 LOC2838 2 19540 XP_211249.1 3 307 CTTGCAACACAA ---- T 3 B c c
GACCCTAGGAGG TCCCTCCTAG TTGTGTTGT
GAGGACG AGGGAGGATC AACACAACG
CCAG T

GAM69 25891 LOC2841 1 6369 XP_211377.1 3 396 TTTTCATAATAA GT GTG 3 B c c
AAAGTTAGGAGG TCCCTCCTA T TTGTTG
GAAACAT AGGGAGGAT A AATAAT
TG AA-

GAM69 25852 LOC2843 1 13773 XP_113978.1 5 218 GCGACGACTACG --- --- - 3 B c c
ACCACTAGGAGA TCC CTCCTAGT TGT GTTGTTG
GCGGACG AGG GAGGATCA GCA CAGCAGC
CGA CCA T

GAM69 25848 LOC2847 1 6746 XP_211629.1 3 585 TTTGCAATTGTC T - TT- 3 B c c
ACAACTAGGAGA CC CTCCTAGTTGTG GTTG
GG GG GAGGATCAACAC TAAC
- A TGT

GAM69 25807 LOC2849 1 20140 XP_209397.1 3 1488 GCATAAATAATA G G- 3 B c c
AAAAGTAGGAGG TCCCTCCTA TT TGTTGTT
GGTGGAG GGGGAGGAT AA ATAATAA
G AA

GAM69 25860 LOC2849 2 6769 XP_211715.1 5 368 TAAGCCAACAAC C A G 3 B c c
AACAGAACAGGG TCC TCCT GTT TGTTGTTG
TGGAGTG AGG GGGA CAA ACAACAAC
T - G

GAM69 25860 LOC2849 2 13185 XP_211715.1 5 368 GCCAACAACAAC C A G 3 B c c
AGAACAGGGTGG TCC TCCT GTT TGTTGTTG
AGTGAGT AGG GGGA CAA ACAACAAC
T - G

GAM69 25814 LOC2850 2 6769 XP_211734.1 5 707 TAAGCCAACAAC C A G 3 B c c
AACAGAACAGGG TCC TCCT GTT TGTTGTTG
TGGAGTG AGG GGGA CAA ACAACAAC
T - G

GAM69 25814 LOC2850 2 13185 XP_211734.1 5 707 GCCAACAACAAC C A G 3 B c c
AGAACAGGGTGG TCC TCCT GTT TGTTGTTG
AGTGAGT AGG GGGA CAA ACAACAAC
T - G

GAM69 25832 LOC2850 2 6769 XP_211740.1 5 853 TAAGCCAACAAC C A G 3 B c c
AACAGAACAGGG TCC TCCT GTT TGTTGTTG
TGGAGTG AGG GGGA CAA ACAACAAC
T - G

GAM69 25832 LOC2850 2 13185 XP_211740.1 5 853 GCCAACAACAAC C A G 3 B c c
AGAACAGGGTGG TCC TCCT GTT TGTTGTTG
AGTGAGT AGG GGGA CAA ACAACAAC
T - G

GAM69 258 LOC2850 1 5718 XP_211744.1 3 177 AAGGCAGTCAAC C AG - 3 B c c

45 ACAAGAGGGATG TCC TCCT TTGTGTTG TTG
GATCATT AGG AGGG AACACAAC GAC
T AG T

GAM69 258 LOC2855 1 8400 XP_211946.2 3 208 CACAGCAACAAC ----- A - 3 B c c
94 AGCAAGACCATG TCCCTC CT GTTGT GTTGTTG
GGGGAGT AGGGGG GA CGACA CAACGAC
TACCA A A

GAM69 258 LOC2857 1 18052 XP_212019.1 5 9 TTTCAGAGAAAC TA GTT 3 B c c
67 ACAACGGAGGGA TCCCTCC GTTGTGTT
AGGAGCC AGGGAGG CAACACAA
-- AGA

GAM69 258 LOC2858 1 6565 XP_209776.1 3 62 AGCAAGACGAAA A T G 3 B c c
46 ACACACAGGAGG TCCCTCCT GT GTGTT TTG
GAAAATC AGGGAGGA CA CACAA AGC
- - A

GAM69 258 LOC2860 1 18326 XP_212134.1 3 188 GAAGGCAACAAC C AGT 3 B c c

08 ATATAGAGGGTG TCC TCCT TGTGTTGTTG
GAAGAAT AGG GGGA ATACAACAAC
T GAT

GAM69 258 LOC3395 1 3748 XP_294985.1 3 1762 TCCAGCTGAACA T----- TT T 3 B c c

05 TCACCTAGGAGG CCCTCCTAG GTG TGTT
GCCATGC GGGAGGATC CAC ACAA
CGTACC -- T

GAM69 258 LOC3396 1 7222 XP_295032.1 5 741 GGGACACACAGC A----- T 3 B c c
85 CAGGCAAGGAGG TCCCTCCT GTTGTGT GTT
GAGCTCA AGGGAGGA CGACACA CAG
ACGGAC -

GAM69 258 LOC3405 1 7740 XP_291337.1 3 26 GTTACGGAAATA A T 3 B c c
61 CGCGACAGGAGG TCCCTCCT GTTGTGT GTT
GAGTATG AGGGAGGA CAGCGCA TAA
- -

GAM69 258 LOC3478 1 14650 XP_300269.1 3 272 ATGGCAATATAC AG TG - 3 B c c

67 ATGGAGAGGAGG TCCCTCCT T TGT TGTTG
GACTCTT AGGGAGGA G ACA ATAAC
GA GT T

GAM69 258 LOC3479 1 8274 XP_302565.1 5 35 AATTCCAACAAC C -- A 3 B c c
29 ACAACCAGCAGA TC CTC CT GTTGTGTTGTTG
GTGACAC AG GAG GA CAACACAACAAC
T AC C

GAM69 258 LOC3484 1 6566 XP_290913.2 5 61 GAGAGGCAGCGA AGTT 3 B c c
83 CATCGGAGGAGG TCCCTCCT GTGTTGTTG
GAGAGGC AGGGAGGA TACAGCGAC
GGC-

GAM69 258 LOC3488 1 1722 XP_302893.1 3 127 AAAAAGGAACAA C -- G 3 B c c
08 GTAACTAGGAGA TC CTCCTAGTTG TGTT TT
GAAAAAT AG GAGGATCAAT ACAA GA
A GA G

GAM69 258 LOC3490 1 9734 XP_302959.1 5 1603 GGCCTACACAGA AG- G T 3 B c c
92 CAAATCAGGAGG TCCCTCCT TTGT TTGT
GAACAGA AGGGAGGA AACA GACA
CTA - C
GAM69 258 LOC3492 2 4719 XP_303013.1 3 1197 ACCAGGAACAAC C- T-- 3 B c c
72 ACACATCTGGGA TCC TCCTAG TGTGTTGTT
CAGGAGG AGG AGGGTC ACACAACAA
AC TAC
GAM69 258 LOC3492 2 11989 XP_303013.1 3 1197 ACAACACACATC ----- T T 3 B c c
72 TGGGACAGGAGG TCCCTCCT AG TGTGT GTTG
GAATCCG AGGGAGGA TC ACACA CAAC
CAGGG T -
GAM69 258 LOC3492 2 4719 XP_303015.1 3 1197 ACCAGGAACAAC C- T-- 3 B c c
79 ACACATCTGGGA TCC TCCTAG TGTGTTGTT
CAGGAGG AGG AGGGTC ACACAACAA
AC TAC
GAM69 258 LOC3492 2 7545 XP_303015.1 3 1197 ACAACACACATC ----- T T 3 B c c
79 TGGGACAGGAGG TCCCTCCT AG TGTGT GTTG
GAATGCG AGGGAGGA TC ACACA CAAC
CAGGG T -
GAM69 258 LOC3493 2 4719 XP_303022.1 3 1172 ACCAGGAACAAC C- T-- 3 B c c
01 ACACATCTGGGA TCC TCCTAG TGTGTTGTT
CAGGAGG AGG AGGGTC ACACAACAA
AC TAC
GAM69 258 LOC3493 2 11989 XP_303022.1 3 1172 ACAACACACATC ----- T T 3 B c c
01 TGGGACAGGAGG TCCCTCCT AG TGTGT GTTG
GAATCCG AGGGAGGA TC ACACA CAAC
CAGGG T -
GAM69 258 LOC3493 2 4719 XP_303023.1 3 1197 ACCAGGAACAAC C- T-- 3 B c c
06 ACACATCTGGGA TCC TCCTAG TGTGTTGTT
CAGGAGG AGG AGGGTC ACACAACAA
AC TAC
GAM69 258 LOC3493 2 11989 XP_303023.1 3 1197 ACAACACACATC ----- T T 3 B c c
06 TGGGACAGGAGG TCCCTCCT AG TGTGT GTTG
GAATCCG AGGGAGGA TC ACACA CAAC
CAGGG T -
GAM69 258 LOC9256 1 6853 XP_045852.1 3 1580 CAAACAAACAAA C- G 3 B c c
8 ACAACTAGCTAG TCCCT CTAGTTGT TTGTT
GGATGGT AGGGA GATCAACA AACAA
TC A
GAM69 258 LSM1 1 11524 NP_055277.1 5 106 CGAGGCGGCGAC G - 3 B c c
TGCGGTAGGAGG TCCCTCCTA TTGT GTTGTTG
GAAGAGG AGGGAGGAT GGCG CAGCGGC
- T
GAM69 258 MECP2 1 15395 NP_004983.1 3 5056 AGGTGTGAGGGC AGT TG 3 B c c
AGTGCAAGGAGG TCCCTCCT TG TTGTT
GAGCACA AGGGAGGA AC GACGG
--- GT

GAM69 258 MGC1133 1 3597 NP_116107.2 3 480 AGTTAAATTCCA - TT 3 B c c
2 TACACTAGGAGG TCCCTCCTAGT TGTG GTT
GAGTTTT AGGGAGGATCA ATAC TAA
C CT
GAM69 258 MGC1233 1 12974 NP_116133.1 3 121 GGAGGAACATAG ---- G 3 B c c
5 CAAAGTAGGAGG TCCCTCCTA GTTGTGTT TT
GACAGAG AGGGAGGAT CGATACAA GA
GAAA G
GAM69 258 MGC4263 1 7740 NP_848662.1 3 26 GTTACGGAAATA A T 3 B c c
8 CGCGACAGGAGG TCCCTCCT GTTGTGT GTT
GAGTATG AGGGAGGA CAGCGCA TAA
- -
GAM69 258 MRAS 1 17599 NP_036351.1 5 21 TCCTCACCGGCG - T 3 B c c
CAGGCTAGGAGG TCCCTCCTAGT TGTGTTG TG
GGGCGGC GGGGAGGATCG ACGCGGC AC
G C
GAM69 258 NQO2 1 17356 NP_000895.1 3 48 TCACGTAAGCAG TC----- T 3 B c c
CACACTAGGAGG CCTCCTAGT GTGTTGTT
CCCAGGC GGAGGATCA CACGACGA
CGGACCC -
GAM69 258 NR3C2 1 18170 NP_000892.1 3 1218 TCATTTGACAAC - GT T 3 B c c
ACATGTGGGAGA TCC CTCCTA TGTGTTGT
GGAGGTC AGG GAGGGT ACACAACA
A GT G
GAM69 258 p100 1 7791 NP_055205.1 3 9 AATTTGGCTACA T T T 3 B c c
GCCGCTAGGAGG TCCCTCCTAGT G GTTGT
GGATCGG GGGGAGGATCG C CGACA
- - T
GAM69 258 PAK1 1 4638 NP_002567.2 5 255 ACGGCAGCGACA A--- - 3 B c c
GCGGGCAGGAGG TCCCTCCT GTTGT GTTGTTG
GAGAAAG AGGGAGGA CGACA CGACGGC
CGGG G
GAM69 258 PDGFB 1 6199 NP_002599.1 3 1190 TGGCTGGAGTGG G T TG 3 B c c
CCAAATAGGAGG TCCCTCCTA TTG GT TT
GAGACTG AGGGAGGAT AAC CG GA
A - GT
GAM69 258 PDGFB 1 6199 NP_148937.1 3 1190 TGGCTGGAGTGG G T TG 3 B c c
CCAAATAGGAGG TCCCTCCTA TTG GT TT
GAGACTG AGGGAGGAT AAC CG GA
A - GT
GAM69 258 PRO2015 1 18651 NP_060982.1 3 235 GGTTTCAAACAG G G GT 3 B c
c
TGGGATAGGAGG TCCCTCCTA TT T TGTT
GACACTT AGGGAGGAT AG G ACAA
- G TG
GAM69 258 PROZ 1 10472 NP_003882.1 3 46 AGAATGAACAAC --- TA 3 B c c
ACAACCGGAAGC TCCC TCC GTTGTGTTGTT
GGGATTC AGGG AGG CAACACAACAA

CGA C-

GAM69 258 PTK7 1 14002 NP_690622.1 3 540 CGTGGACAGCAA AGTTG-- 3 B c c
GCCGTGAGGAGG TCCCTCCT TGTTGTT
GAGCCCG AGGGAGGA ACGACAG
GTGCCGA

GAM69 258 PTPN7 1 17270 NP_002823.2 3 1036 CTCAGCATCAAC CCT T 3 B c c
ACAATTTCCAGG TCCCT AGTTGTGTTG TG
GGACCTC GGGGA TTAACACAAC AC
CCT T

GAM69 258 PTPN7 1 17270 NP_542155.1 3 1036 CTCAGCATCAAC CCT T 3 B c c
ACAATTTCCAGG TCCCT AGTTGTGTTG TG
GGACCTC GGGGA TTAACACAAC AC
CCT T

GAM69 258 PTPN7 1 17270 NP_542156.1 3 949 CTCAGCATCAAC CCT T 3 B c c
ACAATTTCCAGG TCCCT AGTTGTGTTG TG
GGACCTC GGGGA TTAACACAAC AC
CCT T

GAM69 258 RNF3 1 11664 NP_006306.2 3 1104 GTGAGCAGCTGA GT--- 3 B c c
AGGGCTAGGAGG TCCCTCCTAGTT GTTGTT
GAAGCCG AGGGAGGATCGG CGACGA
GAAGT

GAM69 258 SF3A3 1 12715 NP_006793.1 3 870 CCAACAAACAAG CC G--- - 3 B c c
GGAACTAGGACC TC TCCTAGTT TGTT GTTG
GACAGTG AG AGGATCAA ACAA CAAC
CC GGGA A

GAM69 258 SPATA2 1 8049 NP_006029.1 3 2000 GAATGACTAACA T- TT 3 B c c
CATCCTAGGAGG TCCCTCCTAG TGTGTTG
GAAAGTC AGGGAGGATC ACACAAT
CT CA

GAM69 258 SUFU 1 5078 NP_057253.2 3 381 CCTGCCGCACAG A T T 3 B c c
CCCAGCAGGAGG TCCCTCCT GTTG GTTGT
GAGGCGG AGGGAGGA CGAC CGACA
- C C

GAM69 258 TUBB-5 1 18195 NP_115914.1 3 318 CAAGCATGTCTG G ----- 3 B c c
CAAATTAGGAGG TCCCTCCTAGTT TGT TGTT
GAGTTAG AGGGAGGATTAA ACG ACGA
- TCTGT

GAM69 258 USP9Y 1 4718 NP_004645.1 5 597 AAGACACACCAG TT----- T 3 B c c
ATATTTAGGAGG TCCCTCCTAG GTGT GTT
GAATTAG AGGGAGGATT CACA CAG
TATAGAC -

GAM69 258 UXS1 1 7888 NP_079352.1 5 681 GGACTGGAGCAG A G 3 B c c
ACGACGAGGAGG TCCCTCCT GTTGT TTGTT
GAAGAGT AGGGAGGA CAGCA GACGA
G -

GAM70 358 C1QTNF6 1 561 NM_031910.2 3 TGAGGGGGTCAG ACC GAA 3 C c
c

ACACAGGCCC GGGCCTGTG TTGA CCTCA
CCCGGACAC GACT GGAGT
A-- GGG

GAM70 358 DKFZP43 1 10873 NM_014549.1 3 TGACCAGCAAGG G AGAACC 3 C c c

4P211 TCAGAGGCCC GGGCCT TGACCTTG TCA

CCCGGA ACTGGAAC AGT

G GACC--

GAM70 358 FLJ1329 1 16725 NM_032178.1 3 GAGGTTCTGCCA C ACCTTG A 3 C c c

1 CATGCCC GGGC TGTG AGAACCTC

CCCG ACAC TCTTGGAG

T CG---- -

GAM70 358 FLJ1495 1 1848 3 TGAGGTTCTCAA 3 C a a

0 GGTCACAGGCCC GGGCCTGTGACCTTGAGAACCTCA

CCCGGACACTGGAACTCTTGGAGT

GAM70 358 LOC2549 1 10060 XM_171204.2 3 TGAGATCGTGGG TGA AC 3 C c c

56 TCACAGGCCC GGGCCTGTGACCT GA CTCA

CCCGGACACTGGG CT GAGT

TG- A-

GAM70 358 LOC9114 1 503 XM_036480.1 3 TGAGGCTCACCA ACCT- AA 3 C c c

9 GCCACAGGCCT GGGCCTGTG TGAG CCTCA

TCCGGACAC ACTC GGAGT

CGACC --

GAM70 358 SPINT1 1 1381 NM_003710.1 3 AGGTTCTCCAAC C CC - CA 3 C c c

ATCACAGCCC GGGC TGTGA TTG AGAACCT

CCCG ACACT AAC TCTTGGA

- AC C --

GAM71 257 ABCD4 1 8201 NM_020323.1 3 GCCCCTGCCCTC TA GAC 3 C c c

AGG CCTG AGGGCAGGGGC

GGAC TCCCGTCCCCG

-- ---

GAM71 257 ABTB1 1 7271 NM_032548.2 5 CTCCTTCCTGCC A C C 3 C c c

CAGGTA TACCTGG CAGGG AGGGG

ATGGACC GTCCT TCCTC

C - -

GAM71 257 ADAMTS1 1 16850 NM_006988.2 3 CCCCTGTTTCCT T CAG C 3 C c c

GGTA TACC GGA GGCAGGGG

ATGG CCT TTGTCCCC

T --- -

GAM71 257 ADAMTS1 1 7432 NM_139025.1 5 GCCCCTGCCCTG TA GA 3 C c c

3 GCAGG CCTG CAGGGCAGGGGC

GGAC GTCCCGTCCCCG

-- G-

GAM71 257 AFAP 1 5293 NM_021638.2 3 GCCCCTGCATTC CAGG 3 C c c

AGGTG TACCTGGA GCAGGGGC

GTGGACTT CGTCCCCG

A---

GAM71 257 ASB16 1 1294 NM_080863.4 3 GCCTCTGCCTCC C ACA 3 C c c

CAAGTA TAC TGG GGGCAGGGGC

ATG ACC TCCGTCTCCG
A C--
GAM71 257 ATP8B2 1 18449 XM_290875.1 3 GCCCCTGCCCTG TA T A 3 C c c
CCTGGG CC GG CAGGGCAGGGGC
GG CC GTCCCGTCCCCG
G- T -
GAM71 257 AXL 1 3749 NM_021913.2 5 CCCCTGATTGTC GG C 3 C c c
CAGGTG TACCTGGACAG CAGGGG
GTGGACCTGTT GTCCCC
A- -
GAM71 257 BACE 2 1238 NM_138973.1 3 CCCGCTGCTTCC CAG - C 3 C c c
AGGTA TACCTGGA GGCAG GGG
ATGGACCT TCGTC CCC
--- G -
GAM71 257 BACE 2 12874 NM_138973.1 3 CCCCTAAGCTCC CAGG -- C 3 C c c
AGGTG TACCTGGA GC AGGGG
GTGGACCT CG TCCCC
---- AA -
GAM71 257 BCL2 1 8286 NM_000633.1 3 CCCTGGGGCCCT CA --- GC 3 C c c
CCAGGTA TACCTGGA GGGC AGGG
ATGGACCT CCCG TCCC
-- GGG --
GAM71 257 C14orf1 1 18564 NM_007176.1 3 GCCCCTGCCCTG TA GG 3 C c c
TGGG CCT ACAGGGCAGGGGC
GGG TGTCCCGTCCCCG
-- --
GAM71 257 CGR11 1 13993 NM_006569.1 3 CCCCTGTCTGGT CT A C 3 C c c
CCCAGTA TAC GGAC GGGCAGGGG
ATG CCTG TCTGTCCCC
AC G -
GAM71 257 COL4A6 1 11540 NM_001847.1 3 GCCCACTGTGTC TA AGG - 3 C c c
TAGG CCTGGAC GCAG GGGC
GGATCTG TGTC CCCG
-- --- A
GAM71 257 CSRP1 1 14791 NM_004078.1 3 GCCCCTGCTTCT TA CA 3 C c c
CCAGG CCTGGA GGGCAGGGGC
GGACCT TTCGTCCCCG
-- C-
GAM71 257 DAG1 1 11861 NM_004393.1 3 GCCCCTCTCCCC T C A C-- 3 C c c
TGCCCAAGT AC TGG CAGGG AGGGGC
TG ACC GTCCC TCCCCG
- A C CTC
GAM71 257 DCI 1 1497 NM_001919.1 3 GCCCCTGTGGGT TA - AGG 3 C c c
CCCAGG CCTGG AC GCAGGGGC
GGACC TG TGTCCCCG
-- C GG-
GAM71 257 DKFZP43 1 11454 NM_015644.1 3 CCCCTGCCCCTT TG -- C 3 C c c
4B103 GTTGGTA TACC GACA GGGCAGGGG
ATGG TTGT CCCGTCCCC
-- TC -

GAM71 257 DKFZp43 1 15728 3 CCCCTGCCCTGT C 3 C b b
4G0920 CCAGGTG TACCTGGACAGGGCAGGGG
GTGGACCTGTCCCGTCCCC
-
GAM71 257 DKFZp43 1 14410 NM_017558.1 3 GCCTCTCCTATT C GC 3 C c c
4L0850 CAGGTA TACCTGGA AGG AGGGGC
ATGGACTT TCC TCTCCG
A --
GAM71 257 DKFZp54 1 18786 5 GCCCCTGCCCCC TA ACA 3 C c c
7H236 AGG CCTGG GGGCAGGGGC
GGACC CCCGTCCCCG
-- ---
GAM71 257 DKFZp54 1 15410 3 GCCCCTGCCCTA GGAC 3 C c c
7M072 GGGGTG TACCT AGGGCAGGGGC
GTGGG TCCCGTCCCCG
GA--
GAM71 257 DKFZP58 1 457 NM_080730.1 3 GCCCCTCACCTT C C- 3 C c c
6I2223 GTCCACGTA TAC TGGACAGGG AGGGGC
ATG ACCTGTTCC TCCCCG
C AC
GAM71 257 DKFZP58 1 7051 NM_031294.1 3 CCCCTGGAGCTA C GG- C 3 C c c
6M1120 TCCGGGTA TACCTGGA AG CAGGGG
ATGGGCCT TC GTCCCC
A GAG -
GAM71 257 DUSP7 1 19651 XM_037430.5 3 GCCTCATCCTGT TA CA 3 C c c
CCAGG CCTGGACAGGG GGGGC
GGACCTGTCCT CTCCG
-- A-
GAM71 257 EGLN2 1 16027 NM_080732.1 3 GCCTATGCCACC ACAG G 3 C c c
AGGTA TACCTGG GGCA GGGC
ATGGACC CCGT TCCG
A--- A
GAM71 257 EMP1 1 13208 NM_001423.1 3 GCCCCTGCCCTG TA GGA 3 C c c
GGG CCT CAGGGCAGGGGC
GGG GTCCCGTCCCCG
-- ---
GAM71 257 FCER2 1 9196 NM_002002.2 3 GCCCCTGCCTTC TA AC 3 C c c
CCAGG CCTGG AGGGCAGGGGC
GGACC TTCCGTCCCCG
-- C-
GAM71 257 FLJ0000 1 6511 XM_088525.2 3 CCCCTGCCCCCG T ACA C 3 C c c
1 GTG TACC GG GGGCAGGGG
GTGG CC CCCGTCCCC
- --- -
GAM71 257 FLJ1019 1 6887 NM_018019.2 3 GCCCCTGGCTCC T CAG G 3 C c c
3 AGGT ACCTGGA G CAGGGGC
TGGACCT C GTCCCCG
- --- G
GAM71 257 FLJ1060 1 753 5 GCCCCTGCCCCT TA - A - 3 C c c
4 GCTGCGG CC TGG CAGGG CAGGGGC

GG GTC GTCCC GTCCCCG
-- C - C
GAM71 257 FLJ1074 1 10397 NM_018201.2 3 GCCCCTGCTTTC TA A -- 3 C c c
3 TGCCCAGG CCTGG CAG GGCAGGGGC
GGACC GTC TCGTCCCCG
-- C TT
GAM71 257 FLJ1119 1 9608 NM_018356.1 3 GCCCCTGCCCTT TA C 3 C c c
3 TTAGG CCTGGA AGGGCAGGGGC
GGATTT TCCCGTCCCCG
-- -
GAM71 257 FLJ1212 1 10593 5 GCCCCTGCCAGC T ACAG 3 C c c
2 TCAGGT ACCTGG GGCAGGGGC
TGGACT CCGTCCCCG
- CGA-
GAM71 257 FLJ1315 1 4589 3 GCCCCTGTGATC T CAGG 3 C c c
3 CAGGT ACCTGGA GCAGGGGC
TGGACCT TGTCCCCG
- AG--
GAM71 257 FLJ1410 1 12679 NM_025025.1 3 GCCCTCTGTCCT TA CA - 3 C c c
0 CCAGG CCTGGA GGGCAG GGGC
GGACCT CCTGTC CCCG
-- -- T
GAM71 257 FLJ2020 1 4760 NM_017711.2 3 GCCCTCTGCCCA GGACA - 3 C c c
7 GGTG TACCT GGGCAG GGGC
GTGGA CCCGTC CCCG
----- T
GAM71 257 FLJ2159 1 827 NM_024823.1 3 CCCTCCCTCCAG CA C GC 3 C c c
6 GTA TACCTGGA GGG AGGG
ATGGACCT CCC TCCC
-- - --
GAM71 257 FLJ2237 1 5148 NM_025078.1 3 GCCCCTGCCGTG T G AG 3 C c c
8 CAGGT ACCTG AC GGCAGGGGC
TGGAC TG CCGTCCCCG
- G --
GAM71 257 FLJ3286 1 14411 NM_144613.1 3 GCCCCTGCTCCA TA ACA 3 C c c
5 CCAGG CCTGG GGGCAGGGGC
GGACC CTCGTCCCCG
-- AC-
GAM71 257 GIT2 1 16979 NM_014776.2 3 GCCCCTGCTGTC TA - GG 3 C c c
CCAGG CCTGG ACA GCAGGGGC
GGACC TGT CGTCCCCG
-- C --
GAM71 257 GNAI2 1 5504 NM_002070.1 3 GCCCCTGCCCCA T C ACA- 3 C c c
GCCCAAGT AC TGG GGGCAGGGGC
TG ACC CCCGTCCCCG
- A CGAC
GAM71 257 GREB1 1 2037 NM_014668.2 3 CCCCAGGGACTG GGCA- C 3 C c c
TCCAGGTG TACCTGGACAG GGGG
GTGGACCTGTC CCCC
AGGGA -

GAM71 257 H-plk 1 11965 NM_015852.1 5 GCCCCTGCCTGA C GACA 3 C c c
TGCATGTA TAC TG GGGCAGGGGC
ATG AC TCCGTCCCCG
T GTAG
GAM71 257 HEMK 1 14603 NM_016173.1 3 GCCTTCTGCCCG TA ACA - 3 C c c
ACCCAGG CCTGG GGGCAGG GGC
GGACC CCCGTCT CCG
-- CAG T
GAM71 257 HIRA 1 1388 NM_003325.3 3 GCCCCTGCTGCT TA GA - 3 C c c
GCAGG CCTG CAG GGCAGGGGC
GGAC GTC TCGTCCCCG
-- -- G
GAM71 257 ID4 1 19992 NM_001546.2 3 GCCGCGCTGTCC G AGG 3 C c c
AGGTG TACCTGGACAG GC GGC
GTGGACCTGTC CG CCG
G ---
GAM71 257 IL27 1 2935 5 GCCCCTGCCCTG TA GGA 3 C c c
AGG CCT CAGGGCAGGGGC
GGA GTCCCGTCCCCG
-- ---
GAM71 257 ITPK1 1 18327 NM_014216.2 3 GCCCCCACCCTG T A CA 3 C c c
CCTGGTG TACC GG CAGGG GGGGC
GTGG CC GTCCC CCCCG
T - AC
GAM71 257 KIAA036 1 10473 XM_036708.9 3 GCCCCTGCCTGA - GGACA 3 C c c
8 AAGTGTA TAC CT GGGCAGGGGC
ATG GA TCCGTCCCCG
T AAG--
GAM71 257 KIAA045 1 14799 NM_014638.1 5 GCCCCTGCATGC TA A GG 3 C c c
0 CCAGG CCTGG CA GCAGGGGC
GGACC GT CGTCCCCG
-- C A-
GAM71 257 KIAA046 1 15128 NM_014851.1 3 GCCCAGCACTGT TA G AG 3 C c c
9 CCAGG CCTGGACAG GC GGGC
GGACCTGTC CG CCCG
-- A A-
GAM71 257 KIAA076 1 10304 XM_027105.3 3 CGCCCCCGCCCT TA A- A - 3 C c c
7 GCCCCAGG CCTGG CAGGGC GGGGC
GGACC GTCCCG CCCCG
-- CC C C
GAM71 257 KIAA077 1 15906 3 GCCCCTGCCTCC TA ACA 3 C c c
5 CAGG CCTGG GGGCAGGGGC
GGACC TCCGTCCCCG
-- C--
GAM71 257 KIAA101 1 17733 XM_050742.5 3 GCCCCTGTTCCT C CA 3 C c c
0 CCAAGTG TAC TGGA GGGCAGGGGC
GTG ACCT CTTGTCCCCG
A C-
GAM71 257 KIAA187 1 15615 XM_056635.4 3 GCCCCTGCACAT A GG- 3 C c c
9 GCCAGGTG TACCTGG CA GCAGGGGC

GTGGACC GT CGTCCCCG
- ACA

GAM71 257 LHFP 1 5024 NM_005780.1 5 CCCCTGCTCTTC T C C 3 C c c
CAGGT ACCTGGA AGGGCAGGGG
TGGACCT TCTCGTCCCC
- - -

GAM71 257 LOC1137 1 14333 3 GCCCCTGCCTGT T GACA 3 C c c
63 AATAGGT ACCTG GGGCAGGGGC
TGGAT TCCGTCCCCG
- AATG

GAM71 257 LOC1184 1 10854 NM_145202.1 3 GCCCCCGCCCTG TA -- A 3 C c c
71 TCCCAAGG CCT GGACAGGGC GGGGC
GGA CCTGTCCCG CCCCG
-- AC C

GAM71 257 LOC1263 1 19761 5 GCCCCCGTGTCC G CAG 3 C c c
64 AGGTG TACCTGGACA GG GGGC
GTGGACCTGT CC CCCG
G ---

GAM71 257 LOC1440 1 9661 XM_096520.3 5 GCCCCTGCCGAC T CAG 3 C c c
17 TCCAGGT ACCTGGA GGCAGGGGC
TGGACCT CCGTCCCCG
- CAG

GAM71 257 LOC1458 1 18672 XM_096881.6 5 GCCTGTGTCCTC CA G 3 C c c
36 CAGGTA TACCTGGA GGGCA GGGC
ATGGACCT CCTGT TCCG
-- G

GAM71 257 LOC1462 1 12330 3 TCCTCCCCTCCA CA C GC 3 C c c
37 GGTA TACCTGGA GGG AGGG
ATGGACCT CCC TCCT
-- C --

GAM71 257 LOC1494 1 10468 3 GCCCCTGCCCCC TA ACA 3 C c c
61 GGG CCTGG GGGCAGGGGC
GGGCC CCCGTCCCCG
-- ---

GAM71 257 LOC1503 1 7786 5 GCCCCTGCCCCA T GACA 3 C c c
78 CACAGGT ACCTG GGGCAGGGGC
TGGAC CCCGTCCCCG
- ACAC

GAM71 257 LOC1522 1 10326 XM_098188.1 5 GCCCCTGCGGGT TA -- AGG 3 C c
c
86 CCCCAGG CCT GGAC GCAGGGGC
GGA CCTG CGTCCCCG
-- CC GG-

GAM71 257 LOC1573 1 15688 3 GCCCCTCATCTC CA GC 3 C c c
49 CAGGTG TACCTGGA GG AGGGGC
GTGGACCT CT TCCCCG
-- AC

GAM71 257 LOC1591 1 9850 XM_088753.1 5 GCCCCTGCGGTT C ---- 3 C c c
10 CCTGTCCGAGTA TAC TGGACAGG GCAGGGGC
ATG GCCTGTCC CGTCCCCG

```
                                        A      TTGG
GAM71   257   LOC1610 1  7787          5      GCCCCTGCCATC TA   - CAG            3  C  c  c
        38                          GCAGG       CCTG GA  GGCAGGGGC
                                     GGAC CT   CCGTCCCCG
                                    --   G  A--
GAM71   257   LOC1652 1  16928         3      GCCCCTGCCCGA    GGACA             3  C  c  c
        46                          GGTG      TACCT    GGGCAGGGGC
                                    GTGGA    CCCGTCCCCG
                                      G----
GAM71   257   LOC1967 1  19133 XM_116865.1  3      GCCCCTGCCCCA     ACAG            3  C  b  b
        61                          GGTG      TACCTGG   GGCAGGGGC
                                    GTGGACC   CCGTCCCCG
                                       ----
GAM71   257   LOC1973 1  772   XM_113869.2  3      GCCCCCACCCGG    GG  A  CA          3  C  c  c
        42                          TGGGTA     TACCT  AC GGG  GGGGC
                                    ATGGG  TG CCC  CCCCG
                                      -- G   AC
GAM71   257   LOC2036 1  16235         3      GCCCCTTCCCGT T      A  C           3  C  c  c
        36                          CCAGGT      ACCTGGAC GGG AGGGGC
                                     TGGACCTG CCC TCCCCG
                                    -      -  T
GAM71   257   LOC2196 1  2165          3      GCCCCTGCCATG TA   GA  G             3  C  c  c
        54                          CAGG        CCTG  CA GGCAGGGGC
                                     GGAC  GT CCGTCCCCG
                                    --   -- A
GAM71   257   LOC2210 1  18299         3      GCCCTTGTTGCC TA    A  GG            3  C  c  c
        60                          CAGG        CCTGG CA  GCAGGGGC
                                     GGACC GT  TGTTCCCG
                                    --    C  --
GAM71   257   LOC2534 1  14098         5      GCCCCTCTGTGT TA      G  C           3  C  c  c
        61                          CCAGG       CCTGGACA GG AGGGGC
                                     GGACCTGT TC TCCCCG
                                    --       G  -
GAM71   257   LOC2541 1  18053         5      GCCATCCTGTCC T         CAGG          3  C  c  c
        82                          AGGT        ACCTGGACAGGG   GGC
                                     TGGACCTGTCCT   CCG
                                    -          A---
GAM71   257   LOC2544 1  19884         3      GCCCCTGCCCTC TA  -   CA            3  C  c  c
        27                          TGTGG       CC TGGA  GGGCAGGGGC
                                     GG GTCT  CCCGTCCCCG
                                    -- T   --
GAM71   257   LOC2552 1  3832          3      GCCCCTGCCCTA TA  T  AC              3  C  c  c
        85                          CCTGG       CC GG  AGGGCAGGGGC
                                     GG CC  TCCCGTCCCCG
                                    -- T  A-
GAM71   257   LOC2554 1  8843          3      CCCCCCTTCCAG      C   CA  GC        3  C  c  c
        81                          GTG       TACCTGGA AGGG  GGG
                                    GTGGACCT TCCC  CCC
                                         -   --  --
GAM71   257   LOC2556 1  9039          3      GCCCTTGTACTC     GAC  GG            3  C  c  c
```

```
          50                          AGGTA      TACCTG  AG  CAGGGGC
                                            ATGGAC  TC  GTTCCCG
                                              --- AT
GAM71   257   LOC2561 1  7930          5       CCCTCACCGTCC       A  GC   GC        3  C  c  c
          58                          AGGTG      TACCTGGAC GG  AGGG
                                            GTGGACCTG CC  TCCC
                                              - AC   --
GAM71   257   LOC2574 1  3853          3       GCCCCTGTTCAT T  C   CA             3  C  c  c
          94                          CCAAGT     AC TGGA  GGGCAGGGGC
                                            TG ACCT  CTTGTCCCCG
                                            - A   A-
GAM71   257   LOC5733 1  882           3       GCCCCCTCCCTG TA       CA          3  C  c  c
          3                           TCCAGG      CCTGGACAGGG  GGGGC
                                             GGACCTGTCCC  CCCCG
                                            --        TC
GAM71   257   LOC9175 1  13656 XM_040467.1  5       CCTCTGCCTGCC     A   G    C        3  C  c  c
          9                           AGGTA      TACCTGG CAGG CAGGGG
                                            ATGGACC GTCC GTCTCC
                                              -   -    -
GAM71   257   LOXL2  1  9639  NM_002318.1  3       CGCCCCCACCCT TAC       CA   -       3  C  c  c
                                      GTCCAG       CTGGACAGGG  GGGGC
                                             GACCTGTCCC  CCCCG
                                            ---        AC   C
GAM71   257   LR8    1  15399 NM_014020.2  5       GCCCCTGCCCCG TA   GG  A            3  C  c  c
                                      TGAAGG       CCT  AC GGGCAGGGGC
                                             GGA  TG CCCGTCCCCG
                                            --  AG  C
GAM71   257   LY6E   1  5766  NM_002346.1  3       GCCCCTGCCTCT   C  A  -            3  C  c  c
                                      GCCCAAGTG    TAC TGG CAG GGCAGGGGC
                                            GTG ACC GTC CCGTCCCCG
                                              A  C  T
GAM71   257   MARKL1  1  3863          5       GCCCCTGCCCCC TA    ACA             3  C  c  c
                                      CGGG         CCTGG   GGGCAGGGGC
                                             GGGCC   CCCGTCCCCG
                                            --    C--
GAM71   257   MGC1541 1  18601 NM_032371.1  5       GCCCCCGTTCCC T      A  - A         3  C  c  c
          6                           GTCCAGGT     ACCTGGAC GGG C GGGGC
                                             TGGACCTG CCT G CCCCG
                                            -       C  T C
GAM71   257   MGC1602 1  14504 NM_032923.1  3       GCCCCTGCCCTC    TGGAC              3  C  c
c
          5                           GGTG       TACC    AGGGCAGGGGC
                                            GTGG    TCCCGTCCCCG
                                              C----
GAM71   257   MKRN1   1  17691 NM_013446.2  3       CCCCTGAGCTTT       C GG    C        3  C  c  c
                                      CAGGTA       TACCTGGA AG  CAGGGG
                                            ATGGACTT TC  GTCCCC
                                              - GA    -
GAM71   257   MLN    1  13955 NM_002418.1  3       GCCCCTCCTGCC   C  A   GC           3  C  c  c
                                      CAAGTG       TAC TGG CAGG  AGGGGC
```

GTG ACC GTCC TCCCCG
A C --
GAM71 257 MSF 1 16611 NM_006640.2 3 CCCCTGCCCTGC --- - C 3 C c c
TCCTAAGGGTA TACCT GGA CAGGGCAGGGG
ATGGG CCT GTCCCGTCCCC
AAT C -
GAM71 257 NAGA 1 8596 NM_000262.1 3 GCCCCTGCTGTG T A G 3 C c c
CCTGGTA TACC GG CA GGCAGGGGC
ATGG CC GT TCGTCCCCG
T - G
GAM71 257 P4HA2 1 2032 NM_004199.1 5 TTCCTGCCTCAG GACA C 3 C c c
GTA TACCTG GGGCAGGGG
ATGGAC TCCGTCCTT
---- -
GAM71 257 PBX2 1 11494 NM_002586.3 3 GCCCCCCTGGCT TA -- CAG 3 C c c
CCAGG CCTGGA CAGGG GGGC
GGACCT GTCCC CCCG
-- CG ---
GAM71 257 PCDH16 2 6276 NM_003737.1 3 GCCCCTGCCCCT TAC A - 3 C c c
GCCCAG CTGG CAGGG CAGGGGC
GACC GTCCC GTCCCCG
--- C C
GAM71 257 PCDH16 2 16682 NM_003737.1 3 GCCCCTGCCCAG T C ACA- 3 C c c
AACCAAGT AC TGG GGGCAGGGGC
TG ACC CCCGTCCCCG
- A AAGA
GAM71 257 PIP5K1C 2 11489 XM_047620.3 3 GCCCCTCCACTC TA A C-- 3 C c c
TGCCCAGG CCTGG CAGGG AGGGGC
GGACC GTCTC TCCCCG
-- C ACC
GAM71 257 PIP5K1C 2 16584 XM_047620.3 3 CGCCCCCGCCCT TA ------ A - 3 C c c
GTCCCTCCGAAG CCT GGACAGGGC GGGGC
G GGA CCTGTCCCG CCCCG
-- AGCCTC C C
GAM71 257 PRKWNK2 1 19227 3 GCCCCTGCAGGT AGG 3 C b b
CCAGGTG TACCTGGAC GCAGGGGC
GTGGACCTG CGTCCCCG
GA-
GAM71 257 PRO2730 1 5236 NM_025222.2 3 CCCCTGGCTTTT C G C 3 C c c
CCGGGTA TACCTGGA AGG CAGGGG
ATGGGCCT TTC GTCCCC
T G -
GAM71 257 PSKH1 1 8943 NM_006742.1 3 GCCCCTGCCATT TA GA - 3 C c c
GCAGG CCTG CAG GGCAGGGGC
GGAC GTT CCGTCCCCG
-- -- A
GAM71 257 PTPN1 1 487 NM_002827.2 3 GCCCAGCCTGTC T GCAG 3 C c c
CTGGTA TACC GGACAGG GGGC
ATGG CCTGTCC CCCG

T GA--

GAM71 257 RARA 1 3568 NM_000964.1 3 GCCCCCACCTGC TA AC ---- 3 C c c

CCTCCCGGG CCTGG AGGGCA GGGGC

GGGCC TCCCGT CCCCG

-- C- CCAC

GAM71 257 RNPEP 1 8256 NM_020216.2 3 GCCCCTGCCTCT TA CA 3 C c c

TCAGG CCTGGA GGGCAGGGGC

GGACTT TCCGTCCCCG

-- C-

GAM71 257 SLC15A1 1 19682 NM_005073.1 3 CCTCTGCCCCCA ACA C 3 C c c

GGTA TACCTGG GGGCAGGGG

ATGGACC CCCGTCTCC

--- -

GAM71 257 SLC21A9 1 5348 NM_007256.1 3 GCCATCTCCTGT G CAGG 3 C c c

CAGGTA TACCTG ACAGGG GGC

ATGGAC TGTCCT CCG

- CTA-

GAM71 257 SLC2A10 1 1738 NM_030777.2 3 GCCCCTGCCCCC GGACA 3 C c c

AAAGGTG TACCT GGGCAGGGGC

GTGGA CCCGTCCCCG

AACC-

GAM71 257 SLC5A6 1 19138 NM_021095.1 5 GCCCCTGCCCTA TAC AC- 3 C c c

CCCCAG CTGG AGGGCAGGGGC

GACC TCCCGTCCCCG

--- CCA

GAM71 257 SLC6A2 1 3434 NM_001043.1 3 CCCCATGCCAAT T G- - C 3 C c c

GTCCAGGT ACCTGGACA GGCA GGGG

TGGACCTGT CCGT CCCC

- AA A -

GAM71 257 SLC9A3R 1 16392 NM_004785.1 3 GCCCCTGCCCAC ACA 3 C b b

2 CAGGTA TACCTGG GGGCAGGGGC

ATGGACC CCCGTCCCCG

A--

GAM71 257 SSB-4 1 7581 5 GCCCCTGCCGCA T ACAG 3 C c c

GCCCGGTA TACC GG GGCAGGGGC

ATGG CC CCGTCCCCG

C GACG

GAM71 257 STK10 1 13156 NM_005990.1 3 GCCTCTTCTGCC A GC 3 C c c

CAGGTG TACCTGG CAGG AGGGGC

GTGGACC GTCT TCTCCG

C --

GAM71 257 SYNGR1 2 11048 NM_004711.2 3 GCCCCTGCTCCT TA A - 3 C c c

GCCCAGG CCTGG CAGG GCAGGGGC

GGACC GTCC CGTCCCCG

-- C T

GAM71 257 SYNGR1 2 13235 NM_004711.2 3 GCCCAACTCTGT T CAG 3 C c c

CCGGTA TACC GGACAGGG GGGC

ATGG CCTGTCTC CCCG

- AA-

GAM71 257 TFAP4 1 18694 NM_003223.1 3 GCCCCCACCTCT T -- - CA 3 C c c
GCCTCCAGGT ACCTGGA CAG GG GGGGC
TGGACCT GTC CC CCCCG
- CC T AC
GAM71 257 TGIF2 1 6058 NM_021809.2 3 GCCCCTGCCCAG TAC GA -- 3 C c c
TGAACAG CTG CA GGGCAGGGGC
GAC GT CCCGTCCCCG
--- AA GA
GAM71 257 UCP3 1 4639 NM_003356.2 5 GCCCCTGCCGTG TA GA G 3 C c c
GCAGG CCTG CA GGCAGGGGC
GGAC GT CCGTCCCCG
-- G- G
GAM71 257 UREB1 1 5654 NM_031407.2 5 GCCTTTTGCTGT T GGC 3 C c c
CCTGGTA TACC GGACAG AGGGGC
ATGG CCTGTC TTTCCG
T GT-
GAM71 257 USP21 1 3093 NM_012475.2 3 GCCCCTGCCCAT TAC G - 3 C c c
GTACAG CTG ACA GGGCAGGGGC
GAC TGT CCCGTCCCCG
--- A A
GAM72 342 AKAP11 1 10091 NM_016248.2 3 TCACGCCTGTAA AA G A 3 C c c
TCCCAGAACT AGT CTGGGATTACAGGC TGA
TCA GACCCTAATGTCCG ACT
-- A C
GAM72 342 ALOX15B 1 407 NM_001141.1 3 TCATGCCCATAA CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA GGCATGA
TTTCACGACCCTAAT CCGTACT
AC
GAM72 342 AP1GBP1 1 8213 NM_080550.1 3 TCACACCTGTAA C CA 3 C c c
TCTCAACGCTTT AAAGTG TGGGATTACAGG TGA
TTTCGC ACTCTAATGTCC ACT
A AC
GAM72 342 APOL1 1 11403 NM_145343.1 3 TCATGCCTGTAA G 3 C b b
TCCGAGCACTTT AAAGTGCT GGATTACAGGCATGA
TTTCACGA CCTAATGTCCGTACT
G
GAM72 342 ARSD 1 14037 NM_001669.1 3 TCATGCCTTTAA C 3 C b b
TCCCAGCATTTT AAAGTGCTGGGATTA AGGCATGA
TTTTACGACCCTAAT TCCGTACT
T
GAM72 342 BPHL 1 16204 NM_004332.1 3 TCACAGCTATAA CA A- 3 C c c
TCTCAGCACTTT AAAGTGCTGGGATTA GGC TGA
TTTCACGACTCTAAT TCG ACT
A- AC
GAM72 342 BRCA2 1 2407 NM_000059.1 5 TCATGCCTGTAA C 3 C b b
TCCCAACACTTT AAAGTG TGGGATTACAGGCATGA
TTTCAC ACCCTAATGTCCGTACT
A
GAM72 342 C1orf24 1 12135 NM_052966.1 3 CCTATAATCCCA C CATGA 3 C c c
GCACTTT AAAGTGCTGGGATTA AGG

TTTCACGACCCTAAT TCC
A -----
GAM72 342 C1orf33 1 13080 NM_016183.2 3 TCACGCCTGGAA A A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATT CAGGC TGA
TTTCACGACCCTAA GTCCG ACT
G C
GAM72 342 C1QTNF2 1 9609 NM_031908.2 3 TCATGCCTATAA G C 3 C b b
TCCCAGGACTTT AAAGT CTGGGATTA AGGCATGA
TTTCA GACCCTAAT TCCGTACT
G A
GAM72 342 C20orf1 2 11104 3 TCATGCTGTAAT C G 3 C b b
06 CCCATCACTTT AAAGTG TGGGATTACAG CATGA
TTTCAC ACCCTAATGTC GTACT
T -
GAM72 342 C20orf1 2 16007 3 TCATGCCTGTGG G 3 C b b
06 TCCCAGAACTTT AAAGT CTGGGATTACAGGCATGA
TTTCA GACCCTGGTGTCCGTACT
A
GAM72 342 C20orf1 1 19248 XM_300782.1 3 TCACACCTATAA TG C CA 3 C c c
42 TCCTGGCACTTT AAAGTGC GGATTA AGG TGA
TTTCACG CCTAAT TCC ACT
GT A AC
GAM72 342 C21orf5 1 17560 NM_005128.1 5 TCACACCTGTAA CA 3 C b b
TCTCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACTCTAATGTCC ACT
AC
GAM72 342 C22orf2 1 15306 NM_025225.2 3 CTGTAATCCCAG GCATGA 3 C c c
0 CACTTT AAAGTGCTGGGATTACAG
TTTCACGACCCTAATGTC

GAM72 342 C4S-2 1 10076 NM_018641.2 3 TCAGGCAGGTAA G AG A 3 C c c
TCCCAGAACTTT AAAGT CTGGGATTAC GC TGA
TTTCA GACCCTAATG CG ACT
A GA G
GAM72 342 C6orf10 1 2589 NM_006781.1 5 TCACGCCTGTAA A C A 3 C c c
TCCCATCATTT AAGTG TGGGATTACAGGC TGA
TTTAC ACCCTAATGTCCG ACT
- T C
GAM72 342 C6orf29 1 9517 NM_032794.1 3 TCACGCCTGTAA CTG A 3 C c c
TCCAACACTTT AAAGTG GGATTACAGGC TGA
TTTCAC CCTAATGTCCG ACT
AA- C
GAM72 342 CASP10 1 13216 NM_032974.1 3 TCATGCCTGTAA AA 3 C b b
TCCCAGTACT AGTGCTGGGATTACAGGCATGA
TCATGACCCTAATGTCCGTACT
--
GAM72 342 CASP8 1 10165 NM_001228.2 3 TCATGTCTATAA C 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
TTTCACGACCCTAAT TCTGTACT
A

GAM72 342 CENTA2 1 10588 NM_018404.1 3 TCATGCCCATAA T CA 3 C b b
TCCCAGCCCTTT AAAG GCTGGGATTA GGCATGA
TTTC CGACCCTAAT CCGTACT
C AC
GAM72 342 CHST3 1 8037 NM_004273.2 3 TCATACCTGTAA A C 3 C b b
TCCCAGCATTT AAGTGCTGGGATTACAGG ATGA
TTTACGACCCTAATGTCC TACT
- A
GAM72 342 CNGB1 1 8665 NM_001297.1 3 TCATGCCTATAA TG C 3 C b b
TCCCAGTGCTTT AAAG CTGGGATTA AGGCATGA
TTTC GACCCTAAT TCCGTACT
GT A
GAM72 342 CNNM1 1 14071 NM_020348.1 3 TCACACCTGTAA G C CA 3 C c c
TCCCAACAGTTT AAA TG TGGGATTACAGG TGA
TTT AC ACCCTAATGTCC ACT
G A AC
GAM72 342 CPM 1 2111 NM_001874.1 3 TCACACCTTGTA - CA 3 C b b
ATCCCAGCACTT AAAGTGCTGGGATTACA GG TGA
T TTTCACGACCCTAATGT CC ACT
T AC
GAM72 342 CPR2 1 14297 NM_030900.1 3 TCACGTCTGTAA G A 3 C b b
TCCCAGCAGTTT AAA TGCTGGGATTACAGGC TGA
TTT ACGACCCTAATGTCTG ACT
G C
GAM72 342 CROT 1 14662 NM_021151.1 3 TCATGCCTATAA C 3 C b b
TCTTAGCACTTT AAAGTGCTGGGATTA AGGCATGA
TTTCACGATTCTAAT TCCGTACT
A
GAM72 342 CSL4 1 16124 NM_016046.2 3 TCATGTTTGTAA - 3 C b b
ATCCCAGCACTT AAAGTGCTGGGATT ACAGGCATGA
T TTTCACGACCCTAA TGTTTGTACT
A
GAM72 342 CTSS 1 2354 NM_004079.3 3 TCACGCCTGTAA A A 3 C b b
TCCCAGTACTT AAGTGCTGGGATTACAGGC TGA
TTCATGACCCTAATGTCCG ACT
- C
GAM72 342 CYorf14 1 4714 NM_018542.1 3 TCACACCCTGTA CA- 3 C b b
ATCCCAGCACTT AAAGTGCTGGGATTACAGG TGA
T TTTCACGACCCTAATGTCC ACT
CAC
GAM72 342 CYP3A4 1 15095 NM_017460.3 3 TCACGCCTGTAA G A 3 C b b
TCCTAGCAGTTT AAA TGCTGGGATTACAGGC TGA
TTT ACGATCCTAATGTCCG ACT
G C
GAM72 342 DAPP1 1 8299 NM_014395.1 3 TCATGCCTGTAA G 3 C b b
TCCCAGGACTTT AAAGT CTGGGATTACAGGCATGA
TTTCA GACCCTAATGTCCGTACT
G
GAM72 342 DCLRE1C 1 10284 NM_022487.1 3 TCATGCCTGTAA AAAGT 3 C c c

TCCCAGCTAC GCTGGGATTACAGGCATGA
CGACCCTAATGTCCGTACT
CAT--

GAM72 342 DCOHM 1 7474 NM_032151.2 3 TCACGCCTGTAA T A 3 C b b
TCCCTGCACTTT AAAGTGC GGGATTACAGGC TGA
TTTCACG CCCTAATGTCCG ACT
T C

GAM72 342 DHFR 1 3036 NM_000791.2 3 TCACACCTGTAA CA 3 C b b
TCCCAGCGCTTT AAAGTGCTGGGATTACAGG TGA
TTTCGCGACCCTAATGTCC ACT
AC

GAM72 342 DIS3 1 17479 NM_014953.2 3 TCATGCCTGTAA 3 C b b
TCCTAGCATTTT AAAGTGCTGGGATTACAGGCATGA
TTTTACGATCCTAATGTCCGTACT

GAM72 342 DJ122O8 1 4695 NM_020466.3 3 TCATGCTTGTAA 3 C b b
.2 TCCCAGTACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCATGACCCTAATGTTCGTACT

GAM72 342 DKFZp43 2 9845 3 TCACACTTATAA C CA 3 C c b
4E0519 TCCCAGCACTTT AAAGTGCTGGGATTA AGG TGA
TTTCACGACCCTAAT TTC ACT
A AC

GAM72 342 DKFZp43 2 18481 3 TCATGCCTGTAA 3 C b b
4E0519 TCCTAGTACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCATGATCCTAATGTCCGTACT

GAM72 342 DKFZP43 1 1252 NM_015590.1 3 TCACATTTGTAA CA 3 C b b
4F1735 TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAATGTTT ACT
AC

GAM72 342 DKFZP43 1 16090 XM_113763.3 3 CCTGTAATTCCA CATGA 3 C c c
4I1735 GCACTTT AAAGTGCTGGGATTACAGG
TTTCACGACCTTAATGTCC

GAM72 342 DKFZP43 1 8281 5 TCACGTCTGTAA A 3 C b b
4N161 TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAATGTCTG ACT
C

GAM72 342 DKFZp54 1 6974 NM_018704.1 3 TCATGCCTGTAA C 3 C b b
7A023 TCTTATCACTTT AAAGTG TGGGATTACAGGCATGA
TTTCAC ATTCTAATGTCCGTACT
T

GAM72 342 DKFZp54 1 12489 NM_018705.1 3 TCACGCCTGTAA A 3 C b b
7G183 TTCTAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGATCTTAATGTCCG ACT
C

GAM72 342 DKFZP56 1 8696 NM_030954.2 3 TCACGCCTGTAA A 3 C b b
4A022 TCCTAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGATCCTAATGTCCG ACT

```
                                                                C
GAM72   342   DKFZp56 1  8472  NM_032121.1  3       GCCTGTAATCTC              ATGA      3  C  c  c
        4K142                                AGCACTTT    AAAGTGCTGGGATTACAGGC
                                                  TTTCACGACTCTAATGTCCG
                                                                ----
GAM72   342   DKFZP56 1  2862  NM_031208.1  3       TCACGCCTGTAA       G       A       3  C  b  b
        6J2046                               TCGCAGCACTTT AAAGTGCTG GATTACAGGC TGA
                                                  TTTCACGAC CTAATGTCCG ACT
                                                        G       C
GAM72   342   DKFZP58 2  5423          3       TCACACCTGTAA              CA       3  C  b  b
        6D2223                               TCCTAGCGCTTT AAAGTGCTGGGATTACAGG  TGA
                                                  TTTCGCGATCCTAATGTCC  ACT
                                                              AC
GAM72   342   DKFZP58 2  19726         3       TCACACCTGTAA     C        CA       3  C  c  b
        6D2223                               TTCCAACACTTT AAAGTG TGGGATTACAGG  TGA
                                                  TTTCAC ACCTTAATGTCC  ACT
                                                     A         AC
GAM72   342   DKFZP66 1  1610          3       TCATGCCTATAA          C           3  C  b  b
        7O116                                TCCCGGCACTTT AAAGTGCTGGGATTA AGGCATGA
                                                  TTTCACGGCCCTAAT TCCGTACT
                                                              A
GAM72   342   DKFZP76 1  1611  NM_031474.1  5       TCATGCCTGTAA                    3  C  a  a
        1G1913                               TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
                                                  TTTCACGACCCTAATGTCCGTACT

GAM72   342   DNASE2  2  1193  NM_001375.1  3       TCACGTATGTAA           G A      3  C  b  b
                                     TCCCAGCACTTT AAAGTGCTGGGATTACA GC TGA
                                           TTTCACGACCCTAATGT TG ACT
                                                        A  C
GAM72   342   DNASE2  2  14261 NM_001375.1  3       TCACATCTGTAA        A     CA       3  C  c  b
                                     CCCCAGCACTTT AAAGTGCTGGG TTACAGG  TGA
                                           TTTCACGACCC AATGTCT  ACT
                                                     C     AC
GAM72   342   EIF2S1  1  3165  NM_004094.2  3       TCATGCCTGTAA A     TG  A           3  C  c  c
                                     CCCTGGCACTT   AAGTGC  GG TTACAGGCATGA
                                           TTCACG  CC AATGTCCGTACT
                                           -     GT  C
GAM72   342   ET     1  15878 NM_024311.1  3       TCATGCCTGTGG                    3  C  b  b
                                     TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
                                           TTTCACGACCCTGGTGTCCGTACT

GAM72   342   F2RL3  2  16469 NM_003950.1  3       TCACGCCTATAA AA         C   A       3  C  c  b
                                     TCTCAGCACT    AGTGCTGGGATTA AGGC TGA
                                           TCACGACTCTAAT TCCG ACT
                                           --          A   C
GAM72   342   F2RL3  2  17466 NM_003950.1  3       TCACACCTGCAA          A   CA       3  C  b  b
                                     TCCCAGCACTTT AAAGTGCTGGGATT CAGG  TGA
                                           TTTCACGACCCTAA GTCC  ACT
                                                     C   AC
GAM72   342   FANCD2  1  5050  NM_033084.2  3       TCATGCTTGTAA                    3  C  b  b
```

TCCTAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGATCCTAATGTTCGTACT

GAM72 342 FBXO26 1 1376 NM_024907.5 3 TCACACCTGTGG A -- CA 3 C c c
AATCCCAGCACT AAGTGCTGGGAT TACAGG TGA
T TTCACGACCCTA GTGTCC ACT
- AG AC

GAM72 342 FBXO27 1 4320 XM_059045.1 3 TCACACCTGTAA T CA 3 C c c
TCCCTGCACTTT AAAGTGC GGGATTACAGG TGA
TTTCACG CCCTAATGTCC ACT
T AC

GAM72 342 FBXO9 1 14249 NM_033481.1 3 TCACACCTATAA C C CA 3 C c c
TCCCAATACTTT AAAGTG TGGGATTA AGG TGA
TTTCAT ACCCTAAT TCC ACT
A A AC

GAM72 342 FCMD 1 3598 NM_006731.1 3 TCACACCTGTAA G G CA 3 C c c
TACCAGCAGTTT AAA TGCTGG ATTACAGG TGA
TTT ACGACC TAATGTCC ACT
G A AC

GAM72 342 FGF2 1 11990 NM_002006.2 3 TCATGCCTATAT T T C 3 C c c
TCCCTGCACTTT AAAGTGC GGGA TA AGGCATGA
TTTCACG CCCT AT TCCGTACT
T T A

GAM72 342 FKSG17 1 9662 NM_032031.1 3 TCATGCCTGAAT A 3 C b b
CTCAGCACTTT AAAGTGCTGGGATT CAGGCATGA
TTTCACGACTCTAA GTCCGTACT
-

GAM72 342 FLJ0006 1 11930 XM_028154.2 3 TCATGTCTGTAA AA 3 C b b
0 TCCCAGCACT AGTGCTGGGATTACAGGCATGA
TCACGACCCTAATGTCTGTACT
--

GAM72 342 FLJ1013 1 17526 NM_018005.1 3 TCACACCTATAA G C CA 3 C c c
9 TCCTAGGACTTT AAAGT CTGGGATTA AGG TGA
TTTCA GATCCTAAT TCC ACT
G A AC

GAM72 342 FLJ1046 1 2166 NM_018097.1 3 TCACACCTGTAA A C CA 3 C c c
0 TCCTAACACTT AAGTG TGGGATTACAGG TGA
TTCAC ATCCTAATGTCC ACT
- A AC

GAM72 342 FLJ1080 1 9700 NM_018224.1 3 TCACACCGGTAA A CA 3 C c c
3 TCCCAGCACTTT AAAGTGCTGGGATTAC GG TGA
TTTCACGACCCTAATG CC ACT
G AC

GAM72 342 FLJ1083 1 18345 3 TCACACCTATAA G G C CA 3 C c c
0 TCGAGCACTTT AAAGTGCT G ATTA AGG TGA
TTTCACGA C TAAT TCC ACT
G - A AC

GAM72 342 FLJ1089 1 2260 NM_018260.1 3 TCACGCCTGTAA A A 3 C b b
1 ACCCAGCACTTT AAAGTGCTGGG TTACAGGC TGA
TTTCACGACCC AATGTCCG ACT

A C

GAM72 342 FLJ1101 1 6799 NM_018301.1 3 TCACGCCTGAAA A A 3 C b b
6 TCTCAGCACTTT AAAGTGCTGGGATT CAGGC TGA
TTTCACGACTCTAA GTCCG ACT

A C

GAM72 342 FLJ1125 1 1365 NM_018370.1 3 TCACACCTGTAT T CA 3 C b b
9 TCCCAGCACTTT AAAGTGCTGGGA TACAGG TGA
TTTCACGACCCT ATGTCC ACT

T AC

GAM72 342 FLJ1137 1 20041 NM_024961.1 3 TCATACCTGTAA G C 3 C b b
0 TCCCAGCAGTTT AAA TGCTGGGATTACAGG ATGA
TTT ACGACCCTAATGTCC TACT

G A

GAM72 342 FLJ1146 1 7995 NM_024963.2 3 ATCACACCTGTG ----- CA - 3 C c c
7 AGTGGCTCCCAG AAAGTGCTGGGA TTACAGG TGA
CACTTT TTTCACGACCCT AGTGTCC ACT

CGGTG AC A

GAM72 342 FLJ1157 1 13792 NM_025159.1 3 TCACGCCTGTAA A A 3 C b b
7 TCCCAGCATTT AAGTGCTGGGATTACAGGC TGA
TTTACGACCCTAATGTCCG ACT

- C

GAM72 342 FLJ1171 1 6725 NM_024564.1 3 TCATGCCCGTAA CT A 3 C c c
5 TTCTCACATTTT AAAGTG GGGATTAC GGCATGA
TTTTAC TCTTAATG CCGTACT

AC C

GAM72 342 FLJ1213 1 1822 NM_024980.2 3 CCCGTAATCCCA A CATGA 3 C c c
2 GCACTTT AAAGTGCTGGGATTAC GG
TTTCACGACCCTAATG CC

C -----

GAM72 342 FLJ1219 1 15565 NM_025071.1 3 TCACGCATGTAA C G A 3 C c c
0 TCCTAACACTTT AAAGTG TGGGATTACA GC TGA
TTTCAC ATCCTAATGT CG ACT

A A C

GAM72 342 FLJ1229 1 18537 NM_025100.1 5 TCACACCTGTAA A CA 3 C b b
4 ACCCAGCACTTT AAAGTGCTGGG TTACAGG TGA
TTTCACGACCC AATGTCC ACT

A AC

GAM72 342 FLJ1240 1 19647 NM_025105.1 3 TCACACCTGTAA AA A CA 3 C c c
9 CCCCAGCACT AGTGCTGGG TTACAGG TGA
TCACGACCC AATGTCC ACT

-- C AC

GAM72 342 FLJ1244 1 1090 NM_022895.1 3 TCATGCCTGTAA G 3 C b b
8 TCCAAGCATTTT AAAGTGCT GGATTACAGGCATGA
TTTTACGA CCTAATGTCCGTACT

A

GAM72 342 FLJ1267 1 8146 NM_030980.1 3 TCACGCCTGTAG A C A 3 C c c
1 TCCCAACACTT AAGTG TGGGATTACAGGC TGA
TTCAC ACCCTGATGTCCG ACT

- A C

GAM72 342 FLJ1292 1 17641 NM_024875.1 3 TCACGCCGGTAA A A 3 C b b

```
         1                          TCCCAGCACTTT AAAGTGCTGGGATTAC GGC TGA
                                           TTTCACGACCCTAATG CCG ACT
                                                     G   C
GAM72    342  FLJ1319 2  6059          3       TCATGTGTGTAA AA          G          3  C  c  c
         3                          TCCCAGCACT    AGTGCTGGGATTACA GCATGA
                                           TCACGACCCTAATGT TGTACT
                                           --           G
GAM72    342  FLJ1319 2  19618         3       CATGCCTATAAT AA  -       C     A     3  C  c  c
         3                          CCCGGCTACT    AGT GCTGGGATTA AGGCATG
                                           TCA CGGCCCTAAT TCCGTAC
                                           --  T       A     -
GAM72    342  FLJ1333 1  15073 NM_025091.2 3       TCACACCTGTAA  A  T         CA       3  C  c  c
         0                          TCTCAGCCTCC  A AG GCTGGGATTACAGG  TGA
                                           C TC CGACTCTAATGTCC  ACT
                                           C  -          AC
GAM72    342  FLJ1335 1  9233  NM_024592.1 3       TCACACCTGTTA A         -  CA       3  C  c  c
         2                          ATCCCAGCACTT  AAGTGCTGGGATTA CAGG  TGA
                                           TTCACGACCCTAAT GTCC  ACT
                                           -          T   AC
GAM72    342  FLJ1339 1  19961         3       TCACACCTGAAA          A   CA       3  C  b  b
         0                          TCCCAGCACTTT AAAGTGCTGGGATT CAGG  TGA
                                           TTTCACGACCCTAA GTCC  ACT
                                                A   AC
GAM72    342  FLJ1345 1  13553 XM_038291.5 3       TCTTGCCTGTAA AA            T       3  C  c  c
         6                          TCCCAGCATT    AGTGCTGGGATTACAGGCA GA
                                           TTACGACCCTAATGTCCGT CT
                                           --           T
GAM72    342  FLJ1354 1  17984 NM_025008.1 3       TCACACCTGTCA          T   CA       3  C  b  b
         4                          TCCCAGCACTTT AAAGTGCTGGGAT ACAGG  TGA
                                           TTTCACGACCCTA TGTCC  ACT
                                                C   AC
GAM72    342  FLJ1362 1  1377  NM_025009.1 3       TCATGCCTGTAA       G             3  C  b  b
         1                          TCGCAGCACTTT AAAGTGCTG GATTACAGGCATGA
                                           TTTCACGAC CTAATGTCCGTACT
                                              G
GAM72    342  FLJ1384 1  3884  NM_024771.1 5       CCTGTAATCCCA             CATGA      3  C  c  c
         8                          GCACTTT     AAAGTGCTGGGATTACAGG
                                           TTTCACGACCCTAATGTCC
                                                    -----
GAM72    342  FLJ1398 1  11483 NM_024770.1 3       TCGCACCTGTAA             CA       3  C  b  b
         4                          TCCCAGCACTTT AAAGTGCTGGGATTACAGG  TGA
                                           TTTCACGACCCTAATGTCC  GCT
                                                AC
GAM72    342  FLJ1401 1  9324  NM_022103.1 3       CCTGTAACCCCA        A     CATGA      3  C  c  c
         1                          GCACTTT     AAAGTGCTGGG TTACAGG
                                           TTTCACGACCC AATGTCC
                                              C     -----
GAM72    342  FLJ1408 1  6567  NM_025024.1 3       TCATGCCCGTAA           A          3  C  b  b
         2                          TCCCAGCACTTT AAAGTGCTGGGATTAC GGCATGA
                                           TTTCACGACCCTAATG CCGTACT
```

C

GAM72 342 FLJ1425 1 2884 5 TCACACCTGTAA CA 3 C b b
1 TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAATGTCC ACT
AC

GAM72 342 FLJ1428 1 15839 NM_024886.1 3 TCACGCCTGGAA AA A A 3 C c c
0 TCCCAGCACT AGTGCTGGGATT CAGGC TGA
TCACGACCCTAA GTCCG ACT
-- G C

GAM72 342 FLJ1432 1 18652 3 TCACGCCTGTAA AAA A 3 C c c
6 TCCCAGCAC GTGCTGGGATTACAGGC TGA
CACGACCCTAATGTCCG ACT
--- C

GAM72 342 FLJ1432 1 1971 NM_024912.1 3 TCATGCCTACAA A AC 3 C c c
7 TCCCAGCATTT AAGTGCTGGGATT AGGCATGA
TTTACGACCCTAA TCCGTACT
- CA

GAM72 342 FLJ1439 1 16157 NM_032779.1 3 TCACGCCTGTAA G A 3 C b b
7 TCCAGCACTTT AAAGTGCTGG ATTACAGGC TGA
TTTCACGACC TAATGTCCG ACT
- C

GAM72 342 FLJ1439 1 2000 NM_032780.1 3 TCACGCCTGTAA AA G A 3 C c c
9 TACCAGCACT AGTGCTGG ATTACAGGC TGA
TCACGACC TAATGTCCG ACT
-- A C

GAM72 342 FLJ1445 1 6993 NM_032788.1 3 TCACGCCTGTAA A A 3 C b b
7 CCTCAGCACTTT AAAGTGCTGGG TTACAGGC TGA
TTTCACGACTC AATGTCCG ACT
C C

GAM72 342 FLJ1446 1 12835 NM_032790.1 3 TCACGCCTGTAA T A 3 C b b
6 TCCTAGCCCTTT AAAG GCTGGGATTACAGGC TGA
TTTC CGATCCTAATGTCCG ACT
C C

GAM72 342 FLJ2000 2 16023 3 TCACGCCTGTAA C A 3 C b b
4 TCTCAACACTTT AAAGTG TGGGATTACAGGC TGA
TTTCAC ACTCTAATGTCCG ACT
A C

GAM72 342 FLJ2000 2 19735 3 CATGCCTGTAAT A 3 C b b
4 CCCAGCACTTT AAAGTGCTGGGATTACAGGCATG
TTTCACGACCCTAATGTCCGTAC
-

GAM72 342 FLJ2000 1 9107 NM_017618.1 3 TCGGGCCTGTAA A 3 C b b
6 TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAATGTCCG GCT
G

GAM72 342 FLJ2001 2 3892 NM_017621.2 3 TCACACCTGTAA C CA 3 C c c
3 TCCTAACACTTT AAAGTG TGGGATTACAGG TGA
TTTCAC ATCCTAATGTCC ACT
A AC

GAM72 342 FLJ2001 2 4741 NM_017621.2 3 TCACACCTGTAA G CA 3 C c c

3 TCCGAGTACTTT AAAGTGCT GGATTACAGG TGA
TTTCATGA CCTAATGTCC ACT
G AC

GAM72 342 FLJ2004 1 10035 NM_017638.1 3 TCACACCTCTAA C CA 3 C b b
5 TCCCAGCACTTT AAAGTGCTGGGATTA AGG TGA
TTTCACGACCCTAAT TCC ACT
C AC

GAM72 342 FLJ2005 1 9258 NM_017644.1 3 TCACGCCTGTGG A 3 C b b
9 TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTGGTGTCCG ACT
C

GAM72 342 FLJ2006 1 11616 NM_017651.2 3 TCATGCCTGTAA AAA 3 C c c
9 TCCTAGCAC GTGCTGGGATTACAGGCATGA
CACGATCCTAATGTCCGTACT

GAM72 342 FLJ2013 1 12730 3 TCGCACCTGTAA CA 3 C b b
9 TCCCAGCATTTT AAAGTGCTGGGATTACAGG TGA
TTTTACGACCCTAATGTCC GCT
AC

GAM72 342 FLJ2017 1 14813 NM_017699.1 3 TCACGCCTGTAA AA TG -- A 3 C c c
4 TCCCAAAGTGCT AG CT GGGATTACAGGC TGA
TC GA CCCTAATGTCCG ACT
-- GT AA C

GAM72 342 FLJ2020 1 2707 NM_017708.1 3 TCATGCCTGTAA T 3 C b b
0 TCCCTGCACTTT AAAGTGC GGGATTACAGGCATGA
TTTCACG CCCTAATGTCCGTACT
T

GAM72 342 FLJ2034 1 19249 3 TCACACCCGTAA A CA 3 C c c
0 TCCCAGCACTTT AAAGTGCTGGGATTAC GG TGA
TTTCACGACCCTAATG CC ACT
C AC

GAM72 342 FLJ2041 1 16863 NM_017808.1 3 TCATGCCTGTAA A G 3 C b b
3 TCCGAGCACTT AAGTGCT GGATTACAGGCATGA
TTCACGA CCTAATGTCCGTACT
- G

GAM72 342 FLJ2046 1 402 NM_017834.1 5 TCACGCCTGTTA T A 3 C b b
4 TCCCAGCACTTT AAAGTGCTGGGAT ACAGGC TGA
TTTCACGACCCTA TGTCCG ACT
T C

GAM72 342 FLJ2054 1 17595 NM_017872.2 3 TCACGTCTGTAA AAA A 3 C c c
6 TCCCAGCAC GTGCTGGGATTACAGGC TGA
CACGACCCTAATGTCTG ACT
--- C

GAM72 342 FLJ2069 1 16458 NM_017928.1 3 TCACCCCCTGTA CA- 3 C b b
4 ATCCCAGCACTT AAAGTGCTGGGATTACAGG TGA
T TTTCACGACCCTAATGTCC ACT
CCC

GAM72 342 FLJ2070 1 13236 NM_017932.1 3 TCACGCCTGTAA AA A A 3 C c c
0 CCTCAGCACT AGTGCTGGG TTACAGGC TGA
TCACGACTC AATGTCCG ACT

```
                                        --      C      C
GAM72   342   FLJ2078 1  13950          5      TCACGCCTGTAA             A       3  C  b  b
        3                          TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
                                        TTTCACGACCCTAATGTCCG ACT
                                              C
GAM72   342   FLJ2080 1  991   NM_017960.1  3      TCACACCCATAA          CA CA       3  C  c  c
        8                          TCCCAGCACTTT AAAGTGCTGGGATTA  GG  TGA
                                        TTTCACGACCCTAAT  CC  ACT
                                             AC  AC
GAM72   342   FLJ2082 1  14966 NM_017962.1  3      TCATGCCTGTAA A   TGC              3  C  c  c
        5                          TCCCAACTCTT   AAG   TGGGATTACAGGCATGA
                                        TTC   ACCCTAATGTCCGTACT
                                        -   TCA
GAM72   342   FLJ2110 1  7533  NM_025097.1  5      GCCTGTAATCCC             ATGA      3  C  c  c
        6                          AGCACTTT    AAAGTGCTGGGATTACAGGC
                                        TTTCACGACCCTAATGTCCG
                                              ----
GAM72   342   FLJ2116 1  9315           5      TCATGCCTATAA          C          3  C  b  b
        2                          TCCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
                                        TTTCACGACCCTAAT TCCGTACT
                                             A
GAM72   342   FLJ2127 1  2503  NM_025032.1  3      TCATGCCTGTAA AAAG                3  C  c  c
        2                          TCCCAGCA       TGCTGGGATTACAGGCATGA
                                          ACGACCCTAATGTCCGTACT
                                        ----
GAM72   342   FLJ2136 1  18241 NM_024802.1  3      TCATGCCTGTAA        A            3  C  b  b
        9                          ACCCAGCACTTT AAAGTGCTGGG TTACAGGCATGA
                                        TTTCACGACCC AATGTCCGTACT
                                           A
GAM72   342   FLJ2155 1  6940  NM_024801.1  3      TCATGCCTGTAA     C   A           3  C  b  b
        1                          GCCCAACACTTT AAAGTG TGGG TTACAGGCATGA
                                        TTTCAC ACCC AATGTCCGTACT
                                          A   G
GAM72   342   FLJ2200 1  1350           3      TCACGCTTGTAA       G       A        3  C  b  b
        9                          TCGCAGCACTTT AAAGTGCTG GATTACAGGC TGA
                                        TTTCACGAC CTAATGTTCG ACT
                                             G       C
GAM72   342   FLJ2247 1  17883          3      TCACGCCTGCAG          A   A        3  C  b  b
        4                          TCCCAGCACTTT AAAGTGCTGGGATT CAGGC TGA
                                        TTTCACGACCCTGA GTCCG ACT
                                             C   C
GAM72   342   FLJ2269 1  16683 NM_025049.1  3      TCACTCTTGTAA    GC       CA       3  C  c  c
        2                          TCCCAAAACTTT AAAGT  TGGGATTACAGG  TGA
                                        TTTCA  ACCCTAATGTTC  ACT
                                          AA         TC
GAM72   342   FLJ2281 1  458   NM_024916.1  3      TCACGCCTGTCA          T    A       3  C  b  b
        4                          TCTCAGCACTTT AAAGTGCTGGGAT ACAGGC TGA
                                        TTTCACGACTCTA TGTCCG ACT
                                             C    C
GAM72   342   FLJ2304 1  15539 NM_025174.1  3      TCACGCTTATAA          C   A       3  C  b  b
```

0 TCCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACCCTAAT TTCG ACT
A C

GAM72 342 FLJ2304 1 1823 3 CCTGTAATCCTA CATGA 3 C c c
2 GCACTTT AAAGTGCTGGGATTACAGG
TTTCACGATCCTAATGTCC

GAM72 342 FLJ2311 1 11044 NM_024929.1 3 GTCTAATCCCAG AC ATGA 3 C c c
2 CACTTT AAAGTGCTGGGATT AGGC
TTTCACGACCCTAA TCTG
-- ----

GAM72 342 FLJ2312 1 18218 3 TCATGCCTCCAA AC 3 C b b
0 TCCCAGCACTTT AAAGTGCTGGGATT AGGCATGA
TTTCACGACCCTAA TCCGTACT
CC

GAM72 342 FLJ2347 1 8812 NM_024640.1 3 TCATGCCTGTAA AA C 3 C c c
6 TCCCAACATT AGTG TGGGATTACAGGCATGA
TTAC ACCCTAATGTCCGTACT
-- A

GAM72 342 FLJ2349 2 10255 NM_022761.1 3 TCACGCCTGTAA AA - A 3 C c b
9 TCCCAGCTACT AGT GCTGGGATTACAGGC TGA
TCA CGACCCTAATGTCCG ACT
-- T C

GAM72 342 FLJ2349 2 10849 NM_022761.1 3 TCACACCTAATC AC CA 3 C b b
9 CCAGCACTTT AAAGTGCTGGGATT AGG TGA
TTTCACGACCCTAA TCC ACT
-- AC

GAM72 342 FLJ2353 1 6332 NM_024889.1 3 TCATGCCTATAA TGC C 3 C c c
7 TTCCAACCCTTT AAAG TGGGATTA AGGCATGA
TTTC ACCTTAAT TCCGTACT
CCA A

GAM72 342 FLJ2501 1 19167 3 TCATGCCTGTAA G 3 C b b
2 TCCAGTACTTT AAAGTGCTGG ATTACAGGCATGA
TTTCATGACC TAATGTCCGTACT
-

GAM72 342 FLJ3068 1 6277 XM_166291.2 3 CACGCCTCTAAT C A A 3 C c c
1 CCCAGCACTTT AAAGTGCTGGGATTA AGGC TG
TTTCACGACCCTAAT TCCG AC
C C -

GAM72 342 FLJ3116 1 12604 3 TCACACCTGTAA AAA CA 3 C c c
8 TCCTAGCAC GTGCTGGGATTACAGG TGA
CACGATCCTAATGTCC ACT
--- AC

GAM72 342 FLRT2 1 10151 NM_013231.2 5 TCACGTCTGTAA AA A 3 C c c
TCCCAGCGCT AGTGCTGGGATTACAGGC TGA
TCGCGACCCTAATGTCTG ACT
-- C

GAM72 342 GALNT3 1 2190 NM_004482.2 3 TCAGCTTCTAAT C A 3 C b b
CCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACCCTAAT TTCG ACT

C -
GAM72 342 GALNT6 1 14948 NM_007210.2 3 TCATGCCTGAAA A 3 C b b
TCCTAGCACTTT AAAGTGCTGGGATT CAGGCATGA
TTTCACGATCCTAA GTCCGTACT
A
GAM72 342 GAS7 1 17657 NM_005890.1 3 TCACGCCTGTAA T A 3 C b b
TCCCAGCTCTTT AAAG GCTGGGATTACAGGC TGA
TTTC CGACCCTAATGTCCG ACT
T C
GAM72 342 GCN2 1 11455 3 TCACACCTTTAA C CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA AGG TGA
TTTCACGACCCTAAT TCC ACT
T AC
GAM72 342 GGA2 1 16227 NM_015044.2 3 TCACGCCTGTAG A 3 C b b
TCCCAGCATTTT AAAGTGCTGGGATTACAGGC TGA
TTTTACGACCCTGATGTCCG ACT
C
GAM72 342 GPRK7 1 5505 NM_139209.1 3 TCATGCCTGCAA A 3 C b b
TTCCAGCACTTT AAAGTGCTGGGATT CAGGCATGA
TTTCACGACCTTAA GTCCGTACT
C
GAM72 342 HIP1 2 14256 NM_005338.3 3 CATGCCTGTAAT G A 3 C b b
CCCAGAACTTT AAAGT CTGGGATTACAGGCATG
TTTCA GACCCTAATGTCCGTAC
A -
GAM72 342 HIP1 2 17600 NM_005338.3 3 CACGTTTAATCC CA A A 3 C c b
CAGCACTTT AAAGTGCTGGGATTA GGC TG
TTTCACGACCCTAAT TTG AC
-- C -
GAM72 342 HLA-E 1 1460 NM_005516.3 5 TCATGCCTGTAA A 3 C b b
TCCCAGCACTT AAGTGCTGGGATTACAGGCATGA
TTCACGACCCTAATGTCCGTACT
-
GAM72 342 HSC3 1 2408 NM_145174.1 3 TCACACCTGTAA AAA CA 3 C c c
TCCTAGCAT GTGCTGGGATTACAGG TGA
TACGATCCTAATGTCC ACT
--- AC
GAM72 342 HSH2 1 5998 NM_032855.1 3 TCATGCCTGTAG AA 3 C b b
TCCCAGCACT AGTGCTGGGATTACAGGCATGA
TCACGACCCTGATGTCCGTACT
--
GAM72 342 HSMPP8 1 11227 XM_167894.2 3 TCACACCTATAA C CA 3 C c c
TCCCAGCGCTTT AAAGTGCTGGGATTA AGG TGA
TTTCGCGACCCTAAT TCC ACT
A AC
GAM72 342 HSPA5 1 3420 NM_005347.2 3 CAATATTGTAAT GCA A 3 C c c
CCTAGCACTTT AAAGTGCTGGGATTACAG TG
TTTCACGATCCTAATGTT AC
ATA -
GAM72 342 HSPC031 1 3773 NM_016101.1 3 TCGCGCCTGTAA A 3 C b b

TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAATGTCCG GCT
C
GAM72 342 HYPK 1 17104 NM_016400.2 3 TCACGCCTCTAA C A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACCCTAAT TCCG ACT
C C
GAM72 342 IFRD1 1 6054 NM_001550.1 3 TCATGCCTATAA AA GG C 3 C c c
TCAGCACT AGTGCT GATTA AGGCATGA
TCACGA CTAAT TCCGTACT
-- -- A
GAM72 342 IL10RB 1 8908 NM_000628.3 3 TCACGCCTGTAA AAA G A 3 C c c
TACCAGCAC GTGCTGG ATTACAGGC TGA
CACGACC TAATGTCCG ACT
--- A C
GAM72 342 IL11 1 11693 NM_000641.2 3 TCACGCCTGTAA TG A 3 C b b
TCCTGGCACTTT AAAGTGC GGATTACAGGC TGA
TTTCACG CCTAATGTCCG ACT
GT C
GAM72 342 IL13RA1 1 1465 NM_001560.2 3 TCACGCCTGTAA AAAG A 3 C c c
TCCCAGCA TGCTGGGATTACAGGC TGA
ACGACCCTAATGTCCG ACT
---- C
GAM72 342 IL18 1 19198 NM_001562.2 3 TCACGCCTGTAA T A 3 C b b
TCCCAGCCCTTT AAAG GCTGGGATTACAGGC TGA
TTTC CGACCCTAATGTCCG ACT
C C
GAM72 342 IPP 1 19290 NM_005897.1 3 TCACGCCTGTAG A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTGATGTCCG ACT
C
GAM72 342 IRAK4 1 13012 NM_016123.1 3 TCATACCTGTAA - C 3 C b b
ATCCCAGCACTT AAAGTGCTGGGATT ACAGG ATGA
T TTTCACGACCCTAA TGTCC TACT
A A
GAM72 342 ITCH 1 13485 NM_031483.3 3 TCATACCTGTAA AA C 3 C c c
TCCTAGCACT AGTGCTGGGATTACAGG ATGA
TCACGATCCTAATGTCC TACT
-- A
GAM72 342 KBRAS2 1 16138 NM_017595.2 5 TCACCCCTGTAA CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAATGTCC ACT
CC
GAM72 342 KCNA7 2 13270 NM_031886.2 5 TCATGCCTGTAA A 3 C b b
CCCCAGCACTTT AAAGTGCTGGG TTACAGGCATGA
TTTCACGACCC AATGTCCGTACT
C
GAM72 342 KCNA7 2 15078 NM_031886.2 3 CATGCCTGTAAT AA A 3 C c b
CTCAGCACT AGTGCTGGGATTACAGGCATG
TCACGACTCTAATGTCCGTAC

```
                                                  --              -
GAM72   342   KCNJ5  1  12729  NM_000890.3  3      TCACACCTGTGA             CA       3  C  b  b
                                TCCCAGCATTTT AAAGTGCTGGGATTACAGG  TGA
                                      TTTTACGACCCTAGTGTCC  ACT
                                                    AC
GAM72   342   KCNK6  1  4740   NM_004823.1  3      TCACGCCTATAC        AT  C   A       3  C  c  c
                                ACCCAGCACTTT AAAGTGCTGGG  TA AGGC TGA
                                      TTTCACGACCC  AT TCCG ACT
                                           AC  A   C
GAM72   342   KIAA005 1  8437          3      GCCTGTTATCCC          T    ATGA     3  C  c  c
        7                       AGCACTTT    AAAGTGCTGGGAT ACAGGC
                                      TTTCACGACCCTA TGTCCG
                                                 T    ----
GAM72   342   KIAA009 1  5892   NM_015047.1  3      TCAAGCCTATAA           C   A       3  C  b  b
        0                       TCCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
                                      TTTCACGACCCTAAT TCCG ACT
                                                  A   A
GAM72   342   KIAA039 1  19903  NM_014672.1  3      TCATACCTGTTA          -  C       3  C  b  b
        1                       ATTCCAGCACTT AAAGTGCTGGGATTA CAGG ATGA
                                T         TTTCACGACCTTAAT GTCC TACT
                                                  T   A
GAM72   342   KIAA041 1  11980  NM_014711.1  3      TCACACCTGTAC          T    CA       3  C  c  c
        9                       TCCCAGCATTTT AAAGTGCTGGGA TACAGG  TGA
                                      TTTTACGACCCT ATGTCC  ACT
                                                  C    AC
GAM72   342   KIAA044 1  7417          3      TCACGCCTCTAA       G   C   A       3  C  c  c
        7                       TCGCAGCACTTT AAAGTGCTG GATTA AGGC TGA
                                      TTTCACGAC CTAAT TCCG ACT
                                                G   C   C
GAM72   342   KIAA045 1  3255          5      CCTGTAATCCCA   T          CATGA     3  C  c  c
        1                       GCTCTTT    AAAG GCTGGGATTACAGG
                                      TTTC CGACCCTAATGTCC
                                                 T          -----
GAM72   342   KIAA047 1  587   XM_301133.1  3      TCATGCCTGTCA A         T           3  C  b  b
        5                       TCCCAGCATTT   AAGTGCTGGGAT ACAGGCATGA
                                      TTTACGACCCTA TGTCCGTACT
                                                -         C
GAM72   342   KIAA054 1  1327          3      TCACGCCTATAA           C   A       3  C  b  b
        7                       TTCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
                                      TTTCACGACCTTAAT TCCG ACT
                                                  A   C
GAM72   342   KIAA056 1  16513  XM_039912.4  3      TCAAACCTATAA           C  CA       3  C  b  b
        5                       TCCCAGCACTTT AAAGTGCTGGGATTA AGG  TGA
                                      TTTCACGACCCTAAT TCC  ACT
                                                  A   AA
GAM72   342   KIAA059 1  19199          5      TCAAGCCTGTAA              A       3  C  b  b
        6                       TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
                                      TTTCACGACCCTAATGTCCG ACT
                                                    A
GAM72   342   KIAA062 1  8071   NM_014789.1  3      TCATGCCTGTAT          --          3  C  b  b
```

8 AATCCCAGCACT AAAGTGCTGGGAT TACAGGCATGA
TT TTTCACGACCCTA ATGTCCGTACT
AT

GAM72 3424 KIAA0691 13722 XM_051970.3 3 CATGCCTATAAT C C A 3 C c c
CCCAATACTTT AAAGTG TGGGATTA AGGCATG
TTTCAT ACCCTAAT TCCGTAC
A A -

GAM72 3421 KIAA0832 6562 NM_014924.1 5 TCATGCCTGTAA 3 C b b
TCCTAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGATCCTAATGTCCGTACT

GAM72 3421 KIAA0832 19089 NM_014924.1 5 TCACGCCTGTAA A 3 C b b
TCCCGGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGGCCCTAATGTCCG ACT
C

GAM72 3424 KIAA0881 7518 XM_046660.4 5 TCACGCCTGTCA T A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGAT ACAGGC TGA
TTTCACGACCCTA TGTCCG ACT
C C

GAM72 3429 KIAA0881 17820 NM_152257.1 3 TCATGTCTCTAA C 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
TTTCACGACCCTAAT TCTGTACT
C

GAM72 3423 KIAA0951 7972 XM_039733.2 3 TCACACCTGTGA C CA 3 C c c
TCCCAACATTTT AAAGTG TGGGATTACAGG TGA
TTTTAC ACCCTAGTGTCC ACT
A AC

GAM72 3421 KIAA0981 18398 XM_028867.2 3 TCACGCCTATAA C C A 3 C c c
TCCTATCACTTT AAAGTG TGGGATTA AGGC TGA
TTTCAC ATCCTAAT TCCG ACT
T A C

GAM72 3421 KIAA1001 3031 NM_014960.1 3 TCACACCTGTAG CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTGATGTCC ACT
AC

GAM72 3426 KIAA1081 10445 XM_047610.1 3 TCATGCCTTTAA C 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
TTTCACGACCCTAAT TCCGTACT
T

GAM72 3423 KIAA1141 3668 XM_044014.3 3 TCATGCTTGTAA C 3 C b b
TCCCAACACTTT AAAGTG TGGGATTACAGGCATGA
TTTCAC ACCCTAATGTTCGTACT
A

GAM72 3424 KIAA1161 16893 XM_045358.2 3 TCATGCCTGTAA 3 C b b
TCCCAGTACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCATGACCCTAATGTCCGTACT

GAM72 3422 KIAA1201 1103 XM_050478.2 3 TCACGCCTGAAA A A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATT CAGGC TGA
TTTCACGACCCTAA GTCCG ACT

```
                                                A    C
GAM72   342   KIAA120 1   19727          3       TCACATCTGTAA     C         CA        3  C  c  c
        4                                TCCCAACACTTT AAAGTG TGGGATTACAGG  TGA
                                                 TTTCAC ACCCTAATGTCT  ACT
                                                    A         AC
GAM72   342   KIAA125 1   16508          3       TCACCCTTGTAA             CA        3  C  b  b
        3                                TCCCAGCACTTT AAAGTGCTGGGATTACAGG  TGA
                                                 TTTCACGACCCTAATGTTC  ACT
                                                       CC
GAM72   342   KIAA125 1   8495   XM_031577.3  3       TCACGCCTGTAA     CT        A        3  C  c  c
        7                                TCCCTACACTTT AAAGTG  GGGATTACAGGC TGA
                                                 TTTCAC  CCCTAATGTCCG ACT
                                                    AT         C
GAM72   342   KIAA127 1   13081  XM_039169.1  3       TCACGCCTGTAA     C         A        3  C  b  b
        6                                TCCCATCACTTT AAAGTG TGGGATTACAGGC TGA
                                                 TTTCAC ACCCTAATGTCCG ACT
                                                    T         C
GAM72   342   KIAA134 1   8164   XM_043826.5  3       GCCTGTAATCCC AA           ATGA      3  C  c  c
        8                                AGCACT       AGTGCTGGGATTACAGGC
                                                  TCACGACCCTAATGTCCG
                                                 --           ----
GAM72   342   KIAA142 1   2123   XM_029703.1  3       TCACATCTGTAA     C         CA        3  C  c  c
        3                                TCTCAACACTTT AAAGTG TGGGATTACAGG  TGA
                                                 TTTCAC ACTCTAATGTCT  ACT
                                                    A         AC
GAM72   342   KIAA145 1   767    XM_040100.4  3       TCACACCTGTAC A       T    CA        3  C  c  c
        6                                TCCCAGCACTT   AAGTGCTGGGA TACAGG  TGA
                                                  TTCACGACCCT ATGTCC  ACT
                                                 -        C     AC
GAM72   342   KIAA148 1   1131   XM_041126.5  3       TCACGCCTGTAA AA           A        3  C  c  c
        6                                TCCCAGCACT    AGTGCTGGGATTACAGGC TGA
                                                  TCACGACCCTAATGTCCG ACT
                                                 --           C
GAM72   342   KIAA150 1   6930   XM_290952.1  3       TCACACCTTTAA          C  CA        3  C  c  c
        8                                TCCTAGCACTTT AAAGTGCTGGGATTA AGG  TGA
                                                 TTTCACGATCCTAAT TCC  ACT
                                                    T   AC
GAM72   342   KIAA161 1   18444  XM_046531.1  5       TCATGCCTGTAA     G                3  C  b  b
        4                                TCCCAGAACTTT AAAGT CTGGGATTACAGGCATGA
                                                 TTTCA GACCCTAATGTCCGTACT
                                                    A
GAM72   342   KIAA164 1   1772   XM_087167.3  3       TCATGCCTGTAT         T           3  C  b  b
        1                                TCTCAGCACTTT AAAGTGCTGGGA TACAGGCATGA
                                                 TTTCACGACTCT ATGTCCGTACT
                                                       T
GAM72   342   KIAA164 2   6163           3       TCACGCCTGTGA             A        3  C  b  b
        9                                TCCCGGCACTTT AAAGTGCTGGGATTACAGGC TGA
                                                 TTTCACGGCCCTAGTGTCCG ACT
                                                       C
GAM72   342   KIAA164 2   12470          3       TCATGCCTCTTG          TAC          3  C  b  b
```

9 TCCCAGCACTTT AAAGTGCTGGGAT AGGCATGA
TTTCACGACCCTG TCCGTACT
TTC

GAM72 342 KIAA171 1 11201 XM_042834.2 3 TCACGCCTGTAA AG A 3 C c c
5 TCCCAGCAAGTT AA TGCTGGGATTACAGGC TGA
TT ACGACCCTAATGTCCG ACT
GA C

GAM72 342 KIAA172 1 17480 XM_034262.6 3 TCATGCCTGTAA G 3 C b b
7 TCCAGCACTTT AAAGTGCTGG ATTACAGGCATGA
TTTCACGACC TAATGTCCGTACT
-

GAM72 342 KIAA182 1 13832 3 TCACGCCTGTAA A A 3 C b b
1 TCCTAGCACTT AAGTGCTGGGATTACAGGC TGA
TTCACGATCCTAATGTCCG ACT
- C

GAM72 342 KIAA182 1 1448 XM_030378.2 3 TCACGCCTGTAA G A 3 C b b
9 TCCGAGCACTTT AAAGTGCT GGATTACAGGC TGA
TTTCACGA CCTAATGTCCG ACT
G C

GAM72 342 KIAA184 1 17999 XM_087056.4 3 TCACGCCAGTAA A A 3 C b b
1 TCCCAGCACTTT AAAGTGCTGGGATTAC GGC TGA
TTTCACGACCCTAATG CCG ACT
A C

GAM72 342 KIAA187 1 3023 XM_290737.1 3 CCTGTAATCCAG G CATGA 3 C c c
1 CACTTT AAAGTGCTGG ATTACAGG
TTTCACGACC TAATGTCC
- -----

GAM72 342 KIAA187 1 19477 NM_033064.1 3 TCACGCCTGTAA G A 3 C b b
2 TCCCAGACTTT AAAGT CTGGGATTACAGGC TGA
TTTCA GACCCTAATGTCCG ACT
- C

GAM72 342 KIAA194 1 10715 3 CATGCCTGTAAA A A 3 C b b
8 TCCAGCACTTT AAAGTGCTGGG TTACAGGCATG
TTTCACGACCT AATGTCCGTAC
A -

GAM72 342 KIF1B 1 17155 NM_015074.1 3 TCACGCCTGTAA A G A 3 C c c
TCCAAGCACTT AAGTGCT GGATTACAGGC TGA
TTCACGA CCTAATGTCCG ACT
- A C

GAM72 342 KIF3B 1 406 NM_004798.1 3 TCATGCCTGTAA TG 3 C b b
TCCTGGCACTTT AAAGTGC GGATTACAGGCATGA
TTTCACG CCTAATGTCCGTACT
GT

GAM72 342 KLHL6 1 7713 NM_130446.1 3 TCACGCCTGTAA AA T A 3 C c c
TCCCAGCCCT AG GCTGGGATTACAGGC TGA
TC CGACCCTAATGTCCG ACT
-- C C

GAM72 342 KR18 1 11484 NM_033288.1 3 TCACACCTGTGA CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAGTGTCC ACT

```
                                                    AC
GAM72   342   LOC1135 1  11541          3       TCATGCCTGTAA A    C                3  C  b  b
        23                          TCCTAACACTT   AAGTG TGGGATTACAGGCATGA
                                          TTCAC ATCCTAATGTCCGTACT
                                        -    A
GAM72   342   LOC1151 1  16505 XM_055292.1  3       TCACACCTATAA    T       C  CA       3  C  c  c
        29                          TCCCAGCCCTTT AAAG GCTGGGATTA AGG  TGA
                                          TTTC CGACCCTAAT TCC  ACT
                                            C        A  AC
GAM72   342   LOC1151 1  16754          3       TCATGCCTATAA     C      C           3  C  b  b
        96                          TCCTAACACTTT AAAGTG TGGGATTA AGGCATGA
                                          TTTCAC ATCCTAAT TCCGTACT
                                             A      A
GAM72   342   LOC1152 1  8356           3       TCACGCCTGTAA              A        3  C  b  b
        73                          TCCTAGCATTTT AAAGTGCTGGGATTACAGGC TGA
                                          TTTTACGATCCTAATGTCCG ACT
                                                C
GAM72   342   LOC1157 1  3024           3       TCATGCCTGTAA                      3  C  b  b
        57                          TTCTAGCACTTT AAAGTGCTGGGATTACAGGCATGA
                                          TTTCACGATCTTAATGTCCGTACT

GAM72   342   LOC1158 1  8383  NM_138454.1  3       CCTGTAATCCCA A            CATGA      3  C  c  c
        61                          GCACTT       AAGTGCTGGGATTACAGG
                                          TTCACGACCCTAATGTCC
                                        -            -----
GAM72   342   LOC1161 1  8282  NM_138458.1  3       TCACGCCTGTAA              A        3  C  b  b
        43                          TTCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
                                          TTTCACGACCTTAATGTCCG ACT
                                                C
GAM72   342   LOC1162 1  10907 XM_057674.5  3       CACACCTATAAT           C  CA A      3  C  c  c
        36                          CTCAGCACTTT  AAAGTGCTGGGATTA AGG  TG
                                          TTTCACGACTCTAAT TCC  AC
                                             A  AC  -
GAM72   342   LOC1184 1  14292 NM_145202.1  3       TCACCTCTGTAA              CA       3  C  b  b
        71                          TCCCAGCACTTT AAAGTGCTGGGATTACAGG  TGA
                                          TTTCACGACCCTAATGTCT  ACT
                                                CC
GAM72   342   LOC1229 1  17020          3       TCACACCTGTAA              CA       3  C  b  b
        70                          TCCCAGTACTTT AAAGTGCTGGGATTACAGG  TGA
                                          TTTCATGACCCTAATGTCC  ACT
                                                AC
GAM72   342   LOC1262 1  18753          3       TCACTACTCTAA           C  GCA       3  C  c  c
        82                          TTCCAGCACTTT AAAGTGCTGGGATTA AG   TGA
                                          TTTCACGACCTTAAT TC   ACT
                                                C  ATC
GAM72   342   LOC1264 1  3331  XM_059046.7  3       TCATGCCTGTAA     C               3  C  b  b
        32                          TCCCAACATTTT AAAGTG TGGGATTACAGGCATGA
                                          TTTTAC ACCCTAATGTCCGTACT
                                             A
GAM72   342   LOC1272 1  13265 XM_072073.6  3       TCATGCCTGTAA                     3  C  b  b
```

```
          62                    TCCCAGCATTTT AAAGTGCTGGGATTACAGGCATGA
                                      TTTTACGACCCTAATGTCCGTACT

GAM72   342   LOC1272 1  14191        3      TCACGCCTGTAA  G          A       3  C  b  b
          94                  TCCCAGTAGTTT AAA TGCTGGGATTACAGGC TGA
                                      TTT ATGACCCTAATGTCCG ACT
                                        G           C
GAM72   342   LOC1274 1  14475        3      TCATGCCTATAA          C          3  C  b  b
          28                  TCCCAGCGCTTT AAAGTGCTGGGATTA AGGCATGA
                                      TTTCGCGACCCTAAT TCCGTACT
                                          A
GAM72   342   LOC1305 1  6355         3      TCATGCCTGTAA AAA                  3  C  b  b
          35                  TCCCAGCAC     GTGCTGGGATTACAGGCATGA
                                        CACGACCCTAATGTCCGTACT
                                      ---
GAM72   342   LOC1319 1  3563         3      TCATGCCTATAA        A  C          3  C  b  b
          65                  CCCCAGCACTTT AAAGTGCTGGG TTA AGGCATGA
                                      TTTCACGACCC AAT TCCGTACT
                                          C  A
GAM72   342   LOC1326 1  8924         3      ATGCCTGTAATC     C          GA     3  C  c  c
          25                  CCAACACTTT   AAAGTG TGGGATTACAGGCAT
                                      TTTCAC ACCCTAATGTCCGTA
                                        A          --
GAM72   342   LOC1339 1  6976  XM_059674.5  3      TCATGCCTGTAA                    3  C  b  b
          26                  TCCCAGCGCTTT AAAGTGCTGGGATTACAGGCATGA
                                      TTTCGCGACCCTAATGTCCGTACT

GAM72   342   LOC1383 1  11357        3      TCATACTTGTAA     T       C        3  C  b  b
          89                  TCCCTGCACTTT AAAGTGC GGGATTACAGG ATGA
                                      TTTCACG CCCTAATGTTC TACT
                                        T        A
GAM72   342   LOC1394 1  19244 XM_066687.3  3      TCACACCTGTAA             CA       3  C  b  b
          22                  TCCTAGCACTTT AAAGTGCTGGGATTACAGG  TGA
                                      TTTCACGATCCTAATGTCC  ACT
                                          AC
GAM72   342   LOC1429 1  8177  XM_096364.1  3      TCACGCCTGTAA     T       A        3  C  b  b
          48                  TCCCTGCATTTT AAAGTGC GGGATTACAGGC TGA
                                      TTTTACG CCCTAATGTCCG ACT
                                        T        C
GAM72   342   LOC1444 1  16349        3      TCATGCCTGTAA    GC                3  C  b  b
          65                  TCCCAAAACTTT AAAGT  TGGGATTACAGGCATGA
                                      TTTCA  ACCCTAATGTCCGTACT
                                        AA
GAM72   342   LOC1445 1  20141        5      CATGTGTAATCC          AG   A      3  C  c  c
          24                  CAGCATTTT   AAAGTGCTGGGATTAC  GCATG
                                      TTTTACGACCCTAATG  TGTAC
                                          --   -
GAM72   342   LOC1453 1  11469 XM_096791.1  3      CATGCCTGTTAT A        T       A      3  C  c  c
          87                  CCCAGCACTT   AAGTGCTGGGAT ACAGGCATG
                                      TTCACGACCCTA TGTCCGTAC
```

```
                                        -         T       -
GAM72   342   LOC1459 1  7470  XM_085290.7  5       TCACGCCTGTAA A    CT         A        3  C  c  c
        88                          TCCCCACACTT   AAGTG  GGGATTACAGGC TGA
                                          TTCAC  CCCTAATGTCCG ACT
                                        -    AC          C
GAM72   342   LOC1461 1  3209           3       TCACACCTGGAA           A   CA        3  C  c  c
        59                          TCCCAGCATTTT AAAGTGCTGGGATT CAGG  TGA
                                          TTTTACGACCCTAA GTCC  ACT
                                                 G   AC
GAM72   342   LOC1465 1  16974          3       TCACACCTGTGA AA            CA        3  C  c  c
        40                          TCCCAGCACT    AGTGCTGGGATTACAGG  TGA
                                          TCACGACCCTAGTGTCC  ACT
                                        --             AC
GAM72   342   LOC1466 1  4213  XM_085536.1  3       TCACACCTGTGA       ---        CA      3  C  c  c
        56                          TCCCCCCAGCAC AAAGTGCT   GGGATTACAGG  TGA
                                    TTT        TTTCACGA   CCCTAGTGTCC  ACT
                                          CCC         AC
GAM72   342   LOC1466 1  8777           3       TCACGCCTGTAA AA      G       A        3  C  c  c
        69                          TCCAGCACT     AGTGCTGG ATTACAGGC TGA
                                          TCACGACC TAATGTCCG ACT
                                        --       -       C
GAM72   342   LOC1467 1  3515  XM_097074.1  3       TCACGCCTATAA   G C      C   A        3  C  c  c
        28                          TCCCAACAGTTT AAA TG TGGGATTA AGGC TGA
                                          TTT AC ACCCTAAT TCCG ACT
                                           G A       A   C
GAM72   342   LOC1467 1  10771          3       TCATGCCTGTAA A     T                3  C  b  b
        80                          TCCCTGCACTT   AAGTGC GGGATTACAGGCATGA
                                          TTCACG CCCTAATGTCCGTACT
                                        -     T
GAM72   342   LOC1469 1  18219 XM_097121.1  3       TCACACCTGTAA      T        CA        3  C  c  c
        01                          TCCCCGCACTTT AAAGTGC GGGATTACAGG  TGA
                                          TTTCACG CCCTAATGTCC  ACT
                                             C         AC
GAM72   342   LOC1469 1  8050  XM_097142.1  3       CCTGTAATACCA        G      CATGA      3  C  c  c
        58                          GCACTTT     AAAGTGCTGG ATTACAGG
                                          TTTCACGACC TAATGTCC
                                             A       -----
GAM72   342   LOC1469 1  8141           5       TCACACCTATAA           C  CA        3  C  b  b
        75                          TCCCAGCACTTT AAAGTGCTGGGATTA AGG  TGA
                                          TTTCACGACCCTAAT TCC  ACT
                                                A  AC
GAM72   342   LOC1470 1  4511  XM_097182.1  3       TCAGGCCTGTAA A             A        3  C  b  b
        80                          TCCCAGCACTT   AAGTGCTGGGATTACAGGC TGA
                                          TTCACGACCCTAATGTCCG ACT
                                        -              G
GAM72   342   LOC1476 1  2584  XM_097262.1  3       CACACCTGTAAT             CA A      3  C  b  b
        69                          CCCAGCACTTT  AAAGTGCTGGGATTACAGG  TG
                                          TTTCACGACCCTAATGTCC  AC
                                                      AC  -
GAM72   342   LOC1477 1  18394 XM_085862.6  5       TCACGTTTGTAA               A        3  C  b  b
```

27 TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAATGTTTG ACT
C

GAM72 342 LOC1482 1 17321 3 TCATACCTATAG C C 3 C b b
67 TCCCAGCACTTT AAAGTGCTGGGATTA AGG ATGA
TTTCACGACCCTGAT TCC TACT
A A

GAM72 342 LOC1482 1 15074 3 TCATGCCTGTAA - 3 C b b
93 TCTCAAGCACTT AAAGTGCT GGGATTACAGGCATGA
T TTTCACGA CTCTAATGTCCGTACT
A

GAM72 342 LOC1483 1 5999 3 TCATGCCTGTAA T 3 C b b
43 TCCCCGCACTTT AAAGTGC GGGATTACAGGCATGA
TTTCACG CCCTAATGTCCGTACT
C

GAM72 342 LOC1483 1 7273 3 TCACGCCTGTAA AA A 3 C c c
97 TCCCGGCACT AGTGCTGGGATTACAGGC TGA
TCACGGCCCTAATGTCCG ACT
-- C

GAM72 342 LOC1489 1 18844 XM_086361.5 5 TCACACCTGTAA A CA 3 C c c
18 CCCTAGCACTTT AAAGTGCTGGG TTACAGG TGA
TTTCACGATCC AATGTCC ACT
C AC

GAM72 342 LOC1494 1 4860 XM_097645.4 3 TCATGCCTGTAT C T 3 C b b
64 TCCCACCACTTT AAAGTG TGGGA TACAGGCATGA
TTTCAC ACCCT ATGTCCGTACT
C T

GAM72 342 LOC1497 1 19797 5 TCACACCTATAA C CA 3 C c c
11 TCCTAGCGCTTT AAAGTGCTGGGATTA AGG TGA
TTTCGCGATCCTAAT TCC ACT
A AC

GAM72 342 LOC1501 1 6506 3 TCATGCCTGTAA AAAGT 3 C c c
39 TCCCAGC GCTGGGATTACAGGCATGA
CGACCCTAATGTCCGTACT

GAM72 342 LOC1501 1 9701 XM_086791.3 5 TCACGCCTAGAA AC A 3 C b b
42 TCCCAGCACTTT AAAGTGCTGGGATT AGGC TGA
TTTCACGACCCTAA TCCG ACT
GA C

GAM72 342 LOC1502 1 16037 XM_097870.1 3 TCACACCTGTAA G CA 3 C c c
25 TTGCAGCACTTT AAAGTGCTG GATTACAGG TGA
TTTCACGAC TTAATGTCC ACT
G AC

GAM72 342 LOC1502 1 7735 3 TCACACCGGTAA A C A CA 3 C c c
45 TCCCAACACTT AAGTG TGGGATTAC GG TGA
TTCAC ACCCTAATG CC ACT
- A G AC

GAM72 342 LOC1502 1 20103 XM_097869.2 3 TCATGCCTGTAA A 3 C b b
99 CCTCAGCACTTT AAAGTGCTGGG TTACAGGCATGA
TTTCACGACTC AATGTCCGTACT

C

GAM72 342 LOC1506 1 7681 XM_097931.1 5 CCTGTAAGCCCA A CATGA 3 C c c

30 GCACTTT AAAGTGCTGGG TTACAGG

TTTCACGACCC AATGTCC

G -----

GAM72 342 LOC1509 1 7643 3 TCATGCCTCTAA C 3 C b b

60 TCCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA

TTTCACGACCCTAAT TCCGTACT

C

GAM72 342 LOC1509 1 14192 3 TCACCCCTGTAA CA 3 C b b

98 TCCCAGTACTTT AAAGTGCTGGGATTACAGG TGA

TTTCATGACCCTAATGTCC ACT

CC

GAM72 342 LOC1512 1 3564 3 TCAAGCCCATAA CA A 3 C b b

48 TCCCAGCACTTT AAAGTGCTGGGATTA GGC TGA

TTTCACGACCCTAAT CCG ACT

AC A

GAM72 342 LOC1514 1 17658 3 TCATGCCTGTAA T 3 C b b

29 TCCCAGCCCTTT AAAG GCTGGGATTACAGGCATGA

TTTC CGACCCTAATGTCCGTACT

C

GAM72 342 LOC1514 1 729 XM_098060.1 3 TGCCTGTAATCG G TGA 3 C c c

38 CAGCACTTT AAAGTGCTG GATTACAGGCA

TTTCACGAC CTAATGTCCGT

G ---

GAM72 342 LOC1520 1 5871 3 TCAAGCCTGTAA C A 3 C b b

02 TCCCAACACTTT AAAGTG TGGGATTACAGGC TGA

TTTCAC ACCCTAATGTCCG ACT

A A

GAM72 342 LOC1521 1 14066 3 TGCCTGTAATCC C TGA 3 C c c

06 CAACACTTT AAAGTG TGGGATTACAGGCA

TTTCAC ACCCTAATGTCCGT

A ---

GAM72 342 LOC1522 1 18445 3 TCATGCCTGTCA T 3 C b b

83 TCCCAGCACTTT AAAGTGCTGGGAT ACAGGCATGA

TTTCACGACCCTA TGTCCGTACT

C

GAM72 342 LOC1524 1 10381 3 TCATGCCTGTGA CT 3 C b b

41 TCCCTACACTTT AAAGTG GGGATTACAGGCATGA

TTTCAC CCCTAGTGTCCGTACT

AT

GAM72 342 LOC1524 1 733 XM_098231.1 3 TCACACCTGTAA G CA 3 C c c

45 TCCCAGCAGTTT AAA TGCTGGGATTACAGG TGA

TTT ACGACCCTAATGTCC ACT

G AC

GAM72 342 LOC1524 2 6507 3 TCACGCCTGTAA A C A 3 C c b

53 TCCCAACACTT AAGTG TGGGATTACAGGC TGA

TTCAC ACCCTAATGTCCG ACT

- A C

GAM72 342 LOC1524 2 7673 3 CACGCCTGTAAT A A 3 C b b
53 CCCAGCACTTT AAAGTGCTGGGATTACAGGC TG
TTTCACGACCCTAATGTCCG AC
C -
GAM72 342 LOC1526 1 16737 XM_087495.1 5 TCATACCTGTAA AAAG C 3 C c c
27 TCCCAGCA TGCTGGGATTACAGG ATGA
ACGACCCTAATGTCC TACT
---- A
GAM72 342 LOC1528 1 11713 XM_098266.5 3 TCATGCCTGGAA A 3 C b b
04 TCCCAGCACTTT AAAGTGCTGGGATT CAGGCATGA
TTTCACGACCCTAA GTCCGTACT
G
GAM72 342 LOC1530 1 4690 XM_098307.1 3 TCACGTCTGTAA AAAG A 3 C c c
77 TCCCAGCA TGCTGGGATTACAGGC TGA
ACGACCCTAATGTCTG ACT
---- C
GAM72 342 LOC1535 1 8086 XM_087708.6 3 TCATGCCTGTGA 3 C b b
61 TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACCCTAGTGTCCGTACT

GAM72 342 LOC1536 1 1185 3 TCACACCTGTAA G CA 3 C c c
42 TCCCAGGACTTT AAAGT CTGGGATTACAGG TGA
TTTCA GACCCTAATGTCC ACT
G AC
GAM72 342 LOC1536 1 6747 XM_098412.1 3 TGCTATAATCCT CA TGA 3 C c c
84 AGCACTTT AAAGTGCTGGGATTA GGCA
TTTCACGATCCTAAT TCGT
A- ---
GAM72 342 LOC1537 2 5172 XM_098422.1 3 TCATGCCTGTAA 3 C b b
27 TCTCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACTCTAATGTCCGTACT

GAM72 342 LOC1537 2 18363 XM_098422.1 3 TCATGCCTGTAA A - 3 C b b
27 TCTCAGCTACTT AAGT GCTGGGATTACAGGCATGA
TTCA CGACTCTAATGTCCGTACT
- T
GAM72 342 LOC1537 1 5167 3 TCATGCTTGTAA 3 C b b
33 TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACCCTAATGTTCGTACT

GAM72 342 LOC1540 1 8087 3 TCGTGCCTGTAA 3 C b b
89 TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACCCTAATGTCCGTGCT

GAM72 342 LOC1540 1 8225 XM_098466.1 3 CACATCTGTAAT CA A 3 C c c
92 CCCAGCACTTT AAAGTGCTGGGATTACAGG TG
TTTCACGACCCTAATGTCT AC
AC -
GAM72 342 LOC1544 1 7519 3 TCACGCCTGTAA G A 3 C b b
03 TCCCAGAACTTT AAAGT CTGGGATTACAGGC TGA

```
                                                TTTCA GACCCTAATGTCCG ACT
                                                  A           C
GAM72   342   LOC1547 1  9325  XM_098602.1  5       CCTGTAATCCCA              CATGA       3  C  c  c
        39                                      GCATTTT     AAAGTGCTGGGATTACAGG
                                                TTTTACGACCCTAATGTCC
                                                -----
GAM72   342   LOC1549 1  16364          3       TCACATTCGTAA            AG CA        3  C  c  c
        92                                  TCCCAGCACTTT AAAGTGCTGGGATTAC  G  TGA
                                                TTTCACGACCCTAATG  T  ACT
                                                   CT AC
GAM72   342   LOC1553 1  17561          3       TCACACTTGTAA              CA        3  C  b  b
        76                                  TCCCAGCACTTT AAAGTGCTGGGATTACAGG  TGA
                                                TTTCACGACCCTAATGTTC  ACT
                                                  AC
GAM72   342   LOC1554 1  5623  XM_098722.1  3       TCACACCTGTAA AAA           CA        3  C  c  c
        38                                      TCCCAGTAC     GTGCTGGGATTACAGG  TGA
                                                  CATGACCCTAATGTCC  ACT
                                                ---           AC
GAM72   342   LOC1572 1  5887          5       TCATGCCTATAT          T  C          3  C  b  b
        47                                  TCCCAGCACTTT AAAGTGCTGGGA TA AGGCATGA
                                                TTTCACGACCCT AT TCCGTACT
                                                   T  A
GAM72   342   LOC1575 1  12425 XM_098779.1  5       TCACATCTGTAA       G        CA        3  C  c  c
        62                                      TCCAAGCACTTT AAAGTGCT GGATTACAGG  TGA
                                                TTTCACGA CCTAATGTCT  ACT
                                                    A        AC
GAM72   342   LOC1581 1  10160 XM_054490.2  5       TCATGCCTATAA           C          3  C  b  b
        60                                      TTCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
                                                TTTCACGACCTTAAT TCCGTACT
                                                   A
GAM72   342   LOC1582 1  13710          3       TCACGCCTGTAA       G       A        3  C  c  c
        35                                  TCACAGTATTTT AAAGTGCTG GATTACAGGC TGA
                                                TTTTATGAC CTAATGTCCG ACT
                                                    A        C
GAM72   342   LOC1582 1  15611 XM_098912.2  3       TCACGCCTGTAA       G       A        3  C  b  b
        88                                      TCACAGCACTTT AAAGTGCTG GATTACAGGC TGA
                                                TTTCACGAC CTAATGTCCG ACT
                                                    A        C
GAM72   342   LOC1583 1  427   XM_098931.4  5       TCACACCTATAG AA         C  CA        3  C  c  c
        82                                      TCCCAGCACT    AGTGCTGGGATTA AGG  TGA
                                                  TCACGACCCTGAT TCC  ACT
                                                --          A   AC
GAM72   342   LOC1584 1  5974  XM_098939.1  3       TGTGCCTGTAAT               A      3  C  b  b
        34                                      CTCAGCACTTT  AAAGTGCTGGGATTACAGGCATG
                                                TTTCACGACTCTAATGTCCGTGT
                                                -
GAM72   342   LOC1586 1  9473          5       TGCCTGTAATCC              TGA       3  C  b  b
        77                                      CAGCACTTT    AAAGTGCTGGGATTACAGGCA
                                                TTTCACGACCCTAATGTCCGT
                                                ---
```

```
GAM72   342   LOC1588 1  4611  XM_098999.2  3      TCACACCTGTAA     C        CA       3  C  c  c
        63                                   TCCCAACACTTT AAAGTG TGGGATTACAGG  TGA
                                                  TTTCAC ACCCTAATGTCC  ACT
                                                     A         AC
GAM72   342   LOC1589 1  10126                3      TCACACCTGTTA         T   CA       3  C  b  b
        87                                   TCCCAGCACTTT AAAGTGCTGGGAT ACAGG  TGA
                                                  TTTCACGACCCTA TGTCC  ACT
                                                        T    AC
GAM72   342   LOC1590 1  14881 XM_099021.1  3      GCCTGTAATCCC     G         ATGA     3  C  c  c
        53                                   AGGACTTT    AAAGT CTGGGATTACAGGC
                                                  TTTCA GACCCTAATGTCCG
                                                     G          ----
GAM72   342   LOC1591 1  16091                3      TCTGTAATCCCA            CATGA     3  C  c  c
        16                                   GCACTTT     AAAGTGCTGGGATTACAGG
                                                  TTTCACGACCCTAATGTCT
                                                           -----
GAM72   342   LOC1606 1  15754                3      TCACACCTGTAA             CA       3  C  b  b
        46                                   TCTCAGCATTTT AAAGTGCTGGGATTACAGG  TGA
                                                  TTTTACGACTCTAATGTCC  ACT
                                                        AC
GAM72   342   LOC1662 1  9359                 3      TCACGCCAGGAA          ACA  A       3  C  c  c
        19                                   TCCCAGCACTTT AAAGTGCTGGGATT   GGC TGA
                                                  TTTCACGACCCTAA   CCG ACT
                                                     GGA   C
GAM72   342   LOC1960 1  13986                3      TCATGCTTGTAA                    3  C  b  b
        27                                   TCCCGGCACTTT AAAGTGCTGGGATTACAGGCATGA
                                                  TTTCACGGCCCTAATGTTCGTACT

GAM72   342   LOC1967 1  17150 XM_116865.1  3      TCAAGCCTGTAA             A       3  C  b  b
        61                                   TCCCAGTACTTT AAAGTGCTGGGATTACAGGC TGA
                                                  TTTCATGACCCTAATGTCCG ACT
                                                        A
GAM72   342   LOC1971 1  8418                 3      TCATGTTTGTAA                    3  C  b  b
        96                                   TCCTAGCACTTT AAAGTGCTGGGATTACAGGCATGA
                                                  TTTCACGATCCTAATGTTTGTACT

GAM72   342   LOC1973 1  19926                3      TCAGGCCTGTAA     C        A       3  C  b  b
        19                                   TCCCAACACTTT AAAGTG TGGGATTACAGGC TGA
                                                  TTTCAC ACCCTAATGTCCG ACT
                                                     A         G
GAM72   342   LOC1973 1  12694                3      TCATGCCTGTGA AA                 3  C  b  b
        35                                   TCCCAGCACT    AGTGCTGGGATTACAGGCATGA
                                                   TCACGACCCTAGTGTCCGTACT
                                                  --
GAM72   342   LOC1974 1  13833                5      CACACCTGTAAT   G         CA A     3  C  c  c
        08                                   CCCAGCAGTTT  AAA TGCTGGGATTACAGG  TG
                                                  TTT ACGACCCTAATGTCC  AC
                                                    G          AC  -
GAM72   342   LOC2000 1  19993                3      TCACGCCTGTAA     C        A       3  C  b  b
        14                                   TCCCACCACTTT AAAGTG TGGGATTACAGGC TGA
```

TTTCAC ACCCTAATGTCCG ACT
C C
GAM72 342 LOC2002 1 13981 3 TCATGCCTATAA C 3 C b b
82 TCTCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
TTTCACGACTCTAAT TCCGTACT
A
GAM72 342 LOC2007 1 10206 XM_117268.1 3 TCACACCTGTAA AAAG CA 3 C c c
31 TCCCAGCA TGCTGGGATTACAGG TGA
ACGACCCTAATGTCC ACT
---- AC
GAM72 342 LOC2008 1 7883 3 TCATGCCTGTAA C 3 C b b
03 TCCCACCACTTT AAAGTG TGGGATTACAGGCATGA
TTTCAC ACCCTAATGTCCGTACT
C
GAM72 342 LOC2018 1 6971 XM_114393.2 3 TCACGCCTGTAA G A 3 C b b
68 TCCCAGAATTTT AAAGT CTGGGATTACAGGC TGA
TTTTA GACCCTAATGTCCG ACT
A C
GAM72 342 LOC2019 1 19292 3 TCATGCCTGTAA 3 C b b
31 TCTTAGTACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCATGATTCTAATGTCCGTACT
GAM72 342 LOC2021 1 8165 XM_117365.5 5 TCAGACCTATAA C CA 3 C b b
34 TCCCAGCACTTT AAAGTGCTGGGATTA AGG TGA
TTTCACGACCCTAAT TCC ACT
A AG
GAM72 342 LOC2027 1 15090 XM_117455.3 3 TCACGCCTGTAA TGC A 3 C c c
81 TCCTATCCTTT AAAG TGGGATTACAGGC TGA
TTTC ATCCTAATGTCCG ACT
CT- C
GAM72 342 LOC2033 1 12836 3 TCATACCTTTAA C C 3 C b b
50 TCCCAGCACTTT AAAGTGCTGGGATTA AGG ATGA
TTTCACGACCCTAAT TCC TACT
T A
GAM72 342 LOC2033 2 8136 3 TCACACCTGTAA CA 3 C b b
78 TCCCGGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGGCCCTAATGTCC ACT
AC
GAM72 342 LOC2033 2 19699 3 CCTGTAATCCCA C CATGA 3 C c b
78 CACTTT AAAGTG TGGGATTACAGG
TTTCAC ACCCTAATGTCC
- -----
GAM72 342 LOC2033 1 2611 3 TCACACCTGTAA AAA CA 3 C c c
97 TCTCAGCAC GTGCTGGGATTACAGG TGA
CACGACTCTAATGTCC ACT
--- AC
GAM72 342 LOC2196 1 17944 XM_167562.1 3 TCATGCCTATAA AAA C 3 C c c
49 TCCCAGCAC GTGCTGGGATTA AGGCATGA
CACGACCCTAAT TCCGTACT

```
                                        ---          A
GAM72   342   LOC2203 1  10212          3       TCATGCCTGTAA AA   C               3  C  c  c
        70                          TCCCAACACT    AGTG TGGGATTACAGGCATGA
                                      TCAC ACCCTAATGTCCGTACT
                                        --   A
GAM72   342   LOC2206 1  14876          3       CACGCCTGTAAT A   -          A A     3  C  c  c
        62                          CCCAGCTACTT   AAGT GCTGGGATTACAGGC TG
                                      TTCA CGACCCTAATGTCCG AC
                                        -   T          C -
GAM72   342   LOC2210 1  877           3       TCATGCCTGTAA     C                3  C  b  b
        69                          TCCTAACACTTT AAAGTG TGGGATTACAGGCATGA
                                      TTTCAC ATCCTAATGTCCGTACT
                                          A
GAM72   342   LOC2212 1  18966          3       TCACACCTGTAA AA  -          CA       3  C  c  c
        71                          TCCCAGCTACT   AGT GCTGGGATTACAGG  TGA
                                      TCA CGACCCTAATGTCC  ACT
                                        --  T          AC
GAM72   342   LOC2216 1  4135          3       TCACACTTATCA          TAC  CA       3  C  c  c
        41                          TCTCAGCACTTT AAAGTGCTGGGAT   AGG  TGA
                                      TTTCACGACTCTA   TTC  ACT
                                             CTA   AC
GAM72   342   LOC2219 1  17821 XM_168343.1  5       CCTGGAATCCCA          A   CATGA      3  C  c
c
        43                          GCACTTT     AAAGTGCTGGGATT CAGG
                                      TTTCACGACCCTAA GTCC
                                             G   -----
GAM72   342   LOC2219 1  18979 XM_168340.2  3       TCATACGTGTAA            GGC        3  C  c  c
        46                          TCCCAGTACTTT AAAGTGCTGGGATTACA   ATGA
                                      TTTCATGACCCTAATGT   TACT
                                           GCA
GAM72   342   LOC2220 1  8977  XM_168427.2  5       TCATGCCTGTAA         A            3  C  b  b
        60                          GCCCAGCACTTT AAAGTGCTGGG TTACAGGCATGA
                                      TTTCACGACCC AATGTCCGTACT
                                           G
GAM72   342   LOC2220 2  11966          3       TCACGCCTGTAA       G       A        3  C  b  b
        66                          TCGCGGCACTTT AAAGTGCTG GATTACAGGC TGA
                                      TTTCACGGC CTAATGTCCG ACT
                                          G       C
GAM72   342   LOC2220 2  14380          3       TCACACCTGTGA A            CA        3  C  c  b
        66                          TCCCAGCACTT   AAGTGCTGGGATTACAGG  TGA
                                      TTCACGACCCTAGTGTCC  ACT
                                        -             AC
GAM72   342   LOC2221 2  4691  XM_168431.1  3       TCATGCCTGTAA                    3  C  b  b
        60                          TCTCAGTACTTT AAAGTGCTGGGATTACAGGCATGA
                                      TTTCATGACTCTAATGTCCGTACT

GAM72   342   LOC2221 2  6925  XM_168431.1  5       ATGCCTGTAATC              GA      3  C  b  b
        60                          CCAGCACTTT   AAAGTGCTGGGATTACAGGCAT
                                      TTTCACGACCCTAATGTCCGTA
                                             --
```

GAM72 342 LOC2222 1 10341 3 TCATGCCTATAA C - C 3 C b b
37 TACCCACACTTT AAAGTG TGGG ATTA AGGCATGA
TTTCAC ACCC TAAT TCCGTACT
- A A
GAM72 342 LOC2222 1 15689 3 TCATGCCTGTAA G 3 C b b
56 TGCCAGCACTTT AAAGTGCTGG ATTACAGGCATGA
TTTCACGACC TAATGTCCGTACT
G
GAM72 342 LOC2538 1 10077 3 TGTGCCTGTAAT G A 3 C c c
40 CCCAGAACTTT AAAGT CTGGGATTACAGGCATG
TTTCA GACCCTAATGTCCGTGT
A -
GAM72 342 LOC2540 1 7566 3 TCATGCCTGTAA C 3 C b b
45 TCCCAATACTTT AAAGTG TGGGATTACAGGCATGA
TTTCAT ACCCTAATGTCCGTACT
A
GAM72 342 LOC2541 1 1555 XM_172851.1 3 TCACGCCTGTAA AAA A A 3 C c c
00 CCCCAGCAC GTGCTGGG TTACAGGC TGA
CACGACCC AATGTCCG ACT
--- C C
GAM72 342 LOC2550 1 4612 XM_173187.2 3 CTTGTAATCCTA CATGA 3 C c c
31 GCACTTT AAAGTGCTGGGATTACAGG
TTTCACGATCCTAATGTTC

GAM72 342 LOC2550 1 18961 3 TCATGCCTGAAA T A 3 C b b
42 TCCCTGCACTTT AAAGTGC GGGATT CAGGCATGA
TTTCACG CCCTAA GTCCGTACT
T A
GAM72 342 LOC2553 1 16738 3 TCACGCCTGTAA AA G A 3 C c c
26 TCCCAGACT AGT CTGGGATTACAGGC TGA
TCA GACCCTAATGTCCG ACT
-- - C
GAM72 342 LOC2553 1 4607 XM_172920.1 3 TCATGTCTGTAA 3 C b b
28 TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACCCTAATGTCTGTACT

GAM72 342 LOC2554 1 11708 3 TCATGCCTGAAA C A 3 C b b
63 TCCCAACACTTT AAAGTG TGGGATT CAGGCATGA
TTTCAC ACCCTAA GTCCGTACT
A A
GAM72 342 LOC2557 1 18840 XM_173087.2 3 TCATGCCTATAA AAA G C 3 C c c
98 TCCAAGCAC GTGCT GGATTA AGGCATGA
CACGA CCTAAT TCCGTACT
--- A A
GAM72 342 LOC2559 1 1366 3 TCACACCTGTAA T CA 3 C c c
37 TCCCAGCTCTTT AAAG GCTGGGATTACAGG TGA
TTTC CGACCCTAATGTCC ACT
T AC
GAM72 342 LOC2559 1 15032 XM_172907.1 3 GCCTATAATCCC C ATGA 3 C c c
71 AGCACTTT AAAGTGCTGGGATTA AGGC

TTTCACGACCCTAAT TCCG
A ----

GAM72 342 LOC2565 1 16314 XM_172866.1 3 TCACACCTGTGA AAA CA 3 C c c
15 TCTCAGCAC GTGCTGGGATTACAGG TGA
CACGACTCTAGTGTCC ACT
--- AC

GAM72 342 LOC2565 1 15534 3 TCACGCCTATAA C A 3 C b b
20 TCTCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACTCTAAT TCCG ACT
A C

GAM72 342 LOC2565 1 3768 3 TCACGCCTGTGA A 3 C b b
44 TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAGTGTCCG ACT
C

GAM72 342 LOC2573 1 14050 5 TCATGCCTATAA C C 3 C b b
54 TCCCAACACTTT AAAGTG TGGGATTA AGGCATGA
TTTCAC ACCCTAAT TCCGTACT
A A

GAM72 342 LOC2574 1 14619 3 TCAAGCCTATAA A C A 3 C c c
48 TCCCAGCACTT AAGTGCTGGGATTA AGGC TGA
TTCACGACCCTAAT TCCG ACT
- A A

GAM72 342 LOC2575 1 10276 5 TCACACCTGTAA AA CA 3 C c c
96 TCCCAGCACT AGTGCTGGGATTACAGG TGA
TCACGACCCTAATGTCC ACT
-- AC

GAM72 342 LOC5112 1 15769 NM_016094.1 3 TCATGCCAGTTA T A 3 C b b
2 TCCCAGCACTTT AAAGTGCTGGGAT AC GGCATGA
TTTCACGACCCTA TG CCGTACT
T A

GAM72 342 LOC5114 1 19694 NM_016158.1 3 TCATGCCTGTAA G 3 C b b
5 TCTCAGAACTTT AAAGT CTGGGATTACAGGCATGA
TTTCA GACTCTAATGTCCGTACT
A

GAM72 342 LOC5121 1 3156 NM_016380.1 3 TCATGCCTATCA TAC 3 C b b
2 TCCCAGCACTTT AAAGTGCTGGGAT AGGCATGA
TTTCACGACCCTA TCCGTACT
CTA

GAM72 342 LOC5127 1 16733 NM_016546.1 3 TCACGCCTGTAA AAA C A 3 C c c
9 TCCCAACAC GTG TGGGATTACAGGC TGA
CAC ACCCTAATGTCCG ACT
--- A C

GAM72 342 LOC5133 1 8944 NM_016643.1 3 TCATGCCTGTAA - 3 C b b
3 TCTCCAGCACTT AAAGTGCTGG GATTACAGGCATGA
T TTTCACGACC CTAATGTCCGTACT
T

GAM72 342 LOC5171 1 8066 3 TCATGCCTGTAA AAAG T 3 C c c
6 TCCCTGCA TGC GGGATTACAGGCATGA
ACG CCCTAATGTCCGTACT
---- T

GAM72 342 LOC8995 1 4295 XM_027627.4 3 TCACGCCTGGAA A A A 3 C c c
8 TCCCAGCACTT AAGTGCTGGGATT CAGGC TGA
TTCACGACCCTAA GTCCG ACT
- G C
GAM72 342 LOC9009 1 5975 3 TCACACCTGTAA A CA 3 C b b
2 TCCCAGCACTT AAGTGCTGGGATTACAGG TGA
TTCACGACCCTAATGTCC ACT
- AC
GAM72 342 LOC9014 1 3769 3 TCATGCCTACAA AC 3 C b b
1 TCCCAGCACTTT AAAGTGCTGGGATT AGGCATGA
TTTCACGACCCTAA TCCGTACT
CA
GAM72 342 LOC9033 1 4608 XM_030958.6 3 TCATGCCTGTAA 3 C b b
3 TTCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACCTTAATGTCCGTACT

GAM72 342 LOC9057 1 8294 XM_032669.1 3 TCATGCCTGTAA A - 3 C b b
3 TCCTAGCAGCTT AAG TGCTGGGATTACAGGCATGA
TTC ACGATCCTAATGTCCGTACT
- G
GAM72 342 LOC9058 1 8082 NM_145233.1 3 TCATGCCTGTGG 3 C b b
9 TCCCAGCGCTTT AAAGTGCTGGGATTACAGGCATGA
TTTCGCGACCCTGGTGTCCGTACT

GAM72 342 LOC9062 1 4899 XM_033003.4 3 TCACACCTGTAA T CA 3 C b b
4 TCCCGCACTTT AAAGTGC GGGATTACAGG TGA
TTTCACG CCCTAATGTCC ACT
- AC
GAM72 342 LOC9077 1 18233 3 TCACGCCTATAA AAA C A 3 C c c
7 TCTCAGCAC GTGCTGGGATTA AGGC TGA
CACGACTCTAAT TCCG ACT
--- A C
GAM72 342 LOC9078 1 8897 XM_034109.2 5 TCACGCTTACAG AC A 3 C c c
4 TCCCAGCACTTT AAAGTGCTGGGATT AGGC TGA
TTTCACGACCCTGA TTCG ACT
CA C
GAM72 342 LOC9138 1 15283 3 ATGCCTGTAATC GA 3 C b b
0 CCGGCACTTT AAAGTGCTGGGATTACAGGCAT
TTTCACGGCCCTAATGTCCGTA
--
GAM72 342 LOC9139 1 18139 XM_038219.2 3 TCATGCCTGTAG A 3 C b b
7 TCCCAGCACTCG A AGTGCTGGGATTACAGGCATGA
G TCACGACCCTGATGTCCGTACT
C
GAM72 342 LOC9144 1 4045 3 TCACGCCTCTAA C A 3 C b b
2 TCTCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACTCTAAT TCCG ACT
C C
GAM72 342 LOC9156 1 19839 XM_039231.1 5 TCTTGCCTGTAA T 3 C b b
5 TCCCAGCACTTT AAAGTGCTGGGATTACAGGCA GA

TTTCACGACCCTAATGTCCGT CT
T

GAM72	342	LOC9186	1	14448	NM_052858.1	3	TCACACCTGTAA	A	CA	3	C	b	b
	2				CCCCAGCACTTT AAAGTGCTGGG TTACAGG TGA								
					TTTCACGACCC AATGTCC ACT								
					C AC								
GAM72	342	LOC9194	1	17556	XM_041723.1	3	TCATGCCTATAA	C----		3	C	b	b
	8				TTAATCCCAGTA AAAGTGCTGGGATTA AGGCATGA								
					CTTT TTTCATGACCCTAAT TCCGTACT								
					TAATA								
GAM72	342	LOC9222	1	10868	3	TCACACCTGTAA	T	CA	3	C	c	c	
	3				TCCCTGCATTTT AAAGTGC GGGATTACAGG TGA								
					TTTTACG CCCTAATGTCC ACT								
					T AC								
GAM72	342	LOC9246	1	16877	5	GCCTATAATCCC	C	ATGA	3	C	c	c	
	5				AGTACTTT AAAGTGCTGGGATTA AGGC								
					TTTCATGACCCTAAT TCCG								
					A ----								
GAM72	342	LOC9256	1	12413	XM_045852.1	3	TCATGCCAGCAA	ACA		3	C	b	b
	8				TCCTAGCACTTT AAAGTGCTGGGATT GGCATGA								
					TTTCACGATCCTAA CCGTACT								
					CGA								
GAM72	342	LOC9266	1	16307	5	CATGCCTATAAT AAAG	C	A	3	C	c	c	
	1				CCCAGCA TGCTGGGATTA AGGCATG								
					ACGACCCTAAT TCCGTAC								
					---- A -								
GAM72	342	LOC9277	1	8166	3	TCATGCCCGTAA	T GG	A	3	C	c	c	
	1				TTTCTGCACTTT AAAGTGC G ATTAC GGCATGA								
					TTTCACG C TAATG CCGTACT								
					T TT C								
GAM72	342	LOC9313	1	2241	XM_049396.2	3	TCTGTAATCCTA	CATGA		3	C	c	c
	2				GCACTTT AAAGTGCTGGGATTACAGG								
					TTTCACGATCCTAATGTCT								

GAM72	342	LOC9659	1	18099	XM_039922.2	5	TCAGGCCTGTAA A	A	A	3	C	c	c
	7				CCCCAGCACTT AAGTGCTGGG TTACAGGC TGA								
					TTCACGACCC AATGTCCG ACT								
					- C G								
GAM72	342	LRRFIP1	1	15700	NM_004735.1	3	TCATGCCTGTAA AAA			3	C	c	c
					TCTCAGTAC GTGCTGGGATTACAGGCATGA								
					CATGACTCTAATGTCCGTACT								

GAM72	342	LSR68	1	4233	3	TCACGCCTGTAA	G	A	3	C	b	b	
					TGCCAGCACTTT AAAGTGCTGG ATTACAGGC TGA								
					TTTCACGACC TAATGTCCG ACT								
					G C								
GAM72	342	MASP1	1	9106	NM_001879.3	3	TGTGCCAATCCC A	ACA	A	3	C	c	c
					AGCACTCC A AGTGCTGGGATT GGCATG								
					C TCACGACCCTAA CCGTGT								
					C --- -								

GAM72 342 MAWBP 1 1896 NM_022129.1 3 TCATGCCTGTAA G 3 C b b
TCGTAGCACTTT AAAGTGCTG GATTACAGGCATGA
TTTCACGAT CTAATGTCCGTACT
G
GAM72 342 MED6 1 14033 NM_005466.1 3 TCACTCCTGTAA CA 3 C b b
TCCCGGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGGCCCTAATGTCC ACT
TC
GAM72 342 MESDC2 1 5973 XM_051854.3 5 TCACGCCTGTAA A 3 C b b
TCCCAGTACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCATGACCCTAATGTCCG ACT
C
GAM72 342 MGC1099 1 15448 NM_032307.1 3 TATGCCTGTAAT AA A 3 C c c
9 CCCAGCACT AGTGCTGGGATTACAGGCATG
TCACGACCCTAATGTCCGTAT
-- -
GAM72 342 MGC1128 1 4413 5 TCACGTCTATAA AA C A 3 C c c
7 TCCCAGCACT AGTGCTGGGATTA AGGC TGA
TCACGACCCTAAT TCTG ACT
-- A C
GAM72 342 MGC1563 1 2277 NM_032753.2 3 TCATGCCTGTAA TG 3 C b b
1 TCCCAGTGCTTT AAAG CTGGGATTACAGGCATGA
TTTC GACCCTAATGTCCGTACT
GT
GAM72 342 MGC1603 1 11316 NM_032887.1 3 TCAGGCCTGTAA AA A 3 C c c
7 TCCCAGCACT AGTGCTGGGATTACAGGC TGA
TCACGACCCTAATGTCCG ACT
-- G
GAM72 342 MGC2023 1 8637 NM_145041.1 3 CCTGTAATCCCA CATGA 3 C c c
5 GTACTTT AAAGTGCTGGGATTACAGG
TTTCATGACCCTAATGTCC

GAM72 342 MGC2664 1 14080 NM_144971.1 3 TCATGCCTGACA A TA 3 C c c
1 TCTCAGCACTT AAGTGCTGGGAT CAGGCATGA
TTCACGACTCTA GTCCGTACT
- CA
GAM72 342 MGC2989 1 20056 NM_144618.1 3 TCACGCCTGTAG C A 3 C b b
1 TCCCAACACTTT AAAGTG TGGGATTACAGGC TGA
TTTCAC ACCCTGATGTCCG ACT
A C
GAM72 342 MGC3169 1 403 NM_024074.1 3 TCATGCCTATAA C 3 C b b
TCCTAGCACTTT AAAGTGCTGGGATTA AGGCATGA
TTTCACGATCCTAAT TCCGTACT
A
GAM72 342 MGC3935 1 16509 NM_144970.1 3 TCACACCTGTAA - CA 3 C b b
0 TCCCCAGCACTT AAAGTGCTGGG ATTACAGG TGA
T TTTCACGACCC TAATGTCC ACT
C AC
GAM72 342 MGC4368 1 8406 NM_024510.2 3 TCATGCCAGTAA A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTAC GGCATGA

TTTCACGACCCTAATG CCGTACT
A
GAM72 342 MGC4562 1 12121 NM_133375.1 3 TCACGCCTGTAA A A 3 C b b
CCCCAGCACTTT AAAGTGCTGGG TTACAGGC TGA
TTTCACGACCC AATGTCCG ACT
C C
GAM72 342 MGC4771 1 18399 NM_032668.1 3 TCACGCTTGTAA A 3 C b b
TTCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCTTAATGTTCG ACT
C
GAM72 342 MGC4840 1 18803 NM_031490.1 3 TCACACCTGTAA CA 3 C b b
TTCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCTTAATGTCC ACT
AC
GAM72 342 MGC5457 1 17297 NM_032633.1 3 TCACACCTTAAT C CA 3 C b b
CCCAGCACTTT AAAGTGCTGGGATTA AGG TGA
TTTCACGACCCTAAT TCC ACT
- AC
GAM72 342 MIR16 1 10113 NM_016641.2 3 TCATGCCGATAA AAAG CA 3 C c c
TCCCAGCA TGCTGGGATTA GGCATGA
ACGACCCTAAT CCGTACT
---- AG
GAM72 342 MLLT4 1 14447 NM_005936.1 3 TCACACCTGTAA CA 3 C b b
TCCCAGCATTTT AAAGTGCTGGGATTACAGG TGA
TTTTACGACCCTAATGTCC ACT
AC
GAM72 342 MRPL56 1 9134 3 TCACGCCTGTAA C A 3 C b b
TCCCAACACTTT AAAGTG TGGGATTACAGGC TGA
TTTCAC ACCCTAATGTCCG ACT
A C
GAM72 342 MRPS18B 1 18538 NM_014046.2 3 TCACTCCTGTAA CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAATGTCC ACT
TC
GAM72 342 MYO1B 1 9604 XM_290989.1 3 TCACACCTATAA A C C CA 3 C c c
TCCCAACACTT AAGTG TGGGATTA AGG TGA
TTCAC ACCCTAAT TCC ACT
- A A AC
GAM72 342 NBR2 1 6975 NM_005821.2 3 TCATGCCTGTAG 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGGCATGA
TTTCACGACCCTGATGTCCGTACT

GAM72 342 NPHS1 1 19090 NM_004646.1 5 TCACGCCTATAA C A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACCCTAAT TCCG ACT
A C
GAM72 342 Nrap 1 915 NM_006175.2 3 TCATGCTTGTAA A C 3 C b b
TCCCAACACTT AAGTG TGGGATTACAGGCATGA
TTCAC ACCCTAATGTTCGTACT
- A

GAM72 342 NUP62 1 16510 NM_012346.2 3 TCACCCCTGTAA CA 3 C b b
TCTCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACTCTAATGTCC ACT
CC
GAM72 342 OASL 1 17989 NM_003733.1 3 TCACACCTGTAA G CA 3 C c c
TCCCAGAACTTT AAAGT CTGGGATTACAGG TGA
TTTCA GACCCTAATGTCC ACT
A AC
GAM72 342 OPA3 1 2498 NM_025136.1 3 TCACGCCTGTAA AAA A 3 C c c
TCCTAGCAC GTGCTGGGATTACAGGC TGA
CACGATCCTAATGTCCG ACT
--- C
GAM72 342 P2RX7 1 17467 NM_002562.3 3 TCACGTCTGTAA A 3 C b b
TCCCAGCGCTTT AAAGTGCTGGGATTACAGGC TGA
TTTCGCGACCCTAATGTCTG ACT
C
GAM72 342 P2RY6 1 2502 NM_176796.1 3 TCATGCCTGTAA AAAG 3 C c c
TCTCAGCA TGCTGGGATTACAGGCATGA
ACGACTCTAATGTCCGTACT

GAM72 342 PB1 1 12116 NM_018165.1 3 TCACGCCTGTAA A 3 C b b
TCCCAGCATTTT AAAGTGCTGGGATTACAGGC TGA
TTTTACGACCCTAATGTCCG ACT
C
GAM72 342 PCDH11Y 1 12339 NM_032972.1 3 TCATACCTGTAA C 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG ATGA
TTTCACGACCCTAATGTCC TACT
A
GAM72 342 PCDHB9 1 8982 NM_019119.3 3 TCATTCCTGTAA C 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG ATGA
TTTCACGACCCTAATGTCC TACT
T
GAM72 342 PDE4C 1 16348 NM_000923.1 3 CATGCCTATAAT C A 3 C b b
CCCAGCACTTT AAAGTGCTGGGATTA AGGCATG
TTTCACGACCCTAAT TCCGTAC
A -
GAM72 342 PIWIL2 1 6875 NM_018068.2 3 TCACACCTGTAA G CA 3 C b b
TCCAAGCACTTT AAAGTGCT GGATTACAGG TGA
TTTCACGA CCTAATGTCC ACT
A AC
GAM72 342 PLA2G2D 1 4938 NM_012400.2 3 TCATGCCTGTAA A C 3 C b b
TCCCAACACTT AAGTG TGGGATTACAGGCATGA
TTCAC ACCCTAATGTCCGTACT
- A
GAM72 342 POLH 2 12030 NM_006502.1 3 TCACGCCTGTAA C A 3 C b b
TCCTAACACTTT AAAGTG TGGGATTACAGGC TGA
TTTCAC ATCCTAATGTCCG ACT
A C
GAM72 342 POLH 2 19397 NM_006502.1 3 TCATACCTGTAA G C 3 C b b
TGCCAGCACTTT AAAGTGCTGG ATTACAGG ATGA

TTTCACGACC TAATGTCC TACT
G A
GAM72 342 POLK 1 6167 NM_016218.1 3 TCACACCTGTAA T G CA 3 C c c
TGCCAGCCCTTT AAAG GCTGG ATTACAGG TGA
TTTC CGACC TAATGTCC ACT
C G AC
GAM72 342 PP591 1 5542 NM_025207.2 5 TCACACCTATAA C CA 3 C c c
TTCCAGCACTTT AAAGTGCTGGGATTA AGG TGA
TTTCACGACCTTAAT TCC ACT
A AC
GAM72 342 PPP1R3B 2 9817 NM_024607.1 3 TATGCCTGTAAT T A 3 C b b
CCCTGCACTTT AAAGTGC GGGATTACAGGCATG
TTTCACG CCCTAATGTCCGTAT
T -
GAM72 342 PPP1R3B 2 12619 NM_024607.1 5 TATGCCTGTAAT A 3 C b b
CCCAGCACTTT AAAGTGCTGGGATTACAGGCATG
TTTCACGACCCTAATGTCCGTAT
-
GAM72 342 PRIC285 1 17244 NM_033405.1 3 TCACGCCCATAA G CA A 3 C c c
TCCAGCACTTT AAAGTGCTGG ATTA GGC TGA
TTTCACGACC TAAT CCG ACT
- AC C
GAM72 342 PRKY 1 4590 NM_002760.1 3 TCATGCCTGCAA A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATT CAGGCATGA
TTTCACGACCCTAA GTCCGTACT
C
GAM72 342 PRO0038 1 3005 NM_014113.1 3 TCATGCCTATAA AAA C C 3 C c c
TCCCAACAC GTG TGGGATTA AGGCATGA
CAC ACCCTAAT TCCGTACT
--- A A
GAM72 342 PRO0255 1 7528 NM_014124.1 3 TCACGCCTGTAA A 3 C b b
TCTCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACTCTAATGTCCG ACT
C
GAM72 342 PRO0456 1 19460 NM_014127.1 3 TCACGCCTGTAA C A A 3 C c c
CCCCATCACTTT AAAGTG TGGG TTACAGGC TGA
TTTCAC ACCC AATGTCCG ACT
T C C
GAM72 342 PRO0478 1 16168 NM_014129.1 3 TCACACCTGTAA AA T CA 3 C c c
TCCCAGCCT AG GCTGGGATTACAGG TGA
TC CGACCCTAATGTCC ACT
-- - AC
GAM72 342 PRO0628 1 15616 NM_014134.1 3 TCACGCATGTAA G A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACA GC TGA
TTTCACGACCCTAATGT CG ACT
A C
GAM72 342 PRO1048 1 18804 NM_018497.1 5 TCACATCTGTAA CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAATGTCT ACT
AC

GAM72 342 PRO1777 1 16858 3 TCATGCCTGTAA AA 3 C b b
TCCCAGCATT AGTGCTGGGATTACAGGCATGA
TTACGACCCTAATGTCCGTACT
--
GAM72 342 PRO2015 1 11837 NM_018512.1 5 TCACGCCTGTAA A A 3 C b b
TCCCAGCACTT AAGTGCTGGGATTACAGGC TGA
TTCACGACCCTAATGTCCG ACT
- C
GAM72 342 PRO2893 1 4610 3 TCAAGCCTGTAA G A 3 C b b
TCCCAGCAGTTT AAA TGCTGGGATTACAGGC TGA
TTT ACGACCCTAATGTCCG ACT
G A
GAM72 342 PSD 1 14038 NM_002779.2 5 GCCTGCAATCCC A ATGA 3 C c c
AGCACTTT AAAGTGCTGGGATT CAGGC
TTTCACGACCCTAA GTCCG
C ----
GAM72 342 PTRF 1 12748 NM_012232.1 3 TATGCCTGTAAC A A 3 C b b
CCCAGCACTTT AAAGTGCTGGG TTACAGGCATG
TTTCACGACCC AATGTCCGTAT
C -
GAM72 342 RAD18 1 923 NM_020165.2 3 CATGCCTGTGTT A - GG T A 3 C c c
ACAGCAGCTCC A AG TGCTG AT ACAGGCATG
C TC ACGAC TG TGTCCGTAC
C G AT - -
GAM72 342 RAD51 1 11450 NM_002875.2 3 CCTGTACTCCCA T CATGA 3 C c c
GCACTTT AAAGTGCTGGGA TACAGG
TTTCACGACCCT ATGTCC
C -----
GAM72 342 RAD51L1 1 19291 NM_133509.1 5 TCACGCCTGTAA A 3 C b b
TCCCAGCGCTTT AAAGTGCTGGGATTACAGGC TGA
TTTCGCGACCCTAATGTCCG ACT
C
GAM72 342 RBBP9 1 12889 NM_006606.2 3 TCATGCCTGTAA AA 3 C b b
TCCCAGCACT AGTGCTGGGATTACAGGCATGA
TCACGACCCTAATGTCCGTACT
--
GAM72 342 RBL1 1 3943 NM_002895.1 3 TCACGCCTCTAA G C A 3 C c c
TCCCAGGACTTT AAAGT CTGGGATTA AGGC TGA
TTTCA GACCCTAAT TCCG ACT
G C C
GAM72 342 RECQL5 1 16624 NM_004259.2 3 TCATACCTGTTA GATT C 3 C c c
TACCAGCACTTT AAAGTGCTGG ACAGG ATGA
TTTCACGACC TGTCC TACT
ATAT A
GAM72 342 RHOBTB3 1 14678 NM_014899.1 3 TCAGGCCTGTAA A 3 C b b
TCCCAGCATTTT AAAGTGCTGGGATTACAGGC TGA
TTTTACGACCCTAATGTCCG ACT
G
GAM72 342 RNO2 1 8096 3 TCATGTATGTAA A G 3 C c c
TCCTAGCACTT AAGTGCTGGGATTACA GCATGA

TTCACGATCCTAATGT TGTACT
- A
GAM72 342 RoXaN 2 1449 NM_017590.4 3 TCACACCTATAA AA C CA 3 C c c
TCCCAGCACT AGTGCTGGGATTA AGG TGA
TCACGACCCTAAT TCC ACT
-- A AC
GAM72 342 RoXaN 2 7925 NM_017590.4 3 TCACGCCAGTAA AAA A A 3 C c c
TCCCAGCAC GTGCTGGGATTAC GGC TGA
CACGACCCTAATG CCG ACT
--- A C
GAM72 342 RPL13 1 7469 NM_000977.2 3 TCACAGCTGTAA GCA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAG TGA
TTTCACGACCCTAATGTC ACT
GAC
GAM72 342 Rpo1-2 2 1072 3 TCACGCCACTAA C CA A 3 C c c
TCCCAACATTTT AAAGTG TGGGATTA GGC TGA
TTTTAC ACCCTAAT CCG ACT
A CA C
GAM72 342 Rpo1-2 2 1849 3 TCACACCCATAA C CA CA 3 C c c
TCCCAACACTTT AAAGTG TGGGATTA GG TGA
TTTCAC ACCCTAAT CC ACT
A AC AC
GAM72 342 RRP4 1 15765 NM_014285.3 3 TCACGCCTATAA A C A 3 C c c
TCCCAGCACTT AAGTGCTGGGATTA AGGC TGA
TTCACGACCCTAAT TCCG ACT
- A C
GAM72 342 S164 1 19587 XM_027330.10 5 CATGGGAATCCC A ACAGG A 3 C c c

AGCACTCC A AGTGCTGGGATT CATG
C TCACGACCCTAA GTAC
C GG--- -
GAM72 342 SAC2 1 9886 NM_014937.1 3 TCACACCTATAA C C CA 3 C c c
TCCCAACACTTT AAAGTG TGGGATTA AGG TGA
TTTCAC ACCCTAAT TCC ACT
A A AC
GAM72 342 SCYA5 2 9538 3 CACGCCTGTAAT AA - A A 3 C c c
CCCAGCTACT AGT GCTGGGATTACAGGC TG
TCA CGACCCTAATGTCCG AC
-- T C -
GAM72 342 SCYA5 2 19472 3 CTTGTAATCCCA CATGA 3 C c c
GCACTTT AAAGTGCTGGGATTACAGG
TTTCACGACCCTAATGTTC

GAM72 342 SERF1B 1 12529 NM_022978.1 3 TCATGCCTGTAA G 3 C b b
TCTGAGCACTTT AAAGTGCT GGATTACAGGCATGA
TTTCACGA TCTAATGTCCGTACT
G
GAM72 342 SFRS2IP 1 6699 NM_004719.1 5 TCACGCCTGTAT G T A 3 C c c
TCCCAGCAGTTT AAA TGCTGGGA TACAGGC TGA
TTT ACGACCCT ATGTCCG ACT

G T C

GAM72 342 SGKL 1 5761 NM_013257.3 3 TCATGCCTATAA AC-- 3 C b b
AATTCCAGCACT AAAGTGCTGGGATT AGGCATGA
TT TTTCACGACCTTAA TCCGTACT
AATA

GAM72 342 SH2D3A 1 15487 NM_005490.1 3 TCAGGCCTGTAA A 3 C b b
TCTCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACTCTAATGTCCG ACT
G

GAM72 342 SIAT4A 1 9442 NM_173344.1 3 TCACACCTGTAA CTG CA 3 C c c
TCTGAACACTTT AAAGTG GGATTACAGG TGA
TTTCAC TCTAATGTCC ACT
AAG AC

GAM72 342 SIGLEC1 1 5392 NM_052884.1 3 TCACGCCTGTGG A 3 C b b
1 TCTCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACTCTGGTGTCCG ACT
C

GAM72 342 SLC2A11 1 14546 NM_030807.2 3 TCATGACTGTAA G 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAG CATGA
TTTCACGACCCTAATGTC GTACT
A

GAM72 342 SMA3 1 5456 NM_006780.1 3 TCACGCCTGTAA G A 3 C b b
TACCAGCACTTT AAAGTGCTGG ATTACAGGC TGA
TTTCACGACC TAATGTCCG ACT
A C

GAM72 342 SMCR5 1 10816 NM_144774.1 3 TCACACTGTAAT G GCA 3 C c c
GCCAGCACTTT AAAGTGCTGG ATTACAG TGA
TTTCACGACC TAATGTC ACT
G AC-

GAM72 342 SNAPC1 1 6354 NM_003082.2 3 CATGCCTGTAAT A 3 C b b
CCCAGCATTTT AAAGTGCTGGGATTACAGGCATG
TTTTACGACCCTAATGTCCGTAC
-

GAM72 342 SPRY4 1 10205 NM_030964.2 3 TCACGCCTGTAA A 3 C b b
TCTTAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGATTCTAATGTCCG ACT
C

GAM72 342 SRGAP1 1 18079 XM_051143.3 5 TCACGCCTGTAA C A 3 C b b
TCCCAACATTTT AAAGTG TGGGATTACAGGC TGA
TTTTAC ACCCTAATGTCCG ACT
A C

GAM72 342 STX12 1 2278 NM_177424.1 3 TCACACTTGTAA C CA 3 C c c
TCCCAACACTTT AAAGTG TGGGATTACAGG TGA
TTTCAC ACCCTAATGTTC ACT
A AC

GAM72 342 SUDD 1 13818 NM_145906.1 3 TCAAACCTGTAA CA 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGG TGA
TTTCACGACCCTAATGTCC ACT
AA

GAM72 342 SYAP1 1 19134 NM_032796.2 3 TCAGGCCTGTAA A 3 C b b

TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAATGTCCG ACT
G

GAM72 342 SYNJ2BP 1 7272 NM_018373.1 3 TCATGCCTGTAA - 3 C b b
ATCCCAGCACTT AAAGTGCTGGGATT ACAGGCATGA
T TTTCACGACCCTAA TGTCCGTACT
A

GAM72 342 SYNPO2 1 9657 XM_050219.6 3 TCATGCCTGGAA A 3 C b b
TCCTAGCACTTT AAAGTGCTGGGATT CAGGCATGA
TTTCACGATCCTAA GTCCGTACT
G

GAM72 342 TBX6 1 7788 NM_004608.2 3 TCACGCATGTAA AA G A 3 C c c
TCCCAGCACT AGTGCTGGGATTACA GC TGA
TCACGACCCTAATGT CG ACT
-- A C

GAM72 342 TDG 1 16585 NM_003211.1 5 TCATGCCTGTAA AA CTG 3 C c c
TCCAACATT AGTG GGATTACAGGCATGA
TTAC CCTAATGTCCGTACT
-- AA-

GAM72 342 TDP1 1 3718 NM_018319.2 5 TCACGCCTGTCA T A 3 C b b
TCCTAGCACTTT AAAGTGCTGGGAT ACAGGC TGA
TTTCACGATCCTA TGTCCG ACT
C C

GAM72 342 TEP1 1 7532 NM_007110.3 5 TCACGCTTGTAA A 3 C b b
TCCCAGCACTTT AAAGTGCTGGGATTACAGGC TGA
TTTCACGACCCTAATGTTCG ACT
C

GAM72 342 TES 1 12134 NM_015641.2 3 CATGCCTGACCC C- ATTA A 3 C c c
ACACACTTT AAAGTG TGGG CAGGCATG
TTTCAC ACCC GTCCGTAC
AC A--- -

GAM72 342 TM7SF3 1 572 NM_016551.1 3 TCACACCTGTAA AA C CA 3 C c c
TCCCAATACT AGTG TGGGATTACAGG TGA
TCAT ACCCTAATGTCC ACT
-- A AC

GAM72 342 TNFRSF1 1 6162 NM_001066.2 3 TCACGCCTATGA C A 3 C b b
B TCCCAGCACTTT AAAGTGCTGGGATTA AGGC TGA
TTTCACGACCCTAGT TCCG ACT
A C

GAM72 342 TNFSF10 1 15311 NM_003810.2 3 TCACACCTGTAA C CA 3 C c c
TCCCAACATTTT AAAGTG TGGGATTACAGG TGA
TTTTAC ACCCTAATGTCC ACT
A AC

GAM72 342 TPM4 1 11140 NM_003290.1 3 GCCTGTAATCCC C ATGA 3 C c c
AACACTTT AAAGTG TGGGATTACAGGC
TTTCAC ACCCTAATGTCCG
A ----

GAM72 342 TRIM9 1 12950 NM_015163.3 5 CATGCCTGTAAT AAAGT A 3 C c c
CCCAGC GCTGGGATTACAGGCATG
CGACCCTAATGTCCGTAC

```
                                                -----            -
GAM72   342   TSN    1  11699  NM_004622.2  3       TCACACCTGTAA AAA          CA       3  C  c  c
                                                TCCCAGCAC     GTGCTGGGATTACAGG  TGA
                                                      CACGACCCTAATGTCC  ACT
                                                ---            AC
GAM72   342   UBCE7IP 1  504    NM_014948.1  3       TCATGCCTATTA          TAC          3  C  b  b
        5                                       TCCCAGCACTTT AAAGTGCTGGGAT   AGGCATGA
                                                      TTTCACGACCCTA   TCCGTACT
                                                            TTA
GAM72   342   UBE2B  1  19646  NM_003337.1  3       CCTGTAGTCCCA              CATGA      3  C  c  c
                                                GCACTTT     AAAGTGCTGGGATTACAGG
                                                      TTTCACGACCCTGATGTCC
                                                -----
GAM72   342   UBE2G2 1  7019   NM_003343.2  3       TCACGCCTGCAA          A   A        3  C  b  b
                                                TCCCAGCACTTT AAAGTGCTGGGATT CAGGC TGA
                                                      TTTCACGACCCTAA GTCCG ACT
                                                            C   C
GAM72   342   VDR    1  16133  NM_000376.1  3       TCACGCCTGTAA   G          A        3  C  b  b
                                                TCCCAGCAGTTT AAA TGCTGGGATTACAGGC TGA
                                                      TTT ACGACCCTAATGTCCG ACT
                                                        G           C
GAM72   342   VHL    1  11294  NM_000551.1  3       GCCTGTAATCCC              ATGA       3  C  c  c
                                                AGTACTTT    AAAGTGCTGGGATTACAGGC
                                                      TTTCATGACCCTAATGTCCG
                                                ----
GAM72   342   VPS41  1  16653  NM_014396.2  3       TCACGCCCGTAA    G       A  A        3  C  c  c
                                                TCCCAGGGCTTT AAAGT CTGGGATTAC GGC TGA
                                                      TTTCG GACCCTAATG CCG ACT
                                                         G        C  C
GAM72   342   WW45   1  16137          3       TCACTCCTGTAA              CA        3  C  b  b
                                                TCCCAGCATTTT AAAGTGCTGGGATTACAGG  TGA
                                                      TTTTACGACCCTAATGTCC  ACT
                                                            TC
GAM72   342   XRCC2  1  12295  NM_005431.1  3       TCATGCCTGTGA                    3  C  b  b
                                                TCCTAGCACTTT AAAGTGCTGGGATTACAGGCATGA
                                                      TTTCACGATCCTAGTGTCCGTACT

GAM72   342   ZFD25  1  2054   NM_016220.1  3       TCACATCTGTAA        G      CA        3  C  c  c
                                                TGCCAGCACTTT AAAGTGCTGG ATTACAGG  TGA
                                                      TTTCACGACC TAATGTCT  ACT
                                                            G       AC
GAM72   342   ZIM3   1  14398  NM_052882.1  3       ATGCCTGTAATC              GA       3  C  b  b
                                                CCAGTACTTT   AAAGTGCTGGGATTACAGGCAT
                                                      TTTCATGACCCTAATGTCCGTA
                                                --
GAM72   342   ZNF14  1  14474  NM_021030.1  3       TCATGCCTATAG          C          3  C  b  b
                                                TCCCAGCACTTT AAAGTGCTGGGATTA AGGCATGA
                                                      TTTCACGACCCTGAT TCCGTACT
                                                            A
GAM73   264   C17orf2 1  3694   NM_139177.1  3       TCCGCCCCTCCT  A    A  AACA     T      3  C  c  c
```

6 GCTCCA TG GAGCA GGG GGGCGGA
AC CTCGT CCT CCCGCCT
- - C--- -

GAM73 264 GAB2 1 18529 NM_080491.1 3 ATCCGCCCTCTG TGA G ACA 3 C c c

TTGCTC GAGCAA GGA GGGCGGAT
CTCGTT TCT CCCGCCTA
--- G ---

GAM73 264 LOC1442 1 10663 XM_084786.1 5 ATCCACCCTTAT GGAAC C 3 C c c

48 TTGCTCTCA TGAGAGCAAG AGGG GGAT
ACTCTCGTTT TCCC CCTA
AT--- A

GAM73 264 LOC1970 1 7418 3 ATCTGCTCCCCT CA- AACA 3 C c c
03 CAACTCTCA TGAGAG AGGG GGGCGGAT
ACTCTC TCCC CTCGTCTA
AAC ----

GAM73 264 MSN 1 8419 NM_002444.1 3 CCCCCACCCCTT AACA C AT 3 C c c
GCTCTCA TGAGAGCAAGGG GGG GG
ACTCTCGTTCCC CCC CC
CA-- - --

GAM73 264 RPH3A 1 13411 NM_014954.1 3 CCTAGCCTCACC AACA -- AT 3 C c c
CCCTTGCTCTCA TGAGAGCAAGGG GGGC GG
ACTCTCGTTCCC TCCG CC
CCAC AT --

GAM73 264 STK29 1 15075 NM_003957.1 3 CCGCGCCTCCCT A ACA - AT 3 C c c
TGCCTCA TGAG GCAAGGGA GG GCGG
ACTC CGTTCCCT CC CGCC
- --- G --

GAM73 264 TRPC5 1 6129 NM_012471.1 3 ATCTGTAATTTC CAGG 3 C c c
CTTGCTCTCA TGAGAGCAAGGGAA GCGGAT
ACTCTCGTTCCTTT TGTCTA
AA--

GAM74 254 DKFZp43 1 3282 3 AGGAGCATTGCT CAGTT - G 3 C c c
4G171 TGAA TTCAGGCAA TG TCCT
AAGTTCGTT AC AGGA
----- G -

GAM74 254 FBXO9 1 12849 NM_033481.1 3 AGGAGAATTGCC CAGT G G 3 C c c

TGAG TTCAGGCAA TT TCCT
GAGTCCGTT AA AGGA
---- G -

GAM74 254 FGFRL1 1 2185 NM_021923.2 3 AGGACATGCTGC ACA T G 3 C c c
CTGAA TTCAGGCA GT TGTCCT
AAGTCCGT CG ACAGGA
--- T -

GAM74 254 FLJ0002 1 16152 XM_033361.2 3 CAGGTAGATTCT AC T 3 C c c
4 GCCTGAA TTCAGGCA AGTTTG CCTG
AAGTCCGT TTAGAT GGAC
C- -

GAM74 254 FLJ1113 1 3962 3 CAGGACTCGTTC AC TTT-- 3 C c c
6 TACTGCCTGGA TTCAGGCA AG GTCCTG
AGGTCCGT TC CAGGAC
CA TTGCT
GAM74 254 FLJ1289 1 1091 NM_024950.1 5 CAGGACAAGCCA T CAACA 3 C c c
1 CCTGA TCAGG GTTTGTCCTG
AGTCC CGAACAGGAC
- AC---
GAM74 254 FLJ1319 1 12499 NM_022906.1 3 CAGGACAAGCTG GCAA 3 C c c
5 ACTGAA TTCAG CAGTTTGTCCTG
AAGTC GTCGAACAGGAC
A---
GAM74 254 FLJ1414 1 11084 NM_024709.1 3 AGGGGCTGTTGC G TTG G 3 C c c
6 TGAA TTCAG CAACAGT TCCT
AAGTC GTTGTCG GGGA
- --- -
GAM74 254 FLJ2021 1 2327 NM_017713.1 3 AGGAGAATTGCC CAGT G G 3 C c c
1 TGAA TTCAGGCAA TT TCCT
AAGTCCGTT AA AGGA
---- G -
GAM74 254 HLCS 1 10828 NM_000411.3 3 CAGGCTGACGTT T A T T 3 C c c
GCCTGA TCAGGCAAC GTT G CCTG
AGTCCGTTG CAG C GGAC
- - T -
GAM74 254 KIAA097 1 1934 NM_014929.1 3 CAGGATGTTTGT A TT 3 C c c
1 TGCCAGAA TTC GGCAACAG TGTCCTG
AAG CCGTTGTT GTAGGAC
A T-
GAM74 254 LOC1479 1 11680 XM_085932.5 5 CAGGCACTATTG C TT T 3 C c c
20 CCTGGA TTCAGGCAA AGT G CCTG
AGGTCCGTT TCA C GGAC
A -- -
GAM74 254 LOC1582 1 7124 XM_088517.1 3 CAGGATGGGAGC GCAA -- 3 C c c
30 TGCTGAA TTCAG CAGTTT GTCCTG
AAGTC GTCGAG TAGGAC
---- GG
GAM74 254 LOC1649 1 7799 XM_092265.4 5 CAGGACCTGCTC AC TT 3 C c c
55 CTGCCTGAA TTCAGGCA AGT GTCCTG
AAGTCCGT TCG CAGGAC
CC TC
GAM74 254 LOC1959 1 12998 XM_113625.3 3 CAGGCTTTTGTT G TTT T 3 C c c
77 GCTGAA TTCAG CAACAG G CCTG
AAGTC GTTGTT C GGAC
- TT- -
GAM74 254 LOC2207 1 1233 3 CAGGACTGGATC CA-- - 3 C c c
76 CCATTGCCTGGA TTCAGGCAA GTTT GTCCTG
AGGTCCGTT TAGG CAGGAC
ACCC T
GAM74 254 LOC2575 1 18100 5 AGGTAAATTGTC CA T G 3 C c c
76 CTGAA TTCAGG ACAGTTTG CCT

AAGTCC TGTTAAAT GGA
-- - -

GAM74 254 LOC9284 1 13076 NM_138393.1 3 CAGCACTACTGG A TT C 3 C c c
0 TGCCTGAA TTCAGGCA CAGT GT CTG
AAGTCCGT GTCA CA GAC
G T- C

GAM74 254 LTBR 1 2499 NM_002342.1 3 CAGGACTCTCCC AC TTT-- 3 C c c
TACTGCCTGAG TTCAGGCA AG GTCCTG
GAGTCCGT TC CAGGAC
CA CCTCT

GAM74 254 MGC1442 1 9928 NM_032903.1 3 CAGGACAACACT GCAAC - 3 C c c
5 TCTACTGAA TTCAG AGT TTGTCCTG
AAGTC TCA AACAGGAC
ATCT- C

GAM74 254 MGC1603 1 6563 NM_032887.1 3 CAGCCTGGCCAA ACA T --- 3 C c c
7 CTGCCTGAA TTCAGGCA GTT GTC CTG
AAGTCCGT CAA CGG GAC
--- C TCC

GAM74 254 P53AIP1 1 13522 NM_022112.1 3 CAGGACAACTGG A-- T 3 C c c
CCTGCCTGAG TTCAGGCA CAGTT GTCCTG
GAGTCCGT GTCAA CAGGAC
CCG -

GAM74 254 PRC1 1 14663 NM_003981.1 3 CAGGACAGCCTT CAAC T 3 C c c
CCTCCTGAA TTCAGG AG TTGTCCTG
AAGTCC TC GACAGGAC
TCCT C

GAM74 254 RYBP 1 15729 NM_012234.3 5 CAGGACAAAGAG CAACAG 3 C c c
AAACCTGAG TTCAGG TTTGTCCTG
GAGTCC AAACAGGAC
AAAGAG

GAM74 254 SLC37A1 1 6854 NM_018964.2 3 CAGGAACTGCTG A TTG 3 C c c
CCTGAG TTCAGGCA CAGT TCCTG
GAGTCCGT GTCA AGGAC
C ---

GAM74 254 SLC38A5 1 1536 NM_033518.1 5 CAGGCCTCTCTG AC TTT T 3 C c c
CCTGAA TTCAGGCA AG G CCTG
AAGTCCGT TC C GGAC
C- TC- -

GAM74 254 SLC7A6 1 11061 NM_003983.1 3 AGGCTGACTTGC AC T T G 3 C c c
CTGAA TTCAGGCA AGTT G CCT
AAGTCCGT TCAG C GGA
-- T - -

GAM74 254 SMA3 1 6849 NM_006780.1 3 CAGGAAGAATTG ACA G 3 C c c
CTTGAA TTCAGGCA GTTT TCCTG
AAGTTCGT TAAG AGGAC
--- A

GAM74 254 SPOCK 1 10327 NM_004598.2 3 CAGTCGGCATTG CAGTT -- 3 C c c
CCTGAA TTCAGGCAA TGTC CTG
AAGTCCGTT ACGG GAC

```
                                                  -----  CT
GAM74   254   THY1   1  7884  NM_006288.2  3       CAGGCATGGCTG       A   - T          3  C  c  c
                                  GTGCCTGAA   TTCAGGCA CAGTT TG CCTG
                                        AAGTCCGT GTCGG AC GGAC
                                           G    T -
GAM74   254   UBTF   1  14273 NM_014233.1  3       CAGGAAGGAGCT       ACA   G-          3  C  c  c
                                  GCCTGGA     TTCAGGCA   GTTT  TCCTG
                                        AGGTCCGT   CGAG  AGGAC
                                           ---   GA
GAM75   210   ADCY7  1  15427 NM_001114.1  3       GCAAGAAGGCGG CA       GG   C  C        3  C  c
c
                                  GGAGCAG       CTGCTCTCC  GCCT TC TGC
                                        GACGAGGGG  CGGA AG ACG
                                        --        --   - A
GAM75   210   BPESC1 1  12031 NM_021812.1  3       GCAAGAGTTCTG    G    -- GC   CC       3  C  c
c
                                  TGGAGAGAGTG  CACT CTCTCC  GG  CTCT  TGC
                                        GTGA GAGAGG  TC  GAGA  ACG
                                           -     TG  TT   --
GAM75   210   C22orf3 1  12551 NM_012265.1  3       GCAGGAGAGGCC CAC    CTCC             3  C  c
c
                                  CCCCAGCA       TGCT    GGGCCTCTCCTGC
                                           ACGA    CCCGGAGAGGACG
                                        ---   CCC-
GAM75   210   CMRF-35 1  5740  XM_046925.4  3       GCAGGGCTGGGG CA        -    ---       3  C  c  c
        H                          GCTCCGGAGAGC   CTGCTCTCCGG GCCTCT   CCTGC
                                  AG          GACGAGAGGCC CGGGGG   GGACG
                                        --         T     TCG
GAM75   210   CREBL2 1  4609  NM_001310.2  3       CAGGAGCAGGGA C      CCGGG   -    C      3  C  c
 c
                                  AGAGCAGT     ACTGCTCT     CCT CTCCTG
                                           TGACGAGA     GGA GAGGAC
                                        -       AG---  C     -
GAM75   210   D123   1  17716          5       GCAGGAGAGGGA CA    T  CCGGG            3  C  c  c
                                  AAGGCAG       CTGC CT     CCTCTCCTGC
                                           GACG GA     GGAGAGGACG
                                        --    -  AAG--
GAM75   210   ENG    1  2762  NM_000118.1  3       GCAGGAGAGACT CA     TCC  GC           3  C  c  c
                                  GAGCAG       CTGCTC   GG  CTCTCCTGC
                                           GACGAG   TC  GAGAGGACG
                                        --     --- A-
GAM75   210   FLJ1493 1  2656  NM_032864.2  3       CAGGAGAATTAG    G     GGGCC     C      3  C  c
c
        6                          GAGAGAGTG    CACT CTCTCC     TCTCCTG
                                           GTGA GAGAGG     AGAGGAC
                                           -     ATTA-      -
GAM75   210   FLJ3233 1  16169 NM_144641.1  3       CAGTCAGGGCCA        CG    CTC   C      3  C  c
c
        2                          AGAGAGCAGTG  CACTGCTCTC  GGCCT   CTG
                                           GTGACGAGAG  CCGGG   GAC
```

AA ACT -
GAM75 210 GCK 1 4463 NM_000162.2 3 GCTCAAGAGGCC C C CCT 3 C c c
CAGGGAGCAATG CA TGCTCTC GGGCCTCT GC
GT ACGAGGG CCCGGAGA CG
A A ACT
GAM75 210 GORASP1 1 17619 NM_031899.2 3 CAGGAGGGAGAG - CGGG T C 3 C c c
AGAGGCAGTG CACTGC TCTC CC CTCCTG
GTGACG AGAG GG GAGGAC
G AGA- - -
GAM75 210 LANP-L 1 11358 5 GCAGGAAAGGGA C GGG-- C 3 C c c
AAAGGAGAGTAG ACTGCTCTCC CCT TCCTGC
T TGATGAGAGG GGA AGGACG
- AAAAG A
GAM75 210 LOC1430 1 1402 5 GCAGGGTGTCCG CT T 3 C c c
98 GAGAGCGGTG CACTGCTCTCCGGGC C CCTGC
GTGGCGAGAGGCCTG G GGACG
T- -
GAM75 210 LOC1459 1 14081 XM_085290.7 5 CAGGGGGCCCAA C CC T T C 3 C c c
88 GGAGCAGT ACTGCTCT GGGCC C CCTG
TGACGAGG CCCGG G GGAC
- AA - - -
GAM75 210 LOC1999 1 13578 3 GCAGATACCACC T CCTCTC 3 C c c
36 CGGAGGCAGTG CACTGC CTCCGGG CTGC
GTGACG GAGGCCC GACG
- ACCATA
GAM75 210 LOC2215 1 3621 5 GCAGGAGCATCA CA C CCT-- 3 C c c
83 CCCAGAGAGCAG CTGCTCTC GGG CTCCTGC
GACGAGAG CCC GAGGACG
-- A ACTAC
GAM75 210 LOC2563 1 5809 3 GCAGGAGGAGGA CA CCGGG - 3 C c c
10 AGAGCGG CTGCTCT CCTC TCCTGC
GGCGAGA GGAG AGGACG
-- A---- G
GAM75 210 LOC9334 1 4761 NM_138402.2 3 GCAGTGTGATCC C CC TC- 3 C c c
9 AGAGAGCAGTG CACTGCTCTC GGG TC CTGC
GTGACGAGAG CCT AG GACG
A -- TGT
GAM75 210 MMP13 1 15931 NM_002427.2 3 CAGGAGACAAAA CCGGGCC C 3 C c c
GAGCAGTG CACTGCTCT TCTCCTG
GTGACGAGA AGAGGAC
AAAC--- -
GAM75 210 OSBPL5 1 10114 NM_145638.1 3 CAGCCAGGCCAC CA - CTC C 3 C c c
GGAGAGCAG CTGCTCTCCG GGCCT CTG
GACGAGAGGC CCGGA GAC
-- A CC- -
GAM75 210 RAD52 1 8804 NM_002879.2 3 CAGGAAAAAGGT CCG C-- C 3 C c c

TGGAGCAGTG CACTGCTCT GGCCT TCCTG
GTGACGAGG TTGGA AGGAC
--- AAA -

GAM76 292 ARHGEF5 1 1425 NM_005435.2 3 TCATGGCAAGGG T GAACAC 3 C c c

CTGGCCCCA TGGGGTCA GCC CCATGA
ACCCCGGT CGG GGTACT
- GAAC--

GAM76 292 CHRNB4 1 13256 NM_000750.1 5 TCACGGGTGCCC GCCGAA A 3 C c c

TGTGACCCCA TGGGGTCAT CACCC TGA
ACCCCAGTG GTGGG ACT
TCCC-- C

GAM76 292 FLJ1045 1 15495 NM_018095.2 5 TCGTGAGGTGAG CGAA - 3 C c c
0 CGTGATCCTA TGGGGTCATGC CACC CATGA
ATCCTAGTGCG GTGG GTGCT
A--- A

GAM76 292 FLJ2197 1 15840 NM_032213.2 3 TCATGAGGTGGG G GAA - 3 C b b
7 ATGGCCCCA TGGGGTCAT CC CACC CATGA
ACCCCGGTA GG GTGG GTACT
- --- A

GAM76 292 HD 1 4994 NM_002111.3 5 TCATGCTGGCCG T AA CC 3 C c c
GCGTGGCCCC GGGGTCATGCCG CA CATGA
CCCCGGTGCGGC GT GTACT
- CG C-

GAM76 292 KIAA051 1 7751 NM_014732.1 3 CATGGGCCCGGG T GAACA A 3 C c c

3 GCCTGACCCCA TGGGGTCA GCC CCCATG
ACCCCAGT CGG GGGTAC
C GGCCC -

GAM76 292 KIAA132 1 9539 XM_029429.5 3 TCACAGGTGCTC -- C A CA 3 C c c
8 TGCTCGTGGCCC TGGGGTCAT GC GA CACC TGA
CA ACCCCGGTG CG CT GTGG ACT
CT T C AC

GAM76 292 LOC1443 1 17369 3 TCATGGGTGTTA T T CG-- 3 C c c
05 CCTGCTGGCCCT GGGGTCA GC AACACCCATGA
TCCCGGT CG TTGTGGGTACT
- - TCCA

GAM76 292 LOC1463 1 16285 NM_174903.1 5 TCATGGGTGGCG GAA 3 C c c
10 GGTATGATCTCA TGGGGTCATGCC CACCCATGA
ACTCTAGTATGG GTGGGTACT
GCG

GAM76 292 LOC1482 1 12443 3 TCATGGGTGCCT T TGCC A- 3 C c c
23 CCTGCCCCA TGGGG CA GA CACCCATGA
ACCCC GT CT GTGGGTACT
- C--- CC

GAM76 292 LOC1624 1 9518 3 CATGCCAGCTGG GAACACC A 3 C c c
17 GCATGACCCCA TGGGGTCATGCC CATG
ACCCCAGTACGG GTAC
GTCGACC -

GAM76 292 LOC2205 1 18814 5 TCGTGGGCCGCG T - AACA 3 C c c
65 CATGGCCCT GGGGTCATGC CG CCCATGA
TCCCGGTACG GC GGGTGCT
- C C---
GAM76 292 LOC2547 1 18587 3 TCATGGCCATTT G CAC 3 C c c
78 GGCATGATTGCA TG GGTCATGCCGAA CCATGA
AC TTAGTACGGTTT GGTACT
G ACC
GAM76 292 LYPLA2 1 2075 NM_007260.2 3 TCATGAATGTGG T - GA CC 3 C c c
CCATGGCCCC GGGGTCATG CC ACA CATGA
CCCCGGTAC GG TGT GTACT
- C -- AA
GAM76 292 PRTN3 1 15181 NM_002777.2 5 TCGTGGGTGCAC ATGCCGAA 3 C c
c
CCTGGACCCCA TGGGGTC CACCCATGA
ACCCCAG GTGGGTGCT
GTCCCAC-
GAM76 292 SC65 1 6668 NM_006455.1 3 CATGGGTGCTGC CAT CGAA A 3 C c c

ACCCCA TGGGGT GC CACCCATG
ACCCCA CG GTGGGTAC
--- TC-- -
GAM76 292 SMTN 1 16350 NM_134269.1 3 TCATGGGCAAGA T CGAACA 3 C c c

AGCCTGACCCCA TGGGGTCA GC CCCATGA
ACCCCAGT CG GGGTACT
C AAGAAC
GAM77 390 FLJ1259 1 16765 NM_024994.1 3 ATCTTGCAGTGC CA TGA 3 C c c
5 TGCAACCTGGA TTCAGGT CA GTTGCAAGAT
AGGTCCA GT TGACGTTCTA
AC CG-
GAM77 390 LOC1497 1 17357 5 ATCTTGGCCAAT A GA TG 3 C c c
11 GTGACCCGAA TTC GGTCACAT GT CAAGAT
AAG CCAGTGTA CG GTTCTA
C AC --
GAM77 390 RRAS 1 7350 NM_006270.2 3 CTTGCTGTGTGA AGTT AT 3 C c c
CCTGAG TTCAGGTCACATG GCAAG
GAGTCCAGTGTGT CGTTC
---- --
GAM77 390 SLC26A7 1 8226 NM_052832.2 3 ATCTAGTGCTCA CA T A 3 C c c
CATGATCTGAA TTCAGGTCA TGAGT GC AGAT
AAGTCTAGT ACTCG TG TCTA
AC - A
GAM78 277 GOSR2 1 5872 NM_054022.1 3 CTAGTTTGGAAT C CTTA 3 C c c
AAAAATTGCAGA TCTGCAATT TTATTCT TAG
AGACGTTAA AATAAGG ATC
A TTTG
GAM78 277 MRPL13 1 11681 NM_014078.3 3 GAGAATAAGAAT TTATAG 3 C c c
TGCAGA TCTGCAATTCTTATTCTC
AGACGTTAAGAATAAGAG

```
                                                                  ------
GAM79   352   FLJ1137 1   18758 NM_024961.1  3       TGCATGGACCCG      G  ACATGA      C       3  C  c
c
          0                          GTGCAA      TTGCAC CGG      CCATGCA
                                            AACGTG GCC      GGTACGT
                                              -  CA----       -
GAM79   352   NPTXR  1   16236 NM_058178.1  3       GTGCATGGTCCT     AC  GGA  T            3  C  c  c

                                    GGGGCAGCAA   TTGC  GC   CA GACCATGCAC
                                            AACG  CG   GT CTGGTACGTG
                                              A-  GG-  C
GAM80   362   LOC1322 1   15123 XM_059583.7  5       AACATGTCTCGG        T  AC       C       3  C  c  c
          41                          CCCCTGTCCCC  GGGGACAGG GT  AGACATGTT
                                            CCCCTGTCC CG  TCTGTACAA
                                               C  GC       -
GAM80   362   SYK    1   7456  NM_003177.2  3       GAACATGCCCAC   -     GTACAGA          3  C  c  c
                                    AACTTGTCACCC GGG GACAGGT      CATGTTC
                                            CCC CTGTTCA      GTACAAG
                                              A      ACACCC-
GAM81   256   CNTFR  1   13128 NM_001842.3  3       ACCCCATGAGGA  A      -    -  T       3  C  c  c
                                    CATGCAGAGCAC AG TGCTCTGC TGTCCT GTG GGT
                                    CT         TC ACGAGACG ACAGGA TAC CCA
                                              C       T     G   C
GAM81   256   LOC2211 1   17596          5       CCACACAGAACC   A   C  CT  C      T      3  C  c  c
          91                           AAGCACT     AG TGCT TG  GT CTGTGTGG
                                            TC ACGA AC  CA GACACACC
                                              -   -  --  A       -
GAM81   256   LOC2215 1   7033           5       ACCACACCTTGC   A      - TCCT-          3  C  c  c
          35                           CATGCAGAGCAC AG TGCTCTGC TG    GTGTGGT
                                    CT         TC ACGAGACG AC     CACACCA
                                              C       T  CGTTC
GAM81   256   SLC25A1 1   13421 NM_003562.2  3       CACACAGGACAG A   GC          GT       3  C  c  c

          1                          CAGAAGATC     GAT  TCTGCTGTCCTGTGTG
                                              CTA  AGACGACAGGACACAC
                                            -  GA             --
GAM82   333   ADAMTS5 1   9498  NM_007038.1  3       ACCTTTCCATTG   C      - TGAT          3  C  c  c
                                    TTGCATCTT    AAG TGCAACAA GG    AAAGGT
                                            TTC ACGTTGTT CC    TTTCCA
                                              T       A  ----
GAM82   333   CSNK2A1 1   8339  NM_177560.1  3       ACCCTCTCCTTG       A    T  TAAA        3  C  c  c
                                    ATGCAGCTT    AAGCTGCA CAAGG GA    GGT
                                            TTCGACGT GTTCC CT    CCA
                                               A    T  C---
GAM82   333   KLHL4  1   11049 NM_019117.3  3       ACCTTTATCGCC      CAACAA            3  C  c  c
                                    AATGCACAGCTT AAGCTG     GGTGATAAAGGT
                                            TTCGAC     CCGCTATTTCCA
                                               ACGTAA
GAM82   333   LOC1386 1   8881           5       CCTTTCATCCTA       ACA  -  TA   T      3  C  c  c
          39                           TGCAGCTT    AAGCTGCA   AGG TGA  AAGG
```

TTCGACGT TCC ACT TTCC
A-- T -- -

GAM83 287 ACE 1 2830 NP_690044.1 3 141 CGTGGGCCGCCA T TGT - 1 A c c
GATCTGCACCAC AAGGTGGTG CA TTTGG GG
CTTCGAGC TTCCACCAC GT AGACC CC
- CT- G

GAM83 287 ANP32E 2 11390 NP_112182.1 3 316 CCCATAATTAAA GT ------ 1 A c c
ACATGATCACTT AAGGTG GTCATGTTT TGGG
TTACACAG TTTCAC TAGTACAAA ACCC
-- ATTAAT

GAM83 287 ANP32E 2 16172 NP_112182.1 3 1737 GGAATCCCCAAA G ATG 1 A c
c
AAGATAACATTT AAGGTG TGTC TTTTGGGG
TTCTTCTG TTTTAC ATAG AAAACCCC
A A--

GAM83 287 AP3M2 1 17766 NP_006794.1 3 841 TTCTAACCCAAA T TCA----- 1 A c c
ACAGTTCTACTC AAGG GGTG TGTTTTGGG
ACTTCCTT TTCC TCAC ACAAAACCC
T TCATCTTG

GAM83 287 ARHGEF1 1 6308 NP_056128.1 3 2806 GTAATTTAACAT - TT- 1 A c c
2 CATGATTACCAC AAGGTGGTG TCATG TTGGG
CTTCGAAG TTCCACCAT AGTAC AATTT
T TAC

GAM83 287 ASPH 1 11418 NP_064549.1 3 496 CTCCCCAGGCTC T-- T- 1 A c c
ATGTGCCACCAC AAGGTGGTG CATG TTTGGGG
CTTCCCTC TTCCACCAC GTAC GGACCCC
CGT TC

GAM83 287 ASPH 1 11418 NP_115856.1 3 496 CTCCCCAGGCTC T-- T- 1 A c c
ATGTGCCACCAC AAGGTGGTG CATG TTTGGGG
CTTCCCTC TTCCACCAC GTAC GGACCCC
CGT TC

GAM83 287 ATP1B3 1 9521 NP_001670.1 3 96 TCCATTCTAGAA G - 1 A c c
TTATGAGACCAC AAGGTGGT TCATG TTTTGGGG
CTTGGAGA TTCCACCA AGTAT AAGATCTT
G T

GAM83 287 ATP2C1 1 9108 NP_055197.1 3 290 TTAAAAAGGCAA G T GG 1 A c c
AACCTGAACCAC AAGGTGGT TCA GTTTTG
CTTCTGCA TTCCACCA AGT CAAAAC
- C GG

GAM83 287 BACH2 1 13836 NP_068585.1 3 5262 TGAGCCATTCAA CA 1 A c c
GGCAAGCACCAC AAGGTGGTGT TGTTTTGGG
CTTTGCTA TTCCACCACG ACGGAACTT
A-

GAM83 287 BHC80 1 7380 NP_057705.2 5 176 AGTTTCCCCAAA ---- T- AT 1 A c c
ATTGGACTTCTC AAGGT GG GTC GTTTTGGGG
AGAACCTT TTCCA TC CAG TAAAACCCC
AGAC TT GT

GAM83 287 C14orf2 1 831 NP_775878.1 3 1824 AATAGTTCTAAA -- GT- 1 A c c
4 ACATGCTAACCT AAGGT GGT CATGTTTTGGGG
GACCTTTT TTCCA CCA GTACAAAATCTT

GT ATC

GAM83 287 C14orf3 1 10766 NP_777638.1 3 91 TTATTGCTTAAA TG G- 1 A c c
9 ACATGAAGACTG AAGG GT TCATGTTTTGGG
CTTTCTTT TTTC CA AGTACAAAATTC
GT GA

GAM83 287 C14orf7 1 11042 XP_290629.1 3 357 ATACCCAACAGA TGGT -- 1 A c c
8 ACATGACTGTTT AAGG GTCATGTTTTG GGG
CTTTGAGG TTCT CAGTACAAGAC CCC
TTGT AA

GAM83 287 C21orf5 1 15819 NP_060303.1 5 83 GACCTCCCTTGC - TTTT 1 A c c
5 CATGATAACCAC AAGGTGGT GTCATG GGGG
CTTCGCAG TTCCACCA TAGTAC TCCC
A CGT-

GAM83 287 C5orf4 2 2131 NP_115761.1 3 1200 CCACCTCCATGG G T -- 1 A c c
GACTGACACCAT AA GTGGTGTCA GTTT TGGGG
GTTCAAGC TT TACCACAGT CAGG ACCTC
G - GT

GAM83 287 C5orf4 2 16902 NP_057432.1 5 200 ACCATCTCCCAC - TTT 1 A c c
TGTGGCTACCAC AAGGTGGT GTCATG TGGGG
CTTCCCTT TTCCACCA CGGTGT ACCCT
T C--

GAM83 287 C5orf4 2 16902 NP_115761.1 3 306 ACCATCTCCCAC - TTT 1 A c c
TGTGGCTACCAC AAGGTGGT GTCATG TGGGG
CTTCCCTT TTCCACCA CGGTGT ACCCT
T C--

GAM83 287 CASP10 1 18232 NP_116756.1 3 103 GGAAACCTCCCT CA TTT 1 A c c

TTACAGCACCAC AAGGTGGTGT TGT GGGG
CTTGCGAT TTCCACCACG ACA TCCC
-- TT-

GAM83 287 CCKBR 1 6458 NP_000722.2 3 243 TGGCCCATAGAA - --- 1 A b b
ACATGACACTGA AAGGT GGTGTCATGTTT TGGG
CCTTGGAG TTCCA TCACAGTACAAA ACCC
G GAT

GAM83 287 CCKBR 1 6458 NP_795344.1 3 243 TGGCCCATAGAA - --- 1 A b b
ACATGACACTGA AAGGT GGTGTCATGTTT TGGG
CCTTGGAG TTCCA TCACAGTACAAA ACCC
G GAT

GAM83 287 COLQ 1 9718 NP_536803.1 3 286 TGAACACCCAAA TG TCA 1 A c c
ACGCCATTGCCT AAGG GTG TGTTTTGGG
TCCGCAGA TTCC TAC GCAAAACCC
GT C--

GAM83 287 COLQ 1 9718 NP_536804.1 3 34 TGAACACCCAAA TG TCA 1 A c c
ACGCCATTGCCT AAGG GTG TGTTTTGGG
TCCGCAGA TTCC TAC GCAAAACCC
GT C--

GAM83 287 CR1 1 10491 NP_000564.1 3 822 GTCCGCCTCCCG TGT 1 A c c
GGTTGACACCAT AAGGTGGTGTCA TTTGGGG
TTTCCTGC TTTTACCACAGT GGGCCCT
T--

GAM83 287 CX3CR1 1 10405 NP_001328.1 3 444 CCCCCAGACTTT G ---- 1 A c c
ACATGACACAGC AAGGT GTGTCATGT TTTGGGG
TTTATCAC TTTCG CACAGTACA AGACCCC
A TTTC
GAM83 287 CYLD 1 11043 NP_056062.1 5 260 ATCTTAATACAA G - --- 1 A c c
CATGGACACCAC AA GTGGTGTC ATGTT TTGGGG
GTTGCTGA TT CACCACAG TACAA AATTCT
G G CAT
GAM83 287 DHCR24 1 14070 NP_055577.1 3 142 CCCACCCTGACA CAT - TG 1 A c
c
GCCCAACACCAC AAGGTGGTGT GTT T GGG
CTTCCTCC TTCCACCACA CGA A CCC
ACC C GT
GAM83 287 DIRAS2 2 14097 NP_060064.2 3 71 CTCACTCCCCCA AA---- - GT 1 A c c
AAATGACACCCA GGTGG TGTCAT TTTGGGG
CCGTCGTC CCACC ACAGTA AAACCCC
CTGCTG C --
GAM83 287 DIRAS2 2 16186 NP_060064.2 3 71 CACTCCCCCAAA AA------ - GT 1 A c c
ATGACACCCACC GGTGG TGTCAT TTTGGGG
GTCGTCAG CCACC ACAGTA AAACCCC
GACTGCTG C --
GAM83 287 DKFZp54 1 2790 NP_115531.1 5 238 CACCTGCCCAAA G CAT-- 1 A c c
7I094 ACCAAACGCAGC AAGGTG TGT GTTTTGGG
ATCTTCCC TTCTAC ACG CAAAACCC
G CAAAC
GAM83 287 DKFZP56 1 1156 XP_166254.2 3 3186 CATCCTCAGCCC TCAT TTT 1 A c
c
4O0423 CTCTGCCACCAC AAGGTGGTG GT GGGG
CTTAAATA TTCCACCAC CG CCCC
---- TCT
GAM83 287 DKFZP58 1 12701 XP_291242.1 3 63 TCTACTTTTACA GTCATGTT 1 A c
c
6F2423 TCCCCAAACCAC AAGGTGGT TTGGGG
CTTTGTCA TTCCACCA AACCCC

GAM83 287 DKFZp76 1 19365 NP_775734.1 3 2427 CTACAGTTCTGA - T 1 A c c
1B107 GCATGACACTAG AAGG TGGTGTCATGTTT GGG
CCTTCTCT TTCC ATCACAGTACGAG CTT
G T
GAM83 287 E2F3 1 13295 NP_001940.1 3 1826 TGGGGTCAAGAC - - -- G 1 A c c
AGATGACACCAG AAG G TGGTGTCA TGTTTTGG
CACTTTAA TTC C ACCACAGT ACAGAACT
A G AG G
GAM83 287 EDG2 1 10299 NP_001392.2 3 976 ATATCACAACCC GTCATG 1 A c c
AGAAGTAACCAC AAGGTGGT TTTTGGG
CTTTAAAA TTCCACCA AAGACCC
ATG---
GAM83 287 EDG2 1 10299 NP_476500.1 3 976 ATATCACAACCC GTCATG 1 A c c

AGAAGTAACCAC AAGGTGGT TTTTGGG
CTTTAAAA TTCCACCA AAGACCC
ATG---

GAM83 287 FKBP2 1 11911 NP_004461.2 3 175 CTCAGCTCCAGC TCA T 1 A c c
ATACCCCACCAC AAGGTGGTG TGT TTGGGG
CTTCTCCT TTCCACCAC ATA GACCTC
CCC C

GAM83 287 FKBP2 1 11911 NP_476433.1 3 175 CTCAGCTCCAGC TCA T 1 A c c
ATACCCCACCAC AAGGTGGTG TGT TTGGGG
CTTCTCCT TTCCACCAC ATA GACCTC
CCC C

GAM83 287 FLJ1094 1 3221 NP_060750.1 3 919 GATGCTCAGACT TGT-- 1 A c c
5 CCCTGATACCAC AAGGTGGTGTCA TTTGGG
CTTTCCTG TTCCACCATAGT AGACTC
CCCTC

GAM83 287 FLJ1173 1 13471 NP_073593.1 3 319 GTCTCCCCCAAA G T--- 1 A c c
0 ACTGGCTGGCAC AAG TGGTGTCA GTTTTGGGG
CAGCTTCA TTC ACCACGGT CAAAACCCC
G CGGT

GAM83 287 FLJ1187 1 18221 NP_079393.1 3 1432 AGACCACTCAAA - - --- 1 A c c
1 ACATGCTTACAC AAG GT GGTGT CATGTTTTGGG
TAACACTT TTC CA TCACA GTACAAAACTC
A A TTC

GAM83 287 FLJ1242 1 7079 XP_098290.1 3 2103 TTTTTAAACAAA GG GG 1 A c c
5 ACATGACAACCT AAGGT TGTCATGTTTTG
TGGCTTTT TTCCA ACAGTACAAAAC
-- AA

GAM83 287 FLJ1252 1 17806 NP_079087.2 3 1844 TTTGTTTTTACT GTTT 1 A c c
9 CAATGACACCAT AAGGTGGTGTCAT TGGG
TTTTAGTT TTTTACCACAGTA ACTC

GAM83 287 FLJ1308 1 10552 NP_079229.1 3 56 CTCTGCAACAGA GG 1 A c c
9 ATATGACACCAT AAGGTGGTGTCATGTTTTG
CTTCCCAG TTCTACCACAGTATAAGAC
AA

GAM83 287 FLJ1384 1 19252 NP_079047.1 3 2176 TTCATTTCCAAA TGTC 1 A c c
8 ACATCCATCTTT AAGGTGG ATGTTTTGGGG
CTCCACTT TTCTACC TACAAAACCTT

GAM83 287 FLJ1472 1 14879 NP_116218.1 3 753 GCACCTTGTCCA ATG 1 A c c
1 AGGAGACACCAC AAGGTGGTGTC TTTTGGG
TTTCACCC TTTCACCACAG GGAACCT
A--

GAM83 287 FLJ2085 1 3537 NP_079419.1 5 425 CTCTTCCCCAAA CAT 1 A c c
6 ATCCAGCACCAC AAGGTGGTGT GTTTTGGGG
CTTGGTTA TTCCACCACG TAAAACCCC
ACC

GAM83 287 FLJ2115 1 485 NP_078878.1 3 626 TCTCAACACACA T ----- T 1 A c c
6 AAGTGCCACCAC AAGGTGGTG CA TGT TTGGGG
CTTCCCTG TTCCACCAC GT ACA AACTCT

C GAAAC C

GAM83 287 FLJ2351 1 11473 NP_079001.2 3 144 ATTTTGTTTAAA GT 1 A c c
8 ACATGATTATCT AAGGTG GTCATGTTTTGGG
TAATTCCT TTCTAT TAGTACAAAATTT
--

GAM83 287 FLJ2553 1 1034 NP_694966.2 3 2017 ATGACTTCCTCA T T 1 A b b
4 AACTGACACCAT AAGGTGGTGTCA GTTT GGGG
CTTAATTA TTCTACCACAGT CAAA CTCC
- -

GAM83 287 FLJ3053 1 1559 NP_653325.1 3 853 ACACCTAGGGAA T G --- 1 A c c
2 ACATGAGGCCCC AAGG GGT TCATGTTTT GGG
TTATGGGA TTCC CCG AGTACAAAG TCC
- G GGA

GAM83 287 FLJ3206 1 19969 NP_694578.1 3 604 CTTCCGGAACAT T---- 1 A c c
9 GTTCTTCACCAC AAGGTGGTG CATGTTTTGGGG
CTTTTGGA TTCCACCAC GTACAAGGCCTT
TTCTT

GAM83 287 FLJ3231 1 6992 NP_653310.1 3 378 TTCCCTCCACAA C G - 1 A c c
2 GAGATATACCAC AAGGTGGTGT AT TTTTG GGG
CTTTAAAA TTCCACCATA TA AGAAC CCT
- G A

GAM83 287 FLJ3404 1 5426 NP_775940.1 3 1821 AACAAACAACTC CAT T 1 A c c
7 CGGGCACACCAC AAGGTGGTGT GTTT GGGG
CTTTAAGA TTCCACCACA CGGG CCTC
--- -

GAM83 287 FLJ3963 1 7460 XP_290687.1 3 246 GCTGACCCCAAA - TGTCAT 1 A c c
9 ACCCTTCCACAC AAG GTGG GTTTTGGGG
TTTATTAG TTC CACC CAAAACCCC
A TTCC--

GAM83 287 FLJ4028 1 15256 NP_775953.1 3 503 CAGTCCCCAGGA - A 1 A c c
8 CAGGGTCACCAC AAGGTGGTG TC TGTTTTGGGG
CTTTCTCT TTCCACCAC GG ACAGGACCCC
T G

GAM83 287 FNBP4 1 13556 NP_056123.1 3 700 CCCTGTTCCAAA T TCA-- 1 A c c
ACAAAATTCACC AAGG GGTG TGTTTTGGGG
TCCTTTCT TTCC CCAC ACAAAACCTT
T TTAAA

GAM83 287 GAS8 1 6978 NP_001472.1 3 68 TAGGAACACTCG T TG 1 A c c
GGATGACACCCC AAGG GGTGTCA TTTTGGG
TTATCACA TTCC CCACAGT AGGGCTC
- --

GAM83 287 GATA2 1 2059 NP_116027.2 3 92 GCATTTCCCGAA A AT G 1 A c c
GGCCGACACCAC A GGTGGTGTC GTTTT GGG
TCCTGCCA C TCACCACAG CGGAA CCC
C C- G

GAM83 287 GPLD1 1 17577 NP_001494.2 3 736 TGTAACAAACCC G TTTT 1 A c c
CCATGACACACC AAGGTG TGTCATG GGGG
TTTATGTA TTCCAC ACAGTAC CCCC
- ----

GAM83 287 GPR68 1 4765 NP_003476.1 5 242 AGCCCTTGGTAG G T ---- 1 A c c
AGCTTGAACCAC AAGGTGGT TCA GTTTT GGGG
CTTCTATA TTCCACCA AGT CGAGA TCCC
- T TGGT
GAM83 287 GPR77 1 2326 NP_060955.1 5 40 AGGACTCCCAAA A ---- AT-- 1 A c c
ACCAGAGACACC AGGT GGTGTC GTTTTGGGG
AGGAGCCT TCCG CCACAG CAAAACCCT
- AGGA AGAC
GAM83 287 GW112 1 17202 NP_006409.2 5 251 CTCTGTTTCCCT A TTTT 1 A c c
GCCAGACACCAC AAGGTGGTGTC TG GGGG
CTTTCCCG TTCCACCACAG AC CCCT
- CGT-
GAM83 287 HAVCR1 1 1838 NP_036338.1 3 274 GTTTTCTCTCAA GTG T 1 A c c
ACATGAACACTT AAGGTG TCATGTTT GGGG
TAGAATTG TTTCAC AGTACAAA TCTC
A-- C
GAM83 287 HOXB7 1 14802 NP_004493.2 3 499 GGGAGCCCCAAA A TCAT 1 A c
c
ACCTACCACTCG A GGTGGTG GTTTTGGGG
CGTGTTCC G TCACCAT CAAAACCCC
C C---
GAM83 287 HPS3 1 10776 NP_115759.2 3 355 CTGTTGTTGGAG - G 1 A c c
ACATGACAATCA AAGGTGGT GTCATGTTTT GG
TTTTCATC TTTTACTA CAGTACAGAG TT
A G
GAM83 287 HSPC133 1 19037 NP_054887.1 3 324 CAGACCAGAAAT ---- G G 1 A c c
GACTCACACCAC AAGGTGGT GTCAT TTTTGG
CTTATAGC TTCCACCA CAGTA AAGACC
CACT - A
GAM83 287 HT001 1 2559 NP_054784.1 5 164 AGCTCTGGCCAA TCA G 1 A c c
AGCGCGTACCAC AAGGTGGTG TGTTTTGG
CTTTCATC TTCCACCAT GCGAAACC
GC- G
GAM83 287 ICK 1 4546 NP_055735.1 3 3801 AAGGTGTTTAAA GG T 1 A c c
ACATGTCAACCT AAGGT TG CATGTTTTGGG
TATGTAAG TTCCA AC GTACAAAATTT
-- T
GAM83 287 ICK 1 4546 NP_057597.2 3 3801 AAGGTGTTTAAA GG T 1 A c c
ACATGTCAACCT AAGGT TG CATGTTTTGGG
TATGTAAG TTCCA AC GTACAAAATTT
-- T
GAM83 287 IGF2R 1 11950 NP_000867.1 3 944 CTCTTCAGGTTC T--- 1 A c c
TCATGATACCAC AAGGTGGTGTCATG TTTGGGG
CTTTACTG TTCCACCATAGTAC GGACTTC
TCTT
GAM83 287 IL28RA 1 3043 NP_775088.1 3 181 GCTTCCAGCCCT G - TTT 1 A c c
ACATTGAACCAC AAGGTGGT TCA TGT GGGG
CTTCTTTC TTCCACCA AGT ACA TCCC
- T ---
GAM83 287 IMMP2L 1 2346 NP_115938.1 3 251 AATGCCCCCAAA GG T 1 A c c

ATATGCAGACCT AAGGT TG CATGTTTTGGGG
TTGGGAAT TTCCA AC GTATAAAACCCC
G- -

GAM83 287 INPP5E 1 17360 NP_063945.1 3 854 GCTGGAAGTTCA T TG 1 A c c
GGATGCCACCAC AAGGTGGTG CA TTTTGGG
CTTGAACA TTCCACCAC GT AGGACTT
C --

GAM83 287 ITK 1 1134 NP_005537.3 5 48 GAGGTGATGCCC T GT 1 A c c
AAGGTGCACCAC AAGGTGGTG CAT TTTGGG
CTTTCAAG TTCCACCAC GTG GAACCC
- --

GAM83 287 KIAA039 1 728 NP_055487.1 5 196 AGTAGCCCCAAA GG CATG 1 A c
c
1 AGCAGAACCTTG AAGGT TGT TTTTGGGG
ATTTGTCT TTCCA ACG AAAACCCC
AG ----

GAM83 287 KIAA052 1 2007 XP_041964.5 3 242 CCTCCTCAGACA A AT- - 1 A c c
3 CTCAGACACCAC A GGTGGTGTC GT TTTGGGG
TCCAGGCT C TCACCACAG CA AGACTCC
C ACT C

GAM83 287 KIAA078 1 1640 XP_033113.1 3 764 GTGACCTTGAGA T- TG 1 A c c
9 TCCTGATACCAC AAGGTGGTGTCA GTTT GGG
CTTCAAGG TTCCACCATAGT TAGA TCC
CC GT

GAM83 287 KIAA098 1 12474 XP_037557.2 3 1952 CCAAAGTTAAGC -- ----- G 1 A c c
4 AAATGACACCAT AAGGTGGTGTCA TGT TTTGG
TTTCTTCC TTTTACCACAGT ACG AAACC
AA AATTG -

GAM83 287 KIAA133 1 12318 XP_048774.2 3 1597 CCTAATTTCAAA CA TT- 1 A c c
2 ACATCACCTTGC AAGGTGGTGT TG TTGGG
CACCCTGA TTCCACTACA AC AATCC
AA TTT

GAM83 287 KIAA168 1 12907 XP_290806.1 3 264 AAAACTAAAAAC CAT T G 1 A c c
4 CAAACACACCAC AAGGTGGTGT GTTT GG
CTTCCTTG TTCCACCACA CAAA CC
--- - A

GAM83 287 KIAA172 1 15787 NP_085148.1 3 589 CTGTGTGCCTCC ATG 1 A c c
0 GGAAGACACCAC AAGGTGGTGTC TTTTGGGG
CTTTCCCT TTCCACCACAG AAGGCCTC

GAM83 287 KIAA192 1 8388 XP_085210.1 5 2053 GGCACCCCAGTA A----- - T - 1 A c c
0 GCTGGCCACCAC AGGTGGTG TCA GTT TTGGGG
CTGCAGTT TCCACCAC GGT CGA GACCCC
TTGACG C - T

GAM83 287 KIAA194 1 8568 NP_803237.1 3 734 GAGAACCCAGAG A---- - - 1 A c c
6 CAATGACACCAG AGG TGGTGTCAT GTTTTGGG
TCTGGACT TCT ACCACAGTA CGAGACCC
TCAGG G A

GAM83 287 KPNA6 1 16094 NP_036448.1 3 2150 AAAATCCCACCC T-- TTT 1 A c c
ATGTTGTACCAC AAGGTGGTG CATG TGGGG

CTTGGTGA TTCCACCAT GTAC ACCCT
GTT CC-
GAM83 287 LARGE 1 14179 NP_004728.1 3 1162 ACCTGTCCAAGG - ATG 1 A c c
GTAGGCAACCAC AAGGTGGT GTC TTTTGGG
CTTCACCT TTCCACCA CGG GGAACCT
A ATG
GAM83 287 LARGE 1 14179 NP_598397.1 3 1162 ACCTGTCCAAGG - ATG 1 A c c
GTAGGCAACCAC AAGGTGGT GTC TTTTGGG
CTTCACCT TTCCACCA CGG GGAACCT
A ATG
GAM83 287 LAX 1 9263 NP_060243.1 3 548 CCAGCCTGGCCA T -- TG 1 A c c
ACATGACCCATC AAGGTGG GTCATGTT T GG
TTTACTAA TTCTACC CAGTACAA G CC
- CC GT
GAM83 287 LDOC1 1 2933 NP_036449.1 3 457 CACATCCCACCT - A TT- 1 A c c
ACAGACTACCAC AAGGTGGT GTC TGT TGGGG
CTTTCGAG TTCCACCA CAG ACA ACCCT
T - TCC
GAM83 287 LHFP 1 12839 NP_005771.1 3 79 GGAGAGGTCAAA - TC G 1 A c c
ACATCCACCTAC AAGGT GGTG ATGTTTTGG
CTTCAAAA TTCCA CCAC TACAAAACT
T C- G
GAM83 287 LIN7A 1 3012 NP_004655.1 5 50 AGCTTTCTTCTC TCAT TT 1 A c c
CACCACCACCAC AAGGTGGTG GT TGGGG
CTTCCTTC TTCCACCAC CA ACCTC
---- CC
GAM83 287 LOC1189 1 9092 NP_776152.1 3 176 TTTCCAGTAAAA G TG GG-- 1 A c
c
87 ACATGACCAGCT AAG TGG TCATGTTTT GG
TACAAAAA TTC ACC AGTACAAAA CC
G -- ATGA
GAM83 287 LOC1260 1 19476 XP_064903.7 3 766 TCTGGCCAACAA G -- G 1 A c c
17 ACATGAGCCACT AAGGTGGT TCATGTTT TGG
TTTCCCAG TTTCACCG AGTACAAA ACC
- CA G
GAM83 287 LOC1267 1 18542 NP_660300.1 3 307 AATCTTTTAAGA ---- - 1 A c c
31 TACTGACACCAA AAGGT GGTGTCA TGTTTTGGGG
ATGCCTTT TTCCG CCACAGT ATAGAATTTT
TAAA C
GAM83 287 LOC1307 1 10734 XP_059468.3 3 286 TCCAAATCAGAT ------- A T 1 A c c
52 TCCTCAAACCAC AAGGTGGT GTC TG TTTGGG
CTTTGAAA TTCCACCA TAG AC AAACCT
AACTCCT - T
GAM83 287 LOC1444 1 16849 XP_096608.1 3 546 GAGTTGCCCAAA TCAT 1 A c c
86 ACCATTACTTTT AAGGTGGTG GTTTTGGG
AAACGCTG TTTCATTAC CAAAACCC

GAM83 287 LOC1450 1 16596 XP_096714.1 3 1471 TCCTTGTTCAAA GTC 1 A c c
53 ACATTTAATCAT AAGGTGGT ATGTTTTGGG
CTTAAGCA TTCTACTA TACAAAACTT

```
                                                ATT
GAM83   287   LOC1452 1  18659 XP_096730.1  3  1184  AAATGTATTTCC       TCATGT          1  A  c
c
        16                          AAATACCACCAC AAGGTGGTG     TTTGGGG
                                   CTTAAGGG    TTCCACCAC     AAACCTT
                                               CAT---
GAM83   287   LOC1462 1  1810  XP_085374.2  3  799   GGATATGCTCCC       CATG T          1  A  c  c

        27                          CATAAATACCAC AAGGTGGTGT   TT TGGGG
                                   CTTGCCAC    TTCCACCATA    AA ACCCC
                                               ---- T
GAM83   287   LOC1464 1  15013 XP_085461.6  3  171   TGGTGCCCCAAA A----      - CAT          1  A  c
c
        43                          ACTTCACAACCA     AGGTGGT GT   GTTTTGGGG
                                   CCTAGACA        TCCACCA CA   CAAAACCCC
                                           ACAGA      A  CTT
GAM83   287   LOC1467 1  16534 XP_097074.1  5  490   TCTCAGCACCAC       CAT  TT -        1  A  c
c
        28                          CTAACGCACCAC AAGGTGGTGT   GTT  GG GG
                                   CTTGCCCT    TTCCACCACG   CAA  CC CC
                                               ---  T-  A
GAM83   287   LOC1468 1  17740 XP_096086.1  3  447   TGGGGTCAAGAC  - -      --      G      1  A  c  c
        56                          AGGTGACACCAG AAG G TGGTGTCA  TGTTTTGG
                                   CACTTTAA    TTC C ACCACAGT  ACAGAACT
                                           A G       GG       G
GAM83   287   LOC1479 1  6702  XP_085974.1  3  1019  ATTATTGACCCA   G       GTTT          1  A  c  c

        47                          TAGTGACACCAG AAG TGGTGTCAT    TGGG
                                   TTTTGGGA    TTT ACCACAGTG    ACCC
                                           G       AT--
GAM83   287   LOC1484 1  18524 XP_086210.2  5  1200  ATTTTTCCCAAA     -- T  CA           1  A  c  c
        90                          ACAAAGCCCATG AAGGT  GG GT  TGTTTTGGGG
                                   CCTTGCTC    TTCCG  CC CG  ACAAAACCCT
                                           TA  -  AA
GAM83   287   LOC1494 1  19107 NP_690048.1  5  134   CACTGCTTCAGA       G A   -         1  A  c  c
        20                          GACACGAACCAC AAGGTGGT TC TGTTT TGGGG
                                   CTTGAGTG    TTCCACCA AG ACAGA ACTTC
                                           -  C    G
GAM83   287   LOC1512 1  1944  XP_087137.2  3  105   ATCCCAACACAA A-----       CA     ----   1  A  c  c
        42                          AACAAACACCAC      AGGTGGTGT  TGTTTTG    GGG
                                   CTCCGATT         TCCACCACA  ACAAAAC    CCC
                                           TTAGCC        A-       ACAA
GAM83   287   LOC1516 1  12037 XP_087245.1  5  396   GGGTGTTGTCTG       TCAT     G        1  A  c
c
        10                          CAGAACCACCAC AAGGTGGTG    GTTTTG GG
                                   CTTGAAAG    TTCCACCAC    CAAGAC TC
                                               ----     G
GAM83   287   LOC1525 1  12979 XP_087483.3  3  566   TTGAGCTCAGGA       G  ATG-          1  A  c  c

        19                          GTTCGAGACCAC AAGGTGGT TC    TTTTGGG
```

CTTGGGCC TTCCACCA AG AGGACTC
G CTTG
GAM83 287 LOC1530 1 16808 XP_098307.1 3 2756 TTATGGGCTTAA G- ATG 1 A c c
77 GAAGAAGACCAC AAGGTGGT TC TTTTGGG
CTTGTCTA TTCCACCA AG AGAATTC
GA A--
GAM83 287 LOC1575 1 3461 XP_098772.1 3 124 AGAGGCCCAGTA A----- T -- 1 A c c
31 GACATGCACCAC AGGTGGTG CATGTTT TGGG
CTGCTTGA TCCACCAC GTACAGA ACCC
AGTTCG - TG
GAM83 287 LOC1581 1 8554 XP_088492.2 3 12 GACCCTCAAACC GTCA --- 1 A c c
25 TACACCAACCAC AAGGTGGT TGT TTTGGGG
CTTAGATG TTCCACCA ACA AAACTCC
ACC- TCC
GAM83 287 LOC2027 1 9377 XP_117455.1 3 1328 ATCCTTAAATTT T T--- 1 A c c
81 TTATGACACCCT AAGG GGTGTCATG TTTGGGG
TTGTAATC TTTC CCACAGTAT AAATTCC
- TTTT
GAM83 287 LOC2196 1 690 XP_168585.2 5 1884 AGGCCTCAGTGA TC --- 1 A c c
12 GGCATCTACCAC AAGGTGGTG ATGTTT TGGGG
CTTCTACA TTCCACCAT TACGGA ACTCC
C- GTG
GAM83 287 LOC2197 1 5054 XP_167596.1 5 228 GCCTCAACCTGG G T ---- 1 A c c
31 ACCTGACACCAA AAG TGGTGTCA GTT TTGGGG
CTTCGCCG TTC ACCACAGT CAG AACTCC
A C GTCC
GAM83 287 LOC2199 1 15995 XP_167788.1 3 103 AGAAACAAACTC CAT T 1 A c c
14 CAGACGCACCAC AAGGTGGTGT GTTT GGGG
CTTAAGAG TTCCACCACG CAGA CCTC
--- -
GAM83 287 LOC2199 1 10767 XP_167790.1 3 279 AGAAATAATCCC CATGT 1 A c c
42 AAGTCACACCAC AAGGTGGTGT TTTGGGG
CTTCTATT TTCCACCACA GAACCCT
CT---
GAM83 287 LOC2829 1 2531 XP_210838.1 3 642 ACAAATGTTCAG TCAT 1 A c c
76 AATTCTCACCAC AAGGTGGTG GTTTTGGG
CTTCTGGT TTCCACCAC TAAGACTT
TCT-
GAM83 287 LOC2833 1 19120 XP_210969.1 3 118 AAGGAAACTCCA A----- CA 1 A c c
14 GGACAGCACCAC AGGTGGTGT TGTTTTGGGG
CTCCCCTA TCCACCACG ACAGGACCTC
ATCCCC --
GAM83 287 LOC2833 1 7249 XP_300560.1 3 1278 TCCTCTCTGCTC TCAT T 1 A c c
37 CAATACCACCAC AAGGTGGTG GT TTGGGG
CTTGTCCA TTCCACCAC CA AACCTC
---- T
GAM83 287 LOC2834 1 17012 XP_211053.1 3 427 CTATCCTCCAAA G- A- 1 A c c

```
          84                    ACAGAGGGAGCC AAGGTGGT  TC  TGTTTTGGGG
                                ATTTTATA    TTTTACCG  GG  ACAAAACCTC
                                          AG  AG
GAM83     287   LOC2837 1  1502  XP_208835.1  3  788   GGCCGCCCCAAA      G  ATG          1  A  c  c

          67                    AGAGCCGCTTTG AAGGTGGT TC   TTTTGGGG
                                ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                          -  ---
GAM83     287   LOC2837 1  14021 XP_211196.1  5  258   AACTAACAACTC       CAT   T        1  A  c  c
          76                    CAGACGCACCAC AAGGTGGTGT   GTTT GGGG
                                CTTTATGA    TTCCACCACG   CAGA CCTC
                                          ---   -
GAM83     287   LOC2838 1  3222  XP_211218.1  5  7     TAAAACATGCTT    T     T  ---       1  A  c  c
          18                    CAGAAGAACTGG AAGG GGTGTCA GTTT   TGGGG
                                CACCCCTT    TTCC CCACGGT CAAG   ACTTC
                                          -     -   AAG
GAM83     287   LOC2839 1  19383 XP_211254.1  5  124   CTCACATCCTTT      TG   G  TG        1  A  c  c

          06                    GAAGATGACCAC AAGGTGG  TCAT TTT  GGG
                                CTTGAAGA    TTCCACC  AGTA AAG  TCC
                                          --   G   TT
GAM83     287   LOC2840 1  1826  XP_208982.1  3  221   GCTCAGAGACCT        A   TT        1  A  c  c
          31                    GGCAGACACCAC AAGGTGGTGTC TGTT  GGG
                                CTTAACCC    TTCCACCACAG ACGG  TCC
                                          -   --
GAM83     287   LOC2844 1  17281 XP_211475.1  3  330   TCTGTGACTCCC       T-  GTTT        1  A  c  c

          62                    AGTGTTCACCAC AAGGTGGTG  CAT   TGGGG
                                CTTCCTGA    TTCCACCAC  GTG   ACCCT
                                          TT  ----
GAM83     287   LOC2844 1  7971  XP_211474.1  3  161   TGCGCCCGGCAG      -  TG -        1  A  c  c
          73                    TCTGGCGACCAC AAGGTGGT GTCA  TT TTGGG
                                CTTGCGGG    TTCCACCA CGGT  GA GGCCC
                                          G   CT  C
GAM83     287   LOC2845 1  13654 XP_211526.1  5  3     TGTTCTCTGCAT       TCATGTTTT         1  A  c
c
          78                    CCCCTCACCACC AAGGTGGTG       GGGG
                                TTCCTTTG    TTCCACCAC       CCCC
                                          T--------
GAM83     287   LOC2846 1  1698  XP_209313.2  3  2332  CCTAAGAAATGC      GTCA     G       1  A  c
c
          71                    CAGAACAACCAC AAGGTGGT   TGTTTTGG
                                CTTATTTC    TTCCACCA   ACAAGACC
                                          ----       G
GAM83     287   LOC2846 1  2205  XP_209316.1  3  79    CTCTTGCCCTCC       TC  TTTT        1  A  c  c
          84                    CCATCCCACCAC AAGGTGGTG  ATG   GGG
                                CTTGGAGC    TTCCACCAC  TAC   CCC
                                          CC  CCCT
GAM83     287   LOC2847 1  19513 XP_211635.1  3  481   AAATATATCAAA      -  ---      G     1  A  c  c
          75                    ACATGTAAACGC AAGGTGG TGT   CATGTTTTGG
```

CCACCTTA TTCCACC GCA GTACAAAACT
C AAT A
GAM83 287 LOC2847 1 18378 XP_211639.1 3 265 ACGCGACCCAAA AA--- T --- 1 A c c
98 ACCAAATGACCC GGTGG GTCAT GTTTTGGG
ACCACCAC CCACC CAGTA CAAAACCC
CACCA - AAC
GAM83 287 LOC2853 1 7404 XP_211856.1 5 1021 TCCAACCCCAAA - TCA 1 A c c
51 ACACCACTGGCC AAGGT GGTG TGTTTTGGGG
TTCTTTCA TTCCG TCAC ACAAAACCCC
G C--
GAM83 287 LOC2854 1 2002 XP_211885.1 3 1067 CCACTCCCCAAA A----- - T T 1 A c c
04 ACTGACCCCAAT AGGT GG GTCA GTTTTGGGG
CTCTGTGT TCTA CC CAGT CAAAACCCC
TGTGTC A C -
GAM83 287 LOC2854 1 5221 XP_211894.1 3 1577 ATACTCAATGAT G -- - 1 A c c
22 TGATGACACCAG AAG TGGTGTCAT GTT TTGGG
TTTTGGCT TTT ACCACAGTA TAG AACTC
G GT T
GAM83 287 LOC2854 1 18486 XP_211897.1 3 617 TTCAGAAGCCCT GTC 1 A b b
41 AAAACATACCAC AAGGTGGT ATGTTTTGGGG
CTTGGCTA TTCCACCA TACAAAATCCC

GAM83 287 LOC2855 1 3710 XP_211936.1 3 189 TTCAGCCCCAAA - TC- 1 A c c
48 ACATCTCTGCCT AAGGT GGTG ATGTTTTGGGG
GCCTTTAT TTCCG CCGT TACAAAACCCC
T CTC
GAM83 287 LOC2856 1 1605 XP_211958.1 3 435 ATGGCCAACAAA GTG -- 1 A c c
23 ACATGAAACACC AAGGTG TCATGTTTTG GG
TTGAACCC TTCCAC AGTACAAAAC CC
AA- AA
GAM83 287 LOC2857 1 16029 XP_209742.1 3 1382 CTGGGACTGTAA - - TG 1 A c c
47 ACATGACAGCCG AAG GTGG TGTCATGTTT GG
CACTTCAC TTC CGCC ACAGTACAAA TC
A G TG
GAM83 287 LOC2859 1 19964 XP_212103.1 3 2130 AGCCTCCTCACA G - T 1 A c c
46 ACATGACAGCTG AAG TGG TGTCATGTT TGGGG
GCTTAGTA TTC GTC ACAGTACAA ACTCC
G G C
GAM83 287 LOC2863 1 1540 XP_210021.1 5 27 GGCTTCCCCAAA G --- A 1 A c c
45 ATGGGCAACTTC AAG TGG TGTC TGTTTTGGGG
AGCTTAAG TTC ACT ACGG GTAAAACCCC
G TCA -
GAM83 287 LOC2864 1 17170 XP_212323.1 5 70 ACACTCCCCAAA T CATGT 1 A c
c
52 ACACCCCTTTCC AAGG GGTGT TTTGGGG
AGTTACAA TTCC CCACA AAACCCC
- -----
GAM83 287 LOC2864 1 14618 XP_208434.1 5 459 ATAGAAGACCAG - ATG G 1 A c c

```
          84                          AAAGGCGACCAC AAGGTGGT GTC   TTTTGG
                                     CTTGTGAA    TTCCACCA CGG   AAGACC
                                                 G   A--     A
GAM83     287   LOC3385 1   10340 XP_294659.1  5  682   GCTGAAGAATAT         ----      G-       1  A  c  c
          88                          GAGAGACACCAC AAGGTGGTGTC   ATGTTTT  GG
                                     CTTTTAAA    TTCCACCACAG    TATAAGA  TC
                                                   AGAG      AG
GAM83     287   LOC3389 1   1502  XP_290663.1  3  788   GGCCGCCCCAAA       G  ATG           1  A  c  c

          91                          AGAGCCGCTTTG AAGGTGGT TC   TTTTGGGG
                                     ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                                 -  ---
GAM83     287   LOC3389 1   1502  XP_290659.1  3  788   GGCCGCCCCAAA       G  ATG           1  A  c  c

          99                          AGAGCCGCTTTG AAGGTGGT TC   TTTTGGGG
                                     ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                                 -  ---
GAM83     287   LOC3391 1   7871  XP_294835.1  5  667   CAGCAGCTCCTC        T  T  TT          1  A  c  c
          61                          CAGCTGCACCAC AAGGTGGTG CA GT  TGGGG
                                     CTTCAGCA    TTCCACCAC GT CG  ACCTC
                                                 -  -  --
GAM83     287   LOC3391 1   5261  XP_290743.1  3  840   GGCTGTGTCCAC        --     TTT         1  A  c  c
          84                          ATGAGCTACCAC AAGGTGGTG  TCATGT   GGG
                                     CTTGCGTT    TTCCACCAT  AGTACA   CCT
                                                   CG     ---
GAM83     287   LOC3394 1   19567 XP_290899.1  5  147   AGAGATTCTAAA      G  T-              1  A  c  c
          37                          ACATGTTCAGCA AAGGTG TG  CATGTTTTGGGG
                                     CTTTCTGG    TTTCAC AC  GTACAAAATCTT
                                                   G  TT
GAM83     287   LOC3404 1   2003  XP_295258.1  5  119   GCACTCCCCAAA       TGTC             1  A  c  c
          78                          ACATCCCATTTT AAGGTGG    ATGTTTTGGGG
                                     GCAGGTGT    TTTTACC    TACAAAACCCC
                                                 C---
GAM83     287   LOC3417 1   11667 XP_296409.1  3  146   GAGTCCCAACCA A-  -    TCA      -       1  A  c  c

          44                          CCGAAACACCAC   AGG TGGTG   TGTTTTGG GG
                                     CATCCTGT      TCC ACCAC   ACAAAGCC CC
                                               TG   T    C--       A
GAM83     287   LOC3481 1   1502  XP_300623.1  3  788   GGCCGCCCCAAA       G  ATG           1  A  c  c

          13                          AGAGCCGCTTTG AAGGTGGT TC   TTTTGGGG
                                     ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                                 -  ---
GAM83     287   LOC3481 1   10142 XP_300635.1  3  789   GGCCGCCCCAAA       G  ATG           1  A  c
c
          37                          AGAGCCACTTTG AAGGTGGT TC   TTTTGGGG
                                     ACCAGGCT    TTTCACCG AG   AAAACCCC
                                                 -  ---
GAM83     287   LOC3481 1   1502  XP_300636.1  3  788   GGCCGCCCCAAA       G  ATG           1  A  c  c
```

```
          42                    AGAGCCGCTTTG AAGGTGGT TC   TTTTGGGG
                                ACCAGGCT    TTTCGCCG AG   AAAACCCC
                                          - ---
GAM83   287   LOC3481 1  18221 XP_300638.1  3  1406  AGACCACTCAAA  - -   ---          1  A  c  c
          44                    ACATGCTTACAC AAG GT GGTGT  CATGTTTTGGG
                                TAACACTT    TTC CA TCACA  GTACAAAACTC
                                     A A    TTC
GAM83   287   LOC3481 1  11592 XP_302676.1  5  655   GCTCAGTTCCAG      G A  -          1  A  c  c
          82                    TAGCAGAACCAC AAGGTGGT TC TGTT TTGGGG
                                CTTAGTTG    TTCCACCA AG ACGA GACCTT
                                          - -  T
GAM83   287   LOC3487 1  14195 XP_302883.1  3  222   CCATGGTCCCCC A-----      T   TT       1  A  c  c

          68                    AGCGTGCACCAC      AGGTGGTG CATGT  TGGGG
                                CTGGCCCG          TCCACCAC GTGCG  ACCCC
                                     GCCCGG       -   --
GAM83   287   LOC3501 1  3208  XP_303867.1  5  81    TGAGCATTTAAA  - GTG            1  A  c  c
          32                    ACATGAAAACAC AAG GTG  TCATGTTTTGGG
                                TCTTGTTT    TTC CAC   AGTACAAAATTT
                                     T  AAA
GAM83   287   LOC3501 1  15430 XP_303825.1  5  110   CAAATAATAACA      TC     GG       1  A  c  c
          47                    AAGCATTACCAC AAGGTGGTG  ATGTTTTG
                                CTTGTGTC    TTCCACCAT  TACGAAAC
                                          --      AA
GAM83   287   LOC3510 1  8285  XP_304632.1  5  0     CCCCAAAACATC A---------  ---   TC       1  A  c  c
          42                    ACCAGTCCCTAC        AGG  TGGTG  ATGTTTTG
                                TACTTGCT            TCC  ACCAC  TACAAAAC
                                     TCGTTCATCA  CTG   --

                                     GGG
                                     CCC

GAM83   287   LOC5710 1  5002  NP_065114.2  3  1527  CCCTCCCCCAAA      GTC  --          1  A  c  c
          7                     AGTTATAAAACC AAGGTGGT  ATG  TTTTGGGG
                                ATTTTATC    TTTTACCA   TAT  AAAACCCC
                                          AAA  TG
GAM83   287   LOC9014 1  4641  XP_029430.1  3  766   AAGGAGAAACCT        A   TT         1  A  c  c
          8                     GGCAGATACCAC AAGGTGGTGTC TGTT  GGG
                                CTTAACCA    TTCCACCATAG ACGG  TCC
                                          -   --
GAM83   287   LOC9297 1  14969 XP_048529.2  5  3132  CTCCAGTGTCCT   G       TT-----       1  A  c  c

          3                     CCATGACACCAG AAG TGGTGTCATG      TTGGGG
                                CTTTCTCC    TTC ACCACAGTAC      GACCTC
                                     G        CTCCTGT
GAM83   287   LOC9334 1  17460 NP_612411.2  3  498   AGTCCCCACTCA         - TT-        1  A  c  c
          9                     CGGTGACACCAC AAGGTGGTGTCAT GT   TGGGG
                                CTTCCTGA    TTCCACCACAGTG CA   ACCCC
                                          G  CTC
GAM83   287   LSM10  1  918   NP_116270.1  3  142   AAGCTGGTGTCC A-----       A   TT       1  A  c  c
```

AACAGACACCAC AGGTGGTGTC TGT TGGG
CTGTCAAA TCCACCACAG ACA ACCT
AAACTG - --

GAM83 287 LTA 1 3286 NP_000586.2 5 133 CCTTGGTTCTCC A----- TTTT 1 A c c
CCATGACACCAC AGGTGGTGTCATG GGGG
CTGAACGT TCCACCACAGTAC CCCT
TGCAAG ----

GAM83 287 MECP2 1 689 NP_004983.1 3 7972 TGGGCTCCCAAA A--- T - -- 1 A c c
ACACCTGACAGC AGG GG TGTCA TGTTTTGGGG
CCCTCCCT TCC CC ACAGT ACAAAACCCT
TCCC - G CC

GAM83 287 MEIS1 1 12764 NP_002389.1 3 1074 TTGTCCCCATGC TCA T-- 1 A c c
AACAACCACCAC AAGGTGGTG TGTT TGGGG
CTTATACA TTCCACCAC ACAA ACCCC
CA- CGT

GAM83 287 MFAP2 1 2746 NP_002394.1 3 380 ACAGCCCCCGTG G - 1 A c c
GGCATGGACCAC AAGGTGGT TCATGTTT TGGGG
CTTTATTT TTCCACCA GGTACGGG GCCCC
- T

GAM83 287 MFAP2 1 2746 NP_059453.1 3 380 ACAGCCCCCGTG G - 1 A c c
GGCATGGACCAC AAGGTGGT TCATGTTT TGGGG
CTTTATTT TTCCACCA GGTACGGG GCCCC
- T

GAM83 287 MGC1064 1 5646 NP_116082.1 3 156 ACTCTTAACTCT GTCA - 1 A c c
6 ATAAACAACCAC AAGGTGGT TGTTT TGGGG
CTTTCACA TTCCACCA ACAAA ATCTC
---- T

GAM83 287 MGC1243 1 7109 NP_113615.1 3 191 TTTCTCCCCAAA - --- T 1 A c c
5 ACTGGTAATGCC AAGGT GGTGT CA GTTTTGGGG
AACCTTAT TTCCA CCGTA GT CAAAACCCC
A ATG -

GAM83 287 MGC1307 1 8673 NP_116078.2 3 1492 AGCCCCGATGAT C TT--- 1 A c c

1 TCGTAACACCAC AAGGTGGTGT ATG TTGGGG
CTTTCGCC TTCCACCACA TGC AGCCCC
A TTAGT

GAM83 287 MGC1751 1 16554 NP_689684.1 5 311 TTTCTCCCCAAA --- CATG 1 A c
c
5 AATACATCCTAG AAGGT GGTGT TTTTGGGG
CCTTAATG TTCCG CTACA AAAACCCC
ATC TA--

GAM83 287 MGC2306 1 2059 NP_002041.2 3 92 GCATTTCCCGAA A AT G 1 A c c
GGCCGACACCAC A GGTGGTGTC GTTTT GGG
TCCTGCCA C TCACCACAG CGGAA CCC
C C- G

GAM83 287 MGC3101 1 6021 NP_076948.1 3 561 AGCGGCCCCAAA TGTCAT 1 A c
c
ATTCCCACCTTG AAGGTGG GTTTTGGGG
ATTTCCAT TTCCACC TAAAACCCC
CT----

GAM83 287 MGC3321 1 9985 NP_722517.1 3 736 CCCACAACCAAA T GTCA G 1 A c c
5 ACAACCCCTTTT AAGG GGT TGTTTTGG
AAAAGAGT TTCC CCA ACAAAACC
- ---- A
GAM83 287 MGC3397 1 19531 NP_699181.1 3 714 GTCCGCCCCAAA - TGTCAT 1 A c c
4 ACCCGGCCTTGG AAGGT GG GTTTTGGGG
TCCCTGGC TTCCG CC CAAAACCCC
G ------
GAM83 287 MGC3544 1 1776 NP_694952.1 3 592 ACTGGGACCCCA A----- T T 1 A c c
0 GGCATGCACCAC AGGTGGTG CATGTTT GGGG
CTCACCAA TCCACCAC GTACGGA CCCC
AACCAC - -
GAM83 287 MOCS3 1 4326 NP_055299.1 3 857 GTTTACCAAAAT G A-- G 1 A c c
AAAGGAAACCAC AAGGTGGT TC TGTTTTGG
CTTTGTAG TTCCACCA AG ATAAAACC
A GAA A
GAM83 287 MRPL21 1 1724 NP_852616.1 5 199 CTAAAACATCCC --- ---- G 1 A c c
TGAGTTCACCAC AAGGTGGTG TCA TGTTTTGG
CTTGGCCA TTCCACCAC AGT ACAAAATC
TTG CCCT -
GAM83 287 MRPL30 1 8553 NP_660213.1 3 1016 AAGCTGACCAAA TG- G 1 A c c
ACATGGTCCCCA AAGGTGG TCATGTTTTGG
CCTTTTGG TTCCACC GGTACAAAACC
CCT A
GAM83 287 MYL9 1 1500 NP_006088.2 3 243 CTGACCCCTCCA GTCATG 1 A c c
AGGAAAGACCAC AAGGTGGT TTTTGGGG
CTTCTGGG TTCCACCA GGAACCTC
GAAA--
GAM83 287 MYL9 1 1500 NP_852667.1 3 243 CTGACCCCTCCA GTCATG 1 A c c
AGGAAAGACCAC AAGGTGGT TTTTGGGG
CTTCTGGG TTCCACCA GGAACCTC
GAAA--
GAM83 287 NCAM2 1 15637 NP_004531.1 3 1691 TACAGCAGGACA TG GG 1 A c c
GAATATGACCAC AAGGTGG TCATGTTTTG
CTTCGTTT TTCCACC AGTATAAGAC
-- AG
GAM83 287 NEK6 1 1469 NP_055212.2 3 141 AGGTTCCCCAAA -- - ATG 1 A c c
AGGCTGCCCAGC AAGGT GGT GTC TTTTGGGG
CTTACAGC TTCCG CCG CGG AAAACCCC
AC T ---
GAM83 287 NFASC 1 8725 XP_046808.8 3 101 GACCTACCACGA TCAT - 1 A c c
AGCCACCACCAC AAGGTGGTG GTTTTG GG
CTTCAGTA TTCCACCAC CGAAGC CC
CAC- A
GAM83 287 NK4 1 19318 NP_004212.3 3 21 CTCAAAATGAGA ------ 1 A c c
TACTGACACCAC AAGGTGGTGTCA TGTTTTGGG

CTTTGCCC TTCCACCACAGT GTAAAACTC
CATAGA
GAM83 287 NP220 1 9969 NP_055312.2 5 256 TTGCCTCACATG ----- TTT 1 A c c
GTTCAACACCAC AAGGTGGTGT CATGT GGGG
CTTATACT TTCCACCACA GTACA CTCC
ACTTG ---
GAM83 287 NPTXR 1 3192 NP_055108.2 3 1979 AGATGCTTTCCA ----- TT 1 A c c
ACATGACACCTG AAGGT GGTGTCATGT TGGGG
AACATCTT TTCTA CCACAGTACA ACCTT
CAAGT --
GAM83 287 NPTXR 1 3192 NP_478058.1 3 1979 AGATGCTTTCCA ----- TT 1 A c c
ACATGACACCTG AAGGT GGTGTCATGT TGGGG
AACATCTT TTCTA CCACAGTACA ACCTT
CAAGT --
GAM83 287 P2RX5 1 4268 NP_002552.2 3 507 TACTCTCTCTCC ATGT 1 A c c
TAAAGACACCAC AAGGTGGTGTC TTTGGGG
CTTCCTGC TTCCACCACAG AAATCCT

GAM83 287 P2RX5 1 4268 NP_778255.1 3 507 TACTCTCTCTCC ATGT 1 A c c
TAAAGACACCAC AAGGTGGTGTC TTTGGGG
CTTCCTGC TTCCACCACAG AAATCCT

GAM83 287 PDE5A 1 19020 NP_246273.1 5 61 CACCCAAAGGCA GG ---- 1 A c c
ACATGACGGAAC AAGGT TGTCATGTT TTGGG
CTTGCCAA TTCCA GCAGTACAA AACCC
AG CGGA
GAM83 287 PELI2 1 7435 NP_067078.1 3 2160 ATATCCCCCAAA TG GT 1 A c c
ATGAAGTTACCT AAGGTGG TCAT TTTGGGG
TCCAAGTT TTCCATT AGTA AAACCCC
GA --
GAM83 287 PEPD 1 4327 NP_000276.1 3 202 TAATTACCCTTT A TTT 1 A c c
TGCAGGCACCAC AAGGTGGTGTC TGT GGGG
CTTTAATC TTCCACCACGG ACG TCCC
- TTT
GAM83 287 PILRB 1 5459 NP_038468.3 5 1258 CAGCAGCCCCTG CAT TTT 1 A c c
CGCCAACACCAC AAGGTGGTGT GT GGGG
CTTCTGCT TTCCACCACA CG CCCC
AC- CGT
GAM83 287 PILRB 1 5459 NP_778212.2 5 1320 CAGCAGCCCCTG CAT TTT 1 A c c
CGCCAACACCAC AAGGTGGTGT GT GGGG
CTTCTGCT TTCCACCACA CG CCCC
AC- CGT
GAM83 287 POGZ 1 11143 NP_055915.1 3 704 GGCTTTAAAAAT G --- 1 A c c
GCATGAAACCAC AAGGTGGT TCATGT TTTGGGG
CTTTAATT TTCCACCA AGTACG AAATTTC
A TAA
GAM83 287 POLR2D 1 4052 NP_004796.1 3 58 CCACATCCCCAG C T 1 A b b
GCATAACACCAC AAGGTGGTGT ATGTTT GGGG

CTTCCCAC TTCCACCACA TACGGA CCCC
A -
GAM83 287 POU2AF1 1 16639 NP_006226.1 5 143 TTCCCACAGCTT ---- T T 1 A c c
GCCCCACACCAC AAGGTGGTGT CA GTT TGGGG
CTTCACAC TTCCACCACA GT CGA ACCCT
CCCC T C
GAM83 287 PPP1R3A 1 20165 NP_002702.1 3 1407 TTCCTTCATAAA - -- --- 1 A c c
ACATGTAACACT AAGGT GGTGT CATGTTTTG GGG
GATCTTCA TTCTA TCACA GTACAAAAT TCC
G AT ACT
GAM83 287 PRDM2 1 12854 NP_056950.2 3 30 AAAGCCCCCAAA GG CA 1 A c c
ACAAAACAAACC AAGGT TGT TGTTTTGGGG
TTAATTGA TTCCA ACA ACAAAACCCC
A- AA
GAM83 287 PRKCN 1 19159 NP_005804.1 3 845 TATGCATGTTCT T TT 1 A c c
GACTGACACCAT AAGGTGGTGTCA GTT GGG
CTTGATGC TTCTACCACAGT CAG CTT
- T-
GAM83 287 PRO0461 1 19001 NP_112558.1 5 864 GCTCACTTCCAG G A - 1 A c c
TAGCAGAACCAC AAGGTGGT TC TGTT TTGGGG
CTTAGTTG TTCCACCA AG ACGA GACCTT
- - T
GAM83 287 PYCR1 2 7092 NP_008838.2 3 257 GCTCCCAAACCA --- T T 1 A c c
TGTCAGGACCAC AAGGTGGT G CATG TTTGGGG
CTTCCTCT TTCCACCA C GTAC AAACCCT
GGA T C
GAM83 287 PYCR1 2 17062 NP_008838.2 3 38 GCCTGACCACCA T TGTTT - 1 A c c
TCCTGCCACCAC AAGGTGGTG CA TGG GG
CTTCTCTT TTCCACCAC GT ACC CC
C CCT-- A
GAM83 287 Rab11-F 1 7165 NP_055719.1 3 774 TCTTTCCCCAAA --- GT G-- 1 A c c
IP2 AGTGATGATCTC AAGG TG GTCAT TTTTGGGG
AAGTCCTT TTCC AC TAGTA AAAACCCC
TGA TC GTG
GAM83 287 RAB39B 1 14419 NP_741995.1 3 1409 ACCCACCCCAAA A--- ---- GT 1 A c c
ATGACCTTGGCC AGGTGGT GTCAT TTTGGGG
ACCTGTCT TCCACCG CAGTA AAACCCC
TCTG GTTC --
GAM83 287 RAP1B 1 7459 NP_056461.1 3 604 CTTGTCTTTAAA TGG 1 A c c
ACATGATAGTCC AAGG TGTCATGTTTTGGGG
TTTCAGTA TTCC ATAGTACAAAATTTC
TG-
GAM83 287 RAP2A 1 12939 NP_066361.1 3 1925 TTATAATCCTCA G TT 1 A c c
ATTATGAACCAC AAGGTGGT TCATG TTGGGG
CTTGTTTA TTCCACCA AGTAT AACTCC
- T-
GAM83 287 RASGRP2 1 18244 NP_005816.2 5 32 CCTCTCCCCAAA TGTC 1 A c c

ATATTCCCATCT AAGGTGG ATGTTTTGGGG
TGTCCTAG TTCTACC TATAAAACCCC
CT--

GAM83 287 RASGRP2 1 18244 NP_722541.1 5 32 CCTCTCCCCAAA TGTC 1 A c c

ATATTCCCATCT AAGGTGG ATGTTTTGGGG
TGTCCTAG TTCTACC TATAAAACCCC
CT--

GAM83 287 RING1 1 11106 NP_002922.1 5 23 CCCTTTCCCTCT CAT TT 1 A c c
AACCCACACCAC AAGGTGGTGT GTT GGGG
CTTTCTAC TTCCACCACA CAA TCCC
CC- TC

GAM83 287 RNF39 1 5743 NP_079512.1 3 157 TTTCGCCCCAAA A-- -- G - 1 A c c
ATAATGAGACCT AGGT GGT TCAT GTTTTGGGG
CACCTGGT TCCA CCA AGTA TAAAACCCC
TGG CT G A

GAM83 287 RNF39 1 5743 NP_739575.1 3 157 TTTCGCCCCAAA A-- -- G - 1 A c c
ATAATGAGACCT AGGT GGT TCAT GTTTTGGGG
CACCTGGT TCCA CCA AGTA TAAAACCCC
TGG CT G A

GAM83 287 SALPR 1 1044 NP_057652.1 5 329 TTGTCCCCCAGA A ------ T 1 A c c
ACATGACCTAGA AGGT GG GTCATGTTTTGGGG
GGTACCTG TCCA TC CAGTACAAGACCCC
G TGGAGA -

GAM83 287 SCA1 1 17933 NP_000323.1 3 2587 TGGACTCAGAAA CATG-- 1 A c c
AACACACACCAC AAGGTGGTGT TTTTGGG
CTTTTGGC TTCCACCACA AAGACTC
CACAAA

GAM83 287 SCNN1A 1 16640 NP_001029.1 3 816 GTCTTCCCCAAA T--- T 1 A c c
ATTGATCACTCC AAGGTGG GTCA GTTTTGGGG
GCCTTCTC TTCCGCC TAGT TAAAACCCC
TCAC -

GAM83 287 SEMA4C 1 13121 NP_060259.2 5 351 GGACACCTCCTG CA TT 1 A c c

GCACAACACCAC AAGGTGGTGT TGTT GGGG
CTTCTTTG TTCCACCACA ACGG CTCC
AC TC

GAM83 287 SFRS2IP 1 13515 NP_004710.1 3 602 TTAGTGTTCAAA - GTG - 1 A c c
ACATTGAAACAC AAG GTG TCA TGTTTTGGG
TCTTCACC TTC CAC AGT ACAAAACTT
T AA- T

GAM83 287 SIAT6 1 8130 NP_006270.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777623.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777624.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c

TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777625.1 3 582 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777626.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777627.1 3 582 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777628.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777629.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777630.1 3 582 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777631.1 3 563 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SIAT6 1 8130 NP_777632.1 3 1153 GCCCCCTCCAGC ----- TT 1 A c c
TCATGACACTGT AAGGT GGTGTCATG TTGGGG
TTGGCCTT TTCCG TCACAGTAC GACCTC
GTTTG TC

GAM83 287 SLC30A7 1 7436 NP_598003.1 3 80 GTACGATCCAAA G T - - 1 A c c
ACATTGTACCCA AAG TGG GT CA TGTTTTGGG
GCTTTTTA TTC ACC CA GT ACAAAACCT
G - T T

GAM83 287 SNTG2 1 9285 NP_061841.1 3 136 GATACCAATAAA G T -- 1 A c c
ACATGTCACTAG AAG TGGTG CATGTTTTG GG
TTTCCAAA TTT ATCAC GTACAAAAT CC
G T AA

GAM83 287 SOX4 1 9249 NP_003098.1 3 469 GTCTCCCCCTTC TC TTT-- 1 A c c
CTGCATCACCAC AAGGTGGTG ATGT GGGG
CTTGGTTT TTCCACCAC TACG CCCC
-- TCCTT

GAM83 287 SOX7 1 4922 NP_113627.1 3 1542 CCTGCCCCCAAA TGTC 1 A c c
ATATTTTCATCT AAGGTGG ATGTTTTGGGG
TTCCCCCA TTCTACT TATAAAACCCC

TT--

GAM83 287 SPRR4 1 1276 NP_775103.1 3 187 CGTACCCTTCCC GTC TT 1 A c c
CACACATACCAC AAGGTGGT ATGT TGGGG
CTTGGCTT TTCCACCA TACA ACCCC

--- C-

GAM83 287 SRPR 1 14130 NP_003130.2 3 475 TCCCCAGGACCT A---- - ---- 1 A c c
GGATGACACCCG AGGTGG TGTCAT GTTTTGGGG
CCTCACTG TCCGCC ACAGTA CAGGACCCC

GTCAC C GGTC

GAM83 287 SSA1 1 18743 NP_003132.2 3 93 TTTTCCCCATGA G T- - 1 A c c
ACTCTGAACCAC AAGGTGGT TCA GTTT TGGGG
CTTTGTCT TTCCACCA AGT CAAG ACCCC

- CT T

GAM83 287 STAT1 1 15202 NP_644671.1 3 243 AATTTTCCCAAA T T 1 A c c
ACTGATACCCTT AAGG GGTGTCA GTTTTGGGG
TGAAAAAG TTTC CCATAGT CAAAACCCT

- -

GAM83 287 STHM 1 1189 NP_006447.1 3 684 GTCCCATTAGAG T-- G -- 1 A c c
ATGTATCACCAC AAGGTGGTG CAT TTT TGGGG
CTTGTCAC TTCCACCAC GTA AGA ACCCT

TAT G TT

GAM83 287 SUPT4H1 1 16861 NP_003159.1 3 346 AAGTTCTGAAGG - - G 1 A c c
CCATGACACCTG AAGGT GGTGTCATG TTTT GGG
CCTTGCCT TTCCG CCACAGTAC GGAA TCT

T C G

GAM83 287 SVIL 1 2228 NP_003165.1 3 699 TATCTCCCCAAA G - G 1 A c c
AATGTATAGTGC AAGGTG TGT CAT TTTTGGGG
CTTGTTTT TTCCGT ATA GTA AAAACCCC

G T -

GAM83 287 SVIL 1 2228 NP_068506.1 3 699 TATCTCCCCAAA G - G 1 A c c
AATGTATAGTGC AAGGTG TGT CAT TTTTGGGG
CTTGTTTT TTCCGT ATA GTA AAAACCCC

G T -

GAM83 287 TARSH 1 14655 NP_079077.1 3 371 AGAATCCCCAAA G T G 1 A c c
AGTGTCATGCTT AAGGTG TG CAT TTTTGGGG
TTAAACAA TTTCGT AC GTG AAAACCCC

- T -

GAM83 287 TCOF1 1 12765 NP_000347.1 3 347 AAAGGCCTCGGG TCAT 1 A c c
ACTTCCCACCAC AAGGTGGTG GTTTTGGGG
CTTGCTCC TTCCACCAC CAGGGCTCC

CCTT

GAM83 287 TD-60 1 17170 NP_061185.1 3 360 ACACTCCCCAAA T CATGT 1 A c c
ACACCCCTTTCC AAGG GGTGT TTTGGGG
AGTTACAA TTCC CCACA AAACCCC

- -----

GAM83 287 TNRC6 1 3142 NP_055309.1 3 154 GTTTTCCCCAAA G GTC 1 A c c
ACATATCAGTTT AAG TGGT ATGTTTTGGGG
GAATACTT TTT ACTA TACAAAACCCC

G ---

GAM83 287 TNRC6 1 3142 NP_065898.1 3 154 GTTTTCCCCAAA G GTC 1 A c c

ACATATCAGTTT AAG TGGT ATGTTTTGGGG
GAATACTT TTT ACTA TACAAAACCCC
G ---

GAM83 287 TP53I11 1 10684 NP_006025.1 3 582 TCCCCAACCCCA TG A T 1 A c c
AATCAAGACCAC AAGGTGG TC TG TTTGGGG
CTTTCTTC TTCCACC AG AC AAACCCC
-- A T

GAM83 287 TRIM37 1 19079 NP_056109.1 3 926 AATTAGCCCAAA -- TCA 1 A c c
ACAGTTGCCAAA AAGGT GGTG TGTTTTGGG
CTTTGCCA TTTCA CCGT ACAAAACCC
AA TG-

GAM83 287 TRIP-Br 2 1237 NP_055570.1 3 3611 TTAAAGCTTAAA G T- 1 A c c
2 TTTATGAACCAC AAGGTGGT TCATG TTTGGG
CTTTGTGG TTCCACCA AGTAT AAATTC
- TT

GAM83 287 TRIP-Br 2 18572 NP_055570.1 3 1511 TTTTACCCCAAA GG AT- 1 A c c
2 ACTCAGACAGGA AAGGT TGTC GTTTTGGGG
CTTTCTAT TTTCA ACAG CAAAACCCC
GG ACT

GAM83 287 TUBA3 1 7845 NP_006000.2 3 153 CTATGCTCTAAA GGTG 1 A c c
ACATGAATGCTT AAGGT TCATGTTTTGGGG
TGTTACAG TTTCG AGTACAAAATCTC
TA--

GAM83 287 TWISTNB 1 8569 XP_166508.1 3 2569 AATGTAAAAGAC ATGTTT 1 A c
c
CTCAGGCACCAC AAGGTGGTGTC TGGGG
CTTCGCAT TTCCACCACGG ACTCC

GAM83 287 UBE2V1 1 8971 NP_003340.1 3 772 ACCCAACACCTT T TT----- 1 A c c
CCATGACACTTC AAGG GGTGTCATG TTGGG
CTTGCTTT TTCC TCACAGTAC AACCC
T CTTCCAC

GAM83 287 UBE2V1 1 8971 NP_068823.1 3 772 ACCCAACACCTT T TT----- 1 A c c
CCATGACACTTC AAGG GGTGTCATG TTGGG
CTTGCTTT TTCC TCACAGTAC AACCC
T CTTCCAC

GAM83 287 UBE2V1 1 8971 NP_071887.1 3 772 ACCCAACACCTT T TT----- 1 A c c
CCATGACACTTC AAGG GGTGTCATG TTGGG
CTTGCTTT TTCC TCACAGTAC AACCC
T CTTCCAC

GAM83 287 UBN1 1 17578 NP_058632.1 3 592 TTTCTCCTCGGA - GG--- 1 A c c
ACATGACAATGA AAG GT TGTCATGTTTTGGGG
AGCTCTTT TTC CG ACAGTACAAGGCTCC
T AAGTA

GAM83 287 WBP3 1 1501 NP_783863.2 3 2772 TATTTCCCCAAA G T CA 1 A c c
ACAACCCAGCTT AAG TGG GT TGTTTTGGGG
CACCCCAT TTC ACC CA ACAAAACCCC
G - --

GAM83 287 YWHAG 1 15404 NP_036611.2 3 1556 TCCCGAGACGTG - ----- 1 A c c
TAATGACACCAC AAG GTGGTGTCAT GTTTTGGGG

ACTTGTTT TTC CACCACAGTA CAGAGCCCT
A ATGTG

GAM83 287 ZFYVE26 1 7546 XP_031077.1 3 1862 AACACCACCAAA G - A - 1 A c c
ACAGATACCCAT AA GTGG TGTC TGTTTTGG GG
GTTGAGGG TT TACC ATAG ACAAAACC CC
G C - A

GAM84 204 APPD 1 10016 3 GGTGCCACCAGG ACCA C 3 C b b
CCCAGGGA TCCCTGG GCC GGTGGCACC
AGGGACC CGG CCACCGTGG
---- A

GAM84 204 DGCR2 1 6302 NM_005137.1 3 GGTGCAGTGTGC C C C G G 3 C c c
TGTCCAGAGA TC CTGGAC AGC CG TG CACC
AG GACCTG TCG GT AC GTGG
A - T G -

GAM84 204 FCGR2B 2 7555 NM_004001.2 5 GGCGCCAGCTCG CC- CCGG A 3 C c
c
CTCCAGGGA TCCCTGGA AGC TGGC CC
AGGGACCT TCG ACCG GG
CGC ---- C

GAM84 204 FCGR2B 2 19509 NM_004001.2 5 GGGCCAGCTCGC CC- CCGG A 3 C c
c
TCCAGGGA TCCCTGGA AGC TGGC CC
AGGGACCT TCG ACCG GG
CGC ---- -

GAM84 204 FLJ1111 1 6333 NM_018329.1 3 GGGCACCGATGA CT ----- G A 3 C c c
7 GGGCTGGTCCTA TCC GGACCAGCCC GGTG C CC
GGA AGG CCTGGTCGGG CCAC G GG
AT AGTAG - -

GAM84 204 FLJ2027 1 11122 NM_017738.1 3 GCCATAAGTGGT G CCG ACC 3 C c
c
6 CCAGGGA TCCCTGGACCA C GTGGC
AGGGACCTGGT G TACCG
- AA- ---

GAM84 204 FLJ3065 2 6164 NM_144643.1 5 GGCGCCACCGTC C CCAGCC A 3 C c
c
5 TCCAAGGA TCC TGGA CGGTGGC CC
AGG ACCT GCCACCG GG
A CT---- C

GAM84 204 FLJ3065 2 6278 NM_144643.1 5 GGGCCACCGTCT C CCAGCC A 3 C c
c
5 CCAAGGA TCC TGGA CGGTGGC CC
AGG ACCT GCCACCG GG
A CT---- -

GAM84 204 HTRA3 1 1600 NM_053044.2 3 GGCACCACCCCC CC CCC CA 3 C c
c
TCATCCAGGGA TCCCTGGA AG GGTGG CC
AGGGACCT TC CCACC GG
AC CC- AC

GAM84 204 KIAA098 1 6334 NM_014023.1 3 GGTCTTCAGGAG C - GGT C 3 C c c
2 CTGGTCCAAGGA TCC TGGACCAGC CC GG ACC

AGG ACCTGGTCG GG TC TGG
A A ACT -
GAM84 204 LOC1272 1 19840 3 GTGCCGCCAGTG C G CC C 3 C c c
94 GTCCAAGGA TCC TGGACCA C GGTGGCAC
AGG ACCTGGT G CCGCCGTG
A - A- -
GAM84 204 LOC1337 1 8467 XM_068500.1 5 GTGCCACCGGAA C G CAGC C 3 C c
c
28 GTGCAAGGA TCC TG AC CCGGTGGCAC
AGG AC TG GGCCACCGTG
A G AA-- -
GAM84 204 LOC1489 1 10115 XM_086361.5 5 GCTCTGGGCTGC C T ACC 3 C c c

18 TCCAGGGA TCCCTGGA CAGCCCGG GGC
AGGGACCT GTCGGGTC TCG
C - ---
GAM84 204 LOC1511 1 2757 XM_098006.2 5 GTGCCTACCTCT C CCC - C 3 C c c
24 GGTCTAGAGA TC CTGGACCAG GGT GGCAC
AG GATCTGGTC CCA CCGTG
A T-- T -
GAM84 204 OR2C3 1 15199 XM_060575.2 3 GGTGTTTGTGGA C GT 3 C c c
CTGGTTCAGGGA TCCCTGGACCAG CCG GGCACC
AGGGACTTGGTC GGT TTGTGG
A GT
GAM84 204 OXCT2 1 5349 NM_022120.1 3 GGTGCCACCGGG ACC 3 C b b
TTCCCCAGGGG TCCCTGG AGCCCGGTGGCACC
GGGGACC TTGGGCCACCGTGG
CC-
GAM84 204 RPL13A 1 3006 NM_012423.2 3 GGTGCCACAGGC T ACCA CG 3 C c
c
AGCCCTGGGA TCCC GG GCC GTGGCACC
AGGG CC CGG CACCGTGG
T CGA- A-
GAM84 204 TXN2 1 12500 NM_012473.3 3 GGTGCTGCTGCT C CC TG 3 C c c
GATCCGGGGA TCCCTGGA CAGC GG GCACC
AGGGGCCT GTCG TC CGTGG
A -- GT
GAM85 227 DKFZP43 1 7457 NM_031476.1 3 AGGCCCTTCATC G CACAAT 3 C c
c
4B044 TTCATGGCC GG CATGAAGAT GGGCCT
CC GTACTTCTA CCCGGA
G CTT---
GAM85 227 PCDHGA6 1 13203 NM_018919.2 3 AGGCCCATCCAT AA CACA 3 C c
c
CCCATGCCT GGGCATG GAT ATGGGCCT
TCCGTAC CTA TACCCGGA
C- CC--
GAM85 227 PSKH1 1 9017 NM_006742.1 3 AGACCCACTTGG G AT A - C 3 C c c
GCCTTCATGCC GGCATGAAG C CAA TGGG CT
CCGTACTTC G GTT ACCC GA

- CG - C A
GAM86 3820 FLJ2034 1 15070 3 GAGTCTAGTGCA T TA A- 3 C c c
GACCCGTGAT GTCACG GGTC CACTAGACTC
TAGTGC CCAG GTGATCTGAG
- -- AC
GAM87 3661 ADAMDEC 1 3369 NM_014479.2 3 GCTCTTTGTTTA C CTCA 3 C c c
GGCCTAATCTT AAGATTAGGCCT AAAGAGC
TTCTAATCCGGA TTTCTCG
- TTTG
GAM87 3663 KIAA066 1 2132 NM_014827.1 3 CTCTTTGGACCT - TCTCA C 3 C c c
GATCTTG CAAGATTAGG CC AAAGAG
GTTCTAGTCC GG TTTCTC
A ----- -
GAM87 3661 KIAA157 1 15798 XM_027744.1 3 GCTTTGGTGAGA GCC AA 3 C c c
AAACTAATCTTG CAAGATTAG TCTCA AGAGC
GTTCTAATC AGAGT TTTCG
AAA GG
GAM87 3667 KIAA167 1 10201 XM_040383.5 3 GCTCTTTTGAGA CA - CC 3 C c c
ATTCATAATTT AGATTA GG TCTCAAAAGAGC
TTTAAT CT AGAGTTTTCTCG
-- A TA
GAM87 3660 LOC9105 1 7289 3 CTCCTTTGAGAG ATT - A C 3 C c c
GCGCTCCTTG CAAG AG GCCTCTCAAA GAG
GTTC TC CGGAGAGTTT CTC
C-- G C -
GAM87 366 PDGFC 1 2292 NM_016205.1 3 GCTCTTTTGAGA CAAGA --- 3 C c c
GGAGGCCTAA TTAGGCCTC TCAAAAGAGC
AATCCGGAG AGTTTTCTCG
----- GAG
GAM88 310 AIP1 1 19267 NP_036433.2 3 1699 AAAAGCAATTTC C- TGTC 3 B c c
CAAAAATGAAAC ATGG TTC TTGGAAATT
CCATTCAT TACC AAG AACCTTTAA
CA TAAA
GAM88 310 BCL2L12 1 2744 NP_443074.2 5 141 CCAAAACATTTC C-- C T 3 B c c
CAACACAGAACT ATGG TTCTGT TTGGAAAT
TCCATTCA TACC AAGACA AACCTTTA
TTC C C
GAM88 310 BCL2L12 1 2744 NP_619580.1 5 141 CCAAAACATTTC C-- C T 3 B c c
CAACACAGAACT ATGG TTCTGT TTGGAAAT
TCCATTCA TACC AAGACA AACCTTTA
TTC C C
GAM88 310 C18orf1 1 1225 NP_004329.1 3 3350 TCCAAAATTTAC T C - 3 B c c
TAATACAGAAGC A GGCTTCTGT TTGG AAATTT
TTGACAAG G TCGAAGACA AATC TTTAAA
T T A
GAM88 310 CACNA1S 1 476 NP_000060.1 5 207 AGAAAGCCAGAT TGT A 3 B c c
TCCCAGGGAAGC ATGGCTTC CTTGG AATTT
CATGGAGC TACCGAAG GGACC TTAGA
--- C
GAM88 310 D15Wsu7 1 15739 XP_039495.1 3 143 TTTTTAAATTTC - GT - 3 B c c

5e CCAGGGAAGGAG ATGG CTTCT CTTGG AAATTT
ACCGTCAG TGCC GAGGA GGACC TTTAAA
A AG C

GAM88 310 DKFZP43 1 13554 NP_055364.1 3 3210 ACCATAAATTTC A ----- - 3 B c c
4P211 CAGGATCAGACT TGGCT TCTG TCTTGGAAATTT
AACGGCTA ATCGG AGAC AGGACCTTTAAA
- CAATC T

GAM88 310 DKFZP76 1 18171 XP_040560.4 3 343 CAAAATGATTTC GC TC 3 B c c
2N2316 CAAAGCAGAACA ATG TTCTG TTGGAAATT
TGGAACTT TAC AAGAC AACCTTTAG
-- GA

GAM88 310 FLJ1310 1 5327 XP_291109.1 5 196 TTCCATCTTCCA - - ATT 3 B c c
5 GAGACATGAAGC ATGGCTTC TGTCT TGGAA
CATTATTA TACCGAAG ACAGA ACCTT
T G CTA

GAM88 310 FLJ2145 1 2930 NP_079126.1 3 111 TCTCAGAGTTTC GC- T 3 B c c
8 CAAGCAGGGAAA ATG TTCTG CTTGGAAATTT
CATTACTG TAC GGGAC GAACCTTTGAG
AAA -

GAM88 310 FLJ2257 2 12117 NP_079140.1 3 236 GATTTGTTAATT GTCT 3 B c c
8 TCCATGGGAAGC ATGGCTTCT TGGAAATT
CATGATGG TACCGAAGG ACCTTTAA
GT--

GAM88 310 FLJ2257 2 16393 NP_079140.1 3 236 TTTGTTAATTTC GTCT 3 B c c
8 CATGGGAAGCCA ATGGCTTCT TGGAAATT
TGATGGCC TACCGAAGG ACCTTTAA
GT--

GAM88 310 FLJ3079 1 885 NP_689740.1 3 731 AGTAATGATTTC CTT 3 B c c
4 CTTAGCAGAAGC ATGGCTTCTGT GGAAATT
CGTATTTG TGCCGAAGACG CCTTTAG
ATT

GAM88 310 FLJ3423 1 2585 NP_775965.1 3 1534 AACATAATTTCA TCTTG- 3 B c c
3 GTTATCAGAAGC ATGGCTTCTG GAAATT
CATTCCAT TACCGAAGAC CTTTAA
TATTGA

GAM88 310 GLCCI1 1 10955 XP_166529.2 3 2328 CATGTAAATTTC TG TCTT 3 B c c

CCAGAAGTTGTT A GCTTCTG GGAAATTT
GAGCTCAA T TGAAGAC CCTTTAAA
GT ----

GAM88 310 HMBS 1 12118 NP_000181.2 5 132 CAGCCTACTTTC T T TT 3 B c c
CAAGCGGAGCCA ATGGCT CTG CTTGGAAA
TGTCTGGT TACCGA GGC GAACCTTT
- - CA

GAM88 310 JAK3 1 10674 NP_000206.1 3 209 TTTGTTAAGGTT G - AA 3 B c c
CAAGACAGATGG ATG CT TCTGTCTTGGA TT
GCATATGT TAC GG AGACAGAACTT AA
G T GG

GAM88 310 KCNMB2 1 6564 NP_005823.1 3 613 AAAACTAATTTC C C 3 B c c
CAAAATATAAGC ATGGCTT TGT TTGGAAATT

TGTTTTCA TGTCGAA ATA AACCTTTAA
T A

GAM88 310 KCNMB2 1 6564 NP_852006.1 3 613 AAAACTAATTTC C C 3 B c c
CAAAATATAAGC ATGGCTT TGT TTGGAAATT
TGTTTTCA TGTCGAA ATA AACCTTTAA
T A

GAM88 310 LOC1237 1 10477 XP_058721.2 3 326 ATCTTGAGTTTC T - -- 3 B c c
22 CAAGACCTAGAG A GGCT TCT GTCTTGGAAATTT
AGCTTGGG G TCGA AGA CAGAACCTTTGAG
T G TC

GAM88 310 LOC1490 1 11398 XP_097577.1 5 1145 TCCAGCAATTTC T C- 3 B c c
73 CAAAAGCTGGAG ATGGCTTC GT TTGGAAATT
CTGTGTAA TGTCGAGG CG AACCTTTAA
T AA

GAM88 310 LOC1501 1 13554 XP_086802.2 3 3211 ACCATAAATTTC A ----- - 3 B c c
74 CAGGATCAGACT TGGCT TCTG TCTTGGAAATTT
AACGGCTA ATCGG AGAC AGGACCTTTAAA
- CAATC T

GAM88 310 LOC1502 1 13554 XP_059324.1 3 3211 ACCATAAATTTC A ----- - 3 B c c
13 CAGGATCAGACT TGGCT TCTG TCTTGGAAATTT
AACGGCTA ATCGG AGAC AGGACCTTTAAA
- CAATC T

GAM88 310 LOC1533 1 17717 XP_098369.1 5 895 AACAAGGATTTC - GT- 3 B c c
87 CAAGCTAAGCAA ATGGCTT CT CTTGGAAATTT
GTCATCAG TACTGAA GA GAACCTTTAGG
C ATC

GAM88 310 LOC1542 1 18214 XP_098497.1 3 1722 TGGAGCAATTTC TG CT 3 B c c

22 CAGCAGAAGTTG A GCTTCTGT TGGAAATT
TGGCTTGC T TGAAGACG ACCTTTAA
GT --

GAM88 310 LOC1576 1 10850 XP_088347.2 3 136 CTCATTAATTTC GG T 3 B c c
27 CAGGTGGAGGAA AT CTTCTG CTTGGAAATT
ATGGAGGA TA GGAGGT GGACCTTTAA
AA -

GAM88 310 LOC2011 1 18000 XP_113312.3 3 22 CATCTTAATTTC C TGT 3 B c c
73 CAAGGAAACTAT ATGG TTC CTTGGAAATT
ATTTCTTA TATC AAG GAACCTTTAA
A ---

GAM88 310 LOC2548 2 14223 XP_173188.1 3 625 TGAAATTTCCAT A----- G T--- 3 B c c
26 ATTGAGAGAAGC TGGCTTCT TC TGGAAATTT
CAAACATT ACCGAAGA AG ACCTTTAAA
TTACAA G TTAT

GAM88 310 LOC2548 2 15375 XP_173188.1 3 625 TTCTGAAATTTC A-- G T--- 3 B c c
26 CATATTGAGAGA TGGCTTCT TC TGGAAATTT
AGCCAAAC ACCGAAGA AG ACCTTTAAA
CAA G TTAT

GAM88 310 LOC2564 1 12508 XP_170877.1 5 121 AGGCGGAGTTTC T -- 3 B c c
47 CAAGACTTGGGT ATGGC TCT GTCTTGGAAATTT
GTCATCAT TACTG GGG CAGAACCTTTGAG

T TT

GAM88 310 LOC2832 1 9088 XP_208583.2 5 143 GAGAGCGATTTC TG 3 B c c
44 TGGGATGGAAGC ATGGCTTCTGTCT GAAATT
CATCTGCC TACCGAAGGTAGG CTTTAG
GT

GAM88 310 LOC2839 1 11156 XP_211259.2 5 1756 CTCCTTCATTTC T --- T 3 B c c
11 CAATATGGCAGG ATGGCT CTGTC TTGGAAAT
GCCATGAG TACCGG GACGG AACCTTTA
- TAT C

GAM88 310 LOC2842 1 17038 XP_209102.1 3 1645 TTAAAATTTTAA A ------ -- 3 B c c
77 CAAGACAGGGCT TGGCTT CTGTCTTG GAAATTT
AAGAGCCA ACCGAG GACAGAAC TTTTAAA
- AATCGG AA

GAM88 310 LOC2849 1 16684 XP_209402.1 3 121 TGCTACAATTTC GC CT 3 B c c
06 CATTACAGAGAC ATG TTCTGT TGGAAATT
ATCTGTTG TAC GAGACA ACCTTTAA
A- TT

GAM88 310 LOC2853 1 5638 XP_208313.1 3 307 AGCATAGTTTCT - 3 B b b
21 TAAGACAGAGGC ATGGCTTCTGTCTTG GAAATT
CATTTGGT TACCGGAGACAGAAT CTTTGA
T

GAM88 310 LOC2853 1 13211 XP_209588.1 3 1116 GCATTTGATTTC - - T 3 B c c
87 CAAGTCAGGTAG ATGG CT TCTG CTTGGAAATT
ATCATTGG TACT GA GGAC GAACCTTTAG
A T T

GAM88 310 LOC2859 1 16051 XP_212126.1 5 540 GGATAAAATTTC C G T-- 3 B c c
92 CTTTGGAAAGAA ATGG TTCT TCT GGAAATTT
CCCATGGA TACC AAGA AGG CCTTTAAA
C A TTT

GAM88 310 LOC2860 1 9088 XP_209872.1 5 143 GAGAGCGATTTC TG 3 B c c
47 TGGGATGGAAGC ATGGCTTCTGTCT GAAATT
CATCTGCC TACCGAAGGTAGG CTTTAG
GT

GAM88 310 LOC2863 1 6130 XP_212273.1 5 519 AAAGGGAGTTTC T 3 B b b
32 CAGGCCAGAAGC ATGGCTTCTG CTTGGAAATTT
CATCCCTG TACCGAAGAC GGACCTTTGAG
C

GAM88 310 LOC2863 1 6130 XP_212271.1 5 519 AAAGGGAGTTTC T 3 B b b
33 CAGGCCAGAAGC ATGGCTTCTG CTTGGAAATTT
CATCCCTG TACCGAAGAC GGACCTTTGAG
C

GAM88 310 LOC3387 1 6075 XP_294696.2 3 1121 AGGAATTAAAAT TCT A 3 B c c
69 ATCTGTAGAAGC ATGGCTTCTG TGGA ATTT
CATGGCTT TACCGAAGAT GTCT TAAA
--- A

GAM88 310 LOC3395 1 8415 XP_290951.1 3 244 ACTGACAGTTTC TG 3 B c c
56 TGAGGCAGAAGC ATGGCTTCTGTCT GAAATT
CGTATCAT TGCCGAAGACGGA CTTTGA
GT

GAM88 310 LOC3398 1 3921 XP_295079.1 3 217 CTTACCAATTTC C---- T 3 B c c

32 CAAGTAGAAATT ATGG TTCTG CTTGGAAATT
ATCCATTA TACC AAGAT GAACCTTTAA
TATTA -
GAM88 310 LOC3402 1 4434 XP_295199.1 5 462 AGATATAATTTC CTTC C 3 B c c
69 CAATATACCATT ATGG TGT TTGGAAATT
CAACTACA TACC ATA AACCTTTAA
---- T
GAM88 310 LOC3416 1 10681 XP_296347.1 5 185 CAGACAAGTTTC GC TG 3 B c c
25 CAAGAGTGGAAC ATG TTC TCTTGGAAATTT
ATGGTGTC TAC AGG AGAACCTTTGAA
A- TG
GAM88 310 LOC3454 1 6432 XP_298816.1 5 70 TGGCCAAATTTC - - CTT 3 B c c
84 CTACAGCGAGAT ATGG CTT CTGT GGAAATTT
TATGAAAC TATT GAG GACA CCTTTAAA
A C T--
GAM88 310 LOC3479 1 14547 XP_029423.1 5 70 GCACCCAATTTC CTTC -- 3 B c c
39 CAAAAGACATTT ATGG TGTCT TGGAAATT
CATGAAAC TACT ACAGA ACCTTTAA
TT-- AA
GAM88 310 LOC3484 1 7632 XP_209299.2 3 623 GAATCAAATTTC G - G T 3 B c c
74 CAGAGGTAAGTG AT GCTT CT TCT GGAAATTT
GTGAAAGG TG TGAA GG AGA CCTTTAAA
G T - -
GAM88 310 LOC3490 1 18214 XP_302946.1 3 1722 TGGAGCAATTTC TG CT 3 B c c
59 CAGCAGAAGTTG A GCTTCTGT TGGAAATT
TGGCTTGC T TGAAGACG ACCTTTAA
GT --
GAM88 310 LOC3491 2 1659 XP_302972.1 3 722 ATGATGAAATTT AT-- --- T 3 B c c
60 CCAGACAGAAAG GGCT TCTGTCT GGAAATTT
AGCCCTTT CCGA AGACAGA CCTTTAAA
TTTC GAA -
GAM88 310 LOC3491 2 18539 XP_302972.1 3 722 TGATGAAATTTC AT--- --- T 3 B c c
60 CAGACAGAAAGA GGCT TCTGTCT GGAAATTT
GCCCTTTT CCGA AGACAGA CCTTTAAA
TTTTC GAA -
GAM88 310 LOC9023 1 11676 NP_612356.1 3 219 ACTGCCAATTTC T TG 3 B c c
3 TGAGGCTGAAGC ATGGCTTC GTCT GAAATT
CATTTCAC TACCGAAG CGGA CTTTAA
T GT
GAM88 310 LOC9166 1 3125 NP_612382.1 3 866 GTCAGTAATTTC G -- 3 B c c
3 CAATGGGCGGGA ATG CTTCTGTCT TGGAAATT
GGCATTAA TAC GAGGGCGGG ACCTTTAA
G TA
GAM88 310 MESDC2 1 10030 XP_051854.1 3 1447 GATCTTAATTTA T GG 3 B c c
AAAGACAGAGGC A GGCTTCTGTCTT AAATT
TCCAAAAT C TCGGAGACAGAA TTTAA
C AA
GAM88 310 MGC4057 1 17677 NP_689989.1 3 731 GAATTTAATTTC GC C -- 3 B c c

9 CAAGTTACAAAA ATG TT TGT CTTGGAAATT
TCATTATC TAC AA ACA GAACCTTTAA
TA - TT

GAM88 310 MGC4779 1 1116 NP_775816.1 3 1723 ATATGAAATTTC CT--- C 3 B c c
9 CAAAACAGGCAA ATGG TCTGT TTGGAAATTT
ATCCATAA TACC GGACA AACCTTTAAA
TAAAC A

GAM88 310 NCYM 1 3893 NP_006307.1 5 282 GAGGGAATTTCT CTT- 3 B c c
TTTCGCAGAAGC ATGGCTTCTGT GGAAATTT
CATTACTC TACCGAAGACG TCTTTAAG
CTTT

GAM88 310 NUDT4 1 13312 NP_061967.2 3 515 ATTCAAAATTTC CT T 3 B c c
CAGATTTGGGCT ATGGCTT GTCT GGAAATTT
ATTTCTGT TATCGGG TAGA CCTTTAAA
TT -

GAM88 310 PCDH10 1 17410 NP_065866.1 5 680 AGTAAGATTTTT A---- - - 3 B c c
AAAGACAGAAAG TGGCTT CTGTCTT GGAAATTT
CCACAGGA ACCGAA GACAGAA TTTTTAGA
AGGAC A A

GAM88 310 PCDH10 1 17410 NP_116586.1 5 680 AGTAAGATTTTT A---- - - 3 B c c
AAAGACAGAAAG TGGCTT CTGTCTT GGAAATTT
CCACAGGA ACCGAA GACAGAA TTTTTAGA
AGGAC A A

GAM88 310 POFUT1 1 1461 NP_056167.1 3 972 AGAAGATGCCCA -- AA 3 B c c
GGGCCCAGAAGC ATGGCTTCT GTCTTGG ATTT
CATCAGAA TACCGAAGA CGGGACC TAGA
CC CG

GAM88 310 PRO1768 1 3744 NP_054818.1 3 360 GGGCGGAGTTTC TC 3 B c c
CAAGATAACAGC ATGGCT TGTCTTGGAAATTT
TATTGTGT TATCGA ATAGAACCTTTGAG
CA

GAM88 310 RAB11A 1 6694 NP_004654.1 3 807 TATAATAATTTC - T T 3 B c c
CAAGCGGTAGAT ATGG CT CTG CTTGGAAATT
TATGTGGC TATT GA GGC GAACCTTTAA
A T -

GAM88 310 RBM3 1 8083 NP_006734.1 5 252 CGTTTTAATTTC -- T- 3 B c c
CAGGACTTGAAC ATGGC TTC GTCTTGGAAATT
TGCCATGT TACCG AAG CAGGACCTTTAA
TC TT

GAM88 310 SAS 1 15612 NP_005972.1 5 56 GCCTCGATTTAA GG- 3 B c c
AGAGACAGAAGC ATGGCTTCTGTCTT AAATT
TGTCGGGG TGTCGAAGACAGAG TTTAG
AAA

GAM88 310 SOX9 1 9040 NP_000337.1 3 201 TACCCAAATTTC GC C 3 B c c
CAAGACACAAAC ATG TT TGTCTTGGAAATTT
ATGACCTA TAC AA ACAGAACCTTTAAA
A- C

GAM88 310 TAF1L 1 5793 NP_722516.1 3 458 AAAGAAAATTTC CT - T 3 B c c
CAAGCATGGTAT ATGG TC TG CTTGGAAATTT
CATCTCAC TACT GG AC GAACCTTTAAA

AT T -

GAM88 310 TU12B1- 1 16898 NP_057659.1 3 4599 AACTTGATTTAC TC - 3 B c c
TY CAAGACAAGCTG ATGGCT TGTCTTGG AAATT
TGGGCTGT TGTCGA ACAGAACC TTTAG
-- A

GAM88 310 USP13 1 8813 NP_003931.1 3 37 ATATAAAAATTG GTC GA 3 B c c
GCGAAAAGAAGC ATGGCTTCT TTG AATTT
CATACGCC TACCGAAGA AGC TTAAA
AA- GG

GAM88 310 ZNF211 1 8415 NP_006376.1 3 244 ACTGACAGTTTC TG 3 B c c
TGAGGCAGAAGC ATGGCTTCTGTCT GAAATT
CGTATCAT TGCCGAAGACGGA CTTTGA
GT

GAM88 310 ZNF211 1 8415 XP_290823.1 3 244 ACTGACAGTTTC TG 3 B c c
TGAGGCAGAAGC ATGGCTTCTGTCT GAAATT
CGTATCAT TGCCGAAGACGGA CTTTGA
GT

GAM89 235 AP1GBP1 1 17343 NM_080550.1 3 CAAAATGAAATC CATTTTGT 3 C c
c
CAGTGAAG CTTCAC TTTCATTTTG
GAAGTG AAAGTAAAAC
ACCT----

GAM89 235 KIAA124 1 5953 NM_020340.1 3 CAAAATGAAAGT C A TTG 3 C c c
4 AATGGAGAA TTC CCATT TTTTCATTTTG
AAG GGTAA GAAAGTAAAAC
- A T--

GAM89 235 LOC1532 1 1873 XM_087628.1 3 CAAAATGAGAGA CCA - 3 C c c
18 CAAAAATGAAG CTTCA TTTTGTTT TCATTTTG
GAAGT AAAACAGA AGTAAAAC
A-- G

GAM89 235 LOC2566 1 16637 3 CAAAATGAAAAC C CCA- 3 C c c
91 AAAGCAAATGAA TTCA TTTTGTTTTCATTTTG
AAGT GAAACAAAAGTAAAAC
- AAAC

GAM90 374 AF02059 1 16052 NM_014480.1 5 GATGAGGAAACT CA AG 3 C c c
1 GAGGCCTGGAGA TC CAG TTTAGTTTCCTCATT
AG GTC GAGTCAAAGGAGTAG
AG CG

GAM90 374 BANP 1 18199 NM_017869.2 5 GGTGAGGCAAGA A AG T 3 C c c
AGCTCTGGGGA TCC CAGAGTTT TT CCTCATT
AGG GTCTCGAA AA GGAGTGG
G G- C

GAM90 374 BCL6 1 9018 NM_001706.2 3 AATGAGGAATGT TT GT-- 3 C c c
ATATGTTTTGTG TCCACAGAG TA TTCCTCATT
GG GGGTGTTTT AT AAGGAGTAA
GT ATGT

GAM90 374 CIAS1 1 19841 NM_004895.2 5 GATGAGGAAACT A AG 3 C c c
GAAGTTGAGGA TCC CAG TTTAGTTTCCTCATT
AGG GTT AAGTCAAAGGAGTAG
A G-

GAM90 374 CTCFL 1 16845 NM_080618.2 3 ATGAGATTTAAA TTTC T 3 C c c
TTCTGTGGG TCCACAGAGTTTAG CTCAT
GGGTGTCTTAAATT GAGTA
TA-- -
GAM90 374 DKFZp43 1 12460 NM_178123.1 5 ATGAGGAAGATC G TTTAG T 3 C c
c
4O0515 TTGTGGA TCCACA AG TTTCCTCAT
AGGTGT TC GAAGGAGTA
- TA--- -
GAM90 374 E2IG4 1 10835 NM_015516.1 3 GATGGGGAAACT - C AG 3 C c c
GAGGCCTTGAGA TC CA AG TTTAGTTTCCTCATT
AG GT TC GAGTCAAAGGGGTAG
A - CG
GAM90 374 EBAG9 1 768 NM_004215.2 5 GGTGAGGAAACT A AGTT 3 C c c
GCGACTGGGA TCC CAG TAGTTTCCTCATT
AGG GTC GTCAAAGGAGTGG
- AGC-
GAM90 374 FLJ1396 1 10501 3 GATGAAGACTTA G - CC 3 C c c
4 GAATCTGTGGA TCCACAGA TTTA GTTT TCATT
AGGTGTCT AGAT CAGA AGTAG
A T --
GAM90 374 FLJ2191 1 6125 3 AGTGGGGAGATT AGTTT 3 C c c
6 TCCACTGTGGA TCCACAG AGTTTCCTCATT
AGGTGTC TTAGAGGGGTGA
ACCT-
GAM90 374 GAB2 1 12509 NM_080491.1 5 AGTGAGGGAATT T C A 3 C c c
AGACCTTTGG CCA AG GTTTAGTTTCCTCATT
GGT TC CAGATTAAGGGAGTGA
- T -
GAM90 374 GARP 1 10589 NM_005512.1 3 GATGGGGAAACT ACA - 3 C c c
GAGGCTTAGGA TCC GAGT TTAGTTTCCTCATT
AGG TTCG AGTCAAAGGGGTAG
A-- G
GAM90 374 HCC8 1 19979 NM_016516.1 3 AGTGTTGGGAAA A -- 3 C c c
CTGGATTCAGTG TCCAC GAGTTTAGTTTCCT CATT
GG GGGTG CTTAGGTCAAAGGG GTGA
A TT
GAM90 374 HMP19 1 1334 NM_015980.1 3 AGTGAAGAGCAC A - C 3 C c c
AGACTCTGTGGG TCCACAGAGTTT GT TTC TCATT
GGGTGTCTCAGA CA GAG AGTGA
- C A
GAM90 374 IRF1 1 622 NM_002198.1 3 GGTGCAGAGAAG - - - 3 C c c
CTGGACTTCTGT TCCACAGA GTTTAGTTTC CT CATT
GGG GGGTGTCT CAGGTCGAAG GA GTGG
T A C
GAM90 374 KIAA028 1 5713 XM_166238.1 3 AATGAGGAAACA CAG TT A 3 C c c
0 GGTTATGGA TCCA AG T GTTTCCTCATT
AGGT TT A CAAAGGAGTAA
A-- GG -
GAM90 374 KIAA121 1 9549 XM_028835.7 3 AATGGGGATGCA G --- T 3 C c c

9 AATAAAGTTTGT TCCACAGA TTTA GT TCCTCATT
GGG GGGTGTTT AAAT CG AGGGGTAA
G AAA T

GAM90 374 KIAA134 1 17198 XM_044836.7 3 AATGTTGACAAT C - CT 3 C c c
0 TAGATTCTTGGA TCCA AGAGTTTAGTT TC CATT
AGGT TCTTAGATTAA AG GTAA
- C TT

GAM90 374 KIAA171 1 2627 XM_042834.2 3 ATAGGAAACTGA - CATT 3 C c c
5 AACTCTGTGGA TCCACAGAGTT TAGTTTCCT
AGGTGTCTCAA GTCAAAGGA
A TA--

GAM90 374 LOC1244 1 14538 XM_058805.5 5 AGTGCAGGGAGT C GT - 3 C c c
46 TGAACTTTTGGA TCCA AGAGTTTA TTCCT CATT
AGGT TTTCAAGT AGGGA GTGA
- TG C

GAM90 374 LOC1476 1 15549 3 GGTGCTGGGAGA A -- 3 C c c
85 CTGAGCCTGTGG TCCACAG GTTTAGTTTCCT CATT
G GGGTGTC CGAGTCAGAGGG GTGG
- TC

GAM90 374 LOC1485 1 16878 3 GATGAGGAAACT C AG 3 C c c
08 GAAGCTTGGA TCCA AG TTTAGTTTCCTCATT
AGGT TC AAGTCAAAGGAGTAG
- G-

GAM90 374 LOC1509 1 18871 3 GATGGGGGACAA G A TT T 3 C c c
98 GCTGTGTGGA TCCACA AGTTT GT CC CATT
AGGTGT TCGAA CA GG GTAG
G - GG -

GAM90 374 LOC1591 1 16647 5 GATGGGGAGGCC A TA 3 C c c
99 TGGCTCTGGGA TCC CAGAGTT GTTTCCTCATT
AGG GTCTCGG CGGAGGGGTAG
- TC

GAM90 374 LOC1997 1 5506 3 GATGAGGAAACT A-- AG 3 C c c
86 GAGGCTGAGCGG TCC CAG TTTAGTTTCCTCATT
G GGG GTC GAGTCAAAGGAGTAG
CGA G-

GAM90 374 LOC2002 1 13733 XM_114152.1 3 GATGGGGAGGCT A AG 3 C c c
05 GGGGCCTGGGG TCC CAG TTTAGTTTCCTCATT
GGG GTC GGGTCGGAGGGGTAG
- CG

GAM90 374 LOC2205 1 10285 XM_018306.6 3 GATGAGGAAGAG A AG 3 C c c
22 GACTTTGGGG TCC CAGAGTTT TTTCCTCATT
GGG GTTTCAGG GAAGGAGTAG
- A-

GAM90 374 LOC2228 1 2424 5 AATGAGGAAGTG C -- G 3 C c c
03 AGTGTTCTTGGA TCCA AGAG TTTA TTTCCTCATT
AGGT TCTT GAGT GAAGGAGTAA
- GT -

GAM90 374 LOC2541 1 16296 5 AGTGGGGATCTC C - TT 3 C c c
32 AAGCTCTTGGA TCCA AGAGTTT AG TCCTCATT
AGGT TCTCGAA TC AGGGGTGA

```
                                                  -      C  T-
GAM90   374   LOC2575 1  13098          3       AGTGAGGGCACT    C    TT  T          3  C  c  c
        54                              GCTCTTGGA   TCCA AGAGT  AGT TCCTCATT
                                              AGGT TCTCG  TCA GGGAGTGA
                                                -    --  C
GAM90   374   LOC5127 1  954    NM_016546.1  3       AATGAGGAAACT   ACA   -            3  C  c  c
        9                               GAGGCTCAGGGG TCC   GAGT TTAGTTTCCTCATT
                                              GGG   CTCG AGTCAAAGGAGTAA
                                                GA-   G
GAM90   374   LOC8029 1  18667  NM_025198.2  5       GATGAGGACAAG       GTTTAGTT          3  C  c
c
        8                               ATCTGTGGG   TCCACAGA      TCCTCATT
                                              GGGTGTCT      AGGAGTAG
                                                 AGAAC---
GAM90   374   LOC9166 1  10541          5       ATGATGGTTAAA          TTT  -   T     3  C  c  c
        0                               CTCTGTGGG   TCCACAGAGTTTAG   CC TCAT
                                              GGGTGTCTCAAATT   GG AGTA
                                                   ---  T   -
GAM90   374   MGC1203 1  6223   NM_024296.1  3       GGTGAGGGAACT TC    A              3  C  c  c
                                AAACCTGTG     CACAG GTTTAGTTTCCTCATT
                                              GTGTC CAAATCAAGGGAGTGG
                                             --    -
GAM90   374   MGC3035 1  11606  NM_024293.1  5       GATGAGGAGGCT    C  GTTT           3  C  c
c
                                TCTATCTTGGA  TCCA AGA   AGTTTCCTCATT
                                              AGGT TCT    TCGGAGGAGTAG
                                                -  ATCT
GAM90   374   MIR16   1  3695   NM_016641.2  3       AATGAGGAAACT                    3  C  a  a
                                AAACTCTGTGGA TCCACAGAGTTTAGTTTCCTCATT
                                              AGGTGTCTCAAATCAAAGGAGTAA

GAM90   374   NFE2L1  1  19520  NM_003204.1  5       AGTGAGGAAGTG     GAGTT   ---        3  C  c  c
                                ACTGTATGTGGA TCCACA    TAGTT   TCCTCATT
                                              AGGTGT    GTCAG   AGGAGTGA
                                                 AT---    TGA
GAM90   374   NLGN1   1  8799   NM_014932.1  5       GATGAGGGGGCT       TTT  TT         3  C  c  c
                                CCCTCTGTGGA  TCCACAGAG   AGT  CCTCATT
                                              AGGTGTCTC   TCG  GGAGTAG
                                                 CC-   GG
GAM90   374   NRXN2   1  10578  NM_138732.1  3       GATGGGGAAGCT    A-  AGTT           3  C  c  c
                                GCTGGAGGA    TCC  CAG    TAGTTTCCTCATT
                                              AGG  GTC    GTCGAAGGGGTAG
                                                AG   ----
GAM90   374   NUMB    1  13662  NM_003744.3  5       AATGAGGAAACT TC   A   -            3  C  c  c
                                GAGGCTTGGTG    CAC GAGT TTAGTTTCCTCATT
                                              GTG TTCG AGTCAAAGGAGTAA
                                             --  G   G
GAM90   374   PARVA   1  14808  NM_018222.2  3       GATGAGGAAACT    C AG            3  C  c  c
                                AAGGCTTGGA   TCCA AG  TTTAGTTTCCTCATT
                                              AGGT TC  GAATCAAAGGAGTAG
```

- G-

GAM90 374 PRO1496 1 1444 NM_018603.1 3 GGTGAGGACGGG G AGTT 3 C c c

ATCTGTGGA TCCACAGA TTT TCCTCATT

AGGTGTCT AGG AGGAGTGG

- GC--

GAM90 374 PTPRT 1 2885 NM_007050.3 3 GATGAGGAAACT T ACA - 3 C c c

AAGGCTCCTAGG CC GAGT TTAGTTTCCTCATT

GG CTCG AATCAAAGGAGTAG

- ATC G

GAM90 374 RELB 1 9956 NM_006509.1 3 GATGAGGAAACT ACA G 3 C c c

GAGTCCGGA TCC GA TTTAGTTTCCTCATT

AGG CT GAGTCAAAGGAGTAG

C-- -

GAM90 374 ROCK2 1 4807 NM_004850.2 3 GATGTAAACTAG T CCT 3 C c c

CTTTGTGGA TCCACAGAGTT AGTTT CATT

AGGTGTTTCGA TCAAA GTAG

- T--

GAM90 374 WNT10B 1 5168 NM_003394.2 3 GGTGGGGGTCAG A G -- 3 C c c

GTGGACTCTGGG TCC CAGAGTTTA TT TCCTCATT

A AGG GTCTCAGGT GA GGGGGTGG

- G CT

GAM91 336 AQP6 1 14082 NM_053286.1 3 ATCCTCCTCCAG - - CA A 3 C c c

GGACTGCTGTGA TCGCAGCAG CCC GGA GGA GAT

AGTGTCGTC GGG CCT CCT CTA

A A -- C

GAM91 336 C20orf7 1 17422 XM_114180.1 3 ATCTCCCTCCAG TC -- - CA A 3 C c c

0 GAAGCTGCTGC GCAGCAGC CC GGA GG AGAT

CGTCGTCG GG CCT CC TCTA

-- AA A -- C

GAM91 336 FAF1 1 899 NM_131917.1 5 ATCTTCCTGTCC 3 C a a

GGGCTGCTGCGA TCGCAGCAGCCCGGACAGGAAGAT

AGCGTCGTCGGGCCTGTCCTTCTA

GAM91 336 FLJ2020 1 3833 NM_017711.2 5 ATCTTCCCACCC TC G ACA 3 C c c

7 GGGCTGTGC GCA CAGCCCGG GGAAGAT

CGT GTCGGGCC CCTTCTA

-- - CAC

GAM91 336 FLJ2240 1 18346 NM_024794.1 3 CTTCCTGTCCCT CA- CCC AT 3 C c c

8 GCCTTCGA TCG GCAG GGACAGGAAG

AGC CGTC CCTGTCCTTC

TTC --- --

GAM91 336 HPCAL1 1 4354 NM_002149.2 3 ATCCTCCCATCC GCC CA A 3 C c c

GTGTTGTGA TCGCAGCA CGGA GGA GAT

AGTGTTGT GCCT CCT CTA

--- AC C

GAM91 336 LIMD1 1 19473 NM_014240.1 3 ATCCTCCTGTCC G C CCC A 3 C c c

CCTCTGGGA TC CAG AG GGACAGGA GAT

AG GTC TC CCTGTCCT CTA

G - C-- C

GAM92 308 LOC1581 1 16734 3 TAAATAGACTAG G - TA 3 C c c
56 TCATGTCCTT AAGGA CATGAT AG TCTATTTA
TTCCT GTACTG TC AGATAAAT
- A --

GAM93 397 FLJ3233 1 19780 NM_144565.1 3 TGCACAGCAACC C ATA TA 3 C c c
4 CAGCCTT AAGGCTGGG TGCTG TGTA
TTCCGACCC ACGAC ACGT
A --- --

GAM93 397 PKP2 1 7334 NM_004572.1 3 TACATTATCAGC - - TA 3 C b b
CAGCCCAGCCTT AAGGCTGGGCTG CTGATA TGTA
TTCCGACCCGAC GACTAT ACAT
C T --

GAM93 397 PROL1 1 11105 NM_021225.1 3 TATATTAAGCAG - TATA 3 C c c
CCCAGCCTT AAGGCTGGGCTGCT GATATG
TTCCGACCCGACGA TTATAT
A ----

GAM94 332 ABCA1 1 8991 NP_005493.2 5 179 TGTCAAGGGGTA - - 3 B c c
GGAGAAAGAGAC TTGT TTTCTTTCTCCT CTTCT
GCAAACAC AACG AGAGAAAGAGGA GGGGA
C T

GAM94 332 ABR 1 18596 NP_001083.1 5 16 GGAGGAGGAAGA C 3 B c c
GGAGGCGATAG TTGTTTTCTTT TCCTCTTCT
AGCGGAGGAGA AGGAGGAGG
-

GAM94 332 ACE 1 10322 NP_690044.1 3 211 GGAAGAGGCTGC TG ------ 3 B c c
TGAGAAAGAGAA T TTTTCTTTCT CCTCTTCT
TGAGAAGA A AAGAGAAAGA GGAGAAGG
GT GTCGTC

GAM94 332 ACTR6 1 17448 NP_071941.1 5 10 AGCAGAGGGGTC C --- 3 B c c
GGAAAGGGAAAA TTGTTTTCTTT TCC TCTTCT
CAACTACG AACAAAAGGGA AGG GGGAGA
A CTG

GAM94 332 ACTR8 1 7335 NP_075050.1 3 672 GTGAGCTTAGAG - TCT 3 B c c
GAAGAAAGAAAA TTGTTTTCTTTCT CCTCT
CAATTTTT AACAAAAGAAAGA GGAGA
A TTC

GAM94 332 ADAM10 1 19754 NP_001101.1 5 197 GGGGAGAGAAGA -- C 3 B c c
GGGAACGAGCAA TTGTTT TCTTTCT CTCTTCT
GGGAAGGA AACGAG AGGGAGA GAGAGGG
CA A

GAM94 332 ADAMTS8 1 19214 NP_008968.2 3 188 TAAGGGGGAAGA --- 3 B c c
GGAGAGGGTATG TTGTTTT CTTTCTCCTCTTCT
GGGCGGCA GGCGGGG GGGAGAGGAGAAGG
TAT

GAM94 332 AFG3L1 1 13711 NP_001123.1 5 314 AATACTTTAAGA T TC 3 B c c
GGAGTGGAAGGA TTGT TTCTTTC CTCTTCT
ACACAAAC AACA AAGGAAG GAGGAGA
C GT

GAM94 332 AKAP2 1 6726 NP_009134.1 3 1121 AAAGGGAGGGAA ---- -- 3 B c c

GGAGAAAGAATG TTGTTT TCTTTCTCCT CTTCT
GGAATAAA AATAAG AGAAAGAGGA GGAGG
GGTA AG

GAM94 332 AKAP2 1 6726 NP_671492.1 3 1121 AAAGGGAGGGAA ---- -- 3 B c c
GGAGAAAGAATG TTGTTT TCTTTCTCCT CTTCT
GGAATAAA AATAAG AGAAAGAGGA GGAGG
GGTA AG

GAM94 332 ALEX3 1 15945 NP_057691.1 5 204 GGCAAAAGAAGA TT TC 3 B c c
GGAAGGAATTTA TTG TTCTT TCCTCTTCT
ATCCTAAT AAT AAGGA AGGAGAAGA
TT --

GAM94 332 ALEX3 1 15945 NP_808816.1 5 176 GGCAAAAGAAGA TT TC 3 B c c
GGAAGGAATTTA TTG TTCTT TCCTCTTCT
ATCCTAAT AAT AAGGA AGGAGAAGA
TT --

GAM94 332 ALEX3 1 15945 NP_808817.1 5 127 GGCAAAAGAAGA TT TC 3 B c c
GGAAGGAATTTA TTG TTCTT TCCTCTTCT
ATCCTAAT AAT AAGGA AGGAGAAGA
TT --

GAM94 332 ALK7 1 1036 NP_660302.1 3 1104 AGAAAAGGAAGA T---- - 3 B c c
GGAAGGAAGGAA TGTTTTCTTTCT CCTCTTCT
ATATTTTG ATAAAGGAAGGA GGAGAAGG
GTTTT A

GAM94 332 ANK1 1 1839 NP_000028.2 3 316 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A

GAM94 332 ANK1 1 1839 NP_065208.1 3 253 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A

GAM94 332 ANK1 1 1839 NP_065209.1 3 253 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A

GAM94 332 ANK1 1 1839 NP_065210.1 3 253 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A

GAM94 332 ANK1 1 1839 NP_065211.1 3 318 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A

GAM94 332 ANK1 1 1839 NP_065212.1 3 318 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A

GAM94 332 ANK1 1 1839 NP_065213.1 3 255 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG

TA A
GAM94 332 ANK1 1 1839 NP_065214.1 3 318 GCGGGGAGAGAG -- - 3 B c c
AGGGATAGAAAA TTGTTTTCT TTCTC CTCTTCT
CAAGCGCA AACAAAAGA GGGAG GAGAGGG
TA A
GAM94 332 AP1S3 1 6748 XP_291023.1 5 11 GAAAGGGGAAAG CC 3 B c c
GAAGAAAGAAGG TTGTTTTCTTTCT TCTTCT
AGAGCAGG GACGAGAGGAAGA AGAAGG
A-
GAM94 332 APLN 1 3649 NP_059109.2 3 1333 GGTTCCCAGGAG -- T 3 B c c
GGAGAAAGAGAA TTGTTTTCTT TCTCC CTTCT
GACAAGAG AACAGAAGAG AGAGG GAGGA
AA -
GAM94 332 APOA5 1 14854 NP_443200.1 3 490 GGGGAATAGAAG T----- T 3 B c c
GGAGAAAGAGAA TGTTTTCTTTCTCC CTTCTA
TATCATGG ATAAGAGAAAGAGG GAAGAT
GGTACT -
GAM94 332 AQP1 1 19824 NP_000376.1 3 270 AGTTGTGGAGGA G T 3 B c c
GGTGAAAGAAAG TT TTTTCTTTC CCTCTTCTA
GGACCCAC AG GAAAGAAAG GGAGGAGGT
G T
GAM94 332 ARCN1 1 10942 NP_001646.2 3 28 ATACCAAGAAGA G T- T 3 B c c
GGGAGCTGAAAA TT TTTTC TTC CCTCTTCT
GGAAAATT AG AAAAG GAG GGAGAAGA
G TC -
GAM94 332 ARHGEF1 1 3599 NP_056128.1 3 534 AGGTTAAGAAGA - 3 B c c
2 GGAGGAAGTGAG TTGTTTT CTTTCTCCTCTTCT
ACGGGGAA GGCAGAG GAAGGAGGAGAAGA
T
GAM94 332 ARHGEF9 1 14362 NP_056000.1 5 720 ACAGGGAAAGAG TT - - 3 B c c
AGAGAAAGAACA TTGT TCTTTCTC CTCTT CT
AGCTTTCT AACA AGAAAGAG GAGAA GG
-- A A
GAM94 332 ASTN 1 14476 XP_045113.1 3 3115 CTACTGCAGAAG T C T 3 B c c
GAAGAAAGAATA TTGT TTCTTTCT C CTTCT
TAATATGA AATA AAGAAAGA G GAAGA
T A -
GAM94 332 ATP6V1G 1 2763 NP_569730.1 5 205 CGAGCTGGAGGA TC 3 B c c
2 GGAGAAGTAAGC TTGTTT TTTCTCCTCTTCTA
GGTGGGGG GGCGAA GAAGAGGAGGAGGT
T-
GAM94 332 BACE 1 19344 NP_036236.1 3 605 CGGCTGGAAAGA G - 3 B c c
GGAGAAGGAGAG TT TTTTCTTTCTCCTCTT CTA
GGAGTACA AG GAGAGGAAGAGGAGAA GGT
G A
GAM94 332 BACE 1 19344 NP_620427.1 3 605 CGGCTGGAAAGA G - 3 B c c
GGAGAAGGAGAG TT TTTTCTTTCTCCTCTT CTA
GGAGTACA AG GAGAGGAAGAGGAGAA GGT
G A
GAM94 332 BACE 1 19344 NP_620428.1 3 605 CGGCTGGAAAGA G - 3 B c c

GGAGAAGGAGAG TT TTTTCTTTCTCCTCTT CTA
GGAGTACA AG GAGAGGAAGAGGAGAA GGT
G A

GAM94 332 BACE 1 19344 NP_620429.1 3 605 CGGCTGGAAAGA G - 3 B c c
GGAGAAGGAGAG TT TTTTCTTTCTCCTCTT CTA
GGAGTACA AG GAGAGGAAGAGGAGAA GGT
G A

GAM94 332 BACH2 1 17333 NP_068585.1 5 222 ACGCGGGGAAGA G T 3 B c c
GGAGGCGGAAAA TT TTTTCT TCTCCTCTTCT
GGACGCAA AG AAAAGG GGAGGAGAAGG
G C

GAM94 332 BAZ2A 1 16323 NP_038477.1 5 153 GAGGGTGGAAGA G --- 3 B c c
GGAGAGGGTGGA TT TTTTCT TTCTCCTCTTCTA
AGGGGAAT AG GGAAGG GAGAGGAGAAGGT
G TGG

GAM94 332 BCL11B 2 3630 NP_075049.1 3 3157 GTCAGATGTAGA T T - 3 B c c
GGAGAGAGAGCG TGTTTTCTT CTC CTCTTCT
AGAGAACA ACAAGAGAG GAG GAGAGGA
- C A

GAM94 332 BCL11B 2 17597 NP_075049.1 5 79 AGAAGAAGAAGA G 3 B c c
GGAGGAAGAGAG TT TTTTCTTTCTCCTCTTCT
GGAAAGAG AG GAGAGAAGGAGGAGAAGA
G

GAM94 332 BCL11B 2 17597 NP_612808.1 5 79 AGAAGAAGAAGA G 3 B c c
GGAGGAAGAGAG TT TTTTCTTTCTCCTCTTCT
GGAAAGAG AG GAGAGAAGGAGGAGAAGA
G

GAM94 332 BDKRB2 1 14045 NP_000614.1 3 2271 CAGTAAGTATCT TCTT- 3 B c c

GGAGGAAGAAAA TTGTTTTCTTTCTCC CT
CAGGTGAA GACAAAAGAAGGAGG GA
TCTAT

GAM94 332 BM-002 1 19641 NP_057701.1 3 1160 GTAGAAGAAGGC -- - - 3 B c c
AGTTAGAGAAAA TTGTTTTCTTT CT CCT CTTCTA
CAAAGTAT AACAAAAGAGA GA GGA GAAGAT
TT C A

GAM94 332 BMP4 4 11479 NP_001193.1 5 18 CGCCGGGGAAGA G 3 B b b
GGAGGAGGAAGG TT TTTTCTTTCTCCTCTTCT
AAAGAAAG AA AAAGGAAGGAGGAGGAGA
G

GAM94 332 BMP4 4 11479 NP_570911.1 5 18 CGCCGGGGAAGA G 3 B b b
GGAGGAGGAAGG TT TTTTCTTTCTCCTCTTCT
AAAGAAAG AA AAAGGAAGGAGGAGGAGA
G

GAM94 332 BMP4 4 15443 NP_001193.1 5 54 GGGAGGGAAAGA --- - 3 B c b
GGAGGAAGGAAG TTGT TTTCTTTCTCCTCTT CT
ATGCGAGA AGCG AAGGAAGGAGGAGAA GG
TAG A

GAM94 332 BMP4 4 15443 NP_570911.1 5 54 GGGAGGGAAAGA --- - 3 B c b
GGAGGAAGGAAG TTGT TTTCTTTCTCCTCTT CT

ATGCGAGA AGCG AAGGAAGGAGGAGAA GG
TAG A

GAM94 332 BMP4 4 16063 NP_001193.1 5 28 GGAGGAGGAAGG ------ 3 B c b
AAAGAAAGAAAG TTGTTTTCTTTC TCCTCTTCT
CGAGGGAG AGCGAAAGAAAG AGGAGGAGG
AAAGGA

GAM94 332 BMP4 4 16063 NP_570911.1 5 28 GGAGGAGGAAGG ------ 3 B c b
AAAGAAAGAAAG TTGTTTTCTTTC TCCTCTTCT
CGAGGGAG AGCGAAAGAAAG AGGAGGAGG
AAAGGA

GAM94 332 BMP4 4 17767 NP_001193.1 5 19 AAGAGGAGGAGG G 3 B b b
AAGGAAAGAAAG TT TTTTCTTTCTCCTCTTCT
AAAGCGAG AA AAAGGAAGGAGGAGGAGA
G

GAM94 332 BMP4 4 17767 NP_570911.1 5 19 AAGAGGAGGAGG G 3 B b b
AAGGAAAGAAAG TT TTTTCTTTCTCCTCTTCT
AAAGCGAG AA AAAGGAAGGAGGAGGAGA
G

GAM94 332 BTEB1 2 6904 NP_001197.1 5 580 TGACTGGCAGGG T - 3 B c c
GGAGAAAGTAAA TTGTTT CTTTCTCCTCTT CTA
CAGAGTTG GACAAA GAAAGAGGGGGA GGT
T C

GAM94 332 BTEB1 2 12461 NP_001197.1 3 2224 CTCACAGAAAGA TCC - 3 B c c
AACGAAAGAAAG TTGTTTTCTTTC TCTT CT
CAAAGCAA AACGAAAGAAAG AGAA GA
CAA A

GAM94 332 BTN2A1 1 2586 NP_008980.1 5 143 CGAGAACCAGCG -- - T --- 3 B c c
GAGAAAAGAAAA TTGT TTTCTTT CTCC CT TCT
AGCAACGT AACG AAAGAAA GAGG GA AGA
AA A C CCA

GAM94 332 BTN2A1 1 2586 NP_510961.1 5 143 CGAGAACCAGCG -- - T --- 3 B c c
GAGAAAAGAAAA TTGT TTTCTTT CTCC CT TCT
AGCAACGT AACG AAAGAAA GAGG GA AGA
AA A C CCA

GAM94 332 BY55 1 11183 NP_008984.1 3 428 ACTGCAAAGGAA CTC 3 B c c
AGAGAGAGAAAA TTGTTTTCTTTCTC TTCT
CAAGCAAA AACAAAAGAGAGAG AAGG
A--

GAM94 332 C10orf5 1 12775 XP_172843.1 3 2148 AGAAGGAAGGAA G -- 3 B c c
GGAGAAAGAGAA TT TTTTCTTTCTCCT CTTCT
GGAAAGAA AG AAGAGAAAGAGGA GAAGG
G AG

GAM94 332 C14orf7 1 7433 XP_096733.1 5 138 GGGTGTGGAAGA CT- C 3 B c c
2 GGAAAGTGTGAA TTGTTTT TT TCCTCTTCTA
GCAAGGGA AACGAAG GA AGGAGAAGGT
TGT A

GAM94 332 C1orf16 2 4187 NP_055652.2 3 1267 CATTTTGGAAGA G TC 3 B c c
GACGAAAGAAAG TT TTTTCTTTC CTCTTCTA
GAAAATAA AA GAAAGAAAG GAGAAGGT
G CA

GAM94 332 C1orf16 2 7627 NP_055652.2 3 1113 ACAGTCTGAAGA TTC T 3 B c c
GGAAGGAAGCAG TTGTTTTCT TCCTCTTC
CAGTATCT GACGAAGGA AGGAGAAG
--- T
GAM94 332 C1orf2 1 1834 NP_006580.1 3 265 TCTTATAGCACT TCTT 3 B c c
GGAGGAGGAAAA TTGTTTTCTTTCTCC CTA
CAAATTCT AACAAAAGGAGGAGG GAT
TCAC
GAM94 332 C1orf21 1 15376 NP_110433.1 3 4387 CCTGGGAGAAGA T C 3 B c c
GGAAAAAGGAGC TTG TTTCTTT TCCTCTTCT
TAATATTT AAT GAGGAAA AGGAGAAGA
C A
GAM94 332 C1orf9 1 19770 NP_055098.1 5 201 GGGGAAGAAGGA TG T - 3 B c c
GGAGAAGATGAA T TTTTCTT CTCCT CTTCT
GAAGCACC A AGAAGAG GAGGA GAAGG
GT - A
GAM94 332 C20orf1 2 14428 NP_689515.1 5 491 GATGCTAGAAGA TCT TC 3 B c c
58 GCTGAACAAACA TTGTTT TTC CTCTTCTA
GATCGAGG GACAAA AAG GAGAAGAT
C-- TC
GAM94 332 C20orf1 2 14515 NP_689515.1 5 182 TCTAGAGGAAGA T C 3 B c c
58 GGAGGACGACAG TTGTT TCTTTCTC TCTTCTA
GCCATACG GACAG AGGAGGAG AGGAGAT
C A
GAM94 332 C20orf1 1 14077 XP_066058.2 3 1249 TTCCACGGGAGA G TC- 3 B c c
74 GGAGAAACTTAA TT TTT TTTCTCCTCTTCT
AGAGGTTT GA AAA AAAGAGGAGAGGG
G TTC
GAM94 332 C3orf4 1 12175 NP_063948.1 3 305 TGGGAGTAGGAA TT ---- - 3 B c c
TGTGACCGAAAA TTGTTTTC TC TCCT CTTCTA
CAAGTTGT AACAAAAG AG AGGA GAGGGT
CC TGTA T
GAM94 332 C5orf4 1 1351 NP_057432.1 3 1362 GGTAGGAGATAA TT --- 3 B c c
GGAGAAAGAACA TTGT TCTTTCTCC TCTTCTA
GATACGGT GACA AGAAAGAGG AGAGGAT
-- AAT
GAM94 332 C5orf4 1 1351 NP_115761.1 3 2868 GGTAGGAGATAA TT --- 3 B c c
GGAGAAAGAACA TTGT TCTTTCTCC TCTTCTA
GATACGGT GACA AGAAAGAGG AGAGGAT
-- AAT
GAM94 332 C6orf49 1 5100 NP_060071.1 5 725 AGGGGGAAAGAA G - - 3 B c c
GGAGAAAGGAAA TT TTTTCTTTCTCCT CTT CT
GAAAAACC AA AAAGGAAAGAGGA GAA GG
G A A
GAM94 332 C6orf84 2 5543 NP_055710.1 3 289 GCTAGAAATAGA G CCTC 3 B c c
AAGAAAAGAAAA TT TTTTCTTTCT TTCTA
TTGAACAT AA AAAAGAAAGA AAGAT
G TA--
GAM94 332 C6orf84 2 16947 NP_055710.1 3 289 TGTATGCTAGAA G CCTC 3 B c c
ATAGAAAGAAAA TT TTTTCTTTCT TTCTA

GAAAATTG AA AAAAGAAAGA AAGAT
G TA--
GAM94 332 C8orf17 1 4088 NP_064622.1 5 626 TGCGGTAGAAGA T------- TC 3 B c c
GGAAGGGAAACA TGTTTTCTT TCCTCTTCTA
CGAACAAA ACAAAGGGA AGGAGAAGAT
AAACAAGC --
GAM94 332 CA10 1 3311 NP_064563.1 3 451 CCAAAAGAGAGA TTTC - 3 B c c
GGAGAAAATACA TTGT TTTCTCCTCT TCT
GCTCTGAT GACA AAAGAGGAGA AGA
TA-- G
GAM94 332 CALCR 1 16744 NP_001733.1 3 1717 TAATATAGTAGG CT T 3 B c c
GGTTGAAGAAAA TTGTTTTCTTT CCTCT CTA
CAAAATAG AACAAAAGAAG GGGGA GAT
TT T
GAM94 332 CASK 1 11580 NP_003679.1 3 171 GAATAGATAGGA CT CT 3 B c c
GGAGAAAAACAA TTGTTTT TTCTCCT TCTA
TTACACAC AACAAAA AGGAGGA AGAT
AG T-
GAM94 332 CCNI 1 1699 NP_006826.1 5 484 GGAGGAAGAGGA TTT-- 3 B c c
GGAGAAGGTAGC TTGT CTTTCTCCTCTTCT
TACAGCAA GACA GGAAGAGGAGGAGA
TCGAT
GAM94 332 CCNL2 1 9923 NP_112199.1 5 633 CCTGGAGGAAGA TT TC 3 B c c
GGAAGAGGAACC TTG TTCTT TCCTCTTCT
CAAGAGGA AAC AAGGA AGGAGAAGG
CC GA
GAM94 332 CCRL1 1 19245 NP_057641.1 3 178 AAGCCAAGAAGA T TC- 3 B c c
GGAAACAAGATA TTGTT TCTT TCCTCTTCT
ATAAATGT AATAA AGAA AGGAGAAGA
T CAA
GAM94 332 CCRL1 1 19245 NP_848540.1 3 178 AAGCCAAGAAGA T TC- 3 B c c
GGAAACAAGATA TTGTT TCTT TCCTCTTCT
ATAAATGT AATAA AGAA AGGAGAAGA
T CAA
GAM94 332 CD28 1 5373 NP_006130.1 3 288 TGACTGAGAAGT TT CT- 3 B c c
TAGGGTAGAAAA TTGTTTTCT CTC CTTCT
CAAAAAGG AACAAAAGA GGG GAAGA
T- ATT
GAM94 332 CDC14A 1 15163 NP_201570.1 3 155 TAGCAAGAAGCA T TC - 3 B c c
GAGGAAAGAAAC TTG TTTCTTTC CT CTTCT
CAATTGCC AAC AAAGAAAG GA GAAGA
C GA C
GAM94 332 CDC25A 1 910 NP_001780.1 3 346 CATGAGGGGAGA G T 3 B c c
GGAGACGGAGGG TT TTTTCT TCTCCTCTTCT
GAGTAGAG GA GGGAGG AGAGGAGAGGG
G C
GAM94 332 CDC2L1 2 9626 NP_277022.1 5 331 ATGGAAGACAGA TG T - 3 B c c
GGAGAAGAAGAT T TTTTCTT CTCCTCT TCT
GATTCTTT A AGAAGAA GAGGAGA AGA
GT - C

GAM94 332 CDC2L1 2 9626 NP_277025.1 5 331 ATGGAAGACAGA TG T - 3 B c c
GGAGAAGAAGAT T TTTTCTT CTCCTCT TCT
GATTCTTT A AGAAGAA GAGGAGA AGA
GT - C
GAM94 332 CDC2L1 2 11887 NP_277022.1 5 183 GAAGGAACAAGA -- CT 3 B c c
GGAGAAAGCAGA TTGTTTT CTTTCTCCTCTT
GATAAAAC AATAGAG GAAAGAGGAGAA
AC CA
GAM94 332 CDC2L1 2 11887 NP_277023.1 5 183 GAAGGAACAAGA -- CT 3 B c c
GGAGAAAGCAGA TTGTTTT CTTTCTCCTCTT
GATAAAAC AATAGAG GAAAGAGGAGAA
AC CA
GAM94 332 CDC2L1 2 11887 NP_277024.1 5 183 GAAGGAACAAGA -- CT 3 B c c
GGAGAAAGCAGA TTGTTTT CTTTCTCCTCTT
GATAAAAC AATAGAG GAAAGAGGAGAA
AC CA
GAM94 332 CDC2L1 2 11887 NP_277025.1 5 183 GAAGGAACAAGA -- CT 3 B c c
GGAGAAAGCAGA TTGTTTT CTTTCTCCTCTT
GATAAAAC AATAGAG GAAAGAGGAGAA
AC CA
GAM94 332 CDC2L2 5 2681 NP_277069.1 5 964 GGAGGAGGAAGA T TT 3 B c c
GGAGGAGGAGGA TGTT CTTTCTCCTCTTCT
AGGGAGCA ACGA GAAGGAGGAGGAGG
- GG
GAM94 332 CDC2L2 5 2681 NP_277074.1 5 1003 GGAGGAGGAAGA T TT 3 B c c
GGAGGAGGAGGA TGTT CTTTCTCCTCTTCT
AGGGAGCA ACGA GAAGGAGGAGGAGG
- GG
GAM94 332 CDC2L2 5 9626 NP_277069.1 5 299 ATGGAAGACAGA TG T - 3 B c c
GGAGAAGAAGAT T TTTTCTT CTCCTCT TCT
GATTCTTT A AGAAGAA GAGGAGA AGA
GT - C
GAM94 332 CDC2L2 5 9626 NP_277074.1 5 299 ATGGAAGACAGA TG T - 3 B c c
GGAGAAGAAGAT T TTTTCTT CTCCTCT TCT
GATTCTTT A AGAAGAA GAGGAGA AGA
GT - C
GAM94 332 CDC2L2 5 11887 NP_277069.1 5 151 GAAGGAACAAGA -- CT 3 B c c
GGAGAAAGCAGA TTGTTTT CTTTCTCCTCTT
GATAAAAC AATAGAG GAAAGAGGAGAA
AC CA
GAM94 332 CDC2L2 5 11887 NP_277074.1 5 151 GAAGGAACAAGA -- CT 3 B c c
GGAGAAAGCAGA TTGTTTT CTTTCTCCTCTT
GATAAAAC AATAGAG GAAAGAGGAGAA
AC CA
GAM94 332 CDC2L2 5 14067 NP_277069.1 5 946 TGAGGAAGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
AGAGGAGG AG AGAAGGAGGAGGAGGAGA
G
GAM94 332 CDC2L2 5 14067 NP_277074.1 5 985 TGAGGAAGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT

AGAGGAGG AG AGAAGGAGGAGGAGGAGA
G
GAM94 332 CDC2L2 5 17841 NP_277069.1 5 278 CCGTATAGAAGA T----- C 3 B c c
GAAGACTCAATG TTGTTTTCT TCT CTCTTCTA
GAAGACAG GACAGAAGG AGA GAGAAGAT
TAACTC A
GAM94 332 CDC2L2 5 17841 NP_277074.1 5 278 CCGTATAGAAGA T----- C 3 B c c
GAAGACTCAATG TTGTTTTCT TCT CTCTTCTA
GAAGACAG GACAGAAGG AGA GAGAAGAT
TAACTC A
GAM94 332 CDGAP 1 657 XP_291085.1 3 188 TTTGCTAGAAGA - --- TC 3 B c c
GTGGTCAAGGGA TTGTTTT CTTT C CTCTTCTA
AAAACGAG AGCAAAA GGGA G GAGAAGAT
A ACT GT
GAM94 332 CDH1 1 15908 NP_004351.1 3 1975 TTCTTTGGGGGT C T 3 B c c
GGAAAAGGAAAA TTGTTTTCTTT TCC CTTCTA
CAATTCAA AACAAAAGGAA AGG GGGGGT
A T
GAM94 332 CDH18 1 14157 NP_004925.1 5 7 ATAGACTGAAGA ---- T T 3 B c c
GGAGCAAGAACA TTGTTT TCTT CTCCTCTTC
GAAACAGG GACAAA AGAA GAGGAGAAG
GACA C T
GAM94 332 CDKN2C 1 5149 NP_523240.1 5 364 GCAAAGGAAAGG - C - 3 B c c
GGAAAAAGAAAA TTGTTTT CTTT TCCTCTT CT
ACGACTAA AGCAAAA GAAA AGGGGAA GG
A A A
GAM94 332 CDT6 1 7162 NP_066969.1 5 91 CAAAGAGCAAGG -- C- 3 B c c
AAAGAGAGAAAA TTGTTTTCTTTC TCCT TTCT
CAACAAAG AACAAAAGAGAG AGGA GAGA
AA AC
GAM94 332 CGI-104 1 18497 NP_057230.1 5 145 GCGGGAGGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGCTG AG AGGAGGAGGAGGAGAAGG
G
GAM94 332 CGI-85 1 5217 NP_057112.2 3 611 TAAAGATGGAAA T C 3 B c c
GGAGAAAGAAGC TTGTTT CTTTCTCCT TTCTA
AACCTCTG AACGAA GAAAGAGGA AAGGT
- -
GAM94 332 CHD1L 1 18799 NP_078844.1 3 90 GAGACTCATAGA C- ----- 3 B c c
GGAGAAGAAGAG TTGTTTT TTTCTCCTCT TCT
GCAAAAGG AACGGAG GAAGAGGAGA AGA
AA TACTC
GAM94 332 CHRM5 1 18498 NP_036257.1 5 248 GCCAAGAAGAGC -- TC 3 B c c
TGAAATAGAAAA TTGTTTTCT TTC CTCTTCT
CAGCCTAG GACAAAAGA AAG GAGAAGA
TA TC
GAM94 332 CHRNB2 1 17099 NP_000739.1 3 388 CATGGGAGAAGA CTTT 3 B c c
GGGGTATAGGAC TTGTTTT CTCCTCTTCT
AAGGGGTG AACAGGA GGGGAGAAGA

TAT-

GAM94 332 CHST1 1 11016 NP_003645.1 5 275 GTCGGAGGAAGA G TT 3 B c c
GGAGGGAGGAGG TT TTTTCT CTCCTCTTCT
GAGGCCGA GA GGAGGA GAGGAGAAGG
G GG

GAM94 332 CKLFSF6 2 1874 NP_060271.1 3 259 TTGGTGGGAGGA T CT 3 B c c
GGAGAAAACAAT TTGTTTTCTT CTCCTCTT
TGTTTTTA AACAAAAGAG GAGGAGGG
- TG

GAM94 332 CKLFSF6 2 14312 NP_060271.1 3 259 GATTTTGGTGGG T CT 3 B c c
AGGAGGAGAAAA TTGTTTTCTT CTCCTCTT
CAATTGTT AACAAAAGAG GAGGAGGG
- TG

GAM94 332 CLCN4 1 12401 NP_001821.1 3 1673 TAAGTGGGAAGA T TT - 3 B c c
GGAAGGGAGAGG TTGTTT CT CT CCTCTTCT
CAAGCAAC AACGGA GA GA GGAGAAGG
- GG A

GAM94 332 CLDN14 1 5051 NP_652763.1 5 629 GCTTTCTTGGAA T CC 3 B c c
GAAGAAAGAAAC TTGTTT CTTTCT TCTTCTA
AAAAACTG AACAAA GAAAGA AGAAGGT
- --

GAM94 332 CLK3 1 18588 NP_001283.1 3 94 AATCAAGGAGAA C - 3 B b b
GGACAAAGAAAA TTGTTTTCTTT TCCT CTTCT
CAAGTTCC AACAAAAGAAA AGGA GAGGA
C A

GAM94 332 CNNM1 2 1194 NP_065081.1 3 1491 GAAAGAAAGAAA G - C- - 3 B c c
GAGAAAAGAAAA TT TTTTCTTT CTC TCTT CT
GAAAAGCA AA AAAAGAAA GAG AGAA GA
G A AA A

GAM94 332 CNNM1 2 7736 NP_065081.1 3 1491 AAAGAAAGAGAA - - C-- - 3 B c c
AAGAAAAGAAAA TTGTTTT CTTT CT CTCTT CT
GCAACCAC AACGAAA GAAA GA GAGAA GA
A A AAA A

GAM94 332 CNOT4 1 9013 NP_037448.1 3 987 ATTGAAAAGACA T - CT 3 B c c
GGAGAAAAGCAA TTGTTT CTTT CTCCT TCT
ACAGAAAC GACAAA GAAA GAGGA AGA
C A C-

GAM94 332 CNR2 1 15470 NP_001832.1 5 6 CAGGTCCTGGGA TTC 3 B c c
GAGGACAGAAAA TTGTTTTCT TCCTCTTCTA
CAACTGGA AACAAAAGA AGGAGAGGGT
C--

GAM94 332 COL17A1 1 4162 NP_000485.2 3 755 AAAGGGAGAAGA TT--- --- T 3 B c c
GGGAAAACAGAA GTTTTCT TTC CCTCTTCT
AACCTGAT CAAAAGA AAG GGAGAAGA
TAGTC CAA -

GAM94 332 COL17A1 1 4162 NP_570134.1 3 145 AAAGGGAGAAGA TT--- --- T 3 B c c
GGGAAAACAGAA GTTTTCT TTC CCTCTTCT
AACCTGAT CAAAAGA AAG GGAGAAGA
TAGTC CAA -

GAM94 332 COL19A1 1 19736 NP_001849.1 3 4270 AGGCTTTGAAGA T-- 3 B c c

GGAGGAGATGCA TTGTTTTCT TCTCCTCTTCT
GAAGATAA AATAGAAGA AGAGGAGGAGA
CGT

GAM94 332 COL22A1 1 17151 XP_291257.2 3 552 AAAGAAGCAGAA T-- --- - 3 B c c
AGAGAAAGAATT TTGT TTCTTTCTC CT CTTCT
TGCAACCA AACG AAGAAAGAG GA GAAGA
TTT AAA C

GAM94 332 CRAMP1L 1 17653 XP_034570.4 3 769 AGACATGGAAGA CTTTC 3 B c c

GGAAGAACAAAG TTGTTTT TCCTCTTCTA
TCCCCTCT AACAAGA AGGAGAAGGT

GAM94 332 CREG2 1 5574 NP_722578.1 3 1744 TTAGAAAAATGG ----- ---- 3 B c c
GGAGAAAGCTGG TTGTTTT CTTTCTCCTC TTCTA
AAGAACAA AACAAGA GAAAGAGGGG AAGAT
AGGTC TAAA

GAM94 332 CRIM1 1 18711 NP_057525.1 3 819 GTGACAGGAAGA TG TT 3 B c c
GGAGGGAGAGGG T TTTTCT CTCCTCTTCT
TGACGAAC A GGGAGA GAGGAGAAGG
GT GG

GAM94 332 CRK7 1 16784 NP_057591.1 3 341 ACTGGTCGGAAG TT C 3 B c c
AGAGAAAGAACA TTGT TCTTTCTC TCTTCT
GTTTCAGT GACA AGAAAGAG AGAAGG
-- -

GAM94 332 CRN 1 19629 NP_006578.2 5 31 GGGACACGTAGA C ----- 3 B c c
GGAGAGAAAAGC TTGTTTT TTTCTCCTCT TCT
GACCAAGA AGCGAAA AGAGAGGAGA AGG
- TGCAC

GAM94 332 CSF1R 5 1086 NP_005202.2 5 59 GAAGAGAGAAGA G TC 3 B c c
GGAAGAGGAAGA TT TTTTCTT TCCTCTTCT
GGAAGAGA AG AGAAGGA AGGAGAAGA
G GA

GAM94 332 CSF1R 5 2612 NP_005202.2 5 141 GGAGGAGGAAGA TC 3 B c c
GGAAAACAAGAC TTGTTTTCTT TCCTCTTCT
AAACAGCC AACAAAAGGA AGGAGGAGG
GA

GAM94 332 CSF1R 5 6055 NP_005202.2 5 68 AGAAGAGGAAGA TT - 3 B c c
GGAAGAGGAAGA GTTTTCTTTCT CCTCTTCT
GAGGAAGC CGAAGGAGAGA GGAGAAGG
-- A

GAM94 332 CSF1R 5 9658 NP_005202.2 5 140 GCCCAAGGAGGA TC 3 B c c
GGAAGAGGAAAA TTGTTTTCTT TCCTCTTCT
CAAGACAA AACAAAAGGA AGGAGGAGG
GA

GAM94 332 CSF1R 5 15322 NP_005202.2 5 68 GGAAGAGGAAGA - 3 B c c
GGAAGAGAGGAA TTGTTTTCTTTCT CCTCTTCT
GCGGAGGG GGCGAAGGAGAGA GGAGAAGG
A

GAM94 332 CSPG3 1 5105 NP_004377.1 3 1757 GGACTCTGGAGA - TT T 3 B c c
GGAGATTGAAAT TTGT TTTC TCTCCTCTTC

ATAATTGC AATA AAAG AGAGGAGAGG
T TT T
GAM94 332 CXCL1 1 10919 NP_001502.1 3 87 AGGAACAGAAGA - C 3 B c c
GGAAAGAGAGAC TTGT TTTCTTT TCCTCTTCT
ACAGCTGC GACA AGAGAGA AGGAGAAGA
C A
GAM94 332 CXCL2 1 10919 NP_002080.1 3 86 AGGAACAGAAGA - C 3 B c c
GGAAAGAGAGAC TTGT TTTCTTT TCCTCTTCT
ACAGCTGC GACA AGAGAGA AGGAGAAGA
C A
GAM94 332 CYorf14 1 8844 NP_061012.1 3 391 AAGTAAAAGAAA C CTC 3 B c c
AAGAAAAGAAAA TTGTTTTCTTT TC TTCT
TAACTCCC AATAAAAGAAA AG AAGA
- AAA
GAM94 332 CYP3A7 1 13918 NP_000756.1 5 71 AAAAGACTCAGA G T --- 3 B c c
GGAGAGAGATAA TT TT TCTTTCTCCTCT TCT
GGAAGGAA AG AA AGAGAGAGGAGA AGA
G T CTC
GAM94 332 CYP4F3 2 17402 NP_000887.1 3 2932 AGAAAGAAAGAA G CCTC 3 B c
c
AAGAAAAGAAAA TT TTTTCTTTCT TTCT
TCCCTTTT AA AAAAGAAAGA AAGA
G ----
GAM94 332 CYP4F3 2 18277 NP_000887.1 3 2927 AGGAAAGAAAGA G CC - 3 B c c
AAGAAAAGAAAA TT TTTTCTTTCT TCTT CT
GAAAATCC AA AAAAGAAAGA AGAA GG
G A- A
GAM94 332 CYP7B1 1 4296 NP_004811.1 3 27 TTAAGAAGCTAA CCT--- 3 B c c
AAGGAAAGAAAA TTGTTTTCTTTCT CTTCT
TAAATCTA AATAAAAGAAAGG GAAGA
AAAATC
GAM94 332 DCLRE1A 1 13586 NP_055696.1 3 291 AGCCTTAGAAGA CT C 3 B c c
GGAAGCAAAGGC TTGTTTT TT TCCTCTTCTA
AGATTCAG GACGGAA GA AGGAGAAGAT
AC -
GAM94 332 DCT 1 12756 NP_001913.2 5 338 AGTAGAAGATAA TT- - --- 3 B c c
GGAGAAAAGTAC TTGTT CTTT CTCC TCTTCTA
GACAGAGA GACAG GAAA GAGG AGAAGAT
CAT A AAT
GAM94 332 DDX11 1 14293 NP_085913.1 3 252 AGAAGCCAAAGA - - 3 B c c
GGAGGAGGCAGG TTGTT TTCTT TCTCCTCTTCT
AGAAGCAG GACGA GAGGA GGAGGAGGAGA
A C
GAM94 332 DEPP 1 12438 NP_008952.1 3 929 GGGACAGAGAGA TT -- 3 B c c
GGAGAGGAGGAA GTTT TCTTTCTCCTCTTCT
GATTGAGC CGAG AGAAGGAGGAGAGGA
-- TT
GAM94 332 DES 2 5424 NP_001918.2 3 646 GAAGAGAGGAGA ---- 3 B c c

GGAGAGAGGCAG TTGTTTTCT TTCTCCTCTTCT
AGAGCGGT GGCGAGAGA GAGAGGAGAGGA
CGGA

GAM94 332 DES 2 9797 NP_001918.2 3 639 CTGGAGAAGAGA TTT 3 B c c
GGAGAGGAGAGA TTGT CTTTCTCCTCTTCT
GGCAGAGA GACG GAGAGAGGAGAGGA

GAM94 332 DIO1 1 5841 NP_000783.2 3 557 GGAGTTGGAAGA C-- TT 3 B c c
GGAGGGATTAGA TTGTTTT T CTCCTCTTCTA
AACAGGAG GACAAAG A GAGGAGAAGGT
ATT GG

GAM94 332 DJ102H1 1 13535 NP_071367.1 3 95 ACGGATGGAAGA TTTC--- 3 B c c
9.4 GGAAAACACTGA TTGTTTTC TCCTCTTCTA
GAACAACA AACAAGAG AGGAGAAGGT
TCACAAA

GAM94 332 DKFZP43 1 14982 XP_168185.1 3 256 AAAAGAAGAGCA - --- 3 B b b
4A0225 AGAGAAAGAGAA TTGTT TTCTTTCTC CTCTTCT
ACAAAAAT AACAA GAGAAAGAG GAGAAGA
A AAC

GAM94 332 DKFZP43 2 4715 XP_044070.6 3 967 GAAGAAGGAAGA G --- 3 B c c
4L187 GGAAAGGGAGGA TT TTTTCTTTC TCCTCTTCT
GGAGGATT AG AGGAGGAGG AGGAGAAGG
G GAA

GAM94 332 DKFZP43 2 8955 XP_044070.6 5 459 AGAGGAAGAAGA T--- -- T 3 B c c
4L187 GGAGATGGCTGA TGTTTT CT TCTCCTCTTCT
AACATATA ACAAAG GG AGAGGAGAAGA
ATAT TC T

GAM94 332 DKFZp45 1 18054 NP_694967.1 3 1574 GGAGGGAGAAGG T C 3 B c c

1A175 GAAGAAAGAAAC TTGTTT CTTTCT CTCTTCT
AATGTCTA AACAAA GAAAGA GGGAAGA
- A

GAM94 332 DKFZp54 1 1986 NP_061175.1 3 1857 AGGATTAGAAGA CT C 3 B c c
7G183 GGAAACAGAAAC TTGTTTT TT TCCTCTTCTA
AGGTAACA GACAAAG AA AGGAGAAGAT
AC -

GAM94 332 DKFZp56 1 18835 NP_056234.1 3 927 GAGGAGGTGAGA TT TC 3 B c
c
4I1922 GGAGAGGAAGGA GTTTTCTT TCCTCTTCT
GAAAACTG CAAAAGAG AGGAGAGGA
GT GA

GAM94 332 DKFZp76 1 14715 NP_115663.1 3 501 TGAGCAATGAGG TT T 3 B c c
1O17121 AGGAGTGGAAAA TTGTTTTCT CTCCTCTTC
CAAAACCC AACAAAAGG GAGGAGGAG
T- T

GAM94 332 DKK2 1 8609 NP_055236.1 5 259 TAGGAAAAGAGA C CT 3 B c c
GGAGAGAAAAGC TTGTTTT TTTCTCCTCTT
AACTGAGT AACGAAA AGAGAGGAGAG
- AA

GAM94 332 DLX1 1 12176 NP_835221.1 3 972 GGCAAATGGGGA C T 3 B c c

GTAGAGAGAAAA TTGTTTTCTTTCT CTCTTC
CAGGCGAG GACAAAAGAGAGA GAGGGG
T T

GAM94 332 DMD 1 10078 NP_000100.2 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_003997.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_003998.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004000.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004001.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004002.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004003.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004004.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004005.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004006.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004007.1 3 1492 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T

GAM94 332 DMD 1 10078 NP_004008.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA

AT- T
GAM94 332 DMD 1 10078 NP_004009.1 3 1492 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T
GAM94 332 DMD 1 10078 NP_004011.1 3 1578 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T
GAM94 332 DMD 1 10078 NP_004012.1 3 1492 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T
GAM94 332 DMD 1 10078 NP_004013.1 3 1492 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T
GAM94 332 DMD 1 10078 NP_004014.1 3 1492 TTTGTAAGTAAG CCT - 3 B c c
TAAGAAAGAAGG TTGTTTTCTTTCT CTT CT
CAAATTGA AACGGAAGAAAGA GAA GA
AT- T
GAM94 332 DNAJA1 1 9846 NP_001530.1 5 75 GCAGTAGAAGAT T T - 3 B c c
GGTGAAAGAAAC TTGTTT CTTTC CC TCTTCTA
AACTTACT AACAAA GAAAG GG AGAAGAT
- T T
GAM94 332 DNAJB5 1 17549 NP_036398.2 3 544 TGTGCCTCTCTG CC 3 B c c
GGAGAAAGGAGA TTGTTTTCTTTCT TCTTCTA
GAGGATAA AATAGGAGAGAGG AGAGGGT
AA
GAM94 332 DNAM-1 1 2229 NP_006557.1 3 1182 GTACAGGCAACA T C - 3 B c c
GGAGAAAGGAAT TTG TTTCTTTCTCCT TT CT
CAAACCAC AAC AAGGAAAGAGGA AA GG
T C C
GAM94 332 DPF3 1 16598 NP_036206.1 3 693 GGCTGAGGGGTC T- 3 B c c
GGGGGAAGAAAA TTGTTTTCTTTCTCC CTTCT
CAGATGAC GACAAAAGAAGGGGG GGGGA
CT
GAM94 332 DPYSL3 1 13744 NP_001378.1 3 2425 TACAAAAGGTTT C CT- 3 B c c
AGGAAAAGAAAA TTGTTTTCTTT TCCT TCT
CAATGGTG AACAAAAGAAA AGGA GGA
- TTT
GAM94 332 DRD3 1 11135 NP_387507.1 3 99 TTCCAAGAAAGA G T- 3 B c c
GGAGGAGAGTTG TT TTTTC TTCTCCTCTTCT
AAAAGAGA GA AAAAG GAGAGGAGGAGA
G TT
GAM94 332 DUSP16 1 7912 XP_039106.1 5 97 CTGAAAAGAAGA 3 B b b
GGAGGAGGAGAG TTGTTTTCTTTCTCCTCTTCT
CGACGGGA AGCGAGAGGAGGAGGAGAAGA

GAM94 332 EGR1 1 2968 NP_001955.1 3 25 TGCTAAGGGAAA G C 3 B c c

GGGGAAAGAAAG TT TTTTCTTTCTCCT TTCT
GGAAAAGG AG GAAAGAAAGGGGA AGGG
G A

GAM94 332 EIF4G3 1 12862 NP_003751.2 3 0 CAGAAGAGGAGT TTT 3 B c c
CTGAGGATAACT TTGTTTTC CTCCTCTTCT
AAACTTCA AATAGGAG GAGGAGAAGA
TCT

GAM94 332 EIF5A 1 3210 NP_001961.1 3 531 GGGGAGGGAAGA G 3 B c c
GGAGGAGAGGGG TT TTTTCTTTCTCCTCTTCT
AGGGGACC AG GGAGGGGAGAGGAGGAGA
G

GAM94 332 EIF5AP1 1 6926 XP_290186.1 3 516 GAGGGAAGAAGA G 3 B c c
GGAGAGGGGAGG TT TTTTCTTTCTCCTCTTCT
GGACCTGC AG GGAGGGGAGAGGAGAAGA
G

GAM94 332 EMR2 1 9659 NP_038475.2 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EMR2 1 9659 NP_690880.1 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EMR2 1 9659 NP_690881.1 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EMR2 1 9659 NP_690882.1 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EMR2 1 9659 NP_690883.1 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EMR2 1 9659 NP_690884.1 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EMR2 1 9659 NP_690885.1 3 2485 GAATTAAAGAAA - TC - 3 B c c
GAGGAAAGAAAC TTGT TTTCTT TCCTCTT CT
ACAAAAAG AACA AAAGAA AGGAGAA GA
C -- A

GAM94 332 EPB41L1 1 16125 NP_818932.1 5 64 CCTAGACATGGA TT --- 3 B c c
GGAGAAGGACTA TTGT TCTTTCTCCTCT TCTA
CAGTGAGG GACA AGGAAGAGGAGG AGAT
TC TAC

GAM94 332 ESDN 1 551 NP_563615.2 3 2847 ATCTCCAGAAGA TT - 3 B c c
GGGGAGCAGAGT TTG TTCT TTCTCCTCTTCT
CCGAGCTT AGC GAGA GAGGGGAGAAGA

CT C

GAM94 332 EVI5 1 9673 NP_005656.2 3 3273 ATCTTTGGAGAA G - T 3 B c c
GGAGAAAGAAAG TT TTTTCTTTCTCCT CTTC
GAAAGAAC AA GAAAGAAAGAGGA GAGG
G A T

GAM94 332 EXT1 1 16470 NP_000118.1 5 571 AAAGACCGAAGG G T- T 3 B c c
GGAGAAAGTTAA TT TTT CTTTCTCCTCTTC
AGAAATCG AA AAA GAAAGAGGGGAAG
G TT C

GAM94 332 FACL4 1 4716 NP_004449.1 3 132 TCTAAAGATAGA CTC - 3 B c c
GTAAAAAGAAAA TTGTTTTCTTT CTCT TCT
CAAAACCA AACAAAAGAAA GAGA AGA
AAT T

GAM94 332 FACL4 1 4716 NP_075266.1 3 132 TCTAAAGATAGA CTC - 3 B c c
GTAAAAAGAAAA TTGTTTTCTTT CTCT TCT
CAAAACCA AACAAAAGAAA GAGA AGA
AAT T

GAM94 332 FGF13 1 4855 NP_004105.1 5 583 ACAAGCAGCGGA G T 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCT CT
GGAGGCGA AG AGGAGGAAGAGGAGG GA
G C

GAM94 332 FKBP10 2 4046 NP_068758.2 3 648 AACCATAGAAGA C 3 B b b
GAGGAAGAAAAC TTGTTTTCTTTCTC TCTTCTA
AAAGGGCA AACAAAAGAAGGAG AGAAGAT
-

GAM94 332 FKBP10 2 13573 NP_068758.2 3 648 GAACCATAGAAG C 3 B b b
AGAGGAAGAAAA TTGTTTTCTTTCTC TCTTCTA
CAAAGGGC AACAAAAGAAGGAG AGAAGAT
-

GAM94 332 FKBP8 2 10546 NP_036313.2 5 20 GGAGGAGGAAGA TG 3 B c c
GGAGGAAGAGGA T TTTTCTTTCTCCTCTTCT
TGACCTGA A AGGAGAAGGAGGAGAAGG
GT

GAM94 332 FKBP8 2 10823 NP_036313.2 5 8 TGAGGAGGAAGA G 3 B c c
GGAGGAGGAAGA TT TTTTCTTTCTCCTCTTCT
GGAGGAAG AG AGAAGGAGGAGGAGAAGG
G

GAM94 332 FLJ1030 1 18087 NP_060521.2 5 425 GACAGAGGGAGA - T 3 B c c
0 GGAGAAGAGACG TTGT TTTCTT CTCCTCTTCT
CAAAAGAC AACG AGAGAA GAGGAGAGGG
C -

GAM94 332 FLJ1041 1 15496 NP_060559.1 3 300 CCAAGCGGAGGA C- 3 B c c
5 GGAGAAAAAGGA TTGTTTT TTTCTCCTCTTCT
ATAAGAAG AATAAGG AAAGAGGAGGAGG
AA

GAM94 332 FLJ1089 2 10943 NP_060730.1 5 94 AAACACGGAAGA TC 3 B c c
1 GGAAGAGGAAAG TTGTTTTCTT TCCTCTTCT
CAAAGGAG AACGAAAGGA AGGAGAAGG
GA

GAM94 332 FLJ1089 2 18909 NP_060730.1 5 95 GGAAGAGGAAGA TC 3 B c c

	1					GGAAAGCAAAGG TTGTTTTCTT TCCTCTTCT AGTCAGGG AACGAAAGGA AGGAGAAGG GA								
GAM94	332 7	FLJ1099	1	14334	NP_060763.1	3 150 GTATAGAAAGTA C TC--- TGGAAAAGAAAA TTGTTTTCTTT TCC TTCTA CAGACAGT GACAAAAGAAA AGG AAGAT - TATGA							3	B c c
GAM94	332 6	FLJ1101	1	15194	NP_060771.1	3 862 ACTGAAAGGAAA TC C GGAGAAACAGAT TTGTTT TTTCTCCT TTCT AAGTCCAT AATAGA AAAGAGGA AGGA C- A							3	B c c
GAM94	332 1	FLJ1102	2	11805	NP_075388.1	5 569 AGATCCAGAAGC T - AGGGAAAGAAAA TTGTTTTCTTTC CCT CTTCT CGGCGGAT GGCAAAAGAAAG GGA GAAGA - C							3	B b b
GAM94	332 1	FLJ1102	2	19145	NP_075388.1	5 203 CGATCAAGGTCA CTCT AGAGAAAGAAAA TTGTTTTCTTTCTC TCT CGAAAGTC AGCAAAAGAAAGAG GGA AACT							3	B c b
GAM94	332 1	FLJ1119	1	19798	NP_060825.1	5 79 AAACCCAGAAGA T --- GGAGAGCAAAGG TTG TTTCTT TCTCCTCTTCT AGTCAGGA GAC GAGGAA AGAGGAGAAGA T ACG							3	B c c
GAM94	332 0	FLJ1170	1	15002	NP_079168.1	3 84 GTGGAGGGCAGA --- - GGAGAGGGGACA TTGTT TTCTTTCTCCTCT TCT AGACAGGG GACAG AGGGGAGAGGAGA GGG AAC C							3	B c c
GAM94	332 6	FLJ1175	1	6613	NP_078882.2	5 112 AACCTGATTTAG TTCTCC AAGAACAGAAAA TTGTTTTCT TCTTCTA CAAAACTA AACAAAAGA AGAAGAT CA----							3	B c c
GAM94	332 8	FLJ1252	1	3405	NP_079426.2	3 209 GTTTGGATGTGA -- T T-- GGAGAATGAAAC TTGT TTTC TTCTCCTC TCTA TACAAAAA AACA AAAG AAGAGGAG AGGT TC T TGT							3	B c c
GAM94	332 0	FLJ1270	1	4392	NP_079186.1	3 1740 GGGCAAGGAAGA TT TT GGAGTTGGCCAA TTGTT CT CTCCTCTTCT CAGGCAGC GACAA GG GAGGAGAAGG CC TT							3	B c c
GAM94	332 4	FLJ1270	1	13847	NP_079274.1	5 369 AGATAAAGGGGA TT C TGAGAAAGAACA TTGT TCTTTCTC TCTTCT GAGCTCCA GACA AGAAAGAG AGGGGA -- T							3	B c c
GAM94	332 1	FLJ1311	1	2017	NP_079358.1	3 496 CAGGGTAGAAGA TT- T- GGCTGAGGGACA TTGT TCTTTC CCTCTTCTA CACAGAGG GACA AGGGAG GGAGAAGAT CAC TC							3	B c c
GAM94	332 9	FLJ1376	1	5258	NP_079288.1	3 2126 TTGATGGATGAG TT - T GGAGAAAGACAC TTGT TCTTTCTCC TC TCTA AGTCAGTT GACA AGAAAGAGG AG AGGT							3	B c c

C- G T

GAM94	3321	FLJ13841	15346	NP_078978.1	5	159	GATAGAAGTGCT CGGGAAAGAAAG TTGTTTTCTTTCTC CAAAGCGG CTCGT	CT--- CTTCTA AACGAAAGAAAGGG GAAGAT	3	B	c	c
GAM94	3326	FLJ14561	5288	NP_116195.2	3	268	GGAGGAGGAAGA GGAGAGGAGGAA TTGTTTTCTT GCAAAGAA G	- TCTCCTCTTCT AACGAAGGAG AGAGGAGAAGG	3	B	b	b
GAM94	3327	FLJ14951	4961	NP_116255.1	3	1489	TGTCGAGGAAGG GAAGAAAGAAAC TTGTTT AGAAGTCA	T C CTTTCT CTCTTCT GACAAA GAAAGA GGGAAGG	3	B	c	c
GAM94	3322	FLJ20231	17592	NP_061881.2	3	1974	AGGTAAGGGAGA GGAGAGGATTGA TTGTT TAGAGTGT TT	T- T TCTT CTCCTCTTCT GATAG AGGA GAGGAGAGGG -	3	B	c	c
GAM94	3323	FLJ20272	10073	NP_061900.1	3	2183	GAAGAAGAAGAG GAAGAAAGAACA TTGT GTAGAAAA	TT - TCTTTCT CCTCTTCT GACA AGAAAGA GGAGAAGA -- A	3	B	c	c
GAM94	3323	FLJ20272	17100	NP_061900.1	3	2183	AGAAGAAGAAGA GGAAGAAAGAAC TTGT AGTAGAAA	TT - TCTTTCT CCTCTTCT GACA AGAAAGA GGAGAAGA -- A	3	B	c	c
GAM94	3328	FLJ20661	10920	NP_060393.1	3	166	TCAAAGAGGAAA GGAGAAAAACAA TTGTTT ACAGACCA CAA	TC- -- TTTCTCC TCTTCT GACAAA AAAGAGG AGGAGA AA	3	B	c	c
GAM94	3329	FLJ21151	19392	NP_079102.1	3	163	TGAAAGAAAAGG AAGCAAAGAAAA TTGTTTTCTTT CT CCT TTCT TAGCTGCC C A A	- - C GATAAAAGAAA GA GGA AAGA	3	B	c	c
GAM94	3320	FLJ21941	2403	NP_073739.1	3	468	ACCTATGAAAAG AAGCGGGGAAAA TTGTT CAACAACA CA-	TTC T TTTCTCC CTTCT AACAA AAAGGGG GAAGA C	3	B	c	c
GAM94	3326	FLJ21981	6727	NP_079189.3	5	295	GATTGGAGTTGG GGAGAAAGAAGA TTGTTTTCTTTCTCCTC CT CAGATTAG TT	TT GACAGAAGAAAGAGGGG GA	3	B	c	c
GAM94	3327	FLJ22031	10902	XP_168215.1	5	228	CAAGGAACTGGA GGAGAAGACAGC TTGTTTTCTT CACGCTCA -	T TC CTCC TTCT GACAGAAGAG GAGG AAGG TC	3	B	c	c
GAM94	3324	FLJ22771	10317	NP_115605.1	3	666	GCATCTGGAAGA GGAAGAAGAGAG TT TTTTCTT GAATGAGA G	G TC TCCTCTTCTA AA GAGAGAA AGGAGAAGGT GA	3	B	c	c
GAM94	332	FLJ25361	14188	NP_689883.1	3	92	GGAGTGCAGAGA	T- CT	3	B	c	c

9 GGAGAACTGAAA TTGTTTTC TTCTCCTCTT
ATAAAACT AATAAAAG AAGAGGAGAG
TC AC

GAM94 3328 FLJ25431 12072 NP_653297.1 3 353 GGAGTCTAAAGA - C CT 3 B c c
AGAGAAAGAAAA TTG TTTTCTTTCTC TCTT
TCAAGATG AAC AAAAGAAAGAG AGAA
T A AT

GAM94 3321 FLJ31131 13536 NP_689748.1 3 395 CCAGAATAGAAG T----- T 3 B c c
GGAGAGAGAAAA TGTTTTCTTTCTCC CTTCTA
CATTTCTA ACAAAAGAGAGAGG GAAGAT
ATCTTT -

GAM94 3329 FLJ31651 2343 NP_694572.1 3 632 TTACCAGGAGGA C 3 B c c
AGAGAAAGAGGA TTGTTTTCTTTCTC TCTTCT
CAAAATCA AACAGGAGAAAGAG AGGAGG
A

GAM94 3323 FLJ32061 8368 NP_694576.1 3 1875 GGTCAGAGAAGA T- C 3 B c c
GGAAAAGAGACT TTG TTTCTTT TCCTCTTCT
CAGAGAAA GAC AGAGAAA AGGAGAAGA
TC -

GAM94 3323 FLJ32201 17014 NP_653232.2 5 225 GGAAGAGGAAGA T 3 B c c
GGAGGAAGGCGA TTGTT TCTTTCTCCTCTTCT
CGGCAACA GGCAG GGAAGGAGGAGAAGG
C

GAM94 3324 FLJ32891 6669 NP_653268.1 3 829 TATTTTAGAAGA G T --- 3 B c c
GAAGGAGCAAGA TT TTTTCTT CTCC TCTTCTA
GAAGAAGA AA AAGAGAA GAGG AGAAGAT
G C AAG

GAM94 3320 FLJ33611 18380 NP_775968.1 3 1129 GAGGGAGGCAGA CTT - 3 B c c
GGAGACTTGAAA TTGTTTT TCTCCTCT TCT
CAGATGGA GACAAAG AGAGGAGA GGA
TTC C

GAM94 3327 FLJ33881 8829 NP_775756.1 5 72 AAGTAGAGGATG - ---- T 3 B c c
CCGAGGAGAAAA TTGTTTTCTT TC TCCTCT CT
CAGCAGGC GACAAAAGAG AG AGGAGA GA
G CCGT T

GAM94 3328 FLJ34271 8967 NP_775873.1 3 735 AGGGAAGGGAGT G T T 3 B c c
AGGAAAAGAAAA TT TTTTCTT CTCC CTTCT
GCATTTTT AA AAAAGGA GAGG GAAGG
G T -

GAM94 3321 FLJ35721 7540 NP_775955.1 5 0 AGAAGAAGAGGA --- - 3 B c c
AGAGAGGCCTGA TTGTTT TCTTTCT CCTCTTCT
GCGAGCAT AGCGAG GGAGAGA GGAGAAGA
TCC A

GAM94 3325 FLJ35781 6827 NP_775884.1 5 191 CAGGAGCGAACA TC ----- 3 B c c
GGAACAGGAAAA TTGTTTTCTT TCCT CTTCT
CAAATGGC AACAAAAGGA AGGA GAGGA
CA CAAGC

GAM94 3326 FLJ35862 4640 XP_300990.1 5 261 GAAGATGTGGCA CC 3 B c c
GGAGAAAGAAAG TTGTTTTCTTTCT TCTTCT

AAAACGGG GGCAAAAGAAAGA AGAGGA
A-

GAM94 3326 FLJ35862 6770 XP_300990.1 5 261 ATGTGGCAGGAG CC 3 B c c
AAAGAAAGAAAA TTGTTTTCTTTCT TCTTCT
CGGGCCGA GGCAAAAGAAAGA AGAGGA
A-

GAM94 3326 FLJ36001 18215 NP_689858.1 5 6 TGTGGACTGAAG CC T 3 B c c
AAGAAAGAAAAC TTGTTTTCTTTCT TCTTC
AATTCAAA AACAAAAGAAAGA AGAAG
-- T

GAM94 3320 FLJ36871 15135 NP_775929.1 5 329 AGGAGAAAATGA G T --- 3 B c c
GGAGAAAGACAA TT TT TCTTTCTCCTC TTCT
GAAATTTC AA AA AGAAAGAGGAG AAGA
G C TAA

GAM94 3325 FLJ37041 3394 NP_787085.1 3 38 ACACTTAGAAGA TTC T 3 B c c
GGGAAAATGACA TTGTT TTTC CCTCTTCTA
AGTTCAGG AACAG AAAG GGAGAAGAT
TA- -

GAM94 3326 FLJ37301 17101 NP_775768.1 3 1214 TCAGGTGGCAGA T T 3 B c c
GGTGAAAGAAAA TTGTTTTCTTTC CCTCT CTA
TAATGTAT AATAAAAGAAAG GGAGA GGT
T C

GAM94 3328 FLJ38561 18616 NP_694984.1 3 103 AGAGTCAGAAGA TTT 3 B c c
GGAGAAGGCCAC TTGT CTTTCTCCTCTTCT
GGTACAGA GGCA GGAAGAGGAGAAGA
CC-

GAM94 3325 FLJ39001 911 NP_848616.1 5 7 CCCGGGGCAAGA TT - 3 B c c
GGAGGGAGAAGG TTGTTTTCT CTCCTCTT CT
CAGGGCCG GACGGAAGA GAGGAGAA GG
GG C

GAM94 3321 FLJ39061 17919 XP_092342.3 5 724 GGGAGAAGAAGA TT C 3 B c c
GGAAGACCACAG TTGT TCTTTCTC TCTTCT
TATTTCTC GACA AGAAGGAG AGAAGA
CC A

GAM94 3321 FLJ39421 11838 NP_848614.1 5 67 AGGCAGCAGGAA G - - 3 B c c
GGAGAAAGGAGG TT TTTTCTTTCTCCT CTT CT
GAAGGTAA AA GGAGGAAAGAGGA GGA GA
G A C

GAM94 3323 FLJ40471 4047 NP_848626.1 3 2044 AGGTGGAGAAGA CT-- 3 B c c
GGTACAAAGGAA TTGTTTTCTTT CCTCTTCT
AACGAGAG AGCAAAAGGAA GGAGAAGA
ACAT

GAM94 332 FLT4 1 15512 NP_002011.1 3 157 AGGAGGACAAGA TT TC- 3 B c c
GGAGCATGAAAG TTGTT CTTTC CTCTTCT
TGGACAAG AACAG GAAAG GAGGAGA
GT TAC

GAM94 332 FOSB 2 2063 NP_006723.1 3 82 GGAGGAGGAGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GAGAGAGG GA AGGAGGAAGAGGAGGAGG
G

GAM94 332 FOSB 2 18954 NP_006723.1 3 70 AGACTTGGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCTA
GGAGAAGG AG AGGAGGAGGAGGAGAAGGT
G
GAM94 332 FZD1 1 9605 NP_003496.1 3 1663 CTGTGAAGAAGA CTT 3 B b b
GGAGAAAAGCAA TTGTTTT TCTCCTCTTCT
TCCTCCTG AACGAAA AGAGGAGAAGA

GAM94 332 GAB2 1 10497 NP_036428.1 3 1356 CAGGCAGGACAA - CT 3 B c c
GGAGAAAGCAGG TTGTTTT CTTTCTCCT TCT
GCAGAATG GACGGGA GAAAGAGGA AGG
C AC
GAM94 332 GAB2 1 10497 NP_536739.1 3 1356 CAGGCAGGACAA - CT 3 B c c
GGAGAAAGCAGG TTGTTTT CTTTCTCCT TCT
GCAGAATG GACGGGA GAAAGAGGA AGG
C AC
GAM94 332 GABBR1 1 9593 NP_001461.1 5 125 GGGACGGGAGGA G - 3 B c c
GGAGAAAGGTGG TT TTT TCTTTCTCCTCTTCT
AGGAGAAG AG AGG GGAAAGAGGAGGAGG
G T
GAM94 332 GABBR1 1 9593 NP_068704.1 5 125 GGGACGGGAGGA G - 3 B c c
GGAGAAAGGTGG TT TTT TCTTTCTCCTCTTCT
AGGAGAAG AG AGG GGAAAGAGGAGGAGG
G T
GAM94 332 GABBR1 1 9593 NP_068705.1 5 125 GGGACGGGAGGA G - 3 B c c
GGAGAAAGGTGG TT TTT TCTTTCTCCTCTTCT
AGGAGAAG AG AGG GGAAAGAGGAGGAGG
G T
GAM94 332 GAPCENA 1 18769 NP_036329.2 5 223 ATAATGGAAGTG - - CT 3 B c c
ATGATGAGAAAA TTGTTTTCTT TC TC CTTCTA
CAGGACTC GACAAAAGAG AG AG GAAGGT
T T T-
GAM94 332 GATS 2 4488 NP_849153.1 3 631 GTTTAAGCAGAG TTC- T 3 B c b
GGCTACAGAAAA TTGTTTTCT TCCTCT CT
CAGGGAAG GACAAAAGA GGGAGA GA
CATC C
GAM94 332 GATS 2 11136 NP_849153.1 3 453 GAAGGTAGAGGA TT 3 B b b
GGAGAAAGAATC TTG TTCTTTCTCCTCTTCTA
CAAAGATT AAC AAGAAAGAGGAGGAGAT
CT
GAM94 332 GDEP 1 4567 NP_477516.1 5 11 GGAGGCAGAAGA CT C 3 B c c
GGAAGTCAGAGC TTGTTTT TT TCCTCTTCT
GATGTGCT AGCGAGA GA AGGAGAAGA
CT -
GAM94 332 GNGT2 1 10664 NP_113686.1 5 147 GGAAGGGAAGGA T - 3 B c c
GGAGAAAGCAGG TTGTTT CTTTCTCCTC TTCT
CGAAGCGG AGCGGA GAAAGAGGAG AAGG
C G
GAM94 332 GNL1 1 14132 NP_005266.1 5 230 AGGAGGTAGAGA CT 3 B c c
GGAGAAAGAGAG TTGTTTTCTTTCTCCTCTT

CAGCCCGG GACGAGAGAAAGAGGAGAG
AT
GAM94 332 GOLGA2L 1 1437 XP_034789.4 5 23 CAGGAGCTAACA - C ----- 3 B c c
Y GGAAAAAGAAAA TTG TTTTCTTT TCCT CTTCT
TCAATGGC AAC AAAAGAAA AGGA GAGGA
T A CAATC
GAM94 332 GOR 1 2708 NP_758439.1 3 3282 GGAGAAGAGTGA TT----- - 3 B c c
GGAGAAAGGAAA GTTTTCTTTCTCCTC TTCT
CTCAAGTC CAAAGGAAAGAGGAG GAGA
CTGAACT T
GAM94 332 GPA33 1 15497 NP_005805.1 5 207 TGGGTGAGAAGA TTTC T 3 B c c
GGGAAAATTGCA TTGT TTTC CCTCTTCT
GGGACCTC GACG AAAG GGAGAAGA
TTA- -
GAM94 332 GPM6B 1 4391 NP_005269.1 5 187 AGAAAAGGAAGA CT 3 B b b
GGAGGAAAAACA TTGTTTT TTCTCCTCTTCT
AGTGTGTG AACAAAA AGGAGGAGAAGG
--
GAM94 332 GPR55 1 4012 NP_005674.1 3 295 GAGCAGAAGAAT TG C-- 3 B c c
TGAGAAAGAGAA T TTTTCTTTCTC TCTTCT
TGAGACCA A AAGAGAAAGAG AGAAGA
GT TTA
GAM94 332 GPR56 1 5025 NP_005673.2 3 1416 AACTGTAGAAGA CT C---- 3 B c c
GAATCAAGAAGA TTGTTTT TTCT CTCTTCTA
AAAATAAA AATAAAA AAGA GAGAAGAT
AG ACTAA
GAM94 332 GPR62 2 14335 NP_543141.1 5 41 GGCTGGGGCAGG T - 3 B c c
GGAGAAAGACAG TTGTT TCTTTCTCCTCT TCT
CAGACTCA GACGA AGAAAGAGGGGA GGG
C C
GAM94 332 GPR62 2 15063 NP_543141.1 5 175 CAAGGGACAAGA TT -- 3 B c c
GGAGCAGAGGAC TTGTTTTCT CTCCTCT TCT
AGGTGATG GACAGGAGA GAGGAGA AGG
C- AC
GAM94 332 GPR72 1 15584 NP_057624.1 3 277 CTCTGAGGAAGA TTT 3 B c c
GGAGCGAGGACA TTGTTTTC CTCCTCTTCT
ACGTTGGC AACAGGAG GAGGAGAAGG
C--
GAM94 332 GRIA3 1 14641 NP_000819.1 5 82 GAGAGAAGAAGA - - 3 B c c
GGAAGAAGAGGA TTGTTTTCTTT CT CCTCTTCT
GGCGGCGG GGCGGAGGAGA GA GGAGAAGA
A A
GAM94 332 GRIN3A 1 13739 NP_597702.1 3 1502 CCACAGGCAGGA G --- - 3 B c c
GGAGAAGCATGA TT TTTTC TTTCTCCTCTT CT
AGAGAAAA AA AGAAG GAAGAGGAGGA GG
G TAC C
GAM94 332 GSC 1 17283 NP_776248.1 3 119 GCGGGAGGGGGT - --- 3 B c c
CGAGAAAGAGGA TTGTTT TCTTTCT CCTCTTCT
ACGAGGAG AGCAAG AGAAAGA GGGGGAGG
G GCT

GAM94 332 HAND2 1 8738 NP_068808.1 3 24 GCAGTGGGAGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGAGA AG AGGAGGAAGAGGAGGAGG
G

GAM94 332 HBXAP 1 5810 NP_057662.2 5 1034 ATTTTTAGAGGA TG CC 3 B c c
ACAGAAAGAAAG T TTTTCTTTCT TCTTCTA
TGAAAAGA A GAAAGAAAGA AGGAGAT
GT CA

GAM94 332 HEMGN 1 18446 NP_060907.1 5 324 GAAATCGAAGAG -- - T 3 B c c
GCAGAAAGAAAC TTGTT TTCTTTCT CCTCTTC
AACAAAAC AACAA AAGAAAGA GGAGAAG
CA C C

GAM94 332 HIC 1 5416 XP_041273.1 5 559 CGGGGCGGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGAAG AG AGGAGGAGGAGGAGAAGG
G

GAM94 332 HIS1 1 3217 NP_006451.1 5 71 GGGAGGAAAAGA TT --- 3 B c c
GGAGGAGACGGA GTTTTCTT TCTCCTCTTCT
GGAGAACT CAAGAGGA AGAGGAGGAGA
T- GGC

GAM94 332 HMGB2 1 15162 NP_002120.1 3 0 AGGAAGAGGATG ---- C 3 B c c
AAGATGAAGAAT TTGTTT TCTTT TCCTCTTCT
AATGGCTA AATAAG AGAAG AGGAGAAGG
AAGT T

GAM94 332 HMP19 1 15566 NP_057064.1 3 335 GTAACAGCAGAA T TC C 3 B c c
AAGGAAAGAAAC TTGTTT CTT TCCT TTCT
AAAGAACA AACAAA GAA AGGA AAGA
- -- A

GAM94 332 HOXA13 1 14274 NP_000513.2 3 117 GAAGAATGGGAA T --- - 3 B c c
AGAGAAAGAGAC TTGTTT CTTTCTC CTC TTCT
AGAGACTG GACAGA GAAAGAG GGG AAGA
- AAA T

GAM94 332 HOXB5 1 18456 NP_002138.1 3 625 GGTATTGAGAAG C 3 B b b
AGAGAAAGAAGA TTGTTTTCTTTCTC TCTTCT
TAGTGAGA GATAGAAGAAAGAG AGAAGA
-

GAM94 332 HOXB6 3 6159 NP_061825.2 3 508 GAAGTAAGAAGA ----- 3 B b b
GGAGCCTCAGAA TTGTTTTCTTT CTCCTCTTCT
GAAAACAA AACAAAAGAAG GAGGAGAAGA
ACTCC

GAM94 332 HOXB6 3 6159 NP_724778.1 3 1823 GAAGTAAGAAGA ----- 3 B b b
GGAGCCTCAGAA TTGTTTTCTTT CTCCTCTTCT
GAAAACAA AACAAAAGAAG GAGGAGAAGA
ACTCC

GAM94 332 HOXB6 3 6159 NP_724779.1 3 508 GAAGTAAGAAGA ----- 3 B b b
GGAGCCTCAGAA TTGTTTTCTTT CTCCTCTTCT
GAAAACAA AACAAAAGAAG GAGGAGAAGA
ACTCC

GAM94 332 HOXB6 3 13497 NP_061825.2 3 509 AAGAAGAGGAGC ----- 3 B b b
CTCAGAAGAAAA TTGTTTTCTTT CTCCTCTTCT

CAAAGTTC AACAAAAGAAG GAGGAGAAGA
ACTCC
GAM94 332 HOXB6 3 13497 NP_724778.1 3 1824 AAGAAGAGGAGC ----- 3 B b b
CTCAGAAGAAAA TTGTTTTCTTT CTCCTCTTCT
CAAAGTTC AACAAAAGAAG GAGGAGAAGA
ACTCC
GAM94 332 HOXB6 3 13497 NP_724779.1 3 509 AAGAAGAGGAGC ----- 3 B b b
CTCAGAAGAAAA TTGTTTTCTTT CTCCTCTTCT
CAAAGTTC AACAAAAGAAG GAGGAGAAGA
ACTCC
GAM94 332 HOXB6 3 15879 NP_724778.1 5 2 GGGAGAGAGAGG G - - 3 B c b
AGAAAGGCGAAG TT TTT TCTTTCTCCTCT TCT
GAGAAGGA AG AAG GGAAAGAGGAGA AGA
G C G
GAM94 332 HOXB6 3 15879 NP_724779.1 5 2 GGGAGAGAGAGG G - - 3 B c b
AGAAAGGCGAAG TT TTT TCTTTCTCCTCT TCT
GAGAAGGA AG AAG GGAAAGAGGAGA AGA
G C G
GAM94 332 HOXC4 1 9089 NP_055435.2 5 455 AATGAGGGAAGA TG C 3 B c c
CGAGAAAGAGAG T TTTTCTTTCTC TCTTCT
TGGGAGAG G GAGAGAAAGAG AGAAGG
GT C
GAM94 332 HOXC6 1 9089 NP_710160.1 5 292 AATGAGGGAAGA TG C 3 B c c
CGAGAAAGAGAG T TTTTCTTTCTC TCTTCT
TGGGAGAG G GAGAGAAAGAG AGAAGG
GT C
GAM94 332 HPCAL4 1 15640 NP_057341.1 3 3342 TGGCGTGGGATG G C 3 B c c
GGGGAAAGAAAA TT TTTTCTTTCTCCT TTCTA
GAAAGAGA AA AAAAGAAAGGGGG AGGGT
G T
GAM94 332 HSPC056 1 15755 NP_054873.1 3 1188 CCTGTAGAAAGA CTTT - 3 B c
c
GGAGTATGGAAC TTGTTTT CTCCTCTT CTA
AACCTTAC AACAAGG GAGGAGAA GAT
TAT- A
GAM94 332 HSPC159 1 5350 NP_054900.1 3 105 AGATCTGGAGAC ------ TCT 3 B c c
TTAAAAAGAAAA TTGTTTTCTT TCTCC TCT
CAAAAACA AACAAAAGAA AGAGG AGA
AAATTC TCT
GAM94 332 ICA1 1 6433 NP_004959.1 5 148 ATCAACAATAGA T----- T CC 3 B c c
AGAAGAAGAAAA TGTTTTCTT CT TCTTCTA
CATGTCAG ACAAAAGAA GA AGAAGAT
GACTGT - --
GAM94 332 ICA1 1 6433 NP_071683.1 5 103 ATCAACAATAGA T----- T CC 3 B c c
AGAAGAAGAAAA TGTTTTCTT CT TCTTCTA
CATGTCAG ACAAAAGAA GA AGAAGAT
GACTGT - --
GAM94 332 IFNAR2 1 15907 NP_000865.2 3 1502 CAGGGTGGGAGC G T - 3 B c c
AGGGAAAGAAAA TT TTTTCTTTC CCT CTTCTA
GGAAAATA AG AAAAGAAAG GGA GAGGGT

G - C

GAM94 332 IGF1 1 12026 NP_000609.1 3 1678 GGAAAAGAAAAA CTT C- 3 B c c
GGAGAAAAACAA TTGTTTT TCTCCT TTCT
AGAGATTT AACAAAA AGAGGA AAGA
--- AA

GAM94 332 IL15RA 1 17728 NP_002180.1 3 91 CGACTGAGAAGA TCT 3 B c c
GGTGCAAGGAAG TTGTTTTCTT CCTCTTCT
CGGGCTCC GGCGAAGGAA GGAGAAGA
CGT

GAM94 332 IL15RA 1 17728 NP_751950.1 3 91 CGACTGAGAAGA TCT 3 B c c
GGTGCAAGGAAG TTGTTTTCTT CCTCTTCT
CGGGCTCC GGCGAAGGAA GGAGAAGA
CGT

GAM94 332 IL19 1 1253 NP_037503.2 5 735 CTATATCTTAAA CC CT 3 B c c
GAAGAAAGAAAA TTGTTTTCTTTCT TCTT
CAATTAAG AACAAAAGAAAGA AGAA
-- AT

GAM94 332 IL1RL1 1 15835 NP_057316.3 5 84 CAGAAAGTTGAG TT - TT 3 B c c
GAAGAAAGAACT TTG TTCTTTCT CCTC CT
CAAGTACA AAC AAGAAAGA GGAG GA
TC A TT

GAM94 332 IL2 1 4856 NP_000577.2 5 104 GTCATCAGAAGA TT - C 3 B c c
GGAAAAATGAAG TTG TTC TTT TCCTCTTCT
GTAATGTT AAT AAG AAA AGGAGAAGA
GG T A

GAM94 332 IL28RA 2 2495 NP_775088.1 3 603 TGAGGAGGAAGA - TT - 3 B c c
GGAGGCGAGGGA TTG TT CTT TCTCCTCTTCT
ATCAGAAA GAC AA GAG GGAGGAGAAGG
T GG C

GAM94 332 IL28RA 2 18482 NP_775088.1 3 134 AGAGGACGAAGA T --- 3 B c c
GGAGGAGGATGA TGTTTTCT TTCTCCTCTTCT
GGAGGACA ACAGGAGG AGGAGGAGGAGA
- AGT

GAM94 332 IL6R 1 10665 NP_000556.1 3 789 AGAGGAAGGAGA TT 3 B c c
GGAGAGGGGCAC TTGT TCTTTCTCCTCTTCT
AGGGTCTC GACA GGGGAGAGGAGAGGA
C-

GAM94 332 IL6R 1 10665 NP_852004.1 3 1004 AGAGGAAGGAGA TT 3 B c c
GGAGAGGGGCAC TTGT TCTTTCTCCTCTTCT
AGGGTCTC GACA GGGGAGAGGAGAGGA
C-

GAM94 332 ING3 1 3094 NP_061944.1 3 87 AAAAAGAAGAGA -- -- 3 B b b
AGAGAAAGAAGA TTGTTT TCTTTCTC CTCTTCT
AACAATGC AACAAA AGAAAGAG GAGAAGA
GA AA

GAM94 332 IPO8 1 3120 NP_006381.1 5 80 GGTCGCGGAAGA - -- 3 B c c
GGAGGCTGAGAG TTG TTTTCTT TCTCCTCTTCT
GGTCAAAA AAC GGGAGAG GGAGGAGAAGG
T TC

GAM94 332 JAK2 1 17718 NP_004963.1 5 15 GAGAGAGGAAGA TT -- 3 B c c

GGAGCAGAAGGG TTGTT CTTT CTCCTCTTCT
GGCAGCAG GACGG GAAG GAGGAGAAGG
GG AC

GAM94 332 KCNA4 1 3266 NP_002224.1 3 205 TCTTGGAGAAGA CT -- 3 B c c
GGGAGGAATAGG TTGTTTT TTCT CCTCTTCT
AGCAAATC AACGAGG AAGG GGAGAAGA
AT AG

GAM94 332 KCNJ15 1 18499 NP_002234.2 3 1246 TGAGGAAGAAGA TT TTT 3 B c c

GGAGCTGAAGGT TTG TTC CTCCTCTTCT
AAGAAACT AAT AAG GAGGAGAAGA
GG TC-

GAM94 332 KCNJ15 1 18499 NP_733932.1 3 1246 TGAGGAAGAAGA TT TTT 3 B c c

GGAGCTGAAGGT TTG TTC CTCCTCTTCT
AAGAAACT AAT AAG GAGGAGAAGA
GG TC-

GAM94 332 KCNJ15 1 18499 NP_733933.1 3 1246 TGAGGAAGAAGA TT TTT 3 B c c

GGAGCTGAAGGT TTG TTC CTCCTCTTCT
AAGAAACT AAT AAG GAGGAGAAGA
GG TC-

GAM94 332 KCNK6 1 2279 NP_004814.1 3 1498 AGAGAAAGAAAG G CC - 3 B c c
AAAGAAAGAAAG TT TTTTCTTTCT TCTT CT
GGAAAGAT AG GAAAGAAAGA AGAA GA
G A- A

GAM94 332 KCNMB3 1 5079 NP_055222.3 5 105 GGCCAGAGAGGA TG 3 B c c
GGAGAAGGAGGG T TTTTCTTTCTCCTCTTCT
TGAGAGGA A GGGAGGAAGAGGAGGAGA
GT

GAM94 332 KCNMB3 1 5079 NP_741981.1 5 347 GGCCAGAGAGGA TG 3 B c c
GGAGAAGGAGGG T TTTTCTTTCTCCTCTTCT
TGAGAGGA A GGGAGGAAGAGGAGGAGA
GT

GAM94 332 KCNN3 1 10793 NP_002240.2 3 240 GGAGCGGGAAGA T--- 3 B c c
GGAGATGACAGG TTGTTTTCT TCTCCTCTTCT
AAGCGACG AGCGAAGGA AGAGGAGAAGG
CAGT

GAM94 332 KCNN3 1 10793 NP_740752.1 3 240 GGAGCGGGAAGA T--- 3 B c c
GGAGATGACAGG TTGTTTTCT TCTCCTCTTCT
AAGCGACG AGCGAAGGA AGAGGAGAAGG
CAGT

GAM94 332 KCNS2 1 7405 XP_043106.1 3 1353 GGGTAGAGGCCA G -- 3 B c c
GGAGAAAGGAAA TT TTTTCTTTCTCCT CTTCTA
GAGTTGTA GA AAAGGAAAGAGGA GGAGAT
G CC

GAM94 332 KIAA006 1 4542 NP_055691.1 3 273 TTAAGAGACAGA - - 3 B c c
3 GGAGAAAGTGGA TTGTTTT CTTTCTCCTCT TCT
GCGGGGAG GGCGAGG GAAAGAGGAGA AGA
T C

GAM94 3322 KIAA0151 9197 NP_055545.1 3 52 GGTGGAGGGGTG T --- 3 B c c
TGGGAAAGAAAC TTG TTTCTTTCTC CTCTTCTA
CAGCCATA GAC AAAGAAAGGG GGGGAGGT
C TGT
GAM94 3323 KIAA0191 18064 NP_055581.2 3 2460 ATTGGGATGGGT T - - 3 B c c
GGAGAAAGACGA TTGTT TCTTTCTCC TCT TCT
CAAGAGAG AACAG AGAAAGAGG GGG AGG
C T T
GAM94 3327 KIAA0232 19421 NP_055562.1 3 1556 GTATCTGGTAGG ---- T 3 B c c
GGAGAAAGCAGC TTGTTTT CTTTCTCCTCT CTA
AGGACAGT GACAGGA GAAAGAGGGGA GGT
CGAC T
GAM94 3327 KIAA0232 20043 NP_055562.1 3 4162 CACGTCAGAAGA - CT 3 B c c
GGTTGGGGCAAA TTGTTTT CTTT CCTCTTCT
ACAAAACA AACAAAA GGGG GGAGAAGA
C TT
GAM94 3320 KIAA0282 16465 XP_166238.1 3 1701 GTCATCAGGAGA TG T 3 B c c
GGAGAATGAGGA T TTTTC TTCTCCTCTTCT
TGAGGCCC A AGGAG AAGAGGAGAGGA
GT T
GAM94 3320 KIAA0282 18800 XP_166238.1 3 1669 AGGAGAGGAAGA TG T 3 B c c
GGAGGAAGACAG T TT TCTTTCTCCTCTTCT
TGGGAGTC G GA AGAAGGAGGAGAAGG
GT C
GAM94 3323 KIAA0301 477 XP_291141.2 3 145 GAGACAGGGGAG - - 3 B c c
AGAGAAAGACAA TTGTTTT CTTTCTCCTCT TCT
AGAGGGGA AACAGAA GAGAGAGGGGA AGA
A C
GAM94 3325 KIAA0371 7737 XP_048462.1 3 446 GTCATCAGAAGA TT - 3 B c c
GGGAGGAGGAGC TTG TTCTTTCTCC TCTTCT
CCAGGCGT GAC GAGGAGGAGG AGAAGA
CC G
GAM94 3326 KIAA0371 19848 XP_037759.2 3 960 AAGCAGGAAATA T - C- 3 B c c
GGAGAAAAGTAA TTGTTT CTTT CTCCT TTCT
ACAACTTT AACAAA GAAA GAGGA AAGG
T A TA
GAM94 3321 KIAA0431 9717 NP_056066.1 5 371 GCACTTAGAAGA TTC 3 B c c
GGACAGGAGATA TTGTTTTCT TCCTCTTCTA
GTAAAAGG GATAGAGGA AGGAGAAGAT
C--
GAM94 3327 KIAA0551 19825 XP_085507.1 3 3992 CTTAGGTAAAGA CTC 3 B c c
AGAGAAAGAGAA TTGTTTTCTTT CTCTTCT
AGCAAATT AACGAAAGAGA GAGAAGA
AA-
GAM94 3320 KIAA0571 17900 XP_291018.1 3 1788 GGAAGAAGAAGA T----- 3 B c c
GGAGGAAGAAGA TGTTTTCTTTCTCCTCTTCT
TATCCTCT ATAGAAGAAGGAGGAGAAGA
TCTCCT
GAM94 3322 KIAA0591 3081 XP_170645.2 5 679 TGATGAGGAAGA - TTC--- 3 B c c
GGATAAAATGGA TTG TTTTCT TCCTCTTCT

AGATCAAA AAC AGAAGG AGGAGAAGG
T TAAAAT

GAM94	332	KIAA092	1	9702	NP_056011.1	5	38	GAATTATAGAAG CTCC			3	B	c c
	2							ATGTGAAGAAAA TTGTTTTCTTT TCTTCTA					
								CAACACAC AACAAAAGAAG AGAAGAT					
								TGT-					
GAM94	332	KIAA093	1	12863	XP_034536.4	3	147	GGAGGAGGAAGA TT--			3	B	c c
	4							GGAGGAGGAAGA GTTTTCTTTCTCCTCTTCT					
								GGACTTCT CAGGAGAAGGAGGAGGAGA					
								TCTT					
GAM94	332	KIAA103	1	11779	XP_038604.4	3	1184	AGAAAGAGAATG TG C -			3	B	c c
	2							AGAGAAAGAGAA T TTTTCTTTCTC TC TTCT					
								TGAGAGAG A AAGAGAAAGAG AG AAGA					
								GT - T					
GAM94	332	KIAA107	1	19836	XP_037523.6	5	65	GGCCAGGGAAGA G			3	B	c c
	6							GGAGGAAGAAGA TT TTTTCTTTCTCCTCTTCT					
								GGAGGAGG AG AGAAGAAGGAGGAGAAGG					
								G					
GAM94	332	KIAA120	4	1445	XP_050478.1	3	1453	AAAGAAAGAAAG G CC -			3	B	c c
	2							AAAGAAAGAAAA TT TTTTCTTTCT TCTT CT					
								GAAAGAAA AA AAAAGAAAGA AGAA GA					
								G A- A					
GAM94	332	KIAA120	4	6664	XP_050478.1	3	1478	AAAGAAAGAAAG CC -			3	B	c c
	2							AAAGAAAGAAAA TTGTTTTCTTTCT TCTT CT					
								CAGTTCCA GACAAAAGAAAGA AGAA GA					
								A- A					
GAM94	332	KIAA120	4	10637	XP_050478.1	3	1477	AAAGAAAGAAAG CC -			3	B	c c
	2							AAAGAAAGAAAG TTGTTTTCTTTCT TCTT CT					
								AAAACAGT GACAAAAGAAAGA AGAA GA					
								A- A					
GAM94	332	KIAA120	4	11414	XP_050478.1	3	1445	AAAGAAAGAAAG G CC -			3	B	c c
	2							AAAGAAAGAAAG TT TTTTCTTTCT TCTT CT					
								AAAAGAAA AA AAAAGAAAGA AGAA GA					
								G A- A					
GAM94	332	KIAA121	2	2528	XP_172801.1	3	1632	AAAAAGGGAGAG TG -			3	B	c c
	0							TGAGAAAGAGGA T TTTTCTTTCTC CTCTTCT					
								TGAGAGGG A AGGAGAAAGAG GAGAGGG					
								GT T					
GAM94	332	KIAA121	2	15805	XP_172801.1	3	693	GTGCTTTAGAAG T--- -- T			3	B	c c
	0							GGAGAAAGCAAA TGTTTT CTTTCTCC CTTCTA					
								AACATTTT ACAAAA GAAAGAGG GAAGAT					
								TTTT AC -					
GAM94	332	KIAA137	1	15428	XP_033042.2	3	728	AAAGAGATAAGA TT --			3	B	c c
	6							GGAGGAAGCTAA TTGTT CTTTCTCCTCT TCT					
								TAAGAGAC AATAA GAAGGAGGAGA AGA					
								TC AT					
GAM94	332	KIAA139	1	9460	XP_046685.4	5	605	AGAGGAGGAAGA T			3	B	c c
	9							GGAGGAGAAGGC TTGTTTTCTT CTCCTCTTCT					
								GAGGCCAC AGCGGAAGAG GAGGAGAAGG					
								-					

GAM94 3326 KIAA141 1 12761 XP_098762.3 3 929 TTCAAAAGGAGA TG 3 B c c
GGAGAAAGGAAA T TTTTCTTTCTCCTCTTCT
TGAGAATG A AAAGGAAAGAGGAGAGGA
GT

GAM94 3327 KIAA144 1 754 XP_290770.2 5 3413 CGAGGAGGAAGA T 3 B c c
GGAGGAGGACAG TTGTT TCTTTCTCCTCTTCT
CGGCCCTC GGCGA AGGAGGAGGAGAAGG
C

GAM94 3320 KIAA155 1 16791 XP_039393.3 3 3130 CTAATGGGAAGA TTC- 3 B c c
GGAAAATGGGAA TTGTTTTCT TCCTCTTCT
ACAATGCA AACAAAGGG AGGAGAAGG
TAAA

GAM94 3324 KIAA168 1 14267 XP_290806.1 3 1366 GATAGGAGAAGA - 3 B c c
GGAGGAGGAGGA TTGTTT TCTTTCTCCTCTTCT
GCGGGGTC GGCGAG AGGAGGAGGAGAAGA
G

GAM94 3329 KIAA172 1 12326 XP_114418.2 3 2218 AAGATATAGAGA TTG - 3 B c c
GGAGAGGAGTGA TTTTCTTT CTCCTCTTCT
AGAAAAGG AAAAGAAG GAGGAGAGGA
GG- T

GAM94 3321 KIAA173 1 6800 XP_290545.1 3 34 GGAAATAGAAGA C- C 3 B c c
GCAGAAGCAAAA TTGTTTT TTTCT CTCTTCTA
GCAATTGG AACGAAA GAAGA GAGAAGAT
AC C

GAM94 3325 KIAA173 1 12832 XP_290496.1 5 229 AAGAAATGGAGG TG - - --- 3 B c c
AAGCAAAGAAAA T TTTTCTTT CT CCTCT TCT
TGATAT A AAAAGAAA GA GGAGG AGA
GT C A TAA

GAM94 3327 KIAA182 2 5677 XP_290834.1 5 398 CAACTTGGAAGA G TC 3 B c c
GGAAAGAAAAGA TT TTTTCTT TCCTCTTCTA
AGTCAGGA AA AAAAGAA AGGAGAAGGT
G --

GAM94 3327 KIAA182 2 6984 XP_290834.1 5 398 AGCAACTTGGAA G TC 3 B c c
GAGGAAAGAAAA TT TTTTCTT TCCTCTTCTA
GAAGTCAG AA AAAAGAA AGGAGAAGGT
G --

GAM94 3323 KIAA185 2 4894 XP_045184.1 5 835 GAGATGAGAAGA T TCT 3 B c c
GGCACAAGAAAC TTGTTT CTT CCTCTTCT
AATCTCGA AACAAA GAA GGAGAAGA
- CAC

GAM94 3323 KIAA185 2 10772 XP_045184.1 3 151 CCTAGGGGAAGA TT T 3 B c c
GGAGAAGAGGGT TTG TTCTT CTCCTCTTCT
AAGGGGGC AAT GAGAA GAGGAGAAGG
GG -

GAM94 3320 KIAA187 1 17798 NP_115537.1 3 61 GAGGAGGGAAGA T -- 3 B c c
GGAAGAGGCAAG TTGTTT CTTTCTC CTCTTCT
GGGAGGGT AACGGA GAAGGAG GGGAGGA
- AA

GAM94 3321 KIAA200 2 3364 XP_291322.1 3 908 GGAGGAAGAAGA T 3 B b b
GGAGGAGGAGAA TTGTTT CTTTCTCCTCTTCT

AGAAGCAG GACGAA GAAAGAGGAGGAGG
-

GAM94 332 KIAA200 2 19659 XP_291322.1 3 910 AGAAGAGGAGGA -- 3 B b b
1 GGAGAAAGAAGC TTGTT TTCTTTCTCCTCTTCT
AGCAACGA AACGA AAGAAAGAGGAGGAGG
CG

GAM94 332 KR18 3 5169 NP_150630.1 5 270 TCTGGAAGAAGA G ---- 3 B c c
GGAAGAGGAAAG TT TTTTCTTTC TCCTCTTCT
AAAAGGAG AG AAAAGAAAG AGGAGAAGA
G GAGA

GAM94 332 KR18 3 8750 NP_150630.1 5 273 GAAGAAGAGGAA G ---- 3 B c c
GAGGAAAGAAAA TT TTTTCTTTC TCCTCTTCT
GGAGTCAG AG AAAAGAAAG AGGAGAAGA
G GAGA

GAM94 332 KR18 3 16888 NP_150630.1 5 275 AGAAGAGGAAGA G ---- 3 B c c
GGAAAGAAAAGG TT TTTTCTTTC TCCTCTTCT
AGTCAGGG AG AAAAGAAAG AGGAGAAGA
G GAGA

GAM94 332 LANO 1 2628 NP_060684.1 3 609 ATTTGTGGAGGA G - C 3 B c c
TGAGAAAGATGA TT TTT TCTTTCTC TCTTCTA
AGAAGACA AA AAG AGAAAGAG AGGAGGT
G T T

GAM94 332 LASS2 1 1787 NP_037516.2 3 115 TCTGGGGAAAAA G C- 3 B c c
GGAGAAAGGAGA TT TTTTCTTTCTCCT TTCT
GGAGAGTT AG AGAGGAAAGAGGA AAGG
G AA

GAM94 332 LEP 1 8384 NP_000221.1 3 2247 ACAGCGAGAGGC -- CT 3 B c c
AGAGAAAGAAGA TTGTT TTCTTTCTC CTTCT
GACAGGAG GACAG AAGAAAGAG GGAGA
AG AC

GAM94 332 LGI4 1 18376 NP_644813.1 5 303 ACAGAAAGACAG - CT 3 B c c
GGAGAAAGAGAA TTGTT TTCTTTCTCCT TCT
ACAGAAAA GACAA GAGAAAGAGGG AGA
A AC

GAM94 332 LIF 1 7255 NP_002300.1 3 1749 TTGCTCCCAAGA -- 3 B c c
GGAGGAGAGGGA TTGT TTTCTTTCTCCTCTTCT
GGCTGCAG GACG GGAGGGAGAGGAGGAGA
TC

GAM94 332 LILRB1 1 9402 NP_006660.1 5 0 GAGGAGGAACAG G - --- T 3 B c c
AAAAGAAAAGAA TT TTTTCTTT C TCCTCTTC
AAGAAAAA AA AAAAGAAA G AGGAGGAG
G A ACA -

GAM94 332 LIMD1 1 573 NP_055055.1 3 117 GGTAGGGGAAGA G -- 3 B c c
GGAGGGGCAGGA TT TTTTCT TTCTCCTCTTCT
GGGAGAGT GA GGAGGA GGGAGGAGAAGG
G CG

GAM94 332 LIPH 1 6330 NP_640341.1 3 771 TAGATAGTGGAT - ---- T - 3 B c c
GAAGAAAGAAGG TTGTT TTCTTTC TCC CT TCTA
ACGAGGAA AGCAG AAGAAAG AGG GA AGAT
G AAGT T T

GAM94 332 LMO7 1 2940 NP_005349.2 5 207 GAGAGTAGAAGA TT TCTC 3 B c c
GAAGGGAGCAAC TTGTT CTT CTCTTCTA
TTATCCTT AACGA GAA GAGAAGAT
GG ----
GAM94 332 LMO7 1 2940 NP_056667.1 5 207 GAGAGTAGAAGA TT TCTC 3 B c c
GAAGGGAGCAAC TTGTT CTT CTCTTCTA
TTATCCTT AACGA GAA GAGAAGAT
GG ----
GAM94 332 LMO7 1 2940 NP_056668.1 5 207 GAGAGTAGAAGA TT TCTC 3 B c c
GAAGGGAGCAAC TTGTT CTT CTCTTCTA
TTATCCTT AACGA GAA GAGAAGAT
GG ----
GAM94 332 LMOD3 1 4830 XP_067529.3 3 204 AGGGGCTGAAGA ---- T 3 B c c
GGAAGGTGGAAG TTGTTTTCTTTC TCCTCTTC
GAGATAAA AATAGAGGAAGG AGGAGAAG
TGGA T
GAM94 332 LOC1149 1 3594 XP_054936.4 3 777 TTTCCTGACAGA TC - - T 3 B c c
71 TGGATAAGAAAA TTGTTTTCTT TCC TCT TC
CAATAGAA AACAAAAGAA AGG AGA AG
T- T C T
GAM94 332 LOC1160 1 6765 NP_612465.2 5 227 AAGGGAGGGGAG ---- 3 B c c
71 CAAGAAAGAAGG TTGTTTTCTTTC TCCTCTTCT
CGAGAGAG AGCGGAAGAAAG AGGGGAGGG
AACG
GAM94 332 LOC1232 1 9559 XP_058693.1 5 130 CTCCCATAAAGA T-- C 3 B c c
64 GGAGGAAAAGGA TGTTTTCTTT TCCTCTTCT
AGATACAG ATAGAAGGAA AGGAGGAGA
GAC A
GAM94 332 LOC1233 1 8234 XP_063630.4 5 153 TATGCAAAGAGA TT C- 3 B c c
97 AGAGAAAGAAGG TTGT TCTTTCT CTCTTCT
ATGCAATG AACG AGGAAGA GAGAAGA
T- AA
GAM94 332 LOC1238 1 15004 XP_058743.4 3 485 AAAGAAAGAGAG G TC 3 B c c
76 GGAGAAAGAGAG TT TTTTCTTTCTCC TTCT
GGAGAAAG AG GAGAGAAAGAGG GAGA
G GA
GAM94 332 LOC1267 1 8295 XP_059080.1 3 256 GAGGAGGGGATG TT - 3 B c c
82 GGAGAAAGTAGG TTGTTTTCT C TCCTCTTCT
GGATGTGG GATGAAAGA G AGGGGAGGA
GG T
GAM94 332 LOC1319 1 13672 XP_067689.1 3 701 GAAATTAGAAGA T TCT 3 B c c
63 GGCAAGAAACAA TTGTTT CTT CCTCTTCTA
CTCCCCAC AACAAA GAA GGAGAAGAT
- C--
GAM94 332 LOC1352 1 6631 XP_072402.4 3 2463 AAATTGTAGAAA TCCTC 3 B c c
93 ACTGAAAGAAAA TTGTTTTCTTTC TTCTA
CAAGACAA AACAAAAGAAAG AAGAT
TCAA-
GAM94 332 LOC1358 1 7298 XP_059804.4 5 274 AAAAGATGGAAC G C-- - 3 B c c

	18				TGAGAAAGAAAA TT TTTTCTTTCTC TCT TCT GGATAT AG AAAAGAAAGAG AGG AGA G TCA T										
GAM94	332 45	LOC1363 1	6912	XP_072455.2	5 18 TAGGAAGAAAGA -- GGAGACAAGGAC TTGTT TTCTT TCTCCTCTT CT AGACAAAT AACAG AGGAA AGAGGAGAA GA AC C A	-	-	3	B	c	c				
GAM94	332 46	LOC1431 1	12827	XP_011844.4	5 499 ACAGAGTTTGGA TAGTAAAGAAAA TTGTTTTCTTT C TCC TTCT CAACAATA AACAAAAGAAA G AGG GAGA T AT TTT	- -- TC-		3	B	c	c				
GAM94	332 10	LOC1433 1	16252	XP_084485.1	3 445 AGAGGTGAGAAG G GGAGAAAGGAGG TT TTTTCTTTCTCC CTTCT GAGTGGGC GA GGAGGAAAGAGG GAAGA G -	T		3	B	c	c				
GAM94	332 81	LOC1433 1	11353	XP_084501.1	3 1692 CGGATGTGGAGA -- GGAGAATGGAAA TTGT TTTCT TTCTCCTCTTC TCGCAGAA GACG AAAGG AAGAGGAGAGG CT T T	-	T	3	B	c	c				
GAM94	332 47	LOC1441 1	16427	XP_049879.1	3 50 TTATTGGAAAGA - GGAGACAGAATG TTGTT TTCT TCTCCTCTT CTA ACAAGATA AACAG AAGA AGAGGAGAA GGT T C A	T	-	3	B	c	c				
GAM94	332 98	LOC1446 1	11632	XP_084939.1	5 15 CTGAGGGAGGCA T- GAAGAAAGAAAT TTG TTTCTTTCT CT CTTCT CCAAGCCT AAC AAAGAAAGA GA GGAGG CT A C	C -		3	B	c	c				
GAM94	332 76	LOC1447 1	15562	XP_084964.1	3 450 AAAGAAATGTGA AGAGAAAGAAGA TTGTTTTCTTTCTC TC TTCT TAATTTTT AATAGAAGAAAGAG AG AAGA A TGTA	C ----		3	B	c	c				
GAM94	332 44	LOC1458 1	10944	XP_085255.1	3 1411 AGCAAGAAAAGT T GAAGAAAGAATG TTGT TTCTTTCT C CT TTCT CAGAATTG GACG AAGAAAGA G GA AAGA T A T A	- - C		3	B	c	c				
GAM94	332 88	LOC1464 1	4919	XP_047748.5	3 304 GGAGGAGAGAGA GGAGAAGGGAGG TTGTTTTCTTTCTCCTCT TCT CAAGGGAG AACGGAGGGAAGAGGAGA AGA G	-		3	B	b	b				
GAM94	332 20	LOC1465 1	19003	XP_085492.1	3 557 GACTTGGTGGGG T AGAGAAAGAATA TTGT TTCTTTCTC CTCT CTA CAGTGAGT GACA AAGAAAGAG GGGG GGT T A T	- T		3	B	c	c				
GAM94	332 13	LOC1467 1	5569	XP_097071.2	3 1532 CTAGCAGGAAGA T C GGACAAAGAGAC TTGTTT CTTT TCCTCTTCT AGAGCCCA GACAGA GAAA AGGAGAAGG - C			3	B	c	c				
GAM94	332 94	LOC1468 2	1807	NP_660316.1	3 1487 GAAAGATGGAGG G AGAAAAAGAAAA TT TTTTCTT TCTCCTCT TCT GGAAGAAA AG AAAAGAA AGAGGAGG AGA	--	-	3	B	c	c				

| | | |

22 GGAGGAGCTGGA TGTTTTCTTT CTCCTCTTCT
GGAAGCAT ACGAAGGAGG GAGGAGGAGA
T TC

GAM94 332 LOC1529 1 17739 XP_087560.1 3 40 TCACCTGGATTT CTCT 3 B c c
24 TGAGAAAGAAAA TTGTTTTCTTTCTC TCTA
TAACTTCT AATAAAAGAAAGAG AGGT
TTTT

GAM94 332 LOC1550 1 1346 XP_088145.2 5 30 GGGTTGAGCAGA TC- T 3 B c c
81 GGAGAAAATCAG TTGTTT TTTCTCCTCT CT
ACAGATGG GACAGA AAAGAGGAGA GA
CTA C

GAM94 332 LOC1572 1 12456 XP_098743.1 5 108 CCATCCAGTAGA ----- T 3 B c c
73 GGAGAAAGACGT TTGTTT TCTTTCTCCTCT CT
CGAGACAG GACAGA AGAAAGAGGAGA GA
GCTGC T

GAM94 332 LOC1573 1 16253 XP_088301.1 3 921 GCAACAAGCAAG - C - 3 B c c
76 AGAGAAAGAAAC TTGT TTTCTTTCTC TCTT CT
ACAGAAAG GACA AAAGAAAGAG AGAA GA
C - C

GAM94 332 LOC1578 2 3986 XP_098833.2 3 1639 GGGATAGGTAGA T - 3 B c c
58 GGAGAGAGACAG TTGTT TCTTTCTCCTCT TCTA
CAAGAAAA AACGA AGAGAGAGGAGA GGAT
C T

GAM94 332 LOC1578 2 19502 XP_098833.2 3 1589 ATGAGGGAGAGA G - 3 B c c
58 GGAGAGAGGAGA TT TTTTCTTTCTCCTCT TCT
GGAAAGGG AG AGAGGAGAGAGGAGA AGG
G G

GAM94 332 LOC1581 1 12067 XP_044880.1 3 452 CAGAAAAGAAGA TC- - 3 B c c
30 GGCAGAAATCCA TTGTTT TTTCT CCTCTTCT
AGCAGAAC GACGAA AAAGA GGAGAAGA
CCT C

GAM94 332 LOC1584 1 14942 NP_612506.1 3 271 AAGAATAACAGA TTT C 3 B c c
35 ATAGGAGGAAAA TTGTTTTC CTCCT TTCT
CAAGGGGA AACAAAAG GAGGA AAGA
--- T

GAM94 332 LOC1590 2 5842 XP_099018.1 3 170 AATGGAGGAAGA T ---- 3 B c c
36 GGAAGTAGGAAG TTGT TTCTTTC TCCTCTTCT
AATGCAGG GACG AAGAAGG AGGAGAAGG
T ATGA

GAM94 332 LOC1590 2 12457 XP_099018.1 5 2 GGAGGAAGAGGA G --- - 3 B c c
36 AGGATGAAGAAA TT TTTTCT TTCT CCTCTTCT
AGGAAGAA AG AAAAGA AGGA GGAGAAGG
G AGT A

GAM94 332 LOC1591 1 11617 XP_010658.4 3 96 GTCCCAAGAAAT TC 3 B c c
84 GGAGGAAGAAAA TTGTTTTCTTTCTCC TTCT
CAAAGAAT AACAAAAGAAGGAGG AAGA
TA

GAM94 332 LOC1629 2 4321 XP_091891.4 3 152 GAGAGGAGAAGA G T 3 B c c
52 GGAGGAGGCAGA TT TTT CTTTCTCCTCTTCT
GGAAGAAA AG AGA GGAGGAGGAGAAGA

G C

GAM94 332 LOC1629 2 9818 XP_091891.4 3 140 GAAGAAGAGAGA ---- - 3 B c c
52 GGAGAAGAGGAG TTGTTTTCTT TCTCCTCT TCT
GAGGCAGA GACGGAGGAG AGAGGAGA AGA
GAGA G

GAM94 332 LOC1699 1 18410 XP_092983.4 5 165 AGAGAAAGAGAA ----- --- - 3 B c c
24 AGAGAAAGACAA TTGTTT TCTTTCTC CTCTT CT
TCAAGCAG GACGAA AGAAAGAG GAGAA GA
CTAAC AAA A

GAM94 332 LOC1973 1 12560 XP_117014.1 5 63 CTCCCAAAAGAA TT CC 3 B c c
17 GAAGAAAGAACA TTGT TCTTTCT TCTTCT
AATCATAA AACA AGAAAGA AGAAGA
-- --

GAM94 332 LOC1973 1 15635 XP_113869.1 3 805 GAAGGAAGGGAC -- --- 3 B c c
42 AGAGAAAGAAGG TTGTT TTCTTTCTC CTCTTCT
GACAGAGG GACAG AAGAAAGAG GGGAAGG
GG ACA

GAM94 332 LOC2004 1 14717 NP_660343.1 3 210 CCGGGGGCTGGA T T- 3 B c c
20 GGAGAAGACAAG TTGTTTTCTT CTCC CTTCT
GAGTTCTT AACAGAAGAG GAGG GGGGG
- TC

GAM94 332 LOC2011 2 886 NP_660344.1 3 79 AGAGGAGAGAGA G - 3 B c c
58 GGAGAGAGGAGA TT TTTTCTTTCTCCTCT TCT
GAGGGAGG GA AGAGGAGAGAGGAGA AGA
G G

GAM94 332 LOC2011 2 2274 NP_660344.1 3 119 TGACGGAGAAGG T CT 3 B c c
58 AGAGAAAGAGAC TTGTTT CTTTCTC CTTCT
GGGAGAGA GGCAGA GAAAGAG GAAGA
- AG

GAM94 332 LOC2011 1 1481 NP_849158.1 3 1220 GACCGGAGGAGA G --- 3 B c c
64 GGAGAGCGGGGA TT TTTTCT TTCTCCTCTTCT
AGAGGAGA AG AGAAGG GAGAGGAGAGGA
G GGC

GAM94 332 LOC2011 1 1481 XP_290750.1 3 1220 GACCGGAGGAGA G --- 3 B c c
64 GGAGAGCGGGGA TT TTTTCT TTCTCCTCTTCT
AGAGGAGA AG AGAAGG GAGAGGAGAGGA
G GGC

GAM94 332 LOC2016 2 5425 XP_117315.1 5 884 AGGGCCGGAAGA T TC 3 B c c
17 GGAAAGAAACCA TTG TTTCTT TCCTCTTCT
GAGTTTCT GAC AAAGAA AGGAGAAGG
C --

GAM94 332 LOC2016 2 12689 XP_117315.1 5 884 GGAGGGCCGGAA T TC 3 B c c
17 GAGGAAAGAAAC TTG TTTCTT TCCTCTTCT
CAGAGTTT GAC AAAGAA AGGAGAAGG
C --

GAM94 332 LOC2034 1 16230 XP_117548.1 5 124 GAAGGGAGAAGA T--- - T- 3 B c c
13 GGCCGAAGAGGA TGTTTTCTTT C CCTCTTCT
AACATGAA ACAAAGGAGA G GGAGAAGA
AAGT A CC

GAM94 332 LOC2038 1 7325 XP_115009.3 5 143 GTCCGAGGAGGA --- 3 B c c
59 GGAGAAGGAGGC TTGT TTTCTTTCTCCTCTTCT
CTGCAGAA GACG GGAGGAAGAGGAGGAGG
TCC
GAM94 332 LOC2200 1 19843 NP_660351.1 3 376 TGAGAAGGGAAA G C T 3 B c c
70 AAGGAAAGAAAA TT TTTTCTTT TCC CTTCT
ATTGAGGG AA AAAGGAAA AGG GAAGA
G A -
GAM94 332 LOC2207 2 14370 XP_055551.1 5 794 TGAGAAAGAAGA T -- - 3 B c c
63 GGAAGATAAAGA TTGTT TCTT TCT CCTCTTCT
TGACGAAG AGCAG AGAA AGA GGAGAAGA
T AT A
GAM94 332 LOC2207 2 18116 XP_055551.1 5 780 AGAAGAGAAAGG G ------ 3 B c c
63 TGAGAAAGAAGA TT TTTTCTTTCTC CTCTTCT
GGAAGATA AG AGAAGAAAGAG GAGAAGA
G TGGAAA
GAM94 332 LOC2212 1 19455 XP_166281.3 5 63 CCTGGAGGAAGA G 3 B c c
18 GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGAAG AG AGGAGGAGGAGGAGAAGG
G
GAM94 332 LOC2215 1 11589 XP_168088.1 5 32 AGCAAGAAAGAA T CC- - 3 B c c
76 AAAGACAGAAAA TTGTTTTCT TCT TCTT CT
CAAATGCG AACAAAAGA AGA AGAA GA
C AAA A
GAM94 332 LOC2217 1 9150 XP_166411.1 3 74 GCCTGAAGACGA TT C T 3 B c c
11 AGAGAAAGAGCA TTGT TCTTTCTC TC TCT
AGGTTATT AACG AGAAAGAG AG AGA
-- A C
GAM94 332 LOC2219 1 7052 XP_166555.2 3 634 GGGAGCAGAAGA TT -- 3 B c c
22 GGGATGAGGGGG TTGTT CTTTC TCCTCTTCT
AGCAGGAG GACGA GGGAG GGGAGAAGA
GG TA
GAM94 332 LOC2219 1 4736 XP_168348.1 5 4 GCAGAGGGAGAG G T 3 B c c
31 GAGACAGGAAGG TT TTTTCT TCTCCTCTTCT
AAAGATGA AA GAAGGA AGAGGAGAGGG
G C
GAM94 332 LOC2219 1 9228 XP_168344.1 3 1245 AAGGTGGAAAGA TTCT - 3 B c c
81 GGAGAACGTAGC TTGTT TTCTCCTCTT CTA
AATCTGGC AACGA AAGAGGAGAA GGT
TGC- A
GAM94 332 LOC2226 2 8126 XP_291197.1 3 38 AGATGAAGAAGA T TT 3 B c c
99 GGGGTGGGGCAA TTGTT TCT CTCCTCTTCT
CAAGTGGT AACAA GGG GGGGAGAAGA
C GT
GAM94 332 LOC2226 2 16962 XP_291197.1 3 539 AGACCACAGAAA G CTC 3 B c c
99 AGAGAAAGAAAA TT TTTTCTTTCTC TTCT
GGAAAGGC AG AAAAGAAAGAG AAGA
G AA-

GAM94 332 48 LOC2531 1 6000 XP_173032.1 5 251 GGCACGGCAAGA TT T - 3 B c c
GGAGCAAGAGCA TTGT TCTT CTCCTCTT CT
AGGACCGC AACG AGAA GAGGAGAA GG
-- C C

GAM94 332 05 LOC2538 1 10542 XP_172854.1 5 257 TGGATGAGAAGA C-- 3 B b b
GGAGAAAAATAA TTGTTTT TTTCTCCTCTTCT
AACAAGGA AACAAAA AAAGAGGAGAAGA
TAA

GAM94 332 39 LOC2538 2 4687 XP_170875.1 5 89 AGAAGAGGAAGA TC 3 B b b
GGAAAGCAAAGG TTGTTTTCTT TCCTCTTCT
AGTCAGGG AACGAAAGGA AGGAGAAGA
GA

GAM94 332 39 LOC2538 2 17089 XP_170875.1 5 87 AAACCCAGAAGA TC 3 B b b
GGAAGAGGAAAG TTGTTTTCTT TCCTCTTCT
CAAAGGAG AACGAAAGGA AGGAGAAGA
GA

GAM94 332 82 LOC2539 2 2355 XP_170804.3 5 354 GGAGAAAGAAGA T T 3 B c c
GGGTGAGGAGGC TTGTTTTCTT C CCTCTTCT
GACAGAGG AGCGGAGGAG G GGAGAAGA
T -

GAM94 332 82 LOC2539 2 17182 XP_170804.3 5 344 AGGCTGCTGGAA G CT 3 B c c
GGAGAAAGAAGA TT TTTTCTTTCTCCT TCTA
GGGTGAGG GG AGAAGAAAGAGGA AGGT
G --

GAM94 332 92 LOC2539 2 12822 XP_172953.2 3 674 TCTGACAGAAGA - T 3 B c c
GGAGCAGGAGAA TTGTT TTCTT CTCCTCTTCT
ACAAATCG AACAA GAGGA GAGGAGAAGA
A C

GAM94 332 92 LOC2539 2 19414 XP_172953.2 3 675 AGAAGAGGAGCA - T 3 B c c
GGAGAAACAAAT TTGTT TTCTT CTCCTCTTCT
CGTTAAAA AACAA GAGGA GAGGAGAAGA
A C

GAM94 332 49 LOC2558 1 7005 XP_172855.1 3 136 ATGTGAGGATGA T T 3 B c c
GGAGACAGAAAA TTGTTTTCT TCTCCTC TCT
CAAGTAGC AACAAAAGA AGAGGAG AGG
C T

GAM94 332 14 LOC2566 1 1367 XP_172864.1 3 1576 GATCTGGAAAGA CC - 3 B c c
AAGGAAGGAAAA TTGTTTTCTTTCT TCTT CTA
CAAAGGCG AACAAAAGGAAGG AGAA GGT
AA A

GAM94 332 58 LOC2573 1 2994 XP_173138.1 3 1334 AGAGAGTGGAGA TT T 3 B c c
GGAGAGAGAGCA TTGT TCTTTCTCCTCTTC
AATATTG AACG AGAGAGAGGAGAGG
-- T

GAM94 332 88 LOC2828 1 11589 XP_212605.1 5 32 AGCAAGAAAGAA T CC- - 3 B c c
AAAGACAGAAAA TTGTTTTCT TCT TCTT CT
CAAATGCG AACAAAAGA AGA AGAA GA
C AAA A

GAM94 332 26 LOC2829 1 11589 XP_212646.1 5 32 AGCAAGAAAGAA T CC- - 3 B c c
AAAGACAGAAAA TTGTTTTCT TCT TCTT CT

CAAATGCG AACAAAAGA AGA AGAA GA
C AAA A

GAM94 332 86 LOC2829 1 15064 XP_208469.1 3 1045 AATTTTGAGGGG T T 3 B c c
AGGGAAAGAAAC TTGTTT CTTTC CCTCTTCT
AATACCTT AACAAA GAAAG GGAGGGGA
- -

GAM94 332 10 LOC2830 1 1988 XP_210848.1 3 331 TTAAAGAGAAGA ---- T 3 B c c
GGCGAGAGCATG TTGTTTTC TTTC CCTCTTCT
AAGATAAA AATAGAAG AGAG GGAGAAGA
TACG C

GAM94 332 32 LOC2830 1 10557 XP_208489.1 3 190 GAGAGAACAGGA G T --- 3 B c c
GGTGAAAGAAAA TT TTTTCTTTC CCTCT TCT
GGGTGAGT GG AAAAGAAAG GGAGG AGA
G T ACA

GAM94 332 47 LOC2830 1 3684 XP_210870.1 3 646 GGAGCTAGAAGA T TT ------- 3 B c c
GTGGCCAGGAGA TGTTTTC TCTCC TCTTCTA
TGAAAGCA ACGAAAG AGAGG AGAAGAT
- T- ACCGGTG

GAM94 332 53 LOC2830 1 1988 XP_210869.1 3 331 TTAAAGAGAAGA ---- T 3 B c c
GGCGAGAGCATG TTGTTTTC TTTC CCTCTTCT
AAGATAAA AATAGAAG AGAG GGAGAAGA
TACG C

GAM94 332 29 LOC2831 1 16555 XP_208524.1 5 234 GATTCTAGAACA C C 3 B c c
GGAGAAATAAAA TTGTTTT TTTCTCCT TTCTA
CAGCTATC GACAAAA AAAGAGGA AAGAT
T C

GAM94 332 67 LOC2831 1 9978 XP_210921.1 3 812 CTTATAAGAAGA TT T- 3 B c c
GGAGATTAGGTC TTGT TCT TCTCCTCTTCT
ACAGACAT GACA GGA AGAGGAGAAGA
CT TT

GAM94 332 94 LOC2831 1 15353 XP_210932.2 5 415 ATCTGGATGTGA C C- T 3 B c c
AGAGAAAGAGAA TTGTTTT TTTCT CTCTTC
AAACAAAA AACAAAA AGAGA GAGAAG
- AA T

GAM94 332 14 LOC2833 1 13566 XP_210969.1 3 868 AGAAGAAGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGAAG AG AGGAGGAGGAGGAGAAGA
G

GAM94 332 15 LOC2833 1 19603 XP_210974.1 5 106 AGAGGGACGTGG T --- 3 B c c
GGAGAAAGAAGC TTG TTTCTTTCTCCTC TTCT
CAGAAGCC GAC GAAGAAAGAGGGG AGGG
C TGC

GAM94 332 29 LOC2833 2 2261 XP_210978.1 5 475 GAGGAGGGGAGA TG 3 B c c
GGAGAAGGGAAA T TTTTCTTTCTCCTCTTCT
TGGAGGTG G AAAGGGAAGAGGAGAGGG
GT

GAM94 332 29 LOC2833 2 3885 XP_210978.1 5 529 GGAGGGAGGAAG ---- - - 3 B c c
AATAGAGGAAAA TTGTTTTCT TTCT CCTCT TCT
CAATGGGC AACAAAAGG AAGA GGAGG AGG
AGAT A G

GAM94 332 LOC2833 2 10870 XP_211006.1 5 94 GCAGCTCGTAGA TT TCT 3 B c c
81 GGAGAGAAAACA TTGTTTTC TCTCCTCT
AGAGTGGA AACAAAAG AGAGGAGA
-- TGC
GAM94 332 LOC2833 2 18381 XP_211006.1 5 94 ATGCAGCTCGTA TT TCT 3 B c c
81 GAGGAGAGAAAA TTGTTTTC TCTCCTCT
CAAGAGTG AACAAAAG AGAGGAGA
-- TGC
GAM94 332 LOC2834 1 11385 XP_211031.1 3 153 TACAAGAGAAGA T- - --- 3 B c c
23 GGAAGGGAGCAG TGTTTTCT TTC TCCTCTTCT
AGAGCACT ACGAGAGA GAG AGGAGAAGA
TC C GGA
GAM94 332 LOC2834 1 15116 XP_211039.1 5 748 AGAGGACTGGGA T --- 3 B c c
39 GGAGAATGGAGG TTGTTTTC TTCTCCTCT TCT
CAAGAAAA AACGGAGG AAGAGGAGG AGG
T GTC
GAM94 332 LOC2835 1 12690 XP_208101.1 5 35 CAAAGAAGGGTG T ---- 3 B c c
58 GCGAGAAGAAAA TTGTTTTCTT CTC CTCTTCT
CGGGCCGT GGCAAAAGAA GAG GGGAAGA
- CGGT
GAM94 332 LOC2836 1 2425 XP_211135.1 3 347 CAGCAGGAGAGA - - 3 B c c
39 GGAGAGGGCAGA TTGTTTT CTTTCTCCTCT TCT
ACAGGATC GACAAGA GGGAGAGGAGA AGG
C G
GAM94 332 LOC2836 1 18438 XP_211149.1 3 1451 GGGAAAAGAAGA - TT --- 3 B c c
67 GGAGGCTTAGGA TTG T TCTT TCTCCTCTTCT
TGGTCAAG AAC G AGGA GGAGGAGAAGA
T GT TTC
GAM94 332 LOC2837 1 6827 XP_208798.2 5 191 CAGGAGCGAACA TC ----- 3 B c c
17 GGAACAGGAAAA TTGTTTTCTT TCCT CTTCT
CAAATGGC AACAAAAGGA AGGA GAGGA
CA CAAGC
GAM94 332 LOC2837 1 15870 XP_211186.1 5 1651 AAAGGGAGAAGA T----- CT 3 B c
c
38 GGGAAAAGGAAG TGTTTTCTTT CCTCTTCT
CACGTCCC ACGAAGGAAA GGAGAAGA
CCCTGC AG
GAM94 332 LOC2837 1 14856 XP_208815.1 3 321 GGGGTTGGTAGC T --- T 3 B c c
43 AGAGAAAGAGAA TTGTTTTCTT CTC CTCT CTA
GAGAACAG GACAAGAGAA GAG GAGA GAT
- AAA C
GAM94 332 LOC2837 1 8147 XP_208835.1 5 36 ACGGGAGCAGGA ---- - 3 B c c
67 GGAGAAGATACG TTGTTTTC TTTCTCCTCTT CT
AGAGCAGG GACGAGAG GAAGAGGAGGA GA
CATA C
GAM94 332 LOC2838 1 632 XP_211225.1 3 1008 TTTAGGAGAAGA TC 3 B c c
34 GGAGAGACAGGC TTGTTT TTTCTCCTCTTCT
AGGAAAGG GACGGA AGAGAGGAGAAGA
C-

GAM94 332 LOC2838 1 6537 XP_211250.1 5 0 GGGAAGAGGAAA C C 3 B c c
94 ATGAGGCAAGAT TTGTTTT TTT TCCTCTTCT
GCTGAGAA AACGGAG AAA AGGAGAAGG
T -
GAM94 332 LOC2839 1 19947 XP_211256.1 5 0 GGGAAGAGGAAA C C 3 B c c
09 ACGAGGCAAGAT TTGTTTT TTT TCCTCTTCT
GCTGAGAA AACGGAG AAA AGGAGAAGG
C -
GAM94 332 LOC2839 1 9286 XP_211275.2 3 1326 TGACAGGGCAGG T C - 3 B c c
63 AAGAGAAGAAAA TTGTTTTCTT CTC TCTT CT
CGGAGGAG GGCAAAAGAA GAG AGGA GG
- A C
GAM94 332 LOC2839 1 11731 XP_211293.1 5 2021 GCATAAAGGAGG -- C 3 B c c
93 GCAGAAAGAAAC TTGT TTTCTTTCT CTCTTCT
AGCAGTGT GACG AAAGAAAGA GGGAGGA
AC C
GAM94 332 LOC2840 1 16812 XP_211306.1 3 850 AAGGAAAGAAGA G TC 3 B c c
36 GAGGAAAGAAAG TT TTTTCTTTC CTCTTCT
GAGGGAAG GA GAAAGAAAG GAGAAGA
G GA
GAM94 332 LOC2840 1 13458 XP_211331.1 3 1705 TCACAGAAACTG - TC- 3 B c c
93 GGGAAGGGAAAA TTGTTTTCT TTCTCC TTCT
CAAACCTT AACAAAAGG AAGGGG AAGA
G TCA
GAM94 332 LOC2841 1 3622 XP_209004.1 3 1311 AGAGAAACGGGG C- -- 3 B c c
06 AGAGAAAGAAAC TTGTTTT TTTCTCCTC TTCT
GATTCTAA AGCAAAG AGAGAGGGG AAGA
AA CA
GAM94 332 LOC2841 1 12668 XP_211330.2 3 508 TGGAGAGACGGA TTT - 3 B c c
09 GGAGAAGGGCAG TTGT CTTTCTCCTCT TCT
GGTTCAGA GACG GGAAGAGGAGG AGA
--- C
GAM94 332 LOC2841 1 14340 XP_209041.1 5 610 GGGGGAGGGGGA G 3 B c c
58 GGAGAAGGGGCA TT TTTTCTTTCTCCTCTTCT
GTTGTGAC GG AAGAGGAGGGGGAGGGGG
G
GAM94 332 LOC2841 1 574 XP_209050.1 5 457 GGAGGAAGAAGA TT C 3 B c c
66 GGCGAGAACGAT TTGTTTTC TCTC TCTTCT
CCCCGAAC AGCAAGAG GGAG AGAAGG
C- A
GAM94 332 LOC2841 1 4956 XP_209051.1 3 766 TAGGCAGAAAGA G C 3 B c c
71 GGAGGACAAAGA TT TTTTCTTT TCCTCTTCT
GGAGGAAA AG AGGAGAAA AGGAGGAGA
G C
GAM94 332 LOC2841 1 11838 XP_209062.2 5 67 AGGCAGCAGGAA G - - 3 B c c
85 GGAGAAAGGAGG TT TTTTCTTTCTCCT CTT CT
GAAGGTAA AA GGAGGAAAGAGGA GGA GA
G A C
GAM94 332 LOC2842 1 14624 XP_209065.1 3 133 TTACTGGGGAGA CC 3 B c c
00 ATAGAAAGAAAA TTGTTTTCTTTCT TCTTCT

CAATTGAC AACAAAAGAAAGA AGAGGG
TA

GAM94 332 LOC2842 1 11892 XP_209102.1 3 827 GGAAAAGAGAAA T- T C 3 B c c
77 AGGGAAAGAAAT TTG TTTCTTTC CCT TTCT
CCAGAGAA GAC AAAGAAAG GGA AAGA
CT - A

GAM94 332 LOC2842 1 12346 XP_211415.1 5 991 AACCCAGGAGAG G - 3 B c c
81 GAAGAAAGAAAG TT TTTTCTTTCT CCTCTTCT
GAGAGAGG GA GAAAGAAAGA GGAGAGGA
G A

GAM94 332 LOC2843 1 911 XP_209116.1 5 7 CCCGGGGCAAGA TT - 3 B c c
13 GGAGGGAGAAGG TTGTTTTCT CTCCTCTT CT
CAGGGCCG GACGGAAGA GAGGAGAA GG
GG C

GAM94 332 LOC2843 2 2133 NP_778233.2 5 321 GGAGGAGCAGAG TT -- 3 B c c
61 GGAGAAAGCGAG TTGTTTTCT CTC CTCTTCT
GGGGCGGG AGCGAAAGA GAG GAGGAGG
GG AC

GAM94 332 LOC2843 2 7597 NP_778233.2 3 780 AAGGAAAAGGTT ---- C 3 B c c
61 TAAGAAAGAAAA TTGTTTTCTTTCT CCT TTCT
CAAAACCA AACAAAAGAAAGA GGA AAGG
ATTT A

GAM94 332 LOC2845 1 7648 XP_209244.1 3 221 AGCCGAGGAAGG TTT 3 B c c
14 GGAGAAAGCCAC TTGT CTTTCTCCTCTTCT
AACCTTCA AACA GAAAGAGGGGAAGG
CC-

GAM94 332 LOC2845 1 4914 XP_211508.1 3 836 AGAGAAACAGAG --- C- --- 3 B c c
26 ACAGAAAGAAAG TTGTT TTCTTTCT CTCT TCT
AGACAGAC GACAG AAGAAAGA GAGA AGA
AGA CA CAA

GAM94 332 LOC2845 1 13941 XP_211528.3 3 763 TGGGGTGGCAGC T T - T 3 B c c
84 AGGGACAGAAAA TTGTTTTCT TC CCT CT CTA
CAACAGAG AACAAAAGA AG GGA GA GGT
C - C C

GAM94 332 LOC2846 1 9049 XP_211551.1 3 89 GAAGGAAGAAGA TT T T 3 B c c
12 GGGAAGAATCCG TTG TTCTT C CCTCTTCT
ACCACTTT AGC AAGAA G GGAGAAGA
CT - -

GAM94 332 LOC2846 1 8361 XP_208227.1 3 35 TGTAGAGAAAAA CT TC-- 3 B c c
21 TGGTGAAGAAAA TTGTTTTCTTT CC TTCT
CAAAGATG AACAAAAGAAG GG AAGA
T- TAAA

GAM94 332 LOC2846 1 7303 XP_211569.1 3 47 GCCAGGGAGGGA -- - 3 B c c
47 GGAGAAAGCCGA TTGTTTT CTTTCTCCTCT TCT
AGCGAAAG AGCGAAG GAAAGAGGAGG AGG
CC G

GAM94 332 LOC2846 2 2955 XP_211581.1 5 1113 CCAGGGAAAGGA --- C 3 B c c
65 GAAAAGAGAAAA TTGTTTTCTT TCTCCT TTCT
CAGGCTGG GACAAAAGAG AGAGGA AGGG
AAA A

GAM94 332 LOC2846 2 10092 XP_211581.1 5 1113 TCCCCAGGGAAA --- C 3 B c c
65 GGAGAAAAGAGA TTGTTTTCTT TCTCCT TTCT
AAACAGGC GACAAAAGAG AGAGGA AGGG
AAA A
GAM94 332 LOC2846 1 16579 XP_211584.1 3 1985 TGATTTTATGGA TTTC T 3 B c c
69 AGTGGGCGAAAA TTGTTTTC TCC CTTCTA
CAATCAAA AACAAAAG GGG GAAGGT
C--- T
GAM94 332 LOC2846 1 11553 XP_209313.2 5 21 GGAGCCAGAAGA TG -- 3 B c c
71 GGGAGGAAAGGA T TTTTCTTTCT CCTCTTCT
GATGAGAT A AGAGGAAAGG GGAGAAGA
GT AG
GAM94 332 LOC2847 1 2392 XP_211622.1 3 586 TAGAGAAGAAGA CT C 3 B c c
51 GGACAAAACAAG TTGTTTT TTCTC TCTTCT
GGAAAAGC AACAAAA AGGAG AGAAGA
C- A
GAM94 332 LOC2848 1 8984 XP_209368.1 3 95 AACAGAAGACCA T C --- 3 B c c
10 GGAGAAAAAGTC TTG TTT TTTCTCC TCTTCT
AAAAAGAA AAC GAA AAAGAGG AGAAGA
T - ACC
GAM94 332 LOC2848 1 15871 XP_211667.1 3 1335 TGATAGGGCAGG - - C 3 B c c
51 AAGAGAAGAAAA TTGTTTTCT TTCT CCT TTCTA
CGGAGGAG GGCAAAAGA GAGA GGA GGGAT
A A C
GAM94 332 LOC2849 1 19372 XP_209402.1 3 161 TTTACGGAAGGG - CT 3 B c c
06 GGAAACAGAAAA TTGTTTTCT TT CCTCTTCT
CAGCCTCC GACAAAAGA AA GGGGAAGG
C AG
GAM94 332 LOC2849 1 15731 XP_209397.1 3 1657 GAGACAAGAAGA T---- -- T 3 B c c
07 GGGAAAGTAGAA TGTTTT CTTTC CCTCTTCT
ATATTCTA ATAAAG GAAAG GGAGAAGA
ATCTT AT -
GAM94 332 LOC2849 1 11375 XP_211684.1 3 1530 GTCTAAAGAAGA G - T 3 B c c
11 GGTGAGAGCAAA TT TTTT CTTTC CCTCTTCT
AGGAATAA AG AAAA GAGAG GGAGAAGA
G C T
GAM94 332 LOC2849 1 14715 XP_209414.1 3 813 TGAGCAATGAGG TT T 3 B c c
25 AGGAGTGGAAAA TTGTTTTCT CTCCTCTTC
CAAAACCC AACAAAAGG GAGGAGGAG
T- T
GAM94 332 LOC2849 1 3044 XP_211700.1 5 609 CGTCTCAGAAAA - C C- 3 B c c
39 AGGAAAAGAAAA TTGTTTT CTTT TCCT TTCT
ACAATCTA AACAAAA GAAA AGGA AAGA
A - AA
GAM94 332 LOC2850 2 1295 XP_211742.1 3 951 CAAGGAGGAGGC CT--- 3 B c c
43 TGCCAAAGAAAA TTGTTTTCTTT CCTCTTCT
CAAAGGCC AACAAAAGAAA GGAGGAGG
CCGTC
GAM94 332 LOC2850 2 1869 XP_211742.1 5 143 GAAACAATGAAG C T T 3 B c c

43 TGGAAAAGAAAA TTGTTTTCTTT TCC CTTC
CAGCTAAA GACAAAAGAAA AGG GAAG
- T T

GAM94 33223 LOC2851 1 13262 XP_211773.1 3 1054 ACTCCCGGAGGA CT-- 3 B c c
GGAGAACAAAGA TTGTTTT TTCTCCTCTTCT
AACGAGGC AGCAAAG AAGAGGAGGAGG
AAAC

GAM94 33226 LOC2852 1 4047 XP_209522.1 3 2044 AGGTGGAGAAGA CT-- 3 B c c
GGTACAAAGGAA TTGTTTTCTTT CCTCTTCT
AACGAGAG AGCAAAAGGAA GGAGAAGA
ACAT

GAM94 33256 LOC2852 1 19463 XP_211818.1 3 1205 CTGCAAGCTGAG T - TT 3 B c c
GAAGAAAGAAGC TTG TTTCTTTCT CCTC CT
CAATAGTA AAC GAAGAAAGA GGAG GA
C A TC

GAM94 33283 LOC2852 1 13463 XP_208017.1 3 585 GAATAGAGAAGA TCT 3 B c c
GGTAAGAAGATA TTGTTTTCTT CCTCTTCT
ATTGTTTT AATAGAAGAA GGAGAAGA
T--

GAM94 33229 LOC2853 1 3250 XP_209569.1 3 1419 TGAGGAAGGAGA TT 3 B c c
GGAGAGGGTGGC TTGTT CTTTCTCCTCTTCT
AATGATGC AACGG GGGAGAGGAGAGGA
T-

GAM94 33259 LOC2853 1 18819 XP_211858.1 3 893 AGAATTGGAAGA G T 3 B c c
GGAGGCAGAAGA TT TTTTCT TCTCCTCTTCTA
GGAGCAGC AG AGAAGA GGAGGAGAAGGT
G C

GAM94 33276 LOC2853 2 4042 XP_211864.1 3 99 CTGCCAGGAAGA G 3 B c c
GGAGGGGAGGAG TT TTTTCTTTCTCCTCTTCT
GAGGAGGA AG AGGAGGAGGAGGGGAGGA
G

GAM94 33276 LOC2853 2 10455 XP_211864.1 3 276 AGGAGGAGGGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAAGCCA AG AGGAGGAAGAGGAGGGGA
G

GAM94 33208 LOC2854 1 19174 XP_211886.3 5 504 TGTGGAAGGTTC C--- 3 B c c
TGAGAAAGAAAA TTGTTTTCTTTCTC TCTTCTA
TAGTTTCC GATAAAAGAAAGAG GGAAGGT
TCTT

GAM94 33261 LOC2855 1 4265 XP_211940.1 5 90 CTTGAGATGGGA T C-- 3 B c c
GGAGAACGGAAG TGTTTTCTTTCT CTCTTCT
GAAAACA ACAAAAGGAAGG GAGGAGG
- CAA

GAM94 33281 LOC2855 1 2844 XP_211942.1 3 580 GCAGATAGACTT TTC T-- 3 B c c
GAGGACAGAAAA TTGTTTTCT TCCTC TCTA
CAAAAACA AACAAAAGA AGGAG AGAT
C-- TTC

GAM94 33293 LOC2855 1 18196 XP_211944.1 5 518 ACAAGGAGAAGA TT T 3 B c c
GGAAGGGAGGAA TTGTT CTTTCTCC CTTCT
GGGAACAG GACAA GAAGGAGG GAAGG

GG -

GAM94 332 LOC2856 1 11670 XP_211959.1 5 563 AGATGACAAAGA -- CT 3 B c c
26 GGAGTGGAAGAA TTGTTTTCTTT CTCCTCTT
GACAGAGA GACAGAAGAAG GAGGAGAA
GT AC

GAM94 332 LOC2857 2 13781 XP_211990.1 5 5 AGAAAAGAAAAG G CC -- 3 B c c
19 AAAAGAAAGAAA TT TTTTCTTTCT TCT TCT
GGAATTAG AA GAAAGAAAGA AGA AGA
G AA AA

GAM94 332 LOC2857 2 16194 XP_211990.1 5 5 GAAAAGAAAAGA G CC -- 3 B c c
19 AAAGAAAGAAAG TT TTTTCTTTCT TCT TCT
GAATTAGG AA GAAAGAAAGA AGA AGA
G AA AA

GAM94 332 LOC2857 1 9830 XP_212000.1 3 759 AGGGTGAGAAGA G T- 3 B c c
27 GGCTGAGAGAGA TT TTTTCTTTC CCTCTTCT
AGGGGAAA GG AAGAGAGAG GGAGAAGA
G TC

GAM94 332 LOC2857 1 19245 XP_208346.1 3 178 AAGCCAAGAAGA T TC- 3 B c c
37 GGAAACAAGATA TTGTT TCTT TCCTCTTCT
ATAAATGT AATAA AGAA AGGAGAAGA
T CAA

GAM94 332 LOC2857 1 14530 XP_209743.1 3 590 CTTATAAGAAGA TT C 3 B c c
44 GGAAAAGACACA TTGT TCTTT TCCTCTTCT
AGGAATGT AACA AGAAA AGGAGAAGA
C- -

GAM94 332 LOC2857 1 10416 XP_209755.1 3 2716 GAGGGAAGGAGA TCT 3 B c c
69 GGAGAGGAACAG TTGTTT TTCTCCTCTTCT
GTTTTGAT GACAAG GAGAGGAGAGGA

GAM94 332 LOC2857 1 3549 XP_209756.1 3 1434 GGTAAAGTAAGG TG - - 3 B c c
78 GGAGAAAGTGAA T TTTT CTTTCTCCTCTT CT
GTGACTTC A GAAG GAAAGAGGGGAA GA
GT T T

GAM94 332 LOC2857 1 12982 XP_212018.1 5 787 GAAGCTGATGCA --- ------- T 3 B c c
81 GGGGAAAGAAAT TTGTT TTCTTTCTCCT CTTC
TAACAACC AACAA AAGAAAGGGGA GAAG
TTA CGTAGTC -

GAM94 332 LOC2858 1 3350 XP_212028.1 3 1967 GGCATCACAGAA - TCCT 3 B c c
06 GTGAAATGAAAA TTGTTTTC TTTC CTTCT
CAAAATTA AACAAAAG AAAG GAAGA
T T---

GAM94 332 LOC2858 1 10315 XP_209770.1 3 801 TTATTGAAAAGA TT- 3 B c c
54 GGAGGGGAAAGG TTGT TCTTTCTCCTCTTCT
TCTATAAA AATA GGAAAGGGGAGGAGA
TCT

GAM94 332 LOC2859 1 1456 XP_212102.1 3 640 ATTAAGAATAAA C-- 3 B c c
33 GGAGGAGGAAAA TTGTTTTCTTTCTCCT TTCT
CAACAAAG AACAAAAGGAGGAGGA AAGA

AAT

GAM94 332 LOC2860 1 7067 XP_212134.1 3 940 AATGGGAGAGGA TT T 3 B c c
08 GGAGAATCAATG TTG TTCTT CTCCTCTTCTA
GGATGTGG AAC AAGAG GAGGAGAGGGT
T- -

GAM94 332 LOC2860 1 2256 NP_775954.1 3 563 TGCACCAGAAGA TC CT 3 B c c
46 GGGAAAATTAAA TTGTTT TTT CCTCTTCT
CAATTAAA AACAAA AAA GGAGAAGA
TT AG

GAM94 332 LOC2860 2 5125 XP_212156.1 5 141 AGGAAGGAAGGG G - 3 B c c
59 AGGGAAAGAAAG TT TTTTCTTTCTC CTCTTCT
GAAGAAAG AA GAAAGAAAGGG GGGAAGG
G A

GAM94 332 LOC2860 2 12587 XP_212156.1 5 167 AGAAAGAGAAAA T ----- - 3 B c c
59 AGAGAAAGAAAC TTGTTT CTTTCTC CTCTT CT
AGAAAGAA GACAAA GAAAGAG GAGAA GA
- AAAAA A

GAM94 332 LOC2861 1 20048 XP_210719.1 5 0 GTGGATGAGGAG CT T 3 B c c
31 AAGAAGCAGGTG TTGTTTT TTCTCCTC TCTA
ACCATGGA GACGAAG AAGAGGAG AGGT
-- T

GAM94 332 LOC2861 1 17161 XP_212213.1 3 1182 AACAAAAGAAGA - C C 3 B c c
80 AGAAAAAGAAAA TTGTTTT CTTT TC TCTTCT
ACAACCAC AACAAAA GAAA AG AGAAGA
A A A

GAM94 332 LOC2861 2 3917 XP_209933.1 3 2090 TTATTAGGAAGA T ----- - 3 B c c
88 GGAAGAAGAGGT TGTTTTCT TTCT CCTCTTCT
AGAAAACA ACAAAAGA AAGA GGAGAAGG
- TGGAG A

GAM94 332 LOC2861 2 12855 XP_209933.1 3 2095 GGAAGAGGAAGA T----- ----- - 3 B c c
88 AGAGGTAGAAAA TGTTTTCT TTCT CCTCTTC
CATATTTT ACAAAAGA AAGA GGAGAAG
TTTTAT TGGAG A

T
G

GAM94 332 LOC2862 1 2441 XP_209953.1 3 1374 TCTAGAAAACAA TCCTC--- 3 B c
c
06 AATGAAAGAAAA TTGTTTTCTTTC TTCTA
CAAATATG AACAAAAGAAAG AAGAT
TAAAACAA

GAM94 332 LOC2862 1 15563 XP_212238.1 3 465 ATGAGTGGGAGG TTT 3 B c c
35 GGAGAAAGCACA TTGT CTTTCTCCTCTTCTA
CAGAGCTC GACA GAAAGAGGGGAGGGT
CAC

GAM94 332 LOC2863 1 12006 XP_212288.1 3 484 TGCAGAATGAGA C 3 B c c
59 GGAGAGAGGGAA TTGTTTTCTTTCTC TCTTCT
GGCAGGTC GACGGAAGGGAGAG AGGAGA
-

GAM94 332 LOC2863 1 7767 XP_212308.1 5 185 CCCTTTCTAAGA T - C 3 B c c
95 GGAGGAAAAATG TTGT TTC TTT TCCTCTTCT
GATGCAAG AACG AGG AAA AGGAGGAGA
T T A
GAM94 332 LOC2864 1 15065 XP_212313.1 5 1011 GGCAGGAGAGAG G -- - 3 B c c
21 GGAAAAAGAAAA TT TTTTCTT TCTC CTCTTCT
GAAGGAAC AA AAAAGAA AGGG GAGAGGA
G AA A
GAM94 332 LOC2864 1 9648 XP_210044.1 3 862 GCTGCTGGAAGA CTCC 3 B c c
30 AATAGAAGAAAA TTGTTTTCTTT TCTTCTA
CAACCCAC AACAAAAGAAG AGAAGGT
ATAA
GAM94 332 LOC2864 1 15291 XP_212322.1 3 1088 GAGGGTGGTAGA CTT T 3 B c
c
48 GGAGATAAGACA TTGTTTT TCTCCTCT CTA
GTAGGGAA GACAGAA AGAGGAGA GGT
T-- T
GAM94 332 LOC2864 1 4136 XP_212321.1 5 87 GGACCAGGAGAA - - C 3 B c c
49 GAGCAAAGAAAA TTGTTTT CTTT CTC TCTTCT
GCAGCCCG GACGAAA GAAA GAG AGAGGA
A C A
GAM94 332 LOC2865 1 1891 XP_208450.1 3 921 GCGGAGGTGAGA TT- T 3 B c c
45 GGAGAGGAGGAG GTTTTCTT CTCCTCTTCT
AAAACTGC CAAAAGAG GAGGAGAGGA
CGT -
GAM94 332 LOC3385 1 20131 XP_294654.1 3 389 AAGTGTAGAAGA T - 3 B c c
62 GGGAGAGAGAAG TTGTTT CTTTCTCC TCTTCTA
CAGGAGAG GACGAA GAGAGAGG AGAAGAT
- G
GAM94 332 LOC3386 1 7298 XP_294661.1 5 617 AAAAGATGGAAC G C-- - 3 B c c
07 TGAGAAAGAAAA TT TTTTCTTTCTC TCT TCT
GGATAT AG AAAAGAAAGAG AGG AGA
G TCA T
GAM94 332 LOC3387 1 16308 XP_290534.1 5 122 GGAGGGCGAAGA G TT 3 B c c
07 GGAGGAGGAAGG TT TT CTTTCTCCTCTTCT
GGAGGACG AG AG GAAGGAGGAGGAGA
G GG
GAM94 332 LOC3387 1 18110 XP_294690.1 3 50 CTTGGGACCAGA TT C -- 3 B c c
39 AGAGAAAGAACC TTG TTCTTTCTC TCT TCT
AAAAAGTG AAC AAGAAAGAG AGA AGG
C- A CC
GAM94 332 LOC3388 1 19080 XP_290588.1 3 1699 AAAGAAAGAGAA G C--- - 3 B c c
17 AAAGAAAGAAAG TT TTTTCTTTCT CTCTT CT
GAAAGAAA AA GAAAGAAAGA GAGAA GA
G AAAA A
GAM94 332 LOC3388 2 6696 XP_290216.1 3 1477 TGAAGAGGAAGA TC T 3 B c c
19 GGAGGACAGTGA TTGTTTTCTT TCCTCTTC
TGAAGATT GACAGGAGGA AGGAGAAG

GA T

GAM94 332 LOC3388 2 12463 XP_290216.1 3 1475 TGACTATGAAGA TC T 3 B c c
19 GGAAGAGGAGGA TTGTTTTCTT TCCTCTTC
CAGTGATG GACAGGAGGA AGGAGAAG
GA T

GAM94 332 LOC3389 1 9380 XP_294757.1 5 190 CCAGAGGGGAGA T-- 3 B c c
63 GGAGAGAGCCTG TTGTTT CTTTCTCCTCTTCT
GACAGCCT GACAGG GAGAGAGGAGAGGG
TCC

GAM94 332 LOC3389 1 6827 XP_290223.1 5 191 CAGGAGCGAACA TC ----- 3 B c c
69 GGAACAGGAAAA TTGTTTTCTT TCCT CTTCT
CAAATGGC AACAAAAGGA AGGA GAGGA
CA CAAGC

GAM94 332 LOC3389 1 8072 XP_208845.3 5 191 CAGGAGCCAAGA TC CT 3 B c c
71 GGAACAGGAAAA TTGTTTTCTT TCCTCTT
CAAATGGC AACAAAAGGA AGGAGAA
CA CC

GAM94 332 LOC3389 1 4715 XP_294762.1 5 1335 GAAGAAGGAAGA G --- 3 B c c
76 GGAAAGGGAGGA TT TTTTCTTTC TCCTCTTCT
GGAGGATT AG AGGAGGAGG AGGAGAAGG
G GAA

GAM94 332 LOC3389 1 8147 XP_290663.1 5 36 ACGGGAGCAGGA ---- - 3 B c c
91 GGAGAAGATACG TTGTTTTC TTTCTCCTCTT CT
AGAGCAGG GACGAGAG GAAGAGGAGGA GA
CATA C

GAM94 332 LOC3389 1 17003 XP_290659.1 5 29 ATGGGAGCAGGA ---- - 3 B c c
99 GGAGAAGATACG TTGTTTTC TTTCTCCTCTT CT
AGAGCAGG GACGAGAG GAAGAGGAGGA GA
CATA C

GAM94 332 LOC3390 1 5473 XP_294775.1 3 270 TTACACGGGAGA TT- - 3 B c c
22 GGAGAATGGATT TTGT TCT TTCTCCTCTTCT
TATAAAGA AATA AGG AAGAGGAGAGGG
TTT T

GAM94 332 LOC3390 1 6907 XP_294800.1 5 1683 GGAAAGGAGAAA TG -- 3 B c c
71 GGAGAAAGAAGG T TTTTCTTTCTCC TCTTCT
TGAAGTCT A GGAAGAAAGAGG AGAGGA
GT AA

GAM94 332 LOC3391 1 7097 XP_294830.1 5 901 GTCTTGGTAGGA - T - 3 B c c
49 GGAGAAGAAACA TTGT TTTCTT CTCCTCTT CTA
CAGGGAAA GACA AAAGAA GAGGAGGA GGT
C - T

GAM94 332 LOC3391 1 14624 XP_290741.1 3 79 TTACTGGGGAGA CC 3 B c c
73 ATAGAAAGAAAA TTGTTTTCTTTCT TCTTCT
CAATTGAC AACAAAAGAAAGA AGAGGG
TA

GAM94 332 LOC3393 1 2772 XP_294913.1 3 161 GGGAGAAAAGGA - --- 3 B c c
16 GGAGAACAGGAG TTGTTTTCT TTCTCCTCT TCT
ACGAGAAG AGCAGAGGA AAGAGGAGG AGA
C AAA

GAM94 332 LOC3393 1 17128 XP_290824.1 3 289 GGCCGTGAAGAA T CC 3 B c c

61 GATAGAAGAAAA TTGTTTTCTT CT TCTTCT
CAACACGC AACAAAAGAA GA AGAAGA
- T-

GAM94 332 LOC3398 1 6920 XP_295076.1 3 509 TACTTTAGAAGA T CT ---- 3 B c c
22 GGATAATGGATA TTG TTT TTC TCCTCTTCTA
AAATCAAT AAC AAA AGG AGGAGAAGAT
T AT TAAT

GAM94 332 LOC3398 1 5741 XP_295078.1 3 1394 GGAAGGAAGGAA G -- 3 B c c
27 GGAGAAAGGAAA TT TTTTCTTTCTCCT CTTCT
GGAAGGCA AG AAAGGAAAGAGGA GAAGG
G AG

GAM94 332 LOC3398 1 12966 XP_295087.1 5 416 CTCTTCAGTGGA --- -- T 3 B c c
56 GGAGAACAAGAA TTGTTT TCTT TCTCCTCT CT
ATAAACAA AACAAA AGAA AGAGGAGG GA
TAA CA T

GAM94 332 LOC3400 1 2275 XP_295149.1 5 2 GAGGAGGGGAGA G T 3 B c c
73 GGAGAGGAAAGT TT TTTTCTTTCTCCTCTTC
GGGAGGAG AG AGAGGAGAGGGGAGGAG
G -

GAM94 332 LOC3400 1 16277 XP_295154.1 5 291 AAGTGAGATTGA T C T- 3 B c c
90 AGAGAATGAAAA TTGTTTTC TTCTC TC TCT
CAAATTTG AACAAAAG AAGAG AG AGA
T A TT

GAM94 332 LOC3400 1 17500 XP_295160.1 3 782 TTTATAAGAAGA TTT C 3 B c c
95 GGAAGAGACATC TTG TCTTT TCCTCTTCT
AGTAATGC GAC AGAGA AGGAGAAGA
TAC -

GAM94 332 LOC3401 1 7442 XP_290379.1 3 13 TCGGCCGGAAGA C C 3 B c c
27 AGATAAAGAAAA TTGTTTTCTTT TC TCTTCT
CAACACGC AACAAAAGAAA AG AGAAGG
T A

GAM94 332 LOC3401 1 5971 XP_295183.1 3 915 GTTATAGCAGGA CTT - 3 B c c
84 GGAGAAAAACAA TTGTTTT TCTCCTCTT CTA
GCCATTTT AACAAAA AGAGGAGGA GAT
--- C

GAM94 332 LOC3404 3 4350 XP_290420.1 3 664 CTTGGAAGAGGA TG -- - 3 B c c
28 TGATAAAGAAAA T TTTTCTT TC TCCTCTTCTA
TGATAAGG A AAAAGAA AG AGGAGAAGGT
GT AT T

GAM94 332 LOC3404 3 15514 XP_290420.1 3 449 CTCAGGACTAGA -- -- 3 B c c
28 GGAGAAGGTCAG TTGTTTT CTTTCTCCTCT TCT
AGCAAAGC AACGAGA GGAAGAGGAGA AGG
CT TC

GAM94 332 LOC3404 3 18623 XP_290420.1 3 664 AGGCTTGGAAGA TG -- - 3 B c c
28 GGATGATAAAGA T TTTTCTT TC TCCTCTTCTA
AAATGATA A AAAAGAA AG AGGAGAAGGT
GT AT T

GAM94 332 LOC3404 1 2708 XP_290424.2 3 3258 GGAGAAGAGTGA TT----- - 3 B c c
49 GGAGAAAGGAAA GTTTTCTTTCTCCTC TTCT
CTCAAGTC CAAAGGAAAGAGGAG GAGA

CTGAACT T

GAM94 332 95 LOC3408 1 9851 XP_295865.1 3 419 TTCCTGGAAGCA G T - 3 B c c
GGAGAAAGATGA TT TT TCTTTCTCCT CTTCTA
GGACTTTG AG AG AGAAAGAGGA GAAGGT
G T C

GAM94 332 92 LOC3416 1 998 XP_292171.1 5 75 TTTCTTGCAGCA CT CC 3 B c c
GAAGAAAGAAGA TTGTTTT TTCT TCTTCT
GACAGGAG GACAGAG AAGA AGAAGA
-- A-

GAM94 332 25 LOC3421 4 5420 XP_292375.1 5 1128 ATTGGAAGAACA - -- --- 3 B c c
GGAGAAAAAGAA TTGTTTT CTT TCTCC TCTTCTA
AAGCAAAA AACGAAA GAA AGAGG AGAAGGT
A AA ACA

GAM94 332 25 LOC3421 4 8505 XP_292375.1 3 765 GAGTGAAGAAGA ---- T 3 B c c
GGAGGAGACGCC TTGTTT TCTT CTCCTCTTCT
AAGCAGAG GACGAA AGAG GAGGAGAAGA
CCGC -

GAM94 332 25 LOC3421 4 16605 XP_292375.1 5 593 CCTGGGAAATGA - C -- 3 B c c
GGATAAAGAAAA TTG TTTTCTTT TCCTC TTCT
TCGAGAGT AGC AAAAGAAA AGGAG AAGG
T T TA

GAM94 332 25 LOC3421 4 19109 XP_292375.1 5 1128 TGGAAGAACAGG - -- --- 3 B c c
AGAAAAAGAAAA TTGTTTT CTT TCTCC TCTTCTA
GCAAAAAC AACGAAA GAA AGAGG AGAAGGT
A AA ACA

GAM94 332 90 LOC3424 2 12046 XP_296905.2 5 393 GAGAGAAGAGGA G 3 B c c
GGAGAAGGGAGG TT TTTTCTTTCTCCTCTTCT
GGGTGGCC GG GGAGGGAAGAGGAGGAGA
G

GAM94 332 90 LOC3424 2 14647 XP_296905.2 5 393 CAAGAGAGAAGA G 3 B c c
GGAGGAGAAGGG TT TTTTCTTTCTCCTCTTCT
AGGGGGTG GG GGAGGGAAGAGGAGGAGA
G

GAM94 332 26 LOC3429 3 5714 XP_292790.2 5 135 CAGAGGAAGAGG G -- 3 B c c
AAAGAAAGAAGA TT TTTTCTTTC TCCTCTTCT
GGAGGGAA AG AGAAGAAAG AGGAGAAGG
G AA

GAM94 332 26 LOC3429 3 10371 XP_292790.2 5 135 AACTCAGAGGAA G -- 3 B c c
GAGGAAAGAAAG TT TTTTCTTTC TCCTCTTCT
AAGAGGAG AG AGAAGAAAG AGGAGAAGG
G AA

GAM94 332 26 LOC3429 3 17495 XP_292790.2 5 135 CTCAGAGGAAGA G -- 3 B c c
GGAAAGAAAGAA TT TTTTCTTTC TCCTCTTCT
GAGGAGGG AG AGAAGAAAG AGGAGAAGG
G AA

GAM94 332 00 LOC3431 1 7081 XP_295344.1 3 194 AGTTATGAGAAA TTT C 3 B c c
GGAGAAAGCTTG TTGT CTTTCTCCT TTCT
CAATGCAT AACG GAAAGAGGA AAGA
TTC -

GAM94 332 LOC3446 1 18489 XP_293499.2 5 815 GGAGGGTCAGAA T CCT 3 B c
c

00 GCAGAAAGAAAT TTG TTTCTTTCT CTTCT
CAAAGCTC AAC AAAGAAAGA GAAGA
T C--
GAM94 332 LOC3451 1 9265 XP_298539.1 5 402 ACGCAGATAGAA TCTCC 3 B c c
19 GATCCAAGAAAA TTGTTTTCTT TCTTCTA
CAATGGAG AACAAAAGAA AGAAGAT
CCT--
GAM94 332 LOC3462 2 658 XP_294161.2 3 230 ATGATAAGAAGA TT----- T - 3 B c c
84 TGGAGAAGAAAA GTTTTCTT CTCC TCTTCT
CCCGCAAA CAAAAGAA GAGG AGAAGA
AAACGCC - T
GAM94 332 LOC3462 2 10841 XP_294161.2 5 1441 TATCCGAGAAGA TG CT 3 B c
c
84 GGAGGGTAGAAA T TTTT TTCTCCTCTTCT
TGAAGGAA A AAAG GGGAGGAGAAGA
GT AT
GAM94 332 LOC3465 1 14088 XP_299537.1 3 3734 TGGGGAGAGGGA G - 3 B c c
39 GGAGAAAGAGGA TT TTTTCTTTCTCCTCT TCT
GGATCTCG AG AGGAGAAAGAGGAGG AGA
G G
GAM94 332 LOC3477 1 734 XP_290475.1 3 390 TGGGCAGGGGAA TG C- 3 B c c
74 AGAGAAAGAAGA T TTTTCTTTCTC TCTTCT
TGAGAGAT A AGAAGAAAGAG AGGGGA
GT AA
GAM94 332 LOC3479 1 7034 XP_302565.1 5 507 AACCAACCAAGA TT-- T 3 B c c
29 GGAGGAGAAAGA GTT TCTTTCTCCTCTTCT
TGACCCAG CAG AGAAAGAGGAGGAGA
GACC T
GAM94 332 LOC3480 2 4715 XP_302652.1 5 1811 GAAGAAGGAAGA G --- 3 B c c
72 GGAAAGGGAGGA TT TTTTCTTTC TCCTCTTCT
GGAGGATT AG AGGAGGAGG AGGAGAAGG
G GAA
GAM94 332 LOC3480 2 8955 XP_302652.1 5 456 AGAGGAAGAAGA T--- -- T 3 B c c
72 GGAGATGGCTGA TGTTTT CT TCTCCTCTTCT
AACATATA ACAAAG GG AGAGGAGAAGA
ATAT TC T
GAM94 332 LOC3480 1 11526 XP_300287.1 5 191 CAGGAGTGAACA TC ----- 3 B c c
73 GGAACAGGAAAA TTGTTTTCTT TCCT CTTCT
CAAATGGC AACAAAAGGA AGGA GAGGA
CA CAAGT
GAM94 332 LOC3481 1 1437 XP_300621.1 5 47 CAGGAGCTAACA - C ----- 3 B c c
08 GGAAAAAGAAAA TTG TTTTCTTT TCCT CTTCT
TCAATGGC AAC AAAAGAAA AGGA GAGGA
T A CAATC
GAM94 332 LOC3481 1 8147 XP_300623.1 5 36 ACGGGAGCAGGA ---- - 3 B c c
13 GGAGAAGATACG TTGTTTTC TTTCTCCTCTT CT
AGAGCAGG GACGAGAG GAAGAGGAGGA GA
CATA C
GAM94 332 LOC3481 1 8147 XP_300636.1 5 36 ACGGGAGCAGGA ---- - 3 B c c

42 GGAGAAGATACG TTGTTTTC TTTCTCCTCTT CT
AGAGCAGG GACGAGAG GAAGAGGAGGA GA
CATA C

GAM94 332 LOC3481 1 15004 XP_300646.1 3 486 AAAGAAAGAGAG G TC 3 B c c
58 GGAGAAAGAGAG TT TTTTCTTTCTCC TTCT
GGAGAAAG AG GAGAGAAAGAGG GAGA
G GA

GAM94 332 LOC3482 1 4919 XP_300304.1 3 304 GGAGGAGAGAGA - 3 B b b
09 GGAGAAGGGAGG TTGTTTTCTTTCTCCTCT TCT
CAAGGGAG AACGGAGGGAAGAGGAGA AGA
G

GAM94 332 LOC3484 1 15845 XP_302745.1 3 776 GGGATGAGGAGA T T 3 B c c
04 GGAGAACAGAGG TTGTTTTCTT CTCCTC TCT
GATGGTGA GACAAGAGGA GAGGAG AGG
- T

GAM94 332 LOC3484 1 5736 XP_301189.1 5 43 GATAGCAGGAAG T----- - - - 3 B c c
66 GCAGAAAGAAAA TGTTTTCTTTCT CCT CTT CTA
CATAAAGA ACAAAAGAAAGA GGA GGA GAT
AGAAAT C A C

GAM94 332 LOC3485 2 9852 XP_302833.1 3 74 ACCATGGAGCGG -- T T 3 B c c
83 AAAGAAAGAAAA TTGTTTTCTTTC TCC CTTC
CAGCATTC GACAAAAGAAAG AGG GAGG
AA C T

GAM94 332 LOC3485 2 13486 XP_302833.1 3 74 AATGACCATGGA -- T T 3 B c c
83 GCGGAAAGAAAG TTGTTTTCTTTC TCC CTTC
AAAACAGC GACAAAAGAAAG AGG GAGG
AA C T

GAM94 332 LOC3487 1 12887 XP_300843.1 3 1146 AAAGAAAGAAAG T- CC - 3 B c c
90 AAAGAAAGAAAG TGTTTTCTTTCT TCTT CT
AAAATATC ATAAAAGAAAGA AGAA GA
CT A- A

GAM94 332 LOC3488 2 7768 XP_302893.1 3 1730 TTCCTAAGAAGA G ---- C 3 B c b
08 GGAAAATAGCAG TT TTTTCT TT TCCTCTTCT
AAGAGAAG AA AGAAGA AA AGGAGAAGA
G CGAT A

GAM94 332 LOC3488 2 19110 XP_302893.1 3 97 TGGACTTAGGAA T C 3 B b b
08 GGAGAAAGAAAC TTGTTT CTTTCTCCT TTCTA
AAGATTAA AACAAA GAAAGAGGA AGGAT
- -

GAM94 332 LOC3488 2 1352 XP_302902.1 5 2375 TAGAAAGAAAGA TC TT - 3 B c c
35 GGAGGGACAAGC TTGTTT T CTCCTCTT CT
AAGCCCAT AACGAA A GAGGAGAA GA
C- GG A

GAM94 332 LOC3488 2 4351 XP_302902.1 5 842 TAGCTAGGAAGG TTCTC 3 B c c
35 GTTTGTAGAAAA TTGTTTTCT CTCTTCT
CAAGATAA AACAAAAGA GGGAAGG
TGTTT

GAM94 332 LOC3489 1 11023 XP_300883.1 3 975 GAGGTGGGAAGA TT C 3 B c c

38 GGATGAGGAGCA TTGT TCTTT TCCTCTTCT
AAGTTGGG AACG AGGAG AGGAGAAGG
-- T

GAM94 33205 LOC3490 1 14229 XP_302242.1 5 3 AGCGGGGAGGAG TT 3 B c c
GAGAAGGATGCA TTGT TCTTTCTCCTCTTCT
GCCGCCGA GACG AGGAAGAGGAGGAGG
T-

GAM94 33261 LOC3493 1 17756 XP_303035.1 5 515 AAAAGAAGAAAG ---- CC 3 B c c
ACACAAAGAAAA TTGTTTTCTT TCT TCTTCT
TAATCTAA AATAAAAGAA AGA AGAAGA
ACAC A-

GAM94 33257 LOC3494 1 1437 XP_291364.1 5 23 CAGGAGCTAACA - C ----- 3 B c c
GGAAAAAGAAAA TTG TTTTCTTT TCCT CTTCT
TCAATGGC AAC AAAAGAAA AGGA GAGGA
T A CAATC

GAM94 33262 LOC3497 1 12514 XP_303541.1 5 65 GAGGGGAAGCTG - -- 3 B c c
GGAGAAAGGAGG TTG TTTTCTTTCTCCT CTTCT
TCGAGGAG AGC GGAGGAAAGAGGG GAAGG
T TC

GAM94 33242 LOC3506 1 15794 XP_301093.1 5 57 GAAGGAGGGGGA G - 3 B c c
GGAGAAGAGAGA TT TTTTCTTT CTCCTCTTCT
AGAAACTG AA AAGAGAGA GAGGAGGGGG
G A

GAM94 33296 LOC3510 1 11443 XP_304287.1 5 46 GGAGATGAGCAC - --- T 3 B c c
GAAGAAAGAAGA TTGTTTTCTTTCT C CTC TCT
CAGTA GACAGAAGAAAGA G GAG AGA
A CAC T

GAM94 33223 LOC3515 1 13224 XP_304883.1 5 10 GAGTACGTTGAA G CC T 3 B c c
GAAGAAAGAAGA TT TTTTCTTTCT TCTTC
GAAAGGTA AA AGAAGAAAGA AGAAG
G -- T

GAM94 33222 LOC3519 1 4818 XP_305261.1 5 64 TATGATGGAAGA TCT 3 B c c
GGAGAGTTGGAT TTGTTT TTCTCCTCTTCTA
AGGCTGTG GATAGG GAGAGGAGAAGGT
TT-

GAM94 33256 LOC5118 1 11318 NP_057387.1 5 210 AAGAAGAATAAG G CC----- 3 B c c
CAAGAAAGAAAA TT TTTTCTTTCT TCTTCT
GAAGGAAG AA AAAAGAAAGA AGAAGA
G ACGAATA

GAM94 33260 LOC5132 1 18717 NP_057710.1 3 929 GGGAGGGAGGAG G TT - 3 B c c
GGAGAAAGGGAT TT TTTTCT CTCCTCT TCT
AATGATGC AG GAAAGA GAGGAGG AGG
G GG G

GAM94 33260 LOC5558 1 16096 NP_060041.1 3 4 TAGAACAGCTGG C C---- 3 B c c
GAAAAAGAAAAT TTGTTTTCTTT TCCT TTCTA
AATCCATT AATAAAAGAAA AGGG AAGAT
A TCGAC

GAM94 332 LOC5586 1 19025 NP_060949.1 5 133 ACGCGGAGAAGA TT- T 3 B c c

2 GGAGAGGACCTA TTGT TCTT CTCCTCTTCT
CAAGAACG AACA AGGA GAGGAGAAGA
TCC -
GAM94 332 LOC9046 1 9094 XP_031852.2 3 1525 ACTTAGAGAAGA TT ---- - 3 B c c
2 GGAAGAGAATAG GTTTTCTT TCT CCTCTTCT
GAAAACCA CAAAAGGA AGA GGAGAAGA
AC TAAG A
GAM94 332 LOC9067 1 15191 XP_033391.5 3 567 TCTTCTAGAAGA G - - 3 B c c
3 GAGAAGGAGGAA TT TTTTCTTTCT C CTCTTCTA
AAGAAGCA AA AAAAGGAGGA G GAGAAGAT
G A A
GAM94 332 LOC9090 2 16489 XP_034809.1 3 4533 ACAGGAGAAAAG TT CC 3 B c
c
6 GGAGAAAGCAAA TTGTTTTCT CT TCTTCT
AAGTTGAA AACGAAAGA GA AGAGGA
GG AA
GAM94 332 LOC9090 2 16963 XP_034809.1 3 4528 GTTTATAAGACA TT CC 3 B c c
6 GGAGAAAAGGGA TTGTTTTCT CT TCTTCT
GAAAGCAA AACGAAAGA GA AGAGGA
GG AA
GAM94 332 LOC9114 1 13502 XP_036480.1 3 720 TTGTCCTTAGAA T-- --- CT 3 B c c
9 GGAGAAAGACAG TGTTT TCTTTCTCCT TCTA
AGACACAT ACAGA AGAAAGAGGA AGAT
TAC GAC --
GAM94 332 LOC9126 1 19186 XP_037264.1 3 1344 GCTAATAGAGAA CT 3 B c c
3 GGAGAAAGGAAA TTGTTTTCTTTCTCCT TCTA
TAAAATAA AATAAAGGAAAGAGGA AGAT
AG
GAM94 332 LOC9156 2 5752 XP_039231.1 3 1001 CCTGTCTCAAAG G CC - 3 B c c
5 AAAGAAAGAAAG TT TTTTCTTTCT TCTT CT
AAAAGAAA AA AAAAGAAAGA AGAA GA
G A- A
GAM94 332 LOC9156 2 8304 XP_039231.1 3 1002 TCTCAAAGAAAG G CC - 3 B c c
5 AAAGAAAGAAAA TT TTTTCTTTCT TCTT CT
GAAAGAAA AA AAAAGAAAGA AGAA GA
G A- A
GAM94 332 LOC9166 2 16542 NP_612381.1 5 52 AAACCTGGAAGA TC 3 B c c
1 GGAAGAGGAAAG TTGTTTTCTT TCCTCTTCTA
CAAAGGAG AACGAAAGGA AGGAGAAGGT
GA
GAM94 332 LOC9166 2 18909 NP_612381.1 5 54 GGAAGAGGAAGA TC 3 B c c
1 GGAAAGCAAAGG TTGTTTTCTT TCCTCTTCT
AGTCAGGG AACGAAAGGA AGGAGAAGG
GA
GAM94 332 LOC9187 1 15925 NP_612385.1 3 49 GAGTGGAGGAGA ---- - 3 B c c
5 GGAGACAAGGCT TTGTTT TCTT TCTCCTCTTCT
CTGGACAG GACAGG GGAA AGAGGAGAGGA
TCTC C
GAM94 332 LOC9201 1 3847 XP_042234.2 3 1310 AGCAGAACCTGA CTT --- 3 B c c
7 GGAGAAAAGCAG TTGTTTT TCTCCTC TTCT

GTGGAAGG GACGAAA AGAGGAG AAGA
--- TCC
GAM94 332 LOC9217 1 12672 NP_612393.1 3 1599 TGTCCTAGAAGA G CT 3 B c c
0 GGGAAGAGGAAG TT TTTTCTTT CCTCTTCTA
GAAGGTGG AA GAAGGAGA GGAGAAGAT
G AG
GAM94 332 LOC9231 4 1665 XP_044166.4 3 1794 GACCAACACAGA TT TCT 3 B c
c
2 GGAGAGAAAACA TTGTTTTC TCTCCTCT
AAAATAGC AACAAAAG AGAGGAGA
-- CAC
GAM94 332 LOC9231 4 8613 XP_044166.4 3 1750 ACAAAATAGAGG T----- C 3 B c c
2 AGAGAAAGAGAG TGTTTTCTTTCTC TCTTCTA
CATGAGAG ACGAGAGAAAGAG AGGAGAT
GAGAGT -
GAM94 332 LOC9231 4 10275 XP_044166.4 3 1750 AGACAAAATAGA T--- C 3 B c c
2 GGAGAGAAAGAG TGTTTTCTTTCTC TCTTCTA
AGCATGAG ACGAGAGAAAGAG AGGAGAT
GAGT -
GAM94 332 LOC9231 4 13054 XP_044166.4 3 1794 GCGACCAACACA TT TCT 3 B c
c
2 GAGGAGAGAAAA TTGTTTTC TCTCCTCT
CAAAAATA AACAAAAG AGAGGAGA
-- CAC
GAM94 332 LTB4R 1 9294 NP_000743.1 3 150 AGTGGAAGAAGA -- T 3 B c c
GGGAGAGATGGA TTGTTT TCTTTC CCTCTTCT
GCAAAGTG AACGAG AGAGAG GGAGAAGA
GT -
GAM94 332 MAEA 1 4163 NP_005873.1 3 21 ACTCTTAGAAGA TTCTC 3 B c c
GAGAAAATAAGG TTGTTTTCT CTCTTCTA
TTTCATAA AATAAAAGA GAGAAGAT

GAM94 332 MAGEA8 1 7752 NP_005355.2 3 2 CTTTGGGAGAGG ---- 3 B c c
AGAAAGGAGTTT TTGT TTTCTTTCTCCTCTTCTA
GGCAGGAG GACG GAGGAAAGAGGAGAGGGT
GTTT
GAM94 332 MAP1B 2 1647 NP_005900.1 3 505 GTGGGGTAAGGA T CT 3 B c c
GGAGAAAATAAA TTGTTTTCTT CTCCT TCT
CCAACAAT AATAAAAGAG GAGGA GGG
- AT
GAM94 332 MAP1B 2 1647 NP_114399.1 3 505 GTGGGGTAAGGA T CT 3 B c c
GGAGAAAATAAA TTGTTTTCTT CTCCT TCT
CCAACAAT AATAAAAGAG GAGGA GGG
- AT
GAM94 332 MAP1B 2 6508 NP_005900.1 3 409 AGAGAGAAAGAA G C- - 3 B c c
TGAGAAAGAAAA TT TTTTCTTTCTC TCTT CT
GGAATGCA AG AAAAGAAAGAG AGAA GA
G TA A
GAM94 332 MAP1B 2 6508 NP_114399.1 3 409 AGAGAGAAAGAA G C- - 3 B c c
TGAGAAAGAAAA TT TTTTCTTTCTC TCTT CT

GGAATGCA AG AAAAGAAAGAG AGAA GA
G TA A
GAM94 332 MAP3K2 1 2581 NP_006600.2 3 386 GTGACGATGGGA TTCTCC 3 B c c
AGACATGGAAAA TTGTTTTCT TCTTCT
CAAGGAGA AACAAAAGG AGAAGG
TAC---
GAM94 332 MEF2C 1 16421 NP_002388.2 5 328 AGGAAACAGGAA G CTC 3 B c c
AGAGAAAGAAAA TT TTTTCTTTCTC TTCT
GGAAGGAA AG AAAAGAAAGAG AAGG
G A--
GAM94 332 MEGF10 1 15932 NP_115822.1 3 2634 TTAGAATGAGAA CTC--- - 3 B c c
TTAAAGAGAAAA TTGTTTTCTTT CTC TTCTA
CAAAAGAA AACAAAAGAGA GAG AAGAT
AATTAA T
GAM94 332 MEIS2 2 2527 NP_002390.1 5 289 TCGGCGGGCAGA -- T 3 B c c
GGAGAGGGAGGC TTGT TTTCTTTCTCCTCT CT
CGCGGAAT GGCG GGAGGGAGAGGAGA GG
CC C
GAM94 332 MEIS2 2 19135 NP_064534.1 5 709 GAGGGGAAGAGA G -- 3 B c c
AGAGAAAGAGGG TT TTTTCTTTCTC CTCTTCT
GGAAAGGA AG GGGAGAAAGAG GAGAAGG
G AA
GAM94 332 MEIS2 2 19135 NP_733774.1 5 709 GAGGGGAAGAGA G -- 3 B c c
AGAGAAAGAGGG TT TTTTCTTTCTC CTCTTCT
GGAAAGGA AG GGGAGAAAGAG GAGAAGG
G AA
GAM94 332 MEIS2 2 19135 NP_733775.1 5 709 GAGGGGAAGAGA G -- 3 B c c
AGAGAAAGAGGG TT TTTTCTTTCTC CTCTTCT
GGAAAGGA AG GGGAGAAAGAG GAGAAGG
G AA
GAM94 332 MEIS2 2 19135 NP_733776.1 5 709 GAGGGGAAGAGA G -- 3 B c c
AGAGAAAGAGGG TT TTTTCTTTCTC CTCTTCT
GGAAAGGA AG GGGAGAAAGAG GAGAAGG
G AA
GAM94 332 MEIS2 2 19135 NP_733777.1 5 709 GAGGGGAAGAGA G -- 3 B c c
AGAGAAAGAGGG TT TTTTCTTTCTC CTCTTCT
GGAAAGGA AG GGGAGAAAGAG GAGAAGG
G AA
GAM94 332 MGC1292 1 13510 NP_116117.1 5 98 CTGGGTGGCAGA TCTT T 3 B c c
1 GGAGATAAACAG TTGTTT TCTCCTCT CTA
CCATGTGC GACAAA AGAGGAGA GGT
T--- C
GAM94 332 MGC1413 1 1773 NP_116299.1 3 305 TGCAGGGTGGGA -- T - 3 B c c
6 GGAGAAGACCAA TTGTTT TCTT CTCCTCTT CT
ACGAAGTA AGCAAA AGAA GAGGAGGG GG
CC - T

GAM94 332 MGC1547 1 524 NP_659493.1 3 674 GGAGGTAGAAGA TG 3 B c c
6 GGGGAAGGAAGA T TTTTCTTTCTCCTCTTCTA
TGGTTTCT G AGAAGGAAGGGGAGAAGAT
GT
GAM94 332 MGC1563 1 17793 NP_116142.1 5 71 AGTCACAGAGAG - CT 3 B c c
1 GGGAAGAGAAAA TTGTTTTCTTT CTCCTCTT
CAGGGACG GACAAAAGAGA GGGGAGAG
A AC
GAM94 332 MGC1604 1 10140 NP_612380.1 5 46 TTACTGAGAAAG - T C 3 B c c
4 GTGAAATGAAAA TTGTTTTC TTTC CCT TTCT
CAAGCTCA AACAAAAG AAAG GGA AAGA
T T -
GAM94 332 MGC1606 1 17265 NP_444275.1 5 394 CATGGAAGAAGA TTT 3 B c c
3 GGGGGAGAGAGT TTGT CTTTCTCCTCTTCT
TACAGGTT GACA GAGAGAGGGGGAGA
TT-
GAM94 332 MGC2398 1 4692 NP_659442.2 3 84 TGACAAGATTTG - TCT 3 B c c
0 GAAGAAAGAAAA TTGTTTTCTTTCT CC TCT
TAACAGAC AATAAAAGAAAGA GG AGA
A TTT
GAM94 332 MGC2499 1 18721 NP_714914.1 3 1 GGAGGAGGAAGA C 3 B c c
5 GGAAACAAGATA TTGTTTTCTTT TCCTCTTCT
TGACAAGG AACAAAGGAGA AGGAGGAGG
-
GAM94 332 MGC2705 1 4995 NP_116090.2 5 40 TGAGGAGGAGGA - T 3 B c c
GGAGAAGCGGAT TTGTT TTCTTTCTCCTCTTC
GAGATCGT GGCGA GAGGAGGAGGAGGAG
A T
GAM94 332 MGC2738 1 10511 XP_294972.1 3 230 CTCAATAGAAGA T-------- TTT 3 B c
c
2 GGAGGAAAACAT TGTTTTC CTCCTCTTCTA
GTTTTTAA ACAAAAG GAGGAGAAGAT
AATTTTTGT ---
GAM94 332 MGC3210 2 3355 NP_653285.1 3 2939 AGGTTGGGAAGA -- C 3 B c c
4 GGATGAAGATTG TTGTTT TCTTT TCCTCTTCT
AATAACTG AATAAG AGAAG AGGAGAAGG
TT T
GAM94 332 MGC3210 2 6076 NP_653285.1 5 68 AGAGAAGGAAGA TC CT 3 B c c
4 GGAAAGCAAAGG TTGTTTTCTT TCCT TCT
AGTCAGGG AACGAAAGGA AGGA AGA
GA AG
GAM94 332 MGC3262 1 8239 NP_076934.1 3 412 CAGGGGAGCAGA G C 3 B c c
AGGAGAAGAAAA TT TTTTCTTTCT CTCTTCT
CTGCCTGT AA AAGAGGAAGA GAGGGGA
G C
GAM94 332 MGC3397 1 16821 NP_699181.1 3 1621 AAAAATTAAGGG - CT 3 B c c
4 GAGAGAGGAAAA TTGTTTTC TTTCTCCTCTT
CAAAACCA AACAAAAG AGAGAGGGGAA
G TT
GAM94 332 MGC3951 1 4349 NP_776183.1 5 165 AGAGGAGTAGAA G - C 3 B c c

8 GGTAAAAGAAAA TT TTTT CTTTCT CTCTTCT
TGCTGGGA AA AAAA GGAAGA GAGGAGA
G T T

GAM94 332 MGC4010 1 20005 NP_689979.1 3 83 GGAGTAAGAAGA - C---- 3 B c c
7 GGATTAAAAAGG TTGT TTTCTTT TCCTCTTCT
AAAGGCAA AACG AAAGGAA AGGAGAAGA
G AAATT

GAM94 332 MGC4016 1 10970 NP_714920.1 3 163 ATTTTGGAGAAG G T 3 B c c
8 GGAGAAAGAAGG TT TTTTCTTTCTCC CTTCT
GAGAGGCA GA GGAAGAAAGAGG GAAGA
G -

GAM94 332 MGC4607 1 10730 NP_113631.1 5 90 CGATATGGAAGA T - -- 3 B c c
GGAGGGCAAGAA TGTT TTCTT TCTCCTCTTCTA
GGGCA ACGG AAGAA GGAGGAGAAGGT
- G CG

GAM94 332 MN1 1 15003 NP_002421.2 3 1210 GGGCTAGAGGAC C- 3 B c c
AGAGAAAGAGAA TTGTTTTCTTTCTC TCTTCTA
TAGAATGA GATAAGAGAAAGAG AGGAGAT
AC

GAM94 332 MOST2 1 677 NP_064635.1 5 2366 AAAAAGAGAAGA TC C-- 3 B c c
GGAAATAAACCA TTGTTT TTT TCCTCTTCT
GACAGTGC GACAGA AAA AGGAGAAGA
CC TAA

GAM94 332 MOT8 1 16345 NP_061324.1 3 303 ACAGAAAGAAGA G CC 3 B c c
AAGGAAAGAAAG TT TTTTCTTTCT TCTTCT
GAACCAGA AA GAAAGAAAGG AGAAGA
G AA

GAM94 332 MSF 1 18395 NP_006631.1 5 140 AGTGTTTTTAGA G - 3 B c c
GGAGAGAGGAGG TT TTTTCTTTCTC CTCTTCTA
AGGAGGAG AG AGGAGGAGGAG GAGGAGAT
G A

GAM94 332 MTMR9 1 15033 NP_056273.2 3 3542 ACTTCTAGATAG T TCC - 3 B c c
AATGAATGAAAA TTGTTTTC TTC TCT TCTA
CAACACAA AACAAAAG AAG AGA AGAT
T TA- T

GAM94 332 MUC17 1 678 XP_168583.2 3 434 CTCAGTTGAAGA TC T 3 B c c
GGACGAGAGGAC TTGTTTTCTT TCCTCTTC
GACCTTCT AGCAGGAGAG AGGAGAAG
C- T

GAM94 332 MXI1 1 1149 NP_005953.2 3 1628 AGGGCTGGGCAA C CT 3 B c c
GGAAAAAGAAAA TTGTTTTCTTT TCCT TCTA
TAAAGACA AATAAAAGAAA AGGA GGGT
A AC

GAM94 332 MXI1 1 1149 NP_569157.1 3 1623 AGGGCTGGGCAA C CT 3 B c c
GGAAAAAGAAAA TTGTTTTCTTT TCCT TCTA
TAAAGACA AATAAAAGAAA AGGA GGGT
A AC

GAM94 332 MYH10 1 4996 XP_290747.1 5 319 AGTTGGCAGAGA C-- T 3 B c c
ATGGAAAGAAAG TTGTTTTCTTTCT CTCT CTA
CAATGGTC AACGAAAGAAAGG GAGA GGT

TAA C

GAM94 332 MYLK 1 786 NP_005956.2 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444253.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444254.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444255.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444256.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444257.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444258.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444259.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYLK 1 786 NP_444260.1 3 1 GGAAGGGGAAGA -- TC 3 B c c
GGAAGAAGAGTG TTGTTT TCTT TCCTCTTCT
AACAAAGC AACAAG AGAA AGGAGAAGG
TG GA

GAM94 332 MYOZ2 1 7967 NP_057683.1 3 786 ATTCTTAGAAGA TCT C- 3 B c c
GTAAGAACAAAT TTGTTT TTCT CTCTTCTA
AAAGTACA AATAAA AAGA GAGAAGAT
C-- AT

GAM94 332 NEFH 1 15071 NP_066554.1 3 21 GGAAGTAGGCAG G TT - - 3 B c c
GGAGAAAGGAAC TT TTTTCT CT CCT CTTCT
ATCCGGAA AA GAAAGA GA GGA GAAGG
G GG C T

GAM94 332 NEU3 1 18396 NP_006647.2 3 899 GGGGCTAGAAGA TT ------ - 3 B c c
GCGAGAAAATTC GTTTTCTT TCTC CTCTTCTA
AAGAAAAT TAAAAGAA AGAG GAGAAGAT
-- CTTAAA C

GAM94 332 NFE2 1 6329 NP_006154.1 3 129 TAGACCAGAAGA T TT-- - 3 B c c

GGATGACAATGG TTGTT TC TC TCCTCTTCT
CAACAAGT AACAA GG AG AGGAGAAGA
C TAAC T

GAM94 332 NFIB 1 9068 NP_005587.1 3 236 AGGAAAGAAACT - CTC 3 B c c
GAAGAAAGAAGA TTGTTTTCTTTCT C TTCT
TAATAGAC AATAGAAGAAAGA G AAGA
A TCA

GAM94 332 NOL3 1 13717 NP_003937.1 3 519 GAGACTAGAAGA G - 3 B c c
GGGGAGCAGAAA TT TTTTCT TTCTCCTCTTCTA
GGGACCTT AG GAAAGA GAGGGGAGAAGAT
G C

GAM94 332 NR1H2 1 14187 NP_009052.1 5 58 AGGGGCTAAAGA - C 3 B c c
GGAGGACGAAGA TTGTTTT CTTT TCCTCTTCT
AAAGCAGA GACGAAA GAAG AGGAGGAGA
A C

GAM94 332 NR4A3 1 15634 NP_775290.1 5 892 GGGGATGAGGTG TT T T 3 B c c
GGAGAAAGCAAC TTGTTTTCT C CCTC TCT
CACAACGT AACGAAAGA G GGAG AGG
GG T T

GAM94 332 NTN4 1 4071 NP_067052.1 5 22 GCAGCCAGAAGA C TT T 3 B c c
GGTGGGAAAAGC TTGTTTT T C CCTCTTCT
GGAGGAGG GGCGAAA A G GGAGAAGA
- GG T

GAM94 332 NUP54 1 16346 NP_059122.2 3 104 GACCACATGGAG C T T 3 B c c
GGAAAAAGAAAA TTGTTTTCTTT TCC CTTC
CAATTCTT AACAAAAGAAA AGG GAGG
A - T

GAM94 332 NX17 1 14516 NP_065716.1 5 12 GAGGTAGAGTCA - --- - 3 B c c
GAGTAGGGAAAA TTGTTTTCTTT CTC CTCT TCT
CAACTAAT AACAAAAGGGA GAG GAGA GGA
T ACT T

GAM94 332 NYX 1 8632 NP_072089.1 5 303 AAGGAATGTGAG - - --- 3 B c c
GAAGAAAGAAAG TTGT TTTCTTTCT CCTC TTCT
GCAGGGCA GACG AAAGAAAGA GGAG AAGG
G A TGT

GAM94 332 OSBPL11 1 7034 NP_073613.2 3 472 AACCAACCAAGA TT-- T 3 B c c
GGAGGAGAAAGA GTT TCTTTCTCCTCTTCT
TGACCCAG CAG AGAAAGAGGAGGAGA
GACC T

GAM94 332 OSBPL3 1 6630 NP_056365.1 3 2329 TTTATAGTTTTA TTC CT 3 B c c
AGAGGAAGAAAA TTGTTTTCT TCCTCTT
CAGAAACG GACAAAAGA AGGAGAA
--- TT

GAM94 332 OSBPL3 1 6630 NP_663160.1 3 2329 TTTATAGTTTTA TTC CT 3 B c c
AGAGGAAGAAAA TTGTTTTCT TCCTCTT
CAGAAACG GACAAAAGA AGGAGAA
--- TT

GAM94 332 OSBPL3 1 6630 NP_663161.1 3 2329 TTTATAGTTTTA TTC CT 3 B c c
AGAGGAAGAAAA TTGTTTTCT TCCTCTT
CAGAAACG GACAAAAGA AGGAGAA

--- TT
GAM94 332 OSBPL3 1 6630 NP_663162.1 3 2329 TTTATAGTTTTA TTC CT 3 B c c
AGAGGAAGAAAA TTGTTTTCT TCCTCTT
CAGAAACG GACAAAAGA AGGAGAA
--- TT
GAM94 332 OSBPL3 1 6630 NP_663163.1 3 3463 TTTATAGTTTTA TTC CT 3 B c c
AGAGGAAGAAAA TTGTTTTCT TCCTCTT
CAGAAACG GACAAAAGA AGGAGAA
--- TT
GAM94 332 OSBPL3 1 6630 NP_663164.1 3 3463 TTTATAGTTTTA TTC CT 3 B c c
AGAGGAAGAAAA TTGTTTTCT TCCTCTT
CAGAAACG GACAAAAGA AGGAGAA
--- TT
GAM94 332 OTX1 1 2466 NP_055377.1 3 33 AGGAATGAAAGA - T CT 3 B c c
GGAGAAGAAACG TTGT TTTCTT CTCCTCTT
CAACTACC AACG AAAGAA GAGGAGAA
C - AG
GAM94 332 PAK7 3 2124 NP_065074.1 3 1023 CACAAAGGGAGA C- 3 B c c
GGAGAGAACAGG TTGTTTT TTTCTCCTCTTCT
GCAAGACG AACGGGA AGAGAGGAGAGGG
CA
GAM94 332 PAK7 3 2124 NP_817127.1 3 1023 CACAAAGGGAGA C- 3 B c c
GGAGAGAACAGG TTGTTTT TTTCTCCTCTTCT
GCAAGACG AACGGGA AGAGAGGAGAGGG
CA
GAM94 332 PAK7 3 12660 NP_065074.1 3 1837 GACTATGTAGAA G CCT 3 B c c
GTAGAAAGAAAA TT TTTTCTTTCT CTTCTA
GAAAAAGA AA AAAAGAAAGA GAAGAT
G T--
GAM94 332 PAK7 3 12660 NP_817127.1 3 1837 GACTATGTAGAA G CCT 3 B c c
GTAGAAAGAAAA TT TTTTCTTTCT CTTCTA
GAAAAAGA AA AAAAGAAAGA GAAGAT
G T--
GAM94 332 PAK7 3 15289 NP_065074.1 3 1838 TGTAGAAGTAGA G CCT 3 B c c
AAGAAAAGAAAA TT TTTTCTTTCT CTTCTA
AGAAAATC AA AAAAGAAAGA GAAGAT
G T--
GAM94 332 PAK7 3 15289 NP_817127.1 3 1838 TGTAGAAGTAGA G CCT 3 B c c
AAGAAAAGAAAA TT TTTTCTTTCT CTTCTA
AGAAAATC AA AAAAGAAAGA GAAGAT
G T--
GAM94 332 PAPOLB 1 2613 NP_064529.2 3 81 CAAAACGGAAGA TTTC-- 3 B c c
GGAGAAACTCAA TTGT TTTCTCCTCTTCT
TACAAAGA AACA AAAGAGGAGAAGG
TAACTC
GAM94 332 PAX2 1 17177 NP_000269.1 3 507 GGGCCAAGGAGA CTCC 3 B c c
TTAAGAAGAAAA TTGTTTTCTTT TCTTCT
CGACTTTC AGCAAAAGAAG AGAGGA
AATT
GAM94 332 PAX2 1 17177 NP_003978.1 3 507 GGGCCAAGGAGA CTCC 3 B c c

TTAAGAAGAAAA TTGTTTTCTTT TCTTCT
CGACTTTC AGCAAAAGAAG AGAGGA
AATT

GAM94 332 PAX2 1 17177 NP_003979.1 3 507 GGGCCAAGGAGA CTCC 3 B c c
TTAAGAAGAAAA TTGTTTTCTTT TCTTCT
CGACTTTC AGCAAAAGAAG AGAGGA
AATT

GAM94 332 PAX2 1 17177 NP_003980.1 3 443 GGGCCAAGGAGA CTCC 3 B c c
TTAAGAAGAAAA TTGTTTTCTTT TCTTCT
CGACTTTC AGCAAAAGAAG AGAGGA
AATT

GAM94 332 PAX2 1 17177 NP_003981.1 3 443 GGGCCAAGGAGA CTCC 3 B c c
TTAAGAAGAAAA TTGTTTTCTTT TCTTCT
CGACTTTC AGCAAAAGAAG AGAGGA
AATT

GAM94 332 PAX7 1 17455 NP_002575.1 5 48 GCGTGGAGAAGA -- TT - 3 B c c
GGGAGGGAGCGA TTGTTTTC T CTCC TCTTCT
GAGCGAGA AGCGAGAG A GAGG AGAAGA
CG GG G

GAM94 332 PAX7 1 17455 NP_039236.1 5 48 GCGTGGAGAAGA -- TT - 3 B c c
GGGAGGGAGCGA TTGTTTTC T CTCC TCTTCT
GAGCGAGA AGCGAGAG A GAGG AGAAGA
CG GG G

GAM94 332 PCDH10 1 11480 NP_065866.1 5 63 AGGGAAAGAGGC --- - 3 B c c
TTGGGAAGAAAA TTGTTTTCTTTCT CCTCTT CT
CAGCAGAA GACAAAAGAAGGG GGAGAA GG
TTC A

GAM94 332 PCDH10 1 11480 NP_116586.1 5 63 AGGGAAAGAGGC --- - 3 B c c
TTGGGAAGAAAA TTGTTTTCTTTCT CCTCTT CT
CAGCAGAA GACAAAAGAAGGG GGAGAA GG
TTC A

GAM94 332 PCF11 1 6695 NP_056969.1 5 211 GGGAGAGGAAGA ---- 3 B c c
GGAGTCGGAAGG TTGTTTTCTTTC TCCTCTTCT
GAGGCGGG GGCGGAGGGAAG AGGAGAAGG
GCTG

GAM94 332 PDE4B 1 7674 NP_002591.1 3 537 TCTTTCTGGAAA T C 3 B c c
AGGGAAAGAAAA TTGTTTTCTTTC CCT TTCTA
TAGTCTTC GATAAAAGAAAG GGA AAGGT
- A

GAM94 332 PDE4C 1 14459 NP_000914.1 3 604 GGGGCAGGAAGA G TT 3 B c c
GGAGCAGAAAAG TT TTTTCT CTCCTCTTCT
AAGGGCTG AA AAAAGA GAGGAGAAGG
G C-

GAM94 332 PDZGEF1 1 15137 NP_055062.1 3 484 ACCCACCAAGGA - CTCC 3 B c
c
AGACAAAGAAAA TTGTTTT CTTT TCTTCT
ACAATGAA AACAAAA GAAA AGAAGG
A C---

GAM94 332 PDZK3 2 4585 NP_055837.2 3 1444 TCATAAAGAGGA TG C 3 B c c
GGAGAAACAGGG T TTTT TTTCTCCTCTTCT

TGAGTCAA A GGGA AAAGAGGAGGAGA
GT C
GAM94 332 PDZK3 2 4585 NP_835260.1 3 1444 TCATAAAGAGGA TG C 3 B c c
GGAGAAACAGGG T TTTT TTTCTCCTCTTCT
TGAGTCAA A GGGA AAAGAGGAGGAGA
GT C
GAM94 332 PDZK3 2 13677 NP_055837.2 3 1444 GGGTCATAAAGA TG C 3 B c c
GGAGGAGAAACA T TTTT TTTCTCCTCTTCT
GGGTGAGT A GGGA AAAGAGGAGGAGA
GT C
GAM94 332 PDZK3 2 13677 NP_835260.1 3 1444 GGGTCATAAAGA TG C 3 B c c
GGAGGAGAAACA T TTTT TTTCTCCTCTTCT
GGGTGAGT A GGGA AAAGAGGAGGAGA
GT C
GAM94 332 PFDN1 2 6722 NP_002613.2 3 553 TAGACAGAAGAG TT - 3 B c c
GAAGAAAGAACA TTGT TCTTTCT CCTCTTCT
GATGTTCA GACA AGAAAGA GGAGAAGA
-- A
GAM94 332 PFDN1 2 13206 NP_002613.2 3 553 GTAGACAGAAGA TT - 3 B c c
GGAAGAAAGAAC TTGT TCTTTCT CCTCTTCT
AGATGTTC GACA AGAAAGA GGAGAAGA
-- A
GAM94 332 PHEMX 1 12316 NP_620591.1 5 113 GAGGGGAGGAGA G - 3 B c c
GGAGAGGAGAGG TT TTTTCTT TCTCCTCTTCT
AACCGTCA GA AGGAGAG AGAGGAGGGGA
G G
GAM94 332 PHEMX 1 12316 NP_620592.1 5 113 GAGGGGAGGAGA G - 3 B c c
GGAGAGGAGAGG TT TTTTCTT TCTCCTCTTCT
AACCGTCA GA AGGAGAG AGAGGAGGGGA
G G
GAM94 332 PHT2 1 13637 NP_057666.1 5 184 GAGGCGGGGAGA G - 3 B c c
GGAGAGGAGAGA TT TTTTCTT TCTCCTCTTCT
AGAGCCGC GA AAGAGAG AGAGGAGAGGG
G G
GAM94 332 PIP5K1B 1 9155 NP_003549.1 5 316 TTCTAGGAGAGA ---- T - 3 B c c
GGTGAAAGAAAC TTGT TTTCTTTC CCTCT TCT
CTGGCAAA AACG AAAGAAAG GGAGA AGG
GTCC T G
GAM94 332 PISD 2 3283 NP_055153.1 5 370 GGGGAAGGGGAG ---- 3 B c c
GAAAGAGGAAAA TTGTTTTCT TTCTCCTCTTCT
CAAAGGGA AACAAAAGG AGGAGGGGAAGG
AGAA
GAM94 332 PISD 2 19454 NP_055153.1 5 160 TGTTTTAGAAGA TT - - 3 B c c
GGCAGAACAGTG TTGTT CT TTCT CCTCTTCTA
ATAAAGAC AATAG GA AAGA GGAGAAGAT
T- C C
GAM94 332 PITX2 1 3506 NP_700475.1 5 321 GAGGGAGGGAGA T 3 B c c
GGAGAGAGAGTG TTGT TTCTTTCTCCTCTTCT
CGAGACCG AGCG GAGAGAGAGGAGAGGG
T

GAM94 332 PITX2 1 3506 NP_700476.1 5 321 GAGGGAGGGAGA T 3 B c c
GGAGAGAGAGTG TTGT TTCTTTCTCCTCTTCT
CGAGACCG AGCG GAGAGAGAGGAGAGGG
T
GAM94 332 PKNOX2 1 2901 NP_071345.1 3 383 TGAGATGGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCTA
GGAGCTGG AG AGGAGGAGGAGGAGAAGGT
G
GAM94 332 PLAC3 1 12261 NP_064714.1 5 904 AGTACAGCAAGA -- - 3 B c c
GGAGAGAGGTCA TTGTTT TCTTTCTCCTCTT CT
AGCGAGAA AGCGAA GGAGAGAGGAGAA GA
CT C
GAM94 332 PLAC3 1 12261 NP_068755.1 5 904 AGTACAGCAAGA -- - 3 B c c
GGAGAGAGGTCA TTGTTT TCTTTCTCCTCTT CT
AGCGAGAA AGCGAA GGAGAGAGGAGAA GA
CT C
GAM94 332 PLCD3 1 3472 NP_588614.1 3 233 TTTCATAGAAGA CTC- 3 B c c
GCCCTGGAGAAG TTGTTTTCTTT CTCTTCTA
ACAGTAGA GACAGAAGAGG GAGAAGAT
TCCC
GAM94 332 PLCD4 1 18501 NP_116115.1 5 19 TGCTGTAGAAGA TT 3 B b b
GGGGAGGAAACA TTGTTTTC TCTCCTCTTCTA
AGCCAGTG AACAAAGG AGGGGAGAAGAT
--
GAM94 332 PLCL2 1 2076 NP_055999.1 5 218 CAAAACAGAAGA C --- 3 B c c
GGGAACGGAAAA TTGTTTT TTTC TCCTCTTCT
AGACAGTC GACAGAA AAGG GGGAGAAGA
A CAA
GAM94 332 PLXNA2 1 18949 NP_079455.1 3 616 AAAAGAGAAAGA TG CT - 3 B c c
GGAGAAGAAGAA T TTTT TTCTCCTCTT CT
TGATGAGC A AAGA AAGAGGAGAA GA
GT AG A
GAM94 332 PLXNB2 1 8876 NP_036533.1 3 462 GAGATGGGAGGA CT 3 B c c
GGAGAAAAAGCG TTGTTTT TTCTCCTCTTCT
GTACGATG GGCGAAA AAGAGGAGGAGG
--
GAM94 332 PMS2L5 1 9051 NP_777590.1 5 170 TGCGGTGAAGAA TTCT - 3 B c c
GATGGTAGAAAA TTGTTTTCT CC TCTTCT
CAGTCTGG GACAAAAGA GG AGAAGA
T--- T
GAM94 332 PNMA5 3 4787 NP_443158.1 3 696 GGAAGAGGGGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
AGAGGGGG AG AAGAGGAGGGGGAGAAGG
G
GAM94 332 PNMA5 3 10336 NP_443158.1 3 626 AGAGAAAGAGGA G --- 3 B c c
GGAGAATTAAGA TT TTTTCTT TCTCCTCTTCT
AGAGGATG AG AGAAGAA AGAGGAGGAGA
G TTA
GAM94 332 PNMA5 3 12546 NP_443158.1 3 658 GGAGGAGGAAGA TC 3 B c c
GGAGAATAAGGA TTGTTTTCTT TCCTCTTCT

GGAGCAGG AATAAGAGGA AGGAGGAGG
GA

GAM94 332 POLK 1 7290 NP_057302.1 5 39 AGCAGGAGGAGC G T 3 B c c
GGAGAAAGGAGA TT TTTTCTTTCTCC CTTCT
GGGCGGGG GG AGAGGAAAGAGG GAGGA
G C

GAM94 332 POU3F2 1 19974 NP_005595.1 5 51 GTGGGAGAGAGA -- T - 3 B c c
GGAGACAGAAAG TTGTTT TCT TCTCCTCT TCT
AGCGAGCG AGCGAG AGA AGAGGAGA AGA
AA C G

GAM94 332 PPFIBP2 1 10296 XP_084578.4 5 337 CCAGTAAGAAGA T- 3 B c c
GGAGGAGGCCAG TTGTTT CTTTCTCCTCTTCT
GCAGGCAA GACGGA GGAGGAGGAGAAGA
CC

GAM94 332 PPM1F 1 10074 NP_055449.1 3 1774 AGGGGGAGGAGA G TT 3 B c c

GGAGAAAGGGAG TT TT CTTTCTCCTCTTCT
GAAGCTGG AA GA GAAAGAGGAGAGGA
G GG

GAM94 332 PPP1R11 2 4808 NP_068778.1 3 124 ATAGAGGGAAGA TC 3 B c c
GGAAGAGGAGGA TTGTTTTCTT TCCTCTTCT
CGAACAGA AGCAGGAGGA AGGAGAAGG
GA

GAM94 332 PPP1R11 2 4808 NP_740751.1 3 436 ATAGAGGGAAGA TC 3 B c c
GGAAGAGGAGGA TTGTTTTCTT TCCTCTTCT
CGAACAGA AGCAGGAGGA AGGAGAAGG
GA

GAM94 332 PPP1R11 2 8137 NP_068778.1 3 125 GGAAGAGGAAGA TC 3 B c c
GGAGGACGAACA TTGTTTTCTT TCCTCTTCT
GAGATCCT AGCAGGAGGA AGGAGAAGG
GA

GAM94 332 PPP1R11 2 8137 NP_740751.1 3 437 GGAAGAGGAAGA TC 3 B c c
GGAGGACGAACA TTGTTTTCTT TCCTCTTCT
GAGATCCT AGCAGGAGGA AGGAGAAGG
GA

GAM94 332 PPP1R3B 1 16205 NP_078883.1 3 2113 CAAGCAAGAAGA - TT 3 B c c
GGAGTGGAAGCA TTGT TTTCT CTCCTCTTCT
CAGTTGCC GACA GAAGG GAGGAGAAGA
C T-

GAM94 332 PPP2R1B 1 18668 NP_002707.2 5 47 CCAGCAGCAGGA --- - 3 B c c
GGAGAAAGAACA TTGTT TTCTTTCTCCTCTT CT
TGGCGGGC GGCGG AAGAAAGAGGAGGA GA
TAC C

GAM94 332 PPP2R2B 1 15433 NP_004567.1 3 591 AAGCTGAGAAGA - TTC 3 B c c
GGATGCAGAATG TTGTT TTCT TCCTCTTCT
ACAAGGAA AACAG AAGA AGGAGAAGA
T CGT

GAM94 332 PPY2 1 19063 NP_066578.1 3 391 GCTTCCAGGTAT T TCT 3 B c c
GGAGAAAGAGAC TTGTTT CTTTCTCC TCT
AAAGAGGA AACAGA GAAAGAGG GGA

- TAT

GAM94 332 PREI3 1 3082 NP_056202.1 3 68 AATTTTAGAAGA TT TT- - 3 B c c
GGAAGTACAGAA TTG TTCT CT CCTCTTCTA
TTCAGTTT GAC AAGA GA GGAGAAGAT
TT CAT A

GAM94 332 PRKCBP1 1 13695 NP_036540.2 5 56 CTTGGCTGAAGA CT C T 3 B c c

GGAAATAAAAAC TTGTTTT TT TCCTCTTC
AGAACAGG GACAAAA AA AGGAGAAG
AT - T

GAM94 332 PRO0327 1 13463 NP_054844.1 3 585 GAATAGAGAAGA TCT 3 B c c
GGTAAGAAGATA TTGTTTTCTT CCTCTTCT
ATTGTTTT AATAGAAGAA GGAGAAGA
T--

GAM94 332 PRO0767 1 14093 NP_054802.1 3 46 AAAACCAAGATG T T 3 B c c
GGGAGAAGAAAA TTGTTTTCTT CTCCTC TCT
CAGCACAA GACAAAAGAA GAGGGG AGA
- T

GAM94 332 PRO0943 1 17160 NP_061038.1 3 127 CATTCAGAAGGG T- C 3 B c c
GAAAATTGAAAA TTGTTTTC TT TCCTCTTCT
CAACAAAA AACAAAAG AA AGGGGAAGA
TT A

GAM94 332 PRO1787 1 16488 NP_061076.1 3 328 TACAATAATGGA C- 3 B c c
AGGGAAAGAAAG TTGTTTTCTTTCT CTCTTCTA
AAGACAAA AACAGAAGAAAGA GGGAAGGT
AA

GAM94 332 PSG1 1 1739 NP_008836.2 3 44 GCATTCAGAGAA TCTC 3 B c c
GAGTCAGGAAAA TTGTTTTCTT CTCTTCT
CAATTGTA AACAAAAGGA GAGAAGA
CT--

GAM94 332 PSPC1 1 2242 NP_060752.1 3 140 ACCTAGGAGAAA T CC-- 3 B c c
CAAGACAGAAAA TTGTTTTCT TCT TCTTCTA
CAAATCTT AACAAAAGA AGA AGAGGAT
C ACAA

GAM94 332 PTGFRN 1 992 XP_040709.3 5 66 GGAGCTGGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCTA
GAGGCGGC GA AGGAGGAGGAGGAGAAGGT
G

GAM94 332 PTK2 1 18787 NP_005598.3 3 400 CATAGTGGAAGA CT- 3 B c c
GGAGAGCATGAA TTGTTTT TTCTCCTCTTCTA
GCAAAGAA AACGAAG GAGAGGAGAAGGT
TAC

GAM94 332 PTK2 1 18787 NP_722560.1 3 400 CATAGTGGAAGA CT- 3 B c c
GGAGAGCATGAA TTGTTTT TTCTCCTCTTCTA
GCAAAGAA AACGAAG GAGAGGAGAAGGT
TAC

GAM94 332 PTPN4 1 6994 NP_002821.1 5 222 GGGGGAGGAAGA G T 3 B c c
GGAGGTGGAGAA TT TTTTCT TCTCCTCTTCT
GGAGGGGG AG AAGAGG GGAGGAGAAGG
G T

GAM94 332 PTPN6 1 5903 NP_536859.1 3 3 GAACAAGAGGGA --- - 3 B c c
GGAGAAAGTGAG TTGTTTT CTTTCTCCTCT TCT
AAGCAGCG GACGAAG GAAAGAGGAGG AGA
AGT G
GAM94 332 PUM2 1 2095 NP_056132.1 3 30 ATTACAGGAGCA CT- 3 B c c
AGAGAAAGAAGA TTGTTTTCTTTCTC CTTCT
TAATTTAA AATAGAAGAAAGAG GAGGA
AAC
GAM94 332 PWP2H 1 17316 NP_005040.1 3 103 GGCCAGCAAAGA TT- 3 B c c
GGAGGGGTCCAG TTGTTTTCT CTCCTCTTCT
AGAACAGC GACAAGAGA GGGGAGGAGA
CCT
GAM94 332 QKI 1 15541 XP_037438.4 5 39 GGAGGAGGAGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGAAG AG AGGAGGAAGAGGAGGAGG
G
GAM94 332 Rab11-F 1 5368 NP_055515.1 3 453 CCTGTTGGGAAG CC 3 B c c
IP3 AAAGGAAGAAAA TTGTTTTCTTTCT TCTTCT
CAGGTCCC GACAAAAGAAGGA AGAAGG
A-
GAM94 332 RAB13 1 19823 NP_002861.1 3 146 TGAGGAGAAAAA - --- ---- 3 B c c
GGAGAAAAGGGA TTGTTTT CT TTCTCC TCTTCT
AAAGCAGA GACGAAA GG AAGAGG AGAGGA
A GAA AAAA
GAM94 332 RAB17 1 18736 NP_071894.1 5 549 GGACCAGAGAGA -- - 3 B c c
GGAGAAAGCGGA TTGTTTT CTTTCTCCTCT TCT
GACAGGTA GACAGAG GAAAGAGGAGA AGA
GC G
GAM94 332 RAB5A 1 18284 NP_004153.2 5 45 GGCGGCGGAGGA G 3 B c c
GGAGAAAGGAAA TT TTTTCTTTCTCCTCTTCT
GAGGAAGG GA AAAGGAAAGAGGAGGAGG
G
GAM94 332 RAD54B 1 8649 NP_602310.1 3 1172 GAAAAGGAGTTA - -- 3 B c c
GGAGAAAGAAGA TTGTTTT CTTTCTCCT CTTCT
GCAGCTGA GACGAGA GAAAGAGGA GAGGA
A TT
GAM94 332 RAGB 1 16756 NP_006055.2 5 350 GCAGTTGAGGGG C - T 3 B c c
TGAAAAAGAAAA TTGTTTTCTTT TC CTCTTC
CAAACAAA AACAAAAGAAA AG GGGGAG
A T T
GAM94 332 RAGB 1 16756 NP_057740.1 5 350 GCAGTTGAGGGG C - T 3 B c c
TGAAAAAGAAAA TTGTTTTCTTT TC CTCTTC
CAAACAAA AACAAAAGAAA AG GGGGAG
A T T
GAM94 332 RASSF2 1 16451 NP_739579.1 5 151 GAACCTAGAAGA TT- C 3 B c c
GGAAAAGGAATG TTG TTCTTT TCCTCTTCTA
TCAGGCTC GAC AAGGAA AGGAGAAGAT
TGT A
GAM94 332 RBL1 1 15482 NP_002886.1 5 12 CGCGCCTGGGAG T T 3 B c c
GGAGAAAGAAGT TTG TTTCTTTCTCC CTTCTA

CGGGGGCC GGC GAAGAAAGAGG GAGGGT
T -
GAM94 332 RBM9 1 13123 NP_055124.1 3 106 GCAAGATGAAGA TC C T 3 B c c
GGAAAAACAAAC TTGTTT TTT TCCTCTTC
AAACAAAC AACAAA AAA AGGAGAAG
C- A T
GAM94 332 RIL 1 16498 NP_003678.2 3 748 CAGAAGGAAGGT G --- -- 3 B c c
TTAGAAAGAAAA TT TTTTCTTTCT CCT CTTCT
GAACACTT AA AAAAGAAAGA GGA GAAGA
G TTT AG
GAM94 332 RORA 1 6954 NP_002934.1 3 165 GCAAAGGAGGGG ---- CT 3 B c c
AAACAATGAAAA TTGTTTTC TTTCTCCTCTT
CAAATAAA AACAAAAG AAAGGGGAGGA
TAAC AA
GAM94 332 RORA 1 6954 NP_599022.1 3 165 GCAAAGGAGGGG ---- CT 3 B c c
AAACAATGAAAA TTGTTTTC TTTCTCCTCTT
CAAATAAA AACAAAAG AAAGGGGAGGA
TAAC AA
GAM94 332 RORA 1 6954 NP_599023.1 3 165 GCAAAGGAGGGG ---- CT 3 B c c
AAACAATGAAAA TTGTTTTC TTTCTCCTCTT
CAAATAAA AACAAAAG AAAGGGGAGGA
TAAC AA
GAM94 332 RORA 1 6954 NP_599024.1 3 165 GCAAAGGAGGGG ---- CT 3 B c c
AAACAATGAAAA TTGTTTTC TTTCTCCTCTT
CAAATAAA AACAAAAG AAAGGGGAGGA
TAAC AA
GAM94 332 RPA2 1 595 NP_002937.1 5 75 AGCATGGGCAGA T T T 3 B c c
GGAGACAGGAAC TTGTTT CT TCTCCTCT CT
AAGCGTAG AACAAG GA AGAGGAGA GG
- C C
GAM94 332 RPL22 1 16388 NP_000974.1 3 0 AAGAAGAGGAGG G T 3 B c c
AAGACGAGGATT TT TT TCTTTCTCCTCTTCT
AATTTCAT AG AG AGAAGGAGGAGAAGA
G C
GAM94 332 RRS1 1 15022 NP_055984.1 3 429 GGAGTGCGGGGG T 3 B b b
AGGGAAAGAAAA TTGTTTTCTTTC CCTCTTCT
CAAACAGT AACAAAAGAAAG GGAGGGGG
-
GAM94 332 SCA1 1 19326 NP_000323.1 3 5093 CCTGATTTGAGA CTCCT 3 B c c
AGCTGAAGAAAA TTGTTTTCTTT CTTCT
CAAAATTT AACAAAAGAAG GAAGA
TC---
GAM94 332 SCAMP5 1 12952 NP_620417.1 3 1308 GGGAAGGTCAGA T -- 3 B c c
GGAGAAGGCAGG TTGTTT CTTTCTCCTCT TCT
CAGGGCCC GACGGA GGAAGAGGAGA GGA
C CT
GAM94 332 SCN4B 1 2309 NP_777594.1 3 241 GTGGAAGATTCA G ---- 3 B c c
GGAGAAAGAAAG TT TTTTCTTTCTCC TCTTCTA
GAGAGGCT GA GAAAGAAAGAGG AGAAGGT
G ACTT

GAM94 332 SEMA3E 1 10055 NP_036563.1 3 2352 AGAGGGAGGGAG - T 3 B c c
AGAGAAAGACGA TTGTTTT CTTTCTCC CTTCT
AGGGAGAG AGCAGAA GAGAGAGG GAGGG
A -
GAM94 332 SERPINB 1 8680 NP_004146.1 3 2232 AAAGCTTTAGAG - TCT 3 B c c
9 GAGGAATGAAAA TTGTTTTC TTTCTCCTCT
CAAAGTGA AACAAAAG AAGGAGGAGA
T TTT
GAM94 332 SFMBT 2 2582 NP_057413.1 5 115 AAAGACGGAAAG CC - 3 B c c
AAAGAAAGAAAA TTGTTTTCTTTCT TCTT CT
CGAGCGCG AGCAAAAGAAAGA AGAA GG
A- A
GAM94 332 SFMBT 2 17462 NP_057413.1 5 110 GCGAAAAGACGG CC - 3 B c c
AAAGAAAGAAAG TTGTTTTCTTTCT TCTT CT
AAAACGAG AGCAAAAGAAAGA AGAA GG
A- A
GAM94 332 SFRP4 1 2316 NP_003005.1 3 307 TACTCTAGAAGA CTC 3 B c c
GTAGGGAAAATA TTGTTTTCTTT CTCTTCTA
ATGCTTGT AATAAAAGGGA GAGAAGAT
T--
GAM94 332 SFRS8 2 1589 NP_689421.1 3 1859 ACCGAGAGAAGA G C 3 B c c
AGAGAAAGAAAA TT TTTTCTTTCTC TCTTCT
GAAAAAGA AA AAAAGAAAGAG AGAAGA
G A
GAM94 332 SFRS8 2 3151 NP_689421.1 3 1860 GAGAAGAAGAGA G C 3 B c c
AAGAAAAGAAAA TT TTTTCTTTCTC TCTTCT
AGAAAAAG AA AAAAGAAAGAG AGAAGA
G A
GAM94 332 SH3BGRL 1 10168 NP_113657.1 3 3428 GCCACATCAGAA T C C 3 B c
c
2 AGCAGAAGAAAA TTGTTTTCTT CT CT TTCT
CAGTATTT GACAAAAGAA GA GA AAGA
- C -
GAM94 332 SIGLEC5 1 18811 NP_003821.1 3 157 GCTCCAAGCAGA C T 3 B c c
GCAGAAAGAAAA TTGTTTTCTTTCT CTCT CT
CAGATGAT GACAAAAGAAAGA GAGA GA
C C
GAM94 332 SIX2 1 9606 NP_058628.2 3 629 GGAGAGGGAAGA C 3 B c c
GGAGAGAAAAGA TTGTTTT TTTCTCCTCTTCT
CAGGGACT GACAGAA AGAGAGGAGAAGG
A
GAM94 332 SLC11A2 1 3415 NP_000608.1 3 617 TGGAAGTTAAGA T CT 3 B c c
GGGGTGAGAAAA TTGTTTTCTT CTCCTCTT
CAAAGAAG AACAAAAGAG GGGGAGAA
T TT
GAM94 332 SLC12A8 1 8454 NP_078904.1 5 32 GGGGGAGGAAGA G C 3 B c c
GGAAGAGAAAAG TT TTTTCTTT TCCTCTTCT
AAGAAGAA AA AAAAGAGA AGGAGAAGG
G -
GAM94 332 SLC14A1 1 9326 NP_056949.1 3 306 TCCAACAGAAGG TTTC - 3 B c c

AGGAAGTGAAAA TTGTTTTC TCCTC TTCT
CAAACTAT AACAAAAG AGGAG AAGA
TGA- G

GAM94 332 SLC17A3 1 9674 NP_006623.1 5 300 TTCACTAGGAGA TTTC 3 B c c
GGAGAAACACAA TTGT TTTCTCCTCTTCTA
TGGCCACC AACA AAAGAGGAGAGGAT
C---

GAM94 332 SLC28A2 1 12812 NP_004203.1 5 53 AGAACAGGAGAT -- C 3 B c c
GGAGAAAGCAAG TTGTTTTCTT TCTCCT TTCT
TGGAAGAC AACGAAAGAG AGAGGA AAGA
GT C

GAM94 332 SLC38A3 1 14679 NP_006832.1 3 106 CCAGTCGGGGGA TT 3 B c c
GGAGAAAGACGC TTGT TCTTTCTCCTCTTCT
GATTAACA AGCG AGAAAGAGGAGGGGG
C-

GAM94 332 SLC38A5 1 13273 NP_277053.1 3 249 GGAGGAAGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGAGGAGG AG AGGAGGAGGAGGAGAAGA
G

GAM94 332 SLC6A8 1 17109 NP_005620.1 3 454 GGAGGAGAGAGA - 3 B c c
GGAGAAGGGAGG TTGTTTTCTTTCTCCTCT TCT
CAGGGGAG GACGGAGGGAAGAGGAGA AGA
G

GAM94 332 SMARCA5 1 8202 NP_003592.2 5 68 TCCAGAGGAAGA TT 3 B c c
GGAGGAGGCGGC TTGTT CTTTCTCCTCTTCT
GAAGCGTT AGCGG GGAGGAGGAGAAGG
C-

GAM94 332 SMARCF1 1 19730 NP_060920.4 3 324 TAAACTAGAAGA G TC 3 B c c

GGAAGAAGAAGA TT TTTTCTT TCCTCTTCTA
GGAAGTAG AG AGAAGAA AGGAGAAGAT
G GA

GAM94 332 SNAPC1 1 11862 NP_003073.1 3 4 CATCCAAGAAGA TTC-- 3 B c c
GGAGAAAACACT TTGTT TTTCTCCTCTTCT
GACAAAGA AACAG AAAGAGGAGAAGA
TCACA

GAM94 332 SNCA 1 11031 NP_000336.1 3 722 AATTTTAGAAGA TG CT 3 B c c
GGTAGAGAAAAT T TTTTCTTT CCTCTTCTA
GGAACATT G AAAAGAGA GGAGAAGAT
GT T-

GAM94 332 SNCA 1 11031 NP_009292.1 3 722 AATTTTAGAAGA TG CT 3 B c c
GGTAGAGAAAAT T TTTTCTTT CCTCTTCTA
GGAACATT G AAAAGAGA GGAGAAGAT
GT T-

GAM94 332 SNW1 1 9744 NP_036377.1 3 4 AAGGCAAGAAGA T--- -- 3 B c c
GGAGGAAGGAAT TGT TTTCTTTCTCCTCTTCT
AGCACAGG ACG AAGGAAGGAGGAGAAGA
GGAC AT

GAM94 332 SNX9 1 16044 NP_057308.1 3 2043 AAGCAGAGGGAA ----- T 3 B c c
TGTGAAAGAAAA TTGTTTTCTTTC TCCTCT CT

TAAGAGAA AATAAAAGAAAG GGGAGA GA
TGTAA C

GAM94 332 SOX9 1 3166 NP_000337.1 5 83 TTCTTTGCAGGA T -- 3 B c c
GGAGAAGAGAAG TTGT TTCTTTCTC CTCTTCT
GGGTGCAA AACG GGGGAAGAG GAGGAGG
T AA

GAM94 332 SPATA1 1 18673 NP_071749.1 3 444 TAGTAGAAGTTA TC --- 3 B c c
AGGATGAGAAAA TTGTTTTCTT TCCT CTTCTA
CAAGCAGT AACAAAAGAG AGGA GAAGAT
T- ATT

GAM94 332 SPRY3 2 9428 NP_005831.1 3 4244 TAATGAGGGAGG - C 3 B c c
GAAGAAAGAAGA TTGTTTT CTTTCT CTCTTCT
ACAAATAA AACAAGA GAAAGA GGGAGGG
A A

GAM94 332 SPRY3 2 15586 NP_005831.1 3 6349 GGGGTCGGGGGA - 3 B c c
GGAGAAAGGGAG TTGTTTTC TTTCTCCTCTTCT
ACAGCAGA GACAGAGG AAAGAGGAGGGGG
G

GAM94 332 SRF 1 844 NP_003122.1 3 740 TTATTTGAGGAG - TC T 3 B c c
ACGAAGTGAAAA TTGTTTTC TTTC CTCTTC
CAAATCTA AACAAAAG GAAG GAGGAG
T CA T

GAM94 332 SRGAP2 1 16111 NP_055665.1 5 46 TCGAAAAGAAAA T C C 3 B c c
GGAGAAATAAAT TTG TTT TTTCTCCT TTCT
CAAACAGC AAC AAA AAAGAGGA AAGA
T T A

GAM94 332 SRL 1 16356 XP_064152.3 5 920 TCCCTCCGAAGA --- T 3 B c c
GGAGTCCGAAGA TTGTTTTCTTT CTCCTCTTC
GGACAGCG GACAGGAGAAG GAGGAGAAG
CCT C

GAM94 332 SRPUL 2 8925 NP_055282.1 5 244 GAAGGAGAAAGA TTG-- 3 B c c
GGAGGAGAGAGA TTTTCTTTCTCCTCTTCT
AAAAGGGC AAAAGAGAGAGGAGGAGA
CGGGA

GAM94 332 SRPUL 2 13474 NP_055282.1 5 232 AGCAGAGAGGAA G - 3 B c c
GGAGAAAGAGGA TT TTTTCTTTCTCCT CTTCT
GGAGAGAG AG AGGAGAAAGAGGA GGAGA
G A

GAM94 332 SSH1 1 1987 NP_061857.1 3 167 CCATAGAGAGGA T T 3 B c c
GGAGAAGAAACT TTG TTTCTT CTCCTCTTCT
AACCAACA AAT AAAGAA GAGGAGGAGA
C -

GAM94 332 SSR2 1 9632 NP_003136.1 3 397 CCTCTCAGAAGA TG -- - 3 B c c
GGGTGGAAGATG T TTT TCTTTC TCCTCTTCT
AAATGAAA A AAA AGAAGG GGGAGAAGA
GT GT T

GAM94 332 STC2 1 19667 NP_003705.1 5 61 GAAGGAGGAAGA G 3 B c c
GGAGGAGGAGGA TT TTTTCTTTCTCCTCTTCT
AGAGGGGA GG AGAAGGAGGAGGAGGAGA
G

GAM94 332 STMN4 1 18271 NP_110422.2 3 236 GGAGAGGGGAGA G T 3 B c c
GGAGAGAGTTTG TT TTTTCTTTCTCCTCTTC
GGAAAGGG GA AGAGGAGAGGGGAGAGG
G -
GAM94 332 SURF6 1 10512 NP_006744.2 3 805 AAATGAGTGCAG T- CTT 3 B c c
GTTGAAAGAAAA TTGTTTTCTTTC CCT CT
CAGGTGAA GACAAAAGAAAG GGA GA
TT CGT
GAM94 332 SV2A 1 17251 NP_055664.1 3 1027 GGGGAGCAGGGG T T 3 B c c
AGGGAAAGAAAC TTG TTTCTTTC CCTCTTCT
CAGGCATC GAC AAAGAAAG GGAGGGGA
C -
GAM94 332 SYNGR1 1 5970 NP_663783.1 3 302 ACAGGCTGGGGA T TT 3 B c c
GGAGAAAACAAA TTGTTTTCTT CTCCTC CT
CACATCAA AACAAAAGAG GAGGGG GG
- TC
GAM94 332 SYT11 1 10869 NP_689493.2 3 1218 AGGACAAGGAGA TT - 3 B c c
GGAGACAAGTGA TTGTT CTT TCTCCTCTTCT
CGACAGCC AGCAG GAA AGAGGAGAGGA
T- C
GAM94 332 TBX15 1 14891 NP_689593.1 3 780 AGAAGCTGAACA - C T 3 B c c
GGAGAAAGACAA TTGTTT TCTTTCTCCT TTC
ACAGAAAG GACAAA AGAAAGAGGA AAG
C C T
GAM94 332 TBX19 1 12762 NP_005140.1 3 943 AAAGAAAGAAAG G CC - 3 B c c
AAAGAAAGAAAG TT TTTTCTTTCT TCTT CT
GAATCCTA AA GAAAGAAAGA AGAA GA
G A- A
GAM94 332 TDGF1 1 5595 NP_003203.1 3 839 GCAAATAGAAGA - TT - 3 B c c
GAGAGGTTGAAA TTGTTTT C TCTC CTCTTCTA
AACAAAAT AACAAAA G GGAG GAGAAGAT
A TT A
GAM94 332 TED 1 8214 NP_056501.1 3 702 GGGGAGAGGAGA TC- 3 B c c
GGAGAAATGTGG TTGTTT TTTCTCCTCTTCT
ACAGAGGG GACAGG AAAGAGGAGAGGA
TGT
GAM94 332 TEM8 1 7297 NP_444262.1 3 25 TACAAGAAGAAG ---- CC 3 B c c
AAAGAAAGAAAT TTGT TTTCTTTCT TCTTCT
CCCACAGA GACA AAAGAAAGA AGAAGA
CCCT A-
GAM94 332 TERF2IP 1 4291 NP_061848.1 3 492 TTGTAGAGGGGG G C-- 3 B c c
ATAAAAAGAAAA TT TTTTCTTT TCCTCTTCTA
GAAATTGG AA AAAAGAAA AGGGGGAGAT
G AAT
GAM94 332 TGFA 1 6056 NP_003227.1 3 2811 TTCCCTGAGAAA TG C C 3 B c c
GGAGAAAAAGAT T TTTT TTTCTCCT TTCT
GGGATTGC G AGAA AAAGAGGA AAGA
GT - -
GAM94 332 TGM3 1 14294 NP_003236.1 5 15 AGCCTGAGAAGA CT - 3 B c c
GGCAGAGGAAGG TTGTTTT TTCT CCTCTTCT

GCGAAACA AGCGGGA GAGA GGAGAAGA
AG C
GAM94 332 THSD2 1 2496 NP_116173.2 5 243 TCAAAAGAAAGA G - 3 B c c
GGAGAAAGGAAG TT TTTTCTTTCTCCTCTT CT
GGAAGCAT AG GAAGGAAAGAGGAGAA GA
G A
GAM94 332 THTPA 1 2304 NP_077304.1 3 598 ACCTGGAGAGGG -- --- T 3 B c c
TTAGAAAGAACC TTGTT TTCTTTCT CCTCTTC
AACAGCTG GACAA AAGAAAGA GGAGAGG
CC TTG T
GAM94 332 TLE1 2 2500 NP_005068.2 5 0 GGCACGAGGAGG TCT T 3 B c c
AGAAGAGCAAAG TTGTTT TTCTCCTCTTC
AAAAGCAG AACGAG AAGAGGAGGAG
--- C
GAM94 332 TLE1 2 12325 NP_005068.2 5 4 CGAGGAGGAGAA TCT T 3 B c c
GAGCAAAGAAAA TTGTTT TTCTCCTCTTC
GCAGTCCG AACGAG AAGAGGAGGAG
--- C
GAM94 332 TM7SF2 1 5692 NP_003264.1 3 39 CCTCAGAGAAGA CTT T 3 B c c
GGTGGTTTAGAG TTGTTTT TC CCTCTTCT
CAAGGAAA AACGAGA GG GGAGAAGA
TTT T
GAM94 332 TMEPAI 1 11793 NP_064567.2 3 85 CTTCTTAGAAGA --- 3 B c c
GGAGTGAGAGGA TTGTTTTCTTT CTCCTCTTCTA
AGGCGGGG GGCGGAAGGAG GAGGAGAAGAT
AGT
GAM94 332 TNFRSF1 1 17895 NP_036584.1 3 145 GAGAGAAACAGA G T --- 3 B c c
3B GGAGACAGAGAG TT TTTTCT TCTCCTCT TCT
GGAGAGAG AG GAGAGA AGAGGAGA AGA
G C CAA
GAM94 332 TPBG 1 3490 NP_006661.1 5 160 GCGGCAGGAAGA TT TTT 3 B c c
GGAGCGGGAGCA TTGTT C CTCCTCTTCT
GGAGCGCG GACGA G GAGGAGAAGG
GG C--
GAM94 332 TRIM38 1 19253 NP_006346.1 3 1234 CCTCTGAGAATA C C 3 B c c
GGAGAAATGAAG TTGTTTT TTTCTCCT TTCT
CAACAGTT AACGAAG AAAGAGGA AAGA
T T
GAM94 332 TRIM56 1 17780 NP_112223.1 5 138 GGAGGAGGAGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGGCAGCT AG AAGAGGAGGAGGAGGAGG
G
GAM94 332 TRIM56 1 17780 XP_168586.1 5 204 GGAGGAGGAGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGGCAGCT AG AAGAGGAGGAGGAGGAGG
G
GAM94 332 TRPM1 2 12837 NP_002411.2 5 204 ACCCAGCAAAAA TC C T 3 B c c
TGAAGAGGAAAA TTGTTT TTT TCCTCTTC
CAAACAGG GACAAA AAA AGGAGAAG
C- - T

GAM94 332 TRPM1 2 13846 NP_002411.2 5 205 CAAAAATGAAGA TC C T 3 B c c
GGAAAACAAACA TTGTTT TTT TCCTCTTC
GGTGGAGA GACAAA AAA AGGAGAAG
C- - T
GAM94 332 TRPM3 1 13071 NP_079247.2 3 1748 AGAAGCTGAAGA -- --- T 3 B c c
GGATAAGAGCAA TTGTTTTCTT TC TCCTCTTC
GGAAACAA AACAAAGGAA AG AGGAGAAG
CG AAT T
GAM94 332 TXK 1 19521 NP_003319.1 3 841 CTTTCCAGAAGA CTT 3 B c c
GGAGACAAAAGC TTGTTTT TCTCCTCTTCT
AAGATAGC AACGAAA AGAGGAGAAGA
AC-
GAM94 332 UBE1 1 2682 NP_003325.2 5 39 CGGCGGGGAGGA G 3 B c c
GGAGAAGGAGGA TT TTTTCTTTCTCCTCTTCT
GGGTGGCG GG AGGAGGAAGAGGAGGAGG
G
GAM94 332 UBE2J1 1 19768 NP_057105.1 3 442 AGGGATAGAAGA --- TC 3 B c c
GTTGAAAAGGGA TTGTTTTCT TTC CTCTTCTA
AAGCAAAA AACGAAAGG AAG GAGAAGAT
GAA TT
GAM94 332 USF1 1 17504 NP_009053.1 5 120 GAGAGATGAAGG TT - T 3 B c c
GGCAGCAGAAAA TTGTTTTCT CT CCTCTTC
CAGCTG GACAAAAGA GA GGGGAAG
C- C T
GAM94 332 USP14 1 1660 NP_005142.1 3 2 TAATGGAAGAGG T TC 3 B c c
AAAGTGAACAGT TTGTTT CTT TCCTCTTCTA
ATCTTCAT GACAAG GAA AGGAGAAGGT
T --
GAM94 332 VDR 1 5451 NP_000367.1 3 2746 CTAGGAGCTGGG G -- -- 3 B c c
AGGAAAAGAAAA TT TTTTCT TTCTCCT CTTCTA
GAGGGGAA GA AAAAGA AGGAGGG GAGGAT
G AA TC
GAM94 332 VEGFB 1 20042 NP_003368.1 3 266 AGAGTTGGAAGA T- 3 B c c
GGAGACTGGGAG TTGTTTTCT TCTCCTCTTCTA
GCAGCAAG GACGGAGGG AGAGGAGAAGGT
TC
GAM94 332 VGLL2 1 1486 NP_703154.1 3 314 TTTCTTGGAACG TG C 3 B c c
GGGGAAAGAAAA T TTTTCTTTCTCCT TTCTA
TGAAACTT A AAAAGAAAGGGGG AAGGT
GT C
GAM94 332 VNN1 1 11888 NP_004657.1 3 609 CATAAAAGAAGA T - T 3 B c c
GGCGAGTAGGGC TTGT TTCT TTC CCTCTTCT
ACAACAGG AACA GGGA GAG GGAGAAGA
C T C
GAM94 332 VPS41 1 18763 NP_055211.1 3 2119 ACTTATAGAAAA TC---- C 3 B c c
GGAGAAAATAAT TTGTTT TTTCTCCT TTCTA
TAAACAGT GACAAA AAAGAGGA AAGAT
TTAATA A
GAM94 332 WDFY2 1 9273 NP_443182.1 3 113 ACATGTGAGAAG T CCT 3 B c c
TAAGAAAGAAAC TTG TTTCTTTCT CTTCT

TAAAGACC AAT AAAGAAAGA GAAGA
C AT-

GAM94 332 WDR22 1 14695 XP_031102.1 3 1284 AGGTTTAGAAGA - CTC 3 B c c
GAAAAGAGCAAC TTGTT TTCTTT CTCTTCTA
AGATTTTC GACAA GAGAAA GAGAAGAT
C A--

GAM94 332 WDR9 2 2792 NP_061836.2 3 241 GTAGGTGGAGAG -- - T 3 B c c
GTGGAAAGAAAA TTGTT TTCTTTCT CCTCTTC
GACAAATG AACAG AAGAAAGG GGAGAGG
AA T T

GAM94 332 WDR9 2 16206 NP_061836.2 3 38 GAATGTAGAAGT TTTCT T 3 B c c
GGCATCTGAAAA TTGTTTTC CC CTTCTA
CAATTGGT AACAAAAG GG GAAGAT
TCTAC T

GAM94 332 WRB 1 17433 NP_004618.2 3 733 CTCTTTAGAATG TTC- TC 3 B c c
GAACACAGAAAA TTGTTTTCT TCC TTCTA
CAAACCTT AACAAAAGA AGG AAGAT
CACA T-

GAM94 332 ZFHX2 1 3631 XP_033370.7 3 515 AAGGCAAAGAAG T 3 B b b
GGGGAAGGAAAA TTGTTTTCTTTCTCC CTTCT
CAAACTTC AACAAAAGGAAGGGG GAAGA
-

GAM94 332 ZIC4 1 4435 NP_115529.2 3 505 TGGTTTGTAAGA G CT 3 B c c
GGGGAAAGAAAA TT TTTTCTTTCTCCTCTT
GGAGAAAG AG AAAAGAAAGGGGAGAA
G TG

GAM94 332 ZNF228 1 17645 NP_037512.1 5 36 CTTTCTCTAGAA G CCTC 3 B c c
AAAGAAAGAAAA TT TTTTCTTTCT TTCTA
GAATGACC AA AAAAGAAAGA AAGAT
G AA--

GAM94 332 ZNF347 3 6828 NP_115973.1 5 36 AGAAGAGGAAGA - ---- 3 B b b
GGAAAGAAAGAC TTGTTTT CTTTC TCCTCTTCT
AAGTCAGG AACAGAA GAAAG AGGAGAAGA
A GAGA

GAM94 332 ZNF347 3 13718 NP_115973.1 5 34 CCTTGAAGAAGA - ---- 3 B b b
GGAAGAGGAAAG TTGTTTT CTTTC TCCTCTTCT
AAAGACAA AACAGAA GAAAG AGGAGAAGA
A GAGA

GAM94 332 ZNF347 3 17666 NP_115973.1 5 34 GAAGAAGAGGAA - ---- 3 B b b
GAGGAAAGAAAG TTGTTTT CTTTC TCCTCTTCT
ACAAGTCA AACAGAA GAAAG AGGAGAAGA
A GAGA

GAM94 332 ZNF396 1 12937 NP_665699.1 3 1087 AGATTAGTAGGA TT - - 3 B c c
GGAGAAGTGAAT TTG TTC TTTCTCCTCTT CTA
GTAAATTT AAT AAG GAAGAGGAGGA GAT
GT T T

GAM94 332 ZNF409 1 18512 NP_055709.1 3 1018 GGAAGGAGGGGA --- 3 B c c
GGAGAAAGGCAA TTGTTT TCTTTCTCCTCTTCT
AAGCAAAC AACGAA GGAAAGAGGAGGGGA
AAC

GAM94 332 ZNF83 1 5124 NP_060770.2 5 166 GGAAGGGGAAGA TC 3 B c c
GGAAAGCAAAGG TTGTTTTCTT TCCTCTTCT
CGTCAGGA AACGAAAGGA AGGGGAAGG
GA
GAM95 27300 LOC1310 1 17288 5 TAAGCAAGGCAT GGAA CA- 3 C c c
GCTGCAGGGAA TTCCTTGCAGCA CC CTTA
AAGGGACGTCGT GG GAAT
AC-- AAC
GAM96 394 ABCA1 1 14553 NP_005493.2 3 3313 GCTGTGACAGTT TA G 1 A c c
CTGTTGGTCTAC TCTGTGG TGACAGAACTG
AGAAA AGACATC GTTGTCTTGAC
TG A
GAM96 394 ABCC1 1 3827 NP_004987.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABCC1 1 3827 NP_063915.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABCC1 1 3827 NP_063953.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABCC1 1 3827 NP_063954.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABCC1 1 3827 NP_063955.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABCC1 1 3827 NP_063956.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABCC1 1 3827 NP_063957.1 3 663 GCTCTACCAGTT G AT-- - 1 A c c
CTCGTTTTGGGC TCT TGGT GAC AGAACTGG
CAGAGGCA GGA ACCG TTG TCTTGACC
G GGTT C
GAM96 394 ABLIM1 2 1918 NP_002304.2 3 3535 CGCTACCCAATT TG-- T- C 1 A c c
CTGTCATCTCCA TC TGG ATGACAGAA TGGG
AGCTGAGT AG ACC TACTGTCTT ACCC
TCGA TC A
GAM96 394 ABLIM1 2 1918 NP_006710.2 3 3535 CGCTACCCAATT TG-- T- C 1 A c c
CTGTCATCTCCA TC TGG ATGACAGAA TGGG
AGCTGAGT AG ACC TACTGTCTT ACCC
TCGA TC A
GAM96 394 ABLIM1 2 1918 NP_006711.2 3 3535 CGCTACCCAATT TG-- T- C 1 A c c
CTGTCATCTCCA TC TGG ATGACAGAA TGGG

AGCTGAGT AG ACC TACTGTCTT ACCC
TCGA TC A
GAM96 394 ABLIM1 2 13766 NP_002304.2 3 2670 TTAAACTCAGTT TG-- T A 1 A c c
CTGCATCCAACT TC TGG ATG CAGAACTGGG
TGAGAAGA AG ACC TAC GTCTTGACTC
TTCA - -
GAM96 394 ABLIM1 2 13766 NP_006710.2 3 2670 TTAAACTCAGTT TG-- T A 1 A c c
CTGCATCCAACT TC TGG ATG CAGAACTGGG
TGAGAAGA AG ACC TAC GTCTTGACTC
TTCA - -
GAM96 394 ABLIM1 2 13766 NP_006711.2 3 2670 TTAAACTCAGTT TG-- T A 1 A c c
CTGCATCCAACT TC TGG ATG CAGAACTGGG
TGAGAAGA AG ACC TAC GTCTTGACTC
TTCA - -
GAM96 394 ADCY6 1 8443 NP_056085.1 3 699 TTAGCCCCAGTT TG TA A - 1 A c c
CCTGCACGCTCC TCTG G TG CAG AACTGGG
AGGGAACG GGAC C AC GTC TTGACCC
CT GC - C
GAM96 394 ADCY6 1 8443 NP_066193.1 3 699 TTAGCCCCAGTT TG TA A - 1 A c c
CCTGCACGCTCC TCTG G TG CAG AACTGGG
AGGGAACG GGAC C AC GTC TTGACCC
CT GC - C
GAM96 394 AKAP13 1 13225 NP_006729.4 3 782 TAGTATCTCATT T --- C 1 A c c
CTGTCATCAGAT TCTG GGT ATGACAGAA TGGG
CCAGAAGA AGAC CTA TACTGTCTT ACTC
- GAC -
GAM96 394 AKAP13 1 13225 NP_009131.2 3 782 TAGTATCTCATT T --- C 1 A c c
CTGTCATCAGAT TCTG GGT ATGACAGAA TGGG
CCAGAAGA AGAC CTA TACTGTCTT ACTC
- GAC -
GAM96 394 AKAP13 1 13225 NP_658913.1 3 782 TAGTATCTCATT T --- C 1 A c c
CTGTCATCAGAT TCTG GGT ATGACAGAA TGGG
CCAGAAGA AGAC CTA TACTGTCTT ACTC
- GAC -
GAM96 394 ALDH1A3 1 9790 NP_000684.1 3 956 TTTTCTCCAGTT --- TA 1 A c c
CTGTTACCCAAT TCTG TGG TGACAGAACTGGG
TTAGATTA AGAT ACC ATTGTCTTGACCT
TTA C-
GAM96 394 ALEX3 1 13767 NP_057691.1 3 314 GTAAGCTCCCTT T T- CT 1 A c c
CTGTCATTTTCA TC GTGG ATGACAGAA GGG
TTGATTTA AG TACT TACTGTCTT CCC
T TT --
GAM96 394 ALEX3 1 13767 NP_808816.1 3 314 GTAAGCTCCCTT T T- CT 1 A c c
CTGTCATTTTCA TC GTGG ATGACAGAA GGG
TTGATTTA AG TACT TACTGTCTT CCC
T TT --
GAM96 394 ALEX3 1 13767 NP_808817.1 3 314 GTAAGCTCCCTT T T- CT 1 A c c
CTGTCATTTTCA TC GTGG ATGACAGAA GGG
TTGATTTA AG TACT TACTGTCTT CCC
T TT --

GAM96 394 ARHGEF1 1 10259 NP_055773.1 3 557 CTCAAGCCAGTT T TAT C 1 A c c
5 CTTCTCTTCCAG TCTG GG GA AGAACTGG
AAGAATTC AGAC CT CT TCTTGACC
- TCT -
GAM96 394 ARHGEF1 1 10259 NP_776089.1 3 557 CTCAAGCCAGTT T TAT C 1 A c c
5 CTTCTCTTCCAG TCTG GG GA AGAACTGG
AAGAATTC AGAC CT CT TCTTGACC
- TCT -
GAM96 394 ARK5 1 16825 NP_055655.1 3 205 CTTCTGCCAGTT -- GT -- 1 A c c
CTGTCAATTGTC TCTG TG A TGACAGAACTGG
AGTCAGAA AGAC AC T ACTGTCTTGACC
TG TG TA
GAM96 394 ASH1 1 16309 NP_060959.1 3 346 GCTTAGGTTTTT T T ---- 1 A c c
CTGTCATCCTCA TCTG GG ATGACAGAA CTGGG
GATCCCAC AGAC CC TACTGTCTT GATTC
T - TTTG
GAM96 394 BACH2 1 13426 NP_068585.1 5 639 CTTCGCCCAGTT GT T A -- 1 A c c
CCCTGCATCCTA TCT GG ATG CA GAACTGGG
AGACTCGA AGA CC TAC GT CTTGACCC
AT - - CC
GAM96 394 BGLAP 1 17362 NP_000702.1 3 53 GCAACCCCAGTT TG TAT - 1 A c c
CTGCTCCTCTCC TCTG G GA CAGAACTGGG
AGGCACCC GGAC C CT GTCTTGACCC
CT TC- C
GAM96 394 C14orf1 1 691 NP_064600.1 3 98 TCAGACCCAGTT G TA- 1 A c c
32 CTGTCAGCTCTA TCT TGG TGACAGAACTGGG
GAGGCACC GGA ATC ACTGTCTTGACCC
G TCG
GAM96 394 C14orf1 1 20031 NP_078919.1 3 254 TCCATTCCAGTT ATGAC 1 A c c
40 CTCTGATTATAG TCTGTGGT AGAACTGGG
AATCCAGA AGATATTA TCTTGACCT
GTC--
GAM96 394 C4orf9 1 4126 XP_035572.1 3 834 CCAGTGTAATTT A ------ 1 A c c
CTGTCAACCACG TCTGTGGT TGACAGA ACTGG
GACGTTTG AGGCACCA ACTGTCT TGACC
- TTAATG
GAM96 394 C6orf31 1 17451 NP_085154.2 3 72 AGGCTCTTTCTG --- CT 1 A c c
CAGTCATACCGC TCTGTGGTATGAC AGAA GGG
GGACCCAA AGGCGCCATACTG TCTT CTC
ACG T-
GAM96 394 C7orf10 1 11807 NP_079004.1 3 100 TTCTCCCCAGTT -- GA 1 A b b
CTGATACCACTA TCT GTGGTAT CAGAACTGGG
AGAAGAAG AGA CACCATA GTCTTGACCC
AT --
GAM96 394 CADPS 1 11125 NP_003707.1 3 100 CATTACCAATTT - -- C- 1 A c c
CTGTCAACTACC TCT GTGGTA TGACAGAA TGG
ATGAGATG AGA TACCAT ACTGTCTT ACC
G CA TA

GAM96 394 CD209 1 18162 NP_066978.1 3 940 CTCTGAACAGTT T- T- G 1 A c c
CTGTCTCTACTA TC GTGGTA GACAGAACTG
CCTGATCT AG CATCAT CTGTCTTGAC
TC CT A
GAM96 394 CHKL 2 8093 NP_689466.1 3 1444 TCGGTTCCAGTT - TATGAC 1 A c c
CTACTTCCAGCA TCTG TGG AGAACTGGG
GAAGGGGC AGAC ACC TCTTGACCT
G TTCA--
GAM96 394 CHKL 2 13794 NP_689466.1 3 4197 TCCCCCTCCCCC A CAGAA 1 A c
c
AGCTCAGACCAC TCTGTGGT TGA CTGGG
AGAGGTGG AGACACCA ACT GACCC
G C----
GAM96 394 CLNS1A 1 3510 NP_001284.1 3 140 CCTGAACCAGTT GG T C 1 A c c
CTTTCTTGAGAC TCTGT TA GA AGAACTGG
AGACTATA AGACA GT CT TCTTGACC
GA T T
GAM96 394 COL11A2 1 6777 NP_542410.1 5 145 GCTCCCTGTCTT T A -- T 1 A c c
CTGTCAGCCTCA TCTG GGT TGACAGA AC GGG
GGGCATCC GGAC CCG ACTGTCT TG CCC
T - TC T
GAM96 394 COL11A2 1 6777 NP_542411.1 5 145 GCTCCCTGTCTT T A -- T 1 A c c
CTGTCAGCCTCA TCTG GGT TGACAGA AC GGG
GGGCATCC GGAC CCG ACTGTCT TG CCC
T - TC T
GAM96 394 COL11A2 1 6777 NP_542412.1 5 145 GCTCCCTGTCTT T A -- T 1 A c c
CTGTCAGCCTCA TCTG GGT TGACAGA AC GGG
GGGCATCC GGAC CCG ACTGTCT TG CCC
T - TC T
GAM96 394 CPT1B 2 8093 NP_689453.1 5 1987 TCGGTTCCAGTT - TATGAC 1 A c
c
CTACTTCCAGCA TCTG TGG AGAACTGGG
GAAGGGGC AGAC ACC TCTTGACCT
G TTCA--
GAM96 394 CPT1B 2 13794 NP_004368.1 3 328 TCCCCCTCCCCC A CAGAA 1 A c
c
AGCTCAGACCAC TCTGTGGT TGA CTGGG
AGAGGTGG AGACACCA ACT GACCC
G C----
GAM96 394 CPT1B 2 13794 NP_689451.1 3 328 TCCCCCTCCCCC A CAGAA 1 A c
c
AGCTCAGACCAC TCTGTGGT TGA CTGGG
AGAGGTGG AGACACCA ACT GACCC
G C----
GAM96 394 CPT1B 2 13794 NP_689452.1 3 74 TCCCCCTCCCCC A CAGAA 1 A c
c
AGCTCAGACCAC TCTGTGGT TGA CTGGG
AGAGGTGG AGACACCA ACT GACCC
G C----

GAM96 394 CPT1B 2 13794 NP_689453.1 3 811 TCCCCCTCCCCC A CAGAA 1 A c c

AGCTCAGACCAC TCTGTGGT TGA CTGGG
AGAGGTGG AGACACCA ACT GACCC
G C----

GAM96 394 CYP2A7 1 15756 NP_000755.2 5 306 GCGGCACCCCTC GA AACT 1 A c c

CTGAAGTACCAC TCTGTGGTAT CAG GGG
AGATTTAG AGACACCATG GTC CCC
AA CT--

GAM96 394 CYP2A7 1 15756 NP_085079.2 5 306 GCGGCACCCCTC GA AACT 1 A c c

CTGAAGTACCAC TCTGTGGTAT CAG GGG
AGATTTAG AGACACCATG GTC CCC
AA CT--

GAM96 394 DAPK2 1 17977 NP_055141.2 3 1217 TGAAGTCTTAAC GA AACT 1 A c c

CCTTGGTACCAC TCTGTGGTAT CAG GGG
AGAATATC AGACACCATG GTT CCC
-- ----

GAM96 394 DHFR 1 4871 NP_000782.1 3 2454 GCTAATCCTCAT T ACT 1 A c c

CTGTCATATCCA TCTG GGTATGACAGA GGG
GAAATCAC AGAC CTATACTGTCT CCT
- ACT

GAM96 394 DIS3 1 16298 NP_055768.2 3 2795 CTAGTGCCAGTT -- AC 1 A c c

CTTATGCTAAGC TCTGT GGTATG AGAACTGG
AGGTTACG GGACG TCGTAT TCTTGACC
AA --

GAM96 394 DKFZP43 1 19187 XP_300993.1 5 82 ACGCCCCCAGTT A ACA 1 A c c
4B204

CCACACCATGGG TCTGTGGT TG GAACTGGG
TGTTGGAT GGGTACCA AC CTTGACCC
C ---

GAM96 394 DKFZp43 1 10751 NP_690047.1 3 841 ATGCTCCCAGTT GGTA 1 A c c

4C1714

CTGTTAGGACAG TCTGT TGACAGAACTGGG
GCATACTG GGACA ATTGTCTTGACCC
GG--

GAM96 394 DKFZP43 1 7012 XP_166383.1 5 318 TTGTGTCTTCCA GA GAA 1 A c c

4G1411

GATGGGTACCAC TCTGTGGTAT CA CTGGG
AGATGGCT AGACACCATG GT GACCT
G- A--

GAM96 394 DKFZP43 1 16671 NP_073744.1 3 895 TGGGGCTGGGTT TAT G 1 A c c

4H0820

CTGTCTTCTACA TCTGTGG GACAGAACT GG
GGCCACCC GGACATC CTGTCTTGG TC
TT- G

GAM96 394 DKFZP43 1 1790 NP_056425.1 3 455 TCAAGGCCAGTT T A A----- 1 A c c
4J154

CTGCAGTGACAG TCTG GGT TG CAGAACTGG
GCCCAGGG GGAC CCG AC GTCTTGACC

```
                                        -  G  AGTGAC
GAM96   394   DKFZP56 1   15475 NP_056236.1  3  386   GAAGTCTCAGTT    T  T---          1  A  c  c
        4K2062                    CTGTCATTTGTC TCTG GG   ATGACAGAACTGGG
                                  CTGGAGCA    AGGT CC   TACTGTCTTGACTC
                                        -  TGTT
GAM96   394   DKFZp58 1  13013 NP_689960.1  3  72    GAAAATGCTCAT     T-     AC       1  A  c  c
        6I1420                    CTGTCATCTTCA TCTGTGG  ATGACAGA  TGGG
                                  TGGATGAA    AGGTACT  TACTGTCT  ACTC
                                        TC      --
GAM96   394   DKFZP58 1  13101 NP_056253.2  3  1801  CTTCCTCCGTGT  T  G      AC        1  A  c
c
        6I2223                    CTGTCATACACT TC GTG TATGACAGA  TGGG
                                  GAGACCAA    AG CAC ATACTGTCT  GCCT
                                        T  -      GT
GAM96   394   DKFZP58 1  13101 NP_542768.1  3  807   CTTCCTCCGTGT  T  G      AC        1  A  c  c

        6I2223                    CTGTCATACACT TC GTG TATGACAGA  TGGG
                                  GAGACCAA    AG CAC ATACTGTCT  GCCT
                                        T  -      GT
GAM96   394   DKFZP58 1  13101 NP_542769.1  3  807   CTTCCTCCGTGT  T  G      AC        1  A  c  c

        6I2223                    CTGTCATACACT TC GTG TATGACAGA  TGGG
                                  GAGACCAA    AG CAC ATACTGTCT  GCCT
                                        T  -      GT
GAM96   394   DKFZp76 1  9980  NP_115672.1  3  809   GCGTGTCCCCTT     TA-----     CT     1  A  c  c

        1A132                     CTGTCAGACAGC TCTGTGG     TGACAGAA  GGG
                                  TTCACAGA    AGACACT     ACTGTCTT  CCC
                                        TCGACAG      C-
GAM96   394   DKFZp76 1  2288  NP_775734.1  3  4367  CCTGTGTGAGTT     TAT      GG       1  A  c
c
        1B107                     CTGTCTTCACAG TCTGTGG  GACAGAACT
                                  ACTCCTCA    AGACACT   CTGTCTTGA
                                        T--       GT
GAM96   394   DKFZp76 1  16727 XP_166582.2  5  20    GCTATCCCAGTT   G   - ACA          1  A  c  c
        1I2123                    CCCCACTGCCAG TCT TGGTA TG  GAACTGGG
                                  GGAACCCC    AGG ACCGT AC  CTTGACCC
                                        G   C  CC-
GAM96   394   DSCR1  1   5007  NP_004405.2  3  140   GAAATCCCAGTT   T  AT  -          1  A  c  c
                                  CATGTTGCTCAG TCTG GGT  GACA GAACTGGG
                                  AAGAGAAT    AGAC TCG  TTGT CTTGACCC
                                        -  --   A
GAM96   394   DUSP18  1  14263 NP_689724.2  3  544   AGTGGCCCAGTT   T  TATGA          1  A  c
c
                                  CTGGTTTTCTAG TCTG GG   CAGAACTGGG
                                  ATTGTACT    AGAT CT   GTCTTGACCC
                                        -  TTTG-
GAM96   394   EIF2S1  1  15812 NP_004085.1  3  903   AGAGCTCCAGTT    GG---    C        1  A  c  c
                                  CTTTATAACAAA TCTGT    TATGA AGAACTGGG
                                  ACAGGGAT    GGACA    ATATT TCTTGACCT
```

AAACA -

GAM96 394 ENTPD3 1 1288 NP_001239.1 3 571 ACAGCCAGGCTT TG- -- 1 A c c
CTGTCATACAGG TCTG GTATGACAGAA CTGG
TAGATCCC AGAT CATACTGTCTT GACC
GGA CG

GAM96 394 EPAC 1 3791 NP_006096.2 5 34 ACTGGCCCAGTT T ACA 1 A c c
CACTGTACCTGG TCTG GGTATG GAACTGGG
ACTTACCC AGGT CCATGT CTTGACCC
- CA-

GAM96 394 EPHB1 1 9482 NP_004432.1 3 551 CCAGATGTTGTT G -- ------ 1 A c c
CTGTCAGTTGCC TCT TGGTA TGACAGAAC TGG
AAAGGACT GGA ACCGT ACTGTCTTG ACC
A TG TTGTAG

GAM96 394 ERAL1 1 18451 NP_005693.1 3 80 AACTGACCAGTT G AT-- 1 A c c
CTGTCCTTGGCT TCT TGGT GACAGAACTGG
GGGGACCC AGG GTCG CTGTCTTGACC
G GTTC

GAM96 394 F13A1 1 5986 NP_000120.1 3 1085 CAGTGCTAGTTC A A-- 1 A c c
TGACCCAACCAC TCTGTGGT TG CAGAACTGG
AGAGGATG AGACACCA AC GTCTTGATC
- CCA

GAM96 394 F9 1 946 NP_000124.1 3 407 TGTTTATTAGTT -- A 1 A c c
CTGTATACAGTA TCTGTG GTATG CAGAACTGG
CAGGATCT GGACAT CATAT GTCTTGATT
GA -

GAM96 394 FBXO22 1 9917 NP_671717.1 3 845 AGCTAGTCATTC - --- A---- 1 A c c
CTGTCATATTCC TCTG TGG TATGACAG ACTGG
CAGTAGAA AGAT ACC ATACTGTC TGATC
G CTT CTTAC

GAM96 394 FETUB 1 5702 NP_055190.1 3 258 CTAAACTGAGCA CA A G 1 A c c
GTCTCATACCAT TCTGTGGTATGA GA CTG
GGAGAGAT AGGTACCATACT CT GAC
-- - G

GAM96 394 FLJ1021 1 10874 XP_290820.1 3 187 CTCCCTTCCTCC TGAC CT 1 A c
c
1 CTTTCTTACCAC TCTGTGGTA AGAA GGG
AGATGGGA AGACACCAT TCTT CCC
---- T-

GAM96 394 FLJ1026 1 3452 NP_060512.2 5 261 GTTTGTCCAGTT G TA ---- -- 1 A c c
0 CTTTGTTCAACA TCT TGG TG ACA GAACTGGG
CGCCAAGA AGA ACC AC TGT CTTGACCT
- GC AACT TT

GAM96 394 FLJ1075 1 18465 NP_060675.1 3 1441 ATGCTCCCAGTT T T- A--- 1 A c c
1 CCCTCGTCCCTG TCTG GGTA GAC GAACTGGG
CCCAGGTC GGAC CCGT CTG CTTGACCC
- CC CTCC

GAM96 394 FLJ1075 1 18465 NP_060709.1 3 1288 ATGCTCCCAGTT T T- A--- 1 A c c
1 CCCTCGTCCCTG TCTG GGTA GAC GAACTGGG
CCCAGGTC GGAC CCGT CTG CTTGACCC
- CC CTCC

GAM96 394 FLJ1101 1 16891 NP_060769.1 3 1346 AAAGGTCCAGTT - GAC 1 A c c
1 CTCAGTACCATG TC TGTGGTAT AGAACTGGG
TGAGTTAA AG GTACCATG TCTTGACCT
T AC-
GAM96 394 FLJ1111 1 582 NP_060799.1 3 568 GACCCTTGAGTT T TA --- 1 A c c
7 CTGTTGGCCCAC TC GTGG TGACAGAACT GGG
TGACTTTA AG CACC GTTGTCTTGA CCC
T CG GTT
GAM96 394 FLJ1132 1 18433 NP_060859.2 3 870 CTTCTCCCAGTT T TATGAC 1 A c
c
0 CTACCTCCCCAG TCTG GG AGAACTGGG
AAGCCTTC AGAC CC TCTTGACCC
C TCCA--
GAM96 394 FLJ1228 1 15505 NP_071762.2 3 307 GATCCTTCAGTT G T A- 1 A c c
7 CTGGCCATTCCA TCT TGG ATG CAGAACTGGG
GGGACCCT AGG ACC TAC GTCTTGACTT
G T CG
GAM96 394 FLJ1259 1 6618 NP_115545.2 5 349 GAACTTTCAGTA TG A 1 A c c
2 CTGTACTACCAC TCTGTGGTA ACAG ACTGGG
AGATTGAT AGACACCAT TGTC TGACTT
CA A
GAM96 394 FLJ1280 1 1666 NP_073742.1 3 497 ATGGGACCAGTT GT TGA 1 A c c
6 CTGCTGCCTAAG TCT GGTA CAGAACTGG
AAGGTCTG AGA CCGT GTCTTGACC
AT C--
GAM96 394 FLJ1480 2 5726 NP_116229.1 3 488 AACCAGTTGCTG ---- ---- 1 A c c
0 CTGTCATACCCC TCTGT GGTATGACAG AACTGG
TGGCAGGG GGACG CCATACTGTC TTGACC
GTCC GTCG
GAM96 394 FLJ1480 2 9483 NP_116229.1 3 79 AGGCACCCAGTT T TATGA - 1 A c c
0 CCTGACTTCCCA TCTG GG CAG AACTGGG
GAGGCTTC AGAC CC GTC TTGACCC
- TTCA- C
GAM96 394 FLJ2032 1 18080 NP_060235.1 5 435 CTTCCCCCAGTT - - A- CA 1 A c c
0 CATCAAAGCCTA TCT GT GGT TGA GAACTGGG
CAAGACGG AGA CA CCG ACT CTTGACCC
A T AA A-
GAM96 394 FLJ2033 1 5583 NP_060242.1 3 238 ATGGGCCCAGTT GGTATGA 1 A c
c
7 CTGGGAGAGGAC TCTGT CAGAACTGGG
AGAAAAGG AGACA GTCTTGACCC
GGAGAGG
GAM96 394 FLJ2050 1 3424 NP_060321.1 5 138 CCAGCCCCAGTT T T C 1 A c c
9 CTTTTATCCCTG TCTG GG ATGA AGAACTGGG
GGCCCAAC GGGT CC TATT TCTTGACCC
C - T
GAM96 394 FLJ2160 1 6263 NP_079038.1 3 343 ACACTGCAGTCC ATGA A 1 A c c
3 AGTCTGGACCAC TCTGTGGT CAGA CTGGG
AGAGTGAG AGACACCA GTCT GACCT
G--- -

GAM96 394 FLJ2235 1 6381 NP_078863.1 3 192 GTCTGCTGGTGG TGA -- TG 1 A c c
3 TCTGCTTACCAC TCTGTGGTA CAGA AC G
AGAATCCT AGACACCAT GTCT TG C
TC- GG GT
GAM96 394 FLJ2238 1 8060 NP_078865.1 3 16 CTACAGACCCTT T A--- CT 1 A c c
6 CTGTCACAGCAC TCTG GGT TGACAGAA GGG
CCAGGAGC GGAC CCA ACTGTCTT CCC
- CGAC --
GAM96 394 FLJ2257 1 15354 NP_079140.1 5 5 GACATTCCAGTT T A A 1 A c c
8 CTGCGGCCCAGA TCTG GGT TG CAGAACTGGG
CGGCAGAA AGAC CCG GC GTCTTGACCT
- - -
GAM96 394 FLJ2316 1 9803 NP_079331.2 3 832 CACGCACCCCGC A A AC 1 A c c
8 TTTGCACACCAC TCTGTGGT TG CAGA TGGG
AGAGTGCC AGACACCA AC GTTT GCCC
C - C-
GAM96 394 FLJ3009 1 7410 NP_659420.1 3 45 TATATACTGAGG T AA G 1 A c c
2 CTGTCATACCCA TCTG GGTATGACAG CT GG
GATTCCCA AGAC CCATACTGTC GA TC
- G- G
GAM96 394 FLJ3031 1 19948 NP_742148.1 3 1028 TACAACTGAGTT T AT G 1 A c c
7 CTGTCTGGCCCA TCTG GGT GACAGAACT GG
GAACCAGC AGAC CCG CTGTCTTGA TC
- GT G
GAM96 394 FLJ3079 1 4121 NP_653295.1 5 378 CTTCCACCAGTT TG TAT 1 A c c
1 CTGTTCTGCAGG TCTG G GACAGAACTGG
TCGGGAGT GGAC C TTGTCTTGACC
GT ---
GAM96 394 FLJ3134 1 2540 NP_689961.1 3 232 ATGTTCCCAGTT ----- A ACA 1 A c c
0 CCAACAAGCCAA TCTG TGGT TG GAACTGGG
ATACCAGA AGAC ACCG AC CTTGACCC
CATAA A AAC
GAM96 394 FLJ3173 1 8026 NP_659421.1 3 163 TAACTCCCAGTT ATGA-- 1 A c c
7 CTGAGAAGAGCC TCTGTGGT CAGAACTGGG
ATAGGAGT GGATACCG GTCTTGACCC
AGAAGA
GAM96 394 FLJ3283 1 16084 NP_689994.1 5 37 CCTCCCCTGTAC C A- T 1 A c c
0 CTCTCGTACCAC TCTGTGGTATGA AG AC GGG
AGAGGACA AGACACCATGCT TC TG CCC
C CA T
GAM96 394 FLJ3586 1 1168 XP_300990.1 5 798 AGAGGACACAGT - T- A G 1 A c c
6 CTGTCATCCCCA TCT GTGG ATGACAGA CTG
CTGGAAAG AGG CACC TACTGTCT GAC
T CC - A
GAM96 394 FLJ3837 1 13942 NP_689911.1 5 46 TCGTCCTCAGTT GGTA A 1 A c c
7 CTGCGGAGACAG TCTGT TG CAGAACTGGG
AGTCCCCA AGACA GC GTCTTGACTC
GAG- -
GAM96 394 FLJ3842 1 13647 NP_775882.1 3 327 CCCATCCTGGCT - -- A TG 1 A c c

6 CTGTCATTTACT TCTGTG GTA TGACAGA C GG
TACAGAAA AGACAT CAT ACTGTCT G CC
T TT C GT
GAM96 394 FLJ3860 1 12240 NP_694947.1 3 545 AAAATACCCAGG A- AGAA 1 A c c

8 GGTTAAGACCAC TCTGTGGT TGAC CTGGG
AGAAGGCT AGACACCA ATTG GACCC
GA GG--
GAM96 394 FLJ3905 1 7832 NP_775851.1 3 2527 AAAACCTCCATT G-- A- C 1 A c c
8 CTGTCAGGGCAG TCTGT GT TGACAGAA TGGG
AACAGAGC AGACA CG ACTGTCTT ACCT
AGA GG -
GAM96 394 FMR2 1 12667 NP_002016.1 3 4642 GCAGGAAGCCAG T AA 1 A c c
CTGTCATATTCG TCTG GGTATGACAG CTGG
GAGGGAAT AGGC TTATACTGTC GACC
- --
GAM96 394 GAB3 1 19604 NP_542179.1 3 1747 CCACAGCCAGTT TC----- - A 1 A c c
CTGCATCACCAC TGTGGT ATG CAGAACTGG
ACACAGCC ACACCA TAC GTCTTGACC
CCGACAC C -
GAM96 394 GALNT2 1 3290 NP_004472.1 3 1413 AGCCTTGGGGTC A A --- 1 A c c
CTGTTAAACCAC TCTGTGGT TGACAG ACT GGG
AGACAGTT AGACACCA ATTGTC TGG TCC
A C GGT
GAM96 394 GARP 1 7696 NP_005503.1 3 1613 GATGACCCCCAT CA AC 1 A c c
CCCTCATACCAT TCTGTGGTATGA GA TGGG
GGAGTCAT AGGTACCATACT CT ACCC
CC --
GAM96 394 GLG1 1 19296 NP_036333.1 3 283 GTAGACAAGTCT - C - GG 1 A c c
CTCTCATACCAA TCTGT GGTATGA AGA ACT
CAGAACTT AGACA CCATACT TCT TGA
A C C AC
GAM96 394 GNB5 1 19704 NP_006569.1 3 316 CCTCAACTCATT - AT C 1 A c c
CTGTCACCAGTA TCTG TGGT GACAGAA TGGG
GAATTCAG AGAT ACCA CTGTCTT ACTC
G -- -
GAM96 394 GNB5 1 19704 NP_057278.2 3 316 CCTCAACTCATT - AT C 1 A c c
CTGTCACCAGTA TCTG TGGT GACAGAA TGGG
GAATTCAG AGAT ACCA CTGTCTT ACTC
G -- -
GAM96 394 GNPNAT1 1 8591 XP_085119.1 3 1376 ACAAAGCTAGTT TGGTAT 1 A c
c
CTGTCTTTTCAG TCTG GACAGAACTGG
AAGTCCTA AGAC CTGTCTTGATC
TTTT--
GAM96 394 GOLGA4 1 12047 NP_002069.2 3 523 TAAAGACCAGTT G A C 1 A c c
CTTTAAGCTAAG TCT TGGT TGA AGAACTGG
ACATGTAA AGA ATCG ATT TCTTGACC
- A -
GAM96 394 GORASP1 1 8526 NP_114105.1 3 2 AGGCCCAGATCT T CA A 1 A c c

CTACCACAGAAT TCTGTGGTA GA GA CTGGG
ACACCCTG AGACACCAT CT CT GACCC
- -- A

GAM96 394 GPM6A 1 14453 NP_005268.1 3 274 CATTTACTAGTT G ATG 1 A c c
CTGTAAAATCAA TCT TGGT ACAGAACTGG
AGATACTA AGA ACTA TGTCTTGATC
A AAA

GAM96 394 GPR26 1 8305 NP_703143.1 3 314 TGACACTCAGTT G GT - 1 A c c
CTGTCACTGTCA TCT TG A TGACAGAACTGGG
AGGATGCA AGG AC T ACTGTCTTGACTC
A TG C

GAM96 394 GPR63 1 9429 NP_110411.1 3 165 GTAATTATAGTT G TG G 1 A c c
CTGTTACCAAGA TCT TGGTA ACAGAACTG
ATAAATAA AGA ACCAT TGTCTTGAT
- -- A

GAM96 394 GPRK2L 1 7782 NP_005298.1 3 27 TGCTGGCACCCC ATGACAGA 1 A c
c
GGTGCGGACCAC TCTGTGGT ACTGGG
AGAGCAGA AGACACCA TGGCCC
GGCG----

GAM96 394 GRCC9 1 4675 NP_116030.1 3 21 CTACCAGTGGCC G A--- 1 A c c
CTGTGATACCAC TCTGTGGTAT ACAG ACTGG
AGACTGTG AGACACCATA TGTC TGACC
G CCGG

GAM96 394 HBS1L 1 17413 NP_006611.1 3 2901 TAACCCACAGTT GT- AT - 1 A c c
CTGTCACCTAAA TCT GGT GACAGAACTG GG
GGTAACTG GGA CCA CTGTCTTGAC CC
AAT -- A

GAM96 394 HIST2H2 1 6859 NP_003519.1 3 523 CGGTCACCAGTT G A 1 A c c
BE CTGCCGTGCGAT TCTGT GTATG CAGAACTGG
GGGGCCTC GGGTA CGTGC GTCTTGACC
G C

GAM96 394 HM13 1 9742 NP_848697.1 3 858 GACAGGCCAGTT TG T AC 1 A c c
CTCCATTCTGCA TCTG G ATG AGAACTGG
GGACTATC GGAC C TAC TCTTGACC
GT T C-

GAM96 394 HTCD37 1 16787 NP_067045.1 3 371 CAGAACCAGTAT T GG - 1 A c c
CTGTCATGGAAC TC GT TATGACAGA ACTGG
TGAACATT AG CA GTACTGTCT TGACC
T AG A

GAM96 394 HUMAGCG 1 10039 NP_037418.2 3 1043 CAGGCCCGTGTC T A- AC 1 A c
c
B CAGTCATACCTA TCTG GGTATGAC GA TGGG
GAGATTTG AGAT CCATACTG CT GCCC
- AC GT

GAM96 394 HUMAGCG 1 10039 XP_291083.2 3 1039 CAGGCCCGTGTC T A- AC 1 A c
c
B CAGTCATACCTA TCTG GGTATGAC GA TGGG
GAGATTTG AGAT CCATACTG CT GCCC
- AC GT

GAM96 394 IDS 1 2510 NP_000193.1 3 309 CAAACTCAAGTT T- G - 1 A c c
ATGTCATACCTT TCTG GGTATGACA AACT GGG
TGGATACG AGGT CCATACTGT TTGA CTC
TT A A
GAM96 394 ILF3 1 12695 NP_036350.2 3 1056 GGGGAGTTGGGG - CA GG 1 A c c
TTCTCATACCAG TCTG TGGTATGA GAACT
CAGATTTC AGAC ACCATACT CTTGG
G -- GG
GAM96 394 KARS 1 13190 NP_005539.1 3 125 GACACCGCAGTT - AT - 1 A c c
CTGTTCAGCCAT TCTG TGGT GACAGAACTG GG
CAGAAGAG AGAC ACCG TTGTCTTGAC CC
T AC G
GAM96 394 KBF2 1 9785 NP_056958.1 3 2656 TATTTTTGGCCA CA C 1 A b b
TTCTCATACCAC TCTGTGGTATGA GAA TGG
AGACAAAA AGACACCATACT CTT ACC
-- -
GAM96 394 KCNA6 1 1371 NP_002226.1 3 263 CATGCCCAGCTT - G- - 1 A c c
CTGTCATATGAA TCT GT GTATGACAGAA CTGGG
TGAGATAT AGA TA TATACTGTCTT GACCC
G AG C
GAM96 394 KCNIP2 1 12228 NP_055406.2 3 614 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNIP2 1 12228 NP_775283.1 3 614 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNIP2 1 12228 NP_775284.1 3 614 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNIP2 1 12228 NP_775285.1 3 614 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNIP2 1 12228 NP_775286.1 3 614 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNIP2 1 12228 NP_775287.1 3 614 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNIP2 1 12228 NP_775464.1 3 1053 CAAGTTCCACAG TGA A - 1 A c c
GTCTGCTACCAC TCTGTGGTA CAGA CTG GG
AGGCCATC GGACACCAT GTCT GAC CC
C-- G A
GAM96 394 KCNQ2 1 13173 NP_004509.2 3 620 GTGTCCCCAGTT -- AT- A 1 A c c

CCGTCTCAGCTA TCT GTGGT GAC GAACTGGG
CCTGGACT AGG CATCG CTG CTTGACCC
TC ACT C

GAM96 394 KIAA005 1 13907 XP_166201.1 5 439 GCCCGCCCAGTT G AC--- 1 A c c
6 CTCTGAGCGTGC TCTGT GTATG AGAACTGGG
GGCGGACG AGGCG CGTGC TCTTGACCC
G GAGTC

GAM96 394 KIAA018 1 13734 NP_066545.1 3 1098 TGGAGTCTTGTT T AT T 1 A c c
6 CTGTCACCCAGG TCTG GGT GACAGAAC GGG
CTGGGGTG GGAC CCA CTGTCTTG TCT
- -- T

GAM96 394 KIAA031 1 17156 XP_045712.5 3 372 AGGAGGCCAGTT G- ATGA 1 A c
c
6 CTGAAAGGCGAG TCTGT GT CAGAACTGG
CAGAACTC AGACG CG GTCTTGACC
AG GAAA

GAM96 394 KIAA045 1 1902 XP_027862.1 3 1229 CACTCTTCAGTT GG GA 1 A c c
9 CTGAAATAGACA TCTGT TAT CAGAACTGGG
GACTTGAG AGACA ATA GTCTTGACTT
G- AA

GAM96 394 KIAA067 1 17472 NP_055858.1 3 1255 CCCCCAGTGGAT AT-- GA- 1 A c
c
6 GTCTAAAACCAC TCTGTGGT GACA ACTGGG
AGATAATA AGACACCA CTGT TGACCC
AAAT AGG

GAM96 394 KIAA082 1 11600 NP_056143.1 3 3020 AATCATCTAGTT T T 1 A c c
8 CTGTCATCTTAC TC GTGG ATGACAGAACTGGG
TGAAAGGA AG CATT TACTGTCTTGATCT
T C

GAM96 394 KIAA083 1 15913 NP_055739.1 3 2264 TCCCATCCAGTT T GA 1 A c c
1 CTGGAGTTCGTA TCTGTGG AT CAGAACTGGG
GAGAGTGA AGATGCT TG GTCTTGACCT
- AG

GAM96 394 KIAA103 1 15246 NP_055724.1 3 485 GTTTCTCCAGTT --- TGA 1 A c c
6 CTGCCTGCCCTG TCTGT GGTA CAGAACTGGG
GCAGAATC AGACG CCGT GTCTTGACCT
GTC CC-

GAM96 394 KIAA104 1 14051 XP_048592.1 3 434 GGCAGGCCAGTT - TATGAC 1 A c
c
5 CTAATTTCCAAT TCTGT GG AGAACTGG
AGATAAGT AGATA CC TCTTGACC
A TTTAA-

GAM96 394 KIAA133 1 419 XP_048774.2 3 516 TTTTTCCCCTTC A- C CT 1 A c c
2 TCTTAAAACCAC TCTGTGGT TGA AGAA GGG
AGAGGACC AGACACCA ATT TCTT CCC
AA C C-

GAM96 394 KIAA157 1 18988 NP_065978.1 3 1704 AATATTCCAGTT G T -- 1 A c c
6 CTGGGTCATTTA TCT TGG ATGAC AGAACTGGG
GAGAGATA AGA ATT TACTG TCTTGACCT
G - GG

GAM96 394 KIAA171 1 18820 XP_042936.1 3 3270 GAGGCCACAGTT GGTATG - 1 A c c
9 CTGTGAGCAGAG TCTGT ACAGAACTG GG
GAAGAGCT AGACG TGTCTTGAC CC
AG---- A
GAM96 394 KIAA173 1 12607 XP_290496.1 3 2267 TAGCTCGGTAAT GAC -- 1 A c c
5 CTCATGTACCAC TCTGTGGTAT AGA ACTGGG
AGGTAATG GGACACCATG TCT TGGCTC
TAC AA
GAM96 394 KIAA176 1 7558 XP_047355.1 3 50 CAGCCCCCAGTT GGTA - 1 A c c
5 CTGCTCAAGGAC TCTGT TGA CAGAACTGGG
AGAGAAAA AGACA ACT GTCTTGACCC
GGA- C
GAM96 394 KIAA192 1 9076 NP_694971.2 3 397 GAGAGCCTTGTT T AT T 1 A c c
4 CTGTCACCTAGG TCTG GGT GACAGAAC GGG
CTGGAATG GGAT CCA CTGTCTTG TCC
- -- T
GAM96 394 KIAA195 1 7520 XP_166532.1 3 1072 TTCGGTCTAGTT G- -- 1 A c c
0 CTGTCAGTTGCT TCT TGGTA TGACAGAACTGGG
GAGAGAGG AGA GTCGT ACTGTCTTGATCT
GA TG
GAM96 394 KIP3 1 7794 NP_473454.1 3 14 CCACATCCGAAT ATG AC 1 A c c
CTGTGGCACCAC TCTGTGGT ACAGA TGGG
AGAGGAGC AGACACCA TGTCT GCCT
CGG AA
GAM96 394 KRT23 1 1919 NP_056330.3 5 525 GGCGGCTCAGTT G GA 1 A c c
CTGCGGTGCCAG TCT TGGTAT CAGAACTGGG
GGAGTGGA AGG ACCGTG GTCTTGACTC
G GC
GAM96 394 LANCL1 1 3104 NP_006046.1 3 1207 CAATTCATCAGT ATGA - 1 A c c
TTCTGAGACCAC TCTGTGGT CAGAA CTGG
AGAATCAG AGACACCA GTCTT GACT
GA-- T
GAM96 394 LANCL2 1 15186 NP_061167.1 3 2419 TAAAAGCCAGTT ----- G 1 A c c
CTGTGGTGATGA TCTGTGG TAT ACAGAACTGG
CCTATGGA AGGTATC GTG TGTCTTGACC
CAGTA G
GAM96 394 LOC1188 1 17463 NP_849154.1 3 167 CCTGCCATTCCA ATGA AA 1 A c c
12 GAACTGGACCAC TCTGTGGT CAG CTGGG
AGAAAAGT AGACACCA GTC GACCT
G--- AA
GAM96 394 LOC1188 1 17463 XP_058346.2 3 167 CCTGCCATTCCA ATGA AA 1 A c c
12 GAACTGGACCAC TCTGTGGT CAG CTGGG
AGAAAAGT AGACACCA GTC GACCT
G--- AA
GAM96 394 LOC1232 1 6644 XP_058692.1 3 83 CTTACCCCAGTT GTA ACA 1 A c c
32 CCCAAACACAGG TCTGTG TG GAACTGGG

AAGTGATT GGACAC AC CTTGACCC
AA- C--
GAM96 394 LOC1306 1 8428 XP_059461.1 3 655 CATGTCTGGTGT --- - TG 1 A c c
12 CTGTCATGCCAA TCTG TGGTATGACAGA AC GG
CCTAGACA AGAT ACCGTACTGTCT TG CT
CCA G GT
GAM96 394 LOC1344 1 18543 XP_068858.3 5 1252 ATACACCTAGTT T ----- 1 A c c
66 CTGTATGATCAT CTGTGGTATGA CAGAACTGGG
ATCATAGT GATACTATACT GTCTTGATCC
T AGTAT
GAM96 394 LOC1391 1 5578 NP_775764.1 3 308 CTTTGCATATCC ATGAC - 1 A c c
35 ATGTTCTACCAC TCTGTGGT AGAAC TGGG
AGGAAGGT GGACACCA TCTTG ACCT
----- T
GAM96 394 LOC1461 1 13043 NP_775772.1 5 217 TCCAGCTCAGTT A --- 1 A c c
74 CTGTGTACAAAC TCTGTGGT TG ACAGAACTGGG
CATGGAGG AGGTACCA AC TGTCTTGACTC
A ATG
GAM96 394 LOC1475 1 8521 XP_097243.1 3 384 AAGAAGCTGCTG ATG TG 1 A c
c
15 GTTCTGTACCAC TCTGTGGT ACAGAAC G
AGGCCTCA GGACACCA TGTCTTG C
--- GT
GAM96 394 LOC1488 1 2847 XP_097527.1 3 248 ATCTTCCAGCTT T A- - 1 A c c
24 CTGTCAGAACTT TCTG GGT TGACAGAA CTGGG
TAGGTCAG GGAT TCA ACTGTCTT GACCT
T AG C
GAM96 394 LOC1500 1 452 XP_097793.1 5 446 TGGATTCAGACT -- AA 1 A c c
35 GAATTATACCAC TCTGTGGTATGA CAG CTGGG
AGGCCTTC GGACACCATATT GTC GACTT
AA A-
GAM96 394 LOC1502 1 2217 XP_086827.2 5 827 CAAATGCCAGTT T TATGA 1 A c
c
12 CTGCCACTGAAG TC GTGG CAGAACTGG
AGCTGGAT AG CACC GTCTTGACC
T -----
GAM96 394 LOC1509 1 1643 XP_097977.2 3 952 TTCCCTGGTTTT G - -- TG 1 A c c
46 CTGTCACTGGCA TCTGTG TA TGACAGA AC GG
CAGGAGGG GGACAC GT ACTGTCT TG CC
G C TT GT
GAM96 394 LOC1532 1 1123 XP_295161.1 5 111 CATGAGCCAATT --- TA-- C 1 A c c
77 CTGTCACAGTCC TCTGT GG TGACAGAA TGG
GAAATAGA AGATA CC ACTGTCTT ACC
AAG TGAC A
GAM96 394 LOC1550 1 3970 XP_088114.2 3 68 CAAGACCCAGTT G T CA 1 A c c
04 CATTCTGCCAAA TCT TGGTA GA GAACTGGG
GGGAAAAG GGA ACCGT CT CTTGACCC
A - TA
GAM96 394 LOC1572 1 18145 XP_033876.1 5 69 CCGGCCTAGTTA AG- 1 A c c

26 CCGTCATACCAC TCTGTGGTATGAC AACTGGG
GGGAGGAG GGGCACCATACTG TTGATCC
CCA

GAM96 39462 LOC1575 1 7115 XP_098779.1 5 624 ACCGCTCCAGTT --- T- C- 1 A c c
CTCATCATCTCC TCTGT GG ATGA AGAACTGGG
CAGGCAGA AGACG CC TACT TCTTGACCT
GAC TC AC

GAM96 39412 LOC1588 1 11303 XP_088679.1 3 12 GAGACCTCAGTT T - G 1 A c c
CTGTGTGTCTCT TCTG GG TAT ACAGAACTGGG
AGAGGTCC AGAT TC GTG TGTCTTGACTC
C T -

GAM96 39413 LOC1588 1 11303 XP_088680.1 3 12 GAGACCTCAGTT T - G 1 A c c
CTGTGTGTCTCT TCTG GG TAT ACAGAACTGGG
AGAGGTCC AGAT TC GTG TGTCTTGACTC
C T -

GAM96 39491 LOC1676 1 8140 XP_094623.1 3 712 GTTAGTTGCTCT -- ----- 1 A c c
CTGTCATAGCCC TCTGTGG TATGACAGA ACTGG
GCAGAAGC AGACGCC ATACTGTCT TGATT
CG CTCGT

GAM96 39483 LOC1964 1 14696 XP_016909.6 5 191 AGCCATCATCTC --- C AC- 1 A c c
TCACGGTACCAC TCTGTGGTA TGA AGA TGG
AGGCCTGG GGACACCAT ACT TCT ACC
GGC C ACT

GAM96 39458 LOC1998 1 11822 XP_114040.1 3 1078 ATCCTATTAGTT G TAT 1 A c c
CTGTCCCTCTAG TCT TGG GACAGAACTGG
AGAACCCC AGA ATC CTGTCTTGATT
G TCC

GAM96 39409 LOC2006 1 1503 XP_117256.1 5 4189 CAAACCTCAGTT ATGA- 1 A c c
CTGAAAGAGCTA TCTGTGGT CAGAACTGGG
CAGAATGC AGACATCG GTCTTGACTC
AGAAA

GAM96 39495 LOC2008 1 11068 NP_789785.1 3 2463 CTAAATCCTCAT G ACT 1 A c c
CTGTCATATCAA TCT TGGTATGACAGA GGG
GAAATCAC AGA ACTATACTGTCT CCT
- ACT

GAM96 39416 LOC2009 1 903 XP_114317.3 3 312 GACACTCTCGTT T AT T- 1 A c c
CTGTCACCCAGG TCTG GGT GACAGAAC GGG
CTGGAGTG GGAC CCA CTGTCTTG CTC
- -- CT

GAM96 39425 LOC2017 1 3356 XP_114370.1 3 121 TGTCCAGCAGTT T - G 1 A c c
CTGTATATACTC TCTG GGTATG ACAGAACTG
AGAATGAA AGAC TCATAT TGTCTTGAC
- A G

GAM96 39419 LOC2199 2 6258 XP_167785.1 5 793 CCTTGCCCCTCT - - ACT 1 A c c
CTGTCATAGCTA TCTGT GGT ATGACAGA GGG
ACAGGAAT GGACA TCG TACTGTCT CCC
A A CT-

GAM96 39419 LOC2199 2 13602 XP_167785.1 5 531 GTCCCTTGAGTT G T ---- --- 1 A c c
CTGTGTCACATT TCT TGG ATG ACAGAACT GGG

CCAGAGGC GGA ACC TAC TGTCTTGA CCC
G T ACTG GTT
GAM96 394 LOC2220 1 6288 XP_166594.2 3 667 TTAGGCCCAGTT G- CAGA 1 A c c
57 CATGCTAAAAGA TCT TGGTATGA ACTGGG
TGGACTCT AGA ATCGTACT TGACCC
AA ----
GAM96 394 LOC2221 1 10483 NP_787083.1 3 75 AAACCCCCAGTT GT A ACA 1 A c c
71 CCAAACCCGAGA TCT GGT TG GAACTGGG
CTTCAGGC AGA CCA AC CTTGACCC
GC A ---
GAM96 394 LOC2535 2 4331 XP_173110.1 3 491 TATAGCCCAGTT G- TGAC 1 A c c
73 CTTACAAGCAGA TCTGT GTA AGAACTGGG
GAAGCCTA AGACG CAT TCTTGACCC
AA ----
GAM96 394 LOC2535 2 18972 XP_173110.1 3 1723 AACTTCCCAGTT T------ T A 1 A c c
73 CTGACATTCACA CTGTGG ATG CAGAACTGGG
GCATGACC GACACT TAC GTCTTGACCC
CCAGTAC - A
GAM96 394 LOC2554 1 18477 XP_172895.1 5 2620 TCGACTCCAGTT TATGA 1 A c c
80 CTGGCTGCCCGC TCTGTGG CAGAACTGGG
GGGCCTCT GGGCGCC GTCTTGACCT
CGTCG
GAM96 394 LOC2562 1 8993 XP_172550.1 5 35 CATCACCAATGT - -- AC- 1 A c c
48 CTGTCATGCTGA TCT GT GGTATGACAGA TGG
GCAAGAGG AGA CG TCGTACTGTCT ACC
A AG GTA
GAM96 394 LOC2831 1 9301 XP_210888.1 5 119 TGCCCCGGGGTT G AT -- 1 A c c
04 CTGTCCACCGGG TCT TGGT GACAGAACT GGG
GAGGAAAG AGG GCCA CTGTCTTGG CCC
G C- GG
GAM96 394 LOC2833 1 3714 XP_210977.1 5 1048 GTTCACCCAGTT -- CAGA 1 A c c
31 CATACTAAGCAG TCTGT GGTATGA ACTGGG
AGCCAGGC AGACG TCATACT TGACCC
AA ----
GAM96 394 LOC2837 1 17874 XP_208806.1 3 1926 GACATGCTGGTG - A TG 1 A c c
24 TTGTCATACCAC TC TGTGGTATGACAG AC G
ACGACACG AG ACACCATACTGTT TG C
C G GT
GAM96 394 LOC2837 1 2171 XP_211184.1 5 175 TCAGCCCCAGTT GTATGACA 1 A c c
31 CAGAACACAGAA TCTGTG GAACTGGG
CTTCACAC AGACAC CTTGACCC
AAGA----
GAM96 394 LOC2838 1 17890 XP_211225.1 3 205 CCGCAGACCTTT G ---- - 1 A c c

```
          34                          CTGTCATGCTGG TCT TGGTATGACAGAA   CTG GG
                                      GAAGTATC    AGG GTCGTACTGTCTT   GAC CC
                                              -          TCCA  G
GAM96     394   LOC2840 1  10544 XP_208983.3  3  508   CCACTCCCAGTT    T  TATG            1  A  c  c

          23                          CTGTGTTCCAGA TCTG GG   ACAGAACTGGG
                                      AATTGAGA    AGAC CT   TGTCTTGACCC
                                                - TG--
GAM96     394   LOC2840 1  14747 XP_208982.1  3  315   ACATTTCTGTGT       ----   --  C G    1  A  c  c
          31                          CATTTCTACCAC TCTGTGGTA   TGACA  GAA TG
                                      AGATGCGC    AGACACCAT   ACTGT  CTT AC
                                                  CTTT    GT  T  A
GAM96     394   LOC2840 1  14039 XP_208987.1  3  552   CTGTTCTCAGCT    TG T      A          1  A  c  c
          54                          CTGTCATCTGCA TCTG  G ATGACAGA CTGGG
                                      GGGCTTCT    GGAC  C TACTGTCT GACTC
                                                GT -       C
GAM96     394   LOC2840 1  19081 XP_208989.1  3  551   CTGTTCTCAGCT    TG T      A          1  A  c  c
          57                          CTGTCATCTGCG TCTG  G ATGACAGA CTGGG
                                      GGGCTTCT    GGGC  C TACTGTCT GACTC
                                                GT -       C
GAM96     394   LOC2841 1  4099  XP_209024.1  3  542   TTCTTAGACATT    ---          ---       1  A  c  c
          17                          TTGTCATACCAT TCT   GTGGTATGACAGAA   CTGGG
                                      TCTAGAAG    AGA   TACCATACTGTTTT   GATTC
                                                  TCT           ACA
GAM96     394   LOC2843 1  11555 XP_211425.1  5  2055  GGTCTCAGCATT T---   --         --      1  A  c  c
          05                          CTGTCATACTCA    CTGT  GGTATGACAGAA  CTGGG
                                      ACAGCTAT        GACA  TCATACTGTCTT  GACTC
                                              TATC    AC          AC
GAM96     394   LOC2843 1  833   XP_209143.1  3  270   TAGGGGCCGCCT   -  GT      AC         1  A  c  c
          25                          CTGTCATCTCAC TCT GTG  ATGACAGA  TGG
                                      TAGACATT    AGA CAC  TACTGTCT  GCC
                                                T  TC       CC
GAM96     394   LOC2844 1  11999 XP_209210.1  5  256   TCATTGTAAGTT       TAT       GG        1  A  c  c

          40                          CTGTCCTACAGA TCTGTGG   GACAGAACT
                                      GAAGTGTG    AGACATC   CTGTCTTGA
                                                  ---         AT
GAM96     394   LOC2844 1  9502  XP_211469.1  5  486   CCCCTTCCCAGT       A  A  GA          1  A  c  c
          52                          CGTGACAACCAC TCTGTGGT TG CA  ACTGGG
                                      AGATGGCC    AGACACCA AC GT  TGACCC
                                                - A  GC
GAM96     394   LOC2844 1  6210  XP_211474.1  3  3999  TGCCTAGCCACA      G-       AA---       1  A  c  c
          73                          CTGTCATAGACA TCTGTG  TATGACAG    CTGGG
                                      CAGACATG    AGACAC  ATACTGTC    GATCC
                                                  AG        ACACC
GAM96     394   LOC2846 1  8522  XP_211548.1  5  613   GCAGGCCCAGTT   G   ATGA-             1  A  c
c
          00                          CTGGAAAGGCCA TCT TGGT    CAGAACTGGG
                                      GGATGTGG    AGG ACCG    GTCTTGACCC
                                                -   GAAAG
```

GAM96 394 LOC2847 1 11795 XP_209363.1 5 198 GGAGCCCCAAGT ATGA GA - 1 A c c
59 CTTGGGGACCAC TCTGTGGT CA ACT GGG
AGAAGATG AGACACCA GT TGA CCC
GGG- TC A
GAM96 394 LOC2848 1 13771 XP_211644.1 5 763 GGGCTCCCAGTT ATGACA- 1 A c c
31 CAGGATGGGCCA TCTGTGGT GAACTGGG
CAGGGCGT GGACACCG CTTGACCC
GGTAGGA
GAM96 394 LOC2850 1 933 XP_211739.1 5 777 CTGAAACAGATT -- --- - G 1 A c c
33 CTGTCATGGAAC TCTGT GGT ATGACAGAA CTG
TCAACAGA AGACA TCA TACTGTCTT GAC
AC AGG A A
GAM96 394 LOC2851 1 17372 XP_211795.1 5 165 TACGCCCCAGTT T T C 1 A c c
73 CTTTCATCTTGG TCTG GG ATGA AGAACTGGG
AATTCTTT AGGT TC TACT TCTTGACCC
- - T
GAM96 394 LOC2851 1 9868 XP_211802.1 5 63 CCACCTCCCACT GG AC 1 A c c
91 CTGTCATGGCGG TCTGT TATGACAGA TGGG
GATTTTTG GGGCG GTACTGTCT ACCC
-- C-
GAM96 394 LOC2852 1 11893 XP_211805.1 3 10 CACTGGCCAGTT ATGAC 1 A c c
05 CTACCATAGACT TCTGTGGT AGAACTGG
TGACTGCA AGATACCA TCTTGACC

GAM96 394 LOC2852 1 8215 XP_211823.1 3 660 CCTCTTTCAGTT GGTATGA 1 A c c
66 CTGACAGAAAAT TCTGT CAGAACTGGG
AATTTATT AGACA GTCTTGACTT

GAM96 394 LOC2852 1 13602 XP_211833.1 5 531 GTCCCTTGAGTT G T ---- --- 1 A c c
95 CTGTGTCACATT TCT TGG ATG ACAGAACT GGG
CCAGAGGC GGA ACC TAC TGTCTTGA CCC
G T ACTG GTT
GAM96 394 LOC2853 2 6068 XP_211839.1 5 793 CCCTGCCCCTCT - - ACT 1 A c c
09 CTGTCATAGCTA TCTGT GGT ATGACAGA GGG
ACAGGAAT GGACA TCG TACTGTCT CCC
A A CT-
GAM96 394 LOC2853 2 13602 XP_211839.1 5 531 GTCCCTTGAGTT G T ---- --- 1 A c c
09 CTGTGTCACATT TCT TGG ATG ACAGAACT GGG
CCAGAGGC GGA ACC TAC TGTCTTGA CCC
G T ACTG GTT
GAM96 394 LOC2855 1 4219 XP_209641.1 3 495 ATTGGACCAGTT GT TGA 1 A c c
06 CTGCTGCCTAAG TCT GGTA CAGAACTGG
AAGGTCTG AGA CCGT GTCTTGACC
AT C--
GAM96 394 LOC2855 1 1124 XP_211939.1 3 385 CATTGTTCAGTC ACAGA 1 A c c

56 AAAACATACCAC TCTGTGGTATG ACTGGG
AGAATGGG AGACACCATAC TGACTT
AAAAC
GAM96 394 LOC2856 1 16938 XP_209693.1 5 3919 TGGAGTCTTGTT T AT T 1 A c c
38 CTGTCACCCAGG TCTG GGT GACAGAAC GGG
CTGGAGTG GGAC CCA CTGTCTTG TCT
- -- T
GAM96 394 LOC2856 1 9819 XP_209720.1 3 1191 ATGGTTACTGTT G T- T 1 A c c
73 CTGTCCCTACAA TCTGT GTA GACAGAAC GG
TAGAATGT AGATA CAT CTGTCTTG TC
A CC -
GAM96 394 LOC2857 1 10189 XP_209743.1 3 1357 GGGAGTCTTGTT T AT T 1 A c c
44 CTGTCACCCAGG TCTG GGT GACAGAAC GGG
CTGGAGTG GGAC CCA CTGTCTTG TCT
- -- T
GAM96 394 LOC2858 1 9838 XP_212039.1 3 2003 GGAACTCCAGTT TGGT GA 1 A c
c
51 CTGGGGTCAGAA TCTG AT CAGAACTGGG
GATTTAAA AGAC TG GTCTTGACCT
---- GG
GAM96 394 LOC2859 1 4449 XP_212090.1 5 56 CTGGGGCCAGTT T AT --- 1 A c c
51 CTTCTGTTTCAC TCTG GGT GACAGA ACTGG
CTAGAATT AGAT CCA TTGTCT TGACC
- CT TCT
GAM96 394 LOC2862 1 2398 XP_212235.1 3 615 GAGACACCAGTT TATGA 1 A c c
18 CTGCCTACAGGA TCTGTGG CAGAACTGG
GTGAGTTT GGACATC GTCTTGACC
C----
GAM96 394 LOC3387 1 9649 XP_290549.1 3 35 AGTTACATCCAT G T AC 1 A c c
46 CTGTCATCTGAA TCT TGG ATGACAGA TGGG
GAAGGAGG AGA GTC TACTGTCT ACCT
A - --
GAM96 394 LOC3387 1 19175 XP_290580.1 5 1178 CAATCTTTCCTT G A CT 1 A c c
99 CTGTCAACGGCA TCTGT GT TGACAGAA GGG
GGGGCAGG GGACG CA ACTGTCTT CCT
G - --
GAM96 394 LOC3388 1 5337 XP_294740.1 3 166 GTAAAATCTCTT GTA CT 1 A c c
99 CTGTCACACACA TCTGTG TGACAGAA GG
GATGAACT AGACAC ACTGTCTT CT
AC- CT
GAM96 394 LOC3390 1 10862 XP_294795.1 5 696 TTTGGACCAGTT ---- AC 1 A c c
62 CTTGTGCCATTG TCTGT GGTATG AGAACTGG
GCAGGATG GGACG CCGTGT TCTTGACC
GTTA --
GAM96 394 LOC3393 1 12281 XP_294921.1 3 486 ATCCTATTAGTT G TAT 1 A c c
73 CTGTCCCTCCAG TCT TGG GACAGAACTGG
AGAACCCT AGA ACC CTGTCTTGATT
G TCC

GAM96 394 LOC3393 1 13147 XP_294923.1 5 374 GGCCAGTGTTGT TG ---- 1 A c c
78 CTGTCATGTGCC TCTG GTATGACAGA ACTGG
AGAAGCTT AGAC TGTACTGTCT TGACC
CG GTTG
GAM96 394 LOC3396 1 4595 XP_295016.1 5 1498 TGGAGTCTCGTT T AT T 1 A c c
22 CTGTCACCCAGG TCTG GGT GACAGAAC GGG
CTGGCGTG GGAC CCA CTGTCTTG CTC
- -- -
GAM96 394 LOC3396 1 4448 XP_290982.1 5 216 AAGAACCAGGGT T---- T- A- 1 A c c
69 CTGTCATCCCCA CTGTGG ATGACAGA CTGG
CAGCCCCT GACACC TACTGTCT GACC
TCCCC CC GG
GAM96 394 LOC3400 1 5987 XP_295148.1 3 1431 TTTGCCCCAGTT A A- 1 A b b
74 CTGGGCAGCCAC TCTGTGGT TG CAGAACTGGG
AGGCCCCC GGACACCG AC GTCTTGACCC
- GG
GAM96 394 LOC3401 1 7614 XP_291160.1 5 1593 ACATGCCCAGTT GT--- GT - 1 A c c
70 CATGTCATCTCT TCT G ATGACA GAACTGGG
CTTAAGAA AGA C TACTGT CTTGACCC
ATTCT TC A
GAM96 394 LOC3403 1 4624 XP_295221.1 3 937 TAGACCCCAGTT G TAT 1 A c c
53 CTGTTTTCCAGG TCT TGG GACAGAACTGGG
AGGAACTC AGG ACC TTGTCTTGACCC
- TT-
GAM96 394 LOC3404 1 6259 XP_291300.1 5 74 GACCTTCCAGTT T TAT 1 A c c
64 CTGTCTCCTCAG TCTG GG GACAGAACTGGG
ATTGCTGT AGAC CC CTGTCTTGACCT
T T--
GAM96 394 LOC3408 1 2511 XP_295799.1 3 1317 GAGCCCCAGGCC GAC- AA 1 A c
c
50 TCGGGATACCAC TCTGTGGTAT AG CTGGG
AGAGAAAC AGACACCATA TC GACCC
GGGC CG
GAM96 394 LOC3478 1 1097 XP_302614.1 3 1556 AGCCTCCCAAGT GA A- - 1 A c c
64 AGCTGGTACCAC TCTGTGGTAT CAG ACT GGG
AGGCGCCA GGACACCATG GTC TGA CCC
-- GA A
GAM96 394 LOC3478 1 3644 XP_302563.1 3 188 CTGGTTCCAGTT -- ATG 1 A c c
88 CTGTAGCCATTC TCTG TGGT ACAGAACTGGG
AGGTCCAG GGAC ACCG TGTCTTGACCT
TT A--
GAM96 394 LOC3485 1 17828 XP_302814.1 3 948 AGGCCCTAGCAG TGA A G 1 A c
c
28 TCCTGCTACCAC TCTGTGGTA CAG ACTG
AGATCCCA AGACACCAT GTC TGAC
C-- C G
GAM96 394 LOC3490 1 19254 XP_300919.1 3 489 GCTATCTCAGTT GGTATG 1 A c
c
49 CTGTAGCAGATC TCTGT ACAGAACTGGG

CCTGGTTC AGACG TGTCTTGACTC
A-----
GAM96 394 LOC3492 1 4813 XP_300987.1 3 308 GCACAACTACCT ATGA AA 1 A c c
34 CGGCCTGACCAC TCTGTGGT CAG CTGGG
AGAGCTCT AGACACCA GTC GGCTC
---- C-
GAM96 394 LOC3492 1 19187 XP_300994.1 5 82 ACGCCCCCAGTT A ACA 1 A c c
56 CCACACCATGGG TCTGTGGT TG GAACTGGG
TGTTGGAT GGGTACCA AC CTTGACCC
C ---
GAM96 394 LOC3493 1 19187 XP_028319.4 5 82 ACGCCCCCAGTT A ACA 1 A c c
51 CCACACCATGGG TCTGTGGT TG GAACTGGG
TGTTGGAT GGGTACCA AC CTTGACCC
C ---
GAM96 394 LOC6392 1 7473 NP_071380.1 3 636 GCAGCCCGGTTC A ACA- 1 A c c
8 CTAACAGACCAC TCTGTGGT TG GAACTGGG
AGACCCCA AGACACCA AC CTTGGCCC
G AATC
GAM96 394 LOC9090 1 5553 XP_034809.1 5 1027 ACTCCTGAAGTT ----- AT -- 1 A c c
6 CTGTTCGACCAA TCTG TGGT GACAGAACT GGG
ACATCAGA AGAC ACCA TTGTCTTGA TCC
TACAA GC AG
GAM96 394 LOC9126 1 4369 XP_037268.1 5 1773 GTTTCCCCATTT G A- C 1 A c c
6 CTGTCAGAGCCA TCT TGGT TGACAGAA TGGG
AGGGCTTG GGG ACCG ACTGTCTT ACCC
A AG T
GAM96 394 LOC9223 1 18989 XP_043733.1 5 321 CCTTTGCCCATT -- A C 1 A c c
0 CTGTCAGGCTGG TCTGT GGT TGACAGAA TGGG
ACGGGAGG GGGCA TCG ACTGTCTT ACCC
GG G -
GAM96 394 MAP6 1 11998 XP_166256.1 3 2763 GGCCTGGGTTTT -- G 1 A c c
GTTGCATACCAC TCTGTGGTATG ACAGAACT GG
AGATTGTC AGACACCATAC TGTTTTGG TC
GT G
GAM96 394 MGA 1 2236 XP_031689.3 3 1373 GTAACCCCTGTT - AT- T 1 A c c
CTGTCTTCATTG TCTGT GGT GACAGAAC GGG
ACAGGATT GGACA TTA CTGTCTTG CCC
G CTT T
GAM96 394 MGC1023 1 12991 NP_689928.1 3 190 CCATTTTTGGGT T ------- C 1 A c c
3 GTTTTCTACCAC TCTGTGGTA GA CAGAA TGG
AGATTGAT AGACACCAT CT GTTTT ACC
- TTTGTGG T
GAM96 394 MGC1081 1 3998 NP_113613.1 3 748 AGGAGACCCCAA ATGA AC 1 A c c
2 ATTTGACACCAC TCTGTGGT CAGA TGGG
AGAAAGCA AGACACCA GTTT ACCC
CA-- AA
GAM96 394 MGC1312 1 5483 NP_116114.1 3 143 TTGTTGAATGCC ATGA 1 A b b

```
          5                          AGTTTTGACCAC TCTGTGGT   CAGAACTGG
                                     AGAAGAAT    AGACACCA   GTTTTGACC
                                           ----
GAM96   394   MGC2474 1  17757 NP_076420.1  5  42   CATCGTCCAGTT      ATGA          1  A  c  c
                                     CTGACCATGGAC TCTGTGGT   CAGAACTGGG
                                     TCGCAGCC    AGGTACCA   GTCTTGACCT
                                           ----
GAM96   394   MGC2673 1  18016 NP_659429.2  5  325  GGAGTATCAGTT      ATGA          1  A  c
c
          3                          CTGAGCCACAGA TCTGTGGT   CAGAACTGG
                                     TGAGGAAA    AGACACCG   GTCTTGACT
                                           A---
GAM96   394   MGC2749 1  680   NP_076974.1  3  121  TGCTGCCCCGTT   T  AT     T        1  A  c  c
                                     CTGTCACCCAGG TCTG GGT  GACAGAAC GGG
                                     GCTCCTAG    GGAC CCA  CTGTCTTG CCC
                                           -  --      C
GAM96   394   MGC3222 1  11500 NP_077310.1  3  1419  TGTGTACCTTTT   T        CT        1  A  c  c
                                     CTGTCATATTCA TCTG GGTATGACAGAA  GG
                                     GAAACCGT    AGAC TTATACTGTCTT  CC
                                           -          TT
GAM96   394   MGC3468 1  1068  NP_689559.1  3  709   GTCACCCTCGTT  T-    T     T-       1  A  c  c
          0                          CTGTCTGCCACC TC  GTGGTA GACAGAAC  GGG
                                     TGAAGGGA    AG  CACCGT CTGTCTTG  CCC
                                           TC    -      CT
GAM96   394   MGC3469 1  14230 NP_775826.1  3  727   GAGCCCCCAGTT   -  G  T--    --       1  A  c  c

          5                          CTCTGTCCCCTA TCT GTG TA   GACAGA  ACTGGG
                                     GCACTAGA    AGA CAC AT   CTGTCT  TGACCC
                                           T  G  CCC     CT
GAM96   394   MGC3520 1  4448  NP_848647.1  5  216   AAGAACCAGGGT T----     T-      A-       1  A  c  c

          6                          CTGTCATCCCCA     CTGTGG  ATGACAGA  CTGG
                                     CAGCCCCT         GACACC  TACTGTCT  GACC
                                           TCCCC     CC       GG
GAM96   394   MGC4253 1  12415 NP_775841.1  3  1104  TGCCAGTAAGGT  T      AC  -----        1  A  c
c
          0                          TCTACATACCAC TC GTGGTATG  AGA     ACTGG
                                     TGACCATC    AG CACCATAC  TCT     TGACC
                                           T       A-   TGGAA
GAM96   394   MGC4734 1  12722 NP_659488.1  3  265   GGGCAGAGAAGC      ATGA      G        1  A  c
c
                                     GGTTCTGACCAC TCTGTGGT   CAGAACTG
                                     AGAGCTCC    AGACACCA   GTCTTGGC
                                           ----       G
GAM96   394   MGC5508 1  15558 NP_076997.1  3  43    CACACACCGCCA   G       AGA          1  A  c
c
                                     GTGTCATACCAA TCT TGGTATGAC   ACTGG
                                     AGAGCTGA    AGA ACCATACTG   TGACC
                                           A        ---
GAM96   394   MLLT2  1  15646 NP_005926.1  3  3702  TTAAACCTGCTT       T  C  -  CT        1  A  c  c
```

GCTTCCTACCAC TCTGTGGTA GA AG AA GGG
AGATTCTT AGACACCAT CT TC TT TCC
C - G CG

GAM96 394 MLR2 1 18894 XP_050988.1 3 419 TAGAAACTACGT G AC 1 A c c
CTGTCATACTGG TCT TGGTATGACAGA TGG
GAGCTTTA AGG GTCATACTGTCT ATC
- GC

GAM96 394 MRPS12 1 9214 NP_066930.1 5 95 AGTTTCCCAGTT - T C 1 A c c
CTTCCTGCGTGC TCTGTG GTA GA AGAACTGGG
GGGCGAGA GGGCGT CGT CT TCTTGACCC
G C -

GAM96 394 MRPS12 1 9214 NP_203527.1 5 95 AGTTTCCCAGTT - T C 1 A c c
CTTCCTGCGTGC TCTGTG GTA GA AGAACTGGG
GGGCGAGA GGGCGT CGT CT TCTTGACCC
G C -

GAM96 394 MSC 1 2216 NP_005089.1 3 1001 CTTGCCCCGAGG - A AAC 1 A c c
CTGCACTACCAC TCTGTGGTA TG CAG TGGG
AGGAAATA GGACACCAT AC GTC GCCC
C - GGA

GAM96 394 NAT5 1 13542 NP_057184.1 3 332 TCCTCCTCAGTT GT ATG 1 A c c
CTGTGCCTGAGA TCT GGT ACAGAACTGGG
ACCACTGC AGA CCG TGTCTTGACTC
GT ---

GAM96 394 NAT5 1 13542 NP_852668.1 3 332 TCCTCCTCAGTT GT ATG 1 A c c
CTGTGCCTGAGA TCT GGT ACAGAACTGGG
ACCACTGC AGA CCG TGTCTTGACTC
GT ---

GAM96 394 NAT5 1 13542 NP_852669.1 3 387 TCCTCCTCAGTT GT ATG 1 A c c
CTGTGCCTGAGA TCT GGT ACAGAACTGGG
ACCACTGC AGA CCG TGTCTTGACTC
GT ---

GAM96 394 NOX1 1 13865 NP_008983.1 5 7 GATAGCACAGTT G TATG G 1 A c c
CTGTCCAGAGAA TCT TGG ACAGAACTG
GGAAGGCG AGA ACC TGTCTTGAC
G ---- A

GAM96 394 NTSR2 1 3637 NP_036476.1 5 63 TGTCTCCCAGTT G TAT ---- 1 A c c
CTAGAGGTTCCC TCT TGG GAC AGAACTGGG
AGAGAAGA AGA ACC TTG TCTTGACCC
G C-- GAGA

GAM96 394 OAS3 1 12448 NP_006178.1 3 2067 TCAGGGCCAGTT G ATGA 1 A c c

CTGGTGGGCAGC TCTGT GT CAGAACTGG
AGAGACCT AGACG CG GTCTTGACC
A GGTG

GAM96 394 P15RS 1 11233 NP_060640.2 3 3121 GTAAGCCCAGTT GTAT C 1 A c c

CTTCTCTGTATA TCTGTG GA AGAACTGGG
GAAAGGAA AGATAT CT TCTTGACCC
GTCT -

GAM96 394 P4HA1 1 3572 NP_000908.1 3 234 AACCTTAAAGTT - --- 1 A c c

CTGTTGGTATCA TCTGTGGTAT GACAGAACT GGG
CAGAAGAC AGACACTATG TTGTCTTGA TCC
G AAT

GAM96 394 PABPC1 1 18105 NP_002559.1 3 373 AGAATGTCAGTT GG-- T 1 A c c
CTGTTTTAAGTA TCTGT TA GACAGAACTGG
ACAGAATT AGACA AT TTGTCTTGACT
ATGA T

GAM96 394 PAICS 1 1992 NP_006443.1 3 1022 ACAATAAACTCT AT A CT 1 A c c
CTTTTGCACCAC TCTGTGGT G CAGAA GGG
AGACTTCT AGACACCA C GTTTT CTC
-- - CT

GAM96 394 PCBP4 1 2715 NP_065151.1 3 554 AGGGGCCCAGTT G A CA 1 A c c
CTCAGCAGCAGA TCTGT GT TGA GAACTGGG
CACTCTGT AGACG CG ACT CTTGACCC
A - --

GAM96 394 PCBP4 1 2715 NP_127501.1 3 554 AGGGGCCCAGTT G A CA 1 A c c
CTCAGCAGCAGA TCTGT GT TGA GAACTGGG
CACTCTGT AGACG CG ACT CTTGACCC
A - --

GAM96 394 PCBP4 1 2715 NP_127502.1 3 554 AGGGGCCCAGTT G A CA 1 A c c
CTCAGCAGCAGA TCTGT GT TGA GAACTGGG
CACTCTGT AGACG CG ACT CTTGACCC
A - --

GAM96 394 PCBP4 1 2715 NP_127503.1 3 554 AGGGGCCCAGTT G A CA 1 A c c
CTCAGCAGCAGA TCTGT GT TGA GAACTGGG
CACTCTGT AGACG CG ACT CTTGACCC
A - --

GAM96 394 PCDHA9 1 7481 NP_054724.1 3 788 AATTCACTTGTT - TA--- T 1 A c c
CTGTCAGTAATC TCT GTGG TGACAGAAC GG
CATAAGAC AGA TACC ACTGTCTTG TC
A TAATG T

GAM96 394 PDK2 1 7892 NP_002602.2 3 135 GATGACCAGGTT TAT - 1 A c c
CTGTCTCTATGG TCTGTGG GACAGAAC TGG
AAGTCACT AGGTATC CTGTCTTG ACC
T-- G

GAM96 394 PEG10 1 11113 NP_055883.1 3 4383 ATTGATCCAGTT -- GA 1 A b b
GTCATCCACCAC TCTGTGGT ATGACA ACTGGG
AGACATCT AGACACCA TACTGT TGACCT
CC --

GAM96 394 PFKFB4 1 10430 NP_004558.1 3 1187 GAAGTCCAGTGT TGT - 1 A c c
CTGTCATGCCCC TC GGTATGACAGA ACTGGG
TGAGTTCT AG CCGTACTGTCT TGACCT
TCC G

GAM96 394 PIGR 1 20111 NP_002635.2 3 1567 GCCGCACCATTT GTA- C 1 A c c
CTGTCACTCACA TCTGTG TGACAGAA TGG
TGGACCCA AGGTAC ACTGTCTT ACC
ACTC T

GAM96 394 PIP5K2B 1 18234 NP_003550.1 5 132 CCAGGCGGGTTT T A ------ 1 A c c
CTGTCAGGCCCG TCTG GGT TGACAGAA CTGG
GGGAGGAG GGGC CCG ACTGTCTT GACC

- G TGGGCG

GAM96 394 PIP5K2B 1 18234 NP_619632.1 5 132 CCAGGCGGGTTT T A ------ 1 A c c
CTGTCAGGCCCG TCTG GGT TGACAGAA CTGG
GGGAGGAG GGGC CCG ACTGTCTT GACC
- G TGGGCG

GAM96 394 PKNOX1 1 12842 NP_004562.2 3 366 TGTCACTTAGTT - T G 1 A c c
CTGTGGTTCCAG TCTG TGG AT ACAGAACTGGG
CAGATCTC AGAC ACC TG TGTCTTGATTC
G T G

GAM96 394 PLA2G4A 1 11581 NP_077734.1 3 404 ACTGACTAGATT - CA - 1 A c c
TATTCATACCAT TCT GTGGTATGA GAA CTGG
GAGACAAC AGA TACCATACT TTT GATC
G TA A

GAM96 394 PLAGL1 1 15766 NP_006709.2 5 740 CCCTGCCAAGTT ATGA - - 1 A c c
TCTGGGCACCAC TCTGTGGT CAGAA CT GG
AGATTGGA AGACACCA GTCTT GA CC
CGG- T A

GAM96 394 PLP1 1 7068 NP_000524.2 3 14 AGGCACCAAGTT TAT - 1 A c c
CTGTCCCCCGTA TCTGTGG GACAGAACT GG
GAAATCCC AGATGCC CTGTCTTGA CC
CC- A

GAM96 394 PMX1 1 2960 NP_008833.1 3 630 CTCTTCCCAGTT TATGAC 1 A c c
CTCTTTATAGAA TCTGTGG AGAACTGGG
GCTCTAGG AGATATT TCTTGACCC
TC----

GAM96 394 PMX1 1 2960 NP_073207.1 3 474 CTCTTCCCAGTT TATGAC 1 A c c
CTCTTTATAGAA TCTGTGG AGAACTGGG
GCTCTAGG AGATATT TCTTGACCC
TC----

GAM96 394 POLS 1 9961 NP_008930.1 3 835 AGGCCGTTGTCC AT - A -- 1 A c c
TGCTCTGACCAC TCTGTGGT GA CAG AC TGG
AGAGTTTT AGACACCA CT GTC TG GCC
GT C C TT

GAM96 394 PPP2R5D 1 19741 NP_006236.1 3 24 CTCTGCCCCTCA TGACA - 1 A c
c
CGTTCCTACCAC TCTGTGGTA GAAC TGGG
AGGGCCAC GGACACCAT CTTG ACTC
C---- C

GAM96 394 PPP2R5D 1 19741 NP_851307.1 3 24 CTCTGCCCCTCA TGACA - 1 A c
c
CGTTCCTACCAC TCTGTGGTA GAAC TGGG
AGGGCCAC GGACACCAT CTTG ACTC
C---- C

GAM96 394 PPP2R5D 1 19741 NP_851308.1 3 24 CTCTGCCCCTCA TGACA - 1 A c
c
CGTTCCTACCAC TCTGTGGTA GAAC TGGG
AGGGCCAC GGACACCAT CTTG ACTC
C---- C

GAM96 394 PROK1 1 18144 NP_115790.1 3 525 GTTAACTCCTTA A CAG 1 A c c
GTTTCAGACCAC TCTGTGGT TGA AACTGGG

AGACTCAA AGACACCA ACT TTGATTC
G ---
GAM96 394 PXF 1 4076 NP_002848.1 3 134 GCCCGCTGCCCT --- T ACT 1 A c c
CTGTCATCCCAT TCT GTGG ATGACAGA GGG
TCAAGATT AGA TACC TACTGTCT CCC
ACT C ---
GAM96 394 PXMP3 1 12286 NP_000309.1 5 297 CAAAAATTCCCA - AAC 1 A c c
CTGTCATAGCTA TCTGTGGT ATGACAG TGGG
TAGGCTGT GGATATCG TACTGTC ACCC
A ---
GAM96 394 RAB22A 1 10718 NP_065724.1 3 159 AATGGACCAGTT G TAT 1 A c c
CTGTTCTCCAAA TCT TGG GACAGAACTGG
GACTGCAG AGA ACC TTGTCTTGACC
A TC-
GAM96 394 RAP1GA1 1 17705 NP_002876.1 3 734 GACCCTCCAGTT TATGA 1 A c
c
CTGCCACAGGTC TCTGTGG CAGAACTGGG
TGCCGATG GGACACC GTCTTGACCT

GAM96 394 RASSF5 1 1440 NP_113625.1 3 158 CGCCCCCAGGCT ATG-- AA 1 A c
c
GTGCCCCACCAC TCTGTGGT ACAG CTGGG
AGATTCTG AGACACCA TGTC GACCC
CCCCG G-
GAM96 394 RDH-E2 1 18476 NP_620419.1 3 502 CATTTTTGTCAT ------- C G 1 A c c
TTCCATTACCAC TCTGTGGTA TGACAGAA TG
AGATGTAA AGACACCAT ACTGTTTT AC
TACCTTT T -
GAM96 394 REN 1 4098 XP_085689.1 5 624 GGAAACCCACTG AT--- AAC 1 A c c
TCTGAAGACCAC TCTGTGGT GACAG TGGG
AGAGGGGT AGACACCA CTGTC ACCC
GAAGT ---
GAM96 394 RP42 1 2138 NP_065691.1 3 2714 TTCTTACAGTCC - --- A- G 1 A c c
CTGTCATATTAC TCTGT GGTA TGACAG ACTG
CAACAGAG AGACA CCAT ACTGTC TGAC
A TAT CC A
GAM96 394 SCN5A 1 18915 NP_000326.2 3 1217 TCAGGCCCAGTT T- CA 1 A c c
CTCGTGCCCTTA TCTG GGTATGA GAACTGGG
GAGGGGAA AGAT CCGTGCT CTTGACCC
TC --
GAM96 394 SEC61B 1 9649 NP_006799.1 3 35 AGTTACATCCAT G T AC 1 A c c
CTGTCATCTGAA TCT TGG ATGACAGA TGGG
GAAGGAGG AGA GTC TACTGTCT ACCT
A - --
GAM96 394 SH3BP2 1 1516 NP_003014.2 3 699 CACTCACCAGTT T TGA 1 A c c
CTGCTGCCTCAG TCTG GGTA CAGAACTGG
GTCAGGCC GGAC CCGT GTCTTGACC
T C--
GAM96 394 SLC4A4 1 12800 NP_003750.1 3 403 GATAACCAAATT GTA---- C- 1 A c c
CTGTCACTCAAG TCTGTG TGACAGAA TGG

ACACAGAC AGACAC ACTGTCTT ACC
AGAACTC AA
GAM96 394 SLC5A6 1 10988 NP_066918.1 3 464 TCAGTACCAGTT T------ A A 1 A c c
CTGCCAGCCACA CTGTGGT TG CAGAACTGG
GTGAGCCC GACACCG AC GTCTTGACC
CCCGAGT - C
GAM96 394 SLC5A8 1 7461 NP_666018.1 5 29 GAGGCTCCAGTT T T C- 1 A c c
CTCATCTGCTCA TCTG GGTA GA AGAACTGGG
GGTGTCCC GGAC TCGT CT TCTTGACCT
- - AC
GAM96 394 SP3 1 18315 XP_092672.2 5 849 CTAACATCCAGA CAGAA 1 A c c
ATCTCATACCAC TCTGTGGTATGA CTGGG
AGACTGGT AGACACCATACT GACCT
CTAA-
GAM96 394 SPRY3 1 11554 NP_005831.1 3 2419 CTCTGCCCAGTT GT A ---- 1 A c c
CTCTGGGTCAAG TCT GGT TGAC AGAACTGGG
CTGGATGG AGG TCG ACTG TCTTGACCC
-- A GGTC
GAM96 394 SRP 1 1261 NP_149976.1 3 496 AGGCCCACAGGT T A - 1 A c c
CTGTCATCCCAT TCTGTGG ATGACAGA CTG GG
AGGCCACC GGATACC TACTGTCT GAC CC
C G A
GAM96 394 STK23 1 7482 NP_055185.1 3 99 TGGGCGCCAGTT A AC- 1 A c c
CTCCACAACCAC TCTGTGGT TG AGAACTGG
AGGGCAGA GGACACCA AC TCTTGACC
- ACC
GAM96 394 T54 1 8102 NP_056513.2 3 56 CTGGTACCAGTT - ATG 1 A b b
CTGTACCATATG TC TGTGGT ACAGAACTGG
AGAAAGTT AG ATACCA TGTCTTGACC
T ---
GAM96 394 TBX4 1 3489 NP_060958.2 3 771 CCAGTAGCATCT TGGT ------ 1 A c c
CTGTCATCATTC TCTG ATGACAGA ACTGG
AGATTTTG AGAC TACTGTCT TGACC
TTAC CTACGA
GAM96 394 TCFL5 1 19813 NP_006593.1 3 636 TTAAATGCCACG G CA - 1 A c c
TTTTCATACCAA TCT TGGTATGA GAAC TGG
GAGTCATT AGA ACCATACT TTTG ACC
- -- C
GAM96 394 TIM50L 1 12301 XP_053074.2 3 325 AAAAATACATCT ATGA ACT 1 A c c
CCCTCTGACCAC TCTGTGGT CAGA GGG
AGACTCCT AGACACCA GTCT CCC
---- ---
GAM96 394 TNFSF9 1 19645 NP_003802.1 3 639 GATGGTCTTGTT --- A T 1 A c c
CTGTCAACCAGG TCTG TGGT TGACAGAAC GGG
CTAGAATG AGAT ACCA ACTGTCTTG TCT
CGG - T
GAM96 394 TPM3 1 8850 NP_689476.1 5 35 CAGTCTCCAGTT TA-- AC 1 A c c
CTCCAGTGTTCA TCTGTGG TG AGAACTGGG
CAGGTGAG GGACACT AC TCTTGACCT

TGTG C-

GAM96 394 TRIM31 1 1342 NP_008959.2 5 96 AGCCCTGTTGTT - - T--- 1 A c c
CTGTCATGGCCA TCTG TGGT ATGACAGAAC GGG
GTGGGCAG GGGT ACCG TACTGTCTTG CCC
G G TTGT

GAM96 394 TRIM31 1 1342 NP_438111.1 5 96 AGCCCTGTTGTT - - T--- 1 A c c
CTGTCATGGCCA TCTG TGGT ATGACAGAAC GGG
GTGGGCAG GGGT ACCG TACTGTCTTG CCC
G G TTGT

GAM96 394 UBAP2 1 11910 NP_680476.1 3 1006 ATGACCAGAGTT GG - G- 1 A c c
CTGTGCATAACA TCTGT TATG ACAGAACT GG
GGATCCCA GGACA ATAC TGTCTTGA CC
-- G GA

GAM96 394 UTX 1 7037 NP_066963.1 3 74 AATAACCCAGTT T AT A 1 A c c
CTGCACCACTGG TC GTGGT G CAGAACTGGG
TTTTTGTA GG CACCA C GTCTTGACCC
T -- -

GAM96 394 VANGL2 1 10530 XP_049695.4 3 1090 TTAAGTCCAGTT T TGAC 1 A c c
CTTTGCCTCAGG TCTG GGTA AGAACTGGG
GGTCTCGT GGAC CCGT TCTTGACCT
T T---

GAM96 394 VAV3 1 17719 NP_006104.3 3 243 CAGCCTGCCAGT G GT - A 1 A c c
CTGTCATTGTCA TCT TG A TGACAGA CTGG
GGGACCAG AGG AC T ACTGTCT GACC
G TG T -

GAM96 394 WBSCR21 1 19321 NP_112585.2 3 498 AACAGCTCAGTT G T 1 A b b
CTGTCATCCAGG TCT TGG ATGACAGAACTGGG
ACATGGCC AGG ACC TACTGTCTTGACTC
- -

GAM96 394 WBSCR21 1 19321 NP_683713.1 3 328 AACAGCTCAGTT G T 1 A b b
CTGTCATCCAGG TCT TGG ATGACAGAACTGGG
ACATGGCC AGG ACC TACTGTCTTGACTC
- -

GAM96 394 ZFP276 1 1176 NP_689500.1 5 176 CCACGCCCAGTT T---- GAC- 1 A c c
CTACCAGTGCCA CTGTGGTAT AGAACTGGG
CAGCCTTC GACACCGTG TCTTGACCC
CTTCC ACCA

GAM96 394 ZFYVE26 1 13984 XP_031077.1 3 251 AGATGGCCAGTT T T C 1 A c c
CTTTCTACCTCA TCTG GGTA GA AGAACTGG
GAGTGAGT AGAC CCAT CT TCTTGACC
T - T

GAM96 394 ZNF297B 1 12416 NP_054726.1 3 1196 ATACTACCAGTT - G- C 1 A c c
CTTTATGAGCAC TCT GTG TATGA AGAACTGG
TGGAATGT AGG CAC GTATT TCTTGACC
T GA -

GAM97 274 ALTE 1 13580 NM_004729.1 3 ACCAACATGGTG G - CAG 3 C c c
AAACCTCGT ATG GGTTTCACCATGTTGGT
TGC CCAAAGTGGTACAACCA
- T ---

GAM97 274 C21orf5 1 16569 NM_005128.1 3 CTGACCAACATG GAT 3 C c c
GTGAGACCC GGGTTTCACCATGTTGGTCAG
CCCAGAGTGGTACAACCAGTC

GAM97 274 CCR6 1 12282 NM_031409.1 3 CTGGCCAACATG T A 3 C b b
GCGAAACCCCTC GA GGGTTTC CCATGTTGGTCAG
CT CCCAAAG GGTACAACCGGTC
C C
GAM97 274 DKFZP43 1 10163 3 CTGGGCAACACA CACCA G 3 C c c
4N161 GCAAGACCCATC GATGGGTTT TGTTG TCAG
CTACCCAGA ACAAC GGTC
ACGAC G
GAM97 274 F2R 1 8374 NM_001992.2 3 CTAACACGGTGA A TCAG 3 C c c
AACCCGTC GATGGGTTTCACC TGTTGG
CTGCCCAAAGTGG ACAATC
C ----
GAM97 274 FLJ1054 1 9138 NM_018134.1 3 GCTGACCAACAT G ------ - 3 C c c
7 GGTGAAATGAAA ATGGG TTTCACCATGTTGGTCAG
CCCCAT TACCC AAAGTGGTACAACCAGTC
- CAAAGT G

GAM97 274 FLJ1199 1 4576 NM_024976.1 3 CTGACCAACATG GATGG 3 C c c
6 GTGAAAT GTTTCACCATGTTGGTCAG
TAAAGTGGTACAACCAGTC

GAM97 274 FLJ1229 1 11796 NM_025100.1 3 CTGGCCAACATG GAT 3 C c c
4 GTGAAACCC GGGTTTCACCATGTTGGTCAG
CCCAAAGTGGTACAACCGGTC

GAM97 274 FLJ1365 1 10768 3 CTGACCAACATG GAT 3 C c c
9 GTGAAATCC GGGTTTCACCATGTTGGTCAG
CCTAAAGTGGTACAACCAGTC

GAM97 274 FLJ1384 1 14972 NM_024771.1 3 CTGGTCAACATG CA- GT 3 C c c
8 GCAAAAGCCCAT GATGGGTTT CCATGTTG CAG
C CTACCCGAA GGTACAAC GTC
AAC TG
GAM97 274 FLJ1412 1 13220 NM_030895.1 3 CTGGCCAACATG GAT CA 3 C c c
9 GCAAAACCC GGGTTT CCATGTTGGTCAG
CCCAAA GGTACAACCGGTC
--- AC
GAM97 274 FLJ1432 1 6959 3 CCAACAGGTGAA - A TCAG 3 C c c
6 ACCCCATC GATGGG TTTCACC TGTTGG
CTACCC AAAGTGG ACAACC
C - ----
GAM97 274 FLJ2000 1 4766 3 CTGGCCAACATG 3 C b b
4 GTGAAACCCATC GATGGGTTTCACCATGTTGGTCAG

CTACCCAAAGTGGTACAACCGGTC

GAM97 2745 FLJ2004 1 665 NM_017638.1 3 CCAAATGGTGAA - G TCAG 3 C c c
ACCCCATC GATGGG TTTCACCAT TTGG
CTACCC AAAGTGGTA AACC
C - ----

GAM97 2747 FLJ2216 1 11162 NM_024533.2 3 CTGGCCAACATA GAT C 3 C c c
GTGAAACCC GGGTTTCAC ATGTTGGTCAG
CCCAAAGTG TACAACCGGTC
--- A

GAM97 2749 FLJ2349 1 7763 NM_022761.1 3 CTGACCAACATG G - 3 C b b
GTGAAACACTGT ATGG GTTTCACCATGTTGGTCAG
TGTC CAAAGTGGTACAACCAGTC
- A

GAM97 2745 FLJ3145 1 12283 NM_144964.1 3 CTGGCCAACATG T 3 C b b
GTGAAACCCTTC GA GGGTTTCACCATGTTGGTCAG
CT CCCAAAGTGGTACAACCGGTC
T

GAM97 274 FRSB 1 17514 NM_005687.2 3 CTGACCAACATG G - C 3 C c c
ATGAAATGCCAT ATGG GTTTCA CATGTTGGTCAG
TACC TAAAGT GTACAACCAGTC
- G A

GAM97 274 FUSIP1 1 10769 NM_006625.3 3 CTGACCAACACG GAT A 3 C c c
GTGAAACCC GGGTTTCACC TGTTGGTCAG
CCCAAAGTGG ACAACCAGTC
--- C

GAM97 274 FUT6 1 6754 NM_000150.1 3 CCAATATGGTGA TCAG 3 C c c
AACCCGTC GATGGGTTTCACCATGTTGG
CTGCCCAAAGTGGTATAACC

GAM97 274 HIP1 1 3689 NM_005338.3 3 CTGTCCAACATG GAT T 3 C c c
GTGAAACCC GGGTTTCACCATGTTGG CAG
CCCAAAGTGGTACAACC GTC
--- T

GAM97 274 IL18 1 13191 NM_001562.2 3 CTGACCAACATG G - 3 C b b
GTGAAACCTCAT ATG GGTTTCACCATGTTGGTCAG
TAC CCAAAGTGGTACAACCAGTC
- T

GAM97 2741 KIAA044 1 11797 NM_014797.1 3 CTGACCAACATA GAT C 3 C c c
GTGAAACCC GGGTTTCAC ATGTTGGTCAG
CCCAAAGTG TACAACCAGTC
--- A

GAM97 2748 KIAA079 1 13756 3 CTGACCAACATG GAT 3 C c c
GTGAGGCCC GGGTTTCACCATGTTGGTCAG
CCCGGAGTGGTACAACCAGTC

GAM97 2742 KIAA087 1 13072 NM_014940.1 3 CTGACCAACATG G - 3 C b b
GTGAAACACCAT ATGG GTTTCACCATGTTGGTCAG
TACC CAAAGTGGTACAACCAGTC
- A

GAM97 274 KIAA145 1 14943 XM_040100.4 5 CTGACCAACATG A 3 C b b
6 GAGAAACCCATC GATGGGTTTC CCATGTTGGTCAG
CTACCCAAAG GGTACAACCAGTC
A
GAM97 274 KIAA161 1 628 XM_046531.1 5 CCACATGGTGAA G T TCAG 3 C c c
4 ACCCAT ATGGGTTTCACCATGT GG
TACCCAAAGTGGTACA CC
- - ----
GAM97 274 KREMEN 1 2640 3 CCAACATGGCGA - A TCAG 3 C c c
AAACCCATC GATGGGTTT C CCATGTTGG
CTACCCAAA G GGTACAACC
A C ----
GAM97 274 LOC1272 1 17509 XM_072073.6 3 CTGGGCAACATG G 3 C b b
62 GTGAAACCCGTC GATGGGTTTCACCATGTTG TCAG
CTGCCCAAAGTGGTACAAC GGTC
G
GAM97 274 LOC1452 1 7110 XM_096730.1 3 CTGACCAACATG GAT CAC 3 C c c
16 ACAAAACCC GGGTTT CATGTTGGTCAG
CCCAAA GTACAACCAGTC
--- ACA
GAM97 274 LOC1452 1 17584 XM_096740.1 3 CTGACCAACATG GATG 3 C c c
31 GTGAAACT GGTTTCACCATGTTGGTCAG
TCAAAGTGGTACAACCAGTC

GAM97 274 LOC1467 1 6711 XM_097085.5 3 CTGACCAACATG G T 3 C b b
56 GTGAAACCTCA A GGGTTTCACCATGTTGGTCAG
A TCCAAAGTGGTACAACCAGTC
- C
GAM97 274 LOC1489 1 13319 3 GGCCAACATGGT AG 3 C b b
46 GAAACCCGTC GATGGGTTTCACCATGTTGGTC
CTGCCCAAAGTGGTACAACCGG
--
GAM97 274 LOC1501 1 13995 3 CTGACCAACATG GAT TC 3 C c c
85 GTAGAACCC GGGTT ACCATGTTGGTCAG
CCCAA TGGTACAACCAGTC
--- GA
GAM97 274 LOC1972 1 9296 XM_113839.4 3 CTGGGCAACATG - A G 3 C c c
01 GCGAAAACCCAT GATGGGTTT C CCATGTTG TCAG
C CTACCCAAA G GGTACAAC GGTC
A C G
GAM97 274 LOC2002 1 18779 5 CTGACCAACACG GAT CCA 3 C c c
51 ATGAAACCC GGGTTTCA TGTTGGTCAG
CCCAAAGT ACAACCAGTC
--- AGC
GAM97 274 LOC2197 1 19631 XM_167593.1 5 CTGACCAACATG GAT 3 C c c
22 GTGAAACTC GGGTTTCACCATGTTGGTCAG
CTCAAAGTGGTACAACCAGTC

GAM97 274 LOC2216 1 4944 5 CTGACCAACATG G - 3 C b b

```
          41                          GTGAAACGCTAT  ATGG GTTTCACCATGTTGGTCAG
                                            TATC CAAAGTGGTACAACCAGTC
                                      -   G
GAM97   274   LOC2219 1   15826 XM_168349.1  5       CTGGCCAACATG                    3  C  b  b
          54                          GTGAAACCCGTC GATGGGTTTCACCATGTTGGTCAG
                                            CTGCCCAAAGTGGTACAACCGGTC

GAM97   274   LOC2545 1   12649 NM_153613.1  5       CTGACCAACATG GAT     CA            3  C  c  c
          31                          GCAAAACCC      GGGTTT  CCATGTTGGTCAG
                                            CCCAAA  GGTACAACCAGTC
                                      ---     AC
GAM97   274   LOC2551 2   10392          3       GGCCAACATGGT GAT             AG      3  C  c  c
          96                          GAAACCC        GGGTTTCACCATGTTGGTC
                                            CCCAAAGTGGTACAACCGG
                                      ---             --
GAM97   274   LOC2551 2   19720          3       CTGGGGAACATA         CC    GG        3  C  c  c
          96                          ATGAGACCCATC GATGGGTTTCA  ATGTT  TCAG
                                            CTACCCAGAGT  TACAA  GGTC
                                                  AA    GG
GAM97   274   LOC2559 1   4791           3       CTGACCAACATG G   -                3  C  b  b
          37                          GTGAAACTCCAT  ATGG GTTTCACCATGTTGGTCAG
                                            TACC CAAAGTGGTACAACCAGTC
                                      -   T
GAM97   274   LOC2575 1   10645          3       CCAACATGGCAA       CA-       TCAG     3  C  c  c
          76                          AAACCCATC   GATGGGTTT   CCATGTTGG
                                            CTACCCAAA   GGTACAACC
                                                AAC       ----
GAM97   274   LOC5711 1   11157          5       CTGACCAACATG GAT                   3  C  b  b
          8                           GTGAAACCC      GGGTTTCACCATGTTGGTCAG
                                            CCCAAAGTGGTACAACCAGTC
                                      ---
GAM97   274   MASP1   1   692    NM_001879.3  3       CTGACCACTTAT        CACCAT  T         3  C  c  c
                                    CAAACCCATC   GATGGGTTT     GT GGTCAG
                                            CTACCCAAA      CA CCAGTC
                                                CTATT-  -
GAM97   274   MGC1076 1   10417  NM_024345.1  3       CTGACCAACATG G   -                3  C  b  b
          5                           GTGAAACGCCAT  ATGG GTTTCACCATGTTGGTCAG
                                            TACC CAAAGTGGTACAACCAGTC
                                      -   G
GAM97   274   MGC1479 1   15396  NM_032336.1  3       GACCAACATGGT GAT             AG      3  C  c
c
          9                           GAAACCC        GGGTTTCACCATGTTGGTC
                                            CCCAAAGTGGTACAACCAG
                                      ---             --
GAM97   274   SLC14A2 1   5703   NM_007163.2  3       CTGGCGAACATG             G         3  C  b  b
                                    GTGAGACCCATC GATGGGTTTCACCATGTT GTCAG
                                            CTACCCAGAGTGGTACAA CGGTC
                                                  G
GAM97   274   TCTA    1   681    NM_022171.1  3       CTGACCAACATG GAT     -            3  C  c  c
                                    GTGAAAACCC     GGGTTT CACCATGTTGGTCAG
```

CCCAAA GTGGTACAACCAGTC
--- A
GAM97 274 ZNF33A 1 11954 NM_006974.1 3 CTGGTCAACATG GAT GT 3 C c c
GTGAAACCC GGGTTTCACCATGTTG CAG
CCCAAAGTGGTACAAC GTC
--- TG
GAM97 274 ZNF347 1 4168 NM_032584.1 3 CTGACCAACATG GAT A 3 C c c
GCGAAACCC GGGTTTC CCATGTTGGTCAG
CCCAAAG GGTACAACCAGTC
--- C
GAM98 344 GAS7 1 8289 NM_005890.1 3 CCTACAAGGCCC T GGAA 3 C c c
ATCGCCACCA TGGTG CGATGGGCC GTAGG
ACCAC GCTACCCGG CATCC
C AA--
GAM98 344 LOC2546 1 19570 5 CCACTCCCGGCC GAT A A 3 C c c
85 TGACACCA TGGTGTC GGGCCGG AGT GG
ACCACAG TCCGGCC TCA CC
--- C -
GAM98 344 LOC9659 1 7069 XM_039922.2 3 CCCACTGGGACC AT - GGA A 3 C c
c
7 CCGACACCA TGGTGTCG GGG CC AGT GG
ACCACAGC CCC GG TCA CC
-- A G-- C
GAM98 344 SLC7A5 1 6778 NM_003486.2 3 CCACTCCCGGCC T GA A A 3 C c c
TAGGCACC GGTGTC TGGGCCGG AGT GG
CCACGG ATCCGGCC TCA CC
- -- C -
GAM99 320 ACTC 1 17458 NP_005150.1 3 20 AATGCTTCTAGA T CCAA 4 A c c
TGCCTTCTCTCT TGGAGAGA AAG GTATC
CCATCTAC ACCTCTCT TTC CGTAG
C ----
GAM99 320 AD-020 1 9059 NP_064526.1 3 1701 CTCAGAGTTGTG -- AGTA 4 A c c
GCTGTTATCTCT TGGAGAGATA AGCCA TC
TCAGGAAT ACTTCTCTAT TCGGT AG
TG GTTG
GAM99 320 AKAP2 1 17496 NP_009134.1 3 3395 ACTGACATGACT - T ATC 4 A c c
TGGCTTTCTCAT TGGA GAGA AAGCCAAGT
CCAGAAAT ACCT CTCT TTCGGTTCA
A - GTA
GAM99 320 ASPA 1 13895 NP_000040.1 3 261 ATACATGATACT GA A AG 4 A c c
TGGGTAGCTCAA TG GAG TA CCAAGTATC
CATTCTTA AC CTC AT GGTTCATAG
AA G G-
GAM99 320 B7 1 11263 NP_008923.1 5 67 AGGAGGAGGACT -- CA A- 4 A c c
GAGCTTATCTGA TGGAG AGATAAGC AGT TCC
CTCCAGAG ACCTC TCTATTCG TCA AGG
AG AG GG
GAM99 320 BASE 1 13840 NP_776258.1 3 545 GGGGAGGATACT G - G 4 A c c
TGGGTTGATTTA TGGA AGAT AA CCAAGTATCC
TCCATTAT ACCT TTTA TT GGTTCATAGG

A G G

GAM99 320 BZW2 1 2127 NP_054757.1 3 97 AGAAGAGAAACT - AT- A 4 A c c
TGGCTTCTGTTT TG GAGAG AAGCCAAGT TC
TCGCAAAG AC CTTTT TTCGGTTCA AG
G GTC A

GAM99 320 C14orf1 1 8362 NP_071940.2 5 100 TGTGTGGATACT - - AAGC 4 A c c
35 TGTTCAATACTG TGGAG AG AT CAAGTATCC
CTCCAAAA ACCTC TC TA GTTCATAGG
G A ACTT

GAM99 320 C15orf5 1 5753 NP_112206.1 3 174 AACAGGAAATAT G GTA- 4 A c c
TGGCTTATCTCT TG AGAGATAAGCCAA TCC
GTAGGAAG AT TCTCTATTCGGTT AGG
G ATAA

GAM99 320 C1orf24 1 19182 NP_443198.1 3 2089 AAATTAGGTTTA CC T- 4 A c c
CTTCTTGTCTCT TGGAGAGATAAG AAGTA CC
CCAAGTGG ACCTCTCTGTTC TTCAT GG
-- TT

GAM99 320 C1QR1 1 4397 NP_036204.1 3 801 TTCACAGATACT - A GC 4 A c c
TGAATTAATTCA TGGA GAG TAA CAAGTATC
TCCAAATG ACCT CTT ATT GTTCATAG
A A AA

GAM99 320 C20orf1 2 1178 NP_036393.1 3 286 CTCATGGTGGCT AT- AT 4 A c c
03 TGGCTTTGACTC TGGAGAG AAGCCAAGT CC
TCCAAAGA ACCTCTC TTCGGTTCG GG
AGT GT

GAM99 320 C20orf1 2 3291 NP_036393.1 3 153 CTGAGGCTTGCT GAG T- 4 A c c
03 TGGCTTGTGTCC TGGA ATAAGCCAAGTA CC
ATGCTTAA ACCT TGTTCGGTTCGT GG
G-- TC

GAM99 320 C20orf4 1 18788 NP_057129.1 3 0 GGGTACTCCAGG AAGCCA 4 A c c

5 TCTCTCCAAACT TGGAGAGAT AGTATCC
GCTATATA ACCTCTCTG TCATGGG
GACC--

GAM99 320 C20orf5 1 481 NP_113612.1 5 105 CCGGATCTCTGG A--- - T 4 A c c
5 CTCCTCATCTCT TGGAGAGAT AGCCA AG ATCC
CCGGTCTC GCCTCTCTA TCGGT TC TAGG
CTCC C -

GAM99 320 C21orf6 1 531 NP_478068.1 3 53 CTGGGGGTTGGG - AAGT 4 A c c
7 GGCTGTGTCTCT TGGAGAGATA AGCC ATCC
CCATCCCT ACCTCTCTGT TCGG TGGG
G GGGT

GAM99 320 CAB2 1 17481 NP_219487.2 3 1168 AAATGGGGATGG TAA A- - 4 A c c
CTGGGGCTCTCT TGGAGAGA GCC AGT ATCC
CCATCCTC ACCTCTCT CGG TCG TAGG
--- GG G

GAM99 320 CCBL1 1 8720 NP_004050.1 3 282 GGTCTTGTGTTG --- ---- T 4 A c c
CTTCTGGTCTCT TGGAGAGAT AAGC CAAG ATC
CCAGGCTT ACCTCTCTG TTCG GTTC TGG
GTC TTGT -

GAM99 320 CDC14B 1 12278 NP_003662.1 3 494 TTTGATACTATT - - --- 4 A c c
TGGCTTAATCAT TGGAGA GAT AAGCCA AGTATC
CTTCACTT ACTTCT CTA TTCGGT TCATAG
A A TTA
GAM99 320 CDC14B 1 12278 NP_201588.1 3 494 TTTGATACTATT - - --- 4 A c c
TGGCTTAATCAT TGGAGA GAT AAGCCA AGTATC
CTTCACTT ACTTCT CTA TTCGGT TCATAG
A A TTA
GAM99 320 CHKL 1 15506 NP_689466.1 3 3695 TGCTCTCGGAAC AA A- A 4 A c c
CCTGGCGTCTCT TGGAGAGAT GCCA GT TCC
CCACCAGC ACCTCTCTG CGGT CA AGG
-- CC -
GAM99 320 CPNE6 1 15300 NP_006023.1 3 148 GTGGTGGGTCCT -- CA T 4 A c c
GCTCCTATCTCT TGGAGAGATA AGC AG ATCC
CCAAACCC ACCTCTCTAT TCG TC TGGG
CC -- C
GAM99 320 CPT1B 1 15506 NP_689453.1 3 309 TGCTCTCGGAAC AA A- A 4 A c c
CCTGGCGTCTCT TGGAGAGAT GCCA GT TCC
CCACCAGC ACCTCTCTG CGGT CA AGG
-- CC -
GAM99 320 CTSK 1 5778 NP_000387.1 3 186 TGATCCTTCCTA TA C TC 4 A c c
CTTTGCTTCTCT TGGAGAGA AGC AAGTA
CCACCCAT ACCTCTCT TCG TTCAT
-- T CC
GAM99 320 CX3CR1 1 15434 NP_001328.1 3 837 AACTCAAATGCT ----- TA C 4 A c c
TGGCTTCTCATA TGGA GAGA AGCCAAGTAT
CGTCCACC ACCT CTCT TCGGTTCGTA
GCATA -- A
GAM99 320 CXCL9 1 5355 NP_002407.1 3 962 TTCTTGGGTGTT AGCC 4 A c c
TATCCTATCTCT TGGAGAGATA AAGTATCC
CCAACCAG ACCTCTCTAT TTTGTGGG
CCTA
GAM99 320 CYP20A1 1 6915 NP_065725.2 3 443 GATCCTAATACT GATAA C 4 A c
c
TGGCCATCTCCA TGGAGA GCCAAGTAT
CACAAGTT ACCTCT CGGTTCATA
AC--- A
GAM99 320 DARP 1 10261 NP_659431.3 3 413 GTTAGGGGGCTT - C AT 4 A c c
GCCTTGCTCTCT TGGAGAGA TAAG CAAGT CC
CCAGGGCC ACCTCTCT GTTC GTTCG GG
C C GG
GAM99 320 DCTN1 1 11619 NP_004073.2 5 29 GGCTAGGGTACT - A 4 A c c
TGGCTTGCTTTG TGG AGAG TAAGCCAAGTATCC
CTATGTGT ATC TTTC GTTCGGTTCATGGG
G -
GAM99 320 DIO1 2 1704 NP_000783.2 3 380 ACTTCTGAGGTA TAA AA 4 A c c
CGGTATCTCTCT TGGAGAGA GCC GTATC
CCAGCCAC ACCTCTCT TGG CATGG
CTA --
GAM99 320 DIO1 2 6987 NP_000783.2 3 379 ACACTTCTGAGG TAA AA 4 A c c

TACGGTATCTCT TGGAGAGA GCC GTATC
CTCCAGCC ACCTCTCT TGG CATGG
CTA --

GAM99 320 DKFZp31 1 13887 XP_113743.3 3 1123 GTCTGCAGGAAT G GTA 4 A c c

3M0720 TGGCTTATTTCT TG AGAGATAAGCCAA TCC
GTATGCCA AT TCTTTATTCGGTT AGG
G A--

GAM99 320 DKFZp43 1 20081 NP_663736.1 3 221 ATTGCTGATACT -- AAGC 4 A c c

4A2417 TGAATAATCAAT TGGAGA GAT CAAGTATC
CTCTACTA ATCTCT CTA GTTCATAG
AA ATAA

GAM99 320 FAT2 1 1177 NP_001438.1 3 64 AAGGACTGGACT T----- A--- 4 A c c
TGGCTTATTTCT GGAGAGATAAGCCAAGT TCC
TCCTGTCT CTTCTTTATTCGGTTCA AGG
TCTGTC GGTC

GAM99 320 FBXL5 1 15662 NP_036293.1 3 622 TTTAGGGATACT A TAA C 4 A c c
TTGTTCTCACCA TGG GAGA GC AAGTATCC
CTGTCCCT ACC CTCT TG TTCATAGG
A --- T

GAM99 320 FBXL5 1 15662 NP_277077.1 3 622 TTTAGGGATACT A TAA C 4 A c c
TTGTTCTCACCA TGG GAGA GC AAGTATCC
CTGTCCCT ACC CTCT TG TTCATAGG
A --- T

GAM99 320 FLJ1020 1 16040 NP_060494.1 3 349 CTGTTTTGGATG AGCC 4 A c c
4 TTTTGTGTCTCT TGGAGAGATA AAGTATCC
CCAGCTAC ACCTCTCTGT TTTGTAGG
GT--

GAM99 320 FLJ1033 1 8822 NP_060531.1 3 1194 TATCCTGGGTCT AGA T T 4 A c c
0 TGGCTTTTCCCC TGG GA AAGCCAAG ATCC
CATTTGTT ACC CT TTCGGTTC TGGG
CC- T -

GAM99 320 FLJ1076 1 14541 NP_060680.1 3 581 GCTGCTGGTGTT A----- 4 A c c
9 TGGCTTATTGAC TGGAG GATAAGCCAAGTATC
ATACTCCA ACCTC TTATTCGGTTTGTGG
ATACAG

GAM99 320 FLJ1126 1 19814 NP_060842.2 3 452 TGTATATGTACT C C 4 A c c
9 TGCTTTATCTCT TGGAGAGATAAG CAAGTAT
TTACCCTT ATTTCTCTATTT GTTCATG
C T

GAM99 320 FLJ1296 1 4577 NP_078914.1 3 497 CTTCTGGATACT G GCC 4 A c c
0 TTTGTCTTCCAC TGGA AGATAA AAGTATCC
CCTGCCCT ACCT TCTGTT TTCATAGG
- ---

GAM99 320 FLJ1339 1 4021 NP_079224.1 3 283 CATTCAGATACT A A --- 4 A c c
7 TGGTCATTTACT TGG GAG TAA GCCAAGTATC
TACCAAAT ACC TTC ATT TGGTTCATAG
A - TAC

GAM99 320 FLJ1472 2 14815 NP_116218.1 3 1066 CTGGAAGCGGTA TAAGCCA 4 A c c

```
          1                    CTGTATCTCTCT TGGAGAGA      AGTATC
                               CCAAGGCC    ACCTCTCT      TCATGG
                                    CTATG--
GAM99   320   FLJ1472 2  16399 NP_116218.1  3  1065  CTCTGGAAGCGG      TAAGCCA          4  A  c
c
          1                    TACTGTATCTCT TGGAGAGA      AGTATC
                               CTCCAAGG    ACCTCTCT      TCATGG
                                    CTATG--
GAM99   320   FLJ2089 1  5699  NP_078876.1  5  574   CGGACTGGGACT     GAT      A        4  A  c  c
          8                    TGGCTTTCTCCG TGGAGA   AAGCCAAGT TCC
                               GATAAGCG    GCCTCT   TTCGGTTCA GGG
                                    ---       -
GAM99   320   FLJ2098 1  5649  NP_078800.2  5  1525  TCAGAGGGTACT   AGA  AA           4  A  c  c

          6                    TGGCATCACCGG TGG   GAT  GCCAAGTATCC
                               TGCACAGC    GCC   CTA  CGGTTCATGGG
                                    A--   --
GAM99   320   FLJ2312 1  15636 NP_079039.1  3  863   ATAATGGATACT    GAGA    C          4  A  c  c

          9                    TTGCTTGGATCC TGGA    TAAGC AAGTATCC
                               AAGTCAAA    ACCT    GTTCG TTCATAGG
                                    AG--     T
GAM99   320   FLJ3293 1  1197  NP_690873.1  3  417   TTAGTGGATACT    G  ATA   -         4  A  c  c
          2                    TGGGCTACTTCC TGGA AG   AGCC AAGTATCC
                               ACCTTTTG    ACCT TC   TCGG TTCATAGG
                                    - A--    G
GAM99   320   FLJ3316 1  20132 NP_689896.1  5  181   TACGTGGGATAG      -  - AAG        4  A  c  c
          7                    GATTTATTCTCT TGGAGAGA TAAG CC   TATCC
                               CCACACTT    ACCTCTCT ATTT GG   ATAGG
                                    T   A ---
GAM99   320   G6PC   1  3569  NP_000142.1  3  173   TGGAGGGTCGCC   A  A     A -        4  A  c  c
                               TGGCTTATTCCC TGG GAG TAAGCCA GT ATCC
                               ATGTGTGA    ACC CTT ATTCGGT CG TGGG
                                    - -      C  C
GAM99   320   GC     1  2597  NP_000574.1  3  130   AACTAGGATACT       TA  CC          4  A  c  c
                               TTCTACTTTTTC TGGAGAGA  AG  AAGTATCC
                               TAGCTACA    ATCTTTTT  TC  TTCATAGG
                                    CA  T-
GAM99   320   GJB6   1  18208 NP_006774.1  3  168   TTGTAGGATACT    AGATAAGC          4  A  c
c
                               TGCTCCATTCAT TGGAG      CAAGTATCC
                               ACACAACG    ACCTC      GTTCATAGG
                                    --------
GAM99   320   GP5    1  15292 NP_004479.1  3  1950  AATTTTTGGTAT       AA  AA         4  A  c  c
                               AGGGTCATCTCT TGGAGAGAT  GCC  GTATC
                               CCACCTTG    ACCTCTCTA  TGG  TATGG
                                    C-  GA
GAM99   320   GPNMB  1  2512  NP_002501.1  3  382   AGGCGGGATACT      ATAAGCC          4  A  c
c
                               TTCAGCTTTCCA TGGAGAG      AAGTATCC
```

TGTAACTG ACCTTTC TTCATAGG
GACT---
GAM99 320 GPR18 1 4838 NP_005283.1 5 271 ACCTGGAAGACT A - --- A- 4 A c c
TGGCTTTACGTA TGG GAG AT AAGCCAAGT TCC
CTCCCAAT ACC CTC TG TTCGGTTCA AGG
- A CAT GA
GAM99 320 HAPIP 1 10617 NP_003938.1 3 247 AATTCGAGGTTG TA CA T 4 A c c
CTGAGCTTCTCT TGGAGAGA AGC AGTA CC
CCAAAGTC ACCTCTCT TCG TCGT GG
-- AG T
GAM99 320 HOXA1 1 9804 NP_705873.1 3 276 AAGGAGGGTCTC AA C T- 4 A c c
TTGCCCATCTCT TGGAGAGAT GC AAG ATCC
CCGGCCAC GCCTCTCTA CG TTC TGGG
CC - TC
GAM99 320 ICA1 1 6344 NP_071682.1 3 588 CTGGTGGAGGAG TA A A 4 A c c
CTGGGCTTCTCT TGGAGAGA AGCC AGT TCC
CCAAGGAC ACCTCTCT TCGG TCG AGG
-- G -
GAM99 320 IL1F10 1 8455 NP_115945.4 5 16 TGGGTTTGAGCT A A ---- 4 A c c
GGGCTTATCCTC TGGAG GATAAGCC AGT ATCC
CAACTGTG ACCTC CTATTCGG TCG TGGG
- G AGTT
GAM99 320 ILF2 1 9869 NP_004506.2 3 175 GGGTTTTGATAT AG A G 4 A c c
TGGCTTAGCTGC TGG AG TAAGCCAA TATC
CAGTCTCC ACC TC ATTCGGTT ATAG
G- G -
GAM99 320 INHBE 1 2641 NP_113667.1 3 190 TGTCTGAGACTC GAG - A 4 A c c
TGGCTTATTCCA TGGA ATAAGCCA AGT TC
GGTTGGCT ACCT TATTCGGT TCA AG
--- C G
GAM99 320 IREB2 1 10640 XP_039114.2 3 119 GTCCCAGTATAC - CCA C 4 A c c
TCACTTATCTCA TGGA GAGATAAG AGTAT
TCCATGGA ACCT CTCTATTC TCATA
A AC- T
GAM99 320 IRF4 1 13735 NP_002451.1 3 1329 CTTAAAATTACT GAT TC 4 A c c
TGGCTTTTTCCA TGGAGA AAGCCAAGTA
AATGCTTC ACCTTT TTCGGTTCAT
--- TA
GAM99 320 JUP 1 3039 NP_002221.1 3 835 TCCAGAAGATGC T CAA 4 A c c
CAGCTTCTCTCT TGGAGAGA AAGC GTATC
CCAGGGTG ACCTCTCT TTCG CGTAG
C AC-
GAM99 320 JUP 1 3039 NP_068831.1 3 537 TCCAGAAGATGC T CAA 4 A c c
CAGCTTCTCTCT TGGAGAGA AAGC GTATC
CCAGGGTG ACCTCTCT TTCG CGTAG
C AC-
GAM99 320 KIAA063 1 9348 XP_290497.1 3 657 CTGAGGGTACGT AA-- CAA 4 A c c

GCCATCATCTCT TGGAGAGAT GC GTATCC
CCAGCCCA ACCTCTCTA CG CATGGG

CTAC TG-

GAM99 320 KIAA084 1 1976 XP_049237.1 3 1018 AATTGGGTTATA TA AG C 4 A c c
1 TCTGGCTTCTCT TGGAGAGA AGCCA TAT
CCAGACCT ACCTCTCT TCGGT ATA
-- CT T

GAM99 320 KIAA106 1 18247 NP_056147.1 3 1424 TCTATGGATACT T ----- G 4 A c c
8 TGGGTTGTGGGG GGAGAG ATAA CCAAGTATCC
GCTCTCTT TCTCTC TGTT GGTTCATAGG
T GGGGG G

GAM99 320 KIAA110 1 18484 XP_034086.1 5 160 AGAAAGAGTGTT G- GTA 4 A c c
7 GGAGTTATCTCT TGGAGAGATAA CCAA TC
CTACTAAT ATCTCTCTATT GGTT AG
GA GTG

GAM99 320 KIAA119 1 10805 XP_041843.1 3 461 AGCTCCCTGCTT - TC 4 A c c
3 GGCTCTGTCTCT TGGAGAGATA AGCCAAGTA
CCACACCC ACCTCTCTGT TCGGTTCGT
C CC

GAM99 320 KIAA157 1 9853 NP_065978.1 3 545 CTCCTAGTAGTA T CC C 4 A c c
6 CTTTTTCTCTCT TGGAGAGA AAG AAGTAT
CCATTTAA ACCTCTCT TTT TTCATG
C -- A

GAM99 320 KIAA191 1 14728 XP_056302.1 3 933 CATTTTGATACT A A C 4 A c c
1 TGTCTATCCTTC TGGAG GATA G CAAGTATC
ATAGTGCC ACTTC CTAT C GTTCATAG
- - T

GAM99 320 KIAA194 1 13001 XP_086981.2 3 2948 GGTTGGTGTACT AGA- - 4 A c c
0 TGGCTTAAGTAC TGGAG TAAGCCAAGTAT CC
TTCATGCT ACTTC ATTCGGTTCATG GG
ATGA T

GAM99 320 KIF1B 1 5704 NP_055889.1 5 72 GCTGAGGAAACT AG A A 4 A c c
TGGCTGTAACTT TGGAG ATA GCCAAGT TCC
CAAAAGAA ACTTC TGT CGGTTCA AGG
AA - A

GAM99 320 KL 1 7411 NP_710150.1 3 1151 TTTGCGGATACT GA C 4 A c c
TTGCTTATTCGT TGGA GATAAGC AAGTATCC
TTAACGAC ATTT TTATTCG TTCATAGG
GC T

GAM99 320 KLK5 1 1827 NP_036559.1 3 115 GAGATGTTGAGA A ----- G 4 A c c
ATGTTCATCTCT TGGAGAGAT AGC CAA TATC
CCAGCCCC ACCTCTCTA TTG GTT GTAG
C TAAGA -

GAM99 320 LDLR 1 18207 NP_000518.1 3 279 CTCCAGGAAGTT TA - TA- 4 A c c
TTGAGTTTCTCT TGGAGAGA AGC CAAG TCC
CCACCGTG ACCTCTCT TTG GTTT AGG
-- A TGA

GAM99 320 LOC1305 1 15914 NP_620156.1 3 307 CATGCTGCTGTT A- -- TC 4 A c c
89 GGCTCCATCTCT TGGAGAGAT AGCCA AGTA
CCACACTG ACCTCTCTA TCGGT TCGT
CC TG CG

GAM99 320 LOC1444 1 6916 XP_096608.1 3 1846 TAAAGGGATACT --- ATAAG 4 A c
c

86 TGGAACAACTTT TGG AGAG CCAAGTATCC
ATGCCAAT ACC TTTC GGTTCATAGG
GTA AACAA
GAM99 320 LOC1448 1 6779 XP_084972.1 3 119 CCTGTGGATACT TG----- T 4 A c c
17 TGGCTTTTCTCT GAGAGA AAGCCAAGTATCC
TGTGGGCA TTCTCT TTCGGTTCATAGG
ACGGGTG T
GAM99 320 LOC1456 1 15776 XP_096838.1 3 188 CACAGGGATACT AGAGA- 4 A c
c
94 TGGCTTGGGAAA TGG TAAGCCAAGTATCC
ACTAAATA ATC GTTCGGTTCATAGG
AAAAGG
GAM99 320 LOC1482 1 15339 XP_086103.2 5 105 ATTCTGGCCATT TAA - AT 4 A c c
29 TGAGCATTCTCT TGGAGAGA GC CAAGT CC
CCAACTCT ACCTCTCT CG GTTTA GG
TA- A CC
GAM99 320 LOC1583 1 3652 XP_098920.1 3 497 TAAAGATGCTCC G - -- 4 A c c
14 TGGCTTATCTTC TG AGA GATAAGCCA AGTATC
TGCATGTC AC TCT CTATTCGGT TCGTAG
G T CC
GAM99 320 LOC1703 1 19448 XP_096329.1 5 1102 GACGCGAGGGCT GA T A- 4 A c
c
94 TGGCTTTTCTCG TG GAGA AAGCCAAGT TC
TCAGCTGC AC CTCT TTCGGTTCG AG
TG T GG
GAM99 320 LOC2021 1 19255 XP_117365.1 3 22 GGTCTGGATACT GATA C 4 A c c
34 TGCTATGATTTT TGGAGA AGC AAGTATCC
CACTTTTT ACTTTT TCG TTCATAGG
AGTA -
GAM99 320 LOC2531 1 7893 XP_173139.1 5 458 AAGATAAGGAAT G CAA - 4 A c c
87 ATGCTTATCTTC TGGA AGATAAGC GTAT CC
CAATTTGA ACCT TCTATTCG TATA GG
- --- A
GAM99 320 LOC2554 1 14608 XP_172895.1 5 2106 AAGGATGCCACT - C- A-- 4 A c c
80 GTTCTTATCTCC TGGAG AGATAAG CA GTATCC
TCCAATTT ACCTC TCTATTC GT CGTAGG
C TT CAC
GAM99 320 LOC2831 1 2178 XP_210889.1 3 198 ATTTCTGTGGAT T- CCAA 4 A c c
07 GCCTTTTTCTCT TGGAGAGA AAG GTATCC
CCAACCTC ACCTCTCT TTC CGTAGG
TT ----
GAM99 320 LOC2832 1 19809 XP_210956.1 5 951 AACTTTTCTATA TA C 4 A c c
70 TTTGGTTTCTCT TGGAGAGA AGCCAAGTAT
CCACACAT ACCTCTCT TTGGTTTATA
-- T
GAM99 320 LOC2836 1 19415 XP_208762.1 5 1571 TAAATGAGGACT AGAG A- 4 A c
c
33 TGGCTTATGACC TGG ATAAGCCAAGT TC

AGTCTGAT ACC TATTCGGTTCA AG
AG-- GG
GAM99 320 LOC2838 1 16591 XP_208899.1 3 221 TGGGTGATGGAT AAG A T 4 A c c
89 CCTGGAATCTCT TGGAGAGAT CCA G ATCC
CCATCCCT ACCTCTCTA GGT C TAGG
A-- - C
GAM99 320 LOC2840 1 10403 XP_208958.2 3 3922 CGTCCAGATACT T--- - AAG- 4 A c c
01 TGGAGACATCTC GGAG AGAT CCAAGTATC
CTCCTCAC CCTC TCTA GGTTCATAG
CACT C CAGA
GAM99 320 LOC2840 1 5062 XP_208970.1 5 576 AATCGGAAAATG A AA A- 4 A c c
24 AGGCTTATCCTC TGGAG GATAAGCC GT TCC
CAGCAGAA ACCTC CTATTCGG TA AGG
- AG AA
GAM99 320 LOC2843 1 13243 XP_209161.1 3 540 ATCTCAGGGGAA TAA A A 4 A c c
44 ATGTGGCTCTCT TGGAGAGA GCCA GT TCC
CCACCTTG ACCTCTCT CGGT TA AGG
--- G A
GAM99 320 LOC2845 2 3690 XP_209254.1 3 276 AGATGAGGTGCT AG T 4 A c c
42 TGGCTTTCTTCC TGG AGA AAGCCAAGTATC
CAGGACCC ACC TCT TTCGGTTCGTGG
CT -
GAM99 320 LOC2845 2 8640 XP_209254.1 3 31 TGACCCCCTACT TAA TC 4 A c c
42 TGGCTCTTTCCA TGGAGAGA GCCAAGTA
GGGAGCAT ACCTTTCT CGGTTCAT
--- CC
GAM99 320 LOC2847 1 2267 XP_211623.1 5 243 GGAGGGGGCACA TAAG -- AT 4 A c c
49 GTTGGATTCTCT TGGAGAGA CCAA GT CC
CCAGTGAA ACCTCTCT GGTT CA GG
TA-- GA CG
GAM99 320 LOC2848 1 3070 XP_211652.1 3 387 TATTCTGATCTT - A T 4 A c c
24 TGGCTTACTACT TGGAG AG TAAGCCAAG ATC
CCATTGCA ACCTC TC ATTCGGTTT TAG
A - C
GAM99 320 LOC2848 1 2009 XP_211680.1 5 657 ACTCTCTCGGAT TA CAAGT 4 A c c
99 CCGTGCTTCTCT TGGAGAGA AGC ATCC
CCATTGTA ACCTCTCT TCG TAGG
-- TGCC-
GAM99 320 LOC2851 1 15571 XP_211773.1 3 1535 CTACCCCAGGAG A CCA A 4 A c c
23 GCTCTTATCTCC TGG GAGATAAG AGT TCC
CCAGCCCC ACC CTCTATTC TCG AGG
C --- G
GAM99 320 LOC2853 1 3373 XP_211845.1 3 1831 AGGATCTTGGAT AAG----- T 4 A c c

32 AGGATCATCTCT TGGAGAGAT CCAAG ATCC
CCAAACTT ACCTCTCTA GGTTC TAGG
CTAGGATA -
GAM99 320 LOC2853 1 1542 XP_209581.1 3 81 GCTTGGGTAGCT AG - 4 A c c
66 TGGCTTATATTC TGGAG ATAAGCCAAGT ATCC
TAGAGCAG ATCTT TATTCGGTTCG TGGG
A- A
GAM99 320 LOC2853 1 19495 XP_208316.1 5 372 ACCACGGTGTTT - CC- 4 A c c
88 CCCCTTATCTCT TGG AGAGATAAG AAGTATC
ACCATGGC ACC TCTCTATTC TTTGTGG
A CCC
GAM99 320 LOC2861 1 16310 XP_209902.1 3 936 GGTGGGAGCCTG AG - TA 4 A c
c
01 TGGCTTATGGCT TGGAG ATAAGCCA AG TCC
TCACTTAC ACTTC TATTCGGT TC AGG
GG G CG
GAM99 320 LOC2861 1 15285 XP_212216.1 3 407 ATCCAGAGACTT G CC- A 4 A c c
84 TATCTTATCTCT TG AGAGATAAG AAGT TC
ACATAACA AC TCTCTATTC TTCA AG
A TAT G
GAM99 320 LOC2861 1 2050 XP_209933.1 3 766 GAATTTGAGCCT TA TA 4 A c c
88 TGGCTTCTTTCC TGGAGAGA AGCCAAG TC
ACCCAGAT ACCTTTCT TCGGTTC AG
-- CG
GAM99 320 LOC3391 1 20117 XP_290759.1 3 1309 CGTGTCGATGTG G A AG 4 A c
c
99 TGGCTTATCCTG TG AG GATAAGCCA TATC
CAGGAGTG AC TC CTATTCGGT GTAG
G - GT
GAM99 320 LOC3403 1 6677 NP_848659.1 3 962 CCTCTTGATTCT T----- A T 4 A c c
71 TGGCTTGCCTCT GGAGAG TAAGCCAAG ATC
CCTCCAAT CCTCTC GTTCGGTTC TAG
TAACCT C T
GAM99 320 LOC3403 1 6677 XP_291255.2 3 962 CCTCTTGATTCT T----- A T 4 A c c
71 TGGCTTGCCTCT GGAGAG TAAGCCAAG ATC
CCTCCAAT CCTCTC GTTCGGTTC TAG
TAACCT C T
GAM99 320 LOC3423 1 6898 XP_296817.2 5 597 ACTGCAGCGGGA TA AGTA 4 A c
c
46 AGTGGCTTCTCT TGGAGAGA AGCCA TCC
CCAGAATA ACCTCTCT TCGGT AGG
-- GA--
GAM99 320 LOC3462 1 18310 XP_294161.2 5 2226 AAGATAAATACT G A C 4 A c c
84 TGGCTAATCTTC TGGA AGAT AGCCAAGTAT
CATTTACA ACCT TCTA TCGGTTCATA
- A A
GAM99 320 LOC3492 1 8523 XP_303005.1 3 922 GTGCCTAGATGC AGCCAA 4 A c
c
28 CTTTGTATCTCT TGGAGAGATA GTATC

CCATGTCA ACCTCTCTAT CGTAG
GTTTC-
GAM99 320 LOC3492 1 4792 XP_301008.1 5 897 GTGTTATGGAGA TAAGCC 4 A c c
82 TGCTTCCTCTCT TGGAGAGA AAGTATC
CCAACCTC ACCTCTCT TTCGTAG
CC----
GAM99 320 LOC3493 1 4792 XP_301024.1 5 897 GTGTTATGGAGA TAAGCC 4 A c c
13 TGCTTCCTCTCT TGGAGAGA AAGTATC
CCAACCTC ACCTCTCT TTCGTAG
CC----
GAM99 320 LOC5720 1 2672 XP_290488.1 3 1919 GTAACATGGTAT - G 4 A c c
9 TGGCTTATCGTT TGGAGA GATAAGCCAA TATC
TTTATCTC ATTTTT CTATTCGGTT ATGG
G -
GAM99 320 LOC6392 1 6406 NP_071373.2 5 37 AGGTTGTTGCGG TAAGCC 4 A c c
0 ATGCTTCTCTCT TGGAGAGA AAGTATCC
CCAGGCGC ACCTCTCT TTCGTAGG
C-----
GAM99 320 LOC9446 1 1169 XP_017293.3 5 16 GAGGGATTGATG T----- G A 4 A c c
8 CTGGTTATCTCT GGAGAGATAA CCA GTATC
CTGAATCT TCTCTCTATT GGT CGTAG
TCTAAG - -
GAM99 320 LPXN 1 9179 NP_004802.1 3 407 GGTCCTGATACT TAAGC 4 A c c
TGTTTCTTTTCA TGGAGAGA CAAGTATC
CGTTTTCC ACTTTTCT GTTCATAG
TT---
GAM99 320 MAGEA4 1 6081 NP_002353.2 3 185 TGGATGACTTGG T- ---- --- - 4 A c c
AGATTTATCTCT GGA GAGATAAG CCAAGT ATCC
GTTTCCTT CCT CTCTATTT GGTTCA TAGG
TT TTGT AGA G
GAM99 320 MAP2K1 1 20080 NP_002746.1 3 695 GTGTGGGATACT A --- 4 A c c
TAGTGGTATGTC TGGAGAGATA GCCA AGTATCC
TCTTTAAG ATTTCTCTGT TGGT TCATAGG
A GAT
GAM99 320 MGC1414 1 3511 NP_116317.1 3 423 GGGGTTAATAAA ---- AG C 4 A c c
1 TGGCTTATCCTT TGGAGAGA TAAGCCA TAT
CTCTCCAA ACCTCTCT ATTCGGT ATA
TCCT AA A
GAM99 320 MGC3464 1 5090 NP_689873.1 3 516 TATAATGGAAGA T- AAGTA 4 A c c
8 GGCTTTCTCTCT TGGAGAGA AAGCC TCC
CCAATAAA ACCTCTCT TTCGG AGG
CT AGA--
GAM99 320 MGC4189 1 9209 NP_115684.1 3 158 GCCTGTGATACT A A-- - 4 A c c
TGGGCTGTGATC TGGAG GAT AGCC AAGTATC
CTCTAGAG ATCTC CTA TCGG TTCATAG
- GTG G

GAM99 320 MLLT2 1 6110 NP_005926.1 3 1726 GGGATGGGAGCG - CAA A 4 A c c

ATGCTTATCTCT TG GAGAGATAAGC GT TCC
CACAGTGT AC CTCTCTATTCG CG GGG
A TAG A

GAM99 320 OAS2 2 4904 NP_002526.1 3 671 CTCCTCAGATAT TAA C 4 A c c
ACTTGGTTCTCT TGGAGAGA GCCAAGTAT
CCACCAGG ACCTCTCT TGGTTCATA
--- T

GAM99 320 OAS2 2 18197 NP_002526.1 3 672 CTCAGATATACT TAA C 4 A c c
TGGTTCTCTCCA TGGAGAGA GCCAAGTAT
CCAGGTTC ACCTCTCT TGGTTCATA
--- T

GAM99 320 PPP2R5C 1 9224 NP_002710.2 3 1708 CTGAGAAACTTG AGC-- A 4 A c c

ACAAGTATCTCT TGGAGAGATA CAAGT TC
CCATTTTA ACCTCTCTAT GTTCA AG
GAACA A

GAM99 320 PPP2R5C 1 9224 NP_848701.1 3 1708 CTGAGAAACTTG AGC-- A 4 A c c

ACAAGTATCTCT TGGAGAGATA CAAGT TC
CCATTTTA ACCTCTCTAT GTTCA AG
GAACA A

GAM99 320 PRKCB1 1 10260 NP_002729.2 3 418 GGGCCTGGAGCT GAG A 4 A c c

TGGCTTGTATCC TGGA ATAAGCCAAGT TCC
AAGTGTAT ACCT TGTTCGGTTCG AGG
A-- -

GAM99 320 PRKCN 1 11840 NP_005804.1 3 1277 TGTAAGAAACAG A- A 4 A c c
TGGCTTATTTCT TGGAGAGATAAGCCA GT TC
TCATTTCT ACTTCTTTATTCGGT CA AG
GA A

GAM99 320 PRPF4 1 6260 NP_004688.2 3 660 ATTCTTGAAACT GAGAT A 4 A c c
TGGCTTTCCATA TGGA AAGCCAAGT TC
ACATGGTA ACCT TTCGGTTCA AG
----- A

GAM99 320 PSG1 1 3147 NP_008836.2 5 88 TTTCTGGATCCT GA A T 4 A c c
AGGCTTATCTCC TG GAGATAAGCC AG ATCC
ACAGAGGA AC CTCTATTCGG TC TAGG
AC A C

GAM99 320 PSG4 1 4422 NP_002771.1 3 455 ATCTCAGGGGAA TAA A A 4 A c c
ATGTGGCTCTCT TGGAGAGA GCCA GT TCC
CCATCTTG ACCTCTCT CGGT TA AGG
--- G A

GAM99 320 PTER 1 10176 NP_109589.2 3 964 CAGCCCGATACT ATAA - 4 A c c
TGAGCCTCCTCT TGGAGAG GC CAAGTATC
TTAAAAGG ATTTCTC CG GTTCATAG
CTC- A

GAM99 320 RAB7L1 1 6897 NP_003920.1 3 25 TGCTATAGTGTT A C 4 A c c
TGGCTTATTTTC TGGAGAG TAAGCCAAGTAT

CATCCCAG ACCTTTT ATTCGGTTTGTG
- A
GAM99 320 RNF8 1 17319 NP_003949.1 3 3174 AGTGTCTGGGAT TAA AGT 4 A c c
TGGTAGCTCTCT TGGAGAGA GCCA ATCC
CCAACTGC ACCTCTCT TGGT TAGG
CGA ---
GAM99 320 SFRP4 1 19985 NP_003005.1 3 1510 CTATTGGATACT AA - 4 A c c
TAGGTGGTTTCT TGGAGAGAT GCC AAGTATCC
TCACTGAC ACTTCTTTG TGG TTCATAGG
G- A
GAM99 320 SLC25A1 1 1242 NP_055067.1 3 1189 CATTTTTCTACT T C TC 4 A c c
5 TTGCTTTTCTCT TGGAGAGA AAGC AAGTA
CCATACTT ACCTCTCT TTCG TTCAT
T T CT
GAM99 320 SLC2A5 1 5294 NP_003030.1 3 203 TTCTTGAAGCTG TA- A A 4 A c c
GGCTGTCTCTCT TGGAGAGA AGCC AGT TC
CCATGTTG ACCTCTCT TCGG TCG AG
CTG G A
GAM99 320 SORBS1 1 5727 NP_056200.1 3 1534 GCTGGAAATACT A AG -- 4 A c c
TGGAATATTTTC TGGAGAG TA CCAAGTA TCC
CAGAGTCT ACCTTTT AT GGTTCAT AGG
- AA AA
GAM99 320 STAG2 1 8903 NP_006594.3 5 72 GGAAGGCGATTG AA-- -- A- 4 A c c
GCATCGATCTCT TGGAGAGAT GCCAA GT TCC
CCATCCCT ACCTCTCTA CGGTT CG AGG
GCTA AG GA
GAM99 320 SWAP2 1 18106 NP_008987.1 3 78 TGTGATGCTGCT GAT -- 4 A c c
GGTTTTATCTCT TGGAGA AAGCCA AGTATC
AGTGAAAT ATCTCT TTTGGT TCGTAG
AT- CG
GAM99 320 TBX19 1 16617 NP_005140.1 3 200 GCTAGTTAGATC AA C - 4 A c c
ATTTGCATCTCT TGGAGAGAT GC AAGT ATC
CCACCATT ACCTCTCTA CG TTTA TAG
-- - C
GAM99 320 TLL2 1 17891 NP_036597.1 3 2176 ACAATGATACTT CC- 4 A c c
CTTTTTATCTCT TGGAGAGATAAG AAGTATC
TTAGTATG ATTTCTCTATTT TTCATAG
TTC
GAM99 320 TNF 1 3783 NP_000585.2 3 380 AGTGGACCTTAG TAA-- - TA 4 A c c
GCCTTCCTCTCT TGGAGAGA GCC AAG TCC
CCAGATGT ACCTCTCT CGG TTC AGG
CCTTC A C-
GAM99 320 TRPC1 1 18535 NP_003295.1 3 1017 ACTAAGGTTCTT A - T 4 A c c
GAGCTTATCTCC TGG GAGATAAGC CAAG ATC
CAAGGTAC ACC CTCTATTCG GTTC TGG
- A T
GAM99 320 TU3A 1 18290 NP_009108.1 5 100 CCTCAGGAAGCT A AT A 4 A c c
TGGCTTCCCTCC TGG GAG AAGCCAAGT TCC
CATGGGAA ACC CTC TTCGGTTCG AGG

- CC A

GAM99 320 UBQLN1 1 17847 NP_038466.2 3 713 GAAAAGCTGATT G A T 4 A c c
CTGGTTATCTCT TGGAGAGATAA CCA G ATC
TTAAGGAC ATTTCTCTATT GGT C TAG
- - T

GAM99 320 UMPS 1 15501 NP_000364.1 3 306 CATTTGAGGATC AGCC T 4 A c c
CTTCCTATCTCT TGGAGAGATA AAG ATCC
CCATGGGA ACCTCTCTAT TTC TAGG
CC-- C

GAM99 320 WASF3 2 7833 NP_006637.2 3 793 ACTCAAGATACT AA C 4 A c c
TGCCAGTCTCTC TGGAGAGAT GC AAGTATC
CAGTGTGG ACCTCTCTG CG TTCATAG
AC -

GAM99 320 WASF3 2 16728 NP_006637.2 3 793 CACTCAAGATAC AA C 4 A c c
TTGCCAGTCTCT TGGAGAGAT GC AAGTATC
CCAGTGTG ACCTCTCTG CG TTCATAG
AC -

GAM99 320 XLKD1 1 11348 NP_006682.1 3 1009 TTTTGATATTTC - - C-- 4 A c c
TAGCTTATCTAC TGGA G AGATAAGC AAGTATC
TTCCAAAC ACCT C TCTATTCG TTTATAG
T A ATC

GAM100 243 ACADSB 1 9071 NP_001600.1 3 1037 TTGGTTTAATAA A AAGC 4 A c
c
TCAGAAAATATT TGAA TATTTTC TGATTA
CAATACAG ACTT ATAAAAG ACTAAT
- ----

GAM100 243 AMD1 1 693 NP_001625.1 3 1063 AAATCAAGTCAG ATATT 4 A c c
CTTGGATCATTC TGAA TTCAAGCTGATT
ACCTTAAC ACTT AGGTTCGACTGA
ACT--

GAM100 243 ARF3 1 11427 NP_001650.1 3 881 CACTCTTATCAG A C T 4 A c c
CTTAGAGTGTTC TGAA TATTTT AAGCTGAT
AACTGATC ACTT GTGAGA TTCGACTA
- - T

GAM100 243 ARHGAP1 1 8456 NP_055598.1 3 135 TAGATTTGCTCT ---- T 4 A c c
1A ATTGAAAATGTT TGAAATATTTTCA AGC GATT
TCATTTTT ACTTTGTAAAAGT TCG TTAG
TATC T

GAM100 243 ATP6V1C 1 15117 NP_653184.1 3 617 TTTATCGGCATT --- - T 4 A c c
2 GTCCAAAATATT TGAAATATTTT CAA GCTGAT
TTATTCTT ATTTTATAAAA GTT CGGCTA
CCT A T

GAM100 243 BACH1 1 4647 NP_001177.1 3 2966 ATCTATTTTGAA TCAA T 4 A c c
TCTGTAAATATT TGAAATATTT GC GATT
TTAAATGT ATTTTATAAA TG CTAA
---- T

GAM100 243 BACH2 1 8027 NP_068585.1 3 1073 AATCTGCTTGAA T------ T 4 A c c
TATTTTTATATT TGAAATAT TTCAAGC GATT
TCACCTCC ACTTTATA AAGTTCG CTAA
TTTTTAT T

GAM100 243 BAG2 1 9686 NP_004273.1 3 248 TCTTGTACTAGG TTTCAA - 4 A c c
ATCTAGCATATT TGAAATAT GCT GATT
TCACTATT ACTTTATA CGA CTAG
------ T
GAM100 243 BLP2 1 6931 NP_079417.1 3 357 AATGTAGTCTGC TA- - T 4 A c c
CTTGAAAAGTCT TGAAA TTTTCAAG C GATTA
TTCAGCTG ACTTT AAAAGTTC G CTGAT
CTG C T
GAM100 243 BLP2 1 6931 NP_510883.1 3 357 AATGTAGTCTGC TA- - T 4 A c c
CTTGAAAAGTCT TGAAA TTTTCAAG C GATTA
TTCAGCTG ACTTT AAAAGTTC G CTGAT
CTG C T
GAM100 243 C10orf5 1 16299 XP_172843.1 3 2478 ACTTTAAATCAA -- GC 4 A c c
ATTGAAAATAAA TGAAA TATTTTCAA TGATT
TTTTATCC ATTTT ATAAAAGTT ACTAA
AA AA
GAM100 243 C14orf1 1 10104 NP_689660.2 5 502 CTCTGAAATCAG - - 4 A c c
46 CTTTGGAGATGC TGAAA TATTTTCAA GCTGATT
TTTCACTC ACTTT GTAGAGGTT CGACTAA
C T
GAM100 243 C20orf6 1 19464 NP_291028.2 3 480 ATAGAATACAGC AA AA- - 4 A c c
4 ATGGAAAATATC TGA TATTTTC GCTG ATT
AGTGTATT ACT ATAAAAG CGAC TAA
-- GTA A
GAM100 243 C6orf15 1 12717 NP_689764.1 3 2070 AAAGGCGATCAG A- TTC 4 A c c
1 CTTCAGTAGATT TGAA TATT AAGCTGATT
CACGGCAG ACTT ATGA TTCGACTAG
AG C--
GAM100 243 C9orf5 1 14642 NP_114401.1 3 169 TTGTTAAGATGG A G 4 A c c
CTTGAAAAGTTT TGAAAT TTTTCAAGCT ATT
CATTTTAT ACTTTG AAAAGTTCGG TAG
- -
GAM100 243 CAMTA1 1 10875 XP_042323.7 3 1088 GGATTATATTAA TCA T 4 A c c
TTGCTAAATATT TGAAATATTT AGC GATTA
TTATTCAC ATTTTATAAA TCG TTAAT
--- -
GAM100 243 CCKBR 1 3824 NP_000722.2 3 440 TTCCCAATCAGC AA- A- 4 A c c
ACTGAAAATACC TGA TATTTTCA GCTGATT
ATCAGGCC ACT ATAAAAGT CGACTAA
ACC CA
GAM100 243 CCKBR 1 3824 NP_795344.1 3 440 TTCCCAATCAGC AA- A- 4 A c c
ACTGAAAATACC TGA TATTTTCA GCTGATT
ATCAGGCC ACT ATAAAAGT CGACTAA
ACC CA
GAM100 243 CCR9 1 2819 NP_006632.2 3 1167 AAATGCATCACC - C T 4 A c c
TTTGAAAATATT TGAAATATTTTCAA G TGAT
TCACATAT ACTTTATAAAAGTT C ACTA
T C C

GAM100 243 CCR9 1 2819 NP_112477.1 3 1167 AAATGCATCACC - C T 4 A c c
TTTGAAAATATT TGAAATATTTTCAA G TGAT
TCACATAT ACTTTATAAAAGTT C ACTA
T C C
GAM100 243 CG012 1 20065 XP_096710.1 5 1048 ACAGAGAATCAG ATT A 4 A c c
CTGGATCATTTC TGAAAT TTCA GCTGATT
AGCTGTCC ACTTTA AGGT CGACTAA
CT- -
GAM100 243 CLDN12 1 8251 NP_036261.1 3 1193 CTTAATCATTGA ----- GC 4 A c c
TCCAGGAATATT TGAAATATTT TCAA TGATTA
TCAACCAG ACTTTATAAG AGTT ACTAAT
GACCT --
GAM100 243 COL21A1 1 15079 NP_110447.2 3 322 CAGTTTTAGTCA CA C 4 A c c
CTGTGAAATATT TGAAATATTTT AG TGATTA
TCACATTC ACTTTATAAAG TC ACTGAT
TG -
GAM100 243 CPGL2 1 10752 NP_116038.4 3 169 TATCTGGATCAG CAA 4 A c c
TAATAAAATATT TGAAATATTTT GCTGATT
TCAAAGGC ACTTTATAAAA TGACTAG
TAA
GAM100 243 CYP7A1 1 2570 NP_000771.1 3 1037 TATTAAGTGCAG TT-- - 4 A c c
CTTGACATTATG TGAAATAT TCAAGCTG ATT
TTTTATTT ATTTTGTA AGTTCGAC TGA
TTAC G
GAM100 243 DKFZp43 1 8438 NP_115626.1 3 764 CATATTAACAAA A AGCT 4 A c c
4A171 TCTGAAAATATG TGA ATATTTTCA GATT
TCAAATTA ACT TATAAAAGT CTAA
G ----
GAM100 243 DKFZp43 1 8864 XP_037555.8 3 614 CTTTTATAATAA AT G G 4 A c c
4N2030 GTTGAAAATTTC TGAAAT TTTCAA CT ATTA
ATATAATT ACTTTA AAAGTT GA TAAT
-- - A
GAM100 243 DKFZP56 1 11086 NP_108648.1 3 483 ACTGATCAGTTC T----- --- 4 A c c
4D166 TCTGAAAATATT GAAATATTTTCA AGCTGATTA
TCCAAAAT CTTTATAAAAGT TTGACTAGT
TAAAAC CTC
GAM100 243 DKFZp56 1 15799 NP_060005.1 5 1457 TTTTAAAATCAG A TTTT 4 A c
c
6H0824 CTTGTCTTGTTC TG AATA CAAGCTGATT
CACAAACT AC TTGT GTTCGACTAA
C TCT-
GAM100 243 DKFZp66 1 13698 XP_290795.1 5 345 CTAGGTGATCAG ATAT 4 A c c
7M2411 CTTGAAATTCAG TGAA TTTCAAGCTGATTA
CTAACCGA ACTT AAAGTTCGACTAGT

GAM100 243 DKFZp76 1 1198 NP_115663.1 3 1321 CTCCCCTTATGA TCA C 4 A c c
1O17121 TTACTAAATATT TGAAATATTT AG TGATTA

TTATTTTG ATTTTATAAA TC ATTAGT
--- -
GAM100 243 DMP1 1 5295 NP_004398.1 3 64 GAGTCTTAGGGA A - ---- 4 A c c
CTTGAAAATGTA TGA ATATTTTCAAG CT GATT
TCATGATA ACT TGTAAAAGTTC GG CTGA
A A GATT
GAM100 243 DTNB 1 17907 NP_149159.1 3 243 TGATTTTAATTG TAT- T 4 A c c
CTTGAAACAACT TGAAA TTTCAAGC GATTA
TTCAGGGT ACTTT AAAGTTCG TTAAT
CAAC -
GAM100 243 DYSF 1 17950 NP_003485.1 3 252 TTTTTGGATCAG T CA 4 A c c
CTCAGACATATT TGAAATAT TT AGCTGATT
TCAGTATA ACTTTATA AG TCGACTAG
C AC
GAM100 243 EFG2 1 14944 NP_115756.2 3 392 AAAGGTTCAATC CAAGC 4 A c c
AATAAAAATATT TGAAATATTTT TGATT
TTATTCAA ATTTTATAAAA ACTAA
ATA--
GAM100 243 EFG2 1 14944 NP_733792.1 3 392 AAAGGTTCAATC CAAGC 4 A c c
AATAAAAATATT TGAAATATTTT TGATT
TTATTCAA ATTTTATAAAA ACTAA
ATA--
GAM100 243 ENAH 1 12776 NP_060682.1 3 617 ATGTTTCTTCAG A TT 4 A c c
CTTGAGAAATTT TGAAAT TTTTCAAGCTGA
TAGAATGA ATTTTA AAGAGTTCGACT
- TC
GAM100 243 FACL1 1 20169 NP_001986.1 5 40 GAGGAGAATCAG AATA - 4 A c c
CTTAGAGAACTA TGA TTTTC AAGCTGATT
TCAACACA ACT AAGAG TTCGACTAA
ATC- A
GAM100 243 FLJ2030 1 16995 NP_060225.2 3 673 TGGGGTTGGGAT T CT 4 A c c
3 CCTTGGAATATT TGAAATATTT CAAG GATT
TCAATAAA ACTTTATAAG GTTC CTAG
- --
GAM100 243 FLJ2383 1 2419 NP_689963.1 5 114 GCATTACCACTG TCAA T 4 A c c
4 TTAGCAAATATT TGAAATATTT GCTGAT
TCATGATA ACTTTATAAA CGATTG
---- T
GAM100 243 FLJ3289 1 3993 NP_653268.1 3 812 TAAGACTATAAT TC CT 4 A c c
4 CCCTTAAATATT TGAAATATTT AAG GATTA
TTAGAAGA ATTTTATAAA TTC CTAAT
-- C-
GAM100 243 FLJ3376 1 4332 NP_775881.1 3 673 GGCCAAGAAGCA - A-- GA 4 A c c
8 TATGAAAATATG TGAA ATATTTTCA GCT TT
TTCAATCT ACTT TATAAAAGT CGA AA
G ATA AG
GAM100 243 FLJ3492 1 14134 NP_689483.1 3 1514 CTAAGAAATCAT T- AGC 4 A c c
2 ATGACCAATATT TGAAATATT TCA TGATT
TCACTTAT ACTTTATAA AGT ACTAA

CC AT-

GAM100 2436 FLJ3910 1 12417 NP_775900.1 3 1095 TCAGAATTAATC C CT 4 A c c
TCTTAAAATATT TGAAATATTTT AAG GATTA
TTACAGAG ATTTTATAAAA TTC CTAAT
- T-

GAM100 2430 FLJ9043 1 14531 NP_848653.1 3 1236 AAATGCAGTACA T ---- - 4 A c c
TTTGAAAATTTT TGAAA ATTTTCAA GCTG ATT
TAGATTAT ATTTT TAAAAGTT TGAC TAA
- TACA G

GAM100 243 GCC185 1 18198 NP_055450.1 3 1567 TAACTAATCATA - C GC 4 A c c
TTTAAATATATT TGAAATAT TTT AA TGATTA
TCACTTTC ACTTTATA AAA TT ACTAAT
T T AT

GAM100 243 GCC185 1 18198 NP_852118.1 3 1567 TAACTAATCATA - C GC 4 A c c
TTTAAATATATT TGAAATAT TTT AA TGATTA
TCACTTTC ACTTTATA AAA TT ACTAAT
T T AT

GAM100 243 GPHN 1 6063 NP_065857.1 3 138 ATAGTCAACATC T- C--- 4 A c c
TTGAACTATATT TGAAATAT TTCAAG TGATTA
TCAAATGA ACTTTATA AAGTTC ACTGAT
TC TACA

GAM100 243 IL5 1 16606 NP_000870.1 3 186 AGCATAAAATTC - C CT 4 A c c
TTAAAATATATT TGAAATAT TTT AAG GATT
TCAGATAT ACTTTATA AAA TTC TTAA
T A --

GAM100 243 IMPG1 1 5063 NP_001554.2 3 145 CTGAGAATCAGC TTTCAA- 4 A c c
ACACACCATATT TGAAATAT GCTGATT
TCAAATAT ACTTTATA CGACTAA
CCACACA

GAM100 243 ITPR2 1 4278 NP_002214.1 3 1963 GTAAAAAGTACA C C - 4 A c c
CTTTAAAATATT TGAAATATTTT AAG TG ATT
TTAATCAG ATTTTATAAAA TTC AC TGA
T - A

GAM100 243 JUB 1 17497 NP_116265.1 3 1287 CTAGTCAGTTTG A T ---- 4 A c c
CTTGAAACTAGT TGAA TA TTTCAAGC TGATTA
TCACCTAA ACTT AT AAAGTTCG ACTGAT
G C TTTG

GAM100 2431 KIAA039 1 8518 NP_055487.1 3 952 CCCTTGATTTCA A A TT 4 A c c
GCTGAAAATATT TGAA TATTTTCA GCTGA
CATGTCTG ACTT ATAAAAGT CGACT
- - TT

GAM100 2438 KIAA073 1 17995 NP_055534.1 3 703 AGAATTAGGGGC AA ---- 4 A c c
CTTGAAAATATG TG ATATTTTCAAG CTGATT
ACAAACTC AC TATAAAAGTTC GATTAA
AG CGGG

GAM100 243 KIAA149 1 17775 NP_065922.1 3 2300 GACAGTTGAATA CAAGC 4 A c c
5 ATCAAAAATATT TGAAATATTTT TGATTA
TTATTAGG ATTTTATAAAA ACTAAT

```
                                                    -----
GAM100  243  KIAA202 1  18881 NP_742067.1  5  157  TGTTTAAATCAG     ATTTTCA          4  A  c
c
        4                          CTGTTTCATGTA TGAAAT      AGCTGATT
                                   TTAGCCTT    ACTTTG      TCGACTAA
                                           -------
GAM100  243  LBR    1  14697 NP_002287.1  3  991  CACAGATCGGTG     -----      --       4  A  c  c
                                   TTTGAAAATTTG TGAAAT    ATTTTCAA  GCTGATT
                                   CCATTTCA    ACTTTA    TAAAAGTT  TGGCTAG
                                               CCGTT       TG
GAM100  243  LGN    1  6174  NP_037428.2  3  110  CACTGTAATACA T-----       C    -      4  A  c  c
                                   GCTTAAAATATT      GAAATATTTT AAGCTG ATTA
                                   TTTAGAAT          TTTTATAAAA TTCGAC TAAT
                                             TAAGAT        -     A
GAM100  243  LOC1135 1  1372  NP_660283.1  3  11   TTGTGCAGTCAT       TCAA -         4  A  c  c
        21                          GTGTTAAATATT TGAAATATTT    GC TGATT
                                   TCACATTT    ACTTTATAAA    TG ACTGA
                                               TTG-  T
GAM100  243  LOC1237 1  15605 XP_058721.2  3  3385  AAGCAGAGTCAG     TATTT            4  A  c
c
        22                          CTTGATTTCAAG TGAAA     TCAAGCTGATT
                                   GACTCTAT    ACTTT     AGTTCGACTGA
                                           -----
GAM100  243  LOC1265 1  13459 XP_059054.1  3  200  CTTGAAACTCAG    AT         TT       4  A  c  c
        36                          CTTGAAGATTTC TGAA  ATTTTCAAGCTGA
                                   AGCAAATG     ACTT  TAGAAGTTCGACT
                                               --          CA
GAM100  243  LOC1266 1  18742 XP_060121.4  3  4568  TTAGTAATTTAA        TCAAG          4  A  c
c
        69                          ATCAGAAATATT TGAAATATTT    CTGATT
                                   TTATAAAA    ATTTTATAAA    GACTAA
                                           -----
GAM100  243  LOC1313 1  14040 NP_778226.1  3  1463  TTTTCTCCAATT      TT  A  T         4  A  c  c
        68                          TGCCTGAATATT TGAAATAT  TCA GC GATT
                                   TCAGGAGG    ACTTTATA  AGT CG TTAA
                                               --  C  T
GAM100  243  LOC1508 1  8784  XP_087028.1  3  22   CCAGTTAGCACA         AA----         4  A  c  c
        68                          AAGGAAAATATT TGAAATATTTTC     GCTGATT
                                   TCAATAAA    ACTTTATAAAAG     CGATTGA
                                               GAAACA
GAM100  243  LOC1515 1  453   XP_098072.2  3  1786  TTCTGCAAATAT        TC    -        4  A  c  c
        12                          GGCTTAAATATT TGAAATATTT  AAGCTG ATT
                                   TCATGGCA    ACTTTATAAA  TTCGGT TAA
                                               --     A
GAM100  243  LOC1531 1  7609  XP_098318.1  5  466  ATCTATAAAATG  -       AAG  G        4  A  c  c
        39                          AGAGAAAATATT TG AAATATTTTC   CT ATT
                                   TGCAATCC    AC TTTATAAAAG   GA TAA
                                             G        A--  G
GAM100  243  LOC1541 1  7609  XP_098488.2  5  466  ATCTATAAAATG  -       AAG  G        4  A  c  c
        84                          AGAGAAAATATT TG AAATATTTTC   CT ATT
```

```
                                    TGCAATCC    AC TTTATAAAAG   GA TAA
                                          G        A--  G
GAM100  243   LOC1584 1  1108  XP_088580.1  5  82   TATAAAAATCAG  A   ---   --        4  A  c  c
        50                          CTCTTGGAATAT TG AATAT   TTTCA  AGCTGATT
                                    ATGTTGCA    AC TTGTA   AAGGT  TCGACTAA
                                          G    TAT    TC
GAM100  243   LOC1589 1  3321  XP_099004.1  3  782   GCCTGAGATCAG  G     TTC           4  A  c  c

        27                          CTTAGTGTTTGA T AAATATT   AAGCTGATT
                                    AATTGCTC    A TTTGTGA   TTCGACTAG
                                          G     ---
GAM100  243   LOC1634 1  6012  XP_088864.3  3  2547  TAATTTAGTCAA     AT     C         4  A  c  c
        04                          CTTGAAAATTTC TGAAAT  TTTCAAG TGATTA
                                    GGTAGTCT    GCTTTA  AAAGTTC ACTGAT
                                          --      A
GAM100  243   LOC1969 1  7822  XP_113796.1  3  2178  ATGGCCTTAGCC          --   TT      4  A  c  c
        96                          TTTGAAAATATT TGAAATATTTTCAA  GCTGA
                                    TTAAAATA    ATTTTATAAAAGTT  CGATT
                                          TC    CC
GAM100  243   LOC2219 1  14341 XP_168344.1  3  1352  TGAGACAATAAT        TCA   G         4  A  c
c
        81                          GAGTTAAATATT TGAAATATTT   AGCT ATTA
                                    TTATTGGA    ATTTTATAAA   TTGA TAAT
                                          ---   G
GAM100  243   LOC2221 1  3184  XP_168421.2  5  148   ACTGATAATCAG      TTTTC           4  A  c  c

        59                          CTTTATTTTACA TGAAATA    AAGCTGATTA
                                    AAAGAGTT    ATTTTAT    TTCGACTAAT
                                          -----
GAM100  243   LOC2550 1  15757 XP_171243.2  3  684   TAGGTCAGCTCT          ----        4  A  c  c
        45                          TTTGAAAATGTT TGAAATATTTTCA   AGCTGATT
                                    TTATTTGA    ATTTTGTAAAAGT   TCGACTGG
                                          TTTC
GAM100  243   LOC2830 1  11284 XP_208500.1  3  886   TTGTTAAATTAA        CAA --        4  A  c  c
        75                          TGCCAAAATATT TGAAATATTTT   GC  TGATT
                                    TTAATTTT    ATTTTATAAAA   CG  ATTAA
                                          C--  TA
GAM100  243   LOC2834 1  3292  XP_211035.1  3  136   CTGAATGCTGGA       TTCAA  TG        4  A  c
c
        35                          ATTGGCAATATT TGAAATATT    GC  ATT
                                    TCAGGTTC    ACTTTATAA    CG  TAA
                                          -----  GT
GAM100  243   LOC2834 1  9750  XP_211053.1  5  169   TATTAGCTTATC  A     CA     T       4  A  c  c
        84                          AGCTAAAATATT TG AATATTTT  AGCTGAT
                                    GCATAGTG    AC TTATAAAA  TCGACTA
                                          G      --      T
GAM100  243   LOC2836 1  12992 XP_211143.1  3  305   AGTAACCAAATC    A      AGCT         4  A  c
c
        65                          TGTGAAAATATT TGAA TATTTTCA   GATT
                                    CACATGAG    ACTT ATAAAAGT   CTAA
```

```
                                                -       GT--
GAM100   243    LOC2836 1   2565   XP_211167.1   3  1527   GTTAAATAATCT         CAA  T          4  A  c  c
         90                                      GCCTAAAATATT TGAAATATTTT   GC GATTA
                                                TTAGAAAT    ATTTTATAAAA   CG CTAAT
                                                            TC-  T
GAM100   243    LOC2838 1   12634  XP_208853.1   3  2282   TTCTAGAGATCT      AT     CT          4  A  c  c

         10                                      TTTGAAAATTTC TGAAAT  TTTCAAG  GATT
                                                ACACGATT    ACTTTA  AAAGTTT  CTAG
                                                        --      T-
GAM100   243    LOC2841 1   16685  XP_209050.1   3  157    TAGTTAAGCACA          AA----  -        4  A  c  c
         66                                      AAGGAAAATATT TGAAATATTTTC     GCT GATTA
                                                TCAATAAA    ACTTTATAAAAG     CGA TTGAT
                                                            GAAACA   A
GAM100   243    LOC2843 1   5700   XP_211426.1   5  273    GTTCAAGATCAG    A    TT-             4  A  c  c
         04                                      CTTGTGCAATGT TGA ATATT   CAAGCTGATT
                                                ATCAAAAC    ACT TGTAA   GTTCGACTAG
                                                        A    CGT
GAM100   243    LOC2849 1   1198   XP_209414.1   3  1633   CTCCCCTTATGA         TCA  C          4  A  c  c

         25                                      TTACTAAATATT TGAAATATTT   AG TGATTA
                                                TTATTTTG    ATTTTATAAA   TC ATTAGT
                                                        --- -
GAM100   243    LOC2851 1   18198  XP_208296.1   3  1617   TAACTAATCATA       -  C  GC          4  A  c  c
         90                                      TTTAAATATATT TGAAATAT TTT AA  TGATTA
                                                TCACTTTC    ACTTTATA AAA TT  ACTAAT
                                                        T   T  AT
GAM100   243    LOC2852 1   12704  XP_211812.1   5  1767   TTAATTGCTTGC         TT-----    T       4  A  c  c
         29                                      TCTGCTAATATT TGAAATATT      CAAGC GATTA
                                                TCAGCTTC    ACTTTATAA      GTTCG TTAAT
                                                        TCGTCTC    -
GAM100   243    LOC2857 1   3743   XP_211998.1   3  79     AAAAGATAATCT        TT    CT-         4  A  c  c
         26                                      ATCTTGAATATT TGAAATAT  TCAAG   GATTA
                                                TCATATGT    ACTTTATA  AGTTC   CTAAT
                                                        --    TAT
GAM100   243    LOC2857 1   7609   XP_212010.1   5  466    ATCTATAAAATG  -       AAG  G         4  A  c  c
         49                                      AGAGAAAATATT TG AAATATTTTC   CT ATT
                                                TGCAATCC    AC TTTATAAAAG   GA TAA
                                                        G        A--  G
GAM100   243    LOC3385 1   16649  XP_290465.1   3  1418   TCTTATAGAGTC         CA  CT          4  A  c
c
         58                                      TCCTAGAATATT TGAAATATTTT  AG  GATT
                                                TCATTGGC    ACTTTATAAGA  TC  CTGA
                                                        --  CT
GAM100   243    LOC3395 1   14625  XP_290935.1   3  223    AAGAATGAATCT          A CT          4  A  c  c
         12                                      TCTGAAAATATT TGAAATATTTTCA G  GATT
                                                TTAAGTGA    ATTTTATAAAAGT C  CTAA
                                                        - TT
GAM100   243    LOC3401 1   15795  XP_291153.1   3  259    ACATGTGACTGA         CAAG           4  A  c
c
```

```
          38                    TTAGGAAATATT TGAAATATTTT  CTGATTA
                                TTATGGTC   ATTTTATAAAG  GATTAGT
                                        ----
GAM100  243  LOC3402 1  14531 XP_291212.1  3  1236  AAATGCAGTACA   T    ----  -     4  A  c  c
          52                    TTTGAAAATTTT TGAAA ATTTTCAA  GCTG ATT
                                TAGATTAT   ATTTT TAAAAGTT  TGAC TAA
                                        -     TACA  G
GAM100  243  LOC3404 1  6289  XP_291294.1  3  2015  AAAGTTAAGCAT     TTTCAAG        4  A  c
 c
          52                    TAATCAGATATT TGAAATAT    CTGATTA
                                TCATTTTT   ACTTTATA    GACTAAT
                                        -------
GAM100  243  LOC3482 1  6032  XP_300670.1  3  1456  ATTGTCCTGTCT     TT   - T     4  A  c  c
          35                    AGTTTGAATATT TGAAATAT  TCAAGCT GAT
                                TCAAGAAC   ACTTTATA  AGTTTGA CTG
                                        --    T  T
GAM100  243  LOC3482 1  6749  XP_302713.1  5  575   AAACTGCTCAAT      CAAGC        4  A  c
c
          90                    CAAAAGAATATT TGAAATATTTT  TGATT
                                TCAACTCT   ACTTTATAAGA   ACTAA
                                        AA---
GAM100  243  LOC3483 1  10842 XP_300729.1  3  1919  TTTGTTTATCAG     T  A   T     4  A  c  c
          96                    CCTGAGCATATT TGAAATAT TTCA GCTGAT
                                TCATTTTA   ACTTTATA GAGT CGACTA
                                        C  C    T
GAM100  243  LOC3486 1  3869  XP_300391.1  3  1595  TAACTAATCATA     -  C GC       4  A  c  c
          55                    TTTAAATATATT TGAAATAT TTT AA  TGATTA
                                TCACTTTG   ACTTTATA AAA TT  ACTAAT
                                        T  T  AT
GAM100  243  LOC3487 1  13038 XP_300396.1  3  758   TAATTTAACAAA  A     AGCT        4  A  c  c

          05                    TCTGAAAATATG TGA ATATTTTCA  GATT
                                TCAAATTA   ACT TATAAAAGT   CTAA
                                        G      ----
GAM100  243  LOC3487 1  10545 XP_302880.1  3  85    CTTGCAACTCAA     TTTCA  G      4  A  c
c
          49                    ATAGGCTATATT TGAAATAT    AGCT ATT
                                TCACAATA   ACTTTATA    TCGG TAA
                                        -----  A
GAM100  243  LOC5133 1  16981 NP_057730.1  5  204   ATTTGATTAGAA   AA     --       4  A  c  c
          6                     TTTGAAAATAAA TGA  TATTTTCAAG  CTGATTA
                                TCACATTT   ACT  ATAAAAGTTT  GATTAGT
                                        AA      AA
GAM100  243  LOC5708 1  15672 NP_065084.1  3  1002  GTCCAAGATGTG   AA     TG       4  A  c
c
          6                     CTTGAAAATACT TGA  TATTTTCAAGC  ATT
                                CATTAGGT   ACT  ATAAAAGTTCG  TAG
                                        C-      TG
GAM100  243  LOC9260 1  20066 XP_046097.1  3  2042  TTTTGTAATCAG     TTTCA        4  A  c
c
```

6 CTACTGTATGTT TGAAATAT AGCTGATTA
TTATTTTA ATTTTGTA TCGACTAAT
TGTCA
GAM100 243 LRAT 1 7406 NP_004735.1 3 1173 GCAAATAAAATT - GC 4 A c c
ATTGAAAATAAT TGAAAT ATTTTCAA TGATT
TTTAAAGT ATTTTA TAAAAGTT ATTAA
A --
GAM100 243 MADH4 1 7427 NP_005350.1 3 86 CTGTTTATAATC -- AGCT 4 A c c
TGAAGATATATT TGAA ATATTTTCA GATTA
TCACTTTT ACTT TATAGAAGT CTAAT
TA ----
GAM100 243 MAP2 1 3835 NP_002365.2 5 142 AAAAGAAAGAAG - AA GA 4 A c c
CCAGAAAATATT TGA AATATTTTC GCT TT
ATCAACCC ACT TTATAAAAG CGA AA
A AC AG
GAM100 243 MAP2 1 3835 NP_114033.1 5 142 AAAAGAAAGAAG - AA GA 4 A c c
CCAGAAAATATT TGA AATATTTTC GCT TT
ATCAACCC ACT TTATAAAAG CGA AA
A AC AG
GAM100 243 MAP2 1 3835 NP_114034.1 5 142 AAAAGAAAGAAG - AA GA 4 A c c
CCAGAAAATATT TGA AATATTTTC GCT TT
ATCAACCC ACT TTATAAAAG CGA AA
A AC AG
GAM100 243 MAP2 1 3835 NP_114035.1 5 142 AAAAGAAAGAAG - AA GA 4 A c c
CCAGAAAATATT TGA AATATTTTC GCT TT
ATCAACCC ACT TTATAAAAG CGA AA
A AC AG
GAM100 243 MCCC1 1 16428 NP_064551.2 3 186 GGTCACTAATTA CA C 4 A c c
TCTCAAAATATT TGAAATATTTT AG TGATTA
TCATACTA ACTTTATAAAA TC ATTAAT
C- T
GAM100 243 MDS024 2 7227 NP_068592.1 3 918 AAATAGGTACGG C - 4 A c c
TTTTAAAATATT TGAAATATTTT AAGCTG ATT
TTATATAG ATTTTATAAAA TTTGGC TGG
T A
GAM100 243 MDS024 2 10207 NP_068592.1 3 100 AATAAAGTAATT AAGC 4 A c c
ATGGAAAATATT TGAAATATTTTC TGATTA
TTAAACTC ATTTTATAAAAG ATTAAT
GT--
GAM100 243 MGC3407 1 13369 NP_689688.1 3 1399 CAAGATAATCAG A A --- 4 A c c
9 CTATATGAAGAA TGA AT TTTTCA AGCTGATTA
TCTCAGCT ACT TA AGAAGT TCGACTAAT
C - ATA
GAM100 243 MGC4899 1 14625 NP_848645.1 3 512 AAGAATGAATCT A CT 4 A c c
8 TCTGAAAATATT TGAAATATTTTCA G GATT
TTAAGTGA ATTTTATAAAAGT C CTAA
- TT
GAM100 243 NPTX1 1 9030 NP_002513.1 3 3028 ACCTATATCTCC - CT- T 4 A c c
CTTGAAAATACT TGAAA TATTTTCAAG GAT

TTCAGGCT ACTTT ATAAAAGTTC CTA
C CCT T
GAM100 243 NUP214 1 18578 NP_005076.2 3 175 GCGCATGATTAC TTT- C 4 A c c

TTGTTTTATATT TGAAATAT CAAG TGATTA
TCATGTTG ACTTTATA GTTC ATTAGT
TTTT -
GAM100 243 NUP214 1 18578 NP_705906.1 3 266 GCGCATGATTAC TTT- C 4 A c c

TTGTTTTATATT TGAAATAT CAAG TGATTA
TCATGTTG ACTTTATA GTTC ATTAGT
TTTT -
GAM100 243 NXT2 1 14988 NP_061168.2 3 473 TCAAATCAGTTC AAA --- 4 A c c
AGTGAAAATAGT TG TATTTTCA AGCTGATT
ACAGATTT AC ATAAAAGT TTGACTAA
ATG GAC
GAM100 243 OGT 1 19937 NP_003596.1 5 333 GTAATCAGTGCA AAT ---- 4 A c c
TTTGAAAATTCA TGA ATTTTCAA GCTGATTA
AGCCAGCA ACT TAAAAGTT TGACTAAT
--- TACG
GAM100 243 P2RY12 1 11851 NP_073625.1 3 27 TAACAAATTAAC A- C 4 A c c
TAAGGAAATATT TGAAATATTTTC AG TGATT
TCAATCTC ACTTTATAAAGG TC ATTAA
AA A
GAM100 243 P2RY12 1 11851 NP_795345.1 3 27 TAACAAATTAAC A- C 4 A c c
TAAGGAAATATT TGAAATATTTTC AG TGATT
TCAATCTC ACTTTATAAAGG TC ATTAA
AA A
GAM100 243 PACE4 1 6407 NP_002561.1 3 1073 ATGTTAATTATT - C 4 A c c
TTGACAAATATT TGAAATATTT TCAAG TGATTA
TCATATAT ACTTTATAAA AGTTT ATTAAT
C T
GAM100 243 PACE4 1 6407 NP_612192.1 3 1073 ATGTTAATTATT - C 4 A c c
TTGACAAATATT TGAAATATTT TCAAG TGATTA
TCATATAT ACTTTATAAA AGTTT ATTAAT
C T
GAM100 243 PARN 1 12302 NP_002573.1 3 938 TCAGATAGATCA T- GC 4 A c c
TTGTTAGATATT TGAAATATTT CAA TGATT
TCACATTT ACTTTATAGA GTT ACTAG
TT --
GAM100 243 PHF11 1 608 NP_057203.1 5 58 CCACAAGCCAAT TCA 4 A c c
CAGTTGGATATT TGAAATATTT AGCTGATT
TCATTCAT ACTTTATAGG TTGACTAA

GAM100 243 PRKDC 1 9408 NP_008835.5 3 300 ATATGTGATCAG - A C- 4 A c c
CTTTCAAAGCAT TG AAAT TTTT AAGCTGATTA
TTACAAGT AC TTTA GAAA TTCGACTAGT
A C CT
GAM100 243 PTGS2 1 10794 NP_000954.1 3 700 ACTACAATTGCT -- T 4 A c c
TGTTAAAATATT TGAAATATTTT CAAGC GATT

TTATAAGT ATTTTATAAAA GTTCG TTAA
TT -
GAM100 243 RAB27A 1 10792 NP_004571.2 3 224 AGCCTGAGAGTT CAAG 4 A c c
AGGAGAAATATT TGAAATATTTT CTGATT
TCAGAGCC ACTTTATAAAG GATTGA
AG--
GAM100 243 RANBP2L 1 3869 NP_005045.1 3 1595 TAACTAATCATA - C GC 4 A c c
1 TTTAAATATATT TGAAATAT TTT AA TGATTA
TCACTTTG ACTTTATA AAA TT ACTAAT
T T AT
GAM100 243 RBBP1 1 15909 NP_002883.2 3 655 TGAGCACACAAT TCAA - 4 A c c
TATGCAAATATT TGAAATATTT GC TGATT
TTAATGTT ATTTTATAAA CG ATTAA
---- T
GAM100 243 RBBP1 1 15909 NP_075376.1 3 655 TGAGCACACAAT TCAA - 4 A c c
TATGCAAATATT TGAAATATTT GC TGATT
TTAATGTT ATTTTATAAA CG ATTAA
---- T
GAM100 243 RBBP1 1 15909 NP_075377.1 3 655 TGAGCACACAAT TCAA - 4 A c c
TATGCAAATATT TGAAATATTT GC TGATT
TTAATGTT ATTTTATAAA CG ATTAA
---- T
GAM100 243 SELE 1 5666 NP_000441.1 3 1801 TTTTAAATTATA C C-- 4 A c c
ACTTAAAATATT TGAAATATTTT AAG TGATT
TTATAATT ATTTTATAAAA TTC ATTAA
- AAT
GAM100 243 SERPINA 1 8073 NP_783866.1 3 14 CTAAAGTGAGTT - -- G 4 A c c
11 GATGAAAATATT TG AAATATTTTCA AGCT ATT
TGCAAAAA AC TTTATAAAAGT TTGA TGA
G AG G
GAM100 243 SERPINB 1 18333 NP_003775.1 3 559 GGATTAGGGACC CA- ---- 4 A c c
7 TACCAAAATATT TGAAATATTTT AG CTGATT
TCATTAAT ACTTTATAAAA TC GATTAG
CCA CAGG
GAM100 243 SH3GLB1 1 19111 NP_057093.1 3 168 CAATAAAGTTGC - A T 4 A c c
ATGGTAAATATT TGAAATATTT TCA GC GATT
TCATTACA ACTTTATAAA GGT CG TTGA
T A -
GAM100 243 SIAH1 1 6318 NP_003022.1 3 656 ATTAATCAGTTC CA--- 4 A c c
ATTAGAAATATT TGAAATATTTT AGCTGATTA
TTAAAATC ATTTTATAAAG TTGACTAAT
ATTAC
GAM100 243 SLC26A4 1 851 NP_000432.1 3 2301 AAATCATGTACA - ---- - 4 A c c
TTTGAAAATATT TG AAATATTTTCAA GC TGATT
TGCACACA AC TTTATAAAAGTT TG ACTAA
G TACA T
GAM100 243 ST18 1 12777 NP_055497.1 3 1962 CAAACGTTTAAT TCA T 4 A c c

TTGCTAAATATT TGAAATATTT AGC GATTA
TTAACAAG ATTTTATAAA TCG TTAAT
--- T

GAM100 243 STOM 1 4767 NP_004090.3 3 2001 TAGTCCAATCAG AA T A 4 A c c
CTGAAATTAAAT TGA TA TTTCA GCTGATT
CACTTGGG ACT AT AAAGT CGACTAA
AA T -

GAM100 243 STX3A 1 8245 NP_004168.1 3 880 AGAATCCTAAGC - --- 4 A c c
TCTGGAAATATT TGAAATATTTTCA AGCT GATT
TCATGACA ACTTTATAAAGGT TCGA CTAA
C ATC

GAM100 243 SURF6 1 11475 NP_006744.2 3 1098 CCAGAAAAGAAG C - GA 4 A c c

TCTTAAGATATT TGAAATATTTT AAG CT TT
TCAAGGAA ACTTTATAGAA TTC GA AA
- T AG

GAM100 243 SV2B 1 2730 NP_055663.1 5 37 CCTAAGAAGTCA T AGC 4 A c c
CATGAACATATT TGAAATAT TTCA TGATT
TCACATTT ACTTTATA AAGT ACTGA
C AC-

GAM100 243 TCP10 1 15502 NP_004601.1 3 677 AAGATATAATTT - T CT 4 A c c
CTTGAAAATCTT TGA AA ATTTTCAAG GATTA
ATCAGAAG ACT TT TAAAAGTTC TTAAT
A C T-

GAM100 243 TGFA 1 4927 NP_003227.1 3 1597 ATGTTAAATTGG TAT TG 4 A c c
CTTGAAATTTTC TGAAA TTTCAAGC ATT
AGAGAATT ACTTT AAAGTTCG TAA
T-- GT

GAM100 243 TNFSF15 1 1209 NP_005109.2 3 328 GGTCAGGATTGA ----- G- 4 A c c
AAGAGAAATATT TGAAATATTT TCAA CTGATT
TCAACACC ACTTTATAAA AGTT GACTGG
GAGAA AG

GAM100 243 TRIM38 1 13589 NP_006346.1 3 691 TAGGACCAATTA T C 4 A c c
CCTTGAAATATT TGAAATATTT CAAG TGATT
TTAAAATC ATTTTATAAA GTTC ATTAA
- C

GAM100 243 UBXD2 1 5517 NP_055422.1 3 1281 CATTTATCAGAA C --- T 4 A c c
ACTTAAAATATT TGAAATATTTT AAG CTGAT
TCATACCG ACTTTATAAAA TTC GACTA
- AAA T

GAM100 243 UTY 1 2880 NP_009056.2 3 1171 CATATAGTCAGT TCAA- 4 A c c
GAAGTAAATATT TGAAATATTT GCTGATTA
TTAAAGGA ATTTTATAAA TGACTGAT
TGAAG

GAM100 243 VPS26 1 11671 NP_004887.2 3 1514 GCATGTAGTAAG A AA G 4 A c c

CCAGAAAATATT TGAA TATTTTC GCT ATTA
CAAAGAGA ACTT ATAAAAG CGA TGAT
- AC A

GAM100 243 WDFY3 1 17077 NP_055806.2 5 270 ACAGAGAATCAG ATT-- A 4 A c c

CTGGAGCCCAGA TGAAAT TTC AGCTGATT
TTTCAAGT ACTTTA GAG TCGACTAA
GACCC G

GAM100 243 ZFP91 1 2399 NP_444251.1 3 3120 TGTAATGGATCA C C 4 A c c
ATTTAAAATATT TGAAATATTTT AAG TGATT
TTATTTCT ATTTTATAAAA TTT ACTAG
- A

GAM100 243 ZID 1 19367 NP_006617.1 3 87 TAGAGATGCAGC TT -- - 4 A c c
ATTTGTAATATT TGAAATATT CAA GCTG ATT
TCATCCCC ACTTTATAA GTT CGAC TAG
T- TA G

GAM100 243 ZNF75A 1 6345 NP_694573.1 3 104 AAAATCACAAAC A C---- 4 A c c
CTTGAAAAATTT TGAAAT TTTTCAAG TGATT
TACATCAG ATTTTA AAAAGTTC ACTAA
- CAAAC

GAM101 302 KPNA6 1 17036 NM_012316.3 3 TCCTTACTGCTG TA TTGC 3 C c c
AACATCCTG CAGGATGTTCAGT AAGGA
GTCCTACAAGTCG TTCCT
-- TCA-

GAM101 302 REG-IV 1 12913 NM_032044.1 5 TCCTTGCACTAG T C TC -- 3 C c c
CTACATCCTCA A AGGATGT AGTT TGCAAGGA
A TCCTACA TCGA ACGTTCCT
- C -- TC

GAM101 302 STK38 1 14993 NM_007271.1 5 TCCTCTCTGTGC TT --- 3 C c c
TGAACATCCTGT TACAGGATGTTCAGT GCA AGGA
G GTGTCCTACAAGTCG TGT TCCT
-- CTC

GAM101 302 USP29 1 1408 NM_020903.1 3 TCCTTGCAAAGA G AG 3 C b b
GAATCCTGTA TACAGGAT TTC TTTGCAAGGA
ATGTCCTA GAG AAACGTTCCT
A --

GAM102 349 LOC1378 1 5436 XM_059923.2 5 ACCCCTCAACCT - T A- 3 C b b
29 GGCTCATCAACA TCTGTTGA GAGCC GGT AGGGGT
GA AGACAACT CTCGG CCA TCCCCA
A T AC

GAM102 349 ZNF323 1 8592 NM_030899.2 5 ACCCCAGGAATG G TGGTAA 3 C c
c
GCTTCAACAGA TCTGTTGA AGCC GGGGT
AGACAACT TCGG CCCCA
- TAAGGA

GAM103 276 FLJ1385 1 14225 NM_023079.2 3 GGGTATTTTTCT A AG- 3 C c c
5 TGGGGGTGGAGT TAC CCACTCCCAAGAAGAATA
A ATG GGTGGGGGTTCTTTTTAT
A GGG

GAM103 276 ITPR3 1 4198 NM_002224.1 3 CTTGTTTTTCTC CTCCCA 3 C c c
CTTTTGGTGTA TACACCA AGAAGAATAAG
ATGTGGT TCTTTTTGTTC
TTTCC-

GAM103 276 KIAA124 1 5226 XM_039676.3 3 TTTATTTTTAGG A AAG 3 C c c
0 GAGTGGGTA TAC CCACTCCC AAGAATAAG

ATG GGTGAGGG TTTTTATTT
- A--

GAM103 276 KIAA171 1 11994 XM_042936.3 3 TCTGTCTTGGGA - ATAAG 3 C c c
9 GTGGTGTA TACACCACTCCCAAGA AGA
ATGTGGTGAGGGTTCT TCT
G -----

GAM103 276 LOC1996 1 7894 NM_145295.1 3 CTTGTTCTTCTG C TCCCA 3 C c c

92 CTGTAGTGTG TACAC AC AGAAGAATAAG
GTGTG TG TCTTCTTGTTC
A TCG--

GAM104 355 ABAT 1 8488 NP_000654.1 3 81 GATTAGTTTGCC A C- 3 B c c
TAATTCATGTTT TGAAAACA GGA GGGCGAATT
TCACTTAA ACTTTTGT CTT TCCGTTTGA
A AA

GAM104 355 ABL2 1 7728 NP_005149.2 3 84 ACTTGTTTTCCT -- C 3 B c c
GTGTTCTTGTTT TGAAAACAAGGAC GGG GAAT
TCAGAAAA ACTTTTGTTCTTG TCC TTTG
TG T

GAM104 355 ABL2 1 7728 NP_009298.1 3 84 ACTTGTTTTCCT -- C 3 B c c
GTGTTCTTGTTT TGAAAACAAGGAC GGG GAAT
TCAGAAAA ACTTTTGTTCTTG TCC TTTG
TG T

GAM104 355 ADCYAP1 1 13625 NP_001108.1 3 328 TTGAAAATTCGC AG ----- 3 B c c

CCGAGCTGTTTA TGAAAACA GAC GGGCGAATT
TGTTTTTA ATTTTTGT TTG CCCGCTTAA
AT TCGAG

GAM104 355 ALS2CR3 1 4241 NP_055864.1 3 623 AGACTCCTATTT A C C 3 B c c
TCCTTTCTGTTT TGAAAACA GGA GGG GAAT
TCAGGCCT ACTTTTGT CTT TCC TTTA
- - T

GAM104 355 ARNT2 1 7789 NP_055677.1 3 1408 GTTTATGAATCC AGGAC C 3 B c
c

ATTCCCCTGTTT TGAAAACA GGG GAAT
TCAGGGAC ACTTTTGT CCC CTTA
----- -

GAM104 355 BART1 1 2233 NP_036238.1 3 617 TCTTAACATTTG AA GG 3 B c c
CAGTCCTTGTGT TGA ACAAGGAC GCGAAT
CACTGTCT ACT TGTTCCTG CGTTTA
G- A-

GAM104 355 BAT1 1 7126 NP_004631.1 5 250 TCCCCTACTCTT ACG C T 3 B c c
CACCCCTTGTTT TGAAAACAAGG GG GAA
TCACCTAT ACTTTTGTTCC CC CTT
--- A C

GAM104 355 BAZ2A 1 6461 NP_038477.1 3 1126 TTCAGTTTCCCC A - -- C T 3 B c c
AAGTACCTGTTT TGAAAACA GG AC GGG GAA
TCATTCCC ACTTTTGT CC TG CCC CTT
- A AA - T

GAM104 355 BCCIP 1 18876 NP_057651.1 3 167 TTCAGAGTTTGA ACGGG 3 B c c

GATACCTTGTTT TGAAAACAAGG CGAATT
TCATTTTT ACTTTTGTTCC GTTTGA
ATAGA

GAM104 355 BIRC5 1 12241 NP_001159.1 3 1055 GATTTGATTCGC AAACA C 3 B c c

CCTCCTCCCTGT TGA AGGA GGGCGAATT
CATAGAGC ACT TCCT CCCGCTTAG
GTCCC -

GAM104 355 C5R1 1 18094 NP_001727.1 3 73 TCCCGGCCATTC AC C 3 B c c

TCCCTCTTGTTT TGAAAACAAGG GGG GAAT
TCACTTCA ACTTTTGTTCT CCC CTTA
-- T

GAM104 355 DAZ 1 2687 NP_004072.1 5 40 CCGAGGGTTCGC T---- - A 3 B c c

CCGCCCTTGGTT GAAAAC AAGG CGGGCGAATT
TTCCTTAC CTTTTG TTCC GCCCGCTTGG
CATTC G C

GAM104 355 DAZ 1 2687 XP_088763.3 5 126 CCGAGGGTTCGC T---- - A 3 B c c

CCGCCCTTGGTT GAAAAC AAGG CGGGCGAATT
TTCCTTAC CTTTTG TTCC GCCCGCTTGG
CATTC G C

GAM104 355 DAZ2 1 2687 NP_065096.1 5 28 CCGAGGGTTCGC T---- - A 3 B c c

CCGCCCTTGGTT GAAAAC AAGG CGGGCGAATT
TTCCTTAC CTTTTG TTCC GCCCGCTTGG
CATTC G C

GAM104 355 DAZ3 1 2687 NP_065097.1 5 20 CCGAGGGTTCGC T---- - A 3 B c c

CCGCCCTTGGTT GAAAAC AAGG CGGGCGAATT
TTCCTTAC CTTTTG TTCC GCCCGCTTGG
CATTC G C

GAM104 355 DKFZP56 1 9349 NP_110443.1 3 481 TAAATATTCCTT A- C 3 B c c
6D1346 CGAGCTTTGTTT TGAAAACAAGG CGGG GAAT
TCATAAAA ACTTTTGTTTC GCTT CTTA
GA C

GAM104 355 DKFZP58 1 2243 XP_045876.1 3 861 ATTTTAATTTTT C 3 B c c
6C1324 CTGTCTTTGTTT TGAAAACAAGGACGGG GAATT
TCATAAGA ACTTTTGTTTCTGTCT TTTAA
T

GAM104 355 DKFZP58 1 15334 NP_056398.1 3 128 ATAAGCTATATT ACG C 3 B c c

6M0622 TTCCCCTTGTTT TGAAAACAAGG GG GAAT
TTAAAAGG ATTTTTGTTCC CC TTTA
--- T

GAM104 355 DKFZp76 1 10890 NP_115673.1 3 1169 TTCTTTTAATTC AGGAC C 3 B c c

1D112 CCCATGATGTTT TGAAAACA GGG GAATT
TCAATTAT ACTTTTGT CCC CTTAA
AGTA- -

GAM104 355 EDN3 1 20067 NP_000105.1 3 533 CAGTGGAGTTCC A ACG C 3 B c c

CAGGCCTTGTTT TG AAACAAGG GG GAATT
GCAGGAAG AC TTTGTTCC CC CTTGA

G GGA -

GAM104 355 FACL4 1 19125 NP_004449.1 3 2653 GAAAAGCTTTGT T 3 B c c
TTGTTCTTGTTT TGAAAACAAGGACGGGCGAA
TTAAGTTT ATTTTTGTTCTTGTTTGTTT
C

GAM104 355 FACL4 1 19125 NP_075266.1 3 2653 GAAAAGCTTTGT T 3 B c c
TTGTTCTTGTTT TGAAAACAAGGACGGGCGAA
TTAAGTTT ATTTTTGTTCTTGTTTGTTT
C

GAM104 355 FBXW8 1 2739 NP_036306.1 3 2415 AGGCGCATTCGC A A C 3 B c c
CCTTCCTAGTTT TG AAAC AGGA GGGCGAAT
GCAGCAAT AC TTTG TCCT CCCGCTTA
G A T

GAM104 355 FBXW8 1 2739 NP_699179.2 3 2415 AGGCGCATTCGC A A C 3 B c c
CCTTCCTAGTTT TG AAAC AGGA GGGCGAAT
GCAGCAAT AC TTTG TCCT CCCGCTTA
G A T

GAM104 3550 FLJ1097 1 11476 NP_060756.1 3 496 ACATTGATTCAC AG -- C 3 B c c
TGGCGTCTGTTT TGAAAACA GACG GG GAATT
TCATTTTA ACTTTTGT CTGC TC CTTAG
-- GG A

GAM104 3555 FLJ1482 1 7343 NP_116236.1 3 61 GTACTGTATTAA --- GCG 3 B c c
TTGTCCTTGTTT TGAA AACAAGGACGG AAT
ACTTCAGA ACTT TTGTTCCTGTT TTA
CAT AA-

GAM104 355 FLJ2044 1 18174 NP_060294.1 3 1708 TATAAAATATAT GACG G 3 B c c
5 TGGCTTTTGTTT TGAAAACAAG GGC AAT
TCAATGTG ACTTTTGTTT TCG TTA
---- G

GAM104 3552 FLJ2346 1 12718 NP_079119.2 3 821 GCACTTTTCCCC -- C T 3 B c c
AAGTTCTTGTTT TGAAAACAAGGAC GGG GAA
TTATTTTT ATTTTTGTTCTTG CCC CTT
AA - T

GAM104 355 FOXE2 1 10393 NP_036317.1 5 1552 AGTGAGATGAGC AACA GA 3 B c c
CCGTCCTTTCAC TGAA AGGACGGGC ATT
CTGCGATC ACTT TCCTGCCCG TAG
---- AG

GAM104 355 GALNT13 1 3213 XP_054951.3 3 2633 TCCCTAATTTCC G A - C 3 B c c
CAGTCCTTGTCT T AA ACAAGGAC GGG GAATT
TGAACAAT A TT TGTTCCTG CCC TTTAA
G C A -

GAM104 355 GOCAP1 1 19496 NP_073572.2 3 1177 GTGATTGGCTAG - -- G 3 B c c
TGATTCTTGTTT TGAAAACAAGGA CG GGC AATT
TCAGAAGG ACTTTTGTTCTT GT TCG TTAG
A GA G

GAM104 355 GRM7 1 862 NP_000835.1 3 463 TGTTTGTTTTCG A GG T 3 B c c
AATGCCTTGTTT TGAAAACAAGG CG CGAA
TCATAGAG ACTTTTGTTCC GT GCTT

- AA T

GAM104 355 H17739 1 10958 NP_542403.1 3 293 GTTGTTTGCCTT - AC--- 3 B c c
TCAACCTTGTTT TG AAAACAAGG GGGCGAAT
TACAGTTC AC TTTTGTTCC TCCGTTTG
A AACTT

GAM104 355 ING1 1 15187 NP_005528.2 3 174 AGTGATTCTGTT GAC 3 B c c
TGCCTTTTGTTT TGAAAACAAG GGGCGAAT
TCATTGGT ACTTTTGTTT TCCGTTTG

GAM104 355 JUND 2 3027 NP_005345.2 3 655 CTTGGTTCGCCC AG -- 3 B c c
GGTTTTCTGTTT TGAAAACA GA CGGGCGAATT
TCAGTAAA ACTTTTGT TT GCCCGCTTGG
CT TG

GAM104 355 JUND 2 15023 NP_005345.2 3 655 TCCTTGGTTCGC AG -- 3 B c c
CCGGTTTTCTGT TGAAAACA GA CGGGCGAATT
TTTCAGTA ACTTTTGT TT GCCCGCTTGG
CT TG

GAM104 355 KIAA124 1 18193 NP_054767.1 3 225 ATGTAGATATTT G C C 3 B c c
3 CTCTTATTGTTT TGAAAACAA GA GGG GAAT
TCATGTAA ACTTTTGTT TT CTC TTTA
A - -

GAM104 355 KIAA145 1 13381 XP_040100.3 3 155 ATTAATTATTTG G G 3 B c c
6 GTTGTTTTGTTT TGAAAACAAG ACGG CGAAT
TCATTTTT ACTTTTGTTT TGTT GTTTA
- G

GAM104 355 KIAA146 1 10494 XP_027396.4 3 1009 CAGATTTTCCTG --- C 3 B c c
5 TTTTCGTTGTTT TGAAAACAA GGACGGG GAATT
TCAAAGAC ACTTTTGTT TTTGTCC TTTAG
GCT T

GAM104 355 KIAA148 1 19705 XP_041126.4 3 142 GATGAGTTCTGG A GG -- 3 B c c
6 CAGTCTGTGTTT TGAAAACA GGAC GC GAATT
TCATTTGA ACTTTTGT TCTG CG CTTGA
G A- GT

GAM104 355 KIAA199 1 17442 XP_068710.3 3 59 AGACAAGAATTT A C C 3 B c c
8 TCCATTCTGTTT TGAAAACA GGA GGG GAATT
TCATAACT ACTTTTGT CTT CCT TTTAA
- A -

GAM104 355 LOC1149 1 17875 NP_612446.1 3 326 GGTTCTCTATTT A GGG 3 B c c

28 GAGTCTGTGTTT TGAAAACA GGAC CGAAT
TCAATAAA ACTTTTGT TCTG GTTTA
G A--

GAM104 355 LOC1438 1 6237 XP_084661.3 3 39 CCCTCTCGTTCC A A C 3 B c c
91 CCGTCCTCGTTT TG AAAC AGGACGGG GAAT
CCAGCATC AC TTTG TCCTGCCC CTTG
C C -

GAM104 355 LOC1583 1 20082 XP_098934.1 3 600 ATGTTACATTCA GACG --- 3 B c
c

76 AAGCTCTTGTTT TGAAAACAAG GGC GAAT
TCATCACA ACTTTTGTTC TCG CTTA

```
                                                ----  AAA
GAM104  355  LOC2829 1  7126  XP_212571.1  3  158   TCCCCTACTCTT        ACG  C  T       3  B  c  c

         21                                      CACCCCTTGTTT TGAAAACAAGG   GG GAA
                                                TCACCTAT    ACTTTTGTTCC   CC CTT
                                                        ---  A   C
GAM104  355  LOC2829 1  7126  XP_212619.1  3  158   TCCCCTACTCTT        ACG  C  T       3  B  c  c

         57                                      CACCCCTTGTTT TGAAAACAAGG   GG GAA
                                                TCACCTAT    ACTTTTGTTCC   CC CTT
                                                        ---  A   C
GAM104  355  LOC2829 1  7981  XP_210834.1  3  360   TAGGGAAAGTTT        GACG           3  B  c  c

         63                                      GTCAATTTGTTT TGAAAACAAG   GGCGAATT
                                                TCACTATA    ACTTTTGTTT    CTGTTTGA
                                                        AA--
GAM104  355  LOC2836 1  2214  XP_211159.2  3  973   TTCTCTGTTTGC T-----       GG          3  B  c  c
         78                                      CCGTGATTGTTT      GAAAACAA  ACGGGCGAAT
                                                TCTTTATT         CTTTTGTT  TGCCCGTTTG
                                                        TTATTT       AG
GAM104  355  LOC2848 1  1220  XP_211673.1  5  229   TCGGCGGATTTG        GGACG  -         3  B  c
c
         92                                      ACCAAATTGTTT TGAAAACAA     GG CGAATT
                                                TCAAGTTC    ACTTTTGTT     CC GTTTAG
                                                        AAA--  A
GAM104  355  LOC2858 1  7126  XP_209780.1  3  158   TCCCCTACTCTT        ACG  C  T       3  B  c  c

         37                                      CACCCCTTGTTT TGAAAACAAGG   GG GAA
                                                TCACCTAT    ACTTTTGTTCC   CC CTT
                                                        ---  A   C
GAM104  355  LOC2859 1  3485  XP_209821.1  3  195   ACAACATTCTCC        A  C-  C         3  B  c  c
         52                                      CTCTCCCTGTTT TGAAAACA GGA  GGG GAAT
                                                TCACTTTC    ACTTTTGT CCT  CCC CTTA
                                                        C   CT   T
GAM104  355  LOC2859 1  14299 XP_209820.1  3  1706  AATAGGGTATTC  A       ACG  -         3  B  c
c
         53                                      TGCCCCTTGTTT TG AAACAAGG   GGC GAAT
                                                CCACAGCT    AC TTTGTTCC   CCG CTTA
                                                        C        ---   T
GAM104  355  LOC3388 1  13795 XP_290216.1  3  1841  GAAACTGTATTT         AC  C         3  B  c  c
         19                                      TTCCTTTTGTTT TGAAAACAAGG  GGG GAAT
                                                TCATTTGA    ACTTTTGTTTT  CCT TTTA
                                                        --   T
GAM104  355  LOC3406 1  2687  XP_291365.1  5  25    CCGAGGGTTCGC T----     -   A         3  B  c  c
         28                                      CCGCCCTTGGTT     GAAAAC AAGG CGGGCGAATT
                                                TTCCTTAC         CTTTTG TTCC GCCCGCTTGG
                                                        CATTC     G   C
GAM104  355  LOC3484 1  6255  XP_302773.1  3  763   AAGTGCAACATT        AG A   C         3  B  c  c
         80                                      CACTCGCTGTTT TGAAAACA  G CGGG GAAT
                                                TCATTCTT    ACTTTTGT  C GCTC CTTA
```

```
                                                  --  -   A
GAM104   355   LOC3486 1   6408   XP_302853.1   3  2075   TATTGTATTGGC     A    ACG  G          3  B  c
c
          87                          CATCCCTTGTTT TGAAA CAAGG   GGC AAT
                                     CATATTCG    ACTTT GTTCC   CCG TTA
                                                 -    CTA   G
GAM104   355   LOC5113 1   11206  NP_057209.2   3  823    AGGTATTCTTTC       GGA   C--         3  B  c
c
          6                           CTGACATTGTTT TGAAAACAA   CGGG   GAAT
                                     TCAGAATA    ACTTTTGTT   GTCC   CTTA
                                                    ACA    TTT
GAM104   355   LoopADR 1   3456   NP_113624.1   3  136    GAGGACGCTTCC   ----      C  C  T     3  B  c  c

                                     CCTTCCTTGTTT TGA    AAACAAGGA GGG GAA
                                     CTGCTCAG    ACT    TTTGTTCCT CCC CTT
                                              CGTC       T  -  C
GAM104   355   MAPKBP1 1   12122  XP_031706.7   3  2275   TCCAGATTTGCC  G      AC-           3  B  c
c
                                     CCCGCCTTGTTT T AAAACAAGG   GGGCGAATT
                                     TGAAAGCC    A TTTTGTTCC   CCCGTTTAG
                                              G       GCC
GAM104   355   MN1    2   5008   NP_002421.2   3  370    ATGACCTCTTTC       G    C  T       3  B  c  c
                                     CTTGTTTTGTTT TGAAAACAAG ACGGG GAA
                                     TCATGCTG    ACTTTTGTTT TGTTC CTT
                                                 -    -  T
GAM104   355   MN1    2   11831  NP_002421.2   3  362    TTTAGATGACCT       G    C  T       3  B  c  c
                                     CTTTCCTTGTTT TGAAAACAAG ACGGG GAA
                                     TGTTTTCA    ACTTTTGTTT TGTTC CTT
                                                 -    -  T
GAM104   355   NAP1L1  1   19810  NP_004528.1   3  131    TATTTGTTGTTT T                  3  B  c  c
                                     GTTTGCTTGTTT  GAAAACAAGGACGGGCGAAT
                                     TTGTTTTT     TTTTTGTTTTTGTTCGTTTG
                                              -
GAM104   355   NAP1L1  1   19810  NP_631946.1   3  805    TATTTGTTGTTT T                  3  B  c  c
                                     GTTTGCTTGTTT  GAAAACAAGGACGGGCGAAT
                                     TTGTTTTT     TTTTTGTTTTTGTTCGTTTG
                                              -
GAM104   355   PCDHB9  1   5387   NP_061992.2   3  431    CTTATTGGTTTG   AA     CG           3  B  c  c
                                     CCATCCTTGTTC TGA  ACAAGGA  GGCGAATT
                                     ATTACAAC    ACT  TGTTCCT  CCGTTTGG
                                                 --      A-
GAM104   355   PLCD4   1   4220   NP_116115.1   3  210    CTCTTTTCTTCC       -  C  C-  T      3  B  c  c
                                     CTTCCTTTGTTT TGAAAACAA GGA GGG  GAA
                                     TCATAAGC    ACTTTTGTT CCT CCC  CTT
                                                 T  T  TT  T
GAM104   355   PTD012  1   10079  NP_054758.2   3  1003   CTAGCCATAATT    A    AC  C          3  B  c  c

                                     CCTCCCTTGTTT TGAAA CAAGG  GGG GAATT
                                     CGATTGCC    GCTTT GTTCC  CTC CTTAA
                                                 -    --  -
```

GAM104 355 RAG1 1 18485 NP_000439.1 3 3196 CCTGTATTTCCA AG- - C 3 B c c
TGTCAAATGTTT TGAAAACA GACG GG GAAT
TCAAATAA ACTTTTGT CTGT CC TTTA
AAA A -
GAM104 355 SCN5A 1 19424 NP_000326.2 3 748 AGGTCCCATTTT - AC C 3 B c c
CCCCCTGTGTTT TGAAAACA AGG GGG GAAT
TCACGCAG ACTTTTGT TCC CCC TTTA
G -- T
GAM104 355 SFPQ 1 9786 NP_005057.1 3 782 GTTGCATTTCCC C- C T 3 B c c
CATTTCTTGTTT TGAAAACAAGGA GGG GAA
TTAAAAGA ATTTTTGTTCTT CCC CTT
TA - T
GAM104 355 TEX11 1 12751 NP_112566.1 3 114 TTTCTGTTTGCT A AC- 3 B c c
CAGACCCTGTTT TGAAAACA GG GGGCGAAT
TCATGTTG ACTTTTGT CC CTCGTTTG
C AGA
GAM104 355 TEX14 1 6837 NP_112562.1 3 197 AGCAGCACATTC GAC GC 3 B c c

AACCATTTGTTT TGAAAACAAG GG GAAT
TCAGTCAG ACTTTTGTTT CC CTTA
A-- AA
GAM104 355 WDR5 1 9726 NP_438172.1 3 648 GCACATGGATTT AC C 3 B c c
TCCCTTTTGTTT TGAAAACAAGG GGG GAATT
TCAGTGTT ACTTTTGTTTT CCC TTTAG
-- T
GAM104 355 ZDHHC2 1 7683 NP_057437.1 3 2016 GTTGTAATTGTT A C C 3 B c c
CCCTTTCTGTTT TGAAAACA GGA GGG GAAT
TCATATAG ACTTTTGT CTT TCC CTTG
- - -
GAM104 355 ZNF339 1 10412 NP_067043.1 3 244 GCTCACATTCAC GACG C 3 B c
c

CAAAGTTTGTTT TGAAAACAAG GG GAAT
TCATGATC ACTTTTGTTT CC CTTA
GAAA A
GAM105 318 ATP10D 1 13724 NM_020453.2 5 CAGACGTGGTAC G G TG -- 3 C c c

CAGACACCAGAG GCT TGGTGTCTGG TG GC CTG
C CGA ACCACAGACC AT TG GAC
G - GG CA
GAM105 318 COL19A1 1 19700 NM_001858.2 3 CAGGGAGCCCAA T C GTGG 3 C c
c

ACACCCAGC GCTG GGTGT TGGGT CCTG
CGAC CCACA ACCCG GGAC
- A AG--
GAM105 318 DKFZP72 1 6512 XM_045308.6 3 CAGACCCACCAG GC G T C 3 C c
c
7G051 ACACCACA TGTGGTGTCTGG TG GG CTG
ACACCACAGACC AC CC GAC
-- - - A
GAM105 318 EYA3 1 15188 NM_001990.2 5 CAGACTCAATAC GTG - C 3 C c c

CAGACACTACAG GCTGTGGTGTCTGG TG G CTG
C CGACATCACAGACC AC C GAC
ATA T A

GAM105 3180 KIAA155 1 16950 XM_039393.3 3 CAGACCACACCC G T C C 3 C c c
ATACCCAAGC GCT TGG GT TGGGTGTGG CTG
CGA ACC CA ACCCACACC GAC
- - T A

GAM105 318 SLC12A7 1 17473 NM_006598.1 3 CAGAGCGTGTCC TGTG - 3 C c c

CAGACATCACAG GCTGTGGTGTCTGGG GC CTG
C CGACACTACAGACCC CG GAC
TGTG A

GAM106 231 AD024 1 14955 NP_065726.1 3 507 TGGTTCCAAGTC A T A 1 B c c
TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -

GAM106 231 AEBP2 1 20032 NP_694939.1 3 2306 AATCATAATCCT C -- C 1 B c c
TTTGCTGCTTAT ATTAG TA TAGCAAAAGG TTA
CTGATGTT TAGTC AT GTCGTTTTCC AAT
T TC T

GAM106 231 C14orf7 1 17031 XP_085101.1 3 454 CAAACCCAGCCT T --- T 1 B c c
7 TTTGCGATTATG AT AGCTATA GCAAAAGGCT
GCTTGTGG TG TCGGTAT CGTTTTCCGA
T TAG C

GAM106 231 C20orf1 1 17640 XP_300782.1 3 334 TCAGGAAAGCCT A---- G - 1 B c c
42 TTATGGTGTGGC TTAGCTATA CA AAAGGCTT
TAAAGGAG AATCGGTGT GT TTTCCGAA
GAGGA G A

GAM106 231 C20orf1 1 4450 NP_689880.1 3 834 GAGCTAGGCTGT G A - 1 B c c
47 TTTGCTAGAGAT ATTA CT TAGCAAAA GGCTTA
AATTGCAA TAAT GA ATCGTTTT TCGGAT
A G G

GAM106 231 CYCS 1 6813 NP_061820.1 3 3179 CTGTTAAGCCCT GCA- A 1 B c c
TGAAATATAGCT ATTAGCTATA AA GGCTTA
AGTGTGAC TGATCGATAT TT CCGAAT
AAAG C

GAM106 231 DKFZP56 1 4872 NP_114431.2 3 712 GCTGAAAATCCT ATA C 1 B c c

4D172 TTTGCCAGCTAA ATTAGCT GCAAAAGG TT
TTGTGAGA TAATCGA CGTTTTCC AA
C-- T

GAM106 231 DKFZp76 1 2068 XP_089143.5 5 36 AATTCCAAGGTT A G 1 B c c
1A078 TTTGCTACAGTT ATTAGCT TAGCAAAAG CTT
AGTTTCTC TGATTGA ATCGTTTTT GAA
C G

GAM106 231 FGF5 1 14955 NP_004455.1 3 4300 TGGTTCCAAGTC A T A 1 B c c
TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -

GAM106 231 FGF5 1 14955 NP_149134.1 3 4631 TGGTTCCAAGTC A T A 1 B c c

TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -

GAM106 231 FLJ1061 1 18157 NP_061940.1 3 809 AGAGCGACTTCT GC ----- 1 B c c
3 TTTGCTATGAGT ATTA TATAGCAAAAG GCTT
AATACATT TAAT GTATCGTTTTC CGAG
GA TTCAG

GAM106 231 FLJ1081 1 5821 NP_060701.1 3 572 CCTGTCAGCCTC AGC - T 1 B c c
5 TTTCCCATAGCT ATTAGCTAT AAA AGGCT
AATAGACA TAATCGATA TTT TCCGA
CCC C C

GAM106 231 FLJ2036 1 9007 NP_060252.1 3 353 AATAGCTTTGTT T ---- T 1 B c c
0 TTTGCTATGCTA ATTAGC ATAGCAAAA GGCT
ATGTCTAG TAATCG TATCGTTTT TCGA
- TGTT T

GAM106 231 FLJ3871 1 19701 NP_689580.1 3 225 CCAGCAAGCATT TA A - 1 B c c
6 TCTGCCCTAGCT ATTAGCTA GCA AAG GCTT
AATTCTCC TAATCGAT CGT TTT CGAA
CC C A

GAM106 231 FLT3 1 20091 NP_004110.1 3 340 AAACAAAAGCAT A----- G 1 B c c
TTTGCTAAGGAG ATTAGCT TAGCAAAA GCTT
AAGCTAAT TAATCGA ATCGTTTT CGAA
AGAGGA A

GAM106 231 GJA4 1 17924 NP_002051.1 3 292 GCCCTCTGGCCT ATA T 1 B c c
TTTGCAGCTGAT ATTAGCT GCAAAAGGCT
CCAGAGGA TAGTCGA CGTTTTCCGG
--- T

GAM106 231 GRPR 1 10332 NP_005305.1 5 126 AATTCTAAGCCT A------- GC 1 B c c
TTTTGTGGCTAA TTAGCTATA AAAAGGCTTA
GTTTTGTT AATCGGTGT TTTTCCGAAT
TTGTTTTG --

GAM106 231 ITGA9 1 4333 NP_002198.1 3 330 AAATATAAGCCT C GCA 1 B c c
TTTATACTGATT ATTAG TATA AAAGGCTTA
ATTCTTTT TAGTC ATAT TTTCCGAAT
- ---

GAM106 231 KIAA114 1 2396 XP_044014.1 3 2762 AGAAGTAAGCCT CAA 1 B c c
3 TGGACTGTAGCT ATTAGCTATAG AAGGCTTA
GATTATAA TAGTCGATGTC TTCCGAAT
AGG

GAM106 231 KIAA119 1 20133 NP_065765.1 3 124 GTGATTAAGCCT CT AA 1 B c c
8 TCAGTTATCCTA ATTAG ATAGC AAGGCTTA
ATTCCCTT TAATC TATTG TTCCGAAT
C- AC

GAM106 231 KIAA176 1 18828 XP_047355.1 3 1680 CCTAATAAGCCT T AG 1 B c c
5 TTTGGATGCTAA ATTAGC AT CAAAAGGCTTA
TCTGGATT TAATCG TA GTTTTCCGAAT
- G-

GAM106 231 LOC1457 1 823 XP_096860.1 5 1687 TACAGAGTTCCT C -- 1 B c c
86 TTTGCTATGTTT ATTAG TATAGCAAAAGG CTT
GGTAACAT TGGTT GTATCGTTTTCC GAG

T TT
GAM106 231 LOC1464 1 4016 XP_047734.7 3 712 TGGTTCAAAGTC A T A 1 B c c
89 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAATGC TAA TG TATCGTTT CTGAA
G T -
GAM106 231 LOC1467 1 14955 XP_097076.1 3 1470 TGGTTCCAAGTC A T A 1 B c c
33 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -
GAM106 231 LOC1540 1 4793 XP_098468.1 5 586 ATATATTAAGCT ----- G 1 B c c
84 TTTGCTGTAGAT ATTAG CTATAGCAAAAG CTTA
TGCCTAGT TGATC GATGTCGTTTTC GAAT
CGTTA -
GAM106 231 LOC1653 1 18910 XP_092518.1 3 395 AGCTGTCTGAGT AGCA 1 B c
c
24 TTTTAAATAGCT ATTAGCTAT AAAGGCTTA
AATACGAC TAATCGATA TTTTTGAGT
AA--
GAM106 231 LOC2836 1 2396 XP_208762.1 5 3190 AGAAGTAAGCCT CAA 1 B c c
33 TGGACTGTAGCT ATTAGCTATAG AAGGCTTA
GATTATAA TAGTCGATGTC TTCCGAAT
AGG
GAM106 231 LOC2844 1 9942 XP_211447.1 3 126 TTTAAATAGCTT GC- T 1 B c c
09 TTTGCTATATGA ATTA TATAGCAAAAGGCT
TAATATAG TAAT ATATCGTTTTTCGA
AGT T
GAM106 231 LOC2849 1 12650 XP_211723.1 3 1118 TGGTTCCAAGTC A T A 1 B c c
97 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAATGC TAA TG TATCGTTT CTGAA
G T -
GAM106 231 LOC2851 1 3357 XP_211786.1 3 574 ATATTTCCGCCT A TT 1 B c c
53 TTTGCTAAGCTA ATTAGCT TAGCAAAAGGC
ATATATAG TAATCGA ATCGTTTTCCG
- CC
GAM106 231 LOC2863 1 14955 XP_212290.1 5 1462 TGGTTCCAAGTC A T A 1 B c c
56 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -
GAM106 231 LOC2864 1 18372 XP_210047.1 5 2682 CATGATGGGACT C A - 1 B c c
35 TATTCTGTAGCT ATTAGCTATAG AA AGG CTTA
AATCTGAT TAATCGATGTC TT TTC GGGT
- A A
GAM106 231 LOC3398 1 13768 XP_295079.1 3 726 ACAGCCAAGCCT - ATAG 1 B c
c
32 TTTGAAGACTAA ATTAG CT CAAAAGGCTT
TTAGAAAA TAATC GA GTTTTCCGAA
A A---

GAM106 231 LOC3398 1 14955 XP_295089.1 3 566 TGGTTCCAAGTC A T A 1 B c c
65 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -
GAM106 231 LOC3482 1 13642 XP_302706.1 3 265 TGGTTCCAAGTC A T A 1 B c c
64 TTTGCTATTGTA ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
A T -
GAM106 231 LOC3482 1 13642 XP_302705.1 3 265 TGGTTCCAAGTC A T A 1 B c c
65 TTTGCTATTGTA ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
A T -
GAM106 231 LOC3487 1 1854 XP_300822.1 3 702 AAAGGAAAGCCT CT C 1 B c c
21 TTTCCTGTCTGA ATTAG ATAG AAAAGGCTT
TCCTGAGA TAGTC TGTC TTTTCCGAA
-- C
GAM106 231 LOC3494 1 18372 XP_301084.1 5 2683 CATGATGGGACT C A - 1 B c c
30 TATTCTGTAGCT ATTAGCTATAG AA AGG CTTA
AATCTGAT TAATCGATGTC TT TTC GGGT
- A A
GAM106 231 LOC3494 1 18372 XP_301086.1 5 616 CATGATGGGACT C A - 1 B c c
32 TATTCTGTAGCT ATTAGCTATAG AA AGG CTTA
AATCTGAT TAATCGATGTC TT TTC GGGT
- A A
GAM106 231 LOC5708 1 14955 NP_065084.1 3 2247 TGGTTCCAAGTC A T A 1 B c c
6 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -
GAM106 231 LZIC 1 14665 NP_115744.2 5 58 AACTTTGAGCCT CT A 1 B c c
TTTGTAGTCCTG ATTAG AT GCAAAAGGCTTA
ATGAATAA TAGTC TG TGTTTTCCGAGT
C- A
GAM106 231 MAP3K7I 1 17213 NP_055908.1 3 739 GTGTAATAGCCT CTA T 1 B c c
P2 TTTGTTAACTAA ATTAG TAGCAAAAGGCT
TTTTCTTT TAATC ATTGTTTTCCGA
A-- T
GAM106 231 MAP3K7I 1 17213 NP_663317.1 3 1420 GTGTAATAGCCT CTA T 1 B c
c
P2 TTTGTTAACTAA ATTAG TAGCAAAAGGCT
TTTTCTTT TAATC ATTGTTTTCCGA
A-- T
GAM106 231 MGC1138 1 5748 NP_116322.1 3 902 GAGTGACAGCCT GC T 1 B c c
6 TTTTATGGTTGG ATTAGCTATA AAAAGGCT
TGTTACTA TGGTTGGTAT TTTTCCGA
-- C
GAM106 231 MGC2700 1 14955 NP_689795.2 3 809 TGGTTCCAAGTC A T A 1 B c c

5 TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -

GAM106 231 MJD 1 18203 NP_004984.2 3 323 CTTGGATCTTTT TA-- C 1 B c c
TGCAGACTAGCT ATTAGCTA GCAAAAGG TT
AATTAGCT TAATCGAT CGTTTTTC AG
CAGA T

GAM106 231 MJD 1 18203 NP_109376.1 3 323 CTTGGATCTTTT TA-- C 1 B c c
TGCAGACTAGCT ATTAGCTA GCAAAAGG TT
AATTAGCT TAATCGAT CGTTTTTC AG
CAGA T

GAM106 231 OPHN1 1 14955 NP_002538.1 3 4238 TGGTTCCAAGTC A T A 1 B c c
TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -

GAM106 231 PDE10A 1 13919 NP_006652.1 3 289 GCAAACCAGCCT A-- C T 1 B c c
TTTCTAATAGGC ATTAGCT TAG AAAAGGCT
TAATATTG TAATCGG ATC TTTTCCGA
ATA - C

GAM106 231 PHKA1 1 9297 NP_002628.1 3 46 TTCTGGGAGCCT ATAG 1 B c c
TTTGACAGCTGG ATTAGCT CAAAAGGCTT
TCCCTGCC TGGTCGA GTTTTCCGAG
CA--

GAM106 231 PTGS2 1 10976 NP_000954.1 3 1527 AAGCAGAGAATT C- GG 1 B c c

TTATTTATAGCT ATTAGCTATAG AAAA CTT
AATTTTAG TAATCGATATT TTTT GAG
TA AA

GAM106 231 RAB3IP 1 13725 NP_071901.2 5 181 TATGATGAGGCT G 1 B b b
TTTGCTATGGCT ATTAGCTATAGCAAAAG CTTA
AATGATCC TAATCGGTATCGTTTTC GAGT
G

GAM106 231 RASGRP3 1 9577 NP_733772.1 3 326 AAATGAAAGCCT C - - 1 B c c
TTTTGCATGTAC ATTAG TATA GCAAAA GGCTT
TTGATACT TAGTT ATGT CGTTTT CCGAA
C A T

GAM106 231 RETNLB 1 14955 NP_115968.1 3 803 TGGTTCCAAGTC A T A 1 B c c
TTTGCTATTGTG ATT GC ATAGCAAA GGCTT
AATAGTGC TAA TG TATCGTTT CTGAA
G T -

GAM106 231 RHBDL 1 4596 NP_003952.1 3 201 CGGTCTGAGCCT C AGC 1 B c c

TTTTGGATAATT ATTAG TAT AAAAGGCTTA
AATAAATA TAATT ATA TTTTCCGAGT
A GGT

GAM106 231 RNF32 1 14433 NP_112198.1 3 398 GTCCTAAAGCCT CT A A 1 B c c
TTGCCATTCCTA ATTAG AT GCAAA GGCTT
ATACTCGT TAATC TA CGTTT CCGAA
CT C -

GAM106 231 S100B 1 14463 NP_006263.1 3 117 GAGCTTTCCAGC AAA T 1 B c c

CGTGTTGTAGCT ATTAGCTATAGCA GGCT
AATTAGGA TAATCGATGTTGT CCGA
G-- C

GAM106 231 STAF42 1 565 NP_444281.1 3 5 CAAGGAGGGGCT T G 1 B c c
TTTGCTGTGCTA ATTAGC ATAGCAAAAG CTT
ATTAGGAT TAATCG TGTCGTTTTC GGG
- G

GAM106 231 STX7 1 10787 NP_003560.1 3 633 ATATAATAAGCT ----- G 1 B c c
TTTGCTGTAGAT ATTAG CTATAGCAAAAG CTTA
TGCCTAGT TGATC GATGTCGTTTTC GAAT
CGTTA -

GAM106 231 SURF5 1 6232 NP_852468.1 3 2451 AAGCTCAAGCCT ATA A 1 B c c
TTGCGAAGCTAA ATTAGCT GCAAA GGCTT
TGACCTGC TAATCGA CGTTT CCGAA
AG- -

GAM106 231 TBC1D2 1 4122 NP_060891.1 5 814 GAATTGAGAGCC AAA 1 B c c
ACTGCTATAGCT ATTAGCTATAGCA GGCTT
GATCCTTC TAGTCGATATCGT CCGAG
CA-

GAM106 231 TLL1 1 5091 NP_036596.3 3 1987 GTAGATGAGCCT ATA - 1 B c c
TTTAGTAGAGCT ATTAGCT GC AAAAGGCTTA
GATTTATT TAGTCGA TG TTTTCCGAGT
GA- A

GAM107 341 BTN2A2 1 19308 NM_006995.2 3 CCCAGGATTTCC TA GG 3 C c c
ACAGCACAC GTGTGCTGT GAA GTTCTGGG
CACACGACA CTT TAGGACCC
C- --

GAM107 341 DLX4 1 489 NM_138281.1 3 CCCAGAACCCTT T TGTTAG 3 C c c
GGTCTTGCCAC GTG GC AAGGGTTCTGGG
CAC CG TTCCCAAGACCC
- TTCTGG

GAM107 341 LOC1275 1 8266 3 CCCATCACCCCC C AGAA TC 3 C c c
34 CAACACACAC GTGTG TGTT GGGT TGGG
CACAC ACAA CCCA ACCC
- CCC- CT

GAM108 298 FLJ2127 1 532 3 CAACACCAGGAT A GACA G 3 C c c
6 GAGGTCCCA TGG ACCT AT TTGGTGTTG
ACC TGGA TA GACCACAAC
C G--- G

GAM108 298 FOXE1 1 9989 NM_004473.3 3 CAACACCAGAGA A ACAATG 3 C c
c
CCAGGATCCA TGGA CCTG TTGGTGTTG
ACCT GGAC GACCACAAC
A CAGA--

GAM108 298 PKIG 1 15790 NM_007066.2 3 CAACACCAACAC ACCT CAA 3 C c c
CTCCTCTCCA TGGA GA TGTTGGTGTTG
ACCT CT ACAACCACAAC
CTC- CC-

GAM109 290 ADAM10 1 14240 NM_001110.1 5 CTGCTGTTAACC CA G AGCA 3 C c
c

CGTGAGG CCT CAC GTTAACAGCAG
GGA GTG CAATTGTCGTC
-- - CC--

GAM109 290 ATP6V0B 1 18127 NM_004047.2 3 CTGCTGCTGACT C C A 3 C c c
CTGTGCAGCTG CA CTGCACAG AGTTA CAGCAG
GT GACGTGTC TCAGT GTCGTC
C - C

GAM109 290 BMF 1 13824 NM_033503.2 3 CTGCCCCCTCTC C TTAACA- 3 C c c
TCTGTGCAGGTG CACCTGCACAG AG GCAG
GTGGACGTGTC TC CGTC
- TCTCCCC

GAM109 290 BOP 1 6290 XM_097915.2 5 CTGCTCACCCAT CAGTTAAC 3 C c c
CTGTGCAGGTG CACCTGCACAG AGCAG
GTGGACGTGTC TCGTC
TACCCAC-

GAM109 290 C20orf1 1 14412 XM_300247.1 3 CTGCTGGCTGTG CA--- TAA 3 C c c
24 TCCATGCAGGTG CACCTGCA GCAGT CAGCAG
GTGGACGT TGTCG GTCGTC
ACCTG ---

GAM109 290 CBFA2T2 1 2361 NM_175864.1 3 CTGCTGGATGTG C GTTAA 3 C c
c
CTGTGCAGGT ACCTGCACAGCA CAGCAG
TGGACGTGTCGT GTCGTC
- GTAG-

GAM109 290 FLJ2170 1 15800 3 CTGCTGGTTGCT C A GTTAA 3 C c c
9 GAGCAAGTG CAC TGC CAGCA CAGCAG
GTG ACG GTCGT GTCGTC
A A TG---

GAM109 290 KIAA111 1 12180 3 CTGCTGTCCTAT C GC TTA 3 C c c
0 GTGCAGGT ACCTGCACA AG ACAGCAG
TGGACGTGT TC TGTCGTC
- A- C--

GAM109 290 KIAA146 1 15690 XM_050285.2 3 CTGCTGTTAAAG C CA AG 3 C c c
6 TTGCAGGT ACCTGCA GC TTAACAGCAG
TGGACGT TG AATTGTCGTC
- -- A-

GAM109 290 KIAA187 1 5187 XM_056635.4 5 CTGCTGTTAACC C -- 3 C b b
9 ATGCTGTGCATG CAC TGCACAGCA GTTAACAGCAG
TG GTG ACGTGTCGT CAATTGTCGTC
T AC

GAM109 290 LOC1318 1 14590 XM_067585.7 5 CTGCTGTTTGTT C C GTT 3 C c c
73 CTGCAAGTG CAC TGCA AGCA AACAGCAG
GTG ACGT TTGT TTGTCGTC
A C ---

GAM109 290 LOC2032 1 2084 5 CTGCTGTTGGCT CA CACA 3 C c c
97 GCACCAGG CCTG GCAGTTAACAGCAG
GGAC CGTCGGTTGTCGTC
-- CA--

GAM109 290 LOC2219 2 4591 XM_166555.1 5 TGCTTACTGCTG CA TAAC G 3 C c
c

22 CAGGTG CACCTGCA GCAGT AGCA
GTGGACGT CGTCA TCGT
-- T--- -
GAM109 290 LOC2219 2 15720 XM_166555.1 5 CTGCTGCCTTCC G TTAA- 3 C c c

22 TGCTGTGAGGTG CACCT CACAGCAG CAGCAG
GTGGA GTGTCGTC GTCGTC
- CTTCC
GAM109 290 LOC9126 1 4492 XM_037268.7 5 CTGCTGTTCCAG C CAGTT 3 C c c

6 CCTCTGCAGGTG CACCTGCA AG AACAGCAG
GTGGACGT TC TTGTCGTC
C CGACC
GAM109 290 TMEPAI 1 1160 NM_020182.2 3 TGCTGGTGACGT AGCA A G 3 C c
c
GCAGGTG CACCTGCAC GTTA CAGCA
GTGGACGTG CAGT GTCGT
---- G -
GAM109 290 VEZATIN 1 3317 NM_017599.2 3 CTGCTGGCCTTG -- CA TTAA 3 C c
c
CTGCAGAAGTG CAC CTGCA GCAG CAGCAG
GTG GACGT CGTT GTCGTC
AA -- CCG-
GAM109 290 ZFP106 1 11274 NM_022473.1 3 CTGCCTGTGTGT C G GTTA - 3 C c c

GTGCAAGTG CAC TGCACA CA ACAG CAG
GTG ACGTGT GT TGTC GTC
A - G--- C
GAM110 375 LOC1476 1 10171 XM_097265.6 5 CGCCAGCTCTGC C ACT - A 3 C c
c
70 AGAGCCCAGA TCT GGGCTCT CAGA CT GCG
AGA CCCGAGA GTCT GA CGC
- C-- C C
GAM111 311 HA-1 1 8389 XM_037574.3 3 GGAAGCTGTCCC GA T CA A 3 C c c
TGCCCAGT ACTG GCA GG ACAGCTTCC
TGAC CGT CC TGTCGAAGG
-- C -- C
GAM111 311 LOC2195 1 3411 5 GAAGCTGTTTGC A - CAGG C 3 C c c
13 AGCAGCTC GA CTG TGCA AACAGCTTC
CT GAC ACGT TTGTCGAAG
C G ---- -
GAM111 311 LOC2574 1 6598 5 GGAAGCCTGCGT A GGAA - 3 C c c
42 GTGCGCAGCTC GA CTGTGCACA CAG CTTCC
CT GACGCGTGT GTC GAAGG
C GC-- C
GAM111 311 LOC9194 1 14120 XM_041721.3 3 GAAGCATCGTGC AG ACA C 3 C c
c
7 ATAGTTC GAACTGTGCAC GA GCTTC
CTTGATACGTG CT CGAAG
-- A-- -

GAM111 311 MGAM 1 11018 NM_004668.1 3 AAGCTTTCTGTG G AC CC 3 C c c
ACAGTTC GAACTGT CACAGGA AGCTT
CTTGACA GTGTCTT TCGAA
- -- --
GAM111 311 PPARA 1 5628 NM_005036.2 5 GAAGCTGTCACC CACAG A C 3 C c
c
ACAGTTC GAACTGTG GA CAGCTTC
CTTGACAC CT GTCGAAG
CA--- - -
GAM112 263 ACTR1A 1 16686 NP_005727.1 3 1216 AGGCCCCTCTGG A TA T 3 B c
c
GCTGATCTTGTG TG TATA ATCAGCCCA GA
CCATTCTT AC GTGT TAGTCGGGT CT
C TC -
GAM112 263 APRIN 1 18895 NP_055847.1 3 1896 GTAATTATGAGA AAT --- 3 B c c
GGCTGTCATATA TGATATAT CAGCC CATGAT
TCAAAGCA ACTATATA GTCGG GTATTA
CT- AGA
GAM112 263 ATP1A2 1 4788 NP_000693.1 3 2146 GCGAGTGCATGG AT C A 3 B c
c
GCTAATTATCAT TGAT ATAAT AGCCCATG
CAATCTTT ACTA TATTA TCGGGTAC
C- A G
GAM112 263 CDX2 1 6285 NP_001256.1 3 723 GAGCTTCTCTGG A T 3 B c c
GCTGAATGTATG TGATATATA TCAGCCCA GA
TCAGTGCT ACTGTATGT AGTCGGGT CT
A -
GAM112 263 CPS1 1 7610 NP_001866.2 3 308 ACTTTTTATGGT ATA--- - 3 B c c
GCTGATTAATGG TGAT TAATCAGC CCATGA
TGATCAAG ACTA ATTAGTCG GGTATT
GTGGTA T
GAM112 263 CYP7A1 1 7483 NP_000771.1 3 628 GGGTTCTTCGGG A - AT- 3 B c c
TGTGATCATATA TGATATAT ATCA GCCC GA
TCATAAAG ACTATATA TAGT TGGG CT
C G CTT
GAM112 263 CYSLTR2 1 8375 NP_065110.1 3 248 AGAGTCCTGTGG ATAA A 3 B c
c
GCTGAAATATCA TGATAT TCAGCCCATG
GACTGGGA ACTATA AGTCGGGTGT
A--- C
GAM112 263 EPB41L4 1 9787 NP_061987.2 3 1849 ATGAGTCATGGT A-- GC- 3 B c c
B CATGATTATAAA TGAT TATAATCA CCATGAT
CATCAGCC ACTA ATATTAGT GGTACTG
CAA ACT
GAM112 263 FLJ1037 1 1040 NP_115615.2 3 789 TGGGCTGCATGG T T T A 3 B c c
8 GCTGCTTTTATT TGA ATA AA CAGCCCATG
CATGGTGG ACT TAT TT GTCGGGTAC
- T C G
GAM112 263 FLJ1171 1 16607 NP_079122.1 3 768 TGCTCCTTATGG - - A- 3 B c c

0 GCTGGGGTGTAA TG ATAT ATA TCAGCCCATGA
TGTGCAGA AC TGTA TGT GGTCGGGTATT
G A GG
GAM112 263 FLJ1292 1 8731 NP_079151.1 3 1099 CAGTTTGCATGG A TAA A 3 B c c
1 GCTGAGTTATAC TG TATA TCAGCCCATG
CAGCTAGA AC ATAT AGTCGGGTAC
C TG- G
GAM112 263 FLJ2202 1 9484 NP_079225.2 5 35 TTCAAGTTTCAT ATA GC 3 B c c
9 GGTGATTATAGC TG TATAATCA CCATGA
ACAGCTCC AC ATATTAGT GGTACT
ACG --
GAM112 263 FLJ3681 1 9912 NP_694992.1 3 137 GATGATACTTCA T AGC A 3 B c c
2 GGAGATTATATT TGA ATATAATC CC TGA
TCACTCAA ACT TATATTAG GG ACT
T A-- -
GAM112 263 GAB2 1 4928 NP_036428.1 3 1423 TTGTGCCCATGG AAT- A 3 B c c
GCTGTGGCGTAT TGATATAT CAGCCCATG
GTCAGATC ACTGTATG GTCGGGTAC
CGGT C
GAM112 263 GAB2 1 4928 NP_536739.1 3 1423 TTGTGCCCATGG AAT- A 3 B c c
GCTGTGGCGTAT TGATATAT CAGCCCATG
GTCAGATC ACTGTATG GTCGGGTAC
CGGT C
GAM112 263 GPHN 1 7304 NP_065857.1 3 217 AGAAAATTCTGT TA CC T 3 B c c
TCTGATTATATC TGATATA ATCAG CA GA
AAGGCAAA ACTATAT TAGTC GT CT
-- TT -
GAM112 263 GPP34R 1 7889 NP_060648.2 3 1183 TGTAAGTTTCAG AA CCA 3 B c
c
TTGCTGAATATA TGATATAT TCAGC TGA
TCAGTATA ACTATATA AGTCG ACT
-- TTG
GAM112 263 HIRIP3 1 7164 NP_003600.2 5 167 GCAGCGTCGCGG T A A 3 B c c
GCTGATTAGGTT TGA AT TAATCAGCCC TGAT
TCACCCAA ACT TG ATTAGTCGGG GCTG
T G C
GAM112 263 HNRPAB 1 1037 NP_004490.1 3 238 GCGCCATCATGG TAT 3 B c c
GCTGATTTTTAT TGATA AATCAGCCCATGAT
TACCAGGT ATTAT TTAGTCGGGTACTA
TT-
GAM112 263 HNRPAB 1 1037 NP_112556.1 3 238 GCGCCATCATGG TAT 3 B c c
GCTGATTTTTAT TGATA AATCAGCCCATGAT
TACCAGGT ATTAT TTAGTCGGGTACTA
TT-
GAM112 263 KIAA049 1 5227 XP_034717.1 5 1820 GGTGGGTGGTGC AA -- G 3 B c c
3 AGGCTGGATATA TGATATAT TCAGCC CAT AT
TCACAGAA ACTATATA GGTCGG GTG TG
-- AC G

GAM112 263 KIAA056 1 15894 XP_038664.6 3 1034 ACACACTCTTGG T- --- T 3 B c c
4 GCTGACCTTTAT TGATA ATAA TCAGCCCA GA
TTTATCAA ACTAT TATT AGTCGGGT CT
TT TCC T
GAM112 263 KIAA179 1 12645 XP_166146.3 3 2010 TTTATATCATGG A AA G 3 B c c
6 GTGAAAGTGATC TGAT TAT TCA CCCATGAT
ATAACATT ACTA GTG AGT GGGTACTA
- AA -
GAM112 263 LAP1B 1 1138 NP_056417.1 3 287 TTTTGATTCTGG TATAA T 3 B c c
GCTGAGTTATTA TGATA TCAGCCCA GA
CAATTATG ATTAT AGTCGGGT CT
TG--- -
GAM112 263 LASP1 1 13445 NP_006139.1 3 1862 CAGTCATCATGG TAT CA 3 B c
c
GTGTTTTTGTCA TGATA AAT GCCCATGAT
ACTGCTTG ACTGT TTG TGGGTACTA
TT- --
GAM112 263 LOC1452 1 13603 XP_096740.1 3 2014 CGTTGCTCATGG A - 3 B c c
31 GCTAGATTGGGT TGATAT TAATC AGCCCATGA
ATCACCTT ACTATG GTTAG TCGGGTACT
G A
GAM112 263 LOC1463 1 10788 XP_085430.1 5 1367 TGGGGACCAGGG T - A A 3 B c
c
46 ACTGATTATTTG TGATA ATAATCAG CCC TG
TCACCTGG ACTGT TATTAGTC GGG AC
T A - C
GAM112 263 LOC2835 1 18815 XP_211120.1 3 1917 CACCATCGTCTT CC- 3 B c c
47 GCTGATTATATG TGATATATAATCAGC ATGAT
TCAAGTTC ACTGTATATTAGTCG TGCTA
TTC
GAM112 263 LOC2843 1 13825 XP_209131.1 3 1715 TAAATCACATTG - C --- 3 B c c
78 GGTTATTATATA TGAT ATATAAT AGCCCA TGAT
ATCATTTC ACTA TATATTA TTGGGT ACTA
A - TAC
GAM112 263 LOC2845 1 5227 XP_209263.1 5 1352 GGTGGGTGGTGC AA -- G 3 B c
c
68 AGGCTGGATATA TGATATAT TCAGCC CAT AT
TCACAGAA ACTATATA GGTCGG GTG TG
-- AC G
GAM112 263 LOC2848 1 7153 XP_209371.1 3 1018 GCTGCTTCATGG ATATA- 3 B c
c
05 GCTGATGTGAGG TGAT ATCAGCCCATGA
ATTAAACA ATTA TAGTCGGGTACT
GGAGTG
GAM112 263 LOC2849 1 20187 XP_208268.1 3 31 TTTTGGTCATGG ATATA 3 B c c
55 GCTGGTCTGGTC TGAT ATCAGCCCATGAT
GGTTTCCC GCTG TGGTCGGGTACTG
GTC--
GAM112 263 LOC2862 1 5356 XP_209941.1 3 750 AGGACCTCAGGC AAT -- A 3 B c
c

07 TGCTGTCATATA TGATATAT CAGC CC TGA
TCACCCGT ACTATATA GTCG GG ACT
CT- TC -
GAM112 263 LOC3456 1 19831 XP_298913.2 5 631 ACAGTCAGCTGG AT A -- 3 B c c

10 GCTGAGTGTATT TG ATATA TCAGCCCA TGAT
CCAAACGG AC TATGT AGTCGGGT ACTG
CT G CG
GAM112 263 LOC3466 1 11576 XP_299603.1 5 12 AGTTTTTCATGG ATAT- - 3 B c c
25 GCATGATTCCAA TGAT AATCA GCCCATGA
AATCAACA ACTA TTAGT CGGGTACT
AAACC A
GAM112 263 LOC3484 1 2541 XP_300733.1 3 965 CTTTCACCATGG T- C- A 3 B c c
16 GCTTCATTATCT TGATA ATAAT AGCCCATG
TGTCAGAA ACTGT TATTA TCGGGTAC
TC CT C
GAM112 263 LOC3488 1 533 XP_300859.1 3 69 ACACCATCATGG TAT AT 3 B c c
36 GCTGTATTTTCA TGA ATA CAGCCCATGAT
AGTTGATT ACT TAT GTCGGGTACTA
TT- --
GAM112 263 LPP 1 11376 NP_005569.1 3 2989 ACTATATCATGG ATAATC--- 3 B c c
GCTCTGCAGAAC TGATAT AGCCCATGAT
ATATCAAA ACTATA TCGGGTACTA
CAAGACGTC
GAM112 263 MGC4677 1 20187 NP_443103.1 3 31 TTTTGGTCATGG ATATA 3 B c
c

GCTGGTCTGGTC TGAT ATCAGCCCATGAT
GGTTTCCC GCTG TGGTCGGGTACTG
GTC--
GAM112 263 MID1 1 3318 NP_000372.1 3 811 TCAAAAATTCAG T--- CA 3 B c c
GCTGATTGTCTT TGATA ATAATCAGCC TGA
TTATCAGA ACTAT TGTTAGTCGG ACT
TTTC --
GAM112 263 MID1 1 3318 NP_150633.1 3 1056 TCAAAAATTCAG T--- CA 3 B c c
GCTGATTGTCTT TGATA ATAATCAGCC TGA
TTATCAGA ACTAT TGTTAGTCGG ACT
TTTC --
GAM112 263 PLAG1 1 11279 NP_002646.1 3 3308 TCAATTGTCCTG A CAT 3 B c c
GCTGATTATGCA TGAT TATAATCAGCC GAT
TCACTCTG ACTA GTATTAGTCGG CTG
C TC-
GAM112 263 SP2 1 9721 NP_003101.2 5 228 CCTATCAATTGG ATA -- 3 B c c
GCTGATGATGTC TGATAT ATCAGCCCA TGAT
AGTGTTCC ACTGTA TAGTCGGGT ACTA
G-- TA
GAM112 263 ZNF216 1 14718 NP_005998.1 3 1096 TGTATTGCATGG A T - A 3 B c c
GCTGCATTATCT TG TA ATAAT CAGCCCATG
ACAGCATT AC AT TATTA GTCGGGTAC
- C C G
GAM113 233 C20orf2 1 12502 NM_017874.1 5 AGCTCCTGCAGC ACTTATTA 3 C c
c

7 CGCCGCCGCTG CAGT GCTGCAGGAGCT
GTCG CGACGTCCTCGA
CCGCCGC-
GAM113 233 LOC2559 1 16326 XM_171083.2 5 AGCTCCTGCCTC ATT CT 3 C c c
75 CAAGTGCTG CAGTACTT AG GCAGGAGCT
GTCGTGAA TC CGTCCTCGA
CC- --
GAM113 233 LOC9201 1 12778 XM_042234.3 5 AGCTGATGCAAC A C GG 3 C c c
7 TAACAAGTACTG CAGTACTT TTAG TGCA AGCT
GTCATGAA AATC ACGT TCGA
C A AG
GAM114 288 ATP10C 1 17918 3 CATCAGCACCAC A A- A A 3 C c c
GTGCCAAGGAG CTTC GGCAC TGGTGCTGATG
GAGG CCGTG ACCACGACTAC
- AA C -
GAM115 229 FLJ2025 1 3143 NM_019606.3 5 TGATGAGGGCCA -- AAGG AC 3 C c
c
7 TGTAGTTCTT AAGAACTACAT CC CATCA
TTCTTGATGTA GG GTAGT
CC GA-- --
GAM115 229 LOC2016 1 10333 3 TTGATGCTTATG A- CCA C 3 C c c
27 TAGTGCCTT AAG ACTACAT AGGCATCAA
TTC TGATGTA TTCGTAGTT
CG --- -
GAM115 229 LOC5101 1 14480 3 GTTAATGTGGAT A AAG C 3 C c c
5 GTAGTGCTT AAG ACTACATCC GCAT AAC
TTC TGATGTAGG TGTA TTG
G --- A
GAM115 229 PRSS21 1 3015 NM_006799.2 3 GTTGATGCCTTG CTACATC 3 C c
c
CAGGGCATTCTT AAGAA CAAGGCATCAAC
TTCTT GTTCCGTAGTTG
ACGGGAC
GAM116 301 ACADL 1 2475 NP_001599.1 3 544 GCTTATGCAGAA T CTAA 3 A c c
CATCTCTGTGAA TTCACAG GG GTTCTGCA
ACGCTGCT AAGTGTC CT CAAGACGT
T A---
GAM116 301 AD023 1 12888 NP_065730.2 3 327 AAAATGGGTAAG - A C 3 A c c
CATAGCCACTGG TTCAC AGTGGCTA GTT TGC
TGGGATAT GGGTG TCACCGAT CGA ATG
G A -
GAM116 301 ADK 1 19386 NP_001114.1 3 8 CCTGAGAAGCCA CT CT 3 A c c
GACTTCCACTGT TTCACAGTGG AAGTT GC
GGAAGAGC AGGTGTCACC TTCAG CG
-- AC
GAM116 301 ADK 1 19386 NP_006712.1 3 8 CCTGAGAAGCCA CT CT 3 A c c
GACTTCCACTGT TTCACAGTGG AAGTT GC
GGAAGAGC AGGTGTCACC TTCAG CG
-- AC
GAM116 301 AMT 1 16729 NP_000472.1 3 92 GCTGAGGCAGAA A GCTA 3 A c c

CTCACTGGGGGT TTC CAGTG AGTTCTGC
GGGCAGTT GGG GTCAC TCAAGACG
- ----

GAM116 301 ANAPC1 1 14212 NP_073153.1 5 122 CTGCTGCGGCCC AAGTT- 3 A c c

AAGAGTCACTGT TTCACAGTGGCT CTGCA
GAAGGACC AAGTGTCACTGA GGCGT
GAACCC

GAM116 301 AP1GBP1 1 1791 NP_009178.2 3 2186 TTGCTGCTGCAG GGCTA T 3 A c c

TATTGAAACTGT TTCACAGT AGT CTGCA
GAAGAACT AAGTGTCA TTA GACGT
AAG-- T

GAM116 301 AP1GBP1 1 1791 NP_542117.1 3 2150 TTGCTGCTGCAG GGCTA T 3 A c c

TATTGAAACTGT TTCACAGT AGT CTGCA
GAAGAACT AAGTGTCA TTA GACGT
AAG-- T

GAM116 301 ARHGEF4 1 12767 NP_056135.2 5 239 CCAGCAGAGACT A-- - 3 A b b

GACAGCCACTGT TTCACAGTGGCT AGT TCTGC
GAGGAACG GAGTGTCACCGA TCA AGACG
CAG G

GAM116 301 ARHGEF4 1 12767 NP_127462.1 5 239 CCAGCAGAGACT A-- - 3 A b b

GACAGCCACTGT TTCACAGTGGCT AGT TCTGC
GAGGAACG GAGTGTCACCGA TCA AGACG
CAG G

GAM116 301 ARNT2 1 6462 NP_055677.1 3 2390 GACCCAGGTGAA - TAA T 3 A c c

CACGCTGACTGT TTCACAGT GGC GTTC GC
GAACCTGC AAGTGTCA TCG CAAG TG
G CA- -

GAM116 301 ARP5 2 5338 NP_114123.2 3 125 TGTCCCACAGAA CT C 3 A c c
CTTCCCACTGTG TTCACAGTGG AAGTTCTG
GATCTGTG AGGTGTCACC TTCAAGAC
C- A

GAM116 301 ARP5 2 6833 NP_114123.2 3 125 GTGTCCCACAGA CT C 3 A c c
ACTTCCCACTGT TTCACAGTGG AAGTTCTG
GGATCTGT AGGTGTCACC TTCAAGAC
C- A

GAM116 301 ATP6V1A 1 6211 NP_001681.2 3 1645 CATATTGCAGAA A T AA 3 A c c

CAGCTCTGAGAG TTC CAG GGCT GTTCTGCA
CAACAGTT GAG GTC TCGA CAAGACGT
A - --

GAM116 301 ATRN 1 8323 NP_647537.1 3 1014 GGAAAGCAGAAA GGCTAAG- 3 A c c

TGAATGAACTGT TTCACAGT TTCTGC
GAAAGCTC AAGTGTCA AAGACG

AGTAAGTA

GAM116 301 B4GALT3 1 13333 NP_003770.1 3 223 GTCTCCTGTAGG GGC 3 A c c

GCTTATGACTGT TTCACAGT TAAGTTCTGCA
GAATCCTT AAGTGTCA ATTCGGGATGT
GT-

GAM116 301 B4GALT4 1 5385 NP_003769.1 5 168 GTTGGAGCAGAA A GGCTA 3 A c c

CTACTGAGAAAA TTC CAGT AGTTCTGC
ACCAGGCA AAG GTCA TCAAGACG
A -----

GAM116 301 BCL6 1 14159 NP_001697.2 5 283 GTTTTGAGCAAA GGCT C 3 A c c

ATTTTGGACTGT TTCACAGT AAGTT TGC
GAAGCAAG AAGTGTCA TTTAA ACG
GGT- A

GAM116 301 BCL6 1 14159 NP_620309.1 5 376 GTTTTGAGCAAA GGCT C 3 A c c

ATTTTGGACTGT TTCACAGT AAGTT TGC
GAAGCAAG AAGTGTCA TTTAA ACG
GGT- A

GAM116 301 BMI1 1 5333 NP_005171.4 3 491 CATTCTATGTAG TAAGTT 3 A c c

CCATGTCACTGT TTCACAGTGGC CTGCA
GAATAACG AAGTGTCACTG GATGT
TACC--

GAM116 301 BTG2 1 8685 NP_006754.1 3 371 GGAGCAAGCAAG G G C 3 A c c

GTTAGCAACTGT TTCACAGT GCTAA TT TGC
GAACAGAG AAGTGTCA CGATT GA ACG
A G -

GAM116 301 C16orf5 1 20128 NP_037531.1 3 1030 CACTGCATGGCC TA- TT - 3 A c c

TCCTGTCACTGT TTCACAGTGGC AG C TGCA
GAATCGTG AAGTGTCACTG TC G ACGT
TCC CG T

GAM116 301 C1orf9 2 15293 NP_055098.1 3 1540 AGCTGTAGTGCC GG -- T 3 A c c

ATTAGAAACTGT TTCACAGT CTAA GT CTGCA
GAATTTCC AAGTGTCA GATT CG GATGT
AA AC T

GAM116 301 C1orf9 2 15293 NP_057311.1 3 1545 AGCTGTAGTGCC GG -- T 3 A c c

ATTAGAAACTGT TTCACAGT CTAA GT CTGCA
GAATTTCC AAGTGTCA GATT CG GATGT
AA AC T

GAM116 301 C1orf9 2 17492 NP_055098.1 5 56 GGCTGCCAGGAC A AA- - 3 A c c

GCGAGCCACTGA TTC CAGTGGCT GTTCTG CA
GGAGCCGC AGG GTCACCGA CAGGAC GT
A GCG C

GAM116 301 C20orf1 1 15419 NP_219489.1 3 31 CTTGCCTAGATT AAGT- -- 3 A c c
61

TAAGGCCACTGT TTCACAGTGGCT TCT GCA
GAGGAGAG GAGTGTCACCGG AGA CGT
AATTT TC

GAM116 301 C21orf1 1 19399 XP_114191.2 3 3298 GTTGCTGCAGAA --- AA 3 A c c
08

CAGTCCATACTG TTCACAGT GGCT GTTCTGCA
TGGGGCTG GGGTGTCA CTGA CAAGACGT

TAC --
GAM116 301 C5orf13 1 900 NP_004763.1 3 223 AAAACGCTCAGA GCT C 3 A c c
ATTTCACACTGT TTCACAGTG AAGTTCTG
GAATCCAC AAGTGTCAC TTTAAGAC
AC- T
GAM116 301 CABIN1 1 16423 NP_036427.1 3 228 GGAGGGGCCCGC G TTCT 3 A c
c
CTTAGCCATGTG TTCACA TGGCTAAG GC
AAGGTGGA AAGTGT ACCGATTC CG
- CGCC
GAM116 301 CASP8 1 10011 NP_203521.1 3 527 CTTTCTGCTGGG AG T 3 A c c
GATGGCCACTGT TTCACAGTGGCTA TTC GCA
GAATAACT AAGTGTCACCGGT GGG CGT
AG T
GAM116 301 CCND1 1 6838 NP_444284.1 3 2246 CCTCATGCTTCA A TCT 3 A c c
CTTAGCCATGGT TTCAC GTGGCTAAGT GCA
GGACCCAG AGGTG TACCGATTCA CGT
G CTT
GAM116 301 CDR2 1 5603 XP_071866.2 3 454 CTTTGCAAACAG GC --- C 3 A c c
TTTGAATACTGT TTCACAGTG TAA GTT TGCA
GAATTCAT AAGTGTCAT GTT CAA ACGT
AA TGA -
GAM116 301 CENTD1 1 10052 NP_056045.2 5 187 TTAAGCAGGTAA AAGT-- 3 A c
c
AGCAGTCACTGT TTCACAGTGGCT TCTGC
GAAGAAAA AAGTGTCACTGA GGACG
CGAAAT
GAM116 301 CHD3 1 773 NP_001263.1 3 261 GCAGATGCTAAG ----- A - 3 A c c
TCTGTAAACTGT TTCACAGT GGCT AGT TCTGC
GAATTAAC AAGTGTCA CTGA TCG AGACG
AATGT A T
GAM116 301 CIDE-3 1 19483 NP_071377.2 5 3 AGAATGTTCTTT TTCT 3 A c c
TGGCCACTGTGA TTCACAGTGGCTAAG GCA
AGCCTCAG AAGTGTCACCGGTTT TGT
TCT-
GAM116 301 COL10A1 1 5855 NP_000484.2 3 484 AACTTTGTAGAA C GC 3 A c c
CTTAAATACTTG TTCA AGTG TAAGTTCTGCA
AATATTCA AAGT TCAT ATTCAAGATGT
- AA
GAM116 301 COL11A2 1 14857 NP_542410.1 3 551 CACCTCACCTGT CTAAGTTC 3 A
c c
CGCACCCACTGT TTCACAGTGG TGC
GAAAGTTG AAGTGTCACC ACG
C-------
GAM116 301 COL11A2 1 14857 NP_542411.1 3 551 CACCTCACCTGT CTAAGTTC 3 A
c c
CGCACCCACTGT TTCACAGTGG TGC
GAAAGTTG AAGTGTCACC ACG
C-------
GAM116 301 COL11A2 1 14857 NP_542412.1 3 551 CACCTCACCTGT CTAAGTTC 3 A
c c

CGCACCCACTGT TTCACAGTGG TGC
GAAAGTTG AAGTGTCACC ACG
C-------
GAM116 301 COL21A1 1 7623 NP_110447.2 3 314 TAGCCAGTCAGT TT - 3 A c c
TTTAGTCACTGT TTCACAGTGGCTAAG CTG C
GAAATATT AAGTGTCACTGATTT GAC G
T- T
GAM116 301 CPLX1 1 3486 NP_006642.1 5 165 TCTGACCCCTGG AAGT G 3 A c c
AGGAGCCACTGT TTCACAGTGGCT TCT CA
GGAAGCAG AGGTGTCACCGA GGA GT
---- G
GAM116 301 CYP1B1 1 11514 NP_000095.1 3 2749 CATGTCCCAGAA T---- C 3 A c c
CTTAGCCTTTAC TTCACAG GGCTAAGTTCTG
CTGTGAAG AAGTGTC CCGATTCAAGAC
CATTT C
GAM116 301 DCTN4 1 7697 NP_057305.1 3 1729 CCACTACCTGCT CTAA - 3 A c c
AGAGCCTACTGT TTCACAGTGG GTTCT GCA
GAAATCAC AAGTGTCATC CGAGA CGT
---- T
GAM116 301 DISC1 1 6142 NP_061132.1 3 3875 TGGCTAAGAACT -- -- 3 A b b
CATGGCCACTGT TTCACAGTGGCTA AGTTCT GC
GGAAATCT AGGTGTCACCGGT TCAAGA CG
AC AT
GAM116 301 DKFZP43 1 4305 NP_056486.1 5 298 TAACCAACGGCA TA C 3 A c c
4J046 AGCTGCCACTGT TTCACAGTGGC AGTT TGC
GGGCAAAG GGGTGTCACCG TCGA ACG
-- -
GAM116 301 DKFZP56 1 8390 NP_110423.2 3 1981 ACTTGGTTAGAA TA C 3 A c c
4K0822 TTGTGCTACTGT TTCACAGTGGC AGTTCTG
GAACGCTG AAGTGTCATCG TTAAGAT
TG T
GAM116 301 DKFZp76 1 19522 NP_689650.1 5 914 CCTTTGTAGTCC - TT 3 A c c
1B128 TTCAGCCACTGT TTCACAGTGGCT AAG CTGCA
GGGCCCTG GGGTGTCACCGA TTC GATGT
C CT
GAM116 301 DKFZp76 1 9943 NP_689874.1 3 1704 GGTCCAGAAAGA A A --- C 3 A c
c
1G0122 CTCAGCCACTGG TTC CAGTGGCT AGT TCTG
AGTCTGTG GAG GTCACCGA TCA AGAC
- C GAA C
GAM116 301 DKK2 1 10328 NP_055236.1 5 480 GTTATTGCAGAA - T T-- 3 A c c
CTTCCTGTCCTG TTCAC AG GGC AAGTTCTGCA
GTGGAGAA AGGTG TC CTG TTCAAGACGT
G - TCC
GAM116 301 DLAT 1 16982 NP_001922.2 3 866 GAACAGAATTTA C---- C 3 A c c
TGACTCCACTGT TTCACAGTGG TAAGTTCTG
GGAAAATG AGGTGTCACC ATTTAAGAC
TCAGT A
GAM116 301 DOT1L 1 5058 NP_115871.1 3 140 AAGGACGGACGG CTA GC 3 A c
c

GAGCTCCACTGT TTCACAGTGG AGTTCT
GAATCGGC AAGTGTCACC TCGAGG
--- GC

GAM116 301 DRIL2 1 4242 NP_006456.1 3 1539 TGTTCAGCAGAA T----- CTAA 3 A c c
CACCACCACTGT TCACAGTGG GTTCTGC
GACATGGG AGTGTCACC CAAGACG
GGGTAC ACCA

GAM116 301 DSCR3 1 16394 NP_006043.1 3 518 AGAGCGCAAAGT A A TC-- 3 A c c

GCTAGCCACTGG TTC CAGTGGCTA GT TGC
AAATGCAT AAG GTCACCGAT CG ACG
- - TGAA

GAM116 301 EYA1 1 8370 NP_000494.2 3 210 AACAGCTGTTGA G - CT-- 3 A c c
CTCTAGTACTGT TTCACAGTG CTA AGTT GC
GAATCCAG AAGTGTCAT GAT TCAG CG
- C TTGT

GAM116 301 EYA1 1 8370 NP_742055.1 3 210 AACAGCTGTTGA G - CT-- 3 A c c
CTCTAGTACTGT TTCACAGTG CTA AGTT GC
GAATCCAG AAGTGTCAT GAT TCAG CG
- C TTGT

GAM116 301 EYA1 1 8370 NP_742056.1 3 210 AACAGCTGTTGA G - CT-- 3 A c c
CTCTAGTACTGT TTCACAGTG CTA AGTT GC
GAATCCAG AAGTGTCAT GAT TCAG CG
- C TTGT

GAM116 301 EYA1 1 8370 NP_742057.1 3 210 AACAGCTGTTGA G - CT-- 3 A c c
CTCTAGTACTGT TTCACAGTG CTA AGTT GC
GAATCCAG AAGTGTCAT GAT TCAG CG
- C TTGT

GAM116 301 F2RL3 1 4749 NP_003941.1 3 1385 TGGCCTGCAGAA GGCTAAGT 3 A c
c

CTGTGAGACAAT TTCACAGT TCTGCA
AAACTCTC GAGTGTCA AGACGT

GAM116 301 FBXO7 1 10093 NP_036311.2 5 108 ACCGAGTGGCAG T----- AA 3 A c c

GGCGGCCACTGT TCACAGTGGCT GTTCTGC
GGCGGGGC GGTGTCACCGG CGGGACG
CGGGGC --

GAM116 301 FLJ1003 1 12536 NP_060444.1 3 298 AATGGCACAGAA ---- G C 3 A c c
5 CTTAGCAACAGC TTCACA GT GCTAAGTTCTG
ATGTGAAT AAGTGT CA CGATTCAAGAC
ACGA A A

GAM116 301 FLJ1114 1 14300 NP_060809.2 3 7 AGCAAAATAATG AA ------- 3 A c c
9 AATGGCCACTGT TTCACAGTGGCT GTTC TGC
GAAAAATT AAGTGTCACCGG TAAG ACG
-- TAATAAA

GAM116 301 FLJ1115 1 8506 NP_060812.1 3 123 TAGCAAATGGAT - A - --- 3 A c c
5 CTCAGCCACTGT TTCA CAGTGGCT AG TTC TGC
TGGAGTGG AGGT GTCACCGA TC AGG ACG
T C T TAA

GAM116 301 FLJ1127 1 7491 NP_060845.1 5 614 CTAAGCACCATT A -- TC 3 A c c
4 TAAAGCCACTGG TTC CAGTGGCT AAGT TGC
AAATTTGT AAG GTCACCGA TTTA ACG
- AA CC
GAM116 301 FLJ1180 1 11823 NP_079250.1 3 1048 TGTTTAGAAGTA AAG 3 A c c
0 GGAAGTCACTGT TTCACAGTGGCT TTCTGC
GAGCAATG GAGTGTCACTGA AGGATG

GAM116 301 FLJ1219 1 15397 NP_079347.1 3 1257 AAGAAGCCAGAT C AGT - 3 A c
c
0 CCTAGCCACTTG TTCA AGTGGCTA TCTG C
GAGCTGCC AGGT TCACCGAT AGAC G
- CCT C
GAM116 301 FLJ1244 1 19826 NP_079106.2 3 2020 GAGTTGGCGGAT GG TA - 3 A c
c
3 ATTCGGAACTGT TTCACAGT C AGT TCTGC
GAATGTAC AAGTGTCA G TTA AGGCG
A- GC T
GAM116 301 FLJ1258 1 2047 NP_078896.2 3 1384 GGATGCTTCTAA A CT-- 3 A c c
6 TTCAGCCACTGT TTCACAGTGGCT AGTT GCA
GAACCATT AAGTGTCACCGA TTAA CGT
C TCTT
GAM116 301 FLJ1265 1 2476 NP_078798.1 3 437 ACCAGCTCTGGG AAG G 3 A c c
0 GAAAGCTACTGT TTCACAGTGGCT TTCT CA
GAACTAGG AAGTGTCATCGA AAGG GT
--- G
GAM116 301 FLJ1280 1 1109 NP_075054.1 3 494 TGAATGCAGAAG AA - 3 A b b
0 CAGAGCCACTGT TTCACAGTGGCT GTT CTGCA
GAAGTAAG AAGTGTCACCGA CGA GACGT
GA A
GAM116 301 FLJ1320 1 13933 NP_079037.2 3 2234 GTTCCCACAGAA C - - C 3 A c c
4 CTTTGGCACATT TTCA AGTG GCTAA GTTCTG
CTGAAGAA AAGT TTAC CGGTT CAAGAC
C A T A
GAM116 301 FLJ1385 1 18367 NP_075567.1 5 232 GGGGCCGCGCTG A TC 3 A c c
5 CTTAGCCACTGG TTC CAGTGGCTAAGT TGC
GACCCCAC AGG GTCACCGATTCG GCG
- TC
GAM116 301 FLJ1408 1 15997 NP_079300.1 3 2026 CTAAGTAGCAGG TAA T 3 A c c
2 CAGTGCCACTGT TTCACAGTGGC GT CTGC
GGACAGTG AGGTGTCACCG CG GACG
TGA -
GAM116 301 FLJ1456 1 8020 NP_115939.1 3 131 AAAAAGCAAAGA G A C- 3 A c c
4 CTGAGGTACTGT TTCACAGTG CT AGTT TGC
GAATGGAG AAGTGTCAT GA TCAG ACG
G G AA
GAM116 301 FLJ2025 1 1289 NP_062552.1 3 487 GGCAGGGAGGCA G AA ----- 3 A c c

7 CGCAGGTACTGT TTCACAGTG CT GT TCTGC
GAAAATCC AAGTGTCAT GA CA GGACG
G CG CGGAG

GAM116 3016 FLJ2071 1 4364 NP_060408.2 3 1464 ACCTTGTAGACA ACA - 3 A c c
CTTAGCCATCAA TTC GTGGCTAAGT TCTGCA
GAATCAAG AAG TACCGATTCA AGATGT
AAC C

GAM116 3010 FLJ2249 1 4123 NP_079066.2 5 0 GGGAACTTCAGC -- - GC 3 A c c
ACTACTGTGAAA TTCACAGTG GCT AAGTTCT
GAGACAAT AAGTGTCAT CGA TTCAAGG
CA C G-

GAM116 3014 FLJ2249 1 11620 NP_079091.1 5 349 AAGGAGGAGGCG G TA 3 A c c
GGGCTGCACTGT TTCACAGTG C AGTTCTGC
GAGCCCGA GAGTGTCAC G TCGGGGCG
- --

GAM116 3014 FLJ2294 1 16245 NP_079421.2 3 997 CTGAGGAGCTGG TA---- G 3 A c c
CCCTGCCACTGT TTCACAGTGGC AGTTCT CA
GGACTGCC AGGTGTCACCG TCGAGG GT
TCCCGG A

GAM116 3013 FLJ3031 1 956 NP_689970.1 3 1190 ACCTCATGCAGG AAGT 3 A c c
TGAAGCCACTGT TTCACAGTGGCT TCTGCA
GGAAACAG AGGTGTCACCGA GGACGT
AGT-

GAM116 3019 FLJ3202 1 16839 NP_775853.2 3 4125 CACCCTTGCACA T TC 3 A c c
TTTTGTTACTGT TTCACAGTGGC AAGT TGCA
GAAGGACT AAGTGTCATTG TTTA ACGT
T C-

GAM116 3018 FLJ3583 1 1616 NP_775803.1 3 285 TGCTAGCCTGAG - G CT 3 A c c
TTGGCACACTGT TTCACAGTG GCTAA TT GC
GAGAACCC GAGTGTCAC CGGTT AG CG
A G TC

GAM116 3014 FLJ3650 1 9901 NP_787106.2 3 1379 AAAAATTGTAGA GG AG- 3 A c c
AATATAGACTGT TTCACAGT CTA TTCTGCA
GAAAAAGA AAGTGTCA GAT AAGATGT
-- ATA

GAM116 3019 FLJ3674 1 16158 NP_775877.1 3 965 AGAAGAAGCTGA GG - T 3 A c c
ACTTCAGACTGT TTCACAGT CT AAGTTC GC
GAAAGGTA AAGTGTCA GA TTCAAG CG
-- C T

GAM116 3018 FLJ3692 1 12357 NP_775822.1 3 444 GGTGCCATCAGC G AAGT 3 A c c
AGGAGGCACTGT TTCACAGTG CT TCTGC
GAAGCACC AAGTGTCAC GA GGACG
G ----

GAM116 3016 FLJ3910 1 4522 NP_775900.1 3 1008 ACCAAACTGTAC C TTC 3 A c c
CTTAGCCACTTT TTCA AGTGGCTAAG TGCA
GGACACAT AGGT TCACCGATTC ATGT

T C--
GAM116 301 FLJ3965 1 8884 NP_787110.1 3 670 ACCCGCACAGAA A T C 3 A c c
4 CTTGGTCTCTGG TTC CAG GGCTAAGTTCTG
AATCCAGC AAG GTC CTGGTTCAAGAC
- T A
GAM116 301 FLRT3 1 3900 NP_037413.1 3 333 TGAGTAAGATGA - T -- - 3 A c c
CTTGTTGACTGT TTCACAGT GGC AAGT TCT GC
GAAAGTGA AAGTGTCA TTG TTCA AGA TG
G - GT A
GAM116 301 FOXA1 1 15349 NP_004487.2 5 306 TGGCTCCAGGAT GG - C 3 A c c
GTTAGGAACTGT TTCACAGT CTAA GTTCTG
GAAGATGG AAGTGTCA GATT TAGGAC
AG G C
GAM116 301 FOXM1 1 15673 NP_068772.1 3 171 TAGCAGTCACAC - A- T--- 3 A c c
CCTAGCCACTGC TTCA CAGTGGCTA GT CTGC
TGGGACCT GGGT GTCACCGAT CA GACG
C CC CACT
GAM116 301 GALNT13 1 16772 XP_054951.3 3 710 AATCCGCAGCAC CT- T 3 A c c
TTCGATCACTGT TTCACAGTGG AAGT CTGC
GAGAGAAC GAGTGTCACT TTCA GACG
AGC C
GAM116 301 GBA 1 8745 NP_000148.1 3 421 AGAGATGCAGAA AGT A 3 A c c
CTGGGCCCGTGG TTCAC GGCT AGTTCTGCA
AGCAGCAG AGGTG CCGG TCAAGACGT
C-- G
GAM116 301 GLTP 1 6571 NP_057517.1 3 74 AAACAGGCAAAC GCTAA C 3 A c c
CAGAATCACTGT TTCACAGTG GTTCTG
GAATCAAG AAGTGTCAC TAAGAC
----- C
GAM116 301 GOR 1 10062 NP_758439.1 3 1561 CAAAAGTACGAA C--- -- - 3 A c c
CTTAGCAACACT TTCA AGTG GCTAAGTTC TGC
ATATTGAG GAGT TCAC CGATTCAAG ATG
TATA AA C
GAM116 301 GPR26 1 8715 NP_703143.1 3 6037 AGGGCTGGAGAA A G G 3 A c c
CTTAGCTGGTGG TTC CA TGGCTAAGTTCT CA
GAAAGGAG AAG GT GTCGATTCAAGA GT
G G G
GAM116 301 HD 1 3274 NP_002102.2 3 2132 TACATTTGTAAG GCTAAG - 3 A c c
AAATAACACTGT TTCACAGTG TTCT GCA
GAATGTAA AAGTGTCAC AAGA TGT
AATA-- A
GAM116 301 HIC2 1 16826 NP_055909.1 3 2309 TCCTTTGCAGAA A GG - 3 A c c
CTTCAGGGACTG TTC CAGT CT AAGTTCTGCA
GGAGCAGA AGG GTCA GA TTCAAGACGT
- GG C
GAM116 301 HIC2 1 16826 XP_036937.2 3 2309 TCCTTTGCAGAA A GG - 3 A c c
CTTCAGGGACTG TTC CAGT CT AAGTTCTGCA
GGAGCAGA AGG GTCA GA TTCAAGACGT

```
                                        -  GG  C
GAM116  301  HSPC039 1  6893  NP_057181.1  3 399  AGTTCCTTGCAA    --      TC       3  A  c  c
                                CTTAGCCATGAT TTCACA  GTGGCTAAGT  TGCA
                                GTGAGTGG   GAGTGT  TACCGATTCA  ACGT
                                        AG       --
GAM116  301  HSPC056 1  6808  NP_054873.1  3 362  GGTGAAGAGCAC     G  AA  TC       3  A  c
c
                                TACAGTGACTGT TTCACAGT GCT  GT  TGC
                                GAATATAT   AAGTGTCA TGA  CA  ACG
                                        G  --  TC
GAM116  301  HT002  1  13026 NP_054785.2  3 625  CAGGATAGTTGC      G  A  TCT       3  A  c  c

                                ACTGAGCACTGT TTCACAGTG CT AGT  GCA
                                GAGGCCCC   GAGTGTCAC GA TCA  CGT
                                        -  G  ---
GAM116  301  HTR4  1  2727  NP_000861.1  3 13   AGCCCAGTGACA  A  T    -  T       3  A  c  c
                                CTTAGCCCCTGG TTC CAG GGCTAAGT TC GC
                                GACAATGA   AGG GTC CCGATTCA AG TG
                                        -  C      C  -
GAM116  301  HUMAGCG 1  466   NP_037418.2  3 3624  CTACACGGCAGG      G  AAG       3  A  c
c
        B                        GGCAGACACTGT TTCACAGTG CT  TTCTGC
                                GAGTATAA   GAGTGTCAC GA  GGGACG
                                        A  CG-
GAM116  301  HUMAGCG 1  466   XP_291083.2  3 3624  CTACACGGCAGG      G  AAG       3  A  c
c
        B                        GGCAGACACTGT TTCACAGTG CT  TTCTGC
                                GAGTATAA   GAGTGTCAC GA  GGGACG
                                        A  CG-
GAM116  301  ICK   1  20049 NP_055735.1  5 289  ACCACTGCAGAA T  ------  CTA       3  A  c  c
                                CTGAACCACTTC  TCAC    AGTGG  AGTTCTGCA
                                GGCCGTGA    AGTG    TCACC  TCAAGACGT
                                        -  CCGGCT   AAG
GAM116  301  ICK   1  20049 NP_057597.2  5 151  ACCACTGCAGAA T  ------  CTA       3  A  c  c
                                CTGAACCACTTC  TCAC    AGTGG  AGTTCTGCA
                                GGCCGTGA    AGTG    TCACC  TCAAGACGT
                                        -  CCGGCT   AAG
GAM116  301  ICK   1  20049 NP_766629.1  5 353  ACCACTGCAGAA T  ------  CTA       3  A  c  c
                                CTGAACCACTTC  TCAC    AGTGG  AGTTCTGCA
                                GGCCGTGA    AGTG    TCACC  TCAAGACGT
                                        -  CCGGCT   AAG
GAM116  301  IL6R  1  12823 NP_000556.1  3 256  GCTAGAGTGAAC      -    T       3  A  b  b
                                TTGGGCCACTGT TTCACAGTGGCT AAGTTC GC
                                GAAGAGAA   AAGTGTCACCGG TTCAAG TG
                                        G    -
GAM116  301  IL6R  1  12823 NP_852004.1  3 471  GCTAGAGTGAAC      -    T       3  A  b  b
                                TTGGGCCACTGT TTCACAGTGGCT AAGTTC GC
                                GAAGAGAA   AAGTGTCACCGG TTCAAG TG
                                        G    -
GAM116  301  INSR  1  8240  NP_000199.1  3 204  TAGTCCTGCAGA      GGCTAAG       3  A  c
c
```

GGATTTAACTGT TTCACAGT TTCTGCA
GAACCTGG AAGTGTCA GAGACGT
ATTTAG-

GAM116 301 ITPR2 1 19491 NP_002214.1 3 603 CAGCTCTAGGAA C G ---- 3 A c c
CTTAGTACTTTG TTCA AGTG CTAAGTTCT GC
GAGCTTTT AGGT TCAT GATTCAAGG CG
T - ATCT

GAM116 301 KCNJ10 1 5460 NP_002232.2 3 549 AAAGAAGCCAGG T TT - 3 A c c
GTTTGCCACTGT TTCACAGTGGC AAG CTG C
GAAGCTTG AAGTGTCACCG TTT GAC G
- GG C

GAM116 301 KCNMA1 1 8898 NP_002238.2 3 2320 GGTTCTGCATGA - A C 3 A c c
CCTAGCCACTGC TTCA CAGTGGCTA GTT TGCA
TGGGGGTT GGGT GTCACCGAT CAG ACGT
C C T

GAM116 301 KIAA006 1 12869 XP_046677.3 3 1316 CTGTAGGCCAGC T---- 3 A c c
2 CTTAGCCACTGT TTCACAGTGGCTAAG TCTGCA
GGAGCCCT AGGTGTCACCGATTC GGATGT
CGACC

GAM116 301 KIAA024 1 18158 XP_166479.2 3 2156 CTCATTGCAGAA A T CT- 3 A c c

0 CTTTATCCCTGG TTC CAG GG AAGTTCTGCA
AAGCCTTC AAG GTC CC TTCAAGACGT
- - TAT

GAM116 301 KIAA031 2 11176 XP_045712.5 3 388 AGGCGAGCAGAA A- T CTA 3 A c
c
6 CTCCCCCTGGGG TTC CAG GG AGTTCTGC
AGGAAGCT GAG GTC CC TCAAGACG
GG - CC-

GAM116 301 KIAA031 2 13615 XP_045712.5 3 1222 GAAAGCTGCCGA A AAG T 3 A c
c
6 AGCAGCCACTGG TTC CAGTGGCT TTC GCA
AAAGAACC AAG GTCACCGA AAG CGT
- CG- C

GAM116 301 KIAA052 1 4493 XP_171054.1 3 2472 GTTTTATTTGTA GG A T 3 A c c
7 GACATGGACTGT TTCACAGT CTA GT CTGCA
GAAATAAA AAGTGTCA GGT CA GATGT
-- A -

GAM116 301 KIAA066 1 15758 NP_055642.1 3 316 GGTGCAAGCGAA C-- G --- 3 A c c
3 CTTAGTGACTCC TTCA AGT GCTAAGTTC TGCA
TTGAGGTG GAGT TCA TGATTCAAG ACGT
TCC G CGA

GAM116 301 KIAA068 1 4750 NP_055667.1 3 471 ACGGCAGCAGAA C- T TA 3 A c c
2 CTGTCTCTTCTG TTCA AG GGC AGTTCTGC
AAAACCAG AAGT TC CTG TCAAGACG
CT T --

GAM116 301 KIAA103 1 3396 NP_055724.1 3 1241 TAAAGGGTGCAG A AA T 3 A c c

6 TGCAGCCACTGA TTC CAGTGGCT GT CTGCA
GGGACAGC GGG GTCACCGA CG GACGT

A -- T

GAM116 301 KIAA105 1 9566 NP_055894.1 3 545 CCCTTGTTCAGA - AG C 3 A c c
5 AATGGCCACTGT TTC ACAGTGGCTA TTCTG
AGGAAAGC AGG TGTCACCGGT AAGAC
A A- T

GAM116 301 KIAA106 1 9350 XP_042635.3 3 3075 ACTGACATGCAT CT TC 3 A c c
9 TATTTTCACTGT TTCACAGTGG AAGT TGCA
GAATTCAC AAGTGTCACT TTTA ACGT
-- TT

GAM116 301 KIAA110 1 12914 XP_044461.6 3 1590 TGCAGAAATTTC A A ----- 3 A c c
2 CTCAGCCACTGG TTC CAGTGGCT AG TTCTGCA
AGGGATTT GAG GTCACCGA TC AAGACGT
- C CTTTA

GAM116 301 KIAA144 1 7053 NP_065887.1 5 34 TCTGCTGGAGAA - ---- G 3 A c c
6 CTTAGCCCAGAG TTCAC AGT GGCTAAGTTCT CA
CTAGTGAA AAGTG TCG CCGATTCAAGA GT
A AGAC G

GAM116 301 KIAA172 1 18595 XP_034262.4 3 2745 AGTGGTGCTTTA T TCT 3 A c c
7 CTTAGCCCTGTG TTCACAG GGCTAAGT GCA
GACAACTT AGGTGTC CCGATTCA CGT
- TTT

GAM116 301 KIAA173 1 19523 NP_219494.1 3 2934 TGAAGTTTTGCA GGC G 3 A c
c
7 GAAATTGACTGT TTCACAGT TAA TTCTGCA
GAAATGTC AAGTGTCA GTT AAGACGT
--- A

GAM116 301 KIAA175 1 530 XP_028810.2 5 188 GAAGCCTGCAGG A AAG 3 A c c
5 GAAAGCCACTGG TTC CAGTGGCT TTCTGCA
AGAGTTTT GAG GTCACCGA GGGACGT
- AA-

GAM116 301 LACE1 1 17474 NP_660358.2 3 69 ACGCAGGCAGAA CTA 3 A c c
CTCCTTATTGTG TTCACAGTGG AGTTCTGC
GGACTTGA GGGTGTTATT TCAAGACG
CC-

GAM116 301 LLGL1 1 4923 NP_004131.2 3 35 AGGAAGGCAGAA A CTA 3 A c c
CTATCCGCTGAG TTC CAGTGG AGTTCTGC
GAACCTGG AGG GTCGCC TCAAGACG
A TA-

GAM116 301 LOC1151 1 18723 XP_055276.1 3 575 ACAGATGCAGAA CA- AA 3 A c
c
23 CAAGTCATATTT TTCA GTGGCT GTTCTGCA
GAAGAATG AAGT TACTGA CAAGACGT
TTA A-

GAM116 301 LOC1161 1 10531 XP_007651.11 3 333 TCTGATGCAGAA C T CT 3 A c
c
66 CTTTCTCTTTTG TTCA AG GG AAGTTCTGCA
AATGTTAA AAGT TT TC TTCAAGACGT
T C T-

GAM116 301 LOC1184 1 2230 XP_058325.1 3 205 CTCTGAACAGAA T---- C 3 A c c
87 CTTGGCCTTTTG TTCACAG GGCTAAGTTCTG

TTGTGAAT AAGTGTT CCGGTTCAAGAC
GTTTT A
GAM116 301 LOC1214 1 6256 XP_062669.7 5 12 CTCCGTGAGCAA G AA TC 3 A c c
98 GATGGCGACTGT TTCACAGT GCT GT TGC
GAAGAGTG AAGTGTCA CGG TA ACG
G -- GA
GAM116 301 LOC1237 1 17925 XP_058721.2 5 51 TTTCTAGCAGAA C T A-- 3 A c c
22 CTCCAGGTCCTC TTCA AG GGCT AGTTCTGC
TGAGTTAA GAGT TC CTGG TCAAGACG
C - ACC
GAM116 301 LOC1378 1 11715 XP_059923.2 3 179 CAGGACTTGGGA ------- C 3 A c c
29 AGCAGTCACTGT TTCACAGTGGCT AAGTTCTG
GAAATGCG AAGTGTCACTGA TTCAGGAC
CGAAGGG -
GAM116 301 LOC1448 1 18252 XP_096680.2 3 2012 ACATTATCAGAA A T - C 3 A c c
09 CTTAAGTCCTGG TTC CAG GGCT AAGTTCTG
AGATCAGA GAG GTC CTGA TTCAAGAC
- - A T
GAM116 301 LOC1488 1 5548 NP_660321.1 5 21 GGAGCTGAGAAA AAG- -- 3 A c c
23 CCGAGTCACTGT TTCACAGTGGCT TTCT GC
GAAAAGAT AAGTGTCACTGA AAGA CG
GCCA GT
GAM116 301 LOC1494 1 16914 XP_097645.1 5 1291 ATGGCTGAACTG - A-- T 3 A c c
64 GGGGCCCACTGT TTCACAGTGG CT AGTTC GC
GGAGAGCT AGGTGTCACC GG TCAAG CG
C GGG T
GAM116 301 LOC1516 1 15421 XP_087245.1 5 398 TTGTCTGCAGAA CA CTAA 3 A c c
10 CCACCACCTTGA TTCA GTGG GTTCTGCA
AAGATCCA AAGT CACC CAAGACGT
TC AC--
GAM116 301 LOC1527 1 18619 XP_087519.1 5 825 TCTGCAGGAGCA --- AAG 3 A c c
65 AGTGAGTACTGT TTCACAGTG GCT TTCTGCA
GAACACCT AAGTGTCAT TGA AGGACGT
GAG ACG
GAM116 301 LOC1532 1 14107 XP_098331.1 5 28 AGATCGCCAGAA A - G- - 3 A c c
32 CTTAGGACACAT TTC CA GTG CTAAGTTCTG C
GGGATGGA AGG GT CAC GATTCAAGAC G
- A AG C
GAM116 301 LOC1535 1 19757 NP_612500.1 3 83 CCCAAGTGCCGT -- TTCT 3 A c c
16 CTTAGCCATTCA TTCAC AGTGGCTAAG GCA
GTGAAGGG AAGTG TTACCGATTC CGT
AC TGC-
GAM116 301 LOC1538 1 12476 XP_087779.2 5 204 GAGGCAGAGCTT T---- - --- 3 A c c
11 GGCAGCCACTGA TCA CAGTGGCT AAGTTCTGC
TGGTGGTA GGT GTCACCGA TTCGAGACG
ATGGT A CGG

GAM116 301 LOC1576 1 13960 XP_088347.2 3 926 TGCTCTGCCCCT - T- TTCT 3 A c c
27 TCTGCTCACTGT TTCACAGTG GC AAG GCA
GAAGGCCG AAGTGTCAC CG TTC CGT
T TC CC--
GAM116 301 LOC1660 1 12164 XP_093643.3 5 317 CTCTCTAGTGAA - T T 3 A c c
77 TTTGCTAACTGT TTCACAGT GGC AAGTTC GC
GAAGAACA AAGTGTCA TCG TTTAAG TG
A - -
GAM116 301 LOC2011 1 3600 NP_849158.1 3 1319 GGTAGAACAGGT ------ AA 3 A c c
64 GTCGTACACTGT TTCACAGTG GCT GTTCTGC
GAAATGTT AAGTGTCAC TGG CAAGATG
ATGCTG A-
GAM116 301 LOC2011 1 3600 XP_290750.1 3 1319 GGTAGAACAGGT ------ AA 3 A c c
64 GTCGTACACTGT TTCACAGTG GCT GTTCTGC
GAAATGTT AAGTGTCAC TGG CAAGATG
ATGCTG A-
GAM116 301 LOC2034 1 2716 XP_114703.1 3 257 AAACTTTGTAAC T- TC 3 A c c
47 TTTTGTTACTGT TTCACAGTGGC AAGT TGCA
GAATTCAA AAGTGTCATTG TTCA ATGT
TT --
GAM116 301 LOC2035 1 11114 XP_117553.1 5 103 CCATACAGGCAA AGT TC 3 A c c
62 CTTAGCTGGTGA TTCAC GGCTAAGT TGC
AAGGACTC AAGTG TCGATTCA ACG
G-- --
GAM116 301 LOC2198 1 19459 XP_167775.1 3 411 GGGCCAGGAGCT GG -- -- 3 A c c
42 TGAAGGAACTGT TTCACAGT CT AAGTTCT GC
GAAATAAA AAGTGTCA GA TTCGAGG CG
AG AG AC
GAM116 301 LOC2206 1 13427 XP_165433.1 3 89 AGTTCGTCAGAA A GC - 3 A c c
35 CTTAAATACTGA TTC CAGTG TAAGTTCTG C
GGAAGAAG AGG GTCAT ATTCAAGAC G
A AA T
GAM116 301 LOC2538 1 11595 XP_171040.2 5 179 AACACTCTGGGC CT TTC 3 A c c
20 ACCTTCCACTGT TTCACAGTGG AAG TGC
GAATGTGA AAGTGTCACC TTC ACG
-- C--
GAM116 301 LOC2829 1 15939 XP_212606.1 5 38 GTTGGCAGCCGC A - T- 3 A c c
05 TTGAGCCACTGC TTC CAGTGGCT AAGT CTGC
GAGGAAAG GAG GTCACCGA TTCG GACG
C G CC
GAM116 301 LOC2829 1 15939 XP_212647.1 5 38 GTTGGCAGCCGC A - T- 3 A c c
43 TTGAGCCACTGC TTC CAGTGGCT AAGT CTGC
GAGGAAAG GAG GTCACCGA TTCG GACG
C G CC
GAM116 301 LOC2832 1 4814 XP_210964.1 3 1098 TTGAGTGCAGAA - AG A 3 A c c

95 CTAGCTAGTAGA TTC AC TGGCTA GTTCTGCA
AGCCAGAT AAG TG ATCGAT CAAGACGT
A -- -

GAM116 301 LOC2836 1 5207 XP_211164.1 3 1184 CCTCTGGGCAAG CTAA - 3 A c c

86 AGCACCCACTGT TTCACAGTGG GTTCT GC
GAAGTCCT AAGTGTCACC CGAGA CG
CA-- A

GAM116 301 LOC2838 1 19503 XP_208899.1 3 338 CCATGGCCAGCA - AAG 3 A c c

89 GGAAGCCACTGA TTCA CAGTGGCT TTCTGC
TGAGGGGA GAGT GTCACCGA AGGACG
A ---

GAM116 301 LOC2839 1 9479 XP_208908.1 5 183 AGGATGGCAGAA A-- T - A 3 A c c

22 CTGGTCCTCTGC TTC CAG GG CTA GTTCTGC
AAGAAACA AAG GTC CC GGT CAAGACG
AAC T T -

GAM116 301 LOC2840 1 11823 XP_208152.1 3 1048 TGTTTAGAAGTA AAG 3 A c c

48 GGAAGTCACTGT TTCACAGTGGCT TTCTGC
GAGCAATG GAGTGTCACTGA AGGATG

GAM116 301 LOC2842 1 19309 XP_211421.1 5 66 AGTTCATAGTGA CT G T 3 A c c

94 AGTTTCCACTGT TTCACAGTGG AA TTC GC
GAGCGGCA GAGTGTCACC TT AAG TG
T- G -

GAM116 301 LOC2844 1 19943 XP_211475.1 3 1298 CTCCCCCAGAGT CTA -- C 3 A c c

62 ACTCCCCACTGT TTCACAGTGG AGT TCTG
GAAAAGAG AAGTGTCACC TCA AGAC
CC- TG C

GAM116 301 LOC2846 1 4242 XP_208231.1 3 2309 TGTTCAGCAGAA T----- CTAA 3 A c c

42 CACCACCACTGT TCACAGTGG GTTCTGC
GACATGGG AGTGTCACC CAAGACG
GGGTAC ACCA

GAM116 301 LOC2848 1 9072 XP_211650.1 5 177 TCGGATGCTAGC GC T - 3 A c c

28 ACTTGACACTGT TTCACAGTG TAAGT CT GCA
GAGCGCAC GAGTGTCAC GTTCA GA CGT
A- C T

GAM116 301 LOC2848 1 1526 XP_211658.1 5 647 AGCCTTTGGAAC AA- ---- 3 A c c

37 GTGAGCCACTGT TTCACAGTGGCT GTTCT GC
GGGCTGGC GGGTGTCACCGA CAAGG CG
GTG TTTC

GAM116 301 LOC2849 1 1527 XP_211705.1 3 190 TATGGCAGAGGC AA- - 3 A c c

47 CACAGCCACTGT TTCACAGTGGCT GT TCTGC
GGGGCACC GGGTGTCACCGA CG AGACG
CAC G

GAM116 301 LOC2850 1 16141 XP_209446.1 5 243 AAGCAGTGGAGG A ---- 3 A c c

35 CTCAGCCACTGT TTCACAGTGGCT AGTT CTGC
GAGGAGGT GAGTGTCACCGA TCGG GACG

```
                                                C   AGGT
GAM116  301   LOC2851 1  15846 XP_211772.1  5  1433  CATCTTGCAGAA   A  TG CT          3  A  c
c
        31                          CTTCTGCTGGAG TTC CAG  G  AAGTTCTGCA
                                   TCGAAATC    GAG GTC  C  TTCAAGACGT
                                           -  GT --
GAM116  301   LOC2854 1  12379 XP_209608.1  3  50    TGTGGACCAGAA     T  CT-     C      3  A  c  c

        34                          CTTTCACCTTGT TTCACAG GG   AAGTTCTG
                                   GAATGCAT    AAGTGTT CC   TTCAAGAC
                                           -  ACT      C
GAM116  301   LOC2855 1  19592 XP_209660.1  3  1110  CTTGGTGCTGAA   ACA        T       3  A  c
c
        60                          CTTAGCCACAAG TTC  GTGGCTAAGTTC GCA
                                   GAGCTGTC    GAG   CACCGATTCAAG CGT
                                           GAA         T
GAM116  301   LOC2857 1  4300  XP_212000.1  3  76    GTCCGGGAGCGG       CTAA          3  A  c  c

        27                          GGCACCCACTGT TTCACAGTGG   GTTCTGC
                                   GGGTCTCC    GGGTGTCACC    CGGGGCG
                                           CA--
GAM116  301   LOC2858 1  15939 XP_212043.1  5  38    GTTGGCAGCCGC   A     -  T-       3  A  c  c
        30                          TTGAGCCACTGC TTC CAGTGGCT AAGT  CTGC
                                   GAGGAAAG    GAG GTCACCGA TTCG  GACG
                                           C      G   CC
GAM116  301   LOC2859 1  3194  XP_208364.1  3  223   AAAATGCTCAGA       GCT      C       3  A  c  c

        39                          ATTTCACACTGT TTCACAGTG   AAGTTCTG
                                   GAATCCAC    AAGTGTCAC   TTTAAGAC
                                           AC-       T
GAM116  301   LOC2860 1  5267  XP_212119.1  5  782   TCGTGGCCAGAA    AG   T     -       3  A  c  c
        26                          CTTGCTGAGGTG TTCAC  TGGC AAGTTCTG C
                                   AAGGCACA    AAGTG  GTCG TTCAAGAC G
                                           GA   -      C
GAM116  301   LOC2861 1  12515 XP_212185.1  3  377   CTGTGTTGCGGA       CT  G          3  A  c  c

        26                          AGTTCTCACTGT TTCACAGTGG  AA TTCTGCA
                                   GAACTTTA    AAGTGTCACT  TT AAGGCGT
                                           C-  G
GAM116  301   LOC2865 1  9848  XP_210080.1  3  1051  ATTGTAAACAAG         -  G  C--       3  A  c  c
        00                          TTCAGCCACTGT TTCACAGTGGCT AA TT   TGCA
                                   GGAAGACA    AGGTGTCACCGA TT AA   ATGT
                                           C  G  CAA
GAM116  301   LOC3389 1  6175  XP_294754.1  5  1749  CCTTTGTTCAGA   -      AG    C       3  A  c  c
        59                          AATGGCCACTGT TTC ACAGTGGCTA  TTCTG
                                   AGAAAGCC    AAG TGTCACCGGT  AAGAC
                                           A        A-    T
GAM116  301   LOC3389 1  3739  XP_290664.1  3  137   ATATGTTGCAAA   -  -        C        3  A  c  c
        87                          CTTAGCCATATG TTC ACA GTGGCTAAGTT TGCA
                                   TAGAGTGG    GAG TGT TACCGATTCAA ACGT
```

```
                                        A  A       -
GAM116  301   LOC3394 1  17103 XP_290925.1  5  133   GTGGTTGCTGCA       C    TCT        3  A  c
c
        94                          CTTGACCACTGT TTCACAGTGG TAAGT   GCA
                                   GAAGACTG    AAGTGTCACC GTTCA   CGT
                                             A    CGT
GAM116  301   LOC3396 1  8835  XP_295016.1  5  1962  TCTGTGAAGCAA     GT      TC         3  A  c  c

        22                          CTTAGCTGATGT TTCACA  GGCTAAGT  TGC
                                   GGAGGAAT    AGGTGT  TCGATTCA  ACG
                                             AG       --
GAM116  301   LOC3396 1  2508  XP_290981.1  3  1097  TGTCATTCAGAA         AA    C        3  A  c  c
        59                          CACAGCCACTGT TTCACAGTGGCT  GTTCTG
                                   GAAAGTGC    AAGTGTCACCGA  CAAGAC
                                             CA     T
GAM116  301   LOC3401 1  2717  XP_295164.2  5  541   TCAGGCCCAGAA     --- T  T      C      3  A  c  c
        28                          CTTGCCCTCCAG TTCAC   AG GGC AAGTTCTG
                                   TGGACCTT    AGGTG   TC CCG TTCAAGAC
                                             ACC  -  -       C
GAM116  301   LOC3404 1  17429 XP_290424.2  3  1537  CACAAGTACGAA    C---  --       -      3  A  c  c
        49                          CTTAGCAACACT TTCA    AGTG  GCTAAGTTC TGC
                                   ATATTGAG    GAGT    TCAC  CGATTCAAG ATG
                                             TATA    AA       C
GAM116  301   LOC3410 1  19443 XP_295977.1  3  164   GGGCAGCCCTGG         A----  TT        3  A  c
c
        41                          AGGAGCCACTGT TTCACAGTGGCT    AG  CTGC
                                   GGGCTCCA    GGGTGTCACCGA    TC  GACG
                                             GGAGG  CC
GAM116  301   LOC3438 1  19387 XP_293260.2  5  238   CTTGGCTCTGAA         AG   T--       3  A  c  c
        38                          GCTGGCCACTGT TTCACAGTGGCTA  TTC   GC
                                   GGGCTGCA    GGGTGTCACCGGT  AAG   CG
                                             CG   TCT
GAM116  301   LOC3446 1  4215  XP_293503.1  5  898   GCAACAGACAGG       G     ---  C      3  A  c  c
        22                          CTTGGCAACTGT TTCACAGT GCTAAGT   TCTG
                                   GAATACCT    AAGTGTCA CGGTTCG   AGAC
                                             A      GAC    A
GAM116  301   LOC3477 1  17800 XP_300531.1  3  1710  TGGATGTGCAAG   A      AA  TC         3  A  c
c
        67                          ACCAGCCACTGG TTC CAGTGGCT  GT  TGCA
                                   AGGTAGCT    GAG GTCACCGA  CA  ACGT
                                             -      C-  GA
GAM116  301   LOC3479 1  18280 XP_300570.1  5  189   AATGTCAGGAAT T        AAG--    -      3  A  c
c
        24                          GGAAGCCACTGT  TCACAGTGGCT    TTCTG CA
                                   GA          AGTGTCACCGA    AGGAC GT
                                             -         AGGTA    T
GAM116  301   LOC3480 1  11344 XP_300595.1  3  169   GGTACTGCAGAA    A -   AA          3  A  c  c

        35                          CAGAGCCTGCAG TTCAC GT GGCT  GTTCTGCA
                                   TGAGACAC    GAGTG CG CCGA  CAAGACGT
```

```
                                        A  T    GA
GAM116  301   LOC3481 1  5461  XP_302676.1  5  247   TCACCGGCCAGA       - AAG   -       3  A  c  c

        82                          GAAGACCACTGT TTCACAGTGG CT   TTCTG C
                                   GAGCATTT    GAGTGTCACC GA   GAGAC G
                                         A  A--    C
GAM116  301   LOC3487 1  13427 XP_300397.1  3  89    AGTTCGTCAGAA   A    GC      -       3  A  c  c
        20                          CTTAAATACTGA TTC CAGTG  TAAGTTCTG C
                                   GGAAGAAG    AGG GTCAT  ATTCAAGAC G
                                         A    AA       T
GAM116  301   LOC3487 1  15606 XP_302869.1  3  1160  GACTTTGCAGAA    AG  - AA          3  A  c
c
        61                          CCGGTCCAAGGT TTCAC  TGG CT  GTTCTGCA
                                   GAGAGTAG    GAGTG  ACC GG  CAAGACGT
                                         GA   T  C-
GAM116  301   LOC3487 1  13427 XP_300403.1  3  197   AGTTCGTCAGAA   A    GC      -       3  A  c  c

        69                          CTTAAATACTGA TTC CAGTG  TAAGTTCTG C
                                   GGAAGAAG    AGG GTCAT  ATTCAAGAC G
                                         A    AA       T
GAM116  301   LOC3487 1  10129 XP_302884.1  5  296   TTAGCTGCAGAA    -  CTAA          3  A  b
b
        80                          CCCACATGTGAA TTCACA GTGG   GTTCTGCA
                                   TCCTTGTA    AAGTGT CACC    CAAGACGT
                                         A    ----
GAM116  301   LOC3492 1  16327 XP_303016.1  5  1705  AATGCAAACTAG         A----   C       3  A  c  c
        77                          TTCAGCCACTGT TTCACAGTGGCT    AGTT TGCA
                                   GGAGAGAA    AGGTGTCACCGA    TCAA ACGT
                                         CTTGA   -
GAM116  301   LOC5618 1  18280 NP_062457.2  5  310   AATGTCAGGAAT T        AAG--   -       3  A  c
c
        1                           GGAAGCCACTGT  TCACAGTGGCT    TTCTG CA
                                   GA         AGTGTCACCGA    AGGAC GT
                                         -        AGGTA    T
GAM116  301   LOC5711 1  3740  NP_065128.2  5  201   TGCGTTTGCAAT        TA   C-         3  A  c  c
        7                           GGCTGCTACTGT TTCACAGTGGC  AGTT  TGCA
                                   GAACTTGG    AAGTGTCATCG  TCGG  ACGT
                                         --   TA
GAM116  301   LOC8369 1  8686  NP_113651.3  3  1526  ATGTCTTCAGAA     GTGG       C       3  A  c
c
        3                           CTTAGATGTGAA TTCACA   CTAAGTTCTG
                                   AATCTACA    AAGTGT   GATTCAAGAC
                                         A---        T
GAM116  301   LOC9176 1  2057  NP_612384.1  3  871   TAACCCTCGCAC       CT-   TCT       3  A  c
c
        8                           TTTCTCCACTGT TTCACAGTGG   AAGT   GC
                                   GGAGATGG    AGGTGTCACC   TTCA   CG
                                         TCT   ---
GAM116  301   LOC9256 1  18855 XP_045852.1  3  839   CCCTCTCCAGTA       CTAA  T         3  A  c
c
```

8 GGCATCCACTGT TTCACAGTGG GT CTGC
GGAAGTGC AGGTGTCACC CG GATG
TA-- -
GAM116 301 LOC9346 1 16757 XP_051528.1 3 272 CGCCTTGCAGAA -- TA 3 A c c
3 CTGTCAGCCTGT TTCACAG TGGC AGTTCTGCA
GGAGTTGT AGGTGTC ACTG TCAAGACGT
CG --
GAM116 301 LOC9410 1 13826 NP_149986.1 5 1174 AAGGGCAGCCCT C TT--- 3 A c
c
5 CCTTACCACTGT TTCACAGTGG TAAG CTGC
GGAAGTCC AGGTGTCACC ATTC GACG
- CTCCC
GAM116 301 LOH11CR 1 12927 NP_055437.1 3 536 ACAGAGACTGCA - AAGT 3 A c
c
2A GGGGTCCACTGT TTCACAGTGG CT TCTGCA
GAGAGGTG GAGTGTCACC GG GGACGT
T ----
GAM116 301 MAP3K7 1 13790 NP_663305.1 3 4 CTAGTTGCAGAA CAG - A 3 A c c
CTGGACCAGGAT TTCA TGG CTA GTTCTGCA
GAAAGGAC AAGT ACC GGT CAAGACGT
AGG A -
GAM116 301 MAP3K7 1 13790 NP_663306.1 3 4 CTAGTTGCAGAA CAG - A 3 A c c
CTGGACCAGGAT TTCA TGG CTA GTTCTGCA
GAAAGGAC AAGT ACC GGT CAAGACGT
AGG A -
GAM116 301 MAPKBP1 1 19619 XP_031706.7 3 705 TCCTGGCCAGAA - - - 3 A b b
CTTGAGCCAGCT TTCACAG TGGCT AAGTTCTG C
GTGGGATG GGGTGTC ACCGA TTCAAGAC G
G G C
GAM116 301 MCL1 1 3273 NP_068779.1 3 1634 AGCCCTTTTAGA G T C 3 A c c
TTTTGGCACTGT TTCACAGTG CTAAG TCTG
GAAACCCC AAGTGTCAC GGTTT AGAT
- T T
GAM116 301 MDFI 1 7809 NP_005577.1 3 343 GCAGCCAGGGCT G- A- - 3 A c c
GGGGAACACTGT TTCACAGTG CT AGTTCTG C
GAAAGTTA AAGTGTCAC GG TCGGGAC G
AA GG C
GAM116 301 MGC1245 1 11264 NP_115704.1 3 381 GAGGGTGCAGAA AC CTAA 3 A
c c
8 CGAACCACTCGA TTC AGTGG GTTCTGCA
AAACGAGT AAG TCACC CAAGACGT
C- AAG-
GAM116 301 MGC1290 1 2673 NP_112496.1 5 227 CCTAAGTATCAA C -- C- 3 A c c
4 CTTAGCCGTACT TTCA AGT GGCTAAGTT TGC
TTGAACTC AAGT TCA CCGATTCAA ATG
T TG CT
GAM116 301 MGC1480 1 7422 NP_116094.1 3 156 GAAGGATGCGGA G AA 3 A c
c
1 GCCCAGCACTGT TTCACAGTG CT GTTCTGCA
GAAGCCTA AAGTGTCAC GA CGAGGCGT

- CC

GAM116 301 MGC1560 1 5629 NP_659474.1 3 221 ATCCAATGTTGA - A CT 3 A c c
6 CTTAGCCATGGT TTC AC GTGGCTAAGTT GCA
AGAACTCT AAG TG TACCGATTCAG TGT
A G T-

GAM116 301 MGC1593 1 12915 NP_542392.2 3 998 TGCCATTGGAAC - ---- 3 A c c
7 TTGGATTACTGT TTCACAGTGG CTAAGTTCT GCA
GAACATTG AAGTGTCATT GGTTCAAGG CGT
A TTAC

GAM116 301 MGC2316 1 16537 NP_689948.1 5 121 GGAGCAGACCTC G --- T 3 A c
c
6 TGTGGGCACTGT TTCACAGTG CTA AG TCTGC
GAGGCGGA GAGTGTCAC GGT TC AGACG
G GTC C

GAM116 301 MGC2499 1 10667 NP_714914.1 5 441 ATCTCTGCAGAA A - CTAA 3 A c
c
5 CAACCAGCTGGA TTC CAG TGG GTTCTGCA
AAAGATCT AAG GTC ACC CAAGACGT
- G AA--

GAM116 301 MGC2671 1 8483 NP_689723.1 3 375 CTCTTCAGCTAT - T- C 3 A c c
0 TTAGACTACTGT TTCACAGTGG CTAAGT CTG
GAAATGTT AAGTGTCATC GATTTA GAC
A TC T

GAM116 301 MGC3969 1 9234 NP_689984.1 5 143 GGGGCCGCAGGG AG 3 A c
c
6 GCTGGCCACTGT TTCACAGTGGCTA TTCTGC
GGGCTCGG GGGTGTCACCGGT GGGACG
CG

GAM116 301 MGC4586 1 14643 NP_689472.2 3 425 CACAGGCAGCGC G- T T 3 A c
c
6 TTTGTAAACTGT TTCACAGT GC AAGT CTGC
GAAGCCAT AAGTGTCA TG TTCG GACG
AA T C

GAM116 301 MGC4673 1 10690 NP_714925.1 3 2204 CTGCAGAAAGGA ---- AAG 3 A c
c
2 GCTACCCACTGT TTCACAGTG GCT TTCTGCA
GGGTCTTC GGGTGTCAC CGA AAGACGT
CCAT GGA

GAM116 301 MGC4833 1 18723 NP_848545.1 3 576 ACAGATGCAGAA CA- AA 3 A c
c
2 CAAGTCATATTT TTCA GTGGCT GTTCTGCA
GAAGAATG AAGT TACTGA CAAGACGT
TTA A-

GAM116 301 MGC5442 1 18618 NP_113622.1 3 459 ACCCGTGCAGAT G AAGT 3 A c
c
TAAAGTAACTGT TTCACAGT GCT TCTGCA
GAAGTTTT AAGTGTCA TGA AGACGT
A AATT

GAM116 301 MGC5721 1 18590 NP_787074.1 5 15 TCTGATGCAGAA AG C A 3 A c
c

1 CGTATCAGTGAA TTCAC TGG TA GTTCTGCA
ACTCCCTC AAGTG ACT AT CAAGACGT
-- - G

GAM116 301 MGC7036 1 5133 NP_659495.1 3 200 CTGGCTGCAGAA CA- G A 3 A c c

CTAGACACCCTT TTCA GTG CTA GTTCTGCA
GAAGATTT AAGT CAC GAT CAAGACGT
TCC A -

GAM116 301 MNT 1 6137 NP_064706.1 3 486 GGGAAAGCAGAA T----- C A- 3 A c c
CTGAAGCCACTT TCA AGTGGCT AGTTCTGC
GGCCCAGA GGT TCACCGA TCAAGACG
AGACCC - AG

GAM116 301 MTMR4 1 6995 NP_004678.2 3 781 GGCAGCTCTTGA ---- - TT 3 A c c
GTTATGCACTGT TTCACAGTG GCT AAG CTGC
GAAGAATG AAGTGTCAC TGA TTC GACG
GTAT G TC

GAM116 301 MYNN 1 18472 NP_061127.1 5 134 AAAATGCAGTAT CTA- T 3 A c c
TCGCACCACTGT TTCACAGTGG AGT CTGCA
GAGC GAGTGTCACC TTA GACGT
ACGC T

GAM116 301 NAV3 1 11894 NP_055718.2 3 160 GAGGCAGCAGAA CAGT A 3 A c c

CTAAGTCTGAAC TTCA GGCT AGTTCTGC
CGCCAAGA AAGT CTGA TCAAGACG
---- A

GAM116 301 NFKBIE 1 6706 NP_004547.1 3 485 GAAGGCTCTGAA A- A T-- 3 A c c
CTGAGCCACTGG TTC CAGTGGCT AGTTC GC
GGAAGGGA AAG GTCACCGA TCAAG CG
GG G TCT

GAM116 301 NGFR 1 774 NP_002498.1 3 125 CGCCTGGCAGAA C TG A 3 A c c
CTGAGCTCCTCT TTCA AG GCT AGTTCTGC
GGGCAGGA GGGT TC CGA TCAAGACG
C CT G

GAM116 301 NIPSNAP 1 16570 NP_003625.1 3 669 CGGAAGGTAGAA AC GG 3 A c c

1 CTTAGAATTCAG TTC AGT CTAAGTTCTGC
AACTTGGG AAG TTA GATTCAAGATG
AC A-

GAM116 301 NODAL 1 3383 NP_060525.2 5 342 CATTGGAGGTGC G - - G 3 A c c
TTGAGTAACTGT TTCACAGT GCT AAGT TCT CA
GAATACAG AAGTGTCA TGA TTCG GGA GT
A G T G

GAM116 301 NRBF-2 1 2507 NP_110386.1 3 172 CAGGACTTGGGA ------- C 3 A c c
AACAGTCACTGT TTCACAGTGGCT AAGTTCTG
GAAATGCG AAGTGTCACTGA TTCAGGAC
CAAAGGG -

GAM116 301 NUP210 1 7611 NP_079199.2 3 664 TGCTGCCCAACC AA-- CT 3 A c c

ATGGGCCACTGT TTCACAGTGGCT GTT GCA
GAACAGAC AAGTGTCACCGG CAA CGT

GTAC CC

GAM116 301 OCRL 1 5246 NP_000267.2 3 1605 CTAGGTGTTGAA A G T 3 A c c
CTTAGTTAATGG TTC CA TGGCTAAGTTC GCA
AAGACTGA AAG GT ATTGATTCAAG TGT
- A T

GAM116 301 OCRL 1 5246 NP_001578.2 3 1605 CTAGGTGTTGAA A G T 3 A c c
CTTAGTTAATGG TTC CA TGGCTAAGTTC GCA
AAGACTGA AAG GT ATTGATTCAAG TGT
- A T

GAM116 301 OSM 1 5982 NP_065391.1 3 125 TTCCCCTCTGCT A A TCT 3 A c c
ACTAGCCACTGA TTC CAGTGGCTA GT GCA
GAAGTGCA AAG GTCACCGAT CA CGT
A - T--

GAM116 301 P101-PI 1 16367 NP_055123.1 3 120 TGTGCAGAGCCA -- A- 3 A c c
3K TAGTCCCACTGT TTCACAGTGG CTA GTTCTGCA
GGGTCCTG GGGTGTCACC GAT CGAGACGT
CT AC

GAM116 301 P24B 1 5315 NP_031390.1 3 267 ACTAGGCCAGGG G - 3 A c c
ATTAGCCACTGT TTCACAGTGGCTAA TTCTG C
GGGAGGGT GGGTGTCACCGATT GGGAC G
A C

GAM116 301 PAFAH2 1 7764 NP_000428.2 3 303 CCCAGGCCCCGG G A T-- 3 A c c

GCTGAGCACTGT TTCACAGTG CT AGTTC GC
GAGGCCTG GAGTGTCAC GA TCGGG CG
- G CCC

GAM116 301 PAIP2 1 13015 NP_057564.2 3 52 GATGTAGCACAA GCT C 3 A c c
TTTCCACACTGT TTCACAGTG AAGTT TGC
GAAGGCAG AAGTGTCAC TTTAA ACG
ACC C

GAM116 301 PAPOLG 1 2310 NP_075045.2 3 325 TGGGAACCAGTT C TT C 3 A c c

CTTAGCCACTTG TTCA AGTGGCTAAG CTG
GACACTGA AGGT TCACCGATTC GAC
- TT C

GAM116 301 PBXIP1 1 11249 NP_065385.2 3 260 TGTGGGCTTGTG ------ T 3 A c c
TTTTGTCACTGT TTCACAGTGGC TAAGTTC GCA
GAAGGGGG AAGTGTCACTG GTTCGGG TGT
TTTTGT -

GAM116 301 PCDH10 1 10950 NP_116586.1 3 217 AAATGTGCAGAA AC- GG - 3 A c
c

CTGTAGAAACTT TTC AGT CTA AGTTCTGCA
TAGAGGCA GAG TCA GAT TCAAGACGT
ATT AA G

GAM116 301 PDE4B 1 13014 NP_002591.1 5 696 CCATCCCAGGCA T----- CTAA 3 A c
c

GAGCACCACTGT TCACAGTGG GTTCTGC
GATTTGTT AGTGTCACC CGAGACG
TTGTTT A---

GAM116 301 PGBD5 1 19715 NP_078830.2 3 320 GAGGCAGCGTGG G A - 3 A c c

ACTGGTGACTGT TTCACAGT GCTA GTTC TGC
GAAGGAAG AAGTGTCA TGGT CAGG GCG
G - T

GAM116 301 PHF5A 1 8541 NP_116147.1 3 364 TCTTCTGCTTGA GGCTA ---- 3 A c c

GGAACTGACTGT TTCACAGT AGTTCT GCA
GAAGCGAC AAGTGTCA TCAAGG CGT
G---- AGTT

GAM116 301 PIGF 1 15112 NP_775097.1 3 0 GCAGGGGGCTTG G -- 3 A c c

GTACTGTGAAAT TTCACAGTG CTAAGT TCTGC
GGTAACTT AAGTGTCAT GGTTCG GGACG
- GG

GAM116 301 PMP22 1 14008 NP_000295.1 5 188 CGCTGAGCAGAA ACA T 3 A c c

CTTGCCGCCAGA TTC GTGGC AAGTTCTGC
ATGCTCCT AAG CGCCG TTCAAGACG
AC- -

GAM116 301 PMP22 1 14008 NP_696996.1 5 158 CGCTGAGCAGAA ACA T 3 A c c

CTTGCCGCCAGA TTC GTGGC AAGTTCTGC
ATGCTCCT AAG CGCCG TTCAAGACG
AC- -

GAM116 301 PMP22 1 14008 NP_696997.1 5 29 CGCTGAGCAGAA ACA T 3 A c c

CTTGCCGCCAGA TTC GTGGC AAGTTCTGC
ATGCTCCT AAG CGCCG TTCAAGACG
AC- -

GAM116 301 PRND 1 18816 NP_036541.1 3 1682 AGCATTGCAGAA - G AA- 3 A c c

CATGAGTGCTGA TTCA CAGTG CT GTTCTGCA
TGAGGGCA GAGT GTCGT GA CAAGACGT
A - GTA

GAM116 301 PRO0461 1 5461 NP_112558.1 5 454 TCACCGGCCAGA - AAG - 3 A c c

GAAGACCACTGT TTCACAGTGG CT TTCTG C
GAGCATTT GAGTGTCACC GA GAGAC G
A A-- C

GAM116 301 PRO2214 1 15420 NP_060987.1 3 648 TTGCTTCCCTAT TTCT---- 3 A c c

CTTGGCTACTGT TTCACAGTGGCTAAG GCA
GAATAATG AAGTGTCATCGGTTC CGT
TATCCCTT

GAM116 301 PROZ 1 4273 NP_003882.1 3 76 ATTCCAAGCTGG TA - T 3 A c c

CACTGCCACTGT TTCACAGTGGC AGT TC GC
GGAGGGCG AGGTGTCACCG TCA GG CG
-- C T

GAM116 301 PRPF4B 1 18328 NP_003904.2 3 3022 TTGTAAGCAGAA CA - 3 A c c

CTCTAGCTATAT TTCA GTGGCTA AGTTCTGC
GGGGTAGA GGGT TATCGAT TCAAGACG
A- C

GAM116 301 PTPRF 1 2806 NP_002831.1 3 424 CGTATCTGCAGA - AA 3 A c c

ATGGGCCACTGT TTC ACAGTGGCT GTTCTGCA

AGGGGTTG GGG TGTCACCGG TAAGACGT
A G-
GAM116 301 PTPRF 1 2806 NP_569707.1 3 424 CGTATCTGCAGA - AA 3 A c c
ATGGGCCACTGT TTC ACAGTGGCT GTTCTGCA
AGGGGTTG GGG TGTCACCGG TAAGACGT
A G-
GAM116 301 RAB9P40 1 6382 NP_005824.1 5 9 GTCGCCGCAGAA A TA 3 A c c
CTGCCACGTGGG TTCAC GTGGC AGTTCTGC
GATGAGAT GGGTG CACCG TCAAGACG
- --
GAM116 301 RAP1B 1 16170 NP_056461.1 3 847 TCTGCAGCTGTA ---- AGTT 3 A c c

GATTCTCACTGT TTCACAGTGG CTA CTGCA
GAATCCCT AAGTGTCACT GAT GACGT
CTTA GTC-
GAM116 301 RGS17 1 16913 NP_036551.3 3 119 GTTTAGCATTCC A- TTC 3 A c c
TCAGGCTACTGT TTCACAGTGGCT AG TGC
GAAAACAC AAGTGTCATCGG TC ACG
AC CTT
GAM116 301 RGS6 1 7127 NP_004287.3 3 112 CTTACGAGGAGA - GC 3 A c c
CTTGGTCACTGT TTCACAGTGGCTAAGT TCT
GAAGGAGA AAGTGTCACTGGTTCA AGG
G AG
GAM116 301 RNF24 1 18774 NP_009150.1 3 833 ACTGCCTCAGAA AAG C 3 A c c
GGGAGCCACTGT TTCACAGTGGCT TTCTG
GAACCTCT AAGTGTCACCGA AAGAC
GGG T
GAM116 301 RPS24 1 4670 NP_001017.1 3 38 AATGATGTTAGC - CT 3 A c c
TGTGGCCACTGT TTCACAGTGGCTA AGTT GCA
GGATTTTT AGGTGTCACCGGT TCGA TGT
G T-
GAM116 301 RPS24 1 4670 NP_148982.1 3 69 AATGATGTTAGC - CT 3 A c c
TGTGGCCACTGT TTCACAGTGGCTA AGTT GCA
GGATTTTT AGGTGTCACCGGT TCGA TGT
G T-
GAM116 301 SCN8A 1 8797 NP_055006.1 3 104 ATCAATGCAGAA GGCTAA 3 A c
c

CAGCTGTGGAGA TTCACAGT GTTCTGCA
CTCTAACC AGGTGTCG CAAGACGT
A-----
GAM116 301 SE57-1 1 19416 NP_079490.1 3 1535 GTAATTTGCCCA - TA CT 3 A c c
GCTGCTAACTGT TTCACAGT GGC AGTT GCA
GAAGCAAA AAGTGTCA TCG TCGA CGT
A -- CC
GAM116 301 SFRP1 1 12977 NP_003003.2 3 2599 TCCTTGGCAGAA C --- A 3 A c c
CTCAGTTAAATC TTCA AG TGGCT AGTTCTGC
TTTGAAGA AAGT TC ATTGA TCAAGACG
T TAA C
GAM116 301 SFXN5 1 13244 NP_653180.1 3 698 AGAGCTGCAGAA ---- T AA 3 A c c
CCAGTCCCTCTG TTCAC AG GGCT GTTCTGCA

AGTGAAGT AAGTG TC CTGA CAAGACGT
AGTC C C-
GAM116 301 SLC16A1 1 1239 NP_061063.2 3 293 GTAAAAAGCAGC GG TT 3 A c c
0 TTTGGAAACTGT TTCACAGT CTAAG CTGC
GAATGATC AAGTGTCA GGTTT GACG
AA C-
GAM116 301 SLC22A1 1 3144 NP_653186.2 5 629 CCGCTGGGCTGG A---- T 3 A c c
2 AGAAGCCACTGT TTCACAGTGGCT AGTTC GC
GGGCACCA GGGTGTCACCGA TCGGG CG
AGAGG T
GAM116 301 SLC22A1 1 3144 NP_700357.1 5 629 CCGCTGGGCTGG A---- T 3 A c c
2 AGAAGCCACTGT TTCACAGTGGCT AGTTC GC
GGGCACCA GGGTGTCACCGA TCGGG CG
AGAGG T
GAM116 301 SLC9A3R 1 11349 NP_004243.1 3 405 CTGACTGCAGAA ---- TA 3 A c c
1 CTGCCGCTCTCA TTCAC AGTGGC AGTTCTGCA
GTGGACAG AGGTG TCGCCG TCAAGACGT
ACTC --
GAM116 301 SORD 1 10531 NP_003095.1 3 99 TCTGATGCAGAA C T CT 3 A c c
CTTTCTCTTTTG TTCA AG GG AAGTTCTGCA
AATGTTAA AAGT TT TC TTCAAGACGT
T C T-
GAM116 301 SOX1 1 17428 NP_005977.2 3 2765 TACAGTAGGCCC - A T- 3 A c c
TGAGCCGACTGT TTCACAGT GGCT AG TCTGC
GAATTCGG AAGTGTCA CCGA TC GGATG
G G CC
GAM116 301 SOX13 1 15099 NP_005677.1 3 394 TGTCCTGGCTGG AA T 3 A c c
ACCAGCCACTGT TTCACAGTGGCT GTTC GC
GGGACCAA GGGTGTCACCGA CAGG CG
C- T
GAM116 301 SPATA2 1 11422 NP_006029.1 3 1598 CTGGCTGAATCC A- -- T 3 A c c
TGAGGCCACTGT TTCACAGTGGCT AG TTC GC
GAATTTGC AAGTGTCACCGG TC AAG CG
AG CT T
GAM116 301 ST14 1 14983 NP_068813.1 3 128 CAGCGCCCCCAG GCTAA C 3 A c
c
AACATACACTGT TTCACAGTG GTTCTG
GAACTCAA AAGTGTCAC CAAGAC
ATA-- C
GAM116 301 TDP1 1 14692 NP_060789.2 3 22 CCTCCTGGAATC G - - C 3 A c c
TTGAGGCACTGT TTCACAGTG CT AAG TTCTG
GAAATTTA AAGTGTCAC GA TTC AAGGT
G G T C
GAM116 301 TEM1 1 14211 NP_065137.1 3 7 AGACCTGCAGAA GTG AA 3 A c c
CCAGCGTGTGTG TTCACA GCT GTTCTGCA
GGGTGCAG GGGTGT CGA CAAGACGT
GTG C-
GAM116 301 THY1 1 13826 NP_006279.2 3 631 AAGGGCAGCCCT C TT--- 3 A c c
CCTTACCACTGT TTCACAGTGG TAAG CTGC

GGAAGTCC AGGTGTCACC ATTC GACG
- CTCCC

GAM116 301 TOR2A 1 12108 NP_569726.1 3 1449 CTGCAGCCTGAG ----- A TT 3 A c c

CCTTCTTACTGT TTCACAGT GGCT AG CTGCA
GAATTATA AAGTGTCA CCGA TC GACGT
TTCTT G C-

GAM116 301 TRAF1 1 4417 NP_005649.1 3 853 ATGCAGGTGAAA AA ---- 3 A c c
CCCAGTCACTGT TTCACAGTGGCT GT TCTGCA
GAGCTCCC GAGTGTCACTGA CA GGACGT
CC AAGT

GAM116 301 TRIM34 1 6774 NP_569073.1 5 222 CCTCTGCCGAGC -- TAA T 3 A c c
CTGCATCACTGT TTCACAGTG GC GTTC GCA
GAGCAACA GAGTGTCAC CG CGAG CGT
TA TC- C

GAM116 301 TSC22 1 16490 NP_006013.1 3 37 GCCCCCGCAGAA - TG TA-- 3 A c c
CTGGCTGCTGCG TTCACA G GC AGTTCTGC
TGTGAACT AAGTGT C CG TCAAGACG
G GT TCGG

GAM116 301 TSNAXIP 1 19890 NP_060900.1 5 389 CCTGAAGGCCAA T CT 3 A c c

1 GCTTGTCACTGT TTCACAGTGGC AAGTT GC
GAATGAGG AAGTGTCACTG TTCGA CG
- AC

GAM116 301 VTI1B 1 18660 NP_006361.1 3 49 TGTGGACCAGAA T CT- C 3 A c c
CTTTGACCTTGT TTCACAG GG AAGTTCTG
GAATGCAT AAGTGTT CC TTCAAGAC
- AGT C

GAM116 301 WNT5A 1 13031 NP_003383.1 3 1248 TTAATGACAGAA A G - 3 A c c
CTTGGCTAATGG TTC CA TGGCTAAGTTCTG CA
AATTCACA AAG GT ATCGGTTCAAGAC GT
- A A

GAM116 301 XT3 1 16618 NP_064593.1 3 742 GGAAAAGGAGTC AAGT - 3 A c c
AGGAGCCACTGT TTCACAGTGGCT TCTG C
GAGGTGAG GAGTGTCACCGA GGAC G
---- T

GAM116 301 XT3 1 16618 NP_071800.1 3 742 GGAAAAGGAGTC AAGT - 3 A c c
AGGAGCCACTGT TTCACAGTGGCT TCTG C
GAGGTGAG GAGTGTCACCGA GGAC G
---- T

GAM116 301 ZNF180 1 10372 NP_037388.1 3 432 TAGTGTTTAGAA A GG C 3 A c c
CTTAGGCTGGAA TTC CAGT CTAAGTTCTG
AACCATAT AAG GTCG GATTCAAGAT
- -- T

GAM116 301 ZNF31 1 9409 NP_660281.1 3 481 AGTTGGCCTAGA AA C 3 A c c
GCAGGCCACTGT TTCACAGTGGCT GTTCTG
GAGCTCAG GAGTGTCACCGG CGAGAT
A- C

GAM116 301 ZNF323 1 5822 NP_112161.2 3 97 GTTCCAGCAGAA --- - A 3 A c c
CTGGACTAATTC TTCACAG TGG CTA GTTCTGC

TGTGGACC AGGTGTC ATC GGT CAAGACG
TTA A -
GAM116 301 ZNF70 1 2508 NP_068735.1 3 1097 TGTCATTCAGAA AA C 3 A c c
CACAGCCACTGT TTCACAGTGGCT GTTCTG
GAAAGTGC AAGTGTCACCGA CAAGAC
CA T
GAM116 301 ZNF70 1 2508 NP_852101.1 3 1097 TGTCATTCAGAA AA C 3 A c c
CACAGCCACTGT TTCACAGTGGCT GTTCTG
GAAAGTGC AAGTGTCACCGA CAAGAC
CA T
GAM117 216 C11orf2 1 11610 NM_031418.1 5 CCTCCGCCTCCC G AAGCT T 3 C c
c
5 TCTCGGGCA TGCCCGAG AG GGT GAGG
ACGGGCTC TC CCG CTCC
- CCT-- C
GAM117 216 C14orf4 1 14295 XM_041104.8 5 CCTCGCCCCCTC T A A CT T 3 C c c
CCCTCGGGC GCCCGAGG GA G GGT GAGG
CGGGCTCC CT C CCG CTCC
- C - CC -
GAM117 216 ELL 1 11377 NM_006532.1 3 CCCAGCCTCTCC A CT A 3 C c c
TCCTTGGGCA TGCCCGAGGAG AG GGTTG GG
ACGGGTTCCTC TC CCGAC CC
C T- -
GAM117 216 ENDO180 1 5722 3 CCTCCCCTGTCC A AGCT TT 3 C c c
CCTCGGGCA TGCCCGAGG GA GG GAGG
ACGGGCTCC CT CC CTCC
C GT-- C-
GAM117 216 FLJ1481 1 9480 NM_032843.1 3 CCTAGCAGCCTC A GTTG 3 C c c
0 TCCTCGGGCA TGCCCGAGGAGA GCTG AGG
ACGGGCTCCTCT CGAC TCC
C GA--
GAM117 216 KIAA049 1 1285 XM_031397.7 5 CCTGGAACACCT GA C G G 3 C c c
5 GTCCTCGGGCA TGCCCGAGGA AG TG TT AGG
ACGGGCTCCT TC AC AG TCC
G- C A G
GAM117 216 LOC1249 1 2231 3 CCAGCTTCTCCT TTGAGG 3 C c c
30 TGGGCA TGCCCGAGGAGAAGCTGG
ACGGGTTCCTCTTCGACC

GAM117 216 LOC1439 1 11372 3 CTCAACTCCCCT A AGCTG G 3 C c c
15 CGGGCA TGCCCGAGG GA GTTGAG
ACGGGCTCC CT CAACTC
C ----- -
GAM117 216 LOC1498 1 17004 NM_177549.1 3 CTCACCCCTACT G AAGCT T G 3 C c
c
30 CGGGCA TGCCCGAG AG GG TGAG
ACGGGCTC TC CC ACTC
A ----- C -
GAM117 216 LOC9163 1 5850 XM_039721.2 3 CCCAACCAGCCG CC AGAA A 3 C c
c

2 GACCTCAGCA TGC GAGG GCTGGTTG GG
ACG CTCC CGACCAAC CC
A- AGGC -
GAM117 216 MAPRE3 1 8716 NM_012326.2 3 CCCACCCCCTGC AGA CT T A 3 C c c
CCCTCGGGCA TGCCCGAGG AG GGT G GG
ACGGGCTCC TC CCA C CC
CCG CC - -
GAM117 267 KIAA023 1 10563 NM_014747.1 3 CTCAACCAACTC CC AAGC 3 C c c
7 CTTTAGCAT ATGC GAGGAG TGGTTGAG
TACG TTCCTC ACCAACTC
AT A---
GAM117 267 KIAA133 1 5038 XM_048774.4 3 TCAACCATGGCC G AGAAGC G 3 C c c
2 TGGGCAT ATGCCC AGG TGGTTGA
TACGGG TCC ACCAACT
- GGT--- -
GAM117 267 LOC1526 1 2005 XM_087495.1 5 CTCTGTCCTTCT CT TT 3 C c c
27 CCTTGGGCAT ATGCCCGAGGAGAAG GG GAG
TACGGGTTCCTCTTC CT CTC
-- GT
GAM117 267 LOC2556 1 12910 5 CTCACCGCCTCC A A C T 3 C c c
96 TCTTCGGGCA TGCCCGAGGAG AG TGGT GAG
ACGGGCTTCTC TC GCCA CTC
- C C -
GAM118 363 JM5 1 1897 NM_007075.1 3 ATCCAACCTGGG A GAA 3 C c c
GATTTTTTAA TTAAAAGATC CT GTTGGAT
AATTTTTTAG GG CAACCTA
- GTC
GAM119 391 KRTAP4- 1 9962 NM_032524.1 3 ATTGAAATATTT ATA C 3 C c c
4 GCTCTCTGCCA TGGCAGA CAAGT ATTTCAAT
ACCGTCT GTTTA TAAAGTTA
CTC -
GAM119 391 LOC2574 1 6487 XM_088028.2 3 ATTGAAATAAAA ATA AGTC 3 C c c
44 TGGATCTGCCA TGGCAGA CA ATTTCAAT
ACCGTCT GT TAAAGTTA
AG- AAAA
GAM120 285 FLJ1052 1 4274 NM_018125.1 3 CGACAGCCACGT TG AAC C 3 C c c
1 GGGCCGAGA TCTCGGCCT GC GGC GTCG
AGAGCCGGG TG CCG CAGC
-- CA- A
GAM120 285 FPGS 1 7363 NM_004957.2 3 ATGGATCAGCCA AACGG CG 3 C c c
AGGCCGAGA TCTCGGCCTTGGC CCGT
AGAGCCGGAACCG GGTA
ACTA- --
GAM120 285 HCC-4 1 1747 NM_138611.1 5 CGACGGCCATTA T CC C C 3 C c c

CCAATCGCGA TC CGG TTGG AA GGCCGTCG
AG GCT AACC TT CCGGCAGC
C -- A A
GAM120 285 LOC2530 1 19769 3 GACGGCCCGCAG TG AAC G 3 C c c
70 GCCGAGA TCTCGGCCT GC GGCCGTC
AGAGCCGGA CG CCGGCAG
-- C-- -
GAM120 285 NTRK2 1 17811 NM_006180.2 5 CGACGGCCGCCG T C- G AA 3 C c
c
CGGAGCTCCGAG CTCGG CTT GC CGGCCGTCG
GAGCC GAG CG GCCGGCAGC
- TC G CC
GAM121 309 ADAM11 1 8088 NM_002390.2 3 GGACCAGGCCTG G AA G - C 3 C c
c
GAGGGCACTT AAGTGCCC CCA GCT TGG CC
TTCACGGG GGT CGG ACC GG
A C- - A -
GAM121 309 ANXA6 1 12042 NM_004033.1 3 GGCCACAGCTTT C 3 C b b
GGCGGGCACTT AAGTGCCCGCCAAAGCTGTGGCC
TTCACGGGCGGTTTCGACACCGG
-
GAM121 309 CST6 1 10154 NM_001323.2 3 GGGCCATGGTGG G AAA 3 C c c
AGGGCACTT AAGTGCCC CC GCTGTGGCCC
TTCACGGG GG TGGTACCGGG
A ---
GAM121 309 FLJ1326 1 18107 NM_025125.1 3 GGGCCACAGCTT GCCCGCCA 3 C c
c
3 AAACAGCTT AAGT AAGCTGTGGCCC
TTCG TTCGACACCGGG
ACAAA---
GAM121 309 HMX1 1 18643 3 GGCCGCGGCCGG A T AAA C 3 C c c
CGGGCCT AG GCCCGCC GCTGTGGCC
TC CGGGCGG CGGCGCCGG
- - C-- -
GAM121 309 KIAA001 1 17252 NM_014665.1 3 GGGCCGCAGTCA AA CAAA 3 C c
c
4 GCGGGCGC GTGCCCGC GCTGTGGCCC
CGCGGGCG TGACGCCGGG
-- AC--
GAM121 309 KIAA014 1 3528 NM_014661.1 3 GGCCACAGCCTT CCC C A C 3 C c
c
0 GCCATTT AAGTG GC AA GCTGTGGCC
TTTAC CG TT CGACACCGG
--- - C -
GAM121 309 LOC2214 1 7844 XM_168060.2 3 GCAACAGCCTTG G A G CC 3 C c c
24 GGGGGCACTT AAGTGCCC CCAA GCTGT GC
TTCACGGG GGTT CGACA CG
G C A --
GAM121 309 LOC2561 1 3086 5 GGCCCAGGCGGG AA AAAGC T C 3 C c c

```
          58                          CAC         GTGCCCGCC    TG GGCC
                                        CACGGGCGG    AC CCGG
                                      --       ----- -   -
GAM121   309   LOC9012 1   7775  XM_291299.1  5      GGACCACAGCTG    G  GCCAA     - C     3  C  c
c
          0                          CCAGGGACTT   AAGT CCC    AGCTGTGG CC
                                        TTCA GGG    TCGACACC GG
                                       -  ACCG-      A -
GAM121   309   NKX2C  1   6138          3      GGGTCACGCGGC AA      AAA  T         3  C  c  c
                                     GGGCAC      GTGCCCGCC   GC GTGGCCC
                                        CACGGGCGG   CG CACTGGG
                                      --       --- -
GAM121   309   SDC3   1   12205 NM_014654.1  3      GGGCCACAGCCC A     GCCAAA-          3  C  c
c
                                     TTTTAGGGCATT  AGTGCCC     GCTGTGGCCC
                                        TTACGGG     CGACACCGGG
                                      -     ATTTTCC
GAM121   309   SDR1   1   11207 NM_004753.1  3      GGGCCACAGCAC AA     CCAAA           3  C  c
c
                                     CTGGGCAC     GTGCCCG    GCTGTGGCCC
                                        CACGGGT    CGACACCGGG
                                      --     CCA--
GAM121   309   STK22D  1   2793  NM_032028.2  3      GGGCCACGGGCT A      CAA  -        3  C  c  c
                                     CGCGGGCACT   AGTGCCCGC   AGCT GTGGCCC
                                        TCACGGGCG   TCGG CACCGGG
                                      -      C--   G
GAM122   337   LOC2549 1   4945          5      CATCCCCCACAG          TCCTC         3  C  c  c
          36                         GGTCCCTGATAA TTATCAGGGGCCCT    GGATG
                                        AATAGTCCCTGGGA    CCTAC
                                           CACCC
GAM123   212   GCSH   1   9934  NM_004483.1  3      CTAATGAAAGAA       CG-- A   C       3  C  c  c
                                     AATGCCCTTTAA TTAAAGGGC   TC TTTC ATTAG
                                        AATTTCCCG   AG AAAG TAATC
                                           TAAA  -   -
GAM124   323   DTX1   1   13928 NM_004416.1  5      TCGGAGAAGGCT    G     C  T  ----      3  C  c  c
                                     CTACAGGGAAGG GACC CTTCCCTG AG GCC   CCGA
                                     GGTC       CTGG GAAGGGAC TC CGG   GGCT
                                          G      A  T  AAGA
GAM124   323   FLJ2069 1   10484         5      CGGAGCCTCTGG          C  T  C  A      3  C  c  c
          5                          GGAGGCGGTC   GACCGCTTCCCTG AG GC CCG
                                        CTGGCGGAGGGGT TC CG GGC
                                           C  -  A  -
GAM124   323   GMFB   1   18850 NM_004124.1  5      CGGGGCAGGAAG GA       GCAG     A      3  C  c
c
                                     GGAGGCGG     CCGCTTCCCT   TGCCCCG
                                        GGCGGAGGGA   ACGGGGC
                                      --       AGG-      -
GAM124   323   LOC1631 1   20129         5      CGGGGCGGGGGG  C       GCAG     A      3  C  c  c
          32                         AAGCGCTC    GA CGCTTCCCT   TGCCCCG
                                        CT GCGAAGGGG   GCGGGGC
```

C G--- -

GAM124 323 SREBF1 1 16586 NM_004176.2 3 TCGGGGCACTGC GACC --- 3 C c c

AGGGGCCGAGC GCTT CCCTGCAGTGCCCCGA

CGAG GGGACGTCACGGGGCT

---- CCG

GAM125 330 F13A1 1 9703 NM_000129.2 3 ACTCAGGTGCTG CC 3 C b b

AAGGGTAATA TATTACCCTTCAGCACCTGAGT

ATAATGGGAAGTCGTGGACTCA

--

GAM125 330 MEGF10 1 7443 NM_032446.1 3 GGACTCAGAATT - T CAC 3 C c c

GTAGGGATAATA TATTA CCCT CAG CTGAGTCC

ATAAT GGGA GTT GACTCAGG

A T AA-

GAM126 312 PAK6 1 7423 NM_020168.3 3 TCTCAATAACCA - T CATAA 3 C c c

GGTCATCAGG CCTG TG ACT TTATTGAGA

GGAC AC TGG AATAACTCT

T - ACC--

GAM127 321 SPK 1 12856 NM_004819.1 5 AACAAAGACCCA CCGAACAG 3 C c c

CACTACTGGACA TGTCCAGTAG TTTGTT

ACAGGTCATC AAACAA

ACACCCAG

GAM127 321 VAPA 2 2734 NM_003574.2 3 AACTGTTCGGCT TGTT 3 C c a

ACTGGACA TGTCCAGTAGCCGAACAGTT

ACAGGTCATCGGCTTGTCAA

GAM127 321 VAPA 2 11936 NM_003574.2 3 AACAAACTGTTC 3 C a a

GGCTACTGGACA TGTCCAGTAGCCGAACAGTTTGTT

ACAGGTCATCGGCTTGTCAAACAA

GAM128 316 ADAMTS8 1 7148 NM_007037.2 3 GACAAGGGTCTC - -- 3 C c c

CACTGTGG TCACAGTGGA ATTC GTC

GGTGTCACCT TGGG CAG

C AA

GAM128 316 9 ATP6M8- 1 6599 3 GACGTGAATCCC A -- 3 C c c

ACTGTGG TCACAGTGG ATTC GTC

GGTGTCACC TAAG CAG

C TG

GAM128 316 HHLA2 1 16378 3 GACATTCCACCA --- TC 3 C c c

TTGTGA TCACA GTGGAAT GTC

AGTGT CACCTTA CAG

TAC --

GAM128 316 5 KIAA051 1 2335 5 GACAAGAGTGGC GA -- 3 C c c

ACTGTGG TCACAGTG ATTC GTC

GGTGTCAC TGAG CAG

GG AA

GAM129 213 ADAM19 1 14108 NM_033274.1 3 CAGGGAGCCTCT CT-- A T 3 C c c

TCCTCAACCC GGG GGAAGA GCT CCCTG

CCC CCTTCT CGA GGGAC

AACT C -
GAM129 213 ADAM8 1 17299 NM_001109.1 3 CAGAGAAGCCAT GAA--- C 3 C c c
GCGTTCCAGCCT GGGCTGGAA GCTTC CTG
TCCGACCTT CGAAG GAC
GCGTAC A
GAM129 213 AQP6 1 3804 NM_053286.1 3 CAGGGAAGCCTC CT AGAA 3 C c c
CTCCC GGG GGA GCTTCCCTG
CCC CCT CGAAGGGAC
T- C---
GAM129 213 ATP5D 1 13370 NM_001687.1 3 CAGGGAAGCTCC G - A A 3 C c c
TCCTCAGCT GGCTG G AG AGCTTCCCTG
TCGAC C TC TCGAAGGGAC
- T C C
GAM129 213 BACE 1 16749 NM_138973.1 5 CAGGGAAGCCGC AAGAA 3 C c c
CACCGGCCC GGGCTGG GCTTCCCTG
CCCGGCC CGAAGGGAC
ACCGC
GAM129 213 BAP1 1 14852 NM_004656.2 3 CAGAAGAGCCTC - A CC 3 C c c
TGTCCAGCCC GGGCTGGA AGA GCTT CTG
CCCGACCT TCT CGAG GAC
G C AA
GAM129 213 BLR1 1 17913 NM_001716.2 3 CAGGGAAGTCCC G AAGAA 3 C c c
CAGGCC GG CTGG GCTTCCCTG
CC GACC TGAAGGGAC
G CC---
GAM129 213 C1orf1 1 1462 NM_001213.1 3 CAGGACAGCTTC G AGA TC 3 C c c
CAGCC GGCTGGA AGCT CCTG
CCGACCT TCGA GGAC
- --- CA
GAM129 213 C1orf17 1 8671 NM_015101.1 3 CAGGGAAGCTCT CTGG- A 3 C c c
TAGAATCCC GGG AAGA GCTTCCCTG
CCC TTCT CGAAGGGAC
TAAGA -
GAM129 213 CD44 1 12215 NM_000610.2 5 AGGGATCCTCCA A AGCT G 3 C c c
GCTC GGGCTGGA GA TCCCT
CTCGACCT CT AGGGA
C ---- -
GAM129 213 CDC14B 1 2869 NM_033332.1 3 CAGAGAAGGGTC AGAAG C 3 C c
c
CAGCTC GGGCTGGA CTTC CTG
CTCGACCT GAAG GAC
GG--- A
GAM129 213 DDM36 1 9225 3 CAGGGAGGCCCT CT AA 3 C c c
TCCCACCC GGG GGAAG GCTTCCCTG
CCC CCTTC CGGAGGGAC
AC C-
GAM129 213 DDX37 1 8055 NM_032656.2 3 CAGGGAGGGCTG AAGA - 3 C c c
CCCAGCCC GGGCTGG AGCT TCCCTG
CCCGACC TCGG AGGGAC

CG-- G
GAM129 213 DKFZP43 1 1216 XM_041116.4 3 CAGGGCCCTCTT G A CTT 3 C c c

4P0111 CAGCCC GGGCTG AAGA G CCCTG
CCCGAC TTCT C GGGAC
- - CC-
GAM129 213 DKFZp43 1 18911 XM_166410.3 3 CAGGGAAGTGGA AGAA-- 3 C c c

4P0531 GCCTCCAGCCC GGGCTGGA GCTTCCCTG
CCCGACCT TGAAGGGAC
CCGAGG
GAM129 213 DKFZp54 1 5182 NM_020224.1 5 CAGGGATGGGCC G AA -- 3 C c c
7O146 TTCCAGCC GGCTGGAAG GCT TCCCTG
CCGACCTTC CGG AGGGAC
- -- GT
GAM129 213 DNTT 1 14883 NM_004088.2 3 CAGGGAAGCTCA G- A A 3 C c c
TCAAAGCCC GGGCT GA GA GCTTCCCTG
CCCGA CT CT CGAAGGGAC
AA A -
GAM129 213 DOCK1 1 8758 NM_001380.1 3 CAGGGAAGCTCC CTGGA A 3 C c
c
TGATTTCCC GGG AG AGCTTCCCTG
CCC TC TCGAAGGGAC
TTTAG C
GAM129 213 DT1P1A1 1 19425 NM_058163.1 3 CAGGAATGCTGC --- A- TTC 3 C c c

0 CTTCCTTCAGCC GGGCT GGAAG AGC CCTG
C CCCGA CCTTC TCG GGAC
CTT CG TAA
GAM129 213 E1B-AP5 1 11392 NM_144732.1 3 CAGGGCTGCCTC A- A TT 3 C c c
CCTCCAGCCC GGGCTGGA GA GC CCCTG
CCCGACCT CT CG GGGAC
CC C TC
GAM129 213 FGFR3 1 7492 NM_000142.2 3 CAGGGAAGCCCC - GAAGAA 3 C c
c
ACATGTCC GGGC TG GCTTCCCTG
CCTG AC CGAAGGGAC
T ACCC--
GAM129 213 FLJ1020 1 18329 NM_018024.1 5 CAGTCGGTCTTC A - TCC 3 C c c
4 CTCCGGCCC GGGCTGGA GAAG CT CTG
CCCGGCCT CTTC GG GAC
C T CT-
GAM129 213 FLJ1136 1 10040 NM_021946.1 3 CAGGAAAGTGGT A A- C 3 C c c
2 CTCCAGCCC GGGCTGGA GA GCTT CCTG
CCCGACCT CT TGAA GGAC
- GG A
GAM129 213 FLJ1278 1 15286 3 CAGAAGGAACCC AGAAGC -- 3 C c c
3 TCCAGTCC GGGCTGGA TTCC CTG
CCTGACCT AAGG GAC
CCC--- AA

GAM129 213 FLJ1424 1 7701 NM_106552.1 3 CAGGGAAGCTTC TGGAA 3 C c c
9 ATGCCC GGGC GAAGCTTCCCTG
CCCG CTTCGAAGGGAC
TA---
GAM129 213 FLJ1459 2 10977 NM_032808.1 3 CAGGGCCCTCTT C A CTT 3 C c c
4 CCAACTC GGG TGGAAGA G CCCTG
CTC ACCTTCT C GGGAC
A - CC-
GAM129 213 FLJ1459 2 13720 NM_032808.1 3 CAGGAAAGGAGG GAAG C 3 C c
c
4 TTCCAGCCC GGGCTGGAA CTT CCTG
CCCGACCTT GAA GGAC
GGAG A
GAM129 213 FLJ2113 1 7521 NM_024866.1 5 CAGGGAGCCCCC AAGAA T 3 C c
c
5 AGCCC GGGCTGG GCT CCCTG
CCCGACC CGA GGGAC
CC--- -
GAM129 213 FLJ2247 1 20015 3 CAGGATGAGCCT AGAA C- 3 C c c
4 CCAGCTC GGGCTGGA GCTT CCTG
CTCGACCT CGAG GGAC
C--- TA
GAM129 213 FLJ2281 1 9345 NM_024916.1 3 CAGACGGCGGCA A A T -- 3 C c c
4 TCCTCCAGCCC GGGCTGGA GA GCT CC CTG
CCCGACCT CT CGG GG GAC
C A C CA
GAM129 213 FLJ3021 1 17139 NM_145008.1 5 CAGGGCATTGTC A AGCTT 3 C c c

3 CTCCAGCCC GGGCTGGA GA CCCTG
CCCGACCT CT GGGAC
C GTTAC
GAM129 213 FLJ3281 1 16718 NM_144685.1 5 CAGGGAAGCAGG C AAGAA 3 C c
c
8 GGCCAACCT GGG TGG GCTTCCCTG
TCC ACC CGAAGGGAC
A GGGGA
GAM129 213 FUS1 1 12680 NM_007275.1 3 AGGTATGCTTTC - TTC G 3 C c c
TTCCAGCCC GGGCTGGAAGAA GC CCT
CCCGACCTTCTT CG GGA
T TAT -
GAM129 213 GAB2 1 9984 NM_080491.1 3 GGAGGCTTCCTT - CTG 3 C c c
CCAGCCC GGGCTGGAAG AAGCTTCC
CCCGACCTTC TTCGGAGG
C ---
GAM129 213 GAB3 1 18513 NM_080612.1 3 CAGGGAAGCTTG GGAAG 3 C c c
GGGCTC GGGCT AAGCTTCCCTG
CTCGG TTCGAAGGGAC
GG---
GAM129 213 GRLF1 1 5059 NM_024342.1 3 CAGGGAAGCGTG GAAGAA 3 C c
c

CAGCCC GGGCTG GCTTCCCTG
CCCGAC CGAAGGGAC
GTG---
GAM129 213 ITGAM 1 578 NM_000632.2 5 CAGGTTCTGGCT G A TC-- 3 C c c
CCTTCCAGCC GGCTGGAAG AGCT CCTG
CCGACCTTC TCGG GGAC
- C TCTT
GAM129 213 KCNK5 1 14609 NM_003740.2 5 CAGGGCGCCCTT AA TT 3 C c c
TCAGCCC GGGCTGGAAG GC CCCTG
CCCGACTTTC CG GGGAC
C- C-
GAM129 213 KIAA001 1 10733 NM_014665.1 3 CAGGGAAGCTGG GGAAGA 3 C c
c
4 GAGTCC GGGCT AGCTTCCCTG
CCTGA TCGAAGGGAC
GGG---
GAM129 213 KIAA054 1 20182 3 CAGGCTCTTCTT CTTC 3 C c c
4 CCAGCCT GGGCTGGAAGAAG CCTG
TCCGACCTTCTTC GGAC
TC--
GAM129 213 KIAA068 1 5701 NM_014852.1 3 CAGGGAAGCCTC GG AA A 3 C c c
2 CCAGC GCTGG GA GCTTCCCTG
CGACC CT CGAAGGGAC
-- -- C
GAM129 213 KIAA108 1 4946 XM_047610.1 3 CAGGGGAGCTCC G AAGA 3 C c c
6 CAGCC GGCTGG AGCTTCCCTG
CCGACC TCGAGGGGAC
- C---
GAM129 213 KIAA150 1 16666 XM_029353.1 3 CAGGAAAGAGGC AGAA- --- 3 C c c
9 CCCCATCCAGCC GGGCTGGA GCTTC CCTG
C CCCGACCT CGGAG GGAC
ACCCC AAA
GAM129 213 LGI3 1 1973 NM_139278.1 5 AGGGAGGTGCCA AAGAA G 3 C c c
GCCC GGGCTGG GCTTCCCT
CCCGACC TGGAGGGA
G---- -
GAM129 213 LHX1 1 20027 NM_005568.1 5 CAGGCGGCGCGC A AA- TC 3 C c c
TCCAGCCC GGGCTGGA G GCT CCTG
CCCGACCT C CGG GGAC
- GCG C-
GAM129 213 LOC1235 1 3821 3 AGGGGCTGTCCA AGA TT G 3 C c c
91 GCCC GGGCTGGA AGC CCCT
CCCGACCT TCG GGGA
G-- -- -
GAM129 213 LOC1333 1 19811 5 AGGGGACCTCCT A C G 3 C c c
83 TCCAGCTC GGGCTGGAAG AG TTCCCT
CTCGACCTTC TC AGGGGA
C C -
GAM129 213 LOC1357 1 19358 NM_138572.1 3 CAGGCTCTGTGC A TTC--- 3 C c c

63 TCCTTCCAGCCC GGGCTGGAAG AGC CCTG
CCCGACCTTC TCG GGAC
C TGTCTC

GAM129 213 LOC1395 1 11437 5 CAGGTGGCGTTC GAA TC 3 C c c
22 CAGCCC GGGCTGGAA GCT CCTG
CCCGACCTT CGG GGAC
G-- T-

GAM129 213 LOC1432 1 6932 XM_096412.1 5 AGAGAAGCTCCA AGAA C G 3 C c
c
86 GCTC GGGCTGGA GCTTC CT
CTCGACCT CGAAG GA
---- A -

GAM129 213 LOC1443 1 916 3 AGGGAGGGCTCA GAAGA - G 3 C c c
08 GCCC GGGCTG AGCT TCCCT
CCCGAC TCGG AGGGA
----- G -

GAM129 213 LOC1456 1 12662 5 CAGGAGAGGGTT A G - 3 C c c
22 CCTTCAGCCC GGGCTGGA GAA CTTC CCTG
CCCGACTT CTT GGAG GGAC
C G A

GAM129 213 LOC1462 1 2022 XM_085396.1 5 CAGGGAAGTCCT AA 3 C b b
72 TCCAGCCT GGGCTGGAAG GCTTCCCTG
TCCGACCTTC TGAAGGGAC
C-

GAM129 213 LOC1468 1 4445 5 CAGGGAAGAATC C AA AG 3 C c c
61 CCACCC GGG TGG GA CTTCCCTG
CCC ACC CT GAAGGGAC
- -- AA

GAM129 213 LOC1471 1 16773 3 CAGGGAAGCTTC AA 3 C c c
18 CTCGGTCT GGGCTGG GAAGCTTCCCTG
TCTGGCT CTTCGAAGGGAC
C-

GAM129 213 LOC1472 1 14610 3 CAGGGTCAGCCT AA T- 3 C c c
76 TCCAGCTC GGGCTGGAAG GCT CCCTG
CTCGACCTTC CGA GGGAC
-- CT

GAM129 213 LOC1480 1 11808 3 CAGGGATGGCCC AAGAA - 3 C c c
89 CCAGCCC GGGCTGG GCT TCCCTG
CCCGACC CGG AGGGAC
CC--- T

GAM129 213 LOC1501 1 14548 XM_086802.3 5 CAGGGCATCCTC A A TTC 3 C c c

74 CAGCTC GGGCTGGA GA GC CCTG
CTCGACCT CT CG GGAC
C A ---

GAM129 213 LOC1502 1 16131 XM_059324.2 5 CAGGGCGTCCTC A AGCTT 3 C c
c
13 CAGCTC GGGCTGGA GA CCCTG
CTCGACCT CT GGGAC
C GC---

GAM129 213 LOC1503 1 5518 XM_086823.1 5 CAGAGAATATTT AAGC C 3 C c c
43 CCAGCCC GGGCTGGAAG TTC CTG
CCCGACCTTT AAG GAC
AT-- A
GAM129 213 LOC1575 1 2356 XM_098772.1 5 CAGGGCCTCGCC AGAA TT-- 3 C c
c
31 CTCCAGCCC GGGCTGGA GC CCCTG
CCCGACCT CG GGGAC
CC-- CTCC
GAM129 213 LOC1617 1 8474 5 CAGAGAAGCTAT G GA-- C 3 C c c
34 AGTTCCAGCC GGCTGGAA AGCTTC CTG
CCGACCTT TCGAAG GAC
- GATA A
GAM129 213 LOC1657 1 11611 5 AGGGGAGCTCCA - AGAA G 3 C c c
41 AGCCC GGGCT GGA GCTTCCCT
CCCGA CCT CGAGGGGA
A ---- -
GAM129 213 LOC2054 1 9598 5 CAGGGAAGGGAC C AGAAG- 3 C c c
18 CCTCCACCC GGG TGGA CTTCCCTG
CCC ACCT GAAGGGAC
- CCCAGG
GAM129 213 LOC2207 1 1430 XM_167548.3 3 CAGGGAAGCCCC AAGAA 3 C b
b
39 AGCCC GGGCTGG GCTTCCCTG
CCCGACC CGAAGGGAC
C----
GAM129 213 LOC2210 1 6809 5 CAGAGAAGTTCC C AA G C 3 C c c
92 CCACCC GGG TGG GAA CTTC CTG
CCC ACC CTT GAAG GAC
- C- - A
GAM129 213 LOC2220 1 14251 XM_166594.4 3 CAGTGGCCTCTT A TCC 3 C c c
57 TCAGCCC GGGCTGGAAGA GCT CTG
CCCGACTTTCT CGG GAC
C T--
GAM129 213 LOC2221 1 10506 5 CAGGGAAGTAGT G AGAA 3 C c c
61 CCAGGCC GG CTGGA GCTTCCCTG
CC GACCT TGAAGGGAC
G GA--
GAM129 213 LOC2542 1 12271 XM_170654.3 3 CAGGCTCTTTCT AG CTTC 3 C c
c
63 CCAGCCC GGGCTGGA AAG CCTG
CCCGACCT TTC GGAC
CT TC--
GAM129 213 LOC2547 1 13709 3 CAGGGTGCCCCT - AA TT 3 C c c
53 GTCCAGCCC GGGCTGGA AG GC CCCTG
CCCGACCT TC CG GGGAC
G CC T-
GAM129 213 LOC2549 1 16435 XM_173170.1 3 CAGTGGGCTCCT G A TT - 3 C c c
44 TCCAGCC GGCTGGAAG AGC CC CTG
CCGACCTTC TCG GG GAC

```
                                        -       C  -- T
GAM129  213  LOC5128 1  3543          5       CAGGGAAGCCTG   C  GA  AA            3  C  c  c
        5                          CATCCC     GGG TG  AG  GCTTCCCTG
                                        CCC AC  TC  CGAAGGGAC
                                          T  G-  --
GAM129  213  LOC5166 1  13920         3       CAGTGGGAGTTC        A     -         3  C  b  b
        7                          CTTCCAGCCC   GGGCTGGAAG AGCTTCC CTG
                                        CCCGACCTTC TTGAGGG GAC
                                             C      T
GAM129  213  LOC5852 1  12229         3       CAGGGTGTCTTC       A   CTT          3  C  c  c
        5                          CTTCAGCCC   GGGCTGGA GAAG   CCCTG
                                        CCCGACTT CTTC   GGGAC
                                           C   TGT
GAM129  213  MAN1A1  1  1824  NM_005907.2  5       CAGGGAGGATCC     GAA  AG           3  C  c
c
                                   GCAGCCC     GGGCTG   GA  CTTCCCTG
                                        CCCGAC   CT  GGAGGGAC
                                          GC-  A-
GAM129  213  MGC1047 1  3302  NM_030818.1  5       CAGGGAAGCCTG   -  GA  AA           3  C  c  c

        1                          TGGACCC     GGG CTG  AG  GCTTCCCTG
                                        CCC GGT  TC  CGAAGGGAC
                                          A  G-  --
GAM129  213  MGC1618 1  15910 NM_032372.1  3       AGGGACTCTCCA       A  AGCT    G        3  C  c
c
        6                          GCCT       GGGCTGGA GA    TCCCT
                                        TCCGACCT CT    AGGGA
                                          - C---    -
GAM129  213  MGC4368 1  2451  NM_024510.2  5       CAGACGGGCTTC   C  A      CC         3  C  c  c

                                   TCCCACCC    GGG TGG AGAAGCTT  CTG
                                        CCC ACC TCTTCGGG  GAC
                                          -  C       CA
GAM129  213  MGC4796 1  3662  XM_029031.7  3       CAGGGAAGCCCC G   T   A AA           3  C  c
c
                                   TCCTGCC      GGC GGA G  GCTTCCCTG
                                        CCG CCT C  CGAAGGGAC
                                        -  T  - CC
GAM129  213  MMP15  1  15972 NM_002428.1  3       CAGGGAAGCAGC     GAAGAA           3  C  c
c
                                   AGCCT      GGGCTG     GCTTCCCTG
                                        TCCGAC     CGAAGGGAC
                                          GA----
GAM129  213  NXPH3  2  2877  NM_007225.1  3       CAGAGGAGCTCT      A  A    C         3  C  c  c
                                   CCAGCCC     GGGCTGGA GA GCTTC CTG
                                        CCCGACCT CT CGAGG GAC
                                          - -    A
GAM129  213  NXPH3  2  3126  NM_007225.1  3       CAGGGCTTCCCT      A---    TTC        3  C  c  c
                                   CTCCAGCCC   GGGCTGGA   GAAGC   CCTG
                                        CCCGACCT   CTTCG   GGAC
```

CTCC ---
GAM129 213 OVCOV1 1 15335 NM_173073.1 5 CAGAGAGCTCCT A A CC 3 C c c

CCAGCCT GGGCTGGA GA GCTT CTG
TCCGACCT CT CGAG GAC
C - A-
GAM129 213 PIP5K1C 1 16602 XM_047620.3 3 AGGGTCTGTCCA - AGCTT G 3 C c
c

GCCC GGGCTGGA AGA CCCT
CCCGACCT TCT GGGA
G ----- -
GAM129 213 PRX 1 18306 NM_020956.1 3 CAGGAAAGCCAG GAA- C 3 C c c
ATTCCAGCCT GGGCTGGAA GCTT CCTG
TCCGACCTT CGAA GGAC
AGAC A
GAM129 213 PTPRN2 1 17373 NM_130842.1 3 CAGGGGAGCCCC C AAGAA 3 C c
c

CACCC GGG TGG GCTTCCCTG
CCC ACC CGAGGGGAC
- CC---
GAM129 213 PYGB 1 19382 NM_002862.2 3 CAGGGAAGGGCC - AAGAAG 3 C c
c

AAGCCC GGGCT GG CTTCCCTG
CCCGA CC GAAGGGAC
A GG----
GAM129 213 RAB30 1 4058 NM_014488.2 5 CAGGGACTGACT AGA CT 3 C c c
CCAGCCC GGGCTGGA AG TCCCTG
CCCGACCT TC AGGGAC
CAG --
GAM129 213 RASSF2 1 13010 NM_014737.1 3 CAGGGAAGCTCT G G A 3 C c c
TTAGGCC GGCT GAAGA GCTTCCCTG
CCGG TTTCT CGAAGGGAC
- A -
GAM129 213 RBMY1A1 1 5003 NM_005058.1 5 CAGGGAAGCTCC G AGAA 3 C c
c

AGCT GGCTGGA GCTTCCCTG
TCGACCT CGAAGGGAC
- ----
GAM129 213 RERE 1 1394 NM_012102.2 5 CAGGGAAGCCCC AAGAA 3 C c c
CTCAGCCC GGGCTGG GCTTCCCTG
CCCGACT CGAAGGGAC
CCCC-
GAM129 213 RFT1 1 9266 NM_052859.1 3 CAGGGAAGCCTG C GA- AA 3 C c c
GACACCC GGG TG AG GCTTCCCTG
CCC AC TC CGAAGGGAC
- AGG --
GAM129 213 RGS19IP 1 2755 NM_005716.1 3 CAGGACCCGAGC AGAA C--- 3 C c
c

1 CTCCAGCCT GGGCTGGA GCTT CCTG
TCCGACCT CGAG GGAC

C--- CCCA
GAM129 213 RIN3 1 17667 NM_024892.1 5 CAGGGGCAGCCT AGAA - 3 C c c
CCAGTCC GGGCTGGA GCT TCCCTG
CCTGACCT CGA GGGGAC
C--- C
GAM129 213 RNF20 1 18452 NM_019592.4 3 CAGTGTTTTCTT CTTCC- 3 C c c
TTTCCAGCCC GGGCTGGAAGAAG CTG
CCCGACCTTTTTC GAC
TTTTGT
GAM129 213 RNTRE 1 12347 NM_014688.1 3 CAGGGAAATGTC G AGC 3 C c c
TTCAGCCC GGGCTG AAGA TTCCCTG
CCCGAC TTCT AAGGGAC
- GTA
GAM129 213 RPP14 1 4118 NM_007042.1 3 CAGGAAATTAGC GA TC--- 3 C c c
TTTCCAGCCC GGGCTGGAA AGCT CCTG
CCCGACCTT TCGA GGAC
-- TTAAA
GAM129 213 RRP22 1 5851 NM_006477.1 3 AGGGAAGTCTCC T AGAA G 3 C c c
GCCC GGGC GGA GCTTCCCT
CCCG CCT TGAAGGGA
- C--- -
GAM129 213 SELB 1 14956 NM_021937.1 3 CAGGAGGGTCTC -- AG TC 3 C c c
TCCTCCAGCCC GGGCTGGA AGA CT CCTG
CCCGACCT TCT GG GGAC
CC CT GA
GAM129 213 SEMA7A 1 13896 NM_003612.1 3 CAGGGCTACCCT - AGCTT- 3 C c
c
CTGTCCAGCCC GGGCTGGA AGA CCCTG
CCCGACCT TCT GGGAC
G CCCATC
GAM129 213 SGT 1 2232 NM_003021.2 3 CAGCGACCTCCC AAGCT C 3 C c c
TTCCAGCCC GGGCTGGAAG TC CTG
CCCGACCTTC AG GAC
CCTCC C
GAM129 213 SLC12A4 1 8109 NM_005072.2 3 CAGGGAGGGAGT AGAAG 3 C c
c
CCAGCCC GGGCTGGA CTTCCCTG
CCCGACCT GGAGGGAC
GAG--
GAM129 213 SRD5A1 1 11202 NM_001047.1 3 GGACTTGTTCCA G CT CTG 3 C c
c
GCCC GGGCTGGAA AAG TCC
CCCGACCTT TTC AGG
G -- ---
GAM129 213 SUPT6H 1 14488 NM_003170.2 3 CAGGGAAGCACT A- AA 3 C b b
GCCCAGCCC GGGCTGG AG GCTTCCCTG
CCCGACC TC CGAAGGGAC
CG A-
GAM129 213 TEAD2 1 18248 NM_003598.1 3 CAGGGAGGGTCC A AG 3 C c c

TCCAGCTC GGGCTGGA GA CTTCCCTG
CTCGACCT CT GGAGGGAC
C G-
GAM129 213 ZDHHC7 1 3493 NM_017740.1 5 CGGGGCCCGCTC AGAA TT- 3 C c c
CAGCCC GGGCTGGA GC CCCTG
CCCGACCT CG GGGGC
---- CCC
GAM130 331 A1BG 1 6105 NP_570602.2 3 1380 TTGAGACAGAAT C CA 3 B c c
TTTGCTCTTGTT GGCAACAAGAGCGAAA TC
GCCCAGGC CCGTTGTTCTCGTTTT AG
A AC
GAM130 331 AAK1 1 7111 NP_055726.2 3 260 TTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCTG CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 AD7C-NT 2 9687 NP_055301.1 5 13 TTGAGATGGAGT - 3 B b b
P TTTCGCTCTTGT GGCAACAAGAGCGAAA CTCCAT
TGCCCA CCGTTGTTCTCGCTTT GAGGTA
T
GAM130 331 AD7C-NT 2 18860 NP_055301.1 5 13 TGAGATGGAGTT - 3 B b b
P TTCGCTCTTGTT GGCAACAAGAGCGAAA CTCCAT
GCCCA CCGTTGTTCTCGCTTT GAGGTA
T
GAM130 331 ANAPC11 1 10495 NP_057560.8 5 75 GCGAGACGGAGT - A G A 3 B c c
TTCGTCATGTTG GGC AACA GA CGAAACTCC
GCCAGGCC CCG TTGT CT GCTTTGAGG
G A - C
GAM130 331 AP1M1 1 4671 NP_115882.1 3 417 GGCCAGCAGGGG G AA A 3 B c c
CGTCGTTTTGTT GGCAACAAGA CGA CTCC
GCCATTTT CCGTTGTTTT GCT GGGG
- GC A
GAM130 331 APM1 1 4972 NP_004788.1 3 1792 TTAAGATGGAGT A C 3 B b b
TTCCCTCTGTTG GGCAACA GAG GAAACTCCAT
CCAGGCTA CCGTTGT CTC CTTTGAGGTA
- C
GAM130 331 APOA5 1 9130 NP_443200.1 3 382 ACATCCTGGAGT AACA G 3 B c c
TTGGCTCTAGTC GGC AGAGC AAACTCCA
ACTTCTGG CTG TCTCG TTTGAGGT
A--- G
GAM130 331 APPBP2 1 6678 NP_006371.2 3 3478 TTCAGACGGAGT A 3 B b b
TTCGCTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAGGC CCGTTGTTCTCGCTTTGAGG
C
GAM130 331 ASB9 1 6639 NP_076992.1 5 118 GGAGCATGGAGT CA AG G 3 B c c
TTGGACTTTGCT GGCAA AG C AAACTCCAT

GAGCAACT TCGTT TC G TTTGAGGTA
-- AG -

GAM130 331 ATP1B2 1 6894 NP_001669.1 3 806 TTGAGATGGAGT 3 B b b
TTCGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGCTTTGAGGTA

GAM130 331 ATP1B4 1 16642 NP_036201.1 3 1861 TTGAGATGGAGT CA G 3 B c c

TTCGCTGTTGTC GG ACAA AGCGAAACTCCAT
ACCCAGGC CC TGTT TCGCTTTGAGGTA
AC G

GAM130 331 BA108L7 1 2887 NP_112233.2 3 1039 TTTTGATGGAGT CAAG C 3 B c c
.2 TTCACTATTTTG GGCAA AG GAAACTCCAT
CCCAGGCT CCGTT TC CTTTGAGGTA
TTA- A

GAM130 331 BAG5 1 770 NP_004864.1 3 2539 TTGACACCGGAT A- G C A 3 B c c
TTAGCTCTTGTC GGC ACAAGAGC AAA TCC
GGCCTTCG CCG TGTTCTCG TTT AGG
GC A - C

GAM130 331 BAGE 1 15169 NP_001178.1 3 79 AGGAGATGGAGT A- AG C 3 B c c
TTCACTGTGTCA GGC ACA AG GAAACTCCAT
GCCAGGAT CCG TGT TC CTTTGAGGTA
AC G- A

GAM130 331 BHD 1 19933 NP_659434.2 3 895 TTGAGAGGGAGT C A 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
A G

GAM130 331 C14orf1 1 11571 NP_060440.1 3 464 TGAGCAGGAGAT A - A 3 B c c
02 TTTGCTCTTGTG GGCA CAAGAGCGAAA CTCC
TTGAGACC TTGT GTTCTCGTTTT GAGG
- A A

GAM130 331 C14orf1 1 19332 NP_060100.1 3 343 TTAAGACTGAGT C CA 3 B c c
13 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A TC

GAM130 331 C21orf5 1 17801 NP_478062.1 3 65 TCCGGATGGAGT ACA-- C- 3 B c c
1 TTCCCCTCTGCG GGCA AGAG GAAACTCCAT
GCTGCCTC CCGT TCTC CTTTGAGGTA
CGGCG CC

GAM130 331 C4orf9 1 6895 XP_035572.1 3 353 TTGAGACGGAGT A 3 B b b
TTTGCTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAGGC CCGTTGTTCTCGTTTTGAGG
C

GAM130 331 C9orf9 1 20130 NP_061829.2 3 840 TTGAGATGGAGT CA A C 3 B c c
TTCACTCTGTCT GG ACA GAG GAAACTCCAT
CCCAGGCT CC TGT CTC CTTTGAGGTA
TC - A

GAM130 331 CAMLG 1 16032 NP_001736.1 3 774 TTGAGACAGAGT CA 3 B b b
TTCGCTCTTGTT GGCAACAAGAGCGAAACTC

GCCCAGGC CCGTTGTTCTCGCTTTGAG
AC
GAM130 331 CARD6 1 2870 NP_115976.2 3 188 TTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 CBFA2T2 1 3576 NP_005084.1 3 1881 TGAGACGGGAGT CA C A 3 B c
c
TTCTCTCTTGTC GG ACAAGAG GAAACTCC
TCCCAGGC CC TGTTCTC CTTTGAGG
TC T G
GAM130 331 CBFA2T2 1 3576 NP_787060.1 3 1881 TGAGACGGGAGT CA C A 3 B c
c
TTCTCTCTTGTC GG ACAAGAG GAAACTCC
TCCCAGGC CC TGTTCTC CTTTGAGG
TC T G
GAM130 331 CCL22 1 18224 NP_002981.2 3 934 TTGAGATGGAGT CA 3 B b b
TTCGCTCTTGTC GG ACAAGAGCGAAACTCCAT
ACCCACGC CC TGTTCTCGCTTTGAGGTA
AC
GAM130 331 CCNF 1 3240 NP_001752.1 3 1276 TTTGGAGACAGT CA ---- 3 B c c
TTTGCTCTTGTC GG ACAAGAGCGAAAC TCCA
TCCCCGGC CC TGTTCTCGTTTTG AGGT
TC ACAG
GAM130 331 CD209 1 7192 NP_066978.1 3 608 TCGAGATGGAGT A C 3 B b b
TTCACTCTTGTC GGC ACAAGAG GAAACTCCAT
GCTCAGGC TCG TGTTCTC CTTTGAGGTA
C A
GAM130 331 CDC14B 1 2262 NP_201589.1 3 615 CAAAGACAGAGT A CA 3 B c c
CTTGCTCTTGTT GGCAACAAGAGCGA ACTC
GTCCAGGC CTGTTGTTCTCGTT TGAG
C AC
GAM130 331 CDKAL1 1 2168 NP_060244.1 3 427 TCCAGATGGAGT CA 3 B b b
TTCGCTCTTGTC GG ACAAGAGCGAAACTCCAT
CCCCAGGC CC TGTTCTCGCTTTGAGGTA
CC
GAM130 331 CECR1 1 15627 NP_059120.2 3 371 TCGAGATGGAGT 3 B b b
TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 CECR1 1 15627 NP_803124.1 3 371 TCGAGATGGAGT 3 B b b
TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 CENPH 1 14626 NP_075060.1 3 247 TTTGAGATGGAG A A 3 B b b
TCTCGCTTTGTT GGCAACA GAGCGA ACTCCAT
GCCCAGAC CCGTTGT TTCGCT TGAGGTA
- C
GAM130 331 CGI-18 1 8151 NP_057031.1 5 2 GAGACGGAGTTT C A 3 B b b
CCCTCTTGTTGC GGCAACAAGAG GAAACTCC

CCAGGCTG CCGTTGTTCTC CTTTGAGG
C C
GAM130 331 CLECSF1 1 16032 NP_072092.2 3 953 TTGAGACAGAGT CA 3 B b b
2 TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGCTTTGAG
AC
GAM130 331 COX15 1 2870 NP_510870.1 3 642 TTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 CPA4 1 14507 NP_057436.1 3 587 TTGAGGCAGAGT CA 3 B c c
TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGTTTTGAG
AC
GAM130 331 CPSF2 1 7534 XP_029311.2 3 2028 TTGAGATGGAGT 3 B b b
TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGAC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 CYCS 2 5106 NP_061820.1 3 2604 TTTTGAGATAAT C ---- CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAA CTC
GCCCAGGC CCGTTGTTCTC CTTT GAG
A AATA TT
GAM130 331 CYCS 2 18712 NP_061820.1 3 1960 TAGAGATGGAGT A AGA 3 B c c

TTTGCCATGTGG GGC ACA GCGAAACTCCAT
TCCCAGGC CTG TGT CGTTTTGAGGTA
G AC-
GAM130 331 DBR1 1 1786 NP_057300.1 3 69 TTGAGATGGAGT CA C 3 B c c
TTCACTCTTGTC GG ACAAGAG GAAACTCCAT
ACCTAGAC CC TGTTCTC CTTTGAGGTA
AC A
GAM130 331 DCTN6 1 807 NP_006562.1 3 164 AACTAATGGAGT --- GAGC 3 B c c
TTCATTGTAACT GGCA ACAA GAAACTCCAT
GTCCTTTG CTGT TGTT CTTTGAGGTA
CAA A---
GAM130 331 DDX11 1 14693 NP_085913.1 3 1272 GCGTGGTGGAGT ---- AG C 3 B c
c

TTTCCTGTGTTT GGC AACA AG GAAACTCCAT
TCGGCCCC CCG TTGT TC TTTTGAGGTG
GCTT G- C
GAM130 331 DFFB 1 11120 NP_004393.1 3 229 TGTAGATGGAGT C 3 B b b
TTCACTTTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTTTC CTTTGAGGTA
A
GAM130 331 DHFR 1 18204 NP_000782.1 3 903 TTTAGACAGCGT TCCA 3 B c c
TTCGCTCTTGTT GGCAACAAGAGCGAAAC
GCCCAGGC CCGTTGTTCTCGCTTTG
CGAC
GAM130 331 DKFZP56 1 1337 NP_056416.1 5 1094 TTGAGACGGAGT A A 3 B b b
4G092 TTCGCTCTTGTC GGC ACAAGAGCGAAACTCC

GCCCAGGC CCG TGTTCTCGCTTTGAGG
C C
GAM130 331 DKFZp66 1 14527 NP_808881.1 3 949 TTGAGATGGAGT C 3 B b b
7B1218 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A
GAM130 331 DKFZp76 1 6176 NP_115656.1 5 1445 TTGAGACAGAGT CA CA 3 B c
c
1J139 TTTGCTCTTGTC GG ACAAGAGCGAAACTC
ACCCAGGC CC TGTTCTCGTTTTGAG
AC AC
GAM130 331 DKFZp76 1 6894 NP_060879.1 5 1514 TTGAGATGGAGT 3 B b b
1O0113 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGCTTTGAGGTA

GAM130 331 DKFZp76 1 2536 NP_689624.1 3 239 CCAAGATGGAGT CA A 3 B c c
2I137 TTTGCTCTGTCA GG ACA GAGCGAAACTCCAT
CCCAGGCT CC TGT CTCGTTTTGAGGTA
AC -
GAM130 331 DSCR6 1 10753 NP_061835.1 3 529 TTGTGACGGAGT CA A 3 B c c
TTTGCTCTTGTC GG ACAAGAGCGAAACTCC
TCCCAGGC CC TGTTCTCGTTTTGAGG
TC C
GAM130 331 DUSP19 1 11650 NP_543152.1 3 621 TTTAGATGGAGT CA G 3 B c c
TTGGCTCTTGTC GG ACAAGAGC AAACTCCAT
ACCCAGGC CC TGTTCTCG TTTGAGGTA
AC G
GAM130 331 EVI5 1 1296 NP_005656.2 3 2365 TAGAGATGGGGT - AG 3 B b b
TTCGCTATGTTG GGC AACA AGCGAAACTCCAT
GCCAGGCT CCG TTGT TCGCTTTGGGGTA
G A-
GAM130 331 FANCF 1 14481 NP_073562.1 3 469 CCTATCTGGAGT C- A G 3 B c c
TTGGCCTTGTTA GG AACAAG GC AAACTCCA
ACCTAGTA CC TTGTTC CG TTTGAGGT
AA - G
GAM130 331 FLJ1071 1 10891 NP_060659.1 3 678 GTAAAATGGTAG A GA - 3 B c c
3 TTGGCTCTTGTG GGCA CAAGAGC AACT CCAT
CTCAATTT TCGT GTTCTCG TTGA GGTA
- G- T
GAM130 331 FLJ1090 1 13320 NP_060736.1 3 506 GTCCTAGGTGGG - CGA 3 B c c

2 GTTCTCTTTGTT GGCAACAA GAG AACTCCAT
GCCTACCA CCGTTGTT CTC TTGGGGTG
T ---
GAM130 331 FLJ1092 1 5661 NP_060743.1 3 2034 TTGAGATGGAGT A 3 B b b
2 TTCGCGCTTGTT GGCAACAAG GCGAAACTCCAT
GCCCAGGC CCGTTGTTC CGCTTTGAGGTA
G
GAM130 331 FLJ1123 1 3449 NP_061906.1 3 413 TTTTGATGGAGT G -- ----- C 3 B c c
5 TTCCTCTCATAG GCAA CA AGAG GAAACTCCAT

TGATTTGC CGTT GT TCTC CTTTGAGGTA
- TA GATAC -

GAM130 331 FLJ1132 1 4059 NP_060860.1 3 81 TCCAAATGGAGT A 3 B b b
3 TTCGCTCTCGTT GGCAAC AGAGCGAAACTCCAT
GCCGAGGC CCGTTG TCTCGCTTTGAGGTA
C

GAM130 331 FLJ1258 1 1864 NP_078896.2 3 571 TAGAGACAGGGT - AG CA 3 B c c
6 TTCGCTATGTTG GGC AACA AGCGAAACTC
GCCAGGCT CCG TTGT TCGCTTTGGG
G A- AC

GAM130 331 FLJ1274 1 11006 XP_290972.1 3 2523 TTGAGATGGAAT CA C 3 B c c
7 TTTGCTCTTGTC GG ACAAGAGCGAAA TCCAT
ACCCAGGC CC TGTTCTCGTTTT AGGTA
AC A

GAM130 331 FLJ1290 1 6673 NP_073590.1 3 1542 TTGAGACGGAGT G A 3 B b b
3 TTCGCTGTTGTT GGCAACAA AGCGAAACTCC
GCCCAGGC CCGTTGTT TCGCTTTGAGG
G C

GAM130 331 FLJ1297 1 2871 NP_079184.1 3 278 TTGAGATGGAGT 3 B b b
3 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 FLJ1297 2 2871 NP_079085.2 3 52 TTGAGATGGAGT 3 B b b
5 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 FLJ1297 2 16538 NP_079085.2 3 489 GTAAAGACGGGG A A 3 B b b
5 TTTCGCCTTGTT GGCAACAAG GCGAAACTCC
GCCCAGGG CCGTTGTTC CGCTTTGGGG
- C

GAM130 331 FLJ1311 1 9782 NP_078817.1 3 761 TAGAGATGGAGT C AGAGC 3 B c
c
4 TTCACCATGTTA GG AACA GAAACTCCAT
CCCAGGAT CC TTGT CTTTGAGGTA
A ACCA-

GAM130 331 FLJ1495 1 11158 NP_116255.1 3 555 TTGAGATGGAGT C 3 B b b
7 TTCATTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCGAGGC CCGTTGTTCTT CTTTGAGGTA
A

GAM130 331 FLJ2007 1 10863 NP_060126.1 3 2020 TTGAAATGGAGT 3 B b b
9 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 FLJ2024 1 7716 NP_060193.1 3 2282 TTGACACAGAGT CA 3 B c c
5 TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGTTTTGAG
AC

GAM130 331 FLJ2307 1 9888 NP_079328.1 5 328 TTTTCATGGAGT AA- A G 3 B c c
4 TTGTTCCTGGTG GGC CA GAGC AAACTCCAT

GCTCAA TCG GT CTTG TTTGAGGTA
GTG C -

GAM130 331 FLJ2323 1 14644 NP_078967.2 3 472 GTCGAATGGAGT AACA G 3 B c c
3 TTTGATCTCGCT GGC AGA CGAAACTCCAT
GAGTTTGG TCG TCT GTTTTGAGGTA
C--- A

GAM130 331 FLJ2355 1 9031 NP_079156.1 3 707 TTGAGATGGAGT CA A 3 B c c
6 TTTGCTCTGTCA GG ACA GAGCGAAACTCCAT
CCCAGGCT CC TGT CTCGTTTTGAGGTA
AC -

GAM130 331 FLJ2356 1 7932 XP_041701.4 3 1707 CTGAAGCAGAGT CG CA 3 B c c
3 TTTACTCTTGTT GGCAACAAGAG AAACTC
GCCCAGGC CCGTTGTTCTC TTTGAG
AT AC

GAM130 331 FLJ3053 1 6894 NP_653325.1 3 174 TTGAGATGGAGT 3 B b b
2 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGCTTTGAGGTA

GAM130 331 FLJ3113 2 7990 NP_775928.1 3 674 TTGACATGGAGT CA 3 B b b
9 TTCGCTCTTGTC GG ACAAGAGCGAAACTCCAT
ACCCAGGC CC TGTTCTCGCTTTGAGGTA
AC

GAM130 331 FLJ3113 2 19702 NP_775928.1 3 380 TTGAGAAGGCGT T A 3 B b b
9 TTCGCTCTTGTT GGCAACAAGAGCGAAAC CC
GCCCAGGC CCGTTGTTCTCGCTTTG GG
C A

GAM130 331 FLJ3116 1 11889 NP_694567.1 3 1123 TTGAGATGGAGT A 3 B b b
6 TTTGCTCTTGTA GGC ACAAGAGCGAAACTCCAT
GCCCAGGC CCG TGTTCTCGTTTTGAGGTA
A

GAM130 331 FLJ3133 1 5852 NP_689682.1 3 251 TTGAGATGGAGT C 3 B b b
8 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCACGC CCGTTGTTCTC CTTTGAGGTA
A

GAM130 331 FLJ3139 1 18530 NP_694569.1 5 124 TTCCAGATGGAG A A 3 B b b
3 TCTCGCTTTGTT GGCAACA GAGCGA ACTCCAT
GCCCAGGC CCGTTGT TTCGCT TGAGGTA
- C

GAM130 331 FLJ3209 1 2283 NP_776156.1 3 1097 TTGAGATGGAGT A 3 B b b
6 TTCGCTCTGTTG GGCAACA GAGCGAAACTCCAT
CCCAGGCT CCGTTGT CTCGCTTTGAGGTA
-

GAM130 331 FLJ3213 1 6894 NP_689671.2 3 1423 TTGAGATGGAGT 3 B b b
0 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGCTTTGAGGTA

GAM130 331 FLJ3286 1 3876 NP_653214.1 3 1231 TTGAGACAGAGT CA CA 3 B c c

5 TTCGCTCTTGTC GG ACAAGAGCGAAACTC
ACCCAGGC CC TGTTCTCGCTTTGAG
AC AC

GAM130 331 FLJ3450 1 17842 NP_775944.1 5 7 TCGGAGTGGAGT A AG- C 3 B c c
3 TTCCTAGCTGGT GGCA CA AG GAAACTCCAT
GCCTGTCC CCGT GT TC CTTTGAGGTG
G CGA -

GAM130 331 FLJ3496 1 2871 XP_114353.1 3 1531 TTGAGATGGAGT 3 B b b
9 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 FLJ3754 1 4619 NP_775938.1 3 61 TGCTCATGGAGT ACA GA- 3 B c c
3 TGCAGTTCTTGC GGCA AGAGC AACTCCAT
CTAACAGG CCGT TCTTG TTGAGGTA
--- ACG

GAM130 331 FLJ3894 2 2995 NP_689574.1 3 1180 ATGCTGTGAGAA C AA- - 3 B c c
4 ATCTCTCTTGTT GGCAACAAGAG GA CTC CA
GCTGTCCT TCGTTGTTCTC CT GAG GT
T AAA T

GAM130 331 FLJ3894 2 16294 NP_689574.1 3 1252 GTGGCTTGGAGT C G 3 B c c
4 TTTGTTGTTGTT GG AACAA AGCGAAACTCCA
TTCTTGGT CT TTGTT TTGTTTTGAGGT
T G

GAM130 331 GPP34R 1 8899 NP_060648.2 3 1018 TTTAGACAAGAG A A CA 3 B c c

TCTCGCTTTGTT GGCAACA GAGCGA ACTC
GCCCAGGC CCGTTGT TTCGCT TGAG
- C AA

GAM130 331 GPR26 1 2669 NP_703143.1 3 1136 CGAGATGGGAGT C C A 3 B c c
TTCACTCTTATT GGCAA AAGAG GAAACTCC
GCCCAGGC CCGTT TTCTC CTTTGAGG
A A G

GAM130 331 GSPT2 1 18829 NP_060564.1 5 80 ACCCCTTGGCCC A ACT 3 B c c
TTCGCTCTTGCT GGCA CAAGAGCGAA CCA
GCCTTAAC CCGT GTTCTCGCTT GGT
C CCC

GAM130 331 HATH6 1 15485 NP_116216.1 3 900 CAGAAAAAGAGT -- C CA 3 B c c
TTTTCTCTTGTT GGC AACAAGAG GAAACTC
CAGCCTGC CCG TTGTTCTC TTTTGAG
AC T AA

GAM130 331 IL12RB1 1 1878 NP_714912.1 3 165 TAGAGATGGAGT AGAGC 3 B c
c

TTCACCATGTTG GGCAACA GAAACTCCAT
CCCAGGCT CCGTTGT CTTTGAGGTA
ACCA-

GAM130 331 IL19 1 8423 NP_037503.2 5 158 TCAGAGATGTGG A A TC 3 B c c
TCTCGCTTTGTT GGCAACA GAGCGA AC CAT
GCCTACAC CCGTTGT TTCGCT TG GTA
- C GT

GAM130 331 IL1RAPL 1 17936 NP_059112.1 5 183 GGCAGCTGGTGT A---- A T 3 B c c

2 TTCGCTCCTGGA GGCA CA GAGCGAAAC CCA
GTGTGCCT CCGT GT CTCGCTTTG GGT
GTGAG C T

GAM130 331 INMT 1 2284 NP_006765.3 3 606 TTGAGACGGAGT A A A 3 B c c
TTCGCTCTGTCG GGC ACA GAGCGAAACTCC
CCCAGGCT CCG TGT CTCGCTTTGAGG
C - C

GAM130 331 KIAA006 1 11890 NP_055691.1 3 610 TTGAGACTGAGT C CA 3 B c c
3 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A TC

GAM130 331 KIAA011 1 10770 XP_290939.1 3 231 TTGAGATGGAGT CA G G 3 B c c

7 TTGGCTGTTGTC GG ACAA AGC AAACTCCAT
TCCCAGGC CC TGTT TCG TTTGAGGTA
TC G G

GAM130 331 KIAA051 1 6082 NP_055547.1 3 3657 TTTAGACGGAGT A 3 B b b
3 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAGGC CCGTTGTTCTCGTTTTGAGG
C

GAM130 331 KIAA052 1 10779 XP_171054.1 3 517 TAGAGATGGAGT - AGAGC 3 B c
c
7 TTCACCATGTTG GGC AACA GAAACTCCAT
GCCAGGCT CCG TTGT CTTTGAGGTA
G ACCA-

GAM130 331 KIAA056 2 3624 NP_055649.1 5 753 TAGAGGCGGAGT - AGA A 3 B c b

3 TTCGCCATGTTG GGC AACA GCGAAACTCC
GTCAGGCT CTG TTGT CGCTTTGAGG
G AC- C

GAM130 331 KIAA056 2 6206 NP_055649.1 5 587 TTGAGATGGAGT C 3 B b b
3 TTCTCTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
T

GAM130 331 KIAA096 1 2870 XP_290942.1 3 1507 TTGAGACAGAGT C CA 3 B c c
2 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC

GAM130 331 KIAA100 1 1603 XP_290584.1 3 298 TTGAGACGGAGT CA A 3 B c c
2 TTCGCTCTTGTC GG ACAAGAGCGAAACTCC
ACCCCAGC CC TGTTCTCGCTTTGAGG
AC C

GAM130 331 KIAA105 1 5630 XP_043493.5 3 3262 TTTAGGTGGAGT A C 3 B b b
4 TTCACTCTGTTG GGCAACA GAG GAAACTCCAT
CCCAGGCT CCGTTGT CTC CTTTGAGGTG
- A

GAM130 331 KIAA117 1 9008 XP_045907.2 3 1228 TTGAGACAGAGT CA 3 B b b
0 TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAAGC CCGTTGTTCTCGCTTTGAG
AC

GAM130 331 KIAA120 1 14482 XP_049683.4 3 2446 ATGTCATGGAGT C AG G 3 B c c
3 TTAGTCCTTGTT GG AACAAG C AAACTCCAT
TCAGGTTT CT TTGTTC G TTTGAGGTA
- CT A
GAM130 331 KIAA125 1 6895 XP_031577.2 3 3549 TTGAGACGGAGT A 3 B b b
7 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAGGC CCGTTGTTCTCGTTTTGAGG
C
GAM130 331 KIAA126 1 14527 XP_291055.1 3 881 TTGAGATGGAGT C 3 B b b
8 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A
GAM130 331 KIAA161 2 19161 NP_066002.1 3 1364 TTTAGACAGAGT CA 3 B c c
5 TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCTAGGC CCGTTGTTCTCGTTTTGAG
AC
GAM130 331 KIAA161 2 19857 NP_066002.1 3 1833 TAGATATGGAGT - AAGAGC 3 B c c
5 TTCACCACGTTG GGC AAC GAAACTCCAT
GCCAAGAC CCG TTG CTTTGAGGTA
G CACCA-
GAM130 331 KIAA171 1 16424 NP_085136.1 3 724 GGGGGATGGAGT G 3 B b b
2 TTCGCTGTTGTT GGCAACAA AGCGAAACTCCAT
GCCCAGGC CCGTTGTT TCGCTTTGAGGTA
G
GAM130 331 KIAA171 1 16424 XP_041497.2 3 724 GGGGGATGGAGT G 3 B b b
2 TTCGCTGTTGTT GGCAACAA AGCGAAACTCCAT
GCCCAGGC CCGTTGTT TCGCTTTGAGGTA
G
GAM130 331 KIAA173 1 6894 NP_219494.1 3 1411 TTGAGATGGAGT 3 B b b
7 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGCTTTGAGGTA

GAM130 331 KIAA192 1 6286 XP_057040.1 5 305 TTGAGACAAAGT CCA 3 B c c
2 TTCGCTCTTGTT GGCAACAAGAGCGAAACT
GCCCAGGC CCGTTGTTCTCGCTTTGA
AAC
GAM130 331 KIAA198 1 14709 XP_113870.1 5 185 TTGAGACAGAGT CA 3 B c c
7 TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGT CCGTTGTTCTCGTTTTGAG
AC
GAM130 331 LAMP3 1 3877 NP_055213.1 3 548 TTGAGACGGAGT CA C A 3 B c c
TTCACTCTTGTC GG ACAAGAG GAAACTCC
ACCCAGGC CC TGTTCTC CTTTGAGG
AC A C
GAM130 331 LNK 1 8277 NP_005466.1 3 1668 TTGAGATGGAGT CA- GC 3 B c c
TTCTCTTGTCAA GG ACAAGA GAAACTCCAT
CCGGGCTG CC TGTTCT CTTTGAGGTA
AAC --

GAM130 331 LOC1193 1 11220 NP_660290.1 3 104 TTGAGACTGAGT CA- CA 3 B c c
92 TTCGCTCTTGTC GG ACAAGAGCGAAACTC
ATCCTGGC CC TGTTCTCGCTTTGAG
TAC TC
GAM130 331 LOC1283 1 13503 XP_059243.2 3 544 TTTTGATGGAGT G 3 B b b
87 TTCGCTGTTGTT GGCAACAA AGCGAAACTCCAT
GCCCAGGC CCGTTGTT TCGCTTTGAGGTA
G
GAM130 331 LOC1358 1 9805 XP_059804.4 3 720 TTGAGACAGGGT CA 3 B c c
18 TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGCC CCGTTGTTCTCGTTTTGGG
AC
GAM130 331 LOC1378 1 16853 XP_059929.3 3 666 TTGATATGGAGT 3 B b b
86 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGAGGTA

GAM130 331 LOC1432 1 4120 NP_620167.1 5 37 TAGGGACGAAGT C ---- A 3 B c c
41 TTCACTCTTGTT GGCAACAAGAG GAAAC TCC
GCCCAGGC CCGTTGTTCTC CTTTG AGG
A AAGC G
GAM130 331 LOC1450 1 6594 XP_096714.1 3 695 GCCTCCTGGAGT ----- GC 3 B c c
53 TTTATTTTGTTT GGCA ACAAGA GAAACTCCA
TTCTGCTT TCGT TGTTTT TTTTGAGGT
CTTTT A-
GAM130 331 LOC1461 1 2870 NP_778229.1 5 182 TTGAGACAGAGT C CA 3 B c c
77 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 LOC1462 2 3994 XP_085387.1 3 2293 TTGAGATGGAGT C 3 B b b
29 TTCATTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCTAGGC CCGTTGTTCTT CTTTGAGGTA
A
GAM130 331 LOC1462 2 8717 XP_085387.1 3 816 TAAACGTTGGGT AGC A T 3 B c b
29 CTCACGTTTGTT GGCAACAAG GA AC CCA
GCCATTAT CCGTTGTTT CT TG GGT
GCA C -
GAM130 331 LOC1467 1 14527 XP_085588.1 5 873 TTGAGATGGAGT C 3 B b b
84 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A
GAM130 331 LOC1470 1 6206 XP_054031.5 5 587 TTGAGATGGAGT C 3 B b b
71 TTCTCTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
T
GAM130 331 LOC1478 1 739 XP_085924.2 3 129 TTGAGACAGAGT C CA 3 B c c
41 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GTCCAGTC CTGTTGTTCTC CTTTGAG
A AC

GAM130 331 LOC1481 1 2081 NP_653293.1 3 2507 TTGAGATGGAGT AGC 3 B b b

37 TTCACCCTTGTT GGCAACAAG GAAACTCCAT
GCCCAGGC CCGTTGTTC CTTTGAGGTA
CCA

GAM130 331 LOC1482 1 10581 XP_086095.1 3 1169 TTGAGATGGAGT C G C 3 B c c

03 TTCACTGTTGTT GG AACAA AG GAAACTCCAT
CCCCAGGC CC TTGTT TC CTTTGAGGTA
C G A

GAM130 331 LOC1487 1 13543 XP_086281.1 3 380 TTGAGACAGAGT A CA 3 B c c

09 TTCGCTCTAGTT GGCAAC AGAGCGAAACTC
GCCCACAC CCGTTG TCTCGCTTTGAG
A AC

GAM130 331 LOC1491 1 18540 XP_097598.1 5 3300 TTGAGACGGAGT A 3 B b b

49 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAAGC CCGTTGTTCTCGCTTTGAGG
C

GAM130 331 LOC1495 1 7438 XP_097661.1 3 3084 TTGAGATGGAGT A- 3 B b b

06 TTTGCTCTTGTC GGC ACAAGAGCGAAACTCCAT
GGCCAGGC CCG TGTTCTCGTTTTGAGGTA
GC

GAM130 331 LOC1505 1 14454 XP_097917.1 5 1600 TTTGAGACGAGT A CA 3 B c c

87 TTCGCTCTGTTG GGCAACA GAGCGAAACTC
CCCAGGCT CCGTTGT CTCGCTTTGAG
- CA

GAM130 331 LOC1526 1 17776 XP_087503.1 5 340 TAATAATGGAGT - AGAGCG 3 B c c

87 TTACCAGTGCTT GGCAA CA AAACTCCAT
GTCAACTA CTGTT GT TTTGAGGTA
C GACCA-

GAM130 331 LOC1533 1 1484 XP_098364.1 5 427 CCATTTGGCTGT C C T- 3 B c c

46 TTCTCTCTTGTT GG AACAAGAG GAAAC CCA
CTCAGACA CT TTGTTCTC CTTTG GGT
C T TC

GAM130 331 LOC1538 1 4924 XP_087779.2 3 2212 GGGGCGTGGAGT A----- G 3 B c c

11 TTTGTCTTGTAT GGC ACAAGA CGAAACTCCAT
TTTGGCCT CCG TGTTCT GTTTTGAGGTG
GTTTTA -

GAM130 331 LOC1576 1 18434 XP_088346.6 3 81 CAGAGATGGAGT CAAGAGC 3 B c c

23 TTCACCATATTG GGCAA GAAACTCCAT
CCCAGGCT CCGTT CTTTGAGGTA
ATACCA-

GAM130 331 LOC1579 1 1338 XP_098842.1 3 210 TCCCTCTGGAGT ACAA C 3 B c c

18 TTCCTTCATCTG GGCA GAG GAAACTCCA
CCCCACAC CCGT TTC CTTTGAGGT

CTAC -

GAM130 331 LOC1624 1 14028 NP_835227.1 3 472 TTTTGAGACAGT A CCA 3 B c c

27 TTCGCTCTGTTG GGCAACA GAGCGAAACT
CCCAGGCT CCGTTGT CTCGCTTTGA
- CAG

GAM130 331 LOC1624 1 14028 XP_091549.3 3 472 TTTTGAGACAGT A CCA 3 B c c

27 TTCGCTCTGTTG GGCAACA GAGCGAAACT
CCCAGGCT CCGTTGT CTCGCTTTGA
- CAG

GAM130 331 LOC1632 1 799 NP_775802.1 3 3341 TTGAGACAGAGT C A CA 3 B c c

27 CTCACTCTTGTT GGCAACAAGAG GA ACTC
GCCCAAGC CCGTTGTTCTC CT TGAG
A C AC

GAM130 331 LOC1640 1 20153 XP_089356.1 3 810 TTTTTGAGGAGT G A 3 B b b
91 TTCGCTCTTGTT G CAACAAGAGCGAAACTCC
GGCTAGGC C GTTGTTCTCGCTTTGAGG
G A

GAM130 331 LOC1696 1 13298 XP_095809.4 3 1104 TTGAGACAGAGT CA 3 B c c
11 TTCGCTTTTGTT GGCAACAAGAGCGAAACTC
GCCCGGGC CCGTTGTTTTCGCTTTGAG
AC

GAM130 331 LOC1973 1 15866 XP_113872.2 3 1695 TTGAGATGGAGT A A 3 B b b
58 CTCGCTCTTGTC GGC ACAAGAGCGA ACTCCAT
GCCCAGGC CCG TGTTCTCGCT TGAGGTA
C C

GAM130 331 LOC2008 1 8785 XP_117289.1 3 632 TTGAGACGGGGT A 3 B b b
60 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCC
GTCCAGGC CTGTTGTTCTCGCTTTGGGG
C

GAM130 331 LOC2008 1 6736 NP_789785.1 3 918 TTGGGACAGAGT C CA 3 B c c
95 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC

GAM130 331 LOC2197 1 1485 XP_167596.1 5 1200 TAGAGACAGAGT A G CA 3 B c
c
31 TTCGTCATGTTG GGCAACA GA CGAAACTC
CCCAGGCT CCGTTGT CT GCTTTGAG
A - AC

GAM130 331 LOC2828 1 14621 XP_212581.1 5 4 GAGACCGGAGTC A A A 3 B c c
90 TTGCTCTTGTCG GGC ACAAGAGCGA ACTCC
CCTCCTGA CCG TGTTCTCGTT TGAGG
C C C

GAM130 331 LOC2829 1 14621 XP_212629.1 5 4 GAGACCGGAGTC A A A 3 B c c
27 TTGCTCTTGTCG GGC ACAAGAGCGA ACTCC
CCTCCTGA CCG TGTTCTCGTT TGAGG
C C C

GAM130 331 LOC2831 1 4745 XP_210903.1 3 968 GTCTGATGGAGG A 3 B b b

77 TTTGCTCTTGTT GGCAACAAGAGCGAA CTCCAT
GCCCAGGC CCGTTGTTCTCGTTT GAGGTA
G
GAM130 331 LOC2832 1 18890 XP_210952.1 5 539 GTAGGGATTGGG A T 3 B b b
62 TTTTGCCTTGTT GGCAACAAG GCGAAAC CCA
GCCCAGGC CCGTTGTTC CGTTTTG GGT
- -
GAM130 331 LOC2832 1 14527 XP_210961.1 3 2031 TTGAGATGGAGT C 3 B b b
78 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A
GAM130 331 LOC2833 1 8110 XP_210973.1 3 386 TTGAGACGGAGT GGCA A 3 B c
c
23 TTCGCTCTTGT ACAAGAGCGAAACTCC
TGTTCTCGCTTTGAGG
---- C
GAM130 331 LOC2833 1 15080 XP_211007.1 3 1617 TAATGATGGAGT AAC 3 B c c
87 TTTGCTCTTACG GGC AAGAGCGAAACTCCAT
CCCAGGCT CCG TTCTCGTTTTGAGGTA
CA-
GAM130 331 LOC2838 2 7323 XP_208875.1 3 1491 AAGAGACAGAGT AG CA 3 B c
c
63 TTCGCTTGTTGC GGCAACA AGCGAAACTC
CCAGGCTG CCGTTGT TCGCTTTGAG
-- AC
GAM130 331 LOC2838 2 10774 XP_208875.1 3 1491 TTAAGAGACAGA AG CA 3 B c
c
63 GTTTCGCTTGTT GGCAACA AGCGAAACTC
GCCCAGGC CCGTTGT TCGCTTTGAG
-- AC
GAM130 331 LOC2839 1 17017 XP_208909.1 5 794 TTGAGACAGAGT CA CA 3 B c
c
28 TTTGCTCTTGTC GG ACAAGAGCGAAACTC
ACCTAGGC CC TGTTCTCGTTTTGAG
AC AC
GAM130 331 LOC2840 1 9226 XP_211298.1 3 0 GATGGAATTTCA C C 3 B b b
16 CTCTTGTTGCCT GGCAACAAGAG GAAA TCCAT
AGCTGGAG CCGTTGTTCTC CTTT AGGTA
A A
GAM130 331 LOC2840 1 13475 XP_211302.1 5 1071 TATGATTGGAGT - A G 3 B c c
19 TTAGTTTATGTT GGC AACA GAGC AAACTCCA
GGCCAGCT CCG TTGT TTTG TTTGAGGT
G A A
GAM130 331 LOC2841 1 17387 XP_211327.3 3 591 TTGAGACGGAGT C A 3 B c c
02 TTCACTTTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTTTC CTTTGAGG
A C
GAM130 331 LOC2841 1 16225 XP_211328.1 3 1230 GGAAGGTGGAGT AG C 3 B c
c

08 TTCCTGCTGTTG GGCAACA AG GAAACTCCAT
CTTGTGAA TCGTTGT TC CTTTGAGGTG
CG -
GAM130 331 LOC2841 1 15416 XP_211353.1 5 353 ACAGGATGGAGT A A 3 B b b
45 TTCGCTCTGTCG GGC ACA GAGCGAAACTCCAT
CCAGGCTG CCG TGT CTCGCTTTGAGGTA
C -
GAM130 331 LOC2841 1 8830 XP_209059.1 5 405 TTGAGATGGAGT A 3 B b b
83 TTTGCTCTCGTT GGCAAC AGAGCGAAACTCCAT
GCCAAGGC CCGTTG TCTCGTTTTGAGGTA
C
GAM130 331 LOC2842 1 19045 XP_209105.1 3 129 TTGAGACGGAGT C A 3 B c c
89 TTTGCTCTTGTT GG AACAAGAGCGAAACTCC
ACCCAGGC CC TTGTTCTCGTTTTGAGG
A C
GAM130 331 LOC2843 1 16485 XP_211426.1 3 298 TTGAGACACAGT C CCA 3 B c
c
04 TTCGCTCTTATT GGCAA AAGAGCGAAACT
GCCCAGGC CCGTT TTCTCGCTTTGA
A CAC
GAM130 331 LOC2843 1 12705 XP_211435.1 3 515 GTGGGATGGAGT CA AGC 3 B c
c
62 TTCACTTGTCAC GG ACAAG GAAACTCCAT
CCAGGCTG CC TGTTC CTTTGAGGTA
AC A--
GAM130 331 LOC2843 1 1561 XP_209154.1 3 1082 TAGAGACTGGGT - AG T 3 B c c

75 TTCGCTGTGTTA GGC AACA AGCGAAAC CCA
GCCTGGAT CCG TTGT TCGCTTTG GGT
A G- -
GAM130 331 LOC2843 1 9009 XP_209157.1 3 647 TTGAGACGGAGT C C A 3 B c c
76 TTCACTCTTATT GGCAA AAGAG GAAACTCC
GCCCAGGC CCGTT TTCTC CTTTGAGG
A A C
GAM130 331 LOC2844 1 4905 XP_209183.2 3 1635 TTGAGATGGAGT CA A G 3 B c
c
05 TTGGTTCTGTCC GG ACA GAGC AAACTCCAT
CCGAGGCC CC TGT CTTG TTTGAGGTA
CC - G
GAM130 331 LOC2844 1 13699 XP_211443.1 3 173 TTGAGATGGAGT CAA- 3 B c c
08 TTTGCTCTTGCA GG CAAGAGCGAAACTCCAT
CTCCATCC CC GTTCTCGTTTTGAGGTA
TCAC
GAM130 331 LOC2846 1 1879 XP_209319.1 5 84 TACTTACGGAGT C A 3 B b b
75 TTCGCTCTTATT GGCAA AAGAGCGAAACTCC
GCCCAGAC CCGTT TTCTCGCTTTGAGG
A C
GAM130 331 LOC2847 1 18764 XP_211602.1 3 456 TTTGAGATGGAG A A 3 B b b
23 TCTCGCTTTGTT GGCAACA GAGCGA ACTCCAT
GCCCAGGC CCGTTGT TTCGCT TGAGGTA

```
                                                  -    C
GAM130  331   LOC2848 1  11995 XP_209371.1  3  1198  GCCTCCCTGAGT    C     A   CA       3  B  c
c
        05                                     CTCGCTCTTTTG GGCAA AAGAGCGA ACTC
                                               CCCAGGCT    CCGTT TTCTCGCT TGAG
                                                     -     C   TC
GAM130  331   LOC2848 1  2803  XP_211661.1  5  429   TTGAGACGGAGT        C     A       3  B  b  b
        39                                     TTCCCTCTTGTT GGCAACAAGAG GAAACTCC
                                               GCCCGGGC    CCGTTGTTCTC CTTTGAGG
                                                        C      C
GAM130  331   LOC2849 1  5893  XP_211696.1  5  641   TTTGGATGGAGT   A    G            3  B  b  b
        34                                     TTCGTTTTGTCG GGC ACAAGA CGAAACTCCAT
                                               CCCAGGCT    CCG TGTTTT GCTTTGAGGTA
                                                     C    -
GAM130  331   LOC2849 1  1947  XP_211721.1  5  686   CAGAGATGGAGT   -  AAGAGC           3  B  c
c
        82                                     TTCACCACGTTG GGC AAC     GAAACTCCAT
                                               GCCAAGCT    CCG TTG     CTTTGAGGTA
                                                        G  CACCA-
GAM130  331   LOC2850 1  5847  XP_211753.1  5  398   GTAGAGATGGGG      A    A          3  B  c  c
        58                                     TCTTGCTTTGTT GGCAACA GAGCGA ACTCCAT
                                               GCCCAGGT    CCGTTGT TTCGTT TGGGGTA
                                                     -    C
GAM130  331   LOC2850 1  2058  XP_209465.1  3  25    TTTAGATGGAGT        C            3  B  b  b
        88                                     TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
                                               GCCCAGGC    CCGTTGTTCTC CTTTGAGGTA
                                                        A
GAM130  331   LOC2851 1  14805 XP_211797.1  3  1822  CTTTACTGGAGT  CA    C            3  B  b  b

        69                                     TTCCTCTTGTCC GG  ACAAGAG GAAACTCCA
                                               ATTTCTGA    CC  TGTTCTC CTTTGAGGT
                                                     --     -
GAM130  331   LOC2852 1  8332  XP_209521.1  5  238   TAGAGATGGGGT  -  AG             3  B  b  b
        21                                     TTCGCTATGTTG GGC AACA  AGCGAAACTCCAT
                                               GCCAAG      CCG TTGT  TCGCTTTGGGGTA
                                                        G   A-
GAM130  331   LOC2852 1  8457  XP_211829.1  5  548   TTGAGACGGAGT  C     C     A       3  B  c  c
        81                                     TTCTCTCTTGTT GG AACAAGAG GAAACTCC
                                               ACCCAGGC    CC TTGTTCTC CTTTGAGG
                                                        A      T      C
GAM130  331   LOC2855 1  2078  XP_209649.1  5  98    GAGGAATGGAGT   AACAA  C           3  B  c
c
        30                                     TTCCTTGATGAG GGC    GAG GAAACTCCAT
                                               CCTGAGAG    CCG    TTC CTTTGAGGTA
                                                        AGTAG  -
GAM130  331   LOC2858 1  2870  XP_212036.1  5  61    TTGAGACAGAGT        C     CA       3  B  c  c
        13                                     TTCACTCTTGTT GGCAACAAGAG GAAACTC
                                               GCCCAGGC    CCGTTGTTCTC CTTTGAG
                                                        A      AC
GAM130  331   LOC2858 1  9981  XP_209788.1  3  246   AACGTTTTGGAG       A   AA          3  B  c  c
```

68 ATTGTGCTTGTT GGCAACAAG GCGA CTCCA
GCTTTGCT TCGTTGTTC TGTT GAGGT
G A-

GAM130 331 LOC2859 1 6287 XP_209816.1 3 578 TTGAGATGAAGT CG C 3 B c c
24 TTTACTCTTGTT GGCAACAAGAG AAACT CAT
GCCCAGGC CCGTTGTTCTC TTTGA GTA
AT A

GAM130 331 LOC2859 1 9180 XP_212105.1 3 429 TAGAGATGGAGT - AG C 3 B c c
72 TTCACTATGTTG GGC AACA AG GAAACTCCAT
GCCAGGCT CCG TTGT TC CTTTGAGGTA
G A- A

GAM130 331 LOC2859 1 16032 XP_212111.1 3 919 TTGAGACAGAGT CA 3 B b b
89 TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGCTTTGAG
AC

GAM130 331 LOC2860 1 10926 XP_212132.1 5 1573 TAATATGGATTT - - C 3 B b b
02 CTGCTCCTTGTT GGCAACAAG AGC GAAA TCCAT
GCTTGCTA TCGTTGTTC TCG CTTT AGGTA
C T -

GAM130 331 LOC2860 1 16758 XP_209867.2 3 597 TTGAGATGGAGT CA- C 3 B c c

32 TTCACTCTTGTC GG ACAAGAG GAAACTCCAT
AACCAGAT CC TGTTCTC CTTTGAGGTA
AAC A

GAM130 331 LOC2860 1 9783 XP_209873.1 5 631 TTGAGACGGAGA C A A 3 B c c
39 TTCACTTTTGTT GGCAACAAGAG GAA CTCC
GCCCAGGC CCGTTGTTTTC CTT GAGG
A A C

GAM130 331 LOC2860 1 13192 XP_212163.1 5 1386 TTGAGATGGAGT A 3 B b b
78 TTCGCTCTGTTG GGCAACA GAGCGAAACTCCAT
CCAGGCTG CCGTTGT CTCGCTTTGAGGTA
-

GAM130 331 LOC2863 1 6947 XP_212278.1 3 396 AGGAGACGGAGT G C A 3 B c c

41 TTCACTGTTGTT GGCAACAA AG GAAACTCC
GCCCAGGC CCGTTGTT TC CTTTGAGG
G A C

GAM130 331 LOC2864 1 15744 XP_212310.1 5 484 TTTAGATGGAAT C C 3 B b b
01 TTCACTCTTGTT GGCAACAAGAG GAAA TCCAT
GCCCAGGC CCGTTGTTCTC CTTT AGGTA
A A

GAM130 331 LOC2864 1 6673 XP_210063.1 3 969 TTGAGACGGAGT G A 3 B b b
67 TTCGCTGTTGTT GGCAACAA AGCGAAACTCC
GCCCAGGC CCGTTGTT TCGCTTTGAGG
G C

GAM130 331 LOC2865 1 4789 XP_212330.2 3 2060 GACCTGGAATCT G-- --- C-- 3 B c c

20 TTTGCTCTTGTT GCA ACAAGAGCGAAA TCCA
TTTGCAGT CGT TGTTCTCGTTTT AGGT
TGA TTT CTA

GAM130 331 LOC3385 1 9751 XP_294653.1 3 1917 TTGAGACAGAGT C CA 3 B c c
65 TTCACTTTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTTTC CTTTGAG
A AC
GAM130 331 LOC3389 1 1240 XP_294742.1 3 423 TTGAGACGGAGA A A A A 3 B c c
23 TTCGCTCTGTCG GGC ACA GAGCGAA CTCC
CCAGGCTG CCG TGT CTCGCTT GAGG
C - A C
GAM130 331 LOC3390 1 4115 XP_294802.2 3 876 TTGAGATGGAGT AAC C - 3 B c c
77 TTTCACTCTTAT GGC AAGAG GAAA CTCCAT
CGCCCAGG CCG TTCTC CTTT GAGGTA
CTA A T
GAM130 331 LOC3393 1 14109 XP_290838.1 3 2375 TTGAGACGGAGT A 3 B b b
24 TTTGTTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAGGC CCGTTGTTCTTGTTTTGAGG
C
GAM130 331 LOC3393 1 1840 XP_294921.1 5 646 TTGAGACAGAGT C CA 3 B c c
73 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCACGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 LOC3394 1 14527 XP_290919.1 3 1370 TTGAGATGGAGT C 3 B b b
92 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A
GAM130 331 LOC3398 1 3269 XP_291031.1 3 711 TAGAGATGGAGT - AG CG 3 B c
c
33 TTTACTATGTTG GGC AACA AG AAACTCCAT
GCCAGGCT CCG TTGT TC TTTGAGGTA
G A- AT
GAM130 331 LOC3398 1 19270 XP_295090.1 3 390 ACTAGTAGGCAG GC -- A 3 B c c
74 GTTTCTCTTGTT GGCAACAAGA GAAACT CC
GTCTAGAC CTGTTGTTCT CTTTGG GG
-- AC A
GAM130 331 LOC3400 1 13921 XP_295137.1 3 21 TTTGAGATGAGT C CA 3 B c c
37 TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A TA
GAM130 331 LOC3403 1 5604 XP_291269.1 3 1366 TTGAGATGGAGT GC 3 B b b
90 TTCAGTCTTGTT GGCAACAAGA GAAACTCCAT
GCCCAGGC CCGTTGTTCT CTTTGAGGTA
GA
GAM130 331 LOC3404 1 9783 XP_291274.1 5 630 TTGAGACGGAGA C A A 3 B c c
08 TTCACTTTTGTT GGCAACAAGAG GAA CTCC
GCCCAGGC CCGTTGTTTTC CTT GAGG
A A C
GAM130 331 LOC3476 1 14621 XP_300206.1 5 4 GAGACCGGAGTC A A A 3 B c c
44 TTGCTCTTGTCG GGC ACAAGAGCGA ACTCC

CCTCCTGA CCG TGTTCTCGTT TGAGG
C C C
GAM130 331 LOC3479 1 8346 XP_302624.1 5 351 TTGACACGGAGT A 3 B b b
05 TTCGCTCTTGTT GGCAACAAGAGCGAAACTCC
GTCCAGGC CTGTTGTTCTCGCTTTGAGG
C
GAM130 331 LOC3481 1 16032 XP_300626.1 5 537 TTGAGACAGAGT CA 3 B b b
15 TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGCTTTGAG
AC
GAM130 331 LOC3484 1 14527 XP_300730.1 3 611 TTGAGATGGAGT C 3 B b b
02 TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A
GAM130 331 LOC3484 1 688 XP_300758.1 3 175 TTGAGACAGGGT AG CA 3 B c c
92 TTCGCTGTGTTG GGCAACA AGCGAAACTC
CTCCAGCT TCGTTGT TCGCTTTGGG
G- AC
GAM130 331 LOC3485 1 19934 XP_302814.1 3 1890 TTGAGACAGAGT CA 3 B b b
28 TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGCC CCGTTGTTCTCGCTTTGAG
AC
GAM130 331 LOC3487 1 1047 XP_300843.1 3 430 TTGAGATGGAGT A 3 B b b
90 TTCGTGCTTGTT GGCAACAAG GCGAAACTCCAT
GCCCAGGC CCGTTGTTC TGCTTTGAGGTA
G
GAM130 331 LOC3487 1 5380 XP_300845.1 5 7 TTCAGATGGAGT 3 B b b
98 TTTGTTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTTGTTTTGAGGTA

GAM130 331 LOC3490 1 3876 XP_300250.1 3 127 TTGAGACAGAGT CA CA 3 B c c

24 TTCGCTCTTGTC GG ACAAGAGCGAAACTC
ACCCAGGC CC TGTTCTCGCTTTGAG
AC AC
GAM130 331 LOC3492 1 19162 XP_300251.1 3 594 TAGAGAGGGAGT - AGA A 3 B c
c
51 TTCGCCATGTTG GGC AACA GCGAAACTCC
GCCAGGCT CCG TTGT CGCTTTGAGG
G AC- G
GAM130 331 LOC5710 1 7276 NP_065114.2 3 570 TTTAGATGTAGT C 3 B b b
7 TTTGCTCTTGTT GGCAACAAGAGCGAAACT CAT
GCCCAGGC CCGTTGTTCTCGTTTTGA GTA
T
GAM130 331 LOC5714 1 1157 NP_065155.2 3 719 TTGTGACGGAGT C A 3 B b b
6 TTCCCTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
C C
GAM130 331 LOC8502 1 5403 NP_116326.1 5 540 TCCTGATGGAGT AG C 3 B b b
6 TTCACTATGTTG GGCAACA AG GAAACTCCAT

CCCAGG CCGTTGT TC CTTTGAGGTA
A- A

GAM130 331 LOC9040 1 6139 XP_031517.1 5 1629 TTGAGATGAAGT C C A C 3 B c c

8 CTCCCTCTTGTT GG AACAAGAG GA ACT CAT
ACCCAGGC CC TTGTTCTC CT TGA GTA
A C C A

GAM130 331 LOC9111 2 6171 XP_036218.1 3 268 TTGAGATGGAGT CA C 3 B c b

5 TTCACTCTTGTC GG ACAAGAG GAAACTCCAT
ACCCAGGC CC TGTTCTC CTTTGAGGTA
AC A

GAM130 331 LOC9111 2 17551 XP_036218.1 3 2127 GTGTGATGGGGT A 3 B b b

5 TTCGCACTTGTT GGCAACAAG GCGAAACTCCAT
GCCCAGGC CCGTTGTTC CGCTTTGGGGTA
A

GAM130 331 LOC9137 1 2713 XP_038063.5 3 1509 TTTAGACGGAGT C A 3 B b b

3 TTCACTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
A C

GAM130 331 LOC9320 1 6707 XP_049838.1 3 784 TTGAGACGGAGT A C A 3 B c c

6 TTCCCTCTGTTG GGCAACA GAG GAAACTCC
CCCAGGCT CCGTTGT CTC CTTTGAGG
- C C

GAM130 331 LZTS1 1 3087 NP_066300.1 3 1596 GTAGGGACGGGG G A A 3 B c c
TCTCGTTTTGTT GGCAACAAGA CGA ACTCC
GCCAAAGC CCGTTGTTTT GCT TGGGG
- C C

GAM130 331 MEF2A 1 10779 NP_005578.1 5 222 TAGAGATGGAGT - AGAGC 3 B c c

TTCACCATGTTG GGC AACA GAAACTCCAT
GCCAGGCT CCG TTGT CTTTGAGGTA
G ACCA-

GAM130 331 MEGF11 1 19297 NP_115821.1 3 2014 CAAGTTTGAAGT C A- C 3 B c c

TTCGCCGCTTTT GGCAA AAG GCGAAACT CA
GTCAACTA CTGTT TTC CGCTTTGA GT
- GC A

GAM130 331 MGC1313 1 19675 NP_219363.1 3 750 GTGTGATGGGGT 3 B b b

8 TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTCTCGTTTTGGGGTA

GAM130 331 MGC1955 1 11634 NP_291029.1 5 850 GCAACATGGAGT A AG -- 3 B c c

6 TCATTGTCCTGT GGCAACA G CGA AACTCCAT
TGCTTACT TCGTTGT C GTT TTGAGGTA
- CT AC

GAM130 331 MGC2167 1 16032 NP_443093.1 3 483 TTGAGACAGAGT CA 3 B b b

5 TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGCTTTGAG
AC

GAM130 331 MGC2474 1 6895 NP_076420.1 3 937 TTGAGACGGAGT A 3 B b b
TTTGCTCTTGTT GGCAACAAGAGCGAAACTCC
GCCCAGGC CCGTTGTTCTCGTTTTGAGG
C
GAM130 331 MGC2670 1 12477 NP_689794.1 3 785 TTTTTATGGAGT AGAGC 3 B c c
6 TTCATGTTGTCC GGCAACA GAAACTCCAT
ACTATAGC CTGTTGT CTTTGAGGTA
A----
GAM130 331 MGC2734 1 18775 XP_300964.1 5 1651 TTGAGACAGAGT C CA 3 B c c
5 TTCATTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGG CCGTTGTTCTT CTTTGAG
A AC
GAM130 331 MGC3329 1 16011 NP_076991.2 3 1580 ATGAGGTGGAGT CG 3 B b b
TTTACTCTTGTT GGCAACAAGAG AAACTCCAT
GTCTAGGC CTGTTGTTCTC TTTGAGGTG
AT
GAM130 331 MGC3546 1 2083 NP_694976.1 3 70 TTGAGACAGAGT A CA 3 B c c
8 TTTGCCCTTGTT GGCAACAAG GCGAAACTC
GCCCAGGC CCGTTGTTC CGTTTTGAG
C AC
GAM130 331 MGC3771 1 17353 NP_112232.1 5 732 AAGAGACGGAGT C C A 3 B c c
TTCGCTCTTCTT GG AA AAGAGCGAAACTCC
CCCATGCT CC TT TTCTCGCTTTGAGG
C C C
GAM130 331 MGC4057 1 16272 NP_689989.1 3 887 TTGAGATGGAGT CA C 3 B c c
9 TTCACTCTTGTC GG ACAAGAG GAAACTCCAT
TCCCAGAC CC TGTTCTC CTTTGAGGTA
TC A
GAM130 331 MGC5045 1 1368 NP_775733.1 3 72 TTGAGACAGAGT C A CA 3 B c c
2 TTCGCACTTCTT GGCAA AAG GCGAAACTC
GCCCAGGC CCGTT TTC CGCTTTGAG
C A AC
GAM130 331 MGRN1 1 16033 XP_048119.4 3 1577 TTGAGATGGAGT A C 3 B b b
TTCACTCTTGCT GGCA CAAGAG GAAACTCCAT
GCCCAGGC CCGT GTTCTC CTTTGAGGTA
C A
GAM130 331 MLANA 1 10945 NP_005502.1 3 594 TTGAGATGGAGT 3 B b b
TTCGCTTTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAGGC CCGTTGTTTTCGCTTTGAGGTA
GAM130 331 MLF1 1 15324 NP_071888.1 5 19 CCGTACTGGAGG A--- GAAA 3 B c c
CTAGCTCTTGTC GGC ACAAGAGC CTCCA
GCGGCCGC CCG TGTTCTCG GAGGT

GCGC ATCG
GAM130 331 NAP4 1 6341 XP_294897.2 3 549 GGAAGGGGGAAT - - AA- A 3 B c c
CTGCCTCTTGTT GGCAACAAGAG C GA CTCC
GCCATGGG CCGTTGTTCTC G CT GGGG
C T AAG A
GAM130 331 NCAG1 1 11087 NP_115536.1 3 3649 TTGGGGATGGAG A C A 3 B c c
TCTCACTTTGTT GGCAACA GAG GA ACTCCAT
GCCCAGGC CCGTTGT TTC CT TGAGGTA
- A C
GAM130 331 NDRG3 1 10779 NP_114402.1 3 1302 TAGAGATGGAGT - AGAGC 3 B c c
TTCACCATGTTG GGC AACA GAAACTCCAT
GCCAGGCT CCG TTGT CTTTGAGGTA
G ACCA-
GAM130 331 NOSIP 1 6878 NP_057037.1 5 36 GTTAGTGAGAGT C - 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTC CAT
GCCTAGGC CCGTTGTTCTC CTTTGAG GTG
A A
GAM130 331 NT5C2 1 20125 NP_036361.1 5 19 CTGGAGCCGAGT ACA CA 3 B c c
TTCGCTCTGCTG GGCA AGAGCGAAACTC
CCCAGGCT CCGT TCTCGCTTTGAG
CG- CC
GAM130 331 NUP43 1 14929 NP_078923.2 3 1537 TTGAGATGGAGT 3 B b b
TTTGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCTGAGGC TCGTTGTTCTCGTTTTGAGGTA
GAM130 331 OSBPL2 1 16028 NP_055650.1 3 1109 TTGAGACGGAGT C A 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
A C
GAM130 331 OSBPL2 1 16028 NP_653081.1 3 1109 TTGAGACGGAGT C A 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
A C
GAM130 331 PASK 1 12272 NP_055963.1 5 788 TTGAGACAGAGT CA 3 B c c
TTCGCTCTTGTT GGCAACAAGAGCGAAACTC
GCTGAGGC TCGTTGTTCTCGCTTTGAG
AC
GAM130 331 PCDHB14 1 2918 NP_061757.1 3 247 TATTAATGGAGT C G - 3 B c c
TATTGCTATTTT GGCAA AA AGCGA AACTCCAT
TGCTGTGA TCGTT TT TCGTT TTGAGGTA
T A A
GAM130 331 PER2 1 2668 NP_073728.1 3 1357 TTTAGATGGAGT AA--- C 3 B c c
TTCTTTTTGCCC GGC CAAGAG GAAACTCCAT
AGGCTGGA TCG GTTTTT CTTTGAGGTA
GACCC -
GAM130 331 PEX5R 1 4446 NP_057643.1 3 681 CCTTGCTGGAGT G 3 B b b
TTTGTTTTGTTG GGCAACAAGA CGAAACTCCA

CTCCAATT TCGTTGTTTT GTTTTGAGGT
-
GAM130 331 PKNOX1 1 14526 NP_004562.2 3 1804 TTGAGACAGAGT CA 3 B c c
TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GCCCAGGC CCGTTGTTCTCGTTTTGAG
AC
GAM130 331 PPEF2 1 6206 NP_006230.2 3 351 TTGAGATGGAGT C 3 B b b
TTCTCTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
T
GAM130 331 PPEF2 1 6206 NP_690910.1 3 983 TTGAGATGGAGT C 3 B b b
TTCTCTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
T
GAM130 331 PPEF2 1 6206 NP_690911.1 3 2196 TTGAGATGGAGT C 3 B b b
TTCTCTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
T
GAM130 331 PRKY 1 9776 NP_002751.1 3 5768 AACACTGGGCAG A AA - A 3 B c c
CCTCGCCTTGTT GGCAACAAG GCGA CT CC
GCCAACGT CCGTTGTTC CGCT GA GG
- CC C G
GAM130 331 PRND 1 2712 NP_036541.1 3 822 TTTAGATGGAGT CG 3 B b b
TTTACTCTTGTT GGCAACAAGAG AAACTCCAT
GCCCAGGC CCGTTGTTCTC TTTGAGGTA
AT
GAM130 331 PTGIS 1 15449 NP_000952.1 3 3252 TTGAGACGGAGT C AGC A 3 B c
c
TTCACGCTTATT GGCAA AAG GAAACTCC
GCCCAGGC CCGTT TTC CTTTGAGG
A GCA C
GAM130 331 PTGS1 1 10350 NP_000953.2 3 2371 ATCAGTTGGAGT AGA G 3 B c
c
TTGTGTCTGTTG GGCAACA GC AAACTCCA
CTTGTAAT TCGTTGT TG TTTGAGGT
CTG -
GAM130 331 PTGS1 1 10350 NP_542158.1 3 2371 ATCAGTTGGAGT AGA G 3 B c
c
TTGTGTCTGTTG GGCAACA GC AAACTCCA
CTTGTAAT TCGTTGT TG TTTGAGGT
CTG -
GAM130 331 PTPRK 1 3473 NP_002835.2 3 1069 AAGGAATGGAGT A A A --- 3 B c c
TTTTCAGCCTGT GGC ACA G GC GAAACTCCAT
GGCCCAGC CCG TGT C CG TTTTGAGGTA
G - - ACT
GAM130 331 RAB36 1 2081 NP_004905.1 3 1391 TTGAGATGGAGT AGC 3 B b b
TTCACCCTTGTT GGCAACAAG GAAACTCCAT
GCCCAGGC CCGTTGTTC CTTTGAGGTA
CCA
GAM130 331 RNF144 1 4275 NP_055561.1 3 3150 TTGAGACGGAGT CA A 3 B c c

TTCGCTTTTGTC GG ACAAGAGCGAAACTCC
CCCCAAGC CC TGTTTTCGCTTTGAGG
CC C
GAM130 331 RP2 1 14528 NP_008846.1 3 1749 TTGAGGTGGAGT C 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAAGC CCGTTGTTCTC CTTTGAGGTG
A
GAM130 331 SCML2 1 15934 NP_006080.1 3 1297 TTGAGATGGAGT A C 3 B b b
TTCACTCTTGTG GGCA CAAGAG GAAACTCCAT
CCCAGGCT CCGT GTTCTC CTTTGAGGTA
- A
GAM130 331 SEDL 1 5004 NP_055378.1 3 1330 TTGAGATGGAGT A 3 B b b
TTCGCTCTGTTG GGCAACA GAGCGAAACTCCAT
TCCAGGCT CTGTTGT CTCGCTTTGAGGTA
-
GAM130 331 SIL 1 7982 NP_003026.1 3 344 TTGAGACGGAGT A A 3 B c c
TTTGCTCTTGTA GGC ACAAGAGCGAAACTCC
GCCCAGGC CCG TGTTCTCGTTTTGAGG
A C
GAM130 331 SIRPB1 1 2065 NP_006056.1 3 2026 TTGAGATGGAGT C C AGC 3 B c
c
TTCACCTTATTC GG AA AAG GAAACTCCAT
CCAGGCTG CC TT TTC CTTTGAGGTA
C A CA-
GAM130 331 SLC15A1 1 2082 NP_005064.1 3 202 TTGAGACAGAGT CA 3 B c c
TTTGCTCTTGTT GGCAACAAGAGCGAAACTC
GTCCAGGC CTGTTGTTCTCGTTTTGAG
AC
GAM130 331 SLC24A1 1 19932 NP_004718.1 3 670 TTGAGACAGAGT G CA 3 B c c
TTGGCTCTTGTT GGCAACAAGAGC AAACTC
GCCCAGGC CCGTTGTTCTCG TTTGAG
G AC
GAM130 331 SLC35E2 1 13221 XP_049733.6 3 1749 GTTGAGCTGGGC A AAC 3 B c
c
TCTCGCTTTGTT GGCAACA GAGCGA TCCA
GCCCAGGC CCGTTGT TTCGCT GGGT
- CTC
GAM130 331 SMARCD1 1 3343 NP_003067.2 3 663 CAGTATTGGAGT C- 3 B c c
TTTGTTCTTTAT GGCAA AAGAGCGAAACTCCA
TGCTCCCT TCGTT TTCTTGTTTTGAGGT
AT
GAM130 331 SMARCD1 1 3343 NP_620710.1 3 663 CAGTATTGGAGT C- 3 B c c
TTTGTTCTTTAT GGCAA AAGAGCGAAACTCCA
TGCTCCCT TCGTT TTCTTGTTTTGAGGT
AT
GAM130 331 SNARK 1 15170 NP_112214.1 3 585 TTGAGACGGAGT A A 3 B b b
TTCGCTCTTGGT GGCA CAAGAGCGAAACTCC
GCCCAGGC CCGT GTTCTCGCTTTGAGG
G C

GAM130 331 SNX22 1 15559 NP_079074.1 3 502 TTGGGGCGGAGT C A 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
A C

GAM130 331 SPN 1 7729 NP_003114.1 3 169 TTGAGACAGAGT A A CA 3 B c c
TTCGCTTTGTCG GGC ACA GAGCGAAACTC
CCCAGGCT CCG TGT TTCGCTTTGAG
C - AC

GAM130 331 SS18 1 16460 NP_005628.1 3 1657 TTGAGATGGAGT A A 3 B b b
CTTGCTCTTGTC GGC ACAAGAGCGA ACTCCAT
GCCCAGGC CCG TGTTCTCGTT TGAGGTA
C C

GAM130 331 ST5 1 6346 NP_005409.2 3 300 CATGGATGAAGT A AAG ---- 3 B c c
TTCGCTGGGTGC GGCA C AGCGAAAC TCCAT
TCGTGACT TCGT G TCGCTTTG AGGTA
- GG- AAGT

GAM130 331 ST5 1 6346 NP_631896.1 3 300 CATGGATGAAGT A AAG ---- 3 B c c
TTCGCTGGGTGC GGCA C AGCGAAAC TCCAT
TCGTGACT TCGT G TCGCTTTG AGGTA
- GG- AAGT

GAM130 331 STARD7 1 20092 NP_064536.1 3 600 TAGAGATGGAGT C A C 3 B c c

TTCACTCTGTTT GG AACA GAG GAAACTCCAT
CCCAGGCT CC TTGT CTC CTTTGAGGTA
T - A

GAM130 331 STARD7 1 20092 NP_644672.1 3 600 TAGAGATGGAGT C A C 3 B c c

TTCACTCTGTTT GG AACA GAG GAAACTCCAT
CCCAGGCT CC TTGT CTC CTTTGAGGTA
T - A

GAM130 331 STAU 1 7149 NP_004593.1 5 258 GCCAGGTGGAGT A 3 B b b
TTTGCTCTTGTC GGC ACAAGAGCGAAACTCCAT
GCCCAGGC CCG TGTTCTCGTTTTGAGGTG
C

GAM130 331 STOM 1 11080 NP_004090.3 3 479 CTGAGATGGAGT C 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCCAT
GCCCAGGC CCGTTGTTCTC CTTTGAGGTA
A

GAM130 331 SYT11 1 11259 NP_689493.2 3 264 TTGAGGTGGAGT 3 B b b
TTCGCTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCGGGC CCGTTGTTCTCGCTTTGAGGTG

GAM130 331 SYT13 1 1756 NP_065877.1 3 1509 TTAGACGGAGTT - A 3 B b b
TTGCTCTTTGTT GGCAACAA GAGCGAAACTCC
GCCCAGGC CCGTTGTT CTCGTTTTGAGG
T C

GAM130 331 TAF11 1 7353 NP_005634.1 3 533 ATGGAGATGGGG A A 3 B c c
TCTTGCTTTGTT GGCAACA GAGCGA ACTCCAT
GCCCAGGC CCGTTGT TTCGTT TGGGGTA
- C

GAM130 331 TBC1D5 1 14371 NP_055559.1 5 906 TTGAAAAGGAGT CA A 3 B b b
TTCGCTCTTGTC GG ACAAGAGCGAAACTCC
CAGGCTGG CC TGTTCTCGCTTTGAGG
-- A
GAM130 331 TERA 1 19045 NP_067061.1 3 123 TTGAGACGGAGT C A 3 B c c
TTTGCTCTTGTT GG AACAAGAGCGAAACTCC
ACCCAGGC CC TTGTTCTCGTTTTGAGG
A C
GAM130 331 TIM50L 1 18544 XP_053074.2 3 1390 TTGAGACGGAGT C A 3 B b b
TTCGCTCTTATT GGCAA AAGAGCGAAACTCC
GCCCAGGC CCGTT TTCTCGCTTTGAGG
A C
GAM130 331 TNFRSF1 1 6834 NP_443177.1 3 185 CCCCCATGGAGT CAAGA G 3 B c
c
3C TTGGTGTGCTTG GGCAA GC AAACTCCAT
CCTTTGGC CCGTT TG TTTGAGGTA
CGTG- G
GAM130 331 TP53 1 3421 NP_000537.2 3 817 TTTGAGACTGGG A A T 3 B c c
TCTCGCTTTGTT GGCAACA GAGCGA AC CCA
GCCCAGGC CCGTTGT TTCGCT TG GGT
- C -
GAM130 331 TPMT 1 5228 NP_000358.1 3 409 TTGAGATGGAGT 3 B b b
TTCGTTCTTGTT GGCAACAAGAGCGAAACTCCAT
GCCCAACC CCGTTGTTCTTGCTTTGAGGTA
GAM130 331 TRIM5 1 4494 NP_149023.1 3 634 TTGAGATGAAGT C C 3 B c c
TTTGCTCTTGTT GG AACAAGAGCGAAACT CAT
CCCCAGGC CC TTGTTCTCGTTTTGA GTA
C A
GAM130 331 TRPM6 1 5183 NP_060132.3 3 840 TTGAGATGGAGT C C C 3 B c c
TTCACTCTTTTT GG AA AAGAG GAAACTCCAT
ACCCAGGC CC TT TTCTC CTTTGAGGTA
A T A
GAM130 331 TRPV1 1 14336 NP_061197.3 3 668 GTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 TRPV1 1 14336 NP_542435.1 3 669 GTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 TRPV1 1 14336 NP_542436.1 3 669 GTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 TRPV1 1 14336 NP_542437.1 3 668 GTGAGACAGAGT C CA 3 B c c
TTCACTCTTGTT GGCAACAAGAG GAAACTC
GCCCAGGC CCGTTGTTCTC CTTTGAG
A AC
GAM130 331 TU12B1- 1 18545 NP_057659.1 3 1288 TTGAGATGGAGT C 3 B b b

TY TTTGCTCTTATT GGCAA AAGAGCGAAACTCCAT
GCCCAGGC CCGTT TTCTCGTTTTGAGGTA
A

GAM130 331 UBE3A 1 11737 NP_000453.2 3 812 AGGACAGGGATT C A 3 B c c
TTTGTTCTTGTT GGCAACAAGAGCGAAA TCC
GTTCTCGT TTGTTGTTCTTGTTTT AGG
T G

GAM130 331 UBE3A 1 11737 NP_570853.1 3 812 AGGACAGGGATT C A 3 B c c
TTTGTTCTTGTT GGCAACAAGAGCGAAA TCC
GTTCTCGT TTGTTGTTCTTGTTTT AGG
T G

GAM130 331 UBE3A 1 11737 NP_570854.1 3 812 AGGACAGGGATT C A 3 B c c
TTTGTTCTTGTT GGCAACAAGAGCGAAA TCC
GTTCTCGT TTGTTGTTCTTGTTTT AGG
T G

GAM130 331 VIK 1 1104 NP_612503.1 3 869 ACAGAGATGGGG A A 3 B c c
TCTTGCTTTGTT GGCAACA GAGCGA ACTCCAT
GCCCAGGC CCGTTGT TTCGTT TGGGGTA
- C

GAM130 331 VTI1A 1 1804 NP_660207.1 3 519 TAGAGATGGAGT - AGAGC 3 B c c
TTCACCATGTTG GGC AACA GAAACTCCAT
GCCAGGAT CCG TTGT CTTTGAGGTA
G ACCA-

GAM130 331 ZNF253 1 6640 NP_066385.1 3 275 TTGAGATGGAGT CA C 3 B c c
TTCACTCTTGTC GG ACAAGAG GAAACTCCAT
ACCGAGGC CC TGTTCTC CTTTGAGGTA
AC A

GAM130 331 ZNF273 1 16028 XP_088082.1 3 826 TTGAGACGGAGT C A 3 B b b
TTCACTCTTGTT GGCAACAAGAG GAAACTCC
GCCCAGGC CCGTTGTTCTC CTTTGAGG
A C

GAM130 331 ZNF432 1 4119 NP_055465.1 3 1753 AAACCACGGAGT A A 3 B c c
TCTGCTCTTGTT GGCAACAAGAGCG AACTCC
GCCCAGGT CCGTTGTTCTCGT TTGAGG
C C

GAM131 313 ASK 1 7247 NM_006716.1 5 AGAGAGGCGGCC G CA GT -- 3 C c c
GTCCTGTCAAC GT ACAGGA CGG GCCTCTCT
CA TGTCCT GCC CGGAGAGA
- AC -- GG

GAM131 313 ATP8B2 1 13187 XM_290875.1 5 AGAGAGGCCTGA AG 3 C b b
ACCTGTTGACT GGTCAACAGG TCGGGCCTCTCT
TCAGTTGTCC AGTCCGGAGAGA
A-

GAM131 313 LGP1 1 18541 NM_032484.2 3 AGAGAGGCCTTG ACA A - 3 C c c
GCCCAGCTGACC GGTCA GG GTCG GGCCTCTCT
CCAGT CC CGGT CCGGAGAGA
CGA - T

GAM131 313 LHX6 1 7257 NM_014368.1 3 AGAGTTGGGGAC A GGG T- 3 C c c
CCCTGTTGGCC GGTCAACAGG GTC CC CTCT
CCGGTTGTCC CAG GG GAGA

C G-- TT

GAM131 313 LOC1431 1 7765 5 AGAGAGGCAGGA A GG 3 C c c
62 TTCCTGCTGACT GGTCA CAGGAGTC GCCTCTCT
TCAGT GTCCTTAG CGGAGAGA
C GA

GAM131 313 LOC1451 1 15702 3 AGAGAGGCCCGC CAA AGT 3 C c c
23 CTGCCCACC GGT CAGG CGGGCCTCTCT
CCA GTCC GCCCGGAGAGA
CCC ---

GAM131 313 LOC1469 1 17527 XM_097149.2 5 AGAGAGGCCCGG AACA A- 3 C c c
90 CCGCCGGCC GGTC GG GTCGGGCCTCTCT
CCGG CC CGGCCCGGAGAGA
---- GC

GAM131 313 PTMA 1 19917 NM_002823.2 3 AGAGAGGCCCGC CAACA A T 3 C c c
CCGCCCACC GGT GG G CGGGCCTCTCT
CCA CC C GCCCGGAGAGA
CCCG- - -

GAM131 313 TGFA 1 3907 NM_003236.1 3 AGAGACGGACTC C GGGCC 3 C c c
CTGTTCACC GGT AACAGGAGTC TCTCT
CCA TTGTCCTCAG AGAGA
C GC---

GAM132 369 CLIC5 1 17752 NM_016929.1 3 TTGGACTGGTGG CT A G A 3 C c c
CATCATG CATGATGT CGC CAGTCCAA
GTACTACG GTG GTCAGGTT
-- - - -

GAM132 369 FLJ1037 1 929 NM_018077.1 3 TGGACTGTGTAC C T GC AA 3 C c c
7 ATCTGA TCA GATGTAC GCAGTCCA
AGT CTACATG TGTCAGGT
- - -- --

GAM132 369 PAX2 1 16012 NM_003987.1 3 TGGACTGCGCGG A A AA 3 C c c
CGCCGTGAG CTCATG TGT CGCGCAGTCCA
GAGTGC GCG GCGCGTCAGGT
C - --

GAM132 369 SMARCE1 1 3854 NM_003079.3 3 TTTGGACCATTT ACGCGCA 3 C c c
AGCATCATGAG CTCATGATGT GTCCAAA
GAGTACTACG CAGGTTT
ATTTAC-

GAM133 211 AFG3L1 1 18205 NP_001123.1 3 1420 AAGGATGACTCA GCTA GC 1 B c c
GCAGGGATGATT TGAAT CCCTGCTG TC
CAGCAGAG ACTTA GGGACGAC AG
GTA- TC

GAM133 211 ARPP-21 1 4699 NP_057384.1 5 48 ATTGTGAGCCTG CCTG - 1 B c c
GAGAAGTAGCAT TGAATGCTAC CT GGCTC
TTAGTTGG ATTTACGATG GG CCGAG
AAGA T

GAM133 211 BCL2L2 1 19697 NP_004041.1 3 1707 AACTCAGAGCCA AA CCT 1 B c c

GCTTGTGGCAAG TG TGCTAC GCTGGCTCT
CAGTTGGG AC ACGGTG CGACCGAGA
GA TT-

GAM133 211 C5orf7 1 10526 NP_057688.1 3 124 CACCCAGAGCCA T---- - C 1 B c c
GTGTGGTCAGTA GAATGCT ACC TGCTGGCTCT
TTCCAAAC CTTATGA TGG GTGACCGAGA
CAAAC C T

GAM133 211 CD109 1 15628 NP_598000.1 3 425 AGAAAACAGCCA T AC- C 1 B c c
GCAGGAGGAGCT TGAA GCT CCTGCTGGCT
TCATCTGT ACTT CGA GGACGACCGA
- GGA C

GAM133 211 CD72 1 3671 NP_001773.1 3 324 GGCCCGGAGCCA T A CT 1 B c c
GCCAGGCAGTTT TGAA GCT CC GCTGGCTCT
TATTGAAA ATTT TGA GG CGACCGAGG
- C AC

GAM133 211 CGI-69 1 11572 NP_057100.1 5 93 AGCCTAGAGCCA T ACCCTG 1 B c c

GGACTGAAGCTT TGAA GCT CTGGCTCT
CAAGATGG ACTT CGA GACCGAGA
- AGTCAG

GAM133 211 CYP24A1 1 6890 NP_000773.1 5 22 AACGCAGCGCCA - ACCCT T 1 B c c

GCAGCATCTCAT TGA ATGCT GCTGGC CT
CTACCCTC ACT TACGA CGACCG GA
C ----- C

GAM133 211 DKFZp43 1 11319 NP_115624.1 3 1008 CCCCAACAGCCA AT C- C 1 B c c

4F1719 GCAGCAGTGGCC TGA GCTAC CTGCTGGCT
CTCATCAC ACT CGGTG GACGACCGA
CC AC C

GAM133 211 DKFZp66 1 10447 XP_290795.1 5 18 CTGTAGGGAATC AC G --- 1 B c c

7M2411 CAGAAGGAGCAT TGAATGCT CCT CTGG CTCT
TCATGAAG ACTTACGA GGA GACC GGGA
-- A TAA

GAM133 211 DKFZp76 1 9664 NP_612212.1 5 740 GGTATGTGCCAG C- T TC 1 B c c

1H2121 CTGGTTTAGCAT TGAATGCTA CC GCTGGC
TCAATATG ACTTACGAT GG CGACCG
TT T TG

GAM133 211 DKFZp76 1 2227 NP_690877.1 3 74 TTGGAGTTTCCA A --- 1 B c c

1L1417 GCAGGGTGGTGT TG ATGCTACCCTGCTGG CTCT
GCACCACT AC TGTGGTGGGACGACC GAGG
G TTT

GAM133 211 EREG 1 11651 NP_001423.1 3 2285 GGCGTGAGCCAC CC -- 1 B c c
CGCACGTAGCAT TGAATGCTAC TGC TGGCTC
TTACATTA ATTTACGATG ACG ACCGAG
C- CC

GAM133 211 EXO70 1 4489 NP_056034.1 3 1508 ACAGGAGAGCCA AATG 1 B c c

GCAGGGTGGATG TG CTACCCTGCTGGCTCT
CAAGGGGC AC GGTGGGACGACCGAGA
GTA-
GAM133 211 FAT2 1 12813 NP_001438.1 3 521 GAGAGGTGAGCA AA A G 1 B c c
GCAGGGGAGCGG TG TGCT CCCTGCTG CTC
GCACAGTC AC GCGA GGGACGAC GAG
GG G -
GAM133 211 FKBPL 1 12297 NP_071393.2 5 85 GGGGCAAGGCTC A ---- G- 1 B c c
CGAGGGCAGCAT TGAATGCT CCCT GCT GCTCT
TCAGTAGC ACTTACGA GGGA CGG CGGGG
C GCCT AA
GAM133 211 FLJ1012 1 10447 NP_060471.1 3 566 CTGTAGGGAATC AC G --- 1 B c c
0 CAGAAGGAGCAT TGAATGCT CCT CTGG CTCT
TCATGAAG ACTTACGA GGA GACC GGGA
-- A TAA
GAM133 211 FLJ1015 1 2393 NP_060483.1 3 1157 GGGTGGAGGATA G C G- 1 B c c
9 ACAGGGTAGATT TGAAT CTACCCTG TG CTCT
CACTTGTG ACTTA GATGGGAC AT GAGG
- A AG
GAM133 211 FLJ1254 1 2066 NP_071764.2 3 220 ATGGGAGAGCCA T--------- GCTA 1 B c
c
1 GCAGGGGTTCTG GAAT CCCTGCTGGCTCT
GAGAAAAA CTTG GGGACGACCGAGA
AAAAAGAGGT ----
GAM133 211 FLJ1264 1 7228 NP_075562.2 5 26 TTTAAGGGCCAG A CTG- 1 B c c
4 GAAAGGAAGCAT TGAATGCT CC CTGGCTCT
TCAGGGAA ACTTACGA GG GACCGGGA
A AAAG
GAM133 211 FLJ1275 1 3004 NP_078943.1 3 1283 GCCCAGGGCCCA AA-- A - 1 B c c
0 GCAGGGGGCAGT TG TGCT CCCTGCTGG CTCT
GGCACCTG AC ACGG GGGACGACC GGGA
GGTG - C
GAM133 211 FLJ2028 1 5478 NP_060212.1 3 500 CAGGAGCAGCCA TACC C 1 B c
c
1 GCAGTGCATTCA TGAATGC CTGCTGGCT
CCCCACTT ACTTACG GACGACCGA
T--- C
GAM133 211 FLJ2071 1 13390 NP_060408.2 3 1017 TGTTGAGACCAG ACCC - - 1 B c
c
6 TCATGACAGCAT TGAATGCT TG CTGG CTC
TCAAGATT ACTTACGA AC GACC GAG
CAGT T A
GAM133 211 FLJ2167 1 18661 NP_112160.1 5 735 TTCAGGGCCTAG A G- - 1 B c c
3 GAAGGGGAGCAT TGAATGCT CCCT CT GGCTCT
TCAGGAAC ACTTACGA GGGA GA CCGGGA
G AG T
GAM133 211 FLJ2506 1 8347 NP_689717.2 3 203 TATGGAGAGCCA T-- G --- 1 B c c
7 GCAGGGTCTGGG GAAT CT ACCCTGCTGGCTCT

AGTTCTCC CTTG GG TGGGACGACCGAGA
CCT A GTC

GAM133 2116 FLJ3116 1 2122 NP_694567.1 5 0 AGATTAGCAGGG TGC C 1 B c c
TGACTTTCACCC TGAA TACCCTGCTGG TCT
TGCAACAG ACTT GTGGGACGATT AGA
TCA -

GAM133 2119 FLJ3206 1 7828 NP_694578.1 5 94 TGCCCAGAGCCA A --- G 1 B c c
GAGGGATGGTGG TGA TGCTACC CT CTGGCTCT
TAGTCACG ACT ATGGTGG GG GACCGAGA
G TAG A

GAM133 2119 FLJ3291 1 1007 NP_653189.2 5 183 CTCACGGAGCCA A G --- 1 B c c
GCGGCCGGGTAG TG AT CTACCC TGCTGGCTCT
GATGCAGA AC TA GATGGG GCGACCGAGG
G G CCG

GAM133 211 FUT1 1 5184 NP_000139.1 3 61 TTTCTAGAGCCA T C-- 1 B b b
GCAGTACGTGGC TGAA GCTAC CTGCTGGCTCT
TTCAGAGG ACTT CGGTG GACGACCGAGA
- CAT

GAM133 211 GALNT10 1 16339 NP_060010.2 3 1156 TTAAAGGAGCCA A C-- - - 1 B c c

GCCAGGTGTAAT TGA TG TAC CCTG CTGGCTCT
ACAGTCAA ACT AC ATG GGAC GACCGAGG
G ATA T C

GAM133 211 GNG11 1 1974 NP_004117.1 5 210 CTGGGGACCGCA A TA -- - 1 B c c
GCAGGGCTGCAG TGA TGC CCCTGCT GG CTCT
TCACATCC ACT ACG GGGACGA CC GGGG
G TC CG A

GAM133 211 HEMK 1 2688 NP_057257.1 3 2392 GAGATGGAGCCA AAT- --- 1 B c c
GCAGGCTGGTAG TG GCTACC CTGCTGGCTCT
CCTGGCAG AC CGATGG GACGACCGAGG
GGTC TCG

GAM133 211 HOXC8 1 15450 NP_073149.1 5 72 CCCGGGGAGCCA G C- T 1 B c c

GCTGGCCTGGGG TGAAT CTA CC GCTGGCTCT
TTCGGTCC GCTTG GGT GG CGACCGAGG
G CC T

GAM133 211 IRF7 2 2970 NP_004021.1 3 274 CACAGACCCCCA T------ C C-- 1 B c c
GCAGGTAGCATT GAATGCTACC TGCTGG TCT
CCCCAGCC CTTACGATGG ACGACC AGA
CCGACCC - CCC

GAM133 211 IRF7 2 19298 NP_004021.1 3 274 CCACAGACCCCC T----- C C-- 1 B c c
AGCAGGTAGCAT GAATGCTACC TGCTGG TCT
TCCCCAGC CTTACGATGG ACGACC AGA
CGACCC - CCC

GAM133 2110 KIAA009 1 9336 NP_055862.1 3 50 AGTGGAGAGCCA --- A TG 1 B c c
GGGGAGTGTGGG TGA ATGCT CCC CTGGCTCT
TCAGATAA ACT TGTGA GGG GACCGAGA
GGG - --

GAM133 2111 KIAA093 1 11269 XP_041191.2 3 3192 ACGGAAGAGCCA -- AC- 1 B c c
GCAGGAGCAGCG TGA ATGCT CCTGCTGGCTCT

TGGTCATT ACT TGCGA GGACGACCGAGA
GG CGA
GAM133 211 KIAA160 1 6810 XP_049351.2 3 2141 GACCTAGAGCCA AT ACC 1 B c c
0 GTAGAAGCTCTC TGA GCT CTGCTGGCTCT
ACAGTGAG ACT CGA GATGACCGAGA
CT A--
GAM133 211 LNK 1 15247 NP_005466.1 3 1383 TCTTGGGTGCCA - ACC T 1 B c c
GCAGAGCCATTC TGAATG CT CTGCTGGC CT
AGTACAAC ACTTAC GA GACGACCG GG
C --- T
GAM133 211 LOC1308 1 11094 XP_065904.1 3 640 TCTTTGAAGCCA -- CCC C 1 B c c
13 GCATCCTAGCAT TGA ATGCTA TGCTGGCT
CTTCAAAT ACT TACGAT ACGACCGA
TC CCT A
GAM133 211 LOC1470 1 18953 XP_097182.1 3 921 CCTTAAGAGGCA CC C- G 1 B c c
80 TCCAAGTAGCAT TGAATGCTAC TG TG CTCT
TCATAGTG ACTTACGATG AC AC GAGA
A- CT G
GAM133 211 LOC1501 1 13132 XP_097823.1 5 1223 ACTTCAGAGCCA AT C 1 B b b
57 GCAGTGTGGCTC TGA GCTAC CTGCTGGCTCT
AGGTGCCA ACT CGGTG GACGACCGAGA
-- T
GAM133 211 LOC1511 1 1582 XP_087117.1 5 146 GCAGAATGGGCT AT CT 1 B c c
78 CCAGGGTAGCTC TGA GCTACCCTG GGCTC
TCAGAACA ACT CGATGGGAC TCGGG
CT C-
GAM133 211 LOC1520 1 16013 XP_087384.2 3 185 TTTTTAGAGCCA CCCT 1 B c c
98 GTCAAATGGTAT TGAATGCTA GCTGGCTCT
TTAAGTTA ATTTATGGT TGACCGAGA
AAAC
GAM133 211 LOC1522 1 17068 XP_098188.1 5 145 AGGGCAGAGGAA AA C GG 1 B c c
86 GCAGGGTACAGA TG TG TACCCTGCT CTCT
CAGGAGAA AC AC ATGGGACGA GAGA
AG - AG
GAM133 211 LOC1538 1 6064 XP_087779.2 3 762 GGGGCCAAGGCA A --- -- 1 B c c
11 AAGGGGAAGCAT TGAATGCT CCCT GCT GGCTCT
TCACAGAC ACTTACGA GGGG CGG CCGGGG
A AAA AA
GAM133 211 LOC2000 1 19333 XP_086515.7 5 342 CCTGAGGAGCCA AA TAC 1 B c c
30 GCGGGCCGCAAG TG TGC CCTGCTGGCTCT
CAAGTTGC AC ACG GGGCGACCGAGG
GA CC-

GAM133 211 LOC2002 1 14264 XP_114152.1 3 711 GCTCAGGAGCCA T----- G A 1 B c c
05 GCAGGGCAGAGT GAAT CT CCCTGCTGGCTCT
TCTGCCTG CTTG GA GGGACGACCGAGG
GTCCGT A C
GAM133 211 LOC2006 1 19040 XP_117256.1 5 3092 AATCAAAAGAGA T----- GG 1 B c c
09 GCAGGGTGGTAT GAATGCTACCCTGCT CTCT
TCTACAAA CTTATGGTGGGACGA GAGA
AAACAT --
GAM133 211 LOC2207 1 13763 XP_167548.3 5 2428 TGTTTTTGGGGGG A CTGG 1 B c c
39 AACAGGGAGCAT TGAATGCT CCCTG CTCT
TCACAGGG ACTTACGA GGGAC GGGG
- AA--
GAM133 211 LOC2230 1 880 NP_667339.1 5 102 CTGCTGGAGCCA AAT TA - 1 B c c
82 GCGAGGGGTGCC TG GC CCCT GCTGGCTCT
TGCAGCCG AC CG GGGA CGACCGAGG
GTC TG G
GAM133 211 LOC2837 1 3741 XP_211199.1 5 4511 GTGGATGGGCAG - G G C 1 B c c
78 AAGGTGTAGCAT TGAATGCTAC CCT CTG CT
TCGGAGAT GCTTACGATG GGA GAC GG
T A G T
GAM133 211 LOC2838 1 16248 XP_211225.1 3 1536 GTAAAAGGGGCA AATG G 1 B c c
34 GCAGGGTAGAGC TG CTACCCTGCTG CTCT
AGGTGATG AC GATGGGACGAC GGGA
GA-- G
GAM133 211 LOC2840 1 12843 XP_211322.1 5 232 GAAGAGGAGCCA CTAC - 1 B c c
80 GCCAGGTCTTCA TGAATG CCTG CTGGCTCT
TTCAAACC ACTTAC GGAC GACCGAGG
TTCT C
GAM133 211 LOC2844 1 2956 XP_211449.1 5 292 AGCACTGAGCCA ATG AC 1 B c c
10 GCAGGAAGGATC TGA CT CCTGCTGGCTC
TCACAGGT ACT GG GGACGACCGAG
CTA AA
GAM133 211 LOC2844 1 4523 XP_209201.1 3 253 CACAGACAGCCA A A C 1 B c c c
31 GCAGGGGGCGTC TGA TGCT CCCTGCTGGCT
GGAGAACT GCT GCGG GGGACGACCGA
- - C
GAM133 211 LOC2846 1 3697 XP_208231.1 3 339 CTTGGCAAGCCA A C C 1 B c c c
42 GCAGGCTGGTAC TGA TGCTA CCTGCTGGCT
TCGGACCG GCT ATGGT GGACGACCGA
C C A
GAM133 211 LOC2848 1 13866 XP_211642.1 3 249 TCCTAAGAGCCA AT C - 1 B c c c
03 GGCATGGTGGCT TGA GCTACC TGC TGGCTCT

CATGCCTG ACT CGGTGG ACG ACCGAGA
-- T G
GAM133 211 LOC2848 1 11970 XP_209378.1 3 209 GATTCAGGGCCA A CT C 1 B c c
34 GCAGGTTTCACT TGA TG ACC TGCTGGCTCT
CAGCTCTC ACT AC TGG ACGACCGGGA
C TT -
GAM133 211 LOC2848 1 8371 XP_211671.1 5 213 CTCTGCTAGCCA A - C C 1 B c c
57 GCAGAGTGAGCA TG ATGCT AC CTGCTGGCT
TGCACAGC AC TACGA TG GACGACCGA
G G A T
GAM133 211 LOC2854 1 10677 XP_211890.1 5 381 GAGCCACAGCCA CT- C- C 1 B c c
19 GCAGTAGTCCTC TGAATG AC CTGCTGGCT
ATTCAACA ACTTAC TG GACGACCGA
TCC AT C
GAM133 211 LOC2857 1 19478 XP_211991.1 5 393 ATCTCCATGCCA T- T TC 1 B c c
17 GCAGGGTGCCTT TGAA GC ACCCTGCTGGC
TTATATCA ATTT CG TGGGACGACCG
TC - TA
GAM133 211 LOC2858 2 5696 XP_212604.1 5 717 CCCTGGAGAGCA T A G 1 B c c
27 GCAGGGGGCCTT TGAA GCT CCCTGCTG CTCT
CACTCCTG ACTT CGG GGGACGAC GAGA
C - -
GAM133 211 LOC2858 2 13487 XP_212038.1 5 717 CCCTGGAGAGCA T A G 1 B c c
27 GCAGGGGGTCTT TGAA GCT CCCTGCTG CTCT
CACTCCTG ACTT TGG GGGACGAC GAGA
C - -
GAM133 211 LOC2858 2 13487 XP_212645.1 5 717 CCCTGGAGAGCA T A G 1 B c c
27 GCAGGGGGTCTT TGAA GCT CCCTGCTG CTCT
CACTCCTG ACTT TGG GGGACGAC GAGA
C - -
GAM133 211 LOC2859 1 20006 XP_212118.1 5 10 CTTTTAGAGCCA CTA G 1 B c c
86 GAGGGAATTATT TGAATG CCCT CTGGCTCT
TATTAAGC ATTTAT GGGA GACCGAGA
TAA -
GAM133 211 LOC2860 1 13488 XP_212119.1 5 462 GACAAGGAGCCA A G CC 1 B c c
26 GCAGTAGGATCA TGA T CTAC TGCTGGCTCT
AGTGACGC ACT A GATG ACGACCGAGG
- G --
GAM133 211 LOC2861 1 11832 XP_212185.1 3 299 GGAAAGGCATCA T T -- C 1 B c c
26 GCAGGGTGCTTT TGAA GC ACCCTGCTG GCT
CAACCACA ACTT CG TGGGACGAC CGG
T - TA A
GAM133 211 LOC2862 1 19909 XP_212257.1 5 270 GCATTCCAGCCA AT A C 1 B c c

```
          99                          GCAGGGCAGTCT TGA  GCT CCCTGCTGGCT
                                     CAGTGTGG    ACT  TGA GGGACGACCGA
                                              C-  C         C
GAM133   211   LOC2863 1   18912  XP_212305.2  5  12    GCATGAGAGACA   ATGCT      G          1  B  c
c
          84                          GCAGGGTTGTCA TGA    ACCCTGCTG CTCT
                                     CAATATTG    ACT    TGGGACGAC GAGA
                                              GT---       A
GAM133   211   LOC3401 1   16425  XP_291158.1  3  2530  ATCTCCATGCCA   T- T       TC       1  B  c
c
          56                          GCAGGGTGCCTT TGAA  GC ACCCTGCTGGC
                                     TTATATGA    ATTT  CG TGGGACGACCG
                                              TC  -         TA
GAM133   211   LOC3402 1   8452   XP_294634.1  5  736   GGACGGGAGCCA      TAC             1  B  c  c

          68                          GCAGGTCGCGTT TGAATGC   CCTGCTGGCTCT
                                     CGATGACT    GCTTGCG   GGACGACCGAGG
                                               CT-
GAM133   211   LOC3403 1   17510  XP_295216.1  3  197   GGCAGAGGTAGC   A-       --   G       1  B  c  c

          19                          TGAGGGTAGCAT TG  ATGCTACCCT  GCTG CTCT
                                     GGCAGAGG    AC  TACGATGGGA  CGAT GAGA
                                              GG        GT   G
GAM133   211   LOC3495 1   20112  XP_301266.1  5  396   ACACATTGGAGC   --      C  CT        1  B  c  c

          57                          CCATGGTAGCAT TGA  ATGCTACC TG  GGCTCT
                                     CCTCAGCA    ACT  TACGATGG AC  CCGAGG
                                              CC       T  --
GAM133   211   LOC5722 1   15721  NP_065200.1  5  267   AAGATGGAGCCA   A   ACCC            1  B  c
c
          8                           GCACAGCACTCA TGA TGCT   TGCTGGCTCT
                                     TTGCAGTT    ACT ACGA   ACGACCGAGG
                                              C   C---
GAM133   211   LOC9047 1   3057   XP_031975.1  5  15    TCTTGGGAGCCA   A    CC            1  B  c  c
          0                           GCGGTATGGCGT TGA TGCTA  CTGCTGGCTCT
                                     CGGGCTGC    GCT GCGGT  GGCGACCGAGG
                                              -    AT
GAM133   211   LUC7A  1   11723  NP_057508.2  3  583   CTGTAACTCGAG  G    ACCCT           1  B  c
c
                                     AGCCAGTAGCAT T AATGCT    GCTGGCTCT
                                     TGGATTGA    G TTACGA    TGACCGAGA
                                              G     -----
GAM133   211   MASP2  1   1650   NP_631947.1  3  64    AAGCCAGAGCCA   AT   CCCT           1  B  c
c
                                     GCCTGCTGGCCT TGA  GCTA   GCTGGCTCT
                                     CAGCTCCG    ACT  CGGT   CGACCGAGA
                                              C-   CGTC
GAM133   211   MGAT4A 1   18765  NP_036346.1  5  33    GGCCTAGAGCCA      TACC  G          1  B  c
c
                                     GGAGTACTGCAT TGAATGC   CT CTGGCTCT
```

TCAGTTGA ACTTACG GA GACCGAGA
TCAT G
GAM133 211 MGC1124 1 8424 NP_077296.1 3 309 ATGGCAGGGCCA AA A 1 B c c

2 GCAGGGAGGTGG TG TGCT CCCTGCTGGCTCT
GCATGGCA AC GTGG GGGACGACCGGGA
GG A
GAM133 211 MGC2817 1 16603 NP_115900.1 5 265 CGCCCGGAGCCA A ACCCT 1 B c c

GCCGCGCAGCAT TG ATGCT GCTGGCTCT
GCACTGGG AC TACGA CGACCGAGG
G CGCGC
GAM133 211 NMU 1 14657 NP_006672.1 3 3 GAAGAAGGTCAG CT C 1 B c c
CAGGGTTCATTT TGAATG ACCCTGCTGGCT
AAATGGAT ATTTAC TGGGACGACTGG
T- A
GAM133 211 NTSR1 1 2175 NP_002522.1 3 1939 GACTCAGAGCCA AT A - 1 B c c
GACAGGGCAGCC TGA GCT CCCTG CTGGCTCT
TCAGACCC ACT CGA GGGAC GACCGAGA
C- C A
GAM133 211 NUMA1 1 9820 NP_006176.1 3 419 GTGGCTGGGCCA AT TA 1 B c c

GCAGGGGCCCTC TGA GC CCCTGCTGGCTC
ACTCTTGA ACT CG GGGACGACCGGG
CC --
GAM133 211 OPA3 1 4447 NP_079412.1 3 187 CCACTGGGACCA - AC- - 1 B c c
GCAGGTGAAGCG TG AATGCT CCTGCTGG CTC
TTGCAACA AC TTGCGA GGACGACC GGG
G AGT A
GAM133 211 OSR1 1 15350 NP_005100.1 3 2430 ATCCTAGAGCCA C CCCT 1 B c c

GCTGATAATATT TGAATG TA GCTGGCTCT
TAATAATC ATTTAT AT CGACCGAGA
A AGT-
GAM133 211 PF20 1 1865 NP_078808.2 3 111 TTAAATGTGCCA C C TC 1 B c c
GCAGGTAACATT TGAATG TACC TGCTGGC
TACAGTCT ATTTAC ATGG ACGACCG
A - TG
GAM133 211 PNMA5 1 13736 NP_443158.1 3 577 AGGGGAGCCCCA A --- CT 1 B c c

GGAAGGCAGCAT TGAATGCT CC CTG GGCTCT
TCATAAGC ACTTACGA GG GAC CCGAGG
C AAG C-
GAM133 211 POMT1 1 15100 NP_009102.2 3 323 AACCCAGGGCCA AT A - 1 B c c
GCAGTGGAAGCC TGA GCT CC CTGCTGGCTCT
TCAAGCAA ACT CGA GG GACGACCGGGA
C- A T
GAM133 211 RANBP3 1 1217 NP_015560.1 5 242 TCGCCCCAGTTA AAT C 1 B c c

GCAGGGTGGCTG TG GCTACCCTGCTGGCT

CATTCCAG AC CGGTGGGACGATTGA
GT- C
GAM133 211 RASGRP4 1 10789 NP_443181.2 3 1915 GAGGGTCGAGCA CTA G 1 B c c
GCAGGGGCCCAT TGAATG CCCTGCTG CTC
TCAGTCCC ACTTAC GGGACGAC GAG
CCG -
GAM133 211 RASGRP4 1 10789 NP_733747.1 3 291 GAGGGTCGAGCA CTA G 1 B c c
GCAGGGGCCCAT TGAATG CCCTGCTG CTC
TCAGTCCC ACTTAC GGGACGAC GAG
CCG -
GAM133 211 RASGRP4 1 10789 NP_733748.1 3 291 GAGGGTCGAGCA CTA G 1 B c c
GCAGGGGCCCAT TGAATG CCCTGCTG CTC
TCAGTCCC ACTTAC GGGACGAC GAG
CCG -
GAM133 211 RNF121 1 8732 NP_060790.2 3 183 GATGGAGAGCCA AT A - - 1 B c c
GCCAGTGGGGCT TGA GCT CC CTG CTGGCTCT
GTCAGCAG ACT CGG GG GAC GACCGAGA
GT - T C
GAM133 211 RPE 1 5773 NP_008847.1 5 21 TTTTGGGAGCCA A CC 1 B c c
GCGGTATGGCGT TGA TGCTA CTGCTGGCTCT
CGGGCTGC GCT GCGGT GGCGACCGAGG
- AT
GAM133 211 SELM 1 15560 NP_536355.1 3 132 GTCCCCGGGCCA G G - 1 B c c
GCAGGGATGGGG T AAT CTA CCCTGCTGGCTC
TTGGGGAG G TTG GGT GGGACGACCGGG
G G A
GAM133 211 SLC9A8 1 17493 XP_030524.2 3 3509 AATAAAGAGCCA CTACCCT 1 B c c
GCCCCCTTCCAT TGAATG GCTGGCTCT
TTAGTCTC ATTTAC CGACCGAGA
CTTCCCC
GAM133 211 TCF7 1 15351 NP_003193.1 3 1271 CAGCCAGAGCCT ACCCT T 1 B c c
GTCTTTCAGCAT TGAATGCT GC GGCTCT
TCAGTCGC ACTTACGA TG CCGAGA
CTTTC T
GAM133 211 TIEG 1 6313 NP_005646.1 5 67 GCCAAGCAGCCA AA CC C 1 B c c
GCAGCCTAGCAG TG TGCTA CTGCTGGCT
CCAGTCAG AC ACGAT GACGACCGA
CG CC C
GAM133 211 UBE2J2 1 7344 NP_477515.1 3 1004 ACGCCAGAGCCA T TA- 1 B c c
GCAGGGGCTGTT TGAA GC CCCTGCTGGCTCT
TCGGGCCG GCTT TG GGGACGACCGAGA
- TCG
GAM133 211 ZNF6 1 740 NP_068838.2 5 433 GGATGAGAGCCA GC C T 1 B c c
GTGGATGAAATT TGAAT TA CC GCTGGCTCT
CACTAATA ACTTA GT GG TGACCGAGA

AA A -
GAM134 339 FLJ1287 1 19411 3 GAAAAAATGGCG TCAC C 3 C c c
6 TGCCTTGTG CACAGGGT CGCCATTT TTC
GTGTTCCG GCGGTAAA AAG
T--- A
GAM134 339 FLJ1384 1 3226 NM_024645.1 3 GAAGAAATGGCG CA TTCA 3 C c c
2 GCCTTG CAGGG CCGCCATTTCTTC
GTTCC GGCGGTAAAGAAG
-- ----
GAM134 339 IL18RAP 1 3711 NM_003853.2 5 GAAGAAATATAG C - CGCC 3 C c c
TAGAACCCTTTG CA AGGGTTC AC ATTTCTTC
GT TCCCAAG TG TAAAGAAG
T A ATA-
GAM134 339 LOC2563 1 19605 XM_171128.2 5 GAAGAGTACCTG CCAT 3 C c c
80 GTGAACCCTGTG CACAGGGTTCACCG TTCTTC
GTGTCCCAAGTGGT GAGAAG
CCAT
GAM134 339 MAP3K7I 1 9771 NM_006116.1 3 GAAGAGGCGCCC C ---- ATT 3 C c c
P1 TGTGAACCCTGT ACAGGGTTCAC CGCC TCTTC
TGTCCCAAGTG GCGG AGAAG
- TCCC ---
GAM134 339 SCIN 1 6572 NM_033128.1 5 GAAGAAGGAAGT C C CG AT 3 C c c
GAACCCTCA A AGGGTTCAC CC TTCTTC
A TCCCAAGTG GG AAGAAG
- C AA --
GAM134 339 SH3BP2 1 4548 NM_003023.2 3 GAAGAGGGGCAG T C A 3 C c c
TGACCCTGTG CACAGGGT CAC GCC TTTCTTC
GTGTCCCA GTG CGG GGAGAAG
- A -
GAM134 339 SOX30 1 7345 NM_007017.1 3 GAAGAAAACTTA CACCGCCA 3 C c
c
AACCCTGTG CACAGGGTT TTTCTTC
GTGTCCCAA AAAGAAG
ATTCA---
GAM135 248 HEM1 1 11852 NM_005337.1 5 CCTCTGCACCTG C C ACAA 3 C c c
CATGAGAACCC GGGTTCTCA GCA CGGAGG
CCCAAGAGT CGT GTCTCC
- A CCAC
GAM135 248 KIAA065 1 11853 NM_014741.1 5 CTCCGTAATGAG CGCAACA G 3 C c
c
2 AGCCCG CGGGTTCTCA ACGGAG
GCCCGAGAGT TGCCTC
AA----- -
GAM135 248 SEMA4B 1 1258 XM_044533.9 3 CCTCCGTTGTTG 3 C a a
CGTGAGAACCCG CGGGTTCTCACGCAACAACGGAGG
GCCCAAGAGTGCGTTGTTGCCTCC
GAM136 279 AAK1 1 3779 NM_014911.2 3 TGGCAAGATCTC A G 3 C b b

GGCTCACTGCAG CTGCAGTGAGCC AGATC TGCCA
GACGTCACTCGG TCTAG ACGGT
C A
GAM136 279 ABLIM 1 19479 3 GCACGTGGCTCA CT AGAT CA 3 C c c
CTGC GCAGTGAGCCA CGTGC
CGTCACTCGGT GCACG
-- ---- --
GAM136 279 ACADSB 1 15884 NM_001609.1 3 TGGCGCGATCTC CA 3 C b b
AGCTCACTGCAG CTGCAGTGAGC AGATCGTGCCA
GACGTCACTCG TCTAGCGCGGT
AC
GAM136 279 ADCY6 1 17168 NM_020983.2 5 TGGCGCGATCTT C C 3 C b b
TGCTCACTGCA TGCAGTGAGC AAGATCGTGCCA
ACGTCACTCG TTCTAGCGCGGT
- T
GAM136 279 AHR 1 4473 NM_001621.2 3 TGGCACAATCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTCTA CACGGT
- A
GAM136 279 AIM1 1 19229 XM_166300.1 3 TGGCACAATCAC AA C 3 C b b
GGCTCACTGCAG CTGCAGTGAGCC GAT GTGCCA
GACGTCACTCGG CTA CACGGT
CA A
GAM136 279 APM1 2 1915 NM_004797.1 3 TGGCATGATCTC C A 3 C c c
GGCTTACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCATTCGG TCTAGTACGGT
- C
GAM136 279 APM1 2 10876 NM_004797.1 3 TGACACGACCTC A A C 3 C c c
GGCTCACTGCAG CTGCAGTGAGCC AG TCGTG CA
GACGTCACTCGG TC AGCAC GT
C C A
GAM136 279 APOL2 1 3227 NM_145637.1 3 TGGCTCAATCTC C A CGT 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GCCA
ACGTCACTCGG TCTA CGGT
- C ACT
GAM136 279 APPBP2 1 15503 NM_006380.2 3 TGGCACCGTCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTCTG CACGGT
- C
GAM136 279 APXL2 1 12429 5 TGGCGCGATCTC C C A 3 C c c
GGCTCACTACA TG AGTGAGCC AGATCGTGCCA
AC TCACTCGG TCTAGCGCGGT
- A C
GAM136 279 ARHF 1 10691 NM_019034.1 5 TGGCATGATCTT C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGATCGTGCCA
ACGTCACTCGGTTCTAGTACGGT
-
GAM136 279 ASB16 1 16106 NM_080863.4 3 TGGCGCTATCTC C A C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TCTA CGCGGT

						- C T						
GAM136	279 1	ATP6V1A	1	2154	NM_001690.2	5 GGCTCACTGCAG CTGCAGTGAGCCAAGATCGTGCCA GACGTCACTCGGTTCTAGTGCGGT	TGGCGTGATCTT				3	C b b
GAM136	279	ATP7A	1	12838	NM_000052.1	3 GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA ACGTCACTCGGTTCTA CACGGT	TGGCACCATCTT C		C		3	C b b
						- C						
GAM136	279	ATP8B2	1	8818	XM_290875.1	5 AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA ACGTCACTCG TCTA CACGGT	TGGCACAATCTC C		CA C		3	C c c
						- AC A						
GAM136	279	B4GALT5	1	16556	NM_004776.2	3 AGCTCACTGCAG CTGCAGTGAGC GATCGTGCCA GACGTCACTCG CTAGCACGGT ACA	TGGCACGATCAC		CAA		3	C b b
GAM136	279 .2	BA108L7	1	411	NM_030971.1	5 GGCTCACTGCA TGCAGTGAGCCAAGATCG CCA ACGTCACTCGGTTCTAGC GGT	TGGTGCGATCTT C			TG	3	C b b
						- GT						
GAM136	279	BCL10	1	5479	NM_003921.2	3 GGCTCACTGCA TGCAGTGAGCC AGA GTGCCA ACGTCACTCGG TCT CGCGGT	TGGCGCATTCTA C		A TC		3	C c c
						- A TA						
GAM136	279	BDKRB1	1	3577	NM_000710.2	5 AGCTCGCTGCAG CTGCAGTGAGC GAT GTGCCA GACGTCGCTCG CTA CACGGT ATA A	TGGCACAATCAT		CAA C		3	C c c
GAM136	279	BTN3A1	1	17443	NM_007048.2	3 AGCTCCCTGCA TGCAG GAGC AGATCG CCA ACGTC CTCG TCTAGC GGT	TGGTGCGATCTC C		T CA	TG	3	C c c
						- C AC GT						
GAM136	279	C14orf1	1	15476	NM_007176.1	3 TCACTGC GCAGTGAG GAT GTGCCA CGTCACTC CTA CACGGT	TGGCACAATCCC CT		CCAA C		3	C c c
						-- C--- A						
GAM136	279 9	C22orf1	1	8914	NM_003678.2	3 GGCTCACTGC GCAGTGAGCC TCGTGCCA CGTCACTCGG AGCACGGT CACA	TGGCACGAACAC CT		AAGA		3	C c c
						--						
GAM136	279	C5orf4	1	7970	NM_032385.1	5 ACTGCAG CTGCAGTG GC GTG CCA GACGTCAC CG CAC GGT C A------ A	TGGACACAGCCC		A CAAGATC	-	3	C c c
GAM136	279	C6orf5	1	18128		3 AGCTCACTGCAG CTGCAGTGAGC AGAT GTG CA	TGACACAGTCTC		CA C C		3	C c c

GACGTCACTCG TCTG CAC GT
AC A A
GAM136 279 C9orf9 1 8425 NM_018956.2 3 TGGCGCAACCTC C A ATC 3 C c c
GGCTCACTGCA TGCAGTGAGCC AG GTGCCA
ACGTCACTCGG TC CGCGGT
- C CAA
GAM136 279 CARD6 1 5983 NM_032587.2 3 TGGCACGATCTC C A A 3 C c c
GGCTCACCGCA TGC GTGAGCC AGATCGTGCCA
ACG CACTCGG TCTAGCACGGT
- C C
GAM136 279 CCRN4L 1 1330 NM_012118.1 3 TGGCCTGATCTC C A T 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGATCG GCCA
ACGTCACTCGG TCTAGT CGGT
- C C
GAM136 279 CDC14B 1 13617 NM_033332.1 3 TGGCGCGATCTA C A 3 C b b
GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TCTAGCGCGGT
- A
GAM136 279 CEACAM8 1 3822 NM_001816.2 3 TGGCACGATCTC C CCA 3 C c c

AACTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGCACGGT
- AAC
GAM136 279 CHRAC1 1 14719 NM_017444.3 3 TGGCGCTGTCTC C CA C 3 C c c

AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTG CGCGGT
- AC T
GAM136 279 CLECSF1 2 10748 NM_022570.2 3 TGGCACAATCTC CCA C 3 C c c

2 GACTCACTGCAG CTGCAGTGAG AGAT GTGCCA
GACGTCACTC TCTA CACGGT
AGC A
GAM136 279 CLECSF1 2 14434 NM_022570.2 3 GGCACGATCTCG C A A A 3 C c c

2 GCTCACCGCA TGC GTGAGCC AGATCGTGCC
ACG CACTCGG TCTAGCACGG
- C C -
GAM136 279 CNN2 1 7340 NM_004368.1 5 TGGCGCCATCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTCTA CGCGGT
- C
GAM136 279 CPSF2 1 5334 XM_029311.2 3 TGGCACACGATC C A A -- 3 C c c
TCGGCTCACCGC TGC GTGAGCC AGATC GTGCCA
A ACG CACTCGG TCTAG CACGGT
- C C CA
GAM136 279 CR1 1 17680 NM_000651.3 3 TGGCGTAATCTC C A CG 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT TGCCA
ACGTCACTCGG TCTA GCGGT
- C AT

GAM136 279 CRTAP 1 18368 NM_006371.2 3 TGGCACGTTCTC C CA T 3 C c c
AGCTCACTGCA TGCAGTGAGC AGA CGTGCCA
ACGTCACTCG TCT GCACGGT
- AC T
GAM136 279 CYP1A2 2 414 NM_000761.2 3 TGGCGCGATCTC C C CA 3 C c c
AGCTCACTACA TG AGTGAGC AGATCGTGCCA
AC TCACTCG TCTAGCGCGGT
- A AC
GAM136 279 CYP1A2 2 6233 NM_000761.2 3 TGGCATCATCTC C CA C 3 C c c
AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTA TACGGT
- AC C
GAM136 279 DBR1 1 3140 NM_016216.1 5 TGGCGTGATCTC C A A 3 C c c
GGCTCACCGCA TGC GTGAGCC AGATCGTGCCA
ACG CACTCGG TCTAGTGCGGT
- C C
GAM136 279 DCOHM 1 2472 NM_032151.2 3 TGGCACGATCTT 3 C a a
GGCTCACTGCAG CTGCAGTGAGCCAAGATCGTGCCA
GACGTCACTCGGTTCTAGCACGGT

GAM136 279 DFFB 1 1322 NM_004402.1 3 TGATGCAATCTT C C GC 3 C c c
GGCTCACTGCA TGCAGTGAGCCAAGAT GT CA
ACGTCACTCGGTTCTA CG GT
- A TA
GAM136 279 DKFZp54 1 5775 NM_020161.1 3 GCGTGATCTCAG C CA CA 3 C c c

7H025 CTCACTGCA TGCAGTGAGC AGATCGTGC
ACGTCACTCG TCTAGTGCG
- AC --
GAM136 279 DKFZP56 1 2023 NM_030658.2 3 TGGCATGATTGT CAA 3 C b b
4D166 AGCTCACTGCAG CTGCAGTGAGC GATCGTGCCA
GACGTCACTCG TTAGTACGGT
ATG
GAM136 279 DKFZP56 1 17506 NM_032040.1 3 TGGCATGATCAT CCAA 3 C b b
4K0322 AACTCACTGCAG CTGCAGTGAG GATCGTGCCA
GACGTCACTC CTAGTACGGT
AATA
GAM136 279 DKFZp76 1 6234 XM_086327.6 3 TGGCGTCATCTC C A CG 3 C c c
1N1114 GGCTCACTGCA TGCAGTGAGCC AGAT TGCCA
ACGTCACTCGG TCTA GCGGT
- C CT
GAM136 279 DKFZp76 1 14313 NM_018409.1 5 TGATGCAATCTT A C GC 3 C c c
1O0113 GGCTCACCGCAG CTGC GTGAGCCAAGAT GT CA
GACG CACTCGGTTCTA CG GT
C A TA
GAM136 279 DSCR6 1 14099 NM_018962.1 3 TGACACAATCTC C A C C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTG CA
ACGTCACTCGG TCTA CAC GT
- C A A
GAM136 279 EPB72 1 5774 3 GCATGATCTCGG C A CA 3 C c c

CTCACTGCA TGCAGTGAGCC AGATCGTGC
ACGTCACTCGG TCTAGTACG
- C --
GAM136 279 F2RL2 1 13299 NM_004101.1 3 TGGCACTATCTT C C 3 C b b
GGCTCATTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTTACTCGGTTCTA CACGGT
- T
GAM136 279 F3 1 5697 NM_001993.2 5 GCACGATCTCGG C A CA 3 C c c
CTCACTGCA TGCAGTGAGCC AGATCGTGC
ACGTCACTCGG TCTAGCACG
- C --
GAM136 279 FBP17 1 13681 3 TGGCATGATCTC C C A 3 C c c
GGCTCACTACA TG AGTGAGCC AGATCGTGCCA
AC TCACTCGG TCTAGTACGGT
- A C
GAM136 279 FCAR 1 14197 NM_002000.2 3 TGGCACGATCTC C CCA 3 C c c
GACTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGCACGGT
- AGC
GAM136 279 FCRH1 1 11769 NM_052938.2 3 TGGCACAATCTT C C C 3 C c c
GCCTCACTGCA TGCAGTGAG CAAGAT GTGCCA
ACGTCACTC GTTCTA CACGGT
- C A
GAM136 279 FER1L4 1 6674 XM_300246.1 3 TGGCACGATCTC C G A 3 C c c
GGCTGACTGCA TGCAGT AGCC AGATCGTGCCA
ACGTCA TCGG TCTAGCACGGT
- G C
GAM136 279 FEZ1 1 4839 NM_005103.3 3 TGGCACAATTTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTTTA CACGGT
- A
GAM136 279 FKBP9 1 19504 NM_007270.1 3 GCACTGTCTCGG A C CA 3 C c c
CTCACTGCAG CTGCAGTGAGCC AGAT GTGC
GACGTCACTCGG TCTG CACG
C T --
GAM136 279 FLJ1095 1 10208 NM_018283.1 3 TGGCACGATCTC CA 3 C b b
6 AGCTCATTGCAG CTGCAGTGAGC AGATCGTGCCA
GACGTTACTCG TCTAGCACGGT
AC
GAM136 279 FLJ1146 1 1757 NM_024963.2 3 TGGCGTGATCAC CAA 3 C b b
7 AGCTCACTGCAG CTGCAGTGAGC GATCGTGCCA
GACGTCACTCG CTAGTGCGGT
ACA
GAM136 279 FLJ1171 1 12430 NM_024846.1 3 TGGCACAATCAA CAA C 3 C c c
0 AGCTCACTGCAG CTGCAGTGAGC GAT GTGCCA
GACGTCACTCG CTA CACGGT
AAA A
GAM136 279 FLJ1180 1 16539 NM_024974.1 3 TGGCACAATCAA AA C 3 C b b
0 GGCTCACTGCAG CTGCAGTGAGCC GAT GTGCCA
GACGTCACTCGG CTA CACGGT

AA A

GAM136 279 FLJ1289 1 15272 NM_024950.1 3 TGGCGCCGTCTC C A C 3 C c c
1 GGCTCACTACAG CTG AGTGAGCC AGAT GTGCCA
GAC TCACTCGG TCTG CGCGGT
A C C

GAM136 279 FLJ1297 1 7618 NM_024908.1 3 GCGCGATCTTGG C A CA 3 C c c
3 CTCACCGCA TGC GTGAGCCAAGATCGTGC
ACG CACTCGGTTCTAGCGCG
- C --

GAM136 279 FLJ1319 1 12298 3 TGGCAGGATCTC CA G 3 C c c
3 AGCTTACTGCAG CTGCAGTGAGC AGATC TGCCA
GACGTCATTCG TCTAG ACGGT
AC G

GAM136 279 FLJ1345 1 19891 XM_038291.5 3 TGGCACAATCAT CCAA C 3 C c c
6 ACCTCACTGCAG CTGCAGTGAG GAT GTGCCA
GACGTCACTC CTA CACGGT
CATA A

GAM136 279 FLJ1435 1 14477 NM_024732.1 3 TGGCAGTGTCAT A CG 3 C c c
1 GGCTCACTGCAG CTGCAGTGAGCCA GAT TGCCA
GACGTCACTCGGT CTG ACGGT
A TG

GAM136 279 FLJ1480 1 5984 NM_032842.1 3 TGGCACGATCTT C C C 3 C c c
3 AGCTCACTACA TG AGTGAGC AAGATCGTGCCA
AC TCACTCG TTCTAGCACGGT
- A A

GAM136 279 FLJ1495 1 16340 NM_032866.1 3 TGGCGCAACCTT C ATC 3 C c c
7 GGCTCACTGCA TGCAGTGAGCCAAG GTGCCA
ACGTCACTCGGTTC CGCGGT
- CAA

GAM136 279 FLJ2000 1 14892 3 TGGCACGATCTG C A 3 C b b
4 GGCTCATTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTTACTCGG TCTAGCACGGT
- G

GAM136 279 FLJ2014 1 15668 NM_017687.1 3 TGACATGATCAT CAA C 3 C c c
7 AGCTCACTGCAG CTGCAGTGAGC GATCGTG CA
GACGTCACTCG CTAGTAC GT
ATA A

GAM136 279 FLJ2034 1 12081 NM_017774.1 3 TGGCACGATCTC C G A- 3 C b b
2 AGGTCACTGCA TGCAGTGA CC AGATCGTGCCA
ACGTCACT GG TCTAGCACGGT
- - AC

GAM136 279 FLJ2070 1 7187 NM_017932.1 3 TGGTGCGACCTC C A A TG 3 C c c
0 GGCTCACTGCA TGCAGTGAGCC AG TCG CCA
ACGTCACTCGG TC AGC GGT
- C C GT

GAM136 279 FLJ2160 1 17662 3 TGGCATAATCTC C A CG 3 C c c
3 GGCTCACTGCA TGCAGTGAGCC AGAT TGCCA
ACGTCACTCGG TCTA ACGGT
- C AT

GAM136 279 FLJ2302 1 8420 NM_014150.1 3 TGGCACAACCTC C CA ATC 3 C c c

4 AGCTCACTGCA TGCAGTGAGC AG GTGCCA
ACGTCACTCG TC CACGGT
- AC CAA

GAM136 279 FLJ2335 1 17951 NM_032237.2 3 TGATCTTGGCTC TGCCA 3 C c c
6 ACTGCAG CTGCAGTGAGCCAAGATCG
GACGTCACTCGGTTCTAGT

GAM136 279 FLJ2339 1 2537 NM_024784.2 3 TGGCGCAATTTC C CA C 3 C c c
2 AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TTTA CGCGGT
- AC A

GAM136 279 FLJ2341 1 5179 NM_032238.1 3 CGATCATGGCTC A TGCCA 3 C c c

6 ACTGCAG CTGCAGTGAGCCA GATCG
GACGTCACTCGGT CTAGC
A -----

GAM136 279 FLJ2355 1 10048 NM_024880.1 3 TGGGATCTCGCC C CCA GTG 3 C c
c
6 TCACTGCA TGCAGTGAG AGATC CCA
ACGTCACTC TCTAG GGT
- CGC ---

GAM136 279 FLJ2356 1 3685 XM_041701.5 3 TGGCACAATCTC C A C 3 C c c
3 GGTTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTTGG TCTA CACGGT
- C A

GAM136 279 FLJ3249 1 8773 NM_144607.1 3 TGGCAAAATCAT A CG 3 C b b
9 GGCTCACTGCAG CTGCAGTGAGCCA GAT TGCCA
GACGTCACTCGGT CTA ACGGT
A AA

GAM136 279 FLJ3286 1 3736 NM_144613.1 3 TGATGCGATCTC C CA GC 3 C c c
5 AGCTCACTGCA TGCAGTGAGC AGATCGT CA
ACGTCACTCG TCTAGCG GT
- AC TA

GAM136 279 GHR 1 15462 NM_000163.1 3 TGGCGCGATCTT C C 3 C b b
GACTCACTGCA TGCAGTGAG CAAGATCGTGCCA
ACGTCACTC GTTCTAGCGCGGT
- A

GAM136 279 GOLGA3 1 10858 NM_005895.1 3 TGGCACACTCTC C CA TC 3 C c
c
CGCTCACTGCA TGCAGTGAGC AGA GTGCCA
ACGTCACTCG TCT CACGGT
- CC CA

GAM136 279 GP5 1 13821 NM_004488.1 3 GGCCGTCTCAGT CA T T A 3 C c c
TCACTGCAG CTGCAGTGAGC AGA CG GCC
GACGTCACTTG TCT GC CGG
AC - - -

GAM136 279 GR6 1 16362 NM_007354.1 5 TGGCATGATCTT CTG 3 C c c
GGCTCACTG CAGTGAGCCAAGATCGTGCCA
GTCACTCGGTTCTAGTACGGT

GAM136 279 GRM6 1 19400 NM_000843.2 3 TGGCACGATCAT CTG CAA 3 C c c

AGCTCACTG CAGTGAGC GATCGTGCCA
GTCACTCG CTAGCACGGT
--- ATA

GAM136 279 GRWD 1 19632 NM_031485.1 3 GCACGATCTTGG C CA 3 C c c
CTCACTGCA TGCAGTGAGCCAAGATCGTGC
ACGTCACTCGGTTCTAGCACG
- --

GAM136 279 GTPBG3 2 14680 NM_032620.1 3 TGGTGCGACCTT C A TG 3 C c c
GGCTCACTGCA TGCAGTGAGCCAAG TCG CCA
ACGTCACTCGGTTC AGC GGT
- C GT

GAM136 279 GTPBG3 2 18851 NM_032620.1 3 TGGTGCGACCTC C A A TG 3 C c
c

GGCTTACTGCA TGCAGTGAGCC AG TCG CCA
ACGTCATTCGG TC AGC GGT
- C C GT

GAM136 279 HCA4 1 5223 3 TGGCACAATCTT C G C 3 C c c
GGCTCAGTGCA TGCA TGAGCCAAGAT GTGCCA
ACGT ACTCGGTTCTA CACGGT
- G A

GAM136 279 HRH4 1 8519 NM_021624.2 3 TGGCATGCTCTC CA T 3 C c c
AGCTCACTGCAG CTGCAGTGAGC AGA CGTGCCA
GACGTCACTCG TCT GTACGGT
AC C

GAM136 279 HSPC065 1 19775 NM_014157.2 3 TGGCATGATCTC C A 3 C c c
GGCTCGCTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCGCTCGG TCTAGTACGGT
- C

GAM136 279 HUNK 1 11495 NM_014586.1 3 TGGCACAATCAC CAA C 3 C c c
AGTTCACTGCAG CTGCAGTGAGC GAT GTGCCA
GACGTCACTTG CTA CACGGT
ACA A

GAM136 279 IGSF2 1 8672 NM_004258.1 3 TGGCAGGACGAC CCAAGA G 3 C c
c

TCACTGCGG CTGCAGTGAG TC TGCCA
GGCGTCACTC AG ACGGT
AGC--- G

GAM136 279 IMPACT 1 19776 NM_018439.1 3 TGGCATGATCAT A 3 C b b
GGCTCACTGCAG CTGCAGTGAGCCA GATCGTGCCA
GACGTCACTCGGT CTAGTACGGT
A

GAM136 279 INMT 1 3823 NM_006774.3 3 TGGCGCGATCTC C CCA 3 C c c
GACTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGCGCGGT
- AGC

GAM136 279 JAM1 1 14909 5 TGGCGCGATTTC C A 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TTTAGCGCGGT

```
                                        -       C
GAM136  279   JM11   1  3482  NM_033626.1  3      GGCGCAATCTCA C       CA   C    A     3  C  c  c
                                  GCTCACTGCA   TGCAGTGAGC  AGAT GTGCC
                                       ACGTCACTCG  TCTA CGCGG
                                        -       AC   A   -
GAM136  279   KIAA006 1  3287  NM_014876.1  3      TGGCACCATCTC C       A   C        3  C  c  c
        3                 GGCTCACTGCA   TGCAGTGAGCC AGAT GTGCCA
                                       ACGTCACTCGG TCTA CACGGT
                                        -       C   C
GAM136  279   KIAA008 1  17094 NM_014769.1  3      TGGCGTGATCTC C       A            3  C  c  c
        7                 GGTTCACTGCA   TGCAGTGAGCC AGATCGTGCCA
                                       ACGTCACTTGG TCTAGTGCGGT
                                        -       C
GAM136  279   KIAA009 1  1552  NM_015047.1  3      TGGCACAGTCAT         CAA  C         3  C  c  c
        0                 AGCTCACTGCAG CTGCAGTGAGC   GAT GTGCCA
                                       GACGTCACTCG   CTG CACGGT
                                            ATA   A
GAM136  279   KIAA016 1  15212         3      TGACAGGATCTC C       A   G C      3  C  c  c
        1                 GGCTCACTGCA   TGCAGTGAGCC AGATC TG CA
                                       ACGTCACTCGG TCTAG AC GT
                                        -       C   G A
GAM136  279   KIAA020 1  11019 NM_014873.1  3      TGGCATAATCTC         CA   CG        3  C  c  c
        5                 AGCTCACTGCAG CTGCAGTGAGC  AGAT  TGCCA
                                       GACGTCACTCG  TCTA  ACGGT
                                            AC   AT
GAM136  279   KIAA021 2  10972         5      TGGCTCGATCTC CT      A    T        3  C  c  c
        0                 GGCTCACTGC    GCAGTGAGCC AGATCG GCCA
                                        CGTCACTCGG TCTAGC CGGT
                                       --       C    T
GAM136  279   KIAA021 2  12431         5      TGGTGCGATCTC C  A    CA    TG       3  C  c  c
        0                 AGCTCACCGCA   TGC GTGAGC  AGATCG  CCA
                                       ACG CACTCG  TCTAGC  GGT
                                       -  C     AC     GT
GAM136  279   KIAA040 1  13524 NM_014657.1  5      TGGCACAATCAC         CAA  C         3  C  c  c
        6                 AGCTCATTGCAG CTGCAGTGAGC   GAT GTGCCA
                                       GACGTTACTCG   CTA CACGGT
                                            ACA   A
GAM136  279   KIAA044 1  1227  NM_014797.1  3      TGGCACAATCAT         CAA  C         3  C  c  c
        1                 TGCTCACTGTAG CTGCAGTGAGC   GAT GTGCCA
                                       GATGTCACTCG   CTA CACGGT
                                            TTA   A
GAM136  279   KIAA044 1  9929          3      TGGCATGATCTT                    3  C  b  b
        7                 GGCTCACTGCAG CTGCAGTGAGCCAAGATCGTGCCA
                                       GACGTCACTCGGTTCTAGTACGGT

GAM136  279   KIAA045 1  16587 XM_027862.7  3      TGGGGCAATCTC C       A   C G      3  C  c  c
        9                 GGCTCACTGCA   TGCAGTGAGCC AGAT GT CCA
                                       ACGTCACTCGG TCTA CG GGT
                                        -       C   A G
GAM136  279   KIAA049 1  16273 XM_034717.8  5      TGACATGATCTT C    G        C      3  C  c  c
```

```
         3                        GGCTGACTGCA  TGCAGT AGCCAAGATCGTG CA
                                        ACGTCA TCGGTTCTAGTAC GT
                                        -    G         A
GAM136   279  KIAA056 1  10973  XM_038150.2  3       GGCGTGATCTCA C       CA       A      3  C  c  c
         1                        GCTCACTGCA   TGCAGTGAGC  AGATCGTGCC
                                        ACGTCACTCG  TCTAGTGCGG
                                        -       AC       -
GAM136   279  KIAA059 1  9870           3       TGGCGTGATCTC C        A             3  C  c  c
         4                        GGCTTACTGCA  TGCAGTGAGCC AGATCGTGCCA
                                        ACGTCATTCGG TCTAGTGCGGT
                                        -       C
GAM136   279  KIAA059 1  18369  XM_085127.6  3       TGGCGTGATCTT C                  3  C  b  b
         9                        GGCTTACTGCA  TGCAGTGAGCCAAGATCGTGCCA
                                        ACGTCATTCGGTTCTAGTGCGGT
                                        -
GAM136   279  KIAA071 1  4700   NM_014867.1  3       CACGAGGCTCAC C       AAGA   CCA      3  C  c
c
         1                        TGCA       TGCAGTGAGCC   TCGTG
                                        ACGTCACTCGG   AGCAC
                                        -       ----    ---
GAM136   279  KIAA084 1  4724   XM_049237.5  3       TGGCATGAACTC C       CA A          3  C  c  c
         1                        AGCTCACTGCA  TGCAGTGAGC  AG TCGTGCCA
                                        ACGTCACTCG  TC AGTACGGT
                                        -       AC  A
GAM136   279  KIAA092 1  3141   NM_014897.1  5       TGGCGTGATCTT C                  3  C  b  b
         4                        GGCTCACTGCA  TGCAGTGAGCCAAGATCGTGCCA
                                        ACGTCACTCGGTTCTAGTGCGGT
                                        -
GAM136   279  KIAA093 1  19082  XM_041191.4  3       TGGGGTCTCGGG       G A   GTG       3  C  c
c
         1                        TCACTGCAG   CTGCAGTGA CC AGATC   CCA
                                        GACGTCACT GG TCTGG   GGT
                                           G C    ---
GAM136   279  KIAA096 1  19593  NM_014898.1  5       TGGCACAGTCTC C       A  C         3  C  c  c
         1                        GGCTCACTGCA  TGCAGTGAGCC AGAT GTGCCA
                                        ACGTCACTCGG TCTG CACGGT
                                        -       C  A
GAM136   279  KIAA102 1  18235          3       TGGCACGATCTT C  C                3  C  b  b
         8                        GGCTCACTCCA  TG AGTGAGCCAAGATCGTGCCA
                                        AC TCACTCGGTTCTAGCACGGT
                                        - C
GAM136   279  KIAA114 1  12426  XM_044014.3  3       TGGCGCGATCTC C       CA          3  C  c  c
         3                        AGCTCACTGCA  TGCAGTGAGC  AGATCGTGCCA
                                        ACGTCACTCG  TCTAGCGCGGT
                                        -       AC
GAM136   279  KIAA116 1  11081          5       TGGCACAATCAG C       CAA  C          3  C  c  c
         1                        CTCACTGCA   TGCAGTGAGC   GAT GTGCCA
                                        ACGTCACTCG   CTA CACGGT
                                        -       A--  A
GAM136   279  KIAA118 1  2134   NM_020710.1  3       TGGCGTGATCTC       GCCA          3  C  c  c
```

5 GAGTCACTGCAG CTGCAGTGA AGATCGTGCCA
GACGTCACT TCTAGTGCGGT
GAGC

GAM136 2793 KIAA1191 18852 XM_041843.2 3 TGGTGCGATCTC C A TG 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGATCG CCA
ACGTCACTCGG TCTAGC GGT
- C GT

GAM136 2790 KIAA1211 4237 XM_172801.1 5 TGGCGCGATCTC C CA 3 C c c
CGCTCACTGCA TGCAGTGAGC AGATCGTGCCA
ACGTCACTCG TCTAGCGCGGT
- CC

GAM136 2794 KIAA1251 2406 3 TGACACGATCTC C CA C 3 C c c
AGCTCACTGCA TGCAGTGAGC AGATCGTG CA
ACGTCACTCG TCTAGCAC GT
- AC A

GAM136 2797 KIAA1252 5979 XM_031577.3 3 TGGCGCGATCTC C A CA 3 C c b
AGCTCACCGCA TGC GTGAGC AGATCGTGCCA
ACG CACTCG TCTAGCGCGGT
- C AC

GAM136 2797 KIAA1252 15885 XM_031577.3 3 TGGCGCGATCTC C A 3 C b b
GGCTCACTACAG CTG AGTGAGCC AGATCGTGCCA
GAC TCACTCGG TCTAGCGCGGT
A C

GAM136 2790 KIAA1281 8845 NM_015691.1 5 TGACGTGGTCAT CAA C 3 C c c
AGCTCACTGCAG CTGCAGTGAGC GATCGTG CA
GACGTCACTCG CTGGTGC GT
ATA A

GAM136 2790 KIAA1531 13682 XM_042661.5 5 TGGCGTGATCTC C A 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TCTAGTGCGGT
- C

GAM136 2799 KIAA1641 16107 3 TGGCACTATCTC C CA C 3 C c c
AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTA CACGGT
- AC T

GAM136 2792 KIAA1711 5693 XM_041497.9 3 GCACGATCTTGG C A CA 3 C c c
CTCACCGCA TGC GTGAGCCAAGATCGTGC
ACG CACTCGGTTCTAGCACG
- C --

GAM136 2797 KIAA1721 5388 XM_034262.6 3 TGGCACAATCAT CAA C 3 C c c
AGCTCACTGCAG CTGCAGTGAGC GAT GTGCCA
GACGTCACTCG CTA CACGGT
ATA A

GAM136 2797 KIAA1731 3552 NM_033426.1 3 TGGGATCTCGGC C A GTG 3 C c c
TCACTGCA TGCAGTGAGCC AGATC CCA
ACGTCACTCGG TCTAG GGT
- C ---

GAM136 2799 KIAA1821 13422 XM_030378.2 3 TGACACAATCAT A C C 3 C c c
GGCTCACTGCAG CTGCAGTGAGCCA GAT GTG CA
GACGTCACTCGGT CTA CAC GT

A A A

GAM136 2792 KIAA1921 13683 XM_057040.1 5 TGGCATGATCTC C CA 3 C c c
AGCTCACTGCA TGCAGTGAGC AGATCGTGCCA
ACGTCACTCG TCTAGTACGGT
- AC

GAM136 2794 KIAA1921 5980 NM_153239.2 3 TGGCGCGATCTT C C 3 C b b
AGCTCACTGCA TGCAGTGAGC AAGATCGTGCCA
ACGTCACTCG TTCTAGCGCGGT
- A

GAM136 2796 KIAA1951 17777 XM_085836.6 3 TGGCACGATCTC CA 3 C b b
AGCTCACTGCAG CTGCAGTGAGC AGATCGTGCCA
GACGTCACTCG TCTAGCACGGT
AC

GAM136 2791 KIAA1971 11033 XM_058720.5 3 TGGCACGATCTT C 3 C b b
GGCTTACTGCA TGCAGTGAGCCAAGATCGTGCCA
ACGTCATTCGGTTCTAGCACGGT
-

GAM136 279 LAMP3 1 13626 NM_014398.1 3 TGGCACGATCTC C A A 3 C c c
GGCTTATGGCA TGC GTGAGCC AGATCGTGCCA
ACG TATTCGG TCTAGCACGGT
- G C

GAM136 279 LILRA3 1 16588 NM_006865.1 3 TGGCGCAATCTG C A C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TCTA CGCGGT
- G A

GAM136 279 LLGL1 1 17511 NM_004140.2 3 TGGCCCCATCTC C CA CGT 3 C c c

TGCTCACTGCA TGCAGTGAGC AGAT GCCA
ACGTCACTCG TCTA CGGT
- TC CCC

GAM136 2792 LOC1127 1 4017 5 GGCAATCTCGGC C A CG A 3 C c c
4 TCACTGCA TGCAGTGAGCC AGAT TGCC
ACGTCACTCGG TCTA ACGG
- C -- -

GAM136 2797 LOC1136 1 5894 5 TGGCACAACCTT C ATC 3 C c c
5 GGCTCACTGCA TGCAGTGAGCCAAG GTGCCA
ACGTCACTCGGTTC CACGGT
- CAA

GAM136 2791 LOC1152 1 1562 XM_055499.4 5 TGGCAGGATCTC C A G 3 C c c
9 GGCTCACTGCA TGCAGTGAGCC AGATC TGCCA
ACGTCACTCGG TCTAG ACGGT
- C G

GAM136 2799 LOC1193 1 3818 NM_145247.1 3 TGGTGCGATCTT C C TG 3 C c c
2 GACTCACTGCA TGCAGTGAG CAAGATCG CCA
ACGTCACTC GTTCTAGC GGT
- A GT

GAM136 2793 LOC1209 1 13240 3 TGGCATGGTCTC C CA 3 C c c
9 AGCTCACTGTA TGCAGTGAGC AGATCGTGCCA
ATGTCACTCG TCTGGTACGGT
- AC

GAM136 279 LOC1261 1 17494 3 TGGCACAATCTC A A C 3 C c c
33 GGCCCACTGCAG CTGCAGTG GCC AGAT GTGCCA
GACGTCAC CGG TCTA CACGGT
C C A
GAM136 279 LOC1266 1 9831 XM_060121.4 5 TGGCGCAATCTT C C 3 C b b
69 GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTCTA CGCGGT
- A
GAM136 279 LOC1283 1 5976 XM_059243.3 5 TGGCACGATCTT C 3 C b b
87 GGCTCACTGCA TGCAGTGAGCCAAGATCGTGCCA
ACGTCACTCGGTTCTAGCACGGT
-
GAM136 279 LOC1313 1 9826 3 TGGCACAATCTT C C C 3 C c c
08 AGCTCACTGCA TGCAGTGAGC AAGAT GTGCCA
ACGTCACTCG TTCTA CACGGT
- A A
GAM136 279 LOC1351 1 5005 NM_145267.1 3 TGGCACTATCCC C CCAA C 3 C c
c
54 AACTCACTGCA TGCAGTGAG GAT GTGCCA
ACGTCACTC CTA CACGGT
- AACC T
GAM136 279 LOC1353 1 11002 3 TGGCATCATTGT CCAA C 3 C c c
98 AACTCACTGCAG CTGCAGTGAG GAT GTGCCA
GACGTCACTC TTA TACGGT
AATG C
GAM136 279 LOC1357 1 3127 NM_138572.1 3 TGGCAAGATCTT C G 3 C b b
63 GGCTCACTGCA TGCAGTGAGCCAAGATC TGCCA
ACGTCACTCGGTTCTAG ACGGT
- A
GAM136 279 LOC1380 1 5749 5 TGGCACCATCTC C C A C 3 C c c
50 GGCTCACTCCA TG AGTGAGCC AGAT GTGCCA
AC TCACTCGG TCTA CACGGT
- C C C
GAM136 279 LOC1381 1 5770 3 TGGCACGATCAT C CAA 3 C c c
99 AGCTCACTGTA TGCAGTGAGC GATCGTGCCA
ATGTCACTCG CTAGCACGGT
- ATA
GAM136 279 LOC1429 1 9930 5 TGGCATGATCTC A A 3 C b b
27 GGCTCACCGCAG CTGC GTGAGCC AGATCGTGCCA
GACG CACTCGG TCTAGTACGGT
C C
GAM136 279 LOC1443 1 14198 XM_084813.4 5 TGGCGCGATCTC C CCA 3 C c c
17 AACTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGCGCGGT
- AAC
GAM136 279 LOC1452 1 6134 XM_085072.1 5 TGACGAGATCTT C G C 3 C c c
68 GGCTCACTGCA TGCAGTGAGCCAAGATC TG CA
ACGTCACTCGGTTCTAG GC GT
- A A
GAM136 279 LOC1456 1 14806 3 TGGCACCATTTC C A C 3 C c c

22 GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TTTA CACGGT
- C C
GAM136 279 LOC1458 1 9548 XM_096873.2 5 TGGCATGTTCAT C A T 3 C c c
13 GGCTCACTGCA TGCAGTGAGCCA GA CGTGCCA
ACGTCACTCGGT CT GTACGGT
- A T
GAM136 279 LOC1462 2 3787 XM_085387.1 3 TGGCGAGATCAC C AA G 3 C c c
29 GGCTCACTGCA TGCAGTGAGCC GATC TGCCA
ACGTCACTCGG CTAG GCGGT
- CA A
GAM136 279 LOC1462 2 12076 XM_085387.1 3 TGGCGCCATCTC C A C 3 C c c
29 GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TCTA CGCGGT
- C C
GAM136 279 LOC1464 1 14100 XM_085461.6 5 TGGCACGATCTC C C AGCCA 3 C c
c
43 CACGCACTACA TG AGTG AGATCGTGCCA
AC TCAC TCTAGCACGGT
- A GCACC
GAM136 279 LOC1464 1 12428 5 TGGCACGATCTC C A 3 C b b
55 GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TCTAGCACGGT
- C
GAM136 279 LOC1469 1 14423 XM_097121.1 3 TGGCATGATCTC C A 3 C c c
01 GGCTCATTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTTACTCGG TCTAGTACGGT
- C
GAM136 279 LOC1469 1 12423 XM_085634.3 3 TGGTACGATCTT C 3 C b b
09 GGCTCACTGCA TGCAGTGAGCCAAGATCGTGCCA
ACGTCACTCGGTTCTAGCATGGT
-
GAM136 279 LOC1472 1 4474 5 TGGTGCAATCTC C CA C TG 3 C c c
76 AGCTCACTGCA TGCAGTGAGC AGAT G CCA
ACGTCACTCG TCTA C GGT
- AC A GT
GAM136 279 LOC1474 1 15647 5 TGGCACGATCCT C A 3 C b b
29 GGCTCACTGCA TGCAGTGAGCCA GATCGTGCCA
ACGTCACTCGGT CTAGCACGGT
- C
GAM136 279 LOC1476 1 10507 3 TGGTGCGATCTT C A C TG 3 C c c
60 GACTCACAGCA TGC GTGAG CAAGATCG CCA
ACG CACTC GTTCTAGC GGT
- A A GT
GAM136 279 LOC1479 1 4469 3 TGGCGCAATCTT C C C 3 C c c
90 GGCTCACTACA TG AGTGAGCCAAGAT GTGCCA
AC TCACTCGGTTCTA CGCGGT
- A A
GAM136 279 LOC1481 1 17632 NM_144692.1 3 TGGCATGATCTC C A A 3 C c c
37 GGCTCACGGCA TGC GTGAGCC AGATCGTGCCA

ACG CACTCGG TCTAGTACGGT
- G C

GAM136 279 LOC1481 1 7424 XM_086087.1 5 TGGCCTGTCTCG C A T T 3 C c c
89 GCTCACTGCA TGCAGTGAGCC AGA CG GCCA
ACGTCACTCGG TCT GT CGGT
- C - C

GAM136 279 LOC1481 2 1164 3 TGATACAATCTT C C 3 C b b
95 GGCTCACTGCAG CTGCAGTGAGCCAAGAT GTG CA
GACGTCACTCGGTTCTA CAT GT
A A

GAM136 279 LOC1481 2 15515 5 TGGCACAAGATT C A -- 3 C c b
95 ATGACTCACTGT CTGCAGTGAG CA GATC GTGCCA
AG GATGTCACTC GT TTAG CACGGT
A A AA

GAM136 279 LOC1486 1 11573 5 TGGCGAGATCAT CAA G 3 C c c
45 AGCTCACTGCAG CTGCAGTGAGC GATC TGCCA
GACGTCACTCG CTAG GCGGT
ATA A

GAM136 279 LOC1488 1 13862 5 TGGCATGATCTC C A 3 C b b
87 GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TCTAGTACGGT
- C

GAM136 279 LOC1491 1 17663 5 TGGCATGATCTC CT A 3 C c c
17 GGCTCACTGCG GCAGTGAGCC AGATCGTGCCA
CGTCACTCGG TCTAGTACGGT
G- C

GAM136 279 LOC1495 1 6703 XM_097661.4 3 TGGCGCTGTCTC C A C 3 C c c
06 GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TCTG CGCGGT
- C T

GAM136 279 LOC1496 1 14807 XM_097706.1 3 TGGCGCCATCTT C C 3 C c c
92 GGCTCACTGTA TGCAGTGAGCCAAGAT GTGCCA
ATGTCACTCGGTTCTA CGCGGT
- C

GAM136 279 LOC1502 1 9366 XM_097870.1 3 TGGCGTGATCTC C CCA 3 C c c
25 CACTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGTGCGGT
- ACC

GAM136 279 LOC1503 1 9404 XM_086907.1 3 TGGCTTGATCTC C A T 3 C c c
97 GGCTCATTGCA TGCAGTGAGCC AGATCG GCCA
ACGTTACTCGG TCTAGT CGGT
- C T

GAM136 279 LOC1510 1 9827 XM_097998.2 5 TGGTGCAATCTC C A C TG 3 C c c
57 GGCTCACTGCA TGCAGTGAGCC AGAT G CCA
ACGTCACTCGG TCTA C GGT
- C A GT

GAM136 279 LOC1512 1 3995 XM_098021.1 3 TGGCGCGATTTC C CA 3 C c c
01 AGCTCACTGCA TGCAGTGAGC AGATCGTGCCA
ACGTCACTCG TTTAGCGCGGT
- AC

GAM136 279 LOC1514 1 19282 XM_098063.1 5 TGGCGCAATCTC C CA C 3 C c c
75 AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTA CGCGGT
- AC A
GAM136 279 LOC1516 1 16085 3 TGGCACGATCGC C AA 3 C b b
02 GGCTCACTGCA TGCAGTGAGCC GATCGTGCCA
ACGTCACTCGG CTAGCACGGT
- CG
GAM136 279 LOC1518 1 9541 3 TGGCGAAATCTC C CA CG 3 C c c
26 AGCTCACTGCA TGCAGTGAGC AGAT TGCCA
ACGTCACTCG TCTA GCGGT
- AC AA
GAM136 279 LOC1521 1 8819 3 TGGTGCAATCTT C C TG 3 C c c
37 GGCTCACTGCA TGCAGTGAGCCAAGAT G CCA
ACGTCACTCGGTTCTA C GGT
- A GT
GAM136 279 LOC1522 1 6805 3 TGACATGATCTC C CA C 3 C c c
20 AGCTCACTGCA TGCAGTGAGC AGATCGTG CA
ACGTCACTCG TCTAGTAC GT
- AC A
GAM136 279 LOC1523 1 412 5 TGGCACGATCTC C CA 3 C b b
00 AGCTCACTGCA TGCAGTGAGC AGATCGTGCCA
ACGTCACTCG TCTAGCACGGT
- AC
GAM136 279 LOC1525 1 10692 5 TGGCATGATCTC C A A 3 C c c
82 GGCTCACCGCA TGC GTGAGCC AGATCGTGCCA
ACG CACTCGG TCTAGTACGGT
- C C
GAM136 279 LOC1527 2 3422 XM_098257.1 5 TGGCGTGATCTC C GCCA 3 C c c
19 AGATCACTGCA TGCAGTGA AGATCGTGCCA
ACGTCACT TCTAGTGCGGT
- AGAC
GAM136 279 LOC1527 2 5750 XM_098257.1 5 TGGCACCATCTC C CA C 3 C c c
19 CGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTA CACGGT
- CC C
GAM136 279 LOC1527 1 8624 XM_087525.1 5 TGGCATGATCTG C - A 3 C b b
94 GTCTCACTGCA TGCAGTGAG CCA GATCGTGCCA
ACGTCACTC GGT CTAGTACGGT
- T -
GAM136 279 LOC1536 1 6383 5 TGGCACGATCCT C A 3 C b b
06 GGTTCACTGCA TGCAGTGAGCCA GATCGTGCCA
ACGTCACTTGGT CTAGCACGGT
- C
GAM136 279 LOC1536 1 11003 3 TGGCAAGATCTC C A G 3 C c c
88 GGCTCACTGCA TGCAGTGAGCC AGATC TGCCA
ACGTCACTCGG TCTAG ACGGT
- C A
GAM136 279 LOC1538 1 12732 XM_087779.2 5 TGGCACAGTCAT A C 3 C c c

11 GGCTCGCTGCAG CTGCAGTGAGCCA GAT GTGCCA
GACGTCGCTCGGT CTG CACGGT
A A

GAM136 279 LOC1538 1 14252 XM_087798.1 5 TGGCACAATCTC C CA C 3 C c c
83 AGTTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTTG TCTA CACGGT
- AC A

GAM136 279 LOC1548 1 9289 XM_098626.4 3 TGGCGTGATCTC C A 3 C c c
77 GGCTCATTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTTACTCGG TCTAGTGCGGT
- C

GAM136 279 LOC1575 1 17205 3 GCACAATCACGG C AA C CA 3 C c c
06 CTCACTGCA TGCAGTGAGCC GAT GTGC
ACGTCACTCGG CTA CACG
- CA A --

GAM136 279 LOC1575 1 15895 5 TGGCATGATGTC C AAG 3 C c c
07 GGCTCACTGCA TGCAGTGAGCC ATCGTGCCA
ACGTCACTCGG TAGTACGGT
- CTG

GAM136 279 LOC1577 1 1563 5 TGGCACGATCTC C CCA 3 C c c
98 GCCTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGCACGGT
- CGC

GAM136 279 LOC1578 1 11827 XM_098833.3 5 GCGCGATCATGG C A CA 3 C c c

58 CTCACTGCA TGCAGTGAGCCA GATCGTGC
ACGTCACTCGGT CTAGCGCG
- A --

GAM136 279 LOC1584 1 413 XM_098936.1 5 TGGCATGATCTC C CA 3 C c c
02 AGCTCACTGTA TGCAGTGAGC AGATCGTGCCA
ATGTCACTCG TCTAGTACGGT
- AC

GAM136 279 LOC1584 1 12077 XM_098955.1 3 TGGCACCATCTC C CA C 3 C c c
76 AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTA CACGGT
- AC C

GAM136 279 LOC1586 1 8440 XM_045161.1 3 TGGCACAATTTC C CA C 3 C c c
68 AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TTTA CACGGT
- AC A

GAM136 279 LOC1620 1 16604 5 GGCCCGAGCCAC A CAAGA T A 3 C c c
22 TGCAG CTGCAGTG GC TCG GCC
GACGTCAC CG AGC CGG
- ----- C -

GAM136 279 LOC1696 1 11646 XM_095809.4 3 TGGCGCGATTCA C CAA 3 C c c
11 GCTCACTGCA TGCAGTGAGC GATCGTGCCA
ACGTCACTCG TTAGCGCGGT
- AC-

GAM136 279 LOC1965 1 5060 3 TGACGTGATCTC C CA C 3 C c c
29 CGCTCACTGCA TGCAGTGAGC AGATCGTG CA

ACGTCACTCG TCTAGTGC GT
- CC A

GAM136 279 LOC1973 2 16351 XM_113872.2 3 TGGCACGATCTC C T CA 3 C c b
58 AGCTCCCTGCA TGCAG GAGC AGATCGTGCCA
ACGTC CTCG TCTAGCACGGT
- C AC

GAM136 279 LOC1973 2 17773 XM_113872.2 3 TGGCATGATCTC CA 3 C b b
58 AGCTCACTGTAG CTGCAGTGAGC AGATCGTGCCA
GATGTCACTCG TCTAGTACGGT
AC

GAM136 279 LOC2000 1 3544 3 TGGCATGATCTC C CA 3 C c c
14 AGCTCGCTGCA TGCAGTGAGC AGATCGTGCCA
ACGTCGCTCG TCTAGTACGGT
- AC

GAM136 279 LOC2001 1 6860 XM_117200.2 5 GCGCAATCTTGG C C CA 3 C c c
69 CTCACTGCA TGCAGTGAGCCAAGAT GTGC
ACGTCACTCGGTTCTA CGCG
- A --

GAM136 279 LOC2003 1 6549 3 TGGCTGGATCTC C CA GT 3 C c c
16 AGCTCACTGCA TGCAGTGAGC AGATC GCCA
ACGTCACTCG TCTAG CGGT
- AC GT

GAM136 279 LOC2011 1 17606 XM_290750.1 3 TGGCACAACCTC C A ATC 3 C c c
64 GGCTCACTGCA TGCAGTGAGCC AG GTGCCA
ACGTCACTCGG TC CACGGT
- C CAA

GAM136 279 LOC2017 1 7983 5 TGGCTCGATCTC C CA T 3 C c c
02 AGCTCACTGCA TGCAGTGAGC AGATCG GCCA
ACGTCACTCG TCTAGC CGGT
- AC T

GAM136 279 LOC2024 1 5848 NM_145303.1 5 GCGTGATCTCTA CCA CA 3 C c c
59 CTCACTGCAG CTGCAGTGAG AGATCGTGC
GACGTCACTC TCTAGTGCG
ATC --

GAM136 279 LOC2031 1 18848 5 TGGCGCGATCTT C 3 C b b
97 GGCTCACTGCA TGCAGTGAGCCAAGATCGTGCCA
ACGTCACTCGGTTCTAGCGCGGT
-

GAM136 279 LOC2034 1 20008 NM_145305.1 3 TGACACAATCAT CAA C C 3 C c c
27 AGCTCACTGCAG CTGCAGTGAGC GAT GTG CA
GACGTCACTCG CTA CAC GT
ATA A A

GAM136 279 LOC2048 1 3925 3 TGGCGTGATCTC CT A 3 C c c
04 GGCTCACTGC GCAGTGAGCC AGATCGTGCCA
CGTCACTCGG TCTAGTGCGGT
-- C

GAM136 279 LOC2196 1 17829 5 TGGTGCAATCTC A C TG 3 C c c
73 GGCTCACTGTAG CTGCAGTGAGCC AGAT G CCA

GATGTCACTCGG TCTA C GGT
C A GT

| | | |

GACGTCACTCGG TCTAGC
C -----

GAM136	279	LOC2554 2	9221		5	TGGCATGATCAT	CAA	3	C	b	b	
	65				AGCTCACTGCAG CTGCAGTGAGC	GATCGTGCCA						
					GACGTCACTCG	CTAGTACGGT						
					ATA							
GAM136	279	LOC2554 2	17676		3	TGGCACAATCTC C	CA C	3	C	c	b	
	65				AGCTCACTGTA	TGCAGTGAGC AGAT GTGCCA						
					ATGTCACTCG	TCTA CACGGT						
					-	AC A						
GAM136	279	LOC2559 1	2135		3	TGGCACGATCTT C T		3	C	b	b	
	19				GGCTTTCTGCA	TGCAG GAGCCAAGATCGTGCCA						
					ACGTC	TTCGGTTCTAGCACGGT						
					- T							
GAM136	279	LOC2569 1	7013		5	TGCCACGATCTT T	C	3	C	b	b	
	23				GGCTCCCTGCAG CTGCAG GAGCCAAGATCGTG CA							
					GACGTC	CTCGGTTCTAGCAC GT						
					C	C						
GAM136	279	LOC2570 2	14524		3	GGCACGGACAAG	A AAGA- A	3	C	c	c	
	54				GGCCACTGCAG	CTGCAGTG GCC TCGTGCC						
					GACGTCAC	CGG GGCACGG						
					-	GAACA -						
GAM136	279	LOC2570 2	18129		5	TGACACAGTTGC	CAA C C	3	C	c	c	
	54				AGCTCACTGCAG CTGCAGTGAGC	GAT GTG CA						
					GACGTCACTCG	TTG CAC GT						
					ACG	A A						
GAM136	279	LOC9048 2	15288	XM_032059.1	3	TGATGCAATCTC C	A C GC	3	C	c	c	
	5				GGCTCACTGCA	TGCAGTGAGCC AGAT GT CA						
					ACGTCACTCGG	TCTA CG GT						
					-	C A TA						
GAM136	279	LOC9048 2	20154	XM_032059.1	3	TGGAGCGATCTC CTG	A G	3	C	c		
	5				GGCTCACTG	CAGTGAGCC AGATCGT CCA						
					GTCACTCGG	TCTAGCG GGT						
					---	C A						
GAM136	279	LOC9059 1	13863	XM_032811.1	3	TGGCGTGATCTC C	CA	3	C	c	c	
	1				AGCTCACTGCA	TGCAGTGAGC AGATCGTGCCA						
					ACGTCACTCG	TCTAGTGCGGT						
					-	AC						
GAM136	279	LOC9111 1	4470	XM_036218.4	5	TGGTACAATCTC C	A C	3	C	c	c	
	5				GGCTCACTGCA	TGCAGTGAGCC AGAT GTGCCA						
					ACGTCACTCGG	TCTA CATGGT						
					-	C A						
GAM136	279	LOC9137 1	18364	XM_038063.8	3	TGGCGTGACCTT C	A	3	C	c	c	
	3				GGCTCACTGCA	TGCAGTGAGCCAAG TCGTGCCA						
					ACGTCACTCGGTTC	AGTGCGGT						
					-	C						
GAM136	279	LOC9154 1	19265	XM_039093.5	3	TGGCATGATCTC	CA	3	C	b	b	
	7				AGCTCACTGCAG CTGCAGTGAGC	AGATCGTGCCA						

GACGTCACTCG TCTAGTACGGT
AC

GAM136 279 LOC9156 1 1319 XM_039218.8 5 TGACACAATCTC C CA C C 3 C c c
1 AGCTCACTGCA TGCAGTGAGC AGAT GTG CA
ACGTCACTCG TCTA CAC GT
- AC A A

GAM136 279 LOC9214 1 15402 XM_043160.9 5 TGGCACGACCTC C CA A 3 C c c
8 TGCTCGCTGCA TGCAGTGAGC AG TCGTGCCA
ACGTCGCTCG TC AGCACGGT
- TC C

GAM136 279 LOC9246 1 10843 3 TGGACGATCTCA C CA G 3 C c c
6 GCTCACTGCA TGCAGTGAGC AGATCGT CCA
ACGTCACTCG TCTAGCA GGT
- AC -

GAM136 279 LOC9269 1 3545 5 TGGCATGATCTC C C A 3 C c c
7 GGCTCGCTACA TG AGTGAGCC AGATCGTGCCA
AC TCGCTCGG TCTAGTACGGT
- A C

GAM136 279 LTB4R 1 2471 NM_000752.1 5 TGGTGCGATCTC CA TG 3 C c c
AGCTCACTGCAG CTGCAGTGAGC AGATCG CCA
GACGTCACTCG TCTAGC GGT
AC GT

GAM136 279 MAIL 1 6513 NM_031419.1 3 TGGCATGATCTT C 3 C b b
GGCTCACTTCAG CTG AGTGAGCCAAGATCGTGCCA
GAC TCACTCGGTTCTAGTACGGT
T

GAM136 279 MAK 1 19152 NM_005906.2 3 TGGCACTATCTT C C 3 C b b
GGCTTACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCATTCGGTTCTA CACGGT
- T

GAM136 279 MANBAL 1 638 NM_022077.2 5 CGACTCATTGGC - - TGCCA 3 C c c
TCACTGCAG CTGCAGTGAGCCAA GA TCG
GACGTCACTCGGTT CT AGC
A C -----

GAM136 279 MGC1020 1 8635 NM_145060.1 3 GGCGCTATCTCG C A C A 3 C c c
0 GCTCGCTGCA TGCAGTGAGCC AGAT GTGCC
ACGTCGCTCGG TCTA CGCGG
- C T -

GAM136 279 MGC1428 1 11444 NM_080660.1 3 TGACGTGATCTC A C 3 C c c
9 GGCTCACTGCAG CTGCAGTGAGCC AGATCGTG CA
GACGTCACTCGG TCTAGTGC GT
C A

GAM136 279 MGC1587 1 2473 NM_032920.1 5 TGGCGCAACCAG CAAGATC 3 C c
c
3 CTCACTGCAG CTGCAGTGAGC GTGCCA
GACGTCACTCG CGCGGT
ACCAA--

GAM136 279 MGC1842 1 7188 XM_037797.4 3 TGGCACGATCTT C C 3 C b b
GGCTTACTACA TG AGTGAGCCAAGATCGTGCCA
AC TCATTCGGTTCTAGCACGGT

- A
GAM136 279 MGC2474 1 15463 NM_023931.1 3 TGGTGCGATCTC C CCA TG 3 C c c
GACTCACTGCA TGCAGTGAG AGATCG CCA
ACGTCACTC TCTAGC GGT
- AGC GT
GAM136 279 MGC3329 1 12427 NM_024086.2 3 TGGTGCGATCTT C C TG 3 C c c
AGCTCACTGCA TGCAGTGAGC AAGATCG CCA
ACGTCACTCG TTCTAGC GGT
- A GT
GAM136 279 MGC4638 1 3737 3 TGACACGATCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGATCGTG CA
ACGTCACTCGGTTCTAGCAC GT
- A
GAM136 279 NDUFB1 1 2538 NM_004545.2 5 TGGCGTCATCTC C CA CG 3 C c c
AGCTCACTGCA TGCAGTGAGC AGAT TGCCA
ACGTCACTCG TCTA GCGGT
- AC CT
GAM136 279 NDUFC2 1 8439 NM_004549.2 3 TGGCGCAATTTC C A C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TTTA CGCGGT
- C A
GAM136 279 NPR2L 1 6977 NM_006545.3 3 TGGCACAATCAC CAA C 3 C c c
AGCTCACTGTAG CTGCAGTGAGC GAT GTGCCA
GATGTCACTCG CTA CACGGT
ACA A
GAM136 279 NXN 1 15417 NM_022463.2 3 TGGCACCATCTT C C C 3 C c c
GGCTCACTTCA TG AGTGAGCCAAGAT GTGCCA
AC TCACTCGGTTCTA CACGGT
- T C
GAM136 279 ORC1L 1 11234 NM_004153.1 3 TGGCACGATCAT A 3 C b b
GGCTCACTGCAG CTGCAGTGAGCCA GATCGTGCCA
GACGTCACTCGGT CTAGCACGGT
A
GAM136 279 PASK 1 17796 NM_015148.1 5 TGGCACCATCTC C CCA C 3 C c c
GTCTCACTGCA TGCAGTGAG AGAT GTGCCA
ACGTCACTC TCTA CACGGT
- TGC C
GAM136 279 PCDHB11 1 17334 NM_018931.2 3 TGGCAGGATCTC C CA G 3 C c c
AGCTCACTGCA TGCAGTGAGC AGATC TGCCA
ACGTCACTCG TCTAG ACGGT
- AC G
GAM136 279 PDCL 1 15813 NM_005388.2 3 GCGTGATCTCGG C A CA 3 C c c
CTCACTGCA TGCAGTGAGCC AGATCGTGC
ACGTCACTCGG TCTAGTGCG
- C --
GAM136 279 PDZK1 1 13616 NM_002614.2 5 TGGTGCGATCTC C A A TG 3 C c c

GGCTCACAGCA TGC GTGAGCC AGATCG CCA
ACG CACTCGG TCTAGC GGT
- A C GT
GAM136 279 PELI1 2 7342 NM_020651.2 5 TGGCACTGATCT C A - 3 C b b
CGGCTCACTGCA TGCAGTGAGCC AGATC GTGCCA
ACGTCACTCGG TCTAG CACGGT
- C T
GAM136 279 PELI1 2 18940 NM_020651.2 5 TGGCGCAATTTT C C 3 C c b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTTTA CGCGGT
- A
GAM136 279 PIK3C2B 1 18311 NM_002646.2 5 TGGCATGATCTC C CCA 3 C c c
GACTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTAGTACGGT
- AGC
GAM136 279 PIK3CD 1 17678 NM_005026.2 3 TGGTGCAATCTT C C TG 3 C c c
GGCTCACTGTA TGCAGTGAGCCAAGAT G CCA
ATGTCACTCGGTTCTA C GGT
- A GT
GAM136 279 PIP3-E 1 12706 3 TGGCACGATTTT C C 3 C b b
AGCTCACTGCA TGCAGTGAGC AAGATCGTGCCA
ACGTCACTCG TTTTAGCACGGT
- A
GAM136 279 PMCHL1 1 17289 NM_031887.2 3 TGGCACGATCTC CTG A 3 C c c
GGCTCACTG CAGTGAGCC AGATCGTGCCA
GTCACTCGG TCTAGCACGGT
--- C
GAM136 279 PPID 1 8817 NM_005038.1 5 TGGCGCAATCTC C A C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TCTA CGCGGT
- C A
GAM136 279 PRKR 1 7341 NM_002759.1 3 TGACACAGTCTT C C C 3 C c c
GGCTCACTGCA TGCAGTGAGCCAAGAT GTG CA
ACGTCACTCGGTTCTG CAC GT
- A A
GAM136 279 PRO0365 1 15753 NM_014126.1 5 GGCACGATCTCA C CA A 3 C c c
GCTCACTGCA TGCAGTGAGC AGATCGTGCC
ACGTCACTCG TCTAGCACGG
- AC -
GAM136 279 PRO1992 1 4868 3 TGGCACAATCTT C C 3 C b b
GACTCGCTGCAG CTGCAGTGAG CAAGAT GTGCCA
GACGTCGCTC GTTCTA CACGGT
A A
GAM136 279 PSMB2 1 15555 NM_002794.3 3 TGGCGTAATCTT C CG 3 C c c
GGCTCACTGCA TGCAGTGAGCCAAGAT TGCCA
ACGTCACTCGGTTCTA GCGGT
- AT
GAM136 279 PSTPIP2 1 2794 NM_024430.2 3 GGCATGATCTCA C CA A 3 C c c
GCTCACTGCA TGCAGTGAGC AGATCGTGCC

ACGTCACTCG TCTAGTACGG
- AC -
GAM136 279 PTGES 1 2996 NM_004878.2 3 TGGTACAATCTG A C 3 C b b
GCTCACTGCAG CTGCAGTGAGCCA GAT GTGCCA
GACGTCACTCGGT CTA CATGGT
- A
GAM136 279 RAB21 1 18931 NM_014999.1 3 TGGCTTGATCTC C A T 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGATCG GCCA
ACGTCACTCGG TCTAGT CGGT
- C T
GAM136 279 RAB39 1 4443 XM_084662.2 3 TGGGGCAATCTT C T C G 3 C c c
GGCTCCCTGCA TGCAG GAGCCAAGAT GT CCA
ACGTC CTCGGTTCTA CG GGT
- C A G
GAM136 279 RASSF2 1 8520 NM_014737.1 3 TGGGATCTCAGC C CA GTG 3 C c
c
TCACTGCA TGCAGTGAGC AGATC CCA
ACGTCACTCG TCTAG GGT
- AC ---
GAM136 279 RBM8A 1 18760 NM_005105.2 3 GCTGATCATAGC CAA T CA 3 C c c
TCACTGCAG CTGCAGTGAGC GATCG GC
GACGTCACTCG CTAGT CG
ATA - --
GAM136 279 RNO2 1 11666 5 GGCACAATCTCA C CA C A 3 C c c
GCTCACTGCA TGCAGTGAGC AGAT GTGCC
ACGTCACTCG TCTA CACGG
- AC A -
GAM136 279 RPP30 2 415 NM_006413.2 3 TGGCTCGATCTC C CA T 3 C c c
TGCTCACTGCA TGCAGTGAGC AGATCG GCCA
ACGTCACTCG TCTAGC CGGT
- TC T
GAM136 279 RPP30 2 669 NM_006413.2 3 TGGCATAATCAC C CAA CG 3 C c c
AGCTCACTGCA TGCAGTGAGC GAT TGCCA
ACGTCACTCG CTA ACGGT
- ACA AT
GAM136 279 SC4MOL 1 8501 NM_006745.2 3 TGGCACAGTCTC C CA C 3 C c c
AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTG CACGGT
- AC A
GAM136 279 SCML2 1 9298 NM_006089.1 3 GCTCGATCTCGG C A T CA 3 C c c
CTCACTGCA TGCAGTGAGCC AGATCG GC
ACGTCACTCGG TCTAGC CG
- C T --
GAM136 279 SCYA22 1 13867 3 TGGCGTGATCTC C C A 3 C c c
GGCTCACTACA TG AGTGAGCC AGATCGTGCCA
AC TCACTCGG TCTAGTGCGGT
- A C
GAM136 279 SEDL 1 18071 NM_014563.1 3 TGGCACAGTCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA

ACGTCACTCGGTTCTG CACGGT
- A
GAM136 279 SEMA5A 1 11943 NM_003966.1 5 GGCCCTTGGCCC A ATCGT A 3 C c c
GCTGCAG CTGCAGTG GCCAAG GCC
GACGTCGC CGGTTC CGG
C C---- -
GAM136 279 SEPN1 1 17169 NM_020451.1 3 TGGCTCGATCTT C T 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGATCG GCCA
ACGTCACTCGGTTCTAGC CGGT
- T
GAM136 279 SERF1B 1 18926 NM_022978.1 3 TGGCGTGATCTC C CA 3 C c c
TGCTCACTGCA TGCAGTGAGC AGATCGTGCCA
ACGTCACTCG TCTAGTGCGGT
- TC
GAM136 279 SERPINB 1 6595 NM_004155.2 3 TGGCATGATCTG C A 3 C b b
9 GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TCTAGTACGGT
- G
GAM136 279 SH3BP2 1 19004 NM_003023.2 3 TGGCGTGATCTC C G A 3 C c c
GGCTCAATGCA TGCA TGAGCC AGATCGTGCCA
ACGT ACTCGG TCTAGTGCGGT
- A C
GAM136 279 SIL 1 10047 NM_003035.1 3 TGGCAGGATCTC C GCCA G 3 C c c
AGATCACTGCA TGCAGTGA AGATC TGCCA
ACGTCACT TCTAG ACGGT
- AGAC G
GAM136 279 SLC14A2 1 9752 NM_007163.2 5 TGGCACTATCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTCTA CACGGT
- T
GAM136 279 SLC16A4 1 17675 NM_004696.1 3 TGGCGCAATCTC C A C 3 C c c
GGCTCACTGTA TGCAGTGAGCC AGAT GTGCCA
ATGTCACTCGG TCTA CGCGGT
- C A
GAM136 279 SLC2A10 1 15101 NM_030777.2 3 TGGCCTGATCTT C T 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGATCG GCCA
ACGTCACTCGGTTCTAGT CGGT
- C
GAM136 279 SMAC 1 11007 NM_138929.1 5 TGGCGAGATCTC C CA G 3 C c c
AGCTCACTGCA TGCAGTGAGC AGATC TGCCA
ACGTCACTCG TCTAG GCGGT
- AC A
GAM136 279 SNAP23 1 3908 NM_003825.2 3 GCGCGATCTGGG C A CA 3 C c c
CTCACTGCA TGCAGTGAGCC AGATCGTGC
ACGTCACTCGG TCTAGCGCG
- G --
GAM136 279 SNX15 1 10190 NM_013306.2 3 TGGGATCGCGGC C AA GTG 3 C c c
TCACTGCA TGCAGTGAGCC GATC CCA

ACGTCACTCGG CTAG GGT
- CG ---
GAM136 279 SQV7L 1 5878 XM_047287.2 5 TGGCATTATCTC C CA C 3 C c c
AGCTCACTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCACTCG TCTA TACGGT
- AC T
GAM136 279 SS-56 1 15880 NM_018073.4 3 TGGCACGATCTC A 3 C b b
GGCTCACTGCAG CTGCAGTGAGCC AGATCGTGCCA
GACGTCACTCGG TCTAGCACGGT
C
GAM136 279 SUN1 1 16363 3 TGGTGCAATCTT C TG 3 C c c
GGCTCACTGCAG CTGCAGTGAGCCAAGAT G CCA
GACGTCACTCGGTTCTA C GGT
A GT
GAM136 279 TAPBP 2 5937 NM_003190.3 3 TGGCACGATCTC C A A 3 C c b
GGCTCACGGCA TGC GTGAGCC AGATCGTGCCA
ACG CACTCGG TCTAGCACGGT
- G C
GAM136 279 TAPBP 2 7038 NM_003190.3 3 TGGCATGATCTT C 3 C b b
GGCTTACTGCA TGCAGTGAGCCAAGATCGTGCCA
ACGTCATTCGGTTCTAGTACGGT
-
GAM136 279 TCL6 1 17772 NM_020553.2 5 TGGCGCGATCTC A 3 C b b
GGCTCACTGCAG CTGCAGTGAGCC AGATCGTGCCA
GACGTCACTCGG TCTAGCGCGGT
C
GAM136 279 TDGF1 1 17005 NM_003212.1 3 TGACGCGATCTT C C 3 C c c
GGTTCACTGCA TGCAGTGAGCCAAGATCGTG CA
ACGTCACTTGGTTCTAGCGC GT
- A
GAM136 279 TERF2 1 17679 NM_005652.2 3 TGGCGTGATCTC CT A 3 C c c
GGCTCACTGCG GCAGTGAGCC AGATCGTGCCA
CGTCACTCGG TCTAGTGCGGT
G- C
GAM136 279 TIM3 1 19281 5 TGGCACAATCTC C A C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTCACTCGG TCTA CACGGT
- C A
GAM136 279 TJP1 1 4867 NM_175610.1 5 TGGTGCAACCTC CA ATC TG 3 C c c
AGCTCACTGCAG CTGCAGTGAGC AG G CCA
GACGTCACTCG TC C GGT
AC CAA GT
GAM136 279 TMC1 1 10094 NM_138691.2 5 TGGTGCGATCTC C T A TG 3 C c c
GGCTCTCTGCA TGCAG GAGCC AGATCG CCA
ACGTC CTCGG TCTAGC GGT
- T C GT
GAM136 279 TNFRSF1 1 16066 NM_147187.1 3 TGGTGCAATCTT C C TG 3 C c c
0B GGCTCACTATAG CTG AGTGAGCCAAGAT G CCA
GAT TCACTCGGTTCTA C GGT
A A GT

GAM136 279 TP53 1 9481 NM_000546.2 3 TGGCGTGATCTT 3 C b b
GGCTTACTGCAG CTGCAGTGAGCCAAGATCGTGCCA
GACGTCATTCGGTTCTAGTGCGGT

GAM136 279 TRIM5 1 18339 NM_033034.1 3 TGGCACGATCTC C A 3 C b b
GGTTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTTGG TCTAGCACGGT
- C

GAM136 279 TRPV1 1 4442 NM_080704.1 3 TGGCACAATTTT C T C 3 C c c
GGCTCCCTGCA TGCAG GAGCCAAGAT GTGCCA
ACGTC CTCGGTTTTA CACGGT
- C A

GAM136 279 TUCAN 1 5981 NM_014959.1 5 TGGTGCGATCTC C CA TG 3 C c c
AGCTCACTGCA TGCAGTGAGC AGATCG CCA
ACGTCACTCG TCTAGC GGT
- AC GT

GAM136 279 TUFT1 1 5698 NM_020127.1 3 GCGCGATCTCAG C CA CA 3 C c c
CTCACTGCA TGCAGTGAGC AGATCGTGC
ACGTCACTCG TCTAGCGCG
- AC --

GAM136 279 TXNL2 1 3614 NM_006541.1 3 TGGCACGATTAT A 3 C b b
GGCTCATTGCAG CTGCAGTGAGCCA GATCGTGCCA
GACGTTACTCGGT TTAGCACGGT
A

GAM136 279 UBF-fl 2 3774 NM_032828.1 3 TGGCACAATCTC C A C 3 C c c
GGCTCATTGCA TGCAGTGAGCC AGAT GTGCCA
ACGTTACTCGG TCTA CACGGT
- C A

GAM136 279 UBF-fl 2 9865 NM_032828.1 3 TGGCATGATTTC C A 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TTTAGTACGGT
- C

GAM136 279 VENTX2 1 1323 NM_014468.1 3 TGACGCAATCTC C A C C 3 C c c
GGCTCACTGCA TGCAGTGAGCC AGAT GTG CA
ACGTCACTCGG TCTA CGC GT
- C A A

GAM136 279 VPS33A 1 6708 NM_022916.2 3 TGGCACGGTCTC C CCA 3 C c c
ACCTCACTGCA TGCAGTGAG AGATCGTGCCA
ACGTCACTC TCTGGCACGGT
- CAC

GAM136 279 WBSCR20 1 18847 NM_148956.1 5 TGGCGCGATCTC C A A 3 C c c

A GGCTCACCGCA TGC GTGAGCC AGATCGTGCCA
ACG CACTCGG TCTAGCGCGGT
- C C

GAM136 279 XRCC2 2 12449 NM_005431.1 3 TGGCACAATCAT A C 3 C b b
GGCTCACTGCAG CTGCAGTGAGCCA GAT GTGCCA
GACGTCACTCGGT CTA CACGGT
A A

GAM136 279 XRCC2 2 13590 NM_005431.1 3 TGGCACAATCTC A A C 3 C c b

GGCCCGCTGCAG CTGCAGTG GCC AGAT GTGCCA
GACGTCGC CGG TCTA CACGGT
C C A

GAM136 279 YES1 1 416 NM_005433.2 5 TGGCGCGATCTC C A 3 C b b
GGCTCACTGCA TGCAGTGAGCC AGATCGTGCCA
ACGTCACTCGG TCTAGCGCGGT
- C

GAM136 279 ZNF133 1 4840 NM_003434.2 5 TGGCACAATCTC C CCA C 3 C c c
AACTCACTGCA TGCAGTGAG AGAT GTGCCA
ACGTCACTC TCTA CACGGT
- AAC A

GAM136 279 ZNF221 1 13245 NM_013359.1 3 TGGCGCTATCTC C CA C 3 C c c
AGCTCGCTGCA TGCAGTGAGC AGAT GTGCCA
ACGTCGCTCG TCTA CGCGGT
- AC T

GAM136 279 ZNF264 1 4725 NM_003417.1 3 TGATGCGATCTC C T A GC 3 C c c
GGCTCTCTGCA TGCAG GAGCC AGATCGT CA
ACGTC CTCGG TCTAGCG GT
- T C TA

GAM136 279 ZNF338 1 4054 3 TGGCGCTATCTT C C 3 C b b
GGCTCACTGCA TGCAGTGAGCCAAGAT GTGCCA
ACGTCACTCGGTTCTA CGCGGT
- T

GAM136 279 ZNF339 1 11496 NM_021220.1 3 TGGCATGATCAT C A 3 C b b
GGCTCACTGCA TGCAGTGAGCCA GATCGTGCCA
ACGTCACTCGGT CTAGTACGGT
- A

GAM136 279 ZTL1 1 20007 3 TGACACGATCTT C C C 3 C c c
GTCTCACTGCA TGCAGTGAG CAAGATCGTG CA
ACGTCACTC GTTCTAGCAC GT
- T A

GAM137 202 BBX 1 2775 NM_020235.2 3 GCCAGTTTGTTC A A-- T 3 C c c
TCTCAGAACCCA TTTGG TTCTGA AAC AACTGGC
GA AGACC AAGACT TTG TTGACCG
C CTC T

GAM137 202 KIAA032 1 8515 XM_032634.1 3 GCCAGTCAACTT -- AACTA 3 C c c
3 CCTGGAATCCAA TTTGGATTCT GAA ACTGGC
G GAACCTAAGG CTT TGACCG
TC CAAC-

GAM137 202 LOC2023 1 3099 XM_117390.1 3 GCCAGTTAGTTC TG ATT A 3 C c c
47 TCAGCTGAG TT G CTGA AACTAACTGGC
GA C GACT TTGATTGACCG
GT --- C

GAM137 202 TCF7 1 8403 NM_003202.1 3 GCCACTGGTTTC - AC 3 C c c
TCAGAATCCAAA TTTGGATTCTGA AAACTA TGGC
AAACCTAAGACT TTTGGT ACCG
C C-

GAM138 222 C6orf33 1 8900 NM_133367.1 3 ACAGACATTAGC GC - CGC 3 C c c
CATCACGCCTG CAGG GTGGTGGCTAA CTGT

GTCC CACTACCGATT GACA
-- G ACA

GAM138 222 C9orf9 1 5771 NM_018956.2 3 ACAGGCGCCCAC GCCA CTAA 3 C c c

CACCC GGGTGGTGG CGCCTGT
CCCACCACC GCGGACA
---- C---

GAM138 222 FLJ1297 1 10308 NM_024908.1 3 ACAGGCACCTGC - TAAC 3 C c c
3 CACCACGCCTGG GCCAGG GTGGTGGC GCCTGT
C CGGTCC CACCACCG CGGACA
G TCCA

GAM138 222 FLJ2013 1 650 NM_017684.1 3 ACAGGCATGAGC AGG AAC 3 C c c

6 CACCACGGC GCC GTGGTGGCT GCCTGT
CGG CACCACCGA CGGACA
--- GTA

GAM138 222 FLJ2014 1 6891 NM_017687.1 3 ACAAGCATGAGC - AAC C 3 C c c
7 CACCACACCTGG GCCAGG GTGGTGGCT GC TGT
C CGGTCC CACCACCGA CG ACA
A GTA A

GAM138 222 FLJ2070 1 8502 NM_017932.1 3 ACAGGCGTGAGC AGG A 3 C c c
0 CACCGCGGC GCC GTGGTGGCT ACGCCTGT
CGG CGCCACCGA TGCGGACA
--- G

GAM138 222 FLJ2072 1 11088 NM_017953.2 3 ACAGGCATCAGC G - AAC 3 C c c
9 CACCACACCTGG CCAGG GTGGTGGCT GCCTGT
GGTCC CACCACCGA CGGACA
- A CTA

GAM138 222 FLJ3286 1 13561 NM_144613.1 3 ACAGGCATGCAC CA - CTAAC 3 C c c

5 CACCACGCCCAG GC GG GTGGTGG GCCTGT
C CG CC CACCACC CGGACA
AC G ACGTA

GAM138 222 KIAA047 1 14834 XM_301133.1 3 ACAGGCATGAGC GGG AAC 3 C c c

5 CACCGTGGC GCCA TGGTGGCT GCCTGT
CGGT GCCACCGA CGGACA
--- GTA

GAM138 222 KIAA125 1 18365 XM_031577.3 3 ACAGGTGCACAC - CTAA 3 C c c
7 CACCACACCTGG GCCAGG GTGGTGG CGCCTGT
C CGGTCC CACCACC GTGGACA
A ACAC

GAM138 222 KIAA144 1 17528 NM_020834.1 3 ACAGGCACCTGC A - TAAC 3 C c c

3 CACCACACCCGG GCC GG GTGGTGGC GCCTGT
C CGG CC CACCACCG CGGACA
C A TCCA

GAM138 222 KIAA166 1 19546 3 ACAGGCGTGAGC A - A 3 C b b
8 CACCACGCCCGG GCC GG GTGGTGGCT ACGCCTGT
C CGG CC CACCACCGA TGCGGACA

C G G

GAM138 222 KLHL3 1 18573 NM_017415.1 5 ACAGTTCAGCAG AACGC- 3 C c c
CTACCACCCTGG GCCAGGGTGGTGGCT CTGT
C CGGTCCCACCATCGA GACA
CGACTT

GAM138 222 LNK 1 18117 NM_005475.1 3 ACAAGCACCAGC G - AAC C 3 C c c
CACCATGCCTGG CCAGG GTGGTGGCT GC TGT
GGTCC TACCACCGA CG ACA
- G CCA A

GAM138 222 LOC1358 1 3223 XM_059804.4 3 ACAGGCGTGAGC - A 3 C b b
18 CACCACACCTGG GCCAGG GTGGTGGCT ACGCCTGT
C CGGTCC CACCACCGA TGCGGACA
A G

GAM138 222 LOC1429 1 13504 5 ACAGGTGTGAGC G A 3 C b b
27 CACCACGCTGGC GCCAG GTGGTGGCT ACGCCTGT
CGGTC CACCACCGA TGTGGACA
G G

GAM138 222 LOC1462 1 9210 XM_085387.1 3 ACAGGCGTGAGC GC GGCTA 3 C c
c
29 CACCCTG CAGGGTGGT ACGCCTGT
GTCCCACCG TGCGGACA
-- AG---

GAM138 222 LOC1501 1 18674 5 ACAGCTATGCCA C TAAC C 3 C c c
47 CCACCCTAGC GC AGGGTGGTGGC GC TGT
CG TCCCACCACCG CG ACA
A TAT- -

GAM138 222 LOC1522 1 12911 3 ACAGGCACCCGC CA - TAAC 3 C c c
20 CACCACACCCAG GC GG GTGGTGGC GCCTGT
C CG CC CACCACCG CGGACA
AC A CCCA

GAM138 222 LOC1548 1 8021 XM_098626.4 3 ACAGATGTGCAC G CTA C 3 C c c
77 CACCACACTGGC GCCAG GTGGTGG ACG CTGT
CGGTC CACCACC TGT GACA
A ACG A

GAM138 222 LOC1965 1 5335 3 ACAGGCATGCGT A - TAAC 3 C c c
29 CACCACGCCGGC GCC GG GTGGTGGC GCCTGT
CGG CC CACCACTG CGGACA
- G CGTA

GAM138 222 LOC2048 1 2980 3 ACAGGCATGCAC - CTAAC 3 C c c
04 CACCACGCCTGG GCCAGG GTGGTGG GCCTGT
C CGGTCC CACCACC CGGACA
G ACGTA

GAM138 222 LOC8993 1 19547 3 ACAGGCATGAGC CA - AAC 3 C c c
2 CACCACGCCCAG GC GG GTGGTGGCT GCCTGT
C CG CC CACCACCGA CGGACA
AC G GTA

GAM138 222 LOC9125 1 14884 XM_037135.1 5 TACAGGCATCAG CA - AAC - 3 C c
c
0 CCACCACACCCA GC GG GTGGTGGCT GCCTGT
GC CG CC CACCACCGA CGGACA

AC A CTA T

GAM138 222 LOC9154 1 3224 XM_039115.8 5 ACAGGTGTGAGC A - A 3 C c c
9 CACCACACCCGG GCC GG GTGGTGGCT ACGCCTGT
C CGG CC CACCACCGA TGTGGACA
C A G

GAM138 222 LOC9334 1 10297 NM_138402.2 3 ACAGGAGTGAGC - A G 3 C b b
9 CACCACACCTGG GCCAGG GTGGTGGCT AC CCTGT
C CGGTCC CACCACCGA TG GGACA
A G A

GAM138 222 MGC1320 1 4720 NM_031465.1 3 ACAGGCACCAGC G - AAC 3 C c c
4 CACCATGCCTGG CCAGG GTGGTGGCT GCCTGT
GGTCC TACCACCGA CGGACA
- G CCA

GAM138 222 MGC2477 2 12814 NM_024099.1 5 ACAGGCGCCCGC AG CTAA 3 C c
c
CACCACGGC GCC GGTGGTGG CGCCTGT
CGG CCACCGCC GCGGACA
CA C---

GAM138 222 MGC2477 2 13562 NM_024099.1 5 ACAGGCGTGCAC A - CTA 3 C c
c
CACCACGCCCGG GCC GG GTGGTGG ACGCCTGT
C CGG CC CACCACC TGCGGACA
C G ACG

GAM138 222 MKRN4 1 6362 NM_030757.1 3 ACAGGCGTCAGC GCCA -- A 3 C c c
CACCATGCCC GGGT GGTGGCT ACGCCTGT
CCCG CCACCGA TGCGGACA
---- TA C

GAM138 222 MRPL49 1 12809 NM_004927.2 3 ACAGGCGCCCAC CAG CTAA 3 C c
c
CACCACAGC GC GGTGGTGG CGCCTGT
CG CCACCACC GCGGACA
ACA C---

GAM138 222 PIK3CD 1 5480 NM_005026.2 3 ACAGGCATGAGC A - AAC 3 C c c
CACCACGCCCGG GCC GG GTGGTGGCT GCCTGT
C CGG CC CACCACCGA CGGACA
C G GTA

GAM138 222 PRKWNK3 1 3228 NM_020922.1 3 ACAGGCGCCAGC G - AA 3 C c c
CACCATGCCTGG CCAGG GTGGTGGCT CGCCTGT
GGTCC TACCACCGA GCGGACA
- G CC

GAM138 222 RPP30 1 1813 NM_006413.2 3 ACAGGCGTTAGC G A - TG 3 C c c
CACTGCGCCCGG CC GG G GTGGCTAACGCCTGT
GG CC C CACCGATTGCGGACA
- C G GT

GAM138 222 SLC24A1 1 14930 NM_004727.1 3 ACAGGCGTCAGC G - A 3 C c c
CACCGCGCCTGG CCAGG GTGGTGGCT ACGCCTGT
GGTCC CGCCACCGA TGCGGACA

```
                                        -  G     C
GAM138  222  TBXA2R 1  15791 NM_001060.2  3      ACAGGCATGAAC    -    CTAAC        3  C  c  c

                                CACCACACCTGG GCCAGG GTGGTGG   GCCTGT
                                C         CGGTCC CACCACC    CGGACA
                                            A      AAGTA
GAM138  222  TUFT1  1  18146 NM_020127.1  3      ACAGGTGTGCCA    -    TA         3  C  b  b
                                CCACGCCTGGC  GCCAGG GTGGTGGC  ACGCCTGT
                                       CGGTCC CACCACCG  TGTGGACA
                                            G      --
GAM138  222  WHSC1  1  13027 NM_133332.1  3      ACAAGCGGCTGC    -    TAA  C      3  C  c  c
                                CACCACACCTGG GCCAGG GTGGTGGC   CGC TGT
                                C         CGGTCC CACCACCG   GCG ACA
                                            A      TCG   A
GAM139  327  ABHD1  1  18435 NP_690609.1  3  124  CCCTACGTTGCG   A    GC    A       1  B  c  c

                                CTGCTCATCACA TGG GCTGTGA  AGCAGC CA
                                GCCCGGGG    GCC CGACACT  TCGTCG GT
                                       -     AC    C
GAM139  327  ADORA2A 1  13460 NP_000666.2  3  611  CAGTCCTCTCCT   -    G    CAC       1  B  c
c
                                GCTGTCACAGCT TGG AGCTGTGA CAGCAG
                                GCCATCCA    ACC TCGACACT GTCGTC
                                          G     -    CTC
GAM139  327  ALDH5A1 2  5625  NP_001071.1  3  1120  CCTGGTGTGGTG    C  T--     G       1  B  c
c
                                CTGCTCCCTCAC TGGAG TG   GAGCAGCA CACA
                                CTCCAAAA    ACCTC AC   CTCGTCGT GTGT
                                          C  TCC      G
GAM139  327  ALDH5A1 2  5625  NP_733936.1  3  1120  CCTGGTGTGGTG    C  T--     G       1  B  c
c
                                CTGCTCCCTCAC TGGAG TG   GAGCAGCA CACA
                                CTCCAAAA    ACCTC AC   CTCGTCGT GTGT
                                          C  TCC      G
GAM139  327  ALDH5A1 2  8267  NP_001071.1  3  1120  GGTGTGGTGCTG    C  T--     G       1  B  c
c
                                CTCCCTCACCTC TGGAG TG   GAGCAGCA CACA
                                CAAAAGAG    ACCTC AC   CTCGTCGT GTGT
                                          C  TCC      G
GAM139  327  ALDH5A1 2  8267  NP_733936.1  3  1120  GGTGTGGTGCTG    C  T--     G       1  B  c
c
                                CTCCCTCACCTC TGGAG TG   GAGCAGCA CACA
                                CAAAAGAG    ACCTC AC   CTCGTCGT GTGT
                                          C  TCC      G
GAM139  327  ANXA9  1  17446 NP_003559.1  5  382   GCTCCTGTGCTG   A-  G  AG          1  B  c  c

                                CTGAGCAGGGCA TGG  GCT TG  CAGCAGCACA
                                ACCAGTAG    ACC  CGG AC  GTCGTCGTGT
                                          AA   G  GA
GAM139  327  AP3M1  1  2765  NP_036227.1  3  591   CAGGGAGCACTG    - T      CAC       1  B  c  c
```

CTGCTCCATGCT TGGAGC TG GAGCAGCAG
CCATTCTC ACCTCG AC CTCGTCGTC
T - ACG

GAM139 327 ARFGAP3 1 917 NP_055385.2 5 86 CCAGCTGCGCCG - A A AC 1 B c c

CGGCTCACAGCT TG GAGCTGTG GC GCAGC
GACGATGG AC CTCGGCGC CG CGTCG
A - - AC

GAM139 327 ARHGAP1 1 18225 NP_004299.1 3 1773 GTGTATCAAGTG A A ------ 1 B c c

TCGCTCACAGCC TGG GCTGTGAGC GCA GCAC
CCATTCAC ACC CGACACTCG TGT TGTG
C C GAACTA

GAM139 327 ARHGDIA 2 15005 NP_004300.1 3 650 TGGGGTGTGCTG A T- C 1 B c c

CTGCTGCTCCCC TGG GCTG GAGCAGCAGCA
AGCCCACC ACC CGAC CTCGTCGTCGT
- CC C

GAM139 327 ARHGDIA 2 15152 NP_004300.1 3 650 GGTGTGCTGCTG A T- C 1 B c c

CTGCTCCCCAGC TGG GCTG GAGCAGCAGCA
CCACCAGT ACC CGAC CTCGTCGTCGT
- CC C

GAM139 327 ARHGDIG 2 6996 NP_001167.1 3 408 GTACTGCTGCTG T-- G C 1 B c c

CTGCTGCTCAGG GGAGCT TGAGCAGCAGCA
GCTTCGTG CTTCGG ACTCGTCGTCGT
GTG G C

GAM139 327 ARHGDIG 2 10749 NP_001167.1 3 405 CCTGTACTGCTG T G C 1 B c c

CTGCTGCTGCTC GGAGCT TGAGCAGCAGCA
AGGGCTTC CTTCGG ACTCGTCGTCGT
- G C

GAM139 327 ARHGEF4 2 2155 NP_056135.2 3 706 TCAGTCTGCCTG TGA- C 1 B c c

CTGCTGTGCGGT TGGAGCTG GCAGCAGCA
AGCTCCAG ACCTCGAT TGTCGTCGT
GGCG C

GAM139 327 ARHGEF4 2 2155 NP_127462.1 3 1357 TCAGTCTGCCTG TGA- C 1 B c c

CTGCTGTGCGGT TGGAGCTG GCAGCAGCA
AGCTCCAG ACCTCGAT TGTCGTCGT
GGCG C

GAM139 327 ARHGEF4 2 7064 NP_056135.2 3 707 GTCTGCCTGCTG TGA- C 1 B c c

CTGTGCGGTAGC TGGAGCTG GCAGCAGCA
TCCAGAAC ACCTCGAT TGTCGTCGT
GGCG C

GAM139 327 ARHGEF4 2 7064 NP_127462.1 3 1358 GTCTGCCTGCTG TGA- C 1 B c c

CTGTGCGGTAGC TGGAGCTG GCAGCAGCA
TCCAGAAC ACCTCGAT TGTCGTCGT
GGCG C

GAM139 327 ARHGEF7 1 8435 NP_663788.1 3 1562 AGCCGGGTCCTG A - C 1 B b b

CTGCTCACAAGC TGG GCT GTGAGCAGCAG AC
CCAGAGCT ACC CGA CACTCGTCGTC TG
- A C

GAM139 327 ARLTS1 1 10485 NP_612459.1 3 775 GAGATTGTGCTG T----- A T -- 1 B c c

CTGCACTCCAGC GG GCTG GA GCAGCAGCACA
CTGGGTGA TC CGAC CT CGTCGTCGTGT
AGTGGG - - CA

GAM139 327 ASB1 2 5956 NP_057198.1 3 98 GCTGTGCTGCTG T---------- - GTG 1 B c c
CTGGTCTCCTGA GGAG CT AGCAGCAGCA
TGGCTGTT CCTC GG TCGTCGTCGT
TTGTCGGTAGT T ---

CA
GT

GAM139 327 ASB1 2 16782 NP_057198.1 3 98 AGTGCTGTGCTG T------- - GTG 1 B c c
CTGCTGGTCTCC GGAG CT AGCAGCAGCACA
TGATGGCT CCTC GG TCGTCGTCGTGT
TCGGTAGT T ---

GAM139 327 ATF3 1 16226 NP_004015.2 3 96 CTAAACCCAGTG T--- C T C 1 B c c
CTGCTCTCCCAT GGAG TG GAG AGCAGCAC
CTCCCATC CCTC AC CTC TCGTCGTG
CTAC T C -

GAM139 327 B4GALT5 1 2957 NP_004767.1 3 1410 AGCCCAGGTGCA AGC CA 1 B c c

CTGCTCACACCC TGG TGTGAGCAG GCAC
CCACCTGC ACC ACACTCGTC CGTG
CCC A-

GAM139 327 BACE2 3 4701 NP_620477.1 3 128 ATCGTCCTGCTG T G C 1 B c c
CTGCTGCCGTTC TGGAGC GT AGCAGCAGCA
CGGTGTCA GCCTTG CG TCGTCGTCGT
C - C

GAM139 327 BACE2 3 5247 NP_620477.1 3 127 TTAATCGTCCTG T G C 1 B c c
CTGCTGCTGCCG TGGAGC GT AGCAGCAGCA
TTCCGGTG GCCTTG CG TCGTCGTCGT
C - C

GAM139 327 BACE2 3 16352 NP_620477.1 3 128 GTCCTGCTGCTG T G C 1 B c c
CTGCCGTTCCGG TGGAGC GT AGCAGCAGCA
TGTCAGCG GCCTTG CG TCGTCGTCGT
C - C

GAM139 327 BAZ2A 1 12267 NP_038477.1 3 2134 CTGCTTTGTGTT T C C 1 B c c
CCTCTCCCAGCT TGGAGCTG GAG AG AGCACA
CCATCTCT ACCTCGAC CTC TC TTGTGT
C - C

GAM139 327 BRI3 1 8333 NP_056194.1 3 184 GAGGCAGTGCTG TG ---- -- 1 B c c
CTGCTCCCGCCC GAGCT GT GAGCAGCAGCAC
GAGGCTCA CTCGG CG CTCGTCGTCGTG
A- AGCC CC
GAM139 327 BRMS1 1 10687 NP_056214.1 3 142 CCTGTGGTGCTG C T ---- 1 B c c
CTGGGCCCTCCC TGGAG TG GAG CAGCAGCAC
ACTCCATC ACCTC AC CTC GTCGTCGTG
- C CCGG
GAM139 327 C14orf1 2 9620 NP_061057.1 5 64 GTGACTGGTCTG - G C 1 B c c
07 CTGCTGCAGGCT TGGAGC TGT AGCAGCAG AC
TCATCTAA ACTTCG ACG TCGTCGTC TG
G - -
GAM139 327 C14orf1 2 17830 NP_061057.1 5 64 ACTGGTCTGCTG - G C 1 B c c
07 CTGCAGGCTTCA TGGAGC TGT AGCAGCAG AC
TCTAAAAC ACTTCG ACG TCGTCGTC TG
G - -
GAM139 327 C14orf9 1 17946 NP_653169.1 3 416 AGGACTTTGCTG C TG -- C 1 B c c
CTGCTATTGCAC TGGAG TG A GCAGCAGCA
TTCACCAG ACTTC AC T CGTCGTCGT
- GT AT T
GAM139 327 C15orf1 1 17482 NP_570971.1 5 22 TGCATGTAGTTG TG CA - 1 B c c
6 TCACTTGCAGCT TGGAGCTG AG GCAGC ACA
CCATTTCC ACCTCGAC TC TGTTG TGT
GT AC A
GAM139 327 C16orf5 1 9004 NP_037531.1 3 845 CTGTTGCTGTGC T-- --- --- C 1 B c c
CTGCTCACACCT GGAGC TGTGAGCAG CAGCA
GCTCCTGC CCTCG ACACTCGTC GTCGT
CGT TCC CGT T
GAM139 327 C20orf1 1 891 XP_029741.1 3 1208 GGCCCCACTGTG T---- G T C 1 B c c
30 CTGCTCTTCAGG GGA CTG GAG AGCAGCACA
TCCCCACA CCT GAC TTC TCGTCGTGT
ACACC G - -
GAM139 327 C20orf4 1 6027 NP_060714.2 3 618 GGATGGTCTCTG - TGT C- 1 B c c
4 CTGCTCTTGCCT TGGAG C GAGCAGCAG AC
CTAGTTCA ATCTC G CTCGTCGTC TG
C TT- TC
GAM139 327 C22orf5 1 1661 NP_036396.1 3 1778 GCCAAAGTGCTG T----- C T - 1 B c c
CTGATTCCCACT GGAG TG GAG CAGCAGCAC
CCCTTGGT CCTC AC CTT GTCGTCGTG
TGGTTC - C A
GAM139 327 C6orf49 1 11971 NP_060071.1 3 149 CACTCCTTGCTG GA C 1 B c c
CTGCCGGCGGTT TGGAGCTGT GCAGCAGCA
CCAGCCTG ACCTTGGCG CGTCGTCGT
GC T
GAM139 327 C8G 1 8475 NP_000597.1 3 21 GAGGAGGTGGGC A A- AG 1 B c c
CGGCACACAGCT TGGAGCTGTG GC GC CAC
CCAGTGCT ACCTCGACAC CG CG GTG
A GC G-
GAM139 327 C9orf14 1 10704 XP_098859.2 5 319 TTTCTCTGTGCC G C CA 1 B c c
CTTTTGACAGCT TGGAGCTGT AG AG GCACA

CCAGGGAT ACCTCGACA TT TC CGTGT
G T C-
GAM139 327 CA12 1 4145 NP_001209.1 3 397 CTGGAAAGTCTG CTGT C 1 B c c
CTGCTTCTCCAA TGGAG GAGCAGCAG AC
GCTTTCAG ACCTC TTCGTCGTC TG
---- -
GAM139 327 CALML3 1 7337 NP_005176.1 5 913 GGGAGGACTCTG G C C 1 B c c

CTGCTTCTTAAG TGGAGCT TGAG AGCAGCA
CTCCAGCG ACCTCGA ATTC TCGTCGT
- T C
GAM139 327 CASP2 1 9375 NP_116765.1 3 339 TGTGGATGGGAA T ----- G- 1 B c c
ACTGCTCCAGCT TGGAGCTG GAGCAG CA CACA
CCAAGAGG ACCTCGAC CTCGTC GT GTGT
- AAAGG AG
GAM139 327 CASP2 1 9375 NP_116766.1 3 339 TGTGGATGGGAA T ----- G- 1 B c c
ACTGCTCCAGCT TGGAGCTG GAGCAG CA CACA
CCAAGAGG ACCTCGAC CTCGTC GT GTGT
- AAAGG AG
GAM139 327 CBFA2T1 1 14704 NP_783554.1 5 30 GCAGTTGTGCTG - C GA--- 1 B c c

CTGCATATAACA TGG AG TGT GCAGCAGCACA
CTACCAAG ACC TC ACA CGTCGTCGTGT
A - ATATA
GAM139 327 CBR1 1 13028 NP_001748.1 3 21 ACAGTGGTGGCT AG - 1 B b b
GGGCTCACAGCT TGGAGCTGTGAGC CAGC AC
CCATCCAT ACCTCGACACTCG GTCG TG
G- G
GAM139 327 CCR8 1 2636 NP_005192.1 5 8 CCAGAGAGGCTG G -- AC 1 B c c
CTGCTCATTGAG TG AGCT GTGAGCAGCAGC
CTGCACTC AC TCGA TACTCGTCGTCG
G GT GA
GAM139 327 CD151 2 5033 NP_004348.2 3 39 TGGGCCTTGCTG AGCT - C 1 B c c
CTGCTGCACCCA TGG GTG AGCAGCAGCA
ACTACTGA ACC CAC TCGTCGTCGT
---- G T
GAM139 327 CD151 2 5033 NP_620599.1 3 39 TGGGCCTTGCTG AGCT - C 1 B c c
CTGCTGCACCCA TGG GTG AGCAGCAGCA
ACTACTGA ACC CAC TCGTCGTCGT
---- G T
GAM139 327 CD151 2 15477 NP_004348.2 3 39 GCCTTGCTGCTG AGCT - C 1 B c c

CTGCACCCAACT TGG GTG AGCAGCAGCA
ACTGAGCT ACC CAC TCGTCGTCGT
---- G T
GAM139 327 CD151 2 15477 NP_620599.1 3 39 GCCTTGCTGCTG AGCT - C 1 B c c

CTGCACCCAACT TGG GTG AGCAGCAGCA
ACTGAGCT ACC CAC TCGTCGTCGT
---- G T

GAM139 327 CD1B 2 6775 NP_001755.1 5 44 AGTGAAATGCTG C TG C 1 B c c
CTGCTGCCATTT TGGAG TG AGCAGCAGCA
CAACTGT ACTTT AC TCGTCGTCGT
- CG A
GAM139 327 CD1B 2 9277 NP_001755.1 5 44 GAAATGCTGCTG C TG C 1 B c c
CTGCCATTTCAA TGGAG TG AGCAGCAGCA
CTGT ACTTT AC TCGTCGTCGT
- CG A
GAM139 327 CD79A 1 9511 NP_001774.1 3 53 CCCCCGCCTGCT -- A - AC 1 B c c
GTGCACCCAGCT TGGAGCT GTG GCAGCAG C
CCAGTGTC ACCTCGA CAC TGTCGTC G
CC G C CC
GAM139 327 CD79A 1 9511 NP_067612.1 3 53 CCCCCGCCTGCT -- A - AC 1 B c c
GTGCACCCAGCT TGGAGCT GTG GCAGCAG C
CCAGTGTC ACCTCGA CAC TGTCGTC G
CC G C CC
GAM139 327 CD80 1 14816 NP_005182.1 3 524 GATTTTATGCTG A --- C 1 B c c
CTGTTTACAAAA TGG GCT GTGAGCAGCAGCA
GCCCAATG ACC CGA CATTTGTCGTCGT
- AAA A
GAM139 327 CD97 1 830 NP_001775.2 3 221 CTGGTCCTGCTG TGT ----- C 1 B c c
CTGGCTGCCTCT TGGAGC GAG CAGCAGCA
CTGCTCCA ACCTCG CTC GTCGTCGT
TCT CGTCG C
GAM139 327 CD97 1 830 NP_510966.1 3 221 CTGGTCCTGCTG TGT ----- C 1 B c c
CTGGCTGCCTCT TGGAGC GAG CAGCAGCA
CTGCTCCA ACCTCG CTC GTCGTCGT
TCT CGTCG C
GAM139 327 CDC42 1 17563 NP_001782.1 3 11 AGGTGTGTGCTG CT ---- - 1 B c c
CTATGACATCTC TGGAG GTG AGCAGCA GCAC
TCCAGAGC ACCTC TAC TCGTCGT TGTG
TC AGTA G
GAM139 327 CDH12 1 12987 NP_004052.2 5 526 CCGTCGGTGCTG T-- - -- 1 B c c
CTGCTCCTGCAG GG AGCTGT GAGCAGCAGCAC
CTGCCTTT CC TCGACG CTCGTCGTCGTG
TTT G TC
GAM139 327 CDKN1A 1 10006 NP_510867.1 5 197 GGGTGTGTGCTG T-- ---- A 1 B c c
CGTTCACAGGTG GGAG CTGTGAGC GCAGCACA
TTTCTGCG TCTT GACACTTG CGTCGTGT
GCG TGTG -
GAM139 327 CDW92 1 14794 NP_536856.2 3 2104 CATGGACTGTTG TGT C 1 B c
c
CTGCTCCCTGTT TGGAGC GAGCAGCAGCA
CCATATGC ACCTTG CTCGTCGTTGT
TCC C
GAM139 327 CLN8 1 2997 NP_061764.2 3 2721 ACGTGTGTGCTG C- - - 1 B c c
CGTGCTTCACAT TGGAG TGTGA GCA GCAGCACA
CCTCTATT ATCTC ACACT CGT CGTCGTGT
CT T G

GAM139 327 CNN1 1 15985 NP_001290.2 3 61 GGGAGGCTGCTG ---- T C 1 B c c
CTGCTCTTGGCT TGG AGCTG GAGCAGCAGCA
GGACCCAG ACC TCGGT CTCGTCGTCGT
CAGG T C
GAM139 327 CPR8 1 4018 NP_004739.2 5 8 CTTTCCGTGCGC A A- A 1 B c c
GAGTGCACAGCT TGGAGCTGTG GC GC GCAC
CCGGAGGC GCCTCGACAC TG CG CGTG
G AG -
GAM139 327 CSK 1 3625 NP_004374.1 3 84 GACCTGGTGCCC A -- CA 1 B c c
CTGCTCACTGGG TGG GCT GTGAGCAG GCAC
CCCGAGCC GCC CGG CACTCGTC CGTG
- GT CC
GAM139 327 DC-TM4F 1 16599 NP_112189.1 3 1264 CCCAGGCTGCAG G- A C 1 B c
c
2 CTGCTCAGAAGC TGGAGCT TGAGCAGC GCA
TCCAGGCA ACCTCGA ACTCGTCG CGT
AG A C
GAM139 327 DDX9 1 7248 NP_085077.1 5 0 CATTGCTGCTGC -- TGTG C 1 B c c
TACCTGCTTTCC TGGA GC AGCAGCAGCA
AGAGCCTT ACCT CG TCGTCGTCGT
TT TCCA T
GAM139 327 DGCR2 2 10100 NP_005128.1 3 1465 TCTGTGGTGCTG ----- G G 1 B c c
CTCGGGGATGGA TGGAG CT TGAGCAGCA CACA
CTCCATGC ACCTC GG GCTCGTCGT GTGT
AGGTA G G
GAM139 327 DGCR2 2 10383 NP_005128.1 3 1465 AGTTCTGTGGTG ----- G G 1 B c c
CTGCTCGGGGAT TGGAG CT TGAGCAGCA CACA
GGACTCCA ACCTC GG GCTCGTCGT GTGT
AGGTA G G
GAM139 327 DIM1 1 5268 NP_006692.1 3 382 ACAGAGATGTGT T----- C G 1 B c c
GCTCTCACAGCT GGAGCTGTGAG AGCA CACA
TTGCAGGC TTTCGACACTC TCGT GTGT
CGGACG - -
GAM139 327 DKFZP43 1 18675 NP_056307.1 5 531 GCCTCCCCTGCC T CA C 1 B c
c
4H132 CCTGCTCCAGCT TGGAGCTG GAGCAG GCA
CCATCCCC ACCTCGAC CTCGTC CGT
- CC C
GAM139 327 DKFZp43 2 4696 NP_115638.1 3 518 CAGGAGCTGCTG G G AC 1 B c
c
4N035 CTGCAGTTGCAG TG AGCTGT AGCAGCAGC
AAGGATAA AC TTGACG TCGTCGTCG
G - AG
GAM139 327 DKFZp43 2 19517 NP_115638.1 3 518 ACGCAGGAGCTG G G AC 1 B c
c
4N035 CTGCTGCAGTTG TG AGCTGT AGCAGCAGC
CAGAAGGA AC TTGACG TCGTCGTCG
G - AG

GAM139 327 DKFZp43 1 5662 XP_097012.2 3 708 TCATTGTGACTG - -- T - 1 B c c
4O0320 CTGCTCTCATTG TGG AGC TG GAGCAGCAG CACA
CTATCATG ACT TCG AC CTCGTCGTC GTGT
A TT T A
GAM139 327 DKFZp54 1 13133 XP_302775.1 3 222 ATGAGTGTGCTG T- ------- G 1 B c c
7I048 CTCACCTTCCCA GGAGCT GTGAGCAGCA CAC
AGTTCTGT TCTTGA CACTCGTCGT GTG
TG ACCCTTC -
GAM139 327 DKFZP56 1 18382 NP_056208.1 3 97 GCCGTGGTGCTG G G --- 1 B c c
4O0823 CTGGTGTTTGGA TG AGCT TGAGCA GCAGCAC
GTTGCAGC AC TTGA GTTTGT CGTCGTG
G G GGT
GAM139 327 DOCK1 1 5679 NP_001371.1 3 48 AAGAGTGTGCTG C T- CA 1 B c c
CCCCTCCCCATC TGGAG TG GAG GCAGCACA
TCCATGCC ACCTC AC CTC CGTCGTGT
T CC CC
GAM139 327 DOCK2 1 17284 NP_004937.1 3 25 CTGTGGCTGCTG G --- G - 1 B c c
CTGACTAGGGCT TG AGCT GT AGCAGCAGC ACA
GCATGGGA AC TCGG CA TCGTCGTCG TGT
G GAT G G
GAM139 327 DOCK2 1 17284 XP_047961.5 3 25 CTGTGGCTGCTG G --- G - 1 B c c
CTGACTAGGGCT TG AGCT GT AGCAGCAGC ACA
GCATGGGA AC TCGG CA TCGTCGTCG TGT
G GAT G G
GAM139 327 ECE2 2 11759 NP_055508.1 3 519 CTCCCAGTGCTG CT G 1 B b b
CTGCTGACCTTC TGGAG GT AGCAGCAGCAC
ACTGACAG ACTTC CA TCGTCGTCGTG
-- G
GAM139 327 ECE2 2 14658 NP_055508.1 3 519 CCAGTGCTGCTG TG ---------- G 1 B c b
CTGACCTTCACT GAGCT GT AGCAGCAGCAC
GACAGCTC CTCGA CA TCGTCGTCGTG
-- CAGTCACTTC G
GAM139 327 EDEM 1 16207 NP_055489.1 3 308 ATCTTTGGATTG G CA 1 B c c
ATGTTCACAGCT TGGAGCTGTGAGCA CAG CA
TTATACTT ATTTCGACACTTGT GTT GT
A AG
GAM139 327 EDN2 1 12597 NP_001947.1 3 265 AGTGCTGGCTGC T----- ---- - 1 B c c
TGGCCCACAGCT GGAGCTGTG AGCAGC AGCAC
CTGCTGGA TCTCGACAC TCGTCG TCGTG
AGGTCG CCGG G
GAM139 327 EGR3 1 18522 NP_004421.2 3 772 GACGCGGTGCTG T A 1 B c c
CTGCCGCCGCTT TGGAGC GTG GCAGCAGCAC
CGGGTTTG GCTTCG CGC CGTCGTCGTG
C -
GAM139 327 EHD2 1 2637 NP_055416.2 3 46 TGGCCCTGCTGT T- A C 1 B c c
GGCTCCCCAGCT TGGAGCTG GAGC GCAGCA
CCAGTCGG ACCTCGAC CTCG TGTCGT

CC G C
GAM139 327 ELL 2 4864 NP_006523.1 3 857 CATTTGTTGCTG GCT C 1 B c c
CTGCTGCTCATT TGGA GTGAGCAGCAGCA
CCACACTG ACCT TACTCGTCGTCGT
--- C
GAM139 327 ELL 2 15398 NP_006523.1 3 857 TTGTTGCTGCTG GCT C 1 B c c
CTGCTCATTCCA TGGA GTGAGCAGCAGCA
CACTGTTG ACCT TACTCGTCGTCGT
--- C
GAM139 327 EPHA1 1 1286 NP_005223.1 3 134 CTATCGGTGCTG T- G C 1 B c c
CTTCTGCCCGCT TGGAGC GT AG AGCAGCAC
TTAAGGAG ATTTCG CG TC TCGTCGTG
CC - T
GAM139 327 FBG3 1 17902 NP_149438.1 3 495 TGCCCCTGTCTG T---- - T C 1 B c c
CTGCTCCCAGTC GGAG CTG GAGCAGCAG ACA
TCTCGCTC TCTC GAC CTCGTCGTC TGT
CTCGC T C -
GAM139 327 FBXW8 1 2670 NP_036306.1 3 353 TTCTGTGTGTCC T CA A- 1 B c c
GCCCTCCCAGCT TGGAGCTG GAG GC GCACA
CCAGCCCT ACCTCGAC CTC CG TGTGT
C C- CC
GAM139 327 FBXW8 1 2670 NP_699179.2 3 353 TTCTGTGTGTCC T CA A- 1 B c c
GCCCTCCCAGCT TGGAGCTG GAG GC GCACA
CCAGCCCT ACCTCGAC CTC CG TGTGT
C C- CC
GAM139 327 FLJ1061 1 15827 NP_061940.1 3 219 GCCACTGTGCCC G CA A-- 1 B c
c
3 AGCCTCACAGCT TG AGCTGTGAG GC GCACA
GCATCTTA AC TCGACACTC CG CGTGT
G -- ACC
GAM139 327 FLJ1240 1 4490 NP_079381.1 3 818 GCAACATGTGGC G CAG 1 B c c
9 CTGTTCACAGCT TG AGCTGTGAGCAG CACA
ACATAATT AC TCGACACTTGTC GTGT
A CG-
GAM139 327 FLJ1274 1 2024 XP_290972.1 3 3290 ACTTATGTGCTG TG ---- - - - 1 B c c
7 CTAGTCTCTACT GAGCT GT GAG C AGCAGCACA
CGAAGTTC CTTGA CA CTC G TCGTCGTGT
-- AGCT T T A
GAM139 327 FLJ1275 1 15623 NP_078943.1 3 568 CTGACCTGGCTG TGT AC 1 B c
c
0 CTGCTCTTGCTT TGGAGC GAGCAGCAGC
CAGAGCCA ACTTCG CTCGTCGTCG
TT- GT
GAM139 327 FLJ1284 1 6207 NP_078872.1 3 40 GGCCTGTGGTGA - A - G 1 B c c
7 CTGCACACAGCT TG GAGCTGTG GCAG CA CACA
CGCAAAAC AC CTCGACAC CGTC GT GTGT
G A A G
GAM139 327 FLJ1324 2 3195 NP_079364.1 3 907 ATGCTCGGCCTG AGC - C 1 B c c

1 CTGCTGCTCTGC TGG TGT GAGCAGCAGCA
ACCCCCAG ACC ACG CTCGTCGTCGT
CCC T C
GAM139 327 FLJ1324 2 10155 NP_079364.1 3 908 CTCGGCCTGCTG AGC - C 1 B c
c
1 CTGCTCTGCACC TGG TGT GAGCAGCAGCA
CCCAGGGC ACC ACG CTCGTCGTCGT
CCC T C
GAM139 327 FLJ1406 1 5034 NP_079299.1 3 282 TCTCTGGTGCTG C - C 1 B c c
9 CTTCTGTATATT TGGAG TGTG AG AGCAGCAC
TCCACAGC ACCTT ATAT TC TCGTCGTG
T G T
GAM139 327 FLJ1493 2 17123 NP_116253.2 3 416 TTTGTGCTGCTG GCTGTG 1 B c
c
6 CTGTTATTCAAA TGGA AGCAGCAGCACA
GATCAAAG ACTT TCGTCGTCGTGT
ATTG--
GAM139 327 FLJ1493 2 18005 NP_116253.2 3 416 GGATTTGTGCTG GCTGTG 1 B c
c
6 CTGCTGTTATTC TGGA AGCAGCAGCACA
AAAGATCA ACTT TCGTCGTCGTGT
ATTG--
GAM139 327 FLJ2031 1 13985 NP_060233.1 3 195 AGGGTGCCGTTT T ---- A 1 B c c
5 CCTGCTCCAGCT TGGAGCTG GAGCAG C GCAC
CCAGACCT ACCTCGAC CTCGTC G CGTG
- CTTT C
GAM139 327 FLJ2055 1 18638 NP_060350.1 3 208 TTTTTGATGCTG - A C 1 B c c
8 CTGTGTACAGTC TGGAG CTGTG GCAGCAGCA
TTCATTAT ACTTC GACAT TGTCGTCGT
T G A
GAM139 327 FLJ2069 2 7805 NP_060401.1 3 657 GTGTGAGTGCTG CTGT G- 1 B c
c
9 CTCTTTCCACCT TGGAG GAGCAGCA CACA
GCCTTGCA ACCTT CTCGTCGT GTGT
T--- GA
GAM139 327 FLJ2069 2 12279 NP_060401.1 3 657 CCAGTGTGAGTG CTGT G- 1 B c
c
9 CTGCTCTTTCCA TGGAG GAGCAGCA CACA
CCTGCCTT ACCTT CTCGTCGT GTGT
T--- GA
GAM139 327 FLJ2116 1 1748 NP_079349.1 5 57 GGGGTGGTGCTG G GTG 1 B c c

8 CTGCTATGAGCT TG AGCT AGCAGCAGCAC
GCACCATC AC TCGA TCGTCGTCGTG
G GTA
GAM139 327 FLJ2267 1 20087 NP_079173.2 5 590 CGTGCTGCGCGC ---- A A- 1 B c c
2 ACACCTTCAGCT TGGAGCT GTG GC GCAGCAC
CCATGTCG ACCTCGA CAC CG CGTCGTG
CTTC A CG
GAM139 327 FLJ2516 1 14009 NP_689679.1 5 268 TAGGTGGTGCTG T------- C T 1 B c c

8 CTGCTCCATTCC GGAG TG GAGCAGCAGCAC
CAAGTAAC CCTT AC CTCGTCGTCGTG
CAATGAAC - -

GAM139 327 FLJ3043 1 14922 NP_694554.1 3 1401 AGCTGTCTGTTC - C C C 1 B c c
0 CTGCTCACACTG TGG AG TGTGAGCAG AGCA
CCAGAATC ACC TC ACACTCGTC TTGT
G - C C

GAM139 327 FLJ3210 2 8172 NP_694579.1 3 1285 CTCTTCATGGTG G --- 1 B c c
4 CTGCTCCTGCTA TGGAGCTGT AGCA GCAGCAC
TGGTTCCA ACCTTGGTA TCGT CGTCGTG
- CCT

GAM139 327 FLJ3210 2 8933 NP_694579.1 3 1287 TTCATGGTGCTG G --- 1 B c c
4 CTCCTGCTATGG TGGAGCTGT AGCA GCAGCAC
TTCCACAG ACCTTGGTA TCGT CGTCGTG
- CCT

GAM139 327 FLJ3241 1 15601 NP_653217.1 5 26 CGGGACCTGCTG ---- T C 1 B c c
6 CTGCTCCAGCCA TGGA GCTG GAGCAGCAGCA
TGTCCATG ACCT CGAC CTCGTCGTCGT
GTAC - C

GAM139 327 FLJ3666 1 19742 NP_689695.1 3 1087 ACTTCTGTGCTG T-- -- - 1 B c c
6 CTTGCAGTCATA GGAGCTGTGA GCA GCAGCACA
GCTTTCCT TTTCGATACT CGT CGTCGTGT
TCC GA T

GAM139 327 FLJ3879 2 6257 NP_848615.1 3 1797 AGGCATCTGCTG - T C 1 B c c
2 CTGCTCCTGGCT TGG AGCTG GAGCAGCAGCA
GCCACTCA ACC TCGGT CTCGTCGTCGT
G C C

GAM139 327 FLJ3879 2 9676 NP_848615.1 3 1797 CACAGGCATCTG - T C 1 B c c
2 CTGCTGCTCCTG TGG AGCTG GAGCAGCAGCA
GCTGCCAC ACC TCGGT CTCGTCGTCGT
G C C

GAM139 327 FLJ4085 2 1395 NP_775948.1 5 143 TGGTGTGGCCTG G - TG -- 1 B c c
2 CTGCTTCCAGGC TG AGC TG AGCAGCAG CACA
TGCAAACC AC TCG AC TCGTCGTC GTGT
G G CT CG

GAM139 327 FLJ4085 2 13085 NP_775948.1 3 1350 CAGTGCTCCTGA T----- ---- C 1 B c c
2 CTCCTCACAGCT GGAGCTGTGAG CAG AGCAC
CTGTTCCT TCTCGACACTC GTC TCGTG
TCCTTG CTCA C

GAM139 327 FLJ9073 1 15777 NP_699206.1 5 262 GGCTCGGTGCTG T--- A- - 1 B c c
4 CTGCTCGTCAGC GG GCTG TGAGCAGCAGCAC
GACCCCAG CC CGAC GCTCGTCGTCGTG
GACC AG T

GAM139 327 FNBP1 1 3529 XP_052666.3 3 2145 GTGAGTGTGGCA A-- A A 1 B c c
GTCCCCACAGCT TGGAGCTGTG GC GC GCAC
CCACAATG ACCTCGACAC TG CG TGTG
CCC A G

GAM139 327 FZD4 1 2318 NP_036325.2 3 2157 CTCCCTGTGCTG T---- GA - 1 B c c
CTTGTAGACAGT GGAGCTGT GCA GCAGCACA
TCCCATAA CCTTGACA TGT CGTCGTGT

AATAC GA T

GAM139 327 GABARAP 1 1612 NP_113600.1 5 25 CCAGCTGTTTTT - ----- AC 1 B c c
L1 GTGCTCACAAGC TGGAGCT GTGAGCA GCAGC
TCTAGCGA ATCTCGA CACTCGT TGTCG
A GTTTT AC

GAM139 327 GABBR1 1 19293 NP_068705.1 3 36 GACTGCTGTGGG - AG 1 B c c
CTGCTCACTGGC TGGAGCT GTGAGCAGC CACA
TTTAGCTG ATTTCGG CACTCGTCG GTGT
T G-

GAM139 327 GAK 1 3648 NP_005246.1 3 37 GTGGTGGTGGCT A A - 1 B b b
GCGCACACAGCT TGGAGCTGTG GC GCAGC AC
CCACAGGT ACCTCGACAC CG CGTCG TG
A - G

GAM139 327 GAS7 1 6544 NP_005881.1 3 1339 CTTTCAGTGCTG TG-- --- 1 B c c
CTGTTTGGCCCA GAGCTG TGAGCAGCAGCAC
GCTCATTA CTCGAC GTTTGTCGTCGTG
ATTA CCG

GAM139 327 GAS8 1 11159 NP_001472.1 3 351 CGCGCTGTGCTG A TGT - - 1 B c c
CCTGTCTTCGCG TGG GC GAG CAG CAGCACA
CCACTGTT ACC CG TTC GTC GTCGTGT
G C-- T C

GAM139 327 GBP5 1 13996 NP_443174.1 5 44 TAAATCTTGCTG G ----- C 1 B c c
CTGCTCACTCTT TGGA CT GTGAGCAGCAGCA
TGGGTCCA ACCT GG CACTCGTCGTCGT
G TTTCT T

GAM139 327 GCNT1 1 7810 NP_001481.2 5 73 CTTTTAAATGTG GCT C 1 B c c
CTGCTCTTCATT TGGA GTGAG AGCAGCACA
TCAAGATG ACTT TACTT TCGTCGTGT
--- C

GAM139 327 GDI2 1 15867 NP_001485.2 3 342 TATGTGCTGCTG ---- G- C 1 B c c
CTGCTCAAGAGC TGGA GCT TGAGCAGCAGCA
TGGATCCA ACCT CGA ACTCGTCGTCGT
AGGT GA C

GAM139 327 GFAP 1 5626 NP_002046.1 3 1662 CTGCTGCTGCTG - T G C 1 B c c
CTGCTGCTAATC TGG AGC GT AGCAGCAGCA
TTCAGGGC ATC TCG CG TCGTCGTCGT
G T - C

GAM139 327 GGA2 1 10502 NP_619581.1 3 974 TCTCAGATGCTG GC - C 1 B c c
CTGCTTGACAAT TGGA TGT GAGCAGCAGCA
CCACACAA ACCT ACA TTCGTCGTCGT
A- G A

GAM139 327 GK001 1 15464 NP_064583.1 3 1298 CAGCATGTGCTG G C TG -- 1 B c
c
CTGCCTTTGTAA TG AG TG A GCAGCAGCACA
CTGCATGG AC TC AT T CGTCGTCGTGT
G A GT TC

GAM139 327 GOLGA1 2 426 NP_002068.1 3 264 CACAGTGCTGCT T GC-- 1 B c c
AATATCCCAGCT TGGAGCTG GA AGCAGCAC
CCAGCCAG ACCTCGAC CT TCGTCGTG
C ATAA

GAM139 327 GOLGA1 2 14520 NP_002068.1 3 264 TCCACAGTGCTG T GC-- 1 B c c

CTAATATCCCAG TGGAGCTG GA AGCAGCAC
CTCCAGCC ACCTCGAC CT TCGTCGTG
C ATAA

GAM139 327 GOSR1 1 16929 NP_004862.1 3 0 TGTTGCTGCTGT T A C 1 B c c

ATGCGTTCCATT TGGAGC GTG GCAGCAGCA
GTGGGACA ACCTTG CGT TGTCGTCGT
- A T

GAM139 327 GPLD1 1 2598 NP_001494.2 5 51 GTCCCAGTGCTG T--------- GTGA 1 B c c

CTGCAGCTCTGA GGAGCT GCAGCAGCAC
GCATTCCC TCTCGA CGTCGTCGTG
CCCTTACGAG ----

GAM139 327 GPR108 2 790 XP_290854.1 5 46 CTTCTGGTGCTG T G---- 1 B c c

CTGCTGGGTGGC TGGAGC GT AGCAGCAGCAC
TGCTCCGG GCCTCG CG TCGTCGTCGTG
T GTGGG

GAM139 327 GPR108 2 14653 XP_290854.1 5 46 CTGGTGCTGCTG T G---- 1 B c c

CTGGGTGGCTGC TGGAGC GT AGCAGCAGCAC
TCCGGGCG GCCTCG CG TCGTCGTCGTG
T GTGGG

GAM139 327 GPR124 1 3798 NP_116166.6 3 549 CACAAGGTGCTG G T C 1 B c c

CTTTTCAGATCC TGGA CTG GAG AGCAGCAC
ACTATGCA ACCT GAC TTT TCGTCGTG
A - -

GAM139 327 GPR35 1 20062 NP_005292.1 5 158 TGACAGGTGCTG T----- A GT - 1 B c c

CTGCCTCTGAGC GG GCT GAG CAGCAGCAC
CCTCCCTG CC CGA CTC GTCGTCGTG
GTCCCT - GT C

GAM139 327 GRIP1 2 7684 XP_290559.2 5 166 ATTCATATGCTG A- G C 1 B c c

CTGCTGCTGCAG TGG GCTGT AGCAGCAGCA
CCACCAGA ACC CGACG TCGTCGTCGT
AC - C

GAM139 327 GRIP1 2 10480 XP_290559.2 5 166 CATATGCTGCTG A- G C 1 B c c

CTGCTGCAGCCA TGG GCTGT AGCAGCAGCA
CCAGAGCA ACC CGACG TCGTCGTCGT
AC - C

GAM139 327 HIP14 1 15808 NP_056151.1 5 247 AGACTTGTGCTG GA A 1 B c c

CGTGCGGCTCCG TGGAGCTGT GC GCAGCACA
GAGCTCTG GCCTCGGCG TG CGTCGTGT
-- -

GAM139 327 HMGA1 1 11875 NP_002122.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665906.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665907.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665908.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665909.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665910.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665911.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HMGA1 1 11875 NP_665912.1 3 1041 CCGTCATTGCTG A TG C 1 B c c

CTGCTACCAGCG TGG GCTG AGCAGCAGCA
CCAAATGT ACC CGAC TCGTCGTCGT
G CA T

GAM139 327 HP43.8K 2 11596 NP_115946.2 5 390 GTCGCGCTGCTG T GA C 1 B c c

D CTGCGGCGCTCC TGGAGC GT GCAGCAGCA
AAGTTCAT ACCTCG CG CGTCGTCGT
- G- C

GAM139 327 HP43.8K 2 13643 NP_115946.2 5 390 CCCGTCGCGCTG T GA C 1 B c c

D CTGCTGCGGCGC TGGAGC GT GCAGCAGCA
TCCAAGTT ACCTCG CG CGTCGTCGT
- G- C

GAM139 327 HPCAL1 1 15809 NP_602293.1 5 326 GTCTCTGGGTTG T - AC 1 B c c
GCTGTTCCAGCT TGGAGCTG GAGCAGC AGC
CCAAAGAG ACCTCGAC CTTGTCG TTG
- G GG

GAM139 327 HPS4 1 14923 NP_071364.4 3 1557 TTCTCTGCTGTG G --- C 1 B c c
GTTGCTGCAGCT TGGAGCTGT AGCA GCAGCA
CCAGGAAG ACCTCGACG TCGT TGTCGT

```
                                                - TGG    C
GAM139  327  HPS4   1  14923 NP_690053.1  3 3202  TTCTCTGCTGTG      G  ---   C     1 B c c
                                GTTGCTGCAGCT TGGAGCTGT AGCA  GCAGCA
                                CCAGGAAG    ACCTCGACG TCGT  TGTCGT
                                                - TGG    C
GAM139  327  HPS4   1  14923 NP_690054.1  3 1557  TTCTCTGCTGTG      G  ---   C     1 B c c
                                GTTGCTGCAGCT TGGAGCTGT AGCA  GCAGCA
                                CCAGGAAG    ACCTCGACG TCGT  TGTCGT
                                                - TGG    C
GAM139  327  HPS4   1  14923 NP_690055.1  3 3402  TTCTCTGCTGTG      G  ---   C     1 B c c
                                GTTGCTGCAGCT TGGAGCTGT AGCA  GCAGCA
                                CCAGGAAG    ACCTCGACG TCGT  TGTCGT
                                                - TGG    C
GAM139  327  HPS4   1  14923 NP_690056.1  3 599   TTCTCTGCTGTG      G  ---   C     1 B c c
                                GTTGCTGCAGCT TGGAGCTGT AGCA  GCAGCA
                                CCAGGAAG    ACCTCGACG TCGT  TGTCGT
                                                - TGG    C
GAM139  327  HSA2508 1  15722 NP_060871.1  3 32    CCACACTTGTTG  G --  -      C     1 B c c
        39                       CTGCTCAACAGG TG AG  CTGT GAGCAGCAGCA
                                ACTGCACT    AC TC  GACA CTCGTCGTTGT
                                        G AG   A        T
GAM139  327  HUMAGCG 1  10384 NP_037418.2  3 1869  TTTACTTGAGCT  -    G G   AC      1 B c
 c
        B                        GTGGTCACAGCT TGG AGCTGTGA CA CAGC
                                GCCAGGTA    ACC TCGACACT GT GTCG
                                        G      G -   AG
GAM139  327  HUMAGCG 1  10384 XP_291083.2  3 1865  TTTACTTGAGCT  -    G G   AC      1 B c
 c
        B                        GTGGTCACAGCT TGG AGCTGTGA CA CAGC
                                GCCAGGTA    ACC TCGACACT GT GTCG
                                        G      G -   AG
GAM139  327  HYOU1  2  3370  NP_006380.1  3 1175  GAGCTAGGGCTG      TGA     AC      1 B c
c
                                CTGCCTCAGCTC TGGAGCTG  GCAGCAGC
                                CAAGACAA    ACCTCGAC  CGTCGTCG
                                        TC-      GG
GAM139  327  HYOU1  2  5055  NP_006380.1  3 1175  GGAGCTAGGGCT      TGA     AC      1 B c
c
                                GCTGCCTCAGCT TGGAGCTG  GCAGCAGC
                                CCAAGACA    ACCTCGAC  CGTCGTCG
                                        TC-      GG
GAM139  327  ICMT   2  6960  NP_733806.1  5 215   CTCAACGCGCTG    T G     AC      1 B c c
                                CTGCTGCTGCTC TGGAGC GT AGCAGCAGC
                                TATCGGCC    ATCTCG CG TCGTCGTCG
                                        T -      CG
GAM139  327  ICMT   2  8391  NP_733806.1  5 215   AACGCGCTGCTG    T G     AC      1 B c c
                                CTGCTGCTCTAT TGGAGC GT AGCAGCAGC
                                CGGCCGCC    ATCTCG CG TCGTCGTCG
                                        T -      CG
GAM139  327  IGSF4  1  15663 NP_055148.2  3 645   AACTCTTTGCTG    T A     C       1 B c c
```

CTGCCCATGTTT TGGAGC GTG GCAGCAGCA
CAAATACT ACTTTG TAC CGTCGTCGT
- C T

GAM139 327 IL-17RE 3 1468 NP_653241.1 3 310 ACTGTGCTGCTG A G---- 1 B c c
CTGTGGAGCGGC TGG GCTGT AGCAGCAGCACA
GCCGACCT GCC CGGCG TCGTCGTCGTGT
G AGGTG

GAM139 327 IL-17RE 3 1468 NP_705615.1 3 310 ACTGTGCTGCTG A G---- 1 B c c
CTGTGGAGCGGC TGG GCTGT AGCAGCAGCACA
GCCGACCT GCC CGGCG TCGTCGTCGTGT
G AGGTG

GAM139 327 IL-17RE 3 14593 NP_653241.1 3 310 GGCACTGTGCTG A G---- 1 B c c
CTGCTGTGGAGC TGG GCTGT AGCAGCAGCACA
GGCGCCGA GCC CGGCG TCGTCGTCGTGT
G AGGTG

GAM139 327 IL-17RE 3 14593 NP_705615.1 3 310 GGCACTGTGCTG A G---- 1 B c c
CTGCTGTGGAGC TGG GCTGT AGCAGCAGCACA
GGCGCCGA GCC CGGCG TCGTCGTCGTGT
G AGGTG

GAM139 327 IL-17RE 3 19627 NP_653241.1 3 410 CGCCCGCTGCTG CT- C 1 B c c
CTGCTCGCTTAC TGGAG GTGAGCAGCAGCA
TTCAGTCG ACTTC CGCTCGTCGTCGT
ATT C

GAM139 327 IL-17RE 3 19627 NP_705615.1 3 410 CGCCCGCTGCTG CT- C 1 B c c
CTGCTCGCTTAC TGGAG GTGAGCAGCAGCA
TTCAGTCG ACTTC CGCTCGTCGTCGT
ATT C

GAM139 327 ILKAP 1 9889 NP_110395.1 5 94 TGTCTGTCGCTG CT A - 1 B c c
CTGCCGCCTCCA TGGAG GTG GCAGCAGC ACA
CCCAGCCT ACCTC CGC CGTCGTCG TGT
-- - C

GAM139 327 ILKAP 1 9889 NP_789769.1 5 94 TGTCTGTCGCTG CT A - 1 B c c
CTGCCGCCTCCA TGGAG GTG GCAGCAGC ACA
CCCAGCCT ACCTC CGC CGTCGTCG TGT
-- - C

GAM139 327 KCNMB1 1 8103 NP_004128.1 5 337 AGAAACTGTCTG AG G C 1 B c
c
CTGCTCAAGACC TGG CT TGAGCAGCAG ACA
CACAGGAC ACC GA ACTCGTCGTC TGT
CA - -

GAM139 327 KCNN2 1 3750 NP_067627.2 5 160 CTGCTGCTGCTG A TG C 1 B c c
CTGCTCGTCGCG TGG GC TGAGCAGCAGCA
CCGGGGCA GCC CG GCTCGTCGTCGT
G CT C

GAM139 327 KIAA018 1 6545 XP_050495.4 3 1657 CCTGTGTGCCGG ---- T A- 1 B c c
2 CTGCTCACTGCT TGG AGC GTGAGCAGC GCACA
GTGACCAG ACC TCG CACTCGTCG CGTGT
AGTG T GC

GAM139 327 KIAA024 1 18761 NP_055549.1 3 1099 GTCCCCGGGTGG GA AG 1 B c
c

	7				CTGCAGGCAGCT TGGAGCTGT GCAGC CAC CCAGCCCG ACCTCGACG CGTCG GTG GA --								
GAM139	327 0	KIAA029	1	8089	NP_055937.1 3 32 CCGCAAATGCTG TGA C CTGCCCCAGCTC TGGAGCTG GCAGCAGCA TACACTGC ATCTCGAC CGTCGTCGT CC- A						1	B	c c
GAM139	327 9	KIAA045	1	9393	XP_027862.1 3 4427 GATCCAGAGCTG T --- T C CTGCTGCTCACT GGA GC GTGAGCAGCAGCA GCCAGTCC CCT CG CACTCGTCGTCGT - GAC T C						1	B	c c
GAM139	327 5	KIAA047	1	14521	NP_055679.1 3 3023 GAGATTGTGCTG T----- A T -- CTGCACTCCAGC GG GCTG GA GCAGCAGCACA CTGGGAGA TC CGAC CT CGTCGTCGTGT AGAGGG - - CA						1	B	c c
GAM139	327 4	KIAA051	2	11461	NP_055511.1 3 2606 GCACAGCTGCTG G G AC CTGACAGGTCTA TGGA CTGT AGCAGCAGC CCTGAAGT ATCT GACA TCGTCGTCG G G AC						1	B	c c
GAM139	327 4	KIAA051	2	14213	NP_055511.1 3 2606 GTTGCACAGCTG G G AC CTGCTGACAGGT TGGA CTGT AGCAGCAGC CTACCTGA ATCT GACA TCGTCGTCG G G AC						1	B	c c
GAM139	327 2	KIAA057	1	7196	XP_291018.1 3 2535 ATGTTGATGCTG A C CTGTTCATGGCA TGG GCTGTGAGCAGCAGCA CTACAAAG ATC CGGTACTTGTCGTCGT A A						1	B	c c
GAM139	327 2	KIAA065	1	7082	NP_055556.1 3 679 CTGCCTGTGCTC ------ G - C AGGTCCTCAGCT TGGAGCTG TGAGCA CAG CA CCATGGGA ACCTCGAC ACTCGT GTC GT TCCTGG - C C						1	B	c c
GAM139	327 3	KIAA068	1	17564	NP_057195.1 3 333 ACGGTGTACCTG A- G --- CTGCTCAGAGCC TGG GCT TGAGCAGCAG CAC CCCAAGGC ACC CGA ACTCGTCGTC GTG CC G CAT						1	B	c c
GAM139	327 3	KIAA086	1	4169	NP_055728.1 3 133 GTCACTGTGCTG --- G - C CTCTGCAGAGTT TGGAG CT TG AG AGCAGCACA ACTTCAGG ACTTC GA AC TC TCGTCGTGT ATT G G -						1	B	c c
GAM139	327 2	KIAA096	1	19480	XP_290942.1 3 448 CCTGCTGTGCTG T - A---- CTGCCATGGCGC GGAGC TGTG GCAGCAGCACA ATGCTCCT CCTCG ACGC CGTCGTCGTGT T T GGTAC						1	B	c c
GAM139	327 3	KIAA122	1	15273	XP_048747.2 3 1104 TAAAATGTGCTG AG---- CA CCCTTCACAGAT TGG CTGTGAG GCAGCACA GACACCAC ACC GACACTT CGTCGTGT						1	B	c c

ACAGTA CC
GAM139 327 KIAA139 2 12571 XP_046685.4 3 870 AGCACAGTTCTG TG G C 1 B c c
9 CTGCTGTGGCTT TGGAGC T AGCAGCAG AC
CAGCTTTG ACTTCG G TCGTCGTC TG
GT - T
GAM139 327 KIAA139 2 17214 XP_046685.4 3 870 ACAGTTCTGCTG TG G C 1 B c c
9 CTGTGGCTTCAG TGGAGC T AGCAGCAG AC
CTTTGGAA ACTTCG G TCGTCGTC TG
GT - T
GAM139 327 KIAA144 2 14694 XP_044921.4 5 51 GCCGGGCTGCTG T G C 1 B c c
2 CTGCTGCTGCTC TGGAGC GT AGCAGCAGCA
CAGGTGCT ACCTCG CG TCGTCGTCGT
T - C
GAM139 327 KIAA144 2 15532 XP_044921.4 5 50 TCGGCCGGGCTG T G C 1 B c c
2 CTGCTGCTGCTG TGGAGC GT AGCAGCAGCA
CTCCAGGT ACCTCG CG TCGTCGTCGT
T - C
GAM139 327 KIAA150 1 9747 XP_029353.1 3 558 GTGAGAGTGCTG T------- C T 1 B c c
9 CTGTTCCATTCC GGAG TG GAGCAGCAGCAC
TGGGGTCC CCTT AC CTTGTCGTCGTG
CCTGGGGT - -
GAM139 327 KIAA184 1 14729 XP_030838.3 3 2484 TTTGGTGTGCTG A - T- G 1 B c c
3 CTTCCCATGCAC TGG GC TG GAGCAGCA CAC
TACTTTGA ATC CG AC TTCGTCGT GTG
A T CC -
GAM139 327 KIAA188 1 12647 XP_170901.1 3 767 AACAGGCTGCTG T---- - T - C 1 B c c
1 CTGCCTCCAGCT GG AGCTG GAG CAGCAGCA
GCCCACCA CC TCGAC CTC GTCGTCGT
ACCAC G - C C
GAM139 327 KIAA192 1 17408 XP_085210.1 3 163 TGCCATTTGCTG AG - A C 1 B c c
0 CTGCCGCCAGGA TGG CTG TG GCAGCAGCA
CCAGAGCA ACC GAC GC CGTCGTCGT
AG C - T
GAM139 327 KIF1B 1 2509 NP_055889.1 3 419 ATGTCTGTGCTG T---- A -- G 1 B c c
CTGTCACCAGGC GG GCT GTGA CAGCAGCACA
ACCTTTGT CC CGG CACT GTCGTCGTGT
TGTTT A AC -
GAM139 327 KREMEN2 2 10367 NP_663323.1 3 34 TCGGTGCTGCTG T--------- T G 1 B c
c
CTGCTGCTCCTG GGAGC GT AGCAGCAGCAC
GGGCTGCT CCTCG CG TCGTCGTCGTG
TCGTCGGGGT T -
GAM139 327 KREMEN2 2 17585 NP_663323.1 3 34 GTCTCGGTGCTG T------ T G 1 B c
c
CTGCTGCTGCTC GGAGC GT AGCAGCAGCAC
CTGGGGCT CCTCG CG TCGTCGTCGTG
TCGGGGT T -

GAM139 327 KRTAP4- 1 2298 NP_149442.1 3 208 GACCATGTGCTG TG-- A A 1 B c c

13 CCGCCCAACCTG TGGAGC TG GC GCAGCACA
CTCTAGTG ATCTCG AC CG CGTCGTGT
TCCA C C

GAM139 327 KRTAP4- 1 2298 NP_115913.1 3 208 GACCATGTGCTG TG-- A A 1 B c c

4 CCGCCCAACCTG TGGAGC TG GC GCAGCACA
CTCTAGTG ATCTCG AC CG CGTCGTGT
TCCA C C

GAM139 327 KRTAP9- 1 19929 NP_114167.2 3 15 GCCTTCTTGCTG T G C 1 B c c
2 CTGTCACGTTCC TGGAGC GTGA CAGCAGCA
AAGAGAAC ACCTTG CACT GTCGTCGT
- - T

GAM139 327 LARP 1 12149 NP_056130.1 5 2330 GGCCCCGTACTG - AGC C 1 B c
c

CTTCCATCAGCT TGGAGCTG TG AGCAG AC
CCAGCCCC ACCTCGAC AC TCGTC TG
T CT- A

GAM139 327 LDB1 1 19322 NP_003884.1 3 489 TCCCTGCTGCCA --- CA C 1 B c c
CTTATCCCAGCT TGGAGCTG TGAG GCAGCA
CCAAGTTT ACCTCGAC ATTC CGTCGT
CCT AC C

GAM139 327 LMAN1L 1 11471 NP_078971.2 3 669 GGGCAGCAGCTG - A AC 1 B c
c

CTGCCACAGCCT TGGAG CTGTG GCAGCAGC
CCAGCGGC ACCTC GACAC CGTCGTCG
C - AC

GAM139 327 LOC1152 1 8746 NP_612453.1 3 864 AAGAGTGCAAGG - G A-- 1 B c c
07 CTGCTCAGGTCT TGGAG CT TGAGCAGC GCAC
CCAAGCGC ACCTC GG ACTCGTCG CGTG
T - GAA

GAM139 327 LOC1214 1 2311 XP_062645.2 5 167 GACAGTGTGAGC CT - A- 1 B c c
56 CTGCTCACCTTC TGGAG GTGAGCAG C GCAC
ATCCTGCT ACTTC CACTCGTC G TGTG
-- C AG

GAM139 327 LOC1305 1 11004 NP_620156.1 3 303 ACTCCCATGCTG GTG C 1 B c
c

89 CTGTTGGCTCCA TGGAGCT AGCAGCAGCA
TCTCTCCA ACCTCGG TTGTCGTCGT
--- A

GAM139 327 LOC1341 1 7606 XP_059689.2 3 685 TGTGGTGTGCTG AG--- AG 1 B c
c

11 CTGTCCACAGAT TGG CTGTG CAGCAGCACA
AAACCAGT ACC GACAC GTCGTCGTGT
AAATA CT

GAM139 327 LOC1346 1 12967 XP_059727.3 3 1133 CTGGAGGGGCTG G T- AC 1 B c
c

37 CTGCTCCTCAGT TG AGCTG GAGCAGCAGC
TGCATTTC AC TTGAC CTCGTCGTCG

G TC GG
GAM139 327 LOC1360 1 15587 XP_072440.1 5 125 CCTTTTGTGTTC T- ---- C 1 B c c
15 CTGCTCACTTCA GGAGCT GTGAGCAG AGCACA
AGCTTCTT CTTCGA CACTCGTC TTGTGT
TT ACTT C
GAM139 327 LOC1429 1 13772 XP_084389.1 3 171 ACTTCTGTGCTG CTGT 1 B c c
55 CTGCTTCTCCTC TGGAG GAGCAGCAGCACA
CATCTTGC ACCTC TTCGTCGTCGTGT
CTC-
GAM139 327 LOC1439 1 5549 NP_849156.1 5 236 CTAGAGATGCTG G A C 1 B c c
03 CTGCCGCGGTTG TG AGCTGTG GCAGCAGCA
CAGTTGTC AC TTGGCGC CGTCGTCGT
G - A
GAM139 327 LOC1439 1 5549 XP_084655.1 5 235 CTAGAGATGCTG G A C 1 B c c
03 CTGCCGCGGTTG TG AGCTGTG GCAGCAGCA
CAGTTGTC AC TTGGCGC CGTCGTCGT
G - A
GAM139 327 LOC1453 1 10022 XP_085128.1 5 78 ACCTCAGTGCTG TGAG 1 B c c
84 CTGGACTCAGTT TGGAGCTG CAGCAGCAC
CCAAGATC ACCTTGAC GTCGTCGTG
TCAG
GAM139 327 LOC1458 2 13581 XP_096879.1 5 944 TATCTTCTGCTG G G C 1 B c c
28 CTGCTTGGAGTT TG AGCT TGAGCAGCAGCA
ACATTTTC AC TTGA GTTCGTCGTCGT
A G C
GAM139 327 LOC1458 2 17903 XP_096879.1 5 944 ATTTATCTTCTG G G C 1 B c c
28 CTGCTGCTTGGA TG AGCT TGAGCAGCAGCA
GTTACATT AC TTGA GTTCGTCGTCGT
A G C
GAM139 327 LOC1463 1 6404 XP_085421.2 5 191 CCTGCAGTGCTG - C TGA 1 B c
c
36 CTGCCCTCGTCT TGG AG TG GCAGCAGCAC
ACCAGTGG ACC TC GC CGTCGTCGTG
A T TCC
GAM139 327 LOC1467 1 10927 XP_085588.1 5 1274 TACCTGTTTCTG G GTG C- 1 B c
c
84 CTGCTAGAAGAT TGGA CT AGCAGCAG ACA
CCAGGAAA ACCT GA TCGTCGTC TGT
A AGA TT
GAM139 327 LOC1467 2 4648 XP_085593.1 5 288 AGCCGATTTGTG A- - C 1 B c c
95 CTGCTCTCAGCA TGG GCTG TGAG AGCAGCACA
GCCACCGG GCC CGAC ACTC TCGTCGTGT
AC G -
GAM139 327 LOC1467 2 11983 XP_085593.1 5 288 CGATTTGTGCTG A- - C 1 B c c
95 CTCTCAGCAGCC TGG GCTG TGAG AGCAGCACA
ACCGGGGA GCC CGAC ACTC TCGTCGTGT
AC G -
GAM139 327 LOC1469 1 4941 XP_097142.1 5 477 TTCCTCCAATGT CAGC 1 B c c

58 GCTTTCACAGCT TGGAGCTGTGAG AGCACA
TCACTTCC ACTTCGACACTT TCGTGT

GAM139 327 LOC1498 2 13423 XP_097747.1 5 637 ACCCTGGTCTTG - C C 1 B c c
37 CTGCTCATATCT TGG AG TGTGAGCAGCAG AC
GCCAGGAA ACC TC ATACTCGTCGTT TG
G T C
GAM139 327 LOC1498 2 16008 XP_097747.1 5 1667 CTGAAGTGCAGG T---- - A- 1 B c c

37 TTGCTCACAGCA GGA GCTGTGAGCAGC GCAC
TCCTACAA CCT CGACACTCGTTG CGTG
AACAT A GA
GAM139 327 LOC1509 1 18977 XP_097971.1 3 247 CTTGTGTGGCTG G GTG - 1 B c
c
33 CTGCTGGGTCCA TGGA CT AGCAGCAGC ACA
GTCCTGGA ACCT GG TCGTCGTCG TGT
G --- G
GAM139 327 LOC1530 1 12321 XP_041221.1 3 531 CCATGGTAGTTG T----- - 1 B c c
27 CTGCTCATGGTT GGAGCTGTGAGCAGCAGC AC
CTGTCTGT TCTTGGTACTCGTCGTTG TG
TGTCTG A
GAM139 327 LOC1540 1 8503 XP_098466.1 3 729 AGGGGTGTGCTG A A G 1 B c c

92 CGTACAGCCCCG TGG GCTGTG GCAGCA CAC
ATGACCAC GCC CGACAT CGTCGT GTG
C G -
GAM139 327 LOC1656 1 8963 XP_093333.6 5 437 GGCAGTGGTGCT T------ A -- G 1 B c
c
22 GGCCTCACAGCC GG GCTGTGAG CAGCA CAC
CTGGCCAT CC CGACACTC GTCGT GTG
TACCGGT - CG G
GAM139 327 LOC1686 1 8774 XP_166592.1 5 112 GGGAATGTGCTG GC AGCA 1 B c
c
67 CCCCACATGTCC TGGA TGTG GCAGCACA
AGGCT ACCT ACAC CGTCGTGT
GT CC--
GAM139 327 LOC2002 1 5316 XP_114166.1 5 108 CTGGACGTGCTG C AG-- 1 B c c

30 CTGATGGTACAC TGGAG TGTG CAGCAGCAC
CTCCAAGT ACCTC ACAT GTCGTCGTG
C GGTA
GAM139 327 LOC2005 3 2414 XP_114265.1 3 146 GTCCTGTAGCTG TG - 1 B c c
83 CTGCTGCTGGCT TGGAGCTG AGCAGCAGC ACA
CCACTCCT ACCTCGGT TCGTCGTCG TGT
CG A
GAM139 327 LOC2005 3 8208 XP_114265.1 3 149 TAGCTGCTGCTG TG AC 1 B c c

83 CTGGCTCCACTC TGGAGCTG AGCAGCAGC
CTGCGGTC ACCTCGGT TCGTCGTCG
CG AT

GAM139 327 LOC2005 3 19716 XP_114265.1 3 146 CTGTAGCTGCTG TG - 1 B c c
83 CTGCTGGCTCCA TGGAGCTG AGCAGCAGC ACA
CTCCTGCG ACCTCGGT TCGTCGTCG TGT
CG A
GAM139 327 LOC2011 1 18447 XP_113916.1 5 34 CTTCCACTGTGC TGA C- 1 B c c
81 TCTCTGTCAGCT TGGAGCTG GCAG AGCACA
CCAGGTCA ACCTCGAC TGTC TCGTGT
--- TC
GAM139 327 LOC2207 1 15658 XP_167548.3 5 899 CAGACTTGGTGC AG CA 1 B c
c
39 CTGAGCGCAGCT TGGAGCTGTG CAG GCAC
CCAGGGAA ACCTCGACGC GTC CGTG
GA --
GAM139 327 LOC2219 1 15096 XP_166530.2 5 75 CTGAGGGTCCTG A GTG C 1 B c
c
33 CTGCTGGCCCCA TGG GCT AGCAGCAG AC
CCAAATAC ACC CGG TCGTCGTC TG
C --- C
GAM139 327 LOC2552 1 1320 XP_170990.1 5 13 TCCTCCCTCTGC GT CA C 1 B c c
90 CTCTGTTCAGCT TGGAGCT GAGCAG GCA
CCACCTTG ACCTCGA CTTGTC CGT
-- TC C
GAM139 327 LOC2571 1 7890 XP_171239.1 5 208 TGTGAGGTGCTG CTGT - 1 B c c
22 CTGTCTCTCCTC TGGAG GAG CAGCAGCAC
CAGCAAGG ACCTC CTC GTCGTCGTG
CT-- T
GAM139 327 LOC2830 1 4301 XP_210857.1 5 147 AGCCCCTTTCTG CTGT - C 1 B c
c
33 CTGCTGCATCCC TGGAG GA GCAGCAGCA
TCCAGTGT ACCTC CT CGTCGTCGT
C--- A C
GAM139 327 LOC2830 1 9388 XP_210877.1 5 1629 TTATAGGTGCCA AGCAGCA 1 B
c c
62 CAGGGCACAGCT TGGAGCTGTG GCAC
CCATCATT ACCTCGACAC CGTG
GGGACAC
GAM139 327 LOC2831 2 14489 XP_208042.1 5 37 TGTCTGCTGCTG G AG C 1 B c c
14 CTGTCCGAGCTT TGGAGCT TG CAGCAGCA
CACAATGC ACTTCGA GC GTCGTCGT
- CT C
GAM139 327 LOC2831 2 17069 XP_208042.1 5 37 CGGTGTCTGCTG G AG C 1 B c
c
14 CTGCTGTCCGAG TGGAGCT TG CAGCAGCA
CTTCACAA ACTTCGA GC GTCGTCGT
- CT C
GAM139 327 LOC2831 1 12328 XP_208550.1 5 495 CCAGCCTGACTG T A - C 1 B c c

98 TGGTTCCCAGCT TGGAGCTG GAGC GCAG CA
CCAGCCCT ACCTCGAC CTTG TGTC GT
C G A C
GAM139 327 LOC2832 1 17363 XP_210956.1 5 2565 CACTGAGCTGCT CT -- AC 1 B c c
70 CTGCTCACCTCT TGGAG GTGAGCA GCAGC
AGATGCTC ATCTC CACTCGT CGTCG
-- CT AG
GAM139 327 LOC2833 1 18990 XP_211003.1 3 286 GGACCGTGTTTC TGA C-- 1 B c c
64 CCTGCACCAGCT TGGAGCTG GCAG AGCAC
CCACGCTG ACCTCGAC CGTC TTGTG
CA- CCT
GAM139 327 LOC2833 1 3288 XP_208656.1 3 201 TCTTCAATACTG A T C 1 B c c
86 CTGCTGCTTACG TGG GC GTGAGCAGCAGCA
CGCCGGGA GCC CG CATTCGTCGTCGT
G - C
GAM139 327 LOC2834 1 15472 XP_211035.1 3 20 GGAGTCTTGCTG GT - C 1 B c c
35 CTGCATGTTCCA TGGAGCT GAGCA GCAGCA
GGCTCCAC ACCTCGG CTTGT CGTCGT
AC A C
GAM139 327 LOC2835 1 6596 XP_211119.1 5 43 TGAATCTTGCTG G ----- C 1 B c c
82 CTGCTCACTCTT TGGA CT GTGAGCAGCAGCA
TGGGTCCA ACCT GG CACTCGTCGTCGT
G TTTCT T
GAM139 327 LOC2836 1 1923 XP_211134.1 3 978 CAACCCTGTCTG G - C 1 B c c
37 CTGCTCCGGAGC TGGAGCT TG AGCAGCAG ACA
TCCGAGCA GCCTCGA GC TCGTCGTC TGT
G C -
GAM139 327 LOC2837 1 14435 XP_211176.1 5 946 TGGTCTGTGCTT - AGC 1 B c c
23 GGTTTAACAGCT TGGAGCTGT GAGC AGCACA
CCAACAAT ACCTCGACA TTTG TCGTGT
A GT-
GAM139 327 LOC2837 1 15242 XP_208120.1 5 13 AGTGTGGTGCTG A -- G G 1 B c c
89 CTAACATTGCCC TGG GC TGT AGCAGCA CACA
AGGCAACA ACC CG ACA TCGTCGT GTGT
- TT A G
GAM139 327 LOC2838 1 8994 XP_211207.1 5 137 CCTTGCCAGGAC T CA---- C 1 B c c
07 CTGCTCCCAGCT TGGAGCTG GAGCAG GCA
CCACGACG ACCTCGAC CTCGTC CGT
C CAGGAC T
GAM139 327 LOC2838 3 12405 XP_211228.1 5 1860 TAGCTGCTGCTG G T G C 1 B c c
52 CTGCTGCTGCTG TG AGC GT AGCAGCAGCA
CAAACTGT AC TCG CG TCGTCGTCGT
G T - C
GAM139 327 LOC2838 3 12663 XP_211228.1 5 1860 CTGCTGCTGCTG G T G C 1 B c c

52 CTGCTGCTGCAA TG AGC GT AGCAGCAGCA
ACTGTACT AC TCG CG TCGTCGTCGT
G T - C
GAM139 327 LOC2838 3 16600 XP_211228.1 5 1860 GACTAGCTGCTG G T G C 1 B c c
52 CTGCTGCTGCTG TG AGC GT AGCAGCAGCA
CTGCAAAC AC TCG CG TCGTCGTCGT
G T - C
GAM139 327 LOC2839 1 18967 XP_211259.2 5 1572 TGTGCCTTCTTG G T ----- 1 B c c
11 CTGCTCTTAGAT TGGA CTG GAGCAGCA GCACA
TTATTTCA ATTT GAT CTCGTCGT CGTGT
A T TCTTC
GAM139 327 LOC2840 1 12620 XP_210324.1 5 168 TTTGCTCCTGTT ----- C C 1 B c c
15 CCCCTCACAGCT TGGAGCTGTGAG CAG AGCA
CCAGACAT ACCTCGACACTC GTC TCGT
CCCTT C T
GAM139 327 LOC2840 1 15556 XP_208153.1 5 29 CCGCTTGTGCTG C A 1 B c c
37 CTGCCATGTCTC TGGAG TGTG GCAGCAGCACA
TAGTGATC ATCTC GTAC CGTCGTCGTGT
T -
GAM139 327 LOC2841 1 8262 XP_209031.1 5 528 TCCATGGCTGGC -- -- AC 1 B c c
30 CTGCTCACAGAG TGGAGCT GTGAGCAG CAGC
CTCTACCT ATCTCGA CACTCGTC GTCG
GA CG GT
GAM139 327 LOC2841 1 20016 XP_208171.1 5 667 TTCAAGTGCTGC AGCT - 1 B c c
67 CTGCTCACTGAC TGG GTGAGCAG CAGCAC
CAACTGCC ACC CACTCGTC GTCGTG
AGT- C
GAM139 327 LOC2841 2 6257 XP_209060.2 3 1797 AGGCATCTGCTG - T C 1 B c c
86 CTGCTCCTGGCT TGG AGCTG GAGCAGCAGCA
GCCACTCA ACC TCGGT CTCGTCGTCGT
G C C
GAM139 327 LOC2841 2 9676 XP_209060.2 3 1797 CACAGGCATCTG - T C 1 B c c
86 CTGCTGCTCCTG TGG AGCTG GAGCAGCAGCA
GCTGCCAC ACC TCGGT CTCGTCGTCGT
G C C
GAM139 327 LOC2842 2 5381 XP_208184.1 3 65 TTTCTGCTGCTG AG---- G C 1 B c c
31 CTGACAGATTAA TGG CTGT AGCAGCAGCA
CCCAACAA ACC GACA TCGTCGTCGT
CAATTA G C
GAM139 327 LOC2842 2 10934 XP_208184.1 3 65 CATTTTCTGCTG AG---- G C 1 B c c
31 CTGCTGACAGAT TGG CTGT AGCAGCAGCA
TAACCCAA ACC GACA TCGTCGTCGT
CAATTA G C
GAM139 327 LOC2844 1 8357 XP_211460.1 3 247 GCCAATATGCTG C T - C 1 B c c
34 CTGTCTCCAATT TGGAG TG GAG CAGCAGCA
TCAATAGA ACTTT AC CTC GTCGTCGT

A - T A

GAM139 327 LOC2846 1 9828 XP_211553.1 3 616 TCAGTTCTGCTG - T -- C 1 B c c
15 CTGTCTTTACTG TG GAGC GTGA GCAGCAGCA
CTCTCAAC AC CTCG CATT TGTCGTCGT
T T TC C

GAM139 327 LOC2846 1 2504 XP_211587.1 3 21 TTTAAGCTGCTG C A-- C 1 B c c
87 CTGCATACACAT TGGAG TGTG GCAGCAGCA
TTCACTTT ACTTT ACAC CGTCGTCGT
- ATA C

GAM139 327 LOC2847 2 1476 XP_211601.1 3 244 AGCCGTCTGCTG G-- - C 1 B c c
19 CTGCTGCAGGAG TGGAGCT TG AGCAGCAGCA
GCTCCACT ACCTCGG AC TCGTCGTCGT
AGG G C

GAM139 327 LOC2847 2 15624 XP_211601.1 3 245 CGTCTGCTGCTG G-- - C 1 B c c
19 CTGCAGGAGGCT TGGAGCT TG AGCAGCAGCA
CCACTTCG ACCTCGG AC TCGTCGTCGT
AGG G C

GAM139 327 LOC2847 1 13956 XP_211609.1 3 880 GTTGGGGTGCTG T----- G - 1 B c c

39 CTTGTTCAGGCT GGAGCT TGAGCA GCAGCAC
CCCCTGAC CCTCGG ACTTGT CGTCGTG
CAGTCC - T

GAM139 327 LOC2848 2 4696 XP_209394.1 5 81 CAGGAGCTGCTG G G AC 1 B c c

74 CTGCAGTTGCAG TG AGCTGT AGCAGCAGC
AAGGATAA AC TTGACG TCGTCGTCG
G - AG

GAM139 327 LOC2848 2 19517 XP_209394.1 5 81 ACGCAGGAGCTG G G AC 1 B c
c
74 CTGCTGCAGTTG TG AGCTGT AGCAGCAGC
CAGAAGGA AC TTGACG TCGTCGTCG
G - AG

GAM139 327 LOC2849 1 19183 XP_209409.1 3 0 TGTCTGTCCCTC A CA C 1 B c c
22 ACAGCACCAAAT TGG GCTGTGAG GCAG ACA
GTTCCCTG ACC CGACACTC TGTC TGT
A CC -

GAM139 327 LOC2850 2 5723 XP_210798.1 3 277 GGCCCCCGTCTG AG AG C 1 B c
c
36 CTGCTGGACACA TGG CTGTG CAGCAGCA
GAGCCATG ACC GACAC GTCGTCGT
GA AG C

GAM139 327 LOC2850 2 16269 XP_210798.1 3 277 CCCCGTCTGCTG AG AG C 1 B c
c
36 CTGGACACAGAG TGG CTGTG CAGCAGCA
CCATGAAG ACC GACAC GTCGTCGT
GA AG C

GAM139 327 LOC2850 1 5269 XP_211758.1 5 424 CAAGGAAGTCTG G --- C 1 B c c
84 CTGCTCCCCGCA TG AGCTGT GAGCAGCAG AC
GCTGCGGA GC TCGACG CTCGTCGTC TG
G CCC -

GAM139 327 LOC2851 1 16353 XP_211766.1 5 35 TTTCCTGTGGAG A TG AG 1 B c c

03 CTGCTCAGTGCC TGG GC TGAGCAGC CACA
CGGCTTAG GCC CG ACTCGTCG GTGT
- TG AG

GAM139 327 LOC2851 1 8814 XP_209475.3 5 268 GGGACGGTGCTG G AG 1 B c c

12 CTGTCCACGGTT TG AGCTGTG CAGCAGCAC
ACAGCCCA AC TTGGCAC GTCGTCGTG
A CT

GAM139 327 LOC2851 1 11345 XP_211783.1 5 179 AACTCTGTGCTG GTGAG- 1 B c c

52 CTGGGTGGAAGC TGGAGCT CAGCAGCACA
TTTATAGT ATTTCGA GTCGTCGTGT
AGGTGG

GAM139 327 LOC2855 1 2468 XP_209669.1 3 511 TAAGTCTTGCTG G ----- C 1 B c c
92 CTGCTCACTCTT TGGA CT GTGAGCAGCAGCA
TGGGTCCA ACCT GG CACTCGTCGTCGT
G TTTCT T

GAM139 327 LOC2856 1 12598 XP_209685.1 5 319 CGGGCCTCAGCT A A AC 1 B c c

24 GCGGCCACAGCT TGGAGCTGTG GC GCAGC
CCAGATCG ACCTCGACAC CG CGTCG
- G AC

GAM139 327 LOC2856 1 19717 XP_209684.1 5 31 CTGCGGTGTCTG CT G - 1 B c c
25 CTGCTACTCTCC TGGAG GT AGCAGCAG CAC
GAGCTTCG GCCTC CA TCGTCGTC GTG
T- - T

GAM139 327 LOC2856 1 4365 XP_211974.1 5 88 GTGTCTGTGCTG G - TG A 1 B c c
51 CGTTTGTGAGCT TG AGCT G AGC GCAGCACA
GCAACGCT AC TCGA T TTG CGTCGTGT
G G GT -

GAM139 327 LOC2857 1 17272 XP_209738.1 5 1137 CCACTTGTGCTG C A A 1 B c c

48 CCGCCATGTCTC TGGAG TGTG GC GCAGCACA
TAGTGATC ATCTC GTAC CG CGTCGTGT
T - C

GAM139 327 LOC2858 1 15998 XP_209767.1 5 637 CTTGTGTGGCTG - - A 1 B c c
01 CTGCGCAGCCTT TGGAG CTGTG AGCAGC GCACA
CAACAACA ACTTC GACGC TCGTCG TGTGT
C G G

GAM139 327 LOC2859 1 12928 XP_212087.1 5 1534 TAACATGGTGAC GA CAG 1 B c c

28 TTGCTCACAGCC TG GCTGTGAGCAG CAC
TCACTGGA AC CGACACTCGTT GTG
TC CA-

GAM139 327 LOC2859 1 17285 XP_212107.1 5 110 TGGCTCTCAGCT A CA AC 1 B c c

68 GCACTCACAGCA TGG GCTGTGAG GCAGC
CCAGTGAG ACC CGACACTC CGTCG

```
                                        A      A-    AC
GAM139  327   LOC2859 2  1701  XP_212126.1  5  220   AGAGGTGCTGTG     TGTG   G          1  B  c
c
          92                      CTGCTCCACAAG TGGAGC   AGCA CAGCAC
                                  GCAAAACA    ACCTCG   TCGT GTCGTG
                                        ----   -
GAM139  327   LOC2859 2  7305  XP_212126.1  5  220   GGTGCTGTGCTG     TGTG   G          1  B  c
c
          92                      CTCCACAAGGCA TGGAGC   AGCA CAGCAC
                                  AAACAAGA    ACCTCG   TCGT GTCGTG
                                        ----   -
GAM139  327   LOC2860 1  943   XP_212163.1  5  372   TGGCCTGTGCTG   A     G           1  B  c  c
          78                      CTGTCACGGTGC TGG GCTGTGA CAGCAGCACA
                                  TAAGGGGC    ATC TGGCACT GTCGTCGTGT
                                        G     -
GAM139  327   LOC2862 1  4239  XP_212235.1  3  1288  CTGGCTGTGCTG    GC   G  -          1  B  c
c
          18                      CTGGCTGCAAAT TGGA  TGT AGC AGCAGCACA
                                  CTATCCCC    ATCT  ACG TCG TCGTCGTGT
                                        AA  -  G
GAM139  327   LOC2865 1  9346  XP_212330.2  3  1872  AGCTGCGTGCTG T--     -  --         1  B  c  c
          20                      CTGCACTCACCG   GGAGCTG TGA  GCAGCAGCAC
                                  GCTTCTTC       CTTCGGC ACT  CGTCGTCGTG
                                        CTT      C   CA
GAM139  327   LOC3385 1  858   XP_290465.1  5  3754  GACTGTGGCCTT         C  C  --       1  B  c  c
          58                      CTTCTCACAGCT TGGAGCTGTGAG AG AG  CACA
                                  CCACTAGG    ACCTCGACACTC TC TC  GTGT
                                        T  T  CG
GAM139  327   LOC3391 1  15658 XP_290714.1  3  488   CAGACTTGGTGC        AG   CA         1  B  c
c
          22                      CTGAGCGCAGCT TGGAGCTGTG  CAG  GCAC
                                  CCAGGGAA    ACCTCGACGC  GTC  CGTG
                                        GA  --
GAM139  327   LOC3391 1  12464 XP_294837.1  5  45    TAACTCTTGCTG    G -----        C    1  B  c  c
          66                      CTGCTCACTGTT TGGA CT    GTGAGCAGCAGCA
                                  TGGGTCCA    ACCT GG    CACTCGTCGTCGT
                                        G  TTTGT          T
GAM139  327   LOC3391 1  2113  XP_290740.1  3  433   TGCCCTGTGGAG T--    ---       AG      1  B  c  c

          72                      CTGCTCACCTAA   GGAGCT   GTGAGCAGC  CACA
                                  GTTCCTGC       CCTTGA   CACTCGTCG  GTGT
                                        CGT      ATC       AG
GAM139  327   LOC3392 1  12801 XP_290771.1  3  236   TGGGGCCCGGTG         CA  ---- A-     1  B  c
c
          30                      TCACTCACAGCT TGGAGCTGTGAG  GCA   GC  CA
                                  CCATCTCT    ACCTCGACACTC  TGT   CG  GT
                                        AC   GGCC  GG
GAM139  327   LOC3393 1  6942  XP_297112.1  5  170   GGACCCCTGCTG T-     T----       C    1  B  c  c

          05                      CTGCTCCTGCTC   GGAGCTG    GAGCAGCAGCA
```

AGCTCCTG CCTCGAC CTCGTCGTCGT
GT TCGTC C

GAM139 327 LOC3399 1 19354 XP_295099.1 5 35 TAAATCTTGCTG G ----- C 1 B c c
14 CTGTTCATTGTT TGGA CT GTGAGCAGCAGCA
TGGGTCCA ACCT GG TACTTGTCGTCGT
G TTTGT T

GAM139 327 LOC3399 1 13382 XP_295107.1 5 2031 GGGCGGGTGTGC T---- - A- G 1 B c
c
42 AGGCTCACAGGC GGAGC TGTGAGC GCA CAC
TCTGGAAA TCTCG ACACTCG CGT GTG
AAAGG G GA -

GAM139 327 LOC3402 1 5180 XP_290385.1 3 293 TATCTGTGTCCA TGA A A-- 1 B c
c
23 GCGGCCCCAGCT TGGAGCTG GC GC GCACA
CCAGCCCA ACCTCGAC CG CG TGTGT
CC- G ACC

GAM139 327 LOC3402 1 3128 XP_295192.1 5 376 TCCATTGTGCTG C- A--- A 1 B c c
39 CCGCCCTCCGCG TGGAG TGTG GC GCAGCACA
CTCTCCAG ACCTC GCGC CG CGTCGTGT
TC CTCC C

GAM139 327 LOC3402 1 3128 XP_295189.1 5 376 TCCATTGTGCTG C- A--- A 1 B c c
40 CCGCCCTCCGCG TGGAG TGTG GC GCAGCACA
CTCTCCAG ACCTC GCGC CG CGTCGTGT
TC CTCC C

GAM139 327 LOC3402 1 1105 XP_290389.1 3 293 TATCTGTGTCCG TGA A A-- 1 B c
c
43 GCGGCCCCAGCT TGGAGCTG GC GC GCACA
CCAGCCCA ACCTCGAC CG CG TGTGT
CC- G GCC

GAM139 327 LOC3403 1 8372 XP_291269.1 5 2262 AGGCCTGTGCTG TG----- T A- 1 B c
c
90 CTGCCCCACGCT GAGC GTG GCAGCAGCACA
CAAACTGT CTCG CAC CGTCGTCGTGT
TGTCAAA - CC

GAM139 327 LOC3405 1 17000 XP_295270.1 3 60 GCGATGTACTAG T ----- - C 1 B c c
81 CTGCTCACAAGC GGAGC TGTGAGCAGC AG ACA
CTGTTCCT CCTTG ACACTCGTCG TC TGT
T TCCGA A A

GAM139 327 LOC3421 1 12881 XP_292413.1 5 2116 ACCTTCTGTTTC G GC-- C 1 B c
c
95 CATGTCACAGCT TGGAGCTGTGA CA AGCA
CCACCATA ACCTCGACACT GT TTGT
- ACCT C

GAM139 327 LOC3423 1 16656 XP_296817.2 3 1462 CCTCTGCTGCTG ---- T A C 1 B c
c
46 CTGCCACCGCTG TGGA GC GTG GCAGCAGCA
ATTCCATC ACCT CG CAC CGTCGTCGT
TAGT C - C

GAM139 327 LOC3424 1 1758 XP_296893.1 5 57 TTCACCTAAGTT A C AC 1 B c c
87 TCTGCCACAGCT TGGAGCTGTG GCAG AGC

CCACATGA ACCTCGACAC CGTC TTG
- T AA
GAM139 327 LOC3445 1 13365 XP_297716.1 5 10 CTGGCTGTGCTG T--- CT -- 1 B c c
63 CTGCTGCTACCC GGAG GTG AGCAGCAGCACA
CTCCCAAG CCTC CAT TCGTCGTCGTGT
GAAC CC CG
GAM139 327 LOC3449 1 17064 XP_298469.1 5 44 CAATCTTGTGAA A CAG 1 B c c
92 TCTGCCACAGCT TGGAGCTGTG GCAG CACA
CCAAGATG ACCTCGACAC CGTC GTGT
- TAA
GAM139 327 LOC3479 1 9115 XP_302635.1 3 129 ACCACCTTTGTG CT G C 1 B c c

59 CTGCTCTAACCT TGGAG GT AG AGCAGCACA
TCAGAGTT ACTTC CA TC TCGTCGTGT
-- A -
GAM139 327 LOC3481 1 15242 XP_300289.1 5 13 AGTGTGGTGCTG A -- G G 1 B c c

18 CTAACATTGCCC TGG GC TGT AGCAGCA CACA
AGGCAACA ACC CG ACA TCGTCGT GTGT
- TT A G
GAM139 327 LOC3484 1 18044 XP_300352.1 3 997 GAATGACACAGC GA AC 1 B c
c
88 TGCTGTGCAGCT TGGAGCTGT GCAGCAGC
CCACTTCG ACCTCGACG TGTCGTCG
-- AC
GAM139 327 LOC3485 1 8733 XP_300770.1 5 81 CTGCTGGTGCTG T------ GC - 1 B c c
09 CTGCTCGTCATC GGA TG TGAGCAGCAGCAC
CTGGCCAG CCT AC GCTCGTCGTCGTG
GACCGGT -- T
GAM139 327 LOC3485 1 19450 XP_211637.1 5 977 GACCCACGTGCT T G AGC 1 B c
c
49 CCAGTCCCAGCT TGGAGCTG GA C AGCAC
CCAAAAGC ACCTCGAC CT G TCGTG
C - ACC
GAM139 327 LOC3485 1 13423 XP_209362.1 3 917 ACCCTGGTCTTG - C C 1 B c c
52 CTGCTCATATCT TGG AG TGTGAGCAGCAG AC
GCCAGGAA ACC TC ATACTCGTCGTT TG
G T C
GAM139 327 LOC3485 2 4696 XP_300383.1 3 521 CAGGAGCTGCTG G G AC 1 B c
c
99 CTGCAGTTGCAG TG AGCTGT AGCAGCAGC
AAGGATAA AC TTGACG TCGTCGTCG
G - AG
GAM139 327 LOC3485 2 19517 XP_300383.1 3 521 ACGCAGGAGCTG G G AC 1 B c
c
99 CTGCTGCAGTTG TG AGCTGT AGCAGCAGC
CAGAAGGA AC TTGACG TCGTCGTCG
G - AG
GAM139 327 LOC3489 1 14383 XP_300875.1 5 36 TATAGCTTGCTG G ----- C 1 B c c
09 CTGCTCACCTTT TGGA CT GTGAGCAGCAGCA

TGGTCCAC ACCT GG CACTCGTCGTCGT
- TTTTC T
GAM139 327 LOC3490 1 17272 XP_300923.1 5 1137 CCACTTGTGCTG C A A 1 B c c

61 CCGCCATGTCTC TGGAG TGTG GC GCAGCACA
TAGTGATC ATCTC GTAC CG CGTCGTGT
T - C
GAM139 327 LOC3490 1 17272 XP_300926.1 5 1137 CCACTTGTGCTG C A A 1 B c c

66 CCGCCATGTCTC TGGAG TGTG GC GCAGCACA
TAGTGATC ATCTC GTAC CG CGTCGTGT
T - C
GAM139 327 LOC3490 1 6029 XP_302959.1 5 1341 CCTGTGTTGCTG AGCT- G 1 B c
c

92 CTGCTGAGGCCA TGG GT AGCAGCAGCACA
AATCACTC ACC CG TCGTCGTTGTGT
GGAGT -
GAM139 327 LOC3491 1 1431 XP_302967.1 3 129 CCTAGGGTTCTC T C - C 1 B c c
51 GTTCTCCCAGCT TGGAGCTG GAG AGC AG AC
CCAGCCTT ACCTCGAC CTC TTG TC TG
C - C T
GAM139 327 LOC3497 1 18662 XP_303482.1 5 6 CGGCTTGTGCTG T- TGT ---- 1 B c c

10 CTCTGCGCTCTC GGAGC GAGC AGCAGCACA
CGCTTCGC CTTCG CTCG TCGTCGTGT
CG CCT CGTC
GAM139 327 LOC9012 1 3855 XP_291299.1 5 1120 TGCCGGTGGCTC - - C - 1 B c c
0 CTGCTCACATGT TGGAG C TGTGAGCAG AGC AC
CTTCGGGT GCTTC G ACACTCGTC TCG TG
T T C G
GAM139 327 LOC9090 1 7354 XP_034809.1 3 2976 CCTCCTGTGCTG A-- T G 1 B c c

6 CTGGTCACTGTA TGG GC GTGA CAGCAGCACA
ACCCACTA ACC TG CACT GTCGTCGTGT
CAA T G
GAM139 327 LOC9166 1 19944 NP_612381.1 3 215 ACTGTTCTGCTG A --- G C 1 B c c

1 CTGATCACGAGG TGG GCT GTGA CAGCAGCA
GCACCAGA ACC CGG CACT GTCGTCGT
A GAG A C
GAM139 327 LOC9194 1 13563 XP_041721.2 3 974 TGGGAGTTGCTG GA C 1 B c c

7 CTGTTTACAGCC TG GCTGTGAGCAGCAGCA
ACAGTCTC AC CGACATTTGTCGTCGT
AC T
GAM139 327 LOC9197 1 706 XP_041974.2 5 2244 TATGTTGTGCTG - T G 1 B b b
4 CTGTCCAGCTGC TGG AGCTG GA CAGCAGCACA
TAAGATCC ATC TCGAC CT GTCGTCGTGT
G - -
GAM139 327 LOC9327 2 2415 XP_050184.1 3 222 CCTTGCACTGTG TG--- G C 1 B c
c

3 CTGCTCTCACAG GA CTGTGAG AGCAGCACA
ATCGGTGT CT GACACTC TCGTCGTGT
TGTGG A -
GAM139 327 LOC9327 2 18095 XP_050184.1 3 222 TGCACTGTGCTG TG------ G C 1 B c
c
3 CTCTCACAGATC GA CTGTGAG AGCAGCACA
GGTGTCTG CT GACACTC TCGTCGTGT
GTCTGTGG A -
GAM139 327 LW-1 1 11543 NP_057237.1 5 678 CAAGGGGTGCTG G C AG 1 B c c
CTGGCCACACTG TG AG TGTG CAGCAGCAC
CACTAGCA AC TC ACAC GTCGTCGTG
G - CG
GAM139 327 MAPRE1 1 19788 NP_036457.1 3 1102 TTTCGGTATCTG T----- C- 1 B c c
CTGTTCACAGCT GGAGCTGTGAGCAGCAG AC
CTCCACTG TCTCGACACTTGTCGTC TG
GTCACC TA
GAM139 327 MAPRE3 1 12646 NP_036458.2 3 297 CCCAGGGTGCTG A T- A 1 B c
c
CTGCCACCCGCC TGG GC GTG GCAGCAGCAC
CCAGCCAG ACC CG CAC CGTCGTCGTG
C CC -
GAM139 327 MBD1 1 14525 NP_002375.1 3 432 AACAATGTGCTG T------ CT - 1 B c c
CTGCTTCACTTC GGAG GTGA GCAGCAGCACA
CGCCCTCC CCTT CACT CGTCGTCGTGT
CCTCCCG -- T
GAM139 327 MBD1 1 14525 NP_056669.1 3 432 AACAATGTGCTG T------ CT - 1 B c c
CTGCTTCACTTC GGAG GTGA GCAGCAGCACA
CGCCCTCC CCTT CACT CGTCGTCGTGT
CCTCCCG -- T
GAM139 327 MBD1 1 14525 NP_056671.2 3 432 AACAATGTGCTG T------ CT - 1 B c c
CTGCTTCACTTC GGAG GTGA GCAGCAGCACA
CGCCCTCC CCTT CACT CGTCGTCGTGT
CCTCCCG -- T
GAM139 327 MBD1 1 14525 NP_056723.2 3 432 AACAATGTGCTG T------ CT - 1 B c c
CTGCTTCACTTC GGAG GTGA GCAGCAGCACA
CGCCCTCC CCTT CACT CGTCGTCGTGT
CCTCCCG -- T
GAM139 327 MGC1071 1 17990 NP_077301.4 3 565 ACAGTGTTGCTG ------- G 1 B c c
5 CTGGCAGAGATG TGGAG CTGT AGCAGCAGCAC
CATTCCAG ACCTT GACG TCGTCGTTGTG
ACGTAGA G
GAM139 327 MGC1251 1 18236 NP_291026.1 5 27 TTGTCTCTCGCT G A AC 1 B c c
8 GCAGTCGCAGCT TGGAGCTGTGA C GCAGC
CCAGGTCT ACCTCGACGCT G CGTCG
- A CT
GAM139 327 MGC1307 1 12254 NP_116078.2 3 1011 GAGTGTGTGCTG AGCT A 1 B c
c
1 CCGTTCATTACC TGG GTGAGC GCAGCACA

ACGGAGAT ACC TACTTG CGTCGTGT
AT-- C
GAM139 327 MGC1539 1 11393 NP_443087.1 3 417 TCTTGGTGTTGC T----- C - 1 B c c

6 ATGCTCACAACT GGAG TGTGAGCA GCAGCAC
CTGCTGAC TCTC ACACTCGT CGTTGTG
CAGTCG A A
GAM139 327 MGC1614 1 6403 NP_116152.1 3 80 CTGCCAGTGCTG AG AG- 1 B c
c

2 CTGGTGCACAGA TGG CTGTG CAGCAGCAC
CCATCTTT ACC GACAC GTCGTCGTG
A- GTG
GAM139 327 MGC1663 1 18557 NP_777593.1 5 203 GCAGGTGTTGTT --- G C 1 B c c

8 CTGACCCCAGCT TGGAGCT GT AG AGCAGCAC
CCACTGTG ACCTCGA CA TC TTGTTGTG
CCC G -
GAM139 327 MGC1733 1 13961 NP_443112.1 3 281 ACAGTGATGCTG - GTG C 1 B c
c

0 CTGCTAAGGGCT TGGA GCT AGCAGCAGCA
TCCAAACA ACCT CGG TCGTCGTCGT
T GAA A
GAM139 327 MGC2499 2 2593 NP_714914.1 5 148 AGCCGGGTGCTG T-- - T -- 1 B c c

5 CTGCTCCTGCTG GG AGC GT GAGCAGCAGCAC
CTGCTGCC TC TCG CG CTCGTCGTCGTG
CCG G T TC
GAM139 327 MGC2499 2 16446 NP_714914.1 5 165 CTCCTGCTGCTG G ----- C 1 B c
c

5 CTGCCGCCACAG TG AGCTGTG AGCAGCAGCA
CTGCACCT AC TCGACAC TCGTCGTCGT
G CGCCG C
GAM139 327 MGC3015 1 14918 NP_689852.1 3 1953 AATCATCTGGGC T G C AC 1 B c
c

6 TCCTGTCCAGCT TGGAGCTG GA CAG AGC
CCACATGT ACCTCGAC CT GTC TCG
- - C GG
GAM139 327 MGC3222 1 3878 NP_077310.1 3 399 TGCCGTGTGCTG G CT C 1 B c
c

CTTCTCATCACT TG AG GTGAG AGCAGCACA
GCACACAA AC TC TACTC TCGTCGTGT
G AC T
GAM139 327 MGC3248 1 10750 NP_115875.1 3 403 GTAGCTGGTGCG -- A 1 B b b
CTGCTCACGGCC TGGA GCTGTGAGCAGC GCAC
ATTCACTG ACTT CGGCACTCGTCG CGTG
AC -
GAM139 327 MGC3502 1 16655 NP_787073.1 3 917 TTGGTCTTGCTG - C G C 1 B c
c

3 CTGATATCTGCC TGG AG TGT AGCAGCAG AC
AGAAAAGG ACC TC ATA TCGTCGTT TG

```
                                        G T  G     C
GAM139  327  MGC3502 1  16655 XP_086685.1  3 917  TTGGTCTTGCTG  - C  G     C       1  B  c
c
         3                          CTGATATCTGCC TGG AG TGT AGCAGCAG AC
                                    AGAAAAGG    ACC TC ATA TCGTCGTT TG
                                        G T  G     C
GAM139  327  MGC3952 1  7717  NP_699195.1  5 167  CCAACACCTGTG      GAG  C         1  B  b
b
         0                          CTCCTGACAGCT TGGAGCTGT  CAG AGCACA
                                    CCATGCAC    ACCTCGACA  GTC TCGTGT
                                          ---  C
GAM139  327  MGC4504 1  10242 NP_077016.1  3 324  CCCCCAGTGCTG  AGC  -----          1  B  c
c
                                    CTGCTAACCCCA TGG  TGTG   AGCAGCAGCAC
                                    CACCACCC    ACC  ACAC   TCGTCGTCGTG
                                        ---  CCCAA
GAM139  327  MGC4898 1  11203 NP_787077.1  5 192  CTGTAGCTGCTG  A  T-----      C    1  B  c
c
         6                          CTGCTCCCTGCC TGG GCTG    GAGCAGCAGCA
                                    CAGCCCCA    ACC CGAC    CTCGTCGTCGT
                                        C  CCGTCC       C
GAM139  327  MGRN1  1  14631 XP_048119.4  3 2118  GGCAGGTGTCTG T---  --      -     1  B  c  c
                                    CTGCTCACCTGG   GGAGCT  GTGAGCAGCAG CAC
                                    CTCTGGAG       TCTCGG  CACTCGTCGTC GTG
                                          GAGG    TC        T
GAM139  327  MME   1  2426  NP_000893.1  3 3050  GGGTCTGTGCTG  -- T  G          1  B  c  c
                                    CTGTTACTGTTA TGG  AGC GTGA CAGCAGCACA
                                    ACCATTTA    ACC  TTG CATT GTCGTCGTGT
                                        AA  T  -
GAM139  327  MME   1  2426  NP_009218.1  3 3050  GGGTCTGTGCTG  -- T  G          1  B  c  c
                                    CTGTTACTGTTA TGG  AGC GTGA CAGCAGCACA
                                    ACCATTTA    ACC  TTG CATT GTCGTCGTGT
                                        AA  T  -
GAM139  327  MME   1  2426  NP_009219.1  3 3050  GGGTCTGTGCTG  -- T  G          1  B  c  c
                                    CTGTTACTGTTA TGG  AGC GTGA CAGCAGCACA
                                    ACCATTTA    ACC  TTG CATT GTCGTCGTGT
                                        AA  T  -
GAM139  327  MME   1  2426  NP_009220.1  3 3050  GGGTCTGTGCTG  -- T  G          1  B  c  c
                                    CTGTTACTGTTA TGG  AGC GTGA CAGCAGCACA
                                    ACCATTTA    ACC  TTG CATT GTCGTCGTGT
                                        AA  T  -
GAM139  327  MNT   1  2618  NP_064706.1  3 1183  GAGCTAGGGCTG     TGT       AC       1  B  c  c

                                    CTGCTTCTGCTC TGGAGC  GAGCAGCAGC
                                    CAGCCCCT    ACCTCG  TTCGTCGTCG
                                          TC-       GG
GAM139  327  MOST2  1  4257  NP_064635.1  5 681  CTCCCAGTGCTG   GCTGT  --          1  B  c
c
                                    CTGTCCTCTGAT TGGA   GAG  CAGCAGCAC
                                    CCACCCTC    ACCT    CTC  GTCGTCGTG
```

AGT-- CT
GAM139 327 MPP2 1 5243 NP_005365.2 3 2246 CAGGTGTGTGCC AGCA-- - 1 B c c

CCCACCACAGCT TGGAGCTGTG GCA GCAC
CTATGACT ATCTCGACAC CGT TGTG
CACCCC G
GAM139 327 MSP 1 13067 NP_114435.1 3 32 CCAGCTGGCCTG A --- CA 1 B c c
CTGCTCTGCACA TGG GCTGT GAGCAGCAG CA
GCACCGGC GCC CGACA CTCGTCGTC GT
A CGT CG
GAM139 327 MUCDHL 2 1008 NP_112555.1 3 1951 CCGGCTCAAGTG -- G C 1 B c c

CTGCTCTGGCAA TGGAGCT GT AG AGCAGCAC
AGCTCCGG GCCTCGA CG TC TCGTCGTG
AA G -
GAM139 327 MUCDHL 2 8074 NP_112555.1 3 1952 GCTCAAGTGCTG -- G C 1 B c c

CTCTGGCAAAGC TGGAGCT GT AG AGCAGCAC
TCCGGAGC GCCTCGA CG TC TCGTCGTG
AA G -
GAM139 327 MYD88 1 13413 NP_002459.1 3 776 ATGCCTGTGGTC T GCAG 1 B c c

ATGCTCTCAGCT TGGAGCTG GAGCA CACA
CCACCTGG ACCTCGAC CTCGT GTGT
T ACTG
GAM139 327 NESH 1 6776 NP_057512.1 3 382 GTTCTAAGGCTG A- --- AC 1 B c c
CTGCTAATTACA TGG GCTGTG AGCAGCAGC
GCCCCCAA ACC CGACAT TCGTCGTCG
CC TAA GA
GAM139 327 NFS1 1 14605 NP_066923.2 3 398 CTTCGTCTTCTG --- GT C 1 B c c
CTGCTGCTCGGC TGG AGCT GAGCAGCAGCA
TGGACCAG ACC TCGG CTCGTCGTCGT
AGG -- C
GAM139 327 NIPSNAP 1 16274 NP_003625.1 3 20 TGCAGTGTGCTG C A G 1 B c c

1 CCTACACCTCCA TGGAG TGTG GCAGCA CAC
CCTCCTTC ACCTC ACAT CGTCGT GTG
C C -
GAM139 327 NPEPL1 2 2446 NP_078939.2 5 122 AGCCGGCCCCTG G -- C 1 B c c
CTGCTGCTCGGG TG AGCTGT GAGCAGCAGCA
CAGCTGCA AC TCGACG CTCGTCGTCGT
G GG C
GAM139 327 NPEPL1 2 7568 NP_078939.2 5 124 CGGCCCCTGCTG G -- C 1 B c c
CTGCTCGGGCAG TG AGCTGT GAGCAGCAGCA
CTGCACCA AC TCGACG CTCGTCGTCGT
G GG C
GAM139 327 NPEPPS 1 2285 NP_006301.2 3 161 GTTAACTGGTTC C C AC 1 B c c

CTGCTCACACTC TGGAG TGTGAGCAG AGC
CAGAATTA ACCTC ACACTCGTC TTG

```
                                        -       C  GT
GAM139  327  NUP133 1  2638  NP_060700.2  3 308   TCCTGGTTCTAG  GA -       - C        1 B c c
                                CTGCTCACATGT TG  GC TGTGAGCAGC AG AC
                                ACAAATCA    AC  TG ACACTCGTCG TC TG
                                         A- T        A T
GAM139  327  OPRD1  1  15006 NP_000902.2  5 9     CTGCGCTGCTCC    --    ----     A     1 B c c
                                TGGCTCACAGCG TGGAGC  TGTGAGC    AGCAGC CA
                                CTCCGGGC    GCCTCG  ACACTCG    TCGTCG GT
                                          CG      GTCC     C
GAM139  327  P5326  1  20183 NP_113638.1  3 257   CCCTTTGTAATG    CTGT      GC         1 B c c

                                CTGCTCCTCTCC TGGAG    GAGCAGCA  ACA
                                ACTGCCCA    ACCTC    CTCGTCGT  TGT
                                          TC--       AA
GAM139  327  PAK6   1  718   NP_064553.1  3 412   CACAGATACCTG       T       CAC        1 B c c
                                CTGTTCTCAGCT TGGAGCTG GAGCAGCAG
                                CCAGCTTC    ACCTCGAC CTTGTCGTC
                                            T       CAT
GAM139  327  PDCD1  1  9612  NP_005009.1  3 346   CTGCTGCTGCTG   A    GA      C        1 B c c
                                CTGCCTGCGGCC TGG GCTGT  GCAGCAGCA
                                CGGGGCTG    GCC CGGCG  CGTCGTCGT
                                          -    TC       C
GAM139  327  PEMT   1  3100  NP_009100.2  3 104   GAATGGTGCCTG TG-----    G       -      1 B c c
                                CTGCTCAGGGCT      GAGCT TGAGCAGCAG CAC
                                CGCCCCCG          CTCGG ACTCGTCGTC GTG
                                        GCCCCCG    G       C
GAM139  327  PEMT   1  3100  NP_680477.1  3 104   GAATGGTGCCTG TG-----    G       -      1 B c c
                                CTGCTCAGGGCT      GAGCT TGAGCAGCAG CAC
                                CGCCCCCG          CTCGG ACTCGTCGTC GTG
                                        GCCCCCG    G       C
GAM139  327  PEMT   1  3100  NP_680478.1  3 104   GAATGGTGCCTG TG-----    G       -      1 B c c
                                CTGCTCAGGGCT      GAGCT TGAGCAGCAG CAC
                                CGCCCCCG          CTCGG ACTCGTCGTC GTG
                                        GCCCCCG    G       C
GAM139  327  PGLS   2  11405 NP_036220.1  3 124   CACGTCGTGCTG  GA-  GTG             1 B c
c
                                CTGCTGGAAGCC TG   GCT   AGCAGCAGCAC
                                AACAGCCT    AC   CGA   TCGTCGTCGTG
                                          AAC   AGG
GAM139  327  PGLS   2  16901 NP_036220.1  3 124   GTCGTGCTGCTG T  -   - ------         1 B c c
                                CTGGAAGCCAAC  GGA GCTG TG     AGCAGCAGCAC
                                AGCCTCCG     CCT CGAC AC     TCGTCGTCGTG
                                        G  C    A  CGAAGG
GAM139  327  PHTF2  1  13764 NP_065165.1  3 696   AAACACTGGGCT        AGC     AC        1 B c
c
                                GTTTGCACAGCT TGGAGCTGTG   AGCAGC
                                CCAACTGT    ACCTCGACAC   TTGTCG
                                          GT-     GG
GAM139  327  PIB5PA 1  19904 NP_055237.1  3 96    GCCTCTCTCCTG  G    T  C     C        1 B c c
                                CTGCTCCTCCAG TG AGCTG GAG AGCAGCA
```

CTGTATCT AT TCGAC CTC TCGTCGT
G - C C
GAM139 327 PIK4CB 1 7503 NP_002642.1 3 466 CTGGCCATGCTG TGA C 1 B c c
CTGCCCAGCTCT TGGAGCTG GCAGCAGCA
ACCCCTCC ATCTCGAC CGTCGTCGT
C-- A
GAM139 327 PLIN 1 5398 NP_002657.1 3 663 AGAGCCAGCTGC GA - AC 1 B c c
TTGCTCACAGCC TG GCTGTGAGCA GCAGC
ACATTTCC AC CGACACTCGT CGTCG
AC T AC
GAM139 327 PNPLA1 1 15703 NP_775947.1 3 172 TAAAATTCCTGC A C C 1 B c c
TCTGCCACAGCT TGGAGCTGTG GCAG AGCA
CCACTCAG ACCTCGACAC CGTC TCGT
- - C
GAM139 327 PP1665 1 463 NP_110419.3 5 516 CCTTTGTGTGTC - -- CA- 1 B c c
CTGCTCACATTG TGGAG C TGTGAGCAG GCACA
TCTCCAGG ACCTC G ACACTCGTC TGTGT
T TT CTG
GAM139 327 PPIL2 1 4077 NP_055152.1 3 931 GAAGTGGCCTTG A GT- --- 1 B c c
CTGCTCTCAGGC TGG GCT GAGCAGCAG CAC
CCGGCCA GCC CGG CTCGTCGTT GTG
- ACT CCG
GAM139 327 PPL 1 3926 NP_002696.2 3 694 TGGATTGTGCTG TG--- 1 B c c
CTGTTAGCCTTA TGGAGCTG AGCAGCAGCACA
GTTTCAGT ACTTTGAT TTGTCGTCGTGT
TCCGA
GAM139 327 PPP3R2 1 14639 NP_671709.1 3 965 GCATTATGTCTG GAG C 1 B c c

TTGCTCACAGAT TG CTGTGAGCAGCAG ACA
GCAGAGAC AC GACACTCGTTGTC TGT
GTA -
GAM139 327 PRO1580 1 1379 NP_060972.2 5 714 TTCCCCCTGCTT GA C C 1 B c c

CTGCCAGCAGCT TGGAGCTGT GCAG AGCA
CCATCTTG ACCTCGACG CGTC TCGT
AC T C
GAM139 327 Prostei 1 16057 NP_149093.1 3 160 CACCCTGTGCTG G AG--- 1 B c c
n CTGAGGTGCGTA TG AGCTGTG CAGCAGCACA
GCTGCACA AC TCGATGC GTCGTCGTGT
G GTGGA
GAM139 327 PRRG1 1 18891 NP_000941.1 3 1459 TGTCATTTCCTG TG CAC 1 B c
c

CTGCTTCCAGCT TGGAGCTG AGCAGCAG
CCATCCCT ACCTCGAC TCGTCGTC
CT CTT
GAM139 327 PSCA 2 3633 NP_005663.1 3 269 CAACCCTCTCTG A -- C 1 B c c
CTGCTGTTTCCA TGG GCTGTG AGCAGCAGCA
TGGCCCAG ACC CGGTAC TTGTCGTCGT
- CT C
GAM139 327 PSCA 2 6007 NP_005663.1 3 269 CCCTCTCTGCTG A -- C 1 B c c

CTGTTTCCATGG TGG GCTGTG AGCAGCAGCA
CCCAGCAT ACC CGGTAC TTGTCGTCGT
- CT C
GAM139 327 PSTPIP1 1 12408 NP_003969.2 5 136 CTCATTTTGCTG A T - C 1 B c c
CTGATTCTAGCC TGG GCTG GAG CAGCAGCA
CCAAACAA ACC CGAT CTT GTCGTCGT
C - A T
GAM139 327 Rab11-F 1 6083 NP_055515.1 3 486 CCAGGGGTGCTG A-- GTGA 1 B c c
IP3 CTGCCTAAGCCA TGG GCT GCAGCAGCAC
CCCACATA ACC CGA CGTCGTCGTG
CAC ATC-
GAM139 327 RAB6IP1 1 6028 XP_290550.1 3 468 ACAGGTGTGCTG A GTGA A 1 B c c
CGCGGGAAGCCC TGG GCT GC GCAGCACA
CATGCTCC ACC CGA CG CGTCGTGT
C AGGG -
GAM139 327 RAB7L1 1 6106 NP_003920.1 3 1105 GAAATAGGTCTG T----- C C 1 B c c
CTCCTCACAGCT GGAGCTGTGAG AGCAG AC
TTGGGAAT TTTCGACACTC TCGTC TG
TAAGGG C -
GAM139 327 RHPN2 1 11438 NP_149094.2 3 1365 AAAGTGTATCTG AG T --- 1 B c c
CTGCTCCTAGGG TGG CTG GAGCAGCAG CAC
CCATGCTT ACC GAT CTCGTCGTC GTG
GG C TAT
GAM139 327 RIS1 1 13282 NP_056259.1 3 181 AGGTTTGTGCTG TG A 1 B c c
CGCTTCCAGTTC TGGAGCTG AGC GCAGCACA
CGAAAAGC GCCTTGAC TCG CGTCGTGT
CT -
GAM139 327 RNF144 1 1841 NP_055561.1 3 2034 CTGAAATTGCTG A --- --- C 1 B c c
CTGCCCATCGCA TGG GCT GTGA GCAGCAGCA
TGAGCCCA ACC CGA CGCT CGTCGTCGT
- GTA ACC T
GAM139 327 RPL13 1 4471 NP_000968.2 3 315 AAGGTTGGGCTG G G AC 1 B c c
GTGCTCACAGCT TG AGCTGTGAGCA CAGC
GTAATCCC AT TCGACACTCGT GTCG
G G GG
GAM139 327 RPL13 1 4471 NP_150254.1 3 315 AAGGTTGGGCTG G G AC 1 B c c
GTGCTCACAGCT TG AGCTGTGAGCA CAGC
GTAATCCC AT TCGACACTCGT GTCG
G G GG
GAM139 327 RPS18 1 14400 NP_072045.1 5 32 CCGCTTGTGCTG C A A 1 B c c
CAGCCATGTCTC TGGAG TGTG GC GCAGCACA
TAGTGATC ATCTC GTAC CG CGTCGTGT
T - A
GAM139 327 RUFY2 1 15232 NP_060457.2 3 142 TCTCCTGTGGCT - A C - 1 B b b
CTGCCATCAGCT TGGAGCTG TG GCAG AGC ACA
CCAATATC ACCTCGAC AC CGTC TCG TGT
T - - G
GAM139 327 RUNX1 1 16964 NP_001745.2 3 4236 GCTGGACTGCTG AG G C 1 B c c

CTGTTCAGGAGC TGG CT TGAGCAGCAGCA
CACCAGAG ACC GG ACTTGTCGTCGT
GA - C

GAM139 327 SARS2 1 10983 NP_060297.1 3 122 ACATCTGTGTTC TGA C--- 1 B c c
TTCCTGTCAGCT TGGAGCTG GCAG AGCACA
CCACGCCC ACCTCGAC TGTC TTGTGT
--- CTTC

GAM139 327 SART3 1 14542 NP_055521.1 3 116 CCTGGTGTGCTG AGC - 1 B c c
CGTGCTCGCAAC TGG TGTGAGCA GCAGCACA
CACAGATG ACC ACGCTCGT CGTCGTGT
A-- G

GAM139 327 SCMH1 1 18639 NP_036368.1 3 233 CCAGGGCTGGTG T T-- C 1 B c c

CTGCTCTTCCCT GGAGCTG GAG AGCAGCAC
CAGCTCTG TCTCGAC CTT TCGTCGTG
G TCC C

GAM139 327 SCO2 2 3615 NP_005129.1 5 85 AGATCCATGCTG A G - C 1 B c c
CTGCTGACTCGG TGG GCT TGAG CAGCAGCA
AGCCCCA ACC CGA GCTC GTCGTCGT
C G A C

GAM139 327 SCO2 2 18670 NP_005129.1 5 85 TCCATGCTGCTG A G - C 1 B c c
CTGACTCGGAGC TGG GCT TGAG CAGCAGCA
CCCA ACC CGA GCTC GTCGTCGT
C G A C

GAM139 327 SDNSF 1 13351 NP_644808.1 3 1149 GACGGTGGCCCT C C --- 1 B c c

CTTCTCACAGCT TGGAGCTGTGAG AG AG CAC
CCACTAGG ACCTCGACACTC TC TC GTG
T - CCG

GAM139 327 SMARCD1 1 10765 NP_003067.2 3 74 GGCCCTGTGCTG T-- - - - 1 B c c
CCTGCCTCATAG GGA GCTGTGAG CAG CAGCACA
TATCTGCC TCT TGATACTC GTC GTCGTGT
CCG A C C

GAM139 327 SMARCD1 1 10765 NP_620710.1 3 74 GGCCCTGTGCTG T-- - - - 1 B c c
CCTGCCTCATAG GGA GCTGTGAG CAG CAGCACA
TATCTGCC TCT TGATACTC GTC GTCGTGT
CCG A C C

GAM139 327 SNCG 1 5579 NP_003078.1 3 171 CCACCTGTGCTG T A T ------- 1 B c c
CTGCACCAACCT GG GC GTGA GCAGCAGCACA
CACTGCCC CC CG CACT CGTCGTCGTGT
- - T CCAACCA

GAM139 327 SNPH 1 2804 NP_055538.1 3 2525 GTGCGGCAGCTG A G AC 1 B c c

CTGCTCAGGTGC TGG GCT TGAGCAGCAGC
CATGCCCT ACC TGG ACTCGTCGTCG
G - AC

GAM139 327 SSH2 1 15268 XP_290798.1 3 3406 CTCTGAGGTACT A - C C 1 B c c
CTGCTCACAGGC TGG GC TGTGAGCAG AG AC
CCCAGACA ACC CG ACACTCGTC TC TG
C G - A

GAM139 327 STIM1 3 7760 NP_003147.2 3 296 TTGCTGTTCCCT T ------ C 1 B c c
CAGCTCCCAGCT TGGAGCTG GAGC AGCAGCA
CCACCTCT ACCTCGAC CTCG TTGTCGT
C ACTCCC T
GAM139 327 STIM1 3 13882 NP_003147.2 3 244 AACCATGGGCTG CT--- -- A 1 B c c
CTGCTGTCACTC TGGAG GTGA GCAGCAGC CA
CCTCTCCA ACCTC CACT CGTCGTCG GT
TCCCT GT G
GAM139 327 STIM1 3 19353 NP_003147.2 3 244 CATGGGCTGCTG CT--- -- A 1 B c c
CTGTCACTCCCT TGGAG GTGA GCAGCAGC CA
CTCCACTT ACCTC CACT CGTCGTCG GT
TCCCT GT G
GAM139 327 STK38L 1 4238 NP_055815.1 3 1639 TAAATGTTGCTG TG- C 1 B c c
CTGGGTAGCTCC TGGAGCTG AGCAGCAGCA
ACAGTGTT ACCTCGAT TCGTCGTTGT
GGG A
GAM139 327 TARSH 1 6078 NP_079077.1 3 1877 TTCTTTATGTGT GCAGC 1 B c c
TTCATTACAGCT TGGAGCTGTGA AGCACA
CCAAAAAG ACCTCGACATT TTGTGT
ACT--
GAM139 327 TBX1 1 4869 NP_005983.1 3 91 ACAGATGTGCTG AG T 1 B c c
CTGTTCCCAGGC TGG CTG GAGCAGCAGCACA
CACCTGCA ACC GAC CTTGTCGTCGTGT
G- C
GAM139 327 TERF2IP 2 15403 NP_061848.1 5 7 CCGCGGCTGCTG AG - AC 1 B c c
CTGCGCAGGCCC TGG CTGTG AGCAGCAGC
AGTGCTGC ACC GACGC TCGTCGTCG
CG G GC
GAM139 327 TERF2IP 2 16058 NP_061848.1 5 7 GCGCCGCGGCTG AG - AC 1 B c
c
CTGCTGCGCAGG TGG CTGTG AGCAGCAGC
CCCAGTGC ACC GACGC TCGTCGTCG
CG G GC
GAM139 327 TF 1 11063 NP_001054.1 5 18 CGACTGTGCTCG T------- A GT - 1 B c c
CTGCTCAGCGCC GG GCT GAGCAGC AGCACA
GCACCCGG CC CGA CTCGTCG TCGTGT
GGCCCACG G -- C
GAM139 327 TGIF2 1 10404 NP_068581.1 3 274 AGCATGGTGCTG T--- T -- 1 B c c
CTGCTTCTGCTG GGAGC GT GAGCAGCAGCAC
CTTCTCCA CTTCG CG TTCGTCGTCGTG
ACCT T TC
GAM139 327 TGOLN2 2 11996 NP_006455.1 3 70 TGGATTGTGCTG T--- --- C 1 B c c
CTCTCGTTTCAG GGAGCTG TGAG AGCAGCACA
CTTTGATT TTTCGAC GCTC TCGTCGTGT
TTAG TTT -
GAM139 327 TGOLN2 2 18006 NP_006455.1 3 70 CAATGGATTGTG T --- C 1 B c c
CTGCTCTCGTTT GGAGCTG TGAG AGCAGCACA
CAGCTTTG TTTCGAC GCTC TCGTCGTGT

G TTT -

GAM139 327 TIMM13 1 1880 NP_036590.1 3 556 AATGTGTTGCTG A T--- -- 1 B c c
CTGCCACCCCTG TGG GC GTG AGCAGCAGCACA
CCCCAAAG ACC CG CAC TCGTCGTTGTGT
C TCCC CG

GAM139 327 TNFRSF1 1 9446 NP_036584.1 3 414 TCCTCGTGCCTG T----- A - 1 B c c
3B CTGCTCACAGCC GG GCTGTGAGCAGCAG CAC
CCCGAGAG CC CGACACTCGTCGTC GTG
GAGAGC C C

GAM139 327 TRAF5 1 5242 NP_665702.1 5 36 CTGTGGGGTGTC CA 1 B c c
CTGCTCACGGTT TGGAGCTGTGAGCAG GCAC
TCATGGAT ACTTTGGCACTCGTC TGTG
C-

GAM139 327 TREX1 2 9722 NP_338597.1 5 1995 ACGGTGCTGCTG A - 1 B b b
CTGCACGGCCTA TGG GCTGTG AGCAGCAGCAC
TCGCAGAA ATC CGGCAC TCGTCGTCGTG
- G

GAM139 327 TREX1 2 9722 NP_338598.1 5 1605 ACGGTGCTGCTG A - 1 B b b
CTGCACGGCCTA TGG GCTGTG AGCAGCAGCAC
TCGCAGAA ATC CGGCAC TCGTCGTCGTG
- G

GAM139 327 TREX1 2 10243 NP_338597.1 5 1995 GACACGGTGCTG A - 1 B b b
CTGCTGCACGGC TGG GCTGTG AGCAGCAGCAC
CTATCGCA ATC CGGCAC TCGTCGTCGTG
- G

GAM139 327 TREX1 2 10243 NP_338598.1 5 1605 GACACGGTGCTG A - 1 B b b
CTGCTGCACGGC TGG GCTGTG AGCAGCAGCAC
CTATCGCA ATC CGGCAC TCGTCGTCGTG
- G

GAM139 327 TRPS1 1 12768 NP_054831.1 5 136 TTTTTGGTGCTG CTGT G 1 B c c

CTGGTTTCTCCA TGGAG GA CAGCAGCAC
GACCTCGC ACCTC TT GTCGTCGTG
T--- G

GAM139 327 TTC7 1 8625 XP_031626.4 5 188 CTGCTGGTGCTG T-- - T -- 1 B c c
CTGCTGCTGCTG GG AGC GTG AGCAGCAGCAC
CTGCCCAC CC TCG CGT TCGTCGTCGTG
CAC G T CG

GAM139 327 TTTY13 1 18081 NP_114137.1 3 78 GTGACCTTATTG CTG ------ 1 B c c
CTGCTCAGACTC TGGAG TGAGCAGCAG CAC
TATGTTCC ATCTC ACTCGTCGTT GTG
AG- ATTCCA

GAM139 327 U5-200K 1 10933 NP_054733.1 5 129 CAGCTGGTTCTG GT C 1 B c c
D CTGCTTGGTTTC TGGAGCT GAGCAGCAG AC
AACACCTT ACTTTGG TTCGTCGTC TG
-- T

GAM139 327 UCK1 1 7394 NP_113620.1 3 982 TTGTGCTATGTG GA A-- -- 1 B c c
GAGCTCACAGCC TG GCTGTGAGC GCA GCACA
TCACATGT AC CGACACTCG TGT CGTGT
TC AGG AT

GAM139 327 USP20 1 3865 NP_006667.2 3 542 AGGGAGTAGCTG --- - - 1 B b b
CTGCTTCACGGC TGGA GCTGTGA GCAGCAGC AC
GTCTCCAC ACCT CGGCACT CGTCGTCG TG
CTG T A
GAM139 327 WDR5B 1 6229 NP_061942.2 5 327 CAAGCCGTGCTG TG ------- 1 B c c
CTGATTCCGTCT GAGCTGTGAG CAGCAGCAC
CACAGTTT TTTGACACTC GTCGTCGTG
-- TGCCTTA
GAM139 327 WNT3A 2 11109 NP_149122.1 3 1446 CCGACTGTGCTG AG GTGA - 1 B
c c
CTCGCGAAGGTC TGG CT GC AGCAGCACA
CCACAGCC ACC GG CG TCGTCGTGT
CT AAG- C
GAM139 327 WNT3A 2 18055 NP_149122.1 3 1446 CCCCCGACTGTG AG GTGA - 1 B
c c
CTGCTCGCGAAG TGG CT GC AGCAGCACA
GTCCCACA ACC GG CG TCGTCGTGT
CT AAG- C
GAM139 327 WNT5B 1 9907 NP_110402.2 3 845 CTTGAGCTGCTG CT -- AC 1 B c c
CTGTCACTCCTC TGGAG GTGA GCAGCAGC
CACCGAGG ACCTC CACT CGTCGTCG
CT GT AG
GAM139 327 WNT5B 1 9907 NP_116031.1 3 845 CTTGAGCTGCTG CT -- AC 1 B c c
CTGTCACTCCTC TGGAG GTGA GCAGCAGC
CACCGAGG ACCTC CACT CGTCGTCG
CT GT AG
GAM139 327 XPO6 2 1450 XP_055195.3 3 51 CACGGACTTCTG A T- A C 1 B c c
CTGCTGCCACCT TGG GC GTG GCAGCAGCA
GCGCCAGC ACC CG CAC CGTCGTCGT
G TC - C
GAM139 327 XPO6 2 14323 XP_055195.3 3 51 GGACTTCTGCTG A T- A C 1 B c c
CTGCCACCTGCG TGG GC GTG GCAGCAGCA
CCAGCCCT ACC CG CAC CGTCGTCGT
G TC - C
GAM139 327 YWHAQ 1 15153 NP_006817.1 3 638 CTTTATTTGCTG - G C 1 B c c
CTGTTTAAGTTG TGG AGCT TGAGCAGCAGCA
CCAACCTC ACC TTGA ATTTGTCGTCGT
G - T
GAM139 327 ZNF408 1 3799 NP_079017.1 3 33 GCTTTGCCTTTT AG ---- C 1 B c c
GCTGACACAGCT TGGAGCTGTG CAGCA GCA
CCATAAAG ACCTCGACAC GTCGT CGT
A- TTTC T
GAM139 327 ZYX 1 1825 NP_003452.1 3 287 GGTTTAGTGCTG G T -- 1 B c c
CTGCTTTCACTG TG AGC GTGA GCAGCAGCAC
CTGCACCC AC TCG CACT CGTCGTCGTG
G T TT
GAM140 295 BRF1 1 17247 NM_001519.2 3 GTCTCCAGCCCA AA A T-- CC 3 C c c
CCCTCCGCA TGC GGAGG GT CTGGAGAC

```
                                        ACG  CCTCC CA   GACCTCTG
                                          --    - CCC      --
GAM140  295   DKFZP43 1  7407  XM_167745.1  3      GGGTCTTCTACT    A   - TCT          3  C  c  c
        4K028                          CCCTCCCTGCA  TGCA GGAGG AGT   GGAGACCC
                                        ACGT CCTCC TCA   CTTCTGGG
                                          C    C  T--
GAM140  295   DKFZP56 1  10329 NM_015544.1  3      GGGTCTCTCCTC      AG  TTCT          3  C  c
c
        4K1964                         TCCCTTGCA   TGCAAGG  GAG   GGAGACCC
                                        ACGTTCC  CTC   TCTCTGGG
                                          CT   C---
GAM140  295   DNASE1L 1  13997 NM_006730.1  5      GGTCTCCAGAGC     GAGGA        C      3  C  c
 c
        1                          GCTTGCA    TGCAAG    GTTCTGGAGACC
                                        ACGTTC    CGAGACCTCTGG
                                          G----          -
GAM140  295   FLJ1107 1  8946  NM_018316.1  3      GGTCTCCAGGGG    -  A AG       C     3  C  c  c
        8                          GTCCCTGTGCA  TGCA AGG GG  TTCTGGAGACC
                                        ACGT TCC CT  GGGACCTCTGG
                                          G  -  GG         -
GAM140  295   FLJ1416 1  17286 NM_024565.2  5      GGGCCTCCAGGA    A  AG       A       3  C  c  c
        6                          TTTGCCTGCA   TGCA GG  GAGTTCTGGAG CCC
                                        ACGT CC  TTTAGGACCTC GGG
                                          -  G-         C
GAM140  295   HBA2    1  14247 NM_000517.3  3      GGGCCCTCCTCC       AGTTCT   A-       3  C  c
c
                                      CCTCCTTGCA   TGCAAGGAGG     GGAG  CCC
                                        ACGTTCCTCC     CCTC  GGG
                                            CCT---    CC
GAM140  295   KIAA072 1  17774 NM_021648.3  3      TCTCCAGCCTCC       AGTT     CCC      3  C  c
c
        1                          TTGTA      TGCAAGGAGG    CTGGAGA
                                        ATGTTCCTCC    GACCTCT
                                            ----      ---
GAM140  295   KIAA093 1  13222 XM_166213.1  3      GGGCCCTCCTCT   CA      TTCT   A-       3  C  c
c
        7                          CCTCCTCACA   TG  AGGAGGAG    GGAG  CCC
                                        AC  TCCTCCTC    CCTC  GGG
                                          AC       T---   CC
GAM140  295   KIAA165 1  15383          5      GGGCTCCAACTC T         TC    A        3  C  b  b
        5                          CTCCTTGC     GCAAGGAGGAGT  TGGAG CCC
                                        CGTTCCTCCTCA  ACCTC GGG
                                        -          --    -
GAM140  295   KIAA169 1  3626  NM_025135.1  3      GGATCTCCAGGA    A  A  G      - C     3  C  c  c
        5                          GTCCCCTGCA   TGCA GG GGA TTCTGGAGA CC
                                        ACGT CC CCT AGGACCTCT GG
                                          -  -  G       A  -
GAM140  295   LOC1996 1  5475  NM_145295.1  3      GGTCTCCAGAAG    AGGA  AG       C      3  C  c
 c
        92                          CCCTGCA     TGCA   GG  TTCTGGAGACC
```

ACGT CC AAGACCTCTGG
---- CG -
GAM140 295 LOC2001 1 3123 5 GGGCCTCCGGGA AA A A 3 C c c
38 CTCCCCCCGCA TGC GG GGAGTTCTGGAG CCC
ACG CC CCTCAGGGCCTC GGG
CC - C
GAM140 295 LOC2563 1 16565 5 GGTCTCCTGTCC A GTTCT C 3 C c c
69 TCCTGCA TGCA GGAGGA GGAGACC
ACGT CCTCCT CCTCTGG
- GT--- -
GAM140 295 MGC1582 1 12150 NM_032882.1 3 GGGCCTCCTCTC CA TTCT A 3 C c
c
7 CTCCTCTCA TG AGGAGGAG GGAG CCC
AC TCCTCCTC CCTC GGG
TC T--- C
GAM140 295 PTPRT 1 3450 NM_007050.3 3 GTCTCCACACTC GAGTTC CC 3 C c
c
TTTGCA TGCAAGGAG TGGAGAC
ACGTTTCTC ACCTCTG
AC---- --
GAM140 295 RARA 1 3866 NM_000964.1 3 GGGTCTCCCCTC A AG TTCT 3 C c c

ACCCCTGCA TGCA GG GAG GGAGACCC
ACGT CC CTC CCTCTGGG
C CA C---
GAM140 295 RBBP7 1 6024 NM_002893.2 3 GGGCCTCCAGAA TGC G A 3 C c c
CTCCTGTTT AAG AGGAGTTCTGGAG CCC
TTT TCCTCAAGACCTC GGG
--- G C
GAM140 295 STK38 1 2689 NM_007271.1 3 GGTCTCCAGAAC TG A A C 3 C c c
CCCTTTG CAAGG GG GTTCTGGAGACC
GTTTC CC CAAGACCTCTGG
-- - - -
GAM140 295 ZNF287 1 3540 NM_020653.1 5 GGGTCTCTTATC A - GTTCT 3 C c c
CATCCCTGCA TGCA GGA GGA GGAGACCC
ACGT CCT CCT TCTCTGGG
C A AT---
GAM141 357 FLJ2115 1 12599 NM_024602.1 3 AGCACAAGCTGC AC A TCA 3 C c
c
6 CAGGCCTG CAGGT TG CAGCTTGTGCT
GTCCG AC GTCGAACACGA
-- G C--
GAM141 357 LOC1164 1 16557 XM_058185.2 5 AGCACAGGGGGA A ACAG 3 C c
c
37 CATGCCTGG CCAGGTATGTC CTTGTGCT
GGTCCGTACAG GGACACGA
- GG--
GAM141 357 ZNF236 1 9704 NM_007345.1 3 AGCACAAGCCAT AG - CACA 3 C c c

ACATCGCAGGT ACC GT ATGT GCTTGTGCT

TGG CG TACA CGAACACGA
A- C TAC-
GAM142 219 ARGBP2 1 16171 NP_003594.1 5 230 CAGGCAGCACCA AATTC - 3 A c c
AAGGTTTTTGTC CAAAA ACCTTTGG GCT
TTGGGAAG GTTTT TGGAAACC CGA
----- A
GAM142 219 ATP6V1E 1 15473 NP_001687.1 3 332 CCGTCTGGCCTA AAAT 3 A c c
1 AAGGTGATGTAT CAAA TCACCTTTGGGCT
TTGGTGTT GTTT AGTGGAAATCCGG
ATGT
GAM142 219 C14orf3 1 4925 XP_085124.2 3 2 CCGACAGCTCTG -- C TG - 3 A c c
7 AAGATGAATTTT CAA AAAATTCA CTT G GCT
GATTGGAC GTT TTTTAAGT GAA C CGA
AG A GT T
GAM142 219 DKFZp43 1 3751 XP_058513.6 5 517 AGTTTCAGTGCC - CC - 3 A c c
4H2111 AGAATGAATTTT CAA AAAATTCA TTTGG GCT
CTTGTTTC GTT TTTTAAGT AGACC TGA
C A- G
GAM142 219 DKFZp58 1 881 XP_098416.1 3 2320 CGTGAGAAGCCA AA- C G 3 A c c
6C0721 AAGGTAGTTTAT CA AAATT ACCTTTGG CTT
GTGAAAGG GT TTTGA TGGAAACC GAA
GTA - -
GAM142 219 DUSP16 1 14144 XP_039106.1 3 960 GGTTTCAAGCCA - C G 3 A c c
AATGTGAATTTA CAAA AAATTCAC TTTGG CTT
TTTGGGTT GTTT TTTAAGTG AAACC GAA
A T -
GAM142 219 FLJ2255 1 15012 NP_078989.1 3 802 TATCTAAGGAAA --- GGG 3 A c c
7 AAGGTGAATATG CAAAAA ATTCACCTTT CTT
TTTTTGTA GTTTTT TAAGTGGAAA GGA
GTA AA-
GAM142 219 FLJ3842 1 4649 NP_775882.1 3 443 ACAAGCTCAAGG A -- - 3 A c c
6 AGTCTGAATTTT C AAAAATTC AC CTTTGGGCTT
TCACTTTA A TTTTTAAG TG GGAACTCGAA
C TC A
GAM142 219 FLJ3942 1 2533 NP_775880.1 5 11 CGATGAAATCCA A CT 3 A c c
6 AAGGTGAATCTT CAAAA ATTCACCTTTGGG
TTGGTTGG GTTTT TAAGTGGAAACCT
C AA
GAM142 219 HRIHFB2 1 2665 NP_619538.1 3 2 CTGCAGGTCTCA AAA - 3 A c c
122 AAGGTGGGATTT CAAA TTCACCTTTG GGCTT
GGCGAGGG GTTT GGGTGGAAAC CTGGA
A-- T
GAM142 219 IL13RA1 1 10120 NP_001551.1 3 711 GGGAAGCTGAGG A -- G 3 A c c
CAGGTGAATTGT CAAA AATTCACCT TT GGCTT
TTGAACCT GTTT TTAAGTGGA GA TCGAA
G CG G
GAM142 219 KIAA195 1 15822 XP_085375.4 3 2207 CCAGAAGACCCA AA--- A - 3 A c c

4 AAGGAGAGTACT CAAA ATTC CCTTTGGG CTT
GGTTTGTG GTTT TGAG GGAAACCC GAA
GGTCA A A

GAM142 219 LOC1160 1 11647 XP_057302.2 3 1225 AAACAAAGGCCA AA ---- G 3 A c c

68 AAGGTGTATAGA CAA AATT CACCTTTGG CTT
TTGCTTGA GTT TTAG GTGGAAACC GAA
CG ATAT G

GAM142 219 LOC1244 1 12342 XP_058804.4 3 3715 AAGGACCAAAGA A ---- G- 3 A c c

11 CAAGTGAATTTT CA AAAATTCAC CTTTGG CTT
CTGAGGGT GT TTTTAAGTG GAAACC GAA
C AACA AG

GAM142 219 LOC1450 1 6065 XP_096714.1 3 739 AATGCCACAAAG A -- - T 3 A c c

53 TTGTGGAATTTT CAAAAA TTCAC CTTTG GGC
TGTGATTA GTTTTT AGGTG GAAAC CCG
A TT A T

GAM142 219 LOC1498 1 8167 XP_097747.1 5 1500 GTTTGGCCCCAA --- -- T 3 A c c

37 GAAGTGAATTTG CAAA AAATTCAC CTT GGGCT
GGTTTGAG GTTT TTTAAGTG GAA CCCGG
GGG AA C

GAM142 219 LOC1525 1 719 XP_087483.3 3 1185 TCTGAAGAAGTC A--- TT 3 A c c

19 CAGGTGAATTCA CAAA AATTCACCT GGGCTT
GCTTTGGA GTTT TTAAGTGGA CCTGAA
CGAC --

GAM142 219 LOC1587 1 9175 XP_088648.1 3 116 GTGTTAAGCCCA A ATT - 3 A c c

09 AAGTGTGTGTTT CA AAA CAC CTTTGGGCTT
CTGGTTGG GT TTT GTG GAAACCCGAA
C GT- T

GAM142 219 LOC2837 1 15741 XP_208803.1 5 527 AGTCTAAGCCCA AA-- ACC 3 A c c

14 AACAGGAATTCC CAA AATTC TTTGGGCTT
TGTTGAAT GTT TTAAG AAACCCGAA
GTCC GAC

GAM142 219 LOC2841 1 1851 XP_211364.1 5 209 CAAGGAAGCCCA AAAT A -- 3 A c c

75 AGTAGGAGATTT CAAA TC CCT TTGGGCTT
GGGAAACA GTTT AG GGA AACCCGAA
---- A TG

GAM142 219 LOC2864 1 9175 XP_301085.1 3 116 GTGTTAAGCCCA A ATT - 3 A c c

34 AAGTGTGTGTTT CA AAA CAC CTTTGGGCTT
CTGGTTGG GT TTT GTG GAAACCCGAA
C GT- T

GAM142 219 LOC3391 1 4620 XP_294845.1 5 364 CAGCTGAGCCTA A- 3 A c c

86 GAGGTGAATTTC CAA AAATTCACCTTTGGGCTT
ATTGGGGA GTT TTTAAGTGGAGATCCGAG
AC

GAM142 219 LOC3392 1 19571 XP_294880.1 5 364 CAGCTGAGCCTA A- 3 A c c

40 GAGGTGAATTTC CAA AAATTCACCTTTGGGCTT
GTTGGGGA GTT TTTAAGTGGAGATCCGAG

GC
GAM142 219 LOC3392 1 19571 XP_294886.1 5 364 CAGCTGAGCCTA A- 3 A c c
58 GAGGTGAATTTC CAA AAATTCACCTTTGGGCTT
GTTGGGGA GTT TTTAAGTGGAGATCCGAG
GC
GAM142 219 LOC3494 1 9175 XP_301083.1 3 116 GTGTTAAGCCCA A ATT - 3 A c c
29 AAGTGTGTGTTT CA AAA CAC CTTTGGGCTT
CTGGTTGG GT TTT GTG GAAACCCGAA
C GT- T
GAM142 219 LOC9338 1 14314 NP_775741.1 3 2476 CCATAGGACTTA AAAT - 3 A c
c
0 AAGGTGATTTGG CAAA TCACCTTTGGG CTT
ATGCGTTG GTTT AGTGGAAATTC GGA
---- A
GAM142 219 NAPB 1 19771 XP_046652.2 3 666 TGGATGAGTGTC -- C - 3 A c c
AAAGTGAATTTG CAAA AAATTCAC TTTGG GCTT
ATTTGTAC GTTT TTTAAGTG AAACT TGAG
AG - G
GAM142 219 NUDT4 1 4920 NP_061967.2 3 218 TAAGCCAAAGCC A ---- G 3 A c c
ATGTGGAATTTT CAAAAA TTCAC CTTTGG CTT
TGTTTAGA GTTTTT AGGTG GAAACC GAA
A TACC -
GAM142 219 PDGFRA 1 1956 NP_006197.1 3 286 AATAGGCCACAG A A - - 3 A c c
AAGGTGAACTTT CA AAA TTCACCT TTG GGCTT
GTGCTTCA GT TTT AAGTGGA GAC CCGGA
G C A A
GAM142 219 PHF3 1 2904 NP_055968.1 3 540 ATCAGAAGCCCA A TCA- 3 A c c
AGGGGTACATTT CAA AAAT CCTTTGGGCTT
ATTGCTTT GTT TTTA GGGAACCCGAA
A CATG
GAM142 219 RECQL5 1 8712 NP_004250.1 3 684 GCTTCAGACTTA AAA - 3 A c c
GAGGTGAATAAA CAA ATTCACCTTTGGG CT
TTGAGGTC GTT TAAGTGGAGATTC GA
AAA A
GAM142 219 SLC12A5 1 3990 NP_065759.1 3 654 CGAGGCCTCGGG -- C --- 3 A c c
AAGCTGAATTTT CAA AAAATTCA CTTT GGGCTT
CCTTGACG GTT TTTTAAGT GAAG TCCGGA
CC C GGC
GAM142 219 SV2A 1 17235 NP_055664.1 3 577 CTGCAAATATGA A CCTTTG 3 A c
c
AGCCTGAATTTT CA AAAATTCA GGCTT
ATGAAATT GT TTTTAAGT CCGAA
A ------
GAM142 219 SYTL4 1 10244 NP_542775.1 3 831 GTCTCACAGCCC A CCTT 3 A c c

ATGCTGAATTTT CA AAAATTCA TGGGCT
CTGCATTT GT TTTTAAGT ACCCGA
C CGT-
GAM142 219 YKT6 1 13499 NP_006546.1 3 235 TTGAGGTCCCCA ATT CT 3 A c c
AAGGTGTATTTT CAAAAA CACCTTTGGG

TGGGCAAA GTTTTT GTGGAAACCC
AT- CT
GAM143 325 FLJ1444 1 8620 NM_032785.1 3 GGAACTCACACG T CATTCA 3 C c c
2 CAGTCC GGACTGCG TGGGTTCC
CCTGACGC ACTCAAGG
- AC----
GAM143 325 KIAA018 1 8498 XM_050495.6 3 GAACCCATGTGT TG - TT C 3 C c c
2 GACAGTC GACTG CGCA CATGGGTTC
CTGAC GTGT GTACCCAAG
-- A -- -
GAM143 325 LOC1452 1 10431 XM_096740.1 3 GGAACCCATGAT C C T 3 C c c
31 TGTTAATTCA TGGA TG GCA TCATGGGTTCC
ACTT AT TGT AGTACCCAAGG
A - T
GAM143 325 LOC1492 1 10413 5 GAACCTATGGAC A CGCA C 3 C c c
96 AGCCCA TGG CTG TTCATGGGTTC
ACC GAC AGGTATCCAAG
C ---- -
GAM143 325 LOC9013 1 4815 NM_130783.1 3 GGAACCCACAGC T C ATTCA 3 C c c
9 GCAATCC GGA TGCGC TGGGTTCC
CCT ACGCG ACCCAAGG
- A AC---
GAM143 325 MUC3B 1 9337 XM_168578.2 3 AACCCACCTGGA CA -- CC 3 C c c
GACGCAGTTCA TGGACTGCG TTCA TGGGTT
ACTTGACGC AGGT ACCCAA
AG CC --
GAM143 325 PFKFB4 1 7569 NM_004567.2 3 GAACCCATAGGC T GCATTC C 3 C c c
AGTCC GGACTGC ATGGGTTC
CCTGACG TACCCAAG
- GA---- -
GAM144 361 AACS 1 18383 NP_076417.1 5 110 GGTCCCCAGCCC TGC A 1 A c c
TCGTCGCAGCCC CTG CTGTGACGAGGG TG
CGGCCGCC GGC GACGCTGCTCCC AC
CCC G
GAM144 361 ABCC13 1 6955 NP_742021.1 3 211 TTATGTCAGCCA T AG A 1 A c c
GTGTTTCAGGCA CTGTGCCTG GACG GG TGA
CAGGAAGT GACACGGAC TTGT CC ACT
T GA G
GAM144 361 ADCY1 1 8386 NP_066939.1 3 186 CGAGGGCCAACC GA AG A 1 A c c
ACCGAGCAGGCA CTGTGCCTGT CG GG TG
CAGCACAG GACACGGACG GC CC AC
A- CA A
GAM144 361 ADCY1 1 8386 XP_166593.2 3 186 CGAGGGCCAACC GA AG A 1 A c c
ACCGAGCAGGCA CTGTGCCTGT CG GG TG

CAGCACAG GACACGGACG GC CC AC
A- CA A
GAM144 361 ALDH3B2 1 3474 NP_000686.1 3 309 GTTGGCCAGGCC G GA A- 1 A c c
CAGTCACAGGGG CTGT CCTGTGAC GGG TG
CAGTGTCA GACG GGACACTG CCC AC
G A- GG
GAM144 361 APM1 1 2427 NP_004788.1 3 300 TGCTCATATCAA GTGACG A 1 A c c
TCCTATAAGGCA CTGTGCCT AGGG TGA
CAGGGAAC GACACGGA TCCT ACT
ATA--- A
GAM144 361 BCAT2 1 14160 NP_001181.1 3 215 GCCCCCAGCCCC T A- 1 A c c
TCGTCGCGGGTT CTG GCCTGTGACGAGGG TG
CAGGTCCG GAC TGGGCGCTGCTCCC AC
T CG
GAM144 361 BCLG 1 16807 NP_110393.1 5 165 AGAGAATTCCTT GT -- G 1 A c c
GAGTCTAAGGCA CTGTGCCT GAC GAGGGAT
CAGGCCCA GACACGGA CTG TTCCTTA
AT AG A
GAM144 361 BCLG 1 16807 NP_620048.1 5 165 AGAGAATTCCTT GT -- G 1 A c c
GAGTCTAAGGCA CTGTGCCT GAC GAGGGAT
CAGGCCCA GACACGGA CTG TTCCTTA
AT AG A
GAM144 361 BMF 1 9278 NP_277038.1 3 1321 GTGTGGCAGCTC GA- A A 1 A c c
CGATAGCAGGCA CTGTGCCTGT CG GGG TG
CAGGGAAT GACACGGACG GC CTC AC
ATA - G
GAM144 361 BTF 1 6208 NP_055554.1 3 2376 CTATTGTTCCTT ---- -- TG 1 A c c
TTGTCACAGGTA CTG TGCCTGTGAC GAGGGA A
AAATCAGT GAC ATGGACACTG TTCCTT T
TAAA TT GT
GAM144 361 BY55 1 9405 NP_008984.1 3 86 GTATCTTTCTCA ------ C 1 A c c
TTACAATAGGCA CTGTGCCT GTGA GAGGGATG
CAGAGAAG GACACGGA TACT CTTTCTAT
TAACAT -
GAM144 361 C14orf6 2 15823 NP_689546.1 3 1007 CAGGGCTTCATC GTG G 1 A b b
9 CCTGTGAAGGCA CTGTGCCT AC AGGGATGA
CAGGGCCT GACACGGA TG TCCCTACT
AG- -
GAM144 361 C14orf6 2 17914 NP_689546.1 3 1007 GGGCTTCATCCC GTG G 1 A b b
9 TGTGAAGGCACA CTGTGCCT AC AGGGATGA
GGGCCTGC GACACGGA TG TCCCTACT
AG- -
GAM144 361 C1orf19 1 9890 NP_443197.1 3 1078 GTTTGTCATCCC G- T G- 1 A c c
TGGGTCTAGGAA CTGT CCTG GAC AGGGATGA
ATAGTCAA GATA GGAT CTG TCCCTACT
AA - GG

GAM144 361 C1orf2 1 6438 NP_006580.1 3 48 ACTGAACACATC - ACGAG 1 A c c
CAGCCACAGGCA CTG TGCCTGTG GGATG
CCAGCTGG GAC ACGGACAC CCTAC
C CGA--
GAM144 361 C21orf2 1 14016 NP_659428.2 3 1836 CAACATCATCTT GTGA-- - 1 A c c
9 GGGAGAGAGGCA CTGTGCCT CGAGG GATG
CAGACCTG GACACGGA GTTCT CTAC
GAGAGG A
GAM144 361 C6orf33 1 4721 NP_588608.1 3 224 TTTGGATCATAG G AC GG 1 A c c
CTTAACAAGGCA CTGTGCCT TG GAG ATGA
CAGGAAGG GACACGGA AC TTC TACT
- AA GA
GAM144 361 C6orf59 1 1948 NP_079205.1 5 488 GTGAATTCATCA GAC G- 1 A c c
GCTCTGCAGGCA CTGTGCCTGT GAG GATGA
CAGACCTT GACACGGACG CTC CTACT
T-- GA
GAM144 361 C6orf64 1 3256 NP_060792.1 3 944 AACCTAGATCCC CT A G 1 A c c
TCGCATGCGCAG CTGTGC GTG CGAGGGAT
TTCACAAT GACGCG TAC GCTCCCTA
-- - G
GAM144 361 CABC1 1 5724 NP_064632.1 3 694 TTCCTTCCTCTG GT--- - T 1 A c c
TCCGGAGAGGCA CTGTGCCT GAC GAGGGA GA
CAGGTGTC GACACGGA CTG CTCCTT CT
GAGGC T C
GAM144 361 CD86 1 8499 NP_008820.1 3 588 AGTTCTCATCCC T G - 1 A c c
TCTGTCAGGGTC CTG GCCT TGAC GAGGGATGA
AGTAAGGA GAC TGGG ACTG CTCCCTACT
- - T
GAM144 361 CD86 1 8499 NP_787058.2 3 588 AGTTCTCATCCC T G - 1 A c c
TCTGTCAGGGTC CTG GCCT TGAC GAGGGATGA
AGTAAGGA GAC TGGG ACTG CTCCCTACT
- - T
GAM144 361 CDC42EP 1 12629 NP_006440.2 3 2023 GTTGGACCACAC C- A GA 1 A c
c
3 CCGTCACAGTTC CTGTG CTGTGACG GG TG
ACAGTTCC GACAC GACACTGC CC AC
TT - AC
GAM144 361 CDH5 2 11221 NP_001786.1 5 77 CAGAAACATCCC C-- AC--- 1 A c c
TCAGCCCCACAG TGTGCCTGTG GAGGGATG
GCACGATC GCACGGACAC CTCCCTAC
CTA CCCGA
GAM144 361 CDH5 2 19978 NP_001786.1 5 77 AAACATCCCTCA C----- AC--- 1 A c c
GCCCCACAGGCA TGTGCCTGTG GAGGGATG
CGATCTGT GCACGGACAC CTCCCTAC
TGTCTA CCCGA
GAM144 361 CECR7 1 8985 XP_086803.1 5 1681 TGCCATGTCCAT --- ACGA 1 A c c
CCTCCACAGGCA CTGT GCCTGTG GGGATG
GAACAGGA GACA CGGACAC TCCTAC
AGA C---

GAM144 361 CHST3 2 16447 NP_004264.2 3 4552 GACATGGTGCCA T CGAG 1 A c c

TCCTCACAGGCC CTG GCCTGTGA GGATG
TAGCTCAT GAT CGGACACT CCTAC
C ----

GAM144 361 CHST3 2 18607 NP_004264.2 3 1226 CGCCTTCTTCCC TG- G- T 1 A c c

TCGTGGACAGGA CTG CCTGT ACGAGGGA GA
GTCAGCCA GAC GGACA TGCTCCCT CT
TGA GG T

GAM144 361 CHST6 1 3167 NP_067628.1 3 1490 TGAATCTGTCCC CC G 1 A c c

TCGTGACAATTA CTGTG TGT ACGAGGGATG
TAGGAGGA GATAT ACA TGCTCCCTGT
TA G

GAM144 361 CLIPR-5 1 2842 NP_056341.1 3 1107 CACCTCAAGCCC - CG A- 1 A c c

9 TATTCACAGGCA CTG TGCCTGTGA AGGG TGA
CCAGGAAA GAC ACGGACACT TCCC ACT
C TA GA

GAM144 361 COL19A1 1 15138 NP_001849.1 3 3596 TTAAGCATCTTT GACG- 1 A c c

ATGAAACAGGCA CTGTGCCTGT AGGGATG
CAGTACCC GACACGGACA TTTCTAC
AAGTA

GAM144 361 COL1A1 1 6641 NP_000079.1 3 739 GCGTGTCATCCC --- -- 1 A c c

TTGTGCCGCAGG CTGT GCCTGTG ACGAGGGATGA
CTGGGCGG GGCG CGGACGC TGTTCCCTACT
GGT CG

GAM144 361 D2S448 1 9361 XP_056455.2 3 1321 TGAGTATCCACC TG AG-- 1 A c c

ATGTGCCAGGCA CTGTGCCTG ACG GGATG
CAGTGCTG GACACGGAC TGT CCTAT
CG ACCA

GAM144 361 DCC 1 1702 NP_005206.1 3 184 TAAGCATTCCTT - C-- 1 A c c

CTTTCACAGGCA CTG TGCCTGTGA GAGGGATG
TCAGGAAT GAC ACGGACACT TTCCTTAC
T TTC

GAM144 361 DDX54 1 11738 NP_076977.2 3 1069 GGCCCACAGCAC GAC GGA 1 A c c

TCTGAACAGGCA CTGTGCCTGT GAG TG
CAGCCCTC GACACGGACA CTC AC
AGT ACG

GAM144 361 dJ55C23 1 5224 NP_439896.1 3 798 GTATTTCATCCC T GACG 1 A c c

.6 TAGAGCAGGTCA CTG GCCTGT AGGGATGA
GCCTCCTT GAC TGGACG TCCCTACT
- AGA-

GAM144 361 DKFZP43 2 4768 NP_056436.1 3 460 GAACCTCATCCC CTGTGACG 1 A c c

4C171 TGCACAGATGAG CTGTGC AGGGATGA
GAAACCAA GACACG TCCCTACT

```
                                                --------
GAM144  361  DKFZP43 2  16009  NP_056436.1  3  1548  GAAAGCATTGTT      T  --  G       1  A  c  c
         4C171                                  TTAGTCCAGGCA CTGTGCCTG GAC  GAG GATG
                                              CAGTGGCT    GACACGGAC CTG  TTT TTAC
                                                        -  AT   G
GAM144  361  DKFZP43 1  19475  XP_114297.2  3  705   CAAGTCAACCTC      T  -  -  A       1  A  c  c
         4D193                                  TCTGTTCAGGCA CTGTGCCTG GAC GAG GG TGA
                                              CAGATCTG    GACACGGAC TTG CTC CC ACT
                                                        -  T  T  A
GAM144  361  DKFZP58 1  12078  NP_056398.1  3  90    ATGTCTTATTTT      GT   --         1  A  c  c
         6M0622                                  ATTTGTCAGGCA CTGTGCCT  GACGAG  GGATGA
                                              CAGATGCT    GACACGGA  CTGTTT  TTTATT
                                                        --    AT
GAM144  361  DKFZp76 1  14315  NP_060893.1  3  330   TAAGCTCATCCC   T   GT  --         1  A  c  c
         1P1010                                  TCCCGTCCGAGG CTG GCCT  GAC  GAGGGATGA
                                              CTAGTTTC    GAT CGGA  CTG  CTCCCTACT
                                                        -   GC   CC
GAM144  361  DNAJC8  1  20028  NP_055095.1  3  24    GAGTGCCGCCCA        GA-  A       1  A  c  c

                                              AGGTCACAGGCA CTGTGCCTGTGAC   GGG TG
                                              CAGAACCT    GACACGGACACTG   CCC GC
                                                          GAA  -
GAM144  361  DNMT3L  1  11497  NP_037501.2  5  363   CTGCGCCGTCCC   T  -  TG          1  A  c  c

                                              TCGTTCCATGGC CTG GCC TG  ACGAGGGATG
                                              CCAGTCCT    GAC CGG AC  TGCTCCCTGC
                                                        C   T  CT
GAM144  361  DNMT3L  1  11497  NP_787063.1  5  363   CTGCGCCGTCCC   T  -  TG          1  A  c  c

                                              TCGTTCCATGGC CTG GCC TG  ACGAGGGATG
                                              CCAGTCCT    GAC CGG AC  TGCTCCCTGC
                                                        C   T  CT
GAM144  361  DPM2   1  5244  NP_003854.1  3  97    GAGCCTGCAGAA      T  G  GA-       1  A  c  c
                                              CCTGTCCAGGCA CTGTGCCTG GAC AGG   TG
                                              CAGTGGCT    GACACGGAC CTG TCC   AC
                                                        -  -  AAG
GAM144  361  DPM2   1  5244  NP_689903.1  3  923   GAGCCTGCAGAA      T  G  GA-       1  A  c  c
                                              CCTGTCCAGGCA CTGTGCCTG GAC AGG   TG
                                              CAGTGGCT    GACACGGAC CTG TCC   AC
                                                        -  -  AAG
GAM144  361  EGFL4  1  2374  XP_290821.1  3  1033  TGGGGTCAGCCC      ----       A      1  A  b  b
                                              TCGTCACACTGC CTGTGCC   TGTGACGAGGG TGA
                                              GGCACAGG    GACACGG   ACACTGCTCCC ACT
                                                        CGTC        G
GAM144  361  EGFL7  1  12268  NP_057299.1  5  290   AGAAGGCCACCC      G  A-  A  A       1  A  c  c

                                              CGCCTGGAGGCA CTGTGCCT TG  CG GGG TG
                                              CAGGCCAT    GACACGGA GT  GC CCC AC
                                                        G  CC  -  -
GAM144  361  EIF4EBP 1  5134  NP_004087.1  5  233   ACAGCCATGTCC   -  T -      -       1  A  c  c
```

```
          2                          TCGTCAGCCGGC CTG TGCC G TGACGAGGG ATG
                                     AGCGGCC     GGC ACGG C ACTGCTCCT TAC
                                           G   C G       G
GAM144   361   EIF5   1  4078  NP_001960.2  5  380   TTATGTCATCCC    GC   T C---          1  A  c  c
                                     TTCTTCTCCAGA CTGT  CTG GA    GAGGGATGA
                                     CAGAAGAT    GACA  GAC CT    TTCCCTACT
                                           --   -  CTTC
GAM144   361   EPSTI1 1   846   NP_150280.1  5  16    CAGCCGCATCCC    GC    AC           1  A  c  c
                                     TCCCGCAGCGAC CTGT  CTGTG  GAGGGATG
                                     GGCGGCCC    GGCA  GACGC  CTCCCTAC
                                           GC    C-
GAM144   361   EYA4   1  5938  NP_004091.2  5  238   GATGTCCTGTTT      ---  CGA-         1  A  c  c
                                     TCACCAGAGGCA CTGTGCCT   GTGA   GGGATG
                                     CAGCGCGA    GACACGGA   CACT   TCCTGT
                                           GAC    TTTG
GAM144   361   EYA4   1  5938  NP_742101.1  5  238   GATGTCCTGTTT      ---  CGA-         1  A  c  c
                                     TCACCAGAGGCA CTGTGCCT   GTGA   GGGATG
                                     CAGCGCGA    GACACGGA   CACT   TCCTGT
                                           GAC    TTTG
GAM144   361   EYA4   1  5938  NP_742102.1  5  238   GATGTCCTGTTT      ---  CGA-         1  A  c  c
                                     TCACCAGAGGCA CTGTGCCT   GTGA   GGGATG
                                     CAGCGCGA    GACACGGA   CACT   TCCTGT
                                           GAC    TTTG
GAM144   361   EYA4   1  5938  NP_742103.1  5  238   GATGTCCTGTTT      ---  CGA-         1  A  c  c
                                     TCACCAGAGGCA CTGTGCCT   GTGA   GGGATG
                                     CAGCGCGA    GACACGGA   CACT   TCCTGT
                                           GAC    TTTG
GAM144   361   FACL1  1  7139  NP_001986.1  3  531   TGCTACTGTCCC  T       C            1  A  c  c
                                     TTCTCACAGGCA C GTGCCTGTGA GAGGGATG
                                     TTCACAGA    C TACGGACACT TTCCCTGT
                                           T       C
GAM144   361   FACL2  1  7139  NP_066945.1  3  534   TGCTACTGTCCC  T       C            1  A  c  c
                                     TTCTCACAGGCA C GTGCCTGTGA GAGGGATG
                                     TTCACAGA    C TACGGACACT TTCCCTGT
                                           T       C
GAM144   361   FANCA  1  5437  NP_000126.1  3  544   CGCCGGCCACAC  G       G --- A      1  A  c  c

                                     TGGTCACAGGCA CT TGCCTGTGAC AG   GG TG
                                     AAGTCCAG    GA ACGGACACTG TC   CC GC
                                           A       G  ACA  G
GAM144   361   FGF23  1  15801 NP_065689.1  3  51    TTAACCCATCCC    CC   GAC          1  A  c  c
                                     TCAGCAAACGCA CTGTG  TGT   GAGGGATG
                                     GCTCTTCC    GACGC  ACG   CTCCCTAC
                                           AA   A--
GAM144   361   FLJ0000 1  6835  XP_088525.2  3  1091  GGCTGCCATCCC   T   GTGA           1  A  c
c
          1                          TCGGGGCCCAGG CTG GCCT    CGAGGGATG
                                     CCCTCACC    GAC CGGG    GCTCCCTAC
                                           C    ----
GAM144   361   FLJ0002 1  18861 NP_203745.1  5  54    GCTGCCGTCCCC      GTG  A-          1  A  c  c
```

4 GCGTGTGAGGCA CTGTGCCT ACG GGGATG
CAGAAGGG GACACGGA TGC CCCTGC
GTG GC
GAM144 361 FLJ0002 1 18861 XP_033361.2 5 70 GCTGCCGTCCCC GTG A- 1 A c c

4 GCGTGTGAGGCA CTGTGCCT ACG GGGATG
CAGAAGGG GACACGGA TGC CCCTGC
GTG GC
GAM144 361 FLJ1045 1 11597 NP_060565.2 3 293 AAGCCTTTTCTC GTGAC GA 1 A c
c

0 AGACCTTAGGCA CTGTGCCT GAGG TGA
CAGCCTCT GACACGGA TTCC ACT
----- AG
GAM144 361 FLJ1103 1 14811 NP_060776.2 5 9 CCGCCCTCCTTG TG ------ A 1 A c c
6 CTGTCACAGGTG CTG CCTGTGAC GAGGG TG
CAGCCTGT GAC GGACACTG CTCCC GC
GT TCGTTC -
GAM144 361 FLJ1248 1 17886 NP_112495.1 3 108 ACCATCCCAAAC T C ---- 1 A c c
8 TCCTCCCAGGCA CTGTGCCTG GA GA GGGATG
CAGTCTGG GACACGGAC CT CT CCCTAC
C C CAAA
GAM144 361 FLJ1255 1 9222 NP_073743.2 3 2422 AGTTTACATCCC --- - C- 1 A c c
2 TCATTCACAGTG CTGT GC CTGTGA GAGGGATG
TAAAGCAG GACG TG GACACT CTCCCTAC
AAA T TA
GAM144 361 FLJ1320 1 4763 NP_079037.2 3 3459 AGCATTCATCCC GCC AC 1 A c
c

4 TTTCCATATAAC CTGT TGTG GAGGGATGA
AGGAGGGA GACA ATAC TTCCCTACT
AT- CT
GAM144 361 FLJ1344 1 7854 NP_076413.1 3 3585 GGTCGCTCTTGG A---- A 1 A c c
1 GAGGCACAGGCA CTGTGCCTGTG CGAGGG TGA
TGGGTGTG GGTACGGACAC GTTCTC GCT
GGAGG -
GAM144 361 FLJ1384 1 1687 NP_079047.1 3 1963 CGTGTTCATCCC ---- GTG 1 A c c
8 TTGTAAGGTGAG CTG TGCCT ACGAGGGATGA
TTCAGTCT GAC GTGGA TGTTCCCTACT
TTGA A--
GAM144 361 FLJ1410 1 589 NP_079343.1 5 29 TTTCTTCCATCT TG CGA 1 A c c
6 CCCTTGCAGGCA CTGTGCCTG A GGGATG
CAGGGCCA GACACGGAC T CTCTAC
GT CC-
GAM144 361 FLJ1445 1 11171 NP_116177.1 3 533 AGGGCTCATCCC - CTG CG 1 A c
c

7 TTATTAAGCATC CTG TGC TGA AGGGATGA
AGAAAATT GAC ACG ATT TCCCTACT
T A-- AT
GAM144 361 FLJ2041 1 4973 NP_060278.1 3 1085 GGATAAGCAGCT G- GA A 1 A c
c

3 CAGTCACAGGCA CT TGCCTGTGAC GGG TG

GAAGAAGG GA ACGGACACTG CTC AC
AG A- G

GAM144 361 FLJ2043 2 12137 NP_060292.1 3 365 ATCATCTCTCAC --- AC---- 1 A c c
6 AAAACACAGGCA CTG TGCCTGTG GAGGGATGA
ACCCAGAC GAC ACGGACAC CTCTCTACT
CCA AAAACA

GAM144 361 FLJ2043 2 15533 NP_060292.1 5 140 ATGCTCTCACCC G G - A 1 A c c
6 TCGTCTGGAGGG CTGT CCT T GACGAGGG TGA
GCAGGAGT GACG GGA G CTGCTCCC ACT
G G T -

GAM144 361 FLJ2048 1 13148 NP_060311.1 3 529 CCTGAGCTGAAT GTGAC G 1 A c
c
7 CCTTCAAAGGCA CTGTGCCT GAGGGAT
CAGCAGGC GACACGGA CTTCCTA
AA--- A

GAM144 361 FLJ2048 1 14840 NP_060312.1 3 237 CCATCTCACTCA T AC--- - - 1 A c c
9 CACACACAGGCA C GTGCCTGTG GAG G GATG
TCCATACA C TACGGACAC CTC C CTAC
C ACACA A T

GAM144 361 FLJ2062 1 17489 NP_060378.1 5 28 TTCGAGCATCCC T GA 1 A c c
6 TCGGATAGGCCG CTG GCCTGT CGAGGGATG
GGTGTCAG GGC CGGATA GCTCCCTAC
- G-

GAM144 361 FLJ2113 1 7806 NP_079142.1 5 476 AAGCTTCACCGG TGAC A- 1 A c
c
5 GCCCTCCAGGCA CTGTGCCTG GAGGG TG
CAGAGGGG GACACGGAC CTCCC GC
---- GG

GAM144 361 FLJ2205 1 12358 NP_073589.1 5 34 GAGGTGCAGGCC G CT GA 1 A c
c
9 TCGTCACCTGCA CT TGC GTGACGAGG TG
GAGGTGCC GA ACG CACTGCTCC AC
G TC GG

GAM144 361 FLJ2241 1 13241 NP_078973.1 5 111 CTCTCAGTCCTG A- G 1 A c c
9 ATGTCACAGGCG CTGTGCCTGTGACG GGGAT
CGGCAAGG GGCGCGGACACTGT TCCTG
AG A

GAM144 361 FLJ3165 1 19250 NP_689971.1 3 289 TAATTATGCATC GTGACGA 1 A c
c
7 CTAGCTAAGGCA CTGTGCCT GGGATG
CAGAAGAC GACACGGA TCCTAC
ATCGA--

GAM144 361 FLJ3379 1 8915 NP_775854.1 3 1206 AAATCTTCACCT T - A A 1 A c c
0 ATGATCCAGGCA CTGTGCCTG GA CG GGG TGA
CAGATGTG GACACGGAC CT GT TCC ACT
- A A -

GAM144 361 FLJ3399 1 639 NP_787090.1 3 1133 TGGGGACATCCC T T C 1 A c c
6 TCTCTAGGCCTA CTG GCCTG GA GAGGGATG
GGCCATGT GAT CGGAT CT CTCCCTAC
C - -

GAM144 361 FLJ3667 1 18877 NP_775893.1 3 1434 ATCCATCATCCC G -- G AC 1 A c c
4 TCACAGAGATGT CT TGC CT TG GAGGGATGA
AGAGGATG GA ATG GA AC CTCCCTACT
G TA G A-
GAM144 361 FLJ3707 1 18330 NP_694588.1 3 773 GATGGCAGCCCA GA- A 1 A c c
8 GGGTCACAGGCA CTGTGCCTGTGAC GGG TG
TAGGATAA GATACGGACACTG CCC AC
GGA G
GAM144 361 FLJ3898 1 3780 NP_689587.1 3 1630 GAGTTTCATCCC -- GACG 1 A c c
4 TGACAGGTGGAT CTGT GCCTGT AGGGATGA
GGGTGAAA GGTA TGGACA TCCCTACT
GG G---
GAM144 361 FUT7 1 7584 NP_004470.1 3 408 CCTGTGGTCCCC A-- A G 1 A c c
GAGACACAGGCA CTGTGCCTGTG CG GGGAT
CGGGTCCC GGCACGGACAC GC CCCTG
AGA - G
GAM144 361 GHITM 1 18194 NP_055209.1 3 678 AAACTGTTCATC GACGA 1 A c c
CTGAAACAGGCA CTGTGCCTGT GGGATGA
CAGGTGAT GACACGGACA TCCTACT
AAG--
GAM144 361 GIOT-2 2 6079 NP_057348.1 3 364 ATCATTCATCCC C------- GAC 1 A c c
TTAACAGGCACA TGTGCCTGT GAGGGATGA
TTAGATCT ACACGGACA TTCCCTACT
TCTAGATT A--
GAM144 361 GIOT-2 2 11250 NP_057348.1 3 364 CCATCATTCATC C----- GAC 1 A c c
CCTTAACAGGCA TGTGCCTGT GAGGGATGA
CATTAGAT ACACGGACA TTCCCTACT
TAGATT A--
GAM144 361 GOLGA1 1 11331 NP_002068.1 5 263 CTGTCTGAATCC - ACGA G 1 A c c
TGAACACAGGCA CTG TGCCTGTG GGGAT
CCAGGACT GAC ACGGACAC TCCTA
C AAG- A
GAM144 361 GOR 1 13612 NP_758439.1 5 200 CCAGCCCTTGCT --- ----- A 1 A c c
TGGTCACAGGTT CTGTG CCTGTGAC GAGGG TG
ACACAGAT GACAC GGACACTG TTCCC AC
ATT GTTCG G
GAM144 361 GREB1 1 8571 NP_683701.1 5 21 CGCATCCTCTTC TGACGA 1 A b b
CATCCCCAGGCA CTGTGCCTG GGGATG
CAGATCAA GACACGGAC CCCTAC

GAM144 361 GRINA 1 12280 XP_291268.1 3 110 TCCCCTCTCTCT T- TG 1 A c c
TGTCCCCAGGCA CTGTGCCTG GACGAGGGA
CAGCCTAG GACACGGAC CTGTTCTCT
CC CT
GAM144 361 GRTP1 1 11191 NP_078995.1 3 9 GACGGGCACCAG A- AG A 1 A c c

TGGGCATAGGCA CTGTGCCTGTG CG GG TG
CAGGATGA GACACGGATAC GT CC AC
GG GA -

GAM144 361 HES2 1 17870 XP_290879.1 3 2539 CGCCAACATCCT ---- ACGA 1 A c c

CCTCCACAGGCA CTGT GCCTGTG GGGATG
GTGGCAGG GACG CGGACAC TCCTAC
GTGA CTCC

GAM144 361 HLCS 1 13731 NP_000402.2 3 1477 AGTCTGTCTACC TGAC -- 1 A c c

TTTAGCCAGGCA CTGTGCCTG GAGG GATG
CAGGACAG GACACGGAC TTCC CTGT
CGAT AT

GAM144 361 HOXC9 1 18430 NP_008828.1 3 404 CCAGGTCATCCC T TGAC 1 A c
c

TCCCCGGGCCTG CTG GCCTG GAGGGATGA
GGGCGCTC GGT CGGGC CTCCCTACT
C CC--

GAM144 361 HSPC129 1 14145 NP_057480.1 3 1329 AACTGCATTAAC T GA -- 1 A c
c

CAGTCACAGGCT CTG GCCTGTGAC GG GATG
CAGACTGT GAC CGGACACTG CC TTAC
T A- AA

GAM144 361 IGF2AS 1 16566 NP_057496.1 3 209 CTGGGGTCGCCT ACG- - G 1 A c
c

GGGCCACAGGCA CTGTGCCTGTG AGG GAT
CAGCAGCT GACACGGACAC TCC CTG
CGGG G G

GAM144 361 IHPK2 1 9050 NP_057375.1 3 52 GAGAGCGACTCT T - A 1 A c c

GTGTCCCAGGCA CTGTGCCTG GACG AGGG TG
CAGCTGTG GACACGGAC CTGT TCTC GC
C G A

GAM144 361 ITPKB 1 2633 NP_002212.1 3 2352 CCTGCCCAGCCC CCT A 1 A c c

TCGTCACCACAG CTGTG GTGACGAGGG TG
GGACTCCT GACAC CACTGCTCCC AC
--- G

GAM144 361 KCNMB4 1 13644 NP_055320.4 3 146 GAGGCTCATCCC GC G--- - 1 A c
c

TCAGTGGCAACA CTGT CTGT AC GAGGGATGA
GAAACAGG GACA GACA TG CTCCCTACT
AA ACGG A

GAM144 361 KIAA019 1 12459 XP_038362.3 5 356 CAGCCATCCCCC T -- T -- 1 A c c
4 TCGTCCAGCCGC CTG GC CTG GACGA GGGATG
CGGGCCAA GGC CG GAC CTGCT CCCTAC
- CC - CC

GAM144 361 KIAA019 1 8741 NP_055661.1 5 229 TTAATCATCCCC T A-- 1 A b b
6 AGTGTCCAGGCA CTGTGCCTG GACG GGGATGA
CAGAGTAG GACACGGAC CTGT CCCTACT
- GAC

GAM144 361 KIAA025 1 7237 NP_055600.1 3 751 CCTGGTCATCCC TGCCT- - 1 A c
c

```
          8                    TCAGTCACTCAT CTG     GTGAC GAGGGATGA
                               ATCAGAGT    GAC     CACTG CTCCCTACT
                                    TATACT    A
GAM144    361   KIAA046 1  18243 NP_055666.1  3  1711  CTCACTCATCCC C--       AC---          1  A  c  c

          9                    TTTGGCCCACAG   TGTGCCTGTG    GAGGGATGA
                               GTACATGT      ACATGGACAC    TTCCCTACT
                                    TGT       CCGGT
GAM144    361   KIAA055 1  15943 XP_085507.1  3  56   GACTCTCATCCC      GTGACG           1  A  c
c
          7                    TGGGCACAGAAT CTGTGCCT     AGGGATGA
                               TCAGGAAA    GACACGGG     TCCCTACT
                                           ------
GAM144    361   KIAA077 1  7991  NP_055505.1  3  1434  CCTCCCCAGCCC  G     A    A         1  A  c  c
          3                    TTGGCACAGGCA CT TGCCTGTG CGAGGG TG
                               GAGTTCGG    GA ACGGACAC GTTCCC AC
                                    G      G    G
GAM144    361   KIAA097 1  4116  NP_055744.1  3  731   TCTGCCCATCCC    CCT--   C          1  A  c  c
          1                    TCTTCATTCACA CTGTG    GTGA GAGGGATG
                               CACAGTTC    GACAC    TACT CTCCCTAC
                                     ACACT   T
GAM144    361   KIAA098 1  19005 NP_036439.1  3  482   AATCATCACAGG       T -  GG---       1  A  c  c
          7                    TCGATCCAGGCA CTGTGCCTG GA CGA    GATGA
                               CAGATCTG    GACACGGAC CT GCT    CTACT
                                         - A  GGACA
GAM144    361   KIAA105 1  19444 XP_043493.5  3  1636  CCTAATGATCCC   T -  TGA     G       1  A  c
c
          4                    TCGCAGAGCTCA CTG GC CTG   CGAGGGAT
                               GACTAAGT    GAC CG GAC   GCTCCCTA
                                    T A  ---      G
GAM144    361   KIAA121 1  3392  XP_172801.1  3  1063  CCCCACGTCGAC   T      G  --        1  A  c  c
          0                    CTGTCACAGGCC CTG GCCTGTGAC AGG  GATG
                               TGGCTGTA    GGT CGGACACTG TCC  CTGC
                                    C       -  AG
GAM144    361   KIAA131 1  15868 XP_098368.2  3  3209  TGTTATCCTTTG        ---          1  A  c  c
          7                    TATTTATAGGCA CTGTGCCTGTG   ACGAGGGATGA
                               CAGTTATC    GACACGGATAT   TGTTTCCTATT
                                           TTA
GAM144    361   KIAA134 1  10596 XP_044836.2  5  203   GGCCGCCATCCC   T CT-  A          1  A  c  c

          0                    TCGGCGCCCCGC CTG GC   GTG CGAGGGATG
                               CCGGAACC    GGC CG   CGC GCTCCCTAC
                                    C  CCC   G
GAM144    361   KIAA137 1  2469  XP_040708.2  5  75    CAGCTGCCATCG   -      ACGA -       1  A  c  c
          7                    CCGCTACAGGCA CTG TGCCTGTG    GG GATG
                               CCAGTGCC    GAC ACGGACAT    CC CTAC
                                    C       CG--  G
GAM144    361   KIAA182 1  4193  XP_041566.2  3  2490  AGCCTAGATCCC     CT  A     G       1  A  c  c

          2                    TCGCATGCACAG CTGTGC  GTG CGAGGGAT
```

TTCATAGT GACACG TAC GCTCCCTA
-- - G
GAM144 361 KIAA190 1 12359 XP_055834.1 5 2403 CCGCTCTCCTCC G A A T 1 A c c
8 CCGGCACAGGCA CT TGCCTGTG CG GGGA GA
GGGGGTCT GG ACGGACAC GC CCCT CT
G G - C
GAM144 361 KIAA192 1 8934 XP_085210.1 5 2853 TGTTCTCATCCC - TGT- G 1 A c c
0 TGGTTCCTTGGC CTGTG CC GAC AGGGATGA
CACGGTGG GGCAC GG TTG TCCCTACT
C TTCC G
GAM144 361 LAD1 1 13558 NP_005549.2 3 233 GACTTTCTCACC C----- GA - A 1 A c c
CTGCGGCAGGCA TGTGCCTGT CG AGGG TGA
CAACAGAT ACACGGACG GC TCCC ACT
TAGACA -- G -
GAM144 361 LDB2 1 8958 NP_001281.1 3 1016 TGTTCCTCCACA ------ AC 1 A c c
CATGTAAAGGCA CTGTGCCT GTG GAGGGATG
CAGTGGCT GACACGGA CAC CTCCTTGT
AATGTA AC
GAM144 361 LGALS9 1 13678 NP_002299.1 3 263 TCCTACCATCCC GACGA 1 A c c
AGGAGGCAGGCA CTGTGCCTGT GGGATG
CAGCCAGG GACACGGACG CCCTAC
GAGGA
GAM144 361 LGALS9 1 13678 NP_033665.1 3 263 TCCTACCATCCC GACGA 1 A c c
AGGAGGCAGGCA CTGTGCCTGT GGGATG
CAGCCAGG GACACGGACG CCCTAC
GAGGA
GAM144 361 LILRB3 1 19524 NP_006855.1 5 7 AGGGCTCATCCC - GAC 1 A c c
TCTGCAGAGCGC CTGTGC CTGT GAGGGATGA
GGGGTCAC GGCGCG GACG CTCCCTACT
A T--
GAM144 361 LMAN1L 1 13160 NP_078971.2 3 646 AGCCCACATCCC G -- C 1 A c c
TCCTTGGGCAGG CTGT CCTGT GA GAGGGATG
GCAGCAGC GACG GGACG TT CTCCCTAC
- GG C
GAM144 361 LOC1250 1 17192 XP_008617.5 3 2009 CTCTTGCATCCC T GAC 1 A c c
58 TCCTGCAGGCCA CTG GCCTGT GAGGGATG
GCCATGGC GAC CGGACG CTCCCTAC
- TC-
GAM144 361 LOC1266 1 12608 XP_059061.2 5 49 CCTTCCTTTCCC -- G TG 1 A c c
61 TAGTCACAGGAT CTGTG CCTGTGAC AGGGA
CGCAGTTT GACGC GGACACTG TCCCT
TA A TT
GAM144 361 LOC1306 1 18606 XP_059465.1 3 8 CCGCTTCATCCC T TG--- C 1 A c c
72 TCTCAAGTATGG CTG GCC TGA GAGGGATGA
CTCAGCTA GAC CGG ACT CTCCCTACT
T TATGA -

GAM144 361 LOC1322 1 3634 XP_067736.5 3 0 TCATTGCTGAGG G G-- G 1 A c c
05 TCAAGGCACAGT CTGTGCCT TGAC AG GATGA
AGAGGAGA GACACGGA ACTG TC TTACT
- GAG G
GAM144 361 LOC1334 1 19600 XP_059655.2 5 9 CTCCCGCATCCC GC- A--- 1 A c c
91 TCGCCTGCACAG CTGT CTGTG CGAGGGATG
TGGGCAGT GACG GACAC GCTCCCTAC
GGT GTCC
GAM144 361 LOC1395 1 7462 XP_066756.4 3 49 AGGCATCATCCC T - CG- 1 A c c
47 TACCTCTGCAGG CTG GCCTGT GA AGGGATGA
CTCAGGTG GAC CGGACG CT TCCCTACT
T T CCA
GAM144 361 LOC1434 2 15233 NP_783860.1 3 1723 TCTGCTCATCCC T C -- C 1 A c c
25 TCCTCATTCAGA C GTG CTG TGA GAGGGATGA
CATCCTCC C TAC GAC ACT CTCCCTACT
C A TT C
GAM144 361 LOC1434 2 15557 NP_783860.1 3 937 ACAGCCATCCCC GTGACGA- 1 A
c c
25 TATAGAAAGGCA CTGTGCCT GGGATG
CAGCTTTT GACACGGA CCCTAC
AAGATATC
GAM144 361 LOC1442 1 6620 XP_084795.1 5 1066 TTGATTCATTGC T GAGG 1 A c
c
66 AGGTCTCAGGCA CTGTGCCTG GAC GATGA
CAGGTTGA GACACGGAC CTG TTACT
T GACG
GAM144 361 LOC1447 1 3867 XP_084949.1 5 349 CTCAAGAATTGC G G 1 A c c
42 TTGTTACAGGCA CTGTGCCTGTGACGAG GAT
CAGTAGCC GACACGGACATTGTTC TTA
G A
GAM144 361 LOC1456 1 5208 XP_096816.1 3 1716 GGGGCACATCCC G GAC 1 A c
c
01 TCAGCAGGACAG CTGT CCTGT GAGGGATG
CAACAGTC GACA GGACG CTCCCTAC
- A--
GAM144 361 LOC1461 1 8484 NP_778229.1 3 371 GACTCCTGCTCA G CGAG 1 A c
c
77 TCCATCAAGGCA CTGTGCCT TGA GGATGA
CAGCTCAA GACACGGA ACT CCTACT
- A---
GAM144 361 LOC1486 1 12242 XP_086257.1 3 8 CTGCTTCATCCC T TG--- C 1 A c c
40 TCTCAAGTATGG CTG GCC TGA GAGGGATGA
CTCAGCTA GAC CGG ACT CTCCCTACT
T TATGA -
GAM144 361 LOC1490 1 1158 XP_086402.1 5 9 AGGGAAAAGCCA TGAC A 1 A c c
18 CCTTCCCAGGCA CTGTGCCTG GAGGG TG
CAGCCATA GACACGGAC CTTCC AC
C--- -

```
GAM144  361   LOC1522 1  20184 XP_098181.1  3  40    GAGAAGCTCACT       TG G   A        1  A  c  c

          25                        CTGTGTTAGGCA CTGTGCCTG  AC AGGG TGA
                                   CAGTGGTG    GACACGGAT  TG TCTC ACT
                                               TG -   -
GAM144  361   LOC1535 1  11300 NP_612500.1  3  1126  TGGAGTGAAATT       TGA A   G        1  A  c
c
          16                        CCACGCCAGGCA CTGTGCCTG   CG GGGAT
                                   CAGAATTT    GACACGGAC   GC CCTTA
                                               C--  A    A
GAM144  361   LOC1548 1  771   XP_098626.1  3  2441  GGGGATTTCAGC       G  A  GA        1  A  c
c
          77                        TGTGTGCAGGCA CTGTGCCTGT ACG GG  TGA
                                   CAGATGCA    GACACGGACG TGT TC  ACT
                                               -  G  G-
GAM144  361   LOC1550 1  14193 XP_098647.1  3  782   CAGAAGTCAGCC       T  CGA-  GA        1  A  c
 c
          32                        GCAATCCAGGCA CTGTGCCTG GA   GG  TGA
                                   CAGGACGA    GACACGGAC CT   CC  ACT
                                               -  AACG  G-
GAM144  361   LOC1641 1  9005  XP_089384.5  3  1     CGTGTGTTTCCT       TGAC     TG       1  A  c  c

          18                        TCCAGGCACAGT CTGTGCCTG   GAGGGA
                                   GATCATTC    GACACGGAC    CTTCCT
                                               ----     TT
GAM144  361   LOC1699 1  18817 XP_093024.3  3  887   AGCTAGAGCCCT  G       -    ATG       1  A  c
c
          81                        CAGTCACAGGCA CT TGCCTGTGAC GAGGG
                                   AAGGCTGG    GA ACGGACACTG CTCCC
                                         A        A    GAG
GAM144  361   LOC1973 1  6172  XP_113869.1  3  1757  TGTCCTCATCCC   -    GACG-          1  A  c
c
          42                        TGCCCAGCAGGC CTGT GCCTGT    AGGGATGA
                                   TGCAGAAC    GACG CGGACG    TCCCTACT
                                         T     ACCCG
GAM144  361   LOC2217 1  3541  XP_166341.3  3  480   CACCCATTCCAG  G      -- GA          1  A  c  c
          49                        GTGCCACAGGCA CT TGCCTGTG  AC  GGGATG
                                   GGGGATGT    GG ACGGACAC  TG  CCTTAC
                                         G      CG  GA
GAM144  361   LOC2219 1  5317  XP_166542.2  3  170   CCAGATCATCCC  G  C T-  --          1  A  c  c
          38                        TCGAGTCCCCAG CT TGC TG  GAC  GAGGGATGA
                                   CGAGAAAG    GA GCG AC  CTG  CTCCCTACT
                                         -  - CC  AG
GAM144  361   LOC2553 1  1604  NP_777595.1  3  53    AGGAAGTAAGCA       GTGAC   -        1  A  b
b
          30                        TCACCTCAGGCA CTGTGCCT    GAGG GATG
                                   CAGAAGAA    GACACGGA    CTCC CTAC
                                               -----  A
GAM144  361   LOC2559 1  448   XP_171190.3  3  191   GCAAGTCATCCC   -  CTGTG -          1  A  c
c
```

```
          26                          TCAGTGAAAGCA CTG TGC    AC GAGGGATGA
                                     CCAGTCTC    GAC ACG    TG CTCCCTACT
                                               C  AAAG-  A
GAM144   361   LOC2559 2  7649  XP_171083.2  5  1239  GCCTCACAACAG         AC   GA         1  A  c
c
          75                          CCTCCACAGGCA CTGTGCCTGTG  GAGG  TG
                                     CAGCTCCA    GACACGGACAC  CTCC  AC
                                                --   G-
GAM144   361   LOC2559 2  10185 XP_171083.2  5  1724  GCCTCACAGTGA       T  C   GA--       1  A  c
c
          75                          CCTCTCCAGGCA CTGTGCCTG GA GAGG   TG
                                     CAGCTCCT    GACACGGAC CT CTCC   AC
                                               -  -   AGTG
GAM144   361   LOC2559 1  11034 XP_172605.1  5  29    TGGAATCATCCC    GCC    G           1  A  c  c

          92                          TGTCATGTAAAT CTGT   TGTGAC AGGGATGA
                                     AGGAAATC    GATA   GTACTG TCCCTACT
                                               AAT     -
GAM144   361   LOC2830 1  15659 XP_210866.1  3  1587  TTAAGACATTCT    G----      GA         1  A  c  c

          45                          AAGTCACAGGAT CTGT    CCTGTGAC  GGGATG
                                     GAGACAGG    GACA    GGACACTG  TCTTAC
                                               GAGTA       AA
GAM144   361   LOC2830 1  3775  XP_210867.1  5  1639  ATACAGCATCCC   G       CGA          1  A  c
c
          48                          ACCTCACAGGCG CT TGCCTGTGA   GGGATG
                                     AGGAAGCT    GG GCGGACACT   CCCTAC
                                               A       CCA
GAM144   361   LOC2831 1  16750 XP_210897.1  3  1148  GTGGCCGAACAT         CGA  G         1  A  c
c
          25                          GCCTCATAGGCA CTGTGCCTGTGA   GG ATG
                                     CAGCTGAC    GACACGGATACT   CC TAC
                                               ---  G
GAM144   361   LOC2832 1  6314  NP_777600.1  3  544   AACCCCAGCTCT   --      CG-   A       1  A  c  c
          32                          GCCTCACAGGCA CTGT  GCCTGTGA   AGGG TG
                                     GGCAGGCC    GACG  CGGACACT   TCTC AC
                                               GA       CCG   G
GAM144   361   LOC2833 1  13039 XP_211005.1  3  572   AAAGAAGGTATC        TGACGA           1  A  c
c
          82                          TCAGGCCAGGCA CTGTGCCTG     GGGATG
                                     CAGTGGCC    GACACGGAC     CTCTAT
                                               CGGA--
GAM144   361   LOC2835 1  5605  XP_208702.1  5  1426  CAGCAGCCCCTC   T      C--    A-       1  A  c  c

          05                          CCATCACAGGCT CTG GCCTGTGA   GAGGG  TG
                                     CAGGGACC    GAC CGGACACT   CTCCC  AC
                                               T       ACC     CG
GAM144   361   LOC2838 1  707   XP_208846.1  5  99    AAATCATCTCCA        T  CGA--          1  A  c  c
          06                          TATTCTCAGGCA CTGTGCCTG GA     GGGATGA
                                     CAGAGAAA    GACACGGAC CT     CTCTACT
```

T TATAC
GAM144 361 LOC2840 1 12322 XP_208995.1 3 141 AGTGGTCACCCC GA A A 1 A c c
65 ATGGGACAGGCA CTGTGCCTGT CG GGG TGA
CAGCTACT GACACGGACA GT CCC ACT
GG A C
GAM144 361 LOC2841 1 12882 XP_211346.1 3 80 TGGCTCCGCCCT GA- A 1 A c c
33 TGGGAACAGGCA CTGTGCCTGT CGAGGG TG
CGGACCAC GGCACGGACA GTTCCC GC
AGG -
GAM144 361 LOC2841 1 8090 XP_211364.1 5 1127 AAGCCATCTCTC GTGAC-- 1 A c c
75 CCCTGTGAGGCA CTGTGCCT GAGGGATG
CAGGTGGC GACACGGA CTCTCTAC
GTGTCCC
GAM144 361 LOC2842 1 10595 XP_208174.2 3 1897 TCTCCCTCCCTC - C- TG 1 A c c
02 TCTCATGAGGCA CTGTGCCT GTGA GAGGGA
CAGCCAAG GACACGGA TACT CTCCCT
G CT CC
GAM144 361 LOC2842 1 16270 XP_211398.1 5 328 TGGGCCATCGCC - ACGA - 1 A c c
42 GCAGCACAGGCA CTG TGCCTGTG GG GATG
GCGGCGGC GGC ACGGACAC CC CTAC
G GACG G
GAM144 361 LOC2842 1 12953 XP_209096.1 3 166 GCAATACCATTC ACGAG 1 A c c
65 AGGACACAGGCA CTGTGCCTGTG GGATG
TGGGCAAG GGTACGGACAC CTTAC
AGGA-
GAM144 361 LOC2846 1 7901 XP_211548.1 3 786 CTGTCTCATCCC T - G A 1 A c c
00 TTGCCAGGAGCT CTG GC CT TG CGAGGGATGA
CAGGGCTG GAC CG GG AC GTTCCCTACT
T A - C
GAM144 361 LOC2848 1 4644 XP_211643.1 5 468 TGGGTGACGTCC - GAG 1 A c c
11 AGGTCACAGGCT CTGT GCCTGTGAC GGATG
GCAGCGAG GACG CGGACACTG CCTGC
T GA-
GAM144 361 LOC2848 1 6675 XP_211654.1 5 246 TCCTCCTCTGAT C ---- - T 1 A c c
36 GCGTCACAGTCA CTGTG CTGTGACG AG GGA GA
CAGGTCCT GACAC GACACTGC TC CCT CT
T GTAG T C
GAM144 361 LOC2849 1 4865 XP_211706.1 5 521 AGCCCTCCCTGG --- G TG 1 A c c
52 TCCCCATAGGCA CTGTGCCTGT GAC AGGGA
CAGTTGGG GACACGGATA CTG TCCCT
CCC G CC
GAM144 361 LOC2849 1 9447 XP_211720.1 3 651 TTTTCAGACCTG -- A- G GA 1 A c c

```
          81                    GACACGGAGGCA CTGTGCCT  GTG  C AGG  TGA
                                CAGGGTGC    GACACGGA  CAC  G TCC  ACT
                                      GG   AG -  AG
GAM144    361   LOC2850 1  4645  XP_210410.3  5  121   CCATGCCTGTGT       ----  -  G      1  A  c  c
          92                    CAGGGACAGGCA CTGTGCCTGT   GACG AGG ATG
                                CAG        GACACGGACA   CTGT TCC TAC
                                     GGGA   G  G
GAM144    361   LOC2856 1  7854  XP_211965.1  5  349   GGTCGCTCTTGG        A----    A      1  A  c  c
          33                    GAGGCACAGGCA CTGTGCCTGTG   CGAGGG TGA
                                TGGGTGTG    GGTACGGACAC    GTTCTC GCT
                                     GGAGG    -
GAM144    361   LOC2856 1  7761  XP_209720.1  5  426   TTTCCTCATCCC   T  T-------   CG       1  A  c  c

          73                    TTCACCTGTGGA CTG GCC      GTGA  AGGGATGA
                                TGGTCAGG    GAC TGG      CACT  TCCCTACT
                                     -  TAGGTGTC   --
GAM144    361   LOC2856 1  7718  XP_209717.1  5  311   TCTCATCATCCC   G   GAC-----        1  A  c
c
          78                    TCTAGGGACAGC CTGT CCTGT      GAGGGATGA
                                AGGGCAGG    GACG GGACG       CTCCCTACT
                                     -   ACAGGGAT
GAM144    361   LOC2858 1  9156  XP_212055.1  3  1444  TCTCCACCTTCT       TGA  A   TG       1  A  c
c
          12                    CCCCGCCAGGCA CTGTGCCTG  CG GGGA
                                CAGGAGCC    GACACGGAC  GC CCCT
                                     C--  -   CT
GAM144    361   LOC2858 1  14829 XP_209779.1  5  30    CATCCATGTCCC  -  - TGTG          1  A  c  c

          53                    TCGTGTTGGACA CT GTG CC   ACGAGGGATG
                                CTAGAGCT    GA CAC GG    TGCTCCCTGT
                                     T  A  TTG-
GAM144    361   LOC2859 1  8104  XP_212089.1  5  1444  TTCTGGCCTTCA  -       ---   AT-     1  A  c  c
          50                    GGGTCACAGGCA CTG TGCCTGTGAC  GAGGG  GA
                                GTAGGGGG    GAT ACGGACACTG  CTTCC  CT
                                     G       GGA    GGT
GAM144    361   LOC2860 1  19106 XP_212150.1  3  210   AAGACCAGCCAC   TG     G  GA--       1  A  c
 c
          44                    CTGTCACAGGTG CTG  CCTGTGAC AGG   TG
                                CAGTTGTC    GAC  GGACACTG TCC   AC
                                     GT      -  ACCG
GAM144    361   LOC2861 1  6568  XP_209925.1  5  2770  AGCTCCCATCCC   T  CT  GA          1  A  c
c
          66                    TCGGGATGCCCA CTG GC  GT  CGAGGGATG
                                GGAGAGGC    GAC CG  TA  GCTCCCTAC
                                     C  --  GG
GAM144    361   LOC2864 1  13002 XP_208420.1  3  971   AGGTGTCATCCC   GC  G   ---         1  A  c
c
          25                    TTTGTGTCAGAG CTGT  CT TGAC  GAGGGATGA
                                ACAGACCC    GACA  GA ACTG  TTCCCTACT
                                     --  G   TGT
```

GAM144 361 LOC2865 1 9313 XP_210501.1 5 101 AAAGACATTCCT G G- 1 A b b
28 GGGTGACAGGCA CTGTGCCTGT AC AGGGATG
CAGTGCAG GACACGGACA TG TCCTTAC
G GG
GAM144 361 LOC3385 1 513 XP_294658.1 5 788 TAGAGCCATCCC G T - - 1 A c c
85 TCAGTCAGCTGG CT TGCC G TGAC GAGGGATG
CAGGGACA GG ACGG C ACTG CTCCCTAC
G T G A
GAM144 361 LOC3386 1 17348 XP_294664.1 3 704 CTCACACATCCC C---- CT- A 1 A c
c
09 TCGCCACTCTGC TGTGC GTG CGAGGGATG
ACATGGCT ACACG CAC GCTCCCTAC
TCGGT TCT C
GAM144 361 LOC3388 1 16575 XP_294729.1 5 90 GTAGCTTCATCC G ACGA 1 A c
c
42 TATCCGGAGGCA CTGTGCCT TG GGGATGA
CAGCACAT GACACGGA GC TCCTACT
G CTA-
GAM144 361 LOC3391 1 16086 XP_294834.2 5 188 GTGCATCATCCC ---- GTGAC 1 A c
c
59 TCATGAGAGGCA CTG TGCCT GAGGGATGA
AGCCCAGA GAC ACGGA CTCCCTACT
CCGA GAGTA
GAM144 361 LOC3393 1 17438 XP_290289.1 3 210 CATGGTTTGCAT C----- A GA 1 A c
c
54 CCTGCACAGGCA TGTGCCTGTG C GGGATG
CAAGCAGC ACACGGACAC G TCCTAC
CGACGA - --
GAM144 361 LOC3393 1 17886 XP_086070.2 3 51 ACCATCCCAAAC T C ---- 1 A c c
81 TCCTCCCAGGCA CTGTGCCTG GA GA GGGATG
CAGTCTGG GACACGGAC CT CT CCCTAC
C C CAAA
GAM144 361 LOC3393 1 11261 XP_290863.1 5 187 GAAGTCTCTCCC G- --- G 1 A c c
85 AGTCAGGAGGCA CTGTGCCT TGAC GAGGGAT
CAGGGGTC GACACGGA ACTG CTCTCTG
GG ACC A
GAM144 361 LOC3397 1 12948 XP_295038.1 3 559 ACGGCCTCTCCT T C TG 1 A c
c
11 TCATCACAGGCC CTG GCCTGTGA GAGGGA
GGGGATTC GGC CGGACACT CTTCCT
- A CT
GAM144 361 LOC3397 1 18301 XP_295040.1 5 2114 TCCTTGTGTCCC C ---- -- 1 A c c
17 TCGTCCCACAGG TGTG CCTGT GACGAGGGATG
AGGACACA ACAC GGACA CTGCTCCCTGT
- AGGA CC
GAM144 361 LOC3404 1 13612 XP_290424.2 5 186 CCAGCCCTTGCT --- ----- A 1 A c c
49 TGGTCACAGGTT CTGTG CCTGTGAC GAGGG TG
ACACAGAT GACAC GGACACTG TTCCC AC
ATT GTTCG G
GAM144 361 LOC3408 1 1020 XP_295865.1 3 468 CTAGCAGCATCC GA G 1 A b b

95 CTGCAGCAGGCA CTGTGCCTGT C AGGGATG
CAGAGCCA GACACGGACG G TCCCTAC
AC -
GAM144 361 LOC3475 1 1558 XP_298101.2 3 363 TCACCCTTTGTT ----- A 1 A c c
46 GGGGGCCAGGCA CTGTGCCTG TGACGAGGG TGA
CAGGGCAT GACACGGAC GTTGTTTCC ACT
CGGGG C
GAM144 361 LOC3480 1 1075 XP_302654.1 3 1588 GACACGTCTTCC GTG G T 1 A c
c
99 CTGTGAAAGGCA CTGTGCCT AC AGGGA GA
CAGGAAGA GACACGGA TG TCCCT CT
AAG - T
GAM144 361 LOC3481 1 9665 XP_300638.1 5 61 CTCTCAGACCTT - - -- GA 1 A c c
44 TTGTCACAGGGC CTGT GCC TGTGAC GAGG TGA
TACAGGAC GACA CGG ACACTG TTCC ACT
T G TT AG
GAM144 361 LOC3484 1 5817 XP_302746.1 3 111 CTGTGACACCCA GACGA- A 1 A c
c
06 GCCAAGCAGGCA CTGTGCCTGT GGG TG
CAGGAGGA GACACGGACG CCC AC
AACCGA -
GAM144 361 LOC3484 1 4302 XP_302764.1 3 999 AGAAATCACATT TGA G 1 A c c
61 TTTGGCCAGGCA CTGTGCCTG CGAGG ATG
CAGTGGCT GACACGGAC GTTTT TAC
CG- -
GAM144 361 LOC3485 2 8859 XP_300779.1 5 2575 TCGCTTTCAACT GTG- GA 1 A c
c
27 TCGTCACAGGAA CT CCTGTGACGAGG TGA
AAAGGAGC GA GGACACTGCTTC ACT
AAAA A-
GAM144 361 LOC3485 2 14241 XP_300779.1 5 494 AAGGTGCCGCCC T C A 1 A c c

27 TCATCACAGGCT CTG GCCTGTGA GAGGG TG
GGGCATGG GGT CGGACACT CTCCC GC
- A -
GAM144 361 LOC3487 1 10838 XP_302883.1 3 170 GGAACATCCCGA G GA-- 1 A c
c
68 GGGTCACAGGGA CTGT CCTGTGAC GGGATG
CAGTGCAG GACA GGACACTG CCCTAC
G GGAG
GAM144 361 LOC3488 1 7649 XP_300861.1 5 368 GCCTCACAACAG AC GA 1 A c c

42 CCTCCACAGGCA CTGTGCCTGTG GAGG TG
CAGCTCCA GACACGGACAC CTCC AC
-- G-
GAM144 361 LOC3492 1 10784 XP_300987.1 3 353 CCAGGCCATCCC T CTGT ---- 1 A c
c
34 TCTCGTGTCTGT CTG GC GAC GAGGGATG
AGCCAGTG GAC CG CTG CTCCCTAC
- ATGT TGCT

GAM144 361 LOC3493 1 6731 XP_301029.1 5 289 TGAGGCCATTCC GTG -- 1 A c c
23 TCGTCATCTAGG CT CCT GTGACGAGGGATG
AGGGGTCT GG GGA TACTGCTCCTTAC
GA- TC
GAM144 361 LOC3519 1 9902 XP_305307.1 5 164 CCCATCCCCACC C----- - A--- 1 A c c
83 CGCTCACAGGCA TGTGCCTGTGA CG GGGATG
CACACTGG ACACGGACACT GC CCCTAC
GGTCAC C CCAC
GAM144 361 LOC9052 1 10023 NP_835223.1 3 1330 GACATCAAGGGT C AGG---- 1 A c
c
9 GCGTCACAGCCA CTGTG CTGTGACG GATG
CAGTGAGG GACAC GACACTGC CTAC
C GTGGGAA
GAM144 361 LOC9166 1 17439 NP_612381.1 3 323 CATCGTTTGCAT C----- A GA 1 A c
c
1 CCTGCACAGGCA TGTGCCTGTG C GGGATG
CAAGCGGC ACACGGACAC G TCCTAC
CGGCGA - --
GAM144 361 LOC9166 2 16097 XP_039908.2 5 271 AGATGTCATCCC CCT - 1 A c c
4 TTGTATACCATC CTGTG GTG ACGAGGGATGA
GTAGACTT GATGC CAT TGTTCCCTACT
TAC A
GAM144 361 LOC9166 2 20155 XP_039908.2 5 439 AGACATCATCCC CCT - 1 A c c
4 TTGTATACCATC CTGTG GTG ACGAGGGATGA
GTAGACTT GATGC CAT TGTTCCCTACT
TAC A
GAM144 361 LOC9309 1 7213 XP_049221.1 5 1410 GAGCCACATCCC T C C 1 A c c
7 TCTTACAGCTAG CTG GC TGTGA GAGGGATG
TGAATGAG GAT CG ACATT CTCCCTAC
- - -
GAM144 361 LOC9659 1 16552 XP_039922.1 5 894 TCATAGCATCCC TG - C---- 1 A c c
7 TCAGCACTCGCC CTG CCTG TGA GAGGGATG
AGGTGCAG GAC GGAC GCT CTCCCTAC
GT C CACGA
GAM144 361 LOXL1 1 14029 NP_005567.1 3 131 GAGGGGCATCCC T- T AC 1 A c c
TCCCTGCCGGCC CTG GCC GTG GAGGGATG
TCAGGGAG GAC CGG CGT CTCCCTAC
TC C CC
GAM144 361 MADCAM1 1 13746 NP_570116.1 3 118 CAAAGTCATCCC GC - - 1 A c
c
TCTGTTCACAGA CTGT CTGTGA C GAGGGATGA
GATGGATG GGTA GACACT G CTCCCTACT
GA T T
GAM144 361 MADCAM1 1 13746 NP_570117.1 3 118 CAAAGTCATCCC GC - - 1 A c
c
TCTGTTCACAGA CTGT CTGTGA C GAGGGATGA
GATGGATG GGTA GACACT G CTCCCTACT

```
                                        GA     T T
GAM144   361    MADCAM1 1   13746 NP_570118.1  3 118   CAAAGTCATCCC    GC    - -          1  A  c
c
                                TCTGTTCACAGA CTGT  CTGTGA C GAGGGATGA
                                GATGGATG    GGTA  GACACT G CTCCCTACT
                                        GA     T T
GAM144   361    MGC1070 1   17096 NP_116052.1  5 32    CCGTCGTATCCC    -  T T  -          1  A  c  c
         2                      TCGGTCCGGCGG CTGT GCC G GAC GAGGGATG
                                CGGCGGCG    GGCG CGG C CTG CTCCCTAT
                                        G  - -  G
GAM144   361    MGC1663 1   14522 NP_777593.1  5 291   AGGCGTTCCTCA    G-      ---          1  A  c  c
         8                      GAGTCACAGGGA CTGT  CCTGTGAC   GAGGGATG
                                ATGGCGGC    GGTA  GGACACTG   CTCCTTGC
                                        AG       AGA
GAM144   361    MGC1779 1   1463  NP_689575.1  3 381   GATTTTCATCCC    -- - A          1  A  b  b
         1                      TCGCACAAGGAC CTGTG  CCT GTG CGAGGGATGA
                                TACGGGTT    GGCAT  GGA CAC GCTCCCTACT
                                        CA   A  -
GAM144   361    MGC2327 1   9116  NP_689859.1  3 99    TCCACAGAAGCC         C    ATG        1  A  c  c

         0                      CTCTCACAGGCA CTGTGCCTGTGA GAGGG
                                TGGCCACC    GGTACGGACACT CTCCC
                                        -    GAA
GAM144   361    MGC2976 1   8792  NP_653255.1  3 165   AATCATCATCCC    CCT   C            1  A  c  c

         1                      TCATCACCCACA CTGTG   GTGA GAGGGATGA
                                GTCGCCCG    GACAC   CACT CTCCCTACT
                                        C--   A
GAM144   361    MGC3169 1   19412 NP_076979.1  3 354   TTAAAATTGCAT        TGACGA           1  A  c
c
                                CTTGACCAGGCA CTGTGCCTG     GGGATG
                                CAGTGGCT    GACACGGAC     TTCTAC
                                        CAG---
GAM144   361    MGC3536 1   13055 NP_689648.1  3 610   AGACACATCATT         AC-  G         1  A  c  c

         6                      TATACACAGGCA CTGTGCCTGTG   GAG GATG
                                CAGGGGCC    GACACGGACAC   TTT CTAC
                                        ATA   A
GAM144   361    MGC4368 1   10795 NP_078786.2  3 776   GCTGCCAGTCCC    G   TG       G        1  A  c
c
                                TCGTTGCAGGAC CTGT CCTG  ACGAGGGAT
                                AGGGTCAT    GACA GGAC  TGCTCCCTG
                                        -   GT       A
GAM144   361    MGC4538 1   1218  NP_597723.1  3 370   AATCTACATCCC    CC  TG  -          1  A  c
c
         0                      TCTGTTGTATAC CTGTG  TG  AC GAGGGATG
                                AGGAATCT    GACAT  AT  TG CTCCCTAC
                                        --  GT  T
GAM144   361    MIRAB13 1   10121 NP_203744.1  3 619   CAAATCCATCCC    CCTGT  C           1  A  c
c
```

TCTCTCCCTCAC CTGTG GA GAGGGATG
AGTTCCAG GACAC CT CTCCCTAC
TCCCT -

GAM144 361 MIRAB13 1 10121 XP_039236.6 3 1184 CAAATCCATCCC CCTGT C 1 A c c

TCTCTCCCTCAC CTGTG GA GAGGGATG
AGTTCCAG GACAC CT CTCCCTAC
TCCCT -

GAM144 361 MKRN1 1 5351 NP_038474.1 3 764 GCTTCTCATCCC GC A G 1 A c c
TGCATAGATGCA CTGT CTGTG C AGGGATGA
GTATTCTT GACG GATAC G TCCCTACT
TA - -

GAM144 361 MPP2 1 15648 NP_005365.2 3 862 GCTCTCCATGGC GACGA -- 1 A c c

CCACAGCAGGCA CTGTGCCTGT GGG ATG
CAGGTCTG GACACGGACG CCC TAC
ACA-- GG

GAM144 361 MUC6 1 19534 XP_290540.1 5 41 GGTCATCATCCC CC ACG 1 A c c

TACCCACACACA CTGTG TGTG AGGGATGA
GATGGCCA GACAC ACAC TCCCTACT
-- CCA

GAM144 361 NAV1 1 1396 NP_065176.2 3 3228 CAACTCCATCCC T -- AC 1 A c c
TCACCACAGTTG CTG GC CTGTG GAGGGATG
TCTAGGAA GAT TG GACAC CTCCCTAC
C TT CA

GAM144 361 NDRG4 1 19945 NP_065198.1 3 265 ATCCCACTCCCG TGA A- - 1 A c c

GCGGCCCAGGCA CTGTGCCTG CG GGGA TG
CAGAAGGG GACACGGAC GC CCCT AC
CCG GG C

GAM144 361 NDRG4 1 19945 NP_075061.1 3 265 ATCCCACTCCCG TGA A- - 1 A c c

GCGGCCCAGGCA CTGTGCCTG CG GGGA TG
CAGAAGGG GACACGGAC GC CCCT AC
CCG GG C

GAM144 361 NEU3 1 4466 NP_006647.2 3 345 TCTTCTCATCCC C GACG 1 A c c
TAGGACAAGCAT CTGTGC TGT AGGGATGA
AGTGCCTG GATACG ACA TCCCTACT
A GGA-

GAM144 361 NFE2L1 1 1538 NP_003195.1 5 445 GGAGCTCATCCC T CTGTG 1 A c c

TTGTGTTCTGCC CTG GC ACGAGGGATGA
AGGGTGGG GAC CG TGTTCCCTACT
- TCTTG

GAM144 361 NIPSNAP 1 8413 NP_003625.1 3 548 TACAAACAAACC T T-- GA 1 A c c

1 TCGTCACCACGG CTG GCC GTGACGAGG TG
TCAGGAGG GAC TGG CACTGCTCC AC
- CAC AA

GAM144 361 NR2E3 1 3895 NP_057430.1 3 147 CCAACATCTATG T AG-- 1 A c c
GTGTCCCAGGCA CTGTGCCTG GACG GGATG
CAGTGCCA GACACGGAC CTGT TCTAC
C GGTA
GAM144 361 NTSR1 1 19566 NP_002522.1 3 1109 GGCCGGCAGCCC -- GA G A 1 A c
c
TGGGCTGAGGCA CTGTGCCT GT C AGGG TG
CAGACTCA GACACGGA CG G TCCC AC
GT G- - G
GAM144 361 NUDT11 1 3712 NP_060629.1 3 1013 AGTTTTCATCCC C--- T C 1 A c c
TTTTCCAGTACA CTGTG CTG GA GAGGGATGA
CACAGCTA GACAC GAC CT TTCCCTACT
ACAT - T
GAM144 361 OR2H1 1 7630 NP_112145.1 5 430 CAGCCTCATCCC C--------- TGAC 1 A c
c
TCCAGGTACAAA TGTGCCTG GAGGGATGA
CAAGAACA ACATGGAC CTCCCTACT
ACAAGAACAA ----
GAM144 361 OXTR 1 15896 NP_000907.1 5 97 ATAGTGCAGCCT TGAC- GA 1 A c
c
CAGCCCCAGGCA CTGTGCCTG GAGG TG
CAGCGCCG GACACGGAC CTCC AC
CCCGA G-
GAM144 361 PACAP 1 6514 NP_057543.1 5 467 ACCAAGTGAAAC T CGAGG 1 A c
c
GTCTCACAGGCC CTG GCCTGTGA GATG
CAGGACTT GAC CGGACACT CTGC
C -----
GAM144 361 PCTP 1 5135 NP_067036.1 3 1090 GTAAGTATTTCT G - GG 1 A c c
ATGTCAAAGGCA CTGTGCCT TGACG AG ATG
CAGCCTTG GACACGGA ACTGT TC TAT
A A TT
GAM144 361 PDLIM2 1 3034 NP_789847.1 3 2356 TCATCAGAGGCA TGAC A 1 A c
c
GCCTTCCAGGCA CTGTGCCTG GAGGG TG
CAGCTCTG GACACGGAC CTTCC AC
---- G
GAM144 361 PIF1 1 19368 XP_290643.1 3 358 CCTGAACATCCC - T C 1 A c c
TCCTTTCAGGCT CTGT GCCTG GA GAGGGATG
GCAGAAGG GACG CGGAC TT CTCCCTAC
T T C
GAM144 361 PKD2L1 1 7698 NP_057196.1 5 198 CATCCGCTCCCT GAC- TG 1 A c
c
CCCCAGCAGGCA CTGTGCCTGT GAGGGA
CAGACATC GACACGGACG CTCCCT
ACCC CG
GAM144 361 PLOD 1 2035 NP_000293.1 3 415 CATGGCCAGAGC T C GA- 1 A c c
TTCTCCCAGGCA CTGTGCCTG GA GAGG TG
CAGGTGTT GACACGGAC CT CTTC AC
C - GAG

GAM144 361 POLH 1 6619 NP_006493.1 3 174 TACGGTCCCATC CG 1 A b b
TCTTCACAGGCA CTGTGCCTGTGA AGGGATG
TGGATTCT GGTACGGACACT TCTCTAC
--
GAM144 361 POMT2 1 15796 NP_037514.1 3 255 TGGGCTGCTCCC C - TG 1 A c c
TCGTGCACAGCG CTGTGC TGTG ACGAGGGA
CAGGGGAG GACGCG ACAC TGCTCCCT
- G CG
GAM144 361 POU2AF1 1 892 NP_006226.1 5 505 AAAGGCAACATC C------ T GA 1 A c
c
CTGTCACAGGCC TG GCCTGTGAC GGGATG
ATGCTCTG AC CGGACACTG TCCTAC
GTCTCGT - --
GAM144 361 PPIB 1 8556 NP_000933.1 3 9 TTTGCCATCGCC GACGA - 1 A c c
AAGGAGTAGGCA CTGTGCCTGT GG GATG
CAGGGACA GACACGGATG CC CTAC
AGGAA G
GAM144 361 PPIE 2 11142 NP_006103.1 3 191 CACAGCCTGGAC TGACGA 1 A c
c
TATTCCCAGGCA CTGTGCCTG GGGATG
CAGCTGTG GACACGGAC CCTTAT

GAM144 361 PPIE 2 18340 NP_006103.1 3 169 CTTGGAGCAGCT GAC A- 1 A c c
CCTCTGCAGGCA CTGTGCCTGT GAGGG TG
CAGCCTGG GACACGGACG CTCCT AC
T-- CG
GAM144 361 PPP1R16 1 14705 NP_056383.1 3 2777 TCCGTCCCTTGG - A---- 1 A c c
B GGACCACAGGCA CTG TGCCTGTG CGAGGGATG
TCAGCAGT GAC ACGGACAC GTTCCCTGC
T CAGGG
GAM144 361 PPP1R3C 1 19147 NP_005389.1 3 949 GATGGTCCACTC T - - - G 1 A c c
TGTACACAGGCA C GTGCCTGTG AC GAG GGAT
TTCCTCCT C TACGGACAC TG CTC CCTG
T A T A G
GAM144 361 Rab11-F 1 14310 NP_055515.1 5 45 TCTCCTCATCCT --- CGA 1 A c c
IP3 GCTTCACAGGCT CTGT GCCTGTGA GGGATGA
CCGCGGCC GGCG CGGACACT TCCTACT
CCT TCG
GAM144 361 RAI17 1 513 NP_065071.1 3 2069 TAGAGCCATCCC G T - - 1 A c c
TCAGTCAGCTGG CT TGCC G TGAC GAGGGATG
CAGGGACA GG ACGG C ACTG CTCCCTAC
G T G A
GAM144 361 RASGRP4 1 10432 NP_443181.2 3 700 GACCTGGTGTCC - A G 1 A c
c
CTGCATGAGGCA CTGTGCCT GTG C AGGGATG
CAGCCCGA GACACGGA TAC G TCCCTGT
G - -
GAM144 361 RECQL5 1 15459 NP_004250.1 3 1926 GAGTGTCTTTTA G- --- 1 A c c

GTGTCACAGGGA CTGT CCTGTGAC GAGGGATG
ACAGTTAT GACA GGACACTG TTTTCTGT
AG TGA

GAM144 361 RGS6 1 5092 NP_004287.3 3 1003 CACGTGGTGGCA GACGA 1 A c c

TCCTGACAGGCA CTGTGCCTGT GGGATG
CAGTGAGA GACACGGACA TCCTAC
G----

GAM144 361 RNF144 1 7933 NP_055561.1 3 833 GGGCCTCATCCC - T-- C 1 A c c
TTCTCTCCCAGG CTG TGCCTG GA GAGGGATGA
TAGCAGAA GAC ATGGAC CT TTCCCTACT
G CCT C

GAM144 361 RORB 1 8536 NP_008845.2 5 20 ACATTGTGGATC GACG - G 1 A c c
CGCTAACAGGCA CTGTGCCTGT AG GGAT
CAGATGTC GACACGGACA TC CCTA
A--- G G

GAM144 361 RPS15 1 18606 NP_001009.1 3 8 CCGCTTCATCCC T TG--- C 1 A c c
TCTCAAGTATGG CTG GCC TGA GAGGGATGA
CTCAGCTA GAC CGG ACT CTCCCTACT
T TATGA -

GAM144 361 SCAM-1 1 8414 NP_005766.2 3 198 ATTCCCACCCAC T -- A A 1 A c c
GACTCACAGGCA C GTGCCTGTGA CG GGG TG
TTCCTCCC C TACGGACACT GC CCC AC
T CA A -

GAM144 361 SCD 1 10595 NP_005054.2 3 1898 TCTCCCTCCCTC - C- TG 1 A c c
TCTCATGAGGCA CTGTGCCT GTGA GAGGGA
CAGCCAAG GACACGGA TACT CTCCCT
G CT CC

GAM144 361 SIGLEC1 1 17706 NP_149121.2 3 437 TGGAGGCATTCT G---- GA 1 A c c

0 AAGTCACAGGAT CTGT CCTGTGAC GGGATG
GAGACAGG GACA GGACACTG TCTTAC
GAGTA AA

GAM144 361 SIT 1 3507 NP_055265.1 3 347 CACGCCTCAGTG T--- --- GA 1 A c c
TCTCCTCAGGCA CTGTGCCTG GAC GAGG TG
CAGGAAGT GACACGGAC CTG CTCC AC
TCCT TGA GC

GAM144 361 SLC12A7 1 8621 NP_006589.1 3 39 CATCACGGCACT GA G A 1 A c c

CTGGGACAGGCA CTGTGCCTGT C AGGG TG
CGGAGGAC GGCACGGACA G TCTC AC
GG - -

GAM144 361 SLC26A2 1 5087 NP_000103.1 3 578 AGTGCCATTCCT GT-- G 1 A c c
GTCCTTAAGGCA CTGTGCCT GAC AGGGATG
CAGTCTCA GACACGGA CTG TCCTTAC
ATTC -

GAM144 361 SLC2A6 1 8775 NP_060055.1 3 115 AGCAGTCATCCC - ----- A G 1 A c c
TGCCACCAGCCA CTGTGC CT GTG C AGGGATGA
GAGCACAG GACACG GA CAC G TCCCTACT
A CCGAC C -

GAM144 361 SLC4A11 1 6573 NP_114423.1 5 24 GGGTTGCATCCC G - GTGA 1 A c c

TCGGAAGAGCGA CT TGC CT CGAGGGATG
AGGAATGA GA GCG GA GCTCCCTAC
A A AG--

GAM144 361 SLC7A5 1 17430 NP_003477.3 3 197 GAATCTCATCCC T GTGAC- 1 A c c

TCAACTGAGGGC CTG GCCT GAGGGATGA
CAGGGACA GAC CGGG CTCCCTACT
- AGTCAA

GAM144 361 SMP3 1 7660 NP_079439.2 3 678 ACACGTCCCCTG - -- A 1 A c c
CCTCAACAGGCA CTGTGCCTGT GA CG GGGATG
CAGCTCTC GACACGGACA CT GT CCCTGC
A CC C

GAM144 361 SMT3H1 1 11346 NP_008867.1 3 491 GACTGTCACTTG A- A 1 A c c
CTGTTACAGGCA CTGTGCCTGTGACG GGG TGA
CAGGTGAT GACACGGACATTGT TTC ACT
CG -

GAM144 361 SRF 1 7478 NP_003122.1 3 449 TCAGCCCTGTGT T ----- A 1 A c c
CTGTCACAGGCT CTG GCCTGTGACG AGGG TGA
GGGTCAAA GGT CGGACACTGT TCCC ACT
- CTGTG G

GAM144 361 SYT3 1 20170 NP_115674.1 5 599 TTGCCCCATCCC TG AC--- 1 A c c
TCCCACACACAG CTG CCTGTG GAGGGATG
GACCAGAC GAC GGACAC CTCCCTAC
CA ACACC

GAM144 361 TCF2 1 15301 NP_006472.1 3 588 TCATGCTGAGCG T C ------ G 1 A c c
CTCTCTTAGGCA CTGTGCCTG GA GAG G ATGA
CAGGCTGG GACACGGAT CT CTC C TACT
T - GCGAGT G

GAM144 361 TCL6 1 13217 NP_055233.1 3 1616 CTTAGGCATTCT G---- GA 1 A c c
AAGTCACAGGAT CTGT CCTGTGAC GGGATG
GAGACAGG GACA GGACACTG TCTTAC
GAGTA AA

GAM144 361 TCL6 1 13217 NP_065575.1 3 783 CTTAGGCATTCT G---- GA 1 A c c
AAGTCACAGGAT CTGT CCTGTGAC GGGATG
GAGACAGG GACA GGACACTG TCTTAC
GAGTA AA

GAM144 361 TGIF2 1 15336 NP_068581.1 3 797 GCATTGGCTTGT ---- G- 1 A c c
CTGCCGCAGGCA CTGTGCCTGT GACGAG GATG
CAGAAGGG GACACGGACG CTGTTC TTAC
CCGT GG

GAM144 361 TIGD6 1 7598 NP_112215.1 3 343 ATCTTTGGTGAC - G G G 1 A c c
GGGTCACAGGCA CTGTG CCTGT AC AGGGAT
TTGGTAGT GACAC GGGCA TG TTTCTA
T G G -

GAM144 361 TIX1 1 720 NP_055850.1 3 2774 AGGTATGTAGCC G G ATG 1 A c c
CTGTCACAGGAC CTGT CCTGTGAC AGGG
AGCTCACT GACA GGACACTG TCCC
- - GAT

GAM144 361 TM4SF6 1 6282 NP_003261.1 3 646 AGATGGCATCCC T -- G C 1 A c c
TCATCAGGGTTG CTG GC CT TGA GAGGGATG
CCAGATGG GAC CG GG ACT CTCCCTAC
- TT G A
GAM144 361 TRAM2 1 12299 NP_036420.1 3 1926 GGCCTTCATCCC - ---- AC 1 A c c
TCTCTACGATAA CTGTG CCT GTG GAGGGATGA
GGTTGCAG GACGT GGA CAT CTCCCTACT
T ATAG CT
GAM144 361 TRIM14 1 3991 NP_055603.2 3 361 GAACCTTCTCCC C A TG 1 A c c
TCGTACAGCACA CTGTGC TGTG CGAGGGA
GGAACCTG GACACG ACAT GCTCCCT
- - CT
GAM144 361 TRIM14 1 3991 NP_150090.1 3 167 GAACCTTCTCCC C A TG 1 A c c
TCGTACAGCACA CTGTGC TGTG CGAGGGA
GGAACCTG GACACG ACAT GCTCCCT
- - CT
GAM144 361 TSARG1 1 9635 NP_620712.2 3 759 AAGGGTCATCCC ---- GTGACG 1 A c
c
TAAAGGCAAAAA CTGT GCCT AGGGATGA
CAGAACTT GACA CGGA TCCCTACT
AAAA AA----
GAM144 361 UMPK 1 2776 NP_036606.2 5 137 AGCGTGCGTCCG - A - 1 A c c
TTCGCACAGGCA CTG TGCCTGTG CGAG GGATG
GCGGGAGG GGC ACGGACAC GCTT CCTGC
G - G
GAM144 361 USP14 1 11260 NP_005142.1 5 90 CCTTTGCCGCCC T GT A 1 A c c
TCGTCAGGCCCA CTG GCCT GACGAGGG TG
GCTCTCCT GAC CGGA CTGCTCCC GC
C -- -
GAM144 361 USP22 1 7093 XP_042698.2 3 1621 AAACCTATTCTT - CG- 1 A c c
AGCTCACAGGCC CTGTG CCTGTGA AGGGATG
ATGGAGAA GGTAC GGACACT TTCTTAT
C CGA
GAM144 361 WFDC1 1 7098 NP_067020.2 5 97 TGCTCCTGTCCC ---- CGA 1 A c c
CACTCACAGGCC CTGT GCCTGTGA GGGATG
CACGCAGC GACG CGGACACT CCCTGT
CACC CAC
GAM144 361 WFDC13 1 5225 NP_742002.1 3 498 CATATCATGAAC GACGA --- 1 A c
c
CCAGGACAGGCA CTGTGCCTGT GGG ATGA
CAGTGGGG GACACGGACA CCC TACT
GGA-- AAG
GAM144 361 XRCC2 2 11760 NP_005422.1 3 1174 GCAGTACCATTC ACGAG 1 A c
c
AGGACATAGGCA CTGTGCCTGTG GGATG
CAGGCAAA GACACGGATAC CTTAC
AGGA-
GAM144 361 XRCC2 2 18231 NP_005422.1 3 1175 CCATTCAGGACA ACGAG 1 A c
c
TAGGCACAGGCA CTGTGCCTGTG GGATG

AAGATTTC GACACGGATAC CTTAC
AGGA-
GAM144 361 ZD52F10 1 10953 NP_201574.1 3 234 TGGCCACCAGCC - CC GA 1 A c c
TCGTCACATACA CTG TG TGTGACGAGG TG
CCAGCATC GAC AC ACACTGCTCC AC
C AT G-
GAM144 361 ZFP64 1 10150 NP_071371.2 5 17 GGGGCGCATCCC CCT A 1 A c c
TCGCCACCCGCG CTGTG GTG CGAGGGATG
GTCGCCCA GGCGC CAC GCTCCCTAC
C-- C
GAM144 361 ZFPM2 1 10564 NP_036214.1 3 808 ATCAGTTTTATC GTGA 1 A c c
TTTTGAAAGGCA CTGTGCCT CGAGGGATGA
CAGTCTAA GACACGGA GTTTTCTATT
AA--
GAM144 361 ZNF19 1 5130 NP_008892.1 3 111 CTGATCCATCCC CCT GAC 1 A c c
TCAAGCCACAGT CTGTG GT GAGGGATG
TAATGATT GACAC CG CTCCCTAC
--- AA-
GAM144 361 ZNF19 1 5130 NP_690871.1 3 111 CTGATCCATCCC CCT GAC 1 A c c
TCAAGCCACAGT CTGTG GT GAGGGATG
TAATGATT GACAC CG CTCCCTAC
--- AA-
GAM144 361 ZNF297 1 408 NP_005444.3 3 325 TTGAACATCCTG TG GA- 1 A c c
CAGTCACAGGGT CTG CCTGTGAC GGGATG
CAGGGGTC GAC GGACACTG TCCTAC
TG ACG
GAM144 361 ZNF313 1 8636 NP_061153.1 3 1114 TGACGAGACATC GTGAC G 1 A c c
GTTCATAAGGCA CTGTGCCT GAG GATG
CAGCACAT GACACGGA CTT CTAC
ATA-- G
GAM145 335 DRIL2 1 6283 NM_006465.1 3 CTGCAGGGTGTG CCA C G T 3 C c c
GGCAGAGAA TTC TGCCC A GC CCTGCAG
AAG ACGGG T TG GGACGTC
AG- - G -
GAM145 335 FLJ1073 1 15643 NM_018198.1 3 CTGCAGTCCAAG CCCCA C--- 3 C c c
7 CTGAACATGGGA TTCCCATG GGCT CTGCAG
A AAGGGTAC TCGA GACGTC
AAG-- ACCT
GAM145 335 FLJ1412 1 9578 NM_030895.1 3 TGGGAGCCTGGG - A CAG 3 C c c
9 GCAGGAGAA TTC CC TGCCCCAGGCTCCTG
AAG GG ACGGGGTCCGAGGGT
A - ---
GAM145 335 GPRK7 1 19163 NM_139209.1 3 CGGGAGCCTGAG - A C CAG 3 C c c
GCAGGAGAA TTC CC TGCC CAGGCTCCTG

AAG GG ACGG GTCCGAGGGC
A - A ---
GAM145 335 KIAA126 1 4524 3 CTGCAAGGGCGA T CCCAG C 3 C c c
6 GCATGGGA TCCCATGC GCTC TGCAG
AGGGTACG CGGG ACGTC
- AG--- A
GAM145 335 KIAA171 1 11841 XM_042834.2 3 CTCAGGAGCCTG - A C C 3 C b b
5 AGGCAGGAGAA TTC CC TGCC CAGGCTCCTG AG
AAG GG ACGG GTCCGAGGAC TC
A - A -
GAM145 335 LOC1227 1 1477 5 CTGCAGGAAACA T C GC-- 3 C c c
26 CTGAGGCTTGGG TTCCCA GCC CAG TCCTGCAG
AA AAGGGT CGG GTC AGGACGTC
T A ACAA
GAM145 335 LOC1293 1 10922 3 CTGCAGGAATTG T AG C 3 C c c
03 GGGGCTGGGAA TTCCCA GCCCC G TCCTGCAG
AAGGGT CGGGG T AGGACGTC
- GT A
GAM145 335 LOC1326 1 847 5 CTGCAGATCGAG T CCA CTC 3 C c c
17 GCATGGGA TCCCATGCC GG CTGCAG
AGGGTACGG CT GACGTC
- AG- A--
GAM145 335 LOC1463 1 14632 3 CAGGAGCCTGGG T - T CAG 3 C c c
32 GCCTGTGGA TCC CA GCCCCAGGCTCCTG
AGG GT CGGGGTCCGAGGAC
- T C ---
GAM145 335 LOC1495 1 20044 XM_059930.8 3 CTGCAAGAGCCT T CC C 3 C b b
01 GGCTGGGAA TTCCCA GCC AGGCTC TGCAG
AAGGGT CGG TCCGAG ACGTC
- -- A
GAM145 335 LOC1503 1 5916 XM_086907.1 3 GCAGGAGCCTGC - CA CCC AG 3 C c
c
97 AGGAGA TTCC TGC AGGCTCCTGC
GAGG ACG TCCGAGGACG
A -- --- --
GAM145 335 LOC2196 1 17991 3 CAGGAGCCCAGG G CA CAG 3 C c c
54 GGATGGGAA TTCCCAT CCC GGCTCCTG
AAGGGTA GGG CCGAGGAC
G AC ---
GAM145 335 LOC2550 1 13776 3 CTCGGGAGCCTG - A C C 3 C c c
42 AGGCAGGAGAA TTC CC TGCC CAGGCTCCTG AG
AAG GG ACGG GTCCGAGGGC TC
A - A -
GAM145 335 MRPS24 1 17157 NM_032014.1 3 CTGCAGAGAATG CC- GG C 3 C c
c
GAAACGTGGGAA TTCCCATG CCA CTC TGCAG
AAGGGTGC GGT GAG ACGTC
AAA AA -
GAM145 335 RAB31 1 3423 NM_006868.1 3 CTGCAGGGGGCG CA AGG 3 C c c

GGGCAGGAA TTCC TGCCCC CTCCTGCAG
AAGG ACGGGG GGGGACGTC
-- CG-

GAM145 335 WHSC1 1 6879 NM_133332.1 3 CTGCAATGACTG T -- GCTCC 3 C c c

CAGGGCTGGGAA TTCCCA GCCC CAG TGCAG
AAGGGT CGGG GTC ACGTC
- AC AGTA-

GAM146 370 ASIC4 1 15460 NM_018674.2 5 GCCACCACTGCC A 3 C b b
ACTCGGGA TTCTGGGTGGCAGTG TGGC
AGGGCTCACCGTCAC ACCG
C

GAM146 370 ATP10D 1 19772 NM_020453.2 3 GCCACCAGTCAT AG A 3 C c c
CCAGAA TTCTGGGTGGC TG TGGC
AAGACCTACTG AC ACCG
-- C

GAM146 370 BACE 1 4746 NM_138973.1 5 GCCACCAGCACC T CAG A 3 C c c
ACCCAGA TCTGGGTGG TG TGGC
AGACCCACC AC ACCG
- ACG C

GAM146 370 BCL2L1 1 4366 NM_001191.2 3 GCCAGCCCCACC CA GA 3 C c c
CAGGA TTCTGGGTGG GT TGGC
AGGACCCACC CG ACCG
C- --

GAM146 370 BDP1 1 15772 NM_018429.1 3 GCCTCTGCCACC T TGAT 3 C c c
CAGA TCTGGGTGGCAG GGC
AGACCCACCGTC CCG
- T---

GAM146 370 BSN 1 7928 NM_003458.1 3 CCTCTGGCCACC AGT T C 3 C c c
CAGGA TTCTGGGTGGC GA GG
AGGACCCACCG CT CC
GT- - -

GAM146 370 C17orf3 1 17622 NM_017575.2 3 GCCACCAATCCA T CAG A 3 C c c
1 CCCAGA TCTGGGTGG TG TGGC
AGACCCACC AC ACCG
- TA- C

GAM146 370 C20orf1 1 13347 XM_037265.3 3 CCTCTCCTGCCA T T T- C 3 C c c
50 CCCAGA TCTGGGTGGCAG GA GG
AGACCCACCGTC CT CC
- - CT -

GAM146 370 C20orf1 1 3334 3 GCCACAGATTCA CAG A 3 C c c
80 CCCAGGA TTCTGGGTGG TG TGGC
AGGACCCACT AC ACCG
TAG -

GAM146 370 C20orf1 1 5330 NM_015638.1 3 GCCCAGGGCCAC AG AT 3 C c c
88 CCAGAG TTCTGGGTGGC TG GGC
GAGACCCACCG AC CCG
GG --

GAM146 370 C6orf31 1 9476 NM_030651.2 5 GCCATCCAGCAC T G AGT 3 C c c
CCAGA TCTGGGTG C GATGGC

AGACCCAC G CTACCG
- - AC-
GAM146 370 CG012 1 19685 XM_096710.2 3 GCCACACTGGCT - A 3 C b b
ACCCAGAA TTCTGGGTGGC AGTG TGGC
AAGACCCATCG TCAC ACCG
G -
GAM146 370 CHRAC1 1 19743 NM_017444.3 3 CAGTTCTGCCAC TGA GC 3 C c
c
CCAGGA TTCTGGGTGGCAG TG
AGGACCCACCGTC AC
TTG --
GAM146 370 CLIPR-5 1 1749 NM_015526.1 3 CCCCATGTCACC GTGA C- 3 C c c
9 CAGAA TTCTGGGTGGCA TGG
AAGACCCACTGT ACC
---- CC
GAM146 370 CSF1R 1 8995 NM_005211.2 3 GCCATCACTGCC TT G 3 C c c
AGTCAG CTGG TGGCAGTGATGGC
GACT ACCGTCACTACCG
-- G
GAM146 370 DIO2 1 18574 NM_000793.2 3 GCCATCACATTG T -- 3 C b b
TCACCCAGA TCTGGGTGGCA GTGATGGC
AGACCCACTGT CACTACCG
- TA
GAM146 370 DKFZP56 1 7189 5 GCCATTCGCACC G AGT 3 C c c
4C1940 CAGGA TTCTGGGTG C GATGGC
AGGACCCAC G TTACCG
- C--
GAM146 370 DKFZP58 1 18201 XM_170681.3 5 GCCACCACCCTC T T CA A 3 C c c
6P0123 CCAGA TCTGGG GG GTG TGGC
AGACCC CC CAC ACCG
- T -- C
GAM146 370 EIF1AY 1 741 NM_004681.1 3 GCCATCATCAAC G GGCA 3 C c c
CAAGAA TTCT GGT GTGATGGC
AAGA CCA TACTACCG
A AC--
GAM146 370 EPB41L1 1 7094 NM_012156.1 3 GCCACCTCTCCA C TGA 3 C c c
CCCAGGA TTCTGGGTGG AG TGGC
AGGACCCACC TC ACCG
- TCC
GAM146 370 FBXW1B 1 13218 NM_033644.1 3 GCCAAACACCTA CA A- 3 C c c
CCCAGAA TTCTGGGTGG GTG TGGC
AAGACCCATC CAC ACCG
-- AA
GAM146 370 FLJ0002 1 8652 XM_036307.7 3 CATTTGCCACCC GT GC 3 C c c
6 AGGA TTCTGGGTGGCA GATG
AGGACCCACCGT TTAC
-- --
GAM146 370 FLJ1005 1 3965 NM_017984.2 3 CCTCCTGCACCC G T T C 3 C c c
7 AGAA TTCTGGGTG CAG GA GG

AAGACCCAC GTC CT CC
- - - -

GAM146 370 FLJ1222 1 5264 XM_031342.1 3 GCCATACTGCCA A 3 C b b
1 CCCAGAA TTCTGGGTGGCAGTG TGGC
AAGACCCACCGTCAT ACCG
-

GAM146 370 FLJ1434 1 9772 NM_025029.1 3 CCTCACTGCCAC T C 3 C b b
6 CCAGAG TTCTGGGTGGCAGTGA GG
GAGACCCACCGTCACT CC
- -

GAM146 370 FLJ2048 1 579 NM_017842.1 5 GCCATCACCCGG - - CA 3 C c c
9 CATCAGAG TTCTGG GT GG GTGATGGC
GAGACT CG CC CACTACCG
A G --

GAM146 370 FLJ2050 1 14324 NM_017851.1 3 GCCTTCTGGCCA AGT T 3 C c c
9 CCCAGAG TTCTGGGTGGC GA GGC
GAGACCCACCG CT CCG
GT- T

GAM146 370 FLJ2054 1 502 NM_017872.2 3 CATCCCTACCAC C T GC 3 C c c
6 CCAGGA TTCTGGGTGG AG GATG
AGGACCCACC TC CTAC
A C --

GAM146 370 FLJ2179 1 5000 3 GCCATCAAATGC GCAG 3 C c c
1 CCAGGA TTCTGGGTG TGATGGC
AGGACCCGT ACTACCG
AA--

GAM146 370 FLJ2286 1 18657 NM_025109.2 5 CCTCCTGCAACC G T T C 3 C c c
5 CAGAA TTCTGGGT GCAG GA GG
AAGACCCA CGTC CT CC
A - - -

GAM146 370 FMO2 1 2634 NM_001460.1 3 GCCATCTTCACC CAGT 3 C c c
CAGAA TTCTGGGTGG GATGGC
AAGACCCACT CTACCG
T---

GAM146 370 GNRH1 1 2156 NM_000825.2 5 GCCATCACCAGC T GG A- 3 C c c
CACAGAGA TCT GTGGC GTGATGGC
AGA CACCG CACTACCG
- GA AC

GAM146 370 HDAC6 1 7208 NM_006044.2 3 CCACTACTCCAG - C A C 3 C c c
CCCAGAA TTCTGGG TGG AGTG TGG
AAGACCC ACC TCAT ACC
G - C -

GAM146 370 HIP-55 1 8753 NM_014063.3 3 GCCACCACTGTT GTG A 3 C c c
TAGAA TTCTGG GCAGTG TGGC
AAGATT TGTCAC ACCG
--- C

GAM146 370 IGFBP1 1 11301 NM_000596.1 5 CCATCACTTGCC TG CA C 3 C c c
CAGAG TTCTGGG G GTGATGG
GAGACCC T CACTACC
GT -- -

GAM146 370 IL-17RC 1 14135 NM_153461.1 5 GCCACCTGGCAC G TGA 3 C c c
CTAGAA TTCTGGGTG CAG TGGC
AAGATCCAC GTC ACCG
G C--
GAM146 370 KCNK10 1 4467 NM_021161.3 5 GCCACCGAGTGC G G- A 3 C c c
ACCCAGGA TTCTGGGTG CA TG TGGC
AGGACCCAC GT GC ACCG
- GA C
GAM146 370 KIAA012 1 19077 NM_014792.2 5 GCCATCAGGCCC CAG- 3 C c c
5 CACCCAGGA TTCTGGGTGG TGATGGC
AGGACCCACC ACTACCG
CCGG
GAM146 370 KIAA023 1 12123 XM_291106.1 3 GCCACCTCATCA GCA -- 3 C c c
2 CCCAGAG TTCTGGGTG GTGA TGGC
GAGACCCAC TACT ACCG
--- CC
GAM146 370 KIAA031 1 9879 XM_088459.6 3 GCCCAGACCACC CAG AT 3 C c c
0 CAGGA TTCTGGGTGG TG GGC
AGGACCCACC AC CCG
AG- --
GAM146 370 KIAA051 1 8846 NM_014696.1 3 GCCATCACTGTC GG 3 C b b
4 ACAAGAA TTCT GTGGCAGTGATGGC
AAGA CACTGTCACTACCG
A-
GAM146 370 KIAA056 1 17026 XM_038150.2 3 GCCACCAGCCTG G -- A 3 C c c
1 ACACCCAGAA TTCTGGGTG CAG TG TGGC
AAGACCCAC GTC AC ACCG
A CG C
GAM146 370 KIAA063 1 12019 3 CTATTACCACCC CAG C 3 C c c
3 AGAA TTCTGGGTGG TGATGG
AAGACCCACC ATTATC
--- -
GAM146 370 KIAA080 1 6315 NM_014703.1 3 GCCATCACTGCT GGGT 3 C c c
0 TGGAAGAG TTCT GGCAGTGATGGC
GAGA TCGTCACTACCG
AGGT
GAM146 370 KIAA116 1 11204 XM_045358.2 5 CCATCATCACCC GCA C 3 C c c
4 AGAA TTCTGGGTG GTGATGG
AAGACCCAC TACTACC
--- -
GAM146 370 KIAA120 1 5977 XM_031054.5 3 GCCATCGCCCAG - CA 3 C b b
0 CCCAGAA TTCTGGG TGG GTGATGGC
AAGACCC ACC CGCTACCG
G --
GAM146 370 KIAA153 1 5181 XM_042661.5 3 GCCATCACCTAA T - GGCA 3 C c c
0 TCCAAGA TCT GGGT GTGATGGC
AGA CCTA CACTACCG
- A ATC-
GAM146 370 LGMN 1 12719 NM_005606.3 5 GCCACCACTGCC TT - A 3 C c c
ACCACGG CTG GGTGGCAGTG TGGC

GGC CCACCGTCAC ACCG
-- A C
GAM146 370 LGP1 1 15097 NM_032484.2 3 CCTCTTGCACCC G T T C 3 C c c
AGAA TTCTGGGTG CAG GA GG
AAGACCCAC GTT CT CC
- - - -
GAM146 370 LOC1152 1 18602 NM_145244.1 3 CCATGCATGCAC T G - G C 3 C c c

65 CCAGA TCTGGGTG CA GT ATGG
AGACCCAC GT CG TACC
- - A - -
GAM146 370 LOC1187 1 9073 5 CCCCCACTGCCA AT C 3 C c c
86 CTCAGAA TTCTGGGTGGCAGTG GG
AAGACTCACCGTCAC CC
CC -
GAM146 370 LOC1237 1 13791 3 GCCAACAAGACC CAG A 3 C c c
92 ATCCAGAA TTCTGGGTGG TG TGGC
AAGACCTACC AC ACCG
AGA A
GAM146 370 LOC1267 1 3954 XM_059074.1 3 GCCATGCTGGCA T G G 3 C c c
55 CCCAGA TCTGGGTG CAGT ATGGC
AGACCCAC GTCG TACCG
- G -
GAM146 370 LOC1318 1 15001 3 GCCATCACTGCC TT GTG 3 C c c
27 CAGG CTGG GCAGTGATGGC
GACC CGTCACTACCG
G- ---
GAM146 370 LOC1363 1 8085 XM_072456.3 3 GCCATCACCTAG T TG A-- 3 C c c
37 CTGCCTGAA TTC GGG GC GTGATGGC
AAG TCC CG CACTACCG
- GT ATC
GAM146 370 LOC1458 1 2375 XM_096873.2 3 GCCATCACGTAT T TG A 3 C c c
13 CCCTGAA TTC GGG GC GTGATGGC
AAG CCC TG CACTACCG
T TA -
GAM146 370 LOC1465 1 13559 XM_085489.1 3 GCCATCAGGCTC T T AG 3 C c c
06 CCAGA TCTGGG GGC TGATGGC
AGACCC TCG ACTACCG
- - G-
GAM146 370 LOC1469 1 3124 XM_085659.3 5 GCCAACCGCCAC A GA 3 C c c
53 CCAGAG TTCTGGGTGGC GT TGGC
GAGACCCACCG CA ACCG
C --
GAM146 370 LOC1479 1 12124 3 GCCATAGCACCC - CA G 3 C c c
90 AGCCCAGAA TTCTGGG TGG GT ATGGC
AAGACCC ACC CG TACCG
G CA A
GAM146 370 LOC1488 1 10650 5 GCCACCACTGCT T A 3 C b b
70 CCCAGGA TTCTGGG GGCAGTG TGGC
AGGACCC TCGTCAC ACCG

| | | |

GAM146 370 LOC2214 1 10719 3 GCCCAGCTGGCC - GAT 3 C c c
86 ACCTAGAA TTCTGGGTGGC AGT GGC
AAGATCCACCG TCG CCG
G AC-
GAM146 370 LOC2548 1 19184 XM_173100.1 5 GCAAAATTCCAC C GATG 3 C c c
08 CCAGAA TTCTGGGTGG AGT GC
AAGACCCACC TTA CG
- AAA-
GAM146 370 LOC2571 1 7095 3 CCATCACTGCCT T T C 3 C c c
09 TCTTGAA TTC GGG GGCAGTGATGG
AAG TCT CCGTCACTACC
T T -
GAM146 370 LOC2572 1 1513 XM_173124.1 3 GCCATCACCCTG GT CA 3 C c c
35 TCAGGA TTCTGG GG GTGATGGC
AGGACT CC CACTACCG
GT --
GAM146 370 LOC9070 1 17610 NM_033280.1 5 GCCGTCTGTGCC GT 3 C c c
1 ACCCAGAG TTCTGGGTGGCA GATGGC
GAGACCCACCGT CTGCCG
GT
GAM146 370 LOC9224 1 19858 XM_043814.2 5 GCCATCACCACC - CAG 3 C c c
9 TCGGAA TTCTG GGTGG TGATGGC
AAGGC CCACC ACTACCG
T ---
GAM146 370 MGC1050 1 17215 NM_031477.2 3 GCTTCCCGCCAC T AGT T 3 C c
c
0 CCGAA TTC GGGTGGC GA GGC
AAG CCCACCG CT TCG
- CC- -
GAM146 370 moblak 1 11256 NM_130807.1 3 GCCACCACGCCC GGCA A 3 C c c
AGGA TTCTGGGT GTG TGGC
AGGACCCG CAC ACCG
---- C
GAM146 370 NPC1L1 1 13102 NM_013389.1 3 GCCAGTCAAGGC AG - 3 C b b
CACCCAGGA TTCTGGGTGGC TGA TGGC
AGGACCCACCG ACT ACCG
GA G
GAM146 370 PDIP 1 13937 NM_006849.1 3 GCCATCACTGCT GG 3 C c c
GGACAGGA TTCTG TGGCAGTGATGGC
AGGAC GTCGTCACTACCG
AG
GAM146 370 PDZD2 1 18141 5 GCCAGGCGGCCA A GA 3 C c c
TCCAGAA TTCTGGGTGGC GT TGGC
AAGACCTACCG CG ACCG
G G-
GAM146 370 PLAG1 1 18558 NM_002655.1 5 GCCGTATTTGGC G TG 3 C c c
ACCCAGAA TTCTGGGTG CAG ATGGC
AAGACCCAC GTT TGCCG
G TA

GAM146 370 PPP1R13 1 4491 NM_015316.1 3 GCCATCACCCCC TT T CA 3 C c c
B TCCAG CTGGG GG GTGATGGC
GACCT CC CACTACCG
-- - CC
GAM146 370 RGS3 1 18411 NM_144488.1 5 CCCTCACCACCC CAG T C 3 C c c
AGGA TTCTGGGTGG TGA GG
AGGACCCACC ACT CC
--- C -
GAM146 370 RNF2 1 16379 NM_007212.1 3 GCCATCACTACC TT G C 3 C c c
AACCAG CTGG TGG AGTGATGGC
GACC ACC TCACTACCG
-- A A
GAM146 370 RXRA 1 11770 NM_002957.3 3 CCAGCGCCACCC A GA C 3 C c c
AGGA TTCTGGGTGGC GT TGG
AGGACCCACCG CG ACC
- -- -
GAM146 370 SCYA28 1 3241 3 GCCCCTTGCCTC T TGAT 3 C c c
CCAGAA TTCTGGG GGCAG GGC
AAGACCC CCGTT CCG
T CC--
GAM146 370 SLC39A4 1 13352 NM_130849.1 5 GCCCTCAGCCAG - AG T 3 C c c
CCCAGAA TTCTGGG TGGC TGA GGC
AAGACCC ACCG ACT CCG
G -- C
GAM146 370 SMCX 1 17633 NM_004187.1 3 GCCATCACCATT - CAG 3 C c c
CCAGAG TTCTGGG TGG TGATGGC
GAGACCT ACC ACTACCG
T ---
GAM146 370 SRM 1 14242 NM_003132.1 3 GCCACCACTGAT --- A 3 C b b
GCCACCCAGGA TTCTGGGTGGCA GTG TGGC
AGGACCCACCGT CAC ACCG
AGT C
GAM146 370 TCF-3 1 16528 3 GCCATCACCATG - G CAG 3 C c c
TGAGAA TTCT G GTGG TGATGGC
AAGA T TACC ACTACCG
G G ---
GAM146 370 TMPRSS3 1 11876 NM_024022.1 3 GCCACCAACAGC AG- A 3 C c c
CACTCAGAA TTCTGGGTGGC TG TGGC
AAGACTCACCG AC ACCG
ACA C
GAM146 370 WHSC1 1 12138 NM_133332.1 3 GCTCTCCTGCCA T T 3 C c c
CCCAGAG TTCTGGGTGGCAG GA GGC
GAGACCCACCGTC CT TCG
- C
GAM146 370 Z39IG 1 10116 NM_007268.1 3 CATCTTGCCACC G T GC 3 C c c
AGAA TTCTGG TGGCAG GATG
AAGACC ACCGTT CTAC
- - --
GAM146 370 ZNF17 1 12073 XM_091895.5 5 GCTTTGTCCACC - TGAT 3 C c c

CAGAA TTCTGGGTGG CAG GGC
AAGACCCACC GTT TCG
T ----

GAM147 298 FLJ2127 1 532 3 CAACACCAGGAT A GACA G 3 C c c
6 GAGGTCCCA TGG ACCT AT TTGGTGTTG
ACC TGGA TA GACCACAAC
C G--- G

GAM147 298 FOXE1 1 9989 NM_004473.3 3 CAACACCAGAGA A ACAATG 3 C c
c
CCAGGATCCA TGGA CCTG TTGGTGTTG
ACCT GGAC GACCACAAC
A CAGA--

GAM147 298 PKIG 1 15790 NM_007066.2 3 CAACACCAACAC ACCT CAA 3 C c c
CTCCTCTCCA TGGA GA TGTTGGTGTTG
ACCT CT ACAACCACAAC
CTC- CC-

GAM148 280 ADORA1 1 3384 NP_000665.1 3 799 GCTCTGAGCCCT T--- -- A 3 B c c
CCTTCTTGCCCT GTTC GGCAAGAAG GAGGGCT
GAGCTTTC CGAG CCGTTCTTC CTCCCGA
CTTT TC -

GAM148 280 ADRA1A 1 1241 NP_000671.1 3 87 CGGAAGGCCAGC GG AG 3 B c
c
TCTTCTTGGAGG TGTTC CAAGAAGAG GGCT
ACAAGACA ACAGG GTTCTTCTC CCGG
AG GA

GAM148 280 ALDH9A1 1 5663 NP_000687.2 5 356 TCTTCGGCCCTC -- AA- A-- 3 B c c
TCCTGTCGCCGC TGTTC GGC GA GAGAGGGCT
CATGAGCA ACGAG CCG CT CTCTCCCGG
TA CCG GTC

GAM148 280 AOC3 1 10641 NP_003725.1 3 527 GTTCCTGCCTTC TC CA 3 B c c
TCTTCTATCCTG TGT GG AGAAGAGAGGGC
CAATTTCT ACG CC TCTTCTCTTCCG
T- TA

GAM148 280 APBA1 1 6310 NP_001154.2 3 1030 CTCCTGGACTCC AGAA A C 3 B c
c
CCTCCCTGCCGA TGTTCGGCA G GAGGG
ACACACAT ACAAGCCGT C CTCCC
---- C C

GAM148 280 ARSA 1 10346 NP_000478.2 5 333 TAGCCCTCCCTC GG - A 3 B c c
TCTTGGGACAGA TGTTC CAAGA AG GAGGGCT
CCCCTCGG ACAGG GTTCT TC CTCCCGA
-- C C

GAM148 280 C10orf3 1 10591 NP_060601.2 3 754 CATGTAGCCCTC CGG AA 3 B c c
TCATTTGATTGA TGTT CAAG GAGAGGGCT
CAGTATTT ACAG GTTT CTCTCCCGA
TTA A-

GAM148 280 C11orf2 1 13424 NP_054863.1 3 2245 ATGAGGGTTCAC T A 3 B c c
1 TCTTCTTGTTGT TGT CGGCAAGAAGAG GGGCT

ACATGCTG ACA GTTGTTCTTCTC CTTGG
T A
GAM148 280 C20orf5 1 12151 NP_212134.1 3 585 GCCCCTGCCCTC TTC A- 3 B c c
4 TCTCCTTTGCCC TG GGCAAG AGAGAGGGC
CTCAGTCT AC CCGTTT TCTCTCCCG
TCC CC
GAM148 280 C5orf4 1 19712 NP_057432.1 3 680 GTTAGAGCCCTC G CA A 3 B c c
TTTCTCCCCGAA T TTCGG AGA GAGAGGGCT
GAAAGAGC A AAGCC TCT TTCTCCCGA
G CC -
GAM148 280 C5orf4 1 19712 NP_115761.1 3 2186 GTTAGAGCCCTC G CA A 3 B c c
TTTCTCCCCGAA T TTCGG AGA GAGAGGGCT
GAAAGAGC A AAGCC TCT TTCTCCCGA
G CC -
GAM148 280 CDH16 1 10351 NP_004053.1 5 2 GAAGGAGCTCTC TC GG 3 B c c
TTCTTGCTTGGC TGT GGCAAGAAGAGAG CT
AGCTGGAC ACG TCGTTCTTCTCTC GG
GT GA
GAM148 280 CHKL 1 18892 NP_689466.1 3 2405 GCAGGAGCCCTC G AGAA 3 B c
c
TCATGGTGAACA TGTTCG CA GAGAGGGCT
GCAACTAT ACAAGT GT CTCTCCCGA
G A---
GAM148 280 CHSY1 1 9095 NP_055733.2 3 200 CCTTTGAACACA -------- GC 3 B c c
TCTTCTTGCTGA TGTTCGGCAAGAAGA GAGG
ACATTATG ACAAGTCGTTCTTCT TTCC
ACACAAGT --
GAM148 280 CNTF 1 15418 NP_000605.1 3 47 TTCCTTGCTTTC GGCA 3 B c c
TCTTCTAATGGA TGTTC AGAAGAGAGGGC
ATATGCGT ATAAG TCTTCTCTTTCG
GTAA
GAM148 280 CNTN3 1 13470 XP_039627.7 3 1058 TAAGGGACCCTC CGG - 3 B c c
TCTTTTTGGATG TGTT CAAGAAGAGAGGG CT
GCAGAGAT ACGG GTTTTTCTCTCCC GG
TAG A
GAM148 280 CPA4 1 869 NP_057436.1 3 118 GTCAGAGCCCTC G AAG 3 B c c
TGGGTTTGTGGA TGTTC GCAAG AGAGGGCT
GCACACAG ACGAG TGTTT TCTCCCGA
G GGG
GAM148 280 CPA6 1 5035 NP_065094.2 5 195 TTTCAACTCCTC CGGC C 3 B c c
TCTTCTTAACAC TGTT AAGAAGAGAGGG
TATGAAGT ACAA TTCTTCTCTCCT
---- C
GAM148 280 DCK 1 18281 NP_000779.1 5 112 CTCCCAGCCCTC AGAA 3 B c c
TTTGCCGGACGA TGTTCGGCA GAGAGGGCT
GCTCTGGG GCAGGCCGT TTCTCCCGA

GAM148 280 DKFZp43 1 15968 XP_038298.1 3 384 CTGGACGGGCCT G AA G 3 B c
c

4E2321 TGTCCTTGCCGA T TTCGGCAAG GA AGGGCT
GGAAACCC A GAGCCGTTC CT TTCCGG
G -- G

GAM148 280 DKFZp43 1 13849 XP_290829.1 3 110 AGCAGCCTCCTC - A -- 3 B b b
4H247 TCTTCCTGCCTG TGTTC GGCA GAAGAGAGG GCT
AGCACCGC ACGAG CCGT CTTCTCTCC CGA
T C TC

GAM148 280 DKFZP43 1 7184 XP_041116.1 3 2050 TGGCCTGGGGTC - ---- 3 B c c
4P0111 TCTTCTTTGCTG TGTTCGGCAA GAAGAGA GGGCT
GACACAGC ACAGGTCGTT CTTCTCT TCCGG
T GGGG

GAM148 280 DKFZP43 1 5600 NP_115510.1 3 37 CCGAGGGCCGTC AAGA G 3 B c c
4P0316 TCTCCCAGCCGA TGTTCGGC AGAGA GGCT
ACACAGCC ACAAGCCG TCTCT CCGG
ACCC G

GAM148 280 DKFZP58 1 7790 NP_056291.1 3 275 TGAGTGCTTTCC CGGC - 3 B c c
6M1523 TCTTCTTCAACA TGTT AAGAAGAG AGGGC
CTCAACCC ACAA TTCTTCTC TTTCG
C--- C

GAM148 280 DRD1 1 2684 NP_000785.1 3 133 AGGAGAGCCCTC C C A - 3 B c c
TGCTGCTTTCCA TGTT GG AAG AG AGAGGGCT
ACACACAA ACAA CC TTC TC TCTCCCGA
- T G G

GAM148 280 DRD2 1 2357 NP_000786.1 3 474 GAGGCAAGCAAG G A AGG 3 B c c
CTCTCTTGCCGA T TTCGGCAAGA GAG GCT
GGAGCCAG A GAGCCGTTCT CTC CGA
G - GAA

GAM148 280 DRD2 1 2357 NP_057658.2 3 474 GAGGCAAGCAAG G A AGG 3 B c c
CTCTCTTGCCGA T TTCGGCAAGA GAG GCT
GGAGCCAG A GAGCCGTTCT CTC CGA
G - GAA

GAM148 280 EGFL4 1 14622 XP_290821.1 3 535 CGCAGGGCCTGC T C A 3 B c c
TCTTCTTCCGGC TGT CGG AAGAAGAG GGGCT
AGGACCAG ACG GCC TTCTTCTC TCCGG
- - G

GAM148 280 EGLN2 1 15451 NP_060025.1 5 840 GTGGCAGCCCTC - CAA 3 B c c
TCTTTCCAGGGC TGTTC GG GAAGAGAGGGCT
AAGGTCTG ACGGG CC TTTCTCTCCCGA
A ---

GAM148 280 EGR2 1 791 NP_000390.2 3 117 TTCCTGTCCCTC A-- - 3 B c c
TCTCCCTTTGTT TGTTCGGCAAG AGAGAGGG C
GGGCAAAG ACGGGTTGTTT TCTCTCCC G
CCC T

GAM148 280 ELOVL3 1 14478 NP_689523.1 3 51 CTCCAGGCTCTC - CA 3 B c c
TCTTCTCCAGGG TGTTC GG AGAAGAGAGGGCT
CACCAAGA ACGGG CC TCTTCTCTCTCGG

A --
GAM148 280 EYA2 1 15962 NP_742109.1 5 96 GTCTGAGTTCTC TC C - 3 B c c
TCTTCCTTCCCC TGT GG AAG AAGAGAGGGCT
TGCATAGA ACG CC TTC TTCTCTCTTGA
TC C C
GAM148 280 FLJ0002 1 5939 NP_203745.1 3 1121 GGCATTCACGTC G AGA 3 B c c
4 CCTTCTTGCAGG TGTTC GCAAGAAG GGGC
GCATTTTA ACGGG CGTTCTTC CCTG
A ---
GAM148 280 FLJ0002 1 5939 XP_033361.2 3 1121 GGCATTCACGTC G AGA 3 B c c
4 CCTTCTTGCAGG TGTTC GCAAGAAG GGGC
GCATTTTA ACGGG CGTTCTTC CCTG
A ---
GAM148 280 FLJ1003 1 7021 NP_110430.4 3 1172 CCACCTGCCCTC T - A- 3 B c c
5 TCTTCCCTGCCT TG TC GGCA GAAGAGAGGGC
GATCACCG AC AG CCGT CTTCTCTCCCG
T T CC
GAM148 280 FLJ1049 1 11635 NP_060584.2 3 1246 CTAGCCTTCCTC C C A - 3 B c c
6 TCTTCCAAACAC TGTT GG AAGA GAG AGGGCT
AGGTTCCG ACAA CC TTCT CTC TTCCGA
A - - C
GAM148 280 FLJ1445 1 19096 NP_116175.1 3 338 CGTCTTGTCCTC CG A 3 B c c
1 TCTTCTGCACAG TGTT GCA GAAGAGAGGGC
CACAGGTT ACGA CGT CTTCTCTCCTG
CA -
GAM148 280 FLJ1477 1 18575 NP_116226.1 5 119 CTCTGTTCCCTC G AA C 3 B c c
5 TCTTCGCGGAGC TGTTC GC GAAGAGAGGG
GGCGCCGC GCGAG CG CTTCTCTCCC
G -- T
GAM148 280 FLJ2027 1 9599 NP_061900.1 3 1258 TAAATGGGCCTC T -- G 3 B c c
3 TCTTCCTTTGCT TGT CGGCAA GAAGAGAGG CT
GTGCACTT ACG GTCGTT CTTCTCTCC GG
T TC G
GAM148 280 FLJ2191 1 19653 NP_075391.2 3 58 TGGACTGCCCTC T- G - 3 B c c
9 TCCTTCTTGGTG TG TCG CAAGAAG AGAGGGC
ATTCAAAG AC AGT GTTCTTC TCTCCCG
TT G C
GAM148 280 FLJ2303 1 496 NP_078962.2 3 636 GGAGCACCCAAT GG A-- - 3 B c c
3 TCTTCTTGAGAA TGTTC CAAGAAGAG GG GCT
CACCAACC ACAAG GTTCTTCTT CC CGA
A- AAC A
GAM148 280 FLJ3110 1 17843 NP_775902.1 5 130 CCCCCGCCCCTC T--- AA-- - 3 B c c
0 TCTTCCCTGGCT GTTCGGC GAAGAGAGGG C
GGACTTGC CAGGTCG CTTCTCTCCC G
CGTT GTCC C
GAM148 280 FLJ3246 1 3196 NP_660090.1 3 426 CCCCACCCCCTC CA- C 3 B c c
8 TCTTTTCCATTG TGTTCGG AGAAGAGAGGG

AACAAACA ACAAGTT TTTTCTCTCCC
ACC C

GAM148 2800 FLJ3278 1 20150 NP_659402.1 3 36 ATCCAGACCCTC G A - 3 B c c
CCTTCTTGCTGG T TTCGGCAAGAAG GAGGG CT
GGAGGGGA A GGGTCGTTCTTC CTCCC GA
G C A

GAM148 2807 FLJ3548 1 18431 NP_776181.1 3 252 AAGTCAGCCCTC T- C A-- --- 3 B c c
TCTATTTCATGT GTT GGCA GA AGAGAGGGCT
GCCAACTC CAA CCGT CT TCTCTCCCGA
CT - GTA TTA

GAM148 2804 FLJ4058 1 10385 XP_069189.2 3 647 TCCATAACCTTC C - - C 3 B c c
TCTTCTATGACC TGTT GG CA AGAAGAGAGGG
CAACAACA ACAA CC GT TCTTCTCTTCC
C A A A

GAM148 280 GPT2 1 580 NP_597700.1 3 190 TGAGAGCGCCTC CG A- - 3 B c c
TCTTTTGAGCAA TGTT GC AGAAGAGAGG GCT
ACAAGCAT ACAA CG TTTTCTCTCC CGA
A- AG G

GAM148 280 GRTP1 1 6509 NP_078995.1 3 101 ATGGCGGCCCTG C- - G 3 B c c
TCTTCTTGGCCC TGTT GGC AAGAAGA AGGGCT
TGGCACTG ACGG CCG TTCTTCT TCCCGG
TC G G

GAM148 280 HIP2 1 8300 NP_005330.1 3 50 GTCAAGCTTGCC GG A- 3 B c c
TCTTCTTGAGGA TGTTC CAAGAAGAG GGGCT
GCACCAAC ACGAG GTTCTTCTC TTCGA
GA CG

GAM148 280 HOXA7 1 6135 NP_008827.2 3 37 TCCGGGGCCCTC CAAGA 3 B c
c
TCTGCACCGGAC TGTTCGG AGAGAGGGCT
AGTCGGAA ACAGGCC TCTCTCCCGG
ACG--

GAM148 280 HRH3 1 6908 NP_009163.1 3 140 TCTGTGGCCCTC C- AG 3 B c c
TCTTAATGCCAC TGTT GGCA AAGAGAGGGCT
GGCAGCCA ACGG CCGT TTCTCTCCCGG
CA AA

GAM148 280 IGF2 1 12962 NP_000603.1 5 75 ACGCCCGCCCTC T---- - AA 3 B c c
TCGCCTTCGCCG GTTCGGC AAG GAGAGGGC
AACCAAAG CAAGCCG TTC CTCTCCCG
GAAAC C CG

GAM148 280 ITGAL 1 15602 NP_002200.1 3 436 TGGAGTCCAGTC T A -- 3 B c c
TCTTCTGCTGGC TGT CGGCA GAAGAGA GGGCT
AGAAAGCA ACG GTCGT CTTCTCT CCTGA
- - GA

GAM148 2802 KIAA006 1 17664 XP_046677.3 3 1623 CGTTTTGTTTTC CGG 3 B c c
TCTTCTTGGGAG TGTT CAAGAAGAGAGGGC
ACATCTGT ACAG GTTCTTCTCTTTTG
AGG

GAM148 2801 KIAA010 1 11332 NP_055551.1 5 52 TCTCCTCTCCTC - C 3 B c c
TCTTCTTGTTTG TGTTCGG CAAGAAGAGAGGG
AACATGGT ACAAGTT GTTCTTCTCTCCT

T C

GAM148 280 KIAA052 1 9466 XP_291345.1 3 1111 AGCCCCAGCTCC TC A 3 B c c
2 TCTTCTTGCCCC TGT GGCAAGAAGAG GGGCT
GCATATCC ACG CCGTTCTTCTC CTCGA
CC -

GAM148 280 KIAA145 1 9176 XP_044434.1 3 139 ATCCCAGCCCTC CGGC - 3 B c c
8 TCTGTCTTAATT TGTT AAGA AGAGAGGGCT
AGCACAAA ACGA TTCT TCTCTCCCGA
TTAA G

GAM148 280 KIAA165 1 7823 XP_038022.1 3 2063 AGTGGAGCCCTC TC A-- A- 3 B c
c
6 TTTCCCTGCAGC TGT GGC AG AGAGAGGGCT
CTACATTG ACA CCG TC TTTCTCCCGA
T- ACG CC

GAM148 280 KIAA190 1 6342 XP_291137.1 5 580 TCCCAGGCCCTC G GAA- 3 B c c
9 TCAGGATTGCAG TGTTC GCAA GAGAGGGCT
AACAACAC ACAAG CGTT CTCTCCCGG
A AGGA

GAM148 280 KIF5A 1 5352 NP_004975.1 5 76 CTGAGAGCCCTC GGCA A 3 B c c
TCCTCTGGAGCA TGTTC AGA GAGAGGGCT
CACACCAC ACGAG TCT CTCTCCCGA
G--- C

GAM148 280 LCX 1 12109 XP_167612.2 3 954 GTAAGAGTGGTC C GG 3 B c c
TCTTCTTATTGA TGTTCGG AAGAAGAGA GCT
ACAACCTC ACAAGTT TTCTTCTCT TGA
A GG

GAM148 280 LOC1221 1 5819 XP_062994.2 5 148 TCCTCGGGCCTC G AA G 3 B c
c
83 TCTTCGTCGAAG T TTCGGC GAAGAGAGG CT
AGTCTCCT A AAGCTG CTTCTCTCC GG
G -- G

GAM148 280 LOC1262 1 3713 XP_059019.2 5 317 GCCGCATCCCTC C AGA C 3 B c
c
99 TCTACCTGCCAA TGTT GGCA AGAGAGGG
CATCCTGT ACAA CCGT TCTCTCCC
- CCA T

GAM148 280 LOC1452 1 10503 XP_085072.1 5 346 AAAAGCCACTTC C - - 3 B c c
68 TCTTCTTCCTGA TGTTCGG AAGAAGAGA G GGCT
GCAGATGG ACGAGTC TTCTTCTCT C CCGA
C T A

GAM148 280 LOC1500 1 553 XP_097805.1 5 475 ACACCTTCCCTC AGA C 3 B c c
95 TCTGAATGCTGA TGTTCGGCA AGAGAGGG
GCAGAGGC ACGAGTCGT TCTCTCCC
AAG T

GAM148 280 LOC1502 1 14830 XP_086894.2 3 861 CAAGCCTCTCTC CAA --- 3 B c c
97 TCTTCCTACTGA TGTTCGG GAAGAGAG GGCT
GCACCTGT ACGAGTC CTTCTCTC CCGA

ATC TCT

GAM148 280 LOC1963 1 18591 XP_113696.1 3 593 AACCCTCCCTCC G - C 3 B c c
37 TCTTCTTGCTGG T TTCGGCAAGAAGAG AGGG
AGGACCTG G AGGTCGTTCTTCTC TCCC
G C T

GAM148 280 LOC1999 1 1048 XP_114052.1 3 138 AGAGGCGCCTTC CA 3 B c c
06 TCTTCTCTGGGC TGTTCGG AGAAGAGAGGGC
ATTCCCCG ACGGGTC TCTTCTCTTCCG
--

GAM148 280 LOC2196 1 1391 XP_167562.1 5 380 TCTCCTGCTCAT GG- A 3 B c c
49 TCTTCTTGACAG TGTTC CAAGAAGAG GGGC
AACAACCA ACAAG GTTCTTCTT CTCG
ACA A

GAM148 280 LOC2830 1 3635 XP_210849.1 5 907 TCAAGCCTTGAC TC G -- 3 B c c
07 TGTTCTTGCCCG TGT GGCAAGAA AG AGGGCT
GCAAGAGA ACG CCGTTCTT TC TTCCGA
GC G AG

GAM148 280 LOC2835 1 9199 XP_211077.1 3 239 ATCTCCCCTTCC G -- C 3 B c c
11 TCTTCTTGATGG TGTTCG CAAGAAGAG AGGG
ACATTTAT ACAGGT GTTCTTCTC TCCC
A CT C

GAM148 280 LOC2837 1 640 XP_208835.1 3 29 CTCTTAGCCCTC T AGAAG 3 B c c

67 TACTGTTGACCA TG TCGGCA AGAGGGCT
ATCACCAA AC AGTTGT TCTCCCGA
C CA---

GAM148 280 LOC2838 1 7128 XP_211243.1 3 274 TCCCCTACCCTC - C 3 B c c
68 TTTTCTTGCCTG TGTTC GGCAAGAAGAGAGGG
AATAGTAC ATAAG CCGTTCTTTTCTCCC
T A

GAM148 280 LOC2841 1 18426 XP_211360.1 5 108 TCGCCTTCCCTC TT CA- C 3 B c
c
69 TCTTCTGTCCCG TG CGG AGAAGAGAGGG
GCCAGGAT AC GCC TCTTCTCTCCC
CG CTG T

GAM148 280 LOC2841 1 1975 XP_211364.1 5 755 TCCCTTTCCCTC - A- C 3 B c c
75 TCTGCTGAGCAT TGTTCGGCA AGA GAGAGGG
TTAACCAT ACGAGTCGT TCT CTTTCCC
C CC T

GAM148 280 LOC2849 1 5418 XP_211689.1 3 320 AAGGAAACCCTC G AA C 3 B c c

27 TCTTCGTGGGGC TGTTC GC GAAGAGAGGG
ACTCTGCC ACGGG TG CTTCTCTCCC
G -- A

GAM148 280 LOC2851 1 16431 XP_211803.1 3 477 TTCGCCTTATGT T----- --- 3 B c c
94 TCTTCTTGCCGG GTTCGGCAAGAAGAG AGGGC
ACTCTTTT CAGGCCGTTCTTCTT TTCCG
TTTTCT GTA

GAM148 280 LOC2855 1 5312 XP_211947.1 3 434 GGATTCTTTCTC C CA C 3 B c c
87 TCTTCTCCCAAC TGTT GG AGAAGAGAGGG

```
                                    AATCCAAA    ACAA CC  TCTTCTCTCTT
                                              C --         T
GAM148  280  LOC2855 1  2211  XP_211946.2  3  277   CTGCCAGCCCTC    CG-  A            3  B  c  c
        94                                   TCTTTGTGCATT TGTT   GCA GAAGAGAGGGCT
                                    AGCAACAG    ACGA   CGT TTTCTCTCCCGA
                                              TTA   G
GAM148  280  LOC2858 1  14325 XP_212034.1  5  2484   GAGAGAGCCCTC    G   AGAA           3  B  c
 c
        43                                   TCCATGCAGGGC TGTTC GCA    GAGAGGGCT
                                    AGATGGAG    ACGGG CGT    CTCTCCCGA
                                              A   AC--
GAM148  280  LOC2860 1  15183 XP_212158.1  3  1489   AAGAGCCTTCTC   T    A      --        3  B  c  c
        58                                   TCTTCCTGTTGA TGT CGGCA GAAGAGAG  GGCT
                                    CACTTGCC    ACA GTTGT CTTCTCTC  CCGA
                                              -   C       TT
GAM148  280  LOC2860 1  1688  XP_212159.1  3  97    TTAAACTCCCTC    GGC--        C       3  B  c  c
        63                                   TCTTCTTAAATG TGTTC    AAGAAGAGAGGG
                                    GAACAGCT    ACAAG    TTCTTCTCTCCC
                                              GTAAA          T
GAM148  280  LOC3388 1  15148 XP_290588.1  3  852   TTTAAGTGCTTT   TC          -        3  B  c  c
        17                                   TCTTCTTGCCCA TGT  GGCAAGAAGAGAGG GCT
                                    CAAACTAG    ACA  CCGTTCTTCTTTTC TGA
                                              C-           G
GAM148  280  LOC3389 1  640   XP_290663.1  3  29    CTCTTAGCCCTC   T    AGAAG           3  B  c  c

        91                                   TACTGTTGACCA TG TCGGCA    AGAGGGCT
                                    ATCACCAA    AC AGTTGT    TCTCCCGA
                                              C     CA---
GAM148  280  LOC3389 1  640   XP_290659.1  3  29    CTCTTAGCCCTC   T    AGAAG           3  B  c  c

        99                                   TACTGTTGACCA TG TCGGCA    AGAGGGCT
                                    ATCACCAA    AC AGTTGT    TCTCCCGA
                                              C     CA---
GAM148  280  LOC3397 1  7535  XP_295040.1  5  1315  CTGCTGAAGCCA   T     AA   G         3  B  c
c
        17                                   TCTCCTTGCCGA TGT CGGCAAG  GAGA GGCT
                                    CAAACACA    ACA GCCGTTC  CTCT CCGA
                                              -     --   A
GAM148  280  LOC3401 1  5873  XP_295167.1  3  1619  TTATCAGCCCTC    CG C--   --          3  B  c  c

        50                                   TCTTTTCTTATA TGTT  G   AAGA  AGAGAGGGCT
                                    TTAAACAG    ACAA  T   TTCT  TCTCTCCCGA
                                              AT ATA    TT
GAM148  280  LOC3403 1  12963 XP_291261.1  5  1061   AAGGAGCCCCTC       A ---      -     3  B  c  c
        85                                   TCTGCTTCCTGT TGTTCGGCA GA   AGAGAGGG CT
                                    TGGGCACC    ACGGGTTGT CT   TCTCTCCC GA
                                              C  TCG       C
GAM148  280  LOC3430 1  5934  XP_291404.1  5  66    CAAGCTCCTTGG    C       --   -       3  B  c  c
        95                                   TCTTCTTGCCAA TGTT GGCAAGAAGA  GAGG GCT
                                    GCAGGAAG    ACGA CCGTTCTTCT  TTCC CGA
```

```
                                        A       GG   T
GAM148  280   LOC3481 1  640   XP_300623.1  3  29    CTCTTAGCCCTC  T    AGAAG          3  B  c  c

        13                          TACTGTTGACCA TG TCGGCA    AGAGGGCT
                                    ATCACCAA    AC AGTTGT    TCTCCCGA
                                            C     CA---
GAM148  280   LOC3481 1  640   XP_300635.1  3  29    CTCTTAGCCCTC  T    AGAAG          3  B  c  c

        37                          TACTGTTGACCA TG TCGGCA    AGAGGGCT
                                    ATCACCAA    AC AGTTGT    TCTCCCGA
                                            C     CA---
GAM148  280   LOC3481 1  640   XP_300636.1  3  29    CTCTTAGCCCTC  T    AGAAG          3  B  c  c

        42                          TACTGTTGACCA TG TCGGCA    AGAGGGCT
                                    ATCACCAA    AC AGTTGT    TCTCCCGA
                                            C     CA---
GAM148  280   LOC3481 1  12165 XP_300650.1  3  81    CGTCACCCCCTC   CG    A     C       3  B  c
c
        80                          TCTGCTTGCAGA TGTT  GCAAG AGAGAGGG
                                    CAGTGCCA    ACAG  CGTTC TCTCTCCC
                                            A-    G       C
GAM148  280   LOC3483 1  624   XP_302730.1  3  17    TCCACGTCCTTA   CG  ---    -        3  B  c  c
        61                          TCTTCTTGATGC TGTT  GCA   AGAAGA GAGGGC
                                    AAGACAAT    ACAG  CGT   TCTTCT TTCCTG
                                            AA   AGT     A
GAM148  280   LOC3483 1  15542 XP_302732.1  5  877   CCGGGAGCCCTC  G   G  A-           3  B  c
c
        69                          TCTTCTCCGCAG T TTC GC  AGAAGAGAGGGCT
                                    AGGAGAGC    A GAG CG  TCTTCTCTCCCGA
                                            G   A  CC
GAM148  280   LOC3489 1  15228 XP_302915.1  5  48    GCCATAGCCTTC T--    - A--          3  B  c  c
        11                          TCTTCTCAGGCG   GTTCG GC   AGAAGAGAGGGCT
                                    TGGACTGC       CAGGT CG   TCTTCTCTTCCGA
                                            CGT    G  GAC
GAM148  280   LOC3492 1  4297  XP_300251.1  3  1137  GAAACATCTCTC    C  CA       C       3  B  c  c

        51                          TCTTCTCCAAGC TGTT GG  AGAAGAGAGGG
                                    ATAAAGGA    ACGA CC  TCTTCTCTCTC
                                            A  --         T
GAM148  280   LOC5592 1  3949  NP_061972.1  5  98    ACCCGGGCCCTC T---    --   A         3  B  c  c
        4                           TCTGTTTGAACC    GTTCGG  CAAG AGAGAGGGCT
                                    GAACCCGA        CAAGCC  GTTT TCTCTCCCGG
                                            AGCC     AA   G
GAM148  280   MAP3K13 1  16657 NP_004712.1  5  5     TTTGGAGCCCTC T-----   -  AAG         3  B  c
c
                                    TCTTAAGTCAGA      GTTC GGC   AAGAGAGGGCT
                                    ACTCTGTC          CAAG CTG   TTCTCTCCCGA
                                            CTGTCT    A   AA-
GAM148  280   MBTPS1  1  10515 NP_003782.1  5  309   AATGAAAGCCTC T-----      AA      G     3  B  c
c
```

TCTTCAGGCTGA GTTCGGC GAAGAGAGG CT
ACCACAAA CAAGTCG CTTCTCTCC GA
AAACAC GA -
GAM148 280 MEP50 1 13864 NP_077007.1 3 76 TGCCCTGCCCTC CG AA 3 B c c
TCAGCTTGTGAG TGTT GCAAG GAGAGGGC
ACAACACA ACAG TGTTC CTCTCCCG
AG GA
GAM148 280 MGC1301 1 18039 NP_542387.1 3 282 GTAAAAGCCCTC TTC A 3 B c
c
7 TTTTCTGTTTTC TG GGCA GAAGAGAGGGCT
AGGTTTTT AC TTGT CTTTTCTCCCGA
TT- -
GAM148 280 MGC1740 1 2263 NP_689847.1 3 949 TTTGGAGCCCTC G - AA 3 B c c
3 TTGCTTAGTTGA T TTCGGC AAG GAGAGGGCT
AGGAGTTT G AAGTTG TTC TTCTCCCGA
G A G-
GAM148 280 MGC3513 1 13560 NP_689640.1 3 68 TCAGCACTGTCG GG - - - 3 B c c
6 TCTTCTTGGAGG TGTTC CAAGAAGA GA GG GCT
GCAAACTT ACGGG GTTCTTCT CT TC CGA
AG G G A
GAM148 280 MTMR3 1 17072 NP_066576.1 3 1094 TTTCTCCTCTTC GG C 3 B c c
TCTTCTTGGGAC TGTTC CAAGAAGAGAGGG
AGGAATAA ACAGG GTTCTTCTCTTCT
-- C
GAM148 280 MTMR3 1 17072 NP_694690.1 3 1094 TTTCTCCTCTTC GG C 3 B c c
TCTTCTTGGGAC TGTTC CAAGAAGAGAGGG
AGGAATAA ACAGG GTTCTTCTCTTCT
-- C
GAM148 280 MTMR3 1 17072 NP_694691.1 3 1094 TTTCTCCTCTTC GG C 3 B c c
TCTTCTTGGGAC TGTTC CAAGAAGAGAGGG
AGGAATAA ACAGG GTTCTTCTCTTCT
-- C
GAM148 280 MYD88 1 10785 NP_002459.1 3 1337 GTTCTCTCCCTC - C A C 3 B c c
TCTCCTTCCCAG TGTTC GG AAG AGAGAGGG
AGCAATTT ACGAG CC TTC TCTCTCCC
A C C T
GAM148 280 NECAB2 1 5818 NP_061938.1 3 56 CCACCAGCCCCT G G A 3 B c c
TCTTCTTGTGAA T TTCG CAAGAAGAG GGGCT
GGAAATCC G AAGT GTTCTTCTT CCCGA
G - C
GAM148 280 NRCAM 1 12857 NP_005001.1 3 86 TTGTCAGCCCTC GCAAGAA 3 B c
c
TCATACTATGAA TGTTCG GAGAGGGCT
CATATGGG ACAAGT CTCTCCCGA
ATCATA-
GAM148 280 NUP50 1 7777 NP_009103.2 5 224 CCGGCGCTCTCG --- AA G 3 B c c
CCTCCCTGCCGA TGTTCGGCA AG GAGAG GCT
ACACAGCG ACAAGCCGT TC CTCTC CGG
CCC CG G

GAM148 280 NUP50 1 7777 NP_710151.1 5 224 CCGGCGCTCTCG --- AA G 3 B c c
CCTCCCTGCCGA TGTTCGGCA AG GAGAG GCT
ACACAGCG ACAAGCCGT TC CTCTC CGG
CCC CG G
GAM148 280 OTP 1 2151 NP_115485.1 3 850 CGTGCAGCCCTC CG -- 3 B c c
TCTTGGCTTGCA TGTT GCAAG AAGAGAGGGCT
AGATAACG ATAG CGTTC TTCTCTCCCGA
AA GG
GAM148 280 PCOLCE 1 4646 NP_002584.1 3 53 CCCTCAGGCCTC C C- G 3 B c c
TCTTCTTATCCA TGTT GG AAGAAGAGAGG CT
AATAAATG ATAA CC TTCTTCTCTCC GA
A TA G
GAM148 280 PLCD1 1 8152 NP_006216.1 3 237 AATGCAGCCCTC C AA A---- 3 B c c
TCCACCCTCCGG TGTT GGC GA GAGAGGGCT
CCAGCGAG GCGA CCG CT CTCTCCCGA
- GC CCCAC
GAM148 280 PP2447 1 10796 NP_079480.1 5 329 GCCTGCTCCCTC G A A C 3 B c c
TCTCTGCAGAAC TGTTC GCA GA GAGAGGG
GGGCTCAT GCAAG CGT CT CTCTCCC
A - - T
GAM148 280 PPP1R11 1 15269 NP_068778.1 3 101 CCTCCTTCCCTC C A C 3 B c c
TCTTCTGCCTGA TGTT GGCA GAAGAGAGGG
TAGAGGGA ATAG CCGT CTTCTCTCCC
T - T
GAM148 280 PPP1R11 1 15269 NP_740751.1 3 413 CCTCCTTCCCTC C A C 3 B c c
TCTTCTGCCTGA TGTT GGCA GAAGAGAGGG
TAGAGGGA ATAG CCGT CTTCTCTCCC
T - T
GAM148 280 PPP2R4 1 14893 NP_821069.1 5 454 GGACCAGCCCTC GG AA 3 B c c
TCGGTTTGGGAA TGTTC CAAG GAGAGGGCT
TAAGGCAT ATAAG GTTT CTCTCCCGA
G- GG
GAM148 280 PROL2 1 17200 NP_006804.1 5 73 CTTCTCCTTCTC - C 3 B c c
TCTTCGTTGCTG TGTTCGGCAA GAAGAGAGGG
AGCGACAA GCGAGTCGTT CTTCTCTCTT
G C
GAM148 280 PTGFRN 1 14508 XP_040709.3 3 3020 CCGGTGGCCCTT TC AG 3 B c c
GCTTCTTGCTTT TGT GGCAAGAAG AGGGCT
GCAGACTG ACG TCGTTCTTC TCCCGG
TT GT
GAM148 280 PTGIS 1 15201 NP_000952.1 3 3679 CTGAGAGCTCTC TC - 3 B c c
TCTTCTCTGTTA TGT GGCA AGAAGAGAGGGCT
CAAAACGA ACA TTGT TCTTCTCTCTCGA
-- C
GAM148 280 PTPNS1 1 9261 NP_542970.1 3 1972 TTCGTCTCCCTC - - CA C 3 B c c

TCTTTTACCCAG TGT TC GG AGAAGAGAGGG
AGACAGCA ACA AG CC TTTTCTCTCCC
G A CA T

GAM148 280 RAD52 1 9644 NP_602295.1 3 359 TCCTGTACTCTC T CA C 3 B c c
TCTTCTCCGTGC TGT CGG AGAAGAGAGGG
ACTCAGTC ACG GCC TCTTCTCTCTC
T -- A

GAM148 280 SBLF 1 5432 NP_006864.2 3 385 TTTCTTCCCATC TT - C 3 B c c
TCTTCTTGCTGC TG CGGCAAGAAGAGA GGG
TTAGTGTC AT GTCGTTCTTCTCT CCC
TC A T

GAM148 280 SCAP1 1 13627 NP_003717.2 3 121 CTTGGACTCCTC G GA C 3 B c c

TCTTTGCTGAAG T TTCGGCAA AGAGAGGG
AGACCCAA A AAGTCGTT TCTCTCCT
G -- C

GAM148 280 SDK1 1 16745 NP_689957.1 3 777 ACGCTGGCCCTC CAA - 3 B b b
TCCTTCCCCGAA TGTTCGG GAAG AGAGGGCT
CACAGCAC ACAAGCC CTTC TCTCCCGG
C-- C

GAM148 280 SLC21A2 1 10394 NP_005621.1 3 386 AAGGGTATCTGC TC AGAG 3 B c
c

CCTTCTTGCCAG TGT GGCAAGA AGGGC
GCAGCTCC ACG CCGTTCT TCCCG
GA ----

GAM148 280 SLC25A1 1 16041 NP_005975.1 3 525 CCTCGGGCCCTC CAAGA 3 B c
c

TCTCCGCCCCGG TGTTCGG AGAGAGGGCT
ACAGGGTG ACAGGCC TCTCTCCCGG
CCGCC

GAM148 280 SMO 1 19323 NP_005622.1 3 73 TACCTTCAAGGC CAA- G 3 B c c
TCTTCTTCCTCA TGTTCGG GAAGA AGGGCT
CCGAGCAT ACGAGCC CTTCT TCTCGG
ACTC -

GAM148 280 SNRPD3 1 2958 NP_004166.1 5 124 TCATCAGCCCTC TG--- A-- 3 B c c
TTTTCCGGTGCC TTCGGCA GAAGAGAGGGCT
GGAACTAT AGGCCGT CTTTTCTCCCGA
TATCA GGC

GAM148 280 SNX27 1 19179 NP_112180.4 3 569 CTTTCAGTTTTC CG A 3 B c c
TCTTCTGTGAAA TGTT GCA GAAGAGAGGGCT
CAGGAAGA ACAA TGT CTTCTCTTTTGA
AG -

GAM148 280 SPON1 1 2566 NP_006099.1 3 470 TGTTTGCCCATC T---- G - - 3 B c c
TCTTCTTAGTGG GTTC GC AAGAAGAGA GGGC
AACTTTAG CAAG TG TTCTTCTCT CCCG
GATTT G A A

GAM148 280 SPRY4 1 18907 NP_112226.2 3 3502 TGCCTTGCTTTC TC --- 3 B c c
TCTTCTTACTGT TGT GGCA AGAAGAGAGGGC
CCCACAGC ACA CTGT TCTTCTCTTTCG
CC CAT

GAM148 280 SPTBN2 1 11121 NP_008877.1 3 194 GGGCAGCCCTTC TT A - 3 B c c

TCTTCTGCTGTT TG CGGCA GAAGAGA GGGCT
TAATTCCA AT GTCGT CTTCTCT CCCGA
TT - T

GAM148 280 SRD5A2 1 13219 NP_000339.1 5 21 GGGGCCGCGCTC GGCA G 3 B c c

TCTTCTGGGAGG TGTTC AGAAGAGAG GC
GCAGCGGC ACGGG TCTTCTCTC CG
AGGG G

GAM148 280 STAR 1 10859 NP_000340.1 3 463 CCTGCAGCCCTC T- AA- -- - 3 B c c
TGCTCCTCCCGG TGT CGGC GA AG AGAGGGCT
CCGCTGCA ACG GCCG CT TC TCTCCCGA
TC GCC CC G

GAM148 280 SYT13 1 9376 NP_065877.1 3 2334 TGACCAGCATTC CGG G 3 B c c
TCTTCTTGGTAA TGTT CAAGAAGAGAG GCT
CATCTACT ACAA GTTCTTCTCTT CGA
TG- A

GAM148 280 TLL1 1 13124 NP_036596.3 5 467 GTGCTTGCCCTC -- CA- A 3 B c c
TCTACTGTCCCG TGT TCGG AG AGAGAGGGC
GCGGCATC ACG GGCC TC TCTCTCCCG
GC CTG A

GAM148 280 TM7SF2 1 11046 NP_003264.1 5 85 GTGAGCGCCCTC G AA - 3 B c c
TCTCTCCGGCGG TGTTC GC GA AGAGAGGGC
AGCGGAGA GCGAG CG CT TCTCTCCCG
G GC C

GAM148 280 TNFRSF1 1 5580 NP_003811.2 5 98 CCTGAGCCCCTC TC AGA - 3 B c c
4 TCTGCTGCCAGA TGT GGCA AGAGAGGG CT
CACCCCCT ACA CCGT TCTCTCCC GA
GA CG- C

GAM148 280 TNKS1BP 1 5658 NP_203754.1 5 126 CTCCAAGTTCTC TC A 3 B c c
1 TCTTCCTGTCCC TGT GGCA GAAGAGAGGGCT
ACACTCTG ACA CTGT CTTCTCTCTTGA
CC C

GAM148 280 TPCN1 1 3418 NP_060371.2 3 37 CCGAAAGCCGTC CG- - G 3 B c c
TCTTCTATGCAA TGTT GCA AGAAGAGA GGCT
TAACACAA ACAA CGT TCTTCTCT CCGA
TAA A G

GAM148 280 TRADD 2 605 NP_700474.1 5 279 GGCGAGAGCCCC C A 3 B b b
TCTTCTTCCCGA TGTTCGG AAGAAGAG GGGCT
GCAGTGGG ACGAGCC TTCTTCTC CCCGA
C -

GAM148 280 TRADD 2 3225 NP_700474.1 5 420 TCGAAGTCCCTC T------- C A - 3 B c b
TCTTTTGCCAAC GTT GGCAAGA GAGAGGG CT
CCTCATTT CAA CCGTTTT CTCTCCC GA
TTTACTCC - - T

GAM148 280 TRAP240 1 596 NP_005112.1 5 77 CGATGAGTGCCT T A A - 3 B c c
CCTTCGTGCCGA GTTCGGCA GAAG GAGG GCT
ACG CAAGCCGT CTTC CTCC TGA

G G - G
GAM148 280 TREX1 1 6080 NP_338598.1 5 1074 CTGTTGGCTTTC CG- A 3 B c c
TCTTCTGCAGCA TGTT GCA GAAGAGAGGGCT
ACAGGTCA ACAA CGT CTTCTCTTTCGG
CGA -
GAM148 280 TSN 1 15704 NP_004613.1 3 1408 AAAAGTGTCACC T - AG 3 B c c
TTTTCTTGCCTG TG TC GGCAAGAAGAG GGC
ATCAACAA AC AG CCGTTCTTTTC CTG
T T CA
GAM148 280 UBAP2 2 3406 NP_680476.1 3 1237 CTAGCAGCCCTC C A- A 3 B c c
TCTCTCAGCTTA TGTT GGC AGA GAGAGGGCT
GCAGTTCG ACGA TCG TCT CTCTCCCGA
T AC -
GAM148 280 UBAP2 2 6591 NP_680476.1 3 1299 CATGCAGCCCTC T- - AA A 3 B c c
TCCTCGAGCACG TGT CG GC GA GAGAGGGCT
TCACACAC ACA GC CG CT CTCTCCCGA
CT A AG C
GAM148 280 UGT2B4 1 8980 NP_066962.1 3 107 AAGAGATTCCTT CG C 3 B c c
TCTTCTTGTGAC TGTT GCAAGAAGAGAGGG
AAAACATC ACAG TGTTCTTCTTTCCT
-- T
GAM148 280 XPNPEP2 1 966 NP_003390.2 3 1037 CTCCCAGCCCTC T--- CA ---- 3 B c
c
TCCTCATTCTCT GTTCGG AGAA GAGAGGGCT
GAACCCAC CAAGTC TCTT CTCTCCCGA
CACC -- ACTC
GAM148 280 ZFP91 1 15418 NP_739574.1 3 622 TTCCTTGCTTTC GGCA 3 B c c
TCTTCTAATGGA TGTTC AGAAGAGAGGGC
ATATGCGT ATAAG TCTTCTCTTTCG
GTAA
GAM149 237 CENTG1 1 18082 NM_014770.1 3 GGACCGCTGGAC AA A AG 3 C c
c
AGACGCAC GTGTGTCT TC TAGTGGTCC
CACGCAGA AG GTCGCCAGG
-- C --
GAM149 237 LCHN 1 6008 XM_098615.2 3 GGACCCCTCACA CTATCA - T 3 C c c
AACACACTT AAGTGTGT GT AG GGTCC
TTCACACA CA TC CCAGG
AA---- C C
GAM149 237 LEPROTL 1 8728 NM_015344.1 3 ACCACTACTGAT G G - CC 3 C c c
1 GAGGGACAGTT AA TGT TCT ATCAGTAGTGGT
TT ACA GGA TAGTCATCACCA
G G G --
GAM149 237 LOC2032 1 5131 5 GCTGTTACTGAT T TG CC 3 C c c
86 AGACACCTT AAG GTGTCTATCAGTAG GT
TTC CACAGATAGTCATT CG
- GT --
GAM150 261 DAPK1 1 11771 NM_004938.1 3 TCCACATGAAAC CAACTC - 3 C c c

CTACACACTGTC TGACAGTGTG TCAT TGGA
A ACTGTCACAC AGTA ACCT
ATCCAA C

GAM150 261 LOC1280 1 16098 5 TCCTGAAGAAAC G AC- - TT 3 C c c
08 TGAACACTGTCA TGACAGTGT CA TCT CA GGA
ACTGTCACA GT AGA GT CCT
A CAA A --

GAM150 261 LOC2213 1 14194 XM_168134.1 5 TCCATGCATTGC A CTCT T 3 C c c
99 ACGCTGCCA TG CAGTGTGCAA CAT GGA
AC GTCGCACGTT GTA CCT
C AC-- -

GAM150 261 LOC2532 1 10298 XM_170765.2 3 TCCAGTGGTCAC - CA TCT 3 C c c
16 ACACTGGTCA TGAC AGTGTG AC CATTGGA
ACTG TCACAC TG GTGACCT
G AC ---

GAM150 261 SLC2A10 1 1592 NM_030777.2 3 TCCAGTAGTTGA G CTC 3 C c c
ACACTGTCA TGACAGTGT CAACT ATTGGA
ACTGTCACA GTTGA TGACCT
A ---

GAM151 205 LOC1518 1 12621 5 CCACAACCACCA A AC - C C 3 C c c
16 CCAGTGCTA TAGTACTGGTG GTGGT G GG
ATCGTGACCAC CACCA C CC
- -- A A -

GAM152 378 ANXA7 1 7738 NM_001156.2 3 CCTCTAAGTCTG C GA A 3 C c c
CTTGATAGAGT ATTCTA CAAGCAGA TGGAGG
TGAGAT GTTCGTCT ATCTCC
A GA -

GAM152 378 CSEN 1 13661 NM_013434.3 3 CCTCCATCTGGG A AGCAG A 3 C c
c
GATGGAGAAT ATTCT CCA AGATGGAGG
TAAGA GGT TCTACCTCC
- AGGGG -

GAM152 378 NLGN1 1 6771 NM_014932.1 3 TCCTCCATCAAT A A GCAGA 3 C c c

TGGCAGAA TTCT CCAA GATGGAGGA
AAGA GGTT CTACCTCCT
- C AA---

GAM153 244 DDIT3 1 6855 NM_004083.2 5 ATCTTCATACAT T C CCAAG 3 C c c
CACCACACC GG GTGGTGA ATGAAGAT
CC CACCACT TACTTCTA
- A ACA--

GAM154 228 HSZFP36 1 3168 XM_290868.1 5 CTCCTCGAGTAA - G C CG 3 C c c
ATCCATGTGA TCACATGGATTT CT GG GGAG
AGTGTACCTAAA GA CT CCTC
T G - --

GAM154 228 LOC2575 1 9823 5 CGCTCCGCCGCC A TTTCTG 3 C c c
41 CCCTCCAGGTGA TCAC TGGA GGCGGAGCG
AGTG ACCT CCGCCTCGC

G CCCCCG
GAM155 207 DKFZp76 1 18570 3 GAAAGAAGGAAA G AGGC 3 C c c
1O17121 TAAAACATCA TGA GT TGTTTCCTTCTTTC
ACT CA ATAAAGGAAGAAAG
A AA--
GAM155 207 KIAA056 1 18220 XM_038664.6 3 GAAAGAAGAAAA A GG-- G C 3 C c c
4 GATAATACCCA TG GGTA CT TTTC TTCTTTC
AC CCAT GA AAAG AAGAAAG
- AATA - -
GAM155 207 LOC1529 1 8587 3 AAAGAAAAGAAA GCT C- C 3 C c c
41 TCTACCTCA TGAGGTAG GTTTC TTCTTT
ACTCCATC TAAAG AAGAAA
--- AA -
GAM155 207 PTGS1 1 19654 NM_000962.2 3 AAAGAAGAAACT CT C C 3 C c c
TTGCCTCA TGAGGTAGG GTTTC TTCTTT
ACTCCGTTT CAAAG AAGAAA
-- - -
GAM156 262 CLTCL1 1 6732 NM_001835.1 3 TCCAGGCCAGTT A C CAG 3 C c c
TGAAGACTACA TG TAGTCT CAG GGCCTGGA
AC ATCAGA GTT CCGGACCT
- A TGA
GAM156 262 DAAM2 1 4578 XM_166434.3 5 TCCAGACCCTGC TGA T --- C 3 C c c
TGAACGAGCTA TAG CTC CAGCAGGG CTGGA
ATC GAG GTCGTCCC GACCT
--- - CAA A
GAM156 262 DKFZP43 1 16713 XM_041116.4 3 TCCAGGCCCTGC A-- TCCA 3 C c
c
4P0111 CCGACCCCATCA TGAT GTC GCAGGGCCTGGA
ACTA CAG CGTCCCGGACCT
CCC CC--
GAM156 262 FLJ1075 1 6060 NM_018207.1 3 CCGTGGCCACTG TA CAG - A 3 C c c
9 GAGACCTCA TGA GTCTCCAG GGCC TGG
ACT CAGAGGTC CCGG GCC
C- A-- T -
GAM156 262 KIAA080 1 15745 XM_031357.4 3 TCCAGGCCCGAG ATA CAGCA 3 C c
c
2 AGACCAGCA TG GTCTC GGGCCTGGA
AC CAGAG CCCGGACCT
GAC AG---
GAM156 262 LOC1488 1 8056 XM_097542.2 5 CCAGTGGCTGGA T AGGGC A 3 C c
c
94 GACTTCA TGA AGTCTCCAGC CTGG
ACT TCAGAGGTCG GACC
- GT--- -
GAM156 262 LOC1999 1 3088 XM_117166.1 5 TCCAGGCTTCAT C CA-- 3 C c c
88 CCTAGAGACTGT TGATAGTCTC AG GGGCCTGGA
CA ACTGTCAGAG TC TTCGGACCT
A CTAC

GAM156 262 SIRPB1 1 16696 NM_006065.1 3 TCCAAGCCTGCT TA C -- C 3 C c c
GCTGGAAACCTC TGA GT TCCAGCAG GGC TGGA
A ACT CA AGGTCGTC CCG ACCT
C- A GT A
GAM156 262 TRIM37 1 19960 NM_015294.1 3 TCCAGGCCCTGC TA CTCCA 3 C c
c
ATGCCGTCA TGA GT GCAGGGCCTGGA
ACT CG CGTCCCGGACCT
GC TA---
GAM157 225 AMOT 1 1662 NM_133265.1 3 TGATGAGGAATC - TACG 3 C c c
TGAGAACTGGAG TCTCCAGTTC CAG CTCATCA
A AGAGGTCAAG GTC GAGTAGT
A TAAG
GAM157 225 CHAF1B 1 17720 NM_005441.1 3 TGATGAGTTTCT T C TAC 3 C c c
GAAACTGGAG CTCCAGTT CAG GCTCATCA
GAGGTCAA GTC TGAGTAGT
- A TT-
GAM157 225 D123 1 2735 3 TGAGCGTACTGT C TCA 3 C c c
AACTGGAGA TCTCCAGTT CAGTACGCTCA
AGAGGTCAA GTCATGCGAGT
T ---
GAM157 225 LOC1499 1 1436 3 TGATGAGCTCAT C GTAC 3 C c c
35 GGAACTTGAGA TCTC AGTTCCA GCTCATCA
AGAG TCAAGGT CGAGTAGT
T ACT-
GAM157 225 LOC2214 1 9737 XM_166344.3 5 GATGAGCATACG CCA C A 3 C c c
91 ACTGGGGA TCTCCAGTT GTA GCTCATC
AGGGGTCAG CAT CGAGTAG
--- A -
GAM158 383 KIAA023 1 13040 NM_014747.1 5 GGAGGCAGCCCC T TTTTGT C 3 C c
c
7 CTGTGA TCAC GG GGCTGCCTCC
AGTG CC CCGACGGAGG
T C----- -
GAM158 383 KIAA104 1 19310 XM_048592.2 3 GGGAGGCAGCCC A TTTTGT 3 C c
c
5 TTCCCAGGGA TC CTGG GGCTGCCTCCC
AG GACC CCGACGGAGGG
G CTTC--
GAM158 383 KIAA111 1 1213 3 GAGGCAGCCACC A TTTT CC 3 C c c
0 CCAGAGA TC CTGG GTGGCTGCCTC
AG GACC CACCGACGGAG
A C--- --
GAM158 383 LOC1246 1 1663 3 GGAAACAGCCGC GTTT CC C 3 C c c
02 ACAGTGA TCACTG TGTGGCTG TCC
AGTGAC ACGCCGAC AGG
---- AA -
GAM158 383 LOC2538 1 11918 5 GGGAGGCAGCCT A TTTGT 3 C c c
66 TCACCAGGGA TC CTGGT GGCTGCCTCCC

AG GACCA CCGACGGAGGG
G CTT--

GAM158 383 LOC9230 1 16687 NM_138385.1 3 GGAGGCAGCCAC T G T C 3 C c c

5 AGGCGAGTG CACT GTTT GTGGCTGCCTCC
GTGA CGGA CACCGACGGAGG
- G - -

GAM158 383 RAB9B 1 12877 NM_016370.1 5 GGAGGCAGCAGG G GTG C 3 C c
c

AGCAGTGA TCACTG TTTT GCTGCCTCC
AGTGAC AGGA CGACGGAGG
G --- -

GAM158 383 STX1A 1 18630 NM_004603.1 3 GGGAGGCAGCCA TG - 3 C c c

GCGGGGCGTGA TCAC GTTTTG TGGCTGCCTCCC
AGTG CGGGGC ACCGACGGAGGG
-- G

GAM158 383 SUN1 1 9645 3 GGAGACAGCCAC GTTTT C C 3 C c c

CCACAGTGA TCACTG GTGGCTG CTCC
AGTGAC CACCGAC GAGG
ACC-- A -

GAM159 230 AF5Q31 1 13598 NM_014423.1 5 CCTTGGCAGCCT AAT TC A 3 B c c

GTCACCGCCC GGG GT TGG GCTGCCAAGG
CCC CA GTC CGACGGTTCC
GC- CT -

GAM159 230 APPD 1 14424 3 CCTTCAGGAAGC AA A G -- 3 B c c

CCCAGAACACCC GGG TGTTCTGG GCT CC AAGG
CCC ACAAGACC CGA GG TTCC
-- C A AC

GAM159 230 DGCR6 1 10368 NM_005675.2 3 CTTGGCAGCTGC AATGTT G G 3 B c
c

AGCCC GGG CTG AGCTGCCAAG
CCC GAC TCGACGGTTC
------ G -

GAM159 230 FLJ1371 1 19395 NM_024817.1 3 CCTTAGCAGCTC A CTG C 3 B c c
0 ACAACATCCC GGGA TGTT GAGCTGC AAGG
CCCT ACAA CTCGACG TTCC
- CA- A

GAM159 230 GATA2 1 13334 3 CCTTAGCAGCCC TT A C 3 B c c

AGCATTTCC GGGAATG CTGG GCTGC AAGG
CCTTTAC GACC CGACG TTCC
-- - A

GAM159 230 HD 1 15165 NM_002111.3 3 CCTTAGCAAGGG - AA G ---- C 3 B c c

GCTCAGAACACC GGG TGTTCTG AGCT GC AAGG
CC CCC ACAAGAC TCGG CG TTCC
C -- - GGAA A

GAM159 230 KIAA095 1 11636 XM_039733.2 3 CCTCAAAGCTTA T --- GCCA 3 B c c
3 TCCAGAACCTTC GGGAA GTTCTGGA GCT AGG
CC CCCTT CAAGACCT CGA TCC
C ATT AAC-

GAM159 230 LOC1514 1 18291 XM_098060.1 5 CCCTGGGGCGCA C GA G A 3 B c c
38 AACATTCCC GGGAATGTT TG GCT CCA GG
CCCTTACAA AC CGG GGT CC
- G- - C
GAM159 230 LOC9174 1 1274 3 CCCTGGCAGCTG ATGT G A 3 B c c
8 CAGATCCC GGGA TCTG AGCTGCCA GG
CCCT AGAC TCGACGGT CC
---- G C
GAM159 230 SDR1 1 19713 NM_004753.1 3 CCTTGACACTTT TG C C 3 B c c
TGAACATTTCC GGGAATGTTC GAG TG CAAGG
CCTTTACAAG TTC AC GTTCC
TT - A
GAM160 343 LOC1322 1 13188 XM_072302.2 3 TTTGGAATCTCT - ACTCTT C 3 C c c
35 GAAGTA TACTTCAG GA TTTCAAA
ATGAAGTC CT AAGGTTT
T ------ -
GAM160 343 TRAF3 1 9111 NM_145725.1 5 GTTTGTCAGAAG AAC T- 3 C c c
ACCCTGAAGTA TACTTCAGG TCTTTT CAAAC
ATGAAGTCC AGAAGA GTTTG
C-- CT
GAM161 304 APM1 1 9908 NM_004797.1 3 GTCACCCAGGCT C C C 3 C c c
GGAGTACAGTGA TTATTG ACTCCAGCC GGG GAC
AGTGAC TGAGGTCGG CCC CTG
A A A
GAM161 304 BCL10 1 8318 NM_003921.2 3 TCGCCCAGGCTG T C C 3 C c c
GAGTGCAGTG TATTGCACTCCAGCC GGGCGA
GTGACGTGAGGTCGG CCCGCT
- A -
GAM161 304 C13orf1 1 12864 NM_020456.1 3 GTCACCCAGGCT T C C C 3 C c c
AGAGTGCAGTG TATTGCACTC AGCC GGG GAC
GTGACGTGAG TCGG CCC CTG
- A A A
GAM161 304 C21orf6 1 12444 NM_058188.1 5 GTCGCCCAGGCT T A C 3 C c c
7 GGAGCGCAATG TATTGC CTCCAGCC GGGCGAC
GTAACG GAGGTCGG CCCGCTG
- C A
GAM161 304 C6orf33 1 14623 NM_133367.1 3 GTCGCCCAGGCT C 3 C b b
GGAGTGCAGTGA TTATTGCACTCCAGCC GGGCGAC
AGTGACGTGAGGTCGG CCCGCTG
A
GAM161 304 C9orf9 1 10257 NM_018956.2 5 GTCGCCCAGGCT T C 3 C c c
GGAGTGCGGTG TATTGCACTCCAGCC GGGCGAC
GTGGCGTGAGGTCGG CCCGCTG
- A
GAM161 304 CDH17 1 1297 NM_004063.2 3 CGTCGCCCAGGC T C C - 3 C c c
TGGAGTACAGTG TATTG ACTCCAGCC GGGCGAC
G GTGAC TGAGGTCGG CCCGCTG
G A A C

GAM161 304 FCAR 1 8313 NM_002000.2 3 GTCACCCAGGCT T C C C 3 C c c
GAAGTGCAGTG TATTGCACT CAGCC GGG GAC
GTGACGTGA GTCGG CCC CTG
- A A A

GAM161 304 FEZ1 1 8241 NM_005103.3 3 TCGCCCAGGCTG T C C 3 C c c
GAGTGCAATG TATTGCACTCCAGCC GGGCGA
GTAACGTGAGGTCGG CCCGCT
- A -

GAM161 304 FLJ1023 1 12255 NM_018033.1 3 GTCACCCAGGCT T C C 3 C c c
2 GGAGTGCGATG TATTGCACTCCAGCC GGG GAC
GTAGCGTGAGGTCGG CCC CTG
- A A

GAM161 304 FLJ1278 1 7408 NM_032175.1 3 TCGCCCAGGCTG C C C 3 C c c
7 GAGTACAGTGA TTATTG ACTCCAGCC GGGCGA
AGTGAC TGAGGTCGG CCCGCT
A A -

GAM161 304 FLJ1311 1 930 NM_024541.1 5 GTCGCCCAGGCT T C C 3 C c c
4 GGAATGCAGTG TATTGCA TCCAGCC GGGCGAC
GTGACGT AGGTCGG CCCGCTG
- A A

GAM161 304 FLJ1318 1 3353 NM_022063.1 3 GTCACCCAGGCT C C C 3 C c c
8 AGAGTGCAGTAG TTATTGCACTC AGCC GGG GAC
GATGACGTGAG TCGG CCC CTG
A A A

GAM161 304 FLJ1345 1 12949 XM_038291.5 3 GTCGCCCAAGCT T CC 3 C c c
6 GGAGTGCAGTG TATTGCACTCCAGC GGGCGAC
GTGACGTGAGGTCG CCCGCTG
- AA

GAM161 304 FLJ2013 1 8713 NM_017684.1 3 CGTCGCCCAGGC T C C - 3 C c c
6 TGGAATGCAGTG TATTGCA TCCAGCC GGGCGAC
G GTGACGT AGGTCGG CCCGCTG
G A A C

GAM161 304 FLJ2050 1 19171 NM_017849.1 3 GTCACCCGGGCT TTA C 3 C c c
7 GGAGTGTAA TTGCACTCCAGCCCGGG GAC
AATGTGAGGTCGGGCCC CTG
--- A

GAM161 304 FLJ3115 1 1064 NM_144600.1 5 GTCACCCAGACT T CCC C 3 C c c
3 GGAGTGCAGTG TATTGCACTCCAG GGG GAC
GTGACGTGAGGTC CCC CTG
- AGA A

GAM161 304 FLJ3286 1 15270 NM_144613.1 3 GTCACCCAGGCT C C C 3 C c c
5 GGAGTACAATGA TTATTG ACTCCAGCC GGG GAC
AGTAAC TGAGGTCGG CCC CTG
A A A

GAM161 304 GR6 1 11991 NM_007354.1 5 GTCACCCAGGCT T C C C 3 C c c
GGAATGCAGTG TATTGCA TCCAGCC GGG GAC
GTGACGT AGGTCGG CCC CTG
- A A A

GAM161 304 H2AV 1 4146 NM_138635.1 3 GTCACCCAGACT T CCC C 3 C c c
GGAGTGCGATG TATTGCACTCCAG GGG GAC

GTAGCGTGAGGTC CCC CTG
- AGA A
GAM161 304 HCA4 1 18806 3 GTCGCCCAGGCT TTAT C 3 C c c
GGAGTGCATTG TGCACTCCAGCC GGGCGAC
ACGTGAGGTCGG CCCGCTG
GTT- A
GAM161 304 HRH4 1 18713 NM_021624.2 3 GTCACCCAGGCT C C 3 C c c
GGAGTGCAGTAG TTATTGCACTCCAGCC GGG GAC
GATGACGTGAGGTCGG CCC CTG
A A
GAM161 304 HTR1E 1 3407 NM_000865.1 5 GTCGCCCAGGCT TTAT C 3 C c c
GGAGTGCAG TGCACTCCAGCC GGGCGAC
ACGTGAGGTCGG CCCGCTG
G--- A
GAM161 304 IFNAR2 1 8000 NM_000874.2 3 CGTCGCCCAAGC T A CC - 3 C c c
TGGAGCGCAATG TATTGC CTCCAGC GGGCGAC
G GTAACG GAGGTCG CCCGCTG
G C AA C
GAM161 304 KIAA016 1 17542 3 GTCCCCCAAGCT C CC C 3 C c c
1 GGAGTACAATGA TTATTG ACTCCAGC GGG GAC
AGTAAC TGAGGTCG CCC CTG
A AA C
GAM161 304 KIAA059 1 6311 XM_085127.6 3 CGTCGCCCAGGC T A C - 3 C c c
9 TGGAGCGCAGTG TATTGC CTCCAGCC GGGCGAC
G GTGACG GAGGTCGG CCCGCTG
G C A C
GAM161 304 KIAA102 1 4329 3 GTCACCCAAGCT T CC C 3 C c c
8 GGAGTGCAGTG TATTGCACTCCAGC GGG GAC
GTGACGTGAGGTCG CCC CTG
- AA A
GAM161 304 KIAA145 1 6378 XM_040100.4 3 GTCGCCCAGGCT TTAT C 3 C c c
6 GGAGTGCA TGCACTCCAGCC GGGCGAC
ACGTGAGGTCGG CCCGCTG
---- A
GAM161 304 KIAA150 1 2567 XM_290952.1 3 GTCACCCAGGCT TT C C 3 C c c
8 GGAGTGCAAT ATTGCACTCCAGCC GGG GAC
TAACGTGAGGTCGG CCC CTG
-- A A
GAM161 304 KIAA165 1 19930 3 GTCGCCCAGGCT T TG C 3 C c c
5 GGAGTGTGGTG TAT CACTCCAGCC GGGCGAC
GTG GTGAGGTCGG CCCGCTG
- GT A
GAM161 304 KIAA187 1 4810 3 CGTCGCCCAGGC T C C - 3 C c c
7 TAGAGTGCAGTG TATTGCACTC AGCC GGGCGAC
G GTGACGTGAG TCGG CCCGCTG
G A A C
GAM161 304 LOC1261 1 13929 3 GTCACCCAGGCT T A C C 3 C c c
33 GGAGCGCAGTG TATTGC CTCCAGCC GGG GAC
GTGACG GAGGTCGG CCC CTG
- C A A

GAM161 304 LOC1280 1 12251 3 GTCGCCCAGGCT T C C 3 C c c
77 AGAGTGCAGTG TATTGCACTC AGCC GGGCGAC
GTGACGTGAG TCGG CCCGCTG
- A A
GAM161 304 LOC1308 1 18432 XM_065904.2 3 GTCGCCTAGGCT TTA CG 3 C c c
13 GGAGTGCAA TTGCACTCCAGCC GGCGAC
AACGTGAGGTCGG CCGCTG
--- AT
GAM161 304 LOC1443 1 12865 XM_084813.4 5 GTCGCCCAGGCT T C 3 C c c
17 GGAGTGCGATG TATTGCACTCCAGCC GGGCGAC
GTAGCGTGAGGTCGG CCCGCTG
- A
GAM161 304 LOC1464 1 12181 3 GTCGCCCAGGCT TT C 3 C c c
55 GGAGTGTAGT ATTGCACTCCAGCC GGGCGAC
TGATGTGAGGTCGG CCCGCTG
-- A
GAM161 304 LOC1481 1 14101 NM_144692.1 3 GTCACCCAGGCT T C C 3 C c c
37 GGAGTGCCATAG TTAT GCACTCCAGCC GGG GAC
GATA CGTGAGGTCGG CCC CTG
C A A
GAM161 304 LOC1512 1 19905 XM_098021.1 3 GTCACCCAGGCT TT C C C 3 C c c
01 GGAGTCCAAT ATTG ACTCCAGCC GGG GAC
TAAC TGAGGTCGG CCC CTG
-- C A A
GAM161 304 LOC1517 1 2777 3 GTCGCCCAGGCT C 3 C b b
01 GGAGTGCAGTAG TTATTGCACTCCAGCC GGGCGAC
GATGACGTGAGGTCGG CCCGCTG
A
GAM161 304 LOC1522 1 6203 XM_098182.1 3 GTCGCCCAGGCT T G C 3 C c c
45 GGAGTGAGTG TATT CACTCCAGCC GGGCGAC
GTGA GTGAGGTCGG CCCGCTG
- - A
GAM161 304 LOC1530 1 11568 XM_098307.1 3 TCACCCAGGCTG T C C C 3 C c c
77 GAGTGCAGTG TATTGCACTCCAGCC GGG GA
GTGACGTGAGGTCGG CCC CT
- A A -
GAM161 304 LOC1536 1 12866 5 GTCACCCAGGCT T C C 3 C c c
88 GGAGTGCAATG TATTGCACTCCAGCC GGG GAC
GTAACGTGAGGTCGG CCC CTG
- A A
GAM161 304 LOC1538 1 16081 XM_087779.2 3 GTCGCCCAGACT CCC 3 C c c
11 GGAGTGCAGTAG TTATTGCACTCCAG GGGCGAC
GATGACGTGAGGTC CCCGCTG
AGA
GAM161 304 LOC1583 1 8794 XM_098919.1 5 CGTCGCCCAGGC T C - 3 C c c
10 TGGAGTGCAGTG TATTGCACTCCAGCC GGGCGAC
G GTGACGTGAGGTCGG CCCGCTG
G A C

GAM161 304 LOC1960 1 1349 5 GTCTCCCAGGCT C C 3 C b b
47 GGAGTGCAATAG TTATTGCACTCCAGCC GGG GAC
GATAACGTGAGGTCGG CCC CTG
A T
GAM161 304 LOC1997 1 11992 3 GTCACCCGGGCT T C 3 C c c
86 GGAGTGCAGTG TATTGCACTCCAGCCCGGG GAC
GTGACGTGAGGTCGGGCCC CTG
- A
GAM161 304 LOC2003 1 15098 5 TCGCCCAGGCTG T C C C 3 C c c
01 GAGTACAGTG TATTG ACTCCAGCC GGGCGA
GTGAC TGAGGTCGG CCCGCT
- A A -
GAM161 304 LOC2003 1 19042 3 GTCGCCCAGACT T C CCC 3 C c c
16 AGAGTGCAATG TATTGCACTC AG GGGCGAC
GTAACGTGAG TC CCCGCTG
- A AGA
GAM161 304 LOC2205 1 18968 3 GTCACCCAGGCC T A C C 3 C c c
75 GGAGTGCAGTG TATTGCACTCC GCC GGG GAC
GTGACGTGAGG CGG CCC CTG
- C A A
GAM161 304 LOC2212 1 6488 3 GTCACTCAGGCT C C 3 C c c
71 GGAGTGCAATGA TTATTGCACTCCAGCC GGG GAC
AGTAACGTGAGGTCGG CTC CTG
A A
GAM161 304 LOC2457 1 14795 5 GTCGCCCAGGCT C C 3 C c c
71 GGAATGCAGTAG TTATTGCA TCCAGCC GGGCGAC
GATGACGT AGGTCGG CCCGCTG
A A
GAM161 304 LOC2540 1 2709 5 GTCGCCCAAGCT T C CC 3 C c c
82 AGAGTGCAGTG TATTGCACTC AGC GGGCGAC
GTGACGTGAG TCG CCCGCTG
- A AA
GAM161 304 LOC2563 1 19369 3 CGTCGCCCAGGC TTAT C - 3 C c c
06 TGGAGTGCAG TGCACTCCAGCC GGGCGAC
ACGTGAGGTCGG CCCGCTG
G--- A C
GAM161 304 LOC5169 1 6670 3 CGTCACCCAGGC C C - 3 C c c
6 TGGAGTGCAGTA TTATTGCACTCCAGCC GGG GAC
G GATGACGTGAGGTCGG CCC CTG
A A C
GAM161 304 MEFV 1 8754 NM_000243.1 5 CGTCACCCAGGC T C C - 3 C c c
TGGAGTGCAGTG TATTGCACTCCAGCC GGG GAC
G GTGACGTGAGGTCGG CCC CTG
G A A C
GAM161 304 MGC1081 1 4141 NM_030568.2 3 GTCGCCCAGGCT T C C 3 C c c
8 GGAGTACAATG TATTG ACTCCAGCC GGGCGAC
GTAAC TGAGGTCGG CCCGCTG
- A A
GAM161 304 MGC1313 1 5265 NM_033410.1 3 GCCCAGGCTGGA C GAC 3 C c
c

8 GTGCAATAG TTATTGCACTCCAGCC GGGC
GATAACGTGAGGTCGG CCCG
A ---
GAM161 304 MGC2989 1 19764 NM_144618.1 3 GTCACCCAGGCT T C C 3 C c c
1 GGAGTGCGGTGG TATTGCACTCCAGCC GGG GAC
GTGGCGTGAGGTCGG CCC CTG
G A A
GAM161 304 MMPL1 1 11792 3 GTCCTCCAGGCT C C 3 C c c
GGAGTGCAATGA TTATTGCACTCCAGCC GGG GAC
AGTAACGTGAGGTCGG CCT CTG
A C
GAM161 304 MRPL44 1 17368 NM_022915.2 3 GTCGCCCAGGCT TTAT C C 3 C c
c
GGACTGCA TGCA TCCAGCC GGGCGAC
ACGT AGGTCGG CCCGCTG
---- C A
GAM161 304 MYCL2 1 8793 NM_005377.1 3 GTCGCCCAGGCT TT CA C 3 C c c
GGAGGTTAAT ATTG CTCCAGCC GGGCGAC
TAAT GAGGTCGG CCCGCTG
-- TG A
GAM161 304 NCOA6 1 19170 NM_014071.1 5 GTCGCCCAGGCT TT C 3 C c c
GGAGTGCAGT ATTGCACTCCAGCC GGGCGAC
TGACGTGAGGTCGG CCCGCTG
-- A
GAM161 304 NCOA6IP 1 4013 NM_024831.5 3 CGCCCAGGCTGG T C AC 3 C c c
AGTGCAGTG TATTGCACTCCAGCC GGGCG
GTGACGTGAGGTCGG CCCGC
- A --
GAM161 304 OFD1 1 10775 NM_003611.1 5 CGCCCGGGCTGG T ACT AC 3 C c c
GCACTAA TTA TGC CCAGCCCGGGCG
AAT ACG GGTCGGGCCCGC
C --- --
GAM161 304 PDCL 1 848 NM_005388.2 3 GTCACCCAGGCT C C C 3 C c c
GGAGTACAATAG TTATTG ACTCCAGCC GGG GAC
GATAAC TGAGGTCGG CCC CTG
A A A
GAM161 304 PDE6B 1 16553 NM_000283.1 3 GTCACCCAGGCT T T C C 3 C c c
GGAGTGCCGTG TAT GCACTCCAGCC GGG GAC
GTG CGTGAGGTCGG CCC CTG
- C A A
GAM161 304 PIGR 1 3992 NM_002644.1 3 GTCACCCAGACT C CCC C 3 C c c
GGAATGCAGTGA TTATTGCA TCCAG GGG GAC
AGTGACGT AGGTC CCC CTG
A AGA A
GAM161 304 PPID 1 9646 NM_005038.1 5 GTCACCCAGGCT T C C 3 C c c
GGAGTGCGGTG TATTGCACTCCAGCC GGG GAC
GTGGCGTGAGGTCGG CCC CTG
- A A

GAM161 304 PRKR 1 5680 NM_002759.1 3 GTTGCCCAGGCT C 3 C b b
GGAGTGCAATGA TTATTGCACTCCAGCC GGGCGAC
AGTAACGTGAGGTCGG CCCGTTG
A
GAM161 304 PRO0902 1 6546 NM_053057.2 5 GTCACCCAGGCT TT C C 3 C c c
GGAGTGTAGT ATTGCACTCCAGCC GGG GAC
TGATGTGAGGTCGG CCC CTG
-- A A
GAM161 304 RAB39 1 10258 XM_084662.2 5 GTCACCCAGGCT T C C 3 C c c
GGAGTGCAGTG TATTGCACTCCAGCC GGG GAC
GTGACGTGAGGTCGG CCC CTG
- A A
GAM161 304 RAP140 1 2756 NM_015224.1 3 CGTCGCCCAAGC T C CC - 3 C c c
TGGAGTACAGTG TATTG ACTCCAGC GGGCGAC
G GTGAC TGAGGTCG CCCGCTG
G A AA C
GAM161 304 RHD 1 10256 NM_016225.2 3 GTCACCCAGGCT T C C C 3 C c c
AGAGTGCAATG TATTGCACTC AGCC GGG GAC
GTAACGTGAG TCGG CCC CTG
- A A A
GAM161 304 SH3BP2 1 12256 NM_003023.2 5 GTCGCCCAGGCT T C 3 C b b
GGAGTGCAATG TATTGCACTCCAGCC GGGCGAC
GTAACGTGAGGTCGG CCCGCTG
- A
GAM161 304 SHOX 1 4418 3 GTCGCCCAGGCT TT A C 3 C c c
GGAGCGCAGT ATTGC CTCCAGCC GGGCGAC
TGACG GAGGTCGG CCCGCTG
-- C A
GAM161 304 SNAP23 1 5601 NM_003825.2 3 GTCCAGGCTGGA C GAC 3 C c c
GTGCAATAG TTATTGCACTCCAGCC GGGC
GATAACGTGAGGTCGG CCTG
A ---
GAM161 304 SNX15 1 19041 NM_013306.2 3 GTCGCCCAGACT T CCC 3 C c c
GGAGTGCAGTG TATTGCACTCCAG GGGCGAC
GTGACGTGAGGTC CCCGCTG
- AGA
GAM161 304 STAF65(1 18839 NM_014860.1 3 CGTCACCCAGGC T C C - 3 C c c
gamma) TGGAGTGCAATG TATTGCACTCCAGCC GGG GAC
G GTAACGTGAGGTCGG CCC CTG
G A A C
GAM161 304 TAPBP 1 9641 NM_003190.3 5 GTCGCCCAGGCT T C 3 C c c
GGAGTGCAGTG TATTGCACTCCAGCC GGGCGAC
GTGACGTGAGGTCGG CCCGCTG
- A
GAM161 304 TCF2 1 4621 NM_000458.1 3 CGTCACCCGAGC T C C - 3 C c c
TGGAGTGCAGTG TATTGCACTCCAGC CGGG GAC
G GTGACGTGAGGTCG GCCC CTG
G A A C
GAM161 304 TDGF1 1 2312 NM_003212.1 3 GTCACCCAGGCT C C C 3 C c c
GGACTGCAATGA TTATTGCA TCCAGCC GGG GAC

AGTAACGT AGGTCGG CCC CTG
C A A
GAM161 304 TGIF2 1 14237 NM_021809.2 3 CGTCACCCGGGC T C - 3 C c c
TGGAGTGCAGTG TATTGCACTCCAGCCCGGG GAC
G GTGACGTGAGGTCGGGCCC CTG
G A C
GAM161 304 TRAF5 1 1063 NM_004619.2 5 GTCACCCAGGCT T C C C 3 C c c
GGAGTACAGTG TATTG ACTCCAGCC GGG GAC
GTGAC TGAGGTCGG CCC CTG
- A A A
GAM161 304 TRPM6 1 12681 NM_017662.3 3 CCCAGGCTGGAG C CGAC 3 C c
c
TGCAATGA TTATTGCACTCCAGCC GGG
AGTAACGTGAGGTCGG CCC
A ----
GAM161 304 VENTX2 1 17401 NM_014468.1 3 GTCACCCAGGCT C C 3 C b b
GGAGTGCAATGA TTATTGCACTCCAGCC GGG GAC
AGTAACGTGAGGTCGG CCC CTG
A A
GAM161 304 WHSC1 1 18202 NM_133332.1 3 GCCAGGCTGGAG CG GAC 3 C c
c
TGCAGTAA TTATTGCACTCCAGCC GGC
AATGACGTGAGGTCGG CCG
A- ---
GAM161 304 ZNF253 1 12566 NM_021047.1 3 GTCACCGAGGCT - GC 3 C b b
GGAGTGCAATGA TTATTGCACTCCAGCC CGG GAC
AGTAACGTGAGGTCGG GCC CTG
A A-
GAM162 376 KIAA158 1 12216 XM_037262.4 5 AACAGTAATGGA G- TTGCGA 3 C c
c
2 AGTGCGGCCA TGGCCGCA TCC ACTGTT
ACCGGCGT AGG TGACAA
GA TAA---
GAM162 376 VRP 1 11972 NM_007063.1 3 AACAACCTGACA CC - AAC 3 C c c
AACTGTGGCCA TGGCCGCAGT TTG CG TGTT
ACCGGTGTCA AAC GT ACAA
-- A CCA
GAM163 249 EDG6 1 859 NM_003775.1 3 GGGTACAGGAAG CA CT T 3 C c c
CTGTGTGCA TGCACACAGCT CTGTACCT
ACGTGTGTCGA GACATGGG
-- AG -
GAM163 249 LOC1128 1 17580 XM_053402.4 3 AAGGTACAGTGT - TCT 3 C c c
68 GTATGTGTGTAT CATGCACACA GC CTGTACCTT
G GTATGTGTGT TG GACATGGAA
A TGT
GAM163 249 OLIG2 1 18460 NM_005806.1 3 AGGTACCGCTGT C TCTCT T 3 C c c
GTGCAT ATGCACACAGC GTACCT
TACGTGTGTCG CATGGA
- C---- -

GAM163 249 PTEN 1 2919 NM_000314.1 3 AAGGTTGTGTAG C CTCTGT 3 C c c
CTGTGTCATG CATG ACACAGCT ACCTT
GTAC TGTGTCGA TGGAA
- TGTGT-
GAM164 322 FLJ2198 1 11076 NM_024913.1 5 CCAGAAATACAG G C-- CC 3 C c c
6 CAGCCACTTTGC TGTAAAGTGGCTG TG TTC GG
A ACGTTTCACCGAC AC AAG CC
G ATA A-
GAM164 322 LIPI 1 15797 3 CCAGAAAGACCA C GC CC 3 C c c
CCACTTTGCA TGTAAAGTGG TGGT TTC GG
ACGTTTCACC ACCA AAG CC
- GA A-
GAM165 270 ARHC 1 15644 NM_175744.1 5 GGAACGCAGAGC T - AGATC C 3 C c
c
ACCGAGG CC CGGTGCTCTGCG TCC
GG GCCACGAGACGC AGG
- A A---- -
GAM165 270 BNIP-S 1 1814 NM_138278.1 5 GGGAGATTGCAG TCCC - GA 3 C c c

AAGCACC GGTGCT CTGC GATCTCCC
CCACGA GACG TTAGAGGG
---- A --
GAM165 270 DKFZp43 1 8421 NM_017600.1 5 GGGAGACCCAGG C GCGAGA 3 C c
c
4M0331 AGCACCTGGA TCC GGTGCTCT TCTCCC
AGG CCACGAGG AGAGGG
T ACCC--
GAM165 270 FLJ1472 1 9157 5 GAGAGGCGAGCA T GAGA CC 3 C c c
8 CCGGGA TCCCGGTGCTC GC TCTC
AGGGCCACGAG CG AGAG
- G--- --
GAM165 270 KIAA196 1 12294 5 GGGAGACCCACA - CT GAGA-- 3 C c c
9 GCTAAGACACCG TCCCGGTG CT GC TCTCCC
GGA AGGGCCAC GA CG AGAGGG
A AT ACACCC
GAM165 270 LOC1997 1 16714 NM_145297.1 5 GGGAGATCCACA - CT GA-- 3 C c c

77 GCTAAGACACCG TCCCGGTG CT GC GATCTCCC
GGA AGGGCCAC GA CG CTAGAGGG
A AT ACAC
GAM165 270 LOC1999 1 18302 XM_114052.1 5 GGGACAGTGCAG AGATC 3 C c
c
06 AGCACCGGGG TCCCGGTGCTCTGCG TCCC
GGGGCCACGAGACGT AGGG
GAC--
GAM165 270 MGC2046 1 17732 NM_053043.1 5 GGAGAGAGAGCA C GCGAGA C 3 C
c c
0 CCGAGA TC CGGTGCTCT TCTCC
AG GCCACGAGA AGAGG
A G----- -

GAM165 270 TBL1X 1 11582 NM_005647.2 5 AGATGCCTCGCA T C -- CCC 3 C c c
GAGCACCAGG CC GGTGCTCTGCGAG ATCT
GG CCACGAGACGCTC TAGA
- A CG ---
GAM166 232 MGC1319 1 1875 3 AGCCCTAATGAT CA CA C 3 C c c
8 GACTGGAAA TTTCCAGTCA CAT AGG GCT
AAAGGTCAGT GTA TCC CGA
A- A- -
GAM166 232 NEBL 1 6830 NM_006393.1 3 GCTGGAGTGTGA A AA GCT 3 C c c
CTGGAAA TTTCCAGTCACAC TC GGC
AAAGGTCAGTGTG AG TCG
- G- ---
GAM167 236 KLF12 1 14666 NM_007249.3 3 TCTGCCAGGTCT AA- A GA 3 C c c
CAAAAATTCA TGAATTTTTGA CTGG CAGA
ACTTAAAAACT GACC GTCT
CTG - --
GAM167 236 LOC1318 1 11445 XM_067585.7 3 TCTCTGTCCAGT T TTTT A 3 C c c
73 TCATTTTC GAA TGAA CTGGACAGAGA
CTT ACTT GACCTGTCTCT
- TT-- -
GAM167 236 LOC6392 1 17904 NM_022098.1 3 TCTCTGCCTATG AAACT A 3 C c
c
9 CAAAAATTCA TGAATTTTTG GG CAGAGA
ACTTAAAAAC CC GTCTCT
GTAT- -
GAM167 236 VIT1 1 16317 3 TCCCTGTGCAGC A A- G A 3 C c c
ATTCAAAAATCA TGA TTTTTGAA CTG ACAG GA
ACT AAAAACTT GAC TGTC CT
- AC G C
GAM168 217 LOC2209 1 3451 XM_167624.3 3 AATTTCCATTTT AC --- T 3 C c c
30 GTAAAAGCTTCT TCAGAAGCT TACA TG GAAATT
GA AGTCTTCGA ATGT AC CTTTAA
AA TTT -
GAM168 217 PIR51 1 14378 NM_006479.2 3 ATTTCAACTAGC CTACATG T 3 C c c
TTCTGA TCAGAAGCTA TGAAAT
AGTCTTCGAT ACTTTA
CA----- -
GAM168 217 PSG4 1 12119 NM_002780.1 3 AATTTCACATGT 3 C a a
AGTAGCTTCTGA TCAGAAGCTACTACATGTGAAATT
AGTCTTCGATGATGTACACTTTAA
GAM168 217 PSG7 1 2562 NM_002783.1 3 TAATTTCACATG ----- - 3 C b b
TAGTATAGGAGC TCAGAAGCT ACTACATGTGAAATT
TTCTGA AGTCTTCGA TGATGTACACTTTAA
GGATA T
GAM169 365 B29 1 9748 NM_031939.2 3 GCAAATGCAAAC G C - C 3 C c c
ATCTCTGC G AGAG ATGTT GCATTTGC
C TCTC TACAA CGTAAACG
G - A -

GAM169 365 BCMP1 1 8815 NM_031442.1 3 GGCAAATGCTGC G CA T 3 C c c
AAACTTCC GGA AG TGT GCATTTGCC
CCT TC ACG CGTAAACGG
- AA T
GAM169 365 CNNM4 1 18090 NM_020184.1 3 GGCAGGTGCACA AGCA - 3 C c c
CACCTCC GGAG TGT TGCATTTGCC
CCTC ACA ACGTGGACGG
C--- C
GAM169 365 COL1A1 1 16271 NM_000088.2 3 GGCTCTTGCAAC A C TTT 3 C c c
ATCTCCC GG GAG ATGTTGCA GCC
CC CTC TACAACGT CGG
- - TCT
GAM169 365 FECH 1 2667 NM_000140.1 3 GGCAAATGCCCA AGCA TT 3 C c c
ACCTCC GGAG TG GCATTTGCC
CCTC AC CGTAAACGG
CA-- C-
GAM169 365 FLJ1116 1 409 3 GCAAATGCTCAG A TT C 3 C c c
0 CTCTCC GGAGAGC TG GCATTTGC
CCTCTCG AC CGTAAACG
- T- -
GAM169 365 FLJ1495 1 12773 3 GGCATTTGAACA GA G TT 3 C c c
0 TGCTCCTC G GAGCATGTT CA TGCC
C CTCGTACAA GT ACGG
TC - TT
GAM169 365 G6PC 1 19886 NM_000151.1 3 GCAAGTGACATG GA TG C 3 C c c
CCATCC GGA GCATGT CATTTGC
CCT CGTACA GTGAACG
AC -- -
GAM169 365 HRLP5 1 7902 NM_054108.1 3 GCAAAAAGAACA G GCA C 3 C c c
TGCTTCC GGA AGCATGTT TTTGC
CCT TCGTACAA AAACG
- GAA -
GAM169 365 HTR3A 1 7644 NM_000869.1 3 GGCTTTAAAACA GCATTT 3 C c c
TGCTCTCT GGAGAGCATGTT GCC
TCTCTCGTACAA CGG
AATTT-
GAM169 365 IDS 1 2619 NM_000202.2 3 GGCAAATGTGAT A TG 3 C c c
GTGCTCCC GG GAGCATGT CATTTGCC
CC CTCGTGTA GTAAACGG
- GT
GAM169 365 KCNK7 1 10339 NM_033347.1 5 GGCAAATGTCTT A TGTT 3 C c c
GCCTCC GGAG GCA GCATTTGCC
CCTC CGT TGTAAACGG
- TC--
GAM169 365 KIAA063 1 19492 3 GCAAATTGAATG GTTGC C 3 C c c
0 CTCTCT GGAGAGCAT ATTTGC
TCTCTCGTA TAAACG
AGT-- -
GAM169 365 KIAA106 1 14654 XM_048786.5 3 GCAGAAAGATGC G GCA C 3 C c c

```
         1                          TCTCC      GGAGAGCAT TT   TTTGC
                                           CCTCTCGTA AA   AGACG
                                              G ---    -
GAM169   365  KIAA157 1  4142  XM_035299.2  3      GGCAAAAGTCCA     -  T- A          3  C  c  c
         7                        CATAGCTCTCC  GGAGAGC ATGT  GC TTTGCC
                                           CCTCTCG TACA  TG AAACGG
                                             A   CC  A
GAM169   365  KMO    1  6772  NM_003679.1  3      GCAAATGCATGA     C  GT      C        3  C  c  c
                                        TTTCTCT     GGAGAG AT  TGCATTTGC
                                           TCTCTT TA  ACGTAAACG
                                             -  GT       -
GAM169   365  LEFTB  1  1639  NM_020997.2  3      CAAATGCTCTGT       TT     CC        3  C  c  c
                                        GCTCTCT     GGAGAGCATG  GCATTTG
                                           TCTCTCGTGT  CGTAAAC
                                              CT      --
GAM169   365  LOC1162 1  18253 NM_138461.1  3      GGCAAATGCTGA     C  GTT             3  C  c  c
         11                       ATATTCTCC   GGAGAG AT   GCATTTGCC
                                           CCTCTT TA   CGTAAACGG
                                             A  AGT
GAM169   365  LOC1457 1  897   XM_085227.1  3      GGCAAAAGCACT       T  T  A          3  C  c  c
         57                       TGCTCTCC    GGAGAGCA GT GC TTTGCC
                                           CCTCTCGT CA CG AAACGG
                                              T  -  A
GAM169   365  LOC1465 1  9963          3      GGCAAATGTGAC    A  AT  TG             3  C  c  c
         12                       CCGCCTCC    GGAG GC  GT  CATTTGCC
                                           CCTC CG  CA  GTAAACGG
                                             -  CC  GT
GAM169   365  LOC1511 1  13174 XM_098006.2  5      GCAAATGCCAAG  G     GTT      C        3  C  c
c
         24                       TGCTCTGC    G AGAGCAT   GCATTTGC
                                           C TCTCGTG   CGTAAACG
                                            G      AAC      -
GAM169   365  LOC1517 1  11154 XM_093395.6  5      GGCAAATGCAGG -   AGCATG             3  C  c
c
         23                       ACTCCC      GGAG     TTGCATTTGCC
                                           CCTC     GACGTAAACGG
                                           C    AG----
GAM169   365  LOC1579 1  8404  XM_098845.1  3      GGCACCACAGAT       G  CATT          3  C  c  c
         31                       GCTCTCC     GGAGAGCAT TTG   TGCC
                                           CCTCTCGTA GAC    ACGG
                                              -  ACC-
GAM169   365  LOC1972 1  18112          3      GCAGAAACATGC          GCA    C        3  C  c  c
         59                       TTTCC       GGAGAGCATGTT   TTTGC
                                           CCTTTCGTACAA   AGACG
                                              ---    -
GAM169   365  LOC2207 1  7258  XM_055551.4  5      GCAAGCTCACAT      -  T- AT   C       3  C  c  c
         63                       TGCTCTCC    GGAGAGCA TGT  GC  TTGC
                                           CCTCTCGT ACA  CG  AACG
                                              T  CT  --   -
GAM169   365  LOC2220 1  15325 XM_166556.3  3      GCAAATGAAAAC     CAT  G-     C       3  C  c  c
```

68 TCTCTCC GGAGAG GTT CATTTGC
CCTCTC CAA GTAAACG
T-- AA -
GAM169 365 LOC2574 1 10209 3 GCAAATGTTGAT A GTT C 3 C c c
86 GCCTCC GGAG GCAT GCATTTGC
CCTC CGTA TGTAAACG
- GT- -
GAM169 365 LRRN3 1 11257 5 CAAATGCAAGCA - ATG CC 3 C c c
TCTTC GGAGA GC TTGCATTTG
CTTCT CG AACGTAAAC
A --- --
GAM169 365 MGC5466 1 9839 NM_030922.1 5 GCATTTGCCAAC T----- TT C 3 C c c
TTACATGCTCTC GGAGAGCATGT GCA TGC
C CCTCTCGTACA CGT ACG
TTCAAC TT -
GAM169 365 MTCH1 1 5849 NM_014341.1 3 GGCAAATGGCCC - A TTG 3 C c c
AGCTCTGCC GG AGAGC TG CATTTGCC
CC TCTCG AC GTAAACGG
G - CCG
GAM169 365 NPR1 1 2666 NM_000906.1 3 GGCACACGCACC T T ATT 3 C c c
TGCTCTCC GGAGAGCA GT GC TGCC
CCTCTCGT CA CG ACGG
C - CAC
GAM169 365 phorbol 1 1815 3 GCAAAGCAGTAT A A C 3 C c c
in-1 GCTCCC GG GAGCATGTTGC TTTGC
CC CTCGTATGACG AAACG
- - -
GAM169 365 PP1665 1 5088 NM_030792.2 5 GCAGTCACCATG T CAT C 3 C c c
CTCTCC GGAGAGCATG TG TTGC
CCTCTCGTAC AC GACG
C T-- -
GAM169 365 PPARGC1 1 16406 NM_013261.2 3 GCAAAATGATGC GTTG - C 3 C c
c
TTTCC GGAGAGCAT CATTT GC
CCTTTCGTA GTAAA CG
---- A -
GAM169 365 RGS19IP 1 5745 NM_005716.1 3 GCAAATGCAATA G A - C 3 C c c
1 ATGCCCTC GAG GCAT GTTGCATTTGC
CTC CGTA TAACGTAAACG
- C A -
GAM169 365 RPF-1 1 12622 NM_007252.1 5 GGCAAATGAGTG GTTG 3 C c c
CTCTTC GGAGAGCAT CATTTGCC
CTTCTCGTG GTAAACGG
A---
GAM169 365 SLA 1 4672 NM_006748.1 3 GGCACCAGGACT T GCATT 3 C c c
GCTCTCC GGAGAGCA GTT TGCC
CCTCTCGT CAG ACGG
- GACC-
GAM169 365 SPOCK 1 16266 NM_004598.2 3 GGCATGCACACA GC - TT 3 C c c
TATCTCC GGAGA ATGT TGCA TGCC

CCTCT TACA ACGT ACGG
A- C --
GAM169 365 UBE2L3 1 9338 NM_003347.1 3 GGCAAATGGGAT A G T G 3 C c c
TGTCCC GG GA CA GTT CATTTGCC
CC CT GT TAG GTAAACGG
- - - G
GAM169 365 WDR7 1 18603 NM_015285.1 3 GGCACGCACACA G - ATT 3 C c c
TGCTCTGC G AGAGCATGT TGC TGCC
C TCTCGTACA ACG ACGG
G C C--
GAM170 283 LOC1214 1 4519 3 TAGGCCAGGCGC TT AAA CC 3 C c c
57 AGTGG CCACTGCGC CTGG CCTA
GGTGACGCG GACC GGAT
-- --- --
GAM170 283 LOC1454 1 5675 3 AGGCCAGGCGCA TT AAA ACC 3 C c c
83 GTGG CCACTGCGC CTGG CCT
GGTGACGCG GACC GGA
-- --- ---
GAM170 283 LOC1501 1 16990 5 GGCAGGTTTCCA A G TC A 3 C c c
13 AGAGCAGGG CC CTGC CT TGGAAACCT CC
GG GACG GA ACCTTTGGA GG
- A -- C
GAM170 283 P2RY6 1 2447 NM_176796.1 3 GGCAGGGGGCGA TGGAAA A 3 C c
c
AGTGCAGTGG CCACTGCGCTTC CCT CC
GGTGACGTGAAG GGA GG
CGGG-- C
GAM170 283 SRp25 1 1331 3 GGCAGGTTTCAG C T G A 3 C c c
GGTGCCAGTGG CCACTG GC TCT GAAACCT CC
GGTGAC CG GGG CTTTGGA GG
- T A C
GAM171 392 DDX6 1 12093 NM_004397.3 3 AAGGGGCCCAGA GAG G CA 3 C c
c
AATCTG CAGGT TTCTGGGCCCCTT
GTCTA AAGACCCGGGGAA
--- - --
GAM171 392 GCKR 1 12938 NM_001486.1 3 AAGGGGCCCAAC GA T TC CA 3 C c
c
CCTGC GCAGG GT TGGGCCCCTT
CGTCC CA ACCCGGGGAA
-- - -- --
GAM171 392 KIAA004 1 5935 3 TGAAAGAAAAAG GGGCCCC 3 C c c
2 AACACTTGCTC GAGCAGGTGTTCT TTCA
CTCGTTCACAAGA AAGT
AAAAGA-
GAM171 392 KIAA103 1 8929 XM_290502.1 3 GAAGGGGCCCAG GAGCA A 3 C c
c
0 AACACC GGTGTTCTGGGCCCCTTC
CCACAAGACCCGGGGAAG
----- -

GAM171 392 KIAA103 1 13086 NM_014909.1 3 AAGGGGCCACAG G TCTG CA 3 C c c

6 CTGCTC GAGCAG TGT GGCCCCTT
CTCGTC ACA CCGGGGAA
G ---- --

GAM171 392 LOC1481 1 8770 3 TGAAGGGACCCG A- T TCT C 3 C c c

13 CTCCCAGCTC GAGC GG GT GGG CCCTTCA
CTCG CC CG CCC GGGAAGT
AC T --- A

GAM172 253 DIO2 1 4073 NM_000793.2 3 AGTTGTTAACTT C TAATTT 3 C c c

CTACATTCA C AATGT AGTTAACAACT
A TTACA TCAATTGTTGA
C TCT---

GAM172 253 PTPRC 1 11527 NM_002838.2 3 AGTTGTTAACTA 3 C a a

AATTAACATTGG CCAATGTTAATTTAGTTAACAACT
GGTTACAATTAAATCAATTGTTGA

GAM172 253 TCFL5 1 11818 NM_006602.1 3 TTGTTAACTAAA -- AA CT 3 C c c

AACAGTTTGG CCAA TGTT TTTAGTTAACAA
GGTT ACAA AAATCAATTGTT
TG -- --

GAM173 208 LOC1491 1 18849 XM_086442.1 3 ATCCACAATCCC A ATA C -- 3 C c c

57 ATTACTGGGA TC CCAGTA GTGG AT TGGAT
AG GGTCAT TACC TA ACCTA
- --- C AC

GAM173 208 SPON1 1 15969 NM_006108.1 3 ATCCAAATGTGT AATA - - 3 C c c

ACCATTGGTGA TCACCAGT GTG GCATT GGAT
AGTGGTTA CAT TGTAA CCTA
C--- G A

GAM174 252 AKAP13 1 2878 NM_007200.2 3 CCCGGAGCCCCC C GCGGA A 3 C c c

GCATATCAGCA TGC GA CGG GGCTCCGGG
ACG CT GCC CCGAGGCCC
A ATAC- C

GAM174 252 D21S205 1 3842 NM_003683.2 3 CCCAGAGCCTCC T AGC A C 3 C c c

6E GCCTGTGGC GCCG GG CGGAGGCTC GGG
CGGT CC GCCTCCGAG CCC
- GT- - A

GAM174 252 DKFZP43 1 7607 NM_015594.1 5 CCCAAAGCCCGG GGA AG CC 3 C c c

4O047 GAGCTTGGCA TGCCGAGC CGG GCT GGG
ACGGTTCG GCC CGA CCC
AGG -- AA

GAM174 252 INHBB 1 4697 NM_002193.1 5 CCCGGAGCCCGG T A GGA AG 3 C c c

AGCCCGGC GCCG GC CGG GCTCCGGG
CGGC CG GCC CGAGGCCC
- C AG- --

GAM174 252 LOC1471 1 15184 XM_294884.1 5 CCCAAAGCCTAG GGACGG CC 3 C c c
65 GAGCTTGGCA TGCCGAGC AGGCT GGG
ACGGTTCG TCCGA CCC
AGGA-- AA
GAM174 252 LOC1624 1 13555 5 CCGGGGCGCCGG C GGA AG G 3 C c c
17 CTCAGCA TGC GAGC CGG GCTCCGG
ACG CTCG GCC CGGGGCC
A --- G- -
GAM174 252 MGC1292 1 2736 NM_032728.1 5 CCCGGAGCCCCG - GGA A 3 C b b
1 CAGCTCGGGCA TGCC GAGC CGG GGCTCCGGG
ACGG CTCG GCC CCGAGGCCC
G AC- -
GAM174 252 MGC1550 1 8930 NM_032751.1 5 CCATTTCTCCGT G CTCC G 3 C c c
4 CGGCTCGGCA TGCCGAGC GACGGAGG GG
ACGGCTCG CTGCCTCT CC
G TTA- -
GAM174 252 PRKWNK2 1 20003 5 CCCGGAGCCCCC T A GA-- A 3 C c c
GCGGACGCCGGC GCCG GCG CGG GGCTCCGGG
CGGC CGC GCC CCGAGGCCC
- - AGGC C
GAM174 252 TPD52L2 1 18571 NM_003288.1 5 CCCGGCGCCGCC T ACGGA T 3 C c c
CGCTCGGC GCCGAGCGG GGC CCGGG
CGGCTCGCC CCG GGCCC
- CG--- C
GAM174 252 USP20 1 554 NM_006676.1 3 CCCGGAGCCCCG TG CGGA A 3 C c c
AAGACTCGG CCGAG CGG GGCTCCGGG
GGCTC GCC CCGAGGCCC
-- AGAA -
GAM175 265 AASDHPP 1 16747 NP_056238.2 3 607 GGAAATTGTTTG CAAG 4 B c c
T ACATAACACAGG GACCCTGTGTT GTTAGG
GTTCAGGG TTGGGACACAA CAGTTT
TA--
GAM175 265 ADAR 1 13257 NP_001102.1 3 2176 CTCTTCTTTAAC C AA 4 B c c
TGGGAACACAGG GA CCTGTGTTC GGTTAGGG
CTCTCACA CT GGACACAAG TCAATTTC
C GG
GAM175 265 ADAR 1 13257 NP_056655.1 3 2176 CTCTTCTTTAAC C AA 4 B c c
TGGGAACACAGG GA CCTGTGTTC GGTTAGGG
CTCTCACA CT GGACACAAG TCAATTTC
C GG
GAM175 265 ADAR 1 13257 NP_056656.1 3 2176 CTCTTCTTTAAC C AA 4 B c c
TGGGAACACAGG GA CCTGTGTTC GGTTAGGG
CTCTCACA CT GGACACAAG TCAATTTC
C GG

GAM175 265 AFAP 1 7185 NP_067651.1 3 3012 TTCCATTCTAAC C - 4 B c c
CTTGAGCCACAG GAC CTGTG TTCAAGGTTAGGG
TGTCACTC CTG GACAC GAGTTCCAATCTT
T C
GAM175 265 ANXA8 1 15378 NP_001621.1 3 390 CCCATTCCCATC G -- TA 4 B c c
TACTGAAACAGG GACCCTGT TTCA AGGT GGG
GTCTCCAC CTGGGACA AAGT TCTA CCC
- CA --
GAM175 265 APAF1 1 12211 NP_001151.1 3 897 CCCTTCTCTTTT G ----- TT 4 B c c
AATGGAGACAGG GACCCTGT TTCA AGG AGGG
GTCTTGCA CTGGGACA AGGT TCT TCCC
G AATTT CT
GAM175 265 APAF1 1 12211 NP_037361.1 3 897 CCCTTCTCTTTT G ----- TT 4 B c c
AATGGAGACAGG GACCCTGT TTCA AGG AGGG
GTCTTGCA CTGGGACA AGGT TCT TCCC
G AATTT CT
GAM175 265 APOL1 1 10954 NP_003652.2 3 1246 GCATGTCCCCTG A --- GT 4 B c c
CTTGAACACTGA G CCCT GTGTTCAAG TAGGG
AGGGCAGG C GGGA CACAAGTTC GTCCC
- AGT --
GAM175 265 APOL1 1 10954 NP_663318.1 3 1246 GCATGTCCCCTG A --- GT 4 B c c
CTTGAACACTGA G CCCT GTGTTCAAG TAGGG
AGGGCAGG C GGGA CACAAGTTC GTCCC
- AGT --
GAM175 265 APOL1 1 10954 NP_663319.1 3 548 GCATGTCCCCTG A --- GT 4 B c c
CTTGAACACTGA G CCCT GTGTTCAAG TAGGG
AGGGCAGG C GGGA CACAAGTTC GTCCC
- AGT --
GAM175 265 ARF4 1 16305 NP_001651.1 3 563 GCCAAACTTAAC TG GTT 4 B c c
CTTGGTGGGGTT GACCC T CAAGGTTAGG
TGGATTTG TTGGG G GTTCCAATTC
GT ---
GAM175 265 ARHGEF2 1 10786 NP_004714.2 3 367 GAGGGCCTTGTC G- ---- T 4 B c c
CTTGAACACTAC ACCCT GTGTTCAAGG TAGGG
TGGGGTAT TGGGG CACAAGTTCC GTTCC
TA TCAT T
GAM175 265 ARHGEF9 1 527 NP_056000.1 3 1214 CTTCAAATTATT GT A G 4 B c c
GACCTGGACAGG GACCCTGT TCA GGTTAG
GTCCAAGT CTGGGACA GGT CCAGTT
-- - A
GAM175 265 ARNT2 1 16746 NP_055677.1 3 3731 CTGTCTCCTAAC T TCA 4 B c c
CTGCCGGGGTCA GACCCTG GT AGGTTAGGG
TTCCCCAC CTGGGGC CG TCCAATCCT
- ---
GAM175 265 ART5 1 13679 NP_443750.2 5 227 GGATCCCGTGCG G A TA-- 4 B c c
CCTGGAGACAGG GACCCTGT TTCA GGT GGG

GTCCAGAT CTGGGACA AGGT CCG CCC
G - CGTG

GAM175 265 C10orf2 1 3494 NP_068602.1 3 140 GAGGGGCCTAAC CTG A 4 B c c
CTAGAGCAGGTT GACC TGTTC AGGTTAGG
TCCATAGT TTGG ACGAG TCCAATCC
--- A

GAM175 265 C14orf3 1 18001 XP_085124.2 3 459 ACTCTACCTACT -- GT 4 B c c
7 TGAAACCACAGG GACCCTGTG TTCAAG TAGG
GTTGTGGG TTGGGACAC AAGTTC ATCC
CA --

GAM175 265 C1orf34 1 10527 XP_027172.1 3 606 GCCAAATCCCTA C- AG 4 B b b
ACTGAACACAGA GAC CTGTGTTCA GTTAGGG
TGTCTCAG CTG GACACAAGT CAATCCC
TA --

GAM175 265 C5orf7 1 449 NP_057688.1 5 396 CCCTACAGTGTT TT------ AG T 4 B c c
CAAGGTCACAGG GACCCTGTG CA GT AGGG
GTCAAAAT CTGGGACAC GT CA TCCC
TGGAACTT GA -

GAM175 265 CCR2 1 13143 NP_000639.1 3 545 CGTGTATTTAAC CT ----- 4 B c c
CTTGAAGGGTTC GACC GTG TTCAAGGTTAGG
ACCAGGTC CTGG CAC AAGTTCCAATTT
AC TTGGG

GAM175 265 CCRN4L 1 708 NP_036250.2 3 290 CGATCTCCTGAC C - - 4 B c c
CTTGAATCACAA GAC CT GTG TTCAAGGTTAGGG
GAGTCTTA CTG GA CAC AAGTTCCAGTCCT
A A T

GAM175 265 CHDC1 1 13850 XP_166260.1 5 362 CTTCAACCTGCC T T 4 B b b
CTTGAACCGGGG GACCCTG GTTCAAGG TAGG
TCTGGAGC CTGGGGC CAAGTTCC GTCC
- C

GAM175 265 CHST5 1 1259 NP_036258.1 5 239 CCTCTGGCTTTC C- ---- 4 B c c
CTGGAACACAGA GAC CTGTGTTC AAGGTTAGGG
TGTCGAGA CTG GACACAAG TTTCGGTCTC
TA GTCC

GAM175 265 COPS7A 1 15229 NP_057403.1 3 148 ACCTCCCCTAAC CC CAA 4 B c
c
CCCAAACATAGA GA CTGTGTT GGTTAGGG
TCACACCT CT GATACAA CCAATCCC
A- ACC

GAM175 265 CSE1L 1 17881 NP_001307.2 3 168 TTTAACCTGAAC -- --- - 4 B c c
CTTGAGCAAATT GACC CTG TGTTCAAGGT TAGG
AGTTGGTT TTGG GAT ACGAGTTCCA GTCC
TT TAA A

GAM175 265 CSE1L 1 17881 NP_803185.1 3 1292 TTTAACCTGAAC -- --- - 4 B c c
CTTGAGCAAATT GACC CTG TGTTCAAGGT TAGG
AGTTGGTT TTGG GAT ACGAGTTCCA GTCC
TT TAA A

GAM175 265 CTNNA2 1 1392 NP_004380.1 3 507 GAACAATTTAAC CCTGTG 4 B c
c
CTTGAAGTCTAT GAC TTCAAGGTTAGG

ATCCGTGA CTG AAGTTCCAATTT

GAM175 265 CTNNBIP 1 17490 NP_064633.1 3 520 CCTATTTTGAAT ------- T 4 B c c
1 GCAGAAAACAGG GACCCTGT GTTCAAGGT AGG
GTCTGGGA CTGGGACA TAAGTTTTA TCC
AAAGACG -
GAM175 265 CTNND1 1 18658 NP_001322.1 3 2491 GACAAAACTAAC AC G G 4 B c
c
CTTGAATAAGGC G CCT TGTTCAAGGTTAG
CCACTGTA C GGA ATAAGTTCCAATC
CC - A
GAM175 265 DAPK1 1 10219 NP_004929.1 3 31 GGGGCAGCCTCT GT G 4 B c c
GGCTTGGACAGG GACCCTGT TCAAG TTAGGG
GTCTGTTT CTGGGACA GGTTC GGTCTC
-- -
GAM175 265 DCLRE1C 1 8700 NP_071932.1 5 214 AAGAGCCCCTAC CTGTG T 4 B c
c
CTTGAAAAGAAG GACC TTCAAGGT AGGG
GTTGGAGT TTGG AAGTTCCA TCCC
AAGAA -
GAM175 265 DIAPH2 1 5513 NP_006720.1 3 202 CAATTATTCTAA CC- A 4 B c c
TCTGAACACAGT GA CTGTGTTCA GGTTAGGG
TATCAGGA CT GACACAAGT CTAATCTT
ATT -
GAM175 265 DKFZp43 1 15093 XP_087065.1 3 2387 TGTCAGTCCCAC C G TA 4 B c
c
4G179 CTTGAAGACAGA GAC CTGT TTCAAGGT GGG
GTTCCAGG TTG GACA AAGTTCCA CCC
A G --
GAM175 265 DKFZP43 1 10923 NP_056307.1 3 370 GGACAACGCAAC TTCA T 4 B c
c
4H132 CTACCTCACAGG GACCCTGTG AGGT AGG
GTTGTTGT TTGGGACAC TCCA TCC
---- -
GAM175 265 DKFZP43 1 2795 NP_115505.1 3 272 AGGGAGGTCCTG TTCAA 4 B c
c
4H2010 GCCGTCCACAGG GACCCTGTG GGTTAGGG
GTCGGCCC CTGGGACAC CCGGTCCT
CTG--
GAM175 265 DKFZp43 1 6806 NP_115632.1 3 386 CAGTTACCTAAC A - TTCA 4 B c c
4K2435 CTATTTCACATG G CCC TGTG AGGTTAGG
GGCGTTTT C GGG ACAC TCCAATCC
- T TTTA
GAM175 265 DKFZp76 1 10041 NP_689874.1 3 401 AACCACCTCCTG A AG 4 B c c
1G0122 GCTGGACACAGG G CCCTGTGTTCA GTTAGGG
GCAAGTTG C GGGACACAGGT CGGTCCT
- --
GAM175 265 ED1 1 3738 NP_001390.1 3 889 CAGGTGCCTAAC CTGT A 4 B c c

CTGGGACCTGTG GACC GTTC AGGTTAGG
GTCATGTG CTGG CAGG TCCAATCC
TGTC G

GAM175 265 EDG1 1 5089 NP_001391.2 5 215 ACCCCGGCTTCC A- TTA-- 4 B c c
TGGGGACACAGG GACCCTGTGTTC AGG GGG
GTTGGCAC TTGGGACACAGG TCC CCC
GG TTCGG

GAM175 265 EPN2 1 3856 NP_055779.1 3 313 CTTGCCCCTAAC - T CA 4 B c c
CTCAGCCCGAGG GACCCT G GTT AGGTTAGGG
GTCTCCAG CTGGGA C CGA TCCAATCCC
G C C-

GAM175 265 EPN2 1 3856 NP_683723.1 3 313 CTTGCCCCTAAC - T CA 4 B c c
CTCAGCCCGAGG GACCCT G GTT AGGTTAGGG
GTCTCCAG CTGGGA C CGA TCCAATCCC
G C C-

GAM175 265 FEM1A 1 18114 NP_061178.1 3 155 CCATCCCCTCTA GTTCA T- 4 B c
c
CCTGCAGACAGG GACCCTGT AGGT AGGG
GTCGGAGG CTGGGACA TCCA TCCC
GACG- TC

GAM175 265 FLJ1052 1 2136 NP_060594.2 3 1143 TGCCTCCCTAAC - TGTTC 4 B c
c
0 CTTTTCTAGGGC GA CCCTG AAGGTTAGGG
TCAGTTTG CT GGGAT TTCCAATCCC
C CTT--

GAM175 265 FLJ1128 1 5419 NP_060851.1 3 833 CTCTGCCCTTTA - GT GTT 4 B c c
6 CTTGAACAGGAG GAC CCTGT TCAAG AGGG
TCTTGATT CTG GGACA AGTTC TCCC
A -- ATT

GAM175 265 FLJ1170 1 12317 NP_079168.1 3 476 GGCCCTTCAGCC G - -- 4 B c c
0 TTTGGGAACAGG GACCCTGT TTCAA GGTT AGGG
GTCAGCAT CTGGGACA GGGTT CCGA TCCC
A T CT

GAM175 265 FLJ1224 1 6997 NP_078957.1 3 359 CTCCCACCCCAC TTCA TA 4 B c
c
2 CTACCTCACAGG GACCCTGTG AGGT GGG
GTTGTTGT TTGGGACAC TCCA CCC
TCCA C-

GAM175 265 FLJ1308 1 16448 NP_079110.1 3 1303 GAAATTGTTAAC G AA G 4 B c c
1 CAAGGAAACAGG GACCCTGT TTC GGTTAG
GTCAGCCT CTGGGACA AGG CCAATT
A AA G

GAM175 265 FLJ1324 1 14121 NP_079364.1 3 678 AGACGTGGCCTT --- GG 4 B c c
1 GAAGCCCACAGG GACCCTGTG TTCAAGGTTA
GTTGATGG TTGGGACAC AAGTTCCGGT
CCG GC

GAM175 265 FLJ1354 1 9579 NP_079284.1 5 102 CATGGCTAGGCC - AA TA 4 B c c
4 CAGAAACACAGG GACCCTGTGTT C GGT GG
GTCCAACC CTGGGACACAA G CCG TC

A AC GA

GAM175 265 FLJ2186 1 10496 NP_073606.1 5 142 CTTCTTGGGGAC --- AGG 4 B c c
8 CTTGAACACTGG GACCCT GTGTTCAAGGTT
AGGGTCAT CTGGGA CACAAGTTCCAG
GGT GGG

GAM175 265 FLJ2216 1 1259 NP_078809.2 5 116 CCTCTGGCTTTC C- ---- 4 B c c
7 CTGGAACACAGA GAC CTGTGTTC AAGGTTAGGG
TGTCGAGA CTG GACACAAG TTTCGGTCTC
TA GTCC

GAM175 265 FLJ2257 1 15094 NP_079140.1 3 518 GGGACTCTGCAC TTCA - 4 B c c

8 CTACCTCACAGG GACCCTGTG AGGT TAGGG
GTTGTTGT TTGGGACAC TCCA GTCTC
TCCA C

GAM175 265 FLJ2375 1 543 NP_689888.1 3 793 AAGAGCTCCAGA TCA AG- 4 B c c

4 AATCTGCACAGG GACCCTGTGT AGGTT GG
GTTCTCTT TTGGGACACG TCTAA CC
--- AGA

GAM175 265 FLJ3692 1 15645 NP_775822.1 3 1004 CCCTCTCCAAGG A - A---- TT 4 B c
c
8 CTGAGACACAGG G CCCTGTGT TCA GG AGGG
GCATGGCC C GGGACACA AGT CC TCCC
- G CGGAA TC

GAM175 265 FLJ3905 1 1228 NP_775851.1 3 314 TTTAGCCTGAAC - GTGT - 4 B c c
8 CTTGAAGGTGTT GAC CCT TCAAGGT TAGG
TGTTCAGA TTG GGA AGTTCCA GTCC
T ---- A

GAM175 265 FLJ3950 1 7439 NP_775754.1 3 271 ACCTGTCCTGTT GT-- --- T 4 B c c
1 TGAGGGAACAGG GACCCTGT TCA AGG TAGG
GTCGACCC CTGGGACA AGT TCC GTCC
AGGG TTG T

GAM175 265 FPGS 1 7959 NP_004948.2 3 796 TTCTGCCCTAAC - G CA 4 B c c
CTGACAGAGGTG GAC CCT TGTT AGGTTAGGG
TCATCCAC CTG GGA ACAG TCCAATCCC
T G --

GAM175 265 GALE 1 6061 NP_000394.1 3 211 TCTCTAACTCTT TTC--- - 4 B c c
ATCTTCCACAGG GACCCTGTG AAG GTTAGGG
GTCCAAGA CTGGGACAC TTC CAATCTC
CTTCTA T

GAM175 265 GFAP 1 3851 NP_002046.1 3 572 GCCTAGGCTGAC - TGT- G 4 B c c
CTTGAACTCCTG GA CCC GTTCAAGGTTAG
GGCTCAAG CT GGG CAAGTTCCAGTC
C TCCT G

GAM175 265 GPR44 1 5220 NP_004769.1 3 679 AGTTTCAGGGCT T AAG G 4 B c c

AACGACCACAGG GACCCTGTG TC GTTAG
GTCTGCAC CTGGGACAC AG CAATC
C --- G

GAM175 265 GSG1 1 8755 NP_722545.1 3 618 GAGAAGGCGCCA TCAAG A 4 B c
c

ACAGCACACAGG GACCCTGTGT GTT GG
GTCAGGGT CTGGGACACA CAA CC
CGA-- -
GAM175 265 HCNGP 1 12212 NP_037392.1 3 187 CGGGAGCCAGGC GT - - TA 4 B c c
GCTGTGGACAGG GACCCTGT TCA AG GT GG
GTCTGTCC CTGGGACA GGT TC CG CC
-- G G GA
GAM175 265 HS6ST2 1 12074 NP_671704.2 3 1808 ATTTTTCCACAC C -- TA 4 B c c
CTTGAAGTCACA GAC CTGTG TTCAAGGT GGG
GTGTTTTA TTG GACAC AAGTTCCA CCT
T TG CA
GAM175 265 IL18BP 1 17825 NP_005690.1 3 263 CAGCAGCACAAC TGT AA 4 B c c
CTTGACCAGAGC GACCC GTTC GGTTAGGG
TTGGGTCC CTGGG CGAG CCAGTTCC
TT- A-
GAM175 265 IL18BP 1 17825 NP_766630.1 3 47 CAGCAGCACAAC TGT AA 4 B c c
CTTGACCAGAGC GACCC GTTC GGTTAGGG
TTGGGTCC CTGGG CGAG CCAGTTCC
TT- A-
GAM175 265 KIAA019 1 7054 NP_055581.2 3 170 CTTGTGTTCCAC C --- TA 4 B c c
3 CTTGAATCTCAC GAC CTGTG TTCAAGGT GGG
AGCGTCCC CTG GACAC AAGTTCCA CCT
C TCT --
GAM175 265 KIAA035 1 6463 NP_055687.1 3 1852 TGTGAGATTAAC -- - G 4 B c c
4 CTTGGGACACAG GACCC TGTGTTC AAGGTTAG
TGGGTTAG TTGGG ACACAGG TTCCAATT
TG G A
GAM175 265 KIAA047 1 4764 NP_055685.1 3 2198 CTGTCACCCAGA A - AA A 4 B c c
8 CTGGAACACAGT G CC CTGTGTTC GGTT GGG
GGCACGAT C GG GACACAAG TCAG CCC
- T G- A
GAM175 265 KIAA049 1 11550 XP_034717.1 3 1210 GTATAACTTAAC C T- 4 B c c
3 CTTGATTTATAA GACC TGTG TCAAGGTTAGG
GGTCTTAA CTGG ATAT AGTTCCAATTC
A TT
GAM175 265 KIAA060 1 9931 NP_055509.1 5 436 GTCCCAGATAAC A T- G --- 4 B c c
5 CTTGAGGCCTGG G CCC GT TTCAAGGTTA GGG
GCACTGGC C GGG CG GAGTTCCAAT CCC
- TC - AGA
GAM175 265 KIAA167 1 6252 XP_037809.1 3 4619 TATTTTCCTAAC TGTGTTC 4 B c c
1 CTTTCTTCTGGG GACCC AAGGTTAGGG
TCCTTCCT CTGGG TTCCAATCCT
TCTTCT-
GAM175 265 KIAA172 1 15320 XP_034262.4 3 1108 CAGAGTTTCACC TCAA T 4 B c c
7 TGCCCACACAGG GACCCTGTGT GG TAGG

GTCCGTTG CTGGGACACA CC GTCC
---- C

GAM175 265 KIAA180 1 13721 NP_115811.1 3 598 AAACTACCTAAC A TGT T 4 B c c

4 CTTGGCTGTGGG G CCC GT CAAGGTTAGG
CCGATAAT C GGG CG GTTCCAATCC
C TGT -

GAM175 265 KIAA185 2 4361 XP_040592.3 3 601 ATGCCTCCTCCC T AG TT 4 B c c

8 TCTGACCACAGG GACCCTGTG TCA G AGGG
GTCATGCC CTGGGACAC AGT C TCCT
C CT CC

GAM175 265 KIAA185 2 7750 XP_040592.3 3 574 AGGCCTCCTCCC T AG TT 4 B c c

8 TCTGACCACAGG GACCCTGTG TCA G AGGG
GTCATGCC CTGGGACAC AGT C TCCT
C CT CC

GAM175 265 KL 1 5056 NP_004786.2 3 1360 CATTGCCAACCT CA-- A 4 B c c
CACTGACACAGG GACCCTGTGTT AGGTT GG
GTCATAGT CTGGGACACAG TCCAA CC
TCAC -

GAM175 265 KL 1 5056 NP_710150.1 3 2796 CATTGCCAACCT CA-- A 4 B c c
CACTGACACAGG GACCCTGTGTT AGGTT GG
GTCATAGT CTGGGACACAG TCCAA CC
TCAC -

GAM175 265 KLHL3 1 2953 NP_059111.1 3 3603 CTTGTCTCTAAC GTG- C 4 B c c
CTTTAAAAGAGG GACCCT TT AAGGTTAGGG
GGTCAATC CTGGGG AA TTCCAATCTC
AGAA T

GAM175 265 KRTAP4- 1 7123 NP_114060.1 3 338 AAAGCCTCCAAC C--- TG- -- 4 B c c

12 CTTGAAGTCCAG GAC CTG TTCAAGGTT AGG
TGAAGTCT CTG GAC AAGTTCCAA TCC
AAGT CTG CC

GAM175 265 LAMA4 1 11842 NP_002281.1 3 192 TGGATTCTTAAC C GT-- 4 B c c
CTTGAATCCAAA GAC CT GTTCAAGGTTAGGG
GTGTCTGC CTG GA TAAGTTCCAATTCT
T AACC

GAM175 265 LAMC1 1 18303 NP_002284.2 3 1808 GATGATCCTAAC - CA 4 B c c
CTGCAGCACGGT GACC CTGTGTT AGGTTAGGG
GGTTTTAC TTGG GGCACGA TCCAATCCT
T CG

GAM175 265 LCP2 1 2817 NP_005556.1 3 124 TGAACCCCTCCC - A TT 4 B c c
CATGAACACAAG GACCCT GTGTTCA GG AGGG
GGTTTTAT TTGGGA CACAAGT CC TCCC
A A CC

GAM175 265 LOC1184 1 9284 XP_060969.2 5 356 GAAACACCTAAC CC TGT 4 B c
c

61 CTTGACAGAATC GA CTG TCAAGGTTAGG
ATCACCAG CT GAC AGTTCCAATCC
AA ---

GAM175 265 LOC1222 1 13483 XP_063046.4 3 1183 CTGGACCCCTGC G AA T 4 B c c
82 TAGGAGGACAGG GACCCTGT TTC GGT AGGG
GTCCCCTC CTGGGACA GAG TCG TCCC
G GA -
GAM175 265 LOC1251 1 16189 XP_064442.3 3 205 GCCCCCACCCTT GTTCA 4 B c c
15 GACCTCAACAGG GACCCTGT AGGTTAGGG
GTCCTGGA CTGGGACA TCCAGTTCC
AC---
GAM175 265 LOC1456 1 4216 XP_096817.1 3 498 CTGAAGCCAGCT - AG A 4 B c c
09 CTGAGTCACAGG GACCCTGTG TTCA GTT GG
GTTGCCTT TTGGGACAC GAGT CGA CC
T CT -
GAM175 265 LOC1473 1 3191 XP_097230.2 5 87 AACGACCCTGGC GA ------- 4 B c c
81 CTTGAACGTCAG CCCTG TGTTCAAGGTTAGGG
AGCCGGGG GGGGC GCAAGTTCCGGTCCC
-- CGAGACT
GAM175 265 LOC1509 1 17201 XP_097971.1 3 1807 TGATCATCTAAC TGT TC 4 B c c
33 CTTACCTGGGTC GACCC GT AAGGTTAGG
CTCAGCTA CTGGG CA TTCCAATCT
TC- --
GAM175 265 LOC1512 1 4667 XP_098021.1 3 845 TGTATACACTTA TGT - 4 B c c
01 CATTTTGACAGG GACCCTG TCAAGGT TAGG
GTCTTCAT CTGGGAC AGTTTTA ATTC
--- C
GAM175 265 LOC1530 1 2394 XP_098307.1 3 474 AATAAAGTTTAA - AA 4 B c c
77 CTGGAACACAGC GACC CTGTGTTC GGTTAGG
GGTTCATG TTGG GACACAAG TCAATTT
C G-
GAM175 265 LOC1533 1 19725 XP_098364.1 3 54 GGCTTTCCCTGA GTT AG 4 B c c
46 CTCTGCGACAGG GACCCTGT CA GTTAGGG
GTCAAACC CTGGGACA GT CAGTCCC
GC- CT
GAM175 265 LOC1578 1 11755 XP_098833.2 3 821 TGAGCCCCTAAC - TGT A 4 B c c
58 CCTGATCCAGGG GA CCCTG TCA GGTTAGGG
ATCGTTGA CT GGGAC AGT CCAATCCC
A CT- C
GAM175 265 LOC1585 1 3708 XP_088606.1 3 795 TAATTGCCCTAC TTCA T 4 B c c
63 CTACCTCACAGG GACCCTGTG AGGT AGGG
GTTGTTGT TTGGGACAC TCCA TCCC
TCCA -
GAM175 265 LOC1588 1 4444 XP_088691.1 3 153 CCTTCTTTGCCT TT TT 4 B c c
33 TCTTGCCACAGG GACCCTGTG CAAGG AGG
GTCCTTAC CTGGGACAC GTTCT TCC
C- --

GAM175 265 LOC1620 1 9512 XP_091339.2 5 1038 CACCGCCTATCC CC A- T 4 B c c
83 TGAGAACACAGT GAC TGTGTTC AGG TAGG
CAGTGAGG CTG ACACAAG TCC ATCC
-- AG T
GAM175 265 LOC1973 1 14413 XP_113869.1 3 2857 TGAGCAGACCTG TTCAA 4 B c c
42 GCTCACCACAGG GACCCTGTG GGTTAGG
GTCCTACT CTGGGACAC TCGGTCC
CAC--
GAM175 265 LOC2001 1 4520 XP_114148.1 3 1385 CTTCTTGCCGAC C G A 4 B c c
97 CTTGAAGCAGAG GAC CTGT TTCAAGGTT GG
TTGACGTT TTG GACG AAGTTCCAG CC
A - -
GAM175 265 LOC2017 1 3083 XP_114370.1 3 494 TATATCCCCAGC GTTCA TA- 4 B c c
25 ACCTAAAACAGG GACCCTGT AGGT GGG
GTCACACA CTGGGACA TCCA CCC
AAA-- CGA
GAM175 265 LOC2197 1 7954 XP_167570.1 3 93 TTCTGCCCTCCC -- A TT 4 B c c
00 TGAGCCCACAGG GACCCTGT GTTCA GG AGGG
GTCAGTCA CTGGGACA CGAGT CC TCCC
CC C --
GAM175 265 LOC2531 1 6541 XP_173229.1 5 154 AAGAATCCTAAC G TTCA 4 B c c
42 CTCAAAGGGTCG GACCCT TG AGGTTAGGG
TGGTGAGA CTGGGA AC TCCAATCCT
A ----
GAM175 265 LOC2829 1 11235 XP_212579.1 3 834 ACACACACCCCA TCAAG TA 4 B c c
15 CAGGCACACAGG GACCCTGTGT GT GGG
GTCAAGAA CTGGGACACA CA CCC
CGGA- C-
GAM175 265 LOC2829 1 11235 XP_212627.1 3 834 ACACACACCCCA TCAAG TA 4 B c c
51 CAGGCACACAGG GACCCTGTGT GT GGG
GTCAAGAA CTGGGACACA CA CCC
CGGA- C-
GAM175 265 LOC2829 1 4866 XP_210838.1 3 747 AATGTGGCCTTA G GTT 4 B c c
76 TTTGGAGACAGG GACCCTGT TTCAAG AGG
GTCTTCAC CTGGGACA AGGTTT TCC
G AT-
GAM175 265 LOC2831 1 17440 XP_210900.1 3 1198 ACCCCAAATCAC T A--- A 4 B c c
26 ACTGCACACAGG GACCCTGTGT CA GGTT GGG
GTCCCTGA CTGGGACACA GT CTAA CCC
C CACA A
GAM175 265 LOC2831 1 2594 XP_210925.1 5 512 TATTTGACTGTA G ---- 4 B c c
42 TTTGGAGACAGG GACCCTGT TTCAA GGTTAGG
GTCTTTAC CTGGGACA AGGTT TCAGTTT

G TATG
GAM175 265 LOC2834 1 15588 XP_211061.1 3 752 GGGGATCTATAA GTT GG 4 B c c
82 TCTTGTAACAGG GACCCTGT CAAGGTTA
GTCTATCT CTGGGACA GTTCTAAT
AT- AT
GAM175 265 LOC2836 1 11064 XP_211152.1 3 258 ATCTCTCTTGCT TTC- T 4 B c c
72 TTTCCCCACAGG GACCCTGTG AAGGT AGGG
GTCAAGGT CTGGGACAC TTTCG TCTC
CCCT T
GAM175 265 LOC2838 1 15537 XP_211235.1 3 900 GGGAACTGGCTT G-- G 4 B c c
59 TGAGATGACAGG GACCCTGT TTCAAGGTTAG
GTCCAGGA CTGGGACA GAGTTTCGGTC
GTA A
GAM175 265 LOC2840 1 17268 XP_211322.1 3 914 ATTGGTCCTGTG G GGT 4 B c c
80 GTTGGAAACAGG GACCCTGT TTCAA TAGGG
GTCAAGTA CTGGGACA AGGTT GTCCT
A GGT
GAM175 265 LOC2841 1 9262 XP_211338.2 5 249 ACGTCTATTTCC - CA T--- 4 B c c
16 CTCAGACACAGG GA CCCTGTGTT AGG TAGG
GATCCTTG CT GGGACACAG TCC ATCT
A AC CTTT
GAM175 265 LOC2842 1 17027 NP_787104.1 3 711 CCCAGCCATCTG GT ------ A 4 B c c
96 ATTGGTGACAGG GACCCTGT TCAA GGTT GGG
GTCAACCC CTGGGACA GGTT CCGA CCC
GT AGTCTA -
GAM175 265 LOC2844 1 5767 XP_211475.1 3 832 CAGGTCCCCAAG TTC TTA-- 4 B c c
62 TCCCTTCACAGG GACCCTGTG AAGG GGG
GTCCCCAC CTGGGACAC TTCC CCC
--- CTGAA
GAM175 265 LOC2845 1 11550 XP_209263.1 3 1035 GTATAACTTAAC C T- 4 B c c
68 CTTGATTTATAA GACC TGTG TCAAGGTTAGG
GGTCTTAA CTGG ATAT AGTTCCAATTC
A TT
GAM175 265 LOC2848 1 8040 XP_211672.1 5 19 CGCAGCTGGGGC TCA A- 4 B c c
65 CTGGCACACAGG GACCCTGTGT AGGTT GG
GTCCCTGT CTGGGACACA TCCGG TC
CGG GG
GAM175 265 LOC2849 1 17065 XP_211721.1 3 91 TACATCACTCAA GA----- A A 4 B c c
82 CCTGAACACAGG CCCTGTGTTCA GGTT GGG
GGAGGCAG GGGACACAAGT CCAA CTC
GACGGAG - -
GAM175 265 LOC2849 1 10924 XP_211722.1 3 38 CTGGATCTTGAC CC T 4 B c c
93 CTTGAACTGGAC GA CTG GTTCAAGGTTAGGG
TCTGTAGG CT GGT CAAGTTCCAGTTCT

CA -

GAM175 265 LOC2850 1 19445 XP_209440.1 3 400 AAATACCCTAAC CCTGT C 4 B c c

26 CTTTAACTGTCT GAC GTT AAGGTTAGGG
TGAATTAT CTG CAA TTCCAATCCC
T---- T

GAM175 265 LOC2852 1 17158 XP_211809.1 3 95 CAGCTTCCTAAC A GTGT 4 B c c

22 CTTGAGGGGCCA G CCCT TCAAGGTTAGGG
GAGAACAA C GGGG AGTTCCAATCCT
C ----

GAM175 265 LOC2852 1 6284 XP_211812.1 5 1969 AGTTTCCTCATT GTT- T 4 B c c

29 TTGTTTGACAGG GACCCTGT CAAGGT AGGG
GTCCTCAG CTGGGACA GTTTTA TCCT
GTTT C

GAM175 265 LOC2852 1 2395 XP_211813.1 3 1231 GGGCCTGAGATC G- A- 4 B c c

31 TTGAGAGACAGG GACCCTGT TTCAAGGTT GGG
GTCTCACT CTGGGACA GAGTTCTAG TCC
GA AG

GAM175 265 LOC2852 1 1260 XP_208303.1 3 12 CAGCCAGTCCCT TCAAG T 4 B c c

46 ACAGCATACAGG GACCCTGTGT GT AGGG
GTCTCCTT CTGGGACATA CA TCCC
CGA-- -

GAM175 265 LOC2853 1 8111 XP_208316.1 5 313 GCGCCATGAATC - TCAA T 4 B c c

88 CTGCCACACAGG GA CCCTGTGT GGT AGGG
GATCAAGG CT GGGACACA CCG TCCT
A ---- -

GAM175 265 LOC2854 1 10871 XP_209613.1 3 905 AGGTGCCCCTGC A T 4 B b b

38 CTGGAGCACAGG GACCCTGTGTTC AGGT AGGG
GTCCCACG CTGGGACACGAG TCCG TCCC
G -

GAM175 265 LOC2854 1 8485 XP_209633.1 5 414 AAGTTCCCTAAC CC CA--- 4 B c c

86 CTCTCCCAACAC GA CTGTGTT AGGTTAGGG
AGCCTCCA CT GACACAA TCCAATCCC
CC CCCTC

GAM175 265 LOC2856 1 12446 XP_209676.1 5 2144 AAGTCTCCTAAC TGTGTTC 4 B c c

02 CTTCCTGGGTCT GACCC AAGGTTAGGG
GTTTTCTT CTGGG TTCCAATCCT
TCC----

GAM175 265 LOC2857 1 19064 XP_212007.1 3 437 GGCCCACCCAAC C GTG A 4 B c c

45 CTTGAAGAGAGT GAC CT TTCAAGGTT GGG
CAAGTCTA CTG GA AAGTTCCAA CCC
A G-- -

GAM175 265 LOC2857 1 1009 XP_209742.1 5 1316 CCTAAGCCTGGC TTCAA 4 B c c

47 CCTATCCACAGG GACCCTGTG GGTTAGG
GTCCCTGG CTGGGACAC CCGGTCC
CTATC
GAM175 265 LOC2857 1 19355 XP_208349.1 3 2537 AAGTCCTCCCAC C G-- TA 4 B c c
86 CTTGAAGAGACA GA CCTGT TTCAAGGT GGG
GGCTCTGA CT GGACA AAGTTCCA CCC
C GAG --
GAM175 265 LOC2858 1 6025 XP_212027.1 5 364 ACGCCCCTGCCC TCAA 4 B c c
05 TGGCCGCACAGG GACCCTGTGT GGTTAGGG
GTTGGGTT TTGGGACACG CCGGTCCC

GAM175 265 LOC2858 1 11235 XP_209790.1 3 830 ACACACACCCCA TCAAG TA 4 B c c
33 CAGGCACACAGG GACCCTGTGT GT GGG
GTCAAGAA CTGGGACACA CA CCC
CGGA- C-
GAM175 265 LOC2859 1 20077 XP_212092.1 5 883 GCTCACTATAAC - TGT- G 4 B c c
45 CTTGAACTCCTG GA CCC GTTCAAGGTTA GG
GGCTCAAG CT GGG CAAGTTCCAAT TC
C TCCT A
GAM175 265 LOC2859 1 9866 XP_212126.1 5 572 GGATGAAGGCTG AA T G 4 B c c
92 CCAGGACACAGG GACCCTGTGTTC GGT AG
GTCTGGCC CTGGGACACAGG CCG TC
A- - G
GAM175 265 LOC2860 1 12015 XP_212132.1 5 1431 ATTTTTCTTAAC C- G 4 B c c
02 CTTGGAGATGGC GAC CTGT TTCAAGGTTAGGG
TGTCTAGG CTG GGTA AGGTTCCAATTCT
TC G
GAM175 265 LOC2861 1 4900 XP_212194.1 5 268 TCGTAGCTCCCC - - TT G 4 B c c
32 ATTGAACACAGG GAC CCTGTGTTCAA GG AG
TGTCATCA CTG GGACACAAGTT CC TC
T A CC G
GAM175 265 LOC2862 1 2319 XP_212231.1 5 52 CACGCCCCTAAC - GTTCAA 4 B c c
14 CCTAACGGGGAT GA CCCTGT GGTTAGGG
CCCAGTCC CT GGGGCA CCAATCCC
A ATC---
GAM175 265 LOC2864 1 5576 XP_210061.1 3 297 GGCGCTCCTAAC A GTTCA 4 B c c
71 CTCCCGAACGGG G CCCTGT AGGTTAGGG
GCGGCTGG C GGGGCA TCCAATCCT
- AGCCC
GAM175 265 LOC3385 1 10504 XP_294653.1 5 148 CGGTCCAGGGCA - AG AG 4 B c c
65 ATGACACACAGG GACCCTGTGT TCA GTT GG
GTCTCGAT CTGGGACACA AGT CGG CC

C AA GA

GAM175 265 LOC3385 1 9293 XP_294658.1 3 392 TCGGGCCTGACC A TCAA- 4 B c c

85 CGTCCACACAGG G CCCTGTGT GGTTAGG

GCCGTGTC C GGGACACA CCAGTCC

C CCTGC

GAM175 265 LOC3390 1 11684 XP_294800.1 5 2277 ATCCATCCCAGC G A TA- 4 B c c

71 ACCTGGAACAGG GACCCTGT TTCA GGT GGG

GTCTGACA CTGGGACA AGGT CCA CCC

- - CGA

GAM175 265 LOC3391 1 18348 XP_294829.1 3 1512 GCAGCCCTCGAC CAAG - 4 B c c

52 AACAAATACAGG GACCCTGTGTT GTT AGGG

GTCTGTTG CTGGGACATAA CAG TCCC

ACAA C

GAM175 265 LOC3396 1 4270 XP_295024.1 5 746 CCATAGGCTGAG - ---- G - 4 B c c

66 ATGAGGCACAGG GACCCTGTGT TCA AG TTA GG

GTCTGGTT CTGGGACACG AGT TC GAT CC

G AGAG G A

GAM175 265 LOC3398 1 7585 XP_295080.1 5 1657 TGGGCTTGCCTG GTTC T 4 B c c

31 CCCTTCAACAGG GACCCTGT AAGG TAGG

GTCTATTG CTGGGACA TTCC GTCC

AC-- C

GAM175 265 LOC3398 1 14967 NP_835467.1 5 21 TCCAAAGTCCTC TGT AGG 4 B c c

34 TAAACTGACAGG GACCCTG TCA TTAGGG

GTCTCATT CTGGGAC AGT AATCTC

--- CA-

GAM175 265 LOC3398 1 14967 XP_291033.1 5 21 TCCAAAGTCCTC TGT AGG 4 B c c

34 TAAACTGACAGG GACCCTG TCA TTAGGG

GTCTCATT CTGGGAC AGT AATCTC

--- CA-

GAM175 265 LOC3398 1 5152 XP_291050.1 3 233 GCCTGCTACAGC - - T ----- 4 B c c

72 CTTGAACTCATG GA CCC TG GTTCAAGGT TAGG

GGCTCAAG CT GGG AC CAAGTTCCG GTCC

C T T ACATC

GAM175 265 LOC3400 1 10984 XP_295154.1 5 595 TTCTTTCTCTAT - CA GT- 4 B c c

90 AACTAACACAGG GA CCCTGTGTT AG TAGGG

GATCACTG CT GGGACACAA TC ATCTC

A -- AAT

GAM175 265 LOC3403 1 11433 XP_295237.1 5 233 CCTGAGCCACCT A-- ---- 4 B c c

97 CAGGGATACAGG GACCCTGTGTTC AGGT TAGG

GTCCCCCA CTGGGACATAGG TCCA GTCC

GAC CCGA

GAM175 265 LOC3404 1 14607 XP_291274.1 5 1262 CCTTTGTTCTTT TTCA TT 4 B c c

08 TCCTGCCACAGG GACCCTGTG AGG AGGG

GTCTTTGC CTGGGACAC TCC TTCT
CG-- TT
GAM175 265 LOC3408 1 10036 XP_295865.1 5 1779 TCCAACTCCAAC A C - A 4 B c c
95 ACTTAACACAGG G CCCTGTGTT AAG GTT GGG
GCCAATGA C GGGACACAA TTC CAA CTC
C - A C
GAM175 265 LOC3421 1 12487 XP_292375.1 3 549 AGGCCTCGACTT -- TA 4 B c c
25 TGCTGGCACAGG GACCCTGTGTT CAAGGT GGG
GTCCCAGG CTGGGACACGG GTTTCA TCC
TC GC
GAM175 265 LOC3472 1 8399 XP_294563.2 5 142 TCCTGCACCAGA G A---- - 4 B c c
40 CGTGGGGACAGG GACCCTGT TTCA GGT TAGGG
GTCCTGAG CTGGGACA GGGT CCA GTCCT
G GCAGA C
GAM175 265 LOC3477 1 5676 XP_084325.1 3 1692 ATGCTTCCTGCC CC - T 4 B c c
59 CTTGAACATCAG GA CTG TGTTCAAGG TAGGG
ACTCCAAG CT GAC ACAAGTTCC GTCCT
CA T C
GAM175 265 LOC3481 2 9642 XP_300646.1 5 382 ATGCTTCCTGCC CC - T 4 B c c
58 CTTGAACATCAG GA CTG TGTTCAAGG TAGGG
ACTCCAGG CT GAC ACAAGTTCC GTCCT
CA T C
GAM175 265 LOC3481 2 17028 XP_300646.1 3 774 GTCACTCCAAAC TG--- A 4 B c c
58 CTTGAAACTGTC GACCCTG TTCAAGGTT GGG
AGGGTCAG CTGGGAC AAGTTCCAA CCT
TGTCA A
GAM175 265 LOC3483 1 11550 XP_300721.1 3 608 GTATAACTTAAC C T- 4 B c c
70 CTTGATTTATAA GACC TGTG TCAAGGTTAGG
GGTCTTAA CTGG ATAT AGTTCCAATTC
A TT
GAM175 265 LOC3483 1 15891 XP_300723.1 3 939 AGGCTACCCTGA TTCAA 4 B c
c
78 CTAAGCCACAGG GACCCTGTG GGTTAGGG
GTTGGCAT TTGGGACAC TCAGTCCC
CGAA-
GAM175 265 LOC3483 1 11550 XP_300726.1 3 1035 GTATAACTTAAC C T- 4 B c c
83 CTTGATTTATAA GACC TGTG TCAAGGTTAGG
GGTCTTAA CTGG ATAT AGTTCCAATTC
A TT
GAM175 265 LOC3512 1 6773 XP_301805.1 5 351 CTAGTGTTTTCT C AGG 4 B c c
56 GATGAACACAGA GAC CTGTGTTCA TTAGGG
GTCTGCAT CTG GACACAAGT AGTCTT
A ---
GAM175 265 LOC9207 1 4921 XP_042684.1 5 526 CACTCCCCTAAC ---- CAA 4 B c c
8 CCATAGCACAGG GAC CCTGTGTT GGTTAGGG
CTGAGTCC CTG GGACACGA CCAATCCC
AGTC TAC
GAM175 265 LOC9659 1 1106 XP_039922.1 5 1617 TCCTCCACCTGA A---- T- 4 B c c

7 GACGAGCACAGG GACCCTGTGTTC AGGT AGGG
GTCTCCAC CTGGGACACGAG TCCA TCCT
CAGAG CC
GAM175 265 LPHN2 1 9096 NP_036434.1 3 991 CCCCTGTTTATT A G T---- 4 B c c
CTTGAACAGAGG G CCCT TGTTCAAGG TAGGG
GCAAAGAG C GGGA ACAAGTTCT GTCCC
- G TATTT
GAM175 265 MGC1124 1 8334 NP_077296.1 3 370 CTTCACCTCCTT --- TT 4 B b b
2 ACTGGACACAGG GACCCTGTGTTCA AGG AGG
GTCAAGGG CTGGGACACAGGT TCC TCC
CAT --
GAM175 265 MGC2078 1 14606 NP_689934.1 3 393 GCAGTCCGCCCA A TA 4 B b
b
5 TCTGAGCACAGG GACCCTGTGTTCA GGT GGG
GTCTGTCC CTGGGACACGAGT CTA CCC
- --
GAM175 265 MGC2201 1 6173 XP_035307.1 3 4687 GACATACTTGAC GTG--- 4 B c
c
4 CTTGAAAAATCT GACCCT TTCAAGGTTAGG
GGGGTCAT CTGGGG AAGTTCCAGTTC
TCTAAA
GAM175 265 MGC2390 1 2079 XP_038290.2 3 1144 CCTACTCTTGGC T--- -- 4 B c c
8 CTTGAACCTACC GACCC GT GTTCAAGGTTAGGG
TCTGGGTT TTGGG CA CAAGTTCCGGTTCT
TCTC TC
GAM175 265 MGC2848 1 12200 NP_116306.1 3 525 ACAGCCTTCAGC C - - 4 B c c
CTTGAACTGCAG GAC CTGT GTTCAAGGTT AGGG
CGTCACCT CTG GACG CAAGTTCCGA TTCC
C T C
GAM175 265 MGC3397 1 10456 NP_699174.1 3 1496 CCAGACTAACTT A CA-- G 4 B c
c
1 GGGCAACACAGG G CCCTGTGTT AGGTTAG
GCGACCCC C GGGACACAA TTCAATC
- CGGG A
GAM175 265 MGC3472 1 14010 NP_689746.1 5 67 GCGTCACATAAG TTCAA A 4 B c
c
8 CCAGCCCACAGG GACCCTGTG GGTT GG
GTCCTGCA CTGGGACAC CCGA CC
----- -
GAM175 265 MGC3932 1 18878 NP_689642.2 3 867 CTTTATTTTTAT G T 4 B c c
0 TTTTGAGACAGG GACCCTGT TTCAAGG TAGGG
GTCTTGTG CTGGGACA GAGTTTT ATTTT
- T
GAM175 265 MGC4005 1 1339 NP_689796.1 3 1706 GCCCAGGATGGC - TGT- ---- 4 B c
c
3 CTTGAACTCCTG GA CCC GTTCAAGGTTA GGG
GGCTCAAG CT GGG CAAGTTCCGGT CCC
C TCCT AGGA
GAM175 265 MGC4368 1 5575 NP_078786.2 3 779 GCCAGTCCCTCG G - GGTT 4 B c
c

TTGCAGGACAGG GACCCTGT TT CAA AGGG
GTCATCAT CTGGGACA GA GTT TCCC
G C GC--
GAM175 265 MIG-6 1 11440 NP_061821.1 3 19 TTTCTCCTTAAC TGTGTT 4 B c c
CTTGGGGTCATG GACCC CAAGGTTAGGG
GTTCAGCA CTGGG GTTCCAATTCC

GAM175 265 MRPS12 1 18531 NP_066930.1 3 75 CCTTCCGCTCCT TTCAA 4 B c
c
GGCTGCCACAGG GACCCTGTG GGTTAGGG
GTCCTCCG CTGGGACAC TCGGTCCT
CG---
GAM175 265 MRPS12 1 18531 NP_203526.1 3 75 CCTTCCGCTCCT TTCAA 4 B c
c
GGCTGCCACAGG GACCCTGTG GGTTAGGG
GTCCTCCG CTGGGACAC TCGGTCCT
CG---
GAM175 265 MRPS12 1 18531 NP_203527.1 3 75 CCTTCCGCTCCT TTCAA 4 B c
c
GGCTGCCACAGG GACCCTGTG GGTTAGGG
GTCCTCCG CTGGGACAC TCGGTCCT
CG---
GAM175 265 MTA3 1 5772 XP_038567.5 3 1245 CTGCCCTCTGTT -- GTT 4 B c c
TGCAGGCACAGG GACCCTGTGTT CAAG AGGG
GTCACAGT CTGGGACACGG GTTT TCCC
AC GTC
GAM175 265 MUM-1 1 17769 XP_300238.1 5 47 GTCTCCCTCATC T AA- T 4 B c c
ACCGACTACAGG GACCCTGTG TC GGT AGGG
GTCCGGTT CTGGGACAT AG CTA TCCC
C CCA C
GAM175 265 MXI1 1 14939 NP_005953.2 3 144 AACAAAACTATA G- GT G 4 B c c
CTTGAACAAAAG GACCCT TGTTCAAG TAG
GGTCAGAG CTGGGA ACAAGTTC ATC
AA AT A
GAM175 265 MXI1 1 14939 NP_569157.1 3 139 AACAAAACTATA G- GT G 4 B c c
CTTGAACAAAAG GACCCT TGTTCAAG TAG
GGTCAGAG CTGGGA ACAAGTTC ATC
AA AT A
GAM175 265 N4BP3 1 18724 XP_038920.2 3 1214 TGGGTGCCCGGC C A TA 4 B c
c
CTGGAACACAGG GA CCTGTGTTC AGGT GG
TTCTGTCT CT GGACACAAG TCCG CC
T G GC
GAM175 265 NAP1L1 1 12445 NP_004528.1 3 239 GTAGAGGCCTAC GT T 4 B c c
CTTGAATTAAGG GACCCT GTTCAAGGT AGG
GTTATACT TTGGGA TAAGTTCCA TCC
AT -
GAM175 265 NAP1L1 1 12445 NP_631946.1 3 913 GTAGAGGCCTAC GT T 4 B c c
CTTGAATTAAGG GACCCT GTTCAAGGT AGG
GTTATACT TTGGGA TAAGTTCCA TCC

AT -
GAM175 265 NCE2 1 5057 NP_057594.2 3 61 GGGAAGCCCGTG AAG - 4 B c c
GCAGGGCACAGG GACCCTGTGTTC GTTA GGG
GTTGTCCC TTGGGACACGGG CGGT CCC
A-- G
GAM175 265 NDRG1 1 5659 NP_006087.1 3 1308 CTGCTCCCTAAC A --- TC 4 B c c
CTTTCGCCGAAT G CCCTGT GT AAGGTTAGGG
GGGGCAGA C GGGGTA CG TTCCAATCCC
- AGC CT
GAM175 265 NUPL1 1 14772 NP_054808.1 5 119 GCCCTGGCCAGA TT A---- 4 B c c
CATGTCCACAGG GACCCTGTG CA GGTTAGGG
GTTCTCCT TTGGGACAC GT CCGGTCCC
CT ACAGA
GAM175 265 NUPL1 1 14772 NP_055593.1 5 135 GCCCTGGCCAGA TT A---- 4 B c c
CATGTCCACAGG GACCCTGTG CA GGTTAGGG
GTTCTCCT TTGGGACAC GT CCGGTCCC
CT ACAGA
GAM175 265 NXT2 2 5917 NP_061168.2 3 1046 CAATAAACCTAA GTTC 4 B b b
CCTTTTAACAGG GACCCTGT AAGGTTAGG
GTCTAACA CTGGGACA TTCCAATCC
ATT-
GAM175 265 NXT2 2 9223 NP_061168.2 3 1046 AATAAACCTAAC GTTC 4 B b b
CTTTTAACAGGG GACCCTGT AAGGTTAGG
TCTAACAT CTGGGACA TTCCAATCC
ATT-
GAM175 265 PASK 1 7891 NP_055963.1 5 275 GCGCCCAGCCTC TTCA--- A 4 B c c
CTTCCCCACAGG GACCCTGTG AGGTT GGG
GTCTCGCC CTGGGACAC TCCGA CCC
CCCTTCC -
GAM175 265 PDE11A 1 16840 NP_058649.2 3 157 CTGGGCTTTCAC C G T 4 B c c
CTTGAAGCATGG GACC TGT TTCAAGGT AGGG
TCAGCAGC CTGG ACG AAGTTCCA TTTC
T - C
GAM175 265 PER3 2 2006 NP_058515.1 3 975 CTTTTGTTTGCC A GT T 4 B c c
CTTGAACAGGGC G CCCTGT TCAAGG TAGG
AGTGTTGT C GGGACA AGTTCC GTTT
- -- C
GAM175 265 PER3 2 3046 NP_058515.1 3 1037 AGCCCAGTTGTC TTCAA T 4 B c c
CTCGCCCACAGG GACCCTGTG GGT AGGG
GTCCTGCA CTGGGACAC CCG TCCT
----- C
GAM175 265 PLA2G3 1 14052 NP_056530.1 3 885 TAAGAATAGCAC TTCA G 4 B c
c
TGATCTCACAGG GACCCTGTG AGGTTAG
GTTGTGAT TTGGGACAC TCTAGTC
---- A
GAM175 265 PMX1 1 10080 NP_008833.1 5 700 TTTTTCTCCTGA G----- G 4 B c c
CTTGAACATAGG ACCCTGTGTTCAAG TTAGGG

GTGACTTT TGGGATACAAGTTC AGTCCT
TTTCAG -
GAM175 265 PMX1 1 10080 NP_073207.1 5 700 TTTTTCTCCTGA G----- G 4 B c c
CTTGAACATAGG ACCCTGTGTTCAAG TTAGGG
GTGACTTT TGGGATACAAGTTC AGTCCT
TTTCAG -
GAM175 265 POLH 1 9909 NP_006493.1 3 646 AATTGCTTTAAC - G 4 B c c
CTTGGAGGCGGA GACC CTGT TTCAAGGTTAGGG
GGTTGCAT TTGG GGCG AGGTTCCAATTTC
A G
GAM175 265 PPARBP 1 18113 NP_004765.2 3 188 AGACCCTATTAA -- AAGGT 4 B c c
AGAAACCACAGG GACCCTGTG TTC TAGGG
GTTTGATT TTGGGACAC AAG ATCCC
CA AAATT
GAM175 265 PPIL2 1 19201 NP_055152.1 3 363 TTGTGGTTTCCT G C TT 4 B c c
CTTTAAGACAGG GACCCTGT TT AAGG AGGG
GTCTTGCT CTGGGACA AA TTTC TCCT
G - --
GAM175 265 PTEN 1 17273 NP_000305.1 3 171 TGTTTTACCCTA TTCAAG - 4 B c c
TACATCCACAGG GACCCTGTG GT TAGGG
GTTTTGAC TTGGGACAC CA ATCCC
CTA--- T
GAM175 265 PTGES2 1 10220 NP_079348.1 3 157 CAGCCCTCTCGC A CA T-- 4 B c c
TTCTAACACAGG G CCCTGTGTT AGGT AGGG
GCACCTGC C GGGACACAA TTCG TCCC
- TC CTC
GAM175 265 RAB11-F 1 12040 NP_116321.2 3 2634 GCTCACCACAAC C T-- AG 4 B c c
IP4 CTTGAACTCCCA GA CCTG GTTCAAGGTT GG
GGCTCAAG CT GGAC CAAGTTCCAA CC
C CCT CA
GAM175 265 RAI17 1 9293 NP_065071.1 3 2987 TCGGGCCTGACC A TCAA- 4 B c c
CGTCCACACAGG G CCCTGTGT GGTTAGG
GCCGTGTC C GGGACACA CCAGTCC
C CCTGC
GAM175 265 RNASE6 1 15669 NP_005606.1 5 171 CTTCCCCTTCCC - TCA- TT 4 B c c
TATACACACAGG GA CCCTGTGT AGG AGGG
GCTCGAAG CT GGGACACA TCC TCCC
C CATA CT
GAM175 265 RPS6KA2 1 4835 NP_066958.2 3 1194 TATTCCCCTGGG A T AGG 4 B c c
TGTGCACACAGG G CCCTGTGT CA TTAGGG
GCGGGTGT C GGGACACA GT GGTCCC
- C GTG
GAM175 265 SCD 1 15911 NP_005054.2 3 2233 ACCACAAACCCT C AG T 4 B c c

GCTGAACACAGT GAC CTGTGTTCA GT AGGG
GTCTGTTC CTG GACACAAGT CG TCCC
T -- -

GAM175 265 SDK1 1 6489 NP_689957.1 3 779 GCCCTCTCCTTC ----- ---- TT 4 B c c
CCCGAACACAGC GACC CTGTGTTC AAGG AGGG
ACACGGTC CTGG GACACAAG TTCC TCCC
CACAC CCCC TC

GAM175 265 SEI1 1 3289 NP_037508.1 3 219 ACCCCCTAGTGA - AAGG- 4 B c c
TGGAATGACAGG GACCCTGT GTTC TTAGGG
GTCTGGTG CTGGGACA TAAG GATCCC
G GTAGT

GAM175 265 SEPN1 1 12396 NP_065184.1 3 760 TCCCACCGCCTA C T 4 B b b
CCTTAGCACAGG GACCCTGTGTT AAGGT AGG
GTCTCTGC CTGGGACACGA TTCCA TCC
- -

GAM175 265 SERP1 1 14919 NP_055260.1 3 343 TTAGTCTAACTC -- T AG 4 B c c
TGCATAGACAGG GACCCTGT GT CA GTTAGG
GTCTAGAT CTGGGACA TA GT CAATCT
GA C CT

GAM175 265 SH3BGRL 1 9406 NP_112576.1 3 121 GTCATTCCTAAC C T- CA 4 B c
c
3 CTAACCTTAGAG GAC CTG GTT AGGTTAGGG
TCCCTCCC CTG GAT CAA TCCAATCCT
A TC --

GAM175 265 SHANK3 1 2299 XP_037493.1 3 1724 AATTTGGGTTTT TTCA 4 B c c
TAACTTTACAGG GACCCTGTG AGGTTAGGG
GTCAGTTC CTGGGACAT TTCAATTTT

GAM175 265 SLC11A2 1 17770 NP_000608.1 3 203 TCCTGACCTAAC G T---- - 4 B c c
CTTAGAACTGGA ACCCTG GTTC AAGGTTAGG
TTAGGGTG TGGGAT CAAG TTCCAATCC
G TAGGT A

GAM175 265 SLC16A6 1 12166 NP_004685.1 5 19 TCTCTTCCCTTC TGT GTT-- 4 B c
c
TAACTTGACAGG GACCCTG TCAAG AGGG
GTCTTGCT CTGGGAC AGTTC TCCC
--- AATCT

GAM175 265 SLC1A4 1 15625 NP_003029.2 3 80 CCAGCCGCCAGT A A GT A 4 B c
c
CATGGACACAGG G CCCTGTGTTCA G T GG
GCACTGCC C GGGACACAGGT C A CC
- A TG -

GAM175 265 SLC39A1 1 12020 NP_055252.2 5 58 TTTATTCTTATT G T 4 B c c
TTTGGAGACAGG GACCCTGT TTCAAGG TAGGG
GTCTCGCT CTGGGACA AGGTTTT ATTCT
G T

GAM175 265 SMURF1 1 17695 NP_065162.1 5 227 CGGAGCCGTAAC A - G G 4 B c
c
CTTGAGGCGGCG G CC CTGT TTCAAGGTTA GG
GCGGCGGG C GG GGCG GAGTTCCAAT CC

```
                                        - C  -      G
GAM175  265  SMURF1  1  17695  NP_851994.1  5  227  CGGAGCCGTAAC  A  -  G      G       4  B  c
c
                                CTTGAGGCGGCG  G  CC  CTGT  TTCAAGGTTA  GG
                                GCGGCGGG    C  GG  GGCG  GAGTTCCAAT  CC
                                        - C  -      G
GAM175  265  SMURF1  1  17695  XP_166483.1  5  251  CGGAGCCGTAAC  A  -  G      G       4  B  c
c
                                CTTGAGGCGGCG  G  CC  CTGT  TTCAAGGTTA  GG
                                GCGGCGGG    C  GG  GGCG  GAGTTCCAAT  CC
                                        - C  -      G
GAM175  265  SOX13  1  17045  NP_005677.1  3  1155  TTATTCCTCCCT        --  TT       4  B  c  c
                                CATGAGCACAGG  GACCCTGTGTTCA  AGG  AGGG
                                GTCGGGGG    CTGGGACACGAGT  TCC  TCCT
                                          AC  C-
GAM175  265  SRR   1  14627  NP_068766.1  3  1131  CCCACACTTAAC  C    GTT          4  B  c  c
                                CTTGTCAATAGG  GA  CCTGT   CAAGGTTAGG
                                TTCTTGAA    CT  GGATA   GTTCCAATTC
                                         T    ACT
GAM175  265  ST7L  1  19906  NP_060214.2  3  95   TGACAGTAACCC       TTCA   T       4  B  c  c
                                CTACCTCACAGG  GACCCTGTG    AGGT  AGGG
                                GTTGTTGT    TTGGGACAC    TCCA  TCCC
                                        ----   -
GAM175  265  ST7L  1  19906  NP_620055.1  3  95   TGACAGTAACCC       TTCA   T       4  B  c  c
                                CTACCTCACAGG  GACCCTGTG    AGGT  AGGG
                                GTTGTTGT    TTGGGACAC    TCCA  TCCC
                                        ----   -
GAM175  265  ST7L  1  19906  NP_620056.1  3  95   TGACAGTAACCC       TTCA   T       4  B  c  c
                                CTACCTCACAGG  GACCCTGTG    AGGT  AGGG
                                GTTGTTGT    TTGGGACAC    TCCA  TCCC
                                        ----   -
GAM175  265  THBD   1  6439   NP_000352.1  3  1558  CAGCTCTAGACA       TCA  -  -       4  B  c  c
                                CTGCCACACAGG  GACCCTGTGT   AG  GTT  AGGG
                                GTCTGCAA    CTGGGACACA   TC  CAG  TCTC
                                          CCG  A   A
GAM175  265  THY1   1  15926  NP_006279.2  3  923   GGTGGAGTCCCA       TCA  G  A       4  B  c  c

                                GAGCTGCACAGG  GACCCTGTGT   AG  TT  GGG
                                GTTTGGCC    TTGGGACACG   TC  AG  CCC
                                        ---  G  A
GAM175  265  TMPRSS2 1  3601   NP_005647.2  3  1319  CTAGGACTTAAC   ---  TGTG          4  B  c
c
                                CTTGAAATGGAA  GAC   CC   TTCAAGGTTAGG
                                AGTCTTGC    CTG   GG   AAGTTCCAATTC
                                          AAA  TA--
GAM175  265  TU12B1- 1  9561   NP_057659.1  3  4191  AGACGAAATTTG        CAA          4  B  c  c
         TY                      GCCAGACACAGG  GACCCTGTGTT   GGTTAGG
                                GTTCCTTG    TTGGGACACAG   CCGGTTT
                                          A--
GAM175  265  TULP4  1  10089  NP_064630.1  3  3680  GGGTCAAGCCTG       TT  AG  T       4  B  c
c
```

CTCTGCCACAGG GACCCTGTG CA GT AGG
GTTGGATG TTGGGACAC GT CG TCC
C- CT -

GAM175 265K UMP-CMP 1 5399 NP_057392.1 3 1307 CACTTACATCAT - -- - 4 B c c
TTGGTACACAGG GACCCTGTGT TCAA GGT TAGG
GTCAAATA CTGGGACACA GGTT CTA ATTC
T TA C

GAM175 265 UNC84B 1 8301 NP_056189.1 3 562 ACCTAGGGAAGC - AG ----- 4 B c c
ATGAACCACAGG GACCCTGTG TTCA GT TAGG
GTCCCTGA CTGGGACAC AAGT CG ATCC
C A- AAGGG

GAM175 265 UNC84B 1 8301 XP_039332.1 3 562 ACCTAGGGAAGC - AG ----- 4 B c c
ATGAACCACAGG GACCCTGTG TTCA GT TAGG
GTCCCTGA CTGGGACAC AAGT CG ATCC
C A- AAGGG

GAM175 265 USP25 1 3776 NP_037528.2 3 73 TAACCCTTGCCT TTC-- T 4 B c c
TCCTGTCACAGG GACCCTGTG AAGGT AGGG
GTTTGCTT TTGGGACAC TTCCG TCCC
TGTCC T

GAM175 265 ZNF313 1 1924 NP_061153.1 3 132 AATGAGCCATGG G G - 4 B c c
CATTGGGACAGG GACCCTGT TTCAA GTTA GG
GTCACTTC CTGGGACA GGGTT CGGT CC
- A A

GAM176 345 MYBL1 1 18625 XM_034274.10 3 TTTCAGTCATAT C AGCC 3 C c c
AATGGTGTG TACACCA TGTG GACTGAAA
GTGTGGT ATAT CTGACTTT
A A---

GAM177 385 BCL7A 1 9800 NM_020993.2 5 GCACCAGCACCT CA CT 3 C c c
TCCTACAA TTGTGG GGAGGTGCTGGTGC
AACATC CTTCCACGACCACG
-- --

GAM177 385 CLONE24 1 4969 NM_015683.1 3 CACCAGCTTTCA T GT C 3 C c c
945 GCCACCATG CAT GTGGCTGGAG GCTGGTG
GTA CACCGACTTT CGACCAC
C -- -

GAM177 385 PTPN3 1 12354 NM_002829.2 3 GCATTCACCCCC A CT 3 C c c
AGTCACAATG CATTGTGGCTGG GGTG GGTGC
GTAACACTGACC CCAC TTACG
C --

GAM178 223 DGCR2 1 17601 NM_005137.1 3 CTGGGAGCACCT - A G A 3 C c c
GTCTGTTGCAGA TCTGCAACA ACA GTG TTC CAG
AGACGTTGT TGT CAC AGG GTC
C C G -

GAM178 223 DYRK1A 1 7463 NM_130436.1 3 CTGTGGCTCTCC AACA T T 3 C c c

CGTTGCAGA TCTGCAAC AG GGT CACAG
AGACGTTG TC TCG GTGTC
CCC- - -

GAM178 223 FLJ1179 1 8358 NM_024669.1 3 CTGTGGGCCACT ACAACA 3 C c c

5 CGCTGCAGA TCTGCA AGTGGTTCACAG
AGACGT TCACCGGGTGTC
CGC---
GAM178 223 JAM1 1 7807 3 CTGTAGGAACTA CA ACAA -- 3 C c c
CTGTCCCAGA TCTG ACA GTGGTTC ACAG
AGAC TGT CATCAAG TGTC
CC ---- GA
GAM178 223 KLHL3 1 5694 NM_017415.1 5 TGCTGAATCACT T ACAA - G 3 C c c
GTTGCTGA TC GCAACA GTGGTTCA CA
AG CGTTGT CACTAAGT GT
T ---- C -
GAM178 223 LOC2215 1 13446 5 CTGTAAGATCAA CAAG C- 3 C c c
96 TACTTGTTGCAG TCTGCAACAA TGGTT ACAG
A AGACGTTGTT ACTAG TGTC
CATA AA
GAM178 223 OGT 1 16443 NM_003605.2 3 CTGTACAGTACC CAAGT TC--- 3 C c c
TTGTTGCAGA TCTGCAACAA GGT ACAG
AGACGTTGTT CCA TGTC
----- TGACA
GAM178 223 PTPRU 1 17915 NM_005704.2 3 CTGCCTGACCCA ACAA T -- 3 C c c
CTGTTGCAGA TCTGCAACA GTGG TCA CAG
AGACGTTGT CACC AGT GTC
---- C CC
GAM179 300 7h3 1 1101 NP_149014.2 3 853 GGCGTGTGGGGC T G T 3 B c c
TCTTTCAGGGAC TGGTC CTTGAAAGAG CTC
CACAGAGG ACCAG GGACTTTCTC GGG
- G T
GAM179 300 ABR 1 16042 NP_001083.1 3 1066 AAGTTGTGGGGG GAA 3 B c c
CTTTTCAAGAGG TGGTCTCTT AGAGGCTCTT
GGCCAGGC ACCGGGGAG TTTTCGGGGG
AAC
GAM179 300 ABR 1 16042 NP_068781.1 3 1066 AAGTTGTGGGGG GAA 3 B c c
CTTTTCAAGAGG TGGTCTCTT AGAGGCTCTT
GGCCAGGC ACCGGGGAG TTTTCGGGGG
AAC
GAM179 300 AP1GBP1 1 16827 NP_009178.2 3 812 TAAGTGAAGATG T A G - 3 B c c
CTCTTCCAGAGA TGGTCTCT GAA GAG C TCTT
CCACCTTC ACCAGAGA CTT CTC G AGAA
C - - T
GAM179 300 AP1GBP1 1 16827 NP_542117.1 3 812 TAAGTGAAGATG T A G - 3 B c c
CTCTTCCAGAGA TGGTCTCT GAA GAG C TCTT
CCACCTTC ACCAGAGA CTT CTC G AGAA
C - - T
GAM179 300 AP1GBP1 1 16827 NP_542118.1 3 674 TAAGTGAAGATG T A G - 3 B c c
CTCTTCCAGAGA TGGTCTCT GAA GAG C TCTT
CCACCTTC ACCAGAGA CTT CTC G AGAA

C - - T

GAM179 300 APRG1 1 15841 NP_848031.1 5 637 AGTAGAGGAGCC TCT - 3 B c c
TCTTCTCATGGC TGGTC TGA AAGAGGCTCTT
CACCATTG ACCGG ACT TTCTCCGAGGA
T-- C

GAM179 300 ATP11B 1 4094 XP_087254.2 3 1046 AAAAGAAGAGCC T CTT 3 B c c
TCTTTCTGCAGC TGG CT GAAAGAGGCTCTT
CGACTTAG GCC GA CTTTCTCCGAGAA
- CGT

GAM179 300 BPI 1 12380 NP_001716.1 3 223 GGATTATGAGCT T T 3 B c c
TCTTTCAAGGGC TGGTC CTTGAAAGAGGCTC
TAAGGCTG ATCGG GAACTTTCTTCGAG
- T

GAM179 300 C14orf9 1 4439 NP_055643.1 3 74 TGTCCAAGAGCC - C TT G 3 B c c
2 TGTTTTTGAAAC TG GT TC GAAA AGGCTCTT
ACAAGCTG AC CA AG TTTT TCCGAGAA
A A T- G

GAM179 300 C20orf1 1 6704 NP_543019.1 3 194 TGCCTCAGAGCC T AAGA- 3 B c c
75 GGTCCTCAGAGA TGGTCTCT GA GGCTCT
CCACGAAG ACCAGAGA CT CCGAGA
- CCTGG

GAM179 300 C4ST3 1 3672 NP_690849.1 3 104 GCCCCAGGACCC T A C- 3 B c c
CTCTTCAAGAGC TGG CTCTTGAA GAGG TCTT
CACTGCGT ACC GAGAACTT CTCC AGGA
- - CC

GAM179 300 CCNT2 1 12201 NP_001232.1 3 1828 TACTTAGGAGCC T----- TG 3 B c c

TCTTTGTAGGGA GGTCTCT AAAGAGGCTCTT
CTGTGCCT TCAGGGA TTTCTCCGAGGA
TCCGTG TG

GAM179 300 CCNT2 1 12201 NP_490595.1 3 1728 TACTTAGGAGCC T----- TG 3 B c c

TCTTTGTAGGGA GGTCTCT AAAGAGGCTCTT
CTGTGCCT TCAGGGA TTTCTCCGAGGA
TCCGTG TG

GAM179 300 CDA 1 17937 NP_001776.1 3 244 TCCTGTGGGCCC T C - T 3 B c c
TCTTTCAAAGTC TGG CT TTGAAAGAGG CTC
CAGCCTAG ACC GA AACTTTCTCC GGG
T - C T

GAM179 300 CRIP1 1 12094 NP_001302.1 3 5 GCCGAGAGCCAC CT A-- 3 B c c
ACTTTCAAGTAA TGGT CTTGAAAG GGCTCTT
CCAGGTGG ACCA GAACTTTC CCGAGAG
AT ACA

GAM179 300 DKFZP43 1 12743 NP_055364.1 3 2011 CTTTCTCAGGAA T AA C 3 B c
c
4P211 CCTTTCAAGCGG TGGTC CTTGA GAGG TCTT
CCAGAACC ACCGG GAACT TTCC AGGA
C -- A

GAM179 300 DKFZp76 1 9021 NP_060880.2 5 693 ATGACAGCCTCT AA--- CT 3 B c c

2E1312 CCCTACAAGAGA TGGTCTCTTG AGAGGCT
CCAGTAGC ACCAGAGAAC TCTCCGA
ATCCC CA
GAM179 300 DKFZP76 1 10781 XP_040560.4 3 317 GCTGTGAGAGAT - G 3 B b b
2N2316 TCTTTCAAGAAG TGGTCT CTTGAAAGAG CTCTT
ACCAAAAT ACCAGA GAACTTTCTT GAGAG
A A
GAM179 300 DNAL4 1 2920 NP_005731.1 3 465 GAAGGAGATGAT - GC- 3 B c c
TCTTTCAAGGGA TG GTCTCTTGAAAGAG TCTT
CACAGGCA AC CAGGGAACTTTCTT AGAG
A AGT
GAM179 300 DNTT 1 13119 NP_004079.2 5 27 GCAGCAGCAGCC - CT A- - 3 B c c
TCTTCCCATGGA TGG TCT TG AAGAGGCT CT
TCCACCAC ACC AGG AC TTCTCCGA GA
T T- CC C
GAM179 300 DOK4 1 15066 NP_060580.2 3 117 CGGCCAAGAGCC G GAAAG 3 B c
c
TGGAGAAAGGGA TG TCTCTT AGGCTCTT
GCAAGCTG AC AGGGAA TCCGAGAA
G AGAGG
GAM179 300 DSCR1 1 18056 NP_004405.2 3 1484 AAGAGGGAGCCG GA A- 3 B c
c
GTTTGGGAGAGA TGGTCTCTT AAG GGCTCTT
CCATTGCA ACCAGAGAG TTT CCGAGGG
GG GG
GAM179 300 ED1 1 7504 NP_001390.1 3 515 AAAGGCAGGTGC T AA T 3 B c c
TTTTGGCAGAGA TGGTCTCT G AGAGGC CTT
CCATAAGA ACCAGAGA C TTTTCG GGA
- GG T
GAM179 300 FBLN1 1 9477 NP_006476.1 3 213 AGCCCAGGAGCC T GAA 3 B c c
TCTCTGAAGGAC TGGTC CTT AGAGGCTCTT
CAGTCTGG ACCAG GAA TCTCCGAGGA
- GTC
GAM179 300 FLJ1011 1 18159 NP_060470.1 3 148 TTAAGCAAGGAA AA GC 3 B c c
6 CTTGTCAAGAGA TGGTCTCTTGA GAG TCTT
TCATGGTT ACTAGAGAACT TTC GGAA
G- AA
GAM179 300 FLJ1030 1 16190 NP_060523.2 3 197 GGGCAGAGGCCT GT - - - 3 B c c
7 CCTTTCAAGGAG TG CTC TTGAAAG AGGC TCT
TTCACAGT AC GAG AACTTTC TCCG AGA
TT G C G
GAM179 300 FLJ1046 1 9026 NP_060569.3 5 227 CAAAAAGGAACC T C 3 B c c
2 TCTTTCAGGAGC TGG CTCTTGAAAGAGG TCTT
TATAAAAG ATC GAGGACTTTCTCC AGGA
- A
GAM179 300 FLJ1321 1 11648 NP_079280.1 3 235 AGACCAGGACTT T - CT 3 B c c
5 TTTATCTAGAGA TGGTCTCT GA AAGAGG CT
CCAGCATG ACCAGAGA CT TTTTTC GA
T A AG

GAM179 300 FLJ1361 1 10037 NP_079390.1 3 124 AAAGAATGAATT - C T 3 B c c
5 TCTTTCAAGAGA TGGT CTCTTGAAAGAGG TC
ACTAATTG ATCA GAGAACTTTCTTT AG
A A T
GAM179 300 FLJ1378 1 9784 NP_079191.1 3 1077 TTCTGGAGAGCC ---- AA 3 B c c
2 TCTGCAGGGGGT TGGT CTCTTG AGAGGCTCTT
TTGCCATC ACCG GGGGAC TCTCCGAGAG
TTTG G-
GAM179 300 FLJ1384 1 15474 NP_078978.1 5 190 GCGGGAGGTGCC C TG - 3 B c c
1 TCTTTAGAAACC TGGT TCT AAAGAGGC TCTT
ACGAAGTG ACCA AGA TTTCTCCG GGAG
A -- T
GAM179 300 FLJ2057 1 6230 NP_060356.1 3 756 GTTCCAAGAGCC T TGA 3 B c c
4 TTTTAGTGATTA TGGTC CT AAGAGGCTCTT
AAATAGAA ATTAG GA TTTTCCGAGAA
T ---
GAM179 300 FLJ2187 1 4419 NP_075392.1 3 1016 ATAAGGGGTTAC GT- -- 3 B c c
0 TCTTTCAAGAGT TG CTCTTGAAAGAG GCTCTT
AACAAAAA AC GAGAACTTTCTC TGGGGA
AAT AT
GAM179 300 FLJ3130 1 792 NP_653240.1 3 723 GGGTCCAGAGCC GT GAAA 3 B c
c
0 TCGTGAGAGGTC TG CTCTT GAGGCTCT
ACCGGGAT AC GAGAG CTCCGAGA
TG TG--
GAM179 300 FLJ3293 1 19512 NP_653223.1 3 242 TCGGCAGGAGCC T TGAA 3 B c
c
4 TCTCAATGGAGT TGG CTCT AGAGGCTCTT
CCACTTCC ACC GAGG TCTCCGAGGA
T TAAC
GAM179 300 FLJ3600 1 6917 NP_787101.1 3 165 TCCTGAGCAGCC T T- - 3 B c c
0 TCTTTTCTAGGA TGGTC CT GAAAGAGGCT CTT
TCAATATG ACTAG GA TTTTCTCCGA GAG
- TC C
GAM179 300 FLJ3860 1 8910 NP_689867.1 3 110 GATGATGTACTC A-- - - T 3 B c c
7 TGGGTCAAGAGA TGGTCTCTTGA AGAG GC TC
CCAGGGAT ACCAGAGAACT TCTC TG AG
GGG A T T
GAM179 300 FLJ3900 1 11931 NP_848616.1 3 1106 TCTCTTAGAGCC C GAA 3 B c c
5 TCTAGAAAGAAC TGGT TCTT AGAGGCTCT
TAGCCCTA ATCA AGAA TCTCCGAGA
- AGA
GAM179 300 FLJ9079 1 660 NP_699198.1 3 341 CCTCTGAGAGCC G T G 3 B c c
8 TCTTTGGGGTGA TG TC CTT AAAGAGGCTCTT
GCAGCCTT AC AG GGG TTTCTCCGAGAG
G T G
GAM179 300 GPR48 1 14773 NP_060960.1 3 1104 TATAAAAGAGCC GT C AG 3 B c
c

TATTCAATAGCT TG CT TTGAA AGGCTCTT
CAGAGGTT AC GA AACTT TCCGAGAA
TC T A-

GAM179 300 GRIPAP1 1 19328 NP_064522.2 3 289 TGCATGAGCTCT T- A - T 3 B c c
CCTTCCCAGAGA TGGTCTCT GAA GAG GCTC
CCAACTCT ACCAGAGA CTT CTC CGAG
CC C T T

GAM179 300 HABP2 1 17826 NP_004123.1 3 105 ACCTCCAGAGCC AAA 3 B b b
TCCAGGGGACCA TGGTCTCTTG GAGGCTCT
CACAGTAG ACCAGGGGAC CTCCGAGA

GAM179 300 IL16 1 9723 NP_004504.3 3 2047 GGTACCAAGAGA TG AA G 3 B c c
CTCCTTGAGAGA TGGTCTCT A GAG CTCTT
CCAGGCAA ACCAGAGA T CTC GAGAA
GT C- A

GAM179 300 IL16 1 9723 NP_757366.1 3 2667 GGTACCAAGAGA TG AA G 3 B c c
CTCCTTGAGAGA TGGTCTCT A GAG CTCTT
CCAGGCAA ACCAGAGA T CTC GAGAA
GT C- A

GAM179 300 IL1B 1 4722 NP_000567.1 3 449 TGTAAAAGAGCC T C -- 3 B c c
TAGTTTTTAATA TGG CT TTGAAAG AGGCTCTT
GCTATGGA ATC GA AATTTTT TCCGAGAA
- T GA

GAM179 300 IQGAP1 1 17358 NP_003861.1 5 237 CAAATAAGAGCC TCTC A 3 B c
c
TCTTATAAACTC TGG TTG AAGAGGCTCTT
CATTCTTG ACC AAT TTCTCCGAGAA
TCA- A

GAM179 300 KCNK4 1 3257 NP_057695.2 3 97 ACCAAAGAGCCC T---- TT- - 3 B c c
TCTTTCCACGAG GGTCTC GAAAGAGG CTCTT
ACTGAAGT TCAGAG CTTTCTCC GAGAA
TGAAG CAC C

GAM179 300 KCNK4 1 3257 NP_201567.1 3 97 ACCAAAGAGCCC T---- TT- - 3 B c c
TCTTTCCACGAG GGTCTC GAAAGAGG CTCTT
ACTGAAGT TCAGAG CTTTCTCC GAGAA
TGAAG CAC C

GAM179 300 KCNK4 1 3257 NP_201568.1 3 92 ACCAAAGAGCCC T---- TT- - 3 B c c
TCTTTCCACGAG GGTCTC GAAAGAGG CTCTT
ACTGAAGT TCAGAG CTTTCTCC GAGAA
TGAAG CAC C

GAM179 300 KIAA028 1 12582 XP_043118.3 3 2826 TCCCACTCAGAT AAGA -- 3 B c
c
6 TGCTTCAAGAGA TGGTCTCTTGA GGC TCT
CCAACAGA ACCAGAGAACT TCG AGA
---- TT

GAM179 300 KIAA117 1 14096 XP_045907.2 3 497 AATTTGGAAGCC C TT - 3 B c c
0 TCTTTCTGAAAT TGGT TC GAAAGAGGCT CT
CATTAGCT ACTA AG CTTTCTCCGA GG
A T- A

GAM179 300 LAK 1 9362 NP_079420.2 3 151 TCCTGCAGAGCC CTCTT 3 B c c

TCTTTCCCTCTG TGGT GAAAGAGGCTCT
CCACAGTT ACCG CTTTCTCCGAGA
TCTCC

GAM179 300 LOC1201 1 12997 XP_061864.2 5 388 ATTGTTAGAGCC --- TGAA 3 B c c

05 TCTGACTGGGGT TGGT CTCT AGAGGCTCT
TCACCATA ACCA GGGG TCTCCGAGA
CTT TCAG

GAM179 300 LOC1250 1 10141 XP_008617.5 3 1594 TGCCTAAGAGCC T------ GA 3 B c c

58 TTTTGAGGAGAC GGTCTCTT AAGAGGCTCTT
CGTCCTGG CCAGAGGA TTTTCCGAGAA
GGTCCTG G-

GAM179 300 LOC1339 1 16799 XP_059674.1 3 285 AACTTGGGAGCC GT-- GA 3 B c c

26 TCTTGAGAGTGT TG CTCTT AAGAGGCTCTT
ACAGCATC AC GAGAG TTCTCCGAGGG
ATGT --

GAM179 300 LOC1431 1 8192 XP_096387.1 5 920 CGGCCAGGGCTG - C - 3 B c c

88 TCTTTCAAAGTG TGGT CT TTGAAAGA GGCTCT
CCATGTTC ACCG GA AACTTTCT TCGGGA
T - G

GAM179 300 LOC1450 1 13315 XP_085022.1 5 264 TTCCTAAGAGCC CTCTT- 3 B c c

98 TCTTTCCTTCAT TGGT GAAAGAGGCTCTT
ACCATCTT ACCA CTTTCTCCGAGAA
TACTTC

GAM179 300 LOC1488 1 3771 XP_097542.1 5 925 AAGAAGGGATCC C -- 3 B c c

94 TCTTTCAAAGGC TGGTCT TTGAAAGAGG CTCTT
TACCTTTA ATCGGA AACTTTCTCC GGGAA
- TA

GAM179 300 LOC1498 1 4055 XP_097747.1 3 995 TAGAAAGGAGCC CTCTT 3 B c c

37 TCTTTCTTAAAA TGGT GAAAGAGGCTCTT
CCAACCAA ACCA CTTTCTCCGAGGA
AAATT

GAM179 300 LOC1501 1 12743 XP_086802.2 3 2004 CTTTCTCAGGAA T AA C 3 B c c

74 CCTTTCAAGCGG TGGTC CTTGA GAGG TCTT
CCAGAACC ACCGG GAACT TTCC AGGA
C -- A

GAM179 300 LOC1502 1 12743 XP_059324.1 3 2005 CTTTCTCAGGAA T AA C 3 B c c

13 CCTTTCAAGCGG TGGTC CTTGA GAGG TCTT
CCAGAACC ACCGG GAACT TTCC AGGA
C -- A

GAM179 300 LOC1511 1 7338 XP_087116.1 5 1439 CCTGCAAGAGCC T T AA 3 B c c

71 TCTCCCAGGGCC TGG C CTTG AGAGGCTCTT
CAGTCCTC ACC G GGAC TCTCCGAGAA

C - CC

GAM179 300 LOC1575 1 18978 XP_098783.1 5 995 AAATCTCTGAGA T AAG C 3 B c c

56 ACCTTCAAGAGC TGG CTCTTGA AGG TCTT

CCAAAAAC ACC GAGAACT TCC AGAG

C --- A

GAM179 300 LOC2209 1 3721 XP_167629.1 5 510 CTGCTTGGGGCC C T 3 B c c

80 TCTTTCTGGAAA TGGT TCT GAAAGAGGCTCT

CCAGATCA ACCA AGG CTTTCTCCGGGG

A T

GAM179 300 LOC2211 1 3664 XP_167908.1 5 233 TCGCGGCCTGCC AA TCT 3 B c c

40 TCTGCCAAGAGA TGGTCTCTTG AGAGGC

CCAGCATC ACCAGAGAAC TCTCCG

CG TCC

GAM179 300 LOC2557 1 14351 XP_170898.2 5 225 CAGGCTTCCAGC T G CT 3 B c c

36 CTGTTTCAGAGA TGGTCTCT GAAA AGGCT

CCACTAGC ACCAGAGA CTTT TCCGA

- G CC

GAM179 300 LOC2830 1 758 XP_208024.1 5 531 ACAGAGGAGTCT T----- A- 3 B c c

16 CTTCCCAAGAGA GGTCTCTTG AAGAGGCTCTT

CTGCTGGC TCAGAGAAC TTCTCTGAGGA

CGGTCG CC

GAM179 300 LOC2830 1 15999 XP_210867.1 5 1987 CTCTCTGGGGCC -- TG-- 3 B c c

48 TCTTTAAATAGG TGGT CTCT AAAGAGGCTCT

GTCACCAA ACCA GGGA TTTCTCCGGGG

CT TAAA

GAM179 300 LOC2831 1 5476 XP_210910.1 3 400 AGGGGAAGAGCC T----- AA 3 B c c

68 TCAGTCAGGAGG GGTCTCTTGA GAGGCTCTT

CTCTGTGG TCGGAGGACT CTCCGAGAA

GGTGTC GA

GAM179 300 LOC2831 1 2829 XP_210903.1 3 652 GTTGTGTGAGCC GT A T 3 B c c

77 TCTTCAGGGGTT TG CTCTTGAA GAGGCTC

CATCCAGC AC GGGGACTT CTCCGAG

TT - T

GAM179 300 LOC2841 1 6917 XP_294862.1 3 729 TCCTGAGCAGCC T T- - 3 B c c

24 TCTTTTCTAGGA TGGTC CT GAAAGAGGCT CTT

TCAATATG ACTAG GA TTTTCTCCGA GAG

- TC C

GAM179 300 LOC2843 1 11931 XP_209116.1 3 1106 TCTCTTAGAGCC C GAA 3 B c c

13 TCTAGAAAGAAC TGGT TCTT AGAGGCTCT

TAGCCCTA ATCA AGAA TCTCCGAGA

- AGA

GAM179 300 LOC2849 1 9507 XP_211684.1 3 1253 AGGGACAGAGCC - TT- 3 B c c

11 TCTTTCTCTGAG TGGT CTC GAAAGAGGCTCT

AACTACCA ATCA GAG CTTTCTCCGAGA
A TCT
GAM179 300 LOC2851 1 4970 XP_209509.1 3 1542 GAGCTGGAATCC CT C- 3 B c c

93 TCTTTCAGGTAC TGGT CTTGAAAGAGG TCT
CAAATGTC ACCA GGACTTTCTCC AGG
T- TA
GAM179 300 LOC2853 1 800 XP_211844.1 3 1590 TGTTTTTAGAGT T AGAG 3 B c c

34 ATGATTCAGAGA TGGTCTCT GAA GCTCT
CCAATTTA ACCAGAGA CTT TGAGA
- AGTA
GAM179 300 LOC2854 1 17899 XP_208319.1 3 593 TGTCTAAGAGCC - C T G 3 B c c

12 TGTTTTGGAAAC TG GT TCT GAAA AGGCTCTT
ACAAGCTG AC CA AGG TTTT TCCGAGAA
A A - G
GAM179 300 LOC2854 1 7608 XP_211898.1 3 1104 TTGGCTAGAGCC TC GAAA 3 B c
c

31 TCATAAAAGACC TGG TCTT GAGGCTCT
CCAGGTTT ACC AGAA CTCCGAGA
CC AATA
GAM179 300 LOC2857 1 5912 XP_212002.1 5 280 TTCTCCAGAGCC AAA- 3 B c c
35 TCCAGATAAGAG TGGTCTCTTG GAGGCTCT
GCCAGGCT ACCGGAGAAT CTCCGAGA
AGAC
GAM179 300 LOC2858 1 13258 XP_212038.1 5 56 GCCCCAGGAGCC T AA 3 B c c
27 TCTCAGGAGTCT TGG CTCTTGA GAGGCTCTT
ACATCCCA ATC GAGGACT CTCCGAGGA
T --
GAM179 300 LOC2858 1 13258 XP_212604.1 5 56 GCCCCAGGAGCC T AA 3 B c c
27 TCTCAGGAGTCT TGG CTCTTGA GAGGCTCTT
ACATCCCA ATC GAGGACT CTCCGAGGA
T --
GAM179 300 LOC2858 1 13258 XP_212645.1 5 56 GCCCCAGGAGCC T AA 3 B c c
27 TCTCAGGAGTCT TGG CTCTTGA GAGGCTCTT
ACATCCCA ATC GAGGACT CTCCGAGGA
T --
GAM179 300 LOC2859 1 17124 NP_777609.1 3 370 TCAAAGAGGAGC AAAGA 3 B c
c

31 TGACACAAGAGA TGGTCTCTTG GGCTCTT
CCACAGTT ACCAGAGAAC TCGAGGA
ACAG-
GAM179 300 LOC2860 1 17023 XP_212158.1 3 3677 CTCCCAAGAGCC C AAA 3 B c
c

58 TCCAAGGCGCCA TGGT TCTTG GAGGCTCTT
TTGGCTTC ACCG GGAAC CTCCGAGAA
C ---
GAM179 300 LOC3398 1 12230 XP_295071.1 3 1686 CCACCCTTCAGG TGAAA 3 B c
c

```
          08                          AGTTTCCAGAGA TGGTCTCT    GAGGCTCTT
                                      CCAAGAAT    ACCAGAGA    CTTTGAGGA
                                              C----
GAM179    300   LOC3462 1  16628 XP_299387.1  5  54   ATCTTAGAACTC T-----      --     GC     3  B  c  c
          59                          TTTCTGAAGAGA     GGTCTCTT  GAAAGAG  TCT
                                      CCTTATCA         CCAGAGAA  CTTTCTC  AGA
                                               ACTATT      GT      A-
GAM179    300   LOC3477 1  13207 XP_300531.1  3  1795  AGGATACAAGGG       TGAAAG          3  B
c  c
          67                          CCTACCCAGAGA TGGTCTCT     AGGCTCTT
                                      CCAGAGAG    ACCAGAGA     TCCGGGAA
                                              CCCA--
GAM179    300   LOC3481 1  12472 XP_211219.1  5  2083  TCCCTGGAAGCC    C  TG      -       3  B  c
c
          55                          TCTTTGGAAACC TGGT TCT  AAAGAGGCT CT
                                      ACATAGAG    ACCA AGG  TTTCTCCGA GG
                                               A  --       A
GAM179    300   LOC3481 1  15435 XP_302676.1  3  698   CACTTCAGAGCC       GAA             3  B  b  b

          82                          TCTGAGGGGCCA TGGTCTCTT   AGAGGCTCT
                                      CCACTTCT    ACCGGGGAG   TCTCCGAGA
                                              ---
GAM179    300   LOC3483 1  3641  XP_300722.1  3  415   TATGAGAGAGCC  G    GAAA            3  B  c
c
          71                          TCAAAAGAGAGG TG TCTCTT    GAGGCTCTT
                                      GCAAGAAT    AC GGAGAG    CTCCGAGAG
                                               G     AAAA
GAM179    300   LOC3484 1  8278  XP_300352.1  3  340   CCAGCGGGGAGC    -      GA          3  B  c  c
          88                          TGTTTCAAGAGT TGGT CTCTTGAAA  GGCTCTT
                                      ACCGGTAC    GCCA GAGAACTTT  TCGAGGG
                                               T       G-
GAM179    300   LOC3493 1  10985 XP_301935.1  5  85    CACTCTCAGAGG         AAGAGG          3  B  c
c
          84                          TACCTCAAGAGA TGGTCTCTTGA     CTCT
                                      CCAAAGAG    ACCAGAGAACT     GAGA
                                              CCATG-
GAM179    300   MAPK4   1  11406 NP_002738.1  5  58    CCAGAAAGAGCC   TCT   A---           3  B  c  c

                                      TCTTGTAACAAG TGG   CTTG    AAGAGGCTCTT
                                      TATTCAAA    ACT   GAAC    TTCTCCGAGAA
                                               TAT    AATG
GAM179    300   MBNL1   1  12912 NP_066368.1  5  28    GGTGCAAGGGCC   TC ---              3  B  c  c
                                      TCTTTCAAAATG TGG  TC   TTGAAAGAGGCTCTT
                                      AACCCACT    ACC  AG   AACTTTCTCCGGGAA
                                               CA  TAA
GAM179    300   MCP     1  17253 NP_002380.3  3  1317  AGCCAAGCAGTT   TC   -      -       3  B  c  c
                                      TCTTTCAAAGAA TGG  TCTT GAAAGAGGCT CTT
                                      GCCAGCAG    ACC  AGAA CTTTCTTTGA GAA
                                               GA   A       C
GAM179    300   MCP     1  17253 NP_722548.1  3  1203  AGCCAAGCAGTT   TC   -      -       3  B  c  c
```

TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758860.1 3 1199 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758861.1 3 1317 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758862.1 3 1317 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758863.1 3 1203 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758864.1 3 1317 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758865.1 3 1317 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758866.1 3 1203 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758867.1 3 1317 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758868.1 3 1199 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758869.1 3 1203 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758870.1 3 1203 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA
GA A C

GAM179 300 MCP 1 17253 NP_758871.1 3 1203 AGCCAAGCAGTT TC - - 3 B c c
TCTTTCAAAGAA TGG TCTT GAAAGAGGCT CTT
GCCAGCAG ACC AGAA CTTTCTTTGA GAA

GA A C
GAM179 300 MGC1098 1 4521 NP_085053.1 3 1765 CGCCTCAGAGCC - GAA 3 B c c
6 TCTCAGGGCAGG TGGTCT CTT AGAGGCTCT
CCAACTTC ACCGGA GGG TCTCCGAGA
C AC-
GAM179 300 MGC2187 1 2320 XP_291105.1 3 1240 TCTCTGGGGTCC TC-- - 3 B c c
4 TCTTTCAAGGAT TGG TCTTGAAAGAGG CTCT
GTCCACGG ACC GGAACTTTCTCC GGGG
TGTA T
GAM179 300 MGC2673 1 16246 NP_659429.2 3 35 CTGGTGGCAGCT AGA - 3 B c c
3 ATGTTTAAGAGA TGGTCTCTTGAA GGCT CT
CCAGCGTC ACCAGAGAATTT TCGA GG
GTA C
GAM179 300 MGC3337 1 12923 NP_653265.1 3 157 TAAGCGTCTCTT GA---- T 3 B c c
1 ACAGCAGAGAGA TGGTCTCTT AAGAGGC CTT
CCAGACCA ACCAGAGAG TTCTCTG GAA
ACGACA C
GAM179 300 MOCS2 1 19765 NP_004522.1 5 284 AAATAACAGGAG T A G 3 B c c
TTCGTTCAGAGA TGGTCTCT GAA GAG CTCTT
CCATTTCT ACCAGAGA CTT CTT GAGGA
- G -
GAM179 300 MS4A4A 1 19413 NP_076926.2 3 79 GACACAAGAGCC ----- T AAA 3 B c c
TCACATGAGAAA TGG TCTC TG GAGGCTCTT
TTACCAGT ACC AGAG AC CTCCGAGAA
ATTAA T A--
GAM179 300 MS4A4A 1 19413 NP_683876.1 3 79 GACACAAGAGCC ----- T AAA 3 B c c
TCACATGAGAAA TGG TCTC TG GAGGCTCTT
TTACCAGT ACC AGAG AC CTCCGAGAA
ATTAA T A--
GAM179 300 MTH2 1 19548 NP_060753.1 3 1151 GTATGCAGAGGA AGG 3 B c c
GTTTTCAAGAGG TGGTCTCTTGAAAG CTCT
CTATCTGG ATCGGAGAACTTTT GAGA
GAG
GAM179 300 MYO1E 1 3663 NP_004989.1 3 223 TAAAAGGTAGCC CT - A - 3 B c c
TCTTCATAGGAA TGGT CT TGAA GAGGCT CTT
CCAGGAGG ACCA GA ACTT CTCCGA GGA
AG T - T
GAM179 300 NCOA1 1 13930 NP_671756.1 3 174 AGCAGAAGAGCC T C A 3 B c c
TCCTTCAGCAGC TGG CT TTGAA GAGGCTCTT
TACTGACT ATC GA GACTT CTCCGAGAA
- C C
GAM179 300 NESG1 1 3220 NP_036469.1 5 155 TGGATGAGAGCC C G 3 B c c
TCTTTGGAGATA TGGT TCTT AAAGAGGCTCTT
TCAAGTCC ACTA AGAG TTTCTCCGAGAG

T G

GAM179 300 NLG1 1 19329 NP_115499.1 3 357 ACTGAAAGAAGA - GAGGC 3 B c c

TATTTCAAGATG TGGTC TCTTGAAA TCTT
ACCATCTG ACCAG AGAACTTT AGAA
T ATAGA

GAM179 300 PIK3R3 1 16643 NP_003620.1 3 356 TGTATTTGGAAG GAA - 3 B c c

CCTCTGAAGAGA TGGTCTCTT AGAGGCT CT
CCATGTCT ACCAGAGAA TCTCCGA GG
G-- A

GAM179 300 PILRB 1 17335 NP_038468.3 3 215 CCTACAAGAGCC T-- AAA- 3 B c c

TTCATCCAGGAG TGG CTCTTG GAGGCTCTT
CATCCACA ACC GAGGAC TTCCGAGAA
TAC CTAC

GAM179 300 PILRB 1 17335 NP_778212.2 3 240 CCTACAAGAGCC T-- AAA- 3 B c c

TTCATCCAGGAG TGG CTCTTG GAGGCTCTT
CATCCACA ACC GAGGAC TTCCGAGAA
TAC CTAC

GAM179 300 PILRB 1 17335 NP_839956.1 3 215 CCTACAAGAGCC T-- AAA- 3 B c c

TTCATCCAGGAG TGG CTCTTG GAGGCTCTT
CATCCACA ACC GAGGAC TTCCGAGAA
TAC CTAC

GAM179 300 PIP5K1B 1 11230 NP_003549.1 3 154 CCTGACTTAAGA TC GAG 3 B c c

GTTTTCAAGATG TGG TCTTGAAA GCTCTT
TCAAACTT ACT AGAACTTT TGAGAA
GT ---

GAM179 300 PLXNC1 1 17920 NP_005752.1 3 140 TTTGGGCACTGT --- - T 3 B c c

CTTTTTAAGAGA TGGTCTCTTGAAAG AG GCTC
CCAAGGCA ACCAGAGAATTTTT TC CGGG
CTG A T

GAM179 300 PP1628 1 5602 NP_079477.1 5 1991 CCAGCTGGAGCC G GA 3 B c c

TCTTGAGGGAGA T GTCTCTT AAGAGGCTCT
TGAGAGGC A TAGAGGG TTCTCCGAGG
G AG

GAM179 300 PPT2 1 5462 NP_005146.3 3 46 CCCAGGAACTCC T AA C-- 3 B c c

TCGGTCCAGAGA TGGTCTCT GA GAGG TCTT
CCAAGTGG ACCAGAGA CT CTCC AGGA
C GG TCA

GAM179 300 PPT2 1 5462 NP_619731.1 3 46 CCCAGGAACTCC T AA C-- 3 B c c

TCGGTCCAGAGA TGGTCTCT GA GAGG TCTT
CCAAGTGG ACCAGAGA CT CTCC AGGA
C GG TCA

GAM179 300 PRB3 1 6636 NP_006240.2 5 16 GACTCCAGAGCC C AAA 3 B c c

TCCAGCAAGATG TGGT TCTTG GAGGCTCT
CTACTGAT ATCG AGAAC CTCCGAGA
T GAC

GAM179 300 PRO0461 1 14706 NP_112558.1 5 1908 CACTTCAGAGCC GAA 3 B b b

TCTGAGGGGCCA TGGTCTCTT AGAGGCTCT
CCACT ACCGGGGAG TCTCCGAGA

GAM179 300 RAB5C 1 590 NP_004574.1 5 67 CCACTAAGTGCC - CT - T 3 B c c
TCTTTGCATAGC TGGT CT TG AAAGAGGC CTT
ACCAGTCC ACCA GA AC TTTCTCCG GAA
C T- G T

GAM179 300 RAD9 1 16284 NP_004575.1 3 660 CAGCTTTGACCT - C T 3 B c c
TTATTCAAGAGA TGGTCTCTTGAA AGAGG TC
CCAGATGG ACCAGAGAACTT TTTCC AG
A - T

GAM179 300 RBBP2 1 19420 NP_005047.1 3 0 TGGAGGATCTTA GA GG 3 B c c
AAGAGACCAGTT TGGTCTCTT AAGA CTCT
ACAGATGC ACCAGAGAA TTCT GAGG
A- AG

GAM179 300 REGL 1 12552 NP_006499.1 3 550 TATAGAAGAGCC CTT AAG 3 B c
c
TTCTGTAGACCA TGGTCT GA AGGCTCTT
TATAGAAA ACCAGA CT TCCGAGAA
TGT ---

GAM179 300 SAE1 1 17602 NP_005491.1 3 734 TTAGAGAGCTTG CT -- 3 B c c
TCTTTCAAGGCC TGGTCT TGAAAGA GGCTCTT
AGGTTCCC ACCGGA ACTTTCT TCGAGAG
-- GT

GAM179 300 SH3BP1 1 14730 NP_061830.2 3 0 GGAGCCTTGCCT T AA- 3 B c c
CAGAGACCAACT TGGTCTCT GA GAGGCTCT
GGTGGCTG ACCAGAGA CT TTCCGAGG
- CCG

GAM179 300 SIAT1 1 10204 NP_003023.1 3 166 ACTTCAAGAGCC C AAG- 3 B c c
TGTGGTCAGGAA TGGT TCTTGA AGGCTCTT
ATCAGGTC ACTA AGGACT TCCGAGAA
A GGTG

GAM179 300 SIAT1 1 10204 NP_775323.1 3 166 ACTTCAAGAGCC C AAG- 3 B c c
TGTGGTCAGGAA TGGT TCTTGA AGGCTCTT
ATCAGGTC ACTA AGGACT TCCGAGAA
A GGTG

GAM179 300 SIAT1 1 10204 NP_775324.1 3 166 ACTTCAAGAGCC C AAG- 3 B c c
TGTGGTCAGGAA TGGT TCTTGA AGGCTCTT
ATCAGGTC ACTA AGGACT TCCGAGAA
A GGTG

GAM179 300 SLC12A7 1 15230 NP_006589.1 3 1196 ACTGAAGAGATA T AGG- 3 B c
c
GCTTTCAAGGGC TGG CTCTTGAAAG CTCTT
CCAACACT ACC GGGAACTTTC GAGAA
C GATA

GAM179 300 SLC37A3 1 14888 NP_115671.1 3 583 GTATTGAGTCTT T -- T 3 B c c
CCTTTCAAGGAC TGGTC CTTGAAAG AGGCTC
CATAAGGT ACCAG GAACTTTC TCTGAG
- CT T

GAM179 300 SMCX 1 8263 NP_004178.1 3 73 CCTCAAGGATCC TCTT C 3 B c c

TCTTTCTGACCA TGGTC GAAAGAGG TCTT
TCAAGCCT ACCAG CTTTCTCC AGGA
T--- T

GAM179 300 SPON1 1 16909 NP_006099.1 3 858 AAGCAAAATTGG TG CT 3 B c c
TCTCTTTAGAGA TGGTCTCT AAAGAGGCT
CCAATTTG ACCAGAGA TTTCTCTGG
-- TT

GAM179 300 SPTLC2 1 16724 NP_004854.1 3 2886 GTTTATAAGACC C C 3 B c c
TCTTTCAGCAGA TGGTCT TTGAAAGAGG TCTT
TCACATCA ACTAGA GACTTTCTCC AGAA
C -

GAM179 300 STAG3 1 5382 NP_076975.1 3 12 ACCCTTAGGAGT GAAA G 3 B c c
TCGATGGAGAGA TGGTCTCTT GAG CTCTT
CCATGAGG ACCAGAGAG CTT GAGGA
GTAG -

GAM179 300 SYTL2 1 7702 NP_116561.1 5 333 CTTCTGAGAGCC C TT A 3 B c c
TCTTCTCGACAC TGGT TC GAA GAGGCTCTT
TATCCCAC ATCA AG CTT CTCCGAGAG
C CT -

GAM179 300 TNR 1 19266 NP_003276.2 3 450 GAGAAAAGAGCC ------ AAA 3 B c c
TCAGCAAGAGAG TGGT CTCTTG GAGGCTCTT
TTTTGCCA ACCG GAGAAC CTCCGAGAA
TTTTGA GA-

GAM179 300 TYROBP 1 12609 NP_003323.1 3 123 CCACAGAGTGCC AAA - T 3 B c c

ATCCCTGAGAGA TGGTCTCTTG GA GGC CTT
CCAGACCG ACCAGAGAGT CT CCG GAG
CC- A T

GAM179 300 UBP1 1 17947 NP_055332.2 3 1179 TATAAGAGTGCC CTCT T 3 B c c

TCTTTCATAAAA TGGT TGAAAGAGGC CTT
CCAAATGC ACCA ACTTTCTCCG GAG
AAAT T

GAM179 300 WBP3 1 18927 NP_783863.2 3 4530 CCCAAAGTGTCT CT - T 3 B c c
GCTTTCAAGCAC TGGT CTTGAAAG AGGC CTT
CACACCCA ACCA GAACTTTC TCTG GAA
C- G T

GAM180 214 3PAP 1 9183 NP_061934.2 3 821 TTCTTTGCCTGA - AT 1 B c c
GATCCTTCCTGA TTTCT GGGAG GTCTCAGGC
GGAGCGTC GAGGA TCCTT TAGAGTCCG
G CC

GAM180 214 ACK1 1 18640 NP_005772.2 3 593 GAAATAGCCTGA AGA GT 1 B c c

GGTGGCTCAGGA TTTCTGGG T CTCAGGCT
AGCGGAGA AAGGACTC G GAGTCCGA
G-- TG

GAM180 214 ACP2 1 16613 NP_001601.1 3 785 GAATAGGGCTGG A G 1 B c c
GGCAGCTCCCAG TTTCTGGGAG TGTCTCAG CT
AGAATGAA AGAGACCCTC ACGGGGTC GG
G G

GAM180 214 ADAM8 1 19901 NP_001100.1 3 430 AGCACAGACGTG A GGC 1 B c c

GGGCATCCCCAG TTTCTGGG GATGTCTCA
AAAGACTC AAAGACCC CTACGGGGT
- GCA

GAM180 214 ADCY5 1 9867 XP_171048.2 5 26 CACTATCCGGCT GT G 1 B c c
GAGGTCTCCCAG TTTCTGGGAGAT CTCAG CT
AGACAGGC AGAGACCCTCTG GAGTC GG
-- -

GAM180 214 AKAP7 1 662 NP_004833.1 3 797 ATTAAAGCCTGA T----- GA- T 1 B c c
GACTCAGGCCAG TTCTGG GA GTCTCAGGCT
AATTAGGA AAGACC CT CAGAGTCCGA
AGGATT GGA -

GAM180 214 AKAP7 1 662 NP_057461.1 3 797 ATTAAAGCCTGA T----- GA- T 1 B c c
GACTCAGGCCAG TTCTGG GA GTCTCAGGCT
AATTAGGA AAGACC CT CAGAGTCCGA
AGGATT GGA -

GAM180 214 AKAP7 1 662 NP_619539.1 3 797 ATTAAAGCCTGA T----- GA- T 1 B c c
GACTCAGGCCAG TTCTGG GA GTCTCAGGCT
AATTAGGA AAGACC CT CAGAGTCCGA
AGGATT GGA -

GAM180 214 ALK7 1 4668 NP_660302.1 3 690 CTGACATCCTGA G AGA C 1 B c c
GACACTGAGAAA TTTCT GG TGTCTCAGG
TGTCCTGA AAAGA TC ACAGAGTCC
G --- T

GAM180 214 ANKFY1 1 13680 NP_057460.2 3 3283 TGCTTCCCTTGG GA C 1 B c c

GACAAGTCCCAG TTTCTGGGA TGTCTCAGG
AAGAACTA GAAGACCCT ACAGGGTTC
GA C

GAM180 214 AP1S3 1 10369 NP_848929.1 3 18 GCAAGAGCCTGA T G 1 B c c
GAAGTTTCCTTG TTTC GGGAGAT TCTCAGGCT
AGGTCTGT GGAG TCCTTTG AGAGTCCGA
T A

GAM180 214 ARIH2 1 6107 NP_006312.1 5 19 ACATCTGCCTGA T----- G G 1 B c c
GAGATCTCCAAG TTCT GGAGAT TCTCAGGC
AATTACAG AAGA CCTCTA AGAGTCCG
GACATT A G

GAM180 214 ASXL1 1 6136 NP_056153.2 3 249 CAGCCAGCCTGA T ------- T T 1 B c c
GCTCTCCTGCAA TTCTG GGAGA G CTCAGGCT
GACAGAGC GAGAC CCTCT C GAGTCCGA
C AGAACGT - -

GAM180 214 AVPR1B 1 10287 NP_000698.1 5 178 TCCCCAGCCTTC TGTCTC 1 B c c

TTTCTCTCCCAG TTTCTGGGAGA AGGCT
AAGCCTCA GAAGACCCTCT TCCGA
CTTTCT

GAM180 214 BACH2 1 9027 NP_068585.1 3 1189 GGAGAGAGTTTG CT - T 1 B c c
GACATCTCACTC TTT GG GAGATGTC CAGGCT
AAAAGTAC AAA TC CTCTACAG GTTTGA

AC A -
GAM180 214 BVES 1 12682 NP_671488.1 5 79 GGTTGTTGGCCA GA CA 1 B c c
GACAAGTCCCAG TTTCTGGGA TGTCT GGCT
AAACTGCC AAAGACCCT ACAGA CCGG
GA --
GAM180 214 C1orf16 1 9607 NP_055652.2 5 8 CGAGGAGCCTGA - AGATG 1 B c c
GAGACCCACGGA TTTC TGGG TCTCAGGCT
GGCTTCGC GAGG ACCC AGAGTCCGA
C AG---
GAM180 214 C1orf24 1 9821 NP_071366.1 3 1013 CAAATAGTCCTG A TC - 1 B c c
GTTCATTCCCAG TTTCTGGGAG TG TCAGG CT
AAGGGCAC GAAGACCCTT AC GGTCC GA
- TT T
GAM180 214 C1orf24 1 9821 NP_443198.1 3 1011 CAAATAGTCCTG A TC - 1 B c c
GTTCATTCCCAG TTTCTGGGAG TG TCAGG CT
AAGGGCAC GAAGACCCTT AC GGTCC GA
- TT T
GAM180 214 C1QR1 1 6733 NP_036204.1 3 3909 TGGGAATCTGAG G- C 1 B c c
ATATGATCCCAG TTTCTGGGA ATGTCTCAGG
AAAACATC AAAGACCCT TATAGAGTCT
AG A
GAM180 214 C20orf2 1 15921 NP_056232.1 3 237 CGCTGAGCCTGA GGAGA 1 B c
c
8 GACGGGAGGCAG TTTCTG TGTCTCAGGCT
GAAAGGGG AAGGAC GCAGAGTCCGA
GGAGG
GAM180 214 C20orf7 1 9329 XP_114180.1 3 140 GTGAAAGCCTGA GAGATGT 1 B c
c
0 GTCCCACCAGAA TTTCTGG CTCAGGCT
GGACCTTC GAAGACC GAGTCCGA
ACCCT--
GAM180 214 CA14 1 11029 NP_036245.1 3 145 CTCCTTCCCCTG T C 1 B c c
GACATCTCCTAG TTTCTGGGAGATGTC CAGG
AGAGGAAT AGAGATCCTCTACAG GTCC
- C
GAM180 214 CALM1 1 13087 NP_008819.1 3 2389 GCTTTAGCCTGA G-- AGAT 1 B c
c
GACTTGCCATAA TTTCT GG GTCTCAGGCT
GAAACTGC AAAGA CC CAGAGTCCGA
ATA GTT-
GAM180 214 CALU 1 544 NP_001210.1 3 419 TTGTAAGCCTGA GGGAGAT 1 B c
c
GATCAATAAGAA TTTCT GTCTCAGGCT
ATGTTCAG AAAGA TAGAGTCCGA
ATAAC--
GAM180 214 CARD9 1 11302 NP_071747.2 5 44 GCAGCCCCGGGC -- A- 1 B c c
AGCATCTCCCAG TTTCTGGGAGATGT CTC GGCT
AGGCTCCG GGAGACCCTCTACG GGG CCGA
AC CC
GAM180 214 CARD9 1 11302 NP_434700.1 5 44 GCAGCCCCGGGC -- A- 1 B c c

AGCATCTCCCAG TTTCTGGGAGATGT CTC GGCT
AGGCTCCG GGAGACCCTCTACG GGG CCGA
AC CC
GAM180 214 CARD9 1 11302 NP_434701.1 5 55 GCAGCCCCGGGC -- A- 1 B c c
AGCATCTCCCAG TTTCTGGGAGATGT CTC GGCT
AGGCTCCG GGAGACCCTCTACG GGG CCGA
AC CC
GAM180 214 CCL11 1 4942 NP_002977.1 5 77 GCAGAGAGGCTG AGAT G 1 B c c

AGACCAACCCAG TTTCTGGG GTCTCAG CT
AAACCACC AAAGACCC CAGAGTC GA
AAC- G
GAM180 214 CCL8 1 6343 NP_005614.2 5 391 GCAGAGAGGTTG AGATG G 1 B c
c
AGAACAACCCAG TTTCTGGG TCTCAG CT
AAACCTTC AAAGACCC AGAGTT GA
AACA- G
GAM180 214 CD22 1 5550 NP_001762.1 3 456 TTCTGCCTCTGA AGATG -- 1 B c c
GGGAAAGCCCAG TTTCTGGG TCTCA GGC
AAAAGGAC AAAGACCC GGAGT CCG
GAAAG CT
GAM180 214 CDK5RAP 1 3530 NP_079473.2 3 1783 CTGATTGAAGCT G TCA 1 B c
c
3 GACATCTCCAAG TTTCT GGAGATGTC GGCT
AGGTACAG GGAGA CCTCTACAG TCGA
A ---
GAM180 214 CDK5RAP 1 3530 NP_788275.1 3 1998 CTGATTGAAGCT G TCA 1 B c
c
3 GACATCTCCAAG TTTCT GGAGATGTC GGCT
AGGTACAG GGAGA CCTCTACAG TCGA
A ---
GAM180 214 CHI3L2 1 13391 NP_003991.1 3 69 TGCCTGGGGCCT T----- 1 B c c
GCTCTCTCCCAG TTTCTGGGAGA GTCTCAGGC
GAATTCTC AAGGACCCTCT CGGGGTCCG
CTCGTC
GAM180 214 CHST3 1 19995 NP_004264.2 3 3798 GCTTCAGCAGGA AT AG 1 B c
c
GATCCTTCCCAG TTTCTGGGAG GTCTC GCT
AAGGTTGA GAAGACCCTT TAGAG CGA
CC GA
GAM180 214 CHST5 1 6807 NP_036258.1 5 262 CACAGATGTCGA T---- - A 1 B c c
GACATCTCCCAT TTC TGGGAGATGTCTC GGC
GGATTTGT AGG ACCCTCTACAGAG CTG
TGTTT T -
GAM180 214 COL4A4 1 5844 NP_000083.1 3 2002 AACTTGGCCTGA TG - 1 B c c
GAACATTTTCTG TTTC GGAGATGT CTCAGGCT
GGAAGAGG AAGG CTTTTACA GAGTCCGG
GT A
GAM180 214 DCAMKL1 1 2905 NP_004725.1 3 952 TACTCAGTGTCA GG CA 1 B c
c

GACATCTACAGG TTTCTG AGATGTCT GGC
AAAGAAAC AAGGAC TCTACAGA CTG
A- --
GAM180 214 DKFZP43 1 7730 XP_291159.1 3 311 GAACCTGCCTGA TT -- - 1 B c c
4F011 GAACATTTCTAA T CTG GGAGATGT CTCAGGC
CGGGGAGC A GGC TCTTTACA GAGTCCG
GG AA A
GAM180 214 DKFZP56 1 8990 XP_166254.2 3 3905 GACACATCTCCT GATG C 1 B c
c
4O0423 GAGGGATCCCAG TTTCTGGGA TCTCAGG
AAAGAACC AAAGACCCT GGAGTCC
AG-- T
GAM180 214 DKFZP58 1 11679 NP_056253.2 5 3 CACCGGTCTGCA - TCT 1 B c c
6I2223 TCTCCCAGCAGA TTT CTGGGAGATG CAGGCT
AGGCGCAG AGA GACCCTCTAC GTCTGG
C ---
GAM180 214 DKFZP58 1 11679 NP_542768.1 5 3 CACCGGTCTGCA - TCT 1 B c c
6I2223 TCTCCCAGCAGA TTT CTGGGAGATG CAGGCT
AGGCGCAG AGA GACCCTCTAC GTCTGG
C ---
GAM180 214 DKFZp76 1 10603 NP_060892.1 5 1031 TCCGTAGCCTGG GATGT 1 B c
c
1K1423 GTGAAGTCCCAG TTTCTGGGA CTCAGGCT
AAGCTGGT GAAGACCCT GGGTCCGA
GAAGT
GAM180 214 DKFZP76 1 898 XP_295135.1 3 82 TAAAAAGCCTGA C GG A 1 B c c
1M1511 GACGCCTTACAA TTT TG AG TGTCTCAGGCT
AAAGCAAG AAA AC TC GCAGAGTCCGA
A AT C
GAM180 214 DKFZp76 1 19364 NP_060880.2 5 618 AGCGAAACCAGC TCTC 1 B c
c
2E1312 TTCATCTCCCAG TTTCTGGGAGATG AGGCT
AGAATGGG AGAGACCCTCTAC TTCGA

GAM180 214 DRD2 1 8911 NP_000786.1 3 366 GCTGGAGCCTGA AGA T 1 B c c
GTCAGGGCCCAG TTTCTGGG TG CTCAGGCT
AGGCTGAG GGAGACCC AC GAGTCCGA
GGG T
GAM180 214 DRD2 1 8911 NP_057658.2 3 366 GCTGGAGCCTGA AGA T 1 B c c
GTCAGGGCCCAG TTTCTGGG TG CTCAGGCT
AGGCTGAG GGAGACCC AC GAGTCCGA
GGG T
GAM180 214 DUSP2 1 13525 NP_004409.1 3 355 TTGGCAGCCTGA G ATG 1 B c c
GAGCTCCAAGGA TTTCT GGAG TCTCAGGCT
ACAAGCTG AAGGA CCTC AGAGTCCGA
A G--
GAM180 214 EFNA3 1 19601 NP_004943.1 3 878 CCTGAGCCGGGA T----- -- A 1 B c c
ACCATCTCCCAG TTCTGGGAGATG TCTC GGCT
GACCTTGC AGGACCCTCTAC AGGG CCGA

CGTTCC CA -

GAM180 214 ELKS 1 787 NP_055879.1 3 405 GGGGAAGCCTGA A- GT- 1 B c c
GGTAGTCAACCC TTTCTGGG GAT CTCAGGCT
AGGAGCCA GAGGACCC CTG GAGTCCGA
AA ATG

GAM180 214 EVC 1 5644 NP_055371.1 3 3298 GAAGTAGCCTGA - AT 1 B b b
GGCCCTCACCAG TTTCTGG GAG GTCTCAGGCT
AAGCAGAC GAAGACC CTC CGGAGTCCGA
A C-

GAM180 214 FGFR1 1 5084 NP_075598.1 3 167 TAGCTCCATATT A T ------ 1 B c c
GGACATCCCCAG TTTCTGGG GATGTC CA GGCT
AAAAGATG AAAGACCC CTACAG GT TCGA
- - TATACC

GAM180 214 FHX 1 12381 NP_060886.1 3 1375 GTGAGGGCCAAG AGAT A--- 1 B c
c
GGGGACCCCCAG TTTCTGGG GTCTC GGCT
AAAAAGGT AAAGACCC CAGGG CCGG
C--- GGAA

GAM180 214 FKSG42 1 17992 NP_114421.1 3 251 GCTTTTAGATGA - ------ 1 B c c
GACATCTTTCCA TTTCTGGGA GATGTCTCA GGC
GGAGTAGA GAGGACCTT CTACAGAGT TCG
T AGATTT

GAM180 214 FLJ1064 1 4717 NP_060637.1 5 108 CCCGGAGCCTGA GG A T 1 B c c
8
GCCACTGACAGG TTTCTG AG TG CTCAGGCT
AGAGGAGA GAGGAC TC AC GAGTCCGA
AG - C

GAM180 214 FLJ1097 1 13268 NP_060756.1 5 58 TTGCTGTTAGAG T- AG 1 B c c
0
GCTCTTTCCCAG TTTCTGGGAGA GTCTC GC
AAGTTGGA GAAGACCCTTT CGGAG TG
CT AT

GAM180 214 FLJ1170 1 3258 NP_079168.1 3 29 AAGTCAGCCTGA AGATG- 1 B c c
0
GGATTTAGCCCA TTTCTGGG TCTCAGGCT
GAGGTGAT GGAGACCC GGAGTCCGA
GATTTA

GAM180 214 FLJ1257 1 7536 NP_112187.1 3 445 GCTCAGGGCACT GATG - 1 B c c
7
GAGAGATCCCAG TTTCTGGGA TCTCAG GCT
AAGGTAAC GAAGACCCT AGAGTC CGG
AG-- A

GAM180 214 FLJ1258 1 1658 NP_071925.2 3 256 TTTGTGGGAAGA -- - AG 1 B c c
7
CATACCTCCCAG TTTCTGGGAG ATGTCT C GC
AGGGGCAT GGAGACCCTC TACAGA G TG
CA A GG

GAM180 214 FLJ1390 1 19221 NP_078929.1 3 190 TTGGGAGCCTGA TT-- T --- 1 B c c
2
GGGGCCATCTCC TC GGGAGATG TCTCAGGCT
CTGACACT AG CCCTCTAC GGAGTCCGA
TCAC T CGG

GAM180 214 FLJ1416 1 3589 NP_078841.1 3 1686 CCTCACAGCCAG AGA - CA 1 B c
c

6 CACGACCCCCAG TTTCTGGG TGT CT GGCT
AAAGAGGC AAAGACCC GCA GA CCGA
CCA C --

GAM180 2149 FLJ1424 1 14831 NP_071905.2 3 610 GCAGGGTCTGGG GT- 1 B c c
TGGGTCTCCCAG TTTCTGGGAGAT CTCAGGCT
GAGAGGAA GAGGACCCTCTG GGGTCTGG
GGT

GAM180 2149 FLJ1424 1 14831 NP_567825.1 3 299 GCAGGGTCTGGG GT- 1 B c c
TGGGTCTCCCAG TTTCTGGGAGAT CTCAGGCT
GAGAGGAA GAGGACCCTCTG GGGTCTGG
GGT

GAM180 2146 FLJ1493 1 6933 NP_115660.1 3 209 GAGGAGTAGGAG - T AG 1 B c c
CCGGTCTCCCAG TTTCTGGGAGAT G CTC GCT
AAGGCGGA GAAGACCCTCTG C GAG TGA
G C GA

GAM180 2144 FLJ2017 1 4747 NP_060169.1 3 569 TGGCACCAGCTA A T CA 1 B c c
GTCACCTCCCAG TTTCTGGGAG TG CT GGCT
AAGAAACT GAAGACCCTC AC GA TCGA
C T --

GAM180 2147 FLJ2029 1 1321 NP_060221.1 3 621 TTCAGGAGCCTA T----- AT C 1 B c c
AGACCCTCCCAG TTCTGGGAG GTCT AGGCT
AGCCCAGG GAGACCCTC CAGA TCCGA
GGACCC C- A

GAM180 2147 FLJ2029 1 1321 NP_060421.1 3 619 TTCAGGAGCCTA T----- AT C 1 B c c
AGACCCTCCCAG TTCTGGGAG GTCT AGGCT
AGCCCAGG GAGACCCTC CAGA TCCGA
GGACCC C- A

GAM180 2148 FLJ2029 1 11216 NP_060222.1 3 815 TCATTAGACCGA GA A - 1 B c c
GACATCACTAGA TTTCTGG GATGTCTC GG CT
AATTCTGG AAAGATC CTACAGAG CC GA
A- - A

GAM180 214 FLJ2051 1 14414 NP_060323.1 3 1042 TTAGCAGGAGCA ---- T AG 1 B c c

1 GATTTTTCCCAG TTTCTGGGAGA TG CTC GCT
AAGCTGCT GAAGACCCTTT AC GAG CGA
TTAG - GA

GAM180 2143 FLJ2057 1 11877 XP_033853.2 5 55 CCTCGTCACCCT - TC C 1 B c c
GACATCTCTCCG TTTCTGG GAGATGTC AGG
GGAAGACT AAGGGCC CTCTACAG TCC
T -- C

GAM180 2146 FLJ2066 1 8314 NP_060392.1 3 172 GAGCTTGTACTA -- CT---- 1 B c c
TACATCTCCCAA TTTCT GGGAGATGT CAGGCT
AGAAACCC AAAGA CCCTCTACA GTTCGA
AA TATCAT

GAM180 2147 FLJ2216 1 6807 NP_078809.2 5 139 CACAGATGTCGA T---- - A 1 B c c
GACATCTCCCAT TTC TGGGAGATGTCTC GGC
GGATTTGT AGG ACCCTCTACAGAG CTG
TGTTT T -

GAM180 2148 FLJ2257 1 8608 NP_079140.1 3 311 AGGGAAAGTTTA GG C 1 B c c
GACATCTGCAGA TTTCTG AGATGTCT AGGCT

GAGGCAGG AGAGAC TCTACAGA TTTGA
G- -

GAM180 214 FLJ2307 1 16835 NP_079328.1 3 322 ATTTACCAATGA - -- C 1 B c c
4 GACATCTTCCTA TTTCTGGGA GATGTCTCA GG
GGAACTGG AAGGATCCT CTACAGAGT CC
T AA A

GAM180 214 FLJ2346 1 7500 NP_079119.2 3 2435 ATTTCCTACCTA - T C C 1 B c c
2 AGCATCTCCCGA TTTCT GGGAGATG CT AGG
GAAAAATA AAAGA CCCTCTAC GA TCC
G - A A

GAM180 214 FLJ3067 1 2972 NP_694562.1 3 697 AGAAGCTTGGCC - TGT 1 B b b
9 TGAGTCTCCCAG TTT CTGGGAGA CTCAGGCT
CAGAGAAA AGA GACCCTCT GAGTCCGG
C ---

GAM180 214 FLJ3245 1 2212 NP_653177.2 3 433 TACCCTGCCTGA A T 1 B c c
2 GATTCCTCAGGA TTTCTGGG GA GTCTCAGGC
GAAAAGGC GAGGACTC CT TAGAGTCCG
- -

GAM180 214 FLJ3465 1 4616 NP_689617.2 3 529 CTCACTGCCTGA -- AT 1 B c c
8 GACCCCTTCCTT TTTCT GGGAG GTCTCAGGC
AGAGAGCA AGAGA CCTTC CAGAGTCCG
TT CC

GAM180 214 FLJ3481 1 1005 NP_689516.1 5 398 GACGTGTCCATG T CA- 1 B c c
7 GACTTCTCCCAG TTTCTGGGAGA GTCT GGC
GAGGAGTG GAGGACCCTCT CAGG CTG
T TAC

GAM180 214 FLJ3995 2 2358 NP_689749.1 5 88 GGAAGGTGGCCG G - TCA 1 B c c
7 GCTATGTCCCAG TTTCTGGGA AT GTC GGCT
AAACCGTC AAAGACCCT TA CGG CCGG
G T ---

GAM180 214 FLJ3995 2 12852 NP_689749.1 5 394 GGCTCCTCTGGG TG- C 1 B c c
7 AGTTTCTCCCAG TTTCTGGGAGA TCTCAGG
AGAAACCA AGAGACCCTCT AGGGTCT
TTG C

GAM180 214 FLJ4023 1 4486 NP_775906.1 3 387 GTCAGTGCCTGA C AGA 1 B c c
5 GATACACCTACA TTT TGGG TGTCTCAGGC
AGAGCGCC GAA ATCC ATAGAGTCCG
C AC-

GAM180 214 FLJ9079 1 14320 NP_699198.1 3 1291 GGAGAAGCCTGA T----- - AGA 1 B c
c
8 GACAAGCCACAG TTCTG GG TGTCTCAGGCT
AACCCCTC AAGAC CC ACAGAGTCCGA
CTCCCC A GA-

GAM180 214 FOXP1 1 19853 NP_116071.2 5 125 CTGCTAACAGCC G TGT A 1 B c
c
AGAGTGTCCCAG TTTCTGGGA A CTC GGCT
AAGCTTTT GAAGACCCT T GAG CCGA
G --- A

GAM180 214 FPR1 1 2325 NP_002020.1 5 1 AGAGCCTGAGTC - - T 1 B c c

ACTCTCCCCAGG TTTCTGGG AGA TG CTCAGGCT
AGACCCAG GAGGACCC TCT AC GAGTCCGA
C C T

GAM180 214 FPRL2 1 13294 NP_002021.2 5 79 CTTAGAGCCTGA - ATGT 1 B c c
GTTGCTCCACAG TTTCTG GGAG CTCAGGCT
GAATCCAG AAGGAC CCTC GAGTCCGA
A GTT-

GAM180 214 FUT3 1 2915 NP_000140.1 3 304 TTACCTGCTGGG AT- GC 1 B c c
ACCTGCTCCCAG TTTCTGGGAG GTCTCAG
AGACCTTG AGAGACCCTC CAGGGTC
GTC GT

GAM180 214 FUT5 1 2915 NP_002025.1 3 354 TTACCTGCTGGG AT- GC 1 B c c
ACCTGCTCCCAG TTTCTGGGAG GTCTCAG
AGACCTTG AGAGACCCTC CAGGGTC
GTC GT

GAM180 214 FUT6 2 5353 NP_000141.1 5 1086 CCGAGTCCCTCT CTC C 1 B c c
AGCATCTCCCAG TTTCTGGGAGATGT AGG
AAGGTGTC GAAGACCCTCTACG TCC
ATC C

GAM180 214 FUT6 2 7499 NP_000141.1 3 371 TTACCTGCTGGG AT- GC 1 B c c
ACCTGCTCCCAG TTTCTGGGAG GTCTCAG
AGACCTTC AGAGACCCTC CAGGGTC
GTC GT

GAM180 214 FXYD3 1 3047 NP_005962.1 3 834 CCAATGTCCTGA C AG- - 1 B c c
GACATGAACCCA TTT TGGG ATGTCTCAGG C
AAAAGAGA AAA ACCC TACAGAGTCC G
A AAG T

GAM180 214 FXYD3 1 3047 NP_068710.1 3 834 CCAATGTCCTGA C AG- - 1 B c c
GACATGAACCCA TTT TGGG ATGTCTCAGG C
AAAAGAGA AAA ACCC TACAGAGTCC G
A AAG T

GAM180 214 GABBR1 1 7008 NP_068705.1 3 345 CCGGACCATTGA - G -- - 1 B c c
GACATTTGCCAA TTTCT GG AGATGTCTCA GG CT
GGAGGAAC GAGGA CC TTTACAGAGT CC GG
A G TA A

GAM180 214 GAC1 1 7458 NP_006329.1 3 240 GCCATTCTGAGG G -- C 1 B c c
AACATCTCCAAG TTTCT GGAGATGT CTCAGG
GAACGGGA AAGGA CCTCTACA GAGTCT
A AG T

GAM180 214 GARP 1 10909 NP_005503.1 3 537 GGATTTGTCTGA TT-- --- 1 B c c
GACATTTCCAAG TCTG GGAGATGTCTCAGGC
CAGACTGT AGAC CCTTTACAGAGTCTG
TGTC GAA

GAM180 214 GLCCI1 1 14024 XP_166529.2 3 2320 CGCTTTGCCATG GTCT - 1 B c c

TAAATTTCCCAG TTTCTGGGAGAT CA GGC
AAGTTGTT GAAGACCCTTTA GT CCG
AAT- A

GAM180 214 GLUL 1 661 NP_002056.2 5 308 CCCTTCTCCATC TGTCTCA 1 B c c
GCCCTCTCCCAG TTTCTGGGAGA GGC

AAAGCTCC AAAGACCCTCT CCG
C------
GAM180 214 gm117 1 1842 XP_086187.1 3 102 GGGTTATTATGC TG CTCA 1 B c c

CACATCTCCATG TTTC GGAGATGT GGC
AAAATGCA AAAG CCTCTACA CCG
TA ----
GAM180 214 GPR124 1 14853 NP_116166.6 3 194 TGGGGTAGCGAC GA CAG 1 B c
c
AGACAATCCCAG TTTCTGGGA TGTCT GCT
AAACACGC AAAGACCCT ACAGA CGA
A- CAG
GAM180 214 HAS3 1 17871 NP_005320.2 3 524 GATTGCGCCTGA AGA-- 1 B c c
GATACAAGGCCC TTTCTGGG TGTCTCAGGC
AGAAGCCT GAAGACCC ATAGAGTCCG
GGAAC
GAM180 214 HD 1 4516 NP_002102.2 3 238 GGCTGAGCCTGA AT 1 B b b
GGCCTTCCAGAA TTTCTGGGAG GTCTCAGGCT
AGCAGGAG AAAGACCTTC CGGAGTCCGA
--
GAM180 214 HIP1 1 17634 NP_005329.2 3 3416 ACAGTGCCCTGA G- AT - 1 B c c
GACCTCTAGAGA TTTCT GGAG GTCTCAGG C
AAAGATGT AAAGA TCTC CAGAGTCC G
GA -- C
GAM180 214 HTATIP 1 20106 NP_006379.1 5 189 GGTCCCGGAAGT --- A C 1 B c c
GACGTCTCCCAG TTTCTGGGAGATGTC TC GG
AGGGGCCG GGAGACCCTCTGCAG AG CC
TGA G C
GAM180 214 IL4I1 1 17359 NP_690863.1 5 46 AGAGCTGGAGAC -- --- A 1 B c c
ACCATCTCCCAC TTTC TGGGAGA TGTCTC GGCT
CGAGAGTC AGAG ACCCTCT ACAGAG TCGA
CC ACC G
GAM180 214 KIAA025 1 10239 NP_055600.1 3 4053 GCTGAGCCAGGA TGT A- 1 B c
c
8 GTCCTCTCCCAG TTTCTGGGAGA CTC GGCT
AAGTTGGG GAAGACCCTCT GAG CCGA
CCT GA
GAM180 214 KIAA051 1 931 NP_055547.1 3 4575 GTTGGTGCCTGA GGAGA 1 B c
c
3 GACACCAAATGG TTTCTG TGTCTCAGGC
AAGAAGCA GAAGGT ACAGAGTCCG
AAACC
GAM180 214 KIAA068 1 12275 NP_055667.1 3 622 GAGGTCTGCCTG A TCT 1 B c c

2 TTTCGTCCCCAG TTTCTGGG GATG CAGGC
AAACTTGA AAAGACCC CTGC GTCCG
- TTT
GAM180 214 KIAA075 1 10688 NP_055619.1 3 1105 AAGAATGCCTGA TT AGA 1 B c
c
3 GACGCCCCCAGG T CTGGG TGTCTCAGGC

GAATAAGG A GACCC GCAGAGTCCG
GG CC-
GAM180 214 KIAA093 1 17230 XP_052620.6 3 885 GCCACAGCCTGA C GATGT 1 B c c
5 GTGAATCCTACA TTT TGGGA CTCAGGCT
AATATTAC AAA ATCCT GAGTCCGA
C AAGT-
GAM180 214 KIAA111 1 15309 XP_171233.1 3 853 GGCAGGTGGAAA ---- CAG- 1 B c c
1 ACCATCTCCCAG TTTCTGGGAGATG TCT GCT
AAACCTGA AAAGACCCTCTAC AGG CGG
CAAA TGGA
GAM180 214 KIAA119 1 5209 NP_056270.2 3 2965 AGATAGGCAGAG G - AG 1 B c c
4 AACATCTCCAGA TTTCTGG AGATGT CTC GCT
AATGTGTG AAAGACC TCTACA GAG CGG
- A A-
GAM180 214 KIAA126 1 16742 XP_291055.1 3 1572 TTCCTTGCCTGA A TG 1 B b b
8 GATCACCTAGAA TTTCTGGG GA TCTCAGGC
AGGAACCC AAAGATCC CT AGAGTCCG
A --
GAM180 214 KIAA176 1 15863 XP_047355.1 3 727 CCCTGAGCCTGA TG-- T 1 B c c
5 GTCATTTCTATG TTTC GGAGATG CTCAGGCT
TGAAGTCA GAAG TCTTTAC GAGTCCGA
TGTA T
GAM180 214 KIAA200 1 16865 XP_291322.1 3 2151 TGAAGGCAGCCC GT CA 1 B c c
1 AAGGTCTCCCAG TTTCTGGGAGAT CT GGCT
AGGCTCGG GGAGACCCTCTG GA CCGA
-- AC
GAM180 214 KIAA202 1 9621 NP_742067.1 3 906 TTAGAAATGCTC A T CA 1 B c c
4 AGACTTCCCCAG TTTCTGGG GA GTCT GGC
AAATGAAC AAAGACCC CT CAGA TCG
- T C-
GAM180 214 KPNB1 1 15603 NP_002256.2 3 1092 TTGTGGCAGTCT AGA C 1 B c c
GAACGCCCCCAG TTTCTGGG TGT TCAGGCT
AAAATTGT AAAGACCC GCA AGTCTGA
CC- -
GAM180 214 LOC1149 1 1173 NP_660284.1 3 1603 GCAGCAGCTGAC T- C -- 1 B c c
87 ACTTTTTCCCAG TTTCTGGGAGA GT TCAG GCT
AAGGGAGA GAAGACCCTTT CA AGTC CGA
TT C GA
GAM180 214 LOC1164 1 1933 XP_058185.1 3 248 GTGCCAGCCTGA GG AT-- 1 B c c
37 GACTCAACTATC TTTCTG AG GTCTCAGGCT
AGGAAAAA AAGGAC TC CAGAGTCCGA
TA AACT
GAM180 214 LOC1261 1 16559 XP_064964.5 3 113 TGCAAACACCTG AG G C 1 B c c

62 GGAGGTACCCAG TTTCTGGG AT TCTCAGG
AAAACAGC AAAGACCC TG AGGGTCC
A- G A
GAM180 214 LOC1267 1 8959 XP_060167.4 5 65 GCAGCAGCCTGA TT - TGT 1 B c c
67 GTGTTCTCACTA T CTGG GAGA CTCAGGCT
GGGGTCAC G GATC CTCT GAGTCCGA
GG A TGT
GAM180 214 LOC1291 1 13916 XP_072197.3 5 565 TCGATGGCCTGA T- AGA 1 B c c
98 GACACACCCCTT TTTC GGG TGTCTCAGGCT
GAGAAGAA AGAG CCC ACAGAGTCCGG
TT CAC
GAM180 214 LOC1429 1 788 XP_096363.1 3 989 TAATGAGTCTGT ATGTCT 1 B c c
41 TCTGGCTCCCAG TTTCTGGGAG CAGGCT
AAGATGCC GAAGACCCTC GTCTGA
GGTCTT
GAM180 214 LOC1433 1 10414 XP_084485.1 5 556 ATCGGATGCCTG ATGTCT 1 B c c
10 CGTGCCTCCCAG TTTCTGGGAG CAGGC
AAGTGGGT GAAGACCCTC GTCCG
CGTGC-
GAM180 214 LOC1439 1 7055 XP_084664.1 5 246 TTGCTTGCCTGT TT ---- T 1 B c c
16 GACATCTCTGTG T CTG GGAGATGTC CAGGC
GCAGGGGT G GAC TCTCTACAG GTCCG
GG GGTG T
GAM180 214 LOC1440 1 2879 XP_096520.1 3 85 CTTCGGCAGCCT AGATG -- 1 B c c
17 TAGGGAACCCAG TTTCTGGG TCTC AGGCT
AAAGTAGT AAAGACCC AGGG TCCGA
A---- AT
GAM180 214 LOC1478 1 1554 XP_085901.1 3 1550 GAGACAGCCTGA --- AG 1 B c c
04 GATATGGCCTCA TTTCT GGG ATGTCTCAGGCT
TGGGAAGG AAGGG TCC TATAGAGTCCGA
TAC GG
GAM180 214 LOC1479 1 19458 XP_097351.2 5 322 TGACTGGCCTGA G-- T 1 B c c
75 GACTCTATACCG TTTCTGG AGA GTCTCAGGCT
GGAGTCTC GAGGGCC TCT CAGAGTCCGG
ATA -
GAM180 214 LOC1484 1 16289 XP_086210.2 5 31 GCACATGCCTCG -- CTC 1 B c c
90 CGTTCTTCCCAG TTTCTGGGA GATGT AGGC
AAAGTCAG AAAGACCCT TTGCG TCCG
TC C--
GAM180 214 LOC1502 1 18952 XP_097870.1 3 5195 GTAAAAGCCCCC AT A-- 1 B c c
25 GAGACCTCCCAG TTTCTGGGAG GTCTC GGCT
AAGCCAAG GAAGACCCTC CAGAG CCGA
-- CCC
GAM180 214 LOC1507 1 1321 XP_032542.1 3 601 TTCAGGAGCCTA T----- AT C 1 B c c

```
          76                      AGACCCTCCCAG      TTCTGGGAG  GTCT AGGCT
                                  AGCCCAGG          GAGACCCTC  CAGA TCCGA
                                        GGACCC        C-    A
GAM180    214   LOC1515 2  5239   NP_612492.1  5  289   CCCCTGCCTGGG  TT      TG-            1  B  c
c
          68                      AGGCTCTCCCAG T  CTGGGAGA   TCTCAGGC
                                  GGGCTGAT    G  GACCCTCT   AGGGTCCG
                                        GG       CGG
GAM180    214   LOC1515 2  15467  NP_612492.1  5  940   AGGAGTGCCTAA       AGA  T  C          1  B  c
c
          68                      GCCAGGACCCAG TTTCTGGG   TG CT AGGC
                                  AAACTCAG    AAAGACCC   AC GA TCCG
                                              AGG  C  A
GAM180    214   LOC1524 1  10081  XP_098231.1  5  20    ATAACAGCCTGA       GA--           1  B  c  c
          45                      GACAGAGGTCCC TTTCTGGGA   TGTCTCAGGCT
                                  AGGAGATC    GAGGACCCT    ACAGAGTCCGA
                                              GGAG
GAM180    214   LOC1620 1  9824   XP_091339.2  5  840   TCTCCAGCAGCC        TGT   A         1  B  b  b

          83                      AGAGTCTCCCAG TTTCTGGGAGA   CTC GGCT
                                  AAAACAAC    AAAGACCCTCT   GAG CCGA
                                              ---   A
GAM180    214   LOC1640 1  7693   XP_089356.1  5  662   CCCACAGCCATG       AG   T T -        1  B  c  c

          91                      GCCATGGCCCAG TTTCTGGG  ATG C CA GGCT
                                  AAACTCAG    AAAGACCC  TAC G GT CCGA
                                              GG   C -  A
GAM180    214   LOC1652 1  1432   XP_092478.3  3  118   ATAACACTTCCT     --       TC   C      1  B  c  c
          57                      GACATCTCCTTT TTTCT  GGGAGATGTC  AGG
                                  GGAAAAGA    AAAGG  TCCTCTACAG  TCC
                                              TT        --   T
GAM180    214   LOC2006 1  1876   XP_117256.1  5  3677  GGCCTAACATAT       G    TC-----       1  B  c  c

          09                      GGCATATCCCAG TTTCTGGGA ATGTC      AGGCT
                                  AAAATGTT    AAAGACCCT TACGG      TCCGG
                                              A    TATACAA
GAM180    214   LOC2015 1  12642  XP_114343.2  3  177   ACATGGGCCTGA       GAT-           1  B  c  c

          62                      GATTTTATTTTA TTTCTGGGA   GTCTCAGGCT
                                  GAAAAAGG    AAAGATTTT    TAGAGTCCGG
                                              ATTT
GAM180    214   LOC2199 1  5660   XP_166197.1  5  369   GCCGAAGCCTGA   -  -  ATG          1  B  c  c

          18                      GGAAGCTCATCA TTTC TGG GAG   TCTCAGGCT
                                  TGAGATTC    AGAG ACT CTC   GGAGTCCGA
                                              T  A  GAA
GAM180    214   LOC2200 1  5660   XP_167848.1  5  371   GCCGAAGCCTGA   -  -  ATG          1  B  c  c

          71                      GGAAGCTCATCA TTTC TGG GAG   TCTCAGGCT
                                  TGAGATTC    AGAG ACT CTC   GGAGTCCGA
```

T A GAA
GAM180 214 LOC2207 1 1949 XP_165466.1 5 643 ATACCAGCCTGA GG GT 1 B c c

58 GGTGTCTCAGGG TTTCT GAGAT CTCAGGCT
GAGGCTGG GAGGG CTCTG GAGTCCGA
GA TG
GAM180 214 LOC2207 1 5457 XP_055551.1 5 1241 GATCTGCCCCTG - C C 1 B c c
63 AACATCTCCCGA TTTCT GGGAGATGT TCAGG
GAAATGCT AAAGA CCCTCTACA AGTCC
G - C
GAM180 214 LOC2215 1 13096 XP_168132.1 5 279 TGGCCGTATGAA GT - --- 1 B c c
84 GGTGTCTCCCAG TTTCTGGGAGAT CT CA GGCT
AAGCATTA GAAGACCCTCTG GA GT CCGG
TG A ATG
GAM180 214 LOC2530 1 11944 XP_172924.2 5 491 GCTTTGTCCTGA GAG - 1 B b b

44 GACATCCGGAAA TTTCTGG ATGTCTCAGG C
GGAAAGGG AAAGGCC TACAGAGTCC G
--- T
GAM180 214 LOC2532 1 12769 XP_173102.1 3 824 GCCTGTGCCCAT T T------ 1 B c c
63 GACATCTCCCTG TTTC GGGAGATGTC CAGGC
AAAGAGGA AAAG CCCTCTACAG GTCCG
T TACCCGT
GAM180 214 LOC2830 1 4836 XP_302599.1 5 800 AAAGAAGCCTGA -- T 1 B b b
38 GACTCTCCAACA TTTCTG GGAGA GTCTCAGGCT
GGAGAGCT GAGGAC CCTCT CAGAGTCCGA
AA -
GAM180 214 LOC2830 1 7112 XP_208509.1 3 1662 CGATTGCAAAGC TGTCTC 1 B c
c
87 CTCCTCTCCCAG TTTCTGGGAGA AGGCT
AGACCCCT AGAGACCCTCT TCCGA
CC----
GAM180 214 LOC2831 1 11320 XP_210911.1 3 202 AGCTGCTTGAGA TG A -- 1 B c c

40 GACATCACCTGG TTTC GG GATGTCTC AGGC
AGAAGAAG AGAG CC CTACAGAG TTCG
GT A AG
GAM180 214 LOC2832 1 11643 XP_208606.1 5 271 CGGAGCCCTTGA G GA -- 1 B c
c
98 GACATCCTTGAG TTTCT G GATGTCTCA GGCT
AAGAGCCA GAAGA T CTACAGAGT CCGA
G TC TC
GAM180 214 LOC2833 1 8912 XP_300560.1 3 1814 TGAAAGTATGAT TC- G 1 B c c
37 TTCATTTCCCAG TTTCTGGGAGATG TCA GCT
AAAATGTA AAAGACCCTTTAC AGT TGA
TTT A
GAM180 214 LOC2835 1 12808 XP_211118.1 3 2575 TACCAGCCCTGA T----- AGA - 1 B c
c
70 GACAGACCCCAG TTCTGGG TGTCTCAGG CT
GATAAGGG AGGACCC ACAGAGTCC GA

GGGAAT CAG C

GAM180 214 LOC2835 1 1593 XP_211099.1 5 229 AGAGCAGCTTAG TC G - 1 B c c
74 AGGATCTCCCAA TT TGGGAGAT TCTC AGGCT
GGATGAAA AG ACCCTCTA GGAG TTCGA
GA - A

GAM180 214 LOC2838 1 3590 XP_208853.1 3 2266 CAGGCAGCCTGA AT 1 B c c
10 GATTGCTTCTAG TTTCTGGGAG GTCTCAGGCT
AGATCTTT AGAGATCTTC TAGAGTCCGA
GT

GAM180 214 LOC2838 1 4669 XP_211224.1 5 1294 GAGCCGCCTGCC TT----- GAT 1 B c
c
31 TGAGGCTCCCAG TCTGGGA GTCTCAGGC
ACAGACTG AGACCCT CGGAGTCCG
GTCAGAC ---

GAM180 214 LOC2839 1 11417 XP_211259.2 5 334 GAGGGAGCCAGA -- T CA 1 B c
c
11 CCTCTGGCCCAG TTTCTGGG AGA GTCT GGCT
AAAGCCAG AAAGACCC TCT CAGA CCGA
GG C --

GAM180 214 LOC2839 1 15803 XP_208908.1 5 679 ATCCCTTCTGAG --- - C 1 B c c
22 ATCATCTCCCCC TTTCT GGGAGATG TCTCAGG
AAGAAAGT AAAGA CCCTCTAC AGAGTCT
ACC T T

GAM180 214 LOC2839 1 10481 XP_208905.2 5 362 CTCAGGACATGA TG GG- 1 B c
c
29 GACATTTCCTGG TTTC GGAGATGTCTCA CT
AAGTGATT GAAG CCTTTACAGAGT GG
GT ACA

GAM180 214 LOC2839 1 6204 XP_208954.1 3 265 CAGCAGGCCAGA -- CA 1 B c c
82 CCAGTCTCCCAG TTTCTGGGAGAT GTCT GGCT
GAGGCTGA GAGGACCCTCTG CAGA CCGG
AC --

GAM180 214 LOC2840 1 15106 XP_210776.1 5 403 ACAGCAGTCGGA GG A 1 B c
c
45 GACATCTGGCAG TTTCTG AGATGTCTC GGCT
AGACAAAT AGAGAC TCTACAGAG CTGA
GG G

GAM180 214 LOC2842 1 16999 XP_211391.1 3 697 AATTTGGCCACT - CTCA 1 B c c

20 AACATCTCCCAT TTTC TGGGAGATGT GGCT
GGAATTGT AAGG ACCCTCTACA CCGG
T ATCA

GAM180 214 LOC2843 1 1154 XP_211433.1 5 165 GTTTGCGCCGAC TCTCA 1 B c
c
60 TCCGTCTCCCAG TTTCTGGGAGATG GGC
AAATCAAC AAAGACCCTCTGC CCG
CTCAG

GAM180 214 LOC2845 1 2382 XP_211514.1 3 164 ACTCACCTGGGG -- T C 1 B c c
49 CCTCCATCCCAG TTTCTGGGA GA GTCTCAGG
AAGCGCAG GAAGACCCT CT CGGGGTCC

```
                                                AC  C       A
GAM180  214   LOC2845 1  1916  XP_209277.2  5  662   TTCCCTGCCTGA      GGAGA              1  B  c
c
          85                      GACACGTATGGA TTTCTG    TGTCTCAGGC
                                 AGCCAAGA    GAAGGT    ACAGAGTCCG
                                          ATGC-
GAM180  214   LOC2847 1  16000 XP_209353.1  3  200   GATGCTGCCCCT       GATG     C        1  B  c
c
          73                      GGGAAATCCCAG TTTCTGGGA   TCTCAGG
                                 AAGAGGAA    GAAGACCCT   AGGGTCC
                                          AA--      C
GAM180  214   LOC2849 1  11231 XP_211705.1  3  269   CAGATGACCTGA       G --     C       1  B  c  c
          47                      GACCGGTGTTCC TTTCTGGGA AT  GTCTCAGG
                                 GGAAACTG    AAAGGCCTT TG  CAGAGTCC
                                          G  GC       A
GAM180  214   LOC2850 1  6831  XP_209440.1  3  3513  TCAATGCCCACT         GTCTCA-          1  B  c
 c
          26                      TAGATCTCCCAG TTTCTGGGAGAT      GGC
                                 AAATAGCA    AAAGACCCTCTA      CCG
                                          GATTCAC
GAM180  214   LOC2850 1  12677 XP_211741.1  5  591   TGTCTGTCTGAC  TT T -      -          1  B  c  c
          29                      GACATCTCTCCT T  C GG GAGATGTC TCAGGC
                                 GGGGTCTG    G  G CC CTCTACAG AGTCTG
                                       GG T  T      C
GAM180  214   LOC2850 1  10528 XP_208283.1  5  704   CAGACAGCCTGA      G   T--           1  B  c  c
          56                      GACTGTTCTCAC TTTCTG GAGA   GTCTCAGGCT
                                 GGAAACAC    AAAGGC CTCT   CAGAGTCCGA
                                          A   TGT
GAM180  214   LOC2852 1  555   XP_211834.1  3  42    TCCCCGGCCATG        ATG  T -        1  B  c  c
          86                      TGGAACTCCCAG TTTCTGGGAG   TC CA GGCT
                                 AGACAGAA    AGAGACCCTC   GG GT CCGG
                                          AA-  T  A
GAM180  214   LOC2853 2  1613  XP_211864.1  3  585   GAAGGTGGCCAG       GAT  C  A         1  B  c
c
          76                      AAACCGTCCCAG TTTCTGGGA   GT TC GGCT
                                 AAACTGCC    AAAGACCCT   CA AG CCGG
                                          GC-  A  A
GAM180  214   LOC2853 2  15389 XP_211864.1  3  881   GTCGTGTCTGGG        TG-           1  B  c  c
          76                      AGTTTCTCCCAG TTTCTGGGAGA   TCTCAGGC
                                 AGAAACCA    AGAGACCCTCT   AGGGTCTG
                                          TTG
GAM180  214   LOC2857 1  7150  XP_208349.1  3  909   GCTTGCTTGATA    ----       --       1  B  c  c
          86                      GACATCTCTTAC TTTC    TGGGAGATGTC  TCAGGC
                                 AGTGAGAC    AGAG    ATTCTCTACAG  AGTTCG
                                          TGAC        AT
GAM180  214   LOC2859 1  8264  XP_212120.1  3  260   GCTCTGCCATCT       A   TCA-          1  B  c  c
          99                      GACAGCTCCCAG TTTCTGGGAG TGTC    GGC
                                 AGGGTTCT    GGAGACCCTC ACAG    CCG
                                          G    TCTA
GAM180  214   LOC3387 1  17540 XP_294683.1  3  150   CCGGAAACCTGA     GG  -      C        1  B  c
c
```

```
          08                    GACATGCTCAAG TTTCT  GAG ATGTCTCAGG
                                GAAGAGCA    GAAGG  CTC TACAGAGTCC
                                      AA  G        A
GAM180    214   LOC3389 1  5719  XP_290664.1  3  101   AGACACCTCTGA       ATGT    C        1  B  c
c
          87                    GTAAACTCCCAG TTTCTGGGAG   CTCAGG
                                AAAGCCTG    AAAGACCCTC   GAGTCT
                                      AAAT     C
GAM180    214   LOC3391 1  11297 XP_294845.1  5  523   CCGAGGGCCTTG       GAT-  TC         1  B  c
c
          86                    GCTGGGTCCCAG TTTCTGGGA   GTC  AGGCT
                                AAATTCCC    AAAGACCCT   CGG  TCCGG
                                      GGGT   T-
GAM180    214   LOC3392 1  11297 XP_294880.1  5  523   CCGAGGGCCTTG       GAT-  TC         1  B  c
c
          40                    GCTGGGTCCCAG TTTCTGGGA   GTC  AGGCT
                                AAATTCCC    AAAGACCCT   CGG  TCCGG
                                      GGGT   T-
GAM180    214   LOC3392 1  11297 XP_294886.1  5  523   CCGAGGGCCTTG       GAT-  TC         1  B  c
c
          58                    GCTGGGTCCCAG TTTCTGGGA   GTC  AGGCT
                                AAATTCCC    AAAGACCCT   CGG  TCCGG
                                      GGGT   T-
GAM180    214   LOC3397 1  9131  XP_295053.1  3  1271  ACCTCCCTTGTT         CT-   C       1  B  c  c
          51                    AGCATCTCCCAG TTTCTGGGAGATGT  CAGG
                                AGAACCTG    AGAGACCCTCTACG  GTTC
                                      ATT    C
GAM180    214   LOC3398 1  2376  XP_295096.1  3  93    CAGCAAGTCTGA        GTC           1  B  c  c
          99                    AGAGTTTCCCAG TTTCTGGGAGAT   TCAGGCT
                                AAGCCCTG    GAAGACCCTTTG   AGTCTGA
                                      AGA
GAM180    214   LOC3400 1  13639 XP_295154.1  5  400   GCTCCAGCCTGA       GAT            1  B  b  b

          90                    GGCTTCCAGAAG TTTCTGGGA   GTCTCAGGCT
                                TGCCCTAC    GAAGACCTT   CGGAGTCCGA
                                      ---
GAM180    214   LOC3423 1  11373 XP_296817.2  5  723   GGCAGTCTGTAG        A  -  -         1  B  c  c
          46                    AGCAGCTCCCAG TTTCTGGGAG TG TCT CAGGCT
                                AGGCTGCC    GGAGACCCTC AC AGA GTCTGA
                                      G  G   T
GAM180    214   LOC3475 1  3508  XP_298101.2  5  385   GGCGTCGCCTGA       AGA  -          1  B  c  c

          46                    GATCAGGGCCCG TTTCTGGG   TG TCTCAGGC
                                GGAAGCCC    AAGGGCCC   AC AGAGTCCG
                                      GGG  T
GAM180    214   LOC3476 1  2916  XP_300226.1  3  1445  GCTCACCTGGGG       -- T     C       1  B  c  c
          48                    CCTCCATCCCAG TTTCTGGGA  GA GTCTCAGG
                                AAGCGCAG    GAAGACCCT  CT CGGGGTCC
                                      AC  C       A
GAM180    214   LOC3478 1  5296  XP_302617.1  3  178   TGGGCCATTGAT         C-  --        1  B  c  c
```

84 AGCATCTCCCAG TTTCTGGGAGATGT TCA GGCT
GAACAACG AAGGACCCTCTACG AGT CCGG
AT TA
GAM180 214 LOC3481 1 14248 XP_302657.1 3 369 TTTGCGTGCATC A G ---- G 1 B c c

12 AGAATCACCCAG TTTCTGGG GAT TCT CA GC
AAAGATGT AAAGACCC CTA AGA GT CG
A - CTAC G
GAM180 214 LOC3484 1 1711 XP_300742.1 5 811 CAGCGTGTCTAC CT---- G 1 B c c
52 AACGTCTCCCAG TTTCTGGGAGATGT CA GCT
AAGCTCTA GAAGACCCTCTGCA GT CGA
ACATCT G
GAM180 214 LOC3490 1 7090 XP_300945.1 5 168 CCACAATCCTGA A T- C 1 B c c
94 GACTTTCCCCCG TTTCTGGG GA GTCTCAGG
GGAGGCAC GAGGGCCC CT CAGAGTCC
C TT T
GAM180 214 LOC3490 1 7090 XP_300940.1 5 168 CCACAATCCTGA A T- C 1 B c c
97 GACTTTCCCCCG TTTCTGGG GA GTCTCAGG
GGAGGCAC GAGGGCCC CT CAGAGTCC
C TT T
GAM180 214 LOC3491 1 7090 XP_300960.1 5 136 CCACAATCCTGA A T- C 1 B c c
38 GACTTTCCCCCG TTTCTGGG GA GTCTCAGG
GGAGGCAC GAGGGCCC CT CAGAGTCC
C TT T
GAM180 214 LOC3493 1 1916 XP_301019.1 5 662 TTCCCTGCCTGA GGAGA 1 B c
c
05 GACACGTATGGA TTTCTG TGTCTCAGGC
AGCCAAGA GAAGGT ACAGAGTCCG
ATGC-
GAM180 214 LOC3512 3 1629 XP_304390.1 3 579 AGTGCAAGTCAG AGA T A 1 B c
c
28 AGCAAAGCCCAG TTTCTGGG TG CTC GGCT
AAAGCAGA AAAGACCC AC GAG CTGA
GAA - A
GAM180 214 LOC3512 3 5030 XP_304390.1 3 853 TCAGATGCCCCT AGAT C 1 B c
c
28 GAGACCACCCAG TTTCTGGG GTCTCAGG
AAATCAAG AAAGACCC CAGAGTCC
AC-- C
GAM180 214 LOC3512 3 17782 XP_304390.1 3 853 AGATGCCCCTGA AGAT C 1 B c
c
28 GACCACCCAGAA TTTCTGGG GTCTCAGG
ATCAAGCG AAAGACCC CAGAGTCC
AC-- C
GAM180 214 LOC9223 1 11492 XP_043739.2 3 422 GTAGAGGCTTCA AGATG ----- 1 B c
c
5 TATGAGACCCAG TTTCTGGG TCTCA GGCT
AAAGTCTA AAAGACCC AGAGT TCGG
----- ATACT
GAM180 214 LOC9271 1 17389 XP_046811.2 3 912 GGGCCTTCCTGA AGA C 1 B c
c

```
          0                          GACACATTCAGA TTTCTGGG  TGTCTCAGG
                                     GAAGGATC    AGAGACTT  ACAGAGTCC
                                               AC-       T
GAM180  214  LY6H   1  16930 NP_002338.1  3  207  CCCAGGCAGCTG    G      T  --       1  B  c  c
                                     GACATCTCCAGG TTTCT GGAGATGTC CAG  GCT
                                     AAACCAGG    AAAGG CCTCTACAG GTC  CGG
                                               A       -  GA
GAM180  214  LYPLA3  1  10576 NP_036452.1  3  1035  AGCTTAGTGCTG      AGAT    -       1  B  c
c
                                     GGACTAGCCCAG TTTCTGGG   GTCTCAG GCT
                                     AAACTTGA    AAAGACCC    CAGGGTC TGA
                                               GAT-      G
GAM180  214  MGC1033 1  1711  NP_085052.1  5  109   CAGCGTGTCTAC          CT---- G      1  B  c
c
          4                          AACGTCTCCCAG TTTCTGGGAGATGT     CA GCT
                                     AAGCTCTA    GAAGACCCTCTGCA     GT CGA
                                                 ACATCT  G
GAM180  214  MGC1033 1  1711  XP_300761.1  5  811   CAGCGTGTCTAC          CT---- G      1  B  c  c

          4                          AACGTCTCCCAG TTTCTGGGAGATGT     CA GCT
                                     AAGCTCTA    GAAGACCCTCTGCA     GT CGA
                                                 ACATCT  G
GAM180  214  MGC3468 1  4811  NP_689559.1  3  490   CGGCCAGCCTGA    -  AGAT          1  B  c
c
          0                          GGCTGCCTGAGG TTTCT GGG   GTCTCAGGCT
                                     AAGGAAGG    AAGGA TCC    CGGAGTCCGA
                                               G   GT--
GAM180  214  MGC4004 1  15660 NP_689726.2  5  102   TGATTAGCCTGA    T    ATG          1  B  c
c
          2                          GGACCTTCCTGA TTTC GGGAG   TCTCAGGCT
                                     GGAGGAAT    GGAG CCTTC   GGAGTCCGA
                                               T    CA-
GAM180  214  MGC4190 1  5085  NP_689687.1  3  145   AGAAATGCCAGA       GAT--   CA       1  B  c
c
          6                          CCTGTATCCCAG TTTCTGGGA    GTCT  GGC
                                     AAAATAAA    AAAGACCCT    CAGA  CCG
                                               ATGTC   --
GAM180  214  MGC4767 1  8947  NP_115690.1  3  215   GAGCTGCTTCAG          T- C        1  B  c  c
                                     TCCATCTCCCAG TTTCTGGGAGATG  CT AGGC
                                     AGGCATTT    GGAGACCCTCTAC  GA TTCG
                                                 CT  C
GAM180  214  MPRA   1  7693  NP_848509.1  5  91    CCCACAGCCATG       AG  T T -       1  B  c  c
                                     GCCATGGCCCAG TTTCTGGG  ATG C CA GGCT
                                     AAACTCAG    AAAGACCC  TAC G GT CCGA
                                               GG   C -  A
GAM180  214  MS4A6A  1  14166 NP_690590.1  3  409   ATCATTCCCAGA          C  A  C       1  B  c  c
                                     AACATTTCCCAG TTTCTGGGAGATGT TC GG
                                     AAAATGTT    AAAGACCCTTTACA AG CC
                                                 A  A  C
GAM180  214  MS4A6A  1  14166 NP_690591.1  3  303   ATCATTCCCAGA          C  A  C       1  B  c  c
```

AACATTTCCCAG TTTCTGGGAGATGT TC GG
AAAATGTT AAAGACCCTTTACA AG CC
A A C
GAM180 214 NCAG1 1 18626 NP_115536.1 3 2664 GATGGTGCCTGA - - AT 1 B c c
GACCCCTGCCTT TTTCTG GG AG GTCTCAGGC
AGAAACAG AAAGAT CC TC CAGAGTCCG
T G CC
GAM180 214 NET-7 1 11703 NP_036471.1 3 309 GGGAGAGCCTGA T----- - T 1 B c c
GGCTCTGCTCAG TTCTGGG AGA GTCTCAGGCT
GGCCCATT GGGACTC TCT CGGAGTCCGA
TTACCC G -
GAM180 214 NFIB 1 13925 NP_005587.1 5 167 AAGATTTTCTTG T C 1 B c c
GGCATCTCCCGG TTTCTGGGAGATGTC CAGG
AAAGTGCG AAAGGCCCTCTACGG GTTC
- T
GAM180 214 NMNAT2 1 8057 NP_055854.1 3 2335 TCAGCAGCTTGG GATG- T 1 B c
c
AAGAAATCCCAG TTTCTGGGA TC CAGGCT
AAGCGGAC GAAGACCCT AG GTTCGA
AAAGA -
GAM180 214 NOS1 1 17856 NP_000611.1 3 1509 AAATTAGTGTCA A CA 1 B c c
GGCAGTTCCCAG TTTCTGGGAG TGTCT GGC
AAAGAGAC AAAGACCCTT ACGGA CTG
G --
GAM180 214 NPR3 1 9247 NP_000899.1 3 49 TTTTCTGCCTGA GG T 1 B c c
GATTCTTTAAGG TTTCT GAGA GTCTCAGGC
AGATAGAC GAGGA TTCT TAGAGTCCG
AT -
GAM180 214 NRLN1 1 15259 NP_660277.1 3 193 TGTCAGCCCTTG ---- C -- 1 B c c
AACATCTCCTCC TTTCT GGGAGATGT TCA GGCT
AAAGAGAC AGAGA TCCTCTACA AGT CCGA
AACC - TC
GAM180 214 OSR1 1 18887 NP_660303.1 3 314 GAGCCGCAGCGG -- TCA-- 1 B c c
CGCCTCTCCCAG TTTCTGGGAGA TGTC GGCT
AAGTATTA GAAGACCCTCT GCGG CCGA
CC CGACG
GAM180 214 P8 1 9958 NP_036517.1 3 247 GGCAGAGCCAGG A G- CA 1 B c c
AAGATCCCCCAG TTTCTGGG GAT TCT GGCT
AAAAGAAA AAAGACCC CTA AGG CCGA
C GA A-
GAM180 214 PDE8B 1 17979 NP_003710.1 3 348 GGTGCCTGTGAG T----- --- T 1 B c c
CTCATCTCCCAG TTCTGGGAGATG TC CAGGC
GATGGTGA AGGACCCTCTAC AG GTCCG
AGTGGT TCG T
GAM180 214 PEX10 1 13341 NP_002608.1 3 696 ATCTCAGCCTGA GGAGA 1 B c
c
GACGCACAGAGA TTTCTG TGTCTCAGGCT
GGTCTCTT AGAGAC GCAGAGTCCGA
AC---
GAM180 214 PEX10 1 13341 NP_722540.1 3 696 ATCTCAGCCTGA GGAGA 1 B c
c

GACGCACAGAGA TTTCTG TGTCTCAGGCT
GGTCTCTT AGAGAC GCAGAGTCCGA
AC---

GAM180 214 PFDN5 1 11809 NP_665903.1 3 249 GCTAAGGCCTGA G TG 1 B c c
GAGTTTTTGCAG TTTCTG GAGA TCTCAGGCT
AAATGGGG AAAGAC TTTT AGAGTCCGG
G TG

GAM180 214 PNMA2 1 10910 NP_009188.1 3 1214 TCCACAGCCTGA --- G G 1 B c c
GAGGTGTCCCCA TTTCT GGGA AT TCTCAGGCT
AAGAAAGG AAAGA CCCT TG AGAGTCCGA
AAC G G

GAM180 214 PPM1F 1 5913 NP_055449.1 3 2383 ACCCTAGCCTGA TG GA T 1 B c
c

GGCTCCACTGGA TTTC G GA GTCTCAGGCT
AGATCTCG GAAG C CT CGGAGTCCGA
GT AC -

GAM180 214 PPP1R1B 1 8599 NP_115568.2 3 30 TAGCACCCAGCC TCT 1 B b b
TGCATCTCCCAG TTTCTGGGAGATG CAGGCT
GAGGAAGT GAGGACCCTCTAC GTCCGA

GAM180 214 PPP1R1B 1 8599 NP_852606.1 3 30 TAGCACCCAGCC TCT 1 B b b
TGCATCTCCCAG TTTCTGGGAGATG CAGGCT
GAGGAAGT GAGGACCCTCTAC GTCCGA

GAM180 214 PRO2086 1 15425 NP_054830.1 5 329 CCTACTGCCTGA GA 1 B c c
GATGGTTCCAGA TTTCTGGGA TGTCTCAGGC
GGCGGTCT GGAGACCTT GTAGAGTCCG
G-

GAM180 214 PRX 1 15552 NP_066007.1 3 1998 AAAGGTGCCTGA T A-- 1 B c c
GATGAAACTTCC TTTC GGGAG TGTCTCAGGC
TGAGATGA AGAG CCTTC GTAGAGTCCG
T AAA

GAM180 214 PSTPIP1 1 1021 NP_003969.2 3 137 GAGAGGGAGCCT TT TCT 1 B c
c

GTCGTCTCCCAG T CTGGGAGATG CAGGCT
GGAATAAA A GACCCTCTGC GTCCGA
GG T--

GAM180 214 RAB17 1 17352 NP_071894.1 3 638 GGAAGATTCTGA T - C 1 B c c
GACATTTCGCCT TTTC GG GAGATGTCTCAGG
GAGATATA AGAG CC CTTTACAGAGTCT
T G T

GAM180 214 RAI14 1 15321 NP_056392.1 3 159 AAGGTTTCTGAG T - C 1 B c c
GACTTCTCCCAG TTTCTGGGAGA GTC TCAGG
GAGAAGAC GAGGACCCTCT CAG AGTCT
T G T

GAM180 214 RDS 1 14017 NP_000313.1 3 107 ACTCCGAAAGTC - GTC 1 B c c
TGAATCTCCCAA TTTCT GGGAGAT TCAGGCT
GGAGGGCA GAGGA CCCTCTA AGTCTGA
A ---

GAM180 214 RERE 1 1004 NP_036234.2 3 227 TCTCCCTGCATG A - T-- C 1 B c c

ACAGTCCCCCAG TTTCTGGG GA TGTC CAGG
AAACTTAG AAAGACCC CT ACAG GTCC
C G TAC C

GAM180 214 RHCG 1 9363 NP_057405.1 3 324 GTGGGTGAACCT T T C 1 B c c
GAGCTCTCCCAG TTTCTGGGAGA G CTCAGG
GAGACAAC GAGGACCCTCT C GAGTCC
- - A

GAM180 214 RNAHP 1 13198 NP_031398.1 3 936 GACCCAGGCTCT GAT - - 1 B c c

GAAGATTCCCAG TTTCTGGGA GTCT CAG GCT
AAGCCACA GAAGACCCT TAGA GTC CGG
--- A T

GAM180 214 RODH-4 1 8216 NP_003699.2 3 517 CATAGGCCTCAG - GT C 1 B c c
GAGTCATCCCAG TTTCTGGGA GAT CT AGGCT
AAGCAGTG GAAGACCCT CTG GA TCCGG
A AG C

GAM180 214 SALL2 1 12473 XP_300608.1 3 961 ATTTCTTGCCAA G CA 1 B c c
GAGGTCTCCCAG TTTCTGGGAGAT TCT GGC
GAGATATT GAGGACCCTCTG AGA CCG
G A-

GAM180 214 SBP1 1 19335 NP_835222.1 5 730 ATGGCACCCTGA AGA C 1 B c c
GACAGCCCAGAG TTTCTGGG TGTCTCAGG
GTGAATAG GGAGACCC ACAGAGTCC
G-- C

GAM180 214 SDNSF 1 5177 NP_644808.1 3 1613 CAGCTGGCTTGA - T C 1 B c c
ATTTCTCCCCAG TTTCTGGG AGA GT TCAGGCT
AAAATGGG AAAGACCC TCT TA AGTTCGG
C T -

GAM180 214 SDPR 1 5176 NP_004648.1 5 90 ACCCGAGCAAGA A TC AG 1 B c c
AGCAGCTCCCAG TTTCTGGGAG TG TC GCT
AGAGAAAG AGAGACCCTC AC AG CGA
G GA AA

GAM180 214 SLC16A1 1 2213 NP_061063.2 5 170 CCTCGGGCCATG T CT - 1 B c c
0 GTGCTCTCCCAG TTTCTGGGAGA GT CA GGCT
GAGGAGCC GAGGACCCTCT CG GT CCGG
- TG A

GAM180 214 SLC4A10 1 7776 NP_071341.1 3 276 TTCGGAGCAGGA ------ A AG 1 B c
c
GACATCCCTGTG TTTCTG GG GATGTCTC GCT
AGCAGAAA AAAGAC CC CTACAGAG CGA
GAGTGT - GA

GAM180 214 SLC4A5 1 15696 NP_201580.2 3 18 GCCTGGATTGCA - C----- 1 B c c
ACATCCTCCCAG TTTCTGGGAG ATGT TCAGGC
AGAAGGAA AGAGACCCTC TACA GGTCCG
C ACGTTA

GAM180 214 SLC5A2 1 3698 NP_003032.1 3 78 TGAGGAGCCTGC A - GT T 1 B c c
GGTGCTCCCCAG TTTCTGGG GA T C CAGGCT
AAAAGGGG AAAGACCC CT G G GTCCGA
- C TG C

GAM180 214 SMCR7 1 15179 NP_631901.2 5 190 CAGACCATGGCA ---- TCA - 1 B c c

GAGTTCTCCCAG TTTCTGGGAGA TGTC GG CT
AAACGGG AAAGACCCTCT ACGG CC GA
TGAG TA- A

GAM180 214 SMCR7 1 15179 NP_683684.1 5 59 CAGACCATGGCA ---- TCA - 1 B c c
GAGTTCTCCCAG TTTCTGGGAGA TGTC GG CT
AAACGGG AAAGACCCTCT ACGG CC GA
TGAG TA- A

GAM180 214 SMPX 1 15935 NP_055147.1 3 128 CTGAATGCCTGA GG T 1 B b b
GACTCTAGCAGA TTTCTG AGA GTCTCAGGC
AATGGCCT AAAGAC TCT CAGAGTCCG
GA -

GAM180 214 SOST 1 5377 NP_079513.1 3 440 CAGAAAGCCTGA T------ AG 1 B c c
GGCGTGCCCAGA TTCTGGG ATGTCTCAGGCT
GCACAAGA GAGACCC TGCGGAGTCCGA
AGAACAC G-

GAM180 214 SPEC1 1 8847 NP_064624.1 3 2153 TCAGTAGCCTGA GA- T 1 B c c
GTGTTATACTAG TTTCTGG GATG CTCAGGCT
AGATCTAA AGAGATC TTGT GAGTCCGA
ATA -

GAM180 214 STX16 1 8099 NP_003754.1 5 12 GCTTGAGCCTGA G GA T 1 B c c
GGCCTTGTCGAG TTTCT G GA GTCTCAGGCT
AAGCTTCC GAAGA C TT CGGAGTCCGA
G TG C

GAM180 214 STX3A 1 15455 NP_004168.1 3 394 CTACCTCATGGA TGT ---- C 1 B c c
GTATTCTCCCAG TTTCTGGGAGA CTC AGG
AAACTGCA AAAGACCCTCT GAG TCC
TAT GTAC A

GAM180 214 SURF5 1 4742 NP_852468.1 3 1994 AGTCTCAGGCAG AGA AG 1 B c
c
GGACAGACCCAG TTTCTGGG TGTCTC GCT
AAAGAACA AAAGACCC ACAGGG CGG
AG- A-

GAM180 214 TCF4 1 12785 NP_003190.1 3 290 TGTACAGGCTGA AGA G 1 B c c
GACACAGCCCAG TTTCTGGG TGTCTCAG CT
AGACTGAA AGAGACCC ACAGAGTC GA
GAC G

GAM180 214 TIAF1 1 16174 NP_510880.2 3 69 TGGCTGCCTGGG T - 1 B b b
CACCTCTCCCAG TTTCTGGGAGA GT CTCAGGC
GAAGTGGT AAGGACCCTCT CA GGGTCCG
C C

GAM180 214 TMEPAI 1 10288 NP_064567.2 3 1330 GTGACAAGCCTG T----- TGT 1 B c
c
GGTTTCTCCCAG TTCTGGGAGA CTCAGGCT
GATAGGTG AGGACCCTCT GGGTCCGA
GTGGAT TT-

GAM180 214 TNRC5 1 1159 NP_006577.1 5 158 CATTAGCTAGAG AGA - A 1 B c c
AGCAAACCCCAG TTTCTGGG TG TCTC GGCT
AAAGCCTA AAAGACCC AC AGAG TCGA
CAA G A

GAM180 214 TOP2A 1 12252 NP_001058.2 3 714 TGCCTCTGAGTC -- GT--- -- 1 B c c

TGAATCTCCCAA TTTCT GGGAGAT CTCA GGC
AGAGAGAA AGAGA CCCTCTA GAGT CCG
AA AGTCT CT

GAM180 214 TP53I11 1 9520 XP_029347.6 3 553 AACTCAAGGGCC ATGTC 1 B c c

TGAAGCTCCCAG TTTCTGGGAG TCAGGCT
AAGCTTCC GAAGACCCTC AGTCCGG
GA---

GAM180 214 TRIAD3 1 18793 NP_061884.2 3 385 AAGGCAGCCGAG - - A 1 B c c
AGCATCTCCCTG TTTCT GGGAGATG TCTC GGCT
GAGGGGCC GGAGG CCCTCTAC AGAG CCGA
T G -

GAM180 214 UBP1 1 3862 NP_055332.2 3 1465 TTTTGAGTTTGA T C 1 B c c
AATCTCTCCCAG TTTCTGGGAGA GT TCAGGCT
AAGACAAA GAAGACCCTCT TA AGTTTGA
C A

GAM180 214 UNC5H2 1 7676 NP_734465.1 3 253 CTCTTGGCCTGA --- TG 1 B c c
GATCTCTGTGCA TTTCTG GGAGA TCTCAGGCT
GGAACCAA AAGGAC TCTCT AGAGTCCGG
GTG --

GAM180 214 VPS39 1 1316 XP_031720.2 3 55 GGATGGACAGCT T CT 1 B c c
TGGCTCTCCCAG TTTCTGGGAGA GT CAGGCT
AGAGGTGA AGAGACCCTCT CG GTTCGA
- --

GAM180 214 WDFY2 1 575 NP_443182.1 3 18 AGTCGTGTCTTG T T - 1 B c c
TGACTCTCCCAG TTTCTGGGAGA GTC CAGG C
GAATCAGA AAGGACCCTCT CAG GTTC G
- T T

GAM180 214 XT3 1 1554 NP_064593.1 3 1629 GAGACAGCCTGA --- AG 1 B c c
GATATGGCCTCA TTTCT GGG ATGTCTCAGGCT
TGGGAAGG AAGGG TCC TATAGAGTCCGA
TAC GG

GAM180 214 XT3 1 1554 NP_071800.1 3 1629 GAGACAGCCTGA --- AG 1 B c c
GATATGGCCTCA TTTCT GGG ATGTCTCAGGCT
TGGGAAGG AAGGG TCC TATAGAGTCCGA
TAC GG

GAM180 214 ZAN 1 17735 NP_775078.1 3 255 GCCTCGAGATGC A ----- - 1 B c c
GCCACCTCCCAG TTTCTGGGAG TG TCTC AGGC
AAAGCCAG AAAGACCCTC AC AGAG TCCG
C CGCGT C

GAM180 214 ZAN 1 17735 NP_775079.1 3 259 GCCTCGAGATGC A ----- - 1 B c c
GCCACCTCCCAG TTTCTGGGAG TG TCTC AGGC
AAAGCCAG AAAGACCCTC AC AGAG TCCG
C CGCGT C

GAM180 214 ZAN 1 17735 NP_775080.1 3 255 GCCTCGAGATGC A ----- - 1 B c c
GCCACCTCCCAG TTTCTGGGAG TG TCTC AGGC
AAAGCCAG AAAGACCCTC AC AGAG TCCG
C CGCGT C

GAM180 214 ZAN 1 17735 NP_775081.1 3 259 GCCTCGAGATGC A ----- - 1 B c c
GCCACCTCCCAG TTTCTGGGAG TG TCTC AGGC

AAAGCCAG AAAGACCCTC AC AGAG TCCG
C CGCGT C

GAM180 214 ZNF235 1 12391 NP_004225.2 5 23 GGTCGGATCTGA TT C 1 B c c
GATATCTCCCAG T CTGGGAGATGTCTCAGG
GGAGGTTC A GACCCTCTATAGAGTCT
GG A

GAM180 214 ZNF258 1 8831 NP_009098.1 5 59 GTTTGAGCCTGA TG A 1 B c c
GACACTCTTTGA TTTC GGAG TGTCTCAGGCT
GGTAAAAA GGAG TCTC ACAGAGTCCGA
TT -

GAM180 214 ZNF258 1 8831 NP_660353.1 5 172 GTTTGAGCCTGA TG A 1 B c c
GACACTCTTTGA TTTC GGAG TGTCTCAGGCT
GGTAAAAA GGAG TCTC ACAGAGTCCGA
TT -

GAM180 214 ZNF347 1 7083 NP_115973.1 3 100 ATTTATGCCTGA T A G 1 B c c
GAGATTCCTTGA TTTC GGGAG T TCTCAGGC
AAATGCAA AAAG TCCTT A AGAGTCCG
T - G

GAM181 395 LOC2001 1 17783 XM_114148.1 3 CATCTGCACCTG CAA ACTT 3 C c c
97 CACTCCCAAA TTTGG AG GGTGCAGATG
AAACC TC CCACGTCTAC
C-- ACGT

GAM181 395 LOC9090 1 2635 XM_034809.1 3 CATTTGTCAGCC A ACTT -- 3 C c c
6 CTTGCCAAA TTTGGCAA G GGT GCAGATG
AAACCGTT C CCG TGTTTAC
- ---- AC

GAM181 395 LOC9113 1 17149 NM_138773.1 3 CATCTGACTTCA GAC TG- 3 C c c
7 ATATTTGCCAAA TTTGGCAAA TTGG CAGATG
AAACCGTTT AACT GTCTAC
AT- TCA

GAM181 395 NET-5 1 464 NM_006675.2 3 CATCTGCATATG G TTG- 3 C c c
CGTATTTGCCAA TTTGGCAAA AC GTGCAGATG
A AAACCGTTT TG TACGTCTAC
A CGTA

GAM181 395 SIMRP7 1 9314 3 CATCTGCAAACG T ACTTGG 3 C c c
CTTTGCCAA TTGGCAAAG TGCAGATG
AACCGTTTC ACGTCTAC
- GCAA--

GAM182 307 AF02059 1 19423 NM_014480.1 3 GACACACACTGG CCC GG - 3 C c c
1 AGGCAAACCCT AGG TGCCTT CA TGTGTGTC
TCC ACGGAG GT ACACACAG
CAA -- C

GAM182 307 CASKIN1 1 7419 NM_020764.1 3 GACAGGGGACCA A - CATGTG 3 C c c
AGGTCAGGGCC GGCCCTG CCTTGG TGTC
CCGGGAC GGAACC ACAG
- T AGGGG-

GAM182 307 KIAA056 1 19085 XM_039912.4 3 GACACACATCCA CC CCT C 3 C c c
5 TGACACAGCCT AGGC TG TGG ATGTGTGTC
TCCG AC ACC TACACACAG
AC AGT -
GAM182 307 LDB3 1 3284 XM_084376.6 3 ACACACGAGGAG C GGCA C 3 C c c
GCAGGACCT AGG CCTGCCTT TGTGTGT
TCC GGACGGAG GCACACA
A GA-- -
GAM182 307 LOC1244 1 12795 3 ACACACCGCAGG C G--- AT C 3 C c c
70 AAAGCCAGGGCC AGGCCCTG CTT GC GTGTGT
T TCCGGGAC GAA CG CACACA
C AGGA C- -
GAM182 307 LOC2562 1 2860 3 GACACACATCCG CC CCT C 3 C c c
07 TGACACAGCCT AGGC TG TGG ATGTGTGTC
TCCG AC GCC TACACACAG
AC AGT -
GAM182 307 SCYA19 1 10974 3 ACCAGCCAGGAC C A T GTC 3 C c c
AGGGCCT AGGCCCTG CTTGGC TG GT
TCCGGGAC GGACCG AC CA
A - - ---
GAM182 307 TGFA 1 9112 NM_003236.1 3 ACACACATGCAG - GC TG C 3 C c c
TGAGAGGCCT AGGCC CT CT GCATGTGTGT
TCCGG GA GA CGTACACACA
A GT -- -
GAM183 240 DKFZP43 1 16705 3 GTTTTGACCTGT AAC- T 3 C c c
4J1813 ATCCTTTATTTA TAAGTAAA GC GGGTCAAAAC
ATTTATTT TG TCCAGTTTTG
CCTA -
GAM183 240 KIAA102 1 5814 XM_034056.6 3 GTTTTCATCTGG - TG C 3 C c c
5 TGTCTTTTATTT TAAGTAAAA ACGC GGT AAAAC
A ATTTATTTT TGTG CTA TTTTG
C GT C
GAM183 240 MGC2280 1 15928 NM_144590.1 3 GTTTTGGAAGAG C GGG 3 C c c
5 CTTTTTATTTA TAAGTAAAAA GCT TCAAAAC
ATTTATTTTT CGA GGTTTTG
- GAA
GAM183 240 PTGS2 1 14372 NM_000963.1 3 GTTTTGACGTCT C TGG 3 C c c
TTTTACTTG TAAGTAAAAA GC GTCAAAAC
GTTCATTTTT TG CAGTTTTG
C ---
GAM184 284 TGFBR2 1 9885 NM_003242.3 3 TTCAAAAAGTGA - CTTTG 3 C c c
AGCCACTTTATA TTATAA GTGGCT TTTTGAA
A AATATT CACCGA AAAACTT
T AGTGA
GAM185 372 GAB2 1 18059 NM_080491.1 3 CAGACCTTCTCC C CAACAA 3 C c c
CTGAACTTAAGA TCTT AGTTC AAGGTCTG
AGAA TCAAG TTCCAGAC

T TCCCTC
GAM185 372 GADD45B 1 9982 NM_015675.1 3 CAGGTCGTTGGA - AAAA GT 3 C c c
GACTGAAGA TCTTCAGT TCCAAC G CTG
AGAAGTCA AGGTTG C GAC
G ---- TG
GAM186 353 LOC1476 1 2416 XM_085844.2 3 CCACACACACAG AATTTC - A 3 C c c
71 GCACCCA TGGGTGCC GTG GTGTGG
ACCCACGG CAC CACACC
A----- A -
GAM186 353 MGC4093 1 15121 NM_030578.1 3 CCACACCCCGGA CCAAT T A 3 C c c
CACCCA TGGGTG TTCG GGTGTGG
ACCCAC AGGC CCACACC
----- C -
GAM186 353 SMAC 1 450 NM_138929.1 5 TCACACACAACT ATTTCG - A 3 C c c
GGCACCCA TGGGTGCCA TG GTGTGG
ACCCACGGT AC CACACT
CA---- A -
GAM186 353 ZRF1 1 12343 XM_168590.3 5 CCACACCACGAA GCCAA A 3 C c c
AGATCCA TGGGT TTTCGTGGTGTGG
ACCTA AAAGCACCACACC
G---- -
GAM187 294 EIF4EBP 1 13732 NM_004096.2 3 TGAGCATTGTGG C A TT C 3 C c c
2 TAGTTGTTCTT AAG ACAACTAC CAC TGC CA
TTC TGTTGATG GTG ACG GT
T - TT A
GAM187 294 FLJ2048 1 6750 NM_017841.1 3 GGCGAAGCAGTT ACACA CA 3 C c c
7 GTGCTT AAGCACAACT CTTTGCC
TTCGTGTTGA GAAGCGG
C---- --
GAM187 294 LOC9325 1 7403 XM_050105.2 5 TGGGCAAAGTTA CAA ACAC 3 C c c
9 AGACTTGCTT AAGCA CT ACTTTGCCCA
TTCGT GA TGAAACGGGT
TCA AT--
GAM187 294 PTGFRN 1 7229 XM_040709.3 3 TGGGCCGGATGA A A CA TT 3 C c c
GTTGTGCT AGCACAACT CA CT GCCCA
TCGTGTTGA GT GG CGGGT
- - A- C-
GAM188 286 DKFZp43 1 4117 NM_017600.1 5 CAGCAGCAGAAA TA - TGG 3 C c c
4M0331 GCTCAAAG CTTTGA CTT TTTGCTGCTG
GAAACT GAA AGACGACGAC
-- C ---
GAM188 286 GAB3 1 5720 NM_080612.1 3 GCAGCAGCAAAG TAC - ---- - 3 C c c
GCACCATAAGTC TTTGACTT TGGT TTGCTGCTG

AAA AAACTGAA ACCA AACGACGAC
--- T CGGA G
GAM188 286 LOC1429 1 12714 XM_084389.4 5 CAGCAACAAACT ACTTT C 3 C c c
55 CACAAAGTA TACTTTG GGTTTG TGCTG
ATGAAAC TCAAAC ACGAC
AC--- A
GAM189 246 15E1.2 1 12868 XP_290596.1 3 1202 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGAC GTGACGTGAGGTCGGACCC
AC
GAM189 246 A1BG 2 2534 NP_570602.2 3 345 CACTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 A1BG 2 18868 NP_570602.2 3 1397 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT
GAM189 246 AASS 1 6339 NP_005754.2 3 356 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 ABCA13 1 7385 NP_689914.2 3 1068 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 ABCC11 1 7022 NP_149163.2 5 57 GGAGATTGCCCA CAG-- 3 B c c
GGATCAAGGGTG CATTGCACTC CCTGGGCAA
CGGTGTTG GTGGCGTGGG GGACCCGTT
AACTA
GAM189 246 ABCD3 1 14444 NP_002849.1 3 579 TCCTTGTGTGTG T- GCCT 3 B c c
TCTTGGAGTGCA CA TGCACTCCA GGGCA
TTTGACTC GT ACGTGAGGT TCTGT
TT ----
GAM189 246 ACADSB 1 16689 NP_001600.1 3 322 CTCTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCGCG GTGACGTGAG TCGGACCC
A AC
GAM189 246 ACP5 1 6638 NP_001602.1 3 263 ACCTTTGCTGAG AGC- G 3 B c c
TTCCGGGGTGCA CATTGCACTCC CT GGCAA
ATGGGGGA GTAACGTGGGG GA TCGTT
CCTT G
GAM189 246 ADAMTS4 2 1651 NP_005090.1 3 670 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCACA GTAACGTGAGGTCGGACCCG
C
GAM189 246 ADAMTS4 2 13757 NP_005090.1 3 166 CCCTAATGCGCA TT CT- G 3 B c b

GGCTGGCCCTGC CA GCA CCAGCCTG GCA
CCTGGTTT GT CGT GGTCGGAC CGT
CC CCC G

GAM189 246 ADCY6 2 15161 NP_056085.1 3 1225 GAGAGATGCCCA G ----- 3 B c b
GGTTGCACAGGA CATT CACTCC AGCCTGGGCA
GTGGGATG GTAG GTGAGG TTGGACCCGT
G ACACG

GAM189 246 ADCY6 2 15161 NP_066193.1 3 1225 GAGAGATGCCCA G ----- 3 B c b
GGTTGCACAGGA CATT CACTCC AGCCTGGGCA
GTGGGATG GTAG GTGAGG TTGGACCCGT
G ACACG

GAM189 246 ADCY6 2 16688 NP_056085.1 5 65 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCG GTAACGTGAGGTCGGACCC
AC

GAM189 246 ADORA2A 1 19456 NP_000666.2 3 164 AAGGGAGCCCCA T A- - A 3 B c c
GGCTGGAGCAGC CAT GC CTCCAGCCTGGG C
ATGAGGCC GTA CG GAGGTCGGACCC G
- AC C A

GAM189 246 AGMAT 1 9193 NP_079034.2 3 436 GCTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC

GAM189 246 AHR 1 8217 NP_001612.1 3 1634 CTCTGCCGCCCA CC A 3 B c c
AACTGGAGTGCA CATTGCACTCCAG TGGGC
GTGGCACA GTGACGTGAGGTC ACCCG
AA C

GAM189 246 AIM1 1 16864 XP_166300.1 3 715 GACAGGATCTCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACTC
TA

GAM189 246 AKR1D1 1 8063 NP_005980.1 3 62 TCCCATGAGTGC CCAGC G 3 B c c
CAAGACGGTGCA CATTGCACT CT GGCA
ATGGGTAG GTAACGTGG GA CCGT
CA--- A

GAM189 246 ALDH1B1 1 2153 NP_000683.3 3 1073 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 ALOX15 1 19939 NP_001131.1 3 412 CTTTGACACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCC GTGACGTGAGGTCGGACCC
AC

GAM189 246 AMID 1 5895 NP_116186.1 3 694 CCCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM189 246 ANKRD6 1 1746 NP_055757.1 3 1478 CTCTGTCACCCA C CA 3 B c c

GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCATG GTGACGTGAGGTC GACCC
A AC

GAM189 246 AP3S2 1 19874 NP_005820.1 3 657 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGTGCA GTG CGTGAGGTCGGACCC
T AC

GAM189 246 APAF1 2 16578 NP_001151.1 3 630 GCTTTGTTGCCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-

GAM189 246 APAF1 2 16578 NP_037361.1 3 630 GCTTTGTTGCCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-

GAM189 246 APAF1 2 19360 NP_001151.1 3 927 CACTATCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATA GTGACGTGAGGTCGGACCC
AC

GAM189 246 APAF1 2 19360 NP_037361.1 3 927 CACTATCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATA GTGACGTGAGGTCGGACCC
AC

GAM189 246 APM1 2 5598 NP_004788.1 3 812 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGACACG GTGAC TGAGGTCGGACCC
A AC

GAM189 246 APM1 2 20035 NP_004788.1 3 3332 TTCTGTGGCCCT C T A 3 B c c
GGCTGGAGTTCA CATTG ACTCCAGCC GGGC
GTGGTGTG GTGAC TGAGGTCGG CCCG
T T G

GAM189 246 APOBEC3 1 5622 NP_660341.2 3 352 CTCTGTCACCCA C CA 3 B c c

F GACTGGAGTGCA CATTGCACTCCAG CTGGG
ATGGCTTG GTAACGTGAGGTC GACCC
A AC

GAM189 246 APOL1 1 9574 NP_003652.2 3 118 GCTCTGTCGCCA CTG A 3 B c c
AGTTGGAGTGCA CATTGCACTCCAGC GGC
ATGGTGCG GTAACGTGAGGTTG CCG
AA- C

GAM189 246 APOL1 1 9574 NP_663318.1 3 118 GCTCTGTCGCCA CTG A 3 B c c
AGTTGGAGTGCA CATTGCACTCCAGC GGC
ATGGTGCG GTAACGTGAGGTTG CCG
AA- C

GAM189 246 APOL2 1 8064 NP_112092.1 3 131 CTCTATCGCCCA G A 3 B c c
GGATGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGCTCA GTGACGTGAGGT GGACCCG
A C

GAM189 246 APOL2 1 8064 NP_663612.1 3 131 CTCTATCGCCCA G A 3 B c c
GGATGGAGTGCA CATTGCACTCCA CCTGGGC

GTGGCTCA GTGACGTGAGGT GGACCCG
A C
GAM189 246 APPBP2 1 4095 NP_006371.2 3 3495 TCTTGTTGCCCA A - 3 B b b
GGCTGGGAGGGC CATTGC CTCC AGCCTGGGCAA
AATGGCAC GTAACG GAGG TCGGACCCGTT
G G
GAM189 246 APPL 1 12068 NP_036228.1 3 2974 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 AQP2 1 18318 NP_000477.1 3 152 CGTGCGCGCCCA T CCA A 3 B c
c
GGCCAGTGCTGT CAT GCACT GCCTGGGC
GAGCAGGC GTG CGTGA CGGACCCG
T C-- C
GAM189 246 AQP6 3 3169 NP_001643.1 3 614 ATCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT
GAM189 246 AQP6 3 3169 NP_445738.1 3 1780 ATCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT
GAM189 246 AQP6 3 7869 NP_445738.1 5 1736 CAGGTCAGCTCA - A-- A 3 B c c
GGCTGGAGCAGG CAT TGC CTCCAGCCTGGGC
CATATGAG GTA ACG GAGGTCGGACTCG
T GAC A
GAM189 246 AQP6 3 8069 NP_001643.1 5 55 CAGGTCAGCTCA - A-- A 3 B c c
GGCTGGAGCAGG CAT TGC CTCCAGCCTGGGC
TATATGAG GTA ATG GAGGTCGGACTCG
T GAC A
GAM189 246 ARCN1 1 13747 NP_001646.2 3 406 CTTTGTAACCCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
ATGGCATG GTAACGT AGGTCGGACCC
A AA
GAM189 246 ARFRP1 1 6901 NP_003215.1 3 335 CTCCAGTGCTCA T - ---- 3 B c c
GGCTGGCTTGGG CAT GCA CT CCAGCCTGGGCA
CTGCATGA GTA CGT GG GGTCGGACTCGT
- C GTTC
GAM189 246 ARHGAP1 1 4096 NP_004299.1 3 1136 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 ARHGAP1 1 17742 NP_055598.1 3 294 CTCTGTCGTCCA A 3 B b b
1A GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCTG
C
GAM189 246 ARK5 1 17859 NP_055655.1 3 2999 GAGTTTTGCCCA TT CTC - 3 B c c

GGCCTGCTGTCT CA GCA CAG CCTGGGCAA

TGAGTACA GT TGT GTC GGACCCGTT
TC C-- C

GAM189 246 ARPP-19 1 944 NP_006619.1 3 3491 CACTCTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 ASB16 1 14722 NP_543139.4 3 143 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCT GTGACGTGAGGTCGGACCCGTT

GAM189 246 ASB6 2 2196 NP_060343.1 3 1136 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
AC

GAM189 246 ASB6 2 2196 NP_821066.1 3 1699 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
AC

GAM189 246 ASB6 2 10305 NP_060343.1 3 1442 CTCTGTCACCTA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGATCC
AC

GAM189 246 ASB6 2 10305 NP_821066.1 3 2005 CTCTGTCACCTA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGATCC
AC

GAM189 246 ASE-1 2 1741 NP_036231.1 3 451 CTCTGTCGCCCA A 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTTGGACCCG
C

GAM189 246 ASE-1 2 3101 NP_036231.1 3 743 TGGTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 ATF7IP2 1 9602 NP_079273.1 3 541 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGTCAC GTGAC TGAGGTCGGACCCGTT
A

GAM189 246 ATM 1 1837 NP_612150.1 3 123 TCTGTCCGCCCA C------ T A 3 B c c
GGCTGGGTGCAG ATTGCAC CCAGCCTGGGC
TCACGGCT TGACGTG GGTCGGACCCG
TCGGCAC - C

GAM189 246 ATP1B2 1 16916 NP_001669.1 3 823 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM189 246 ATP1B4 1 13042 NP_036201.1 3 1878 TGTTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 ATP6V0D 1 15039 NP_689778.1 3 853 CTCTGTCGCCCA C A 3 B b b
2 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
ATGGCGTG GTAACGTGAG TCGGACCCG
A C
GAM189 246 ATP6V1A 1 18868 NP_001681.2 3 676 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM189 246 ATP7A 1 4112 NP_000043.1 3 1061 TTTTGCAGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
A
GAM189 246 ATP8B2 1 8634 XP_290875.1 3 1016 TCTTGTCACCTA CA CA 3 B c c
GGCAAGAGTGCA CATTGCACTC GCCTGGG
ATGGCACA GTAACGTGAG CGGATCC
AA AC
GAM189 246 AXL 1 11802 NP_001690.2 3 471 CTGTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 AXL 1 11802 NP_068713.2 3 471 CTGTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 B4GALT4 1 11028 NP_003769.1 3 654 AGGACCTGCCCA CACTC - 3 B c
c
GGTATGCCTTCC CATTG CA GCCTGGGCA
AGTGATGC GTGAC GT TGGACCCGT
CTTCC A
GAM189 246 B4GALT7 1 18475 NP_009186.1 3 311 TTCACGTGCCCA A TC - 3 B c c

GGCCTGTGGGTA CATTGC C CAG CCTGGGCA
GTGGGGAG GTGATG G GTC GGACCCGT
- GT C
GAM189 246 BA108L7 1 10888 NP_112233.2 3 1055 CTATTTTGCCCA 3 B b b
.2 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAGCGTGAGGTCGGACCCGTT

GAM189 246 BACE2 1 11052 NP_036237.2 3 781 AGACTTTGCCCA --- TCCAG 3 B c
c
GGGTCCTGTGCC CATT GCAC CCTGGGCAA
TGGATGGG GTAG CGTG GGACCCGTT
GTC TCCTG
GAM189 246 BACE2 1 11052 NP_620476.1 3 781 AGACTTTGCCCA --- TCCAG 3 B c
c
GGGTCCTGTGCC CATT GCAC CCTGGGCAA
TGGATGGG GTAG CGTG GGACCCGTT
GTC TCCTG
GAM189 246 BACE2 1 11052 NP_620477.1 3 978 AGACTTTGCCCA --- TCCAG 3 B c
c

GGGTCCTGTGCC CATT GCAC CCTGGGCAA
TGGATGGG GTAG CGTG GGACCCGTT
GTC TCCTG

GAM189 246 BAG5 1 5695 NP_004864.1 3 1870 CTCTGTTGCCCA C 3 B b b
GGCTGCAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGCC GTGACGTGA GTCGGACCCGTT
C

GAM189 246 BART1 1 16830 NP_036238.1 3 1112 GTTTGTATGCTT CC TG 3 B c c
TGGTTTAGTGCA CATTGCACT AGCC GGCA
ATGTGTGG GTAACGTGA TTGG TCGT
T- TT

GAM189 246 BAZ2A 1 8852 NP_038477.1 5 23 TCTTATTGCCCA C 3 B b b
GGCTTGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGACCTG GTAACGTGAG TCGGACCCGTT
T

GAM189 246 BCAP31 1 4861 NP_005736.2 3 467 TGTTTTGTATTT CCTGG- 3 B c c
CTCTGGAGTGCA CATTGCACTCCAG GCAA
ATGGTGCA GTAACGTGAGGTC TGTT
TCTTTA

GAM189 246 BCL10 1 19576 NP_003912.1 3 783 CTCTATCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM189 246 BDP1 1 19556 NP_060899.1 3 153 TTCTGTTGCCCA CA 3 B b b
GGCAAGAGTGCA CATTGCACTC GCCTGGGCAA
GTGGTATG GTGACGTGAG CGGACCCGTT
AA

GAM189 246 BENE 1 6009 NP_005425.1 3 474 CTCTTCCTCCAA - CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGG
GTGACGCG GTGACGTGAGGTCGGA CCT
A CC

GAM189 246 BHD 1 9036 NP_659434.2 3 912 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 BMF 1 759 NP_277038.1 3 2226 TTGCCAGGCCCA T-- T A 3 B c c
GGCTGGGTGCCC CAT GCAC CCAGCCTGGGC
TGTGGCCT GTG CGTG GGTCGGACCCG
TCC - G

GAM189 246 BNIP-S 1 5845 NP_612122.1 3 333 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC

GAM189 246 BRIP1 1 13904 NP_114432.1 3 208 GTCTGTTGCCCA C 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGTGTG GTGACGT AGGTCGGACCCGTT
A

GAM189 246 BTN3A1 1 2067 NP_008979.2 3 1056 ACTCTGTTGCTA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGTGCG GTGACGTGAGGTCGGATC GTT

-

GAM189 246 BXDC1 2 4549 XP_166303.1 3 1357 CTCTGTCGCTCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACTCG
C

GAM189 246 BXDC1 2 12129 XP_166303.1 3 686 TTCTGTCACCTA G CA 3 B c b
GGGTGGAGTGCA CATTGCACTCCA CCTGGG
GTGGCACA GTGACGTGAGGT GGATCC
G AC

GAM189 246 C11orf1 1 11525 NP_065693.2 3 217 CTCTGTTGCCCA 3 B b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 C13orf1 1 5746 NP_065189.1 3 1686 CCTTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCACG GTGACGTGAG TCGGACCC
A AC

GAM189 246 C14orf1 1 12744 NP_009107.1 3 1453 CTCTGTCACCCA C-- CA 3 B c c
GGCTGGGAATTG CATTGCA TCCAGCCTGGG
CAGTGGCA GTGACGT GGGTCGGACCC
TAA AC

GAM189 246 C14orf1 2 5052 NP_060100.1 3 797 CTTCTGTGGTCA CAC G 3 B c b
13 GGCTGGGACAGT CATTG TCCAGCCTGG CA
GAAAGGCA GTGAC GGGTCGGACT GT
A-- G

GAM189 246 C14orf1 2 18863 NP_060100.1 3 360 TCTTGTTGCCCA C 3 B b b
13 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCATG GTAAC TGAGGTCGGACCCGTT
A

GAM189 246 C14orf1 1 17955 NP_660274.1 3 1620 CTTTGTCACCTA C CA 3 B c c
43 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGCGCGA GTGACGTGAGGTCG ATCC
A AC

GAM189 246 C14orf9 1 14861 NP_055643.1 3 968 CTCTGTCACCCA CA 3 B c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM189 246 C1orf24 1 19538 NP_443198.1 3 1462 CTCTGTCGCCAA G A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGTGTG GTGACGTGAGGTCGGA CCG
A C

GAM189 246 C1QTNF6 1 14882 NP_114116.2 3 543 CTCTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGTGCA GTGACGTGAG TCGGACCCGTT
A

GAM189 246 C20orf1 1 16257 NP_689880.1 3 981 CTCTGTCGCCCA T A 3 B c c
47 GGTTGGAGTGCC CAT GCACTCCAGCCTGGGC
ATGGCACC GTA CGTGAGGTTGGACCCG
C C

GAM189 246 C21orf6 1 6569 NP_478068.1 5 158 CGCTGTCGCCCA A A 3 B b b

7 GGCTGGAGCGCA CATTGC CTCCAGCCTGGGC
ATGGCGCG GTAACG GAGGTCGGACCCG
C C

GAM189 246 C22orf1 1 18897 NP_003669.2 3 1825 CTCTGTTGTCCA 3 B b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCTGTT

GAM189 246 C4orf9 1 15574 XP_035572.1 3 370 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 C6orf33 1 6896 NP_588608.1 3 2345 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGATGCA GTGACGTGAGGTCGGACCCG
C

GAM189 246 C6orf5 2 10099 NP_056339.2 3 1428 CTCTGTCGTCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGCTGCA GTGACGTGAGGTCGGACCTG
C

GAM189 246 C6orf5 2 12805 NP_056339.2 3 2320 CACTCTTTCCCA C C CA 3 B c b
GGCTGCAGTACA CATTG ACT CAGCCTGGG
GTGACACA GTGAC TGA GTCGGACCC
A C TT

GAM189 246 C6orf57 1 2114 NP_660310.1 3 501 CTCTCTCACCCA G CA 3 B c c
GGCTGGAGTGGA CATT CACTCCAGCCTGGG
GTGGCGCT GTGA GTGAGGTCGGACCC
G AC

GAM189 246 C7 1 17778 NP_000578.1 3 631 CTTTGTTGCCCA A 3 B b b
GGCTGGAGCGCA CATTGC CTCCAGCCTGGGCAA
GTGGGGTG GTGACG GAGGTCGGACCCGTT
C

GAM189 246 C9orf5 1 14258 NP_114401.1 3 1340 GGTTCTTGGCCA TG A C G 3 B c c

GGCTGTAGGTGG CAT C CT CAGCCTGG CAA
TGGCTCAC GTG G GA GTCGGACC GTT
GT - T G

GAM189 246 C9orf9 2 5477 NP_061829.2 3 856 CTCTGTCTCCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
TC

GAM189 246 C9orf9 2 11520 NP_061829.2 3 217 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGGCGTGAGGTCGGACCCG
C

GAM189 246 CAB2 1 9181 NP_219487.2 3 709 GAGTGTGGGCCA --- C --- 3 B c c
GGCTGAGTGCAT CAT TGCACTC AGCCTGG GCA
AGGTGACA GTG ACGTGAG TCGGACC TGT
GAT - GGG

GAM189 246 CABP4 1 7624 NP_660201.1 5 32 CAAGGGTGCCCA TG CCAG 3 B c
c

GGGGTGTGGTGT CAT CACT CCTGGGCA
CTCTGAGC GTG GTGG GGACCCGT
GT ----

GAM189 246 CALN1 1 17850 NP_113656.1 3 159 GTAAAGAACCCA - C - CA 3 B c c
AGGTTGAGTGCA CA TTGCACTC AGCCT GGG
ACTGGGGT GT AACGTGAG TTGGA CCC
C - A AA

GAM189 246 CAMLG 1 18944 NP_001736.1 3 791 TCTTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCGCC GTAACGTGAG TCGGACCCGTT
A

GAM189 246 CAPN6 1 2208 NP_055104.2 3 671 TGCTTAATCAAG C - ----- 3 B c c
AGCTGGAGTTCA CATTG ACTCCAGC CT GGGCA
ATGAGTCC GTAAC TGAGGTCG GA TTCGT
T A ACTAA

GAM189 246 CAPRI 1 4271 NP_008920.3 3 1974 CTGTGTTGCCCA - 3 B b b
GGCTGGAGTGCA CATT GCACTCCAGCCTGGGCAA
AATGGCTT GTAA CGTGAGGTCGGACCCGTT
A

GAM189 246 CARD6 1 9036 NP_115976.2 3 205 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 CASP2 1 16398 NP_001215.1 3 1634 CTCTGTCGCCCA A A 3 B c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM189 246 CASP2 1 16398 NP_116764.1 3 1245 CTCTGTCGCCCA A A 3 B c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM189 246 CASP2 1 16398 NP_116765.1 3 2059 CTCTGTCGCCCA A A 3 B c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM189 246 CASP2 1 16398 NP_116766.1 3 2059 CTCTGTCGCCCA A A 3 B c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM189 246 CASP8 1 15049 NP_001219.2 3 82 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 CASP8 1 15049 NP_203519.1 3 82 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 CASP8 1 15049 NP_203520.1 3 82 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG

C
GAM189 246 CASP8 1 15049 NP_203521.1 3 827 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 CASPR4 1 13634 NP_620481.1 3 103 CCAGATACTGAA CC C GG 3 B c
c
CAAGTTAGTGCA CATTGCACT AGC TG CA
ATGAAGTA GTAACGTGA TTG AC GT
-- A AA
GAM189 246 CBFA2T2 2 8242 NP_787060.1 5 594 CCCTGTCACTCA CA CA 3 B c c
GGCTGGAGCACA CATTG CTCCAGCCTGGG
GTGGTGTG GTGAC GAGGTCGGACTC
AC AC
GAM189 246 CBFA2T2 2 8572 NP_005084.1 3 1896 TCTTGTCTCCCA C----- CA 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATCGCGCA TAACGTGAGGTCGGACCC
ACGCGC TC
GAM189 246 CBFA2T2 2 8572 NP_787060.1 3 1896 TCTTGTCTCCCA C----- CA 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATCGCGCA TAACGTGAGGTCGGACCC
ACGCGC TC
GAM189 246 CCL16 1 9543 NP_004581.1 3 276 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 CCL22 2 1679 NP_002981.2 3 951 TCTTGTCACCCA C CA 3 B c b
CGCTGGAGTGCA CATTGCACTCCAGC TGGG
ATGGTGTG GTAACGTGAGGTCG ACCC
C AC
GAM189 246 CCL22 2 15049 NP_002981.2 3 1275 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 CCNF 1 17624 NP_001752.1 3 1293 TCTTGTCTCCCC T CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCC GGG
GTGGCATG GTGACGTGAGGTCGG CCC
C TC
GAM189 246 CCRN4L 1 4698 NP_036250.2 3 103 CTCTGTTGCCTA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCCTG GTGAC TGAGGTCGGATCCGTT
A
GAM189 246 CD209 2 4298 NP_066978.1 3 1590 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC
GAM189 246 CD209 2 17051 NP_066978.1 3 625 TCTTGTCGCTCA T A 3 B c b

GGCTGGAGTGCC CAT GCACTCCAGCCTGGGC
ATGGCGCG GTA CGTGAGGTCGGACTCG
C C

GAM189 246 CD24 1 19572 NP_037362.1 3 890 CTTTGTCGCCCA A A 3 B c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGGC
GTGGTGCG GTGACGTGAGG CGGACCCG
C C

GAM189 246 CD5 1 1049 NP_055022.1 5 31 CCCAGCTGCCCA CA------- A C 3 B c c
GGCTGAGGCAAG TTGC CTC AGCCTGGGCA
AGAAGGCC AACG GAG TCGGACCCGT
CCGGAAGAG - -

GAM189 246 CD84 1 514 NP_003865.1 3 1303 TGAATAGTCCTA AC - A 3 B c c
GGCTGGACAGCA CATTGC TCCAGCCTGGG C
ATGGGCTG GTAACG AGGTCGGATCC G
AC T A

GAM189 246 CDC14B 1 17127 NP_201589.1 3 632 TCTTGTTGTCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCTGTT

GAM189 246 CDC2L2 1 15084 NP_296370.1 5 18 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGAG GTAACGTGAGGTCGGACCC
AC

GAM189 246 CDC6 1 9211 NP_001245.1 3 414 CCCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 CDCP1 1 12091 NP_073753.3 3 1772 TTCTGTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGATCCGTT

GAM189 246 CDH1 2 5514 NP_004351.1 3 519 TTCTATCGGCCA GCA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGACC
GGC

GAM189 246 CDH1 2 12580 NP_004351.1 3 825 CTCCATCGCCCA CT - A 3 B c c
GGCCTGGGATGC CATTGCA CCAG CCTGGGC
AGTGATGT GTGACGT GGTC GGACCCG
AG C C

GAM189 246 CDH17 1 13851 NP_004054.2 3 190 CTCTGTCGCCCA C A 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGTGTG GTGAC TGAGGTCGGACCCG
A C

GAM189 246 CDK11 1 8162 XP_166324.1 3 3222 CTCTGTCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACG GTGACGTGAGGTCG ACCC
A AC

GAM189 246 CDKAL1 1 1255 NP_060244.1 3 444 TCTTGTCCCCCA --- CA 3 B c c
GGCTGGAGTGGT CATTGCAC TCCAGCCTGGG
GCAGTGGC GTGACGTG AGGTCGGACCC

```
                                                GTG          CC
GAM189  246  CEACAM8 1  17969 NP_001807.2  3 353   CTCTGTCGCCCA              A        3  B  b  b
                                GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                GTGGCACG    GTGACGTGAGGTCGGACCCG
                                                      C
GAM189  246  CECR1  2  4574  NP_059120.2  3 388   TCTTGTTGCCCA    C                3  B  b  b
                                GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
                                ATGGTGCG    GTAAC TGAGGTCGGACCCGTT
                                           A
GAM189  246  CECR1  2  4574  NP_803124.1  3 388   TCTTGTTGCCCA    C                3  B  b  b
                                GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
                                ATGGTGCG    GTAAC TGAGGTCGGACCCGTT
                                           A
GAM189  246  CECR1  2  9037  NP_059120.2  3 1395  CTCTGTTGCCCA CA-----       G         3  B  c  b

                                GGGTGGAGTGCA      TTGCACTCCA CCTGGGCAA
                                GCGGTGCG          GACGTGAGGT GGACCCGTT
                                        GCGTGGC        G
GAM189  246  CECR1  2  9037  NP_803124.1  3 1395  CTCTGTTGCCCA CA-----       G         3  B  c  b

                                GGGTGGAGTGCA      TTGCACTCCA CCTGGGCAA
                                GCGGTGCG          GACGTGAGGT GGACCCGTT
                                        GCGTGGC        G
GAM189  246  CENPH  1  19549 NP_075060.1  3 263   CTTTGTTGCCCA    A    C           3  B  b  b
                                GACTGGAGGGCA CATTGC CTCCAG CTGGGCAA
                                GTGGCGCG    GTGACG GAGGTC GACCCGTT
                                           G    A
GAM189  246  CENPJ  1  13565 NP_060921.2  5 123   CTGAGCTGCCCA    AC  ----          3  B  c  c
                                GGCTTCACGGAG CATTGC  TCC   AGCCTGGGCA
                                CGGTGTTG    GTGGCG  AGG   TCGGACCCGT
                                           --  CACT
GAM189  246  CGI-150 1  2191  NP_057164.1  5 49    GCTCTGTCATCA            --       3  B  b  b
                                GGCTGGAGTGCA CATTGCACTCCAGCCTG  GGCA
                                GTGGCTCA    GTGACGTGAGGTCGGAC  CTGT
                                              TA
GAM189  246  CGI-18  1  18313 NP_057031.1  5 19    TCTTGTTGCCCA C-    A ----          3  B  c  c
                                GGCTGGAAATGG  ATTGC C   TCCAGCCTGGGCAA
                                CGCGATCT      TAGCG G   AGGTCGGACCCGTT
                                        TC    C GTAA
GAM189  246  CGI-43  1  14860 NP_056437.1  3 376   CTCCGTGACCCA    C        -       3  B  b  b
                                GGCTGGAATGCA CATTGCA TCCAGCCTGGG CA
                                ATGGCTCA    GTAACGT AGGTCGGACCC GT
                                           A        A
GAM189  246  CHC1L  1  15582 NP_001259.1  5 208   AGGGACTGCCCA  - C   C -          3  B  c  c
                                GGACTGAGTCCA CAT TG ACTC AG CCTGGGCA
                                TATGGAAG    GTA AC TGAG TC GGACCCGT
                                          T C   - A
GAM189  246  CHRAC1  1  9475  NP_059140.1  3 960   CTCAGTTGCCCA    C             3  B  b  b
                                GGCTGGATTGCG CATTGCA TCCAGCCTGGGCAA
                                GTGGCGCT    GTGGCGT AGGTCGGACCCGTT
```

T

GAM189 246 CHSY1 1 11924 NP_055733.2 3 639 CTCTGTTACCCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCA GTGACGT AGGTCGGACCC
A AT

GAM189 246 CIAS1 1 13461 NP_004886.2 5 289 CTGTGTCGCCTA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGATCCG
C

GAM189 246 CIP29 2 3509 NP_115740.3 3 164 CTCTGTTGCCCA C 3 B b b
GCTGGAGTGCAG CATTGCACTCCAGC TGGGCAA
TGGTGTGA GTGACGTGAGGTCG ACCCGTT
-

GAM189 246 CIP29 2 20120 NP_115740.3 3 164 GCTCTGTTGCCC C 3 B b b
AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGTGTG GTGACGTGAGGTCG ACCCGTT
-

GAM189 246 CLDN19 1 5914 NP_683763.1 3 1484 CTGGGTGCCTGA CC CT- 3 B c
c
AGCTATAGTGCA CATTGCACT AGC GGGCA
ATGGTTCC GTAACGTGA TCG TCCGT
TA AAG

GAM189 246 CLECSF1 2 15296 NP_072092.2 3 320 CTTTGTTACCCA CA 3 B c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AT

GAM189 246 CLECSF1 2 16192 NP_072092.2 3 970 TCTTGTTGCCCA CA----- 3 B c c
2 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGCACG AACGTGAGGTCGGACCCGTT
GCACGGC

GAM189 246 CLIC5 1 19116 NP_058625.1 5 142 CCCCGCTGCTCG GCA- 3 B c c
GGCTGGAGAATA CATT CTCCAGCCTGGGCA
GATGGTTT GTAG GAGGTCGGGCTCGT
ATAA

GAM189 246 CLN8 1 515 NP_061764.2 3 1639 CTTTGGCTCCCA C CA 3 B c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGTGTG GTGAC TGAGGTCGGACCC
C TC

GAM189 246 CLNS1A 1 18823 NP_001284.1 3 80 GTGCCTCTTCCA ---- CC ----- 3 B c c
CTCTGGAGTGAA CATTG CACTCCAG TGG GCA
GTTAATGA GTAAT GTGAGGTC ACC CGT
TGAA TC TTCTC

GAM189 246 CMAR 2 5053 NP_005191.2 5 232 CGCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCTGCG GTGACGTGAGGTCGGACCC
AC

GAM189 246 CMAR 2 18767 NP_005191.2 5 364 CTGTGTTGCCAA CA----- G 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCT GGCAA
GGCCGCGA GACGTGAGGTCGGA CCGTT
AGCGCCG A

GAM189 246 CNN2 1 9959 NP_004359.1 3 736 GGTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM189 246 CNP 1 606 NP_149124.1 3 561 TGCTATTTCCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCG GTGACGTGAGGTCG ACCC
A TT

GAM189 246 COLEC12 1 11525 NP_110408.2 3 104 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 CORO1C 1 13595 NP_055140.1 3 1013 GCAGCTTGCCCA C C C- 3 B c
c
GCTCTTGAGTAC CATTG ACTC AG CTGGGCAA
AGTGGTGG GTGAC TGAG TC GACCCGTT
A T TC

GAM189 246 COX15 1 7552 NP_510870.1 3 659 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCGTG GTAAC TGAGGTCGGACCCGTT
A

GAM189 246 CPA4 1 8942 NP_057436.1 3 604 TCTTGTTGCCCA TG 3 B b b
GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
ATGGGCTC GTA GTGAGGTCGGACCCGTT
GT

GAM189 246 CPR8 1 13999 NP_065790.1 3 1691 CTTTGTCAGCCA --- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
GTGACACG GTGACGTGAGGTCGGACC TGTT
GAC

GAM189 246 CPS1 1 14493 NP_001866.2 3 668 TCACACTCTCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCT
CT

GAM189 246 CPSF2 2 591 XP_029311.2 3 2045 TCTTGTTGCCCA C 3 B b b
GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCACA GTAACGTGAGGTC GACCCGTT
A

GAM189 246 CPSF2 2 1877 XP_029311.2 3 1220 CAGAGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGAG GTGACGTGAGGTCGGACCC
AC

GAM189 246 CR1 1 17292 NP_000564.1 3 771 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTA GTGACGTGAGGTCGGACCC
TC

GAM189 246 CR1 1 17292 NP_000642.2 3 770 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTA GTGACGTGAGGTCGGACCC
TC

GAM189 246 CRLF3 1 7105 NP_057070.2 3 613 TCTTGTCACTCA CA 3 B c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACTC
AC

GAM189 246 CRSP6 1 7661 NP_004259.3 3 435 CTCTGTAGCCCA C A 3 B c c
GTCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTGTG GTGACGTGAGGTC GACCCG
T A

GAM189 246 CRTAP 1 7107 NP_006362.1 3 267 CTCTCTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 CSE-C 1 2336 NP_061851.1 5 2 GGAGTGCCCAGG G 3 B b b
ATGGAGTGCAGT CATTGCACTCCA CCTGGGCA
GGCTATTC GTGACGTGAGGT GGACCCGT
A

GAM189 246 CSE1L 1 6312 NP_803185.1 3 493 TCTCATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGAGCTA GTGACGTGAGGTCGGACCCGTT

GAM189 246 CSNK2A2 1 15382 NP_001887.1 5 1 TGTCACCCAGGC CA 3 B c c
TGGAGTGCAGTG CATTGCACTCCAGCCTGGG
GCGCAATC GTGACGTGAGGTCGGACCC
AC

GAM189 246 CTEN 1 14746 NP_116254.3 3 767 CACTGTCACCCA CTC CA 3 B c c

GGCTGAACTGCA CATTGCA CAGCCTGGG
GTGGTGTG GTGACGT GTCGGACCC
CAA AC

GAM189 246 CTF1 1 13287 NP_001321.1 3 196 CTCTGTCGCCCA A 3 B b b
GGCTGGGGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGGGGTCGGACCCG
C

GAM189 246 CTSS 1 4517 NP_004070.3 3 1701 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACCCGTT

GAM189 246 CXCL16 1 17688 NP_071342.1 3 340 CTCTGTCATCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCT
AC

GAM189 246 CYCS 3 9339 NP_061820.1 3 2207 CCTTTTCGCCCA C C A 3 B c b
GGCTGAGTACAG CATTG ACTC AGCCTGGGC
TGGTGCAA GTGAC TGAG TCGGACCCG
A - C

GAM189 246 CYCS 3 18868 NP_061820.1 3 2620 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM189 246 CYCS 3 18991 NP_061820.1 3 1817 CTGTGTCGCCAA G A 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC

GTGGTGCG GTGACGTGAGGTCGGA CCG
A C
GAM189 246 CYLC2 1 15540 NP_001331.1 3 731 CTCTGTTGCCCT C T 3 B b b
GGCTGGAGTTCA CATTG ACTCCAGCC GGGCAA
GTGACATG GTGAC TGAGGTCGG CCCGTT
T T
GAM189 246 CYP1A2 3 6637 NP_000752.1 3 788 ACTCTGTTGCCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-
GAM189 246 CYP1A2 3 13576 NP_000752.1 3 418 GTCTGTCACCCA CA 3 B c b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTTGGACCC
AC
GAM189 246 CYP1A2 3 18279 NP_000752.1 3 1085 CTCTGTCTCCTA C CA 3 B c b
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCATC GTGACGTGAGGTCG ATCC
A TC
GAM189 246 CYP2B6 2 2194 NP_000758.1 3 1087 CTCTGTCTCCCA T CA 3 B c b
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
ATGGTGCA GTA CGTGAGGTCGGACCC
T TC
GAM189 246 CYP2B6 2 10618 NP_000758.1 3 276 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 CYP4F3 1 9158 NP_000887.1 3 1396 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM189 246 CYP51A1 1 2152 NP_000777.1 3 884 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 CYP8B1 1 5978 NP_004382.1 3 1006 CTCTGTTGCCCA C 3 B b b
GGCTGCAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGTG GTGACGTGA GTCGGACCCGTT
C
GAM189 246 DBR1 1 7961 NP_057300.1 3 86 TCTTGTCACCTA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
ATGGCGTG GTAACGTGAGGTC GATCC
A AC
GAM189 246 DCX 1 16590 NP_000546.2 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC
GAM189 246 DCX 1 16590 NP_835364.1 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM189 246 DCX 1 16590 NP_835365.1 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC
GAM189 246 DCX 1 16590 NP_835366.1 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC
GAM189 246 DES 1 14498 NP_001918.2 3 295 GGATGGAGCCCA AC A A 3 B c c
GGCGGGAGCGGT CATTGC TCC GCCTGGGC
GGCCCTGT GTGGCG AGG CGGACCCG
-- G A
GAM189 246 DFFB 2 2019 NP_004393.1 3 246 TTTTGTTGCCCA 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGATGTGAGGTCGGACCCGTT

GAM189 246 DFFB 2 9091 NP_004393.1 3 889 CTCTGTCGCTCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGATGCA GTGACGTGAGGTCGGACTCG
C
GAM189 246 DHFR 1 8052 NP_000782.1 3 920 TCTTGTTGCCCA CTCC 3 B b b
GGCTAGCATGCA CATTGCA AGCCTGGGCAA
ATGGTGTG GTAACGT TCGGACCCGTT
ACGA
GAM189 246 DIAPH2 1 14492 NP_006720.1 3 4013 CTCTGTCACCCA C CA 3 B c c
GGCTGCAGTGTA CATTGCACT CAGCCTGGG
GTGGTGCA GTGATGTGA GTCGGACCC
C AC
GAM189 246 DISC1 1 1298 NP_061132.1 3 3218 CTCTGTCACCCA C CA 3 B c c
AGTTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCCCC GTGACGTGAGGTTG ACCC
A AC
GAM189 246 DKFZP43 1 4014 NP_115519.1 3 480 CTTTGTTACCCA C CA 3 B c c
4B1727 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGTGTC GTGAC TGAGGTCGGACCC
A AT
GAM189 246 DKFZp43 1 8235 NP_060068.1 3 861 CTCTGTCACCCA C CA 3 B c c
4C0923 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 DKFZP43 1 8661 XP_044196.3 3 1560 CCCTGTTGCCCA 3 B b b
4C212 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 DKFZP43 1 2209 NP_056410.2 3 810 CTCTGTCGCCCA C C A 3 B c c
4D146 GGCTAGAGTATA CATTG ACTC AGCCTGGGC
GTGGTGTG GTGAT TGAG TCGGACCCG
A A C
GAM189 246 DKFZp43 1 11326 NP_060082.1 5 772 GTCTGTTGCCCA 3 B b b
4E2220 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 DKFZP43 1 16771 NP_110444.1 3 2412 CTCTGTCACCTA - CA 3 B c c
4F0318 GGCTGGAGTTGC CATTGCA CTCCAGCCTGGG
AGTGGTTT GTGACGT GAGGTCGGATCC
T AC
GAM189 246 DKFZp43 1 3951 NP_115624.1 3 1205 TCTTGTTTCCCA CA 3 B b b
4F1719 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGGTGA GTAACGTGAGGTCGGACCC
TT
GAM189 246 DKFZp43 1 4195 NP_060076.1 3 1080 ATTTAGTGCCCA - --- AGC 3 B c c

4K1210 GGGAGTCCAGCG CATT GC ACTCC CTGGGCA
AATGACGT GTAA CG TGAGG GACCCGT
G ACC ---
GAM189 246 DKFZp54 1 14246 NP_064546.1 3 257 CTCCATTGCCCA CA----- C 3 B c c

7H025 GGCTGGACTGCA TTGCA TCCAGCCTGGGCAA
GCAGCGTG GACGT AGGTCGGACCCGTT
GTGCGAC C
GAM189 246 DKFZp54 1 11057 NP_694590.1 3 1544 CACTGTCACCCA CA 3 B c c
7P234 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 DKFZP56 1 2662 NP_056416.1 5 1111 TCTTGTCGCCCA C A 3 B c c
4G092 GGCTGTAGTGCA CATTGCACT CAGCCTGGGC
GTGGTACA GTGACGTGA GTCGGACCCG
T C
GAM189 246 DKFZP56 1 16590 XP_032397.1 3 259 CTCTGTCACCTA CA 3 B c c
4I122 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC
GAM189 246 DKFZP56 1 17964 NP_114429.1 3 215 CTCTGTTGCCCA 3 B b b
4K0322 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM189 246 DKFZp56 1 2663 NP_115497.2 3 696 CTGTGTCACACA --- 3 B b b
4K142 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCGTG GTGACGTGAGGTCGGAC CTGT
ACA
GAM189 246 DKFZP56 1 3686 NP_115496.1 3 226 CTCTGTTGCCCA C 3 B b b
4O0523 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
A
GAM189 246 DKFZP56 1 10539 NP_110443.1 5 181 GCGTTTGTCCCA CA- - - 3 B c c
6D1346 GGCTCGGGGGCT CATTG CTCC AGCCTGGG CAA
CAGTGGGA GTGAC GGGG TCGGACCC GTT
TCG C T
GAM189 246 DKFZP56 1 12353 NP_056226.1 3 714 CTCTGTTGCCCA T C 3 B b b
6I1024 GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA

CTGGTGGT GT ACGTGAG TCGGACCCGTT
C A
GAM189 246 DKFZp58 1 12173 XP_098416.1 3 3009 CTCTGTCACCCA CA 3 B b b
6C0721 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCAAG GTAACGTGAGGTCGGACCC
AC
GAM189 246 DKFZP58 1 11134 NP_056248.1 3 473 CTCTGTCATCCA CA 3 B c c
6D0919 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCT
AC
GAM189 246 DKFZp66 1 15574 NP_808881.1 3 966 TCTTGTTGCCCA 3 B b b
7B1218 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 DKFZp66 1 8492 XP_117353.1 3 296 CTCTGTCAGCCA TG --- 3 B c c
7E0512 GGCTGGAGTGTG CAT CACTCCAGCCTGG GCA
GTGGCACA GTG GTGAGGTCGGACC TGT
GT GAC
GAM189 246 DKFZp76 1 13571 NP_775734.1 3 2765 CTATGTCTCCCA CA 3 B c c
1B107 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM189 246 DKFZp76 1 17969 NP_689650.1 5 1005 CTCTGTCGCCCA A 3 B b b
1B128 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM189 246 DKFZp76 1 7769 XP_046017.3 3 1995 GCCCCCTGCCCA GC-- T 3 B c
c
1G2113 GGCTGGGTAAGA CATT AC CCAGCCTGGGCA
GATGGGCT GTAG TG GGTCGGACCCGT
AGAA -
GAM189 246 DKFZp76 1 15190 NP_061181.1 3 887 ATCTGTCGCCCA C----- A 3 B c c
1H039 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCGTG TGACGTGAGGTCGGACCCG
GTGCGA C
GAM189 246 DKFZp76 1 5768 NP_115656.1 5 1462 TCTTGTCACCCA CA 3 B c c
1J139 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 DKFZp76 1 1317 NP_060892.1 5 136 ACTTCAGCTCCA ACTC - A 3 B c
c
1K1423 GGCTGCAGTAAT CATTGC CAGCCTGG GC
GTGTTGGT GTAATG GTCGGACC CG
AC-- T A
GAM189 246 DKFZp76 1 13529 XP_086327.6 3 1184 ACTCTGTTGCCA C G 3 B b b
1N1114 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTC GTGACGT AGGTCGGACC GTT
A -
GAM189 246 DKFZp76 1 7699 NP_060879.1 5 1531 TCTTGTTGCCCA C 3 B b b
1O0113 GGCTTGAGTGCA CATTGCACTC AGCCTGGGCAA

GTGATGCA GTGACGTGAG TCGGACCCGTT
T
GAM189 246 DKFZp76 1 9147 NP_690870.1 3 740 CTCTGTCACCCA CA 3 B c c
1P1121 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 DKFZp76 1 4056 NP_848637.1 3 168 CTCTGTGGCCCA C A 3 B c c
2C2414 GGCTGAAGTGCA CATTGCACT CAGCCTGGGC
GTGGTGTG GTGACGTGA GTCGGACCCG
A G
GAM189 246 DKFZp76 1 1744 NP_689624.1 3 255 CTCTGTCACCCA CA 3 B c c
2I137 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 DKFZp76 1 6884 NP_689597.1 3 705 CAATGGTGCCCA 3 B b b
2I194 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCGTG GTGACGTGAGGTCGGACCCGT

GAM189 246 DKFZp76 1 9194 NP_061189.2 3 781 TTCTGTTGCCCA AG 3 B b b
2L0311 GGAGGGAGTGCA CATTGCACTCC CCTGGGCAA
GTGGTGCA GTGACGTGAGG GGACCCGTT
GA
GAM189 246 DKK3 1 20069 NP_037385.1 3 27 TAATCTGGACCA GC - G- 3 B c c
GGCTGTGGGTAG CATT ACTC CAGCCTGG CA
ATGTGCAA GTAG TGGG GTCGGACC GT
A- T AG
GAM189 246 DKK3 1 20069 NP_056965.2 3 27 TAATCTGGACCA GC - G- 3 B c c
GGCTGTGGGTAG CATT ACTC CAGCCTGG CA
ATGTGCAA GTAG TGGG GTCGGACC GT
A- T AG
GAM189 246 DNAH11 1 1214 NP_003768.1 3 43 TCCTCTAGCCTC CT A 3 B c c
TGCTGGAGTGCA CATTGCACTCCAGC GGGC
GTGAGGAT GTGACGTGAGGTCG TCCG
TC A
GAM189 246 DNAJB5 1 5815 NP_036398.2 3 231 AGAGCTAGCCCA C A- A 3 B c c
GGCCAGGGGTCA CATTG ACTCC GCCTGGGC
ATGTTCAT GTAAC TGGGG CGGACCCG
- AC A
GAM189 246 DRIM 1 6633 NP_055318.1 3 141 CTCTGTCACCCA A - CA 3 B c c
AGGCGGAGTGCA CATTGCACTCC GCCT GGG
GTGACGAC GTGACGTGAGG CGGA CCC
- A AC
GAM189 246 DRPLA 1 9796 NP_001931.1 5 185 TTCAGCTGCCCA GCA A-- 3 B c c
GGCAGAGGAGAA CATT CTCC GCCTGGGCA
TGGGGTCT GTAA GAGG CGGACCCGT
--- AGA
GAM189 246 DSC3 1 7559 NP_001932.1 3 2049 CTCTGACGCACA G A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTG GC
GTGGCTCC GTGACGTGAGGTCGGAC CG
A C

GAM189 246 DSC3 1 7559 NP_077741.1 3 2263 CTCTGACGCACA G A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTG GC
GTGGCTCC GTGACGTGAGGTCGGAC CG
A C
GAM189 246 DSCR6 1 14954 NP_061835.1 3 546 TCTTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
TC
GAM189 246 DUSP19 2 5768 NP_543152.1 3 638 TCTTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 DUSP19 2 15367 NP_543152.1 3 2293 TCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 EBAF 1 18275 NP_003231.2 3 510 TGAAGGGCTTCA A - A 3 B c c
GGCTGGGGGCAG CATTGC CTCCAGCCTGG GC
TGGACAGG GTGACG GGGGTCGGACT CG
- T G
GAM189 246 EDG8 1 12263 NP_110387.1 3 952 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGGCAC GTAACGTGAGGTCGGACCC
AC
GAM189 246 EEF2K 1 2595 NP_037434.1 3 345 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACATG GTGACGTGAGGTCGGACCC
AC
GAM189 246 EHD1 1 7065 NP_006786.2 3 329 GGCCTTTGCTGT -- - TG 3 B c c
GGCTGGAGCTGG CATTG CA CTCCAGCC GGCAA
ACAGTGCA GTGAC GT GAGGTCGG TCGTT
AG C TG
GAM189 246 EHD2 1 4837 NP_055416.2 3 906 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGAG GTGACGTGAGGTCGGACCCG
C
GAM189 246 EIF2S3 1 1744 NP_001406.1 3 347 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 EIF5A2 1 8340 NP_065123.1 3 975 CTCCATCAGCCA GCA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGACC
GAC
GAM189 246 ELP3 1 14236 NP_060561.3 3 906 CTGTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 EMR2 2 13462 NP_038475.2 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG

GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 13462 NP_690880.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 13462 NP_690881.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 13462 NP_690882.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 13462 NP_690883.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 13462 NP_690884.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 13462 NP_690885.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM189 246 EMR2 2 17743 NP_038475.2 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM189 246 EMR2 2 17743 NP_690880.1 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM189 246 EMR2 2 17743 NP_690881.1 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM189 246 EMR2 2 17743 NP_690882.1 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM189 246 EMR2 2 17743 NP_690883.1 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM189 246 EMR2 2 17743 NP_690884.1 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM189 246 EMR2 2 17743 NP_690885.1 3 1758 CTTTGTCACCCA C C CA 3 B c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC
GAM189 246 ENDOGL1 1 5031 NP_005098.1 3 154 CCGTGTCATCCA CA 3 B c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTGGA GTGGCGTGAGGTCGGACCT
AC
GAM189 246 EPHA8 1 1229 NP_065387.1 3 461 CTTATCCGTTAA - A GG A 3 B c c
GGCTGGAGGCAC CAT TGC CTCCAGCCT GC
ATGTGGGT GTA ACG GAGGTCGGA TG
C - AT C
GAM189 246 EREG 1 17956 NP_001423.1 3 2043 CTCTGTTGCCCA 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTTGGACCCGTT

GAM189 246 EVC 1 18115 NP_055371.1 3 2225 CACTTTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 EVC 1 18115 NP_714928.1 3 2225 CACTTTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 EVI5 2 7219 NP_005656.2 3 516 GTTTGTCACCCA T CA 3 B c b
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGTGTG GTG CGTGAGGTCGGACCC
T AC
GAM189 246 EVI5 2 11607 NP_005656.2 3 2217 TCACTGCACTCA - - 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG G GCA
GTGGTACG GTGACGTGAGGTCGGAC C CGT
T A
GAM189 246 EZH1 1 14083 NP_001982.2 3 288 GAAGCGAGCACA G G A 3 B c c
GGCTGGGGTGGA CATT CACTCCAGCCTG GC
TGACTTAT GTAG GTGGGGTCGGAC CG
- A A
GAM189 246 F11R 1 2664 NP_058642.1 3 2148 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM189 246 F11R 1 2664 NP_653085.1 3 2148 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM189 246 F11R 1 2664 NP_653086.1 3 2150 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM189 246 F11R 1 2664 NP_653087.1 3 2150 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM189 246 F2RL3 1 4234 NP_003941.1 3 3005 CGCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 F3 1 18492 NP_001984.1 3 424 CTCTGTTGCCCA C----- 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCACG TGACGTGAGGTCGGACCCGTT
GCACGA
GAM189 246 F5 1 7269 NP_000121.1 5 47 AAGCGCTGCCCA TG -- 3 B c c
GGTCCTGGGGTG CAT CACTCCAG CCTGGGCA
GTGGCAGC GTG GTGGGGTC GGACCCGT
-- CT
GAM189 246 FABP2 1 2195 NP_000125.1 3 371 CTCTTTCACTCA C CA 3 B c c
GGCTGGAATGTA CATTGCA TCCAGCCTGGG
GTGGAGAG GTGATGT AGGTCGGACTC
A AC
GAM189 246 FANCE 1 5597 NP_068741.1 3 280 CTCTGTCATCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGATGCG GTGACGTGAGGTCGGACCT
AC
GAM189 246 FANCF 1 5816 NP_073562.1 3 738 CTCTGTCACCCA C CA 3 B c c
GTCTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGTG GTGACGTGAGGTC GACCC
T AC
GAM189 246 FAT3 1 8236 XP_061871.5 3 1359 CTCTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCATG GTAACGTGAG TCGGACCC
A AC
GAM189 246 FBXW8 1 11845 NP_036306.1 3 1498 TCACCTAGACTA C GCA 3 B c
c
GACTGGAGTGCA CATTGCACTCCAG CTGG
ATGGCCTG GTAACGTGAGGTC GATC
A AGA
GAM189 246 FBXW8 1 11845 NP_699179.2 3 1498 TCACCTAGACTA C GCA 3 B c
c
GACTGGAGTGCA CATTGCACTCCAG CTGG
ATGGCCTG GTAACGTGAGGTC GATC
A AGA
GAM189 246 FCAR 3 3819 NP_001991.1 3 158 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGAGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 FCAR 3 10448 NP_579803.1 3 158 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 10448 NP_579805.1 3 158 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG

GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 10448 NP_579806.1 3 158 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 10448 NP_579807.1 3 158 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 10448 NP_579808.1 3 282 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 10448 NP_579811.1 3 158 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 10448 NP_579812.1 3 158 CTCTGTCACCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM189 246 FCAR 3 17643 NP_579813.1 3 243 CTCTTTCGCCAA G A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGCACG GTGACGTGAGGTCGGA CCG
A C
GAM189 246 FCAR 3 17643 NP_579814.1 3 243 CTCTTTCGCCAA G A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGCACG GTGACGTGAGGTCGGA CCG
A C
GAM189 246 FCGR2A 1 497 NP_067674.1 3 523 ATCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCT GTGACGTGAGGTCGGACCC
AT
GAM189 246 FER1L4 1 11291 XP_300246.1 3 222 CTCTGTCTCCCA CA 3 B c c
GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTTGGACCC
TC
GAM189 246 FER1L4 1 11291 XP_300246.1 3 371 CTCTGTCTCCCA CA 3 B c c
GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTTGGACCC
TC
GAM189 246 FEZ1 1 5204 NP_072043.1 3 826 TTCTATCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCACA GTAACGTGAGGTCGGACCCG
C
GAM189 246 FGF5 1 14382 NP_004455.1 3 2381 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC

GAM189 246 FGF5 1 14382 NP_149134.1 3 2712 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 FHL2 1 16589 NP_001441.2 5 449 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM189 246 FISH 1 13261 NP_055446.1 5 209 CTCTGTTGCTCA C 3 B b b
GGCTGGATTGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACTCGTT
T
GAM189 246 FKBP9 1 7851 NP_009201.1 3 805 CGTTTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
GTGGTGCC GTGACGTGAGGTCGGACC TGTT
GC
GAM189 246 FLJ0000 1 14844 XP_088525.2 3 1654 AGGGGGCTGCCA - CT G 3 B c
c
1 GGCTGGCTGCCG CATTG CA CCAGCCTGG CA
ATGCTCCG GTAGC GT GGTCGGACC GT
C C- -
GAM189 246 FLJ0006 1 11528 XP_028154.1 5 30 CTCTGTCACCCA CA 3 B c c
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 FLJ1010 1 9189 NP_078994.1 3 253 CTGTGTGGCCCA A 3 B b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
G
GAM189 246 FLJ1023 1 19236 NP_060503.1 3 795 CTCTGTCACCCA CA 3 B c c
2 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
ATGGCGCG GTAGCGTGAGGTCGGACCC
AC
GAM189 246 FLJ1029 1 2615 NP_060520.2 3 183 CTTTGTTGCCCA C----- 3 B c c
8 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCACG TGACGTGAGGTCGGACCCGTT
GCACGA
GAM189 246 FLJ1034 1 19219 NP_060535.1 5 100 CTCTGTCTCCCA C CA 3 B c c
6 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGCACG GTGACGTGA GTCGGACCC
A TC
GAM189 246 FLJ1052 1 4272 NP_060594.2 3 1711 AGTGGTTGCCCA C- CCA 3 B c c
0 GGCCTAGTTTCA CATTG ACT GCCTGGGCAA
GTGGCAGA GTGAC TGA CGGACCCGTT
TT TC-
GAM189 246 FLJ1053 1 9543 NP_060599.1 3 806 CTCTGTCACCCA CA 3 B c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 2460 FLJ1056 1 15591 NP_060608.1 3 190 TTCTGTCGCCCA T A 3 B c c
GGCTGGCGTGCA CATTGCAC CCAGCCTGGGC
GTGGCGCG GTGACGTG GGTCGGACCCG
C C

GAM189 2463 FLJ1071 1 7909 NP_060659.1 3 360 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 2466 FLJ1084 1 11528 NP_060711.1 3 352 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM189 2467 FLJ1084 1 19357 NP_060712.2 3 490 CTCTGTCATGCA --- 3 B b b
GGCTGGAGTGCG CATTGCACTCCAGCCTG GGCA
GTGGTGCG GTGGCGTGAGGTCGGAC CTGT
GTA

GAM189 2462 FLJ1092 1 18818 NP_060743.1 3 2051 GCTTGTTGCCCA C 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
ATGGCGTG GTAACGT AGGTCGGACCCGTT
A

GAM189 2463 FLJ1132 1 2044 NP_060860.1 3 97 TCTCGTTGCCGA C----- G 3 B c c
GGCTGGAGTGTA ATTGCACTCCAGCCT GGCAA
GTAGTGTG TGATGTGAGGTCGGA CCGTT
GTGTGA G

GAM189 2467 FLJ1146 1 834 NP_079239.2 3 145 TCCTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC

GAM189 2460 FLJ1171 1 9688 NP_079122.1 3 1011 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC

GAM189 2465 FLJ1171 1 3305 NP_078840.1 3 898 CACCGTTGCCCA A 3 B b b
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGCAA
GTGACGTG GTGACG GAGGTCGGACCCGTT
G

GAM189 2460 FLJ1180 1 10847 NP_079250.1 3 1242 CACTGTCACCCA A CA 3 B c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
C AC

GAM189 2466 FLJ1207 1 8886 NP_079463.2 3 158 AGGTTGGGCTCA TT T A 3 B c c
GGCTGGGTGCTC CA GCAC CCAGCCTGGGC
TGCCATGG GT CGTG GGTCGGACTCG
CT - G

GAM189 2463 FLJ1236 1 17722 NP_115543.1 3 51 CACCGTCCCCCA T CA 3 B c c
GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
GTGGCGTG GTG CGTGAGGTCGGACCC
C CC

GAM189 2462 FLJ1257 1 17515 NP_075056.2 5 117 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTATA CATTG ACTCCAGCCTGGG

GTGGTGTG GTGAT TGAGGTCGGACCC
A AC

GAM189 2466 FLJ1258 1 10410 NP_078896.2 5 38 CTGTCTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM189 2469 FLJ1264 1 3686 XP_291344.1 3 951 CTCTGTTGCCCA C 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
A

GAM189 2467 FLJ1268 1 3324 NP_079193.2 3 212 CACTCTTGCCCA T 3 B b b
GGCTGGGGTGTC CAT GCACTCCAGCCTGGGCAA
GTGGCGTG GTG TGTGGGGTCGGACCCGTT
C

GAM189 2467 FLJ1274 1 10683 XP_290972.1 3 2540 TCTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCG GTAACGTGAGGTCGGACCC
AC

GAM189 2467 FLJ1278 1 14839 NP_115551.1 3 1020 CTTTATCGCCCA C A 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGATGCA GTGAC TGAGGTCGGACCCG
A C

GAM189 2460 FLJ1280 1 4261 NP_075054.1 3 1087 ACTGGCTGCCCA ACTC 3 B c c
GGCTGAATGGCA CATTGC CAGCCTGGGCA
GTGCCTGG GTGACG GTCGGACCCGT
GTAA

GAM189 2468 FLJ1288 1 17723 NP_079221.1 3 241 CTCTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCATG GTGACGTGAG TCGGACCCGTT
A

GAM189 2463 FLJ1290 1 10224 NP_073590.1 3 1559 TGTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTA GTAACGTGAGGTCGGACCCGTT

GAM189 2460 FLJ1296 1 11523 NP_078914.1 3 1535 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 2463 FLJ1297 1 5230 NP_079184.1 3 294 TCTTGTTGCCCA C----- 3 B b b
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCG TAACGTGAGGTCGGACCCGTT
GCGCGA

GAM189 2465 FLJ1297 1 2409 NP_079085.2 3 355 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCACAA GTGACGTGAGGTCGGACCC
AC

GAM189 2466 FLJ1298 1 6037 XP_290685.1 3 1798 AAACCAAGCCCA A A A 3 B c c
GGCCGGGGGCGG CATTGC CTCC GCCTGGGC
TGGCTCAC GTGGCG GGGG CGGACCCG

- C A

GAM189 246 2 FLJ1307 2 2223 XP_117117.2 3 698 CTCTGTCGGCCA --- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
GGC

GAM189 246 2 FLJ1307 2 13729 XP_117117.2 3 2202 GGAGTGTGCCCA T CTCCA 3 B c b
GGTCACTGCTAT CAT GCA GCCTGGGCA
GGCCTTCG GTA CGT TGGACCCGT
T CAC--

GAM189 246 4 FLJ1311 1 11919 NP_078817.1 3 610 CTCTGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGTG GTGACGT AGGTCGGACCCG
A C

GAM189 246 7 FLJ1319 1 8231 NP_078890.1 3 403 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 2 FLJ1335 2 10493 NP_078868.1 3 519 CAAAATAATAAC T GGCA 3 B c c
AGGCTGGGTGCA CATTGCAC CCAGCCTG
ATGGCTCA GTAACGTG GGTCGGAC
- AATA

GAM189 246 2 FLJ1335 2 13318 NP_078868.1 3 519 AAAATAATAACA T GGCA 3 B c c
GGCTGGGTGCAA CATTGCAC CCAGCCTG
TGGCTCAC GTAACGTG GGTCGGAC
- AATA

GAM189 246 6 FLJ1345 1 8163 XP_038291.5 3 2588 CTCTGTCGCCCA C A 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCACA GTGACGTGAGGTCG ACCCG
A C

GAM189 246 0 FLJ1391 1 7691 NP_073617.1 3 1668 GGGATTGGCCCA T- C A 3 B c c
GCTTGGAGTGCT CAT GCACTCCAG CTGGGC
TGTGTGGT GTG CGTGAGGTT GACCCG
TT C G

GAM189 246 4 FLJ1398 2 4819 NP_079046.1 3 897 ATACAAGTTGTT CCA G 3 B c c
AGGCCAGGTGCA CATTGCACT GCCTGG CAA
ATGGCTCG GTAACGTGG CGGATT GTT
AC- -

GAM189 246 4 FLJ1398 2 10809 NP_079046.1 5 245 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGATCC
AC

GAM189 246 0 FLJ1410 1 12143 NP_079301.1 3 386 TCCTGCCGCCCA T A -- A 3 B c c
GGCCTTGGAGGT CA TGC CTCCA GCCTGGGC
ACTGCTGC GT ATG GAGGT CGGACCCG
C - TC C

GAM189 246 0 FLJ1426 1 921 NP_079303.2 3 414 TGTTTTGCATCA GC-- C - 3 B c c
AGCTGGAGTACT CATT ACTCCAGC TGG GCAA

GGATGGAA GTAG TGAGGTCG ACT CGTT
GTCA A A

GAM189 2461 FLJ1435 1 8586 NP_079008.1 3 317 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCAGT GTGACGTGAGGTCGGACCCG
C

GAM189 2462 FLJ1444 1 16259 NP_116174.1 3 2236 CTCTGTTACCCA C CA 3 B c c
GGCTAGAGTGTA CATTGCACTC AGCCTGGG
GTGGCATG GTGATGTGAG TCGGACCC
A AT

GAM189 2463 FLJ1480 1 939 NP_116231.1 3 437 TCTGTCAACGCA C ---- 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTG GGCA
GTGGCACG GTGACGTGAGGTC GAC CTGT
A GCAA

GAM189 2467 FLJ1495 1 13527 NP_116255.1 3 572 TCTTGTTGCCGA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
ATGGCGCA GTAACGTGAGGTCGGA CCGTT
G

GAM189 2465 FLJ2004 1 12557 NP_060108.1 3 132 CTTTGTTTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
TT

GAM189 2460 FLJ2007 1 7530 NP_060122.1 3 626 CTGAAGAAGTGC CAGCCT 3 B c c
CTTTTGAGTGCA CATTGCACTC GGGCA
ATGAATGT GTAACGTGAG TCCGT
TTT---

GAM189 2469 FLJ2007 1 14265 NP_060126.1 3 2037 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTATG GTAACGTGAGGTCGGACCCGTT

GAM189 2465 FLJ2009 1 7385 NP_060136.1 3 1358 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM189 2466 FLJ2013 1 4536 NP_060154.1 3 461 CTCTGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM189 2467 FLJ2014 1 2624 NP_060157.1 3 399 CTGTGTTGCCCA CA----- C 3 B c c
GGCTAGAGTGCA TTGCACTC AGCCTGGGCAA
GCAGTGAC GACGTGAG TCGGACCCGTT
CAGTGAC A

GAM189 2465 FLJ2024 2 5275 NP_060193.1 3 2299 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGACACG GTAACGTGAGGTCGGACCCGTT

GAM189 2465 FLJ2024 2 8581 NP_060193.1 3 542 TCAGGAGCTCAA TT - A 3 B c b
GGCTGGAGTGTC CA GCACTCCAGCCT GGGC
TTGACAGT GT TGTGAGGTCGGA CTCG

TC A A

GAM189 246 FLJ2025 1 7206 NP_062552.1 3 257 CCCAGCCTCCCA T AC CA 3 B c c

7 GGCTGGATGGCA CAT GC TCCAGCCTGGG

TGGACTGT GTA CG AGGTCGGACCC

- GT TC

GAM189 246 FLJ2034 1 4079 NP_060246.1 3 705 CTCTGTCATCCA CC CA 3 B c c

4 AACTGGAGTGCA CATTGCACTCCAG TGGG

GTGGCACA GTGACGTGAGGTC ACCT

AA AC

GAM189 246 FLJ2035 1 11024 NP_060251.1 3 284 GCCGAGGGCCCA TCCA- A 3 B c

c

9 GGCCCTGTGTGC CATTGCAC GCCTGGGC

GGTGCCCA GTGGCGTG CGGACCCG

TGTCC G

GAM189 246 FLJ2037 1 9357 NP_060264.2 3 181 CATGCCTCCTAA T AGC ---- 3 B c c

5 GAGAGGAGTGCA CA TGCACTCC CT GGGCA

TTGCTTTA GT ACGTGAGG GA TCCGT

T AGA ATCC

GAM189 246 FLJ2051 1 17759 NP_060323.1 3 676 TCTTGTCACCCA CA 3 B c c

1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCGCG GTGACGTGAGGTCGGACCC

AC

GAM189 246 FLJ2052 1 17075 NP_060333.1 5 132 AAGCGGTGCCCA - - - A 3 B c c

7 GGCCGGTGGTGA CA TTG CACT CC GCCTGGGCA

CAACTGGG GT AAC GTGG GG CGGACCCGT

C A T C

GAM189 246 FLJ2067 2 13041 NP_060394.1 3 632 GTTGTCACTTAA C G---- 3 B c b

1 GTTTGGAGTGCA CATTGCACTCCAG CT GGCAA

GTGGCATG GTGACGTGAGGTT GA CTGTT

T ATTCA

GAM189 246 FLJ2067 2 16491 NP_060394.1 3 1539 GTCTGTTGCCCA 3 B b b

1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 FLJ2070 1 18943 NP_060402.1 3 424 CTCTCTCGCCCA A 3 B b b

0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

GTGGTGCG GTGACGTGAGGTCGGACCCG

C

GAM189 246 FLJ2081 1 10574 NP_060431.1 3 96 CTCTTTCACCCA CA 3 B c c

3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCACG GTGACGTGAGGTCGGACCC

AC

GAM189 246 FLJ2112 1 17516 NP_079359.2 3 1349 TGTGTCTGCCCA - ACT- 3 B c c

8 GGCTGGCTGAGC CATT GC CCAGCCTGGGCA

GGGTGGAT GTGG CG GGTCGGACCCGT

G AGTC

GAM189 246 FLJ2160 1 15047 NP_079038.1 3 482 CTCTGTCACCCA C CA 3 B c c

3 GGCTGGAGTACA CATTG ACTCCAGCCTGGG

GTGGCATA GTGAC TGAGGTCGGACCC

A AC

GAM189 2463 FLJ2167 1 1435 NP_112160.1 5 802 TTCTGTCACCTA CA 3 B c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGACATG GTGATGTGAGGTCGGATCC
AC

GAM189 2467 FLJ2177 1 4203 NP_115585.1 3 785 TTGTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCA GTAACGTGAGGTCGGACCC
AC

GAM189 2469 FLJ2232 1 9543 NP_078932.2 3 528 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 2461 FLJ2253 1 5636 NP_078926.2 5 342 CTCTGTTACCCA A CA 3 B c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCGCA GTGACGTGAGG CGGACCC
C AT

GAM189 2464 FLJ2279 1 5559 NP_071357.1 3 256 CTCTGTCGCCTG C TG A 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCC GGC
GTGGTGCG GTGAC TGAGGTCGG CCG
A GT C

GAM189 2465 FLJ2296 1 2808 NP_071384.1 3 232 CTCTTTCGCCCA G A 3 B c c
GGATGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGTGCG GTGACGTGAGGT GGACCCG
A C

GAM189 2464 FLJ2302 1 9682 NP_079212.1 3 330 CTCTGTCTCCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACA GTAACGTGAG TCGGACCC
A TC

GAM189 2463 FLJ2305 1 8693 NP_075058.1 3 212 CTCTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCTCA GTGACGTGAGGTCGGACCCGTT

GAM189 2466 FLJ2318 1 1340 NP_078892.1 3 368 GTTCTGTCGCTT C A 3 B c c
AGCTGGAGTGCG CATTGCACTCCAGC TGGGC
GTGGCGTG GTGGCGTGAGGTCG ATTCG
- C

GAM189 2463 FLJ2326 1 11523 NP_079391.1 5 182 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 2466 FLJ2335 1 12273 NP_115613.1 3 241 CTCTGTTGCTGA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
GTGATGTG GTGACGTGAGGTCGGA TCGTT
G

GAM189 2462 FLJ2339 3 5554 NP_079060.1 3 607 CTCTGTCCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
CC

GAM189 246 FLJ2339 3 9148 NP_079060.1 3 197 CTCTGTCACCCA C CA 3 B c c

2 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCGCG GTGACGTGAGGTC GACCC
A AC

GAM189 2462 FLJ2339 3 20052 NP_079060.1 3 497 CTCTGTCACTGA G CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GG
GTGGCGCA GTGACGTGAGGTCGGA TC
G AC

GAM189 2466 FLJ2341 1 2152 NP_115614.1 3 1323 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 2466 FLJ2355 1 17969 NP_079156.1 3 425 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM189 2463 FLJ2356 1 15048 XP_041701.4 3 1724 TCTTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCACA GTAACGTGAG TCGGACCCGTT
A

GAM189 2467 FLJ2386 1 1374 NP_689875.1 3 1366 GGTGGGGGTCCA -- A- A 3 B c c
GGCTGGAGGGGC CATT GC CTCCAGCCTGGGC
CCAATGTA GTAA CG GAGGTCGGACCTG
CC GG G

GAM189 2466 FLJ2541 1 16915 NP_659455.2 5 107 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
ATGGCATC GTA CGTGAGGTCGGACCC
C AC

GAM189 2465 FLJ2579 1 934 NP_689633.1 3 563 CTCTGTCTCCCA A CA 3 B c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACG GTGACGTGAGG CGGACCC
C TC

GAM189 2467 FLJ3050 1 17957 NP_694555.1 5 68 CCCTGTTGCCCA CAC 3 B c c
GGCTGGAATACA CATTG TCCAGCCTGGGCAA
GTGGCACG GTGAC AGGTCGGACCCGTT
ATA

GAM189 2462 FLJ3053 1 19834 NP_653325.1 3 191 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGTATG GTGAC TGAGGTCGGACCCGTT
A

GAM189 2469 FLJ3113 3 3952 NP_775928.1 3 691 TCTTGTCACCCA A CA 3 B c b
GGCAGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCGTT GTGACGTGAGG CGGACCC
A AC

GAM189 2469 FLJ3113 3 15200 NP_775928.1 5 145 CTCTCTGGCCCA C A 3 B c b
AGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCACG GTGACGTGAGGTCG ACCCG
A G

GAM189 2469 FLJ3113 3 18868 NP_775928.1 3 397 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM189 2463 FLJ3115 1 7373 NP_653201.1 3 275 CTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCACG GTGACGTGAGGTC GACCC
A AC

GAM189 2466 FLJ3116 1 19301 NP_694567.1 3 1140 TCTTGTAGCCCA CT A 3 B c c
GGCTGGGATGCA CATTGCA CCAGCCTGGGC
ATGGCATG GTAACGT GGTCGGACCCG
AG A

GAM189 2468 FLJ3133 1 1672 NP_689682.1 3 268 TCTTGTTGCCCA C 3 B b b
CGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGTGCA GTAACGTGAGGTCG ACCCGTT
C

GAM189 2464 FLJ3138 1 14326 NP_689685.1 3 927 TCTTGCTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCA
ATGGTGCG GTAACGTGAG TCGGACCCGT
A

GAM189 2463 FLJ3139 1 9670 NP_694569.1 5 140 CTTTGTTGCCCA TT 3 B b b
GGCTGGAGTGCC CA GCACTCCAGCCTGGGCAA
TTGGCGCG GT CGTGAGGTCGGACCCGTT
TC

GAM189 2461 FLJ3140 1 16543 NP_689877.1 3 351 CTCTGTTGGCCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGTTCGA GTGACGTGAGGTCGGACC GTT
G

GAM189 2466 FLJ3209 2 1025 NP_776156.1 3 1416 CTTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCCGTT

GAM189 2466 FLJ3209 2 16043 NP_776156.1 3 1113 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAATGTGAGGTCGGACCCGTT

GAM189 2460 FLJ3213 3 2061 NP_689671.2 3 1143 CTCTGTTGCCTG TG 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGGCCCA GTGACGTGAGGTCGG CCGTT
GT

GAM189 2460 FLJ3213 3 4630 NP_689671.2 3 1440 TCTTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCATG GTAACGTGAG TCGGACCCGTT
A

GAM189 2460 FLJ3213 3 15049 NP_689671.2 3 519 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM189 2466 FLJ3220 1 3860 NP_689710.1 3 41 CTCTGTCGCCCA A A 3 B c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCGTG GTGACG GAGGTCGGACCCG
G C

GAM189 246 FLJ3233 1 8493 NP_653166.1 3 1145 TCTCCTGGCCCA T A - - A 3 B c c

4 GGCCTGGCGGGC CA TGC CT CCAG CCTGGGC
ACTGCTTC GT ACG GG GGTC GGACCCG
C - C C G

GAM189 2469 FLJ3249 1 4681 NP_653208.1 3 744 CTCTGTCACCCA C CA 3 B c c
GTCTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCAAA GTGACGTGAGGTC GACCC
T AC

GAM189 2461 FLJ3273 1 16099 NP_689632.1 3 733 AGCCGCTGCCCA T - AG 3 B c c
GGGGAGTGGCTG CAT GC ACTCC CCTGGGCA
TGGGGAGG GTG CG TGAGG GGACCCGT
T G --

GAM189 2463 FLJ3280 1 1856 NP_694584.1 3 643 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGAA GTGACGTGAGGTCGGACCC
AC

GAM189 2465 FLJ3286 1 2146 NP_653214.1 3 1248 TCTTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
ATGATGCG GTAAC TGAGGTCGGACCC
A AC

GAM189 2464 FLJ3289 1 7467 NP_653268.1 3 705 CTCTGTTGTCCA CA----- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGATATG GACGTGAGGTCGGACCTGTT
GTATAGC

GAM189 2462 FLJ3293 1 9555 NP_690873.1 3 604 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 2465 FLJ3350 1 13693 NP_689530.1 3 741 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACGCG GTGACGTGAGGTCGGACCCGTT

GAM189 2465 FLJ3365 1 16113 NP_775912.1 3 326 CTCTGTTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCTTG GT ACGTGAGGTCGGACCCGTT
C

GAM189 2467 FLJ3481 2 4004 NP_689516.1 5 271 CCGCTGGTCCCA T C - A 3 B c c
GGCTGGATTGCC CAT GCA TCCAGCCTGGG C
GTGGCACA GTG CGT AGGTCGGACCC G
C T T G

GAM189 2467 FLJ3481 2 7075 NP_689516.1 3 208 GTCTGCCACCCA C CA 3 B c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
C AC

GAM189 2462 FLJ3492 1 18132 NP_689483.1 5 153 CTTTGACCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
CC

GAM189 2469 FLJ3496 1 581 XP_114353.1 3 1548 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCCGTT

GAM189 2465 FLJ3510 1 18938 NP_689890.1 5 161 CTCTGTCGTCCA T A 3 B c c
GGCTGGAGTGCC CAT GCACTCCAGCCTGGGC
GTGGCGTA GTG CGTGAGGTCGGACCTG
C C

GAM189 2461 FLJ3568 2 1653 NP_787096.1 3 1370 CTCTGTTGCCCA CAC 3 B c c
GGCTGGACTACA CATTG TCCAGCCTGGGCAA
GTGGCACA GTGAC AGGTCGGACCCGTT
ATC

GAM189 2461 FLJ3568 2 11521 NP_787096.1 3 1071 CTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCACA GTGACGTGAGGTC GACCC
A AC

GAM189 2468 FLJ3584 1 14986 XP_290755.1 3 1062 CTTTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCATG GTGACGTGAG TCGGACCC
A AC

GAM189 2465 FLJ3644 1 2147 NP_694965.1 3 231 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGATGTGAGGTCGGACCC
AC

GAM189 2465 FLJ3704 1 9497 NP_787085.1 3 765 CTCTGTCGCCCA C A 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGTGCG GTGAC TGAGGTCGGACCCG
A C

GAM189 2468 FLJ3707 1 11528 NP_694588.1 5 43 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM189 2463 FLJ3743 1 8582 NP_848612.1 3 198 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCC GTGATGTGAGGTCGGACCC
AT

GAM189 2463 FLJ3754 1 5495 NP_775938.1 3 744 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATT GTGACGTGAGGTCGGACCCGTT

GAM189 2461 FLJ3810 1 5589 NP_694993.2 3 742 GCTCTGTTGCCA A G 3 B b b
GGCTGGAGGGCA CATTGC CTCCAGCCTGG CAA
GTGGCACG GTGACG GAGGTCGGACC GTT
G -

GAM189 2469 FLJ3814 3 9373 XP_091919.5 3 259 CTCTGTCTCCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGAGTG GTGACGTGAGGTCGGACCC
TC

GAM189 2469 FLJ3814 3 15044 XP_091919.5 3 1432 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 FLJ3814 3 18971 XP_091919.5 5 26 CTCTATTGCCCA 3 B b b

9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTA GTGACGTGAGGTCGGACCCGTT

GAM189 2461 FLJ3828 2 6885 NP_689814.1 3 109 CTCTGTTGCCCT C----- T 3 B c b
GGCTGGAGTGCA ATTGCACTCCAGCC GGGCAA
GTAGAGTG TGACGTGAGGTCGG CCCGTT
GTGAGA T
GAM189 2461 FLJ3828 2 9492 NP_689814.1 3 1966 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTACG GTGACGTGAGGTCGGACCCG
C
GAM189 2467 FLJ3860 2 7382 NP_689867.1 3 288 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM189 2467 FLJ3860 2 16688 NP_689867.1 3 544 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCG GTAACGTGAGGTCGGACCC
AC
GAM189 2462 FLJ3879 1 14861 NP_848615.1 3 1162 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM189 2469 FLJ3881 2 9791 NP_665872.1 3 1041 CTCTGTCACTCA C CA 3 B c c
TGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCGTG GTGACGTGAGGTCG ACTC
T AC
GAM189 2469 FLJ3881 2 18642 NP_665872.1 3 214 GTCTCTTACCCA C CA 3 B c c
GGCTAGGGTGCA CATTGCACTC AGCCTGGG
GTGGTGTG GTGACGTGGG TCGGACCC
A AT
GAM189 2461 FLJ3899 2 10356 NP_776188.1 3 1037 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGATCC
AC
GAM189 2461 FLJ3899 2 14236 NP_776188.1 3 731 CTGTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM189 2465 FLJ3941 1 11673 NP_775952.1 3 342 GTCTTTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCTGTG GTGACGTGAGGTCGGACCC
AC
GAM189 2469 FLJ3959 2 8232 NP_776164.1 3 1104 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM189 2469 FLJ3959 2 16001 NP_776164.1 3 627 TGCTGTCTCCCC A T CA 3 B c c
GGCTGGAGCGCA CATTGC CTCCAGCC GGG
GTGGCACG GTGACG GAGGTCGG CCC

C C TC

GAM189 246 FLJ3963 1 9190 XP_290687.1 3 682 CTCTGTCGTCCA A 3 B b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGAGGTCGGACCTG
C

GAM189 246 FLJ9023 1 10357 NP_775852.1 3 74 CTTTGTCGCCCA A 3 B b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
C

GAM189 246 FLJ9072 1 19889 NP_787115.1 3 525 CTCTGTCGCCCA A 3 B b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGCCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 FNBP1 1 16354 XP_052666.3 3 1012 CTCTATTGTTCA C 3 B b b
GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATG GTGACGTGAGGTC GACTTGTT
A

GAM189 246 FOXE2 1 15626 NP_036317.1 5 631 AAGCTGCGTCCG T AC A 3 B c c

GGCTGGAGCACT CA TGC TCCAGCCTGGGC
GGAACCCG GT ACG AGGTCGGGCCTG
C -- C

GAM189 246 FOXO1A 1 736 NP_002006.2 3 13 AGCTGGGTGTCA C G 3 B c c
GGCTGGGGTTAG CATTG ACTCCAGCCTGG CA
TGAGCAGG GTGAT TGGGGTCGGACT GT
- -

GAM189 246 FSHPRH1 1 11528 NP_006724.1 5 15 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 FUT1 2 11525 NP_000139.1 3 613 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 FUT1 2 16365 NP_000139.1 3 935 CTCTGTAGCCCA CA A 3 B c b
GGCCAGAGTGCA CATTGCACTC GCCTGGGC
GTGGCGCG GTGACGTGAG CGGACCCG
AC A

GAM189 246 FZD4 1 4487 NP_036325.2 3 3982 CTCTGTCACCCA A CA 3 B c c
GGCTGGGGCGCA CATTGC CTCCAGCCTGGG
ATGGCACG GTAACG GGGGTCGGACCC
C AC

GAM189 246 G2A 1 8714 NP_037477.1 3 1257 CTCTGTTGCCTG CA TG 3 B c c
GGCTGGAGAACA CATTG CTCCAGCC GGCAA
GTGGCACC GTGAC GAGGTCGG CCGTT
AA GT

GAM189 246 G6PC 1 4204 NP_000142.1 3 1429 ACCTATCACCCA G CA 3 B c c
GGCTGGAGTGGA CATT CACTCCAGCCTGGG
GTGGCACG GTGA GTGAGGTCGGACCC
G AC

GAM189 246 GAL3ST-4 1 4518 NP_078913.3 3 252 CTCTGTCCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC
GAM189 246 GATA2 1 16014 NP_116027.2 3 225 GACTGCTGCCCA T ----- G 3 B c c
GGTGGGGTTTCC CAT GC ACTCCA CCTGGGCA
TGCATGGA GTA CG TGGGGT GGACCCGT
- TCCTT -
GAM189 246 GGA2 2 5631 NP_055859.1 3 1712 CTCTGTCACTCA CA 3 B c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTATA GTGGCGTGAGGTCGGACTC
AC
GAM189 246 GGA2 2 5631 NP_619581.1 3 2800 CTCTGTCACTCA CA 3 B c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTATA GTGGCGTGAGGTCGGACTC
AC
GAM189 246 GGA2 2 6391 NP_055859.1 5 66 CCGCAGCGTCGG AC G A 3 B c c
GGCTGGAGCGAT CATTGC TCCAGCCT GGC
GGCGGCGA GTAGCG AGGTCGGG CTG
-- G C
GAM189 246 GGA2 2 6391 NP_619581.1 5 66 CCGCAGCGTCGG AC G A 3 B c c
GGCTGGAGCGAT CATTGC TCCAGCCT GGC
GGCGGCGA GTAGCG AGGTCGGG CTG
-- G C
GAM189 246 GM2A 1 11286 NP_000396.1 3 761 GCTTTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
GTGGTGCA GTGACGTGAGGTCGGACC TGTT
AC
GAM189 246 GNE 1 8367 NP_005467.1 3 618 GCATGAACCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTCA GTGACGTGAGGTCGGACCC
CA
GAM189 246 GNG4 1 559 NP_004476.1 3 608 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC
GAM189 246 GNPNAT1 1 8464 XP_085119.1 3 2471 CTCCATCACCCA C CA 3 B c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGTGTG GTGAC TGAGGTCGGACCC
C AC
GAM189 246 GNRPX 1 12243 NP_060519.1 3 147 CTGTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGTGCC GTGACGTGAG TCGGACCCGTT
A
GAM189 246 GOLGA3 1 15049 NP_005886.2 3 601 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 GP5 1 5681 NP_004479.1 3 596 CTCTGTGGCCCA T A 3 B c c

GGCTGGCGTGCA CATTGCAC CCAGCCTGGGC
GTGGGCCG GTGACGTG GGTCGGACCCG
C G

GAM189 246 GPP34R 1 14203 NP_060648.2 3 870 TGCTCTTGCCCA --- A 3 B c c
GGCAGGAGTACA CATTGC ACTCC GCCTGGGCAA
GTAGTGCA GTGATG TGAGG CGGACCCGTT
ACA A

GAM189 246 GPR26 1 3010 NP_703143.1 3 1152 TCTTATTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGTGCG GTAACGTGAG TCGGACCCGTT
A

GAM189 246 GPR4 1 4965 NP_005273.1 3 280 CTGTGTTGCCCA C----- 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGTGCA TGACGTGAGGTCGGACCCGTT
ACGTGA

GAM189 246 GPR56 1 8622 NP_005673.2 5 25 CTCTGTCACACA --- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGTGTG GTGACGTGAGGTCGGAC CTGT
ACA

GAM189 246 GPR66 1 19237 NP_006047.2 3 530 CTCTGTCGCCCA C A 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCGCG GTGACGTGAG TCGGACCCG
A C

GAM189 246 GPR81 1 13260 NP_115943.1 3 375 CTCTGTGTCCCA - 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG CA
GTGGCACA GTGACGTGAGGTCGGACCC GT
T

GAM189 246 GR6 1 2604 NP_031380.1 5 287 CTCTGTCACCCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCATG GTGACGT AGGTCGGACCC
A AC

GAM189 246 GRAF 1 4362 NP_055886.1 3 2801 CTCTGTGGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
G

GAM189 246 GREB1 3 9792 NP_055483.2 3 1722 TCTTGCTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
ATGGTGCA GTAACGTGAGGTCGGACCCGT

GAM189 246 GREB1 3 11815 NP_055483.2 3 1726 CCCAGGCTGGAG CA 3 B b b

TGCAATGGTGCA CATTGCACTCCAGCCTGGG
ATGATCTC GTAACGTGAGGTCGGACCC
--

GAM189 246 GREB1 3 14861 NP_055483.2 3 1092 CTCTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM189 246 GRID1 1 17390 XP_043613.8 3 2299 GGGAGGTGCCCA C---- --- T G 3 B c
c

GGTGGGTGGACC ATTG CAC CCA CCTGGGCA
AGTACTCC TGAC GTG GGT GGACCCGT
CCTCA CAG - -

GAM189 246 GRINL1A 1 5433 NP_056347.1 3 713 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCAGG GTGACGTGAGGTCGGACCCG
C

GAM189 246 GRM6 1 10398 NP_000834.1 3 2444 CTCAATTTCTTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGATTC
TT

GAM189 246 GRWD 1 7996 NP_113673.2 3 372 GTCTGTCGCCCA C----- A 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCACG TGACGTGAGGTCGGACCCG
GCACGA C

GAM189 246 GSDM 1 3199 NP_835465.1 3 296 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 GSDM 1 3199 XP_209009.1 3 294 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 GSTM1 1 12752 NP_000552.2 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT

GAM189 246 GSTM1 1 12752 NP_666533.1 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT

GAM189 246 GSTM2 1 12752 NP_000839.1 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT

GAM189 246 GSTM4 1 12752 NP_000841.1 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT

GAM189 246 GSTM4 1 12752 NP_671490.1 3 358 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT

GAM189 246 GTF2E1 1 15661 NP_005504.1 3 306 TCTTGTACCCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
CA

GAM189 246 GTF2IRD 1 11522 NP_115579.3 3 143 CTCTGTCGCCCA A 3 B b b
2 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTTGGACCCG

C

GAM189 246 GTF2IRD 1 11522 NP_775808.1 3 143 CTCTGTCGCCCA A 3 B b b
2 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTTGGACCCG
C

GAM189 246 GTPBG3 2 7812 NP_116009.1 3 467 GTCTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 GTPBG3 2 10292 NP_116009.1 3 631 CTCTGTCACCCA C CA 3 B c b

GGCTGGAGTTCA CATTG ACTCCAGCCTGGG
GTGGTGCG GTGAC TGAGGTCGGACCC
T AC

GAM189 246 GYG 1 4258 NP_004121.2 3 443 TAGAATTGCCCA G --- - 3 B b b
GTGCTGCCAGAG CATT CACTC CAGC CTGGGCAA
TGAGTGAG GTGA GTGAG GTCG GACCCGTT
- ACC T

GAM189 246 H-plk 1 12753 NP_056936.1 5 982 GCTGTGTCACCA G -- 3 B b b
GGATGGAGTGCA CATTGCACTCCA CCTGG GCA
GTGGCATG GTGACGTGAGGT GGACC TGT
A AC

GAM189 246 H2AV 1 18864 NP_619541.1 3 585 TCTTGTCACCCA C CA 3 B c c
GACTGGAGTGCG CATTGCACTCCAG CTGGG
ATGGCACG GTAGCGTGAGGTC GACCC
A AC

GAM189 246 H63 1 4554 NP_612432.2 3 465 TCTTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACA GTAACGTGAGGTCGGACCC
TT

GAM189 246 H63 1 4554 NP_816929.1 3 465 TCTTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACA GTAACGTGAGGTCGGACCC
TT

GAM189 246 HAVCR2 1 16260 NP_116171.2 3 497 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 HE9 1 7942 NP_741997.1 3 210 CTCTGTTGCCCA C 3 B b b
GCCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCACA GTAACGTGAGGTC GACCCGTT
C

GAM189 246 HEPH 1 15338 NP_055614.1 5 130 CTGGCGGACTCA -- CA 3 B c c
GGCTGGGGTCTG CATTGC ACTCCAGCCTGGG
CAGTGCAG GTGACG TGGGGTCGGACTC
TC AG

GAM189 246 HEXA 1 14035 NP_000511.1 3 270 AGGGCACAGCCA C GCA 3 B c c

GGCTGGAGTCAG CATTG ACTCCAGCCTGG
TGTCTGCC GTGAC TGAGGTCGGACC

- GAC

GAM189 246 HLCS 1 2142 NP_000402.2 5 180 TTCTGTCGTCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCTG
C

GAM189 246 HMG20A 1 5040 NP_060670.1 3 1222 CTGTGTTGCCCA 3 B b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCTAT GTGGCGTGAGGTCGGACCCGTT

GAM189 246 HPRN 1 12916 NP_071938.1 3 220 TGGCTCTGCCCA G G 3 B c c
GGTGGGGTGGGG CATT CACTCCA CCTGGGCA
TGGCCCAG GTGG GTGGGGT GGACCCGT
G -

GAM189 246 HRH4 2 3116 NP_067637.2 3 1950 CTCTGTTGCCCA A C 3 B b b
CGCAGGAGTGCA CATTGCACTCC GC TGGGCAA
GTGGCATG GTGACGTGAGG CG ACCCGTT
A C

GAM189 246 HRH4 2 18211 NP_067637.2 3 1339 CTGTGTTGCCCA C----- - T C 3 B c b
GCCTGGGTGTCA ATTG CAC CCAG CTGGGCAA
ATAATTAT TAAC GTG GGTC GACCCGTT
TATTAA T - C

GAM189 246 HRMT1L3 1 18437 NP_062828.2 5 195 CCCAGCTGCCCA GCA AG 3 B c c
GGACGGGGCAAG CATT CTCC CCTGGGCA
ATGTCCAA GTAG GGGG GGACCCGT
AAC CA

GAM189 246 HSD3B7 1 2674 NP_079469.2 3 210 CTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGTG GTGACGTGAGGTC GACCC
A AC

GAM189 246 HSMPP8 1 7797 XP_167894.1 3 330 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 HSPA4 1 15189 XP_114482.1 3 1414 GAGTGTTACAGG CC-- - 3 B c c
CTCTAAAGTGCA CATTGCACT AGCCTG GGCA
ATGGAGAA GTAACGTGA TCGGAC TTGT
AATC A

GAM189 246 HSPC065 2 713 NP_054876.2 3 2293 CTCTGTCCCCCA C CA 3 B c b
TGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCATG GTGACGTGAGGTCG ACCC
T CC

GAM189 246 HSPC065 2 4676 NP_054876.2 3 2126 CTCTGTCCCCAA --- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGGCA
GTGGTGCA GTGACGTGAGGTCGGA CCTGT
ACC

GAM189 246 HTR1D 1 2563 NP_000855.1 3 290 GCCCTCTCGCCA GCA 3 B c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGG
GTGGCACA GTGATGTGAGGTCGGACC
GCT

GAM189 246 HUNK 1 17952 NP_055401.1 3 2963 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM189 246 HUS1 1 14238 NP_004498.1 3 1024 TTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGCCACA GTGACGTGAGGTC GACCC
A AC
GAM189 246 HYAL4 1 2143 NP_036401.1 5 83 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM189 246 HYPB 1 14422 NP_036403.1 3 1551 AGAATCCTGAGG -- G CA 3 B c c
ACCTGGAGTGCA CATTGCACTCCAG CCT GG
ATGAGAAT GTAACGTGAGGTC GGA TC
CA G CT
GAM189 246 ICAM1 1 12075 NP_000192.1 3 1135 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 ICK 1 7385 NP_055735.1 3 1470 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 ICK 1 7385 NP_057597.2 3 1470 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 IGF1 1 6279 NP_000609.1 3 5348 CACTGTCCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC
GAM189 246 IGHMBP2 1 17385 NP_002171.1 5 29 TCTAGGGGCCCA A- - A A 3 B c c

GGCCGGCGGCGG CATTGC CT CC GCCTGGGC
CGATGGCC GTAGCG GG GG CGGACCCG
GC C C G
GAM189 246 IGLL1 1 4573 NP_064455.1 5 2 GGCCACATGGAC - - - A 3 B c c
TGGGGTGCAATG CATTGCACTCCAG CC TG GGC
GGACAGCT GTAACGTGGGGTC GG AC CCG
A T A G
GAM189 246 IGLL1 1 4573 NP_690594.1 5 2 GGCCACATGGAC - - - A 3 B c c
TGGGGTGCAATG CATTGCACTCCAG CC TG GGC
GGACAGCT GTAACGTGGGGTC GG AC CCG
A T A G
GAM189 246 IL11 1 11544 NP_000632.1 3 700 CTCTGTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGAGGCA GTGACGTGAGGTCGGATCCGTT

GAM189 246 IL12RB1 1 10756 NP_714912.1 3 315 AGTCTGTTGGCA C----- C -- 3 B c c

GACTGGAGTGCA ATTGCACTCCAG CTG GGCA
ATCATGGC TAACGTGAGGTC GAC TTGT
CGGTAC A GG

GAM189 246 IL16 1 19554 NP_757366.1 5 100 CTCTGTTGCCCA --- 3 B b b
GGCTGGAGTTCA CATTGC ACTCCAGCCTGGGCAA
GCGGTGCA GTGGCG TGAGGTCGGACCCGTT
ACT

GAM189 246 IL21R 1 498 NP_068570.1 3 1362 TCTCGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM189 246 IL21R 1 498 NP_851564.1 3 1362 TCTCGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM189 246 IL21R 1 498 NP_851565.1 3 1362 TCTCGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM189 246 IL28RA 1 7046 NP_734464.1 3 2268 TCTTTTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM189 246 IL28RA 1 7046 NP_775087.1 3 2268 TCTTTTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM189 246 IL28RA 1 7046 NP_775088.1 3 2965 TCTTTTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM189 246 IL5RA 1 8557 NP_000555.2 3 453 CATTTTGCATCA TG-- C - 3 B c c
GCCTGGAGTGAA CAT CACTCCAG CTGG GCAA
CCATGAAC GTA GTGAGGTC GACT CGTT
CCAA C A

GAM189 246 IL5RA 1 8557 NP_783853.1 3 453 CATTTTGCATCA TG-- C - 3 B c c
GCCTGGAGTGAA CAT CACTCCAG CTGG GCAA
CCATGAAC GTA GTGAGGTC GACT CGTT
CCAA C A

GAM189 246 ILF3 1 17287 NP_036350.2 3 581 GGTGTCTGACCC CCA C-- - 3 B c c
ACCAGCAGTGCA CATTGCACT GC TGGG CA
ATGGGCAG GTAACGTGA CG ACCC GT
--- ACC A

GAM189 246 IMPACT 1 8975 NP_060909.1 3 2007 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGATCC
AC

GAM189 246 INHBE 1 16283 NP_113667.1 3 663 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGACACG GTGACGTGAGGTCGGACC TGT

AC
GAM189 246 INMT 2 9149 NP_006765.3 3 445 CTCTGTCACCCA C CA 3 B c b
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACG GTAACGTGAG TCGGACCC
A AC
GAM189 246 INMT 2 11523 NP_006765.3 3 622 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 IRF4 2 1517 NP_002451.1 3 1184 CGGGGACTCCCA T A CA 3 B c c
GGCTGGAGAGCA CA TGC CTCCAGCCTGGG
CTGCCAGG GT ACG GAGGTCGGACCC
C A TC
GAM189 246 IRF4 2 2698 NP_002451.1 3 102 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
TC
GAM189 246 ITGAX 1 559 NP_000878.1 3 396 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC
GAM189 246 JAK3 1 18060 NP_000206.1 3 401 GCTCGTTACCCA G CA 3 B c c
GGGTGGAGTGCA CATTGCACTCCA CCTGGG
GTGGTAGC GTGACGTGAGGT GGACCC
G AT
GAM189 246 JM11 1 10197 NP_296375.1 3 1440 GCTCTGTCACCA CA----- -- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGG GCA
GCGGCGCA GACGTGAGGTCGGACC TGT
ACGCGGC AC
GAM189 246 JRK 1 3927 NP_003715.1 3 1242 CTCTGTTGACCA G G 3 B b b
GGCTGGAGTGAA CATT CACTCCAGCCTGG CAA
GTGGTGTG GTGA GTGAGGTCGGACC GTT
A A
GAM189 246 KCNJ11 1 15049 NP_000516.2 5 53 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 KCNJ16 1 2456 NP_061128.1 3 625 GCTACTTGCCCA -- CCA 3 B c c
GGTAGTGATCAG CATTG CACT GCCTGGGCAA
TGAGAGTT GTGAC GTGA TGGACCCGTT
TA ---
GAM189 246 KCNJ16 1 2456 NP_733937.1 3 625 GCTACTTGCCCA -- CCA 3 B c c
GGTAGTGATCAG CATTG CACT GCCTGGGCAA
TGAGAGTT GTGAC GTGA TGGACCCGTT
TA ---
GAM189 246 KCNJ16 1 2456 NP_733938.1 3 625 GCTACTTGCCCA -- CCA 3 B c c
GGTAGTGATCAG CATTG CACT GCCTGGGCAA
TGAGAGTT GTGAC GTGA TGGACCCGTT
TA ---
GAM189 246 KENAE 1 14862 NP_789786.1 3 211 CTCTGTCACCCA CA 3 B c c

GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTTGGACCC
AC

GAM189 246 KIAA006 1 5884 NP_055691.1 3 627 TCTTGTTGCCCA 3 B b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACC GTAACGTGAGGTCGGACCCGTT

GAM189 246 KIAA008 1 18751 NP_055865.1 3 1279 TCCCCACCCCCA T - - CA 3 B c c

2 GGCTGGCAGTAG CA TGC ACT CCAGCCTGGG
CACTGCTG GT ACG TGA GGTCGGACCC
C A C CC

GAM189 246 KIAA008 2 7956 NP_055584.1 3 1558 GCCCATTTTATG GC ------- A 3 B c c
7 GGCTGGAGTTAA CATT ACTCCAGCCT GGGC
ATGGAAGT GTAA TGAGGTCGGG CCCG
AT TATTTTA -

GAM189 246 KIAA008 2 10179 NP_055584.1 3 2190 TTCTGTCACCCA CA 3 B c c
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 KIAA011 1 9255 XP_290939.1 3 248 TGTTGTCTCCCA CA 3 B c c
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
TC

GAM189 246 KIAA018 1 2218 XP_050495.4 3 2250 GAGGTCTGCCCA A T G 3 B c c
2 GGGTGGGAGCAG CATTGC C CCA CCTGGGCA
TGTCACTG GTGACG G GGT GGACCCGT
A - G

GAM189 246 KIAA018 1 2625 NP_066545.1 3 1108 TTCTGTCACCCA CA 3 B c c
6 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGGGGTCGGACCC
AC

GAM189 246 KIAA020 1 3429 NP_055688.1 3 1258 CTCTGTCACCCA C CA 3 B c c
5 GGCTGTAGTGCA CATTGCACT CAGCCTGGG
GTGGCATA GTGACGTGA GTCGGACCC
T AC

GAM189 246 KIAA023 1 17386 NP_055562.1 3 5053 CCCTGATGCCCA CA------ T 3 B c
c
7 GGCTGGGTGCAG TTGCAC CCAGCCTGGGCA
GCTCTCAT GACGTG GGTCGGACCCGT
TACTCTCG -

GAM189 246 KIAA029 1 10742 XP_042833.2 3 3373 GCTGGAGGCCCG A- A 3 B c c
5 GGCTGGAGGGGC CATTGC CTCCAGCCTGGGC
AGTGTTGC GTGACG GAGGTCGGGCCCG
GG G

GAM189 246 KIAA043 1 5041 NP_055616.1 5 677 CTCTGTCACCCA C CA 3 B c c
5 GTTTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGCA GTGACGTGAGGTT GACCC
T AC

GAM189 246 KIAA044 1 1475 XP_044155.1 5 2280 CACTGTCTCCTA CA 3 B c c

6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGATCC
TC

GAM189 2469 KIAA045 1 4531 XP_027862.1 3 3704 CTTTGTTGCCCA TG 3 B b b
GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
GTGGGGCA GTG GTGAGGTCGGACCCGTT
GT

GAM189 2469 KIAA046 2 9147 NP_055666.1 3 702 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM189 2469 KIAA046 2 9493 NP_055666.1 3 350 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
AC

GAM189 2465 KIAA047 1 16940 NP_055679.1 3 1231 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 2463 KIAA049 1 17206 XP_034717.1 5 926 CTCTCTTACCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGACATG GTGACGTGAGGTCG ACCC
A AT

GAM189 2465 KIAA049 2 5442 XP_031397.1 3 1639 AGATGCCTTCCA C C --- 3 B c b
GGCTGCAGTCAG CATTG ACT CAGCCTGG GCA
TGCAGATG GTGAC TGA GTCGGACC CGT
- C TTC

GAM189 2465 KIAA049 2 14759 XP_031397.1 3 2802 CCCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCG GTAACGTGAGGTCGGACCC
AC

GAM189 2463 KIAA051 1 3931 NP_055547.1 3 3674 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACACA GTGACGTGAGGTCGGACCCGTT

GAM189 2467 KIAA052 1 19745 XP_171054.1 3 365 TGCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGTCCCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 KIAA053 1 12455 XP_047659.6 3 1245 TTCTGTCACCCA C C CA 3 B c c

2 GGCTAGAGTACA CATTG ACTC AGCCTGGG
GTGGGAAC GTGAC TGAG TCGGACCC
A A AC

GAM189 2465 KIAA055 1 5555 NP_055605.1 3 2301 CTCTGTTGCCCA T C 3 B b b
TGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
TTGGCACA GT ACGTGAGGTCG ACCCGTT
T T

GAM189 2461 KIAA056 1 9629 XP_038150.2 3 321 CTCTGTTGCCCG CA----- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA

GCGGCGTG GACGTGAGGTCGGGCCCGTT
GTGCGGC

GAM189 2462 KIAA0561 16544 NP_055519.1 3 2049 CTCTGTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGATCCGTT

GAM189 2463 KIAA0561 16377 NP_055649.1 5 604 TCTTGTTGCCCA C 3 B b b
GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGTTGTG GTGACGTGA GTCGGACCCGTT
A

GAM189 2462 KIAA0681 6522 NP_055667.1 3 32 TGGCACCGAGAG ---- - A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GG GC
GTGGCGTG GTGACGTGAGGTCGGG CC CG
AGAG A G

GAM189 2464 KIAA0801 14656 XP_291080.1 3 453 AGTGGTTGGCCA - C C G 3 B c c
GGCTGCAGTATA CA TTG ACT CAGCCTGG CAA
ACTGAAGC GT AAT TGA GTCGGACC GTT
C A C G

GAM189 2461 KIAA0831 3260 NP_055739.1 3 1918 CTCAGCTGCCCA TG 3 B b b
GGCTGGAGTGTG CAT CACTCCAGCCTGGGCA
GTGGCGCC GTG GTGAGGTCGGACCCGT
GT

GAM189 2461 KIAA0842 5490 XP_049237.1 3 1172 TTCTGTTGCCCA C 3 B b b
AGTTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCATG GTGACGTGAGGTTG ACCCGTT
A

GAM189 2461 KIAA0842 8185 XP_049237.1 3 1521 GGCTGTTTCCCA C CA 3 B c b
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGCATG GTGACGTGA GTCGGACCC
A TT

GAM189 2461 KIAA0861 2153 NP_055893.2 3 955 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C

GAM189 2469 KIAA0881 13271 NP_056192.1 3 736 TCTTGTCCCCCA C CA 3 B c c
GGCTTGAGTGCA CATTGCACTC AGCCTGGG
ATGACTCA GTAACGTGAG TCGGACCC
T CC

GAM189 2464 KIAA0922 7655 NP_055712.1 3 2517 TTCTGTTGCCTG TG 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGGCGTG GTGACGTGAGGTCGG CCGTT
GT

GAM189 2464 KIAA0922 13297 NP_055712.1 3 1717 CTATGTTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCTAT GTGACGTGAG TCGGACCCGTT
A

GAM189 2461 KIAA0931 14272 XP_041191.2 3 162 CTCAGTCGCTCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGTGGG GTAACGTGAGGTCGGACTCG
C

GAM189 2465 KIAA093 1 11958 XP_052620.6 3 1214 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGTCAAG GTGACGTGAGGTCGGACCCG
C

GAM189 2462 KIAA096 1 8976 XP_290942.1 3 1524 TCTTGTTGCCCA G 3 B b b
GGCTGGAGTGAA CATT CACTCCAGCCTGGGCAA
ATGGTGCG GTAA GTGAGGTCGGACCCGTT
A

GAM189 2462 KIAA100 1 12518 XP_290584.1 5 0 CGCCTAGGCTGG T A A 3 B c c
AGCGCCGTGGTA CAT GC CTCCAGCCTGGGC
CAGTCTTG GTG CG GAGGTCGGATCCG
C C C

GAM189 2460 KIAA104 1 11846 XP_051091.3 3 2456 CTCTGTCACCCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACG GTGACGT AGGTCGGACCC
A AC

GAM189 2461 KIAA104 1 3653 NP_055762.1 3 968 CCCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 2464 KIAA105 1 14832 XP_043493.5 3 3278 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGGG GTGACGTGAGGTCGGACCCGTT

GAM189 2465 KIAA111 1 9842 NP_055746.1 3 688 TCCCTCCTCCCA G T CA 3 B c c
GGCTGGTGTGAG CATT CAC CCAGCCTGGG
TGTGCGTG GTGA GTG GGTCGGACCC
- T TC

GAM189 2468 KIAA112 1 5783 NP_061872.1 3 1959 CTCCATTGCCCA CAC 3 B c c
GGCTGGATTACA CATTG TCCAGCCTGGGCAA
GTGGCGCA GTGAC AGGTCGGACCCGTT
ATT

GAM189 2463 KIAA114 1 7385 XP_044014.1 3 3995 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM189 2465 KIAA114 1 17532 NP_065749.1 3 887 AAATATTGCTCA CA------ CT 3 B c c
GGCTGGTTGCAA TTGCA CCAGCCTGGGCAA
ACTCCTTG AACGT GGTCGGACTCGTT
GTTCCTCA T-

GAM189 2465 KIAA115 1 2664 XP_030864.2 3 2954 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC

GAM189 2460 KIAA117 1 10162 XP_045907.2 3 1245 TCTTGTTGCCCA C 3 B b b
AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCACG GTAACGTGAGGTCG ACCCGTT
A

GAM189 246 KIAA118 1 5755 NP_065761.1 3 154 GCTCTGTCGCCA -- 3 B b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTCGGACC TGT
GC

GAM189 2463 KIAA1191 17517 XP_041843.1 3 1645 ACACTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC

GAM189 2468 KIAA1195 12389 NP_065765.1 3 421 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 2468 KIAA1195 12478 NP_065765.1 3 993 CTCTGTTGCCTA G- 3 B b b
GGCTGGAGTGAA CATT CACTCCAGCCTGGGCAA
AGTGGCGC GTGA GTGAGGTCGGATCCGTT
AA

GAM189 2468 KIAA1195 13749 NP_065765.1 3 1272 AGTCCTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 2468 KIAA1195 16088 NP_065765.1 3 3710 TCACTGTTGCCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCACA GTGACGTGAGGTCGGACC GTT
-

GAM189 2468 KIAA1195 16471 NP_065765.1 3 724 TCTGTTGCCCCA - 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG CAA
GTGGTGTG GTGACGTGAGGTCGGACCC GTT
C

GAM189 2469 KIAA1201 8271 XP_027307.2 3 1885 CCCTGTTGCCCA C----- C 3 B c c
AGTTGGAGTGCA ATTGCACTCCAGC TGGGCAA
ATCTTGGC TAACGTGAGGTTG ACCCGTT
CGGTTC A

GAM189 2460 KIAA1211 9144 XP_172801.1 3 105 CTCTGTTACCCA GC CA 3 B c c
GATTGGAGTGCA CATTGCACTCCA CTGGG
GTGGCGCG GTGACGTGAGGT GACCC
TA AT

GAM189 2467 KIAA1252 9032 XP_031577.2 3 3566 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCGCG GTAAC TGAGGTCGGACCCGTT
A

GAM189 2467 KIAA1252 11523 XP_031577.2 3 1695 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 2468 KIAA1261 3236 XP_291055.1 3 898 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 2463 KIAA1272 4555 XP_300760.1 5 675 CTCTGTCCCCCA T C CA 3 B c c
GTCTGGCGTGCA CATTGCAC CCAG CTGGG
ATGGTTTG GTAACGTG GGTC GACCC

C T CC

GAM189 246 KIAA127 2 7374 XP_300760.1 5 380 GTCCAAGCTCAA C- A 3 B c c
3 AGCTGGAGTGCA CATTGCACTCCAGC TGGGC
ATGGCGCA GTAACGTGAGGTCG ACTCG
AA A

GAM189 246 KIAA127 1 1905 XP_039169.1 5 90 GACGGTGGCGCC GCA T - A 3 B c
c
6 GGCTGGAGAATG CATT CTCCAGCC GG GC
GACTGTGA GTAA GAGGTCGG CC CG
--- - G G

GAM189 246 KIAA128 1 9573 NP_065799.1 3 1243 CCCTGTTGCCCA 3 B b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGGATG GTGACGTGAGGTCGGACCCGTT

GAM189 246 KIAA139 1 10123 XP_050793.2 3 1500 CTCTGTTGCCCA CA----- 3 B c c
3 GGCTGGAGTGTA TTGCACTCCAGCCTGGGCAA
GAGACACA GATGTGAGGTCGGACCCGTT
ACACAGA

GAM189 246 KIAA144 1 15171 NP_065885.1 3 712 CTCTGTCGCCCA C A 3 B b b
3 GGCTGTAGTGCA CATTGCACT CAGCCTGGGC
ATGGCGCA GTAACGTGA GTCGGACCCG
T C

GAM189 246 KIAA145 1 5529 XP_040100.3 3 2060 CTCTGTCGCCCA T A 3 B b b
6 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
CTGGCGCG GT ACGTGAGGTCGGACCCG
C C

GAM189 246 KIAA146 1 1667 XP_051160.2 3 1298 CTTTGGTGCCCA GC CCA 3 B c
c
3 GGCCAAGTAGAA CATT ACT GCCTGGGCA
TGAGATGA GTAA TGA CGGACCCGT
GA AC-

GAM189 246 KIAA146 2 18838 XP_027396.4 3 449 GCCAGCCAAGGC T --- G A 3 B c b

5 CAGTGGAGTGCT CAT GCACTCCA GCCT GGC
GTGGGGTC GTG CGTGAGGT CGGA CCG
T GAC A A

GAM189 246 KIAA146 2 18992 XP_027396.4 3 570 GGTCTGTCGCCA -- 3 B b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC

GAM189 246 KIAA149 1 15045 XP_034415.1 3 2966 CTCTGTTGCCCA C C 3 B b b
3 GTCTGGAGTTCA CATTG ACTCCAG CTGGGCAA
GTGGCGCG GTGAC TGAGGTC GACCCGTT
T T

GAM189 246 KIAA150 1 8820 XP_290952.1 3 78 GCTCGTCACCCA C----- CA 3 B c c
8 GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATTGTGCA TAACGTGAGGTCGGACCC
ACGTGT AC

GAM189 246 KIAA151 1 13383 XP_170889.1 3 95 CTCTGTCGCCCA G A 3 B c c
8 GGGTGGAGTGCG CATTGCACTCCA CCTGGGC

GTGGCACG GTGGCGTGAGGT GGACCCG
G C

GAM189 2460 KIAA153 2 4028 XP_042661.5 3 1177 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
ATGGCGTG GTAACGTGAGGTCGGACC TGT
GC

GAM189 2460 KIAA153 2 15284 XP_042661.5 3 818 TGCTCTTACCCA C CA 3 B c b
GGCTGAGTGCAG CATTGCACTC AGCCTGGG
TGGCAGAA GTGACGTGAG TCGGACCC
- AT

GAM189 2460 KIAA155 1 3790 XP_039393.3 3 663 GCAAGCAGCCCA A TC --- A 3 B c c
GGCAGCTGTGGG CATTGC C CA GCCTGGGC
CAGTGCTG GTGACG G GT CGGACCCG
- GT CGA A

GAM189 2469 KIAA155 1 4029 XP_054472.2 3 1629 CTTTGTCCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
CC

GAM189 2461 KIAA157 1 14154 XP_027744.1 3 882 CTGTCTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCCTG GTGACGTGAGGTCGGACCCGTT

GAM189 2465 KIAA161 2 8549 NP_066002.1 3 1381 TCTTGTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGATCCGTT

GAM189 2465 KIAA161 2 10111 NP_066002.1 3 1687 GCTCTGTCACCA A -- 3 B b b
GGCCGGAGTGCA CATTGCACTCC GCCTGG GCA
GTGGTGTC GTGACGTGAGG CGGACC TGT
C AC

GAM189 2461 KIAA167 2 7194 XP_037809.1 3 1742 CTCTGTTGCTCA G C 3 B c b
AGCTGGAGTGGA CATT CACTCCAGC TGGGCAA
GTGGCACG GTGA GTGAGGTCG ACTCGTT
G A

GAM189 2461 KIAA167 2 17191 XP_037809.1 3 4094 CTCTGTTGGCCA C G 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCACA GTGACGT AGGTCGGACC GTT
A G

GAM189 2462 KIAA171 2 1142 NP_085136.1 3 1318 CTCTATTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCGTG GT ACGTGAGGTCGGACCCGTT
C

GAM189 2462 KIAA171 2 1142 XP_041497.2 3 1487 CTCTATTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCGTG GT ACGTGAGGTCGGACCCGTT
C

GAM189 2462 KIAA171 2 14165 NP_085136.1 3 740 TGTTGTTGCCCA C----- 3 B b b
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCACG TAACGTGAGGTCGGACCCGTT

GCACGA

GAM189 246 KIAA171 2 14165 XP_041497.2 3 740 TGTTGTTGCCCA C----- 3 B b b
2 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCACG TAACGTGAGGTCGGACCCGTT
GCACGA

GAM189 246 KIAA172 1 14630 XP_040280.2 5 25 CATCCTTGCCCA T- --- A C 3 B c c
4 GCCGGTGTGGTG CAT GCACT CC GC TGGGCAA
CTTGTGTG GTG CGTGG GG CG ACCCGTT
TT TGT C -

GAM189 246 KIAA173 1 10602 NP_219494.1 3 1428 TCTTGTTGCCCA C A 3 B b b
7 GGCGGAGTACAA CATTG ACTCC GCCTGGGCAA
TGGTGGGA GTAAC TGAGG CGGACCCGTT
A -

GAM189 246 KIAA177 1 1618 NP_149091.1 3 2168 AGGACAAGCCCA T CT A A 3 B c
c
5 GGCAGGGCTGCA CAT GCA CC GCCTGGGC
TGGAGAGG GTA CGT GG CGGACCCG
- CG A A

GAM189 246 KIAA178 1 11058 NP_115820.1 3 342 CTGTGTCACCTA CA 3 B c c
4 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM189 246 KIAA182 1 10095 XP_041566.2 3 992 CGGGGCTGACCA CA- G 3 B c c

2 GGCTGGGGGTCC CATTG CTCCAGCCTGG CA
AGTGAAAC GTGAC GGGGTCGGACC GT
CTG A

GAM189 246 KIAA182 2 2143 XP_290834.1 3 938 CTCTGTTGCCCA 3 B b b
7 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM189 246 KIAA182 2 12636 XP_290834.1 3 1306 CCTTGTCACCCA C CA 3 B c b
7 GGCTGTAGTGCG CATTGCACT CAGCCTGGG
GTGGCGCG GTGGCGTGA GTCGGACCC
T AC

GAM189 246 KIAA182 1 14863 XP_030378.2 3 210 CTCTGTTGCCCA 3 B b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTA GTGACGTGAGGTCGGACCCGTT

GAM189 246 KIAA183 1 12627 XP_114087.2 3 1679 CTCTGCCAGCCA --- 3 B b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC CGT
GAC

GAM189 246 KIAA185 1 19095 XP_045184.1 3 1021 CCCCTCTGCCCA TT ACTC 3 B c
c
3 GGCTGCCACGCC CA GC CAGCCTGGGCA
CTGGATGC GT CG GTCGGACCCGT
CC CACC

GAM189 246 KIAA190 1 16492 XP_056282.1 3 3672 AGCCTGTGTCCA T- A 3 B c c
4 GGCTGGGGAGCC CAT GC CTCCAGCCTGGGCA

CGTGTCTG GTG CG GGGGTCGGACCTGT
CC A

GAM189 2462 KIAA1921 7553 XP_057040.1 5 322 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM189 2464 KIAA1922 1857 NP_694971.2 3 597 CTCTGTCGCCCA G A 3 B c c
GGATGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGCGCG GTGACGTGAGGT GGACCCG
A C

GAM189 2464 KIAA1922 8341 NP_694971.2 3 407 TTCTGTCACCTA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGTGCA GTGACGT AGGTCGGATCC
A AC

GAM189 2467 KIAA1931 2983 XP_057107.3 5 301 ACGCGCTGTCCT GCA T 3 B c c
GGCTGGAGGAGG CATT CTCCAGCC GGGCA
TGGAGCAG GTGG GAGGTCGG CCTGT
AG- T

GAM189 2461 KIAA1972 6902 XP_058720.4 3 214 CTCTGTCGCCCA A 3 B b b
GGCTGGGGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGGGGTCGGACCCG
C

GAM189 2461 KIAA1972 11506 XP_058720.4 3 264 CTCCGCTTCCCA CA 3 B c b
GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGGGGTCGGACCC
TT

GAM189 2467 KIAA1981 7554 XP_113870.1 5 202 TCTTGTTGCCCA C 3 B b b
GGTTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCACG GTGACGTGAG TTGGACCCGTT
A

GAM189 2468 KIAA2021 12100 XP_059415.2 3 1063 TCTGGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCC GTGACGTGAGGTCGGACCCGTT

GAM189 246 KLF12 1 1127 NP_009180.3 3 950 TGGGGCTGCCCA C CCA 3 B c c
GGCAAAGTCAGT CATTG ACT GCCTGGGCA
GAACATGA GTGAC TGA CGGACCCGT
- AA-

GAM189 246 KLRD1 1 2353 NP_002253.1 3 396 TCACACTGCCCA CA 3 B c c
GGCTGGAGCATA CATTG CTCCAGCCTGGGCA
GTGGCAAG GTGAT GAGGTCGGACCCGT
AC

GAM189 246 KLRD1 1 2353 NP_031360.1 3 396 TCACACTGCCCA CA 3 B c c
GGCTGGAGCATA CATTG CTCCAGCCTGGGCA
GTGGCAAG GTGAT GAGGTCGGACCCGT
AC

GAM189 246 KMO 1 6338 NP_003670.1 3 716 CTCTGTTGACCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGTGAG GTGACGTGAGGTCGGACC GTT
A

GAM189 246 LAMP3 1 17760 NP_055213.1 3 565 TCTTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 LARS 1 2620 NP_064502.8 5 54 TTGCACAGTCGG -- --- G 3 B c c
CTGGGCGGTGCA CATTGCACT CCAGCC TG GCAA
ATGGCGGA GTAACGTGG GGTCGG AC CGTT
CG CTG A
GAM189 246 LASP1 1 17709 NP_006139.1 3 840 GCCTGCCTCCTA T AC --- 3 B c c
GGCTGGAAGCCA CAT GC TCCAGCCT GGGCA
TGGTCCCG GTA CG AGGTCGGA TCCGT
C A- TCC
GAM189 246 LCN7 1 15937 NP_071447.1 3 400 CTCCGTTGCCCA 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCCCA GTGACGTGAGGTTGGACCCGTT

GAM189 246 LETM1 1 18695 NP_036450.1 3 1029 GCAGCATGGCCA T A -- G 3 B c c

GGCTGGCCAGGG CAT GC CT CCAGCCTGG CA
CGTGGGCA GTG CG GA GGTCGGACC GT
- G CC G
GAM189 246 LGP2 1 8032 NP_077024.1 5 165 AGAGTGGCACCA GC C - A 3 B c c
GGCTGAGTTAAG CATT ACTC AGCCTGG GC
TGGGACTG GTGA TGAG TCGGACC CG
AT - A G
GAM189 246 LHX2 1 4178 NP_004780.3 5 506 CGCCGTCGCCCA ACTCCA A 3 B c
c
GGCGCCCCGCAA CATTGC GCCTGGGC
TGTAGCTG GTAACG CGGACCCG
CCCCG- C
GAM189 246 LIN-28 1 4726 NP_078950.1 3 2144 CTGTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGAGCTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 Link-GE 1 19936 NP_057423.1 3 677 CCTGCATGCCCA GCA- - - 3 B c c
FII GGCTTGTGAGCC CATT CTC CA GCCTGGGCA
AAGGTGCT GTGG GAG GT CGGACCCGT
AACC T T
GAM189 246 LIPH 1 10379 NP_640341.1 3 3 TTCTTTGCCCAG T - C - 3 B c c
AGTTGCAGTTGT CA TGCA CT CAGC CTGGGCAA
ACTGTTGC GT ATGT GA GTTG GACCCGTT
C T C A
GAM189 246 LLGL2 1 15172 NP_004515.1 3 6 GCTGAGCGTCCA ACTC A 3 B c c
GGCTGCGCGATG CATTGC CAGCCTGGGC
GCACACAC GTAGCG GTCGGACCTG
C--- C
GAM189 246 LNK 2 1866 NP_005466.1 3 1845 CCATGTTGGCCA GCACT G 3 B c c

GGCTGGTCTCGA CATT CCAGCCTGG CAA
ATGTCTGA GTAA GGTCGGACC GTT

GCTCT G

GAM189 246 LNK 2 13992 NP_005466.1 3 1683 TCTTGTCAACCG GCA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGGCC
AAC

GAM189 246 LOC1126 3 793 XP_053145.1 3 1145 AAAACTGGTAAC T GGCA 3 B c c
87 AGGCTGGGTGCA CATTGCAC CCAGCCTG
ATGGCTCA GTAACGTG GGTCGGAC
- AATG

GAM189 246 LOC1126 3 7988 XP_053145.1 3 1145 AAACTGGTAACA T GGCA 3 B c c
87 GGCTGGGTGCAA CATTGCAC CCAGCCTG
TGGCTCAC GTAACGTG GGTCGGAC
- AATG

GAM189 246 LOC1126 3 16673 XP_053145.1 3 169 CCCTGTCACCCA CA 3 B c c
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC1128 1 16256 NP_612422.2 3 419 CTCTGTCACCCA CA 3 B b b
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC

GAM189 246 LOC1134 3 5336 NP_612437.2 3 852 TTCTGTCACCCG CA 3 B c b
44 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGGCCC
AC

GAM189 246 LOC1134 3 15899 NP_612437.2 3 590 CTCTGTCACACA C----- --- 3 B c b
44 GGCTGGAGTGCA ATTGCACTCCAGCCTG GGCA
GTACAATT TGACGTGAGGTCGGAC CTGT
TTAACA ACA

GAM189 246 LOC1134 3 18294 NP_612437.2 3 1177 CTGTATTGCCCA 3 B b b
44 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1138 1 5632 NP_612444.1 5 268 TCCTGCCGCCCA -- C A A 3 B c c
28 GGCAGGATGTCA CATT GCA TCC GCCTGGGC
GATGAGGA GTAG TGT AGG CGGACCCG
AC - A C

GAM189 246 LOC1151 1 15271 XP_055276.1 5 257 CTCTATGGCCCA C A 3 B c c
23 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGACACG GTGAC TGAGGTCGGACCCG
A G

GAM189 246 LOC1152 1 12422 XP_055499.2 5 1755 CTTTGTCCCCCA CA 3 B c c
19 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
ATGGCAGG GTAGCGTGAGGTCGGACCC
CC

GAM189 246 LOC1156 1 7429 NP_663299.1 3 657 GCTCTGTCGCCT T A 3 B c c
48 GGCTGGAGTGCA CATTGCACTCCAGCC GGGC
GTGGTGTG GTGACGTGAGGTCGG TCCG

```
                                                  -  C
GAM189  246  LOC1164 1  14720 XP_058095.1  5  1241  CAATGGTGTCCA                    3  B  b  b
        11                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
                              GTGGCGTG    GTGACGTGAGGTCGGACCTGT

GAM189  246  LOC1184 1  456  XP_060981.3  3  219  CTCTGTTGCCCA CA-----             3  B  c  c
        90                    GGCTGGAGTGCA      TTGCACTCCAGCCTGGGCAA
                              GCGGCATG          GACGTGAGGTCGGACCCGTT
                                    GTACGGC
GAM189  246  LOC1188 1  2649  NP_849154.1  3  581  TACTCTCGCCCA       C      A       3  B  c  c
        12                    GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
                              GTGGCATG    GTGACGTGAG TCGGACCCG
                                          A       C
GAM189  246  LOC1188 1  2649  XP_058346.2  3  581  TACTCTCGCCCA       C      A       3  B  c  c
        12                    GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
                              GTGGCATG    GTGACGTGAG TCGGACCCG
                                          A       C
GAM189  246  LOC1193 1  745  XP_061446.3  5  191  CCCACCCACCCA  T  AC       CA       3  B  c
c
        95                    GGCTGGAGCCAT CAT GC  TCCAGCCTGGG
                              GGATAAAT    GTA CG  AGGTCGGACCC
                                       C  --         AC
GAM189  246  LOC1205 1  17112 XP_058475.1  3  679  CTCTGTCGCGCC          C  -  A      3  B  c  c
        26                    AGCTGGAGTGCA CATTGCACTCCAGC TGG GC
                              GTGCCATG    GTGACGTGAGGTCG ACC CG
                                          -  G  C
GAM189  246  LOC1219 1  9891  XP_062872.2  5  585  CTCTGTCACCCG   T         CA       3  B  c  c
        52                    GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
                              GTGGCTTG    GTG CGTGAGGTCGGGCCC
                                          T          AC
GAM189  246  LOC1242 1  14576 XP_058785.3  5  257  AACTTCAGTCCG   T  A       A       3  B  c  c
        21                    GGCTGGAGGCCG CAT GC CTCCAGCCTGGGC
                              TGCACAAC    GTG CG GAGGTCGGGCCTG
                                       C  -         A
GAM189  246  LOC1250 1  1744  XP_058889.3  3  407  CTCTGTCACCCA            CA       3  B  c  c
        61                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                              GTGGCGTG    GTGACGTGAGGTCGGACCC
                                          AC
GAM189  246  LOC1266 1  3477  XP_060121.4  3  194  CTGTGTTGCCCA                   3  B  b  b
        69                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                              ATGGCGCA    GTAACGTGAGGTCGGACCCGTT

GAM189  246  LOC1272 1  18918 XP_059122.1  3  141  CTTTGTTGCCCA C------     -  AGC       3  B  c
c
        53                    GAGGATGTGCAG      ATTGCAC TCC  CTGGGCAA
                              TTGTCATC          TGACGTG AGG  GACCCGTT
                                    CTACTGT     T  A--
GAM189  246  LOC1278 1  18516 XP_059184.1  5  112  TGGTGTTGCCCA     A  CA-          3  B  c  c

        41                    GGCAGAGAGGGC CATTGC CTC  GCCTGGGCAA
```

AGTGTGGA GTGACG GAG CGGACCCGTT
G AGA
GAM189 246 LOC1283 1 15173 XP_059243.2 3 561 TGTTGTTGCCCA 3 B b b
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC1322 1 509 XP_059583.1 5 83 CTTTGCTTCCCA CA 3 B c c
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
TT
GAM189 246 LOC1352 2 3512 XP_072402.4 3 1277 CTTGCTCTCCCA CA 3 B c b
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTA GTGACGTGAGGTCGGACCC
TC
GAM189 246 LOC1352 2 10443 XP_072402.4 3 564 CTCTGTTGCCCA C 3 B b b
93 GGCTGAAGTGTA CATTGCACT CAGCCTGGGCAA
GTGGCACA GTGATGTGA GTCGGACCCGTT
A
GAM189 246 LOC1357 1 17207 NP_612639.1 3 39 CTCCGTCACCCA CA 3 B c c
63 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCAAG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC1358 1 19136 XP_059804.4 3 736 TCTTGTTGCCCA C----- C 3 B c c
18 GCCTGGAGTGCA ATTGCACTCCAG CTGGGCAA
ATAGCGTG TAACGTGAGGTC GACCCGTT
GTGCGA C
GAM189 246 LOC1378 1 19990 XP_059929.3 3 683 TCTTGTTGCCCA 3 B b b
86 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC1394 1 9489 XP_066687.2 5 64 CTCTGTTGCCCA C 3 B b b
22 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGTGTG GTGACGTGAGGTC GACCCGTT
A
GAM189 246 LOC1432 1 15574 NP_620167.1 5 54 TCTTGTTGCCCA 3 B b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC1442 1 3159 XP_084786.1 5 399 CTCTTTCGCCCA A 3 B b b
48 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGTGTG GTAACGTGAGGTCGGACCCG
C
GAM189 246 LOC1442 1 17498 XP_084795.1 5 1526 ATGCTCAGCCCA TG CA- A 3 B c
c
66 GGCATTGAGTGT CAT CACTC GCCTGGGC
GATGCTGA GTA GTGAG CGGACCCG
GT TTA A
GAM189 246 LOC1444 3 1633 XP_084852.6 3 1294 ATCTGTTACCCA CA 3 B c b
04 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC

AT
GAM189 246 LOC1444 3 5897 XP_084852.6 3 1129 GTCTGTTGCCTA A 3 B b b
04 GGCGGGAGTGCA CATTGCACTCC GCCTGGGCAA
GTGGCATC GTGACGTGAGG CGGATCCGTT
G
GAM189 246 LOC1444 3 15352 XP_084852.6 3 421 TTACCAGGCCCA TG A 3 B c b
04 GGCTGGGGTGGT CAT CACTCCAGCCTGGGC
GTGAACCC GTG GTGGGGTCGGACCCG
TG G
GAM189 246 LOC1444 1 5733 NP_612482.1 5 153 CCTTGAAGCCCA TT CTC A 3 B c c
67 GGCTGATGCTTG CA GCA CAGCCTGGGC
AAGTAACT GT CGT GTCGGACCCG
T- A-- A
GAM189 246 LOC1444 1 19220 XP_096611.2 3 209 CTCTGTCACTCA CA 3 B c c
81 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATA GTGACGTGAGGTCGGACTC
AC
GAM189 246 LOC1446 1 12712 XP_096648.1 3 520 CTCTGTCATCCA A CA 3 B c c
67 GGCTGGAGGGTA CATTGC CTCCAGCCTGGG
GTGGCGTG GTGATG GAGGTCGGACCT
G AC
GAM189 246 LOC1447 1 17736 XP_084949.1 5 57 CTCTGTTGCCTA C 3 B b b
42 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCAAG GTGAC TGAGGTCGGATCCGTT
A
GAM189 246 LOC1447 1 8972 XP_084963.2 5 181 CTTTGTCACCCA C CA 3 B c c
66 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 LOC1447 2 444 XP_084964.1 5 134 CTCCATCACTCA C CA 3 B c b
76 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGCTGAG GTGAC TGAGGTCGGACTC
A AC
GAM189 246 LOC1447 2 16275 XP_084964.1 5 252 TTCTGTTGCCCA 3 B b b
76 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT
GAM189 246 LOC1448 1 12065 XP_084972.1 5 233 CTCTGTCGCCCA A 3 B b b
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC1449 1 12130 XP_084990.1 5 26 CTTCGTGTTTGC TG- CTG 3 B c c
62 TGCTGGAGTGAC CAT CACTCCAGC GGCAA
TGTGTGTT GTG GTGAGGTCG TCGTT
TCA ---
GAM189 246 LOC1450 1 675 XP_085022.1 5 469 TTATAGAGCCTA - A-- A 3 B c c
98 GGCTGGAGGAGG CAT TGC CTCCAGCCTGGGC

TACATGGG GTA ATG GAGGTCGGATCCG
C GAG A

GAM189 246 LOC1452 1 6417 XP_096740.1 3 2362 TTACGAAATGCT CA CTG 3 B c c
31 AGCCAGGGTGCA CATTGCACTC GC GGCA
ATGGCTCA GTAACGTGGG CG TCGT
AC A--

GAM189 246 LOC1452 1 18805 XP_085072.1 5 637 CTCTTTTGCCCA GCA 3 B c c
68 GGCTGGAGCGAA CATT CTCCAGCCTGGGCAA
GTGACGAG GTGA GAGGTCGGACCCGTT
AGC

GAM189 246 LOC1457 1 4773 XP_085211.1 3 988 GCTCTGTCACCA C -- 3 B c c
25 GGCTGGAGTACA CATTG ACTCCAGCCTGG GCA
GTGATGAC GTGAC TGAGGTCGGACC TGT
A AC

GAM189 246 LOC1457 2 7370 XP_085227.1 5 95 CTCTGTCGCCCA A 3 B b b
57 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGGCGTGAGGTCGGACCCG
C

GAM189 246 LOC1457 2 11523 XP_085227.1 5 213 CTCTGTCGCCCA A 3 B b b
57 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC1457 1 2196 XP_085231.2 5 1119 CTCTGTCACCCA CA 3 B b b
83 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
AC

GAM189 246 LOC1458 1 16256 XP_096873.1 5 60 CTCTGTCACCCA CA 3 B b b
13 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC

GAM189 246 LOC1459 1 11009 XP_085290.3 5 555 CTCTGTCACCCA GCC CA 3 B c c
88 AGATGGAGTGCA CATTGCACTCCA TGGG
ATGGCACG GTAACGTGAGGT ACCC
AGA AC

GAM189 246 LOC1461 1 16175 NP_778229.1 5 198 TCTTGTTGCCCA C----- 3 B c c
77 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCACT TGACGTGAGGTCGGACCCGTT
TCACGA

GAM189 246 LOC1462 4 1644 XP_085387.1 3 3210 CTCTGTCGCCCA C A 3 B c b
29 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCACA GTGACGTGAG TCGGACCCG
A C

GAM189 246 LOC1462 4 5551 XP_085387.1 3 1707 CTCTGTCGCCCA A 3 B b b
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC1462 4 5672 XP_085387.1 3 4034 CTCTGTTGCCTA C 3 B b b
29 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA

GTGGTGCA GTGAC TGAGGTCGGATCCGTT
A

GAM189 246 LOC1462 4 8706 XP_085387.1 3 2310 TCTTGTTGCCTA 3 B b b
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGAG GTAACGTGAGGTCGGATCCGTT

GAM189 246 LOC1463 2 5798 XP_085430.1 5 736 ACTCGTTGCCCA 3 B b b
46 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1463 2 17670 XP_085430.1 5 388 ACTCCGTTGCCA T G 3 B b b
46 GGCTGGAGTGCT CAT GCACTCCAGCCTGG CAA
GTGGCGCT GTG CGTGAGGTCGGACC GTT
T -

GAM189 246 LOC1464 1 2457 XP_096998.2 5 536 GCTCTGTCACCA -- 3 B b b
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGTG GTGACGTGAGGTCGGACC TGT
AC

GAM189 246 LOC1464 1 813 XP_085461.6 5 101 ACTTGTCACCCA CA 3 B b b
43 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGTG GTAACGTGAGGTCGGACCC
AC

GAM189 246 LOC1464 1 9246 XP_097006.1 5 119 AAGCCCACGTGA TG ----- A 3 B c c

75 GGCTGGAGTGAT CAT CACTCCAGCCT GGGC
GTGGCCAC GTG GTGAGGTCGGA CCCG
TA GTGCA A

GAM189 246 LOC1465 1 3374 XP_097013.1 3 40 TGGGAGGTCCCA -- TC - A 3 B c c
13 GGCTGTGTGCAC CAT TGCAC CAGCCTGGG C
AGTGACAG GTG ACGTG GTCGGACCC G
AC T- T G

GAM189 246 LOC1466 1 7382 XP_085514.2 5 1114 CTCTGTCGCCCA A 3 B b b
03 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC1467 1 13448 XP_085588.1 5 890 TCTTGTTGCCCA 3 B b b
84 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGGCGTGAGGTCGGACCCGTT

GAM189 246 LOC1468 1 1745 XP_097107.1 3 677 CTCTGTTGCCCA 3 B b b
39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1468 1 8315 NP_660316.1 3 1177 TGCTGCTGCCCA 3 B b b
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACG GTGACGTGAGGTCGGACCCGT

GAM189 246 LOC1468 1 8232 XP_097120.1 5 550 CTCTGTCACCCA CA 3 B c c
95 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC

AC
GAM189 246 LOC1469 1 6392 XP_097121.1 3 1204 TGTCAAAAATCA GCA 3 B c c
01 GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGCATG GTGACGTGAGGTCGGACT
AAA
GAM189 246 LOC1469 2 9492 XP_085634.2 3 662 CTCTGTCGCCCA A 3 B b b
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTACG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC1469 2 19550 XP_085634.2 3 995 CTCTGTCGCCCA A 3 B b b
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGGC GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC1470 1 16699 XP_054031.5 5 604 TCTTGTTGCCCA C 3 B b b
71 GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
ATGTTGTG GTAACGTGA GTCGGACCCGTT
A
GAM189 246 LOC1470 1 12558 XP_097182.1 5 18 CTCTGTCCGCCA --- 3 B b b
80 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GCC
GAM189 246 LOC1471 1 10618 XP_085722.2 3 252 CACTGTTGCCCA 3 B b b
66 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1473 1 19915 XP_097230.2 3 1189 TTGATCTGCCCA T CT AG- 3 B c
c
81 GGAAAGGGATGC CA TGCA CC CCTGGGCA
ATTGACAC GT ACGT GG GGACCCGT
T AG AAA
GAM189 246 LOC1474 1 12065 XP_084000.1 3 143 CTCTGTCGCCCA A 3 B b b
07 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC1478 2 1634 XP_085903.1 3 281 CTCTGTCACCCA G C CA 3 B c b

17 GGCTGTAGTGGA CATT CACT CAGCCTGGG
GTGGTGTG GTGA GTGA GTCGGACCC
G T AC
GAM189 246 LOC1478 2 19233 XP_085903.1 3 445 CTCTGTCGCCCA A 3 B b b
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCG GTAACGTGAGGTCGGACCCG
C
GAM189 246 LOC1478 2 8642 XP_085924.2 3 146 TCTTGTTGTCCA C 3 B b b
41 GTCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCACA GTAACGTGAGGTC GACCTGTT
T
GAM189 246 LOC1478 2 12065 XP_085924.2 3 458 CTCTGTCGCCCA A 3 B b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG

C

GAM189 246 LOC1479 1 17952 XP_085974.1 3 579 CTCTGTCACCCA CA 3 B c c
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC1481 2 5784 NP_653293.1 3 2524 CCTTGTTGCCCA C C 3 B b b
37 GGCTGTAGTACA CATTG ACT CAGCCTGGGCAA
ATGGCATG GTAAC TGA GTCGGACCCGTT
A T

GAM189 246 LOC1481 2 17935 NP_653293.1 3 2097 CTCTGTCACCCA --- CA 3 B c b
37 GGCTGGAGTGCC CATT GCACTCCAGCCTGGG
ATAGTGTG GTGA CGTGAGGTCGGACCC
TAC AC

GAM189 246 LOC1481 1 11563 XP_047554.4 3 983 GTCGCCCACCCA C CA 3 B c c
98 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC

GAM189 246 LOC1487 1 15671 XP_086286.4 3 1372 CTCTGTCGCCCA A 3 B b b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC1487 2 6922 XP_086281.1 3 397 TCTAGTTGCCCA C CC 3 B b b
09 CACTAGAGTGCA CATTGCACTC AG TGGGCAA
ATGGCGCA GTAACGTGAG TC ACCCGTT
A AC

GAM189 246 LOC1487 2 9201 XP_086281.1 5 143 CTCTGGTACTCA CA 3 B c b
09 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTGTG GTGGCGTGAGGTCGGACTC
AT

GAM189 246 LOC1491 1 2184 XP_097598.1 5 3317 TCTTGTTGCCCA C 3 B b b
49 AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCGCG GTGACGTGAGGTCG ACCCGTT
A

GAM189 246 LOC1491 1 12637 XP_086458.1 3 41 TTTTGTTGCCCA C----- CACT 3 B c
c
94 GGCTGGTCTCCA ATTG CCAGCCTGGGCAA
ATTTCTGG TAAC GGTCGGACCCGTT
GGTCTT CTCT

GAM189 246 LOC1493 1 13354 NP_787072.1 3 371 CCCCGTCGCACA G A 3 B c c
71 GGCTGGAGTGCA CATTGCACTCCAGCCTG GC
GTGGCAAA GTGACGTGAGGTCGGAC CG
A C

GAM189 246 LOC1494 1 16260 XP_086546.1 3 564 CTCTGTTGCCCA 3 B b b
66 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC1494 1 5016 XP_086536.1 3 76 CTCTGTCGTCGA G A 3 B c c
78 GGCTGGAGTGTA CATTGCACTCCAGCCT GGC

GTGGTGCG GTGATGTGAGGTCGGA CTG
G C
GAM189 246 LOC1495 1 2139 XP_097661.1 3 1639 CGCTGTTGCCCA C 3 B b b
06 GGCTGTAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGCG GTGACGTGA GTCGGACCCGTT
T
GAM189 246 LOC1496 1 8887 XP_086600.1 3 1141 AGATTTTGCCCA GC AGC 3 B c
c
06 GAGGAGTAAATG CATT ACTCC CTGGGCAA
GAGGTGGG GTAA TGAGG GACCCGTT
A- A--
GAM189 246 LOC1496 1 11025 XP_097706.1 3 613 CTCTGTCACCCA CA 3 B c c
92 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC1497 1 10508 XP_097719.1 5 453 TTCTGCTGCCCA - C 3 B b b
03 AGCTGGAGTGGC CATTGC ACTCCAGC TGGGCA
AGTGGCAT GTGACG TGAGGTCG ACCCGT
G A
GAM189 246 LOC1498 1 17917 XP_097733.1 5 13 GGTAGTTTGACC CT CT - 3 B c c
32 TCCGTTGGTGCA CATTGCA CCAGC GGG CAA
ATGCCAGA GTAACGT GGTTG TCC GTT
-- CC A
GAM189 246 LOC1500 1 5157 XP_097797.1 5 593 CTCTGTCGCCCA A 3 B b b
54 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCC GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC1502 1 7207 XP_097870.1 3 1704 CTCTGTCGCTCA A 3 B b b
25 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACTCG
C
GAM189 246 LOC1503 1 7485 XP_097894.1 5 386 ATGGAGCCTGCC - AG T 3 B c c
84 TTGGGGAGTGCA CAT TGCACTCC CC GGGCA
TGTGTTGG GTG ACGTGAGG GG TCCGT
T -- T
GAM189 246 LOC1503 1 19467 XP_086907.1 3 479 CTCTGTCGTCCA C A 3 B c c
97 GGTTAGAGTGCA CATTGCACTC AGCCTGGGC
ATGGCTTG GTAACGTGAG TTGGACCTG
A C
GAM189 246 LOC1505 1 16940 XP_097917.1 5 1616 CTCTGTTGCCCA 3 B b b
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1510 1 12075 XP_097998.1 3 1067 CTCTGTCACCCA CA 3 B c c
57 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC1511 1 19774 XP_098019.1 3 458 AAATGTACACCA T --- 3 B c c
96 GGCTGGGTGCGG CATTGCAC CCAGCCTGG GCA

TGGCTCAC GTGGCGTG GGTCGGACC TGT
- ACA

GAM189 246 LOC1512 2 2572 XP_098021.1 3 1785 TTCTGTCACCCA C CA 3 B c b
01 GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
ATGGGGCG GTAAC TGAGGTCGGACCC
C AC

GAM189 246 LOC1512 2 12725 XP_098021.1 3 367 ACGCTGTCACCA -- 3 B b b
01 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC

GAM189 246 LOC1514 2 4174 XP_098063.1 5 739 CTCTGTCATCCA CA 3 B c b
75 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCT
AC

GAM189 246 LOC1514 2 4371 XP_098063.1 5 100 CTCTGTGGCCCA A 3 B b b
75 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGATGTGAGGTCGGACCCG
G

GAM189 246 LOC1516 1 2599 XP_087245.1 5 765 TGAGCCTGCACA CCA - G 3 B c
c
10 GAGCCAGGTGCA CATTGCACT GC CTG GCA
ATGGGCAG GTAACGTGG CG GAC CGT
AC- A A

GAM189 246 LOC1516 3 2693 NP_612144.1 3 222 CTCTGTCGCTCG C A 3 B c c
36 CGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCATG GTGACGTGAGGTCG GCTCG
C C

GAM189 246 LOC1516 3 4151 NP_612144.1 3 2151 CTGTGTCCCCCA CA 3 B c c
36 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
CC

GAM189 246 LOC1516 3 14731 NP_612144.1 3 891 CTCTGTCACCCA C CA 3 B c c
36 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGTGTG GTGACGT AGGTCGGACCC
A AC

GAM189 246 LOC1516 1 4248 XP_098100.2 5 2082 CTGTGTCACCAA C----- A - -- 3 B c c
57 GGCTGGAGGGCA ATTGC CTCCAGCCT GG GCA
ATAGCATG TAACG GAGGTCGGA CC TGT
GTACGA G A AC

GAM189 246 LOC1518 1 4677 XP_098132.1 3 897 CTGTGTTGCCCA TT C C----- 3 B c c
77 GGCTAATATCGA CA GCA TC AGCCTGGGCAA
ATGCTTGG GT CGT AG TCGGACCCGTT
T- A CTATAA

GAM189 246 LOC1522 1 9470 XP_098182.1 3 1274 CTCTGTCGCCCA ---- A 3 B c c
45 GGCTGGAGTGAG CATTGCAC TCCAGCCTGGGC
TGCAGTGG GTGACGTG AGGTCGGACCCG
AGTG C

GAM189 246 LOC1524 1 2922 XP_098231.1 3 524 ATCTGTTGCCCA 3 B b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGAGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1526 1 1745 XP_011108.2 3 709 CTCTGTTGCCCA 3 B b b
20 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1527 2 11919 XP_098257.1 5 116 CTCTGTCGCCCA C A 3 B c c
19 GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGTG GTGACGT AGGTCGGACCCG
A C
GAM189 246 LOC1527 2 17637 XP_098257.1 5 423 CTCTGTCGCCCA C A 3 B c c
19 GCCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGCACC GTGACGTGAGGTC GACCCG
C C
GAM189 246 LOC1527 1 2010 XP_087525.1 5 422 GTCTGTTACCCA CA 3 B c c
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT
GAM189 246 LOC1528 1 9568 XP_098266.2 3 1700 TTTCTCGCACAG - G A 3 B c c
04 GCTTGGAGTGCA CATTGCACTCCA GCCTG GC
GTGGTGCG GTGACGTGAGGT CGGAC CG
T A C
GAM189 246 LOC1530 1 5304 XP_098307.1 3 805 TGATATCACCCA CA 3 B c c
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC1538 3 9683 XP_087779.2 3 42 CTCTGTCACCCA A CA 3 B c b
11 GGCAGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
A AC
GAM189 246 LOC1538 3 17512 XP_087779.2 3 1384 CTCTGTTGCCCA C 3 B b b
11 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGTGTA GTGACGTGAGGTC GACCCGTT
A
GAM189 246 LOC1538 3 19665 XP_087779.2 3 962 ACCTGGTGCCCA - G 3 B b b
11 GGTGGAGGTGCA CATTGCAC TCCA CCTGGGCA
GTGGGGGT GTGACGTG AGGT GGACCCGT
G -
GAM189 246 LOC1538 1 15929 XP_087798.1 5 128 TTCTTTTGCCCA 3 B b b
83 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1539 1 2882 XP_087801.1 5 188 CTCTGTAGCCCA C A 3 B c c
10 GTCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTACA GTGACGTGAGGTC GACCCG
T A
GAM189 246 LOC1542 1 4307 XP_098505.1 5 117 GCTCTGTCGCCA -- 3 B b b
82 GGTTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTTGGACC TGT
GC

GAM189 246 LOC1548 1 19205 XP_098618.3 5 2827 CTTTGTCAGCCA --- 3 B b b
22 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
ATGTGCAA GTAACGTGAGGTCGGACC TGTT
GAC
GAM189 246 LOC1548 3 3200 XP_098626.1 5 110 CTCTGTTGCCCA C 3 B b b
77 GTCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCGCA GTGACGTGAGGTC GACCCGTT
T
GAM189 246 LOC1548 3 16089 XP_098626.1 3 1270 CTCTGTCGCCCA G A 3 B c b
77 GGGTGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGCGTG GTGACGTGAGGT GGACCCG
G C
GAM189 246 LOC1548 3 17731 XP_098626.1 3 3542 CCTCTGTTGCCA T C G 3 B c b
77 GGCTGGAATGCC CAT GCA TCCAGCCTGG CAA
GTGGCGCA GTG CGT AGGTCGGACC GTT
C A -
GAM189 246 LOC1550 1 17980 XP_088142.4 3 57 TGCTCCGGCCCA C A-- A 3 B c c
66 GGCGGGGGAGTC CATTG ACTCC GCCTGGGC
AGTGCCCA GTGAC TGAGG CGGACCCG
- GGG G
GAM189 246 LOC1580 1 2542 XP_088442.1 5 3580 TCTTGTCACCCA CA 3 B c c
14 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGATGTGAGGTCGGACCC
AC
GAM189 246 LOC1582 1 5779 XP_098903.4 3 1267 CTCTTTCGCCCA C A A 3 B c c
28 GGCCGGACTGCA CATTGCA TCC GCCTGGGC
GTGGCAGG GTGACGT AGG CGGACCCG
C C C
GAM189 246 LOC1583 1 14859 XP_098919.1 5 371 CTCTGTCGCCCA A 3 B b b
10 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC1583 1 6212 XP_048461.1 5 2535 TTGTGGAGGTTT T ----- GG 3 B c c
81 TGTTGGTGTGCA CATTGCAC CCA GCCT GCAA
ATGGAGGA GTAACGTG GGT TGGA TGTT
T TGTTT GG
GAM189 246 LOC1584 1 17964 XP_098936.1 5 140 CTCTGTTGCCCA 3 B b b
02 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT
GAM189 246 LOC1584 1 1263 XP_098942.1 3 643 CTCTGTCACTCA CA 3 B c c
36 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACTC
AC
GAM189 246 LOC1584 1 935 XP_098955.1 3 893 CTCTGTCGCCCA A 3 B b b
76 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC1585 1 12003 XP_088608.1 3 908 GGACTCTGCCCA TT TCCA 3 B c c
72 GGCCAGCGTGTT CA GCAC GCCTGGGCA
CTGAAAAT GT TGTG CGGACCCGT
CT CGAC
GAM189 246 LOC1586 1 16260 XP_045161.1 3 426 CTCTGTTGCCCA 3 B b b
68 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC1608 1 17208 XP_090573.3 5 537 CTCCGTAGCCCA A 3 B b b
97 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
A
GAM189 246 LOC1624 2 8231 NP_835227.1 3 823 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1624 2 8231 XP_091549.3 3 817 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1624 2 12068 NP_835227.1 3 488 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1624 2 12068 XP_091549.3 3 488 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC1629 1 3249 XP_091886.7 3 255 TCTCTGTCGCCA C -- 3 B b b
62 GGCTGGAATGCA CATTGCA TCCAGCCTGG GCA
GTGCAGTG GTGACGT AGGTCGGACC TGT
A GC
GAM189 246 LOC1629 1 13831 XP_091890.6 3 380 CTCTGTCGCCCA C A 3 B c c
67 CGTTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGATGTG GTGACGTGAGGTTG ACCCG
C C
GAM189 246 LOC1632 2 9147 NP_775802.1 3 1668 CTCTGTCACCCA CA 3 B c b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC1632 2 11854 NP_775802.1 3 3358 TCTTGTTGCCCA C 3 B b b
27 AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGTGCA GTGACGTGAGGTCG ACCCGTT
A
GAM189 246 LOC1640 1 7989 XP_089356.1 3 827 TCTTGTTGGCTA GC G 3 B c c
91 GGCTGGAGTAAA CATT ACTCCAGCCTGG CAA
ATGGTGCG GTAA TGAGGTCGGATC GTT
AA G
GAM189 246 LOC1684 1 19786 XP_095114.2 3 696 CTCTGTAACCCA CA 3 B c c

51 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCCTG GTGACGTGAGGTCGGACCC
AA

GAM189 246 LOC1704 1 15561 XP_096330.1 5 66 CAGCCTCATAAG T ----- A 3 B c c
09 GGCTGGAGTGCT CAT GCACTCCAGCCT GGGC
GTGGTGCC GTG CGTGAGGTCGGG TCCG
T AATAC A

GAM189 246 LOC1962 1 2452 XP_113683.1 3 810 ACTCTGTCGCCA -- 3 B b b
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGTG GTGACGTGAGGTCGGACC TGT
GC

GAM189 246 LOC1973 1 2432 XP_113869.1 3 2117 AAGAGAGGCCCA TT A- A 3 B c
c
42 GGCTGGGGCAGC CA GC CTCCAGCCTGGGC
CCTGAGAG GT CG GGGGTCGGACCCG
CC AC G

GAM189 246 LOC1973 2 4625 XP_113872.2 3 1712 TCTTGTCGCCCA A 3 B b b
58 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC1973 2 6387 XP_113872.2 3 2114 ATCTGTCACCCA CA 3 B c b
58 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC1997 1 10884 XP_117119.1 5 143 CTCTGTCACCTA C CA 3 B c c
25 GGCTGGATTGCA CATTGCA TCCAGCCTGGG
ATGGTGCA GTAACGT AGGTCGGATCC
T AC

GAM189 246 LOC1998 2 5253 XP_117153.1 5 184 CTCTGTGTCTCA C - 3 B b b
99 GGCTGGAGTACA CATTG ACTCCAGCCTG GGCA
GTGGTGCA GTGAC TGAGGTCGGAC CTGT
A T

GAM189 246 LOC1998 2 8292 XP_117153.1 3 67 CTTTGTCGCCCA C A 3 B c b
99 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGTGCG GTGAC TGAGGTCGGACCCG
A C

GAM189 246 LOC1999 1 19756 XP_114052.1 3 1225 CTGTGTTGTCCA 3 B b b
06 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCTGTT

GAM189 246 LOC2001 2 5066 XP_211599.1 3 1 CTGTCGTCCAGG C------- A 3 B c c
69 CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC
ACGCAATC TGACGTGAGGTCGGACCTG
CTAACGCA C

GAM189 246 LOC2001 2 6122 XP_117200.1 5 523 TTCTGTCGTCCA C----- A 3 B c c
69 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCGCA TGACGTGAGGTCGGACCTG
ACGCGA C

GAM189 246 LOC2008 1 16540 XP_114306.1 5 176 GGGCACCGCGGA A- GG A 3 B c
c

44 GGCTGGAGCCGC CATTGC CTCCAGCCT GC
AATGGTGC GTAACG GAGGTCGGA CG
CC GG C

GAM189 246 LOC2008 2 4175 XP_117289.1 3 649 TCTTGTTGTCCA 3 B b b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCTGTT

GAM189 246 LOC2008 2 12075 XP_117289.1 3 1713 CTCTGTCACCCA CA 3 B c b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2008 2 11863 NP_789785.1 3 935 TCTTGTTGCCCA A 3 B b b
95 GGCGGAGTGCAG CATTGCACTCC GCCTGGGCAA
TGGAACAA GTGACGTGAGG CGGACCCGTT
-

GAM189 246 LOC2008 2 17681 NP_789785.1 3 935 CTCTTGTTGCCC A 3 B b b
95 AGGCGGAGTGCA CATTGCACTCC GCCTGGGCAA
GTGGAACA GTGACGTGAGG CGGACCCGTT
-

GAM189 246 LOC2009 1 3465 XP_114317.3 3 322 TTCTGTCACCCA CA 3 B c c
16 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACTCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2011 2 13384 XP_290750.1 3 824 CTCTGTGGCCCA A 3 B b b
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
G

GAM189 246 LOC2011 2 16993 NP_849158.1 3 824 CTCTGTGGCCCA A 3 B b b
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
G

GAM189 246 LOC2012 1 4556 NP_775818.1 3 677 CTCTGTCACTCA C CA 3 B c c
92 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACA GTGAC TGAGGTCGGACTC
A AC

GAM189 246 LOC2015 1 15044 XP_114343.2 3 1575 CTCTGTTGCCCA 3 B b b
62 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2017 1 5492 XP_114370.1 3 1955 CTCTATTGCTCA TG 3 B b b
25 GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
GTGGCAGG GTG GTGAGGTCGGACTCGTT
GT

GAM189 246 LOC2024 1 9145 XP_117397.1 5 32 CTCTGTCGCCCA A 3 B b b
00 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC2024 1 18628 XP_114481.4 3 52 CTCTGTTGCCCA 3 B b b
04 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2024 1 16450 XP_114493.1 5 2041 GCTCTGTCACCA -- 3 B b b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGAGGC GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 LOC2029 2 1729 XP_117486.2 3 1523 CTCTGTCACCCA C CA 3 B c b
34 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 LOC2029 2 4820 XP_117486.2 3 2743 GCTCTGTCACCA -- 3 B b b
34 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 LOC2035 2 2351 XP_114719.1 3 2894 CCTTCTTGCCCA CA----- 3 B c b
47 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
AGGGCGCA AACGTGAGGTCGGACCCGTT
ACGCGGG
GAM189 246 LOC2035 2 9545 XP_114719.1 3 1379 CTCTGTTGCCCA 3 B b b
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2042 1 10724 XP_115295.1 3 931 CTCTGTCTCCCA TG CA 3 B c c

88 GGCTGGAGTGTG CAT CACTCCAGCCTGGG
ATGGCGTG GTA GTGAGGTCGGACCC
GT TC
GAM189 246 LOC2192 1 19361 XP_166599.2 3 1203 CTTGCTCGCCCA G A 3 B c c
93 GGGTGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGTGTG GTGACGTGAGGT GGACCCG
G C
GAM189 246 LOC2197 1 2410 XP_167570.1 5 94 AGGAGTGCTGAG G G- 3 B c c
00 GGCTGGAGTGGG CATT CACTCCAGCCT GGCA
TGGGCCCT GTGG GTGAGGTCGGG TCGT
- AG
GAM189 246 LOC2197 1 4678 XP_167596.1 5 1058 CTCTGTCATCCA CA 3 B c c
31 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCAAA GTGACGTGAGGTCGGACCT
AC
GAM189 246 LOC2197 1 18913 XP_167601.1 3 868 CTCTGTTGCCCA C----- 3 B c c
35 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTCGCACA TGACGTGAGGTCGGACCCGTT
ACACGC
GAM189 246 LOC2198 1 14588 XP_167782.1 3 1073 TCTGTTGCCCCA - 3 B b b
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG CAA
GTGGCGTG GTGACGTGAGGTCGGACCC GTT
C
GAM189 246 LOC2200 3 6497 NP_660352.1 3 213 CTCTGTCACACA --- 3 B b b
74 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCACG GTGACGTGAGGTCGGAC CTGT
ACA

GAM189 246 LOC2200 3 9147 NP_660352.1 3 543 CTCTGTCACCCA CA 3 B c b
74 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2200 3 16838 NP_660352.1 3 383 ACTCGTCACCCC C CA 3 B c b
74 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCG GTGACGTGAGGTCG ACCC
- CA
GAM189 246 LOC2211 1 17256 XP_167915.1 5 38 AGAAGCTGAAAA CTG--- A 3 B c c
74 AGCTGGAGTGCA CATTGCACTCCAGC GGC
ATGGCACC GTAACGTGAGGTCG TCG
AAAAAG A
GAM189 246 LOC2216 1 1939 XP_168131.1 5 811 CTCTGTTGCCAA G 3 B b b
63 GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
GTGGAACG GTGACGTGAGGTCGGA CCGTT
A
GAM189 246 LOC2219 1 15948 XP_168340.1 3 921 GAGAATCGCTTG CT A 3 B c c
46 AGCTGGAGTGCA CATTGCACTCCAGC GGGC
GTGGTGCA GTGACGTGAGGTCG TTCG
AG C
GAM189 246 LOC2219 1 14860 XP_165859.1 3 376 CTCCGTGACCCA C - 3 B b b
60 GGCTGGAATGCA CATTGCA TCCAGCCTGGG CA
ATGGCTCA GTAACGT AGGTCGGACCC GT
A A
GAM189 246 LOC2219 1 17029 XP_168342.1 3 57 CTCTGTCTCCCA C CA 3 B c c
64 GGCTGGACTGCA CATTGCA TCCAGCCTGGG
GTGGTGCG GTGACGT AGGTCGGACCC
C TC
GAM189 246 LOC2220 1 12803 XP_166594.2 5 744 TCTGTTGTCCAA C----- - 3 B c c
57 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM189 246 LOC2220 1 3232 XP_166556.1 3 655 TCTTGTCGCCCA A 3 B b b
68 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGTG GTAACGTGAGGTCGGACCCG
C
GAM189 246 LOC2221 1 16228 XP_212100.1 5 76 CGCAGGCTGCCA C T G 3 B c c
59 GGCTGGCGTACA CATTG AC CCAGCCTGG CA
GTGGCGCA GTGAC TG GGTCGGACC GT
A C -
GAM189 246 LOC2529 1 2959 XP_170858.2 3 279 CTCTGTCGCCCA C----- A 3 B c c
83 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
ATACTGCA TAACGTGAGGTCGGACCCG
ACGTCA C
GAM189 246 LOC2536 1 5487 XP_172985.2 5 301 CTCTGTCTCCCA CA 3 B c c
12 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGCACA GTGGCGTGAGGTCGGACCC

TC

GAM189 24605 LOC2538 1 4532 XP_172854.1 3 1254 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGATGTG GTGACGTGAGGTCGGACCCGTT

GAM189 24675 LOC2548 1 6188 XP_171170.1 3 281 TGGAGAAATTCA T CA 3 B c c
GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA

GAM189 24631 LOC2550 1 3261 XP_173187.1 3 221 GCACGGGGCCCA C A 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCGTG GTGACGTGAG TCGGACCCG
A G

GAM189 24677 LOC2551 1 6294 XP_172941.1 3 613 TCTCGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 24658 LOC2554 1 6365 XP_173150.1 5 386 CAAAGCCCTTCA C --- A 3 B c c
GGCTGGAGTATA CATTG ACTCCAGCCT GGGC
GTGGCATG GTGAT TGAGGTCGGA CCCG
A CTT A

GAM189 24688 LOC2554 1 3150 XP_172581.2 3 2634 CTTTGTCACCCA A CA 3 B c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCATG GTGACGTGAGG CGGACCC
C AC

GAM189 24675 LOC2559 1 12803 XP_171083.2 5 864 TCTGTTGTCCAA C----- - 3 B c c
GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM189 24614 LOC2566 1 7385 XP_172864.1 3 861 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM189 24605 LOC2829 1 986 XP_212606.1 5 165 CTCTGTCGCCAA CTG A 3 B c c
AGTTGGAGTGCA CATTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C

GAM189 24643 LOC2829 1 986 XP_212647.1 5 165 CTCTGTCGCCAA CTG A 3 B c c
AGTTGGAGTGCA CATTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C

GAM189 24663 LOC2829 1 814 XP_210834.1 3 1912 ATGGCCATGCTG T - TG G 3 B c c
GGCTGGAGTGGC CAT GC ACTCCAGCC G CA
TGTGGGGT GTG CG TGAGGTCGG C GT
T G GT -

GAM189 24672 LOC2829 1 18172 XP_210837.1 3 862 CTCTGTCTCCTA A CA 3 B c c
GGCTGGAGCGCA CATTGC CTCCAGCCTGGG
GTGGTGCA GTGACG GAGGTCGGATCC
C TC

GAM189 246 LOC2829 2 12068 XP_210845.1 3 528 CTCTGTTGCCCA 3 B b b
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2829 2 16541 XP_210845.1 5 34 CTTTGTCACCCA C CA 3 B c b
87 GGCTGGAGTATA CATTG ACTCCAGCCTGGG
GTGGCACA GTGAT TGAGGTCGGACCC
A AC
GAM189 246 LOC2829 1 11798 XP_208473.1 3 987 CCCTGTTGCCCA A 3 B b b
97 GGCTGGAGAGCA CATTGC CTCCAGCCTGGGCAA
GTGGTGCA GTGACG GAGGTCGGACCCGTT
A
GAM189 246 LOC2830 1 17587 XP_210870.1 3 415 CAGAGTAGTTCA A -- A 3 B c c
47 GGCTGGGTGGAG CATTGC CT CCAGCCTGGGC
CAGTGGGA GTGACG GG GGTCGGACTTG
A TG A
GAM189 246 LOC2830 1 7252 XP_210875.1 3 1388 GTTTGTCACCCA CA 3 B c c
61 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2830 1 4176 XP_208509.1 3 178 TTGTGTTCCCCA C CA 3 B c c
87 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGCATG GTGACGTGA GTCGGACCC
A CT
GAM189 246 LOC2830 1 2219 XP_210885.1 5 1721 CTCTGTCGCCCA C A 3 B c c
89 GGCTCGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCATG GTGACGTGAG TCGGACCCG
C C
GAM189 246 LOC2831 1 16397 XP_210895.1 3 712 CTCTCTTGCCCA 3 B b b
19 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTATG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2831 1 5323 XP_208525.3 3 380 CTCTGTCACCCA C CA 3 B c c
30 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGTG GTGACGT AGGTCGGACCC
A AC
GAM189 246 LOC2831 1 12544 XP_210911.1 3 454 ACCCTGTTGCCA C G 3 B b b
40 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGCG GTGACGT AGGTCGGACC GTT
A -
GAM189 246 LOC2831 1 19977 XP_210925.1 3 177 ATCTTCTCAGGC C--- CA 3 B c c

42 TCACTGAGTGCA CATTGCACTC AGCCTGGG
ATGTCTGC GTAACGTGAG TCGGACTC
TCAC TT
GAM189 246 LOC2831 1 2650 XP_210920.1 3 2296 ACTCTGTCACCA -- 3 B b b
43 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 LOC2831 1 19812 XP_210917.2 5 317 CTCTGTCATCCA CA 3 B c c

52 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCT
AC

GAM189 246 LOC2831 1 4979 XP_208535.1 3 649 CTCTGTTGCCCA 3 B b b
70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGAG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2831 1 15574 XP_210903.1 3 985 TCTTGTTGCCCA 3 B b b
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2832 1 10112 XP_208555.2 3 1675 TACTGTTGTCCA C----- A 3 B c c
15 GGCTGGAGCGCA ATTGC CTCCAGCCTGGGCAA
GTTGATTG TGACG GAGGTCGGACCTGTT
GTTAGT C

GAM189 246 LOC2832 1 9525 NP_787089.1 5 63 CTCTGTCGCCCA A 3 B b b
41 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTTGGACCCG
C

GAM189 246 LOC2832 1 4496 XP_208583.2 3 1432 ACAGCAGCCCTG T G -- A 3 B c c

44 GGGGTGGGTGCA CATTGCAC CCA CCT GGGC
ATGAGGAT GTAACGTG GGT GGG CCCG
- G GT A

GAM189 246 LOC2832 1 8223 XP_210952.1 5 554 CCTTGTTGCCCA TTG CT- 3 B c
c
62 GGCTGGTCTTGA CA CA CCAGCCTGGGCAA
ACTGGGCT GT GT GGTCGGACCCGTT
CAA TCT

GAM189 246 LOC2832 1 9036 XP_210961.1 3 2048 TCTTGTTGCCCA 3 B b b
78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2832 1 17952 XP_210962.1 3 346 CTCTGTCACCCA CA 3 B c c
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2832 1 9585 XP_210965.1 5 438 CTCTGTCTCCGA --- 3 B b b
99 GGCTGGAGTGCA CATTGCACTCCAGCCT GGGCA
ATGTTGCA GTAACGTGAGGTCGGA TCTGT
GCC

GAM189 246 LOC2833 1 2201 XP_210978.1 5 938 CTCTGTCGCCCA C A 3 B b b
29 GACTGGAGTGCA CATTGCACTCCAG CTGGGC
ATGGTGCG GTAACGTGAGGTC GACCCG
A C

GAM189 246 LOC2833 2 2143 XP_210981.1 3 1369 CTCTGTTGCCCA 3 B b b
35 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM189 246 LOC2833 2 16144 XP_210981.1 3 1637 CTCTGTCACCCA A CA 3 B c b

35 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGTGCG GTGACGTGAGG CGGACCC
C AC

GAM189 246 LOC2833 1 8232 XP_208647.1 3 808 CTCTGTCACCCA CA 3 B c c
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2833 1 7265 XP_211007.1 3 1634 CTCTTACGCCCA G C A 3 B c c
87 GGCTGGAATGAA CATT CA TCCAGCCTGGGC
GTGGCATG GTGA GT AGGTCGGACCCG
A A C

GAM189 246 LOC2833 1 1730 XP_211021.1 5 134 CTCTGTTGCCCA C 3 B b b
94 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCACA GTGAC TGAGGTCGGACCCGTT
A

GAM189 246 LOC2833 1 9003 XP_211020.1 3 528 ACTCTGTTGCTA G 3 B b b
95 GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCACA GTGACGTGAGGTCGGATC GTT
-

GAM189 246 LOC2834 1 19206 XP_211024.1 5 444 CTCTGTCGCCAA A G A 3 B c c
00 GGCTGGAGGGCA CATTGC CTCCAGCCT GGC
ATGGCATG GTAACG GAGGTCGGA CCG
G A C

GAM189 246 LOC2834 1 16658 XP_211032.1 5 1943 GCTGTATTGCCA C G 3 B b b
32 GACTGGAGTGCA CATTGCACTCCAG CTGG CAA
GTGGCGTG GTGACGTGAGGTC GACC GTT
A -

GAM189 246 LOC2834 1 2220 XP_211043.1 3 165 CTCTGTCGCCCA C A 3 B c c
41 GGCTGCAGTGCG CATTGCACT CAGCCTGGGC
GTGGTGCG GTGGCGTGA GTCGGACCCG
C C

GAM189 246 LOC2834 1 10032 XP_211037.1 5 974 CACCTCTTGCCA C --- -- G 3 B c c
42 GGCTGCAGAGCT ATTGCA CTC CAGCCTGG CAA
ATGCAGTC TGACGT GAG GTCGGACC GTT
C ATC AC -

GAM189 246 LOC2834 1 5683 XP_211044.1 5 306 CTGTGTCATGCA --- 3 B b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCATG GTGACGTGAGGTCGGAC CTGT
GTA

GAM189 246 LOC2834 1 7397 XP_208679.1 5 490 GTCTGACACCTG TG CA 3 B c c

52 GGCTGGAGTGCA CATTGCACTCCAGCC GG
GTGGTGCA GTGACGTGAGGTCGG CC
GT AC

GAM189 246 LOC2834 1 14861 XP_211049.1 5 128 CTCTGTCACCCA CA 3 B c c
54 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2834 1 13967 XP_211050.1 3 1034 AAACCTTTGTCA A T G 3 B c c
67 GGCTGGGCGCGG CATTGC C CCAGCCTGG CAA

TGGCTCAC GTGGCG G GGTCGGACT GTT
C - -

GAM189 246 LOC2834 1 9892 XP_211056.1 3 1714 TTCTCTTGCCCA 3 B b b
75 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2834 1 17710 XP_211053.1 5 1048 CTCTGTCCCCTG --- 3 B b b
84 GGCTGGAGTGCA CATTGCACTCCAGCCT GGGCA
ATGGTGCG GTAACGTGAGGTCGGG CCTGT
TCC

GAM189 246 LOC2834 1 7371 XP_211062.1 3 676 CTCTGTTACCCA C CA 3 B c c
87 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCGTG GTAACGTGAG TCGGACCC
A AT

GAM189 246 LOC2835 1 12075 XP_211075.1 3 1820 CTCTGTCACCCA CA 3 B c c
07 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2835 1 3199 XP_211083.1 3 3279 CTCTGTCACCCA CA 3 B c c
34 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2835 1 13652 XP_211118.1 3 37 CTCTGCTCCCCA G C CA 3 B c c

70 GGCTTGAGTGAG CATT CACTC AGCCTGGG
TGTGTGCC GTGA GTGAG TCGGACCC
- T CT

GAM189 246 LOC2835 2 6183 XP_211095.1 5 421 CTCTGTTGCCCA CAT----- C 3 B c c

75 GGCTAGAGTGCA TGCACTC AGCCTGGGCAA
CTAATACA ACGTGAG TCGGACCCGTT
ACATAATC A

GAM189 246 LOC2835 2 10067 XP_211095.1 5 885 CTCTGTTGCCCA C TC 3 B c c
75 GGCTGAGGTACA CATTG AC CAGCCTGGGCAA
GTGGCGTG GTGAC TG GTCGGACCCGTT
A GA

GAM189 246 LOC2835 1 10466 XP_294741.1 5 480 CTCTGTCACCCA T C CA 3 B c c

85 AGCTGGAGTGCA CA TGCACTCCAGC TGGG
CTGGCATG GT ACGTGAGGTCG ACCC
C A AC

GAM189 246 LOC2835 1 10638 NP_787093.1 3 911 CTCTGTTGCCCA 3 B b b
88 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGACTC GTGGCGTGAGGTCGGACCCGTT

GAM189 246 LOC2836 1 4420 XP_211126.1 5 3889 CTCTGTTGCCCA C 3 B b b
24 GGCTGGAGTCCA CATTG ACTCCAGCCTGGGCAA
GTGGCATG GTGAC TGAGGTCGGACCCGTT
C

GAM189 246 LOC2836 2 3581 XP_211134.1 5 1238 CTCTGTCGCCCA C A 3 B c b

37 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGTATG GTGACGTGAG TCGGACCCG
A C
GAM189 246 LOC2836 2 14859 XP_211134.1 5 361 CTCTGTCGCCCA A 3 B b b
37 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC2836 1 17964 XP_208764.1 3 227 CTCTGTTGCCCA 3 B b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2836 1 16674 XP_211147.1 5 893 CTCTGTCGCCCA CAC A 3 B c
c
63 GGCTGGACTACA CATTG TCCAGCCTGGGC
ATGGCACG GTAAC AGGTCGGACCCG
ATC C
GAM189 246 LOC2836 1 8450 XP_208773.1 5 12 TTTTGTCACCCA T CA 3 B c c
64 GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
ATGGCACG GTA CGTGAGGTCGGACCC
C AC
GAM189 246 LOC2836 1 1730 XP_211152.1 5 19 CTCTGTTGCCCA C 3 B b b
72 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCACA GTGAC TGAGGTCGGACCCGTT
A
GAM189 246 LOC2836 1 11904 NP_787094.1 3 1229 TTTTGTCACCGA G CA 3 B c c

87 GGCTGGAGTGCA CATTGCACTCCAGCCT GG
ATGGCCCG GTAACGTGAGGTCGGA CC
G AC
GAM189 246 LOC2836 1 5305 XP_208788.1 3 334 AGAAATTTGTCA T G 3 B b b
93 GGCTGGGTGCAG CATTGCAC CCAGCCTGG CAA
TGGCTCAT GTGACGTG GGTCGGACT GTT
- -
GAM189 246 LOC2837 2 13716 XP_211170.3 3 1559 CCTTCTTCCCCA G - CA 3 B c b

01 GGCTGGGAGTGG CATT CACTCC AGCCTGGG
GTGAGACG GTGG GTGAGG TCGGACCC
- G CT
GAM189 246 LOC2837 2 14381 XP_211170.3 3 3386 GCTCTGTCACCA -- 3 B b b
01 GGCTGGAGTGCG CATTGCACTCCAGCCTGG GCA
GTGGCATA GTGGCGTGAGGTCGGACC TGT
AC
GAM189 246 LOC2837 1 9256 XP_211176.1 5 751 AAAAATTTGAAC CC - GG 3 B c c

23 GAGGCTAGTGCA CATTGCACT AGCCT G CAA
ATGTTTTG GTAACGTGA TCGGA C GTT
-- G AA
GAM189 246 LOC2837 1 11523 XP_208115.1 3 290 CTCTGTCGCCCA A 3 B b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG

C

GAM189 246 LOC2837 1 12479 XP_208835.1 3 299 CGCTGTTGCCCA CC 3 B b b
67 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC

GAM189 246 LOC2837 1 4370 XP_211199.1 5 1257 CTCTGTCGCCCA A 3 B b b
78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGGG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC2837 1 17644 XP_211198.1 3 2590 ACGACAGACCCA T ---- CA 3 B c
c
79 GGCTGGAGTCTT CAT GC ACTCCAGCCTGGG
GGCTGTGC GTG CG TGAGGTCGGACCC
T GTTC AG

GAM189 246 LOC2838 1 6265 XP_208122.1 3 1461 TAGTGTTGCCCA 3 B b b
01 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGC GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2838 1 16700 XP_208850.1 3 949 CTCTGTCATCCA CA 3 B c c
02 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCT
AC

GAM189 246 LOC2838 1 9546 XP_211218.1 3 256 CTCTGTCACCCC T CA 3 B c c
18 GGCTGGAGTGCA CATTGCACTCCAGCC GGG
GTGGTGTG GTGACGTGAGGTCGG CCC
C AC

GAM189 246 LOC2838 1 4308 NP_848611.1 5 92 TGGAGTTGCCCA GCA - -- 3 B c c
49 GGCCCTGTGAGC CATT CTC CA GCCTGGGCAA
AAGTGGCA GTGA GAG GT CGGACCCGTT
AC- T CC

GAM189 246 LOC2838 1 4308 XP_208870.1 5 92 TGGAGTTGCCCA GCA - -- 3 B c c
49 GGCCCTGTGAGC CATT CTC CA GCCTGGGCAA
AAGTGGCA GTGA GAG GT CGGACCCGTT
AC- T CC

GAM189 246 LOC2838 1 4974 XP_211229.1 3 679 CTCTGTCACCGA G CA 3 B c c
51 GGTTGGAGTGCA CATTGCACTCCAGCCT GG
GTGGTATG GTGACGTGAGGTTGGA CC
G AC

GAM189 246 LOC2838 1 6184 XP_211233.1 3 694 AAAGACTGAAGA GGG 3 B c c
56 GGCTGGAGTGCA CATTGCACTCCAGCCT CA
GTGGCGCA GTGACGTGAGGTCGGA GT
GAA

GAM189 246 LOC2838 2 1401 NP_787095.1 3 713 CTCTGTCGTCCA A 3 B b b
61 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCTG
C

GAM189 246 LOC2838 2 1635 NP_787095.1 3 1035 CTCTGTCGACCA CA----- --- 3 B c b

61 GGCTGGAGTGCA TTGCACTCCAGCCTGG GCA
GGGGCACA GACGTGAGGTCGGACC TGT

ACACGGG AGC
GAM189 246 LOC2838 1 13285 XP_208875.1 3 1506 GCTTGTTGCCCA 3 B b b
63 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2838 1 18993 XP_211248.2 5 724 CTCTGTCTCCCG CA 3 B c c
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGGCCC
TC
GAM189 246 LOC2838 2 11072 XP_211249.1 3 1413 GTCCCAGCTCCA CA - A 3 B c
b
88 GGCTGGAGCCAG CATTG CTCCAGCCTGG GC
TGAAGGGT GTGAC GAGGTCGGACC CG
C- T A
GAM189 246 LOC2838 2 14104 XP_211249.1 3 1551 CTCTGCTGCCCA C 3 B b b
88 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCA
GTGGTGCC GTGACGT AGGTCGGACCCGT
A
GAM189 246 LOC2838 2 3899 XP_208899.1 3 784 TTCTGTCACCCA A CA 3 B c c
89 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGTGTA GTGACGTGAGG CGGACCC
C AC
GAM189 246 LOC2838 2 10739 XP_208899.1 5 290 ATTCTAGGCAGA C GG A 3 B c
c
89 GGCTGGAATGCA CATTGCA TCCAGCCT GC
ATGATGCG GTAACGT AGGTCGGA CG
A GA G
GAM189 246 LOC2839 2 4703 XP_208909.1 5 2420 TTCTGCTGCCCA 3 B b b
28 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACG GTGACGTGAGGTTGGACCCGT

GAM189 246 LOC2839 2 20101 XP_208909.1 5 2716 CTCTGTTGCCCA 3 B b b
28 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGTCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2839 1 15775 XP_208905.2 5 920 CTCCGTCACCCA CA 3 B c c
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2839 1 19569 XP_208145.2 3 1458 TAGTGTCACCCA CA 3 B c c
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGATCCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2840 2 11764 XP_208958.2 3 2380 ATCATGGGTCCA ACTC A 3 B c
c
01 GGCTGATAGCAA CATTGC CAGCCTGGGC
TGGACAGA GTAACG GTCGGACCTG
ATA- G
GAM189 246 LOC2840 2 18161 XP_208958.2 3 1485 CACTGTCGCCCA T CC A 3 B c
c

```
        01                      ATCTGGAGTGCA CA TGCACTCCAG  TGGGC
                                CTGGCGCT    GT ACGTGAGGTC  ACCCG
                                      C       TA    C
GAM189  246  LOC2840 1  3244  XP_211298.1  3  17    CTCTTGTTGCCT          C          3  B  b  b
        16                      AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
                                ATGGCGCA    GTAACGTGAGGTCG ATCCGTT
                                            -
GAM189  246  LOC2840 1  18610 XP_208961.1  3  354   CTCTGTAACTCA            CA       3  B  c  c
        17                      GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                GTGGCGCG    GTGACGTGAGGTCGGACTC
                                              AA
GAM189  246  LOC2840 1  10124 XP_211302.1  3  2841  CTCTGTTGCCCT    C      T          3  B  b  b
        19                      GGCTGGAGTACA CATTG ACTCCAGCC GGGCAA
                                GTGGCATG    GTGAC TGAGGTCGG CCCGTT
                                      A       T
GAM189  246  LOC2840 2  14597 XP_208983.3  3  1018  CTGTGTCGCCCA            A        3  B  b  b
        23                      GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                GTGGCGTG    GTGACGTGAGGTCGGACCCG
                                              C
GAM189  246  LOC2840 2  17953 XP_208983.3  3  1473  CTCTGTTGCCCA          C          3  B  b  b
        23                      GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
                                GTGGCGTG    GTGACGTGAGGTC GACCCGTT
                                            A
GAM189  246  LOC2840 1  10847 XP_208152.1  3  1242  CACTGTCACCCA        A     CA       3  B  c  c

        48                      GGCCGGAGTGCA CATTGCACTCC GCCTGGG
                                GTGGCACA    GTGACGTGAGG CGGACCC
                                          C      AC
GAM189  246  LOC2840 2  1596  XP_211321.1  3  58    CCCTGTTGCCCA        C          3  B  b  b
        74                      GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
                                GTGGTGCG    GTGACGTGA GTCGGACCCGTT
                                      A
GAM189  246  LOC2840 2  15531 XP_211321.1  3  983   CTCAGTCGCCCA            A        3  B  b  b
        74                      GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                GTGGCATG    GTGACGTGAGGTCGGACCCG
                                              C
GAM189  246  LOC2840 1  18527 XP_211323.1  3  2     CTGTCACCCAGG        C      CA       3  B  c  c
        82                      CTGAAGTGCAGT CATTGCACT CAGCCTGGG
                                GCAGGACC    GTGACGTGA GTCGGACCC
                                      A       AC
GAM189  246  LOC2840 3  7333  XP_211324.1  3  845   CTCTGTCACCCT          T  CA       3  B  c  b
        95                      GGCTGGAGTGCG CATTGCACTCCAGCC GGG
                                GTGGCGAT    GTGGCGTGAGGTCGG CCC
                                        T   AC
GAM189  246  LOC2840 3  11799 XP_211324.1  3  1043  CTCTTTCGCCCA      C  A      A       3  B  c  b

        95                      GGCCGGACTGCA CATTGCA TCC GCCTGGGC
                                GTGGCGCA    GTGACGT AGG CGGACCCG
                                      C  C       C
GAM189  246  LOC2840 3  15513 XP_211324.1  3  143   CTCTGTCATTCA            ---        3  B  b  b
```

95 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGTGCA GTGACGTGAGGTCGGAC CTGT
TTA

GAM189 24698 LOC284001 8582 XP_209008.3 3 198 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCC GTGATGTGAGGTCGGACCC
AT

GAM189 24600 LOC284101 1777 XP_209015.1 3 1541 TCCAGTGCTCCA T A - 3 B c c
GGCTGGGGGCCG CAT GC CTCCAGCCTGG GCA
TGGATCCT GTG CG GGGGTCGGACC CGT
C - T

GAM189 24601 LOC284101 19537 XP_209019.1 5 411 CTCTGTTGCCCA --- 3 B b b
GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA

GAM189 24602 LOC284103 3233 XP_211327.3 3 608 TTTTGTTGCCCA CA----- 3 B c b
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGCGCG AACGTGAGGTCGGACCCGTT
GCGCGGC

GAM189 24602 LOC284103 7745 XP_211327.3 5 862 CTTTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 24602 LOC284103 18149 XP_211327.3 5 46 TCTTGCCGTCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGTG GTAACGTGAGGTCGGACCTG
C

GAM189 24628 LOC284102 1966 XP_211342.1 3 461 CCCTGTCGCCCA T A 3 B b b
GGCTGGAGTGCC CAT GCACTCCAGCCTGGGC
ATGGCGCG GTA CGTGAGGTCGGACCCG
C C

GAM189 24628 LOC284102 17271 XP_211342.1 3 0 TCGCCCAGGCTG A 3 B b b
GAGTGCAGTGGT CATTGCACTCCAGCCTGGGC
AGATCAGG GTGACGTGAGGTCGGACCCG
C

GAM189 24635 LOC284101 12779 XP_209032.1 3 540 GACTGTTGCCCA 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
ATGGCGCC GTAATGTGAGGTCGGACCCGTT

GAM189 24645 LOC284101 4102 XP_211353.1 5 368 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
ATGGCGCG GTAACGTGAGGTCGGACC TGT
GC

GAM189 24671 LOC284101 11530 XP_209051.1 3 1095 TGTTGTCGCCTA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGATGCG GTAACGTGAGGTCGGATCCG
C

GAM189 24683 LOC284102 1111 XP_209059.1 5 422 TCTCGTTGCCAA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
ATGGCACG GTAACGTGAGGTCGGA CCGTT

A

GAM189 24683 LOC2841 2 9456 XP_209059.1 5 922 ATCGATAGCCCA C A A 3 B c b
GGCAGGAGTACA CATTG ACTCC GCCTGGGC
GTGGCACA GTGAC TGAGG CGGACCCG
A A A

GAM189 24686 LOC2841 1 14861 XP_209060.2 3 1162 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM189 24691 LOC2841 1 4421 XP_211377.1 5 64 TCTTGTCGCCCA CA----- A 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGC
ACGGTATG AACGTGAGGTCGGACCCG
GTATGGC C

GAM189 24602 LOC2842 1 3800 XP_208174.2 3 2063 TCAGTGCTCTCA - CT- 3 B c c
GCTGGCAGTGCA CATTGCACT CCAGC GGGCA
ATGCTTGT GTAACGTGA GGTCG CTCGT
C ACT

GAM189 24667 LOC2842 1 8494 XP_211411.1 5 1562 ATCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC

GAM189 24676 LOC2842 1 1026 XP_211412.1 5 1027 CTTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC

GAM189 24686 LOC2842 1 19875 XP_211419.1 3 1829 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
TC

GAM189 24689 LOC2842 2 1885 XP_209105.1 3 146 TCTTGTTACCCA A CA 3 B c c
GGCAGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCGTG GTGACGTGAGG CGGACCC
A AT

GAM189 24689 LOC2842 2 16648 XP_209105.1 3 311 CCACATTGGCCA GCACT G 3 B c c
GGCTGGTCTCAA CATT CCAGCCTGG CAA
ATGACCCT GTAA GGTCGGACC GTT
ACTCT G

GAM189 24697 LOC2842 1 1751 XP_209112.1 3 1370 GGTGCCTGCCCA GCA - AG- 3 B c c
GGATGGGTAGGA CATT CT CC CCTGGGCA
AATGCTGA GTAA GA GG GGACCCGT
AG- T GTA

GAM189 24604 LOC2843 1 4849 XP_211426.1 3 315 TCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACGAG GTGACGTGAGGTCGGACCCGTT

GAM189 24617 LOC2843 2 3386 XP_209162.1 3 1766 CTCTCTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG

C

GAM189 246 LOC2843 2 7077 XP_209162.1 3 813 TTCTGTCACACA T C --- 3 B c b
17 GTCTGGAGTGCT CAT GCACTCCAG CTG GGCA
GTGGTGCA GTG CGTGAGGTC GAC CTGT
T T ACA

GAM189 246 LOC2843 1 1731 XP_209143.1 3 1033 TTCTGTCGTCCA A 3 B c c
25 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGGCGTGAGGTCGGACCTG
C

GAM189 246 LOC2843 1 11986 XP_211437.1 3 437 CTTTGTGCCCTA C - 3 B b b
56 GACTGGAGTGCA CATTGCACTCCAG CT GGGCA
ATGGCGCC GTAACGTGAGGTC GA CCCGT
A T

GAM189 246 LOC2843 1 18898 XP_211435.1 3 530 ACTTGTCACCCA CA 3 B c c
62 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2843 1 16701 XP_209154.1 3 931 CTCTGTCATCCA CA 3 B c c
75 GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTTGGACCT
AC

GAM189 246 LOC2843 1 19718 XP_209157.1 3 664 TCTTATTGCCCA 3 B b b
76 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2843 1 9312 XP_209163.1 3 384 CTCTATTGCCCA C 3 B b b
79 GTCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATG GTGACGTGAGGTC GACCCGTT
T

GAM189 246 LOC2843 1 16459 XP_211454.1 5 125 CTGTTTGGCCCA T ACT - A 3 B c
c
95 GGCCTGGGCCAT CAT GC CCAG CCTGGGC
GACGGATG GTA CG GGTC GGACCCG
C --- C G

GAM189 246 LOC2843 1 10399 XP_211452.1 3 1675 CTGTGTTGTCCA 3 B b b
96 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGTG GTAACGTGAGGTCGGACCTGTT

GAM189 246 LOC2844 2 2645 XP_209183.2 3 1651 TTCTGTCCCCGA A --- 3 B b b
05 GGCCGGAGTGCA CATTGCACTCC GCCT GGGCA
ATGGCGTG GTAACGTGAGG CGGA CCTGT
C GCC

GAM189 246 LOC2844 2 19462 XP_209183.2 3 908 CTCTGTCACCCA C C CA 3 B c
b
05 GGCTGTAGTACA CATTG ACT CAGCCTGGG
GTGGTGCC GTGAC TGA GTCGGACCC
A T AC

GAM189 246 LOC2844 1 14364 XP_211443.1 5 367 CTCTGTTGCCCA T 3 B b b
08 GGCTGGTGTGTA CATTGCAC CCAGCCTGGGCAA
GTGATCTC GTGATGTG GGTCGGACCCGTT

T

GAM189 246 LOC2844 1 17304 XP_211449.1 3 638 GTGGTTGCTGAA TG- G- 3 B c c

10 GGCTGGAGTGGG CAT CACTCCAGCCT GGCAA
TGTGGCAA GTG GTGAGGTCGGA TCGTT
TGG AG

GAM189 246 LOC2844 2 4533 XP_209200.1 5 1199 CTCTGTTGCCCG 3 B b b

21 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGGCCCGTT

GAM189 246 LOC2844 2 15844 XP_209200.1 5 1328 CTATGTTGCCCA CA------ CT 3 B c b

21 GGCTGGTTGCAA TTGCA CCAGCCTGGGCAA
ACTTCTGG AACGT GGTCGGACCCGTT
GGTCTTCA T-

GAM189 246 LOC2844 2 15844 XP_209200.1 5 1372 CTATGTTGCCCA CA------ CT 3 B c b

21 GGCTGGTTGCAA TTGCA CCAGCCTGGGCAA
ACTTCTGG AACGT GGTCGGACCCGTT
GGTCTTCA T-

GAM189 246 LOC2844 3 4975 XP_209198.1 3 476 TGCTGCTGCCCA 3 B b b

26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGTGCA GTGACGTGAGGTCGGACCCGT

GAM189 246 LOC2844 3 5357 XP_209198.1 3 311 CTCTGTCGCCCA A 3 B b b

26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGACATG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC2844 3 13177 XP_209198.1 3 877 CTCTGTCGCCCA C A 3 B c b

26 GGTTTGAGTGCA CATTGCACTC AGCCTGGGC
ATGGCACA GTAACGTGAG TTGGACCCG
T C

GAM189 246 LOC2844 1 8752 XP_209210.1 3 761 CCTCTGTCACCA -- 3 B b b

40 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
AC

GAM189 246 LOC2844 3 3999 XP_209216.1 5 680 CACTGTCACCCG CA 3 B c b

54 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCTCG GTAACGTGAGGTCGGGCCC
AC

GAM189 246 LOC2844 3 16031 XP_209216.1 5 1116 CTCTGTTGCCCA C 3 B b b

54 GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGTG GTGACGTGA GTCGGACCCGTT
A

GAM189 246 LOC2844 3 19117 XP_209216.1 5 1282 CCATCTTGGCCA TG- T G 3 B c b

54 GGCTGGTGTGAT CAT CAC CCAGCCTGG CAA
CATGGCTC GTA GTG GGTCGGACC GTT
CTA T G

GAM189 246 LOC2844 1 18777 XP_211470.1 3 256 CTCTGTTATCCA T CA 3 B c c

56 GGCTGGTGTGCA CATTGCAC CCAGCCTGGG
GTGATACA GTGACGTG GGTCGGACCT
T AT
GAM189 246 LOC2844 1 19286 XP_209225.1 3 1168 CTCTGTCACCCA CT CA 3 B c c
71 GGCTGGGATGCA CATTGCA CCAGCCTGGG
GTGGCTTC GTGACGT GGTCGGACCC
AG AC
GAM189 246 LOC2845 1 14119 XP_211500.1 3 1747 CTCTGTCGCCCA CA A 3 B c c
12 GGCTGGAGCCCA CATTG CTCCAGCCTGGGC
GTGGCGAG GTGAC GAGGTCGGACCCG
CC C
GAM189 246 LOC2845 1 18865 XP_211502.1 5 908 CCCAATAGCCCA A 3 B b b
13 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCAGA GTGACGTGAGGTCGGACCCG
A
GAM189 246 LOC2845 1 19112 XP_211514.1 5 89 CCTTGCCCTTTG TT - --- 3 B c c
49 GGCTGGAGATGC CA GCA CTCCAGCCT GGGCAA
TTTGCCAG GT CGT GAGGTCGGG CCCGTT
TT A TTT
GAM189 246 LOC2845 1 9493 XP_211515.1 3 1303 CTCTGTCACCCA CA 3 B c c
51 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2845 1 19533 XP_211522.1 3 7 CTCTGTCTCCCA G C CA 3 B c c
77 GACTGGAGTGAG CATT CACTCCAG CTGGG
TGGTGTGA GTGA GTGAGGTC GACCC
- A TC
GAM189 246 LOC2845 1 12803 XP_209278.3 5 73 TCTGTTGTCCAA C----- - 3 B c c
87 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM189 246 LOC2846 1 12497 XP_211552.1 3 977 CTCGGTCACCTA CA 3 B c c
11 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGATGTGAGGTCGGATCC
AC
GAM189 246 LOC2846 1 18882 XP_211561.1 5 505 CTCTGTTGCCTA C 3 B b b
28 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCGTG GTAACGTGAGGTC GATCCGTT
A
GAM189 246 LOC2846 2 501 XP_209319.1 5 101 TCTTATTGCCCA C C 3 B b b
75 GACTAGAGTGCG CATTGCACTC AG CTGGGCAA
ATGGTGCG GTAGCGTGAG TC GACCCGTT
A A
GAM189 246 LOC2846 2 2389 XP_209319.1 5 558 CTCTGTCACCCA -- CA 3 B c b
75 GGCTGGAGTGTG CATTGCAC TCCAGCCTGGG
CAGTGGCG GTGACGTG AGGTCGGACCC
TG AC
GAM189 246 LOC2846 1 5926 XP_208236.1 3 488 AGAGACTGTAGC T AGC A 3 B c c

83 TCAGGGCGTGCA CATTGCAC CC CTGGGC
ATGTGAGG GTAACGTG GG GACTCG
C --- A

GAM189 24601 LOC2847 1 12803 XP_294994.1 5 866 TCTGTTGTCCAA C----- - 3 B c c
GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM189 24608 LOC2847 1 5153 XP_209332.1 3 524 CTCTGTTGCCCA CA------ T 3 B c c
GGCTGGGTGCAG TTGCAC CCAGCCTGGGCAA
CGGTGCGA GACGTG GGTCGGACCCGTT
AGCGTGGC -

GAM189 24623 LOC2847 3 2215 XP_211602.1 3 637 CTGTGTTGGCCA G CT- G 3 B c b
GGCTGGTCTTGA CATT CA CCAGCCTGG CAA
ATGCCTGA GTAA GT GGTCGGACC GTT
- TCT G

GAM189 24623 LOC2847 3 3182 XP_211602.1 3 472 CTTTGTTGCCCA 3 B b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGGCGTGAGGTCGGACCCGTT

GAM189 24623 LOC2847 3 6498 XP_211602.1 3 61 CTCTGCCACCCA C CA 3 B c b
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACG GTGACGTGAGGTCG ACCC
A AC

GAM189 24605 LOC2848 3 853 XP_209371.1 3 1213 TTTGCCCAGGCT ---- 3 B b b
GGATGGAGTGCA CATTGCACTCCA GCCTGGGCAA
GTGGCGTG GTGACGTGAGGT CGGACCCGTT
AGGT

GAM189 24605 LOC2848 3 1544 XP_209371.1 3 1111 CTCTGCTGCTCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGTGCA GTGACGTGAGGTCGGACTCGT

GAM189 24605 LOC2848 3 8046 XP_209371.1 3 1213 CTCTTTTGCCCA ---- 3 B b b
GGCTGGATGGAG CATTGCACTCCA GCCTGGGCAA
TGCAGTGG GTGACGTGAGGT CGGACCCGTT
AGGT

GAM189 24639 LOC2848 1 19401 XP_211661.1 5 446 TCTTGTTGCCCG 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGGCCCGTT

GAM189 24653 LOC2848 1 3582 XP_209383.1 3 138 CTCTGTCACCCA A CA 3 B c c
GGCTGGAGCGTA CATTGC CTCCAGCCTGGG
ATGGCACA GTAATG GAGGTCGGACCC
C AC

GAM189 24656 LOC2848 1 12736 XP_211668.2 3 619 TCTTGTCCCCCA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
ATGGCACG GTAACGTGAGGTC GACCC
A CC

GAM189 24656 LOC2848 1 12736 XP_302835.1 3 108 TCTTGTCCCCCA C CA 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG

ATGGCACG GTAACGTGAGGTC GACCC
A CC
GAM189 246 LOC2848 1 16785 XP_209384.2 3 315 GATGGAGGCAGT G TGG A 3 B c c
59 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM189 246 LOC2848 1 16785 XP_211670.2 5 289 GATGGAGGCAGT G TGG A 3 B c c
61 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM189 246 LOC2848 1 1645 XP_211672.1 3 70 CTCTGTTGCCCA 3 B b b
65 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAGCGTGAGGTCGGACCCGTT
GAM189 246 LOC2848 1 16785 XP_209412.1 3 1421 GATGGAGGCAGT G TGG A 3 B c c
73 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM189 246 LOC2848 2 3846 XP_209394.1 3 1070 GCTCTGTCGCCA C -- 3 B c c
74 GGCTGGAGTACA CATTG ACTCCAGCCTGG GCA
GTGGTGTG GTGAC TGAGGTCGGACC TGT
A GC
GAM189 246 LOC2848 2 16244 XP_209394.1 3 616 GCTCTGCGCCCA G A 3 B c c
74 GGATGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGCATG GTGACGTGAGGT GGACCCG
A C
GAM189 246 LOC2849 1 14894 XP_211696.1 5 657 TTTTGTCGCCCA A 3 B b b
34 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC2849 1 5465 XP_211705.1 3 1141 TCTTGTCTCTCA CT CA 3 B c c
47 GGCTGGGTTGCA CATTGCA CCAGCCTGGG
ATGGCACA GTAACGT GGTCGGACTC
TG TC
GAM189 246 LOC2849 1 4025 XP_211703.1 3 163 ACTCTGTCGCCA -- 3 B b b
50 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTCGGACC TGT
GC
GAM189 246 LOC2850 1 3500 XP_211731.2 3 639 TGTGTGACCTTA - - 3 B b b
02 GGCTGGAGTGCA CATTGCACTCCAGCCTG GG CA
ATGGCATG GTAACGTGAGGTCGGAT CC GT
T A
GAM189 246 LOC2850 1 17523 XP_209440.1 3 2382 CTCTGTCACCCA C CA 3 B c c
26 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGCG GTGACGTGAGGTC GACCC
A AC

GAM189 246 LOC2850 1 2174 XP_211751.1 3 866 TTCTGTCACCCA A C CA 3 B c c
52 GGCTAGAGCGCA CATTGC CTC AGCCTGGG
GTGGCAAG GTGACG GAG TCGGACCC
C A AC
GAM189 246 LOC2850 1 20023 XP_211753.1 5 236 TGTCACCCAGGT C --- CA 3 B c c
58 GGCTGGAGTACA CATTG ACTCCAGCC TGGG
GTGGCCTG GTGAC TGAGGTCGG ACCC
A TGG AC
GAM189 246 LOC2850 1 5667 XP_209464.1 3 987 CTCTATCACCCA C CA 3 B c c
83 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGTACG GTGACGTGA GTCGGACCC
A AC
GAM189 246 LOC2850 1 6092 XP_209465.1 3 42 TCTTGTTGCCCA CA 3 B b b
88 GGCCAGAGTGCA CATTGCACTC GCCTGGGCAA
ATGGCGTG GTAACGTGAG CGGACCCGTT
AC
GAM189 246 LOC2851 1 17113 XP_211773.1 3 843 GGGGATGAGCCA CA G- 3 B c
c
23 GGCTGGGGACAG CATTG CTCCAGCCTGG CA
TGGGGCTG GTGAC GGGGTCGGACC GT
A- GA
GAM189 246 LOC2851 2 5921 XP_211771.1 3 578 CTCTGTCACCCA CA 3 B c c
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCCCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2851 2 11528 XP_211771.1 3 145 CTCTGTCACCCA CA 3 B c c
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2851 1 4283 XP_211791.1 3 1871 TGCAGATTCCCA T CA 3 B c c
66 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACCC
- TT
GAM189 246 LOC2851 1 7860 XP_209500.1 3 170 CTCTTTTGCCCA C----- G C 3 B c c
76 GACTGGAGTGAA ATT CACTCCAG CTGGGCAA
GTAGCATG TGA GTGAGGTC GACCCGTT
GTACGA A A
GAM189 246 LOC2851 1 1745 XP_209509.1 3 678 CTCTGTTGCCCA 3 B b b
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2852 1 13597 XP_209521.1 5 78 ATCTGTCACCCA A CA 3 B c c
21 GGCTGGAGCGCA CATTGC CTCCAGCCTGGG
GTGGTGTG GTGACG GAGGTCGGACCC
C AC
GAM189 246 LOC2852 3 8001 XP_211813.1 3 723 CTCTGTCACCCA C CA 3 B c c
31 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCC
A AC

GAM189 246 LOC2852 3 8001 XP_211813.1 3 889 CTCTGTCACCCA C CA 3 B c c
31 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCC
A AC
GAM189 246 LOC2852 3 9352 XP_211813.1 3 1425 CTATCTTGCCCA C--------- CTCC 3 B c
c
31 GGCTTGCAATTT ATTGCA AGCCTGGGCAA
ATAGAGCT TAACGT TCGGACCCGTT
TCGAGATATT ----
GAM189 246 LOC2852 3 15366 XP_211813.1 3 1260 CACTGTCACCCA G C CA 3 B c
c
31 GTCTGGAGTGGA CATT CACTCCAG CTGGG
GTGGCATA GTGA GTGAGGTC GACCC
G T AC
GAM189 246 LOC2852 1 15575 XP_211829.1 5 565 TCTTGTTACCCA CA 3 B b b
81 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACG GTAACGTGAGGTCGGACCC
AT
GAM189 246 LOC2852 1 9374 XP_209554.1 3 399 CTATGTCACTCA CA 3 B c c
99 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACTC
AC
GAM189 246 LOC2853 1 1027 XP_211844.1 3 477 CTCTGTCTCCCA - CA 3 B c c
34 GGCTGGAGTTGC CATTGCA CTCCAGCCTGGG
AGTGGTGC GTGACGT GAGGTCGGACCC
T TC
GAM189 246 LOC2853 2 556 XP_211854.1 3 1258 CTCTGTTACCCA C CA 3 B c b
45 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCGCG GTGACGTGAG TCGGACCC
A AT
GAM189 246 LOC2853 2 18883 XP_211854.1 3 869 CAGGGTTGCCCA G 3 B b b
45 GGGTGGAGTGCA CATTGCACTCCA CCTGGGCAA
GTGGCAGG GTGACGTGAGGT GGACCCGTT
G
GAM189 246 LOC2853 1 6117 XP_209581.1 3 515 CTCTGTCACCCA CA 3 B c c
66 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGGGGTCGGACCC
AC
GAM189 246 LOC2853 1 10352 XP_211861.3 3 251 CTTTGTCACCCA CA 3 B c c
69 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2853 1 19692 XP_211873.1 3 1012 CTCTCTCGCCAT TG A 3 B c c

89 GGTTGGAGTGCA CATTGCACTCCAGCC GGC
GTGGTGCG GTGACGTGAGGTTGG CCG
TA C
GAM189 246 LOC2853 2 9688 XP_211879.1 3 41 CTCTGTCTCCCA CA 3 B c b
92 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC

TC

GAM189 246 LOC2853 2 17969 XP_211879.1 3 344 CTCTGTCGCCCA A 3 B b b
92 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC2853 2 4655 XP_209593.1 3 1208 TCCTCTCGCCCA A 3 B b b
98 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTC GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC2853 2 13286 XP_209593.1 3 906 CTCTGTCGCCCA C----- A 3 B c b
98 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCGCG TGACGTGAGGTCGGACCCG
GCGCGA C

GAM189 246 LOC2854 1 4171 XP_209607.3 3 1518 TTCTGTCGCCCA A 3 B b b
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC2854 1 13804 XP_211914.1 5 572 CACTGTCGCCCA A 3 B b b
88 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGGCGTGAGGTCGGACCCG
C

GAM189 246 LOC2854 1 11239 XP_211917.1 3 164 CTCTGTCCCTCA C----- --- 3 B c c
91 GGCTGGAGTGCA ATTGCACTCCAGCCT GGGCA
GTAGCGTG TGACGTGAGGTCGGA CCTGT
GTGCGA CTC

GAM189 246 LOC2855 1 3519 XP_211923.1 5 176 TACTTTCATTCA CA 3 B c c
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACTT
AC

GAM189 246 LOC2855 1 14552 XP_209643.1 3 12 CTCTTTTTGCAC C G 3 B b b
10 AGGCTGAGTGCA CATTGCACTC AGCCTG GCAA
ATGCCGTG GTAACGTGAG TCGGAC CGTT
- A

GAM189 246 LOC2855 2 6961 XP_209654.1 5 8 CTGTGTCGCCCA - A 3 B b b
40 GGCTGGAGTGCA CATT GCACTCCAGCCTGGGC
AGTGGCAT GTGA CGTGAGGTCGGACCCG
A C

GAM189 246 LOC2855 2 9543 XP_209654.1 5 1535 CTCTGTCACCCA CA 3 B c b
40 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2855 1 8718 XP_209660.1 3 436 CACTCTTGCCCA T C 3 B b b
60 GGCTGTAGTGCT CAT GCACT CAGCCTGGGCAA
GTGGCACG GTG CGTGA GTCGGACCCGTT
T T

GAM189 246 LOC2855 2 12804 XP_209671.1 3 721 CTCTGTCGCCAG - -- 3 B b b
89 GACTGGAGTGCA CATTGCACTCCAG CCTGG GCA
GTGACACG GTGACGTGAGGTC GGACC TGT
A GC

GAM189 246 LOC2855 2 17087 XP_209671.1 3 267 CTTGATCACCCA C CA 3 B c b

89 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCGTG GTGACGTGAG TCGGACCC
A AC

GAM189 246 LOC2856 1 13843 XP_211959.1 5 850 CTCTGTTGCCCA C 3 B b b
26 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGATACG GTGACGT AGGTCGGACCCGTT
A

GAM189 246 LOC2856 1 4949 XP_209693.1 5 3929 TTCTGTCACCCA CA 3 B c c
38 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2856 1 19299 XP_209719.2 3 204 CTCTGTTGCTCA 3 B b b
79 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACTCGTT

GAM189 246 LOC2856 1 17726 XP_209724.1 3 1089 CTCTGTTGCCCA 3 B b b
89 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2856 1 16940 XP_211981.1 5 24 CTCTGTTGCCCA 3 B b b
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2857 1 18012 XP_211997.1 5 350 CTCTGTCAACCA --- 3 B b b
22 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGACTCT GTGACGTGAGGTCGGACC TGT
AAC

GAM189 246 LOC2857 1 11141 XP_209743.1 3 1367 TTCTGTCACCCA CA 3 B c c
44 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2857 1 11528 XP_209742.1 3 2434 CTCTGTCACCCA CA 3 B c c
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2857 1 13412 XP_209750.1 3 371 CACTCTTGCCCA - A 3 B b b
60 GGCTGGAGCGCA CATT GC CTCCAGCCTGGGCAA
AGTGGCGC GTGA CG GAGGTCGGACCCGTT
A C

GAM189 246 LOC2857 1 16810 XP_212013.1 5 230 CTATGGTCCACA T -- - - A 3 B c c
77 GGCTGGAGGGTG CAT GCAC TCCAGCCTG GG C
CATGGAAC GTA CGTG AGGTCGGAC CC G
- GG A T G

GAM189 246 LOC2858 1 559 XP_212055.1 3 719 CTCTGTCACCCA CA 3 B b b
12 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC

GAM189 246 LOC2858 1 12389 XP_212036.1 5 78 TCTTGTTGCCCA 3 B b b
13 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2858 2 1847 XP_209777.1 3 237 CTCTGTTGCCCA C G 3 B b b
22 GGATGGAATGCA CATTGCA TCCA CCTGGGCAA
GTGGCACA GTGACGT AGGT GGACCCGTT
A A
GAM189 246 LOC2858 2 9753 XP_209777.1 5 1360 CTGTGTCACCCA CA 3 B c b
22 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2858 1 986 XP_212043.1 5 165 CTCTGTCGCCAA CTG A 3 B c c
30 AGTTGGAGTGCA CATTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C
GAM189 246 LOC2858 1 17964 XP_212034.1 3 188 CTCTGTTGCCCA 3 B b b
43 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2858 1 18945 XP_212045.1 5 732 CTCTGTCACCCG CA 3 B c c
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGGCCC
AC
GAM189 246 LOC2858 1 10885 XP_212061.1 3 687 TTCTGTAACCCA CA 3 B c c
72 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCCTG GTGACGTGAGGTCGGACCC
AA
GAM189 246 LOC2859 1 6188 XP_209810.1 3 304 TGGAGAAATTCA T CA 3 B c c
14 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA
GAM189 246 LOC2859 1 19536 XP_212104.1 3 41 CTATGTTGCCCA 3 B b b
23 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2859 1 17126 XP_209816.1 3 595 TCTTGTTGCCCA GCAC --- 3 B c
c
24 GGCTATGGGAAG CATT TCC AGCCTGGGCAA
AAATGAAA GTAA AGG TCGGACCCGTT
AGA- GTA
GAM189 246 LOC2859 1 12075 XP_212092.1 5 845 CTCTGTCACCCA CA 3 B c c
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2859 1 15323 XP_209821.1 3 680 TGCTGTTGCCCA 3 B b b
52 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2859 1 2604 XP_209833.1 5 934 CTCTGTCACCCA C CA 3 B c c
61 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCATG GTGACGT AGGTCGGACCC
A AC

GAM189 246 LOC2859 1 5318 XP_212105.1 3 866 TCGTGTTGCCCC T 3 B b b
72 GGCTGGAGTGCA CATTGCACTCCAGCC GGGCAA
GTGGCGCT GTGACGTGAGGTCGG CCCGTT
C
GAM189 246 LOC2859 2 1397 XP_212117.1 5 4 TACTGTCATACA C----- T --- 3 B c b
79 GGCTGGCGTGCA ATTGCAC CCAGCCTG GGCA
GTAGTGGG TGACGTG GGTCGGAC CTGT
GGGTGA C ATA
GAM189 246 LOC2859 2 6388 XP_212117.1 5 548 CTCTGTCAGCCA --- 3 B b b
79 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
ATGGCATG GTAACGTGAGGTCGGACC TGT
GAC
GAM189 246 LOC2859 1 11742 XP_212111.1 3 936 TCTTGTTGCCCA C A 3 B b b
89 GGCAGGAGTACA CATTG ACTCC GCCTGGGCAA
ATGGCAGG GTAAC TGAGG CGGACCCGTT
A A
GAM189 246 LOC2859 1 3647 XP_212120.1 3 774 CTATGTTGCCCA C-- ACT--- 3 B c c
99 GGCTGGCCTCAA ATTGC CCAGCCTGGGCAA
GCAATCCT TAACG GGTCGGACCCGTT
TCC AACTCC
GAM189 246 LOC2860 1 15231 XP_209866.1 3 1642 AATCGTCACCCA CC CA 3 B c
c
29 CATTGGAGTGCA CATTGCACTCCAG TGGG
GTGGTACG GTGACGTGAGGTT ACCC
AC AC
GAM189 246 LOC2860 1 2244 XP_209868.1 5 640 TTTTGTTGCGCA G 3 B b b
30 GGCTGGAGTGCA CATTGCACTCCAGCCTG GCAA
ATGGTGCA GTAACGTGAGGTCGGAC CGTT
G
GAM189 246 LOC2860 1 11035 XP_209873.1 5 648 TTTTGTTGCCCA 3 B b b
39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2860 1 9367 XP_212152.1 3 1054 CTCTGTTGTCCA 3 B b b
52 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACCTGTT

GAM189 246 LOC2860 1 17965 NP_776192.1 5 66 CTCTGTTGCCCA C 3 B b b
75 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCGTG GTGAC TGAGGTCGGACCCGTT
A
GAM189 246 LOC2860 5 3810 XP_212163.1 3 451 CTCTGTCGCCCA A 3 B b b
78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGAGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC2860 5 13100 XP_212163.1 5 790 CTGTCTTGCCCA CA----- C 3 B c b
78 GGCTGGAGTTCA TTG ACTCCAGCCTGGGCAA
GGGGCTAT GAC TGAGGTCGGACCCGTT

TATCGGG T

GAM189 246 LOC2860 5 15083 XP_212163.1 3 760 CTCTGTCACCCA G CA 3 B c b

78 GGATGGAGTGCA CATTGCACTCCA CCTGGG
GTGTTGTG GTGACGTGAGGT GGACCC
A AC

GAM189 246 LOC2860 5 15589 XP_212163.1 5 1402 GCTCTGTTGCCA T G 3 B b b

78 GGCTGGAGTGCA CA TGCACTCCAGCCTGG CAA
CTGGGGCT GT ACGTGAGGTCGGACC GTT
C -

GAM189 246 LOC2860 5 16716 XP_212163.1 5 84 CTGGGCTGCCCA TG CCAG 3 B c b

78 GGGGTGTGATGT CAT CACT CCTGGGCA
GGAGCTGG GTA GTGG GGACCCGT
GT ----

GAM189 246 LOC2860 1 16409 XP_212166.3 5 142 GCCATGTGGAAC ----- TG-- A 3 B c c

90 TGCTGGAGTGCA CATTGCACTCCAGC C GGC
GTGGCATG GTGACGTGAGGTCG G CCG
TCAAG TGTA -

GAM189 246 LOC2861 1 7847 XP_212185.1 3 991 CTCTGCCACCCA CA 3 B c c

26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2861 1 7113 XP_212194.1 5 446 TTTTGTCACCCA CA 3 B c c

32 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2861 1 9746 XP_212196.1 3 1354 CCATATTGCCCA GCACT 3 B c c

35 GGCTGGTCTCGA CATT CCAGCCTGGGCAA
ATGCCTGG GTAA GGTCGGACCCGTT
GCTCT

GAM189 246 LOC2861 1 3927 XP_209925.1 5 1001 CTCTGTTGACCA G G 3 B b b

66 GGCTGGAGTGAA CATT CACTCCAGCCTGG CAA
GTGGTGTG GTGA GTGAGGTCGGACC GTT
A A

GAM189 246 LOC2861 1 8426 XP_212211.1 5 1936 GCTGTGTCACCA AC -- 3 B b b

70 GGCTGGAGCAGT CATTGC TCCAGCCTGG GCA
GGCACGAT GTGACG AGGTCGGACC TGT
-- AC

GAM189 246 LOC2861 2 3430 XP_212219.1 5 148 CTTTGTCACCCA C CA 3 B c c

86 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM189 246 LOC2861 2 18020 XP_212219.1 3 390 CTCTATCACCCA CA 3 B c c

86 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTGGCT GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2862 1 2600 XP_209953.1 3 1535 CTCTGTTGCCCA C 3 B b b

06 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCACA GTGACGT AGGTCGGACCCGTT
A

GAM189 246 LOC2862 1 19893 XP_209941.1 3 913 CTCTGTCACCCA C CA 3 B c c
07 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGCCACA GTGACGTGAGGTC GACCC
A AC

GAM189 246 LOC2862 3 2849 XP_212230.1 3 1658 CTCTGTCACCCA CA 3 B c b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC2862 3 4372 XP_212230.1 3 1457 CTCTGTCGCCCA C A 3 B c b
08 GGCTGGAGTTCA CATTG ACTCCAGCCTGGGC
GTGGCGCG GTGAC TGAGGTCGGACCCG
T C

GAM189 246 LOC2862 3 9724 XP_212230.1 3 2282 CTCTGTAGCCCA A 3 B b b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGTGGCA GTGACGTGAGGTCGGACCCG
A

GAM189 246 LOC2862 1 19240 XP_212228.1 5 554 CTCTGTCAACCA T --- 3 B b b
15 GGCTGGAGTGCA CA TGCACTCCAGCCTGG GCA
CTGGCGCA GT ACGTGAGGTCGGACC TGT
C AAC

GAM189 246 LOC2862 1 7774 XP_212233.1 5 65 TGCCCCCTGCCA CA TC G 3 B c
c
21 GGCTGAGGGACA CATTG C CAGCCTGG CA
GTGACACA GTGAC G GTCGGACC GT
AG GA -

GAM189 246 LOC2862 1 6118 XP_209956.1 3 768 TGGCCATGCCCA TTGC T - 3 B c
c
23 GGGCTGGTGTTG CA AC CCAGCC TGGGCA
GTTGAGGA GT TG GGTCGG ACCCGT
TGGT T G

GAM189 246 LOC2862 1 6868 XP_212244.1 5 238 CTCTGTCGCTCA A A 3 B c c
45 GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGTGCA GTGGCG GAGGTCGGACTCG
A C

GAM189 246 LOC2863 1 15975 XP_212278.1 3 413 TGTTGTTGCCCA 3 B b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2863 1 522 XP_208408.1 5 131 TCCCCACTGGCC GC C G 3 B c c

47 AGCTGGAGTAGA CATT ACTCCAGC TGG CA
TGAAGTTC GTAG TGAGGTCG ACC GT
A- - G

GAM189 246 LOC2863 1 15730 XP_212286.1 5 688 GCTCTGTCACCA A -- 3 B c c
54 GGCTGGAGGGCA CATTGC CTCCAGCCTGG GCA
GTGGCGCC GTGACG GAGGTCGGACC TGT
G AC

GAM189 246 LOC2863 1 7385 XP_212290.1 5 1101 CTCTGTCACCCA CA 3 B c c
56 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC2863 1 14974 XP_212285.1 5 14 CAATGTTGCCCA 3 B b b
57 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC2863 1 3785 XP_212291.1 3 157 TTCTGGTGTCCA TGC- C 3 B c c

71 GGCTGAAGTCCT CAT ACT CAGCCTGGGCA
CGTGTGAC GTG TGA GTCGGACCTGT
CTCC A
GAM189 246 LOC2863 1 2722 XP_212308.1 5 5808 CCCTGTTGCCCA CC 3 B b b
95 GGCTACAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCATG GTAACGTGA TCGGACCCGTT
CA
GAM189 246 LOC2864 1 1038 XP_212310.1 5 501 TCTTGTTGCCCA A C 3 B b b
01 GGCTAGAGGGCA CATTGC CTC AGCCTGGGCAA
ATGGTGCA GTAACG GAG TCGGACCCGTT
G A
GAM189 246 LOC2864 1 2754 XP_212319.1 3 55 GTGCTGTTTCCT T -- 3 B c c
41 GGCTGGAGTGCA CATTGCACTCCAGCC GG GCA
GTGGCATG GTGACGTGAGGTCGG CC TGT
T TT
GAM189 246 LOC2864 1 9580 XP_210063.1 3 986 TGTTGTTGCCCA 3 B b b
67 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC2865 1 3183 XP_212340.1 3 892 CTTTGTCGCCCA A 3 B b b
53 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC2865 1 9264 XP_210106.1 3 99 CTCTGTAGACCA A --- 3 B c c
58 GGCTGGAGCGCA CATTGC CTCCAGCCTGG GCA
GTGGCAGG GTGACG GAGGTCGGACC TGT
C AGA
GAM189 246 LOC2865 1 9264 XP_210108.1 3 99 CTCTGTAGACCA A --- 3 B c c
64 GGCTGGAGCGCA CATTGC CTCCAGCCTGG GCA
GTGGCAGG GTGACG GAGGTCGGACC TGT
C AGA
GAM189 246 LOC3385 1 13760 XP_294654.1 3 1173 GCTCCATCACCA GCA 3 B c
c
62 GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCG GTGACGTGAGGTCGGACC
ACT
GAM189 246 LOC3385 1 12867 XP_294653.1 3 1934 TTTTGTTGCCCA C 3 B b b
65 GGCTGGAGTTCA CATTG ACTCCAGCCTGGGCAA
GTGGCGTG GTGAC TGAGGTCGGACCCGTT
T

GAM189 246 LOC3385 1 14074 XP_290473.1 3 981 CTATATTGCCCA CC C 3 B b b
75 AGCTACAGTGCA CATTGCACT AGC TGGGCAA
ATGATTAA GTAACGTGA TCG ACCCGTT
CA A
GAM189 246 LOC3385 1 4528 XP_290472.1 3 1085 CCCTGTCACCCA C CA 3 B c c
79 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
ATGGCACG GTAACGT AGGTCGGACCC
A AC
GAM189 246 LOC3385 1 7523 XP_294658.1 5 203 CACTTTGTTTCA T-- T-- - 3 B c c
85 GGCTGGTCTGTG CAT GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM189 246 LOC3386 1 6626 XP_290494.1 3 2436 TCTTGTTGCCCA 3 B b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGAGCG GTAACGTGAGGTCGGACCCGTT
GAM189 246 LOC3387 1 12803 XP_211595.2 5 683 TCTGTTGTCCAA C----- - 3 B c c
09 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM189 246 LOC3387 1 6518 XP_294688.1 3 517 ACTCCAGGCTCA TG A- A 3 B c c
31 GGCTGGAGCCGT CAT C CTCCAGCCTGGGC
GATGGCAC GTA G GAGGTCGGACTCG
GT CC G
GAM189 246 LOC3387 2 14732 XP_294690.1 3 117 TTCTGATGCCCA 3 B b b
39 GGTTGGGGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACA GTGACGTGGGGTTGGACCCGT
GAM189 246 LOC3387 2 15044 XP_294690.1 3 528 CTCTGTTGCCCA 3 B b b
39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT
GAM189 246 LOC3387 1 16493 XP_290570.1 3 878 GTCTGTCACCCA CA 3 B c c
73 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC3388 1 11507 XP_290216.1 3 337 TTTTATTGCCCA TT CCA 3 B c c
19 GGCAGTGCTCTG CA GCACT GCCTGGGCAA
GGCAGGAA GT CGTGA CGGACCCGTT
CT ---
GAM189 246 LOC3388 1 12341 XP_294740.1 5 562 CTCTGTCACCAA T - -- 3 B c c
99 GGCTGGAGTGCA CA TGCACTCCAGCCT GG GCA
TTGGTGCA GT ACGTGAGGTCGGA CC TGT
T A AC
GAM189 246 LOC3389 2 4298 XP_294742.1 3 438 GCTCTGTCGCCA -- 3 B b b
23 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT

GC

GAM189 246 LOC3389 2 8559 XP_294742.1 3 2044 TTCTGTCACTCA CA 3 B c b
23 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACTC
AC

GAM189 246 LOC3389 1 3348 XP_294757.1 3 1068 ACTGAAGTCCCA - - - A 3 B c c
63 GGCTGGGGGTGT CATTG CACTCC AGCCTGGG C
CAATGGAC GTAAC GTGGGG TCGGACCC G
T G T A

GAM189 246 LOC3389 1 12479 XP_290663.1 3 299 CGCTGTTGCCCA CC 3 B b b
91 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC

GAM189 246 LOC3389 1 12479 XP_290659.1 3 299 CGCTGTTGCCCA CC 3 B b b
99 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC

GAM189 246 LOC3390 1 17484 XP_294802.2 3 894 TCTTATCGCCCA A 3 B b b
77 GGCTGGGGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCA GTAACGTGGGGTCGGACCCG
C

GAM189 246 LOC3390 1 9543 XP_290692.1 3 851 CTCTGTCACCCA CA 3 B c c
78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC3390 1 1843 XP_290697.2 5 868 AAAAGAATATTG T G CA 3 B c c
83 AGGCTGGGTGCA CATTGCAC CCAGCCT GG
ATGCATCA GTAACGTG GGTCGGA TT
- G AT

GAM189 246 LOC3391 1 14266 XP_290711.1 5 144 TTTGGCTGCCCA TT ACTCC 3 B c
c
08 GGCTCGCCTTGA CA GC AGCCTGGGCA
CTCCAAAT GT CG TCGGACCCGT
TC C----

GAM189 246 LOC3391 1 15614 XP_294825.1 5 449 GCTCTGTTGCCA G 3 B b b
46 GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGTGCG GTGACGTGAGGTCGGACC GTT
-

GAM189 246 LOC3391 1 16261 XP_290742.1 3 674 CTCTGTCACCCA C CA 3 B c c
78 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
ATGGCGTG GTAAC TGAGGTCGGACCC
A AC

GAM189 246 LOC3392 1 4056 XP_290756.1 3 357 CTCTGTGGCCCA C A 3 B c c
01 GGCTGAAGTGCA CATTGCACT CAGCCTGGGC
GTGGTGTG GTGACGTGA GTCGGACCCG
A G

GAM189 246 LOC3392 1 19537 XP_290762.2 5 411 CTCTGTTGCCCA --- 3 B b b
16 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA

GAM189 246 LOC3392 1 19597 XP_294879.1 3 545 TGGAAGCCTTCA TC -- A 3 B c c
48 GGTTGCTGTGCA CATTGCAC CAGCCTG GGC
ATGGAATA GTAACGTG GTTGGAC CCG
TC TT A
GAM189 246 LOC3392 1 19597 XP_294883.1 3 545 TGGAAGCCTTCA TC -- A 3 B c c
50 GGTTGCTGTGCA CATTGCAC CAGCCTG GGC
ATGGAATA GTAACGTG GTTGGAC CCG
TC TT A
GAM189 246 LOC3392 1 19537 XP_294900.2 5 411 CTCTGTTGCCCA --- 3 B b b
82 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA
GAM189 246 LOC3392 1 11314 XP_294899.2 5 1180 CTCTGTTGCCCA --- 3 B b b
83 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAATGCC GTAACG TGAGGTTGGACCCGTT
ACA
GAM189 246 LOC3393 1 9544 XP_290838.1 3 2392 TCTTGTTGCCCA C 3 B b b
24 GGCTGCAGTGCA CATTGCACT CAGCCTGGGCAA
ATGGCACA GTAACGTGA GTCGGACCCGTT
C
GAM189 246 LOC3393 2 16940 XP_290830.1 3 372 CTCTGTTGCCCA 3 B b b
25 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC3393 2 17114 XP_290830.1 3 143 AGCCTTTCTCCA A CA 3 B c b
25 GGTGGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCATG GTGACGTGAGG TGGACCT
G CT
GAM189 246 LOC3394 1 2027 XP_294944.1 5 627 CTCTGTTGCCCA CA----- 3 B c c
17 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GGGGCGTA GACGTGAGGTCGGACCCGTT
ATGCGGG
GAM189 246 LOC3394 1 10679 XP_290902.1 3 308 TCTTGTCGCCCA A 3 B b b
48 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCA GTAACGTGAGGTCGGACCCG
C
GAM189 246 LOC3394 1 5488 XP_290911.1 3 1340 CTCTGTCGCCCA A 3 B b b
58 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACT GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC3394 1 13513 XP_290907.2 3 838 CTCTGTCGCCTA A 3 B b b
59 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGATCCG
C
GAM189 246 LOC3394 3 695 XP_290919.1 3 1557 CCATGTTGGCCA GCACT G 3 B c
b
92 GGCTGGTCTCGA CATT CCAGCCTGG CAA
ATGCCTGG GTAA GGTCGGACC GTT
GCTCT G
GAM189 246 LOC3394 3 7386 XP_290919.1 3 1081 CTCTGTCGCGCA G G A 3 B c b

92 GGGTGGAGTGCG CATTGCACTCCA CCTG GC
GTGGCACG GTGGCGTGAGGT GGAC CG
G G C

GAM189 246 LOC3394 3 8590 XP_290919.1 3 1387 TCTTGTTGCCCA T 3 B b b
92 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
TTGGCGTG GT GCGTGAGGTCGGACCCGTT
T

GAM189 246 LOC3395 2 12075 XP_295005.1 3 1040 CTCTGTCACCCA CA 3 B c c
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC3395 2 14733 XP_295005.1 3 1187 CTACGTGACCCA C----- - 3 B c c
77 GGCTGGAGTGTA ATTGCACTCCAGCCTGGG CA
GTAGCTAT TGATGTGAGGTCGGACCC GT
TATCGA A

GAM189 246 LOC3396 1 15295 XP_295014.1 3 1461 CTCTGTCACTTA CA 3 B c c
00 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGATTC
AC

GAM189 246 LOC3396 1 17076 XP_290981.1 3 1596 GCCCTGTTGCCA C G 3 B b b

59 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -

GAM189 246 LOC3396 1 1982 XP_295032.1 5 166 CTCTACCACCCA CA 3 B c c
85 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC3396 1 15954 XP_295035.1 5 835 AGACAGGGTCTT CCT A 3 B c
c

94 GACTGGAGTGCA CATTGCACTCCAG GGGC
GTGGTGCG GTGACGTGAGGTC TCTG
AGT G

GAM189 246 LOC3397 1 11528 XP_295038.1 3 1272 CTCTGTCACCCA CA 3 B c c
11 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC3397 1 16942 XP_295041.1 5 880 CTCTGTCGCCCA A 3 B b b
20 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC3398 1 13337 XP_295072.1 3 1492 GTCTGTCACCCA CA 3 B c c
03 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC3398 1 6146 XP_295071.1 3 813 CTTACCATTTTG TCCA G 3 B c c

08 CTAGGGTGTGCA CATTGCAC GCCT GGCAA
ATGCCCAC GTAACGTG TGGG TCGTT
---- A

GAM189 246 LOC3398 2 1744 XP_291020.1 5 1637 CTCTGTCACCCA CA 3 B c c
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 LOC3398 2 17750 XP_291020.1 5 1174 CACTGTCACCTA CA 3 B c c
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTAAA GTGACGTGAGGTCGGATCC
AC
GAM189 246 LOC3398 2 7633 XP_291031.1 5 575 CTCTGTTGCCCA C 3 B b b
33 GCCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATT GTGACGTGAGGTC GACCCGTT
C
GAM189 246 LOC3398 2 10421 XP_291031.1 3 561 CTGTGATGCCGA G G 3 B b b
33 GGGTGGAGTGCA CATTGCACTCCA CCT GGCA
GTGGCACA GTGACGTGAGGT GGA CCGT
G G
GAM189 246 LOC3398 1 14645 NP_835467.1 5 48 TTCTGTCGCCCA A 3 B b b
34 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGACGCG GTGATGTGAGGTCGGACCCG
C
GAM189 246 LOC3398 1 14645 XP_291033.1 5 48 TTCTGTCGCCCA A 3 B b b
34 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGACGCG GTGATGTGAGGTCGGACCCG
C
GAM189 246 LOC3398 3 4026 XP_291050.1 3 183 CTGTGTTGCCCA C----- 3 B c b
72 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCTAT TGACGTGAGGTCGGACCCGTT
TATCGA
GAM189 246 LOC3398 3 5858 XP_291050.1 5 768 CTCAGTCGCTCA A 3 B b b
72 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACTCG
C
GAM189 246 LOC3398 3 9299 XP_291050.1 5 471 GTCTGTTGCCCA 3 B b b
72 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGGG GTGACGTGAGGTTGGACCCGTT

GAM189 246 LOC3398 1 1081 XP_295095.1 5 133 CTCTGTTGCCCA C 3 B b b
94 GGTTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCTTG GTGACGTGAG TTGGACCCGTT
A
GAM189 246 LOC3399 1 3425 XP_291065.1 3 1461 CTCTGTTGCCCA CA----- 3 B c c
07 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GGGGCACG GACGTGAGGTCGGACCCGTT
GCACGGG
GAM189 246 LOC3399 1 10709 XP_291069.1 5 122 CTCTGTTGCCCA 3 B b b
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC3399 1 714 XP_295099.1 5 595 CAGAATCGCCCA - - T- A- A 3 B c c
14 GGCCAGGCTGTG CAT TGC AC CC GCCTGGGC

GCAGATGA GTA ACG TG GG CGGACCCG
G G TC AC C

GAM189 246 LOC3399 1 16942 XP_291095.1 3 714 CTCTGTCGCCCA A 3 B b b
70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC3400 1 12244 XP_295137.1 3 37 TCTTGTTGCCCA 3 B b b
37 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGCGCGA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC3401 1 12803 XP_291150.1 5 683 TCTGTTGTCCAA C----- - 3 B c c
25 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM189 246 LOC3401 1 11753 XP_291153.1 3 2141 CTCTGTCACTCA CA 3 B c c
38 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGACGTG GTAACGTGAGGTCGGACTC
AC

GAM189 246 LOC3401 1 10096 XP_291158.1 3 1441 GCTCTGTCACGA - - 3 B b b
56 GGCTGGAGTGCA CATTGCACTCCAGCCT G GGCA
GTGGCCCC GTGACGTGAGGTCGGA C CTGT
G A

GAM189 246 LOC3402 1 12803 XP_291203.1 5 683 TCTGTTGTCCAA C----- - 3 B c c
27 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM189 246 LOC3402 1 2179 XP_295188.1 5 340 TCCAGCGGCCCA CA A A 3 B c
c
38 GGCGGGGGACAG CATTG CTCC GCCTGGGC
TGCCGTTC GTGAC GGGG CGGACCCG
AG - G

GAM189 246 LOC3402 1 18147 XP_295190.1 5 998 CTGTGTGGCCTA A 3 B b b
59 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCA GTAACGTGAGGTTGGATCCG
G

GAM189 246 LOC3402 1 15740 XP_291214.1 5 1350 TCTCTTGTCCAA C----- - 3 B c c
90 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM189 246 LOC3403 1 18868 XP_291269.1 3 1383 TCTTGTTGCCCA 3 B b b
90 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC3404 1 1309 XP_291274.1 5 647 TTTTGTTGCCCA 3 B b b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGATGCA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC3404 1 1744 XP_295240.1 3 174 CTCTGTCACCCA CA 3 B c c
14 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC

AC

GAM189 246 LOC3404 1 1744 XP_295252.1 5 244 CTCTGTCACCCA CA 3 B c c
50 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC

AC

GAM189 246 LOC3405 1 13053 XP_295268.1 5 225 TCTCTGTAGCCA C----- A -- 3 B c c
28 GGCTGGAGGGCA ATTGC CTCCAGCCTGG GCA
ATTGTACA TAACG GAGGTCGGACC TGT
ACATGT G GA

GAM189 246 LOC3429 1 13464 XP_292790.2 3 811 CTCTGTCACCCA CA 3 B c c
26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC

AC

GAM189 246 LOC3434 1 439 XP_295563.1 5 222 TGTTCATGCCCA --- CTC -- 3 B c c
35 GGATCTGCTGCG CAT TGCA CAG CCTGGGCA
CTCATGGA GTA GCGT GTC GGACCCGT
CTC C-- TA

GAM189 246 LOC3452 1 523 NP_835236.1 3 952 CTCTTTCGCCCA A 3 B b b
75 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTATG GTGACGTGAGGTCGGACCCG

C

GAM189 246 LOC3458 1 12611 XP_293993.2 5 33 AGGAGATGTCCA TG A C 3 B c c

78 GGCTGAAGGTGG CAT C CT CAGCCTGGGCA
TGATTTGA GTG G GA GTCGGACCTGT
GT - A

GAM189 246 LOC3466 1 17927 XP_294357.2 3 372 GCTCTGTCTCCA C -- 3 B c c
53 GGCTGGAGTACA CATTG ACTCCAGCCTGG GCA
GTGGTGCG GTGAC TGAGGTCGGACC TGT
A TC

GAM189 246 LOC3476 1 9837 XP_300226.1 3 110 CATTGCCCTTCG TT - --- 3 B c c
48 GGCTGGAGATGC CA GCA CTCCAGCCT GGGCAA
TTTGCCGG GT CGT GAGGTCGGG CCCGTT
TT A CTT

GAM189 246 LOC3477 1 11420 XP_300530.1 5 15 AACTATCACCTG TG CA 3 B c c
64 GGCTGGAGTGCG CATTGCACTCCAGCC GG
ATGGCATG GTAGCGTGAGGTCGG CC
GT AC

GAM189 246 LOC3479 1 9505 XP_302624.1 5 368 TCTTGTTGTCCA C 3 B b b
05 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCATG GTAACGTGAG TCGGACCTGTT
A

GAM189 246 LOC3479 1 17689 XP_300565.1 5 189 TTTTATTGCCCA 3 B b b
18 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGATGTGAGGTCGGACCCGTT

GAM189 246 LOC3480 2 13716 XP_302653.1 3 1556 CCTTCTTCCCCA G - CA 3 B c b

75 GGCTGGGAGTGG CATT CACTCC AGCCTGGG
GTGAGACG GTGG GTGAGG TCGGACCC

```
                                        -    G      CT
GAM189  246  LOC3480 2  14381  XP_302653.1  3  3385  GCTCTGTCACCA          --       3  B  b  b
        75                      GGCTGGAGTGCG CATTGCACTCCAGCCTGG  GCA
                               GTGGCATA    GTGGCGTGAGGTCGGACC  TGT
                                             AC
GAM189  246  LOC3480 2  13332  XP_300615.1  3  234   TCCCGTCCAACA    C      ---  A     3  B  c  c
        94                      GGCTGGAGTACA CATTG ACTCCAGCCT   GGGC
                               ATGGCGAG    GTAAC TGAGGTCGGA   CCTG
                                           A       CAA   C
GAM189  246  LOC3480 2  16473  XP_300615.1  5  57    GAGACCGACGGC  T       CTG  A       3  B  c
c
        94                      CGCTGGAGTGCA CA TGCACTCCAGC   GGC
                               CTGGCATG    GT ACGTGAGGTCG   CCG
                                           C        ---  G
GAM189  246  LOC3481 1  12479  XP_300623.1  3  299   CGCTGTTGCCCA       CC           3  B  b  b
        13                      GGCTCTAGTGCA CATTGCACT  AGCCTGGGCAA
                               ATGGCACG    GTAACGTGA  TCGGACCCGTT
                                             TC
GAM189  246  LOC3481 1  13705  XP_300626.1  5  554   TCTTGTTGCCCA       CA           3  B  b  b
        15                      GGCCCGAGTGCA CATTGCACTC  GCCTGGGCAA
                               GTGGTGCG    GTGACGTGAG  CGGACCCGTT
                                             CC
GAM189  246  LOC3481 1  12479  XP_300635.1  3  299   CGCTGTTGCCCA       CC           3  B  b  b
        37                      GGCTCTAGTGCA CATTGCACT  AGCCTGGGCAA
                               ATGGCACG    GTAACGTGA  TCGGACCCGTT
                                             TC
GAM189  246  LOC3481 1  12479  XP_300636.1  3  299   CGCTGTTGCCCA       CC           3  B  b  b
        42                      GGCTCTAGTGCA CATTGCACT  AGCCTGGGCAA
                               ATGGCACG    GTAACGTGA  TCGGACCCGTT
                                             TC
GAM189  246  LOC3482 1  15852  XP_300670.1  3  1531  CTCTGTTGCCCA     C            3  B  b  b
        35                      GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
                               GTGGTACG    GTGACGT AGGTCGGACCCGTT
                                             A
GAM189  246  LOC3482 1  7306   XP_300683.1  5  58    CTCTGTTGCCTG          TG         3  B  b  b
        62                      GGCTGGAGTGCA CATTGCACTCCAGCC  GGCAA
                               GTGCCACG    GTGACGTGAGGTCGG  CCGTT
                                             GT
GAM189  246  LOC3483 1  16669  XP_302716.1  5  317   CTTTGTTGCCCA                  3  B  b  b
        14                      GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
                               GTGGCGTG    GTGGCGTGAGGTCGGACCCGTT

GAM189  246  LOC3483 1  19778  XP_300696.1  3  1763  AGTCTGTCACCA          --       3  B  b  b
        26                      GGCTGGAGTGCA CATTGCACTCCAGCCTGG  GCA
                               GTGGCATG    GTGACGTGAGGTCGGACC  TGT
                                             AC
GAM189  246  LOC3483 1  8820   XP_030209.2  3  79    GCTCGTCACCCA C-----          CA    3  B  c  c
        27                      GGCTGGAGTGCA     ATTGCACTCCAGCCTGGG
                               ATTGTGCA        TAACGTGAGGTCGGACCC
                                       ACGTGT            AC
```

GAM189 246 LOC3483 2 872 XP_302741.1 3 1206 CGCCGTTGCCCA 3 B b b
93 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM189 246 LOC3483 2 11192 XP_302741.1 3 744 CTAGGAGGCCCA TG A 3 B c b

93 GGCTGGAGTGAG CAT CACTCCAGCCTGGGC
GTGGCACG GTG GTGAGGTCGGACCCG
GA G
GAM189 246 LOC3483 3 1569 XP_300729.1 5 150 CTCTGTCACCCA C CA 3 B c b
96 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGCAGTG GTGACGT AGGTCGGACCC
A AC
GAM189 246 LOC3483 3 9545 XP_300729.1 3 184 CTCTGTTGCCCA 3 B b b
96 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC3483 3 10270 XP_300729.1 3 1031 TCTTGTTATCCA CA 3 B c b
96 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCG GTAACGTGGGGTCGGACCT
AT
GAM189 246 LOC3484 3 695 XP_300730.1 3 798 CCATGTTGGCCA GCACT G 3 B c
b
02 GGCTGGTCTCGA CATT CCAGCCTGG CAA
ATGCCTGG GTAA GGTCGGACC GTT
GCTCT G
GAM189 246 LOC3484 3 7386 XP_300730.1 3 322 CTCTGTCGCGCA G G A 3 B c b
02 GGGTGGAGTGCG CATTGCACTCCA CCTG GC
GTGGCACG GTGGCGTGAGGT GGAC CG
G G C
GAM189 246 LOC3484 3 8590 XP_300730.1 3 628 TCTTGTTGCCCA T 3 B b b
02 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
TTGGCGTG GT GCGTGAGGTCGGACCCGTT
T
GAM189 246 LOC3484 1 19778 XP_300738.1 3 1763 AGTCTGTCACCA -- 3 B b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 LOC3484 1 15049 XP_302760.1 3 2633 CTCTGTCGCCCA A 3 B b b
55 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC3484 2 4143 XP_300743.1 3 130 ACTCTGTCACCA -- 3 B b b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 LOC3484 2 13465 XP_300743.1 5 247 CTCTGTCACCCA C CA 3 B c b
60 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACC GTAACGTGAG TCGGACCC
A AC

GAM189 246 LOC3484 1 17206 XP_209299.2 3 230 CTCTCTTACCCA C CA 3 B c c
74 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGACATG GTGACGTGAGGTCG ACCC
A AT
GAM189 246 LOC3484 1 6119 XP_302789.1 5 27 CTCTGTCACCCA CA 3 B b b
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCC GTAACGTGAGGTCGGACCC
AC
GAM189 246 LOC3485 1 19361 XP_300762.1 3 1203 CTTGCTCGCCCA G A 3 B c c
03 GGGTGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGTGTG GTGACGTGAGGT GGACCCG
G C
GAM189 246 LOC3485 1 12803 XP_302806.1 5 745 TCTGTTGTCCAA C----- - 3 B c c
08 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM189 246 LOC3485 1 5488 XP_300778.1 3 1340 CTCTGTCGCCCA A 3 B b b
25 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACT GTGACGTGAGGTCGGACCCG
C
GAM189 246 LOC3485 2 872 XP_302818.1 3 1206 CGCCGTTGCCCA 3 B b b
32 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM189 246 LOC3485 2 11192 XP_302818.1 3 744 CTAGGAGGCCCA TG A 3 B c b

32 GGCTGGAGTGAG CAT CACTCCAGCCTGGGC
GTGGCACG GTG GTGAGGTCGGACCCG
GA G
GAM189 246 LOC3485 1 8544 XP_302833.1 3 313 TGGAGTCTCGCT CCT A 3 B c c

83 CTCTGGAGTGCA CATTGCACTCCAG GGGC
ATGGCGCA GTAACGTGAGGTC CTCG
T-- C
GAM189 246 LOC3485 1 16785 XP_302834.1 5 1212 GATGGAGGCAGT G TGG A 3 B c
c
94 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM189 246 LOC3485 1 16785 XP_302837.1 3 1593 GATGGAGGCAGT G TGG A 3 B c
c
95 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM189 246 LOC3486 1 16785 XP_302844.1 5 289 GATGGAGGCAGT G TGG A 3 B c
c
03 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM189 246 LOC3486 1 16785 XP_300793.1 3 1421 GATGGAGGCAGT G TGG A 3 B c
c

05 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G

GAM189 246 LOC3487 1 7387 XP_300808.1 5 298 CTCTGTCACCCA C CA 3 B c c
02 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC

GAM189 246 LOC3487 1 810 XP_300843.1 3 447 GCTTGTTGCCCA 3 B b b
90 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 LOC3487 1 7741 XP_302888.1 3 342 TGCTCTCGCCCA A 3 B b b
97 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGGTGG GTGACGTGAGGTCGGACCCG
C

GAM189 246 LOC3487 1 19402 XP_300845.1 5 24 TCTTGTTGCCCA C 3 B b b
98 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
ATGGCGCG GTAACGT AGGTCGGACCCGTT
A

GAM189 246 LOC3488 1 15126 XP_300853.1 5 279 CCCTGTTGCCCA --- 3 B b b
25 GGCTGGAGTATA CATTGC ACTCCAGCCTGGGCAA
GTAGTGCA GTGATG TGAGGTCGGACCCGTT
ATA

GAM189 246 LOC3488 1 12803 XP_300861.1 5 475 TCTGTTGTCCAA C----- - 3 B c c
42 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM189 246 LOC3489 1 8605 XP_302929.1 3 301 TTCTGTCGCCCT G T A 3 B c c
47 GGCTGGAGTGGA CATT CACTCCAGCC GGGC
ATGCCGTG GTAA GTGAGGTCGG CCCG
G T C

GAM189 246 LOC3489 1 1900 XP_300434.1 3 607 AGAGTCTTGCTC CT 3 B c c
95 TGCTGGAGTGCG CATTGCACTCCAGC GGGCAA
GTGGTGCA GTGGCGTGAGGTCG CTCGTT
T-

GAM189 246 LOC3490 2 1746 XP_300250.1 5 533 CTCTGTCACCCA C CA 3 B c c
24 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCATG GTGACGTGAGGTC GACCC
A AC

GAM189 246 LOC3490 2 4617 XP_300250.1 3 144 TCTTGTCACCCA CA 3 B c c
24 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 LOC3490 1 16022 XP_300932.1 3 177 CTCTGTCACCCA C CA 3 B c c
75 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGTACA GTGACGTGA GTCGGACCC
A AC

GAM189 246 LOC3490 1 6188 XP_300937.1 3 287 TGGAGAAATTCA T CA 3 B c c
96 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT

```
                                                  -        AA
GAM189  246  LOC3491 1  12803  XP_302960.1  5  184   TCTGTTGTCCAA C-----          -       3  B  c  c
        14                                    GGCTGGAGTGTA      ATTGCACTCCAGCCT GGGCAA
                                             GTAGTGCT          TGATGTGAGGTCGGA CCTGTT
                                                     TCGTGA             A
GAM189  246  LOC3491 5  958   XP_300969.1  3  1370  CTCTATTACTCA    GC          CA       3  B  c  b
        70                                    GGCTGGAGTAAA CATT  ACTCCAGCCTGGG
                                             ATGGTGCC    GTAA  TGAGGTCGGACTC
                                                       AA           AT
GAM189  246  LOC3491 5  3349  XP_300969.1  3  832   CCCTATTGCCCA                        3  B  b  b
        70                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                             ATGGCGTG    GTAACGTGAGGTCGGACCCGTT

GAM189  246  LOC3491 5  9545  XP_300969.1  3  469   CTCTGTTGCCCA                        3  B  b  b
        70                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                             GTGGTGCA    GTGACGTGAGGTCGGACCCGTT

GAM189  246  LOC3491 5  11508  XP_300969.1  5  1053  CTCTGCCAGCCA  T       C   ---       3  B  c  b

        70                                    GACTGGAGTGCA CA TGCACTCCAG CTGG   GCA
                                             TTGGCGAG    GT ACGTGAGGTC GACC   CGT
                                                       T        A    GAC
GAM189  246  LOC3491 5  18074  XP_300969.1  5  147   TTCTGTGGCCCA                A       3  B  b  b
        70                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                             GTGGCTGT    GTGACGTGAGGTCGGACCCG
                                                                G
GAM189  246  LOC3492 2  2323  XP_300251.1  5  413   GGGGCATGCCCA CA---  -    CA          3  B  c
c
        51                                    GGCAGAGTGACA     TTG CACTC  GCCTGGGCA
                                             GGAGAG          GAC GTGAG  CGGACCCGT
                                                     GAGAG  A    A-
GAM189  246  LOC3492 2  4454  XP_300251.1  3  444   CACTATCACCCA     A  C      CA       3  B  c  c
        51                                    GGCTAGAGGGCA CATTGC CTC AGCCTGGG
                                             GTGGCACA    GTGACG GAG TCGGACCC
                                                       G  A       AC
GAM189  246  LOC3493 1  10639  XP_088528.1  5  447   TCTGGTTGCCCA    C                   3  B  b  b
        60                                    GGCTGGGGTACA CATTG ACTCCAGCCTGGGCAA
                                             GTGGTGGA    GTGAC TGGGGTCGGACCCGTT
                                                       A
GAM189  246  LOC3494 1  13466  XP_303044.1  5  14    CTCCGTTGCCCA    C                   3  B  b  b
        08                                    GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
                                             ATGGTGCG    GTAAC TGAGGTCGGACCCGTT
                                                       A
GAM189  246  LOC3494 1  4112  XP_300513.1  3  1060  TTTTGCAGCCCA                A       3  B  b  b
        40                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                             GTGGCACC    GTGACGTGAGGTCGGACCCG
                                                                A
GAM189  246  LOC3501 1  18715  XP_303810.1  5  16    TCCCTCTGCCCA  T A   G             3  B  c  c
        06                                    GGTGGGGGCCGT CAT GC CTCCA CCTGGGCA
                                             GGCTGGAA    GTG CG GGGGT GGACCCGT
```

C - -

GAM189 246 LOC3509 1 19860 XP_304556.1 5 119 AAGGAATGCCCA - A CAG 3 B c c

14 GGAGAGAGCACA CAT TGC CTC CCTGGGCA

TGGTTG GTA ACG GAG GGACCCGT

C A A--

GAM189 246 LOC5105 1 5678 NP_056995.1 3 405 GTGAACTGCTTA T A 3 B c c

8 GGTAGGAGTGCA CA TGCACTCC GCCTGGGCA

CTGCAGTT GT ACGTGAGG TGGATTCGT

C A

GAM189 246 LOC5119 2 3111 NP_057415.1 5 98 TCCTGTTACCCA CA CA 3 B c b

3 GGCTGGAGGACA CATTG CTCCAGCCTGGG

GTGATGTG GTGAC GAGGTCGGACCC

AG AT

GAM189 246 LOC5119 2 14721 NP_057415.1 3 733 TTCTGTTGTCCA G 3 B b b

3 GGATGGAGTGCA CATTGCACTCCA CCTGGGCAA

GTGGTTGA GTGACGTGAGGT GGACCTGTT

A

GAM189 246 LOC5125 1 14855 NP_057580.2 5 156 CTCTGTTACCCA CA 3 B c c

7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGTGTG GTGACGTGAGGTCGGACCC

AT

GAM189 246 LOC5133 1 8243 NP_057728.1 5 337 CTCTGTTGCCCA C 3 B b b

4 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA

ATGGCACA GTAACGTGAG TCGGACCCGTT

A

GAM189 246 LOC5133 1 18703 NP_057730.1 3 665 CTCTGTTACCCA CA 3 B b b

6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

ATGGAGTG GTAACGTGAGGTCGGACCC

AT

GAM189 246 LOC5595 1 17853 NP_061976.1 5 0 GTCACCCAGGCT CA 3 B c c

4 GGAGTGTAGTGG CATTGCACTCCAGCCTGGG

CGCAATCT GTGATGTGAGGTCGGACCC

AC

GAM189 246 LOC5690 1 5945 NP_064528.1 3 518 CTTTGTCACCCA C CA 3 B c c

2 GGCTAGAGTGCA CATTGCACTC AGCCTGGG

GTGGTGCA GTGACGTGAG TCGGACCC

A AC

GAM189 246 LOC5692 1 8643 NP_064555.1 3 1847 GTCTGGGGCTCA G T A 3 B c c

6 GGCTGGTGTGGG CATT CAC CCAGCCTGGGC

ATGCAGCC GTAG GTG GGTCGGACTCG

G T G

GAM189 246 LOC5710 1 16916 NP_065114.2 3 587 TCTTGTTGCCCA 3 B b b

7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC5714 1 11036 NP_065155.2 3 736 TCTTGTTGCCCA CA----- 3 B c c

6 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA

ACGGTGCA AACGTGAGGTCGGACCCGTT

ACGTGGC

GAM189 246 LOC8989 1 14184 NP_612350.1 5 445 CCATGTTTGCCA G CT- G 3 B c c

4 GGCTGGTCCTGA CATT CA CCAGCCTGG CAA

ATGCCTGA GTAA GT GGTCGGACC GTT

- CCT -

GAM189 246 LOC9040 1 7704 XP_031517.1 5 1646 TCTTGTTACCCA CA 3 B c c

8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCGCG GTGACGTGAGGTCGGACCC

AT

GAM189 246 LOC9048 2 6896 XP_032059.1 3 1341 CTCTGTCGCCCA A 3 B b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

GTGATGCA GTGACGTGAGGTCGGACCCG

C

GAM189 246 LOC9048 2 18698 XP_032059.1 3 1183 CTCTGTCACCCA C CA 3 B c b

5 GGCTAGAGTGCA CATTGCACTC AGCCTGGG

GTGGAGCG GTGACGTGAG TCGGACCC

A AC

GAM189 246 LOC9071 1 13994 XP_033704.1 3 121 AGTCACATCCCA G - CA 3 B c c

9 GGCTGGGGATGG CATT CA CTCCAGCCTGGG

ATGCTCTG GTAG GT GGGGTCGGACCC

- A TA

GAM189 246 LOC9099 1 15038 XP_035410.1 3 115 CTCTGTTGCCCA C 3 B b b

9 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA

GTGGCACG GTGAC TGAGGTCGGACCCGTT

A

GAM189 246 LOC9111 3 12591 XP_036218.1 3 758 GTCTTTCACCCA T CA 3 B c b

5 GGCTGGAGTGCT CAT GCACTCCAGCCTGGG

GTGGCACG GTG CGTGAGGTCGGACCC

T AC

GAM189 246 LOC9111 3 17831 XP_036218.1 3 2144 ACTTGTTGCCCA 3 B b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

ATGGTACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 LOC9111 3 19989 XP_036218.1 3 285 TCTTGTCACCCA CA 3 B b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

ATGGCACG GTAACGTGAGGTCGGACCC

AC

GAM189 246 LOC9117 1 16178 XP_036612.1 5 209 CTTTGTCGCCCG A A 3 B c c

0 GGCAGGAGTGCA CATTGCACTCC GCCTGGGC

GTGGCTCA GTGACGTGAGG CGGGCCCG

A C

GAM189 246 LOC9125 1 8577 XP_037135.1 5 2207 CTCTGTCACCCA C- CA 3 B c c

0 GGCTGGAGTTAT CATTG ACTCCAGCCTGGG

AGTGACGT GTGAT TGAGGTCGGACCC

AT AC

GAM189 246 LOC9126 1 18355 XP_037268.1 5 267 GCAGGATGCCCA C---- AC - - 3 B c c

6 GGGCTCGGAAGC ATTGC TCC AGCC TGGGCA
AGTAAGGA TGACG AGG TCGG ACCCGT
AGGAA A- C G
GAM189 246 LOC9137 1 9077 XP_038063.5 3 1526 TCTTGTTGCCCA G 3 B b b
3 GGCTGGAGTGAA CATT CACTCCAGCCTGGGCAA
GTGGCGTG GTGA GTGAGGTCGGACCCGTT
A
GAM189 246 LOC9154 1 17238 XP_039115.1 5 1290 GCCCTGTGGCTG TG G 3 B c
c
9 GGCTGGAGTGCA CATTGCACTCCAGCC G CA
ATGGCGCG GTAACGTGAGGTCGG C GT
GT G
GAM189 246 LOC9166 1 8303 NP_612381.1 3 517 CTCTGTCGGCCA C --- 3 B b b
1 GGCTGGAATGCA CATTGCA TCCAGCCTGG GCA
ATGGTGCC GTAACGT AGGTCGGACC TGT
A GGC
GAM189 246 LOC9166 1 8075 NP_612382.1 3 339 CTCTGTGGCCCA A 3 B b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
G
GAM189 246 LOC9189 1 14589 XP_041340.1 3 205 CTCTGCCGCCCA A A 3 B c c
3 GGCGGGAGTGCA CATTGCACTCC GCCTGGGC
GTGGCAGT GTGACGTGAGG CGGACCCG
G C
GAM189 246 LOC9214 1 4097 XP_043160.1 5 761 CCCTGCCGCCCA C A 3 B c c
8 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCACG GTGACGTGAG TCGGACCCG
A C
GAM189 246 LOC9259 1 19339 NP_775739.1 3 3527 CTCTGTTGCCCG C 3 B b b
7 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCATG GTAAC TGAGGTCGGGCCCGTT
A
GAM189 246 LOC9313 1 9953 XP_049396.1 5 1234 GCTCTGTCACCA A -- 3 B c c
2 GGCTGGAGGGCA CATTGC CTCCAGCCTGG GCA
GTGGTGCG GTGACG GAGGTCGGACC TGT
G AC
GAM189 246 LSS 1 6091 NP_002331.2 3 1071 GTCTCATGCCCA TT T G 3 B c c
GGTGGGTGCTCT CA GCAC CCA CCTGGGCA
GGGCTGGA GT CGTG GGT GGACCCGT
CT - -
GAM189 246 LTB4R 1 1022 NP_000743.1 5 303 CTCTGTCATTCA --- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGTGCG GTGACGTGAGGTCGGAC CTGT
TTA
GAM189 246 LTB4R2 1 15504 NP_062813.1 5 1345 CAGTTTTGCCCA --- TCCAGC 3 B c
c
GATGTGCTAGAA CATT GCAC CTGGGCAA
TGGGGCTG GTAA CGTG GACCCGTT
GAT TA----
GAM189 246 LY75 1 17724 NP_002340.1 3 573 CTCTGTTGCCCA C 3 B b b

GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCGTG GTAAC TGAGGTCGGACCCGTT
A

GAM189 246 LYZ 1 7382 NP_000230.1 3 331 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM189 246 LZTS1 1 4518 NP_066300.1 3 1445 CTCTGTCCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC

GAM189 246 MAC30 1 5069 XP_031536.2 3 228 CTCTGTTGCCCA ----- 3 B b b
GGCTGGAGTAAA CATTGC ACTCCAGCCTGGGCAA
GGGCAGTG GTGACG TGAGGTCGGACCCGTT
GGAAA

GAM189 246 MAIL 1 2338 NP_113607.1 3 872 CTCTGGCGCCCA C A 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGCATG GTGAC TGAGGTCGGACCCG
A C

GAM189 246 MAK 1 1989 NP_005897.1 3 644 CTCTTGTGTCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACT GTGACGTGAGGTCGGACCTGT

GAM189 246 MAPA 1 5231 NP_660299.1 3 806 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGCTGCG GTAACGTGAGGTCGGACCC
AC

GAM189 246 MAPK8IP 1 14298 NP_203750.1 3 1043 CCCTGTGCTCAG GCA- - 3 B c c
3 GGCTGGAGAGAG CATT CTCCAGCC TGGGCA
GGTGGCGG GTGG GAGGTCGG ACTCGT
GAGA G

GAM189 246 MCLC 1 7270 NP_055942.1 3 316 CTCTGTCACCCA TG CA 3 B c c
GGCTGGAGTGAG CAT CACTCCAGCCTGGG
GTGGTACA GTG GTGAGGTCGGACCC
GA AC

GAM189 246 MDM2 1 6671 NP_002383.1 3 355 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM189 246 MDM2 1 6671 NP_006869.1 3 355 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM189 246 MDM2 1 6671 NP_006870.1 3 355 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM189 246 MDM2 1 6671 NP_006871.1 3 355 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM189 246 MDM2 1 6671 NP_006872.1 3 355 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM189 246 MDM2 1 6671 NP_006873.1 3 299 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM189 246 MDM4 1 7078 NP_002384.1 3 548 TTCTGTCTCCCA C CA 3 B c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGAGTCA GTGACGTGA GTCGGACCC
A TC
GAM189 246 MEFV 2 5443 NP_000234.1 3 511 CTCTGTGGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
G
GAM189 246 MEFV 2 19829 NP_000234.1 3 823 TCTTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 MESDC2 1 6523 XP_051854.1 3 74 GCTCTTTGCCCA - G C-- 3 B c c
GCTCCTGGGGTG CA TT CACTCCAG CTGGGCAA
GGAGTGGT GT AG GTGGGGTC GACCCGTT
G G CTC
GAM189 246 MFTC 1 16545 NP_110407.2 3 548 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 MGAT2 1 9699 NP_079374.1 3 986 TCTTGTCGCTCA C A 3 B c c
GCCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGAGCTG GTGACGTGAGGTC GACTCG
C C
GAM189 246 MGC1077 1 5386 NP_085044.2 5 225 CTAGAGATGCCC G CC 3 B c c
2 ATCTGGAGTGAG CATT CACTCCAG TGGGCA
TGCAGGAC GTGA GTGAGGTC ACCCGT
- T-
GAM189 246 MGC1081 1 2199 NP_085045.2 3 89 CTCTGTCGCCCA C A 3 B b b
8 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
ATGGTGCG GTAAC TGAGGTCGGACCCG
A C
GAM189 246 MGC1110 1 17609 NP_115701.2 3 1315 CTGTGTTGCTCA 3 B b b
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACTCGTT
GAM189 246 MGC1226 1 12220 NP_116085.1 5 203 TGATGTTGCCCA C 3 B b b
2 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCACA GTGACGTGAG TCGGACCCGTT

A

GAM189 246 MGC1251 1 18251 NP_291026.1 3 0 CCCCAGGTTGGA CA 3 B c c
8 GTGCAGTGGCGT CATTGCACTCCAGCCTGGG
GTCTTGGG GTGACGTGAGGTTGGACCC
C-

GAM189 246 MGC1301 1 11562 NP_542387.1 3 458 CTCTGTTGCCCA CCA 3 B b b
7 GGCAGTAGTGCA CATTGCACT GCCTGGGCAA
GTGGCGCG GTGACGTGA CGGACCCGTT
TGA

GAM189 246 MGC1302 1 13564 NP_689501.1 3 433 GTCTGTTTCCCA CA 3 B c c
4 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGATACA GTGATGTGAGGTCGGACCC
TT

GAM189 246 MGC1313 2 6646 NP_219363.1 3 766 TCTTGTTGCCCA C----- 3 B b b
8 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCA TAACGTGAGGTCGGACCCGTT
ACGCGA

GAM189 246 MGC1313 2 9543 NP_219363.1 3 456 CTCTGTCACCCA CA 3 B c b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 MGC1317 1 20116 NP_116101.1 3 289 CACTTCTGCCCA G CA-- 3 B c c
0 GGCAGCAGGGTG CATT CACTC GCCTGGGCA
GGTGGGTA GTGG GTGGG CGGACCCGT
- ACGA

GAM189 246 MGC1320 1 9494 NP_113653.1 3 129 CTCTGTTGCCCA 3 B b b
4 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTATG GTGACGTGAGGTCGGACCCGTT

GAM189 246 MGC1428 1 3677 NP_542391.1 3 452 CTCTGTTGCCCA 3 B b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 MGC1443 1 17347 NP_116286.1 5 825 CCCTGTCACCCA C CA 3 B c c
6 GGCTGGGGTACG CATTG ACTCCAGCCTGGG
GTGGCATG GTGGC TGGGGTCGGACCC
A AC

GAM189 246 MGC1483 1 15044 NP_219480.1 3 381 CTCTGTTGCCCA 3 B b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 MGC1541 1 15115 NP_079011.2 3 1453 TCCCATTGCCCA T- CC C 3 B c c
9 GCCTCAGTGCAT CA TGCACT AG CTGGGCAA
TTGGCAAA GT ACGTGA TC GACCCGTT
TT C- C

GAM189 246 MGC1560 1 10968 NP_659474.1 5 287 CTCTGTTGCCCA T C 3 B b b

6 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
TTGGTGTG GT AC TGAGGTCGGACCCGTT
T A
GAM189 246 MGC1566 1 3620 NP_116145.1 3 25 CTAGGATGCCCA CA----- T - 3 B c c

8 GGGCTGGGTGCA TTGCAC CCAGCC TGGGCA
GCCAGCTG GACGTG GGTCGG ACCCGT
GTCGACC - G
GAM189 246 MGC1587 1 2894 NP_116309.1 5 81 CTCTGTCGCCCA G T A 3 B c c
3 GGCTGGCGTGAA CATT CAC CCAGCCTGGGC
GTGGCGCA GTGA GTG GGTCGGACCCG
A C C
GAM189 246 MGC1842 1 15046 XP_037797.2 3 1420 CTCTGTTGCCCA C 3 B b b
GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCACG GTGACGTGAGGTC GACCCGTT
A
GAM189 246 MGC2167 1 16916 NP_443093.1 3 500 TCTTGTTGCCCA 3 B b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM189 246 MGC2173 1 8134 NP_659481.1 3 997 GGGATGCTGATG -- -- 3 B c c
8 GGTTGGAGTGCC CATT GCACTCCAGCCTG GGCA
TAATGGCT GTAA CGTGAGGTTGGGT TCGT
TC AG
GAM189 246 MGC2306 1 7160 NP_002041.2 3 225 GACCGCTGCCCA T ----- G 3 B c c

GGTGGGGTTTCC CAT GC ACTCCA CCTGGGCA
TGCATGGA GTA CG TGGGGT GGACCCGT
- TCCTT -
GAM189 246 MGC2474 2 7797 NP_076420.1 3 954 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 MGC2474 2 18665 NP_076420.1 3 1312 GCTCCTCACCCA C CA 3 B c
b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGTGTG GTGACGT AGGTCGGACCC
A AC
GAM189 246 MGC2477 3 5609 NP_077004.1 5 1480 CTCTGTTGCCCA C 3 B b b
GCTGGAGTGCAG CATTGCACTCCAGC TGGGCAA
TGGCGTGA GTGACGTGAGGTCG ACCCGTT
-
GAM189 246 MGC2477 3 8610 NP_077004.1 5 1291 TCTGTCGCCCAG - A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCC TGGGC
GTGGCGCG GTGACGTGAGGTCGG ACCCG
G C
GAM189 246 MGC2477 3 19729 NP_077004.1 5 1480 ACTCTGTTGCCC C 3 B b b
AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCGTG GTGACGTGAGGTCG ACCCGTT
-

GAM189 246 MGC2603 1 5845 NP_076942.1 3 419 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC
GAM189 246 MGC2718 1 3976 NP_076972.2 3 437 GAGCTGAGCCCA ACTC A 3 B c
c
GGCTGCGTAGTG CATTGC CAGCCTGGGC
ACCACAAG GTGATG GTCGGACCCG
C--- A
GAM189 246 MGC2734 2 18352 XP_300964.1 5 1668 TCTTGTTGCCCA - 3 B b b
5 GGGCTGGAGTGC CATTGCACTCCAGCC TGGGCAA
AGTGGCAT GTGACGTGAGGTCGG ACCCGTT
G
GAM189 246 MGC2734 2 19385 XP_300964.1 5 1668 CTTGTTGCCCAG - 3 B b b
5 GGCTGGAGTGCA CATTGCACTCCAGCC TGGGCAA
GTGGCATG GTGACGTGAGGTCGG ACCCGTT
G
GAM189 246 MGC2989 1 14858 NP_653219.1 3 606 CTCTGTCACCCA CA 3 B c c
1 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTGCA GTGGCGTGAGGTCGGACCC
AC
GAM189 246 MGC2989 1 16672 NP_659485.1 3 503 CTTTGTTGCCCA C 3 B b b
8 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATA GTGACGTGAGGTC GACCCGTT
A
GAM189 246 MGC3113 1 10136 NP_076940.1 3 713 CTCTGTTCCCCA A CA 3 B c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGTACG GTGACGTGAGG CGGACCC
C CT
GAM189 246 MGC3207 2 5157 NP_115661.1 3 1437 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCC GTGACGTGAGGTCGGACCCG
C
GAM189 246 MGC3207 2 13812 NP_115661.1 3 788 ACTCGTTGCCCA CA----- 3 B c b
GGCTGGAGTGTA TTGCACTCCAGCCTGGGCAA
GAGGCGAG GATGTGAGGTCGGACCCGTT
GAGCGGA
GAM189 246 MGC3329 1 4477 NP_076991.2 3 1597 TCTTGTTGTCTA T 3 B b b
GGCTGGAGTGCC CAT GCACTCCAGCCTGGGCAA
GTGGTGCG GTG CGTGAGGTCGGATCTGTT
C
GAM189 246 MGC3363 1 12069 NP_689809.1 3 684 CTCTGTCACCCA CA 3 B c c
7 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGTA GTGATGTGAGGTCGGACCC
AC
GAM189 246 MGC3388 1 8724 NP_659473.1 3 49 ATGCAATTTCCA T TCC ----- 3 B c c
7 GGCTGTGCTGTG CAT GCAC AGCCTGG GCA

GACTTCTT GTG CGTG TCGGACC CGT
T --- TTTAA

GAM189 246 MGC3403 1 9529 NP_694956.1 5 278 TTCAGCAGTCCA CTC A 3 B c c
4 GGCTGATGCAGT CATTGCA CAGCCTGGGC
GGCTTCAA GTGACGT GTCGGACCTG
A-- A

GAM189 246 MGC3407 1 19817 NP_689688.1 3 189 TTCTGTCACCCA CA 3 B c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 MGC3413 2 8232 XP_291029.1 3 501 CTCTGTCACCCA CA 3 B c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM189 246 MGC3413 2 9087 XP_291029.1 3 335 CACTGTCACCCA CA 3 B c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM189 246 MGC3513 1 8535 NP_689640.1 5 174 CTCTCTCACCCA GC CA 3 B c c
6 GGCTGGAGTAGA CATT ACTCCAGCCTGGG
GTGACAAT GTGA TGAGGTCGGACCC
GA AC

GAM189 246 MGC3544 2 6886 NP_694952.1 3 493 CTCTGTCGCCCA C A 3 B c c
0 GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCA GTGACGT AGGTCGGACCCG
A C

GAM189 246 MGC3544 2 7378 NP_694952.1 3 184 CTCTGTCACCCA CA 3 B c c
0 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGCGCA GTGGCGTGAGGTCGGACCC
AC

GAM189 246 MGC3546 1 7484 NP_694976.1 3 87 CCTTGTTGCCCA 3 B b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 MGC3552 1 18741 NP_659502.1 3 487 TCCCACATGCCC TC - CT 3 B c c
1 CGCATGCGTGCA CATTGCAC CA GC GGGCA
ATGCCTCC GTAACGTG GT CG CCCGT
C- A C-

GAM189 246 MGC3771 1 3231 NP_112232.1 5 748 CTCTTCTTCCCA C CA 3 B c c
TGCTGGAGTGCA CATTGCACTCCAGC TGGG
ATGGCGCA GTAACGTGAGGTCG ACCC
T TT

GAM189 246 MGC3932 1 13428 NP_689642.2 3 697 CTGGCTTGCCCA 3 B b b
0 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCTAG GTGGCGTGAGGTCGGACCCGTT

GAM189 246 MGC4015 1 10743 NP_689563.1 3 318 CTGTATTGCCCA TG 3 B b b

7 GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
GTGGCACA GTG GTGAGGTCGGACCCGTT
GT

GAM189 246 MGC4016 1 7220 NP_714920.1 5 285 CTCTGTTGCCAA C G 3 B b b
8 GGCTGGAATGCA CATTGCA TCCAGCCT GGCAA
GTGGCGAG GTGACGT AGGTCGGA CCGTT
A A

GAM189 246 MGC4057 2 16218 NP_689989.1 3 904 TCTTGTCTCCCA C CA 3 B c c
9 GACTGGAGTGCA CATTGCACTCCAG CTGGG
ATGGCATG GTAACGTGAGGTC GACCC
A TC

GAM189 246 MGC4057 2 19220 NP_689989.1 3 333 CTCTGTCACTCA CA 3 B c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATA GTGACGTGAGGTCGGACTC
AC

GAM189 246 MGC4248 1 3338 NP_115709.2 3 277 AATTGACTGCCA T G 3 B b b
GGCTGGGTGCAG CATTGCAC CCAGCCTGG CA
TGGCTCAC GTGACGTG GGTCGGACC GT
- -

GAM189 246 MGC4312 1 12783 NP_775784.1 3 200 CTCTGTCACCCA T CA 3 B c c
2 GGTTGGAGTGCA CA TGCACTCCAGCCTGGG
TTGGTGTG GT ACGTGAGGTTGGACCC
T AC

GAM189 246 MGC5033 1 2959 NP_848604.1 3 279 CTCTGTCGCCCA C----- A 3 B c c
7 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
ATACTGCA TAACGTGAGGTCGGACCCG
ACGTCA C

GAM189 246 MGC5045 1 16867 NP_775733.1 3 89 ACTTCTTGCCCA C 3 B b b
2 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A

GAM189 246 MGC5055 2 11296 NP_776163.1 3 459 ACTTTGCTCCCA C CA 3 B c b
9 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCTAT GTGACGT AGGTCGGACCC
A TC

GAM189 246 MGC5055 2 15151 NP_776163.1 3 561 CTCTGTCGTCCA A 3 B b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGACTCA GTGACGTGAGGTCGGACCTG
C

GAM189 246 MGC9912 1 12221 NP_542395.1 3 351 GCTCTGTCGCCA C -- 3 B b b
GACTGGAGTGCA CATTGCACTCCAG CTGG GCA
GTGGCGCA GTGACGTGAGGTC GACC TGT
A GC

GAM189 246 MGRN1 1 16616 XP_048119.4 3 1594 TCTTGCTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCTCA GTGACGTGAGGTCGGACCCGT

GAM189 246 MHC2TA 3 783 NP_000237.1 3 439 CACTGTTGCCCA T 3 B b b
GGCTGGCGTGCA CATTGCAC CCAGCCTGGGCAA
GTGGTGCG GTGACGTG GGTCGGACCCGTT
C
GAM189 246 MHC2TA 3 922 NP_000237.1 3 809 CAGATTGCAACA CAC G- 3 B c b
GGCTGGGCTTCA CATTG TCCAGCCTG GCAA
GTGGCAGC GTGAC GGGTCGGAC CGTT
TTC AA
GAM189 246 MHC2TA 3 2053 NP_000237.1 3 2660 CTCTTATGCCCA C 3 B b b
CGCTGGAGTGCA CATTGCACTCCAGC TGGGCA
GTGAGCCG GTGACGTGAGGTCG ACCCGT
C
GAM189 246 MIRAB13 1 11523 NP_203744.1 3 1732 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 MIRAB13 1 11523 XP_039236.6 3 2297 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 MKRN4 1 12075 NP_110384.1 3 373 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 MLANA 1 13029 NP_005502.1 3 611 TTTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM189 246 MLC1 2 14833 NP_055981.1 3 825 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACATGGCC GTA CGTGAGGTT GACCCGT
CAC C
GAM189 246 MLC1 2 14833 NP_631941.1 3 825 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACATGGCC GTA CGTGAGGTT GACCCGT
CAC C
GAM189 246 MLC1 2 19859 NP_055981.1 3 775 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM189 246 MLC1 2 19859 NP_055981.1 3 877 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM189 246 MLC1 2 19859 NP_631941.1 3 775 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM189 246 MLC1 2 19859 NP_631941.1 3 877 CTGTCATGCCCA T-- C 3 B c c

GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C

GAM189 246 MLZE 1 9728 NP_113603.1 5 585 CGGAGTTGCCCA CA----- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGCATGG GACGTGAGGTCGGACCCGTT
GGTACGC

GAM189 246 MMPL1 1 4374 NP_004133.1 3 511 TTCTGTCCTCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGACATG GTAACGTGAGGTCGGACCT
CC

GAM189 246 MOAP1 1 1744 NP_071434.2 3 300 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 moblak 1 19657 NP_570719.1 3 1259 CCGGCCTAACCA GCA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGGG GTGACGTGAGGTCGGACC
AAT

GAM189 246 MOCS3 1 12064 NP_055299.1 3 579 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGATGTGAGGTCGGACCCGTT

GAM189 246 MPL 2 11185 NP_005364.1 3 569 CTCTGTCACCCA C CA 3 B c b
GGCTGCAGTGCA CATTGCACT CAGCCTGGG
ATGGCGCG GTAACGTGA GTCGGACCC
C AC

GAM189 246 MPL 2 16608 NP_005364.1 3 750 TGCCTGTTGCCA C G 3 B b b
GACTGGAGTGCA CATTGCACTCCAG CTGG CAA
GTGGCACG GTGACGTGAGGTC GACC GTT
A -

GAM189 246 MRPL35 1 9545 NP_057706.2 3 1060 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 MRPL44 1 14596 NP_075066.1 3 259 CTCTGTCGCCCA C A 3 B c c
GGCTGGACTGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
C C

GAM189 246 MRPL49 1 5438 NP_004918.1 3 324 CTCTGTTGCCCA G 3 B b b
GGGTGGAGTGCA CATTGCACTCCA CCTGGGCAA
GTGGCATG GTGACGTGAGGT GGACCCGTT
G

GAM189 246 MRPS27 1 4179 NP_055899.1 3 430 TTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM189 246 MSTP028 1 12951 NP_114160.1 3 1907 CTCTATTGGCCA G 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGG CAA
GTGGCACC GTGATGTGAGGTCGGACC GTT

G
GAM189 246 MTH2 1 15874 NP_060753.1 3 851 CTCTGTTGCCCA CC 3 B b b
CATTGGAGTGCA CATTGCACTCCAG TGGGCAA
GTGGCACG GTGACGTGAGGTT ACCCGTT
AC
GAM189 246 MYCL2 1 16868 NP_005368.1 3 1431 TCTTGTCGCCCA CA A 3 B c c
GGCTGGAGGTTA CATTG CTCCAGCCTGGGC
ATGGCATG GTAAT GAGGTCGGACCCG
TG C
GAM189 246 MYLC2PL 1 3580 NP_612412.1 5 369 CTCTGTCGCCCA A A 3 B b b
GGCTGGAGCGCA CATTGC CTCCAGCCTGGGC
ATGGCATG GTAACG GAGGTCGGACCCG
C C
GAM189 246 MYO5C 1 4306 NP_061198.1 3 628 GCTCTATCGCCA GCA 3 B c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGG
GTGGCATG GTGATGTGAGGTCGGACC
GCT
GAM189 246 NACT 1 19968 NP_808218.1 3 552 GCAACCTCCCAC - C- CA 3 B c c
TGCTGGAGTGCG CATT GCACTCCAGC TGGG
AGTGGGAA GTGA CGTGAGGTCG ACCC
G TC TC
GAM189 246 Nanog 1 11523 NP_079141.1 3 282 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM189 246 NCAG1 1 3766 NP_115536.1 3 3665 CTTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTCTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 NCOA6 2 12826 NP_054790.1 5 1279 CTCTGTCACCGA G CA 3 B c c

GGCTGGAGTGCA CATTGCACTCCAGCCT GG
GTGGCGCG GTGACGTGAGGTCGGA CC
G AC
GAM189 246 NCOA6 2 19446 NP_054790.1 5 884 CTCTGTCGCCCA C----- A 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTCGTGCC TGACGTGAGGTCGGACCCG
CCGTGC C
GAM189 246 NCOA6IP 2 8841 NP_079107.5 3 280 TTTTACCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGCCATG GTGACGTGAGGTCGGACCCG
C
GAM189 246 NCOA6IP 2 10534 NP_079107.5 3 444 CCATGTTGCCCA CA------ C T 3 B c
b

GGCTGGTGTCAA TTG AC CCAGCCTGGGCAA
ACTCCTGG AAC TG GGTCGGACCCGTT
GGTCCTCA - T
GAM189 246 NDP52 1 15337 NP_005822.1 3 1122 CTCTGTCACCCA T CA 3 B c c
GGCTGGCGTGCA CATTGCAC CCAGCCTGGG
ATGGCGCA GTAACGTG GGTCGGACCC

C AC
GAM189 246 NDRG3 1 15102 NP_114402.1 3 1152 CGCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCA GTAACGTGAGGTCGGACCC
AT
GAM189 246 NDUFC2 1 10192 NP_004540.1 3 1240 GCTCTGTCATCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCGCA GTGACGTGAGGTCGGAC CTGT
TA
GAM189 246 NEU3 1 12075 NP_006647.2 5 71 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 NF2 1 9169 NP_057502.1 5 480 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGTG GTAACGTGAGGTCGGACCCG
C
GAM189 246 NONO 1 17960 NP_031389.2 3 447 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGATGTGAGGTCGGACCCG
C
GAM189 246 NOSIP 1 7311 NP_057037.1 5 53 TCTTGTTGCCTA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGATCCGTT

GAM189 246 NPTXR 1 5189 NP_055108.2 3 3926 CACATGGGCCCA - C A 3 B c c
GGCTGAGTGTGA CATT GCACTC AGCCTGGGC
GTGAGCAT GTGA TGTGAG TCGGACCCG
G - G
GAM189 246 NPTXR 1 5189 NP_478058.1 3 3926 CACATGGGCCCA - C A 3 B c c
GGCTGAGTGTGA CATT GCACTC AGCCTGGGC
GTGAGCAT GTGA TGTGAG TCGGACCCG
G - G
GAM189 246 NQO1 1 14855 NP_000894.1 3 685 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AT
GAM189 246 NR2E1 1 13178 NP_003260.1 5 598 AGGAGCCTTGCA - A --- A 3 B c c
GGCTGGAGGGCG CA TTGC CTCCAGCCTG GGC
GCTGGAGA GT GGCG GAGGTCGGAC CCG
C G GTT A
GAM189 246 NRLN1 1 15825 NP_660277.1 5 22 GGCCAGTGCCCA -- CC 3 B b b
GGTTAGTGAGCA CATTGC ACT AGCCTGGGCA
GTGCCCGG GTGACG TGA TTGGACCCGT
AG --
GAM189 246 NT5C2 1 4030 NP_036361.1 5 35 CTCTGCTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCA
GTGATGTG GTGAC TGAGGTCGGACCCGT
A
GAM189 246 NUDT4 1 18879 NP_061967.2 3 1290 CTTTGTCACCCA CA 3 B b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACA GTAACGTGAGGTCGGACCC
AC

GAM189 246 NUMA1 1 14343 NP_006176.1 5 119 CTTCCACCAGGA --- GCA 3 B c c

GTCTGGAGTGCA CATTGCACTCCAG CCTGG
ATGGCACG GTAACGTGAGGTC GGACC
TGA ACC

GAM189 246 NUP43 1 1900 NP_078923.2 3 606 AGAGTCTTGCTC CT 3 B c c
TGCTGGAGTGCG CATTGCACTCCAGC GGGCAA
GTGGTGCA GTGGCGTGAGGTCG CTCGTT
T-

GAM189 246 NXN 1 935 NP_071908.1 3 876 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
C

GAM189 246 OR51E2 1 4096 NP_110401.1 3 439 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC

GAM189 246 ORC1L 1 17969 NP_004144.1 3 92 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM189 246 OSBPL2 1 7553 NP_055650.1 3 1126 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM189 246 OSBPL2 1 7553 NP_653081.1 3 1126 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM189 246 P2RXL1 1 4425 NP_005437.1 3 954 GCTCTGATCCCA G C CA 3 B c c
GGCTGGATGGAG CATT CA TCCAGCCTGGG
TGGCTGGA GTGA GT AGGTCGGACCC
G - TA

GAM189 246 P2RY1 1 8453 NP_002554.1 3 822 ATTTACTTGCCC TC CCT 3 B c c
CACTGCTGTGCA CATTGCAC CAG GGGCAA
ATGCCTTA GTAACGTG GTC CCCGTT
TC AC-

GAM189 246 P450RAI 1 18160 NP_063938.1 3 48 CAGCCCAGCCCA TG A-- A 3 B c c

-2 GGCAGCGGGGTG CAT CACTCC GCCTGGGC
GTGGTTGT GTG GTGGGG CGGACCCG
-- CGA A

GAM189 246 PAICS 1 16852 NP_006443.1 3 413 CACTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 PASK 1 2769 NP_055963.1 5 805 TCTTGTTGCTGA G 3 B b b

GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
GTGGCACC GTGACGTGAGGTCGGA TCGTT
G

GAM189 246 PCDHA9 2 10427 NP_054724.1 3 1915 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCC GTGACGTGAGGTCGGACCCGTT

GAM189 246 PCDHA9 2 16048 NP_054724.1 3 1315 TTCTGCCACCCA C CA 3 B c b
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC

GAM189 246 PCDHB11 1 10723 NP_061754.1 3 192 TTCTGTCGCCCT T A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCC GGGC
ATGGTGTG GTAACGTGAGGTCGG CCCG
T C

GAM189 246 PCDHB16 1 4617 NP_066008.1 3 581 TCTTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 PCDHB9 1 11523 NP_061992.2 3 527 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 PDE6B 1 936 NP_000274.1 3 197 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
GTGGCACG GTG CGTGAGGTCGGACCC
C AC

GAM189 246 PDGFC 1 905 NP_057289.1 3 45 AGCTCTTGCCCA C-- - 3 B b b
GAGCTGTGCAGT CATTGCACT CAGC CTGGGCAA
GCAGTGGC GTGACGTGA GTCG GACCCGTT
CGT A

GAM189 246 PDLIM2 1 14973 NP_789847.1 3 1201 CTCTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 PDZK1 1 4194 NP_002605.2 5 44 TTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 PDZRN1 1 5270 NP_699202.1 3 522 CACTCTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 PELI1 3 5491 NP_065702.2 5 2686 CTCTGTTGCCCA 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACT GTGACGTGAGGTTGGACCCGTT

GAM189 246 PELI1 3 7382 NP_065702.2 5 2122 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM189 246 PELI1 3 14861 NP_065702.2 5 1442 CTCTGTCACCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM189 246 PER2 1 19703 NP_073728.1 3 1370 TCTTTTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM189 246 PFAS 1 16261 NP_036525.1 3 674 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
ATGGCGTG GTAAC TGAGGTCGGACCC
A AC
GAM189 246 PHAX 1 12159 NP_115553.1 3 698 CCTGAACCCCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCAGG GTGAC TGAGGTCGGACCC
A CC
GAM189 246 PIGR 1 11059 NP_002635.2 3 814 CACTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM189 246 PIK3C2B 1 10488 NP_002637.2 3 1447 GCCCTGTCGCCA -- 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGATGTGAGGTCGGACC TGT
GC
GAM189 246 PIK3C3 1 8874 NP_002638.1 3 2 AGTTTGCCCAGT GCA C- 3 B c c
ACTGGAGAAAAT CATT CTCCAG CTGGGCAA
GAACTGGG GTAA GAGGTC GACCCGTT
AA- AT
GAM189 246 PIK3CD 1 9545 NP_005017.2 3 822 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 PKNOX1 1 8826 NP_004562.2 3 1821 TCTTGTTGCCCA A 3 B b b
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGCAA
ATGGTGCA GTAACG GAGGTCGGACCCGTT
G
GAM189 246 PLA2G6 1 16143 NP_003551.1 3 514 TGGGAAAGCCCA G A--- A 3 B c c

GGCCGCAGGAGT CATT CACTCC GCCTGGGC
GGGATGCC GTAG GTGAGG CGGACCCG
G ACGC A
GAM189 246 PMCHL1 1 16917 NP_114093.1 3 526 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 PMCHL2 1 16917 NP_114094.1 3 524 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 PMPCA 1 7640 NP_055975.1 3 246 TGAAGTGCCCAG CA----- - 3 B c c
CGCTGGAGTGCA TTGCACTCCAGC CTGGGCA
GCGTGCCA GACGTGAGGTCG GACCCGT
ACCGTGC C
GAM189 246 PNMA2 2 8006 NP_009188.1 3 1714 CTCTATCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 PNMA2 2 17067 NP_009188.1 3 265 TCTCATCACCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCACA GTGACGTGAG TCGGACCC
A AC
GAM189 246 POFUT1 1 11287 NP_056167.1 3 1737 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
TC
GAM189 246 POLE3 1 6151 NP_059139.2 3 1144 CTCTGTGGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
G
GAM189 246 POLR2D 2 2798 NP_004796.1 3 520 AACTCTTGTCCA C-- --- 3 B c c
GGCTGGAGGAGT ATTGCACTCC AGCCTGGGCAA
GCAGTCGT TGACGTGAGG TCGGACCTGTT
TGC AGG
GAM189 246 POLR2D 2 5412 NP_004796.1 3 520 TCTTGTCCAGGC C----- --- 3 B c c
TGGAGGAGTGCA ATTGCACTCC AGCCTGGGCAA
GTCGTACA TGACGTGAGG TCGGACCTGTT
ACATGC AGG
GAM189 246 PON1 1 2152 NP_000437.3 3 1197 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 POU2AF1 1 20135 NP_006226.1 3 1375 CTCCATTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A
GAM189 246 POU2F3 1 16114 NP_055167.1 3 1109 TGCTCCAGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
A
GAM189 246 PP1628 1 10180 NP_079477.1 5 1279 ATTGCTCAGCCA - A TC ---- 3 B c c
GGCTGTGGAGCA CA TTGC C CAGCCTGG GCAA
GCTGAGGC GT GACG G GTCGGACC CGTT
C A GT GACT
GAM189 246 PP3111 1 10883 NP_071439.2 3 190 GAGCAGGCCCCA TT C- - A 3 B c
c
GGCTGGACCTGC CA GCA TCCAGCCTGGG C
CCTGTCCT GT CGT AGGTCGGACCC G
CC CC C G

GAM189 246 PP3856 1 10744 NP_660202.1 5 509 TCCAGGTGCCCT C------ C T 3 B c c
GGCTGGAGTCAG ATTG ACTCCAGCC GGGCA
TCCTCATC TGAC TGAGGTCGG CCCGT
CTACTCC - T
GAM189 246 PPAP2C 1 7299 NP_003703.1 3 35 GGACCCCGCCCA T - A- A 3 B c c
GGCAGGGAGCTG CAT GCA CTCC GCCTGGGC
CTGTGAGT GTG CGT GAGG CGGACCCG
T C GA C
GAM189 246 PPAP2C 1 7299 NP_803545.1 3 35 GGACCCCGCCCA T - A- A 3 B c c
GGCAGGGAGCTG CAT GCA CTCC GCCTGGGC
CTGTGAGT GTG CGT GAGG CGGACCCG
T C GA C
GAM189 246 PPAP2C 1 7299 NP_808211.1 3 35 GGACCCCGCCCA T - A- A 3 B c c
GGCAGGGAGCTG CAT GCA CTCC GCCTGGGC
CTGTGAGT GTG CGT GAGG CGGACCCG
T C GA C
GAM189 246 PPEF2 1 2954 NP_006230.2 3 368 TCTTGTTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGGCGCG GT ACGTGAGGTCGGACCCGTT
T
GAM189 246 PPEF2 1 2954 NP_690910.1 3 1000 TCTTGTTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGGCGCG GT ACGTGAGGTCGGACCCGTT
T
GAM189 246 PPEF2 1 2954 NP_690911.1 3 2213 TCTTGTTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGGCGCG GT ACGTGAGGTCGGACCCGTT
T
GAM189 246 PPFIA4 1 16851 XP_046751.3 5 91 CAGTGCTGCCCA GCAC -- 3 B c c
GGACCTGGACCG CATT TCCAG CCTGGGCA
AATGGGGG GTAA AGGTC GGACCCGT
GCC- CA
GAM189 246 PPFIBP1 3 8231 NP_003613.2 3 2295 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 PPFIBP1 3 10708 NP_003613.2 3 1168 TTCTGTTGCCCA C 3 B b b
TGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCGTG GTGACGTGAGGTCG ACCCGTT
T
GAM189 246 PPFIBP1 3 12217 NP_003613.2 3 861 CTCTGTCACCCA T CA 3 B c b
GGTTGGAGTGCC CAT GCACTCCAGCCTGGG
ATGGCATG GTA CGTGAGGTTGGACCC
C AC
GAM189 246 PPID 1 7378 NP_005029.1 3 247 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGCGCA GTGGCGTGAGGTCGGACCC
AC
GAM189 246 PPIL2 1 13122 NP_055152.1 3 392 CTCTGTTGCCCA CC 3 B b b
GGCTCCAGTGCA CATTGCACT AGCCTGGGCAA

GTGGTGTG GTGACGTGA TCGGACCCGTT
CC
GAM189 246 PPP1R12 1 3861 NP_002472.1 3 4497 CTCTCTCGCCCA A 3 B b b
B GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 PPP1R12 1 3861 NP_115288.1 3 4630 CTCTCTCGCCCA A 3 B b b
B GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 PRKR 1 4790 NP_002750.1 3 275 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGACACA GTAACGTGAGGTCGGACCCGTT

GAM189 246 PRKWNK3 1 14862 NP_065973.1 3 639 CTCTGTCACCCA CA 3 B c c

GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTTGGACCC
AC
GAM189 246 PRND 2 1539 NP_036541.1 3 839 TCTTGTTGCCCA CA----- 3 B c b
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGCATG AACGTGAGGTCGGACCCGTT
GTACGGC
GAM189 246 PRND 2 4170 NP_036541.1 3 2764 TTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 PRO0297 1 10574 NP_054800.1 5 53 CTCTTTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 PRO0365 1 18148 NP_054845.1 5 883 GCTCTGTCGCCA C -- 3 B b b
GGCTGAAGTGCA CATTGCACT CAGCCTGG GCA
GTGGCGCA GTGACGTGA GTCGGACC TGT
A GC
GAM189 246 PRO1048 1 12596 NP_060967.1 3 319 CTCTGCTGCCCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCA
GTGGCACA GTGAC TGAGGTCGGACCCGT
A
GAM189 246 PRO2730 1 2048 NP_079498.1 3 320 TGGTCAGGCCCA TG C A 3 B c
c

GGCTGAGTGAGA CAT CACTC AGCCTGGGC
TGAGCTGC GTA GTGAG TCGGACCCG
GA - G
GAM189 246 PROM2 2 2147 NP_653308.1 3 786 CTCTGTCACCCA CA 3 B c b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGATGTGAGGTCGGACCC
AC
GAM189 246 PROM2 2 13176 NP_653308.1 3 951 CCATGTTGCCCA T- - 3 B b b
GGCTGGAAGTGT CAT GCACT CCAGCCTGGGCAA

CTATGTTT GTA TGTGA GGTCGGACCCGTT
TC A
GAM189 246 PRPF31 1 11313 NP_056444.1 3 145 TGGGACTGCCCA TT A AG 3 B c c
GGGAGGAGGCCT CA GC CTCC CCTGGGCA
TGGAAGAG GT CG GAGG GGACCCGT
TC - AG
GAM189 246 PSMD9 1 17758 NP_002804.2 3 752 CTTTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTCGTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 PSPH 1 15044 NP_004568.1 3 276 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 PTGES 1 16070 NP_004869.1 3 528 CTCTGTTGCCCA G C 3 B b b
AGCTGGAGTGAA CATT CACTCCAGC TGGGCAA
GTGGTACA GTGA GTGAGGTCG ACCCGTT
A A
GAM189 246 PTGIS 2 10783 NP_000952.1 3 3269 GCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 PTGIS 2 17361 NP_000952.1 3 2840 CTCTGCTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCA
GTGGCGTG GTGACGTGAG TCGGACCCGT
A
GAM189 246 PTK2 1 10355 NP_005598.3 5 129 CCCAGGCTGCCA G G 3 B b b
GGCTGGAGTGGA CATT CACTCCAGCCTGG CA
GTGGCATG GTGA GTGAGGTCGGACC GT
G -
GAM189 246 PYGM 1 15938 NP_005600.1 5 741 GCTCCACTCCTT A ------ - A 3 B c c
GGCTGGAGGCAG CATTGC CTCCAGCC TGG GC
TGCTGAGG GTGACG GAGGTCGG ACC CG
- TTCCTC T -
GAM189 246 IP4 RAB11-F 1 13848 NP_116321.2 3 2596 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTATG GTGATGTGAGGTCGGACCCGTT

GAM189 246 RAB21 1 7076 NP_055814.1 3 289 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
CTGGCTTG GT ACGTGAGGTCGGACCC
C AC
GAM189 246 RAB33B 1 7910 NP_112586.1 3 839 GCTCTGTCTCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTC GTGACGTGAGGTCGGACC TGT
TC
GAM189 246 RAB36 2 808 NP_004905.1 3 1408 CCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTA GTAACGTGAGGTCGGACCCGTT

GAM189 246 RAB36 2 1652 NP_004905.1 3 1726 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACG GTAACGTGAGGTCGGACCC
AC
GAM189 246 RAB39 1 3754 XP_084662.1 3 753 TTTTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGGCA GTGACGTGAGGTCGGACCC
AC
GAM189 246 RAB4A 1 16568 NP_004569.2 5 27 GCGCCTGCGCGG - C - G 3 B c c
AGCTGGAGTCCG CA TTG ACTCCAGC CTG GCA
GCTGGGCC GT GGC TGAGGTCG GGC CGT
C C A G
GAM189 246 RABL2A 1 2648 NP_038198.1 3 578 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
GC
GAM189 246 RABL2B 1 2648 NP_009012.1 3 585 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
GC
GAM189 246 RAI 1 8937 NP_006654.1 5 22 CAAGTGAGTCTC T A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCC GGGC
GTGGTGCA GTGACGTGAGGTCGG TCTG
C A
GAM189 246 RAI16 1 4335 NP_073586.3 3 417 GTCAGGAGCCCA TG CCA A 3 B c
c
GGCCAGTGAGAT CAT CACT GCCTGGGC
GGGGCCTG GTA GTGA CGGACCCG
GA C-- A
GAM189 246 RAI17 1 7523 NP_065071.1 3 1485 CACTTTGTTTCA T-- T-- - 3 B c c
GGCTGGTCTGTG CAT GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM189 246 RAI17 1 7523 XP_166091.2 3 1485 CACTTTGTTTCA T-- T-- - 3 B c c
GGCTGGTCTGTG CAT GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM189 246 RAI3 1 12784 NP_003970.1 3 343 CTCTGTCACCCA C CA 3 B c c
GGCTTGAGTGCA CATTGCACTC AGCCTGGG
GTGGTGCG GTGACGTGAG TCGGACCC
T AC
GAM189 246 RAP140 1 16472 NP_056039.1 3 1919 CTCTGTCGCCCA C C A 3 B c c
AGCTGGAGTACA CATTG ACTCCAGC TGGGC
GTGGTGCA GTGAC TGAGGTCG ACCCG
A A C
GAM189 246 RARG 1 11090 NP_000957.1 5 41 CGGAGCCTCCCA A T CA 3 B c c
GGCTGGGGCAGT CATTGC C CCAGCCTGGG
GGGCATGG GTGACG G GGTCGGACCC

```
                                                - -        TC
GAM189   246   RASSF2  1   19336 NP_055552.1  3  3347   TTCTGTTTCCCA              CA        3  B  c  c
                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                    GTGGTGGG    GTGACGTGAGGTCGGACCC
                                                  TT
GAM189   246   RASSF2  1   19336 NP_739579.1  3  3573   TTCTGTTTCCCA              CA        3  B  c  c
                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                    GTGGTGGG    GTGACGTGAGGTCGGACCC
                                                  TT
GAM189   246   RASSF2  1   19336 NP_739580.1  3  3347   TTCTGTTTCCCA              CA        3  B  c  c
                                    GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                    GTGGTGGG    GTGACGTGAGGTCGGACCC
                                                  TT
GAM189   246   RBBP1   1   11014 NP_002883.2  3  542    GCAGTGTGCCCA   -   C-  -          3  B  c  c
                                    GGATTGAAGGTG CATT GCACT  CAG CCTGGGCA
                                    TAAATGGG    GTAA TGTGG  GTT GGACCCGT
                                                  A    AA  A
GAM189   246   RBBP1   1   11014 NP_075376.1  3  542    GCAGTGTGCCCA   -   C-  -          3  B  c  c
                                    GGATTGAAGGTG CATT GCACT  CAG CCTGGGCA
                                    TAAATGGG    GTAA TGTGG  GTT GGACCCGT
                                                  A    AA  A
GAM189   246   RBBP1   1   11014 NP_075377.1  3  542    GCAGTGTGCCCA   -   C-  -          3  B  c  c
                                    GGATTGAAGGTG CATT GCACT  CAG CCTGGGCA
                                    TAAATGGG    GTAA TGTGG  GTT GGACCCGT
                                                  A    AA  A
GAM189   246   RBBP9   1   16100 NP_006597.2  3  1856   CTCTGTCTCCCA    CA        CA        3  B  c  c

                                    GGCTGGAGGTCA CATTG  CTCCAGCCTGGG
                                    GTGGCACA    GTGAC  GAGGTCGGACCC
                                                  TG         TC
GAM189   246   RBL2    1   6615  NP_005602.2  3  607    AGTCCTTGATTG      TCCA            3  B  c  c
                                    TTCGGGTGTGCA CATTGCAC    GCCTGGGCAA
                                    ATGTCTGA    GTAACGTG    TGGGCTTGTT
                                                  ----
GAM189   246   RCBTB1  1   13829 NP_060661.2  5  129    CTCTCTTGCCCA    CAC    C           3  B  c
c
                                    GACTGGAATACA CATTG   TCCAG CTGGGCAA
                                    GTGGTGTG    GTGAC   AGGTC GACCCGTT
                                                  ATA    A
GAM189   246   RCD-8   1   13335 NP_055144.2  3  595    CTGCCTTGCCCA  T  AC-   G -         3  B  c  c
                                    GGGGTGGGATGG CA TGC   TCCA CC TGGGCAA
                                    CACTGAAG    GT ACG   GGGT GG ACCCGTT
                                                  C  GTA   G  G
GAM189   246   RDH13   1   9713  NP_612421.1  5  227    ACTCTGTCGCCA C-----    C       --      3  B  c  c
                                    GGCTGGAATGCA      ATTGCA TCCAGCCTGG  GCA
                                    GTAGGGCA          TGACGT AGGTCGGACC  TGT
                                                  ACGGGA     A         GC
GAM189   246   RGS3    1   3344  NP_570613.1  5  61     GTGCTCATGCCA    C   --      G        3  B  c  c
                                    GGCTGACGGGTC CATTG ACTC  CAGCCTGG CA
                                    CAGTGCGG    GTGAC TGGG  GTCGGACC GT
```

C CA -
GAM189 246 RHD 2 4143 NP_057208.2 3 690 ACTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 RHD 2 4143 NP_057309.2 3 779 ACTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 RHD 2 13465 NP_057208.2 3 281 CTCTGTCACCCA C CA 3 B c b
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACC GTAACGTGAG TCGGACCC
A AC
GAM189 246 RHD 2 13465 NP_057309.2 3 370 CTCTGTCACCCA C CA 3 B c b
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACC GTAACGTGAG TCGGACCC
A AC
GAM189 246 RHPN2 1 11803 NP_149094.2 3 890 CTGTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 RIP60 1 5556 NP_037532.1 3 100 GTGCCTGCCTAG C----- - 3 B c c
TGCTGGAGTAGG CATTG ACTCCAGC CTGGGCA
GGACAATG GTAAC TGAGGTCG GATCCGT
AGGGGA T
GAM189 246 RIP60 1 5556 NP_055189.1 3 100 GTGCCTGCCTAG C----- - 3 B c c
TGCTGGAGTAGG CATTG ACTCCAGC CTGGGCA
GGACAATG GTAAC TGAGGTCG GATCCGT
AGGGGA T
GAM189 246 RNF137 2 7446 NP_060543.4 3 163 TCTTTGCTACCA T -- C -- 3 B c b
GGCTGAAGTCTG CAT GC ACT CAGCCTGG GCAA
TCATGAAA GTA TG TGA GTCGGACC CGTT
C TC A AT
GAM189 246 RNF137 2 16940 NP_060543.4 3 829 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 RNF144 1 4727 NP_055561.1 3 3167 TTTTGTCCCCCA C C CA 3 B c c
AGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGACAGG GTAAC TGAGGTCG ACCC
A A CC
GAM189 246 RNF8 2 9745 NP_003949.1 3 959 CCCAAGCTGGAG --- C CA 3 B c c
TACAGTAGTGCA CATTGC ACTCCAGC TGGG
ATCTCAGC GTGATG TGAGGTCG ACCC
ACA A --
GAM189 246 RNF8 2 13778 NP_003949.1 3 954 CTCTGTTGCCCA --- C 3 B c c
AGCTGGAGTACA CATTGC ACTCCAGC TGGGCAA
GTAGTGCA GTGATG TGAGGTCG ACCCGTT
ACA A
GAM189 246 RP2 1 6582 NP_008846.1 3 1766 TCTTGTTGCCCA C 3 B b b

AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCGCG GTAACGTGAGGTCG ACCCGTT
A

GAM189 246 RPH3AL 1 2614 NP_008918.1 3 641 CTTTGTTGCCCA 3 B b b
GGCTGGGGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGGGGTCGGACCCGTT

GAM189 246 RPP30 2 445 NP_006404.1 3 358 CTTTGTTGCTCA C 3 B b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCATA GTGAC TGAGGTCGGACTCGTT
A

GAM189 246 RPP30 2 19325 NP_006404.1 3 1203 CTCTGTCCCCCA CA 3 B c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTCG GTGACGTGAGGTCGGACCC
CC

GAM189 246 S100A15 1 19723 NP_789793.1 3 3404 CTCTGTCGCCCG T A 3 B c c
GGCTGGAGTGCT CAT GCACTCCAGCCTGGGC
GTGAGCTG GTG CGTGAGGTCGGGCCCG
T C

GAM189 246 SARM1 2 4282 NP_055892.1 3 3667 CTCTGTTGTCCA A 3 B b b
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGCAA
GTGACATA GTGACG GAGGTCGGACCTGTT
G

GAM189 246 SARM1 2 7147 NP_055892.1 3 416 AGGCAATGCCCA T A --- A 3 B c b
GGCGGGCCTGGG CA TGC CT CC GCCTGGGCA
CACTGTAT GT ACG GG GG CGGACCCGT
C - TCC G

GAM189 246 SAS 1 17726 NP_005972.1 3 511 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM189 246 SBLF 1 14551 NP_006864.2 3 1609 CTCTGTTGCCCA C 3 B b b
GCCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGTGTCA GTGACGTGAGGTC GACCCGTT
C

GAM189 246 SCAMP-4 1 2153 NP_524558.1 3 873 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 SCAND2 1 7179 NP_071333.2 3 1783 TTCTATCACCCA G CA 3 B c c
GGCTGGAGTGGA CATT CACTCCAGCCTGGG
GTGGTATG GTGA GTGAGGTCGGACCC
G AC

GAM189 246 SCARF1 1 5158 NP_003684.1 3 410 CTCTGTCCCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
CC

GAM189 246 SCD 1 3800 NP_005054.2 3 2066 TCAGTGCTCTCA - CT- 3 B c c
GCTGGCAGTGCA CATTGCACT CCAGC GGGCA
ATGCTTGT GTAACGTGA GGTCG CTCGT

C ACT

GAM189 246 SCML2 1 3898 NP_006080.1 3 1313 CTCTTGTGCCCA C----- 3 B b b
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCA
ATAGCTCG TAACGTGAGGTCGGACCCGT
GCTCGA

GAM189 246 SCN2B 1 13704 NP_004579.1 3 496 GAGCAGCCATCA - - -- A 3 B c c
GGCTGGAGGTGA CATTG CAC TCCAGCCTG GGC
CGATGAGT GTAGC GTG AGGTCGGAC CCG
A G TA A

GAM189 246 SCN3B 1 4399 NP_060870.1 3 2013 CTCTGTCTCCCA C CA 3 B c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGTGCA GTGACGTGAG TCGGACCC
A TC

GAM189 246 SDS-RS1 1 14127 NP_612441.1 5 91 ATCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM189 246 SEDL 3 926 NP_055378.1 3 1000 TCCTGTTGTGCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GCAA
GTGGCACA GTGACGTGAGGTCGGAC TGTT
G

GAM189 246 SEDL 3 11591 NP_055378.1 3 1346 CTCTGTTGTCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCAGT GTAACGTGAGGTCGGACCTGTT

GAM189 246 SEDL 3 15576 NP_055378.1 3 308 ACTCTGTTGCCA G 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCA GTGACGTGAGGTCGGACC GTT
-

GAM189 246 SEMA3E 1 13353 NP_036563.1 3 5 TGCCCAGGCACA G ----- ------ 3 B c c
CGCTGGACTCCT CATT CAC TCCA GCCTGGGC
GTGGGGTG GTGG GTG AGGT CGGACCCG
G TCCTC CGCACA

A
T

GAM189 246 SEPN1 1 18255 NP_065184.1 3 1557 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
ATGGCTCG GTA CGTGAGGTCGGACCC
T AC

GAM189 246 SERF1A 2 9219 NP_068802.1 3 243 ACTCTGTCACCA C -- 3 B b b
GACTGGAGTGCA CATTGCACTCCAG CTGG GCA
GTGGCGCC GTGACGTGAGGTC GACC TGT
A AC

GAM189 246 SERF1A 2 15849 NP_068802.1 3 410 CACTGTTGCCCA C 3 B b b
GGCTGGACTGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
C

GAM189 246 SERF1B 2 9219 NP_075267.1 3 243 ACTCTGTCACCA C -- 3 B b b

GACTGGAGTGCA CATTGCACTCCAG CTGG GCA
GTGGCGCC GTGACGTGAGGTC GACC TGT
A AC

GAM189 246 SERF1B 2 15849 NP_075267.1 3 410 CACTGTTGCCCA C 3 B b b
GGCTGGACTGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
C

GAM189 246 SERPINB 2 4363 NP_004146.1 3 511 CTCTGTCGCCCA A 3 B b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCTCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 SERPINB 2 9152 NP_004146.1 3 2359 CTCTGTCACCCA CA 3 B c b
9 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGCATG GTGATGTGAGGTCGGACCC
AC

GAM189 246 SFXN2 1 3678 NP_849189.1 3 594 CTCTGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGCG GTGACGT AGGTCGGACCCG
A C

GAM189 246 SFXN2 1 3678 XP_058359.2 3 595 CTCTGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGCG GTGACGT AGGTCGGACCCG
A C

GAM189 246 SH3BGRL 1 2741 NP_113657.1 3 3337 ACTGAAGCCACA T ACT - A 3 B c
c
2 GGCTGGTGGCCA CAT GC CCAGCCTG GGC
TGTTCTCT GTA CG GGTCGGAC CCG
C GT- A A

GAM189 246 SH3BP2 3 1122 NP_003014.2 3 3271 CTCTGTCGCCCA TTG C A 3 B c
b
GGCTAGAGTGGA CA CACTC AGCCTGGGC
TTGGCGTG GT GTGAG TCGGACCCG
TAG A C

GAM189 246 SH3BP2 3 3836 NP_003014.2 3 1850 CCCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGCCGTG GTAACGTGAGGTCGGACCCG
C

GAM189 246 SH3BP2 3 9440 NP_003014.2 5 157 CTCAGTTGCCCA A C 3 B b b
GACTGGAGAGCA CATTGC CTCCAG CTGGGCAA
GTGGCCAA GTGACG GAGGTC GACCCGTT
A A

GAM189 246 SHOX 1 4375 NP_006874.1 3 0 GCCCAGGCTGGA C A 3 B b b
GTATAATGGCAT CATTG ACTCCAGCCTGGGC
GTCTCGAC GTAAT TGAGGTCGGACCCG
A -

GAM189 246 SIGLEC8 1 4513 NP_055257.1 3 516 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGGCA GTGACGTGAGGTCGGATCC
AC

GAM189 246 SIL 1 12411 NP_003026.1 3 361 TCTTGTAGCCCA A 3 B b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCAGG GTAACGTGAGGTCGGACCCG
A

GAM189 246 SIRPB1 1 14771 NP_006056.1 3 2041 ACCTTATTCCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGTCGTG GTAACGTGAGGTCGGACCC
TT

GAM189 246 SLA2 1 19573 NP_115590.1 3 689 CCCTGTTGCCCA C 3 B b b
TGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCACG GTAACGTGAGGTCG ACCCGTT
T

GAM189 246 SLA2 1 19573 NP_778252.1 3 792 CCCTGTTGCCCA C 3 B b b
TGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCACG GTAACGTGAGGTCG ACCCGTT
T

GAM189 246 SLC12A8 1 5190 NP_078904.1 3 209 CCTTGTCACCCA C CA 3 B c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGCACA GTGAC TGAGGTCGGACCC
C AC

GAM189 246 SLC13A1 1 4370 NP_071889.2 3 1480 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGGG GTGACGTGAGGTCGGACCCG
C

GAM189 246 SLC14A2 1 4514 NP_009094.2 5 33 CTCTGTCACCCA T C CA 3 B c c
GGCTGGAGTACA CA TG ACTCCAGCCTGGG
CTGGCACT GT AC TGAGGTCGGACCC
C A AC

GAM189 246 SLC15A1 1 18930 NP_005064.1 3 219 TCTTGTTGTCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCTGTT

GAM189 246 SLC16A4 1 611 NP_004687.1 3 183 CTCTTTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM189 246 SLC19A3 1 6713 NP_079519.1 3 1013 ACAGGAGTCAGA G- A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
ATGGCGTG GTAACGTGAGGTCGGA CTG
GA A

GAM189 246 SLC1A5 1 1277 NP_005619.1 3 177 GGGATGCCTGGC - C -- TG 3 B c c

TGCTGGAGTACA CAT TG ACTCCAGC C GGCA
TGTGTTCA GTG AC TGAGGTCG G CCGT
T A TC GT

GAM189 246 SLC24A1 1 10966 NP_004718.1 3 687 TCTTGTTGCCCA T 3 B b b
GGCTGGTGTGCA CATTGCAC CCAGCCTGGGCAA
ATGGCGTG GTAACGTG GGTCGGACCCGTT
T

GAM189 246 SLC30A5 1 3692 NP_076960.1 3 153 CTCCATCGCCCA C A 3 B c c
GGCTGCAGTGCA CATTGCACT CAGCCTGGGC

GTGACACG GTGACGTGA GTCGGACCCG
C C
GAM189 246 SLC30A6 1 5362 NP_060434.2 3 507 CTCTGTCGCCCA C A 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCATG GTGACGT AGGTCGGACCCG
A C
GAM189 246 SLC35E2 1 13336 XP_049733.6 3 1607 GTCTGTCACCCA C CA 3 B c c

GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 SLC39A1 1 9528 NP_055252.2 5 88 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGGCGTGAGGTCGGACCCGTT

GAM189 246 SLC4A11 1 806 NP_114423.1 3 251 AGCTTCTGCCCA - G T G 3 B c c
GGGTGGGTGGGA CA TT CAC CCA CCTGGGCA
CTGAGCAG GT AG GTG GGT GGACCCGT
C G - G
GAM189 246 SLC5A1 1 2571 NP_000334.1 3 123 AAATTTTGCCCA - ----- G 3 B c c
GGTGGATAAATG CAT TGCAC TCCA CCTGGGCAA
TGTACATG GTA ATGTG AGGT GGACCCGTT
C TAAAT -
GAM189 246 SLC6A14 1 13830 NP_009162.1 3 1676 TTCTGTTGCCTG TG 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGGCATG GTGACGTGAGGTCGG CCGTT
GT
GAM189 246 SLC6A3 1 12941 NP_001035.1 3 1594 GTGGGCTCCAGG -- - A 3 B c c
GACTGGAGTGTA CATTGCACTCCAG CCTGG GC
ATGCTCGG GTAATGTGAGGTC GGACC CG
AG T G
GAM189 246 SMAC 2 1861 NP_620308.1 5 482 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGAG GTGACGTGAGGTCGGACCCG
C
GAM189 246 SMAC 2 18165 NP_620308.1 5 656 CTCTGTTGCCCA C 3 B b b
GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGGGCG GTGACGTGA GTCGGACCCGTT
A
GAM189 246 SNAP23 1 19007 NP_003816.2 3 673 CTCTCTTGTCCA C----- 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCG TAACGTGAGGTCGGACCTGTT
GCGCGA
GAM189 246 SNAP23 1 19007 NP_570710.1 3 673 CTCTCTTGTCCA C----- 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCG TAACGTGAGGTCGGACCTGTT
GCGCGA
GAM189 246 SNARK 1 18622 NP_112214.1 3 602 TCTTGGTGCCCA C 3 B b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCA
ATGGCGCG GTAACGTGAG TCGGACCCGT

A

GAM189 246 SNPH 1 15041 NP_055538.1 3 2430 GCCCTGGCCCAG - C- A 3 B c c
CTCTGGAGTGCA CAT TGCACTCCAG CTGGGC
TGTGTGTG GTG ACGTGAGGTC GACCCG
T TC G

GAM189 246 SNX15 1 7625 NP_037438.2 3 270 CTGTGTCGCCCA C A 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTGGG GTGACGTGAGGTC GACCCG
A C

GAM189 246 SNX15 1 7625 NP_680086.1 3 270 CTGTGTCGCCCA C A 3 B c c
GACTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTGGG GTGACGTGAGGTC GACCCG
A C

GAM189 246 SNX22 1 13596 NP_079074.1 3 519 TCTTGTTGCCCA C 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCACG GTGACGT AGGTCGGACCCGTT
A

GAM189 246 SNX27 1 16941 NP_112180.4 3 3109 CTCTGTCGCCCA A 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTTGGACCCG
C

GAM189 246 SPN 1 16209 NP_003114.1 3 185 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGCACGA GTAACGTGAGGTCGGACCCG
C

GAM189 246 SPOP 1 5610 NP_003554.1 5 130 CTCTGTCACCCG CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGGCCC
AC

GAM189 246 SQV7L 1 7375 XP_047287.1 5 1345 CTCTGTTGCCCA C A 3 B b b
GGCAGGAGTACA CATTG ACTCC GCCTGGGCAA
GTGGCATT GTGAC TGAGG CGGACCCGTT
A A

GAM189 246 SRL 1 6681 XP_064152.3 3 585 CTCTGTCGGCCA --- 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTTGGACC TGT
GGC

GAM189 246 SRRM2 1 18975 NP_057417.2 5 1 GCGGCCCAGGCG - A A 3 B c c
GGGTGCGAGTGG CATT GCACTCC GCCTGGGC
CGCAGTCG GTGA CGTGGGG CGGACCCG
G - G

GAM189 246 SS18 1 17762 NP_005628.1 3 1674 TCTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM189 246 STAF65(1 2196 NP_055675.1 3 1380 CTCTGTCACCCA CA 3 B b b
gamma) GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
AC

GAM189 246 STAU 1 3950 NP_004593.1 5 275 TCTTGTCGCCCA A 3 B b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM189 246 STE 1 3303 NP_005411.1 3 196 CTCTGTTGCCTA CA 3 B b b
GGCTGGAGGACA CATTG CTCCAGCCTGGGCAA
GTGGCACA GTGAC GAGGTCGGATCCGTT
AG

GAM189 246 STEAP2 1 9147 NP_694544.1 3 1987 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM189 246 STOM 1 2907 NP_004090.3 3 495 TCTTGTTGCCCA C----- 3 B b b
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCATG TAACGTGAGGTCGGACCCGTT
GTACGA

GAM189 246 STX12 1 12575 NP_803173.1 3 1621 AGTGTGTAGAGA C TGG--- 3 B c
c

TGGCTGAGTGCA CATTGCACTC AGCC GCA
ATGGCTCA GTAACGTGAG TCGG TGT
- TAGAGA

GAM189 246 SYT11 1 9033 NP_689493.2 3 281 TCTTGTTGCCCG 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGAG GTAACGTGAGGTCGGGCCCGTT

GAM189 246 SYT13 1 15294 NP_065877.1 3 1526 CTTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TADA3L 1 9087 NP_597814.1 3 289 CACTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM189 246 TAL1 1 18260 NP_003180.1 3 2375 TTCTGTCACTCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGTGCC GTGAC TGAGGTCGGACTC
A AC

GAM189 246 TAPBP 3 11523 NP_003181.3 3 837 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 TAPBP 3 12247 NP_003181.3 3 230 CTCTTCCGCCCA C A 3 B c b
GGCTGCAGTGCA CATTGCACT CAGCCTGGGC
GTGGCATG GTGACGTGA GTCGGACCCG
C C

GAM189 246 TAPBP 3 16940 NP_003181.3 3 1142 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TAT 1 18942 NP_000344.1 3 779 CTCTGTCGCCCA C A 3 B c c
TGCTGGAGTGCA CATTGCACTCCAGC TGGGC

GTGGCGCG GTGACGTGAGGTCG ACCCG
T C
GAM189 246 TBC1D5 2 14859 NP_055559.1 5 590 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C
GAM189 246 TBC1D5 2 16449 NP_055559.1 5 920 CGCTCTTGTCCA C 3 B b b
GGCTGGAGTATA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAT TGAGGTCGGACCTGTT
A
GAM189 246 TBX3 1 19690 NP_005987.2 5 243 GCCCAGCGCCCC G ------ - A 3 B c c
GCCTGGAGTGGA CATT CACTCCA GC CTGGGC
TGAGCCTC GTAG GTGAGGT CG GACCCG
- CCGCCC C -
GAM189 246 TBX3 1 19690 NP_057653.2 5 243 GCCCAGCGCCCC G ------ - A 3 B c c
GCCTGGAGTGGA CATT CACTCCA GC CTGGGC
TGAGCCTC GTAG GTGAGGT CG GACCCG
- CCGCCC C -
GAM189 246 TCF2 1 625 NP_006472.1 3 2022 CTCTGTCACCCG C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG GCCC
A AC
GAM189 246 TCL6 1 17450 NP_036600.2 5 645 CTCTGTCACTCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM189 246 TCL6 1 17450 NP_055233.1 5 645 CTCTGTCACTCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM189 246 TCL6 1 17450 NP_065575.1 5 645 CTCTGTCACTCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM189 246 TCL6 1 17450 NP_065577.2 5 645 CTCTGTCACTCA C CA 3 B c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM189 246 TDGF1 1 8563 NP_003203.1 3 321 CTCTGTCACCCA C CA 3 B c c
GGCTGGACTGCA CATTGCA TCCAGCCTGGG
ATGACGCG GTAACGT AGGTCGGACCC
C AC
GAM189 246 TERA 2 14491 NP_067061.1 3 305 CCACGTTGGCCA GCACT G 3 B c
c
GGCTGGTCTTAA CATT CCAGCCTGG CAA
ATGACCCT GTAA GGTCGGACC GTT
ATTCT G
GAM189 246 TERA 2 17755 NP_067061.1 3 140 TCTTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC

AT

GAM189 246 TERF1 1 1745 NP_003209.1 3 419 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 TERF1 1 1745 NP_059523.1 3 419 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 TERF2 1 1744 NP_005643.1 3 141 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM189 246 TGIF2 1 6881 NP_068581.1 3 1452 CTCTGTCACCCG CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGGCCC
AC

GAM189 246 TIGD6 1 4933 NP_112215.1 3 909 TTATATTGCCTA C 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGTTAT GTGACGT AGGTCGGATCCGTT
A

GAM189 246 TIM50L 2 5989 XP_053074.2 3 614 CACTGTTGCCCA T 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGATGTG GT ACGTGAGGTCGGACCCGTT
T

GAM189 246 TIM50L 2 10157 XP_053074.2 3 1407 TCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM189 246 TLK1 1 6551 NP_036422.2 5 279 TCCGGGAGGCCC CCAG A 3 B c c

AGGGAAGGTGCA CATTGCACT CCTGGGC
ATGGATGA GTAACGTGG GGACCCG
AAG- G

GAM189 246 TLR5 1 16229 NP_003259.2 5 97 CTCTGCCGCCCA C A 3 B c c
GGCTGGACTGCA CATTGCA TCCAGCCTGGGC
GTGACACA GTGACGT AGGTCGGACCCG
C C

GAM189 246 TMC1 1 2152 NP_619636.2 5 128 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TMEM14A 1 5271 NP_054770.1 5 75 CTCGGGGCTGCA - A 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGC
GTGGGACA GTGACGTGAGGTCGGAC TCG
G G

GAM189 246 TMPRSS3 1 6625 NP_076927.1 3 245 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM189 246 TMPRSS3 1 6625 NP_115777.1 3 245 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM189 246 TMPRSS3 1 6625 NP_115780.1 3 245 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM189 246 TNFAIP2 2 13948 NP_006282.2 3 637 ACGGCCCCTACA CT- ---- A 3 B c b

GGCTGGCCCTGC CATTGCA CCAGCCT GGGC
AATGGGGC GTAACGT GGTCGGA CCCG
CCC CATC G
GAM189 246 TNFAIP2 2 17621 NP_006282.2 3 1221 CTGTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCCTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TNFRSF1 2 4398 NP_003833.3 3 454 CTCTGTCTCCCA CA 3 B b b
0B GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
TC
GAM189 246 TNFRSF1 2 4398 NP_671716.1 3 454 CTCTGTCTCCCA CA 3 B b b
0B GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
TC
GAM189 246 TNFRSF1 2 15107 NP_003833.3 3 2022 CTCTCTCGCCCA CA----- A 3 B c
b
0B GGCTGGAGTGCA TTGCACTCCAGCCTGGGC
ACGGTACG AACGTGAGGTCGGACCCG
GCATGGC C
GAM189 246 TNFRSF1 2 15107 NP_671716.1 3 2022 CTCTCTCGCCCA CA----- A 3 B c
b
0B GGCTGGAGTGCA TTGCACTCCAGCCTGGGC
ACGGTACG AACGTGAGGTCGGACCCG
GCATGGC C
GAM189 246 TNFRSF1 1 2200 NP_003830.1 3 503 GGCTCTGGCCCA C A 3 B c c
1A GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGTGCG GTGACGTGAG TCGGACCCG
A G
GAM189 246 TNFRSF2 1 16759 NP_055267.1 3 747 TAATATGCTCTG GCA TG - 3 B c
c
1 GGCTGGAGAAAT CATT CTCCAGCC G GCA
GAAATCCT GTAA GAGGTCGG C CGT
A-- GT T
GAM189 246 TNFRSF9 1 13464 NP_001552.2 3 227 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC
GAM189 246 TNS 1 8787 NP_072174.2 3 34 GCCCCTTGCCCA T CCAG 3 B c c
GGGCCAGTGCCA CAT GCACT CCTGGGCAA

TGGGGAAG GTA CGTGA GGACCCGTT
C CCG-
GAM189 246 TOLLIP 2 3306 NP_061882.2 3 933 CTGCTGTGCCCA T --- CAG- 3 B c c
GGACGTGGGTTC CAT GC ACTC CCTGGGCA
AGCGTGGG GTG CG TGGG GGACCCGT
- ACT TGCA
GAM189 246 TOLLIP 2 13694 NP_061882.2 3 526 GGCCCCTGCCCA C C - 3 B c c
GGGCTTGGGTCT CATTG ACTC AGCC TGGGCA
GGTGAGCT GTGGT TGGG TCGG ACCCGT
C T G
GAM189 246 TOP3B 1 4495 NP_003926.1 3 39 CTCCCTCACCCA T C CA 3 B c c
GGCTGCAGTGCC CAT GCACT CAGCCTGGG
ATGCAGAC GTA CGTGA GTCGGACCC
C C AC
GAM189 246 TOR1B 1 14221 NP_055321.1 3 180 CTCCGTCATCCA C CA 3 B c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCT
A AC
GAM189 246 TOSO 1 5682 NP_005440.1 3 356 TGTTGCTGCCCA - CA CC 3 B c c
GGCTCTAGATCA CAT TG CT AGCCTGGGCA
CATGGCAT GTA AC GA TCGGACCCGT
C TA TC
GAM189 246 TP53 1 4654 NP_000537.2 3 833 CTTTGTTGCCCA G 3 B b b
GGCTGGAGTGGA CATT CACTCCAGCCTGGGCAA
GTGGCGTG GTGA GTGAGGTCGGACCCGTT
G
GAM189 246 TP53I11 1 14987 XP_029347.6 5 217 CTGCAGAGGCCG GCA-- ----- 3 B c
c
GGCTGGAGGAGA CATT CTCCAGCCTGG GCA
AGATGGCG GTAG GAGGTCGGGCC CGT
AAGAG GGAGA
GAM189 246 TPMT 1 19670 NP_000358.1 3 426 TCTTGTTGCCCA CC 3 B b b
ACCTGGAGTGCA CATTGCACTCCAG TGGGCAA
GTGGTGCG GTGACGTGAGGTC ACCCGTT
CA
GAM189 246 TRAF5 1 7045 NP_004610.1 3 1091 CATTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 TRAF5 1 7045 NP_665702.1 3 1091 CATTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 TRIM16 1 4601 NP_006461.2 3 249 CACTGTTGCCCA A 3 B b b
GGCTGGAGAGCA CATTGC CTCCAGCCTGGGCAA
GTGGCGCG GTGACG GAGGTCGGACCCGTT
A
GAM189 246 TRIM5 1 5879 NP_149023.1 3 651 TCTTGTTCCCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACG GTAACGTGAGGTCGGACCC

CT

GAM189 246 TRIM6 1 13572 NP_477514.1 3 172 CTCTGTCGCCCA T A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
CTGGCGCA GT ACGTGAGGTCGGACCCG
C C

GAM189 246 TRIP-Br 1 19574 NP_055570.1 3 2988 GACAGTTATTGA TC CC GG 3 B c
c
2 CACTGATGTGCA CATTGCAC CAG TG CAA
ATGAAGTG GTAACGTG GTC AC GTT
TA -- A-

GAM189 246 TRPM6 1 18177 NP_060132.3 3 857 TCTTTTTACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGATGCG GTAACGTGAGGTCGGACCC
AT

GAM189 246 TRPV1 2 16980 NP_061197.3 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM189 246 TRPV1 2 16980 NP_542435.1 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM189 246 TRPV1 2 16980 NP_542436.1 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM189 246 TRPV1 2 16980 NP_542437.1 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM189 246 TRPV1 2 19833 NP_061197.3 3 685 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TRPV1 2 19833 NP_542435.1 3 686 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TRPV1 2 19833 NP_542436.1 3 686 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TRPV1 2 19833 NP_542437.1 3 685 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM189 246 TSC1 1 15082 NP_000359.1 3 786 ATTGTGACCACA - T - - 3 B c c
GGCTGGTGTGTA CAT TGCAC CCAGCCTG GG CA
GGTGGTAA GTG ATGTG GGTCGGAC CC GT
G T A A

GAM189 246 TSPYL 1 15042 XP_166325.1 3 658 CTCTGTCGCCCA A 3 B b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTTGGACCCG
C
GAM189 246 TTY7 1 1016 NP_114132.1 5 521 CCCCCATGCCCA G TC G 3 B c c
GGTGTGGTGAAG CATT CAC CA CCTGGGCA
TGAATCCC GTGA GTG GT GGACCCGT
A GT -
GAM189 246 TU12B1-TY 3 4256 NP_057659.1 3 3182 TCTTTTTGCCCA A 3 B b b
GGCCGGAGTGCA CATTGCACTCC GCCTGGGCAA
ATGGCACG GTAACGTGAGG CGGACCCGTT
C
GAM189 246 TU12B1-TY 3 15780 NP_057659.1 3 1305 TCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM189 246 TU12B1-TY 3 16036 NP_057659.1 3 2855 CTCTGTTGCCCA CC 3 B b b
TTCTGGAGTGCA CATTGCACTCCAG TGGGCAA
GTGGTGTG GTGACGTGAGGTC ACCCGTT
TT
GAM189 246 TUCAN 2 7106 NP_055774.1 3 2766 CTCTGTCATCTA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGATCT
AC
GAM189 246 TUCAN 2 9530 NP_055774.1 3 2457 CTCTGTTACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AT
GAM189 246 TXL-2 1 15381 NP_835231.1 5 95 AATTGCCCTGCA CA----- --- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCT GGGCAA
GCGGCATG GACGTGAGGTCGGA CCCGTT
GTACGGC CGT
GAM189 246 TXNL2 2 9147 NP_006532.1 3 68 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 TXNL2 2 19232 NP_006532.1 3 766 AATTAAGTGCCA CA T G 3 B c c
GGCTGGGCACAA CATTG C CCAGCCTGG CA
TGGCTCGT GTAAC G GGTCGGACC GT
AC - -
GAM189 246 U1SNRNP 1 9590 NP_008951.1 5 122 GGGAGTCGCCCA A A 3 B c c

BP GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C
GAM189 246 U1SNRNP 1 9590 NP_851030.1 5 122 GGGAGTCGCCCA A A 3 B c c

BP GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C

GAM189 246 U1SNRNP 1 9590 NP_851034.1 5 122 GGGAGTCGCCCA A A 3 B c c

BP GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C

GAM189 246 UCK1 1 11791 NP_113620.1 3 710 TGTGCGGGGCCA C ---- - ---- 3 B c c
GGCTGGGAGCCC ATTGCA CTCC AGCCTGG GCA
ATGCAGTA TGACGT GAGG TCGGACC CGT
A ACCC G GGGG

GAM189 246 UGDH 1 7909 NP_003350.1 3 153 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM189 246 UGT1A1 1 10967 NP_000454.1 3 534 AATGAATGAATG T - TGGG 3 B c c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM189 246 UGT1A10 1 10967 NP_061948.1 3 535 AATGAATGAATG T - TGGG 3 B c c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM189 246 UGT1A4 1 10967 NP_009051.1 3 534 AATGAATGAATG T - TGGG 3 B c c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM189 246 UGT1A6 1 10967 NP_001063.1 3 533 AATGAATGAATG T - TGGG 3 B c c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM189 246 UGT1A8 1 10967 NP_061949.3 3 535 AATGAATGAATG T - TGGG 3 B c c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM189 246 UGT1A9 1 10967 NP_066307.1 3 534 AATGAATGAATG T - TGGG 3 B c c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM189 246 UMPS 1 2144 NP_000364.1 3 391 CTCTGTTGCCCA G 3 B b b
GGATGGAGTGCA CATTGCACTCCA CCTGGGCAA
GTGGTGAG GTGACGTGAGGT GGACCCGTT
A

GAM189 246 UNC84B 1 13541 NP_056189.1 3 1393 TCTGGAGCATGA C GG- A 3 B c c
GGCTGGATGCAG CATTGCA TCCAGCCT GC

TGGTGGTG GTGACGT AGGTCGGA CG
- GTA A
GAM189 246 UNC84B 1 13541 XP_039332.1 3 1393 TCTGGAGCATGA C GG- A 3 B c c
GGCTGGATGCAG CATTGCA TCCAGCCT GC
TGGTGGTG GTGACGT AGGTCGGA CG
- GTA A
GAM189 246 URG4 1 6788 NP_060390.2 3 565 GACCCCTGCCCA T C CAG 3 B c c
GGAAGAGTTCAC CA TG ACTC CCTGGGCA
TGGTCGCT GT AC TGAG GGACCCGT
C T AA-
GAM189 246 USP22 1 11288 XP_042698.2 3 2025 GTTTGTTGCCCA G 3 B b b
GGCTGGAGTGAG CATT CACTCCAGCCTGGGCAA
TGGCACAG GTGA GTGAGGTCGGACCCGTT
-
GAM189 246 VDU1 1 3187 NP_055832.2 3 278 CTTTGTCACCCA T CA 3 B c c
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGTGTT GTG CGTGAGGTCGGACCC
T AC
GAM189 246 VENTX2 1 19331 NP_055283.1 3 305 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGACGCA GTAACGTGAGGTCGGACCC
AC
GAM189 246 VHL 2 3873 NP_000542.1 3 2569 CTCTGTTGCCCA CA----- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GAGGTGCG GACGTGAGGTCGGACCCGTT
GCGTGGA
GAM189 246 VHL 2 8786 NP_000542.1 3 989 TCTTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM189 246 VIPR2 1 7754 NP_003373.2 3 314 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCCTG GTGACGTGAGGTCGGACCCG
C
GAM189 246 VPS39 1 18246 XP_031720.2 3 1284 CAGAGGTGCACA T ----- G 3 B c c
GGCTGGAGTTTC CA TGC ACTCCAGCCTG GCA
AGGCACTG GT ACG TGAGGTCGGAC CGT
C GACTT A
GAM189 246 VTI1A 1 2313 NP_660207.1 3 358 GCCCTGTCGCCT G T A 3 B c c
GGCTGGAGTGGA CATT CACTCCAGCC GGGC
GTGGCACA GTGA GTGAGGTCGG TCCG
G - C
GAM189 246 WBSCR18 1 2152 NP_115693.2 3 832 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT
GAM189 246 WDR6 1 12628 NP_439891.1 5 93 TCCCAGTGACGG T - GG 3 B c c
GTCTGGAGTGCG CAT GCACTCCAG CCTG CA

TGGGGGAC GTG CGTGAGGTC GGGC GT
- T A-

GAM189 246 WHSC1 1 9245 NP_579889.1 3 3922 CCCTGTTGGCCA C----- G 3 B c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGG CAA
GTAAGTGG TGACGTGAGGTCGGACC GTT
GGTGAA G

GAM189 246 WNT5A 1 10269 NP_003383.1 5 751 GCTTTGGGGATG - T------ A 3 B c c
GCTGGAAGTGCA CATTGCACT CCAGCC GGGC
ATGTCTTC GTAACGTGA GGTCGG TTCG
A TAGGGGT -

GAM189 246 XRCC2 3 9688 NP_005422.1 3 99 CTCTGTCTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC

GAM189 246 XRCC2 3 10148 NP_005422.1 3 278 TGTCTCCCAGGC --- CA 3 B c c
TGCTGGAGTGCA CATTGCACTCCA GCCTGGG
GTGGCACA GTGACGTGAGGT CGGACCC
CGT TC

GAM189 246 XRCC2 3 12605 NP_005422.1 3 278 CTCTGTCTCCCA --- CA 3 B c c
GGCTGCTGGAGT CATTGCACTCCA GCCTGGG
GCAGTGGC GTGACGTGAGGT CGGACCC
CGT TC

GAM189 246 YES1 1 16112 NP_005424.1 3 1378 CTCTGCCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM189 246 ZAP 2 508 NP_064504.2 3 204 TTCTGATGCCCA - CTC---- 3 B c b
GGTTGCACCCCA CATTG CA CAGCCTGGGCA
TGCCAATG GTAAC GT GTTGGACCCGT
C ACCCCAC

GAM189 246 ZAP 2 3071 NP_064504.2 3 308 CTCCATCGTCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCTG
C

GAM189 246 ZFP30 1 9331 NP_055713.1 3 1854 CTCTTTCGCCCA T A 3 B c c
GGCTGGCGTGCA CATTGCAC CCAGCCTGGGC
GTGGCACA GTGACGTG GGTCGGACCCG
C C

GAM189 246 ZFP42 1 10587 NP_777560.1 3 643 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTCTA CATTG ACTCCAGCCTGGG
GTGTCGTG GTGAT TGAGGTCGGACCC
C AC

GAM189 246 ZFP64 1 15043 NP_060667.1 3 151 CTCTGTTTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCT GTGACGTGAGGTCGGACCC
TT

GAM189 246 ZFP64 1 15043 NP_071371.2 3 151 CTCTGTTTCCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCT GTGACGTGAGGTCGGACCC
TT

GAM189 246 ZFYVE26 1 12160 XP_031077.1 3 3 CCCATGGCCCAG TT - --- A 3 B c c
GCTCCAGGAAGT CA GCACT CC AGCCTGGGC
GCCTTGGG GT CGTGA GG TCGGACCCG
TC A ACC G
GAM189 246 ZMYND17 1 456 NP_848546.1 3 219 CTCTGTTGCCCA CA----- 3 B c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGGCATG GACGTGAGGTCGGACCCGTT
GTACGGC
GAM189 246 ZNF18 1 19151 XP_085596.2 5 97 AAGGACTTGCCA CAC G 3 B b b
GGCTGGACAATG CATTG TCCAGCCTGG CAA
CCCGTTGA GTAAC AGGTCGGACC GTT
--- -
GAM189 246 ZNF253 1 19746 NP_066385.1 3 292 TCTTGTCACCGA G CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GG
ATGACATG GTAACGTGAGGTCGGA CC
G AC
GAM189 246 ZNF264 2 3319 NP_003408.1 3 2604 CTCTGTCACCCA T C CA 3 B c c
CGCTGGAGTGCT CAT GCACTCCAGC TGGG
GTGATGCG GTG CGTGAGGTCG ACCC
T C AC
GAM189 246 ZNF264 2 9147 NP_003408.1 3 2978 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM189 246 ZNF273 1 18868 XP_088082.1 3 843 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM189 246 ZNF281 1 16434 NP_036614.1 3 34 CAAAAGTGGCCA CA---- G 3 B c c
GGCTGGAGGTCT CATTG CTCCAGCCTGG CA
TCTAATGT GTAAT GAGGTCGGACC GT
CTTCTG G
GAM189 246 ZNF289 1 13159 NP_115765.2 3 77 CCACAGTTCCCA TT - CA 3 B c c
GGCTGGGGATGC CA GCA CTCCAGCCTGGG
TTTGCCTT GT CGT GGGGTCGGACCC
TT A TT
GAM189 246 ZNF305 1 18505 NP_055539.1 3 2909 TCCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCACG GTAACGTGAGGTCGGACCCG
C
GAM189 246 ZNF334 2 5064 NP_060572.2 5 42 TGTCACCCAGGC C --- CA 3 B c c
TGCTGGAGTACA CATTG ACTCCA GCCTGGG
GTGGCACA GTGAC TGAGGT CGGACCC
A CGT AC
GAM189 246 ZNF334 2 9628 NP_060572.2 5 42 CACTGTCACCCA C --- CA 3 B c c
GGCTGCTGGAGT CATTG ACTCCA GCCTGGG
ACAGTGGC GTGAC TGAGGT CGGACCC
A CGT AC
GAM189 246 ZNF339 1 1729 NP_067043.1 3 655 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG

GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM189 246 ZNF345 1 1011 NP_003410.1 3 601 TCACTGTCACCA -- 3 B b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTCGGACC TGT
AC
GAM189 246 ZNF398 1 8530 NP_065832.1 5 255 CTCTGTCGCCCA C A A 3 B c c
GGCGGGAATGCA CATTGCA TCC GCCTGGGC
GTGGCGCA GTGACGT AGG CGGACCCG
A G C
GAM189 246 ZNF409 1 2388 NP_055709.1 5 10 AGCGAGTGCCCA CACTC G 3 B c
c
GGGTGAATCAAT CATTG CA CCTGGGCA
GGAAACCC GTAAC GT GGACCCGT
TAA-- G
GAM189 246 ZNF431 1 8477 XP_086098.2 3 1487 CTCTTTCGCCCA T A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
TTGGCATG GT ACGTGAGGTCGGACCCG
T C
GAM189 246 ZNF432 1 5065 NP_055465.1 3 1769 TCTTGTTGCCCA C----- 3 B c c
GGTTGGAGTGTA ATTGCACTCCAGCCTGGGCAA
ATAGCACG TAATGTGAGGTTGGACCCGTT
GCACGA
GAM189 246 ZNF440 1 1744 NP_689570.1 3 1224 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM189 246 ZNF70 1 17076 NP_068735.1 3 1596 GCCCTGTTGCCA C G 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM189 246 ZNF70 1 17076 NP_852101.1 3 1596 GCCCTGTTGCCA C G 3 B b b
GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM189 246 ZNF74 1 12340 NP_003417.1 5 610 TGTCACCCAGGC --- A CA 3 B c c
GGGAGTGGTGCA CATTGCAC TCC GCCTGGG
ATGGCTTG GTAACGTG AGG CGGACCC
GTG G AC
GAM190 289 ABCC3 1 1929 NP_064422.1 3 1743 TCAGGCCGCATC T AAGA 3 A c
c
CTGAACTGCTTC G AGCA TTCAGGATGTG
TCCAAGGA C TCGT AAGTCCTACGC
T C---
GAM190 289 ACRC 1 16426 NP_443189.1 5 28 ATCGCAGTTGCT A A ----- 3 A c c
CCGGATCTTTGC GT GCAAAGATTC GGA TGTG
ACACACTC CA CGTTTCTAGG CCT ACGC
- - CGTTG
GAM190 289 ADCY1 1 16609 NP_066939.1 3 3179 CACATGTACATC AAAGA 3 A c
c

CTGGAAGCTGCC GTAGC TTCAGGATGTGC
CAAGGTGT CGTCG AGGTCCTACATG
A----

GAM190 289 AGL 1 9569 NP_000636.1 5 12 AATTTGCACATC AGATTCA 3 A c c
CCAAGTTGCTAT GTAGCAA GGATGTGC
GTGAATAG TATCGTT CCTACACG
GAAC---

GAM190 289 AGS3 1 16761 NP_056412.1 3 47 CCCACCCGCATC AAAG 3 A c c
CTGAGTGGCGCT GTAGC ATTCAGGATGTG
GCAGGGCT CGTCG TGAGTCCTACGC
CGG-

GAM190 289 ANKTM1 1 10754 NP_015628.1 3 1413 TGTTGCATATAC G C - 3 A c c
CTTAATCTTTGA GTA CAAAGATT AGG ATGTGC
TATGAATA TAT GTTTCTAA TCC TATACG
A T A

GAM190 289 ANXA10 1 6862 NP_009124.1 3 210 TTGCCTACTATC CAA - 3 A c c
CTGAATTTGCCT GTAG AGATTCAGGAT GTG
ACTATCTA CATC TTTAAGTCCTA CAT
CG- T

GAM190 289 ARHGAP6 1 2102 NP_001165.1 5 1152 CTACCGCCTCCT T -- T 3 A c c

GGACCTCTTTGC G AGCAAAGA TTCAGGA GTG
TCGTCCTT C TCGTTTCT AGGTCCT CGC
- CC C

GAM190 289 ARHGEF7 1 3061 NP_003890.1 3 1483 CTTTAACTGCAC - - A 3 A c c
CTGAATCCTTTG GTA GCAAAG ATTCAGG TGTG
TGTACTGA CAT TGTTTC TAAGTCC ACGT
G C -

GAM190 289 ATP11B 1 10635 XP_087254.2 3 2215 AGTGTGCTCATC AAGA T 3 A c
c

CTGAACTGTTAC GTAGCA TTCAGGATG GC
TCCAAATC CATTGT AAGTCCTAC CG
C--- T

GAM190 289 ATP6V1G 1 1415 NP_569730.1 3 183 TCCTGCTCACAT G--- -- G 3 A c c
2 CTGAATCTCCTT TAGCAA AGATTCAG ATGTG
GTTGTTCT GTTGTT TCTAAGTC TACAC
TCTT CC -

GAM190 289 ATP6V1G 1 1415 NP_612139.1 3 183 TCCTGCTCACAT G--- -- G 3 A c c
2 CTGAATCTCCTT TAGCAA AGATTCAG ATGTG
GTTGTTCT GTTGTT TCTAAGTC TACAC
TCTT CC -

GAM190 289 ATP7B 1 1270 NP_000044.1 3 619 GACCAATGTCCT - - G 3 A c c
TGTGGTCTTTGC GTAGCAAAGATT CA GGATGT
TGCTGCTC CGTCGTTTCTGG GT CCTGTA
T T A

GAM190 289 B4GALT5 1 2973 NP_004767.1 3 308 CTACCCCACATC TA A TT 3 A c
c

CTGTCTTAGCCG G GC AAGA CAGGATGTG
CAGTCTCC C CG TTCT GTCCTACAC
GC A --

GAM190 289 BAZ2A 1 6467 NP_038477.1 3 167 GTGCCCCACATC CA-- TTCA 3 A c c

CTCTTATTCCTA GTAG AAGA GGATGTG
CATCCCTT CATC TTCT CCTACAC
CTTA ----

GAM190 289 C14orf1 1 10053 NP_064600.1 3 646 AACAGCCAGATC - A --- G 3 A c c
32 CTGAATGTTCTA GT AGCA AGA TTCAGGAT TG
TGTTCACC CA TTGT TCT AAGTCCTA AC
C A TGT G

GAM190 289 C1QTNF5 1 19062 NP_056460.1 3 0 GGCACAGCTCCC T CA -- 3 A c c

CAGTCTTTGCTT G AGCAAAGATT GGA TGTGC
ATGCCCAC A TCGTTTCTGA CCT ACACG
T CC CG

GAM190 289 CARKL 1 13528 NP_037408.1 3 2290 AACAGTCATATG CA G 3 A c c
CTGAATCTTCTA GTAG AAGATTCAG ATGTG
TCTGTGAA TATC TTCTAAGTC TATAC
-- G

GAM190 289 CAS1 1 16002 NP_075051.2 3 621 GGGTATGCAAGC G C ATG 3 A c c

CTAAATCTTTGT GTA CAAAGATT AGG TGC
ACACTTTG CAT GTTTCTAA TCC ACG
- A GA-

GAM190 289 CCNF 1 2161 NP_001752.1 3 1643 TGTCCGCGGCAG TT GA - 3 A c c

CTGTCTTTTTGC GTAGCAAAGA CAG TGT GC
TACTATAA CATCGTTTTT GTC ACG CG
CT G- G

GAM190 289 CCR2 1 8836 NP_000638.1 3 84 GTGATTCACAGT - -- GGA 3 A c c
GTGAATCTTGGT GTAG CA AAGATTCA TGTG
GTCTACGT CATC GT TTCTAAGT ACAC
T GG GTG

GAM190 289 CD209 1 1357 NP_066978.1 3 2395 AACCACTCCTCA TA - --- T 3 A c c
TGTAATCTTTGC G GCAAAGATT CA GGA GTG
CTCTCTCT C CGTTTCTAA GT CCT CAC
TC T ACT -

GAM190 289 CD4 1 4243 NP_000607.1 3 555 CAGACTCACATC A AGAT 3 A c c
CTGACCTTGCAC GT GCAA TCAGGATGTG
AAACAGCC CA CGTT AGTCCTACAC
- CC--

GAM190 289 CDC14A 1 12880 NP_003663.2 3 1200 GAGCGTTACATC AAA---- - 3 A c c

CTGATATCCTTC GTAGC GAT TCAGGATGTG
CAGGCTGC CGTCG CTA AGTCCTACAT
GACCTTC T

GAM190 289 CENTD2 1 5185 NP_056057.1 3 146 ACAACCCACATC - AA TC 3 A c c

CTCCATCCTGAC GTAG CA GAT AGGATGTG
TGCAGCAT CGTC GT CTA TCCTACAC
A C- CC

```
GAM190  289  CENTD2 1  5185  NP_631920.1  3 146   ACAACCCACATC   - AA  TC          3 A c c

                              CTCCATCCTGAC GTAG CA  GAT  AGGATGTG
                              TGCAGCAT    CGTC GT  CTA  TCCTACAC
                                    A C-  CC
GAM190  289  CLCN6  1  15103 NP_001277.1  3 358   AGCAGTGTTCCT       --   TG--      3 A c c
                              GGCCATCTTTGC GTAGCAAAGAT  TCAGGA   TGC
                              TACTTTCC    CATCGTTTCTA  GGTCCT   ACG
                                    CC     TGTG
GAM190  289  CLCN6  1  15103 NP_068503.1  3 358   AGCAGTGTTCCT       --   TG--      3 A c c
                              GGCCATCTTTGC GTAGCAAAGAT  TCAGGA   TGC
                              TACTTTCC    CATCGTTTCTA  GGTCCT   ACG
                                    CC     TGTG
GAM190  289  CLCN6  1  15103 NP_068504.1  3 358   AGCAGTGTTCCT       --   TG--      3 A c c
                              GGCCATCTTTGC GTAGCAAAGAT  TCAGGA   TGC
                              TACTTTCC    CATCGTTTCTA  GGTCCT   ACG
                                    CC     TGTG
GAM190  289  CLCN6  1  15103 NP_068505.1  3 358   AGCAGTGTTCCT       --   TG--      3 A c c
                              GGCCATCTTTGC GTAGCAAAGAT  TCAGGA   TGC
                              TACTTTCC    CATCGTTTCTA  GGTCCT   ACG
                                    CC     TGTG
GAM190  289  CLECSF9 1  15211 NP_055173.1  3 250   TACAAAGCAATT      GATTC  -  ---      3 A c
c
                              CATACCTTTTGC GTAGCAAA    AGG ATG   TGC
                              TACATTTG    CATCGTTT    TCC TAC   ACG
                                    -----  A  TTA
GAM190  289  CLOCK  1  16410 NP_004889.1  3 2734  AGTAAGCACCAG       TT  GAT        3 A c
c
                              CTGCCTCTTTGC GTAGCAAAGA  CAG   GTGC
                              TGCTTTGT    CGTCGTTTCT  GTC   CACG
                                    CC   GAC
GAM190  289  CPA1   1  8808  NP_001859.1  3 0     AGCACACCCTGA    CAAA      A        3 A c c
                              ATCACCCCTACT GTAG    GATTCAGG TGTGC
                              GGCTGACC    CATC    CTAAGTCC ACACG
                                    CCCA       C
GAM190  289  CPA5   1  16798 NP_525124.2  3 0     AGCACACCCTGA    CAAA      A        3 A c c
                              ATCACCCCTACT GTAG    GATTCAGG TGTGC
                              ACAGCACG    CATC    CTAAGTCC ACACG
                                    CCCA       C
GAM190  289  CPNE3  1  16717 NP_003900.1  3 537   CCTGTCTATGCA         CA          3 A c c
                              TCTGATTTTTGC GTAGCAAAGATT  GGATGTG
                              TACAGTTT    CATCGTTTTTAG  TCTACGT
                                    --
GAM190  289  CRYZL1 1  7391  NP_005102.2  3 420   TCAACACCTTCC -       C-   T-       3 A c c
                              TTAAGTCTTTGC G TAGCAAAGATT  AGGA  GTG
                              TGTCATAA    C GTCGTTTCTGA  TCCT  CAC
                                    T        AT    TC
GAM190  289  CRYZL1 1  7391  NP_665857.1  3 1333  TCAACACCTTCC -       C-   T-       3 A c c
                              TTAAGTCTTTGC G TAGCAAAGATT  AGGA  GTG
                              TGTCATAA    C GTCGTTTCTGA  TCCT  CAC
```

```
                                        T        AT   TC
GAM190  289   DGCR2  1  16760 NP_005128.1  3  1222  TTTTAGCACATC   C    TCA          3  A  c  c

                                  CATATCTTTTCT GTAG AAAGAT   GGATGTGC
                                  ACGTTGAA    CATC TTTCTA   CCTACACG
                                        T     TA-
GAM190  289   DKFZp31 1  13429 XP_087728.2  3  1485  GTAAGCAAATTT   G      -  G       3  A  c  c
        3G1735                      ATGAATCTTTGT GTA CAAAGATTCA GGAT TGC
                                  ACACCATA    CAT GTTTCTAAGT TTTA ACG
                                        -       A   A
GAM190  289   DKFZP43 1  14814 NP_110431.1  3  1115  ATGATTACAGTT  A  AA     -        3  A  c  c

        4E2135                      CTGAATCTGTAA GT GCA  GATTCAGGA TGTG
                                  CACTTACA    CA TGT  CTAAGTCTT ACAT
                                        A  --      G
GAM190  289   DKFZp43 1  14147 NP_057697.1  3  2640  AGCTAGGTACAG      G   AGGA         3  A  c
 c
        4L142                       AGGAATGTTTGC GTAGCAAA ATTC    TGTGC
                                  TACCTTTA    CATCGTTT TAAG    ACATG
                                        G   GAG-
GAM190  289   DKFZP58 1  19113 NP_056248.1  3  1362  CTATTGCATTTC      ATTC   T        3  A  c
c
        6D0919                      CTACTCCTTTGC GTAGCAAAG    AGGA GTGC
                                  TACGTGTA    CATCGTTTC    TCCT TACG
                                        CTCA   T
GAM190  289   DKFZP72 1  12451 XP_045308.2  3  393   TGTTCGCACATC  A  AAGATT          3  A  c
 c
        7G051                       CTGTGTGTGCAC GT GCA     CAGGATGTGC
                                  AGCTGTCC     CA CGT     GTCCTACACG
                                        -  GTGT--
GAM190  289   DKFZP72 1  12399 NP_056355.2  3  198   TACCATTACATC T  AA-  -          3  A  c  c
        7M111                       CTGATATCTGGG G AGC   AGAT TCAGGATGTG
                                  GCTTCTGA    C TCG   TCTA AGTCCTACAT
                                        T  GGG   T
GAM190  289   DPF3   1  14462 NP_036206.1  3  3393  ACTACCCACGTA   -  -    GG        3  A  c  c
                                  GTGAATCTTTTG GTAG CAAA GATTCA  ATGTG
                                  TCTGCAAT    CGTC GTTT CTAAGT  TGCAC
                                        T   T    GA
GAM190  289   E2IG5  1  3520  NP_055182.2  3  385   CAGACCACATTC  AG     C-          3  A  c  c
                                  TATAATCTTTGA GT  CAAAGATT  AGGATGTG
                                  ACATGCTG    CA  GTTTCTAA  TCTTACAC
                                        A-      TA
GAM190  289   ESPL1  1  7872  NP_036423.1  5  290   TGTGATGCCATC  A   AGA     T       3  A  c  c
                                  CTGAGGGCTTGC GT GCAA   TTCAGGATG GC
                                  AACCAGCA    CA CGTT   GAGTCCTAC CG
                                        A   CGG      -
GAM190  289   ETV1   1  18488 NP_004947.2  5  264   ATCGCCTCTTGT        ----   T      3  A  c  c
                                  TCGGATTTTTGC GTAGCAAAGATT    CAGGA GTG
                                  TACTACCG    CATCGTTTTTAG    GTTCT CGC
                                        GCTT    C
```

GAM190 289 EXTL2 1 3245 NP_001430.1 3 279 ATTGTTTACATC CAA A 3 A c c
CTGAGACTGTTC GTAG AG TTCAGGATGTG
TACAGTTT CATC TC GAGTCCTACAT
TTG A
GAM190 289 FLJ0000 1 9436 NP_258260.1 3 1673 ACCAGGGACATC AA-- G 3 A c c
7 CTGAGTTTGGTG GTAGC AGATTCAGGATGT
GCTACTTC CATCG TTTGAGTCCTACA
GTGG G
GAM190 289 FLJ1242 1 16869 XP_098290.1 3 1223 CTGCCCACCTGC G ---- A T 3 A c c
5 CATAGTATTTGC GTAGCAAA ATT CAGG TG GC
TACTGAAT CATCGTTT TGA GTCC AC CG
A TACC - C
GAM190 289 FLJ1311 1 6552 NP_078817.1 3 445 TGGAGCTACATC AG - TT - 3 A c c
4 CTGCTTCCTTTG GT CAAAG A CAGGATGT GC
GGCCTGGG CG GTTTC T GTCCTACA CG
G- C TC T
GAM190 289 FLJ1374 1 5728 NP_079287.1 5 226 AGTGATCACATC AAAGAT- 3 A c
c
4 CTGATTGAGTGG GTAGC TCAGGATGTG
CTATGGAC TATCG AGTCCTACAC
GTGAGTT
GAM190 289 FLJ1396 1 3592 NP_079138.1 3 43 TAGGATATGTAG GG- 3 A c c
2 ATGAGTTTTTGC GTAGCAAAGATTCA ATGTG
TACAGAGC CATCGTTTTTGAGT TGTAT
AGA
GAM190 289 FLJ1477 1 10085 NP_116227.1 3 449 TCTGTTTACATC - GAT 3 A c c
9 CTGATTTGTATA GTA GCAAA TCAGGATGTG
CTATTTTA CAT TGTTT AGTCCTACAT
A ---
GAM190 289 FLJ2003 1 7692 NP_060101.2 3 228 TATTTAGTATAC T A A 3 A c c
5 CTGAATCTTGGT G AGC AAGATTCAGG TGTGC
TTCTTTTT C TTG TTCTAAGTCC ATATG
T G -
GAM190 289 FLJ2018 1 6742 NP_060174.1 3 345 ATATCCCACATC G----- 3 A c c
9 CTGGATCTTTGT TAGCAAAGATTCAGGATGTG
TGGGTATT GTTGTTTCTAGGTCCTACAC
TTATGG
GAM190 289 FLJ2061 1 6968 NP_060373.1 3 732 AAGAGTAGGGGC AA ATG- 3 A c
c
8 CTGAATCCTGCT GTAGCA GATTCAGG TGC
ACAACTAT CATCGT CTAAGTCC ATG
C- GGGG
GAM190 289 FLJ2168 1 11614 NP_079135.1 3 377 CCTGCTTGCACA T TC G 3 A c c
7 TGTTATCTTTGC G AGCAAAGAT AG ATGTGC
TTCTGCCG C TCGTTTCTA TT TACACG
T -- G
GAM190 289 FLJ2268 1 18629 NP_079405.2 3 6 CATGCCCTCACC TTCA AT 3 A c c
8 CCACTTCTTTGC GTAGCAAAGA GG GTG

TACCTAGC CATCGTTTCT CC CAC
TCA- C-

GAM190 289 FLJ2295 1 11826 NP_079095.2 3 671 TGCTCCCACATC - A TT 3 A c c
5 CTGCTTATTGCC GTAG CAA GA CAGGATGTG
TGCCACCC CGTC GTT TT GTCCTACAC
C A C-

GAM190 289 FLJ2323 1 2723 NP_079219.1 3 546 TTGTTTGCATTT A - 3 A c c
5 ATGAATCTTGCT GTAGCAA GATTCA GGATGTG
GCCTTTTA CGTCGTT CTAAGT TTTACGT
- A

GAM190 289 FLJ3004 1 2890 NP_653196.1 3 783 GCACTTAATACC G - AT---- 3 A c c
6 TGCAATGTTTGC GTAGCAAA ATT CAGG GTGC
TACTGTAC CATCGTTT TAA GTCC CACG
G C ATAATT

GAM190 289 FLJ3331 1 5940 NP_694961.1 3 1846 AAAGTGGCCATC AAGA-- T 3 A c
c
8 CTGAAACCTAGT GTAGCA TTCAGGATG GC
GTTGCTGT CGTTGT AAGTCCTAC CG
GATCCA -

GAM190 289 FLJ3370 1 7549 NP_775946.1 3 2042 GCTTATAACATC - A AT G 3 A c c
8 CTGACTATGCTT GTA GCA AG TCAGGATGT
ACAAATAT CAT CGT TC AGTCCTACA
T A -- A

GAM190 289 FLJ3886 1 17233 NP_689907.1 3 584 ATTTGCTGCTCC CA AT - 3 A c c
5 CTGAATCTTCTA GTAG AAGATTCAGG GT GC
CTGAACAT CATC TTCTAAGTCC CG CG
-- CT T

GAM190 289 FLJ3937 1 15804 NP_847884.1 3 71 AACGTGCACATC AG - A- 3 A c c
8 CAGGAGTCCTTT GT CAAAG ATTC GGATGTGC
GGACAGTG CA GTTTC TGAG CCTACACG
G- C GA

GAM190 289 FLJ3987 1 16670 NP_776160.1 3 47 TGGAAGATACAC TC A 3 A c c
3 TTTTGTCTTTGC GTAGCAAAGAT AGG TGTG
TATTATAG TATCGTTTCTG TTC ACAT
TT -

GAM190 289 FLJ4059 1 10738 NP_689828.1 3 74 ACAACATGCAAT T TC G 3 A c c
7 CTTTGTCTTTGC G AGCAAAGAT AGGAT TGC
TTCTGGCC C TCGTTTCTG TTCTA ACG
T T- -

GAM190 289 FOXO1A 1 9586 NP_002006.2 3 3248 TACAGACACAAG CAGGA 3 A c
c
AACAATCTTTGC GTAGCAAAGATT TGTG
TATAATTG TATCGTTTCTAA ACAC
CAAGA

GAM190 289 FYCO1 1 17030 NP_078789.1 3 2057 CCCAGAGCAATC G- A G 3 A c c
TAGAATCTTTGA GTA CAAAGATTC GGAT TGC
GTGCTTGG CGT GTTTCTAAG TCTA ACG
GA A -

GAM190 289 GAS2L1 1 11278 NP_006469.2 5 145 GAGCCAGCGATC --- A A G 3 A c c

CTGAACTGTGTT GTAG CA AG TTCAGGAT TGC
CCTGCCCA CGTC GT TC AAGTCCTA GCG
CTT G - -

GAM190 289 GMPPA 1 709 NP_037467.1 3 14 GAGGTGCTCATC -- A- T T 3 A c c
CTGACTCGATTG GTAG CAA GA TCAGGATG GC
TTCTGCCA CGTC GTT CT AGTCCTAC CG
TT AG C T

GAM190 289 GPR56 1 5394 NP_005673.2 3 380 GTCTGGCACATC TA AA- C 3 A c c

CTTAATCCTGTG G GCA GATT AGGATGTGC
CCCCTGCC C CGT CTAA TCCTACACG
CC GTC T

GAM190 289 GRIN3A 1 14895 NP_597702.1 3 3185 TCTCTGCTATTC A - T 3 A c c
ATGAATCTTGCT GTAGCAA GATTCA GGATG GC
ATTGCACA TATCGTT CTAAGT CTTAT CG
- A -

GAM190 289 HDAC6 1 11395 NP_006035.2 3 124 CTGCATCCCATC A --- --- 3 A c c
CTGAATATCCTT GT GCAAAG ATTCAGGATG TGC
TGCAACTC CA CGTTTC TAAGTCCTAC ACG
A CTA CCT

GAM190 289 HECA 1 13430 NP_057301.1 3 260 TTCACTCTTACC G ----- T 3 A c c
AAGAATCTTTGA GTA CAAAGATTC AGGA GTG
TGCAGCTT CGT GTTTCTAAG TTCT CAC
A AACCA -

GAM190 289 HIVEP2 1 3062 NP_006725.2 5 15 CATATGCTCTTC A A TGT 3 A c c
CTGAATCTTGCC GT GCAA GATTCAGGA GC
ACTG CA CGTT CTAAGTCCT CG
C - TCT

GAM190 289 HSPA4 1 10608 XP_114482.1 3 1535 TCTTAGCACATC CAA TTC- 3 A c
c

CTCTGTTCTCTA GTAG AGA AGGATGTGC
CCTGTCAT CATC TCT TCCTACACG
--- TGTC

GAM190 289 IAPP 1 10420 NP_000406.1 5 136 GCAATGGGCATC AAAGA G 3 A c
c

CTGAAGCTGCAA GTAGC TTCAGGATGT
GTAT CGTCG AAGTCCTACG
----- G

GAM190 289 IL10RA 1 2291 NP_001549.1 3 796 GCCACTCACATC ATTC 3 A c c
CTCACTTTGCTG GTAGCAAAG AGGATGTG
CCCCACCA CGTCGTTTC TCCTACAC
AC--

GAM190 289 IL18R1 1 10177 NP_003846.1 3 951 CCTGAGCTCCAG AA GT-- 3 A c c
TCCTGAGTTTGC GTAGCA GATTCAGGAT GC
TACTTACT CATCGT TTGAGTCCTG CG
-- ACCT

GAM190 289 INSRR 1 19916 XP_043563.2 3 285 TCAAGAGCCATC A C T 3 A c c
TTCGATCTTTGC GT GCAAAGATT AGGATG GC
GGCCTGAG CG CGTTTCTAG TTCTAC CG
G C -

GAM190 289 IRS2 1 13393 XP_007095.5 3 930 GTCTCTGCTCTC - A- TGT 3 A c c
CTGAATCTTGGG GTA GC AAGATTCAGGA GC
CATGCCTT CGT CG TTCTAAGTCCT CG
A GG CT-
GAM190 289 ITIH1 1 16797 NP_002206.1 3 77 GAGGACGACATC AAGAT G 3 A c c
CTGACCTGCTGC GTAGCA TCAGGATGT
TGAGGCTG CGTCGT AGTCCTACA
CC--- G
GAM190 289 KCNK5 1 14350 NP_003731.1 3 1042 GCCCACTGTGTC -- --- 3 A c c
CTGAATGTTTTT GTAGCAAAGAT TCAGGAT GTG
GTTATTTT TATTGTTTTTG AGTCCTG CAC
TA TGT
GAM190 289 KEO4 1 12625 NP_006450.1 3 618 GGCCTGCAGGGA A ATG- 3 A c c
CCTGAGCTTTGC GTAGCAAAG TTCAGG TGC
TACCCAAC CATCGTTTC GAGTCC ACG
- AGGG
GAM190 289 KIAA017 2 5898 XP_035973.4 3 199 CGGGCGTCTTGG - ---- G 3 A c c
9 TTGAATCTTTTG GTAGCAAA GATTCA GGATGT
CTACAAAC CATCGTTT CTAAGT TCTGCG
T TGGT G
GAM190 289 KIAA017 2 16659 XP_035973.4 3 199 GGGCGTCTTGGT - ---- G 3 A c c
9 TGAATCTTTTGC GTAGCAAA GATTCA GGATGT
TACAAACC CATCGTTT CTAAGT TCTGCG
T TGGT G
GAM190 289 KIAA100 1 2770 NP_055775.1 3 608 CTCGAGTAGATC CAAA - G 3 A c
c
1 CTGAAATCCTAC GTAG GATT CAGGAT TGC
ATTTCTAT CATC CTAA GTCCTA ATG
---- A G
GAM190 289 KIAA100 1 17180 NP_057368.1 3 35 ATAGGCCACATC CA-- -- 3 A c c
7 CTTGGGGTCTTC GTAG AAGATTC AGGATGTG
TTATTACC CATT TTCTGGG TCCTACAC
ATTC GT
GAM190 289 KIAA102 1 11253 XP_034056.6 3 2235 GAAATGTACAAG AA A-- 3 A c c
5 CCCTGGATTTGC GTAGCA GATTCAGG TGTGC
TACAGAGT CATCGT TTAGGTCC ACATG
-- CGA
GAM190 289 KIAA120 1 8002 XP_031054.4 3 1823 TACCACAGGTTC C AG --- 3 A c c
0 CTGAATAATTCC GTAG AA ATTCAGGA TGTG
TGCAGGGC CGTC TT TAAGTCCT ACAC
C AA TGG
GAM190 289 KIAA143 1 20070 XP_039698.3 5 508 GGAAGGAAAGCC A CAG T 3 A c
c
2 ATTAATCTTTGC GT GCAAAGATT GATG GC
ACAGTACC CA CGTTTCTAA TTAC CG
- --- -
GAM190 289 KIAA161 1 8531 XP_035946.3 3 150 CCCTAGTCATAG GATT A 3 A c c
3 CCTGTCATTTGC GTAGCAAA CAGG TGTG
TACTTTTG CATCGTTT GTCC ATAC

ACT- G

GAM190 289 KIAA181 1 13394 XP_046743.2 5 2733 TTGGGCTTGGGC ATGT- 3 A c c

3 CTGGGTCTTTGC GTAGCAAAGATTCAGG GC
TGCCAGGT CGTCGTTTCTGGGTCC CG
GGGTT

GAM190 289 KIAA189 1 7357 XP_058025.2 3 603 TCCCATTCCAAT C ---- T 3 A c c

4 TTGAATCTTTCT GTAG AAAGATTCA GGA GTG
ATTTCTTT TATC TTTCTAAGT CCT TAC
- TTAA -

GAM190 289 KIAA199 1 4798 XP_114447.2 3 3856 AAAAAGCATACC ATTC- A 3 A c c

9 TTTCAATTTTGC GTAGCAAAG AGG TGTGC
TACTTGGT CATCGTTTT TCC ATACG
AACTT -

GAM190 289 KIAA202 1 7392 XP_059415.2 3 1675 GAGCCTTCATAT TTC 3 A c c

8 TTTCTTCTTTGC GTAGCAAAGA AGGATGTG
TGCCTTCT CGTCGTTTCT TTTTATAC
TC-

GAM190 289 LCHN 1 13962 XP_098615.2 3 2663 CAGGCACAACCT - - A 3 A c c

AGGATCCTTTGC GTAGCAAAG ATTC AGG TGTGC
TACCAGTT CATCGTTTC TAGG TCC ACACG
C A A

GAM190 289 LHX3 1 17614 NP_055379.1 3 986 ACTCCCGCAAAC AA- ATG 3 A c c

CTGAATCTCGAG GTAGC AGATTCAGG TGC
CTACCTAT CATCG TCTAAGTCC ACG
AGC AA-

GAM190 289 LHX3 1 17614 NP_835258.1 3 794 ACTCCCGCAAAC AA- ATG 3 A c c

CTGAATCTCGAG GTAGC AGATTCAGG TGC
CTACCTAT CATCG TCTAAGTCC ACG
AGC AA-

GAM190 289 LOC1128 1 19114 XP_053402.1 3 300 CCTCGCGACATC CAA T - 3 A c c

68 CTGATCTCTCCT GTAG AGAT CAGGATGT GC
GCAATAAC CGTC TCTA GTCCTACA CG
CTC - G

GAM190 289 LOC1222 1 3932 XP_063046.4 3 510 TGTCTTGGCATC ATT T 3 A c c

82 TTCTGCCTTTGC GTAGCAAAG CAGGA GTGC
TACTGAGC CATCGTTTC GTCTT TACG
C-- C

GAM190 289 LOC1300 1 12021 XP_072228.2 3 2462 GCATTGCACATC G- C ---- - 3 A c c

74 CGTGCAGAAATC TAG AAAGATT CA GGATGTGC
TTTCTGAC GTC TTTCTAA GT CCTACACG
CA - AGAC G

GAM190 289 LOC1309 1 12589 NP_620159.2 3 245 TTCATTTTCTTT - --- T 3 A c c

51 AGAATCATTTGC GTAGCAAA GATTC AGGA GTG
TACTGTTT CATCGTTT CTAAG TCTT TAC
A ATT T

GAM190 289 LOC1458 1 17550 XP_085246.1 3 1060 GACATTGACTTC A T G 3 A c c

20 CTGGATCTTTGC GT GCAAAGATTCAGGA GT
GGCCCCAG CG CGTTTCTAGGTCCT CA
G T G
GAM190 289 LOC1468 1 17975 XP_097120.1 5 905 ATCATCTTACAA TT GGA 3 A c
c
95 ATGCCTCTTTGC GTAGCAAAGA CA TGTG
TACTTTGT CATCGTTTCT GT ACAT
CC AA-
GAM190 289 LOC1501 1 16139 XP_086789.1 5 173 CAAAGGGGCAGG AT ATG 3 A c
c
38 GCCTGGCTTTGC GTAGCAAAG TCAGG TGC
TACAAGAT CATCGTTTC GGTCC ACG
-- GGG
GAM190 289 LOC1509 1 802 XP_097971.1 5 128 GACTTGCACATC A--- T- 3 A c c
33 CTGTCATCTGCT GTAGCA AGAT CAGGATGTGC
GTGTTACA CATTGT TCTA GTCCTACACG
GTCG CT
GAM190 289 LOC1519 1 2273 XP_087354.5 5 521 CCTCAGCAGATC A- A -- G 3 A c c
79 CTGAAGATCTTC GT GC AAGAT TCAGGAT TGC
GTGGACAA CA TG TTCTA AGTCCTA ACG
GG C GA G
GAM190 289 LOC1575 1 13070 XP_098783.1 3 541 GGCCACAGTTCC GT----- - -- 3 A c c
56 ATGAATCTTTGC AGCAAAGATTCA GGA TGTG
TCCCTTCC TCGTTTCTAAGT CCT ACAC
CCTTCCC A TG
GAM190 289 LOC1684 1 1886 XP_095122.3 3 275 TGTTGATACATT AGC 3 A c c
74 TTGAATCTTTAG GT AAAGATTCAGGATGTG
ACACTTAC CA TTTCTAAGTTTTACAT
GA-
GAM190 289 LOC1962 1 2140 XP_113683.1 3 2917 GGAGGCCACATC -- AAG-- 3 A c
c
64 CTGAATATGAAT GTAG CA ATTCAGGATGTG
GTTCTACT CATC GT TAAGTCCTACAC
TT AAGTA
GAM190 289 LOC2012 1 8606 XP_113925.1 3 459 TCCACTGGCACT ATT AT- 3 A c c
29 TCCCTGCTTTGC GTAGCAAAG CAGG GTGC
TACCATCG CATCGTTTC GTCC CACG
--- CTT
GAM190 289 LOC2031 1 3628 XP_300975.1 3 69 GCTACCACATTC ATTCA- 3 A c c
07 AATTAACTTTGC GTAGCAAAG GGATGTG
TATTAATT TATCGTTTC CTTACAC
AATTAA
GAM190 289 LOC2221 1 4845 XP_168431.1 5 2030 TTGTCACCCTTT TC---- AT 3 A c c
60 TACCATCTTTGC GTAGCAAAGAT AGG GTG
TATACTAT TATCGTTTCTA TCC CAC
CCATTT --
GAM190 289 LOC2537 1 10609 XP_171023.1 5 76 TACTATTACATC - AAAGA 3 A c c

82 CTGGAGCTGTCG G TAGC TTCAGGATGTG
TTTTATTG C GTCG AGGTCCTACAT
T -----
GAM190 289 LOC2551 1 8769 XP_173156.1 3 757 AATGAGCATTGC A ---- AT 3 A c c
67 CTGAATCAGAGT GTAGC AA GATTCAGG GTGC
TAGCTACT CATCG TT CTAAGTCC TACG
A GAGA GT
GAM190 289 LOC2563 1 4774 XP_170597.1 3 122 CTCACAGTATCC G C- - 3 A c c
74 TATAATCTTTGT GTA CAAAGATT AGGATG TG
GCTCTCAC CGT GTTTCTAA TCCTAT AC
- TA G
GAM190 289 LOC2831 1 19787 XP_210889.1 5 199 TTTCTGCACATC GATTC--- 3 A c
c
07 CTTACCAACATT GTAGCAAA AGGATGTGC
TGTTATTG TATTGTTT TCCTACACG
ACAACCAT
GAM190 289 LOC2831 1 8033 XP_210920.1 3 1605 GTAATCCACATC A- TC 3 A c c
43 CTCCATCTTGAG GTAGC AAGAT AGGATGTG
TTACTCCT CATTG TTCTA TCCTACAC
AG CC
GAM190 289 LOC2832 1 11642 XP_208583.2 3 240 GACACGAATGCA TTCA T 3 A c
c
44 CCTTCTCTTTGC GTAGCAAAGA GGA GTGC
TACCAACA CATCGTTTCT CTT CACG
---- C
GAM190 289 LOC2833 1 19234 XP_210977.1 5 1277 CACTTTCACAGA - C A- 3 A c c
31 CCTAATCTTTGT GTAG CAAAGATT AGG TGTG
TTGCAAAC CGTT GTTTCTAA TCC ACAC
T - AG
GAM190 289 LOC2833 1 11381 XP_210989.1 5 465 CTGCATCGCATC - AA A 3 A c c
52 CTGAAGCTCAGC GTAG C AG TTCAGGATGTG
CTGCCTAC CGTC G TC AAGTCCTACGC
C AC G
GAM190 289 LOC2835 1 19719 XP_211119.1 3 199 GAACGCTATTTC G C T - 3 A c c
82 CTAAATATTTGC GTAGCAAA ATT AGGA GT GC
TACACACA CATCGTTT TAA TCCT TA CG
A A T T
GAM190 289 LOC2836 1 3276 XP_211126.1 5 2796 ACGTGCATACTC --- AA- - 3 A c c
24 CTGAATCGGATG GTA GCA GATTCAGGA TGTGC
TAAATGCA CGT TGT CTAAGTCCT ATACG
AAA AGG C
GAM190 289 LOC2839 1 5990 XP_211259.2 5 2101 CAAGCCGCTACC A AT- 3 A c c
11 CTGAATCTTTGT GT GCAAAGATTCAGG GTG
GGCGGGTT CG TGTTTCTAAGTCC CGC
G CAT
GAM190 289 LOC2840 1 17779 XP_211302.1 3 3279 AATAAATGTCTC AT- - G 3 A c c
19 TGATTACTTTGC GTAGCAAAG TCAG GATGT
TACCTTTA CATCGTTTC AGTC CTGTA
ATT T A

GAM190 289 LOC2841 1 4876 XP_211353.1 3 310 TCTCAGTCACTT TCAG T 3 A c c

45 CAGTATCTTTGC GTAGCAAAGAT GA GTG
TACACAGA CATCGTTTCTA CT CAC
TGA- T

GAM190 289 LOC2842 1 9975 XP_211408.1 5 74 CCTTTTCAATAT -- C G 3 A c c
60 TCTAATCTTTGC GT AGCAAAGATT AGGATGT
TTTGCTGA CG TCGTTTCTAA TCTTATA
TT - A

GAM190 289 LOC2846 1 9976 XP_211581.1 5 919 ACACCAAGCACC CAAA AT 3 A c
c

65 CTGAATCGAGAC GTAG GATTCAGG GTGC
TGCAGGAG CGTC CTAAGTCC CACG
AGAG --

GAM190 289 LOC2846 1 10939 XP_209318.1 3 501 CCCCACCACATC - AGATT 3 A c
c

78 CTGCCATTGCTC GT AGCAA CAGGATGTG
ACCCTTTC CA TCGTT GTCCTACAC
C ACC--

GAM190 289 LOC2847 1 9623 XP_211601.1 3 269 CCACTTCGTCTC ---- TG 3 A c c
19 CTGAATCTTGTT GTAGCA AAGATTCAGGA TG
CTGCTGCC CGTCGT TTCTAAGTCCT GC
CTTG CT

GAM190 289 LOC2849 1 17855 XP_211729.1 5 1061 AAGGCCCACATC AGATTC 3 A c
c

95 CTACAATTGCTA GTAGCAA AGGATGTG
CTTCCTGA CATCGTT TCCTACAC
AACA--

GAM190 289 LOC2850 1 13385 XP_209435.1 5 597 CATGGCCACATC GCA-- G 3 A c
c

09 CTGAATGTTGAC GTA AA ATTCAGGATGTG
AATACCCT CAT TT TAAGTCCTACAC
AACAG G

GAM190 289 LOC2850 1 6445 XP_211737.1 5 1700 GACAAGTATCTA CA AT-- 3 A c c

23 GCCAGTCTTTGC GTAGCAAAGATT GG GTGC
TACAAGTT CATCGTTTCTGA CC TATG
-- GATC

GAM190 289 LOC2850 1 4367 XP_209440.1 3 2955 CAGGTCACAAAC T CA --- 3 A c c

26 TCCAATCTTTGT G AGCAAAGATT GGA TGTG
TTGGGTAG G TTGTTTCTAA CCT ACAC
T -- CAA

GAM190 289 LOC2854 1 12287 XP_211884.1 3 2390 CTCAGTCACATC CA TT 3 A c
c

02 CTGTCTTCCTTA GTAG AAGA CAGGATGTG
CATCTTTG CATT TTCT GTCCTACAC
CC --

GAM190 289 LOC2855 1 7733 XP_211929.1 5 490 AAAACACGACTC T AA -- 3 A c c
31 CTGAATCATGTT G AGCA GATTCAGGA TGTG

CCATTACT C TTGT CTAAGTCCT GCAC
C A- CA
GAM190 289 LOC2857 1 11785 XP_209728.1 5 3 TCTGCCACATCC CAA C 3 A c c
03 TCAATCTCTACC GTAG AGATT AGGATGTG
GGAGGAAC CATC TCTAA TCCTACAC
--- C
GAM190 289 LOC2857 1 12713 XP_212006.1 3 981 GACTGGTTACAT G CA 3 A c c
33 TCCAATCTTTGT GTA CAAAGATT GGATGTG
GCAGGACA CGT GTTTCTAA CTTACAT
- C-
GAM190 289 LOC2859 1 1977 XP_212092.1 5 1457 CACTATCACATC - CAAAG 3 A c
c
45 CTGAATATCACT GT AG ATTCAGGATGTG
CACAGAAT CA TC TAAGTCCTACAC
C ACTA-
GAM190 289 LOC2860 1 3883 XP_209868.1 5 1265 TCTTTGCACATC C TT 3 A c c
30 CTGCTCTTTCTG GTAG AAAGA CAGGATGTGC
CCTGAAAA CGTC TTTCT GTCCTACACG
- C-
GAM190 289 LOC3386 1 10009 XP_294666.1 5 142 TGCGGAGCCATC ---- A T 3 A c c
16 CTGAGGCTTTGA GTAG CAAAG TTCAGGATG GC
CATCTATG TATC GTTTC GAGTCCTAC CG
TACA G -
GAM190 289 LOC3388 1 10133 XP_294736.1 5 424 GAGTACCACATC - AGAT-- 3 A c
c
66 CTGACCCCACTT GTAG CAA TCAGGATGTG
GTTTGCAA CGTT GTT AGTCCTACAC
T CACCCC
GAM190 289 LOC3392 2 1143 XP_294893.1 5 1162 GCAGGTCTCCAG - A ----- G 3 A c c

73 CTGAATCTGTGC GTAG CA AGATTCAG GAT TGC
CTACAAAT CATC GT TCTAAGTC CTG ACG
C G GACCT G
GAM190 289 LOC3392 2 7171 XP_294893.1 5 1280 GCAGGTCTCCAG - A ----- G 3 A c c

73 CTGAATCTGTGC GTAG CA AGATTCAG GAT TGC
CTACGAAT CATC GT TCTAAGTC CTG ACG
C G GACCT G
GAM190 289 LOC3395 1 18173 XP_290946.1 3 1 AACTGGAGCTCC TCA T G 3 A c c

45 ATCTTTGCTGCT GTAGCAAAGAT GGA GT
AGGAAGGC CGTCGTTTCTA CCT CG
--- - A
GAM190 289 LOC3395 1 18173 XP_290949.1 3 1 AACTGGAGCTCC TCA T G 3 A c c

53 ATCTTTGCTGCT GTAGCAAAGAT GGA GT
AGGAAGGC CGTCGTTTCTA CCT CG
--- - A
GAM190 289 LOC3396 1 1952 XP_295035.1 3 871 CTTGTTATATGC A - 3 A c c
94 CAGAATCTTTGC GTAGCAAAGATTC GG ATGTG

TATGTGTT TATCGTTTCTAAG CC TATAT
A G
GAM190 289 LOC3398 2 12990 XP_295088.1 3 762 TTTCAAAACATC G GA G 3 A c c
59 CTGGAGATTTGT GTA CAAA TTCAGGATGT
ACTAAGGC CAT GTTT AGGTCCTACA
- AG A
GAM190 289 LOC3398 2 15811 XP_295088.1 3 962 CTAATCCACATC A GATTC- 3 A c
c
59 CTTATTGATTAG GTAGC AA AGGATGTG
CTACACTG CATCG TT TCCTACAC
A AGTTAT
GAM190 289 LOC3398 1 1545 XP_295090.1 3 698 ATTTCAAATTCA ATTCAG 3 A c
c
74 CATTAGCTTTGC GTAGCAAAG GATGTG
TACCACTA CATCGTTTC TTACAC
GA----
GAM190 289 LOC3399 1 18833 XP_295123.1 3 659 CTTACCCATTAC G AT 3 A c c
87 TTGGATATTTGC GTAGCAAA ATTCAGG GTG
TACGATCC CATCGTTT TAGGTTC TAC
A AT
GAM190 289 LOC3483 1 18880 XP_300696.1 3 645 TGGTTTTGGTCA ATT A 3 A c c
26 TACTTGCTTTGC GTAGCAAAG CAGG TGTG
TACCTAAA CATCGTTTC GTTC ATAC
--- -
GAM190 289 LOC3484 1 18880 XP_300738.1 3 645 TGGTTTTGGTCA ATT A 3 A c c
45 TACTTGCTTTGC GTAGCAAAG CAGG TGTG
TACCTAAA CATCGTTTC GTTC ATAC
--- -
GAM190 289 LOC3484 1 6321 XP_300758.1 3 1 AACTGGAGCTCC TCA T G 3 A c c
92 ATCTTTGCTGCT GTAGCAAAGAT GGA GT
AAGAAGGC CGTCGTTTCTA CCT CG
--- - A
GAM190 289 LOC3485 1 19269 XP_300779.1 5 2607 CGACTCCACATC AAGATTC 3 A
c c
27 CTCTGCACATGC GTAGCA AGGATGTG
TACCTACA CATCGT TCCTACAC
ACACGTC
GAM190 289 LOC3485 1 8957 XP_290329.1 3 101 CTCGCAGTATCC G - - 3 A c c
70 TAGAATCTTTGT GTA CAAAGATTC AGGATG TGC
GCTCTCGC CGT GTTTCTAAG TCCTAT ACG
- A G
GAM190 289 LOC3486 1 18314 XP_302853.1 3 2098 TTCATATTCGTT --- CA- 3 A c c
87 AATAAACTTTGC GTAGCAAAG ATT GGATGTG
TACTTTGC CATCGTTTC TAA CTTATAC
AAA TTG
GAM190 289 LOC3488 1 9714 XP_302893.1 3 334 ATTGACACATTC T TTCA- 3 A c c
08 ATTTTTCTTTGC G AGCAAAGA GGATGTG
TTATTTGA A TCGTTTCT CTTACAC

T TTTTA

GAM190 289 LOC3488 1 3838 XP_302902.1 5 629 GTCCTTACACAT ATT G 3 A c c
35 TGTGTCCTTTGC GTAGCAAAG CA GATGTG
TACCATCA CATCGTTTC GT TTACAC
CT- G

GAM190 289 LOC3492 1 13594 XP_300251.1 3 928 CATAGTATCATC G- G- - 3 A c c
51 CTGAATAGTTTG GTA CAAA ATTCAGGATG TGC
AATGCTCT CGT GTTT TAAGTCCTAC ATG
AA GA T

GAM190 289 LOC3494 1 19652 XP_303044.1 5 28 GGAGTACAATGG - - GG - 3 A c c
08 TGCGATCTTTGC GT AGCAAAGATT CA AT GTGC
TCACTGCA CA TCGTTTCTAG GT TA CATG
C C GG A

GAM190 289 LOC5161 1 4728 NP_057067.1 3 499 CAGAACCACATC T AA --- 3 A c c
9 CTGAGGAGTCTC G AGC AGAT TCAGGATGTG
AGCTTATC A TCG TCTG AGTCCTACAC
T AC AGG

GAM190 289 LOC5720 1 19313 XP_290488.1 3 784 CTCATCACTTCC -- C T 3 A c c
9 TAATTATTTTGC GTAGCAAA GATT AGGA GTG
TACATTTC CATCGTTT TTAA TCCT CAC
TA - T

GAM190 289 LOC6512 1 18173 NP_075389.1 3 1 AACTGGAGCTCC TCA T G 3 A c
c
1 ATCTTTGCTGCT GTAGCAAAGAT GGA GT
AGGAAGGC CGTCGTTTCTA CCT CG
--- - A

GAM190 289 LOC6512 1 18173 NP_075390.1 3 1 AACTGGAGCTCC TCA T G 3 A c
c
2 ATCTTTGCTGCT GTAGCAAAGAT GGA GT
AGGAAGGC CGTCGTTTCTA CCT CG
--- - A

GAM190 289 LOC9017 1 16015 XP_029589.1 5 1101 CCCTATCTGGCA ATT G 3 A c
c
0 GTCCTGCTTTGC GTAGCAAAG CAGGAT TGC
TACTTGCT CATCGTTTC GTCCTG ACG
--- -

GAM190 289 LOC9075 1 3453 XP_033868.1 3 1705 TGAAGTCACATC - AAG 3 A c c
0 CTGAATGTGCAT GTA GCA ATTCAGGATGTG
GCCAGACA CGT CGT TAAGTCCTACAC
A G--

GAM190 289 LOC9125 1 4751 XP_037135.1 5 53 AGACTGTTTTGC TTCAG 3 A c c
0 ATCACTCTTTGC GTAGCAAAGA GATGTG
TATTGAAG TATCGTTTCT CTACGT
CA---

GAM190 289 LOC9224 1 14921 XP_043814.1 3 22 GTGTGTACAAAC - - GA 3 A c c
9 TGATATCTTTGC GTAG CAAAGAT TCAG TGTGC
CTACCAGC CATC GTTTCTA AGTC ACATG
C T AA

GAM190 289 LRP1B 1 12085 NP_061027.1 3 976 ATTACGTGAACG G----- TTCA 3 A c
c

CATCCTCTTTGC TAGCAAAGA GGATGTG
TAGGTCAA ATCGTTTCT CCTACGC
AACTGG ----

GAM190 289 LRP4 1 16297 XP_035037.2 3 812 CCAGTACCTTTC T C T-- 3 A c c
CTAAGTCTTTGC G AGCAAAGATT AGGA GTGC
TCAAATTA C TCGTTTCTGA TCCT CATG
- A TTC

GAM190 289 MAP3K13 1 9282 NP_004712.1 3 33 GGAATACACATC - A- -- 3 A c c
CTGAAGATCTCG GTAG CA AGAT TCAGGATGTG
TGACTATA TATC GT TCTA AGTCCTACAC
A GC GA

GAM190 289 MAPKBP1 1 2864 XP_031706.7 3 861 TCTCCCTGCATC T AAG 3 A c
c
CTGAATGATGCT G AGCA ATTCAGGATGTG
TAGTCAGA A TCGT TAAGTCCTACGT
T AG-

GAM190 289 MBD4 1 6949 NP_003916.1 3 168 TGTGTGCCAATG GG -- TG 3 A c c
GTGGATCTTTGC GTAGCAAAGATTCA AT G C
TACTGAAT CATCGTTTCTAGGT TA C G
GG AC GT

GAM190 289 MGC1305 1 7515 NP_116099.1 3 208 CCCTCAAGCATC T GAT G 3 A c
c
3 CTGATTTGTTCG G AGCAAA TCAGGATGT
TTCTCTCT C TTGTTT AGTCCTACG
- --- A

GAM190 289 MGC1543 1 8619 NP_116263.2 3 713 CCGCCGCCCCGC ATT AT 3 A c
c
8 TCCCTGCTTTGC GTAGCAAAG CAGG GTG
TACACAAA CATCGTTTC GTCC CGC
--- CT

GAM190 289 MGC1798 1 5825 NP_705836.1 3 703 TGAATCCACATC AAAGA 3 A c
c
6 CTGAAGGGAGGC GTAGC TTCAGGATGTG
TACAACTG CATCG AAGTCCTACAC
GAGGG

GAM190 289 MGC3530 1 17665 NP_694987.1 3 685 TTCACACATTTT G C-- 3 A c c
4 AAAAATGTTTGC GTAGCAAA ATT AGGATGTG
TACTTGTT CATCGTTT TAA TTTTACAC
G AAA

GAM190 289 MGC4571 1 8478 NP_689677.1 3 266 CAGTACCTCTTC G AA T--- 3 A c
c
4 CTGAATCTGGTA GTA CA GATTCAGGA GTGC
CCCATCTG CAT GT CTAAGTCCT CATG
G -- TCTC

GAM190 289 MGC5466 1 3145 NP_112184.1 3 675 AGCCAGCACATC A- ATT 3 A c
c
CTGCCTGCTGTT GTAGCA AG CAGGATGTGC
GCAGCCTG CGTTGT TC GTCCTACACG
CG C--

GAM190 289 MLC1SA 1 4844 NP_002466.1 3 6 TTGAAACACATC A- TC-- 3 A c c

CTAAGCGTCTGG GTAGCA AGAT AGGATGTG
TGCTGCAG CGTCGT TCTG TCCTACAC
GG CGAA

GAM190 289 MOG 1 6547 NP_002424.1 3 108 TTGCACACTCAC - - - 3 A b b
TGGCATCTTTGC GTAGCAAAGAT TCAG GA TGTGC
TATGGGGA TATCGTTTCTA GGTC CT ACACG
C A C

GAM190 289 MORF4L2 1 17588 NP_036418.1 3 494 TGTTCTTAGGCA T TC G 3 A c c
TTCTATCTTTGC G AGCAAAGAT AGGATGT
TCAAATTG C TCGTTTCTA TCTTACG
- -- G

GAM190 289 MPHOSPH 1 8003 NP_073619.1 5 58 CTGCTACACATC C ATTC 3 A c c
9 CTCGTGCTTTTT GTAG AAAG AGGATGTG
ACCTCAGT CATT TTTC TCCTACAC
- GTGC

GAM190 289 MSL3L1 1 17050 NP_523352.1 3 1283 CTTGTGTACATC A AA TT 3 A c c
CTGTCCCTGCCA GT GCA GA CAGGATGTGC
CATCCATA CA CGT CT GTCCTACATG
C CC --

GAM190 289 MT1F 1 17234 NP_005940.1 3 90 TTTATACCACCT GAT- AT 3 A c c
TGACCCATTTGC GTAGCAAA TCAGG GTG
TACATTCC CATCGTTT AGTTC CAC
ACCC --

GAM190 289 MT1G 1 4199 NP_005941.1 3 94 TTGCTACAATCT AT- - 3 A c c
TGACCCCTTTGC GTAGCAAAG TCAGGAT GTG
TACATTCC CATCGTTTC AGTTCTA CAT
CCC A

GAM190 289 MT1H 1 6444 NP_005942.1 3 90 TTTCTACAACTC - T A -- 3 A c c
CGACTCATTTGC GTAGCAAA GA TC GGA TGTG
TACATTCC CATCGTTT CT AG CCT ACAT
A C - CA

GAM190 289 MT1L 1 17203 NP_002441.2 3 89 TTTTCTACAACC GA A- 3 A c c
CTGAGCATTTGC GTAGCAAA TTCAGG TGTG
TACATACT CATCGTTT GAGTCC ACAT
AC CA

GAM190 289 MT1X 1 7997 NP_005943.1 3 99 TTTGTACAACCC GAT- A- 3 A c c
TGACCCGTTTGC GTAGCAAA TCAGG TGTGC
TACATCTT CATCGTTT AGTCC ACATG
GCCC CA

GAM190 289 MYRIP 1 14896 NP_056275.1 3 304 ACATATTTTCCC ATT- ---- 3 A c c
TGTTTGCTTTGC GTAGCAAAG CAGG ATGTG
TACTGTAT CATCGTTTC GTCC TATAC
GTTT CTTT

GAM190 289 NALP2 1 2364 NP_060322.1 3 184 CCTGCACACATC TC 3 A b b
CTTATCTTTGTT GTAGCAAAGAT AGGATGTG
ACATATGA CATTGTTTCTA TCCTACAC
T-

GAM190 289 NCK1 1 17015 NP_006144.1 3 318 AATAATGCATAT GC AG 3 A c c
CAGAATCTTTAT GTA AAAGATTC GATGTGC
ATGGAAGA TAT TTTCTAAG CTATACG
A- A-
GAM190 289 NKX3-1 1 8119 NP_006158.2 3 1335 CTGACAATCCTT - --- - G 3 A c c
GAGAATCTTTGC GTA GCAAAGATTC AGGAT GT
ATGCAGAG CGT CGTTTCTAAG TCCTA CA
A AGT A G
GAM190 289 NLGN1 1 8186 NP_055747.1 3 1464 AAAGAGCACATC GCAAAGAT 3 A c c
CTGATAAATACT GTA TCAGGATGTGC
TTCTCTCT CAT AGTCCTACACG
AAAT----
GAM190 289 NOTCH1 1 11588 NP_060087.2 3 733 ATGGTACCAATC T G -- 3 A c c
ATGAATCTTTGT G AGCAAAGATTCA GAT GTGC
TTCAGGTT C TTGTTTCTAAGT CTA CATG
T A AC
GAM190 289 NOX1 1 8938 NP_008983.1 5 151 GAATCCGGATTG --- - G 3 A c c
CTGAATCTTCCC GTAGCA AAGATTCAG GAT TG
TGTTGCCT CGTTGT TTCTAAGTC TTA GC
CCC G G
GAM190 289 NOX1 1 8938 NP_039248.1 5 15 GAATCCGGATTG --- - G 3 A c c
CTGAATCTTCCC GTAGCA AAGATTCAG GAT TG
TGTTGCCT CGTTGT TTCTAAGTC TTA GC
CCC G G
GAM190 289 NOX1 1 8938 NP_039249.1 5 15 GAATCCGGATTG --- - G 3 A c c
CTGAATCTTCCC GTAGCA AAGATTCAG GAT TG
TGTTGCCT CGTTGT TTCTAAGTC TTA GC
CCC G G
GAM190 289 NPTX2 1 4797 NP_002514.1 3 1192 GACATGCCCATC AA- - T 3 A c c
CTGACATTGTAT GTAGCA GAT TCAGGATG GC
GCTACGAG CATCGT TTA AGTCCTAC CG
ATG C C
GAM190 289 NPTXR 1 13368 NP_055108.2 3 2863 CCCAGTCACATC AAAGAT 3 A c c
CTGAGCTGCTCC GTAGC TCAGGATGTG
TGGCTGAT CGTCG AGTCCTACAC

GAM190 289 NPTXR 1 13368 NP_478058.1 3 2863 CCCAGTCACATC AAAGAT 3 A c c
CTGAGCTGCTCC GTAGC TCAGGATGTG
TGGCTGAT CGTCG AGTCCTACAC

GAM190 289 NRG1 1 17541 NP_039252.1 3 370 AATGACCACATC AAGA- 3 A c c
CTGAAAAGGGTG GTAGCA TTCAGGATGTG
TTGCTAAG CGTTGT AAGTCCTACAC
GGGAA
GAM190 289 NRG1 1 17541 NP_039253.1 3 370 AATGACCACATC AAGA- 3 A c c
CTGAAAAGGGTG GTAGCA TTCAGGATGTG
TTGCTAAG CGTTGT AAGTCCTACAC

```
                                        GGGAA
GAM190  289  NRG1   1  17541 NP_039256.1  3 370   AATGACCACATC     AAGA-          3 A c c
                                CTGAAAAGGGTG GTAGCA    TTCAGGATGTG
                                TTGCTAAG    CGTTGT    AAGTCCTACAC
                                        GGGAA
GAM190  289  NRXN3  1  14089 NP_004787.2  3 69    CTATCCACGCCT  AG       -- A       3 A c c
                                ATGAATCTTTGG GT  CAAAGATTCA  GG TGTG
                                ACGGTGAG    CA  GTTTCTAAGT  CC GCAC
                                        G-        AT  -
GAM190  289  NRXN3  1  14089 NP_620426.1  3 69    CTATCCACGCCT  AG       -- A       3 A c c
                                ATGAATCTTTGG GT  CAAAGATTCA  GG TGTG
                                ACGGTGAG    CA  GTTTCTAAGT  CC GCAC
                                        G-        AT  -
GAM190  289  OLR1   1  2011  NP_002534.1  3 703   TGTTACCACTTC     AAA      T        3 A c c
                                CTGAATCAGTTA GTAGC   GATTCAGGA GTG
                                TTATTTCT    TATTG   CTAAGTCCT CAC
                                        A--       T
GAM190  289  OSBPL3 1  18511 NP_056365.1  3 3266  ACACCGGCATAA       TCA  --       3 A c c

                                ATCTATTTTTGC GTAGCAAAGAT   GGAT  GTGC
                                TACCAGAT    CATCGTTTTTA   TCTA  TACG
                                        ---   AA
GAM190  289  OSBPL3 1  18511 NP_663160.1  3 3266  ACACCGGCATAA       TCA  --       3 A c c

                                ATCTATTTTTGC GTAGCAAAGAT   GGAT  GTGC
                                TACCAGAT    CATCGTTTTTA   TCTA  TACG
                                        ---   AA
GAM190  289  OSBPL3 1  18511 NP_663161.1  3 3266  ACACCGGCATAA       TCA  --       3 A c c

                                ATCTATTTTTGC GTAGCAAAGAT   GGAT  GTGC
                                TACCAGAT    CATCGTTTTTA   TCTA  TACG
                                        ---   AA
GAM190  289  OSBPL3 1  18511 NP_663162.1  3 3266  ACACCGGCATAA       TCA  --       3 A c c

                                ATCTATTTTTGC GTAGCAAAGAT   GGAT  GTGC
                                TACCAGAT    CATCGTTTTTA   TCTA  TACG
                                        ---   AA
GAM190  289  OSBPL3 1  18511 NP_663163.1  3 4400  ACACCGGCATAA       TCA  --       3 A c c

                                ATCTATTTTTGC GTAGCAAAGAT   GGAT  GTGC
                                TACCAGAT    CATCGTTTTTA   TCTA  TACG
                                        ---   AA
GAM190  289  OSBPL3 1  18511 NP_663164.1  3 4400  ACACCGGCATAA       TCA  --       3 A c c

                                ATCTATTTTTGC GTAGCAAAGAT   GGAT  GTGC
                                TACCAGAT    CATCGTTTTTA   TCTA  TACG
                                        ---   AA
GAM190  289  PADI3  1  16411 NP_057317.1  3 968   CGTTTCCACATC     A ATT          3 A c c
                                CTGCTCTGCTGC GTAGCA AG   CAGGATGTG
                                AGGAGAGG    CGTCGT TC   GTCCTACAC
```

C ---

GAM190 289 PHTF2 1 13802 NP_065165.1 3 89 GAAAGCTTGTCA T T - T 3 A c c
CTGATTCTTTGC G AGCAAAGA TCAG GATG GC
TTCAGGAG C TCGTTTCT AGTC CTGT CG
T T A T

GAM190 289 POLR3D 1 17860 NP_001713.1 3 222 AGATGGCACATC AAGATTC 3 A c c
CTTGCTGCTGGG GTAGCA AGGATGTGC
GACTTGGC CGTCGT TCCTACACG

GAM190 289 PPIA 1 8957 NP_066953.1 3 101 CTCGCAGTATCC G - - 3 A c c
TAGAATCTTTGT GTA CAAAGATTC AGGATG TGC
GCTCTCGC CGT GTTTCTAAG TCCTAT ACG
- A G

GAM190 289 PSMD5 1 8408 NP_005038.1 3 268 TCCTTTCACTGC A C AT 3 A c c
CTTAATCTTTGC GT GCAAAGATT AGG GTG
AACAGGGT CA CGTTTCTAA TCC CAC
A T GT

GAM190 289 PTGS1 1 9441 NP_000953.2 3 569 AGAATGCATTCC - A AT 3 A c c
CTGAATCTGTGC GTAG CA AGATTCAGG GTGC
CTGCACTG CGTC GT TCTAAGTCC TACG
C G CT

GAM190 289 PTGS1 1 9441 NP_542158.1 3 569 AGAATGCATTCC - A AT 3 A c c
CTGAATCTGTGC GTAG CA AGATTCAGG GTGC
CTGCACTG CGTC GT TCTAAGTCC TACG
C G CT

GAM190 289 RERE 1 16468 NP_036234.2 3 2518 GGCAGCGTGCAC AA A GA 3 A c c
ACTCGGATTTGC GTAGCA GATTC G TGTGC
TACGTTTC CATCGT TTAGG C ACACG
-- - TC

GAM190 289 RIMS2 1 14112 NP_055492.1 5 35 GCTGCACGGGTA CA GA-- 3 A c c
CTGAATCTTCTA GTAG AAGATTCAG TGTGC
CGACTGAA CATC TTCTAAGTC GCACG
-- ATGG

GAM190 289 SEMA6D 1 13936 NP_705872.1 3 30 TGTCCTCATCAC T AT 3 A c c
CTGTGTCTTTGC GTAGCAAAGAT CAGG GTG
TGCTTTTG CGTCGTTTCTG GTCC TAC
T AC

GAM190 289 SLC9A1 1 7514 NP_003038.2 5 494 TCTTCCCACTTG AT GAT 3 A c c
CTGACCCTTTGC GTAGCAAAG TCAG GTG
TACCTATG CATCGTTTC AGTC CAC
CC GTT

GAM190 289 SNX24 1 12825 NP_054754.1 3 372 GAAAATCATATC AG AA-- 3 A c c
CTGAATCATACT GT CA GATTCAGGATGTG
GAGACTGA CA GT CTAAGTCCTATAC
GA CATA

GAM190 289 SOCS1 1 10166 NP_003736.1 3 315 TTTACATATACC A TCA- - 3 A c c
CAGTATCTTTGC GT GCAAAGAT GG ATGTG
ACAAACCA CA CGTTTCTA CC TATAC

```
                                                -      TGAC  A
GAM190  289  SPON1  1  13425 NP_006099.1  3  1486  CATAGTATAGTC   G  AAG     -        3  A  c
c
                                                CTGAATATGTAC GTA CA   ATTCAGGA TGTGC
                                                TTTTAACA    CAT GT   TAAGTCCT ATATG
                                                        - A--       G
GAM190  289  SPRY3  1  14598 NP_005831.1  3  1602  TTCGCCATTGCA       TTCA          3  A  c  c
                                                TCTACTCTTTGC GTAGCAAAGA   GGATGTG
                                                TGCACACA    CGTCGTTTCT   TCTACGT
                                                        CA--
GAM190  289  SSH-3  1  17604 NP_060327.2  3  558   ACCTCCACCGGT        CA  --       3  A  c  c
                                                CCAGGTCTTTGC GTAGCAAAGATT  GGAT  GTG
                                                TGCTGTCC    CGTCGTTTCTGG  CCTG  CAC
                                                        A-   GC
GAM190  289  SSH-3  1  17604 NP_060746.2  3  1024  ACCTCCACCGGT        CA  --       3  A  c  c
                                                CCAGGTCTTTGC GTAGCAAAGATT  GGAT  GTG
                                                TGCTGTCC    CGTCGTTTCTGG  CCTG  CAC
                                                        A-   GC
GAM190  289  SUFU  1  12371 NP_057253.2  3  444   CAGCTCATCTCT       A--   -  T      3  A  c  c
                                                GGAAGCCTTTGC GTAGCAAAG   TTCAG GATG GC
                                                TACTCAAG    CATCGTTTC   AGGTC CTAC CG
                                                        CGA    T   T
GAM190  289  SURB7  1  3571  NP_004255.2  3  665   TTTTTCTACATC    C    ---          3  A  c  c
                                                CTGAACTATTTT GTAG AAAGAT   TCAGGATGTG
                                                TCCTATTT    TATC TTTTTA   AGTCCTACAT
                                                        C     TCA
GAM190  289  SUV39H2 1  3837  NP_078946.1  3  430   GCAAATCTACAG       TT   -        3  A  c  c
                                                TTCTGTTTTTGC GTAGCAAAGA  CAGGA TGTG
                                                TACTCTAT    CATCGTTTTT  GTCTT ACAT
                                                        --    G
GAM190  289  TPH2   1  11938 NP_775489.1  3  878   TTTGTTACAATC GT-----          -     3  A  c  c
                                                CTGAATCTTTGC       AGCAAAGATTCAGGAT GTG
                                                TTTTTGCA          TCGTTTCTAAGTCCTA CAT
                                                        ACGTTTT            A
GAM190  289  TRO    1  7155  NP_808223.1  3  317   AAAGTACATCCT  A-       --         3  A  c  c
                                                TGGAATCTTTGT GT  GCAAAGATTC  AGGATGTGC
                                                CCACACAG    CA  TGTTTCTAAG  TCCTACATG
                                                        CC        GT
GAM190  289  TRO    1  7155  NP_808226.1  3  317   AAAGTACATCCT  A-       --         3  A  c  c
                                                TGGAATCTTTGT GT  GCAAAGATTC  AGGATGTGC
                                                CCACACAG    CA  TGTTTCTAAG  TCCTACATG
                                                        CC        GT
GAM190  289  TRPV3  1  668   NP_659505.1  3  213   GTGGGAAACATC      A        G       3  A  c  c
                                                CTGGATTTTGTT GTAGCAA GATTCAGGATGT
                                                ACTTGGCA    CATTGTT TTAGGTCCTACA
                                                        -         A
GAM190  289  UBQLN2 1  17562 NP_038472.2  3  931   ACTGTATATGAC   G      C  --        3  A  c  c
                                                CTTAATCTTTGT GTA CAAAGATT AGG  ATGTGC
                                                GCAGCCTG    CGT GTTTCTAA TCC  TATATG
                                                        -      T  AG
```

GAM190 289 UNC5C 1 19876 NP_003719.2 3 513 TACAGAGAAATC GATTC GA 3 A c c

ACAGACTTTTGC GTAGCAAA AG TGTG
TACAAATC CATCGTTT TC ACAC
----- AG

GAM190 289 WDR17 1 1039 NP_733828.2 3 81 GGTTAGCATTAC C AT 3 A c c
CTTAATCTTTGT GTAGCAAAGATT AGG GTGC
TGCTCAAG CGTTGTTTCTAA TCC TACG
T AT

GAM190 289 ZBTB2 1 12940 NP_065912.1 3 723 TTAATGCACATC G---- -- TC 3 A c c
CTTATCTCATTG TAGCAA AGAT AGGATGTGC
CTGGCTTC GTCGTT TCTA TCCTACACG
CTTCG AC T-

GAM190 289 ZNF179 1 13355 NP_009079.1 3 671 TGTCTGTGCATC G- ---- TG 3 A c c
CTGAACCACTCT TAGCAAAGA TTCAGGATG C
TTGCTGGG GTCGTTTCT AAGTCCTAC G
GG CACC GT

GAM190 289 ZNF213 1 6621 XP_036493.1 3 65 CCACGGCACATC - ATT 3 A b b
CTGCTTTGTTCA GT AGCAAAG CAGGATGTGC
CCACTGGG CA TTGTTTC GTCCTACACG
C ---

GAM190 289 ZNF264 1 15761 NP_003408.1 3 3979 TTTGTACACCTT T TT T 3 A c c
CTGTTTCTTTGC G AGCAAAGA CAGGA GTG
TTATTTTT A TCGTTTCT GTCTT CAC
T TT C

GAM191 389 PRO1048 1 7282 NM_018497.1 3 TGTTGAGATGCA TA TTAT 3 C c c

GATTCCTCA TG GAATCT TATCTCAACA
AC CTTAGA GTAGAGTTGT
TC C---

GAM192 393 AKAP2 1 7475 3 AGGGCCACTTAG ACTT TT 3 C c c
AGAGCAGTA TATTGCTCTCTAA TG CCT
ATGACGAGAGATT AC GGA
C--- CG

GAM192 393 KIAA133 1 4284 NM_020779.1 3 AGGAACAAGGAG C AAA 3 C c c
6 AAAGCAATG TATTGCT TCT CTTTGTTCCT
GTAACGA AGA GGAACAAGGA
A ---

GAM193 268 AHRR 1 2984 NP_065782.1 3 188 GGAGCCTATCCT GCTA - 4 A c c
GAATTTTGTAAA TATT AGAATTCAGG TAG
ATATCCCA ATAA TTTTAAGTCC ATC
AATG T

GAM193 268 AKR7A3 1 11149 NP_036199.1 3 100 AACTGCCTCAGT G C---- 4 A c c
AAATTCTTAGGG TATT CTAAGAATT AGGTAGT
ATGGAAGT GTAG GATTCTTAA TCCGTCA
G ATGAC

GAM193 268 AMOTL1 1 14975 NP_570899.1 3 620 CTTAGCTTTTCT TA T- 4 A c c
GAATTCTGCAGT TATTGC AGAATTCAGG AGT
ATTTTCTA ATGACG TCTTAAGTCT TCG
-- TT

GAM193 268 BCL2L13 1 14529 NP_056182.1 3 1281 GCATCTTCACCT CT AG 4 A c c
GAATTCTTCAAT TATTG AAGAATTCAGGT
GCCAGGGT GTAAC TTCTTAAGTCCA
-- CT
GAM193 268 C2orf7 1 11975 NP_115695.1 3 428 TAAACCCTCACT T GT 4 A c c
GACTTTTTAGCA TATTGCTAAGAA TCAG AG
ATAAAGCT ATAACGATTTTT AGTC TC
C AC
GAM193 268 C4ST 1 18004 NP_060883.1 3 5 GCCAAGCTACCT G GAA 4 A c c
GAAATTGGAATA TATT CTAA TTCAGGTAGT
AGGGGGTG ATAA GGTT AAGTCCATCG
- A--
GAM193 268 CACNB2 1 11254 NP_000715.1 3 157 ATTATTGCTGTT AGAA G 4 A c c
GCTTGAATAGCA TATTGCTA TTCAGGTA
ATAGCATG ATAACGAT AAGTTCGT
---- T
GAM193 268 CAPN2 1 4529 NP_001739.1 3 314 TTACACACTTTC A TT T- 4 A c c
CTGTTCATAGCA TATTGCTA GAA CAGG AGT
ATATTAAA ATAACGAT CTT GTCC TCA
A -- TT
GAM193 268 CPD 1 7505 NP_001295.2 3 3334 TACCCATTTATC TCA 4 A c c
CTATTTTTAGCA TATTGCTAAGAAT GGTAG
ATAATTCG ATAACGATTTTTA CTATT
TC-
GAM193 268 DKFZp43 1 16786 NP_060070.1 5 753 CCCCTTTACCTT AG - 4 A c c
4M0331 GAGTTGATAGCA TATTGCTA AATTCA GGTAG
ATAGAGCA ATAACGAT TTGAGT CCATT
AG T
GAM193 268 DSCR1L1 1 3399 NP_005813.1 3 1562 GTCCGTTTTACT AGA - 4 A c c
GTGAATATAGCA TATTGCTA ATTCA GGTAG
ATATAGTA ATAACGAT TAAGT TCATT
A-- G
GAM193 268 ETV5 1 10755 NP_004445.1 3 1995 GAATGGATTTAT ATT - 4 A c c
GCTGTCTTAGCA TATTGCTAAGA CAG GTAG
ATATGACA ATAACGATTCT GTC TATT
--- G
GAM193 268 FHOD2 1 8919 XP_057927.2 3 1839 TATTAATGGGCC TT AG 4 A c c
TGCTTCTTAGCA TATTGCTAAGAA CAGGT
ATATTAGA ATAACGATTCTT GTCCG
C- GG
GAM193 268 FLJ1082 1 13628 XP_051956.8 3 444 GATTATACTTCA A GGT 4 A c c
4 TGAGTCTTAGCA TATTGCTAAGA TTCA AGT
ATATGGGA ATAACGATTCT GAGT TCA
- ACT
GAM193 268 FLJ2026 1 15924 NP_060203.2 3 128 ACTGCTCTACCT A ---- 4 A c c
5 GAATTTAGACTA TATTGCT AG AATTCAGGTAG
AGCAGTAA ATGACGA TC TTAAGTCCATC

A AGAT

GAM193 268 FLJ2130 1 17809 NP_075052.1 3 251 ATACTAGCACTA TCA 4 A c c
2 CTATTCTTAGCA TATTGCTAAGAAT GGTAGT
GTGCTTGG GTGACGATTCTTA TCATCA

GAM193 268 GAS41 1 14327 NP_006521.1 3 142 CTGTTGACCATG - - AG 4 A c c
AATTTCTTAGCA TATTGCTAAGAA TTCA GGT
ATAGGAAT ATAACGATTCTT AAGT CCA
T A GT

GAM193 268 GRIN2B 1 16251 NP_000825.1 3 893 CATGTATTACCT T A 4 A c c
GAATTTTGGCTG TAT GCTAAGA TTCAGGTAGT
TGTCTCCC GTG CGGTTTT AAGTCCATTA
T -

GAM193 268 GTF2H2 1 8307 NP_001506.1 3 195 ACAGAAATACCT AA - G 4 A c c
GAAATTCAGTAG TATTGCT GAATT CAGGTA
TACTTCAT ATGATGA CTTAA GTCCAT
-- A A

GAM193 268 GYG2 1 9556 NP_003909.1 3 1276 AGGAACCTGCCT T A 4 A c c
GAATTTATGGCA TA TGCTA GAATTCAGGTAG
TTAGTGGT AT ACGGT TTTAAGTCCGTC
T A

GAM193 268 HSPC230 1 9132 NP_057571.1 3 23 TAAATAATGGAT ATTCA 4 A c c
TGCTTTTTAGCA TATTGCTAAGA GGTAGT
ATAGAGCT ATAACGATTTT TCGTTA

GAM193 268 IRTA1 1 7687 NP_112572.1 3 854 GAAATAATTACC AATTCA 4 A c c
AACCCCTTAGCA TATTGCTAAG GGTAGT
ATAAGCAC ATAACGATTC CCATTA
CCCAA-

GAM193 268 ITGAV 1 12126 NP_002201.1 3 1147 CAACTCACTGAT -- - T GT 4 A c c
TTACTTCTAGCA TATTGCTA AG AA TCAG AGT
ATAGCATG ATAACGAT TC TT AGTC TCA
CT A T AC

GAM193 268 KIAA055 1 6266 NP_055605.1 3 1943 AAGCTACTTGGG GAA--- 4 A c c
5 ACATTATTAGCA TATTGCTAA TTCAGGTAGT
ATAAAAAT ATAACGATT GGGTTCATCG
ATTACA

GAM193 268 KIAA104 1 17833 NP_055743.1 3 639 CAGCCTATTAAC ATT --- 4 A c c
6 TGTGTCTTAGCA TATTGCTAAGA CAG GTAG
ATGTTGTA GTAACGATTCT GTC TATC
GT- AAT

GAM193 268 KIAA126 1 8735 XP_047707.1 3 1288 CATGTTTATCCT C- - 4 A c c
5 GAATTTTTACTT TATTG TAAGAATTCAGG TAG
AATAATTT ATAAT ATTTTTAAGTCC ATT
TC T

GAM193 268 KIAA193 1 5530 XP_087672.1 3 831 CTGGCTGTTCCT G C -- 4 A c c
5 AAATTCTTAGGA TATT CTAAGAATT AGG TAGT
TATGTCCC ATAG GATTCTTAA TCC GTCG
- A TT

GAM193 268 KIDINS2 1 5248 XP_291015.1 3 821 CAACTTTTCTAA AA GG 4 A c c

20 GTGAGCTTAGCA TATTGCTAAG TTCA TAG
ATGAGAAG GTAACGATTC GAGT ATC
-- GA
GAM193 268 KIT 1 17832 NP_000213.1 3 358 GATAGTTTACCT AGA 4 A c c
GAATAAATGGTA TATTGCTA ATTCAGGTAG
GTAATCAC ATGATGGT TAAGTCCATT
AAA
GAM193 268 LAMP2 1 1978 NP_054701.1 3 568 GCTGGTATTATT TCA 4 A c c
ATGTTCTTAGCA TATTGCTAAGAAT GGTAGT
ATAAATGC ATAACGATTCTTG TTATTA
TA-
GAM193 268 LOC1155 1 13272 XP_291142.1 3 1715 CAGCAGAAAATC AATTCA 4 A c
c
48 TACTCTTTAGCA TATTGCTAAG GGTAG
ATATATAA ATAACGATTT TCATC
C-----
GAM193 268 LOC1429 1 5300 XP_084389.1 5 333 CCTGACTCTCCT G AG T- 4 A c c

55 GAATTACTAGAA TATT CTA AATTCAGG AGT
TGTCAGCA GTAA GAT TTAAGTCC TCA
- CA TC
GAM193 268 LOC1465 1 19666 XP_085491.1 3 1937 CTAATCCTACCT T ------ AT 4 A c c

17 GATCTTTAACAA TA TGCT AAGA TCAGGTAG
AGCATTAA AT ACGA TTCT AGTCCATC
T AACAAT --
GAM193 268 LOC1496 1 17873 XP_097710.1 3 579 GGTGCGGGCTCC CT A T 4 A c
c
84 GAATTCTTTCCA TATTG AAGAATTC GG AGT
ATAGTCTG ATAAC TTCTTAAG CC TCG
CT - -
GAM193 268 LOC1522 1 17088 XP_098174.1 3 1395 TTCTTAGATATC TC G 4 A c c
00 TTATTCTTAGTA TATTGCTAAGAAT AGGTA
ATACTACT ATAATGATTCTTA TCTAT
T- A
GAM193 268 LOC2193 1 19644 XP_165921.1 5 258 AAAGAACTGCCT TAAG 4 A c c

92 GAATTACTGCAA TATTGC AATTCAGGTAGT
TGAAATAG GTAACG TTAAGTCCGTCA
TCA-
GAM193 268 LOC2541 1 8379 XP_172851.1 3 323 CAGCCCTACCCT CTAA - 4 A c c

00 GAATTCCTCAGT TATTG GAATTCAGG TAG
GCGCCGAC GTGAC CTTAAGTCC ATC
TC-- C
GAM193 268 LOC2840 1 12022 XP_208151.1 3 256 TAAATCTGGCTG A- T G 4 A c c
20 TATTCAGTAGCA TATTGCTA GAAT CAG TAG
ATACAAAA ATAACGAT CTTA GTC GTC
GA T G
GAM193 268 LOC3385 1 13628 XP_290482.1 3 419 GATTATACTTCA A GGT 4 A c c

97 TGAGTCTTAGCA TATTGCTAAGA TTCA AGT
ATATGGGA ATAACGATTCT GAGT TCA
- ACT

GAM193 268 LOC3387 1 17845 XP_294690.1 3 874 TATGGATTACTT AA - 4 A c c
39 TGAAACTTAGCA TATTGCTAAG TTCAG GTAGT
ATGAGAGT GTAACGATTC AAGTT CATTA
A- T

GAM193 268 LOC3389 1 12926 XP_294753.1 3 172 GAAATTTTATCT TAA 4 A c c
61 GAATTCCGTAAT TATTGC GAATTCAGGTAG
GAATATAC GTAATG CTTAAGTCTATT
C--

GAM193 268 LOC3390 1 10159 XP_290660.1 5 258 AAAGAACTGCCT TA - 4 A c c
03 GAATTGCTGCAA TATTGC AG AATTCAGGTAGT
TGAAATAG GTAACG TC TTAAGTCCGTCA
-- G

GAM193 268 LOC3399 1 2352 XP_295110.1 5 1319 CTAAACTTCCCT - -- T- 4 A c c
52 GAATTGGCTTAG TATTG CTAAG AATTCAGG AGT
TCAATGCC GTAAC GATTC TTAAGTCC TCA
T GG CT

GAM193 268 LOC3477 1 13628 XP_290475.1 3 419 GATTATACTTCA A GGT 4 A c c

74 TGAGTCTTAGCA TATTGCTAAGA TTCA AGT
ATATGGGA ATAACGATTCT GAGT TCA
- ACT

GAM193 268 LOC3492 1 3953 XP_303016.1 5 3219 CTAAACTTCCCT - -- T- 4 A c c
77 GAATTGGCTTGG TATTG CTAAG AATTCAGG AGT
TCAATGCC GTAAC GGTTC TTAAGTCC TCA
T GG CT

GAM193 268 LOC3492 1 3953 XP_303021.1 5 3215 CTAAACTTCCCT - -- T- 4 A c c
99 GAATTGGCTTGG TATTG CTAAG AATTCAGG AGT
TCAATGCC GTAAC GGTTC TTAAGTCC TCA
T GG CT

GAM193 268 LOC5410 1 12980 XP_168508.4 3 1815 TTACTCCTTTGA CT- ---- T 4 A c c
3 GAATTCTTTAAC TATTG AAGAATTC AGG AGT
AATATTTA ATAAC TTCTTAAG TCC TCA
AAT AGTT -

GAM193 268 LOC9114 1 6578 XP_036480.1 3 2905 TAATATTACAGG G - AG 4 A c c
9 AAATTCTTAGGA TATT CTAAGAATT C GTAGT
TATACCAT ATAG GATTCTTAA G CATTA
- A GA

GAM193 268 LOC9249 1 16786 XP_045436.1 5 847 CCCCTTTACCTT AG - 4 A c c
7 GAGTTGATAGCA TATTGCTA AATTCA GGTAG
ATAGAGCA ATAACGAT TTGAGT CCATT
AG T

GAM193 268 LPP 1 14339 NP_005569.1 3 838 TCCGCACTACCT T GAA 4 A c c
GAACATTGTAAT TATTGC AA TTCAGGTAGT
ACAGACAA ATAATG TT AAGTCCATCA
- AC-

GAM193 268 MECP2 1 10015 NP_004983.1 3 6219 CATTTGCTTTTG ---- - -- 4 A c c
TAATTCTTAATG TATTGCT AAGAATT CA GGTAG

AGCAATAT ATAACGA TTCTTAA GT TCGTT
GTAA T TT
GAM193 268 MGC1435 1 10146 NP_116120.1 3 90 ACTTGCTTTGAA --- - 4 A c c
3 TTCATGTTAGCA TATTGCTAA GAATTCAG GTAG
ATAAATGA ATAACGATT CTTAAGTT CGTT
GTA T
GAM193 268 MGC2776 1 2621 NP_079541.1 3 361 CTGATTTTACCT AGAA 4 A c c
GAAAATGGTAGT TATTGCTA TTCAGGTAG
AGTTTACA ATGATGGT AAGTCCATT
AA--
GAM193 268 MKRN3 1 3557 NP_005655.1 3 907 GCACTATATTGG C -- - 4 A c c
TAATTCTTACAA TATTG TAAGAAT TCAG GTAGT
TGGCATTA GTAAC ATTCTTA GGTT TATCA
- AT A
GAM193 268 MU 1 2785 NP_071368.1 3 106 TTAGCCTCTGCT AATTC 4 A c c
TCAAGCTTAGCA TATTGCTAAG AGGTAG
ATATATTC ATAACGATTC TTCGTC
GAAC-
GAM193 268 NLGN4Y 1 6577 NP_055708.1 3 1836 GTCCAGCTACCT T- AT 4 A c c
GACTCTTTTGCA TATTGC AAGA TCAGGTAGT
ATAACAAC ATAACG TTCT AGTCCATCG
TT C-
GAM193 268 NPY 1 549 NP_000896.1 3 120 AGCCACTGTGCT TA - 4 A c c
GAATTCTGCAAT TATTGC AGAATTCAG GTAGT
GTTTTCCT GTAACG TCTTAAGTC TGTCA
-- G
GAM193 268 P114-RH 1 6818 NP_056133.1 3 1947 AGAACTTAAGAC A T AG 4 A c c
O-GEF CTGATTCTAGCA TATTGCTA GAAT CAGGT
ATAAACGT ATAACGAT CTTA GTCCA
- - GA
GAM193 268 PDK3 1 13449 NP_005382.1 3 87 TCACTGTTCCAG T A- -- 4 A c c
GAATTCTTGCAG TATTGC AAGAATTC GG TAGT
TGTAGAGG GTGACG TTCTTAAG CC GTCA
- GA TT
GAM193 268 PKIA 1 11912 NP_006814.1 3 203 TTTTCCCTACCT GA TC 4 A c c
CTGTCATTAGCA TATTGCTAA AT AGGTAG
ATGGTTGA GTAACGATT TG TCCATC
AC TC
GAM193 268 POU2AF1 1 3129 NP_006226.1 3 446 GAGGTAATTATA A AG 4 A c c
GGGATTTTAGCA TATTGCTAAGA TTC GTAGT
ATAACATT ATAACGATTTT AGG TATTA
- GA
GAM193 268 RCBTB1 1 13748 NP_060661.2 3 1428 ATGCTACAACTA TCA 4 A c c
CTATTTTTAGCA TATTGCTAAGAAT GGTAGT
ATGTTTTT GTAACGATTTTTA TCATCA

GAM193 268 RSN 1 9415 NP_002947.1 3 534 TTTGCACTACCT AA ATT 4 A c c
GTTATCAGTAGT TATTGCT GA CAGGTAGT

GCCTTTAC GTGATGA CT GTCCATCA
-- ATT
GAM193 268 SEL1L 1 1707 NP_005056.3 3 994 CATCACCTTCCT GCT T 4 A c c
GAATTCTTTAAA TATT AAGAATTCAGG AG
TATGAAAT ATAA TTCTTAAGTCC TC
AT- T
GAM193 268 SGKL 1 19551 NP_037389.4 3 260 ATTTAAAAGCTA T TCA 4 A c c
TTATTCTTAGCA TA TGCTAAGAAT GGTAGT
TTAACCTA AT ACGATTCTTA TTATCG
T ---
GAM193 268 SGKL 1 19551 NP_733827.2 3 260 ATTTAAAAGCTA T TCA 4 A c c
TTATTCTTAGCA TA TGCTAAGAAT GGTAGT
TTAACCTA AT ACGATTCTTA TTATCG
T ---
GAM193 268 SIMP 1 20030 XP_114346.2 3 399 TTTATTTGAATT AG----- 4 A c c
ACCCGAATAGCA TATTGCTA AATTCAGGTAG
ATATGTAA ATAACGAT TTAAGTTTATT
AAGCCCA
GAM193 268 SLC12A2 1 2850 NP_001037.1 3 280 TTTTCCTTTGCT AGAA 4 A c c
ACTTGAATAGCA TATTGCTA TTCAGGTAGT
ATAAAAGC ATAACGAT AAGTTCATCG

GAM193 268 SLC16A6 1 2622 NP_004685.1 3 272 TAAATCTGGCTG A- T G 4 A c c
TATTCAGTAGCA TATTGCTA GAAT CAG TAG
ATACAAGA ATAACGAT CTTA GTC GTC
GA T G
GAM193 268 SLC6A3 1 9121 NP_001035.1 3 1394 TTTTGTTTACAA GA AG 4 A c c
GAATAATTAGCA TATTGCTAA ATTC GTAG
ATACTGAG ATAACGATT TAAG CATT
AA AA
GAM193 268 SMARCAD 1 8809 NP_064544.1 3 177 TTGCCACTAACT GCT G 4 A c
c
1 GAATTCTTCAAA TATT AAGAATTCAG TAGT
TACTCACA ATAA TTCTTAAGTC ATCA
AC- A
GAM193 268 ST18 1 4579 NP_055497.1 3 692 CAGCCTGCTCAG - A- 4 A c c
AATTTGTTAGCA TATTGCTAA GAATTC GGTAG
ATAATTAA ATAACGATT TTTAAG TCGTC
G AC
GAM193 268 STAU2 1 19453 NP_055208.1 3 1940 GGACCACTACCT A AATT 4 A c
c
GCAGCTAAGCAG TATTGCT AG CAGGTAGT
TGAGCAGA GTGACGA TC GTCCATCA
A GAC-
GAM193 268 STC2 1 696 NP_003705.1 3 1249 CAGATCCTAATT AA G 4 A c c
GGAAATTTAGCA TATTGCTAAG TTCAG TAG
ATAAGGAG ATAACGATTT AGGTT ATC
AA A
GAM193 268 TINAG 1 12710 NP_055279.1 3 67 AACCCCCTAAAT AA G- 4 A c c
TGAAGTTTAGCA TATTGCTAAG TTCAG TAG

ATATGACA ATAACGATTT AAGTT ATC
G- AA

GAM193 268 ULK2 1 17181 NP_055498.2 3 2173 AGAGATTTTGCC AGA - 4 A c c
TTGAGTATAGCA TATTGCTA ATTCA GGTAG
ATAATAAA ATAACGAT TGAGT CCGTT
A-- T

GAM193 268 ZAK 1 7242 NP_598407.1 3 2306 GAAGTACTACCT - - AAT 4 A c c
GACTTGAGTCAA TATTG CT AAG TCAGGTAGT
TGCACCCA GTAAC GA TTC AGTCCATCA
T G ---

GAM194 350 6 FLJ1071 1 11429 NM_018191.2 3 CATATTAGATTA 3 C a a
CTAAGTCATTTG CAAATGACTTAGTAATCTAATATG
GTTTACTGAATCATTAGATTATAC

GAM195 334 ATPIF1 1 13146 NP_057395.1 3 62 ATTGCCCACTTC TA A--- 3 B c c
TGTGTAGACATG AACCATGTTT GCATA TGGG
GTTCTGGT TTGGTACAGA TGTGT ACCC
-- CTTC

GAM195 334 ATPIF1 1 13146 NP_835497.1 3 243 ATTGCCCACTTC TA A--- 3 B c c
TGTGTAGACATG AACCATGTTT GCATA TGGG
GTTCTGGT TTGGTACAGA TGTGT ACCC
-- CTTC

GAM195 334 ATPIF1 1 13146 NP_835498.1 3 1584 ATTGCCCACTTC TA A--- 3 B c c
TGTGTAGACATG AACCATGTTT GCATA TGGG
GTTCTGGT TTGGTACAGA TGTGT ACCC
-- CTTC

GAM195 334 CECR7 1 4000 XP_086803.1 3 571 TTTCCTCCATTG - GC 3 B c c
TTGTAAAACATG AAC CATGTTTTA ATAATGGG
TGTTTTGC TTG GTACAAAAT TGTTACCT
T GT

GAM195 334 DSC1 1 19861 NP_004939.1 3 1019 AATATGTTTCGT TT T 3 B c c
TTGCTCAACATG AACCATGTT AGCA AATGGG
GTTTACTA TTGGTACAA TCGT TTGCTT
C- -

GAM195 334 DSC1 1 19861 NP_077739.1 3 811 AATATGTTTCGT TT T 3 B c c
TTGCTCAACATG AACCATGTT AGCA AATGGG
GTTTACTA TTGGTACAA TCGT TTGCTT
C- -

GAM195 334 FGF2 1 18914 NP_001997.3 3 1884 AGATTTGCCCAT T ATA 3 B c c
AGGTTAAACATG AACCATGTTT AGC ATGGG
GTTAGAAA TTGGTACAAA TTG TACCC
- GA-

GAM195 334 7 FLJ1278 1 1139 NP_115551.1 3 179 AGTACCCGTTTT GCAT- 3 B c c
AAGTAAGACATG AACCATGTTTTA AATGGG
GTTTTCCA TTGGTACAGAAT TTGCCC
GAATT

GAM195 334 6 FLJ2008 1 11844 NP_060131.1 3 1732 CTGTAGCTATTA C TT- 3 B c c
TGCTTTTAATAT AAC ATGTT AGCATAATGG
TGTTTTAA TTG TATAA TCGTATTATC
T TTT

GAM195 334 FLJ2072 1 18778 NP_060414.2 3 94 GTAGTGCCATTT TA AT- 3 B c c
7 TGGCCGGACATG AACCATGTTT GC AATGG
GTTGGGGT TTGGTACAGG CG TTACC
C- GTT
GAM195 334 FLJ2126 1 2872 NP_079383.1 3 133 TCATGAGTTCCA ATAA 3 B c c
9 AGTTGAAACATG AACCATGTTTTAGC TGGG
GTTGTGCA TTGGTACAAAGTTG ACCT
A---
GAM195 334 FLJ2374 1 1179 NP_689484.1 3 1040 GTTAGATCACCA T AA 3 B c c
9 TGCTGCAACATG AACCATGTT TAGCAT TGG
GTTTATAT TTGGTACAA GTCGTA ACT
C CC
GAM195 334 GJB2 2 11557 NP_003995.1 3 1259 AATATTGCCATT TT 3 B b b
ATGCTTGACATG AACCATGTT AGCATAATGG
GTTTCCAA TTGGTACAG TCGTATTACC
T-
GAM195 334 GJB2 2 18295 NP_003995.1 3 1259 ATATTGCCATTA TT 3 B b b
TGCTTGACATGG AACCATGTT AGCATAATGG
TTTCCAAA TTGGTACAG TCGTATTACC
T-
GAM195 334 GPC3 1 10408 NP_004475.1 3 292 CCTATGTTTGGC TA----- 3 B c c
TGCTAGAACATG AACCATGTTTTAGCA ATGGG
GTTACCAT TTGGTACAAGATCGT TATCC
CGGTTTG
GAM195 334 KCNJ16 1 3607 NP_061128.1 5 373 TTATACCATGGA G A- 3 B c c
TGCTAAAAATGG AACCAT TTTTAGCAT ATGG
TTCTAACT TTGGTA AAAATCGTA TACC
- GG
GAM195 334 KCNJ16 1 3607 NP_733937.1 5 292 TTATACCATGGA G A- 3 B c c
TGCTAAAAATGG AACCAT TTTTAGCAT ATGG
TTCTAACT TTGGTA AAAATCGTA TACC
- GG
GAM195 334 KCNJ16 1 3607 NP_733938.1 5 380 TTATACCATGGA G A- 3 B c c
TGCTAAAAATGG AACCAT TTTTAGCAT ATGG
TTCTAACT TTGGTA AAAATCGTA TACC
- GG
GAM195 334 KIAA017 1 8331 NP_055455.1 3 859 TTTCTCTATAGT TA- A 3 B c c
3 GCAACAAACATG AACCATGTTT GCAT ATGGG
GTTTCTCA TTGGTACAAA CGTG TATCT
CAA A
GAM195 334 KIAA195 1 16208 XP_085375.4 3 2087 AGGAACTCATTA T TTT 3 B c c
4 TGCTACTGGTTG AACCA GT AGCATAATGGG
TTTGGGGA TTGGT CA TCGTATTACTC
- ---
GAM195 334 KIAA197 1 3715 XP_166279.1 3 144 GGCCAGATTTTA A------ G ---- 3 B c c
2 TGCTAAAAATGG ACCAT TTTTAGCATAA TGG
TAGTTTGT TGGTA AAAATCGTATT ACC
TGTTTGA - TTAG
GAM195 334 LOC1438 1 17605 XP_084661.3 3 1470 AGAATGCCATCT AGCATA 3 B c
c

```
          91                    ATTAAAAACATG AACCATGTTTT    ATGG
                                GTTAATAT    TTGGTACAAAA    TACC
                                            ATTATC
GAM195    334   LOC1454 1  1564  XP_085120.1  3  1233  AAGCACCAGCTA      TTTA   A-        3  B  c
c
          53                    TGTAATCACATG AACCATGT   GCATA  TGG
                                GTTGTTCT    TTGGTACA   TGTAT  ACC
                                          CTAA    CG
GAM195    334   LOC1464 1  4001  XP_085461.6  5  679   GCCCGTGAATAG       AG  A----       3  B  c  c

          43                    TGACAAAACATG AACCATGTTTT  CAT    ATGGG
                                GTTTGCAG    TTGGTACAAAA  GTG    TGCCC
                                            CA   ATAAG
GAM195    334   LOC1510 1  13828 XP_097998.1  3  861   TAAACCCCATTA    T  TTT  C          3  B  c  c

          57                    TACTTCCACTGG AACCA GT   AG ATAATGGG
                                TTATCTCC    TTGGT CA   TC TATTACCC
                                          - CCT  A
GAM195    334   LOC2842 1  4846  XP_208184.1  5  146   GTGCCGTTATTC A-----          ---       3  B  c  c
          31                    TGCTGGAACATG      ACCATGTTTTAGCA   TAATGG
                                GTGCCAAT          TGGTACAAGGTCGT   ATTGCC
                                        TAACCG            CTT
GAM195    334   LOC2843 1  13621 XP_211452.1  3  778   ACGGTCCCTTTA      GT-       T        3  B  c  c
          96                    TGCTAAGTCAGT AACCAT   TTTAGCATAA GGG
                                GGTTCTCA    TTGGTG   GAATCGTATT CCC
                                          ACT        T
GAM195    334   LOC2849 1  1922  XP_211689.1  3  795   AGTTCCAACTTC     T       T --        3  B  c  c
          27                    TGCTAAAATTGG AACCA GTTTTAGCA AA  TGGG
                                TTAATTGG    TTGGT TAAAATCGT TT  ACCT
                                          -       C  CA
GAM195    334   LOC2859 1  2646  XP_209820.1  3  2072  AATCTACCCAAT       TTA  TAA--        3  B  c
c
          53                    AATTGCAACATG AACCATGTT   GCA    TGGG
                                GTTCTTTG    TTGGTACAA  CGT    ACCC
                                          --- TAATA
GAM195    334   LOC2864 1  1532  XP_212325.1  3  485   GCCACTTAGTCG        GCA----  -       3  B  c  c

          70                    GGATAGAACATG AACCATGTTTTA      TAA TGG
                                GTTCGCAA    TTGGTACAAGAT      ATT ACC
                                            AGGGCTG   C
GAM195    334   LOC3397 1  17583 XP_295061.1  3  90    ACTGTGCCATTA    A  T  A           3  B  c  c
          78                    TGTAAATACAGG AACC TGT TT GCATAATGG
                                TTATTCCC    TTGG ACA AA TGTATTACC
                                          -  T  A
GAM195    334   MTL5   1  16748 NP_004914.1  3  705   TATTATTATTGT         ---  -         3  B  c  c
                                TTGTAAAACATG AACCATGTTTTA  GCA TAATGG
                                GTTCACAT    TTGGTACAAAAT  TGT ATTATT
                                            GTT   T
GAM195    334   NRCAM  1  1144  NP_005001.1  3  366   ACCCGTGTATGT        ---     -        3  B  c  c
                                TATGAAAACATG AACCATGTTT   TAGCATA ATGGG
```

GTTTGATA TTGGTACAAA ATTGTAT TGCCC
AGT G
GAM195 334 NUCKS 1 19959 NP_073568.1 3 344 AGAACCTACTTA GCA - 3 B c c
AGATAGAACATG AACCATGTTTTA TAA TGGG
GTTTTGGC TTGGTACAAGAT ATT ATCC
AGA C
GAM195 334 OPHN1 1 1488 NP_002538.1 3 2211 CCACAGTCCCTT AGCA T 3 B c
c
TAAAGAAACATG AACCATGTTTT TAA GGG
GTTTGACT TTGGTACAAAG ATT CCC
AA-- T
GAM195 334 P450RAI 1 14707 NP_063938.1 3 2764 GAATTTTGCTCT TAGC 3 B c c
-2 ATTGTAAACATG AACCATGTTT ATAATGGG
GTTCAAAA TTGGTACAAA TGTTATCT

GAM195 334 PDIP1 1 8489 NP_849194.1 3 189 CCCAACCCCATT A----- - TA 3 B c c
GCTAACAACATG ACCATGTT TTAGCA ATGGG
GTACATTC TGGTACAA AATCGT TACCC
CTTACA C --
GAM195 334 PDIP1 1 8489 XP_170803.1 3 189 CCCAACCCCATT A----- - TA 3 B c c
GCTAACAACATG ACCATGTT TTAGCA ATGGG
GTACATTC TGGTACAA AATCGT TACCC
CTTACA C --
GAM195 334 PLGL 1 2694 NP_002656.1 3 571 TTTTTGGCACCA G ATA 3 B c c
TAGTAGAACATG AACCATGTTTTA C ATGG
GTTGCTTT TTGGTACAAGAT G TACC
- A--
GAM195 334 RNF41 1 14646 NP_005776.1 3 740 ACTCCTAGCTTT TAA-- 3 B c c
TGCTAAAATATG AACCATGTTTTAGCA TGGG
GTTGGCAC TTGGTATAAAATCGT ATCC
TTTCG
GAM195 334 SHANK2 1 11675 NP_036441.1 3 1591 GCCCATCTCTAA GCATA---- 3 B c
c
TTATAAAACATG AACCATGTTTTA ATGGG
GTTTTGTT TTGGTACAAAAT TACCC
ATTAATCTC
GAM195 334 SLC38A2 1 451 NP_061849.2 3 1646 AAGGGCCAGAAA A AA- 3 B c c
TGTGGAGACATG AACCATGTTTT GCAT TGG
GTTTTTGT TTGGTACAGAG TGTA ACC
G AAG
GAM195 334 TRIM9 1 10464 NP_443210.1 3 1058 AGTCACCCTAAA TTT AAT- 3 B c
c
ATGCTTCACATG AACCATGT AGCAT GGG
GTTAAAAA TTGGTACA TCGTA CCC
CT- AAAT
GAM195 334 WASF3 1 12232 NP_006637.2 3 1135 TTCACCCTGTTC --- C AT 3 B c c
TAGAAGCACATG AACCATGT TTTAG ATA GGG
GTTGTCCT TTGGTACA AGATC TGT CCC
CGA T --

GAM195 334 ZNF2 1 8545 NP_066574.1 3 733 TCTTTACCATTA GTTTT 3 B c c
TGCTCGATGGTT AACCAT AGCATAATGG
TGTTTGTT TTGGTA TCGTATTACC
GC---
GAM196 209 AP1M1 1 18556 NM_032493.2 3 GCCCAGGGACCC T AA AA-- 3 C c c
CTGCCTTCCCC GGGGAAGG CAGG GGTCC GC
CCCCTTCC GTCC CCAGG CG
- -- GACC
GAM196 209 AP1S1 1 1717 NM_057089.1 3 GCCTGGACCCCC TC AA A 3 C c c
CTCTTTCTCC GGGGAAGG AGG GGTCCA GC
CCTCTTTC TCC CCAGGT CG
-- CC C
GAM196 209 CLCN6 1 17159 NM_021735.1 3 GCTTGGACTTTT G 3 C b b
CTGACTTCCCC GGGGAAG TCAGGAAGGTCCAAGC
CCCCTTC AGTCTTTTCAGGTTCG
-
GAM196 209 FLJ1172 1 1140 NM_024970.1 3 GCTTTGACCCCC CA AA C 3 C c c
2 AACCTTCTCC GGGGAAGGT GG GGTC AAGC
CCTCTTCCA CC CCAG TTCG
AC -- T
GAM196 209 FLJ1410 1 17744 NM_025026.1 3 GCTCCCACCCCT AA CCA 3 C c c
7 GACCTTCTCC GGGGAAGGTCAGG GGT AGC
CCTCTTCCAGTCC CCA TCG
-- CCC
GAM196 209 FLJ1428 1 2799 NM_024886.1 3 GCCTGGACCTCC TC A A 3 C c c
0 CTCCTTCCTC GGGGAAGG AGG AGGTCCA GC
CTCCTTCC TCC TCCAGGT CG
-- C C
GAM196 209 FLJ2344 1 7447 NM_024825.1 5 GCTTGGAAGACG T GAAGG 3 C c
c
7 CTGCCTTCCCC GGGGAAGG CAG TCCAAGC
CCCCTTCC GTC AGGTTCG
- GCAGA
GAM196 209 KIAA169 1 14970 XM_166523.1 3 GCCTGGGCATCT A AAG A 3 C c c
1 GACCTCCCC GGGGA GGTCAGG GTCCA GC
CCCCT CCAGTCT CGGGT CG
- A-- C
GAM196 209 KIAA194 1 12635 XM_086981.2 3 GCTTGGACATGA A AGGAAG 3 C c
c
0 AGACCCTCCCC GGGGA GGTC GTCCAAGC
CCCCT CCAG CAGGTTCG
C AAGTA-
GAM196 209 LOC1381 1 16109 5 GCCCGGACCTCG A AGGA AA 3 C c c
28 GCCTCCCC GGGGA GGTC AGGTCC GC
CCCCT CCGG TCCAGG CG
- C--- CC
GAM196 209 LOC1496 1 10864 XM_097702.2 3 GCTCCCCTTCCT A TCCA 3 C c c
57 GGCCCTCCCC GGGGA GGTCAGGAAGG AGC

CCCCT CCGGTCCTTCC TCG
C CC--

GAM196 209 LOC1508 1 9457 XM_087019.1 3 CTTGGACTGTAG TCAGGAA C 3 C c c
37 TCCTTCCCC GGGGAAGG GGTCCAAG
CCCCTTCC TCAGGTTC
TGATG-- -

GAM196 209 LOC1515 1 2480 5 GCCTGGTTACTG GAAGGT A 3 C c c
56 ACCTTTCCC GGGGAAGGTCAG CCA GC
CCCTTTCCAGTC GGT CG
ATT--- C

GAM196 209 LOC2540 1 17846 3 GCTGGGTCCCCC CA AA GT A 3 C c c
16 CAACCTTCCCC GGGGAAGGT GG G CCA GC
CCCCTTCCA CC C GGT CG
AC CC TG -

GAM196 209 Nrap 1 5880 NM_006175.2 3 GCCTGGACCTCC GGT A A 3 C c c
CTGCGATTTCCC GGGGAA CAGG AGGTCCA GC
CCCTTT GTCC TCCAGGT CG
AGC C C

GAM196 209 SHB 1 5017 NM_003028.1 5 GCTCGGACCTTC AG CA A 3 C c c
CGCTCTCCCC GGGGA GT GGAAGGTCC AGC
CCCCT CG CCTTCCAGG TCG
CT -- C

GAM196 209 TSLP 1 8451 NM_033035.2 5 GCTCCTCCCTGA A TCCA 3 C c c
CCTTCCTC GGGGAAGGTCAGG AGG AGC
CTCCTTCCAGTCC TCC TCG
C ----

GAM281 278 1 13946 NP_444285.1 3 355 CCTATGTGCCAG TCCA G- 3 B c c
AGGTACTGTGCA CACTGCAC GCCT GGCA
GTGCTGGA GTGACGTG TGGA CCGT
TCA- GA

GAM281 278 15E1.2 1 12868 XP_290596.1 3 1202 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGAC GTGACGTGAGGTCGGACCC
AC

GAM281 278 A1BG 2 2534 NP_570602.2 3 345 CACTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGTTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 A1BG 2 18868 NP_570602.2 3 1397 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 AASS 1 6339 NP_005754.2 3 356 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 ABCA13 1 7385 NP_689914.2 3 1068 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC

AC
GAM281 278 ABCC11 1 7022 NP_149163.2 5 57 GGAGATTGCCCA CAG-- 3 B c c
GGATCAAGGGTG CACTGCACTC CCTGGGCAA
CGGTGTTG GTGGCGTGGG GGACCCGTT
AACTA
GAM281 278 ABLIM2 1 3488 NP_115808.1 5 113 CGAGCGGCTGCT CAGC G 3 B c
c
GAGATGAGTGCA CACTGCACTC CT GGCA
GTGTCGCA GTGACGTGAG GA TCGT
TA-- G
GAM281 278 ACADSB 1 16689 NP_001600.1 3 322 CTCTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCGCG GTGACGTGAG TCGGACCC
A AC
GAM281 278 ADAMTS3 1 16811 NP_055058.1 5 1 GCTTTGCCCAGT GCAC -- 3 B c
c
AGTTGGAAAGTG CACT TCCAGC CTGGGCAA
AACTCGAC GTGA AGGTTG GACCCGTT
A--- AT
GAM281 278 ADAMTS4 2 1651 NP_005090.1 3 670 CTCTGTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCACA GT ACGTGAGGTCGGACCCG
A C
GAM281 278 ADAMTS4 2 13757 NP_005090.1 3 166 CCCTAATGCGCA CT CT- G 3 B c
b
GGCTGGCCCTGC CA GCA CCAGCCTG GCA
CCTGGTTT GT CGT GGTCGGAC CGT
CC CCC G
GAM281 278 ADARB1 1 12610 NP_056648.1 3 1353 AGAAGTGCTCTG C- CCT 3 B c
c
CCTGCCAGTGCA CACTGCACT CAG GGGCA
GTGCCCAG GTGACGTGA GTC CTCGT
CC CGT
GAM281 278 ADCY1 1 6261 NP_066939.1 3 1739 GGGCTTTGCAGG -- A GG 3 B c c
GCGGCCAGTGCA CACTGCACT CC GCCT GCAA
GTGATGCC GTGACGTGA GG CGGG CGTT
CC - A-
GAM281 278 ADCY6 1 16688 NP_056085.1 5 65 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGCG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 ADORA2A 1 19456 NP_000666.2 3 164 AAGGGAGCCCCA C A- - A 3 B c
c
GGCTGGAGCAGC CA TGC CTCCAGCCTGGG C
ATGAGGCC GT ACG GAGGTCGGACCC G
- AC C A
GAM281 278 AGMAT 1 9193 NP_079034.2 3 436 GCTTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG

ATGGCATG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 AGTRAP 1 3359 NP_065083.2 3 501 CTAGGGATGCAG ---- A GG 3 B c c
GGCTGGAGGCCA CACT GC CTCCAGCCT GCA
GAGGTGTC GTGG CG GAGGTCGGG CGT
AGAC - A-
GAM281 278 AHR 1 8217 NP_001612.1 3 1634 CTCTGCCGCCCA CC A 3 B c c
AACTGGAGTGCA CACTGCACTCCAG TGGGC
GTGGCACA GTGACGTGAGGTC ACCCG
AA C
GAM281 278 AIM1 1 16864 XP_166300.1 3 715 GACAGGATCTCA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACTC
TA
GAM281 278 ALDH1B1 1 2153 NP_000683.3 3 1073 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 ALOX15 1 19939 NP_001131.1 3 412 CTTTGACACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCC GTGACGTGAGGTCGGACCC
AC
GAM281 278 AMID 1 5895 NP_116186.1 3 694 CCCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM281 278 ANKRD6 1 1746 NP_055757.1 3 1478 CTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGCATG GTGACGTGAGGTC GACCC
A AC
GAM281 278 ANPEP 1 6737 NP_001141.1 5 5 AATTTTTGCCCA T CTC C 3 B c c
GTCTGCCTGTTG CAC GCA CAG CTGGGCAA
TGGGGCTC GTG TGT GTC GACCCGTT
T CC- T
GAM281 278 AP1S3 1 10109 XP_291023.1 3 1017 CTCTGTCACCCA C----- CA 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGCACG TGACGTGAGGTCGGACCC
GCACGA AC
GAM281 278 AP3S2 1 19874 NP_005820.1 3 657 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCT CAC GCACTCCAGCCTGGG
GTGGTGCA GTG CGTGAGGTCGGACCC
T AC
GAM281 278 APAF1 2 16578 NP_001151.1 3 630 GCTTTGTTGCCA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-
GAM281 278 APAF1 2 16578 NP_037361.1 3 630 GCTTTGTTGCCA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA

GTGGCGCG GTGACGTGAGGTCGGACC GTT

-

GAM281 278 APAF1 2 19360 NP_001151.1 3 927 CACTATCACCCA CA 3 B b b

GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGCATA GTGACGTGAGGTCGGACCC

AC

GAM281 278 APAF1 2 19360 NP_037361.1 3 927 CACTATCACCCA CA 3 B b b

GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGCATA GTGACGTGAGGTCGGACCC

AC

GAM281 278 APG-1 1 17324 NP_055093.2 5 34 GGGAAAGACCCA A- - CA 3 B c c

GGCTGCGGGACG CACTGC CTC CAGCCTGGG

CGGTGCAG GTGGCG GGG GTCGGACCC

CA C AG

GAM281 278 APM1 3 5598 NP_004788.1 3 812 CTCTGTCACCCA C CA 3 B c b

GGCTGGAGTACA CACTG ACTCCAGCCTGGG

GTGACACG GTGAC TGAGGTCGGACCC

A AC

GAM281 278 APM1 3 11707 NP_004788.1 3 1808 CCTCTGTTGCCA C G 3 B b b

GGCTAGAGTGCA CACTGCACTC AGCCTGG CAA

GTGGCATG GTGACGTGAG TCGGACC GTT

A -

GAM281 278 APM1 3 20035 NP_004788.1 3 3332 TTCTGTGGCCCT C T A 3 B c b

GGCTGGAGTTCA CACTG ACTCCAGCC GGGC

GTGGTGTG GTGAC TGAGGTCGG CCCG

T T G

GAM281 278 APOBEC3 1 5622 NP_660341.2 3 352 CTCTGTCACCCA C C CA 3 B c c

F GACTGGAGTGCA CA TGCACTCCAG CTGGG

ATGGCTTG GT ACGTGAGGTC GACCC

A A AC

GAM281 278 APOL2 1 8064 NP_112092.1 3 131 CTCTATCGCCCA G A 3 B b b

GGATGGAGTGCA CACTGCACTCCA CCTGGGC

GTGGCTCA GTGACGTGAGGT GGACCCG

A C

GAM281 278 APOL2 1 8064 NP_663612.1 3 131 CTCTATCGCCCA G A 3 B b b

GGATGGAGTGCA CACTGCACTCCA CCTGGGC

GTGGCTCA GTGACGTGAGGT GGACCCG

A C

GAM281 278 APPBP2 1 4095 NP_006371.2 3 3495 TCTTGTTGCCCA C A - 3 B b b

GGCTGGGAGGGC CA TGC CTCC AGCCTGGGCAA

AATGGCAC GT ACG GAGG TCGGACCCGTT

A G G

GAM281 278 APPL 1 12068 NP_036228.1 3 2974 CTCTGTTGCCCA 3 B b b

GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 AQP2 1 18318 NP_000477.1 3 152 CGTGCGCGCCCA T CCA A 3 B c c

GGCCAGTGCTGT CAC GCACT GCCTGGGC

GAGCAGGC GTG CGTGA CGGACCCG
T C-- C
GAM281 278 AQP6 1 3169 NP_001643.1 3 614 ATCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT
GAM281 278 AQP6 1 3169 NP_445738.1 3 1780 ATCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT
GAM281 278 ARCN1 1 13747 NP_001646.2 3 406 CTTTGTAACCCA C C CA 3 B c c
GGCTGGAATGCA CA TGCA TCCAGCCTGGG
ATGGCATG GT ACGT AGGTCGGACCC
A A AA
GAM281 278 ARFRP1 1 6901 NP_003215.1 3 335 CTCCAGTGCTCA C - ---- 3 B c c
GGCTGGCTTGGG CA TGCA CT CCAGCCTGGGCA
CTGCATGA GT ACGT GG GGTCGGACTCGT
- C GTTC
GAM281 278 ARHF 1 7962 NP_061907.1 3 1092 TTCTGTCACTCA C CA 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCATG GTGACGTGAG TCGGACTC
A AC
GAM281 278 ARHGAP1 1 4096 NP_004299.1 3 1136 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC
GAM281 278 ARHGAP1 1 17742 NP_055598.1 3 294 CTCTGTCGTCCA A 3 B b b
1A GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCTG
C
GAM281 278 ARHGEF4 1 14328 NP_056135.2 3 903 ACCCACAGCCCA T CA- A 3 B c
c
GGCAGCGGGTGT CAC GCACTC GCCTGGGC
GTGGAGAT GTG TGTGGG CGGACCCG
- CGA A
GAM281 278 ARHGEF4 1 14328 NP_127462.1 3 1554 ACCCACAGCCCA T CA- A 3 B c
c
GGCAGCGGGTGT CAC GCACTC GCCTGGGC
GTGGAGAT GTG TGTGGG CGGACCCG
- CGA A
GAM281 278 ARPP-19 1 944 NP_006619.1 3 3491 CACTCTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 ARSB 1 13855 NP_000037.1 5 23 GGACCTGCCACA CA - ----- - 3 B c c
GGCTGGGCTCTT CT GCAC TCCAGCCTG GGCA
GTGCTAGA GA CGTG GGGTCGGAC CCGT
A- T TTCTC A
GAM281 278 ASB16 1 14722 NP_543139.4 3 143 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGGCGCT GTGACGTGAGGTCGGACCCGTT

GAM281 278 ASB6 2 2196 NP_060343.1 3 1136 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCA GT ACGTGAGGTCGGACCC
A AC
GAM281 278 ASB6 2 2196 NP_821066.1 3 1699 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCA GT ACGTGAGGTCGGACCC
A AC
GAM281 278 ASB6 2 10305 NP_060343.1 3 1442 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGATCC
AC
GAM281 278 ASB6 2 10305 NP_821066.1 3 2005 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGATCC
AC
GAM281 278 ASE-1 2 1741 NP_036231.1 3 451 CTCTGTCGCCCA A 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTTGGACCCG
C
GAM281 278 ASE-1 2 3101 NP_036231.1 3 743 TGGTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 ATF7IP2 1 9602 NP_079273.1 3 541 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGTCAC GTGAC TGAGGTCGGACCCGTT
A
GAM281 278 ATM 2 1837 NP_612150.1 3 123 TCTGTCCGCCCA C------ T A 3 B c c
GGCTGGGTGCAG ACTGCAC CCAGCCTGGGC
TCACGGCT TGACGTG GGTCGGACCCG
TCGGCAC - C
GAM281 278 ATM 2 12000 NP_000042.2 5 50 TACTACTTTGAC CAGCCT - 3 B c c
CTTCCGAGTGCA CACTGCACTC GGG CAA
GTGAGGCA GTGACGTGAG TCC GTT
CCT--- A
GAM281 278 ATP1B2 1 16916 NP_001669.1 3 823 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 ATP1B4 1 13042 NP_036201.1 3 1878 TGTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 ATP6V0D 2 15039 NP_689778.1 3 853 CTCTGTCGCCCA C C A 3 B c c

2 GGCTAGAGTGCA CA TGCACTC AGCCTGGGC
ATGGCGTG GT ACGTGAG TCGGACCCG

A A C
GAM281 278 ATP6V0D 2 17102 NP_689778.1 3 437 CTCTGTCACCTA CC CA 3 B c c
2 GGCTACAGTGCA CACTGCACT AGCCTGGG
GTGGTGTG GTGACGTGA TCGGATCC
CA AC
GAM281 278 ATP6V1A 1 18868 NP_001681.2 3 676 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 ATP7A 1 4112 NP_000043.1 3 1061 TTTTGCAGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
A
GAM281 278 AXL 1 11802 NP_001690.2 3 471 CTGTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 AXL 1 11802 NP_068713.2 3 471 CTGTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 B4GALT4 1 11028 NP_003769.1 3 654 AGGACCTGCCCA CACTC - 3 B c c
GGTATGCCTTCC CACTG CA GCCTGGGCA
AGTGATGC GTGAC GT TGGACCCGT
CTTCC A
GAM281 278 B4GALT5 1 16140 NP_004767.1 3 1488 CTCTGTCGCCTA TG C A 3 B c c
AGCTGGAGTGTG CAC CACTCCAGC TGGGC
GTGGCACG GTG GTGAGGTCG ATCCG
GT A C
GAM281 278 B4GALT7 1 18475 NP_009186.1 3 311 TTCACGTGCCCA A TC - 3 B c c
GGCCTGTGGGTA CACTGC C CAG CCTGGGCA
GTGGGGAG GTGATG G GTC GGACCCGT
- GT C
GAM281 278 BA108L7 1 10888 NP_112233.2 3 1055 CTATTTTGCCCA C 3 B b b
.2 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
ATGGTGCG GT GCGTGAGGTCGGACCCGTT
A
GAM281 278 BACE 1 16660 NP_036236.1 5 182 GCCCGCTGCCCA T ACT-- 3 B c c
GGCTGGCCGCCG CAC GC CCAGCCTGGGCA
CCGTGCCG GTG CG GGTCGGACCCGT
C CCGCC
GAM281 278 BACE 1 16660 NP_620427.1 5 182 GCCCGCTGCCCA T ACT-- 3 B c c
GGCTGGCCGCCG CAC GC CCAGCCTGGGCA
CCGTGCCG GTG CG GGTCGGACCCGT
C CCGCC
GAM281 278 BACE 1 16660 NP_620428.1 5 182 GCCCGCTGCCCA T ACT-- 3 B c c

GGCTGGCCGCCG CAC GC CCAGCCTGGGCA
CCGTGCCG GTG CG GGTCGGACCCGT
C CCGCC

GAM281 278 BACE 1 16660 NP_620429.1 5 182 GCCCGCTGCCCA T ACT-- 3 B c c
GGCTGGCCGCCG CAC GC CCAGCCTGGGCA
CCGTGCCG GTG CG GGTCGGACCCGT
C CCGCC

GAM281 278 BACH2 1 2573 NP_068585.1 3 228 ACCCCTTGCCCA AC---- A- 3 B c c
GGCAAGGAAAGA CACTGC TCC GCCTGGGCAA
CAGCAGTG GTGACG AGG CGGACCCGTT
ACAGAA AA

GAM281 278 BAG5 1 5695 NP_004864.1 3 1870 CTCTGTTGCCCA C 3 B b b
GGCTGCAGTGCA CACTGCACT CAGCCTGGGCAA
GTGGTGCC GTGACGTGA GTCGGACCCGTT
C

GAM281 278 BAZ2A 1 8852 NP_038477.1 5 23 TCTTATTGCCCA C C 3 B b b
GGCTTGAGTGCA CA TGCACTC AGCCTGGGCAA
ATGACCTG GT ACGTGAG TCGGACCCGTT
A T

GAM281 278 BCHE 1 7089 NP_000046.1 5 49 GTCCAATTTACA - A- ------- A 3 B c c
GGCTGGAGCAGC CA CTGC CTCCAGCCT GGGC
AGCTGCAT GT GACG GAGGTCGGA CCTG
C AC CATTTAA -

GAM281 278 BCL10 1 19576 NP_003912.1 3 783 CTCTATCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 BDKRB1 1 8663 NP_000701.2 5 92 TCCGTCGGCCCA C C A 3 B c c
GACTGAAGTGCA CACTGCACT CAG CTGGGC
GTGGCACA GTGACGTGA GTC GACCCG
A A G

GAM281 278 BDKRB2 1 15590 NP_000614.1 3 1234 CGGTCTTGCCCA CAC AGC 3 B c c
GAGGATCACAGT CACTG TCC CTGGGCAA
GCTGAGAC GTGAC AGG GACCCGTT
ACT A--

GAM281 278 BDP1 1 19556 NP_060899.1 3 153 TTCTGTTGCCCA CA 3 B b b
GGCAAGAGTGCA CACTGCACTC GCCTGGGCAA
GTGGTATG GTGACGTGAG CGGACCCGTT
AA

GAM281 278 BENE 1 6009 NP_005425.1 3 474 CTCTTCCTCCAA - CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCT GGG
GTGACGCG GTGACGTGAGGTCGGA CCT
A CC

GAM281 278 BHD 1 9036 NP_659434.2 3 912 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 BIA2 1 6389 NP_056246.1 3 819 TATAAGACCTTA T -- CA 3 B c c
AGGCTGGGTGCA CACTGCAC CCAGCCT GGG

GTGGCTCA GTGACGTG GGTCGGA TCC
- AT AG

GAM281 278 BID 1 10620 NP_001187.1 5 128 CCGCGCTGCCCA C- G -- -- 3 B c c
GGCCATGGACTG ACT CAC TCCA GCCTGGGCA
TGAGGTCA TGG GTG AGGT CGGACCCGT
AC A TC AC

GAM281 278 BMF 1 759 NP_277038.1 3 2226 TTGCCAGGCCCA T-- T A 3 B c c
GGCTGGGTGCCC CAC GCAC CCAGCCTGGGC
TGTGGCCT GTG CGTG GGTCGGACCCG
TCC - G

GAM281 278 BMP6 1 6882 NP_001709.1 3 588 GTTGTATGTTCG - --- C 3 B c c
TGCTGGAGTTTT CACTG C ACTCCAGC TGGGCA
GTTGGTGT GTGGT G TGAGGTCG GCTTGT
T TTT T

GAM281 278 BNIP-S 1 5845 NP_612122.1 3 333 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC

GAM281 278 BRIP1 1 13904 NP_114432.1 3 208 GTCTGTTGCCCA C 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGTGTG GTGACGT AGGTCGGACCCGTT
A

GAM281 278 BRPF3 1 7755 XP_166450.1 3 879 GGGCTCCTATCA - - ----- A 3 B c c
GGCTGGGTGTGC CACT GCAC TCCAGCCTG GGC
GAGTGTCC GTGA CGTG GGGTCGGAC TCG
G T TATCC G

GAM281 278 BTN3A1 1 2067 NP_008979.2 3 1056 ACTCTGTTGCTA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGTGCG GTGACGTGAGGTCGGATC GTT
-

GAM281 278 BXDC1 2 4549 XP_166303.1 3 1357 CTCTGTCGCTCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACTCG
C

GAM281 278 BXDC1 2 12129 XP_166303.1 3 686 TTCTGTCACCTA G CA 3 B c b
GGGTGGAGTGCA CACTGCACTCCA CCTGGG
GTGGCACA GTGACGTGAGGT GGATCC
G AC

GAM281 278 BY55 1 7101 NP_008984.1 5 46 CACTGTCAACCA CA --- 3 B c c
GGCCAGAGTGCA CACTGCACTC GCCTGG GCA
GTGAAGAT GTGACGTGAG CGGACC TGT
AC AAC

GAM281 278 C11orf1 1 3521 NP_003466.1 3 127 TTGGCCTCAGGA AG--- - A 3 B c c
3 GCTGGGGGTGCA CACTGCACTCC CCTG GGC
GTGGGGGA GTGACGTGGGG GGAC CCG
GTCGA T G

GAM281 278 C11orf1 1 11525 NP_065693.2 3 217 CTCTGTTGCCCA 3 B b b
7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 C13orf1 1 5746 NP_065189.1 3 1686 CCTTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCACG GTGACGTGAG TCGGACCC
A AC
GAM281 278 C14orf1 1 12744 NP_009107.1 3 1453 CTCTGTCACCCA C-- CA 3 B c c
GGCTGGGAATTG CACTGCA TCCAGCCTGGG
CAGTGGCA GTGACGT GGGTCGGACCC
TAA AC
GAM281 278 C14orf1 2 5052 NP_060100.1 3 797 CTTCTGTGGTCA CAC G 3 B c b
13 GGCTGGGACAGT CACTG TCCAGCCTGG CA
GAAAGGCA GTGAC GGGTCGGACT GT
A-- G
GAM281 278 C14orf1 2 18863 NP_060100.1 3 360 TCTTGTTGCCCA C C 3 B b b
13 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGCATG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 C14orf1 1 1480 NP_060698.1 5 81 TTAAATGTCCCA A G -- - 3 B c c
15 GGCTGGAAGGTG C CT CAC TCCAGCCTGGG CA
GAGCGAGA G GA GTG AGGTCGGACCC GT
C G GA T
GAM281 278 C14orf1 1 17955 NP_660274.1 3 1620 CTTTGTCACCTA C CA 3 B c c
43 AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGCGCGA GTGACGTGAGGTCG ATCC
A AC
GAM281 278 C14orf9 1 14861 NP_055643.1 3 968 CTCTGTCACCCA CA 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 C16orf7 1 16110 NP_004904.1 3 374 GCCCCCAGAAGA -- ----- CA 3 B c c
AGCTGGAGTGCA CACT GCACTCCAGC CTGGG
TAGTGCGG GTGA CGTGAGGTCG GACCC
TA AAGAA CC
GAM281 278 C1orf24 1 19538 NP_443198.1 3 1462 CTCTGTCGCCAA G A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGC
GTGGTGTG GTGACGTGAGGTCGGA CCG
A C
GAM281 278 C1QTNF6 1 14882 NP_114116.2 3 543 CTCTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGTGCA GTGACGTGAG TCGGACCCGTT
A
GAM281 278 C20orf1 1 16257 NP_689880.1 3 981 CTCTGTCGCCCA CT A 3 B c c
47 GGTTGGAGTGCC CA GCACTCCAGCCTGGGC
ATGGCACC GT CGTGAGGTTGGACCCG
AC C
GAM281 278 C21orf6 1 6569 NP_478068.1 5 158 CGCTGTCGCCCA C A A 3 B c c
7 GGCTGGAGCGCA CA TGC CTCCAGCCTGGGC
ATGGCGCG GT ACG GAGGTCGGACCCG
A C C
GAM281 278 C22orf1 1 18897 NP_003669.2 3 1825 CTCTGTTGTCCA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGGCACG GTGACGTGAGGTCGGACCTGTT

GAM281 278 C3IP1 1 2482 NP_067646.1 3 132 CGGGTGATTACA CCA GG-- 3 B c c
GGCACCAGTGCA CACTGCACT GCCTG CA
GTGATGAT GTGACGTGA CGGAC GT
CCA ATTA

GAM281 278 C4orf9 1 15574 XP_035572.1 3 370 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACA GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 C6orf33 1 6896 NP_588608.1 3 2345 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGATGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 C6orf5 2 10099 NP_056339.2 3 1428 CTCTGTCGTCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGCTGCA GTGACGTGAGGTCGGACCTG
C

GAM281 278 C6orf5 2 12805 NP_056339.2 3 2320 CACTCTTTCCCA C C CA 3 B c b
GGCTGCAGTACA CACTG ACT CAGCCTGGG
GTGACACA GTGAC TGA GTCGGACCC
A C TT

GAM281 278 C6orf57 1 2114 NP_660310.1 3 501 CTCTCTCACCCA G CA 3 B c c
GGCTGGAGTGGA CACT CACTCCAGCCTGGG
GTGGCGCT GTGA GTGAGGTCGGACCC
G AC

GAM281 278 C7 2 9684 NP_000578.1 3 245 AGCCTTTGCACA T CT G 3 B c b
GGCTGGCTGCGT CAC GCA CCAGCCTG GCAA
GTTCTTGA GTG CGT GGTCGGAC CGTT
- C- A

GAM281 278 C7 2 17778 NP_000578.1 3 631 CTTTGTTGCCCA A 3 B b b
GGCTGGAGCGCA CACTGC CTCCAGCCTGGGCAA
GTGGGGTG GTGACG GAGGTCGGACCCGTT
C

GAM281 278 C9orf5 1 14258 NP_114401.1 3 1340 GGTTCTTGGCCA TG A C G 3 B c c

GGCTGTAGGTGG CAC C CT CAGCCTGG CAA
TGGCTCAC GTG G GA GTCGGACC GTT
GT - T G

GAM281 278 C9orf9 2 5477 NP_061829.2 3 856 CTCTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
TC

GAM281 278 C9orf9 2 11520 NP_061829.2 3 217 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCG CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGGCGTGAGGTCGGACCCG
C

GAM281 278 CAB2 1 9181 NP_219487.2 3 709 GAGTGTGGGCCA --- C --- 3 B c c
GGCTGAGTGCAT CACT GCACTC AGCCTGG GCA
AGGTGACA GTGG CGTGAG TCGGACC TGT

ATA - GGG
GAM281 278 CABP4 1 7624 NP_660201.1 5 32 CAAGGGTGCCCA TG CCAG 3 B c c
GGGGTGTGGTGT CAC CACT CCTGGGCA
CTCTGAGC GTG GTGG GGACCCGT
GT ----
GAM281 278 CAMLG 1 18944 NP_001736.1 3 791 TCTTGTTGCCCA C C 3 B b b
GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA
ATGGCGCC GT ACGTGAG TCGGACCCGTT
A A
GAM281 278 CAPRI 1 4271 NP_008920.3 3 1973 CTGTGTTGCCCA CAC----- 3 B c c
GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
AATGGCTT ACGTGAGGTCGGACCCGTT
TTCGGTAA
GAM281 278 CARD6 1 9036 NP_115976.2 3 205 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 CASP2 1 16398 NP_001215.1 3 1634 CTCTGTCGCCCA A A 3 B b b
GGCTGGAGGGCA CACTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C
GAM281 278 CASP2 1 16398 NP_116764.1 3 1245 CTCTGTCGCCCA A A 3 B b b
GGCTGGAGGGCA CACTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C
GAM281 278 CASP2 1 16398 NP_116765.1 3 2059 CTCTGTCGCCCA A A 3 B b b
GGCTGGAGGGCA CACTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C
GAM281 278 CASP2 1 16398 NP_116766.1 3 2059 CTCTGTCGCCCA A A 3 B b b
GGCTGGAGGGCA CACTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C
GAM281 278 CASP8 1 15049 NP_001219.2 3 82 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 CASP8 1 15049 NP_203519.1 3 82 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 CASP8 1 15049 NP_203520.1 3 82 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 CASP8 1 15049 NP_203521.1 3 827 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM281 278 CBFA2T2 1 8242 NP_787060.1 5 594 CCCTGTCACTCA CA CA 3 B c c
GGCTGGAGCACA CACTG CTCCAGCCTGGG
GTGGTGTG GTGAC GAGGTCGGACTC
AC AC
GAM281 278 CCL16 1 9543 NP_004581.1 3 276 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 CCL22 2 1679 NP_002981.2 3 951 TCTTGTCACCCA C C CA 3 B c b
CGCTGGAGTGCA CA TGCACTCCAGC TGGG
ATGGTGTG GT ACGTGAGGTCG ACCC
A C AC
GAM281 278 CCL22 2 15049 NP_002981.2 3 1275 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 CCNF 1 17624 NP_001752.1 3 1293 TCTTGTCTCCCC T CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCC GGG
GTGGCATG GTGACGTGAGGTCGG CCC
C TC
GAM281 278 CCRN4L 1 4698 NP_036250.2 3 103 CTCTGTTGCCTA C 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGCCTG GTGAC TGAGGTCGGATCCGTT
A
GAM281 278 CD209 2 4298 NP_066978.1 3 1590 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 CD209 2 17051 NP_066978.1 3 625 TCTTGTCGCTCA CT A 3 B c b
GGCTGGAGTGCC CA GCACTCCAGCCTGGGC
ATGGCGCG GT CGTGAGGTCGGACTCG
AC C
GAM281 278 CD24 1 19572 NP_037362.1 3 890 CTTTGTCGCCCA A A 3 B b b
GGCCGGAGTGCA CACTGCACTCC GCCTGGGC
GTGGTGCG GTGACGTGAGG CGGACCCG
C C
GAM281 278 CDC14B 1 17127 NP_201589.1 3 632 TCTTGTTGTCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCTGTT
GAM281 278 CDC2L2 1 15084 NP_296370.1 5 18 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGAG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 CDC6 1 9211 NP_001245.1 3 414 CCCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 CDCP1 1 12091 NP_073753.3 3 1772 TTCTGTTGCCTA 3 B b b

GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGATCCGTT

GAM281 278 CDH1 2 5514 NP_004351.1 3 519 TTCTATCGGCCA GCA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGACC
GGC
GAM281 278 CDH1 2 12580 NP_004351.1 3 825 CTCCATCGCCCA CT - A 3 B c c
GGCCTGGGATGC CACTGCA CCAG CCTGGGC
AGTGATGT GTGACGT GGTC GGACCCG
AG C C
GAM281 278 CDH17 1 13851 NP_004054.2 3 190 CTCTGTCGCCCA C A 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGC
GTGGTGTG GTGAC TGAGGTCGGACCCG
A C
GAM281 278 CDK11 1 8162 XP_166324.1 3 3222 CTCTGTCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACG GTGACGTGAGGTCG ACCC
A AC
GAM281 278 CDKAL1 2 1255 NP_060244.1 3 444 TCTTGTCCCCCA --- CA 3 B c c
GGCTGGAGTGGT CACTGCAC TCCAGCCTGGG
GCAGTGGC GTGACGTG AGGTCGGACCC
GTG CC
GAM281 278 CDKAL1 2 3603 NP_060244.1 3 444 TGTCCCCCAGGC --- CA 3 B c c
TGGAGTGGTGCA CACTGCAC TCCAGCCTGGG
GTGGCACG GTGACGTG AGGTCGGACCC
GTG CC
GAM281 278 CDT6 1 18500 NP_066969.1 3 577 GGAACTGACCCA CA---- C- - 3 B c c
GGCTGGACTTGC CTGCA TCCAGCCTGGG CA
GGGGAGGA GGCGT AGGTCGGACCC GT
AGGAGG TC A
GAM281 278 CEACAM8 1 17969 NP_001807.2 3 353 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 CECR1 2 4574 NP_059120.2 3 388 TCTTGTTGCCCA C C 3 B b b
GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGTGCG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 CECR1 2 4574 NP_803124.1 3 388 TCTTGTTGCCCA C C 3 B b b
GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGTGCG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 CECR1 2 9037 NP_059120.2 3 1395 CTCTGTTGCCCA A G 3 B b b
GGGTGGAGTGCA C CTGCACTCCA CCTGGGCAA
GCGGTGCG G GACGTGAGGT GGACCCGTT
C G
GAM281 278 CECR1 2 9037 NP_803124.1 3 1395 CTCTGTTGCCCA A G 3 B b b
GGGTGGAGTGCA C CTGCACTCCA CCTGGGCAA
GCGGTGCG G GACGTGAGGT GGACCCGTT

C G
GAM281 278 CENPH 1 19549 NP_075060.1 3 263 CTTTGTTGCCCA A C 3 B b b
GACTGGAGGGCA CACTGC CTCCAG CTGGGCAA
GTGGCGCG GTGACG GAGGTC GACCCGTT
G A
GAM281 278 CENPJ 1 13565 NP_060921.2 5 123 CTGAGCTGCCCA AC ---- 3 B b b
GGCTTCACGGAG CACTGC TCC AGCCTGGGCA
CGGTGTTG GTGGCG AGG TCGGACCCGT
-- CACT
GAM281 278 CGI-150 1 2191 NP_057164.1 5 49 GCTCTGTCATCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGCTCA GTGACGTGAGGTCGGAC CTGT
TA
GAM281 278 CGI-43 1 14860 NP_056437.1 3 376 CTCCGTGACCCA C C - 3 B b b
GGCTGGAATGCA CA TGCA TCCAGCCTGGG CA
ATGGCTCA GT ACGT AGGTCGGACCC GT
A A A
GAM281 278 CHD5 1 2568 NP_056372.1 3 686 CCTTCCTGCCAA ----- A G 3 B c c
GGCTGGAGGCCG CACT GC CTCCAGCCT GGCA
CCAGGTGT GTGG CG GAGGTCGGA CCGT
ACCGC - A
GAM281 278 CHRAC1 1 9475 NP_059140.1 3 960 CTCAGTTGCCCA C 3 B b b
GGCTGGATTGCG CACTGCA TCCAGCCTGGGCAA
GTGGCGCT GTGGCGT AGGTCGGACCCGTT
T
GAM281 278 CHSY1 1 11924 NP_055733.2 3 639 CTCTGTTACCCA C CA 3 B c c
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCGCA GTGACGT AGGTCGGACCC
A AT
GAM281 278 CIAS1 1 13461 NP_004886.2 5 289 CTGTGTCGCCTA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGATCCG
C
GAM281 278 CIP29 2 3509 NP_115740.3 3 164 CTCTGTTGCCCA C 3 B b b
GCTGGAGTGCAG CACTGCACTCCAGC TGGGCAA
TGGTGTGA GTGACGTGAGGTCG ACCCGTT
-
GAM281 278 CIP29 2 20120 NP_115740.3 3 164 GCTCTGTTGCCC C 3 B b b
AGCTGGAGTGCA CACTGCACTCCAGC TGGGCAA
GTGGTGTG GTGACGTGAGGTCG ACCCGTT
-
GAM281 278 CLDN14 1 3558 NP_652763.1 5 247 AGGAGATGCCCA -- CC 3 B c c
GGTTCAGGTGTA CAC TGCACT AGCCTGGGCA
TCGTGCAT GTG ATGTGG TTGGACCCGT
CT AC
GAM281 278 CLECSF1 2 15296 NP_072092.2 3 320 CTTTGTTACCCA CA 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AT
GAM281 278 CLECSF1 2 16192 NP_072092.2 3 970 TCTTGTTGCCCA CAC----- 3 B c
b

2 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ACGGCACG ACGTGAGGTCGGACCCGTT
GCACGGCA
GAM281 278 CLIC5 1 19116 NP_058625.1 5 141 CCCCGCTGCTCG - CA 3 B c c
GGCTGGAGAATA CA CTG CTCCAGCCTGGGCA
GATGGTTT GT GAT GAGGTCGGGCTCGT
A AA
GAM281 278 CLN6 1 19830 NP_060352.1 3 875 TGCATTCCTGGG G -- --- --- 3 B c c
GGCTGGAGGGTG CACT CAC TCCAGCCT GG GCA
GGGTGCCA GTGG GTG AGGTCGGG CC CGT
G GG GGT TTA
GAM281 278 CLN8 1 515 NP_061764.2 3 1639 CTTTGGCTCCCA C CA 3 B c c
GGCTGGAGTCCA CACTG ACTCCAGCCTGGG
GTGGTGTG GTGAC TGAGGTCGGACCC
C TC
GAM281 278 CMAR 2 5053 NP_005191.2 5 232 CGCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGCTGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 CMAR 2 18767 NP_005191.2 5 364 CTGTGTTGCCAA CA----- G 3 B c b
GGCTGGAGTGCA CTGCACTCCAGCCT GGCAA
GGCCGCGA GACGTGAGGTCGGA CCGTT
AGCGCCG A
GAM281 278 CNN2 1 9959 NP_004359.1 3 736 GGTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM281 278 CNP 1 606 NP_149124.1 3 561 TGCTATTTCCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGTGCG GTGACGTGAGGTCG ACCC
A TT
GAM281 278 COL4A4 1 12506 NP_000083.1 5 201 TCCGGGGGCCCA G - A- A 3 B c
c
GGCGGGGAAGTG CACT CACT CC GCCTGGGC
GGGTGCGG GTGG GTGA GG CGGACCCG
G A GG G
GAM281 278 COLEC12 2 11525 NP_110408.2 3 104 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 COLEC12 2 12507 NP_110408.2 3 538 CTCTGTCACCCA --- C CA 3 B c
b
GGCTGGAATGAC CACT G CA TCCAGCCTGGG
GAAGTGAA GTGA C GT AGGTCGGACCC
AG A A AC
GAM281 278 COQ4 1 14708 NP_057119.1 3 276 CTGGGCTCATGC --- C A 3 B c c
TGGGATTGTGCA CACTGCAC TCCAGC TGGGC
GTGCTCCT GTGACGTG GGGTCG ACTCG
TTA T G
GAM281 278 CORO1C 1 13595 NP_055140.1 3 1013 GCAGCTTGCCCA C C C- 3 B c
c

GCTCTTGAGTAC CACTG ACTC AG CTGGGCAA
AGTGGTGG GTGAC TGAG TC GACCCGTT
A T TC

GAM281 278 COX15 1 7552 NP_510870.1 3 659 TCTTGTTGCCCA C C 3 B b b
GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGCGTG GT AC TGAGGTCGGACCCGTT
A A

GAM281 278 CPA4 1 8942 NP_057436.1 3 604 TCTTGTTGCCCA CT 3 B b b
GGCTGGAGTGTG CA GCACTCCAGCCTGGGCAA
ATGGGCTC GT TGTGAGGTCGGACCCGTT
AG

GAM281 278 CPR8 1 13999 NP_065790.1 3 1691 CTTTGTCAGCCA --- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCAA
GTGACACG GTGACGTGAGGTCGGACC TGTT
GAC

GAM281 278 CPS1 1 14493 NP_001866.2 3 668 TCACACTCTCCA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCT
CT

GAM281 278 CPSF2 2 591 XP_029311.2 3 2045 TCTTGTTGCCCA C C 3 B b b
GACTGGAGTGCA CA TGCACTCCAG CTGGGCAA
ATGGCACA GT ACGTGAGGTC GACCCGTT
A A

GAM281 278 CPSF2 2 1877 XP_029311.2 3 1220 CAGAGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGAG GTGACGTGAGGTCGGACCC
AC

GAM281 278 CR1 1 17292 NP_000564.1 3 771 CTCTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTA GTGACGTGAGGTCGGACCC
TC

GAM281 278 CR1 1 17292 NP_000642.2 3 770 CTCTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTA GTGACGTGAGGTCGGACCC
TC

GAM281 278 CRLF3 1 7105 NP_057070.2 3 613 TCTTGTCACTCA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACTC
AC

GAM281 278 CRSP6 1 7661 NP_004259.3 3 435 CTCTGTAGCCCA C A 3 B b b
GTCTGGAGTGCA CACTGCACTCCAG CTGGGC
GTGGTGTG GTGACGTGAGGTC GACCCG
T A

GAM281 278 CRTAP 1 7107 NP_006362.1 3 267 CTCTCTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 CSAD 1 7030 NP_057073.2 3 94 TCCCAGCCTTTG T A --- A 3 B c c
AGGCCGGGTGCA CACTGCAC CC GCCT GGGC
GTGGCTCA GTGACGTG GG CGGA TCCG

- C GTT A

GAM281 278 CSE-C 1 2336 NP_061851.1 5 2 GGAGTGCCCAGG G 3 B b b
ATGGAGTGCAGT CACTGCACTCCA CCTGGGCA
GGCTATTC GTGACGTGAGGT GGACCCGT
A

GAM281 278 CSE1L 1 6312 NP_803185.1 3 493 TCTCATTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGAGCTA GTGACGTGAGGTCGGACCCGTT

GAM281 278 CSNK1G2 1 14869 NP_001310.2 3 1019 GGGCCGTGCCCA T ACT AG 3 B c c
GGGCGGTGGCTG CAC GC CC CCTGGGCA
TGAGTCTA GTG CG GG GGACCCGT
T GT- CG

GAM281 278 CSNK2A2 1 15382 NP_001887.1 5 1 TGTCACCCAGGC CA 3 B b b
TGGAGTGCAGTG CACTGCACTCCAGCCTGGG
GCGCAATC GTGACGTGAGGTCGGACCC
AC

GAM281 278 CST 1 9756 NP_004852.1 5 76 TGTGTCATCCAG A - CA 3 B c c
AGCTGGAGTGCA C CTGCACTCCAGC CTGGG
GCGGCACA G GACGTGAGGTCG GACCT
C A AC

GAM281 278 CTEN 1 14746 NP_116254.3 3 767 CACTGTCACCCA CTC CA 3 B c c
GGCTGAACTGCA CACTGCA CAGCCTGGG
GTGGTGTG GTGACGT GTCGGACCC
CAA AC

GAM281 278 CTF1 1 13287 NP_001321.1 3 196 CTCTGTCGCCCA A 3 B b b
GGCTGGGGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGGGGTCGGACCCG
C

GAM281 278 CTSB 1 12465 NP_680090.1 5 118 GCTGCAGCGCTG T TG - A 3 B c c
GGCTGGTGTGCA CACTGCAC CCAGCC G GC
GTGGTGCG GTGACGTG GGTCGG C CG
T GT G A

GAM281 278 CTSB 1 12465 NP_680092.1 5 118 GCTGCAGCGCTG T TG - A 3 B c c
GGCTGGTGTGCA CACTGCAC CCAGCC G GC
GTGGTGCG GTGACGTG GGTCGG C CG
T GT G A

GAM281 278 CTSS 1 4517 NP_004070.3 3 1701 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACCCGTT

GAM281 278 CXCL16 1 17688 NP_071342.1 3 340 CTCTGTCATCCA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCT
AC

GAM281 278 CXCL6 1 4626 NP_002984.1 3 51 TAAAATTGCCCA C-- AC A ------ 3 B c c
GTCTTCAGCGGA ACTGC TCC GC CTGGGCAA
GCAGTTTT TGACG AGG CG GACCCGTT

TTT -- - ACTTCT

GAM281 278 CXorf12 1 4704 NP_003483.1 3 174 TTCGGTGTGGAG T G GG- 3 B c c
GGGTGGAGTGCT CAC GCACTCCA CCT GCA
GTGATCTC GTG CGTGAGGT GGG TGT
T G AGG

GAM281 278 CYCS 3 9339 NP_061820.1 3 2207 CCTTTTCGCCCA C C A 3 B c b
GGCTGAGTACAG CACTG ACTC AGCCTGGGC
TGGTGCAA GTGAC TGAG TCGGACCCG
A - C

GAM281 278 CYCS 3 18868 NP_061820.1 3 2620 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 CYCS 3 18991 NP_061820.1 3 1817 CTGTGTCGCCAA G A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGC
GTGGTGCG GTGACGTGAGGTCGGA CCG
A C

GAM281 278 CYLC2 1 15540 NP_001331.1 3 731 CTCTGTTGCCCT C T 3 B b b
GGCTGGAGTTCA CACTG ACTCCAGCC GGGCAA
GTGACATG GTGAC TGAGGTCGG CCCGTT
T T

GAM281 278 CYP1A2 3 6637 NP_000752.1 3 788 ACTCTGTTGCCA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-

GAM281 278 CYP1A2 3 13576 NP_000752.1 3 418 GTCTGTCACCCA CA 3 B c b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTTGGACCC
AC

GAM281 278 CYP1A2 3 18279 NP_000752.1 3 1085 CTCTGTCTCCTA C CA 3 B c b
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCATC GTGACGTGAGGTCG ATCC
A TC

GAM281 278 CYP2B6 2 2194 NP_000758.1 3 1087 CTCTGTCTCCCA --- CA 3 B c b
GGCTGGAGTGCT CACT GCACTCCAGCCTGGG
ATGGTGCA GTGG CGTGAGGTCGGACCC
TAT TC

GAM281 278 CYP2B6 2 10618 NP_000758.1 3 276 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 CYP4F3 1 9158 NP_000887.1 3 1396 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM281 278 CYP51A1 1 2152 NP_000777.1 3 884 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 CYP8B1 1 5978 NP_004382.1 3 1006 CTCTGTTGCCCA C 3 B b b

GGCTGCAGTGCA CACTGCACT CAGCCTGGGCAA
GTGGTGTG GTGACGTGA GTCGGACCCGTT
C

GAM281 278 D2S448 1 11750 XP_056455.2 3 580 ACAGGGACACTG CCAG TG 3 B c c

TCTGGGGGTGCA CACTGCACT CC GGCA
GTGCAAGC GTGACGTGG GG CTGT
---- GT

GAM281 278 DBC-1 1 12841 NP_066997.3 3 172 GGCAGGCCATCA T A -- A 3 B c c
GGCTGGGGGCTG CAC GC CTCCAGCCTG GGC
TGCTATGT GTG CG GGGGTCGGAC CCG
T - TA G

GAM281 278 DBR1 1 7961 NP_057300.1 3 86 TCTTGTCACCTA C C CA 3 B c c
GACTGGAGTGCA CA TGCACTCCAG CTGGG
ATGGCGTG GT ACGTGAGGTC GATCC
A A AC

GAM281 278 DCK 1 3487 NP_000779.1 3 956 TAGTTTGTTTAG T AGC- 3 B c c
TTAAGGTGTGCA CACTGCAC CC CTGGGCAA
GTGTTTTT GTGACGTG GG GATTTGTT
T AATT

GAM281 278 DCX 1 16590 NP_000546.2 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM281 278 DCX 1 16590 NP_835364.1 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM281 278 DCX 1 16590 NP_835365.1 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM281 278 DCX 1 16590 NP_835366.1 3 4962 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM281 278 DDX31 1 16338 NP_619526.1 3 189 TTGATTGTCCCT C----- G T- 3 B c c
GGATGGAGTGCA ACTGCACTCCA CC GGGCAA
GTCACCTT TGACGTGAGGT GG CCTGTT
TTCCAC A TC

GAM281 278 DES 1 14498 NP_001918.2 3 295 GGATGGAGCCCA AC A A 3 B c c
GGCGGGAGCGGT CACTGC TCC GCCTGGGC
GGCCCTGT GTGGCG AGG CGGACCCG
-- G A

GAM281 278 DFFB 2 2019 NP_004393.1 3 246 TTTTGTTGCCCA 3 B b b
GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGATGTGAGGTCGGACCCGTT

GAM281 278 DFFB 2 9091 NP_004393.1 3 889 CTCTGTCGCTCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC

GTGATGCA GTGACGTGAGGTCGGACTCG
C
GAM281 278 DHFR 1 8052 NP_000782.1 3 920 TCTTGTTGCCCA C CTCC 3 B c c
GGCTAGCATGCA CA TGCA AGCCTGGGCAA
ATGGTGTG GT ACGT TCGGACCCGTT
A ACGA
GAM281 278 DIAPH2 1 14492 NP_006720.1 3 4013 CTCTGTCACCCA C CA 3 B c c
GGCTGCAGTGTA CACTGCACT CAGCCTGGG
GTGGTGCA GTGATGTGA GTCGGACCC
C AC
GAM281 278 DISC1 2 1298 NP_061132.1 3 3218 CTCTGTCACCCA C CA 3 B c c
AGTTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCCCC GTGACGTGAGGTTG ACCC
A AC
GAM281 278 DISC1 2 11285 NP_061132.1 3 1279 TGCAGTGCTCAA - AGCC 3 B c c

TAAGGCAGTGCA CACTGCACT CC TGGGCA
GTGCTCAG GTGACGTGA GG ACTCGT
C AATA
GAM281 278 DKFZP43 1 4080 NP_113664.1 3 2101 CTCTGTTGCCCA CA - 3 B b b
4B044 AGGTAGAGTGCA CACTGCACTC GCCT GGGCAA
GTGGCGTG GTGACGTGAG TGGA CCCGTT
A- A
GAM281 278 DKFZP43 1 4014 NP_115519.1 3 480 CTTTGTTACCCA C CA 3 B c c
4B1727 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGTGTC GTGAC TGAGGTCGGACCC
A AT
GAM281 278 DKFZp43 1 8235 NP_060068.1 3 861 CTCTGTCACCCA C CA 3 B c c
4C0923 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC
GAM281 278 DKFZP43 1 8661 XP_044196.3 3 1560 CCCTGTTGCCCA C 3 B b b
4C212 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 DKFZP43 1 2209 NP_056410.2 3 810 CTCTGTCGCCCA C C A 3 B c c
4D146 GGCTAGAGTATA CACTG ACTC AGCCTGGGC
GTGGTGTG GTGAT TGAG TCGGACCCG
A A C
GAM281 278 DKFZp43 1 11326 NP_060082.1 5 772 GTCTGTTGCCCA 3 B b b
4E2220 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 DKFZP43 1 16771 NP_110444.1 3 2412 CTCTGTCACCTA - CA 3 B c c
4F0318 GGCTGGAGTTGC CACTGCA CTCCAGCCTGGG
AGTGGTTT GTGACGT GAGGTCGGATCC
T AC
GAM281 278 DKFZp43 1 3951 NP_115624.1 3 1205 TCTTGTTTCCCA C CA 3 B c c
4F1719 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGGTGA GT ACGTGAGGTCGGACCC

A TT
GAM281 278 DKFZp43 1 4195 NP_060076.1 3 1080 ATTTAGTGCCCA A C AGC 3 B c c
4K1210 GGGAGTCCAGCG C CTG ACTCC CTGGGCA
AATGACGT G GAC TGAGG GACCCGT
C C ---
GAM281 278 DKFZp54 1 14246 NP_064546.1 3 257 CTCCATTGCCCA CA----- C 3 B c c
7H025 GGCTGGACTGCA CTGCA TCCAGCCTGGGCAA
GCAGCGTG GACGT AGGTCGGACCCGTT
GTGCGAC C
GAM281 278 DKFZp54 1 1180 NP_115531.1 3 64 CCACACGTTTGT A C CT 3 B c c
7I094 CTGTTGAGTGCA C CTGCACTC AGC GGGCAA
GCGACAAG G GACGTGAG TTG TCTGTT
C - --
GAM281 278 DKFZp54 1 11057 NP_694590.1 3 1544 CACTGTCACCCA CA 3 B b b
7P234 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 DKFZP56 1 17204 NP_108648.1 3 922 TTCTGTTGCCTA CA 3 B b b
4D166 GGCCAGAGTGCA CACTGCACTC GCCTGGGCAA
GTGGCATG GTGACGTGAG CGGATCCGTT
AC
GAM281 278 DKFZP56 1 2662 NP_056416.1 5 1111 TCTTGTCGCCCA C A 3 B b b
4G092 GGCTGTAGTGCA CACTGCACT CAGCCTGGGC
GTGGTACA GTGACGTGA GTCGGACCCG
T C
GAM281 278 DKFZP56 1 16590 XP_032397.1 3 259 CTCTGTCACCTA CA 3 B c c
4I122 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC
GAM281 278 DKFZP56 1 1067 NP_056274.1 3 522 GCTCTGTCACCA C -- 3 B b b
4J0863 GGCTTGAGTGCA CACTGCACTC AGCCTGG GCA
GTGGTGTG GTGACGTGAG TCGGACC TGT
T AC
GAM281 278 DKFZP56 1 18768 NP_060927.1 5 32 GCAGCAAGCCCA ACTCCA A 3 B c c
4J157 GGCGGCGGTGGA CACTGC GCCTGGGC
AAGGCTAA GTGGCG CGGACCCG
G----- A
GAM281 278 DKFZP56 1 17964 NP_114429.1 3 215 CTCTGTTGCCCA 3 B b b
4K0322 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT
GAM281 278 DKFZp56 1 2663 NP_115497.2 3 696 CTGTGTCACACA --- 3 B b b
4K142 GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGCGTG GTGACGTGAGGTCGGAC CTGT
ACA
GAM281 278 DKFZP56 1 10819 XP_166254.2 3 1562 CAGCAGCCAGCA A- -- A 3 B c c

4O0423 GGCTGGGGGAGC CACTGC CTCCAGCCTG GGC
AGTGAGGG GTGACG GGGGTCGGAC CCG
AG GA A
GAM281 278 DKFZP56 1 3686 NP_115496.1 3 226 CTCTGTTGCCCA C 3 B b b
4O0523 GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
A
GAM281 278 DKFZP56 1 10539 NP_110443.1 5 181 GCGTTTGTCCCA CA- - - 3 B c c
6D1346 GGCTCGGGGGCT CACTG CTCC AGCCTGGG CAA
CAGTGGGA GTGAC GGGG TCGGACCC GTT
TCG C T
GAM281 278 DKFZP56 1 12353 NP_056226.1 3 714 CTCTGTTGCCCA --- C 3 B b b
6I1024 GGCTAGAGTGCA CACT GCACTC AGCCTGGGCAA
CTGGTGGT GTGG CGTGAG TCGGACCCGTT
TCA A
GAM281 278 DKFZp58 1 12173 XP_098416.1 3 3009 CTCTGTCACCCA C CA 3 B c c

6C0721 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCAAG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 DKFZP58 1 11134 NP_056248.1 3 473 CTCTGTCATCCA CA 3 B c c
6D0919 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCT
AC
GAM281 278 DKFZp66 1 15574 NP_808881.1 3 966 TCTTGTTGCCCA C 3 B b b
7B1218 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 DKFZp66 1 8492 XP_117353.1 3 296 CTCTGTCAGCCA TG --- 3 B c c
7E0512 GGCTGGAGTGTG CAC CACTCCAGCCTGG GCA
GTGGCACA GTG GTGAGGTCGGACC TGT
GT GAC
GAM281 278 DKFZp76 1 13571 NP_775734.1 3 2765 CTATGTCTCCCA CA 3 B b b
1B107 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM281 278 DKFZp76 1 17969 NP_689650.1 5 1005 CTCTGTCGCCCA A 3 B b b
1B128 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 DKFZp76 1 15190 NP_061181.1 3 887 ATCTGTCGCCCA C----- A 3 B c c
1H039 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGC
GTAGCGTG TGACGTGAGGTCGGACCCG
GTGCGA C
GAM281 278 DKFZp76 1 12187 XP_166582.2 3 1000 AAAATCTGAACA CCAG GG 3 B c
c

1I2123 GGGCCAGGTGCA CACTGCACT CCTG CA
GTGGCTCA GTGACGTGG GGAC GT
ACCG AA
GAM281 278 DKFZp76 1 5768 NP_115656.1 5 1462 TCTTGTCACCCA CA 3 B b b

1J139 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 DKFZp76 1 7711 NP_060892.1 5 37 TGTTTGAGTGAG C TGGG 3 B c c

1K1423 TGGCTGAGTGCA CACTGCACTC AGCC CA
GTGTCTTT GTGACGTGAG TCGG GT
- TGA-

GAM281 278 DKFZp76 1 13529 XP_086327.6 3 1184 ACTCTGTTGCCA C G 3 B b b

1N1114 GGCTGGAATGCA CACTGCA TCCAGCCTGG CAA
GTGGCGTC GTGACGT AGGTCGGACC GTT
A -

GAM281 278 DKFZp76 1 7699 NP_060879.1 5 1531 TCTTGTTGCCCA C 3 B b b

1O0113 GGCTTGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGATGCA GTGACGTGAG TCGGACCCGTT
T

GAM281 278 DKFZp76 1 9147 NP_690870.1 3 740 CTCTGTCACCCA CA 3 B b b

1P1121 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 DKFZp76 1 4056 NP_848637.1 3 168 CTCTGTGGCCCA C A 3 B b b

2C2414 GGCTGAAGTGCA CACTGCACT CAGCCTGGGC
GTGGTGTG GTGACGTGA GTCGGACCCG
A G

GAM281 278 DKFZp76 1 13803 XP_172976.2 3 1898 CTCTGTCGCCCA CA----- A 3 B c c

2H185 GGCTGGAGTGCA CTGCACTCCAGCCTGGGC
GAGGTGCG GACGTGAGGTCGGACCCG
GCGTGGA C

GAM281 278 DKFZp76 1 1744 NP_689624.1 3 255 CTCTGTCACCCA CA 3 B b b

2I137 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 DKFZp76 1 6884 NP_689597.1 3 705 CAATGGTGCCCA 3 B b b

2I194 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCGTG GTGACGTGAGGTCGGACCCGT

GAM281 278 DKFZp76 1 9194 NP_061189.2 3 781 TTCTGTTGCCCA AG 3 B b b

2L0311 GGAGGGAGTGCA CACTGCACTCC CCTGGGCAA
GTGGTGCA GTGACGTGAGG GGACCCGTT
GA

GAM281 278 DLG2 1 9202 NP_001355.1 5 197 AGCACATGCCCA T TCCAG 3 B c c

GGATCGTGTGTG CAC GCAC CCTGGGCA
TGGGGCTT GTG TGTG GGACCCGT
- TGCTA

GAM281 278 DNAH11 1 1214 NP_003768.1 3 43 TCCTCTAGCCTC CT A 3 B c c

TGCTGGAGTGCA CACTGCACTCCAGC GGGC
GTGAGGAT GTGACGTGAGGTCG TCCG
TC A

GAM281 278 DNAJB5 1 5815 NP_036398.2 3 231 AGAGCTAGCCCA C C A- A 3 B c c

GGCCAGGGGTCA CA TG ACTCC GCCTGGGC
ATGTTCAT GT AC TGGGG CGGACCCG
A - AC A

GAM281 278 DNCL2A 1 949 NP_808853.1 3 681 AGGGTTTGCCCA - CTCC C 3 B c c

GTTTGCAGATGA CA CTGCA AGC TGGGCAA
GAAACCCA GT GACGT TTG ACCCGTT
A ---- -

GAM281 278 DPM2 1 3466 NP_689903.1 3 285 GTTGGTTATTGC CCAGCC 3 B c c

TTAAGAAGTGCA CACTGCACT TGGGCAA
GTGTGTCT GTGACGTGA ATTCGTT
AGA---

GAM281 278 DRIM 1 6633 NP_055318.1 3 141 CTCTGTCACCCA A - CA 3 B c c
AGGCGGAGTGCA CACTGCACTCC GCCT GGG
GTGACGAC GTGACGTGAGG CGGA CCC
- A AC

GAM281 278 DRPLA 1 9796 NP_001931.1 5 185 TTCAGCTGCCCA C- G -- A-- 3 B c c
GGCAGAGGAGAA ACT CA CTCC GCCTGGGCA
TGGGGTCT TGG GT GAGG CGGACCCGT
TC G AA AGA

GAM281 278 DSC3 1 7559 NP_001932.1 3 2049 CTCTGACGCACA G A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GC
GTGGCTCC GTGACGTGAGGTCGGAC CG
A C

GAM281 278 DSC3 1 7559 NP_077741.1 3 2263 CTCTGACGCACA G A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GC
GTGGCTCC GTGACGTGAGGTCGGAC CG
A C

GAM281 278 DSCR6 1 14954 NP_061835.1 3 546 TCTTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
TC

GAM281 278 DUPLIN 1 6863 XP_208760.3 3 181 TCTCTCACCCAG C - CA 3 B c c
GCCTGAAGTGCA CACTGCACT CAG CCTGGG
GTGGCATG GTGACGTGA GTC GGACCC
A C AC

GAM281 278 DUSP19 2 5768 NP_543152.1 3 638 TCTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 DUSP19 2 15367 NP_543152.1 3 2293 TCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 DYRK1A 1 10913 NP_567824.1 5 63 CGCCATCGTCCC C T A 3 B c c
GGCTGAAGTGCA CACTGCACT CAGCC GGGC
GTGGCACG GTGACGTGA GTCGG CCTG

A C C
GAM281 278 EBAF 1 18275 NP_003231.2 3 510 TGAAGGGCTTCA A - A 3 B c c
GGCTGGGGGCAG CACTGC CTCCAGCCTGG GC
TGGACAGG GTGACG GGGGTCGGACT CG
- T G
GAM281 278 EDG8 1 12263 NP_110387.1 3 952 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGGCAC GT ACGTGAGGTCGGACCC
A AC
GAM281 278 EEF2K 1 2595 NP_037434.1 3 345 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGACATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 EGFL4 1 5780 XP_290821.1 5 41 AGGACTGTGGCC TCCA - G 3 B c c
ATGGTGTGTGCA CACTGCAC GCC TGG CA
GTGGCCCC GTGACGTG TGG ACC GT
TG-- T G
GAM281 278 EHD1 1 7065 NP_006786.2 3 329 GGCCTTTGCTGT -- - TG 3 B c c
GGCTGGAGCTGG CACTG CA CTCCAGCC GGCAA
ACAGTGCA GTGAC GT GAGGTCGG TCGTT
AG C TG
GAM281 278 EHD2 1 4837 NP_055416.2 3 906 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGAG GTGACGTGAGGTCGGACCCG
C
GAM281 278 EIF2C1 1 2761 NP_036331.1 3 1955 AGACCTAGCCCA - CA - A 3 B c c
GGCTTGGAGGCC CA CTG CTCCA GCCTGGGC
AGCTGGAG GT GAC GAGGT CGGACCCG
C CG T A
GAM281 278 EIF2S3 1 1744 NP_001406.1 3 347 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 EIF5A2 1 8340 NP_065123.1 3 975 CTCCATCAGCCA GCA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGACC
GAC
GAM281 278 ELP3 1 14236 NP_060561.3 3 906 CTGTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 EMR2 1 13462 NP_038475.2 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM281 278 EMR2 1 13462 NP_690880.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM281 278 EMR2 1 13462 NP_690881.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM281 278 EMR2 1 13462 NP_690882.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM281 278 EMR2 1 13462 NP_690883.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM281 278 EMR2 1 13462 NP_690884.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM281 278 EMR2 1 13462 NP_690885.1 5 151 CTCTATCACCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM281 278 ENDOGL1 1 5031 NP_005098.1 3 154 CCGTGTCATCCA CA 3 B c c
GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGTGGA GTGGCGTGAGGTCGGACCT
AC

GAM281 278 EREG 1 17956 NP_001423.1 3 2043 CTCTGTTGCCCA 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTTGGACCCGTT

GAM281 278 ERN2 1 12665 NP_150296.1 5 47 TGCAGCTGCCCA C -- ---- 3 B c c
GGCGCTATGGCG ACTGCACT CCA GCCTGGGCA
AGTGCGGT TGGCGTGA GGT CGGACCCGT
- GC ATCG

GAM281 278 ERO1L 1 11477 NP_055399.1 5 37 GGCACGTCCACA -- - T - - A 3 B c c
GGCTGGGTCGCG CACT GC AC CCAGCCTG GG C
AGGTGGCG GTGG CG TG GGTCGGAC CC G
AG C - A T C

GAM281 278 ESPL1 1 20090 NP_036423.1 5 510 GCCCCTCCATGC CC CT 3 B c c
CTGCTTGGTGCA CACTGCACT AGC GGGCA
GTGCTCTC GTGACGTGG TCG TCCGT
T- --

GAM281 278 EVC 1 18115 NP_055371.1 3 2225 CACTTTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 EVC 1 18115 NP_714928.1 3 2225 CACTTTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 EVER1 1 14255 NP_009198.3 3 145 CAGCTGCGCCTA G--- - A 3 B c c
GGCTGGAGCTGG CACT CA CTCCAGCCTGGGC

AAGGGTGG GTGG GT GAGGTCGGATCCG
GAAG C C
GAM281 278 EVI5 2 7219 NP_005656.2 3 516 GTTTGTCACCCA T CA 3 B c b
GGCTGGAGTGCT CAC GCACTCCAGCCTGGG
GTGGTGTG GTG CGTGAGGTCGGACCC
T AC
GAM281 278 EVI5 2 11607 NP_005656.2 3 2217 TCACTGCACTCA - - 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG G GCA
GTGGTACG GTGACGTGAGGTCGGAC C CGT
T A
GAM281 278 F11R 1 2664 NP_058642.1 3 2148 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 F11R 1 2664 NP_653085.1 3 2148 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 F11R 1 2664 NP_653086.1 3 2150 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 F11R 1 2664 NP_653087.1 3 2150 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 F2RL2 1 10122 NP_004092.1 3 201 CTTTATCACCCA T C CA 3 B c c
GACTGGCGTGCA CACTGCAC CCAG CTGGG
GTGGCACT GTGACGTG GGTC GACCC
C A AC
GAM281 278 F2RL3 1 4234 NP_003941.1 3 3005 CGCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 F3 1 18492 NP_001984.1 3 424 CTCTGTTGCCCA C----- 3 B b b
GGCTGGAGTGCA ACTGCACTCCAGCCTGGGCAA
GTAGCACG TGACGTGAGGTCGGACCCGTT
GCACGA
GAM281 278 F5 1 7269 NP_000121.1 5 47 AAGCGCTGCCCA TG -- 3 B b b
GGTCCTGGGGTG CAC CACTCCAG CCTGGGCA
GTGGCAGC GTG GTGGGGTC GGACCCGT
-- CT
GAM281 278 FABP2 1 2195 NP_000125.1 3 371 CTCTTTCACTCA C CA 3 B c c
GGCTGGAATGTA CACTGCA TCCAGCCTGGG
GTGGAGAG GTGATGT AGGTCGGACTC
A AC
GAM281 278 FAM13A1 1 9972 NP_055698.1 3 625 GCATCTGCCCAC C----- - GCC 3 B c
c
GATGGCAGTGCA ACTGCACT CCA TGGGCA
GTCATCAT TGACGTGA GGT ACCCGT

TACTAC C AGC

GAM281 278 FANCC 1 15368 NP_000127.1 3 791 AAAGAATTGGCC T T A 3 B c c
TGGCTGGGTGCA CACTGCAC CCAGCC GGGC
GTGGCTCA GTGACGTG GGTCGG TCCG
- - G

GAM281 278 FANCE 1 5597 NP_068741.1 3 280 CTCTGTCATCCA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGATGCG GTGACGTGAGGTCGGACCT
AC

GAM281 278 FANCF 1 5816 NP_073562.1 3 738 CTCTGTCACCCA C CA 3 B c c
GTCTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGTGTG GTGACGTGAGGTC GACCC
T AC

GAM281 278 FAT3 1 8236 XP_061871.5 3 1359 CTCTGTCACCCA C C CA 3 B c c
GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCATG GT ACGTGAG TCGGACCC
A A AC

GAM281 278 FBXL7 1 11584 NP_036436.1 3 967 CCTCTTTTGCCA C------ T C G 3 B c c
GGCTGGATGCTG AC GCA TCCAGCCTGG CAA
TCGTCTCT TG CGT AGGTCGGACC GTT
TCTCTGC T - -

GAM281 278 FBXO27 1 16526 NP_849142.1 3 1113 CATTTGTGCCCA --- A C 3 B b b
GGTTGAGGCTAT CACT GC CTC AGCCTGGGCA
AGTGAGCC GTGA CG GAG TTGGACCCGT
TAT - -

GAM281 278 FBXO27 1 16526 XP_059045.1 3 1113 CATTTGTGCCCA --- A C 3 B b b
GGTTGAGGCTAT CACT GC CTC AGCCTGGGCA
AGTGAGCC GTGA CG GAG TTGGACCCGT
TAT - -

GAM281 278 FCAR 3 3819 NP_001991.1 3 158 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGAGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 FCAR 3 10448 NP_579803.1 3 158 CTCTGTCACCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 10448 NP_579805.1 3 158 CTCTGTCACCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 10448 NP_579806.1 3 158 CTCTGTCACCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 10448 NP_579807.1 3 158 CTCTGTCACCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 10448 NP_579808.1 3 282 CTCTGTCACCCA C CA 3 B c b

GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 10448 NP_579811.1 3 158 CTCTGTCACCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 10448 NP_579812.1 3 158 CTCTGTCACCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM281 278 FCAR 3 17643 NP_579813.1 3 243 CTCTTTCGCCAA G A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGC
GTGGCACG GTGACGTGAGGTCGGA CCG
A C

GAM281 278 FCAR 3 17643 NP_579814.1 3 243 CTCTTTCGCCAA G A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGC
GTGGCACG GTGACGTGAGGTCGGA CCG
A C

GAM281 278 FCGR2A 1 497 NP_067674.1 3 523 ATCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCT GTGACGTGAGGTCGGACCC
AT

GAM281 278 FCMD 1 2141 NP_006722.1 3 5021 AAATCCCTGCTT T CCT 3 B c c
CTTTTGGGTGCA CACTGCAC CCAG GGGCA
GTGGCTCA GTGACGTG GGTT TTCGT
- TTC

GAM281 278 FER1L4 1 11291 XP_300246.1 3 222 CTCTGTCTCCCA CA 3 B c c
GGTTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTTGGACCC
TC

GAM281 278 FER1L4 1 11291 XP_300246.1 3 371 CTCTGTCTCCCA CA 3 B c c
GGTTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTTGGACCC
TC

GAM281 278 FEZ1 1 5204 NP_072043.1 3 826 TTCTATCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCACA GT ACGTGAGGTCGGACCCG
A C

GAM281 278 FGF2 1 11604 NP_001997.3 3 1930 AAAGAAAAATCT T A CA 3 B c c
AGGCCGGGTGCA CACTGCAC CC GCCTGGG
GTGGCTCA GTGACGTG GG CGGATCT
- C AA

GAM281 278 FGF5 1 14382 NP_004455.1 3 2381 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 FGF5 1 14382 NP_149134.1 3 2712 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT

AC
GAM281 278 FHL2 1 16589 NP_001441.2 5 449 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 FISH 1 13261 NP_055446.1 5 209 CTCTGTTGCTCA C 3 B b b
GGCTGGATTGCA CACTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACTCGTT
T
GAM281 278 FKBP9 1 7851 NP_009201.1 3 805 CGTTTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCAA
GTGGTGCC GTGACGTGAGGTCGGACC TGTT
GC
GAM281 278 FLJ0006 1 11528 XP_028154.1 5 30 CTCTGTCACCCA CA 3 B b b
0 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 FLJ1010 1 9189 NP_078994.1 3 253 CTGTGTGGCCCA A 3 B b b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
G
GAM281 278 FLJ1023 1 19236 NP_060503.1 3 795 CTCTGTCACCCA C CA 3 B c c
2 GGCTGGAGTGCG CA TGCACTCCAGCCTGGG
ATGGCGCG GT GCGTGAGGTCGGACCC
A AC
GAM281 278 FLJ1029 1 2615 NP_060520.2 3 183 CTTTGTTGCCCA C----- 3 B b b
8 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGCAA
GTAGCACG TGACGTGAGGTCGGACCCGTT
GCACGA
GAM281 278 FLJ1034 1 19219 NP_060535.1 5 100 CTCTGTCTCCCA C CA 3 B c c
6 GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGCACG GTGACGTGA GTCGGACCC
A TC
GAM281 278 FLJ1052 1 4272 NP_060594.2 3 1711 AGTGGTTGCCCA C- CCA 3 B c c
0 GGCCTAGTTTCA CACTG ACT GCCTGGGCAA
GTGGCAGA GTGAC TGA CGGACCCGTT
TT TC-
GAM281 278 FLJ1053 1 9543 NP_060599.1 3 806 CTCTGTCACCCA CA 3 B b b
5 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 FLJ1056 1 15591 NP_060608.1 3 190 TTCTGTCGCCCA T A 3 B b b
0 GGCTGGCGTGCA CACTGCAC CCAGCCTGGGC
GTGGCGCG GTGACGTG GGTCGGACCCG
C C
GAM281 278 FLJ1056 1 11899 NP_060612.1 5 55 CATGTCTGCCCA C----- - C AG 3 B c c
9 GGGGGACTGCGA ACT GCA TCC CCTGGGCA
GTTCCTGG TGA CGT AGG GGACCCGT

GGTCCT G C G-

GAM281 278 FLJ1064 1 18109 NP_061896.1 5 69 ACTCTGCTGCCT C 3 B b b
0 AGGCTGAGTGCA CACTGCACTC AGCCTGGGCA
GTGGTGTG GTGACGTGAG TCGGATCCGT
-

GAM281 278 FLJ1071 1 7909 NP_060659.1 3 360 CACTGTTGCCCA 3 B b b
3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 FLJ1076 1 12257 NP_060680.1 3 888 TTGAGGCATGCT CCA TG G 3 B c
c
9 GGGCCTGGTGCA CACTGCACT GCC G CA
GTGATGGC GTGACGTGG CGG C GT
TC- GT -

GAM281 278 FLJ1084 1 11528 NP_060711.1 3 352 CTCTGTCACCCA CA 3 B b b
6 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ1084 1 19357 NP_060712.2 3 490 CTCTGTCATGCA --- 3 B b b
7 GGCTGGAGTGCG CACTGCACTCCAGCCTG GGCA
GTGGTGCG GTGGCGTGAGGTCGGAC CTGT
GTA

GAM281 278 FLJ1089 1 7243 NP_060733.1 3 811 CCCTGTGTTGTT TCC - 3 B c c
8 ACAGGCTGTGCA CACTGCAC AGCCTG GGCAA
GTGCAACA GTGACGTG TCGGAC TTGTT
--- A

GAM281 278 FLJ1092 1 18818 NP_060743.1 3 2051 GCTTGTTGCCCA C C 3 B b b
2 GGCTGGAATGCA CA TGCA TCCAGCCTGGGCAA
ATGGCGTG GT ACGT AGGTCGGACCCGTT
A A

GAM281 278 FLJ1093 1 4934 NP_060747.1 3 1050 AAAAGCTCAGGG CA-- - A 3 B c c
2 CGGTCGAGTGCA CACTGCACTC GCC TGGGC
GTGGCTCG GTGACGTGAG CGG ACTCG
CTGG G A

GAM281 278 FLJ1093 1 7238 NP_060749.2 3 1386 CACTGTGGCCCA CA ----- A 3 B c c

6 GGCTGGACTCCA CACTG C TCCAGCCTGGGC
GCACAGTG GTGAC G AGGTCGGACCCG
AC ACCTC G

GAM281 278 FLJ1102 1 3089 NP_060774.1 3 76 GATAAAAACACC T C CA 3 B c c
9 CAGCTGGGTGCA CACTGCAC CCAGC TGGG
GTGGCTCG GTGACGTG GGTCG ACCC
- - AC

GAM281 278 FLJ1132 1 2044 NP_060860.1 3 97 TCTCGTTGCCGA C----- G 3 B c c
3 GGCTGGAGTGTA ACTGCACTCCAGCCT GGCAA
GTAGTGTG TGATGTGAGGTCGGA CCGTT
GTGTGA G

GAM281 278 FLJ1146 1 834 NP_079239.2 3 145 TCCTGTCACCCA C CA 3 B c c
7 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC

A AC

GAM281 278 FLJ1171 2 2245 NP_079122.1 3 1178 CTTTGTTGCCCA TG----- CT 3 B c b

0 GGCTGGTTGAAC CAC CA CCAGCCTGGGCAA
TCCCGTGA GTG GT GGTCGGACCCGTT
CCCTCAA T-

GAM281 278 FLJ1171 2 9688 NP_079122.1 3 1011 CTCTGTCTCCCA CA 3 B b b

0 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC

GAM281 278 FLJ1171 1 3305 NP_078840.1 3 898 CACCGTTGCCCA A 3 B b b

5 GGCTGGAGGGCA CACTGC CTCCAGCCTGGGCAA
GTGACGTG GTGACG GAGGTCGGACCCGTT
G

GAM281 278 FLJ1180 1 10847 NP_079250.1 3 1242 CACTGTCACCCA A CA 3 B c c

0 GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
C AC

GAM281 278 FLJ1207 1 8886 NP_079463.2 3 158 AGGTTGGGCTCA CT T A 3 B c c

6 GGCTGGGTGCTC CA GCAC CCAGCCTGGGC
TGCCATGG GT CGTG GGTCGGACTCG
CT - G

GAM281 278 FLJ1236 1 17722 NP_115543.1 3 51 CACCGTCCCCCA T CA 3 B c c

3 GGCTGGAGTGCC CAC GCACTCCAGCCTGGG
GTGGCGTG GTG CGTGAGGTCGGACCC
C CC

GAM281 278 FLJ1244 1 8405 NP_075046.1 3 844 AGTAGAAGCTTG T A - A 3 B c c

8 TGGCCGGGTGCA CACTGCAC CC GCC TGGGC
GTGGCTCA GTGACGTG GG CGG GTTCG
- C T A

GAM281 278 FLJ1257 1 17515 NP_075056.2 5 117 CTCTGTCACCCA C CA 3 B c c

2 GGCTGGAGTATA CACTG ACTCCAGCCTGGG
GTGGTGTG GTGAT TGAGGTCGGACCC
A AC

GAM281 278 FLJ1258 1 10410 NP_078896.2 5 38 CTGTCTCACCCA CA 3 B b b

6 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ1264 1 3686 XP_291344.1 3 951 CTCTGTTGCCCA C 3 B b b

9 GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
A

GAM281 278 FLJ1268 1 3324 NP_079193.2 3 212 CACTCTTGCCCA T 3 B b b

7 GGCTGGGGTGTC CAC GCACTCCAGCCTGGGCAA
GTGGCGTG GTG TGTGGGGTCGGACCCGTT
C

GAM281 278 FLJ1274 1 10683 XP_290972.1 3 2540 TCTTGTCACCCA C CA 3 B c c

7 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGCG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 FLJ1278 1 14839 NP_115551.1 3 1020 CTTTATCGCCCA C A 3 B b b
7 GGCTGGAGTACA CACTG ACTCCAGCCTGGGC
GTGATGCA GTGAC TGAGGTCGGACCCG
A C
GAM281 278 FLJ1280 1 4261 NP_075054.1 3 1087 ACTGGCTGCCCA ACTC 3 B b b
0 GGCTGAATGGCA CACTGC CAGCCTGGGCA
GTGCCTGG GTGACG GTCGGACCCGT
GTAA
GAM281 278 FLJ1288 1 17723 NP_079221.1 3 241 CTCTGTTGCCCA C 3 B b b
8 GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCATG GTGACGTGAG TCGGACCCGTT
A
GAM281 278 FLJ1290 1 10224 NP_073590.1 3 1559 TGTTGTTGCCCA C 3 B b b
3 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 FLJ1296 1 11523 NP_078914.1 3 1535 CTCTGTCGCCCA A 3 B b b
0 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 FLJ1297 1 5230 NP_079184.1 3 294 TCTTGTTGCCCA CAC----- 3 B c c
3 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCGCG ACGTGAGGTCGGACCCGTT
GCGCGATA
GAM281 278 FLJ1297 1 2409 NP_079085.2 3 355 CTCTGTCACCCA CA 3 B b b
5 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGCACAA GTGACGTGAGGTCGGACCC
AC
GAM281 278 FLJ1298 2 6037 XP_290685.1 3 1798 AAACCAAGCCCA A A A 3 B c c
6 GGCCGGGGGCGG CACTGC CTCC GCCTGGGC
TGGCTCAC GTGGCG GGGG CGGACCCG
- C A
GAM281 278 FLJ1298 2 11396 XP_290685.1 3 8 CCCTTGGGCCCT T CCT A 3 B c c
6 GCCTGGAGTGTG CAC GCACTCCAG GGGC
TGCCGCCT GTG TGTGAGGTC CCCG
- CGT G
GAM281 278 FLJ1307 1 2223 XP_117117.2 3 698 CTCTGTCGGCCA --- 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
GGC
GAM281 278 FLJ1311 1 11919 NP_078817.1 3 610 CTCTGTCGCCCA C A 3 B b b
4 GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGCGTG GTGACGT AGGTCGGACCCG
A C
GAM281 278 FLJ1318 1 4530 NP_079158.1 3 2176 AACTTTGCTTCA ACT - 3 B c c
9 GGCTGGGTAGTG CACTGC CCAGCCTGG GCAA
GTAGAGGT GTGATG GGTCGGACT CGTT
--- T
GAM281 278 FLJ1319 1 8231 NP_078890.1 3 403 CTCTGTTGCCCA 3 B b b

7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 FLJ1344 2 3478 NP_076413.1 3 2560 CTACGGAGATGA TCCA GG- 3 B c c
1 GACAGGCGTGCA CACTGCAC GCCTG CA
GTGTGCGC GTGACGTG CGGAC GT
---- AGA
GAM281 278 FLJ1344 2 12452 NP_076413.1 3 3479 GGTGTGTGGCCA T - -- G 3 B c c
1 GGCTGCAGAGCT CAC GCA CTC CAGCCTGG CA
GCGTGCCG GTG CGT GAG GTCGGACC GT
- C AC G
GAM281 278 FLJ1345 1 8163 XP_038291.5 3 2588 CTCTGTCGCCCA C A 3 B b b
6 AGCTGGAGTGCA CACTGCACTCCAGC TGGGC
GTGGCACA GTGACGTGAGGTCG ACCCG
A C
GAM281 278 FLJ1359 1 7813 NP_079116.2 5 98 CCCGCAAAATCA C ---- A 3 B c c
0 GGCTTGAGTGCA CACTGCACTC AGCCTGG GC
GTGGCGCA GTGACGTGAG TCGGACT CG
T AAAA C
GAM281 278 FLJ1374 1 6185 NP_079287.1 3 1773 AGCCCAAGCCCA CTCCA A 3 B c c
4 GGCATTGCAGTG CACTGCA GCCTGGGC
CACAGAGC GTGACGT CGGACCCG
TA--- A
GAM281 278 FLJ1391 1 7691 NP_073617.1 3 1668 GGGATTGGCCCA T- C A 3 B c c
0 GCTTGGAGTGCT CAC GCACTCCAG CTGGGC
TGTGTGGT GTG CGTGAGGTT GACCCG
TT C G
GAM281 278 FLJ1398 1 10809 NP_079046.1 5 245 CTCTGTCACCTA CA 3 B c c
4 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGATCC
AC
GAM281 278 FLJ1410 1 12143 NP_079301.1 3 386 TCCTGCCGCCCA C A -- A 3 B c c
0 GGCCTTGGAGGT CA TGC CTCCA GCCTGGGC
ACTGCTGC GT ATG GAGGT CGGACCCG
C - TC C
GAM281 278 FLJ1435 1 8586 NP_079008.1 3 317 CTTTGTCGCCCA A 3 B b b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCAGT GTGACGTGAGGTCGGACCCG
C
GAM281 278 FLJ1444 1 16259 NP_116174.1 3 2236 CTCTGTTACCCA C CA 3 B c c
2 GGCTAGAGTGTA CACTGCACTC AGCCTGGG
GTGGCATG GTGATGTGAG TCGGACCC
A AT
GAM281 278 FLJ1467 1 16071 NP_116212.3 3 250 CTCCTGCCCTGG - G -- T 3 B c c
5 ATCTGGAGTGGA CA CT CACTCCAG CC GGGCA
GCTGCTCT GT GA GTGAGGTC GG CCCGT
C G TA T
GAM281 278 FLJ1480 1 939 NP_116231.1 3 437 TCTGTCAACGCA C ---- 3 B b b

	3			GACTGGAGTGCA CACTGCACTCCAG CTG GGCA GTGGCACG GTGACGTGAGGTC GAC CTGT A GCAA						
GAM281	278 7	FLJ1495 1	13527	NP_116255.1 3 572 TCTTGTTGCCGA C G GGCTGGAGTGCA CA TGCACTCCAGCCT GGCAA ATGGCGCA GT ACGTGAGGTCGGA CCGTT A G					3	B b b
GAM281	278 5	FLJ2004 1	12557	NP_060108.1 3 132 CTTTGTTTCCCA CA GGCTGGAGTGCA CACTGCACTCCAGCCTGGG GTGGCACG GTGACGTGAGGTCGGACCC TT					3	B b b
GAM281	278 9	FLJ2007 1	14265	NP_060126.1 3 2037 TCTTGTTGCCCA C GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA ATGGTATG GT ACGTGAGGTCGGACCCGTT A					3	B b b
GAM281	278 5	FLJ2009 1	7385	NP_060136.1 3 1358 CTCTGTCACCCA CA GGCTGGAGTGCA CACTGCACTCCAGCCTGGG GTGGCGCG GTGACGTGAGGTCGGACCC AC					3	B b b
GAM281	278 3	FLJ2012 1	17513	NP_060144.1 5 309 GCACGGTGCCCA -- CT--- GGTTGGCCTCCT CACT GCA CCAGCCTGGGCA GCTGGGTG GTGG CGT GGTTGGACCCGT GT CCTCC					3	B c c
GAM281	278 6	FLJ2013 1	4536	NP_060154.1 3 461 CTCTGTCGCCCA C A GGCTGGAATGCA CACTGCA TCCAGCCTGGGC GTGGTGCG GTGACGT AGGTCGGACCCG A C					3	B b b
GAM281	278 7	FLJ2014 1	2624	NP_060157.1 3 399 CTGTGTTGCCCA CA----- C GGCTAGAGTGCA CTGCACTC AGCCTGGGCAA GCAGTGAC GACGTGAG TCGGACCCGTT CAGTGAC A					3	B c c
GAM281 c	278 7	FLJ2020 1	14870	NP_060181.2 5 50 GGGCTGTGCCCA CA ---- CA-- GGCCACAGAGCA CTGCA CTC GCCTGGGCA GCTGCAGG GACGT GAG CGGACCCGT G- CGAC ACAC					3	B c
GAM281	278 5	FLJ2024 2	5275	NP_060193.1 3 2299 TCTTGTTGCCCA C GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA ATGACACG GT ACGTGAGGTCGGACCCGTT A					3	B b b
GAM281	278 5	FLJ2024 2	8581	NP_060193.1 3 542 TCAGGAGCTCAA CT - A GGCTGGAGTGTC CA GCACTCCAGCCT GGGC TTGACAGT GT TGTGAGGTCGGA CTCG TC A A					3	B c b
GAM281 c	278 7	FLJ2025 1	7206	NP_062552.1 3 257 CCCAGCCTCCCA C AC CA GGCTGGATGGCA CA TGC TCCAGCCTGGG TGGACTGT GT ACG AGGTCGGACCC - GT TC					3	B c
GAM281	278	FLJ2030 1	5413	NP_060228.1 3 704 TTGGGCTGCTGA -- AG G					3	B c c

8 GGGGCTAGTGCA CACTGCACT CC CCT GGCA
GTGGTCCT GTGACGTGA GG GGA TCGT
TC -- G

GAM281 278 FLJ2032 1 16994 NP_060235.1 5 79 GAGGACGCCGAG G - G A 3 B c c

0 GCCTGGAGTGGG CACT CACTCCAG CCT GGC
TGGTAGCC GTGG GTGAGGTC GGA CCG
- C G C

GAM281 278 FLJ2034 1 4079 NP_060246.1 3 705 CTCTGTCATCCA CC CA 3 B c c

4 AACTGGAGTGCA CACTGCACTCCAG TGGG
GTGGCACA GTGACGTGAGGTC ACCT
AA AC

GAM281 278 FLJ2035 1 11024 NP_060251.1 3 284 GCCGAGGGCCCA TCCA- A 3 B c
c

9 GGCCCTGTGTGC CACTGCAC GCCTGGGC
GGTGCCCA GTGGCGTG CGGACCCG
TGTCC G

GAM281 278 FLJ2037 1 9357 NP_060264.2 3 181 CATGCCTCCTAA C AGC ---- 3 B c c

5 GAGAGGAGTGCA CA TGCACTCC CT GGGCA
TTGCTTTA GT ACGTGAGG GA TCCGT
T AGA ATCC

GAM281 278 FLJ2050 1 3211 NP_060319.1 3 2329 CTCTGTCACCCG -- CA 3 B c c

7 GGCTGGAGTGTA CAC TGCACTCCAGCCTGGG
ACGTGGCA GTG ATGTGAGGTCGGGCCC
CA AC

GAM281 278 FLJ2051 1 17759 NP_060323.1 3 676 TCTTGTCACCCA CA 3 B b b

1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ2067 2 13041 NP_060394.1 3 632 GTTGTCACTTAA C G---- 3 B c b

1 GTTTGGAGTGCA CACTGCACTCCAG CT GGCAA
GTGGCATG GTGACGTGAGGTT GA CTGTT
T ATTCA

GAM281 278 FLJ2067 2 16491 NP_060394.1 3 1539 GTCTGTTGCCCA 3 B b b

1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 FLJ2070 1 18943 NP_060402.1 3 424 CTCTCTCGCCCA A 3 B b b

0 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 FLJ2081 1 10574 NP_060431.1 3 96 CTCTTTCACCCA CA 3 B b b

3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ2082 2 3016 NP_060432.1 5 19 ACAGGTGCAGAA CCA GG- 3 B c
c

5 GGTGCAGGTGCA CACTGCACT GCCT GCA
GTGGGTAC GTGACGTGG TGGA CGT
ACG AGA

GAM281 278 FLJ2082 2 19008 NP_060432.1 5 180 ACAAGTGCAGAA CCA GG- 3 B c c
5 GGTGCAGGTGCA CACTGCACT GCCT GCA
GTGGGTAC GTGACGTGG TGGA CGT
ACG AGA
GAM281 278 FLJ2088 1 5155 NP_079475.1 5 234 ACTGCTTGCCCA - C G 3 B c c
6 GGGTGCAGTGTG CACT GCACT CA CCTGGGCAA
AGTGTGAT GTGA TGTGA GT GGACCCGTT
G C G
GAM281 278 FLJ2112 1 17516 NP_079359.2 3 1349 TGTGTCTGCCCA - ACT- 3 B c c
8 GGCTGGCTGAGC CACT GC CCAGCCTGGGCA
GGGTGGAT GTGG CG GGTCGGACCCGT
G AGTC
GAM281 278 FLJ2160 1 15047 NP_079038.1 3 482 CTCTGTCACCCA C CA 3 B c c
3 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATA GTGAC TGAGGTCGGACCC
A AC
GAM281 278 FLJ2167 1 1435 NP_112160.1 5 802 TTCTGTCACCTA CA 3 B c c
3 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGACATG GTGATGTGAGGTCGGATCC
AC
GAM281 278 FLJ2177 1 4203 NP_115585.1 3 785 TTGTGTCACCCA C CA 3 B c c
7 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGCA GT ACGTGAGGTCGGACCC
A AC
GAM281 278 FLJ2186 1 13223 NP_073596.1 3 448 CTTCTCTGCCCA - CTCCA 3 B c c
5 GGCCGCTGCAGC CA CTGCA GCCTGGGCA
TGCACAGC GT GACGT CGGACCCGT
C CGC--
GAM281 278 FLJ2202 3 1727 NP_079225.2 3 269 AAATGTTGCCCA - CTCCA ----- 3 B c c
9 GTATGTGCGCAT CACTG CA GC CTGGGCAA
TGCCAGTG GTGAC GT CG GACCCGTT
C TACG- TGTAT
GAM281 278 FLJ2202 3 5439 NP_079225.2 3 497 AGTGTGAGCACA A C G A 3 B c c
9 CGCTGGAGTGCA C CTGCACTCCAGC TG GC
GCGTTCCA G GACGTGAGGTCG AC CG
C C A A
GAM281 278 FLJ2202 3 19447 NP_079225.2 3 2126 AAATCTGTCTCA C-- -- - - 3 B c c
9 GGCTGGTAGTTA ACTGC ACT CCAGCCTG GGCA
GCAGTTGT TGACG TGA GGTCGGAC CTGT
TGT AT T T
GAM281 278 FLJ2216 1 15971 NP_078809.2 5 476 ACTCTTCACTCA C CA 3 B c c
7 GGCTGCAGTGCA CACTGCACT CAGCCTGGG
GTGGCGCA GTGACGTGA GTCGGACTC
C AC
GAM281 278 FLJ2232 1 9543 NP_078932.2 3 528 CTCTGTCACCCA CA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC

AC

GAM281 2781 FLJ2253 1 5636 NP_078926.2 5 342 CTCTGTTACCCA A CA 3 B c c
GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCGCA GTGACGTGAGG CGGACCC
C AT

GAM281 2783 FLJ2269 1 4200 NP_073587.1 5 496 GGCCATGGCCCA - - T A A 3 B c c
GGCCGGCGTCGT CACTG C AC CC GCCTGGGC
CGGTG GTGGC G TG GG CGGACCCG
T C C C G

GAM281 2784 FLJ2279 1 5559 NP_071357.1 3 256 CTCTGTCGCCTG C TG A 3 B c c
GGCTGGAGTACA CACTG ACTCCAGCC GGC
GTGGTGCG GTGAC TGAGGTCGG CCG
A GT C

GAM281 2785 FLJ2295 1 19507 NP_079095.2 3 881 TCTAAAGCCCCA GC T - A 3 B c c
GGCTGGGTTAGG CACT AC CCAGCCTGGG C
TGGTCTAG GTGG TG GGTCGGACCC G
AT - C A

GAM281 2785 FLJ2296 1 2808 NP_071384.1 3 232 CTCTTTCGCCCA G A 3 B b b
GGATGGAGTGCA CACTGCACTCCA CCTGGGC
GTGGTGCG GTGACGTGAGGT GGACCCG
A C

GAM281 2784 FLJ2302 1 9682 NP_079212.1 3 330 CTCTGTCTCCCA C C CA 3 B c c
GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCACA GT ACGTGAG TCGGACCC
A A TC

GAM281 2780 FLJ2304 2 14760 NP_079450.1 3 504 TTGATCATTTTG T G CA 3 B c c
AGGCTGGGTGCA CACTGCAC CCAGCCT GG
GTGGCTCA GTGACGTG GGTCGGA TT
- G TT

GAM281 2780 FLJ2304 2 18256 NP_079450.1 3 112 CTCCATCACCCA CA C CA 3 B c c
AGCCAGAGTGCA CACTGCACTC GC TGGG
GTGGTGAA GTGACGTGAG CG ACCC
AC A AC

GAM281 2783 FLJ2305 1 8693 NP_075058.1 3 212 CTCTATTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCTCA GTGACGTGAGGTCGGACCCGTT

GAM281 2786 FLJ2318 1 1340 NP_078892.1 3 368 GTTCTGTCGCTT C A 3 B c c
AGCTGGAGTGCG CACTGCACTCCAGC TGGGC
GTGGCGTG GTGGCGTGAGGTCG ATTCG
- C

GAM281 2783 FLJ2326 1 11523 NP_079391.1 5 182 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 2786 FLJ2335 1 12273 NP_115613.1 3 241 CTCTGTTGCTGA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGCAA
GTGATGTG GTGACGTGAGGTCGGA TCGTT

G

GAM281 2782 FLJ2339 3 5554 NP_079060.1 3 607 CTCTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
CC

GAM281 2782 FLJ2339 3 9148 NP_079060.1 3 197 CTCTGTCACCCA C CA 3 B c b
GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGCGCG GTGACGTGAGGTC GACCC
A AC

GAM281 2782 FLJ2339 3 20052 NP_079060.1 3 497 CTCTGTCACTGA G CA 3 B c b
GGCTGGAGTGCA CACTGCACTCCAGCCT GG
GTGGCGCA GTGACGTGAGGTCGGA TC
G AC

GAM281 2786 FLJ2341 1 2152 NP_115614.1 3 1323 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 2786 FLJ2355 2 11323 NP_079156.1 3 723 CTCTGTCACCCA C- CA 3 B c b
GGCTGGAGTACC CACTG ACTCCAGCCTGGG
GGTGGTGG GTGGC TGAGGTCGGACCC
CA AC

GAM281 2786 FLJ2355 2 17969 NP_079156.1 3 425 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM281 2783 FLJ2356 1 15048 XP_041701.4 3 1724 TCTTGTTGCCCA C C 3 B b b
GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA
ATGGCACA GT ACGTGAG TCGGACCCGTT
A A

GAM281 2786 FLJ2541 1 16915 NP_659455.2 5 107 CTCTGTCACCCA CT CA 3 B c c
GGCTGGAGTGCC CA GCACTCCAGCCTGGG
ATGGCATC GT CGTGAGGTCGGACCC
AC AC

GAM281 2781 FLJ2542 1 12127 NP_689725.2 5 22 GCCCTTGAGCCT GC T A 3 B c c
GGCTGGAGTAGG CACT ACTCCAGCC GGGC
TGGAATAT GTGG TGAGGTCGG TCCG
A- - A

GAM281 2785 FLJ2579 1 934 NP_689633.1 3 563 CTCTGTCTCCCA A CA 3 B c c
GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCACG GTGACGTGAGG CGGACCC
C TC

GAM281 2787 FLJ3050 1 17957 NP_694555.1 5 68 CCCTGTTGCCCA CAC 3 B b b
GGCTGGAATACA CACTG TCCAGCCTGGGCAA
GTGGCACG GTGAC AGGTCGGACCCGTT
ATA

GAM281 2782 FLJ3053 1 19834 NP_653325.1 3 191 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGTATG GTGAC TGAGGTCGGACCCGTT
A

GAM281 278 FLJ3113 3 3952 NP_775928.1 3 691 TCTTGTCACCCA A CA 3 B c b

9 GGCAGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCGTT GTGACGTGAGG CGGACCC
A AC
GAM281 278 FLJ3113 3 15200 NP_775928.1 5 145 CTCTCTGGCCCA C A 3 B b b
9 AGCTGGAGTGCA CACTGCACTCCAGC TGGGC
GTGGCACG GTGACGTGAGGTCG ACCCG
A G
GAM281 278 FLJ3113 3 18868 NP_775928.1 3 397 TCTTGTTGCCCA C 3 B b b
9 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 FLJ3115 1 7373 NP_653201.1 3 275 CTCTGTCACCCA C CA 3 B c c
3 GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGCACG GTGACGTGAGGTC GACCC
A AC
GAM281 278 FLJ3116 1 19301 NP_694567.1 3 1140 TCTTGTAGCCCA C CT A 3 B c c
6 GGCTGGGATGCA CA TGCA CCAGCCTGGGC
ATGGCATG GT ACGT GGTCGGACCCG
A AG A
GAM281 278 FLJ3132 1 17683 NP_689600.1 3 932 TAAAAACTGCAT T TGG 3 B c c
2 TGGCTGGGTGCA CACTGCAC CCAGCC GCA
GTGGCTCA GTGACGTG GGTCGG CGT
- TTA
GAM281 278 FLJ3133 1 1672 NP_689682.1 3 268 TCTTGTTGCCCA C C 3 B b b
8 CGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
ATGGTGCA GT ACGTGAGGTCG ACCCGTT
A C
GAM281 278 FLJ3138 1 14326 NP_689685.1 3 927 TCTTGCTGCCCA C C 3 B b b
4 GGCTAGAGTGCA CA TGCACTC AGCCTGGGCA
ATGGTGCG GT ACGTGAG TCGGACCCGT
A A
GAM281 278 FLJ3139 1 9670 NP_694569.1 5 140 CTTTGTTGCCCA CT 3 B b b
3 GGCTGGAGTGCC CA GCACTCCAGCCTGGGCAA
TTGGCGCG GT CGTGAGGTCGGACCCGTT
TC
GAM281 278 FLJ3140 1 16543 NP_689877.1 3 351 CTCTGTTGGCCA G 3 B b b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGTTCGA GTGACGTGAGGTCGGACC GTT
G
GAM281 278 FLJ3143 1 9290 NP_689709.1 3 323 AACTCTGCAGCA T--- G- 3 B c c
4 GGCTGGTGCTGT CACTGCAC CCAGCCTG GCA
GTAGTGGC GTGATGTG GGTCGGAC CGT
TCGT GA
GAM281 278 FLJ3209 2 1025 NP_776156.1 3 1416 CTTTGTTGCCCA C 3 B b b
6 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 FLJ3209 2 16043 NP_776156.1 3 1113 CTCTGTTGCCCA C 3 B b b
6 GGCTGGAGTGTA CA TGCACTCCAGCCTGGGCAA

ATGGTGCA GT ATGTGAGGTCGGACCCGTT
A

GAM281 2780 FLJ3213 3 2061 NP_689671.2 3 1143 CTCTGTTGCCTG TG 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCC GGCAA
GTGGCCCA GTGACGTGAGGTCGG CCGTT
GT

GAM281 2780 FLJ3213 3 4630 NP_689671.2 3 1440 TCTTGTTGCCCA C C 3 B b b
GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA
ATGGCATG GT ACGTGAG TCGGACCCGTT
A A

GAM281 2780 FLJ3213 3 15049 NP_689671.2 3 519 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM281 2786 FLJ3220 1 3860 NP_689710.1 3 41 CTCTGTCGCCCA A A 3 B b b
GGCTGGAGGGCA CACTGC CTCCAGCCTGGGC
GTGGCGTG GTGACG GAGGTCGGACCCG
G C

GAM281 2782 FLJ3233 1 12917 NP_653242.1 3 220 GGTCCCCATGTC TCC C 3 B c c
CAGCCTTGTGCA CACTGCAC AG CTGGGCA
GTGAGTTC GTGACGTG TC GACCTGT
T-- C

GAM281 2784 FLJ3233 1 8493 NP_653166.1 3 1145 TCTCCTGGCCCA C A - - A 3 B c c
GGCCTGGCGGGC CA TGC CT CCAG CCTGGGC
ACTGCTTC GT ACG GG GGTC GGACCCG
C - C C G

GAM281 2789 FLJ3249 1 4681 NP_653208.1 3 744 CTCTGTCACCCA C CA 3 B c c
GTCTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGCAAA GTGACGTGAGGTC GACCC
T AC

GAM281 2781 FLJ3273 1 16099 NP_689632.1 3 733 AGCCGCTGCCCA T - AG 3 B b b
GGGGAGTGGCTG CAC GC ACTCC CCTGGGCA
TGGGGAGG GTG CG TGAGG GGACCCGT
T G --

GAM281 2783 FLJ3280 1 1856 NP_694584.1 3 643 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGAA GTGACGTGAGGTCGGACCC
AC

GAM281 2785 FLJ3286 1 2146 NP_653214.1 3 1248 TCTTGTCACCCA C C CA 3 B c c
GGCTGGAGTACA CA TG ACTCCAGCCTGGG
ATGATGCG GT AC TGAGGTCGGACCC
A A AC

GAM281 2784 FLJ3289 1 7467 NP_653268.1 3 705 CTCTGTTGTCCA A 3 B b b
GGCTGGAGTGCA C CTGCACTCCAGCCTGGGCAA
GCGATATG G GACGTGAGGTCGGACCTGTT
C

GAM281 2782 FLJ3293 1 9555 NP_690873.1 3 604 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGCTGTG GTGACGTGAGGTCGGACCC
AC

GAM281 2785 FLJ3350 1 13693 NP_689530.1 3 741 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGACGCG GTGACGTGAGGTCGGACCCGTT

GAM281 2785 FLJ3365 1 16113 NP_775912.1 3 326 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCTTG GT ACGTGAGGTCGGACCCGTT
C

GAM281 2787 FLJ3481 2 4004 NP_689516.1 5 271 CCGCTGGTCCCA T C - A 3 B c c
GGCTGGATTGCC CAC GCA TCCAGCCTGGG C
GTGGCACA GTG CGT AGGTCGGACCC G
C T T G

GAM281 2787 FLJ3481 2 7075 NP_689516.1 3 208 GTCTGCCACCCA C CA 3 B c c
GGCTGGAGTCCA CACTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
C AC

GAM281 2782 FLJ3492 1 18132 NP_689483.1 5 153 CTTTGACCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
CC

GAM281 2789 FLJ3496 1 581 XP_114353.1 3 1548 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCA GT ACGTGAGGTCGGACCCGTT
A

GAM281 2785 FLJ3510 1 18938 NP_689890.1 5 161 CTCTGTCGTCCA T A 3 B c c
GGCTGGAGTGCC CAC GCACTCCAGCCTGGGC
GTGGCGTA GTG CGTGAGGTCGGACCTG
C C

GAM281 2787 FLJ3548 1 12556 NP_776181.1 3 522 TTCTGTCACTCA C C CA 3 B c c
AGCTGTAGTGCA CACTGCACT CAGC TGGG
GTGGTGCC GTGACGTGA GTCG ACTC
T A AC

GAM281 2781 FLJ3568 2 1653 NP_787096.1 3 1370 CTCTGTTGCCCA CAC 3 B b b
GGCTGGACTACA CACTG TCCAGCCTGGGCAA
GTGGCACA GTGAC AGGTCGGACCCGTT
ATC

GAM281 2781 FLJ3568 2 11521 NP_787096.1 3 1071 CTCTGTCACCCA C CA 3 B c b
GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGCACA GTGACGTGAGGTC GACCC
A AC

GAM281 2788 FLJ3584 1 14986 XP_290755.1 3 1062 CTTTGTCACCCA C CA 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCATG GTGACGTGAG TCGGACCC
A AC

GAM281 2782 FLJ3611 1 6601 NP_775950.1 3 318 ATAGCATTTGCC G CT 3 B b b
CTGTGGGGTGCA CACTGCACTCCA C GGGCAA
GTGTTACC GTGACGTGGGGT G CCCGTT
- T-

GAM281 278 FLJ3644 1 2147 NP_694965.1 3 231 CTCTGTCACCCA CA 3 B c c
5 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGATGTGAGGTCGGACCC
AC
GAM281 278 FLJ3704 1 9497 NP_787085.1 3 765 CTCTGTCGCCCA C A 3 B b b
5 GGCTGGAGTACA CACTG ACTCCAGCCTGGGC
GTGGTGCG GTGAC TGAGGTCGGACCCG
A C
GAM281 278 FLJ3707 1 11528 NP_694588.1 5 43 CTCTGTCACCCA CA 3 B b b
8 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 FLJ3726 1 4602 NP_787088.1 3 1284 ACTCCTTGCCTA CA--- C-- 3 B c c
6 GGCTGGAGTTTA CTG ACTCCAGCCTGGGCAA
CAGAGACA GAC TGAGGTCGGATCCGTT
ACAGA ATT
GAM281 278 FLJ3743 1 8582 NP_848612.1 3 198 CTCTGTTACCCA CA 3 B c c
3 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGTGCC GTGATGTGAGGTCGGACCC
AT
GAM281 278 FLJ3754 1 5495 NP_775938.1 3 744 CTCTGTTGCCCA 3 B b b
3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCATT GTGACGTGAGGTCGGACCCGTT

GAM281 278 FLJ3810 1 5589 NP_694993.2 3 742 GCTCTGTTGCCA A G 3 B b b
1 GGCTGGAGGGCA CACTGC CTCCAGCCTGG CAA
GTGGCACG GTGACG GAGGTCGGACC GTT
G -
GAM281 278 FLJ3814 3 9373 XP_091919.5 3 259 CTCTGTCTCCCA CA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGAGTG GTGACGTGAGGTCGGACCC
TC
GAM281 278 FLJ3814 3 15044 XP_091919.5 3 1432 CTCTGTTGCCCA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 FLJ3814 3 18971 XP_091919.5 5 26 CTCTATTGCCCA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTA GTGACGTGAGGTCGGACCCGTT

GAM281 278 FLJ3828 2 6885 NP_689814.1 3 109 CTCTGTTGCCCT C----- T 3 B c b
1 GGCTGGAGTGCA ACTGCACTCCAGCC GGGCAA
GTAGAGTG TGACGTGAGGTCGG CCCGTT
GTGAGA T
GAM281 278 FLJ3828 2 9492 NP_689814.1 3 1966 CTCTGTCGCCCA A 3 B b b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 FLJ3860 2 7382 NP_689867.1 3 288 CTCTGTCGCCCA A 3 B b b
7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC

GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 FLJ3860 2 16688 NP_689867.1 3 544 CTCTGTCACCCA C CA 3 B c b
7 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGCG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 FLJ3879 1 14861 NP_848615.1 3 1162 CTCTGTCACCCA CA 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ3881 2 9791 NP_665872.1 3 1041 CTCTGTCACTCA C CA 3 B c c
9 TGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCGTG GTGACGTGAGGTCG ACTC
T AC

GAM281 278 FLJ3881 2 18642 NP_665872.1 3 214 GTCTCTTACCCA C CA 3 B c c
9 GGCTAGGGTGCA CACTGCACTC AGCCTGGG
GTGGTGTG GTGACGTGGG TCGGACCC
A AT

GAM281 278 FLJ3899 2 10356 NP_776188.1 3 1037 CTCTGTCACCTA CA 3 B c b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGATCC
AC

GAM281 278 FLJ3899 2 14236 NP_776188.1 3 731 CTGTGTCACCCA CA 3 B b b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ3941 1 11673 NP_775952.1 3 342 GTCTTTCACCCA CA 3 B b b
5 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGCTGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ3944 1 7388 XP_084736.6 3 2971 CACTGCACTCCA CA----- - T --- 3 B c c
1 GGCTGGGTGACA CTG CAC CCAGCCTGG GCA
GAGCGAGA GAC GTG GGTCGGACC CGT
AGAGCGA A - TCA

GAM281 278 FLJ3959 3 2845 NP_776164.1 3 808 CTCTGTCGCCCA C----- C A 3 B c b
9 GGCTGGAATGCA ACTGCA TCCAGCCTGGGC
GTTGTGAG TGACGT AGGTCGGACCCG
GAGTGT A C

GAM281 278 FLJ3959 3 8232 NP_776164.1 3 1104 CTCTGTCACCCA CA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM281 278 FLJ3959 3 16001 NP_776164.1 3 627 TGCTGTCTCCCC A T CA 3 B c b
9 GGCTGGAGCGCA CACTGC CTCCAGCC GGG
GTGGCACG GTGACG GAGGTCGG CCC
C C TC

GAM281 278 FLJ3963 2 6883 XP_290687.1 3 1662 CACCAAGAACAA ------ G CA 3 B c b

9 TGCTGGAGTGCA CACTGCACTCCAGC CT GG
GTGGCGTG GTGACGTGAGGTCG GA CC

TAACAA A AC

GAM281 278 FLJ3963 2 9190 XP_290687.1 3 682 CTCTGTCGTCCA A 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGAGGTCGGACCTG
C

GAM281 278 FLJ3982 1 17406 NP_775971.1 3 612 CTCTGTCACCTA C CA 3 B c c
1 GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGTGCG GTGACGTGAG TCGGATCC
A AC

GAM281 278 FLJ9023 1 10357 NP_775852.1 3 74 CTTTGTCGCCCA A 3 B b b
1 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
C

GAM281 278 FLJ9058 1 2786 NP_699176.1 3 751 CTCTCCTGCCCA C--- A C -- 3 B c c
6 GGGGCTAGAGAG ACTGC CTC AGCCT GGGCA
CAGTCTCC TGACG GAG TCGGG CCCGT
CCTC A A GA

GAM281 278 FLJ9072 1 19889 NP_787115.1 3 525 CTCTGTCGCCCA A 3 B b b
3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGCCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 FNBP1 1 16354 XP_052666.3 3 1012 CTCTATTGTTCA C 3 B b b
GACTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCATG GTGACGTGAGGTC GACTTGTT
A

GAM281 278 FOXE2 1 15626 NP_036317.1 5 631 AAGCTGCGTCCG C AC A 3 B c c

GGCTGGAGCACT CA TGC TCCAGCCTGGGC
GGAACCCG GT ACG AGGTCGGGCCTG
C -- C

GAM281 278 FOXO1A 1 736 NP_002006.2 3 13 AGCTGGGTGTCA C G 3 B c c
GGCTGGGGTTAG CACTG ACTCCAGCCTGG CA
TGAGCAGG GTGAT TGGGGTCGGACT GT
- -

GAM281 278 FSHPRH1 1 11528 NP_006724.1 5 15 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 FSTL1 1 11213 NP_009016.1 3 253 ATGGTGCTCTGG C----- - A -- 3 B c c
GGCTGGAGGCTA ACT GC CTCCAGCCT GGGCA
GTAAGGAA TGA CG GAGGTCGGG CTCGT
AAGGAA T - GT

GAM281 278 FUT1 2 11525 NP_000139.1 3 613 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 FUT1 2 16365 NP_000139.1 3 935 CTCTGTAGCCCA CA A 3 B c b
GGCCAGAGTGCA CACTGCACTC GCCTGGGC
GTGGCGCG GTGACGTGAG CGGACCCG
AC A

GAM281 278 FZD4 1 4487 NP_036325.2 3 3982 CTCTGTCACCCA C A CA 3 B c c
GGCTGGGGCGCA CA TGC CTCCAGCCTGGG
ATGGCACG GT ACG GGGGTCGGACCC
A C AC
GAM281 278 G1P3 1 724 NP_002029.3 3 136 CTATATTGTCCA C 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCTAT GTGACGTGAG TCGGACCTGTT
A
GAM281 278 G1P3 1 724 NP_075010.1 3 136 CTATATTGTCCA C 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCTAT GTGACGTGAG TCGGACCTGTT
A
GAM281 278 G1P3 1 724 NP_075011.1 3 136 CTATATTGTCCA C 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCTAT GTGACGTGAG TCGGACCTGTT
A
GAM281 278 G2A 1 8714 NP_037477.1 3 1257 CTCTGTTGCCTG CA TG 3 B c c
GGCTGGAGAACA CACTG CTCCAGCC GGCAA
GTGGCACC GTGAC GAGGTCGG CCGTT
AA GT
GAM281 278 G6PC 1 4204 NP_000142.1 3 1429 ACCTATCACCCA G CA 3 B c c
GGCTGGAGTGGA CACT CACTCCAGCCTGGG
GTGGCACG GTGA GTGAGGTCGGACCC
G AC
GAM281 278 GAL3ST-4 1 4518 NP_078913.3 3 252 CTCTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC
GAM281 278 GATA2 1 16014 NP_116027.2 3 225 GACTGCTGCCCA C ----- G 3 B c c
GGTGGGGTTTCC CA TGC ACTCCA CCTGGGCA
TGCATGGA GT ACG TGGGGT GGACCCGT
- TCCTT -
GAM281 278 GBP4 1 15052 NP_443173.2 3 1418 CTTTGACACCCA C----- CA 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGCACA TGACGTGAGGTCGGACCC
ACACGA AC
GAM281 278 GGA2 1 5631 NP_055859.1 3 1712 CTCTGTCACTCA CA 3 B c c
GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGTATA GTGGCGTGAGGTCGGACTC
AC
GAM281 278 GGA2 1 5631 NP_619581.1 3 2800 CTCTGTCACTCA CA 3 B c c
GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGTATA GTGGCGTGAGGTCGGACTC
AC
GAM281 278 GGT1 1 13688 NP_005256.1 5 23 TGCCGTCATCCA C -- CA 3 B c c
GGCTGGACAGTT CACTG AC TCCAGCCTGGG
CAGTGATT GTGAC TG AGGTCGGACCT
T AC AC
GAM281 278 GGT1 1 13688 NP_038265.1 5 442 TGCCGTCATCCA C -- CA 3 B c c
GGCTGGACAGTT CACTG AC TCCAGCCTGGG

CAGTGATT GTGAC TG AGGTCGGACCT
T AC AC
GAM281 278 GGT1 1 13688 NP_038347.1 5 152 TGCCGTCATCCA C -- CA 3 B c c
GGCTGGACAGTT CACTG AC TCCAGCCTGGG
CAGTGATT GTGAC TG AGGTCGGACCT
T AC AC
GAM281 278 GGT2 1 13688 XP_290331.1 5 26 TGCCGTCATCCA C -- CA 3 B c c
GGCTGGACAGTT CACTG AC TCCAGCCTGGG
CAGTGATT GTGAC TG AGGTCGGACCT
T AC AC
GAM281 278 GM2A 1 11286 NP_000396.1 3 761 GCTTTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCAA
GTGGTGCA GTGACGTGAGGTCGGACC TGTT
AC
GAM281 278 GNE 1 8367 NP_005467.1 3 618 GCATGAACCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCTCA GTGACGTGAGGTCGGACCC
CA
GAM281 278 GNG4 1 559 NP_004476.1 3 608 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGTG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 GNPNAT1 2 854 XP_085119.1 3 1473 ATTAGCCTGGTA T A ---- A 3 B c c

AGGCCGGGTGCA CACTGCAC CC GCCT GGGC
GTGGCTCA GTGACGTG GG CGGA TCCG
- C ATGG A
GAM281 278 GNPNAT1 2 8464 XP_085119.1 3 2471 CTCCATCACCCA C CA 3 B c
c
GGCTGGAGTCCA CACTG ACTCCAGCCTGGG
GTGGTGTG GTGAC TGAGGTCGGACCC
C AC
GAM281 278 GNRPX 1 12243 NP_060519.1 3 147 CTGTGTTGCCCA C 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGTGCC GTGACGTGAG TCGGACCCGTT
A
GAM281 278 GOLGA1 1 12206 NP_002068.1 3 913 TGGCACTGCTCC C CCT 3 B c
c
CTCTGAAGTGCA CACTGCACT CAG GGGCA
GTGGGATC GTGACGTGA GTC CTCGT
A TCC
GAM281 278 GOLGA3 1 15049 NP_005886.2 3 601 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 GOLGIN- 1 4244 NP_851421.1 5 607 TAGGAGGCTCTG - A TG - A 3 B c
c
67 GGCGGAGGTGCA CACTGCAC TCC GCC G GC
GTGACCCC GTGACGTG AGG CGG C CG
G - GT T G

GAM281 278 GP5 1 5681 NP_004479.1 3 596 CTCTGTGGCCCA T A 3 B b b
GGCTGGCGTGCA CACTGCAC CCAGCCTGGGC
GTGGGCCG GTGACGTG GGTCGGACCCG
C G
GAM281 278 GPP34R 1 14203 NP_060648.2 3 870 TGCTCTTGCCCA --- A 3 B b b
GGCAGGAGTACA CACTGC ACTCC GCCTGGGCAA
GTAGTGCA GTGATG TGAGG CGGACCCGTT
ACA A
GAM281 278 GPR114 1 10636 NP_722579.1 3 911 TGAATTTGCCCA G- T A 3 B c c
GGTAGGCGTGAG CACT CAC CC GCCTGGGCAA
AGTGTGGG GTGA GTG GG TGGACCCGTT
GA C A
GAM281 278 GPR26 1 3010 NP_703143.1 3 1152 TCTTATTGCCCA C C 3 B b b
GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA
ATGGTGCG GT ACGTGAG TCGGACCCGTT
A A
GAM281 278 GPR4 1 4965 NP_005273.1 3 280 CTGTGTTGCCCA C----- 3 B b b
GGCTGGAGTGCA ACTGCACTCCAGCCTGGGCAA
GTAGTGCA TGACGTGAGGTCGGACCCGTT
ACGTGA
GAM281 278 GPR56 1 8622 NP_005673.2 5 25 CTCTGTCACACA --- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGTGTG GTGACGTGAGGTCGGAC CTGT
ACA
GAM281 278 GPR61 1 15604 NP_114142.2 3 4 CCGCCTCACCCC - C T CA 3 B c c
GGCTGGAGTCAT CAC TG ACTCCAGCC GGG
GTGGGCCG GTG AC TGAGGTCGG CCC
T - C AC
GAM281 278 GPR66 1 19237 NP_006047.2 3 530 CTCTGTCGCCCA C A 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCGCG GTGACGTGAG TCGGACCCG
A C
GAM281 278 GPR81 1 13260 NP_115943.1 3 375 CTCTGTGTCCCA - 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG CA
GTGGCACA GTGACGTGAGGTCGGACCC GT
T
GAM281 278 GR6 1 2604 NP_031380.1 5 287 CTCTGTCACCCA C CA 3 B c c
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCATG GTGACGT AGGTCGGACCC
A AC
GAM281 278 GRAF 2 4362 NP_055886.1 3 2801 CTCTGTGGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
G
GAM281 278 GRAF 2 13350 NP_055886.1 3 3769 TAAAGAATGCCA T A TG 3 B c b
TGGCCGGGTGCA CACTGCAC CC GCC GGCA
GTGGCTCA GTGACGTG GG CGG CCGT
- C TA
GAM281 278 GREB1 3 9792 NP_055483.2 3 1722 TCTTGCTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCA

ATGGTGCA GT ACGTGAGGTCGGACCCGT
A
GAM281 278 GREB1 3 14113 NP_055483.2 3 1898 CCAGGTTGGCCA TGCACT G 3 B c b
GGCTGGTCTTGT CAC CCAGCCTGG CAA
GAACTCCT GTG GGTCGGACC GTT
TTCT-- G
GAM281 278 GREB1 3 14861 NP_055483.2 3 1092 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 GRID1 1 17390 XP_043613.8 3 2299 GGGAGGTGCCCA C---- --- T G 3 B c c
GGTGGGTGGACC ACTG CAC CCA CCTGGGCA
AGTACTCC TGAC GTG GGT GGACCCGT
CCTCA CAG - -
GAM281 278 GRINL1A 1 5433 NP_056347.1 3 713 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCAGG GTGACGTGAGGTCGGACCCG
C
GAM281 278 GRM6 1 10398 NP_000834.1 3 2444 CTCAATTTCTTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGATTC
TT
GAM281 278 GRWD 1 7996 NP_113673.2 3 372 GTCTGTCGCCCA C----- A 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGGC
GTAGCACG TGACGTGAGGTCGGACCCG
GCACGA C
GAM281 278 GSDM 1 3199 NP_835465.1 3 296 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 GSDM 1 3199 XP_209009.1 3 294 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 GSTM1 1 12752 NP_000552.2 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA CTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM281 278 GSTM1 1 12752 NP_666533.1 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA CTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM281 278 GSTM2 1 12752 NP_000839.1 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA CTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM281 278 GSTM4 1 12752 NP_000841.1 3 71 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA CTGC CT CAGCCTGGGCA

CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM281 278 GSTM4 1 12752 NP_671490.1 3 358 GCCTGCTGCCCA - A C-- 3 B c c
GGCTGTGCAGCG CA CTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM281 278 GTF2E1 1 15661 NP_005504.1 3 306 TCTTGTACCCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGTG GT ACGTGAGGTCGGACCC
A CA
GAM281 278 GTF2IRD 1 11522 NP_115579.3 3 143 CTCTGTCGCCCA A 3 B b b
2 GGTTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTTGGACCCG
C
GAM281 278 GTF2IRD 1 11522 NP_775808.1 3 143 CTCTGTCGCCCA A 3 B b b
2 GGTTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTTGGACCCG
C
GAM281 278 GTPBG3 2 7812 NP_116009.1 3 467 GTCTATTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 GTPBG3 2 10292 NP_116009.1 3 631 CTCTGTCACCCA C CA 3 B c b

GGCTGGAGTTCA CACTG ACTCCAGCCTGGG
GTGGTGCG GTGAC TGAGGTCGGACCC
T AC
GAM281 278 GYG 1 4258 NP_004121.2 3 443 TAGAATTGCCCA G --- - 3 B b b
GTGCTGCCAGAG CACT CACTC CAGC CTGGGCAA
TGAGTGAG GTGA GTGAG GTCG GACCCGTT
- ACC T
GAM281 278 H-plk 1 12753 NP_056936.1 5 982 GCTGTGTCACCA G -- 3 B b b
GGATGGAGTGCA CACTGCACTCCA CCTGG GCA
GTGGCATG GTGACGTGAGGT GGACC TGT
A AC
GAM281 278 H2AV 1 18864 NP_619541.1 3 585 TCTTGTCACCCA C C CA 3 B c c
GACTGGAGTGCG CA TGCACTCCAG CTGGG
ATGGCACG GT GCGTGAGGTC GACCC
A A AC
GAM281 278 H63 1 4554 NP_612432.2 3 465 TCTTGTTTCCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCACA GT ACGTGAGGTCGGACCC
A TT
GAM281 278 H63 1 4554 NP_816929.1 3 465 TCTTGTTTCCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCACA GT ACGTGAGGTCGGACCC
A TT
GAM281 278 HAVCR2 1 16260 NP_116171.2 3 497 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACA GT ACGTGAGGTCGGACCCGTT

A

GAM281 278 HCK 1 7142 NP_002101.2 3 52 AGGGGGTGCCCA -- - - G 3 B c c
GGTGGTGGCTGC CACT GCA CT CCA CCTGGGCA
AAGGTGGC GTGG CGT GG GGT GGACCCGT
AA C T -

GAM281 278 HE9 1 7942 NP_741997.1 3 210 CTCTGTTGCCCA C C 3 B b b
GCCTGGAGTGCA CA TGCACTCCAG CTGGGCAA
ATGGCACA GT ACGTGAGGTC GACCCGTT
A C

GAM281 278 HECA 1 17954 NP_057301.1 3 1529 TCTTGTCACCCA C----- CA 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGTGCG TGACGTGAGGTCGGACCC
GCGTGA AC

GAM281 278 HEMK 1 6468 NP_057257.1 3 1820 GATGTTGCACCA CAGC - 3 B c c

GAAGAGAGTGCA CACTGCACTC CTGG GCAA
GTGTTGGA GTGACGTGAG GACC CGTT
AGAA A

GAM281 278 HEPH 1 15338 NP_055614.1 5 130 CTGGCGGACTCA -- CA 3 B c c
GGCTGGGGTCTG CACTGC ACTCCAGCCTGGG
CAGTGCAG GTGACG TGGGGTCGGACTC
TC AG

GAM281 278 HEXA 1 14035 NP_000511.1 3 270 AGGGCACAGCCA C GCA 3 B c c

GGCTGGAGTCAG CACTG ACTCCAGCCTGG
TGTCTGCC GTGAC TGAGGTCGGACC
- GAC

GAM281 278 HHLA3 1 13713 NP_009002.1 5 17 GTTTCCGCCCAG - C--- - A 3 B c c
AGCTGGAGTCTC CA CTG ACTCCAGC CTGGGC
CCAGCTGC GT GAC TGAGGTCG GACCCG
C CCTC A C

GAM281 278 HHLA3 1 13713 XP_294968.1 5 34 GTTTCCGCCCAG - C--- - A 3 B c c
AGCTGGAGTCTC CA CTG ACTCCAGC CTGGGC
CCAGCTGC GT GAC TGAGGTCG GACCCG
C CCTC A C

GAM281 278 HIC 1 488 XP_041273.1 5 356 CGCAGGGGAGCC - G TG A 3 B c c
GGCTGGAGTGAG CA CT CACTCCAGCC GGC
CTGGCTGG GT GA GTGAGGTCGG CCG
C - -- A

GAM281 278 HLCS 1 2142 NP_000402.2 5 180 TTCTGTCGTCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCTG
C

GAM281 278 HMG20A 1 5040 NP_060670.1 3 1222 CTGTGTTGCCCA 3 B b b
GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGCTAT GTGGCGTGAGGTCGGACCCGTT

GAM281 278 HPRN 1 12916 NP_071938.1 3 220 TGGCTCTGCCCA G G 3 B b b
GGTGGGGTGGGG CACT CACTCCA CCTGGGCA
TGGCCCAG GTGG GTGGGGT GGACCCGT

G -

GAM281 278 HRH4 3 3116 NP_067637.2 3 1950 CTCTGTTGCCCA A C 3 B b b
CGCAGGAGTGCA CACTGCACTCC GC TGGGCAA
GTGGCATG GTGACGTGAGG CG ACCCGTT
A C

GAM281 278 HRH4 3 5301 NP_067637.2 3 1416 CTCTGTCACCCA C----- CA 3 B c b
GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGCATG TGACGTGAGGTCGGACCC
GTACGA AC

GAM281 278 HRH4 3 5358 NP_067637.2 3 496 GGCATGTGCCCA T TCCA---- 3 B c b

GGTGAGCTCCTG CAC GCAC GCCTGGGCA
TGTGTGTC GTG TGTG TGGACCCGT
- TCCTCGAG

GAM281 278 HSC3 1 1095 NP_660157.1 3 704 TAGAAATAGACT T C CA 3 B c c
TAGCTGGGTGCA CACTGCAC CCAGC TGGG
GTGGCTCA GTGACGTG GGTCG ATTC
- - AG

GAM281 278 HSD3B7 1 2674 NP_079469.2 3 210 CTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGTGTG GTGACGTGAGGTC GACCC
A AC

GAM281 278 HSMPP8 1 7797 XP_167894.1 3 330 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 HSNOV1 2 849 NP_059985.2 3 372 GCAGGCTGTCCA CA -- ---- 3 B c c
GGCTGGGCTTGG CTG CACT CCAGCCTGGGCA
TGGTCAGG GAC GTGG GGTCGGACCTGT
G- TG TTCG

GAM281 278 HSNOV1 2 12942 NP_059985.2 3 662 TTGAGATGCAGA C C GG 3 B c
c

GTCTAGAGTGCA CACTGCACTC AG CT GCA
GTGGTGCA GTGACGTGAG TC GA CGT
A T GA

GAM281 278 HSPC065 2 713 NP_054876.2 3 2293 CTCTGTCCCCCA C CA 3 B c b
TGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCATG GTGACGTGAGGTCG ACCC
T CC

GAM281 278 HSPC065 2 4676 NP_054876.2 3 2126 CTCTGTCCCCAA --- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGGCA
GTGGTGCA GTGACGTGAGGTCGGA CCTGT
ACC

GAM281 278 HTR1D 1 2563 NP_000855.1 3 290 GCCCTCTCGCCA GCA 3 B c c
GGCTGGAGTGTA CACTGCACTCCAGCCTGG
GTGGCACA GTGATGTGAGGTCGGACC
GCT

GAM281 278 HTR1E 1 538 NP_000856.1 5 138 CTCAGTCGCCCA CA----- A 3 B c c
GGCTGGAGTGCA CTGCACTCCAGCCTGGGC
GCAGCACA GACGTGAGGTCGGACCCG

ACACGAC C

GAM281 278 HTR3B 1 656 NP_006019.1 5 57 GGGATCTGCCCA GC TC G- 3 B c c
GGAATGTTGTCA CACT AC CA CCTGGGCA
AGTGTAAT GTGA TG GT GGACCCGT
AC TT AA

GAM281 278 HUNK 1 17952 NP_055401.1 3 2963 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM281 278 HUS1 1 14238 NP_004498.1 3 1024 TTCTGTCACCCA C CA 3 B c c
GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGCCACA GTGACGTGAGGTC GACCC
A AC

GAM281 278 HYAL1 1 1192 NP_695018.1 5 140 GGCCCAGGGGGC TG ------ A 3 B c c

AGCTGGAGTGGT CAC CACTCCAGC CTGGGC
GCTCTGGG GTG GTGAGGTCG GACCCG
-- ACGGGG G

GAM281 278 HYAL4 1 2143 NP_036401.1 5 83 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM281 278 ICAM1 1 12075 NP_000192.1 3 1135 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 ICK 1 7385 NP_055735.1 3 1470 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM281 278 ICK 1 7385 NP_057597.2 3 1470 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM281 278 IGF1 1 6279 NP_000609.1 3 5348 CACTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC

GAM281 278 IL11 1 11544 NP_000632.1 3 700 CTCTGTTGCCTA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGAGGCA GTGACGTGAGGTCGGATCCGTT

GAM281 278 IL16 1 19554 NP_757366.1 5 100 CTCTGTTGCCCA --- 3 B b b
GGCTGGAGTTCA CACTGC ACTCCAGCCTGGGCAA
GCGGTGCA GTGGCG TGAGGTCGGACCCGTT
ACT

GAM281 278 IL21R 1 498 NP_068570.1 3 1362 TCTCGTCGCCCA C A 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM281 278 IL21R 1 498 NP_851564.1 3 1362 TCTCGTCGCCCA C A 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM281 278 IL21R 1 498 NP_851565.1 3 1362 TCTCGTCGCCCA C A 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C

GAM281 278 IL28RA 1 7046 NP_734464.1 3 2268 TCTTTTTGCCTA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM281 278 IL28RA 1 7046 NP_775087.1 3 2268 TCTTTTTGCCTA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM281 278 IL28RA 1 7046 NP_775088.1 3 2965 TCTTTTTGCCTA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM281 278 IMPACT 1 8975 NP_060909.1 3 2007 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGATCC
AC

GAM281 278 INHBE 1 16283 NP_113667.1 3 663 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGACACG GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 INMT 2 9149 NP_006765.3 3 445 CTCTGTCACCCA C C CA 3 B c b
GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCACG GT ACGTGAG TCGGACCC
A A AC

GAM281 278 INMT 2 11523 NP_006765.3 3 622 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 IRF4 2 1517 NP_002451.1 3 1184 CGGGGACTCCCA C A CA 3 B c b
GGCTGGAGAGCA CA TGC CTCCAGCCTGGG
CTGCCAGG GT ACG GAGGTCGGACCC
C A TC

GAM281 278 IRF4 2 2698 NP_002451.1 3 102 CTCTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
TC

GAM281 278 IRTA2 1 19371 NP_112571.1 5 50 TGTGCTCCTTGG T - --- 3 B c c
AGCTGGTGTGCA CACTGCAC CCAGC CT GGGCA
GTGTCCTG GTGACGTG GGTCG GG CTCGT
T A TTC

GAM281 278 ITGAD 1 2749 XP_113880.1 3 311 CTTGCCTAGGGG ----- AG 3 B c c
GCAGAGGGTGCA CACTGCACT CC CCTGGGCAA

GTGGCAGT GTGACGTGG GG GGATCCGTT
GAGAC G-
GAM281 278 ITGAM 1 5922 NP_000623.1 3 301 TGTGCGTGTGTC TCCA C 3 B c c

CATGTGTGTGCA CACTGCAC GC TGGGCA
GTGTGTGC GTGACGTG TG ACCTGT
TG-- T
GAM281 278 ITGAX 1 559 NP_000878.1 3 396 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGTG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 ITPR2 1 20047 NP_002214.1 3 273 GCTTGCCCAAAA CA--- A-- --- 3 B c c
GGCTGGAGAGGG CTGC CTCCAGCCT GGGCAA
CAGGGAGC GACG GAGGTCGGA CCCGTT
CGAGG GGA AAA
GAM281 278 JAK3 1 18060 NP_000206.1 3 401 GCTCGTTACCCA G CA 3 B c c
GGGTGGAGTGCA CACTGCACTCCA CCTGGG
GTGGTAGC GTGACGTGAGGT GGACCC
G AT
GAM281 278 JDP2 1 2088 NP_569736.1 3 597 CCTCGCCAGCCC T -- CT A 3 B c c
TGCTGGAGTTTG CAC GC ACTCCAGC GGGC
CTGTGGGC GTG CG TGAGGTCG CCCG
T TT T- A
GAM281 278 JM11 1 10197 NP_296375.1 3 1440 GCTCTGTCACCA A -- 3 B b b
GGCTGGAGTGCA C CTGCACTCCAGCCTGG GCA
GCGGCGCA G GACGTGAGGTCGGACC TGT
C AC
GAM281 278 JRK 1 3927 NP_003715.1 3 1242 CTCTGTTGACCA G G 3 B b b
GGCTGGAGTGAA CACT CACTCCAGCCTGG CAA
GTGGTGTG GTGA GTGAGGTCGGACC GTT
A A
GAM281 278 JWA 1 8446 NP_006398.1 3 526 ACTTTGCCACCT - C CTG- 3 B c c
GTTTGATGTGCA CACTGCAC TC AGC GGCAA
GTGGAAAC GTGACGTG AG TTG CCGTT
T T TCCA
GAM281 278 KCNJ11 1 15049 NP_000516.2 5 53 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 KCNJ16 1 2456 NP_061128.1 3 625 GCTACTTGCCCA -- CCA 3 B b b
GGTAGTGATCAG CACTG CACT GCCTGGGCAA
TGAGAGTT GTGAC GTGA TGGACCCGTT
TA ---
GAM281 278 KCNJ16 1 2456 NP_733937.1 3 625 GCTACTTGCCCA -- CCA 3 B b b
GGTAGTGATCAG CACTG CACT GCCTGGGCAA
TGAGAGTT GTGAC GTGA TGGACCCGTT
TA ---
GAM281 278 KCNJ16 1 2456 NP_733938.1 3 625 GCTACTTGCCCA -- CCA 3 B b b
GGTAGTGATCAG CACTG CACT GCCTGGGCAA
TGAGAGTT GTGAC GTGA TGGACCCGTT

TA ---

GAM281 278 KCNK3 1 16912 NP_002237.1 3 1001 GCAAAGGGGTGG T GG A 3 B c c

GGGCTGGGTGCA CACTGCAC CCAGCCT GC

GTGGCTCA GTGACGTG GGTCGGG TG

\- GG G

GAM281 278 KENAE 1 14862 NP_789786.1 3 211 CTCTGTCACCCA CA 3 B c c

GGTTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGTGTG GTGACGTGAGGTTGGACCC

AC

GAM281 278 KIAA006 1 5884 NP_055691.1 3 627 TCTTGTTGCCCA C 3 B b b

3 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA

ATGGCACC GT ACGTGAGGTCGGACCCGTT

A

GAM281 278 KIAA008 1 18751 NP_055865.1 3 1279 TCCCCACCCCCA C - - CA 3 B c c

2 GGCTGGCAGTAG CA TGC ACT CCAGCCTGGG

CACTGCTG GT ACG TGA GGTCGGACCC

C A C CC

GAM281 278 KIAA008 1 10179 NP_055584.1 3 2190 TTCTGTCACCCA CA 3 B b b

7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGCGTG GTGACGTGAGGTCGGACCC

AC

GAM281 278 KIAA011 1 9255 XP_290939.1 3 248 TGTTGTCTCCCA CA 3 B b b

7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGCGTG GTGACGTGAGGTCGGACCC

TC

GAM281 278 KIAA018 1 2218 XP_050495.4 3 2250 GAGGTCTGCCCA A T G 3 B b b

2 GGGTGGGAGCAG CACTGC C CCA CCTGGGCA

TGTCACTG GTGACG G GGT GGACCCGT

A - G

GAM281 278 KIAA018 1 2625 NP_066545.1 3 1108 TTCTGTCACCCA CA 3 B c c

6 GGCTGGGGTGCA CACTGCACTCCAGCCTGGG

GTGGCGTG GTGACGTGGGGTCGGACCC

AC

GAM281 278 KIAA020 1 3429 NP_055688.1 3 1258 CTCTGTCACCCA C CA 3 B c c

5 GGCTGTAGTGCA CACTGCACT CAGCCTGGG

GTGGCATA GTGACGTGA GTCGGACCC

T AC

GAM281 278 KIAA023 1 17386 NP_055562.1 3 5053 CCCTGATGCCCA CA------ T 3 B c c

7 GGCTGGGTGCAG CTGCAC CCAGCCTGGGCA

GCTCTCAT GACGTG GGTCGGACCCGT

TACTCTCG -

GAM281 278 KIAA025 1 9416 NP_055600.1 3 3704 GCCTGCTCTCTG GCA --- 3 B c c

8 GGCTGGAGCAGG CACT CTCCAGCCT GGGCA

TGGATTCG GTGG GAGGTCGGG CTCGT

AC- TCT

GAM281 278 KIAA029 1 10742 XP_042833.2 3 3373 GCTGGAGGCCCG A- A 3 B c c

5 GGCTGGAGGGGC CACTGC CTCCAGCCTGGGC

AGTGTTGC GTGACG GAGGTCGGGCCCG
GG G

GAM281 278 KIAA031 1 13450 XP_044334.1 3 1771 AAACTGCTGAAA T CTG--- 3 B c c
8 AAGCTGGGTGCA CACTGCAC CCAGC GGCA
GTGAAATG GTGACGTG GGTCG TCGT
- AAAAAG

GAM281 278 KIAA043 1 5041 NP_055616.1 5 677 CTCTGTCACCCA C CA 3 B c c
5 GTTTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGTGCA GTGACGTGAGGTT GACCC
T AC

GAM281 278 KIAA044 1 1475 XP_044155.1 5 2280 CACTGTCTCCTA CA 3 B c c
6 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGATCC
TC

GAM281 278 KIAA045 1 4531 XP_027862.1 3 3704 CTTTGTTGCCCA TG 3 B b b
9 GGCTGGAGTGTG CAC CACTCCAGCCTGGGCAA
GTGGGGCA GTG GTGAGGTCGGACCCGTT
GT

GAM281 278 KIAA046 2 9147 NP_055666.1 3 702 CTCTGTCACCCA CA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 KIAA046 2 9493 NP_055666.1 3 350 CTCTGTCACCCA CA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
AC

GAM281 278 KIAA047 1 16940 NP_055679.1 3 1231 CTCTGTTGCCCA 3 B b b
5 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA049 1 17206 XP_034717.1 5 926 CTCTCTTACCCA C CA 3 B c c
3 AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGACATG GTGACGTGAGGTCG ACCC
A AT

GAM281 278 KIAA049 1 14759 XP_031397.1 3 2802 CCCTGTCACCCA C CA 3 B c c
5 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 KIAA051 1 3931 NP_055547.1 3 3674 TCTTGTTGCCCA 3 B b b
3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGACACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA052 1 19745 XP_171054.1 3 365 TGCTGTTGCCCA 3 B b b
7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGTCCCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA053 1 12455 XP_047659.6 3 1245 TTCTGTCACCCA C C CA 3 B c c
2 GGCTAGAGTACA CACTG ACTC AGCCTGGG

GTGGGAAC GTGAC TGAG TCGGACCC
A A AC

GAM281 2785 KIAA055 1 5555 NP_055605.1 3 2301 CTCTGTTGCCCA C C 3 B b b
TGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
TTGGCACA GT ACGTGAGGTCG ACCCGTT
T T

GAM281 2787 KIAA055 1 2234 XP_085507.1 3 165 TTGGGATGCCCA - GCA CA-- 3 B c c
GGCCGCAGAGGA CA CT CTC GCCTGGGCA
AGCTGGGC GT GA GAG CGGACCCGT
C AG- ACGC

GAM281 2781 KIAA056 1 9629 XP_038150.2 3 321 CTCTGTTGCCCG A 3 B b b
GGCTGGAGTGCA C CTGCACTCCAGCCTGGGCAA
GCGGCGTG G GACGTGAGGTCGGGCCCGTT
C

GAM281 2782 KIAA056 1 16544 NP_055519.1 3 2049 CTCTGTTGCCTA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGATCCGTT

GAM281 2783 KIAA056 1 16377 NP_055649.1 5 604 TCTTGTTGCCCA C 3 B b b
GGCTGAAGTGCA CACTGCACT CAGCCTGGGCAA
GTGTTGTG GTGACGTGA GTCGGACCCGTT
A

GAM281 2782 KIAA068 1 6522 NP_055667.1 3 32 TGGCACCGAGAG ---- - A 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCT GG GC
GTGGCGTG GTGACGTGAGGTCGGG CC CG
AGAG A G

GAM281 2783 KIAA068 1 18206 NP_057195.1 3 450 GCTCACAGCCCA T T A A 3 B c c
GGCAGGGTGTGT CAC GCAC CC GCCTGGGC
GGCTCCTG GTG TGTG GG CGGACCCG
- - A A

GAM281 2781 KIAA083 1 3260 NP_055739.1 3 1918 CTCAGCTGCCCA TG 3 B b b
GGCTGGAGTGTG CAC CACTCCAGCCTGGGCA
GTGGCGCC GTG GTGAGGTCGGACCCGT
GT

GAM281 2781 KIAA084 2 5490 XP_049237.1 3 1172 TTCTGTTGCCCA C 3 B b b
AGTTGGAGTGCA CACTGCACTCCAGC TGGGCAA
GTGGCATG GTGACGTGAGGTTG ACCCGTT
A

GAM281 2781 KIAA084 2 8185 XP_049237.1 3 1521 GGCTGTTTCCCA C CA 3 B c b
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGCATG GTGACGTGA GTCGGACCC
A TT

GAM281 2781 KIAA086 1 2153 NP_055893.2 3 955 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C

GAM281 278 KIAA088 1 13271 NP_056192.1 3 736 TCTTGTCCCCCA C C CA 3 B c c

	9				GGCTTGAGTGCA CA TGCACTC AGCCTGGG ATGACTCA GT ACGTGAG TCGGACCC A T CC						
GAM281	2784	KIAA092	2	7655	NP_055712.1	3 2517	TTCTGTTGCCTG GGCTGGAGTGCA CACTGCACTCCAGCC GGCAA GTGGCGTG GTGACGTGAGGTCGG CCGTT GT	TG	3	B	b b
GAM281	2784	KIAA092	2	13297	NP_055712.1	3 1717	CTATGTTGCCCA GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA GTGGCTAT GTGACGTGAG TCGGACCCGTT A	C	3	B	b b
GAM281	2781	KIAA093	1	14272	XP_041191.2	3 162	CTCAGTCGCTCA GGCTGGAGTGCA CACT GCACTCCAGCCTGGGC ATGGTGGG GTGG CGTGAGGTCGGACTCG TAA C	--- A	3	B	c c
GAM281	2785	KIAA093	1	11958	XP_052620.6	3 1214	CTCTGTCGCCCA GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC GTGTCAAG GTGACGTGAGGTCGGACCCG C	A	3	B	b b
GAM281	2782	KIAA096	1	8976	XP_290942.1	3 1524	TCTTGTTGCCCA GGCTGGAGTGAA CACTG CACTCCAGCCTGGGCAA ATGGTGCG GTGGT GTGAGGTCGGACCCGTT AAA	---	3	B	b b
GAM281	2782	KIAA100	1	12518	XP_290584.1	5 0	CGCCTAGGCTGG T A AGCGCCGTGGTA CAC GC CTCCAGCCTGGGC CAGTCTTG GTG CG GAGGTCGGATCCG C C C	A	3	B	c c
GAM281	2782	KIAA103	1	1326	XP_038604.4	3 1349	TTACAGTGACCT C--- GGCTGGAGTTAC CACTG ACTCCAGCC GGG CA CTGGTGCA GTGGT TGAGGTCGG TCC GT CCAT - A	T -	3	B	c c
GAM281	2780	KIAA104	1	11846	XP_051091.3	3 2456	CTCTGTCACCCA GGCTGGAATGCA CACTGCA TCCAGCCTGGG GTGGCACG GTGACGT AGGTCGGACCC A AC	C CA	3	B	c c
GAM281	2781	KIAA104	1	3653	NP_055762.1	3 968	CCCTGTTGCCCA GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA GTGGCACG GTGACGTGAGGTCGGACCCGTT		3	B	b b
GAM281	2782	KIAA105	1	919	NP_055771.1	5 227	CTCTGTCACTCA GGCTGCAGTGCA CACTGCACT CAGCCTGGG GTGGCATG GTGACGTGA GTCGGACTC C AC	C CA	3	B	c c
GAM281	2784	KIAA105	1	14832	XP_043493.5	3 3278	CTCTGTTGCCCA GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA GTGGTGGG GTGACGTGAGGTCGGACCCGTT		3	B	b b
GAM281	2785	KIAA111	1	9842	NP_055746.1	3 688	TCCCTCCTCCCA G T GGCTGGTGTGAG CACT CAC CCAGCCTGGG TGTGCGTG GTGA GTG GGTCGGACCC	CA	3	B	c c

- T TC

GAM281 278 KIAA112 1 10583 XP_050325.1 3 3198 GTGGGCTGTGCA --- ACT G 3 B c c

6 GGCTGGTGGCCT CACT GC CCAGCCTG GCA

GGGTGCCT GTGG CG GGTCGGAC TGT

GTC GT- G

GAM281 278 KIAA112 1 5783 NP_061872.1 3 1959 CTCCATTGCCCA CAC 3 B b b

8 GGCTGGATTACA CACTG TCCAGCCTGGGCAA

GTGGCGCA GTGAC AGGTCGGACCCGTT

ATT

GAM281 278 KIAA114 1 7385 XP_044014.1 3 3995 CTCTGTCACCCA CA 3 B b b

3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGCGCG GTGACGTGAGGTCGGACCC

AC

GAM281 278 KIAA115 1 2664 XP_030864.2 3 2954 CTCTGTCACCCA CA 3 B b b

5 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGTATG GTGACGTGAGGTCGGACCC

AC

GAM281 278 KIAA117 1 10162 XP_045907.2 3 1245 TCTTGTTGCCCA C C 3 B b b

0 AGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA

ATGGCACG GT ACGTGAGGTCG ACCCGTT

A A

GAM281 278 KIAA118 1 5755 NP_065761.1 3 154 GCTCTGTCGCCA -- 3 B b b

5 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA

GTGGCGTG GTGACGTGAGGTCGGACC TGT

GC

GAM281 278 KIAA119 1 17517 XP_041843.1 3 1645 ACACTGTCGCCA -- 3 B b b

3 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA

GTGGTGCG GTGACGTGAGGTCGGACC TGT

GC

GAM281 278 KIAA119 5 12389 NP_065765.1 3 421 TCTTGTTGCCCA 3 B b b

8 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA119 5 12478 NP_065765.1 3 994 CTCTGTTGCCTA G- 3 B b b

8 GGCTGGAGTGAA CACT CACTCCAGCCTGGGCAA

AGTGGCGC GTGA GTGAGGTCGGATCCGTT

AA

GAM281 278 KIAA119 5 13749 NP_065765.1 3 1272 AGTCCTTGCCCA 3 B b b

8 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA119 5 16088 NP_065765.1 3 3710 TCACTGTTGCCA G 3 B b b

8 GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA

GTGGCACA GTGACGTGAGGTCGGACC GTT

-

GAM281 278 KIAA119 5 16471 NP_065765.1 3 724 TCTGTTGCCCCA - 3 B b b

8 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG CAA

GTGGTGTG GTGACGTGAGGTCGGACCC GTT

C

GAM281 278 KIAA121 1 9144 XP_172801.1 3 105 CTCTGTTACCCA GC CA 3 B c c
0 GATTGGAGTGCA CACTGCACTCCA CTGGG
GTGGCGCG GTGACGTGAGGT GACCC
TA AT
GAM281 278 KIAA125 3 8196 XP_031577.2 3 1026 CTCTCTCACCCA - CA 3 B c b
7 GGCTGGAGTGTA CACT GCACTCCAGCCTGGG
AGTGACAT GTGA TGTGAGGTCGGACCC
A AC
GAM281 278 KIAA125 3 9032 XP_031577.2 3 3566 TCTTGTTGCCCA C C 3 B b b
7 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGCGCG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 KIAA125 3 11523 XP_031577.2 3 1695 CTCTGTCGCCCA A 3 B b b
7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 KIAA126 1 3236 XP_291055.1 3 898 TCTTGTTGCCCA C 3 B b b
8 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 KIAA127 1 7374 XP_300760.1 5 380 GTCCAAGCTCAA C C- A 3 B c c
3 AGCTGGAGTGCA CA TGCACTCCAGC TGGGC
ATGGCGCA GT ACGTGAGGTCG ACTCG
A AA A
GAM281 278 KIAA128 1 9573 NP_065799.1 3 1243 CCCTGTTGCCCA 3 B b b
7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGGATG GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA139 1 10123 XP_050793.2 3 1500 CTCTGTTGCCCA CA----- 3 B c c
3 GGCTGGAGTGTA CTGCACTCCAGCCTGGGCAA
GAGACACA GATGTGAGGTCGGACCCGTT
ACACAGA
GAM281 278 KIAA144 1 15171 NP_065885.1 3 712 CTCTGTCGCCCA C C A 3 B c c
3 GGCTGTAGTGCA CA TGCACT CAGCCTGGGC
ATGGCGCA GT ACGTGA GTCGGACCCG
A T C
GAM281 278 KIAA145 1 5529 XP_040100.3 3 2060 CTCTGTCGCCCA C A 3 B b b
6 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
CTGGCGCG GT ACGTGAGGTCGGACCCG
C C
GAM281 278 KIAA146 2 18838 XP_027396.4 3 449 GCCAGCCAAGGC T --- G A 3 B c b

5 CAGTGGAGTGCT CAC GCACTCCA GCCT GGC
GTGGGGTC GTG CGTGAGGT CGGA CCG
T GAC A A
GAM281 278 KIAA146 2 18992 XP_027396.4 3 570 GGTCTGTCGCCA -- 3 B b b
5 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 KIAA149 1 15045 XP_034415.1 3 2966 CTCTGTTGCCCA C C 3 B b b

3 GTCTGGAGTTCA CACTG ACTCCAG CTGGGCAA
GTGGCGCG GTGAC TGAGGTC GACCCGTT
T T

GAM281 2788 KIAA150 1 8820 XP_290952.1 3 78 GCTCGTCACCCA --- CA 3 B c c
GGCTGGAGTGCA CAC TGCACTCCAGCCTGGG
ATTGTGCA GTG ACGTGAGGTCGGACCC
TTA AC

GAM281 2788 KIAA151 1 13383 XP_170889.1 3 95 CTCTGTCGCCCA G A 3 B c c
GGGTGGAGTGCG CACTGCACTCCA CCTGGGC
GTGGCACG GTGGCGTGAGGT GGACCCG
G C

GAM281 2780 KIAA153 3 4028 XP_042661.5 3 1177 GCTCTGTCGCCA C -- 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGG GCA
ATGGCGTG GT ACGTGAGGTCGGACC TGT
A GC

GAM281 2780 KIAA153 3 12345 XP_042661.5 3 818 TTGCTCTTACCC C CA 3 B c b
AGGCTGAGTGCA CACTGCACTC AGCCTGGG
GTGGCAGA GTGACGTGAG TCGGACCC
- AT

GAM281 2780 KIAA153 3 15284 XP_042661.5 3 818 TGCTCTTACCCA C CA 3 B c b
GGCTGAGTGCAG CACTGCACTC AGCCTGGG
TGGCAGAA GTGACGTGAG TCGGACCC
- AT

GAM281 2780 KIAA155 1 3790 XP_039393.3 3 663 GCAAGCAGCCCA A TC --- A 3 B c c
GGCAGCTGTGGG CACTGC C CA GCCTGGGC
CAGTGCTG GTGACG G GT CGGACCCG
- GT CGA A

GAM281 2789 KIAA155 1 4029 XP_054472.2 3 1629 CTTTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
CC

GAM281 2781 KIAA157 1 14154 XP_027744.1 3 882 CTGTCTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCCTG GTGACGTGAGGTCGGACCCGTT

GAM281 2785 KIAA161 2 8549 NP_066002.1 3 1381 TCTTGTTGCCTA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGATCCGTT

GAM281 2785 KIAA161 2 10111 NP_066002.1 3 1687 GCTCTGTCACCA A -- 3 B b b
GGCCGGAGTGCA CACTGCACTCC GCCTGG GCA
GTGGTGTC GTGACGTGAGG CGGACC TGT
C AC

GAM281 2781 KIAA167 2 7194 XP_037809.1 3 1742 CTCTGTTGCTCA G C 3 B b b
AGCTGGAGTGGA CACT CACTCCAGC TGGGCAA
GTGGCACG GTGA GTGAGGTCG ACTCGTT
G A

GAM281 2781 KIAA167 2 17191 XP_037809.1 3 4094 CTCTGTTGGCCA C G 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGG CAA

GTGGCACA GTGACGT AGGTCGGACC GTT
A G
GAM281 278 KIAA167 1 5094 XP_046570.3 3 455 CCCGCCTGCTAA TC- CTG 3 B c c
9 GCTGTGTGTGCA CACTGCAC CAGC GGCA
GTGATGGC GTGACGTG GTCG TCGT
TGT AA-
GAM281 278 KIAA171 2 1142 NP_085136.1 3 1318 CTCTATTGCCCA C 3 B b b
2 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCGTG GT ACGTGAGGTCGGACCCGTT
C
GAM281 278 KIAA171 2 1142 XP_041497.2 3 1487 CTCTATTGCCCA C 3 B b b
2 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCGTG GT ACGTGAGGTCGGACCCGTT
C
GAM281 278 KIAA171 2 14165 NP_085136.1 3 740 TGTTGTTGCCCA CAC----- 3 B c b
2 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCACG ACGTGAGGTCGGACCCGTT
GCACGATA
GAM281 278 KIAA171 2 14165 XP_041497.2 3 740 TGTTGTTGCCCA CAC----- 3 B c b
2 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCACG ACGTGAGGTCGGACCCGTT
GCACGATA
GAM281 278 KIAA172 2 14630 XP_040280.2 5 25 CATCCTTGCCCA T- --- A C 3 B c c
4 GCCGGTGTGGTG CAC GCACT CC GC TGGGCAA
CTTGTGTG GTG CGTGG GG CG ACCCGTT
TT TGT C -
GAM281 278 KIAA172 2 15040 XP_040280.2 3 6011 TCATTGGTCTGT TCCAG TG 3 B c c
4 CTGGGACGTGCA CACTGCAC CC GGCA
GTGTTCAT GTGACGTG GG CTGT
CA--- GT
GAM281 278 KIAA173 1 10602 NP_219494.1 3 1428 TCTTGTTGCCCA --- C A 3 B c c
7 GGCGGAGTACAA CACT G ACTCC GCCTGGGCAA
TGGTGGGA GTGG C TGAGG CGGACCCGTT
TAA A -
GAM281 278 KIAA177 2 1618 NP_149091.1 3 2168 AGGACAAGCCCA C CT A A 3 B c c
5 GGCAGGGCTGCA CA TGCA CC GCCTGGGC
TGGAGAGG GT ACGT GG CGGACCCG
- CG A A
GAM281 278 KIAA177 2 17949 NP_149091.1 3 499 AGCACTGTCTCA A CA - 3 B c c
5 GGCTGGAGGTCA C CTG CTCCAGCCTG GGCA
GCGAACCT G GAC GAGGTCGGAC CTGT
C TG T
GAM281 278 KIAA178 1 11058 NP_115820.1 3 342 CTGTGTCACCTA CA 3 B c c
4 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC
GAM281 278 KIAA182 1 10095 XP_041566.2 3 992 CGGGGCTGACCA CA- G 3 B c c

2 GGCTGGGGGTCC CACTG CTCCAGCCTGG CA
AGTGAAAC GTGAC GGGGTCGGACC GT
CTG A

GAM281 278 KIAA182 2 2143 XP_290834.1 3 938 CTCTGTTGCCCA 3 B b b
7 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM281 278 KIAA182 2 12636 XP_290834.1 3 1306 CCTTGTCACCCA C CA 3 B c b
7 GGCTGTAGTGCG CACTGCACT CAGCCTGGG
GTGGCGCG GTGGCGTGA GTCGGACCC
T AC

GAM281 278 KIAA182 1 14863 XP_030378.2 3 210 CTCTGTTGCCCA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTA GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIAA183 1 12627 XP_114087.2 3 1679 CTCTGCCAGCCA --- 3 B b b
6 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC CGT
GAC

GAM281 278 KIAA185 1 19095 XP_045184.1 3 1021 CCCCTCTGCCCA CT ACTC 3 B c
c

3 GGCTGCCACGCC CA GC CAGCCTGGGCA
CTGGATGC GT CG GTCGGACCCGT
CC CACC

GAM281 278 KIAA186 1 16627 XP_044212.4 3 53 CTGCTCGTTCTT TCCAG G 3 B c
c

2 GCCGAGGGTGCA CACTGCAC CCT GGCAA
GTGGTGGC GTGACGTG GGA CCGTT
----- G

GAM281 278 KIAA190 1 16492 XP_056282.1 3 3672 AGCCTGTGTCCA T- A 3 B c c
4 GGCTGGGGAGCC CAC GC CTCCAGCCTGGGCA
CGTGTCTG GTG CG GGGGTCGGACCTGT
CC A

GAM281 278 KIAA192 1 7553 XP_057040.1 5 322 TCTTGTTGCCCA C 3 B b b
2 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCATG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 KIAA192 2 1857 NP_694971.2 3 597 CTCTGTCGCCCA G A 3 B b b
4 GGATGGAGTGCA CACTGCACTCCA CCTGGGC
GTGGCGCG GTGACGTGAGGT GGACCCG
A C

GAM281 278 KIAA192 2 8341 NP_694971.2 3 407 TTCTGTCACCTA C CA 3 B c b
4 GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGTGCA GTGACGT AGGTCGGATCC
A AC

GAM281 278 KIAA193 1 2983 XP_057107.3 5 301 ACGCGCTGTCCT GCA T 3 B c c
7 GGCTGGAGGAGG CACT CTCCAGCC GGGCA
TGGAGCAG GTGG GAGGTCGG CCTGT
AG- T

GAM281 278 KIAA197 3 5820 XP_058720.4 3 562 CTCTGTCATCCA C CA 3 B c b

1 GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCACG GTGACGTGAG TCGGACCT
A AC

GAM281 278 KIAA197 3 6902 XP_058720.4 3 214 CTCTGTCGCCCA A 3 B b b
1 GGCTGGGGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGGGGTCGGACCCG
C

GAM281 278 KIAA197 3 11506 XP_058720.4 3 264 CTCCGCTTCCCA CA 3 B c b
1 GGCTGGGGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGGGGTCGGACCC
TT

GAM281 278 KIAA198 1 7554 XP_113870.1 5 202 TCTTGTTGCCCA C 3 B b b
7 GGTTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCACG GTGACGTGAG TTGGACCCGTT
A

GAM281 278 KIAA202 1 12100 XP_059415.2 3 1063 TCTGGTTGCCCA 3 B b b
8 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCC GTGACGTGAGGTCGGACCCGTT

GAM281 278 KIF25 1 17138 NP_005346.2 5 14 AAACAGGCGGCA C G- A 3 B c c
GGCTGGGGTTGG CACTG ACTCCAGCCTG GC
TGGGGCTT GTGGT TGGGGTCGGAC CG
- GG G

GAM281 278 KIF25 1 17138 NP_085118.1 5 14 AAACAGGCGGCA C G- A 3 B c c
GGCTGGGGTTGG CACTG ACTCCAGCCTG GC
TGGGGCTT GTGGT TGGGGTCGGAC CG
- GG G

GAM281 278 KIP2 1 4201 NP_006374.1 3 525 TCACAATGTGAA - C GG 3 B c c
GCTGTGGGTGCA CACTGCACTC CAGC T GCA
GTGGCGCC GTGACGTGGG GTCG A TGT
T - AG

GAM281 278 KLF12 1 1127 NP_009180.3 3 950 TGGGGCTGCCCA C CCA 3 B b b
GGCAAAGTCAGT CACTG ACT GCCTGGGCA
GAACATGA GTGAC TGA CGGACCCGT
- AA-

GAM281 278 KLRD1 1 2353 NP_002253.1 3 396 TCACACTGCCCA CA 3 B b b
GGCTGGAGCATA CACTG CTCCAGCCTGGGCA
GTGGCAAG GTGAT GAGGTCGGACCCGT
AC

GAM281 278 KLRD1 1 2353 NP_031360.1 3 396 TCACACTGCCCA CA 3 B b b
GGCTGGAGCATA CACTG CTCCAGCCTGGGCA
GTGGCAAG GTGAT GAGGTCGGACCCGT
AC

GAM281 278 KMO 1 6338 NP_003670.1 3 716 CTCTGTTGACCA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGTGAG GTGACGTGAGGTCGGACC GTT
A

GAM281 278 LAMP3 1 17760 NP_055213.1 3 565 TCTTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC

A AC

GAM281 278 LCN7 1 15937 NP_071447.1 3 400 CTCCGTTGCCCA 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCCCA GTGACGTGAGGTTGGACCCGTT

GAM281 278 LCX 1 2891 XP_167612.2 3 44 CCTCTTAATGCC CC CT 3 B c c
TTTGCTAGTGCA CACTGCACT AGC GGGCA
GTGTATTT GTGACGTGA TCG TCCGT
-- TT

GAM281 278 LEPROTL 1 1871 NP_056159.1 3 1958 TTTTCTGTTCTG C- G T 3 B c c
1 GATGTCAGTGCA CACTGCACT CA CC GGGCA
GTGCACTG GTGACGTGA GT GG CTTGT
CT A T

GAM281 278 LETM1 1 18695 NP_036450.1 3 1029 GCAGCATGGCCA T A -- G 3 B c c

GGCTGGCCAGGG CAC GC CT CCAGCCTGG CA
CGTGGGCA GTG CG GA GGTCGGACC GT
- G CC G

GAM281 278 LGP1 1 16610 NP_115873.1 5 32 CTCTGTTGCCCA C 3 B b b
AGCTGGGGTGCA CACTGCACTCCAGC TGGGCAA
GTGGCACG GTGACGTGGGGTCG ACCCGTT
A

GAM281 278 LGP2 1 8032 NP_077024.1 5 165 AGAGTGGCACCA GC C - A 3 B c c
GGCTGAGTTAAG CACT ACTC AGCCTGG GC
TGGGACTG GTGA TGAG TCGGACC CG
AT - A G

GAM281 278 LIN-28 1 4726 NP_078950.1 3 2144 CTGTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGAGCTG GTGACGTGAGGTCGGACCCG
C

GAM281 278 Link-GE 1 19936 NP_057423.1 3 677 CCTGCATGCCCA GCA- - - 3 B c c
FII GGCTTGTGAGCC CACT CTC CA GCCTGGGCA
AAGGTGCT GTGG GAG GT CGGACCCGT
AACC T T

GAM281 278 LIPH 1 10379 NP_640341.1 3 3 TTCTTTGCCCAG C - C - 3 B c c
AGTTGCAGTTGT CA TGCA CT CAGC CTGGGCAA
ACTGTTGC GT ATGT GA GTTG GACCCGTT
C T C A

GAM281 278 LNK 1 13992 NP_005466.1 3 1683 TCTTGTCAACCG GCA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGGCC
AAC

GAM281 278 LOC1126 1 16673 XP_053145.1 3 169 CCCTGTCACCCA CA 3 B b b
87 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC1128 1 16256 NP_612422.2 3 419 CTCTGTCACCCA C CA 3 B c c
17 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCATG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 LOC1128 1 12772 XP_053402.1 5 341 CCCCTGGGCACA A ---- G A 3 B c c
68 GGCTGGGATCAG CACTGC CT CCAGCCTG GC
GGCAGTGA GTGACG GA GGTCGGAC CG
G CTAG A G
GAM281 278 LOC1134 3 5336 NP_612437.2 3 852 TTCTGTCACCCG CA 3 B c b
44 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGGCCC
AC
GAM281 278 LOC1134 3 15899 NP_612437.2 3 590 CTCTGTCACACA C----- --- 3 B c b
44 GGCTGGAGTGCA ACTGCACTCCAGCCTG GGCA
GTACAATT TGACGTGAGGTCGGAC CTGT
TTAACA ACA
GAM281 278 LOC1134 3 18294 NP_612437.2 3 1177 CTGTATTGCCCA 3 B b b
44 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1138 1 5632 NP_612444.1 5 268 TCCTGCCGCCCA - C - A A 3 B c c
28 GGCAGGATGTCA CA CTG AC TCC GCCTGGGC
GATGAGGA GT GAC TG AGG CGGACCCG
A - T A C
GAM281 278 LOC1151 1 15271 XP_055276.1 5 257 CTCTATGGCCCA C A 3 B b b
23 GGCTGGAGTACA CACTG ACTCCAGCCTGGGC
GTGACACG GTGAC TGAGGTCGGACCCG
A G
GAM281 278 LOC1152 1 12422 XP_055499.2 5 1755 CTTTGTCCCCCA C CA 3 B c c

19 GGCTGGAGTGCG CA TGCACTCCAGCCTGGG
ATGGCAGG GT GCGTGAGGTCGGACCC
A CC
GAM281 278 LOC1156 1 7429 NP_663299.1 3 657 GCTCTGTCGCCT T A 3 B b b
48 GGCTGGAGTGCA CACTGCACTCCAGCC GGGC
GTGGTGTG GTGACGTGAGGTCGG TCCG
- C
GAM281 278 LOC1164 1 14720 XP_058095.1 5 1241 CAATGGTGTCCA 3 B b b
11 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCGTG GTGACGTGAGGTCGGACCTGT

GAM281 278 LOC1184 1 456 XP_060981.3 3 219 CTCTGTTGCCCA A 3 B b b
90 GGCTGGAGTGCA C CTGCACTCCAGCCTGGGCAA
GCGGCATG G GACGTGAGGTCGGACCCGTT
C
GAM281 278 LOC1188 1 2649 NP_849154.1 3 581 TACTCTCGCCCA C A 3 B b b
12 GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCATG GTGACGTGAG TCGGACCCG
A C
GAM281 278 LOC1188 1 2649 XP_058346.2 3 581 TACTCTCGCCCA C A 3 B b b
12 GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCATG GTGACGTGAG TCGGACCCG
A C

GAM281 278 LOC1205 1 17112 XP_058475.1 3 679 CTCTGTCGCGCC C - A 3 B b b
26 AGCTGGAGTGCA CACTGCACTCCAGC TGG GC
GTGCCATG GTGACGTGAGGTCG ACC CG
- G C
GAM281 278 LOC1219 1 9891 XP_062872.2 5 585 CTCTGTCACCCG T CA 3 B c c
52 GGCTGGAGTGCT CAC GCACTCCAGCCTGGG
GTGGCTTG GTG CGTGAGGTCGGGCCC
T AC
GAM281 278 LOC1242 1 14576 XP_058785.3 5 257 AACTTCAGTCCG T A A 3 B c c
21 GGCTGGAGGCCG CAC GC CTCCAGCCTGGGC
TGCACAAC GTG CG GAGGTCGGGCCTG
C - A
GAM281 278 LOC1250 1 1744 XP_058889.3 3 407 CTCTGTCACCCA CA 3 B b b
61 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC1266 2 3477 XP_060121.4 3 194 CTGTGTTGCCCA C 3 B b b
69 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC1266 2 17906 XP_060121.4 3 3860 TCCTTCCAGGGT AG---- CA 3 B c
b
69 TTAGGGAGTGCA CACTGCACTCC CCTGGG
GTGATGTC GTGACGTGAGG GGACCT
GATTTG TC
GAM281 278 LOC1272 1 18918 XP_059122.1 3 141 CTTTGTTGCCCA C------ - AGC 3 B c
c
53 GAGGATGTGCAG ACTGCAC TCC CTGGGCAA
TTGTCATC TGACGTG AGG GACCCGTT
CTACTGT T A--
GAM281 278 LOC1278 1 18516 XP_059184.1 5 112 TGGTGTTGCCCA A CA- 3 B c c
41 GGCAGAGAGGGC CACTGC CTC GCCTGGGCAA
AGTGTGGA GTGACG GAG CGGACCCGTT
G AGA
GAM281 278 LOC1283 1 15173 XP_059243.2 3 561 TGTTGTTGCCCA C 3 B b b
87 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC1308 1 12052 XP_065904.1 3 931 CACTGTCGCCTA --- A 3 B c c
13 GGCTGGAGTGCA CACT GCACTCCAGCCTGGGC
ACAGTGTG GTGA CGTGAGGTCGGATCCG
CAA C
GAM281 278 LOC1322 1 509 XP_059583.1 5 83 CTTTGCTTCCCA CA 3 B b b
41 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
TT
GAM281 278 LOC1352 2 3512 XP_072402.4 3 1277 CTTGCTCTCCCA CA 3 B b b
93 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTA GTGACGTGAGGTCGGACCC

TC
GAM281 278 LOC1352 2 10443 XP_072402.4 3 564 CTCTGTTGCCCA C 3 B b b
93 GGCTGAAGTGTA CACTGCACT CAGCCTGGGCAA
GTGGCACA GTGATGTGA GTCGGACCCGTT
A
GAM281 278 LOC1357 1 17207 NP_612639.1 3 39 CTCCGTCACCCA CA 3 B b b
63 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCAAG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC1358 1 19136 XP_059804.4 3 736 TCTTGTTGCCCA CAC----- C 3 B c
c
18 GCCTGGAGTGCA TGCACTCCAG CTGGGCAA
ATAGCGTG ACGTGAGGTC GACCCGTT
GTGCGATA C
GAM281 278 LOC1378 1 19990 XP_059929.3 3 683 TCTTGTTGCCCA C 3 B b b
86 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCATA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC1384 1 3277 XP_059972.1 3 311 ATGCTGGCTTGG T A -- A 3 B c c
28 AGGCCGGGTGCA CACTGCAC CC GCCT GGGC
GTGGCTCA GTGACGTG GG CGGA TTCG
- C GG G
GAM281 278 LOC1394 1 9489 XP_066687.2 5 64 CTCTGTTGCCCA C 3 B b b
22 GACTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGTGTG GTGACGTGAGGTC GACCCGTT
A
GAM281 278 LOC1429 1 2999 XP_096365.1 3 0 GTGCCCAGGAAG AC AG-- 3 B c c
46 AGGAAGTAGTGT CACTGC TCC CCTGGGCA
ACGATACA GTGATG AGG GGACCCGT
A- AGAA
GAM281 278 LOC1432 1 15574 NP_620167.1 5 54 TCTTGTTGCCCA C 3 B b b
41 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC1442 1 3159 XP_084786.1 5 399 CTCTTTCGCCCA C A 3 B b b
48 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGTGTG GT ACGTGAGGTCGGACCCG
A C
GAM281 278 LOC1444 1 3665 NP_705898.1 3 1010 ACAAGGTGCACA TGC-- - G 3 B c
c
02 GGCTGGAAGTCT CAC ACT CCAGCCTG GCA
TTTGTGAA GTG TGA GGTCGGAC CGT
TTTTC A A
GAM281 278 LOC1444 3 1633 XP_084852.6 3 1294 ATCTGTTACCCA CA 3 B b b
04 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
AT
GAM281 278 LOC1444 3 5897 XP_084852.6 3 1129 GTCTGTTGCCTA A 3 B b b
04 GGCGGGAGTGCA CACTGCACTCC GCCTGGGCAA

GTGGCATC GTGACGTGAGG CGGATCCGTT
G
GAM281 278 LOC1444 3 15352 XP_084852.6 3 421 TTACCAGGCCCA TG A 3 B c b
04 GGCTGGGGTGGT CAC CACTCCAGCCTGGGC
GTGAACCC GTG GTGGGGTCGGACCCG
TG G
GAM281 278 LOC1444 1 19220 XP_096611.2 3 209 CTCTGTCACTCA CA 3 B c c
81 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTATA GTGACGTGAGGTCGGACTC
AC
GAM281 278 LOC1446 1 12712 XP_096648.1 3 520 CTCTGTCATCCA A CA 3 B c c
67 GGCTGGAGGGTA CACTGC CTCCAGCCTGGG
GTGGCGTG GTGATG GAGGTCGGACCT
G AC
GAM281 278 LOC1447 1 17736 XP_084949.1 5 57 CTCTGTTGCCTA C 3 B b b
42 GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGCAAG GTGAC TGAGGTCGGATCCGTT
A
GAM281 278 LOC1447 1 12981 XP_084954.1 5 1152 CATTACTGCCCA CA--- - A- 3 B c
c
47 GGTAAGGAGTGC CT GCACTCC GCCTGGGCA
TAGAATCA GA CGTGAGG TGGACCCGT
ACTAA T AA
GAM281 278 LOC1447 1 8972 XP_084963.2 5 181 CTTTGTCACCCA C CA 3 B c c
66 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC
GAM281 278 LOC1447 2 444 XP_084964.1 5 134 CTCCATCACTCA C CA 3 B c b
76 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGCTGAG GTGAC TGAGGTCGGACTC
A AC
GAM281 278 LOC1447 2 16275 XP_084964.1 5 252 TTCTGTTGCCCA C 3 B b b
76 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCATG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC1448 1 12065 XP_084972.1 5 233 CTCTGTCGCCCA A 3 B b b
17 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC1448 1 14506 XP_096698.1 3 383 CTCTGTTGCCCA CA----- 3 B c c
71 GGCTGGAGTGCA CTGCACTCCAGCCTGGGCAA
GGGACACC GACGTGAGGTCGGACCCGTT
CCACAGG
GAM281 278 LOC1449 1 12130 XP_084990.1 5 26 CTTCGTGTTTGC TG- CTG 3 B c
c
62 TGCTGGAGTGAC CAC CACTCCAGC GGCAA
TGTGTGTT GTG GTGAGGTCG TCGTT
TCA ---
GAM281 278 LOC1452 2 6493 XP_085072.1 5 482 TTCCCTTCCACA - CT - CA 3 B c b

68 GGCTGGTTGCAT CAC TGCA CCAGCCTG GG
GTGCCATG GTG ACGT GGTCGGAC CC
T T- A TT

GAM281 278 LOC1452 2 18805 XP_085072.1 5 637 CTCTTTTGCCCA GCA 3 B b b
68 GGCTGGAGCGAA CACT CTCCAGCCTGGGCAA
GTGACGAG GTGA GAGGTCGGACCCGTT
AGC

GAM281 278 LOC1454 1 11939 XP_085120.1 5 319 CTGTGTCATGCA C----- G --- 3 B c c

53 GGCTGGAGTGAA ACT CACTCCAGCCTG GGCA
GTCGTGTG TGA GTGAGGTCGGAC CTGT
GTGTGC A GTA

GAM281 278 LOC1456 1 13897 XP_096829.1 3 498 TAGAGCTGTATG T A GG- 3 B c
c

63 AGGCCGGGTGCA CACTGCAC CC GCCT GCA
GTGGCTCA GTGACGTG GG CGGA TGT
- C GTA

GAM281 278 LOC1457 1 4773 XP_085211.1 3 988 GCTCTGTCACCA C -- 3 B b b
25 GGCTGGAGTACA CACTG ACTCCAGCCTGG GCA
GTGATGAC GTGAC TGAGGTCGGACC TGT
A AC

GAM281 278 LOC1457 2 7370 XP_085227.1 5 95 CTCTGTCGCCCA A 3 B b b
57 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGGCGTGAGGTCGGACCCG
C

GAM281 278 LOC1457 2 11523 XP_085227.1 5 213 CTCTGTCGCCCA A 3 B b b
57 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC1457 1 2196 XP_085231.2 5 1119 CTCTGTCACCCA C CA 3 B c c
83 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCA GT ACGTGAGGTCGGACCC
A AC

GAM281 278 LOC1458 1 16256 XP_096873.1 5 60 CTCTGTCACCCA C CA 3 B c c
13 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCATG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 LOC1461 1 16175 NP_778229.1 5 198 TCTTGTTGCCCA C----- 3 B b b
77 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGCAA
GTAGCACT TGACGTGAGGTCGGACCCGTT
TCACGA

GAM281 278 LOC1462 4 1644 XP_085387.1 3 3210 CTCTGTCGCCCA C A 3 B b b
29 GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCACA GTGACGTGAG TCGGACCCG
A C

GAM281 278 LOC1462 4 5551 XP_085387.1 3 1707 CTCTGTCGCCCA A 3 B b b
29 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC1462 4 5672 XP_085387.1 3 4034 CTCTGTTGCCTA C 3 B b b

29 GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGTGCA GTGAC TGAGGTCGGATCCGTT
A

GAM281 278 LOC1462 4 8706 XP_085387.1 3 2310 TCTTGTTGCCTA C 3 B b b
29 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGAG GT ACGTGAGGTCGGATCCGTT
A

GAM281 278 LOC1463 3 1901 XP_085430.1 5 1413 ACTGTCTGCTCA CA--- - - 3 B c b
46 GGCTGGTGGTGA CTG CACT CCAGCCTGGGCA
CAGGATCC GAC GTGG GGTCGGACTCGT
CCTAG A T

GAM281 278 LOC1463 3 5798 XP_085430.1 5 736 ACTCGTTGCCCA 3 B b b
46 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1463 3 17670 XP_085430.1 5 388 ACTCCGTTGCCA T G 3 B b b
46 GGCTGGAGTGCT CAC GCACTCCAGCCTGG CAA
GTGGCGCT GTG CGTGAGGTCGGACC GTT
T -

GAM281 278 LOC1464 2 2457 XP_096998.2 5 536 GCTCTGTCACCA -- 3 B b b
29 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGTG GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 LOC1464 2 4769 XP_096998.2 5 55 CCCAATCTGCCA C--- T -- G 3 B c b
29 GGCTGGACTGTG AC GCAC TCCAGCCTGG CA
CTGTTCCT TG CGTG AGGTCGGACC GT
TCCT T TC -

GAM281 278 LOC1464 1 813 XP_085461.6 5 101 ACTTGTCACCCA C CA 3 B c c
43 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGTG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 LOC1464 1 9246 XP_097006.1 5 119 AAGCCCACGTGA TG ----- A 3 B c c

75 GGCTGGAGTGAT CAC CACTCCAGCCT GGGC
GTGGCCAC GTG GTGAGGTCGGA CCCG
TA GTGCA A

GAM281 278 LOC1465 1 3374 XP_097013.1 3 40 TGGGAGGTCCCA -- TC - A 3 B c c
13 GGCTGTGTGCAC CACT GCAC CAGCCTGGG C
AGTGACAG GTGA CGTG GTCGGACCC G
CA T- T G

GAM281 278 LOC1466 1 7382 XP_085514.2 5 1114 CTCTGTCGCCCA A 3 B b b
03 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC1467 1 5954 XP_097085.5 3 1653 TTTCAGTGCCCA - AC CAG 3 B c
c

56 GGAAGAAGGCAG CA CTGC TC CCTGGGCA
CTGGGACA GT GACG AG GGACCCGT
C GA AA-

GAM281 278 LOC1467 1 13448 XP_085588.1 5 890 TCTTGTTGCCCA 3 B b b

84 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGTACA GTGGCGTGAGGTCGGACCCGTT

GAM281 278 LOC1468 1 1745 XP_097107.1 3 677 CTCTGTTGCCCA 3 B b b
39 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1468 1 8315 NP_660316.1 3 1177 TGCTGCTGCCCA 3 B b b
94 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCACG GTGACGTGAGGTCGGACCCGT

GAM281 278 LOC1468 1 8232 XP_097120.1 5 550 CTCTGTCACCCA CA 3 B b b
95 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC1469 1 6392 XP_097121.1 3 1204 TGTCAAAAATCA GCA 3 B c c
01 GGCTGGAGTGCA CACTGCACTCCAGCCTGG
GTGGCATG GTGACGTGAGGTCGGACT
AAA
GAM281 278 LOC1469 2 9492 XP_085634.2 3 662 CTCTGTCGCCCA A 3 B b b
09 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC1469 2 19550 XP_085634.2 3 995 CTCTGTCGCCCA A 3 B b b
09 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGGC GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC1470 1 16699 XP_054031.5 5 604 TCTTGTTGCCCA C C 3 B b b
71 GGCTGAAGTGCA CA TGCACT CAGCCTGGGCAA
ATGTTGTG GT ACGTGA GTCGGACCCGTT
A A
GAM281 278 LOC1470 1 12558 XP_097182.1 5 18 CTCTGTCCGCCA --- 3 B b b
80 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GCC
GAM281 278 LOC1471 1 10618 XP_085722.2 3 252 CACTGTTGCCCA 3 B b b
66 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1473 1 19915 XP_097230.2 3 1189 TTGATCTGCCCA C CT AG- 3 B c
c
81 GGAAAGGGATGC CA TGCA CC CCTGGGCA
ATTGACAC GT ACGT GG GGACCCGT
T AG AAA
GAM281 278 LOC1474 1 12065 XP_084000.1 3 143 CTCTGTCGCCCA A 3 B b b
07 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC1476 1 16101 XP_097255.1 3 529 CTCTGTCCCCTA C CA 3 B c c
22 GGCTGCAGTGCA CACTGCACT CAGCCTGGG

GTGGCGCG GTGACGTGA GTCGGATCC
C CC
GAM281 278 LOC1478 2 1634 XP_085903.1 3 281 CTCTGTCACCCA G C CA 3 B c b
17 GGCTGTAGTGGA CACT CACT CAGCCTGGG
GTGGTGTG GTGA GTGA GTCGGACCC
G T AC
GAM281 278 LOC1478 2 19233 XP_085903.1 3 445 CTCTGTCGCCCA C A 3 B b b
17 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCGCG GT ACGTGAGGTCGGACCCG
A C
GAM281 278 LOC1478 2 8642 XP_085924.2 3 146 TCTTGTTGTCCA C C 3 B b b
41 GTCTGGAGTGCA CA TGCACTCCAG CTGGGCAA
ATGGCACA GT ACGTGAGGTC GACCTGTT
A T
GAM281 278 LOC1478 2 12065 XP_085924.2 3 458 CTCTGTCGCCCA A 3 B b b
41 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC1479 1 17952 XP_085974.1 3 579 CTCTGTCACCCA CA 3 B b b
47 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC1481 2 5784 NP_653293.1 3 2524 CCTTGTTGCCCA C C C 3 B c c
37 GGCTGTAGTACA CA TG ACT CAGCCTGGGCAA
ATGGCATG GT AC TGA GTCGGACCCGTT
A A T
GAM281 278 LOC1481 2 17935 NP_653293.1 3 2097 CTCTGTCACCCA --- CA 3 B c c
37 GGCTGGAGTGCC CACT GCACTCCAGCCTGGG
ATAGTGTG GTGA CGTGAGGTCGGACCC
TAC AC
GAM281 278 LOC1481 1 12666 XP_086087.1 5 625 GCTCTGTCACCA T C-- -- 3 B c c
89 GGCTGTACAGTG CAC GCACT CAGCCTGG GCA
CCGTGGCC GTG CGTGA GTCGGACC TGT
C CAT AC
GAM281 278 LOC1481 1 11563 XP_047554.4 3 983 GTCGCCCACCCA C CA 3 B c c
98 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC
GAM281 278 LOC1487 1 15671 XP_086286.4 3 1372 CTCTGTCGCCCA A 3 B b b
08 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC1487 1 9201 XP_086281.1 5 143 CTCTGGTACTCA CA 3 B c c
09 GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGTGTG GTGGCGTGAGGTCGGACTC
AT
GAM281 278 LOC1491 1 2184 XP_097598.1 5 3317 TCTTGTTGCCCA C 3 B b b

```
          49                    AGCTGGAGTGCA CACTGCACTCCAGC TGGGCAA
                                GTGGCGCG    GTGACGTGAGGTCG ACCCGTT
                                          A
GAM281    278   LOC1493 1  13354 NP_787072.1  3 371   CCCCGTCGCACA          G A      3 B b b
          71                    GGCTGGAGTGCA CACTGCACTCCAGCCTG GC
                                GTGGCAAA    GTGACGTGAGGTCGGAC CG
                                          A C
GAM281    278   LOC1494 1  16260 XP_086546.1  3 564   CTCTGTTGCCCA C              3 B b b
          66                    GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
                                ATGGCACA    GT ACGTGAGGTCGGACCCGTT
                                          A
GAM281    278   LOC1494 1  5016  XP_086536.1  3 76    CTCTGTCGTCGA          G A      3 B c c
          78                    GGCTGGAGTGTA CACTGCACTCCAGCCT GGC
                                GTGGTGCG    GTGATGTGAGGTCGGA CTG
                                          G C
GAM281    278   LOC1495 2  1489  XP_097661.1  3 3101  TCTTGTCGGCCA       C    GCA      3 B c
b
          06                    GGCTAGAGTGCA CACTGCACTC AGCCTGG
                                GTGGCGCT    GTGACGTGAG TCGGACC
                                          A     GGC
GAM281    278   LOC1495 2  2139  XP_097661.1  3 1639  CGCTGTTGCCCA       C          3 B b b
          06                    GGCTGTAGTGCA CACTGCACT CAGCCTGGGCAA
                                GTGGTGCG    GTGACGTGA GTCGGACCCGTT
                                          T
GAM281    278   LOC1496 1  11025 XP_097706.1  3 613   CTCTGTCACCCA          CA       3 B b b
          92                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
                                GTGGCGCC    GTGACGTGAGGTCGGACCC
                                          AC
GAM281    278   LOC1497 1  10508 XP_097719.1  5 453   TTCTGCTGCCCA    -     C          3 B b b
          03                    AGCTGGAGTGGC CACTGC ACTCCAGC TGGGCA
                                AGTGGCAT    GTGACG TGAGGTCG ACCCGT
                                          G     A
GAM281    278   LOC1500 1  5157  XP_097797.1  5 593   CTCTGTCGCCCA           A       3 B b b
          54                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
                                GTGGTGCC    GTGACGTGAGGTCGGACCCG
                                          C
GAM281    278   LOC1501 1  8279  XP_097820.1  5 433   AAGCTGTGCCCA  TGC-   AG--       3 B c
c
          50                    GGAAGGGGAGTA CAC   ACTCC   CCTGGGCA
                                ACTGTGCA    GTG   TGAGG   GGACCCGT
                                          TCAA    GGAA
GAM281    278   LOC1501 1  13000 XP_097823.1  3 78    AAAGACAAGGCC      -  CCT   A      3 B c c

          57                    CCTGGCAGTGCA CACTGCACT CCAG   GGGC
                                GTGTTGGA    GTGACGTGA GGTC   CCCG
                                          C   ---   G
GAM281    278   LOC1501 1  19856 XP_097824.1  5 477   TCTCTGTCACCA    CACTC     --       3 B c
c
          66                    GGCTGTATTACA CACTG    CAGCCTGG  GCA
                                GTGGTGCA    GTGAC    GTCGGACC  TGT
```

ATTAT AC

GAM281 278 LOC1502 2 4400 XP_097870.1 3 3097 AGAATTGCTTTG T T-- 3 B c b
25 TGGCTGGGTGCA CACTGCAC CCAGCC GGGCAA
GTGGTTCA GTGACGTG GGTCGG TTCGTT
- TGT

GAM281 278 LOC1502 2 7207 XP_097870.1 3 1704 CTCTGTCGCTCA A 3 B b b
25 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACTCG
C

GAM281 278 LOC1503 1 9922 XP_086884.2 5 21 GCTGCGCCTCCA C---- AC- ---- 3 B c c
56 GGCTGGACCAGC ACTGC TCCAGCCTGG GCA
AGTTCCAG TGACG AGGTCGGACC CGT
GACCT ACC TCCG

GAM281 278 LOC1503 1 826 XP_086905.1 3 8 CCTCAGGGCCCA TG CA A 3 B c c
83 GGCCTGAGTGGT CAC CACTC GCCTGGGC
GCTGCTCA GTG GTGAG CGGACCCG
-- TC G

GAM281 278 LOC1503 1 7485 XP_097894.1 5 386 ATGGAGCCTGCC - AG T 3 B c c
84 TTGGGGAGTGCA CAC TGCACTCC CC GGGCA
TGTGTTGG GTG ACGTGAGG GG TCCGT
T -- T

GAM281 278 LOC1504 1 5756 XP_086906.1 3 531 CTCTGTTGTCCA C 3 B b b
07 GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGTGTG GTGACGTGAG TCGGACCTGTT
A

GAM281 278 LOC1505 1 16940 XP_097917.1 5 1616 CTCTGTTGCCCA 3 B b b
87 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1508 1 18257 XP_097954.1 5 680 CTGTGCCTGCTC C----- CT 3 B c c
19 CTTATGAGTGCA CACTGCACTC AGC GGGCA
GTGGAAGG GTGACGTGAG TCG TCCGT
TATTCC --

GAM281 278 LOC1510 1 12075 XP_097998.1 3 1067 CTCTGTCACCCA CA 3 B b b
57 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC1511 1 19774 XP_098019.1 3 458 AAATGTACACCA T --- 3 B b b
96 GGCTGGGTGCGG CACTGCAC CCAGCCTGG GCA
TGGCTCAC GTGGCGTG GGTCGGACC TGT
- ACA

GAM281 278 LOC1512 2 2572 XP_098021.1 3 1785 TTCTGTCACCCA C C CA 3 B c
b
01 GGCTGGAGTCCA CA TG ACTCCAGCCTGGG
ATGGGGCG GT AC TGAGGTCGGACCC
A C AC

GAM281 278 LOC1512 2 12725 XP_098021.1 3 367 ACGCTGTCACCA -- 3 B b b
01 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA

GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC
GAM281 278 LOC1514 2 4174 XP_098063.1 5 739 CTCTGTCATCCA CA 3 B c b
75 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCT
AC
GAM281 278 LOC1514 2 4371 XP_098063.1 5 100 CTCTGTGGCCCA A 3 B b b
75 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGATGTGAGGTCGGACCCG
G
GAM281 278 LOC1516 3 2693 NP_612144.1 3 222 CTCTGTCGCTCG C A 3 B c b
36 CGCTGGAGTGCA CACTGCACTCCAGC TGGGC
GTGGCATG GTGACGTGAGGTCG GCTCG
C C
GAM281 278 LOC1516 3 4151 NP_612144.1 3 2151 CTGTGTCCCCCA CA 3 B b b
36 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
CC
GAM281 278 LOC1516 3 14731 NP_612144.1 3 891 CTCTGTCACCCA C CA 3 B c b

36 GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGTGTG GTGACGT AGGTCGGACCC
A AC
GAM281 278 LOC1516 1 3130 XP_098103.1 5 180 TCTCACTATGTT T CCTG 3 B c c

58 GTCTGGAGTGCT CAC GCACTCCAG GGCA
GTGGTGGA GTG CGTGAGGTC TTGT
T TG--
GAM281 278 LOC1518 2 4677 XP_098132.1 3 897 CTGTGTTGCCCA CT C C----- 3 B c
c
77 GGCTAATATCGA CA GCA TC AGCCTGGGCAA
ATGCTTGG GT CGT AG TCGGACCCGTT
T- A CTATAA
GAM281 278 LOC1518 2 17499 XP_098132.1 3 732 GTTTACCTCCCA C C CA 3 B c c

77 AGCTGGAGTCCA CACTG ACTCCAGC TGGG
GTGGTGAG GTGAC TGAGGTCG ACCC
C A TC
GAM281 278 LOC1518 1 15127 XP_087329.1 5 958 CTCTATGGCCCA A A A 3 B c c
78 GGCTGGAGCGCA C CTGC CTCCAGCCTGGGC
GCGGT G GACG GAGGTCGGACCCG
C C G
GAM281 278 LOC1522 2 3559 XP_098182.1 3 1274 GTCGCCCAGGCT ---- A 3 B b b
45 GGAGTGAGTGCA CACTGCAC TCCAGCCTGGGC
GTGGCGCA GTGACGTG AGGTCGGACCCG
AGTG C
GAM281 278 LOC1522 2 9470 XP_098182.1 3 1274 CTCTGTCGCCCA ---- A 3 B b b
45 GGCTGGAGTGAG CACTGCAC TCCAGCCTGGGC
TGCAGTGG GTGACGTG AGGTCGGACCCG
AGTG C

GAM281 278 LOC1524 2 2922 XP_098231.1 3 524 ATCTGTTGCCCA 3 B b b
45 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGAGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1524 2 6147 XP_098231.1 3 201 CCCTGTCTCCGA CAC --- 3 B c b
45 GGCTGGAATACG CACTG TCCAGCCT GGGCA
GTGGTGCG GTGGC AGGTCGGA TCTGT
ATA GCC
GAM281 278 LOC1526 1 1745 XP_011108.2 3 709 CTCTGTTGCCCA 3 B b b
20 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1527 2 11919 XP_098257.1 5 116 CTCTGTCGCCCA C A 3 B b b
19 GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGCGTG GTGACGT AGGTCGGACCCG
A C
GAM281 278 LOC1527 2 17637 XP_098257.1 5 423 CTCTGTCGCCCA C A 3 B b b
19 GCCTGGAGTGCA CACTGCACTCCAG CTGGGC
GTGGCACC GTGACGTGAGGTC GACCCG
C C
GAM281 278 LOC1527 1 18605 XP_087519.1 5 896 GGCCCAGTGCCA GCAC G 3 B c
c
65 GGCTGGGCCCAA CACT TCCAGCCTGG CA
GTGTCGAT GTGA GGGTCGGACC GT
ACCC -
GAM281 278 LOC1527 1 2010 XP_087525.1 5 422 GTCTGTTACCCA CA 3 B b b
94 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT
GAM281 278 LOC1528 1 9568 XP_098266.2 3 1700 TTTCTCGCACAG - G A 3 B c c
04 GCTTGGAGTGCA CACTGCACTCCA GCCTG GC
GTGGTGCG GTGACGTGAGGT CGGAC CG
T A C
GAM281 278 LOC1530 1 1646 XP_041221.1 3 428 GGAGCTGCCCCA - CC - 3 B b b
27 GGCTTTAGTGCA CA CTGCACT AGCCTGGG CA
GCTGCCAA GT GACGTGA TCGGACCC GT
C TT C
GAM281 278 LOC1530 1 5304 XP_098307.1 3 805 TGATATCACCCA CA 3 B b b
77 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC1538 4 9170 XP_087779.2 3 1086 CTCTGTCGCCCA C----- C A 3 B c
b
11 GACTGGAGTGCA ACTGCACTCCAG CTGGGC
GTAGCGCC TGACGTGAGGTC GACCCG
CCGCGA A C
GAM281 278 LOC1538 4 9683 XP_087779.2 3 42 CTCTGTCACCCA A CA 3 B c b
11 GGCAGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
A AC

GAM281 278 LOC1538 4 17512 XP_087779.2 3 1384 CTCTGTTGCCCA C 3 B b b
11 GACTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGTGTA GTGACGTGAGGTC GACCCGTT
A
GAM281 278 LOC1538 4 19665 XP_087779.2 3 962 ACCTGGTGCCCA - G 3 B b b
11 GGTGGAGGTGCA CACTGCAC TCCA CCTGGGCA
GTGGGGGT GTGACGTG AGGT GGACCCGT
G -
GAM281 278 LOC1538 1 15929 XP_087798.1 5 128 TTCTTTTGCCCA 3 B b b
83 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1539 1 2882 XP_087801.1 5 188 CTCTGTAGCCCA C A 3 B b b
10 GTCTGGAGTGCA CACTGCACTCCAG CTGGGC
GTGGTACA GTGACGTGAGGTC GACCCG
T A
GAM281 278 LOC1542 1 4307 XP_098505.1 5 117 GCTCTGTCGCCA -- 3 B b b
82 GGTTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTTGGACC TGT
GC
GAM281 278 LOC1548 1 19205 XP_098618.3 5 2827 CTTTGTCAGCCA -- --- 3 B b b
22 GGCTGGAGTGCA CAC TGCACTCCAGCCTGG GCAA
ATGTGCAA GTG ACGTGAGGTCGGACC TGTT
TA GAC
GAM281 278 LOC1548 4 3200 XP_098626.1 5 110 CTCTGTTGCCCA C 3 B b b
77 GTCTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCGCA GTGACGTGAGGTC GACCCGTT
T
GAM281 278 LOC1548 4 12700 XP_098626.1 3 983 TTCTGTCTCGCA CA --- 3 B c b
77 GGCCAGAGTGCA CACTGCACTC GCCTG GGCA
GTGGTGTG GTGACGTGAG CGGAC CTGT
AC GCT
GAM281 278 LOC1548 4 16089 XP_098626.1 3 1270 CTCTGTCGCCCA G A 3 B b b

77 GGGTGGAGTGCA CACTGCACTCCA CCTGGGC
GTGGCGTG GTGACGTGAGGT GGACCCG
G C
GAM281 278 LOC1548 4 17731 XP_098626.1 3 3542 CCTCTGTTGCCA T C G 3 B c b

77 GGCTGGAATGCC CAC GCA TCCAGCCTGG CAA
GTGGCGCA GTG CGT AGGTCGGACC GTT
C A -
GAM281 278 LOC1550 1 17980 XP_088142.4 3 57 TGCTCCGGCCCA C A-- A 3 B c c
66 GGCGGGGGAGTC CACTG ACTCC GCCTGGGC
AGTGCCCA GTGAC TGAGG CGGACCCG
- GGG G
GAM281 278 LOC1579 1 9709 XP_098845.1 3 1816 AGGAATTGCCCA C-- G T ----- 3 B c
c
31 GCAGACGTTGGG ACT CAC CCAGC CTGGGCAA
TGAGTCTG TGA GTG GGTTG GACCCGTT

GTC - - CAGAC

GAM281 278 LOC1580 1 2542 XP_088442.1 5 3580 TCTTGTCACCCA CA 3 B c c
14 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGATGTGAGGTCGGACCC
AC

GAM281 278 LOC1582 1 5779 XP_098903.4 3 1267 CTCTTTCGCCCA C A A 3 B c c
28 GGCCGGACTGCA CACTGCA TCC GCCTGGGC
GTGGCAGG GTGACGT AGG CGGACCCG
C C C

GAM281 278 LOC1583 1 14859 XP_098919.1 5 371 CTCTGTCGCCCA A 3 B b b
10 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC1584 1 17964 XP_098936.1 5 140 CTCTGTTGCCCA 3 B b b
02 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1584 1 1263 XP_098942.1 3 643 CTCTGTCACTCA CA 3 B c c
36 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACTC
AC

GAM281 278 LOC1584 2 935 XP_098955.1 3 893 CTCTGTCGCCCA A 3 B b b
76 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC1584 2 17016 XP_098955.1 3 1219 CTCTGTTGCCCC C CT 3 B c b

76 AGCTTGAGTGCA CACTGCACTC AGC GGGCAA
GTGGCGTG GTGACGTGAG TCG CCCGTT
T AC

GAM281 278 LOC1585 1 3426 XP_088606.1 5 1037 GCTCTATCACCA A GCA 3 B c
c
63 GGTGGGAGTGCA CACTGCACTCC GCCTGG
GTGGCACA GTGACGTGAGG TGGACC
G ACT

GAM281 278 LOC1585 1 12003 XP_088608.1 3 908 GGACTCTGCCCA CT TCCA 3 B c
c
72 GGCCAGCGTGTT CA GCAC GCCTGGGCA
CTGAAAAT GT TGTG CGGACCCGT
CT CGAC

GAM281 278 LOC1586 1 16260 XP_045161.1 3 426 CTCTGTTGCCCA C 3 B b b
68 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACA GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC1608 1 17208 XP_090573.3 5 537 CTCCGTAGCCCA A 3 B b b
97 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
A

GAM281 278 LOC1612 1 16016 XP_090783.3 5 71 ATGTGTAGGGTT ---- GG 3 B c c
47 GGGGAGAGTGCA CACTGCACT CCAGCCT GCA

GTGATGGG GTGACGTGA GGTTGGG TGT
GAGG A-
GAM281 278 LOC1624 2 8231 NP_835227.1 3 823 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1624 2 8231 XP_091549.3 3 817 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1624 2 12068 NP_835227.1 3 488 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1624 2 12068 XP_091549.3 3 488 CTCTGTTGCCCA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC1629 2 3249 XP_091886.7 3 255 TCTCTGTCGCCA C -- 3 B b b
62 GGCTGGAATGCA CACTGCA TCCAGCCTGG GCA
GTGCAGTG GTGACGT AGGTCGGACC TGT
A GC
GAM281 278 LOC1629 2 13131 XP_091886.7 3 256 GTCGCCAGGCTG ----- GCA 3 B c
b
62 GAATGCAGTGCA CACTGCAC TCCAGCCTGG
GTGAGCCA GTGACGTG AGGTCGGACC
ACGTA GCT
GAM281 278 LOC1629 1 13831 XP_091890.6 3 380 CTCTGTCGCCCA C A 3 B c c
67 CGTTGGAGTGCA CACTGCACTCCAGC TGGGC
GTGATGTG GTGACGTGAGGTTG ACCCG
C C
GAM281 278 LOC1632 2 9147 NP_775802.1 3 1668 CTCTGTCACCCA CA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC1632 2 11854 NP_775802.1 3 3358 TCTTGTTGCCCA C 3 B b b
27 AGCTGGAGTGCA CACTGCACTCCAGC TGGGCAA
GTGGTGCA GTGACGTGAGGTCG ACCCGTT
A
GAM281 278 LOC1640 1 7989 XP_089356.1 3 827 TCTTGTTGGCTA C--- G 3 B c c
91 GGCTGGAGTAAA CACTG ACTCCAGCCTGG CAA
ATGGTGCG GTGGT TGAGGTCGGATC GTT
AAAA G
GAM281 278 LOC1680 1 3971 XP_094794.2 3 11 GGTCATGACCAT T - - G 3 B c c
02 GGTGTGGGTGCA CACTGCAC CCA GCC TGG CA
GTGACTGC GTGACGTG GGT TGG ACC GT
- G T A
GAM281 278 LOC1684 1 19786 XP_095114.2 3 696 CTCTGTAACCCA CA 3 B b b
51 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCCTG GTGACGTGAGGTCGGACCC

AA

GAM281 278 LOC1704 1 15561 XP_096330.1 5 66 CAGCCTCATAAG T ----- A 3 B c c
09 GGCTGGAGTGCT CAC GCACTCCAGCCT GGGC
GTGGTGCC GTG CGTGAGGTCGGG TCCG
T AATAC A

GAM281 278 LOC1962 1 2452 XP_113683.1 3 810 ACTCTGTCGCCA -- 3 B b b
64 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGTG GTGACGTGAGGTCGGACC TGT
GC

GAM281 278 LOC1973 2 4625 XP_113872.2 3 1712 TCTTGTCGCCCA A 3 B b b
58 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC1973 2 6387 XP_113872.2 3 2114 ATCTGTCACCCA CA 3 B b b
58 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC1997 1 10884 XP_117119.1 5 143 CTCTGTCACCTA C C CA 3 B c c

25 GGCTGGATTGCA CA TGCA TCCAGCCTGGG
ATGGTGCA GT ACGT AGGTCGGATCC
A T AC

GAM281 278 LOC1998 2 5253 XP_117153.1 5 184 CTCTGTGTCTCA C - 3 B b b
99 GGCTGGAGTACA CACTG ACTCCAGCCTG GGCA
GTGGTGCA GTGAC TGAGGTCGGAC CTGT
A T

GAM281 278 LOC1998 2 8292 XP_117153.1 3 67 CTTTGTCGCCCA C A 3 B b b
99 GGCTGGAGTACA CACTG ACTCCAGCCTGGGC
GTGGTGCG GTGAC TGAGGTCGGACCCG
A C

GAM281 278 LOC1999 1 19756 XP_114052.1 3 1225 CTGTGTTGTCCA 3 B b b
06 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCTGTT

GAM281 278 LOC2001 2 5066 XP_211599.1 3 1 CTGTCGTCCAGG C------- A 3 B c c
69 CTGGAGTGCAGT ACTGCACTCCAGCCTGGGC
ACGCAATC TGACGTGAGGTCGGACCTG
CTAACGCA C

GAM281 278 LOC2001 2 6122 XP_117200.1 5 523 TTCTGTCGTCCA C----- A 3 B c c
69 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGC
GTAGCGCA TGACGTGAGGTCGGACCTG
ACGCGA C

GAM281 278 LOC2008 2 4175 XP_117289.1 3 649 TCTTGTTGTCCA C 3 B b b
60 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCA GT ACGTGAGGTCGGACCTGTT
A

GAM281 278 LOC2008 2 12075 XP_117289.1 3 1713 CTCTGTCACCCA CA 3 B b b
60 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2008 2 11863 NP_789785.1 3 935 TCTTGTTGCCCA A 3 B b b
95 GGCGGAGTGCAG CACTGCACTCC GCCTGGGCAA
TGGAACAA GTGACGTGAGG CGGACCCGTT
-
GAM281 278 LOC2008 2 17681 NP_789785.1 3 935 CTCTTGTTGCCC A 3 B b b
95 AGGCGGAGTGCA CACTGCACTCC GCCTGGGCAA
GTGGAACA GTGACGTGAGG CGGACCCGTT
-
GAM281 278 LOC2009 1 3465 XP_114317.3 3 322 TTCTGTCACCCA CA 3 B b b
16 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGACTCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2011 2 13384 XP_290750.1 3 824 CTCTGTGGCCCA A 3 B b b
64 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
G
GAM281 278 LOC2011 2 16993 NP_849158.1 3 824 CTCTGTGGCCCA A 3 B b b
64 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
G
GAM281 278 LOC2012 1 4556 NP_775818.1 3 677 CTCTGTCACTCA C CA 3 B c c
92 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCACA GTGAC TGAGGTCGGACTC
A AC
GAM281 278 LOC2015 1 15044 XP_114343.2 3 1575 CTCTGTTGCCCA 3 B b b
62 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2017 1 5492 XP_114370.1 3 1955 CTCTATTGCTCA TG 3 B b b
25 GGCTGGAGTGTG CAC CACTCCAGCCTGGGCAA
GTGGCAGG GTG GTGAGGTCGGACTCGTT
GT
GAM281 278 LOC2024 1 9145 XP_117397.1 5 32 CTCTGTCGCCCA A 3 B b b
00 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2024 1 18628 XP_114481.4 3 52 CTCTGTTGCCCA 3 B b b
04 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2024 2 11010 XP_114493.1 5 197 CTACACCGCCCA GC CA A 3 B c
b
60 GGCCAGAGTAGG CACT ACTC GCCTGGGC
GTGGAGCT GTGG TGAG CGGACCCG
GA AC C
GAM281 278 LOC2024 2 16450 XP_114493.1 5 2041 GCTCTGTCACCA -- 3 B b b
60 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGAGGC GTGACGTGAGGTCGGACC TGT
AC
GAM281 278 LOC2029 2 1729 XP_117486.2 3 1523 CTCTGTCACCCA C CA 3 B c b

34 GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM281 278 LOC2029 2 4820 XP_117486.2 3 2743 GCTCTGTCACCA -- 3 B b b
34 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTCGGACC TGT
AC
GAM281 278 LOC2035 2 2351 XP_114719.1 3 2894 CCTTCTTGCCCA CAC----- 3 B c b

47 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
AGGGCGCA ACGTGAGGTCGGACCCGTT
ACGCGGGA
GAM281 278 LOC2035 2 9545 XP_114719.1 3 1379 CTCTGTTGCCCA 3 B b b
47 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2042 1 10724 XP_115295.1 3 931 CTCTGTCTCCCA CT CA 3 B c c

88 GGCTGGAGTGTG CA GCACTCCAGCCTGGG
ATGGCGTG GT TGTGAGGTCGGACCC
AG TC
GAM281 278 LOC2192 1 19361 XP_166599.2 3 1203 CTTGCTCGCCCA G A 3 B b b

93 GGGTGGAGTGCA CACTGCACTCCA CCTGGGC
GTGGTGTG GTGACGTGAGGT GGACCCG
G C
GAM281 278 LOC2197 1 2410 XP_167570.1 5 94 AGGAGTGCTGAG G G- 3 B c c
00 GGCTGGAGTGGG CACT CACTCCAGCCT GGCA
TGGGCCCT GTGG GTGAGGTCGGG TCGT
- AG
GAM281 278 LOC2197 1 4678 XP_167596.1 5 1058 CTCTGTCATCCA CA 3 B c c
31 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCAAA GTGACGTGAGGTCGGACCT
AC
GAM281 278 LOC2197 1 18913 XP_167601.1 3 868 CTCTGTTGCCCA C----- 3 B b b
35 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGCAA
GTCGCACA TGACGTGAGGTCGGACCCGTT
ACACGC
GAM281 278 LOC2198 1 14588 XP_167782.1 3 1073 TCTGTTGCCCCA - 3 B b b
94 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG CAA
GTGGCGTG GTGACGTGAGGTCGGACCC GTT
C
GAM281 278 LOC2200 3 6497 NP_660352.1 3 213 CTCTGTCACACA --- 3 B b b
74 GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGCACG GTGACGTGAGGTCGGAC CTGT
ACA
GAM281 278 LOC2200 3 9147 NP_660352.1 3 543 CTCTGTCACCCA CA 3 B b b
74 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2200 3 16838 NP_660352.1 3 383 ACTCGTCACCCC C CA 3 B c b
74 AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGTGCG GTGACGTGAGGTCG ACCC
- CA
GAM281 278 LOC2216 1 1939 XP_168131.1 5 811 CTCTGTTGCCAA G 3 B b b
63 GGCTGGAGTGCA CACTGCACTCCAGCCT GGCAA
GTGGAACG GTGACGTGAGGTCGGA CCGTT
A
GAM281 278 LOC2218 1 3555 XP_166513.1 3 834 GGCTCGCCTCTC T A T--- A 3 B c c
89 TGGCCGGGTGCA CACTGCAC CC GCC GGGC
GTGAACGG GTGACGTG GG CGG TCCG
- C TCTC C
GAM281 278 LOC2219 1 15948 XP_168340.1 3 921 GAGAATCGCTTG CT A 3 B c c
46 AGCTGGAGTGCA CACTGCACTCCAGC GGGC
GTGGTGCA GTGACGTGAGGTCG TTCG
AG C
GAM281 278 LOC2219 1 14860 XP_165859.1 3 376 CTCCGTGACCCA C C - 3 B b b
60 GGCTGGAATGCA CA TGCA TCCAGCCTGGG CA
ATGGCTCA GT ACGT AGGTCGGACCC GT
A A A
GAM281 278 LOC2219 1 17029 XP_168342.1 3 57 CTCTGTCTCCCA C CA 3 B c c
64 GGCTGGACTGCA CACTGCA TCCAGCCTGGG
GTGGTGCG GTGACGT AGGTCGGACCC
C TC
GAM281 278 LOC2220 1 7700 XP_168371.1 5 63 CTGGCCCTTCAA CAC ---- A 3 B c c
31 GGCTGGAAGCCA CACTG TCCAGCCT GGGC
GTGTCCTA GTGAC AGGTCGGA CCCG
CGA ACTT G
GAM281 278 LOC2220 1 12803 XP_166594.2 5 744 TCTGTTGTCCAA C----- - 3 B c c
57 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM281 278 LOC2220 1 3232 XP_166556.1 3 655 TCTTGTCGCCCA C A 3 B b b
68 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCGTG GT ACGTGAGGTCGGACCCG
A C
GAM281 278 LOC2221 1 16228 XP_212100.1 5 76 CGCAGGCTGCCA C T G 3 B c c
59 GGCTGGCGTACA CACTG AC CCAGCCTGG CA
GTGGCGCA GTGAC TG GGTCGGACC GT
A C -
GAM281 278 LOC2536 1 5487 XP_172985.2 5 301 CTCTGTCTCCCA CA 3 B c c
12 GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGCACA GTGGCGTGAGGTCGGACCC
TC
GAM281 278 LOC2538 1 4532 XP_172854.1 3 1254 CTCTGTTGCCCA 3 B b b
05 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGATGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2539 1 3617 XP_172953.2 5 328 GGCCCATGCCCA CA --- AG--- 3 B c c
92 GGATGAGGGACA CTGCAC TCC CCTGGGCA
GGTGCAGC GACGTG AGG GGACCCGT
C- GAC GAGTA
GAM281 278 LOC2548 2 6188 XP_171170.1 3 281 TGGAGAAATTCA T CA 3 B c c
75 GGCTGGGTGCAG CACTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA
GAM281 278 LOC2548 2 14560 XP_171170.1 3 281 ATGGAGAAATTC T CA 3 B c c
75 AGGCTGGGTGCA CACTGCAC CCAGCCTGGG
GTGGCTCA GTGACGTG GGTCGGACTT
- AA
GAM281 278 LOC2550 2 3261 XP_173187.1 3 221 GCACGGGGCCCA C A 3 B b b
31 GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCGTG GTGACGTGAG TCGGACCCG
A G
GAM281 278 LOC2550 2 13629 XP_173187.1 5 311 AGGCTTTGCAAA - - CCTGG 3 B c b
31 CTGTGAAGTGCA CACTGCACT C CAG GCAA
GTGCCTAC GTGACGTGA G GTC CGTT
A T AAA--
GAM281 278 LOC2551 1 6294 XP_172941.1 3 613 TCTCGTTGCCCA C 3 B b b
77 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC2554 1 6365 XP_173150.1 5 386 CAAAGCCCTTCA C --- A 3 B c c
58 GGCTGGAGTATA CACTG ACTCCAGCCT GGGC
GTGGCATG GTGAT TGAGGTCGGA CCCG
A CTT A
GAM281 278 LOC2554 1 3150 XP_172581.2 3 2634 CTTTGTCACCCA A CA 3 B c c
88 GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCATG GTGACGTGAGG CGGACCC
C AC
GAM281 278 LOC2557 1 2873 XP_170898.2 5 409 GCAGCAAGCCCA ACTCCA A 3 B c c
36 GGCGGCGGTGGA CACTGC GCCTGGGC
AAGGCTGG GTGGCG CGGACCCG
G----- A
GAM281 278 LOC2559 1 12803 XP_171083.2 5 864 TCTGTTGTCCAA C----- - 3 B c c
75 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM281 278 LOC2566 1 7385 XP_172864.1 3 861 CTCTGTCACCCA CA 3 B b b
14 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2829 1 986 XP_212606.1 5 165 CTCTGTCGCCAA CTG A 3 B c c

05 AGTTGGAGTGCA CACTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C

GAM281 278 LOC2829 1 986 XP_212647.1 5 165 CTCTGTCGCCAA CTG A 3 B c c
43 AGTTGGAGTGCA CACTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C

GAM281 278 LOC2829 2 814 XP_210834.1 3 1912 ATGGCCATGCTG T - TG G 3 B c c

63 GGCTGGAGTGGC CAC GC ACTCCAGCC G CA
TGTGGGGT GTG CG TGAGGTCGG C GT
T G GT -

GAM281 278 LOC2829 2 2675 XP_210834.1 3 471 TATGAACCCATT C -- CA 3 B c c
63 GGTTAGAGTGCA CACTGCACTC AGCC TGGG
GTGGCTTC GTGACGTGAG TTGG ACCC
A TT AA

GAM281 278 LOC2829 1 18172 XP_210837.1 3 862 CTCTGTCTCCTA A CA 3 B c c
72 GGCTGGAGCGCA CACTGC CTCCAGCCTGGG
GTGGTGCA GTGACG GAGGTCGGATCC
C TC

GAM281 278 LOC2829 2 12068 XP_210845.1 3 528 CTCTGTTGCCCA 3 B b b
87 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2829 2 16541 XP_210845.1 5 34 CTTTGTCACCCA C CA 3 B c b
87 GGCTGGAGTATA CACTG ACTCCAGCCTGGG
GTGGCACA GTGAT TGAGGTCGGACCC
A AC

GAM281 278 LOC2829 1 11798 XP_208473.1 3 987 CCCTGTTGCCCA A 3 B b b
97 GGCTGGAGAGCA CACTGC CTCCAGCCTGGGCAA
GTGGTGCA GTGACG GAGGTCGGACCCGTT
A

GAM281 278 LOC2830 1 6384 XP_210859.1 3 1821 GCCCAGGCTGAA ------- A 3 B c c
31 GTGTAGAGTGCA CACTGCACTC CAGCCTGGGC
GTGGCATG GTGACGTGAG GTCGGACCCG
ATGTGAA -

GAM281 278 LOC2830 1 1940 XP_208488.1 3 1671 CCCAGGTGATCT ---- ---- CA 3 B c c

35 GGTTACAGTGCA CACTGCACT CCAG CCTGGG
GTGCTGAC GTGACGTGA GGTC GGACCC
CATT TAGT --

GAM281 278 LOC2830 1 17587 XP_210870.1 3 415 CAGAGTAGTTCA A -- A 3 B c c
47 GGCTGGGTGGAG CACTGC CT CCAGCCTGGGC
CAGTGGGA GTGACG GG GGTCGGACTTG
A TG A

GAM281 278 LOC2830 1 7252 XP_210875.1 3 1388 GTTTGTCACCCA CA 3 B b b
61 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2830 1 4176 XP_208509.1 3 178 TTGTGTTCCCCA C CA 3 B c c

87 GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGCATG GTGACGTGA GTCGGACCC
A CT

GAM281 278 LOC2830 1 2219 XP_210885.1 5 1721 CTCTGTCGCCCA C A 3 B b b
89 GGCTCGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCATG GTGACGTGAG TCGGACCCG
C C

GAM281 278 LOC2831 1 16397 XP_210895.1 3 712 CTCTCTTGCCCA 3 B b b
19 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTATG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2831 1 5323 XP_208525.3 3 380 CTCTGTCACCCA C CA 3 B c c
30 GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCGTG GTGACGT AGGTCGGACCC
A AC

GAM281 278 LOC2831 1 12544 XP_210911.1 3 454 ACCCTGTTGCCA C G 3 B b b
40 GGCTGGAATGCA CACTGCA TCCAGCCTGG CAA
GTGGCGCG GTGACGT AGGTCGGACC GTT
A -

GAM281 278 LOC2831 1 2650 XP_210920.1 3 2296 ACTCTGTCACCA -- 3 B b b
43 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 LOC2831 1 19812 XP_210917.2 5 317 CTCTGTCATCCA CA 3 B c c
52 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCT
AC

GAM281 278 LOC2831 1 4979 XP_208535.1 3 649 CTCTGTTGCCCA 3 B b b
70 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGAG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2831 1 15574 XP_210903.1 3 985 TCTTGTTGCCCA C 3 B b b
77 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACA GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC2832 2 8144 XP_208555.2 3 1991 CTATGTCACCGA CC G CA 3 B c
c
15 GGCTACAGTGCA CACTGCACT AGCCT GG
GTGGTTCA GTGACGTGA TCGGA CC
CA G AC

GAM281 278 LOC2832 2 10112 XP_208555.2 3 1675 TACTGTTGTCCA C----- A 3 B c c
15 GGCTGGAGCGCA ACTGC CTCCAGCCTGGGCAA
GTTGATTG TGACG GAGGTCGGACCTGTT
GTTAGT C

GAM281 278 LOC2832 1 9525 NP_787089.1 5 63 CTCTGTCGCCCA A 3 B b b
41 GGTTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTTGGACCCG
C

GAM281 278 LOC2832 1 8223 XP_210952.1 5 555 CCTTGTTGCCCA CTG CT- 3 B c
c

62 GGCTGGTCTTGA CA CA CCAGCCTGGGCAA
ACTGGGCT GT GT GGTCGGACCCGTT
CAA TCT
GAM281 278 LOC2832 1 9036 XP_210961.1 3 2048 TCTTGTTGCCCA C 3 B b b
78 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC2832 1 17952 XP_210962.1 3 346 CTCTGTCACCCA CA 3 B b b
93 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2832 1 9585 XP_210965.1 5 438 CTCTGTCTCCGA C --- 3 B c c
99 GGCTGGAGTGCA CA TGCACTCCAGCCT GGGCA
ATGTTGCA GT ACGTGAGGTCGGA TCTGT
A GCC
GAM281 278 LOC2833 2 2201 XP_210978.1 5 938 CTCTGTCGCCCA C C A 3 B c c
29 GACTGGAGTGCA CA TGCACTCCAG CTGGGC
ATGGTGCG GT ACGTGAGGTC GACCCG
A A C
GAM281 278 LOC2833 2 12183 XP_210978.1 5 371 GTGCTGGCCCCT A----- T- A 3 B c
c
29 GGCTGGAGGGGA CACTGC CTCCAGCC GGGC
GGGCAGTG GTGACG GAGGTCGG CCCG
GGAGGG TC G
GAM281 278 LOC2833 2 2143 XP_210981.1 3 1369 CTCTGTTGCCCA 3 B b b
35 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM281 278 LOC2833 2 16144 XP_210981.1 3 1637 CTCTGTCACCCA A CA 3 B c b

35 GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGTGCG GTGACGTGAGG CGGACCC
C AC
GAM281 278 LOC2833 1 8232 XP_208647.1 3 808 CTCTGTCACCCA CA 3 B b b
77 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2833 1 7265 XP_211007.1 3 1634 CTCTTACGCCCA G C A 3 B c c
87 GGCTGGAATGAA CACT CA TCCAGCCTGGGC
GTGGCATG GTGA GT AGGTCGGACCCG
A A C
GAM281 278 LOC2833 1 1730 XP_211021.1 5 134 CTCTGTTGCCCA C 3 B b b
94 GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGCACA GTGAC TGAGGTCGGACCCGTT
A
GAM281 278 LOC2833 1 9003 XP_211020.1 3 528 ACTCTGTTGCTA G 3 B b b
95 GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGCACA GTGACGTGAGGTCGGATC GTT
-
GAM281 278 LOC2834 1 19206 XP_211024.1 5 444 CTCTGTCGCCAA C A G A 3 B c
c

00 GGCTGGAGGGCA CA TGC CTCCAGCCT GGC
ATGGCATG GT ACG GAGGTCGGA CCG
A G A C

GAM281 278 LOC2834 1 16658 XP_211032.1 5 1943 GCTGTATTGCCA C G 3 B b b
32 GACTGGAGTGCA CACTGCACTCCAG CTGG CAA
GTGGCGTG GTGACGTGAGGTC GACC GTT
A -

GAM281 278 LOC2834 1 16366 XP_211034.1 5 1756 TGCCATCTCAGT C -- ---- 3 B c c
34 TGCTGCAGTGCA CACTGCACT CAGC CTG GGCA
GTGAATTA GTGACGTGA GTCG GAC CCGT
C TT TCTA

GAM281 278 LOC2834 1 2220 XP_211043.1 3 165 CTCTGTCGCCCA C A 3 B c c
41 GGCTGCAGTGCG CACTGCACT CAGCCTGGGC
GTGGTGCG GTGGCGTGA GTCGGACCCG
C C

GAM281 278 LOC2834 1 10032 XP_211037.1 5 974 CACCTCTTGCCA C --- -- G 3 B c c
42 GGCTGCAGAGCT ACTGCA CTC CAGCCTGG CAA
ATGCAGTC TGACGT GAG GTCGGACC GTT
C ATC AC -

GAM281 278 LOC2834 1 5683 XP_211044.1 5 306 CTGTGTCATGCA --- 3 B b b
45 GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGCATG GTGACGTGAGGTCGGAC CTGT
GTA

GAM281 278 LOC2834 1 7397 XP_208679.1 5 490 GTCTGACACCTG TG CA 3 B c c

52 GGCTGGAGTGCA CACTGCACTCCAGCC GG
GTGGTGCA GTGACGTGAGGTCGG CC
GT AC

GAM281 278 LOC2834 1 14861 XP_211049.1 5 128 CTCTGTCACCCA CA 3 B b b
54 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2834 1 13967 XP_211050.1 3 1034 AAACCTTTGTCA A T G 3 B c c
67 GGCTGGGCGCGG CACTGC C CCAGCCTGG CAA
TGGCTCAC GTGGCG G GGTCGGACT GTT
C - -

GAM281 278 LOC2834 1 9892 XP_211056.1 3 1714 TTCTCTTGCCCA 3 B b b
75 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2834 1 17710 XP_211053.1 5 1048 CTCTGTCCCCTG C --- 3 B c c
84 GGCTGGAGTGCA CA TGCACTCCAGCCT GGGCA
ATGGTGCG GT ACGTGAGGTCGGG CCTGT
A TCC

GAM281 278 LOC2834 1 7371 XP_211062.1 3 676 CTCTGTTACCCA C C CA 3 B c c
87 GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCGTG GT ACGTGAG TCGGACCC
A A AT

GAM281 278 LOC2835 1 12075 XP_211075.1 3 1820 CTCTGTCACCCA CA 3 B b b
07 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG

GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2835 1 2025 XP_211071.1 5 621 CAAAGGCCTGAG C - - A 3 B c c
20 AGCTGGAGTCAG CACTG ACTCCAGC CT GGGC
TGTGGTGT GTGAC TGAGGTCG GA TCCG
- A G G
GAM281 278 LOC2835 1 3199 XP_211083.1 3 3279 CTCTGTCACCCA CA 3 B b b
34 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2835 1 15869 XP_211114.1 3 157 TGGGTGGGTGCC TC T 3 B b
b
66 TGGCTGTGTGCA CACTGCAC CAGCC GGGCA
GTGAGGAG GTGACGTG GTCGG TCCGT
T- -
GAM281 278 LOC2835 1 13652 XP_211118.1 3 37 CTCTGCTCCCCA G C CA 3 B c c
70 GGCTTGAGTGAG CACT CACTC AGCCTGGG
TGTGTGCC GTGA GTGAG TCGGACCC
- T CT
GAM281 278 LOC2835 2 6183 XP_211095.1 5 421 CTCTGTTGCCCA CAC----- C 3 B c
b
75 GGCTAGAGTGCA TGCACTC AGCCTGGGCAA
CTAATACA ACGTGAG TCGGACCCGTT
ACATAATC A
GAM281 278 LOC2835 2 10067 XP_211095.1 5 885 CTCTGTTGCCCA C TC 3 B b b
75 GGCTGAGGTACA CACTG AC CAGCCTGGGCAA
GTGGCGTG GTGAC TG GTCGGACCCGTT
A GA
GAM281 278 LOC2835 1 10466 XP_294741.1 5 480 CTCTGTCACCCA C C CA 3 B c
c
85 AGCTGGAGTGCA CA TGCACTCCAGC TGGG
CTGGCATG GT ACGTGAGGTCG ACCC
C A AC
GAM281 278 LOC2835 1 10638 NP_787093.1 3 911 CTCTGTTGCCCA 3 B b b
88 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGACTC GTGGCGTGAGGTCGGACCCGTT
GAM281 278 LOC2836 2 4420 XP_211126.1 5 3889 CTCTGTTGCCCA C 3 B b b
24 GGCTGGAGTCCA CACTG ACTCCAGCCTGGGCAA
GTGGCATG GTGAC TGAGGTCGGACCCGTT
C
GAM281 278 LOC2836 2 15245 XP_211126.1 5 750 CTCTCACACCCA C----- CA 3 B c b
24 GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTCTCAAC TGACGTGAGGTCGGACCC
CAACTC AC
GAM281 278 LOC2836 2 3581 XP_211134.1 5 1238 CTCTGTCGCCCA C A 3 B b b
37 GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGTATG GTGACGTGAG TCGGACCCG

```
                                                A       C
GAM281   278    LOC2836 2   14859  XP_211134.1   5  361    CTCTGTCGCCCA              A        3  B  b  b
         37                                      GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
                                                GTGGTGCA    GTGACGTGAGGTCGGACCCG
                                                          C
GAM281   278    LOC2836 1   17964  XP_208764.1   3  227    CTCTGTTGCCCA                    3  B  b  b
         41                                      GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
                                                GTGGCATG    GTGACGTGAGGTCGGACCCGTT

GAM281   278    LOC2836 1   16674  XP_211147.1   5  893    CTCTGTCGCCCA  C  CAC        A        3  B  c
c
         63                                      GGCTGGACTACA CA TG   TCCAGCCTGGGC
                                                ATGGCACG    GT AC   AGGTCGGACCCG
                                                          A  ATC          C
GAM281   278    LOC2836 1   8450   XP_208773.1   5  12     TTTTGTCACCCA  CT          CA        3  B  c  c
         64                                      GGCTGGAGTGCC CA  GCACTCCAGCCTGGG
                                                ATGGCACG    GT  CGTGAGGTCGGACCC
                                                          AC           AC
GAM281   278    LOC2836 1   1730   XP_211152.1   5  19     CTCTGTTGCCCA     C                3  B  b  b
         72                                      GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
                                                GTGGCACA    GTGAC TGAGGTCGGACCCGTT
                                                          A
GAM281   278    LOC2836 1   11904  NP_787094.1   3  1229   TTTTGTCACCGA  C         G  CA        3  B  c
c
         87                                      GGCTGGAGTGCA CA TGCACTCCAGCCT GG
                                                ATGGCCCG    GT ACGTGAGGTCGGA CC
                                                          A          G  AC
GAM281   278    LOC2836 1   3654   XP_211165.1   5  133    CCTCGGAGCCCA    --  TCCA      A       3  B  c
c
         89                                      GGCAGCTGTGTC CACTG  CAC   GCCTGGGC
                                                CAGTGAGA    GTGAC  GTG   CGGACCCG
                                                          CT   TCGA       A
GAM281   278    LOC2836 2   5305   XP_208788.1   3  334    AGAAATTTGTCA       T       G         3  B  b  b
         93                                      GGCTGGGTGCAG CACTGCAC CCAGCCTGG CAA
                                                TGGCTCAT    GTGACGTG GGTCGGACT GTT
                                                          -       -
GAM281   278    LOC2836 2   16069  XP_208788.1   3  334    AAGAAATTTGTC       T       G         3  B  b  b
         93                                      AGGCTGGGTGCA CACTGCAC CCAGCCTGG CAA
                                                GTGGCTCA    GTGACGTG GGTCGGACT GTT
                                                          -       -
GAM281   278    LOC2837 2   13716  XP_211170.3   3  1559   CCTTCTTCCCCA    G    -     CA        3  B  c  b

         01                                      GGCTGGGAGTGG CACT CACTCC AGCCTGGG
                                                GTGAGACG    GTGG GTGAGG TCGGACCC
                                                          -     G       CT
GAM281   278    LOC2837 2   14381  XP_211170.3   3  3386   GCTCTGTCACCA             --        3  B  b  b
         01                                      GGCTGGAGTGCG CACTGCACTCCAGCCTGG  GCA
                                                GTGGCATA    GTGGCGTGAGGTCGGACC  TGT
                                                          AC
GAM281   278    LOC2837 1   5985   XP_208804.3   3  979    CAGGCTCACCCA    GC-         CA        3  B  c
c
```

06 GGCTGGGGTCTG CACT ACTCCAGCCTGGG
AGTGTCAC GTGA TGGGGTCGGACCC
GTC AC

GAM281 278 LOC2837 1 15912 XP_208800.1 3 502 TTCAGTGTCTGT T A - 3 B c c
15 GGCTGGAGAGTG CAC GC CTCCAGCC TGGGCA
TGTCTTTC GTG TG GAGGTCGG GTCTGT
- A T

GAM281 278 LOC2837 1 11523 XP_208115.1 3 290 CTCTGTCGCCCA A 3 B b b
41 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC2837 1 12479 XP_208835.1 3 299 CGCTGTTGCCCA C CC 3 B b b

67 GGCTCTAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCACG GT ACGTGA TCGGACCCGTT
A TC

GAM281 278 LOC2837 1 4370 XP_211199.1 5 1257 CTCTGTCGCCCA A 3 B b b
78 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGGG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC2837 1 17644 XP_211198.1 3 2588 ACGACAGACCCA T ---- CA 3 B c
c

79 GGCTGGAGTCTT CAC GC ACTCCAGCCTGGG
GGCTGTGC GTG CG TGAGGTCGGACCC
T GTTC AG

GAM281 278 LOC2838 1 6265 XP_208122.1 3 1461 TAGTGTTGCCCA 3 B b b
01 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGC GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2838 1 16700 XP_208850.1 3 949 CTCTGTCATCCA CA 3 B c c
02 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCT
AC

GAM281 278 LOC2838 1 9395 XP_208853.1 5 582 TCCCGCACCCCA A A T CA 3 B c
c

10 GGCTGGGGCAGC C CTGC C CCAGCCTGGG
GAGGGCGT G GACG G GGTCGGACCC
C - - CA

GAM281 278 LOC2838 1 9546 XP_211218.1 3 256 CTCTGTCACCCC T CA 3 B c c
18 GGCTGGAGTGCA CACTGCACTCCAGCC GGG
GTGGTGTG GTGACGTGAGGTCGG CCC
C AC

GAM281 278 LOC2838 1 4974 XP_211229.1 3 679 CTCTGTCACCGA G CA 3 B c c
51 GGTTGGAGTGCA CACTGCACTCCAGCCT GG
GTGGTATG GTGACGTGAGGTTGGA CC
G AC

GAM281 278 LOC2838 1 6184 XP_211233.1 3 694 AAAGACTGAAGA GGG 3 B b b

56 GGCTGGAGTGCA CACTGCACTCCAGCCT CA
GTGGCGCA GTGACGTGAGGTCGGA GT

GAA

GAM281 278 LOC2838 1 10167 XP_211236.1 5 1169 CTCTGTTGCCTA C 3 B b b
57 GGCTAGGGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCACA GTGACGTGGG TCGGATCCGTT
A

GAM281 278 LOC2838 3 1401 NP_787095.1 3 713 CTCTGTCGTCCA A 3 B b b
61 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCTG
C

GAM281 278 LOC2838 3 1635 NP_787095.1 3 1035 CTCTGTCGACCA CA----- --- 3 B c b

61 GGCTGGAGTGCA CTGCACTCCAGCCTGG GCA
GGGGCACA GACGTGAGGTCGGACC TGT
ACACGGG AGC

GAM281 278 LOC2838 3 7476 NP_787095.1 3 287 AAGATGTGCCCA ACT AG 3 B c
b
61 GGAGGTGGCGGT CACTGC CC CCTGGGCA
GGCGCACA GTGGCG GG GGACCCGT
GT- A-

GAM281 278 LOC2838 1 13285 XP_208875.1 3 1506 GCTTGTTGCCCA C 3 B b b
63 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC2838 1 18993 XP_211248.2 5 724 CTCTGTCTCCCG CA 3 B c c
87 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGGCCC
TC

GAM281 278 LOC2838 2 11072 XP_211249.1 3 1413 GTCCCAGCTCCA CA - A 3 B c
b
88 GGCTGGAGCCAG CACTG CTCCAGCCTGG GC
TGAAGGGT GTGAC GAGGTCGGACC CG
C- T A

GAM281 278 LOC2838 2 14104 XP_211249.1 3 1551 CTCTGCTGCCCA C 3 B b b
88 GGCTGGAATGCA CACTGCA TCCAGCCTGGGCA
GTGGTGCC GTGACGT AGGTCGGACCCGT
A

GAM281 278 LOC2838 2 3899 XP_208899.1 3 784 TTCTGTCACCCA A CA 3 B c c
89 GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGTGTA GTGACGTGAGG CGGACCC
C AC

GAM281 278 LOC2838 2 5525 XP_208899.1 5 223 GGCAGTGACTAG - AGCC A 3 B c
c
89 TCCAGGAGTGCA CA CTGCACTCC TGGGC
GCTGGGAG GT GACGTGAGG ACCTG
C ---- A

GAM281 278 LOC2838 1 7156 XP_211250.1 3 176 AAAGTACAAGGC T A TG A 3 B c
c
94 CGGCCGGGTGCA CACTGCAC CC GCC GGC
GTGGCTCA GTGACGTG GG CGG CCG
- C -- G

GAM281 278 LOC2839 1 7156 XP_211256.1 3 176 AAAGTACAAGGC T A TG A 3 B c c
09 CGGCCGGGTGCA CACTGCAC CC GCC GGC
GTGGCTCA GTGACGTG GG CGG CCG
- C -- G
GAM281 278 LOC2839 3 4703 XP_208909.1 5 2420 TTCTGCTGCCCA 3 B b b
28 GGTTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCACG GTGACGTGAGGTTGGACCCGT

GAM281 278 LOC2839 3 11501 XP_208909.1 5 811 TCTTGTCACCTA CA CA 3 B c b
28 GGCCAGAGTGCA CACTGCACTC GCCTGGG
GTGTCATG GTGACGTGAG CGGATCC
AC AC
GAM281 278 LOC2839 3 20101 XP_208909.1 5 2716 CTCTGTTGCCCA 3 B b b
28 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGTCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2839 1 15775 XP_208905.2 5 920 CTCCGTCACCCA CA 3 B b b
29 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2839 1 10461 XP_208931.1 3 56 GTGCAGCTGACC TCCAG G 3 B c c
54 AGGGTTTGTGCA CACTGCAC CCTGG CA
GTGATCTT GTGACGTG GGACC GT
TTTG- A
GAM281 278 LOC2839 1 19569 XP_208145.2 3 1458 TAGTGTCACCCA CA 3 B b b
64 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGATCCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2839 1 4650 XP_211289.1 3 757 CAAAGGCAGGCC T T A 3 B c c
83 TGGCTGGGTGCA CACTGCAC CCAGCC GGGC
GTGGCTCA GTGACGTG GGTCGG TCCG
- - G
GAM281 278 LOC2840 1 18161 XP_208958.2 3 1485 CACTGTCGCCCA C CC A 3 B c c
01 ATCTGGAGTGCA CA TGCACTCCAG TGGGC
CTGGCGCT GT ACGTGAGGTC ACCCG
C TA C
GAM281 278 LOC2840 2 3244 XP_211298.1 3 17 CTCTTGTTGCCT C C 3 B b b
16 AGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
ATGGCGCA GT ACGTGAGGTCG ATCCGTT
A -
GAM281 278 LOC2840 2 17923 XP_211298.1 5 53 GCGGGCTGCCCA CA-------- CCA 3 B c b
16 GGCAGTGCAGAG CTGCACT GCCTGGGCA
CGGAGAGA GACGTGA CGGACCCGT
AGAGAGGCGA ---
GAM281 278 LOC2840 1 18610 XP_208961.1 3 354 CTCTGTAACTCA CA 3 B c c

17 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACTC
AA
GAM281 278 LOC2840 1 10124 XP_211302.1 3 2841 CTCTGTTGCCCT C T 3 B b b
19 GGCTGGAGTACA CACTG ACTCCAGCC GGGCAA
GTGGCATG GTGAC TGAGGTCGG CCCGTT
A T
GAM281 278 LOC2840 2 14597 XP_208983.3 3 1018 CTGTGTCGCCCA A 3 B b b
23 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2840 2 17953 XP_208983.3 3 1473 CTCTGTTGCCCA C 3 B b b
23 GACTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCGTG GTGACGTGAGGTC GACCCGTT
A
GAM281 278 LOC2840 1 10847 XP_208152.1 3 1242 CACTGTCACCCA A CA 3 B c c

48 GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
C AC
GAM281 278 LOC2840 1 6213 XP_208992.1 3 182 CTCTGTTGTCCA C C 3 B b b
63 AGCTAGAGTGCA CACTGCACTC AGC TGGGCAA
GTGATACC GTGACGTGAG TCG ACCTGTT
A A
GAM281 278 LOC2840 2 1596 XP_211321.1 3 58 CCCTGTTGCCCA C 3 B b b
74 GGCTGAAGTGCA CACTGCACT CAGCCTGGGCAA
GTGGTGCG GTGACGTGA GTCGGACCCGTT
A
GAM281 278 LOC2840 2 15531 XP_211321.1 3 983 CTCAGTCGCCCA A 3 B b b
74 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2840 1 18527 XP_211323.1 3 2 CTGTCACCCAGG C CA 3 B c c
82 CTGAAGTGCAGT CACTGCACT CAGCCTGGG
GCAGGACC GTGACGTGA GTCGGACCC
A AC
GAM281 278 LOC2840 3 7333 XP_211324.1 3 845 CTCTGTCACCCT T CA 3 B c b
95 GGCTGGAGTGCG CACTGCACTCCAGCC GGG
GTGGCGAT GTGGCGTGAGGTCGG CCC
T AC
GAM281 278 LOC2840 3 11799 XP_211324.1 3 1043 CTCTTTCGCCCA C A A 3 B c b

95 GGCCGGACTGCA CACTGCA TCC GCCTGGGC
GTGGCGCA GTGACGT AGG CGGACCCG
C C C
GAM281 278 LOC2840 3 15513 XP_211324.1 3 143 CTCTGTCATTCA --- 3 B b b
95 GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGTGCA GTGACGTGAGGTCGGAC CTGT
TTA
GAM281 278 LOC2840 1 8582 XP_209008.3 3 198 CTCTGTTACCCA CA 3 B c c

98 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGTGCC GTGATGTGAGGTCGGACCC
AT

GAM281 278 LOC2841 1 1777 XP_209015.1 3 1541 TCCAGTGCTCCA T A - 3 B c c
00 GGCTGGGGGCCG CAC GC CTCCAGCCTGG GCA
TGGATCCT GTG CG GGGGTCGGACC CGT
C - T

GAM281 278 LOC2841 1 19537 XP_209019.1 5 411 CTCTGTTGCCCA --- 3 B b b
01 GGTTGGAGTACA CACTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA

GAM281 278 LOC2841 3 3233 XP_211327.3 3 608 TTTTGTTGCCCA CAC----- 3 B c b
02 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ACGGCGCG ACGTGAGGTCGGACCCGTT
GCGCGGCA

GAM281 278 LOC2841 3 7745 XP_211327.3 5 862 CTTTGTCACCCA CA 3 B b b
02 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2841 3 18149 XP_211327.3 5 46 TCTTGCCGTCCA C A 3 B c b
02 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCGTG GT ACGTGAGGTCGGACCTG
A C

GAM281 278 LOC2841 1 3725 XP_209024.1 3 57 CTTTGTCGCCCT C----- T A 3 B c c
17 GGCTGGAGTGCA ACTGCACTCCAGCC GGGC
GTTGCGCA TGACGTGAGGTCGG CCCG
ACGCGT T C

GAM281 278 LOC2841 2 1966 XP_211342.1 3 461 CCCTGTCGCCCA CT A 3 B c b
28 GGCTGGAGTGCC CA GCACTCCAGCCTGGGC
ATGGCGCG GT CGTGAGGTCGGACCCG
AC C

GAM281 278 LOC2841 2 17271 XP_211342.1 3 0 TCGCCCAGGCTG A 3 B b b
28 GAGTGCAGTGGT CACTGCACTCCAGCCTGGGC
AGATCAGG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC2841 1 12779 XP_209032.1 3 540 GACTGTTGCCCA C 3 B b b
35 GGCTGGAGTGTA CA TGCACTCCAGCCTGGGCAA
ATGGCGCC GT ATGTGAGGTCGGACCCGTT
A

GAM281 278 LOC2841 1 4102 XP_211353.1 5 368 GCTCTGTCGCCA C -- 3 B b b
45 GGCTGGAGTGCA CA TGCACTCCAGCCTGG GCA
ATGGCGCG GT ACGTGAGGTCGGACC TGT
A GC

GAM281 278 LOC2841 1 11530 XP_209051.1 3 1095 TGTTGTCGCCTA C A 3 B c c
71 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGATGCG GT ACGTGAGGTCGGATCCG
A C

GAM281 278 LOC2841 2 1111 XP_209059.1 5 422 TCTCGTTGCCAA C G 3 B b b
83 GGCTGGAGTGCA CA TGCACTCCAGCCT GGCAA
ATGGCACG GT ACGTGAGGTCGGA CCGTT

```
                                        A          A
GAM281  278  LOC2841 2  9456  XP_209059.1  5 922   ATCGATAGCCCA    C    A     A       3  B  c  b
         83                    GGCAGGAGTACA CACTG ACTCC GCCTGGGC
                              GTGGCACA    GTGAC TGAGG CGGACCCG
                                        A    A       A
GAM281  278  LOC2841 1  14861 XP_209060.2  3 1162  CTCTGTCACCCA            CA       3  B  b  b
         86                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
                              GTGGTGCG    GTGACGTGAGGTCGGACCC
                                          AC
GAM281  278  LOC2842 1  8707  XP_211397.1  5 749   GTCACTTGCCCA     ACTCCA           3  B  c
c
         45                    GGTGCGGTGGCT CACTGC     GCCTGGGCAA
                              CACACCTG    GTGGCG     TGGACCCGTT
                                        ------
GAM281  278  LOC2842 1  8494  XP_211411.1  5 1562  ATCTGTCACCCA  C          CA       3  B  c  c
         67                    GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
                              ATGGCATG    GT ACGTGAGGTCGGACCC
                                        A          AC
GAM281  278  LOC2842 1  1026  XP_211412.1  5 1027  CTTTGTCACCCA  C          CA       3  B  c  c
         76                    GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
                              ATGGCGTG    GT ACGTGAGGTCGGACCC
                                        A          AC
GAM281  278  LOC2842 1  19875 XP_211419.1  3 1829  CTCTGTCTCCCA            CA       3  B  b  b
         86                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
                              GTGGTGCA    GTGACGTGAGGTCGGACCC
                                          TC
GAM281  278  LOC2842 1  1885  XP_209105.1  3 146   TCTTGTTACCCA       A    CA       3  B  c  c
         89                    GGCAGGAGTGCA CACTGCACTCC GCCTGGG
                              GTGGCGTG    GTGACGTGAGG CGGACCC
                                        A     AT
GAM281  278  LOC2843 1  4849  XP_211426.1  3 315   TCTTATTGCCCA                  3  B  b  b
         04                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
                              GTGACGAG    GTGACGTGAGGTCGGACCCGTT

GAM281  278  LOC2843 2  2477  XP_211425.1  5 1682  CTCTGTCACCCA      T   C   CA       3  B  c  c

         05                    TGCTGGTGTGCA CACTGCAC CCAGC TGGG
                              GTGGCGTG    GTGACGTG GGTCG ACCC
                                        T    T   AC
GAM281  278  LOC2843 2  3802  XP_211425.1  5 1275  CTCTGCCACCCA      C   C   CA       3  B  c
c
         05                    GACTGAAGTGCA CACTGCACT CAG CTGGG
                              GTGGTGCG    GTGACGTGA GTC GACCC
                                        A   A    AC
GAM281  278  LOC2843 2  3386  XP_209162.1  3 1766  CTCTCTCGCCCA            A        3  B  b  b
         17                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
                              GTGGCGTG    GTGACGTGAGGTCGGACCCG
                                          C
GAM281  278  LOC2843 2  7077  XP_209162.1  3 813   TTCTGTCACACA   T      C  ---       3  B  c  b
         17                    GTCTGGAGTGCT CAC GCACTCCAG CTG   GGCA
```

GTGGTGCA GTG CGTGAGGTC GAC CTGT
T T ACA
GAM281 278 LOC2843 1 11129 XP_211432.1 5 1 TCTTCCCGAGGC T -- - CA 3 B c c
21 CCTGGAGTGCCG CAC GCACTCCA GCCT GGG
TGCGTGTG GTG CGTGAGGT CGGA CCC
C CC G TT
GAM281 278 LOC2843 1 1731 XP_209143.1 3 1033 TTCTGTCGTCCA A 3 B b b
25 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGGCGTGAGGTCGGACCTG
C
GAM281 278 LOC2843 1 11986 XP_211437.1 3 437 CTTTGTGCCCTA C C - 3 B b b
56 GACTGGAGTGCA CA TGCACTCCAG CT GGGCA
ATGGCGCC GT ACGTGAGGTC GA CCCGT
A A T
GAM281 278 LOC2843 1 18898 XP_211435.1 3 530 ACTTGTCACCCA CA 3 B b b
62 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCTCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2843 1 16701 XP_209154.1 3 931 CTCTGTCATCCA CA 3 B c c
75 GGTTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTTGGACCT
AC
GAM281 278 LOC2843 2 981 XP_209157.1 3 1220 CTCTGTCGCCCA C C A 3 B c b
76 AGCTGAAGTGCA CACTGCACT CAGC TGGGC
GTGGTGCG GTGACGTGA GTCG ACCCG
A A C
GAM281 278 LOC2843 2 19718 XP_209157.1 3 664 TCTTATTGCCCA C 3 B b b
76 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC2843 1 9312 XP_209163.1 3 384 CTCTATTGCCCA C 3 B b b
79 GTCTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCATG GTGACGTGAGGTC GACCCGTT
T
GAM281 278 LOC2843 1 10399 XP_211452.1 3 1675 CTGTGTTGTCCA C 3 B b b
96 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGTG GT ACGTGAGGTCGGACCTGTT
A
GAM281 278 LOC2844 2 2645 XP_209183.2 3 1651 TTCTGTCCCCGA C A --- 3 B c c
05 GGCCGGAGTGCA CA TGCACTCC GCCT GGGCA
ATGGCGTG GT ACGTGAGG CGGA CCTGT
A C GCC
GAM281 278 LOC2844 2 19462 XP_209183.2 3 908 CTCTGTCACCCA C C CA 3 B c
c
05 GGCTGTAGTACA CACTG ACT CAGCCTGGG
GTGGTGCC GTGAC TGA GTCGGACCC
A T AC
GAM281 278 LOC2844 1 14364 XP_211443.1 5 367 CTCTGTTGCCCA T 3 B b b
08 GGCTGGTGTGTA CACTGCAC CCAGCCTGGGCAA
GTGATCTC GTGATGTG GGTCGGACCCGTT

T

GAM281 278 LOC2844 1 17304 XP_211449.1 3 638 GTGGTTGCTGAA G G- 3 B c c
10 GGCTGGAGTGGG CACT CACTCCAGCCT GGCAA
TGTGGCAA GTGG GTGAGGTCGGA TCGTT
- AG

GAM281 278 LOC2844 1 4533 XP_209200.1 5 1199 CTCTGTTGCCCG 3 B b b
21 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGGCCCGTT

GAM281 278 LOC2844 2 4975 XP_209198.1 3 476 TGCTGCTGCCCA 3 B b b
26 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGTGCA GTGACGTGAGGTCGGACCCGT

GAM281 278 LOC2844 2 5357 XP_209198.1 3 311 CTCTGTCGCCCA A 3 B b b
26 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGACATG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC2844 1 16193 XP_290862.1 3 86 CTCTGCTGCCCG C 3 B b b
36 GGCTAGAGTGCA CACTGCACTC AGCCTGGGCA
GTGGTGGG GTGACGTGAG TCGGGCCCGT
A

GAM281 278 LOC2844 1 3825 XP_209204.2 3 197 AAAGCTGGCAGC - C- -- A 3 B c c
39 CCTGGAAGTGCA CACTGCACT CCAG CTG GGC
GTGTTGGG GTGACGTGA GGTC GAC TCG
A CC GG A

GAM281 278 LOC2844 1 8752 XP_209210.1 3 761 CCTCTGTCACCA -- 3 B b b
40 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 LOC2844 3 3999 XP_209216.1 5 680 CACTGTCACCCG C CA 3 B c b
54 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCTCG GT ACGTGAGGTCGGGCCC
A AC

GAM281 278 LOC2844 3 16031 XP_209216.1 5 1116 CTCTGTTGCCCA C 3 B b b
54 GGCTGAAGTGCA CACTGCACT CAGCCTGGGCAA
GTGGTGTG GTGACGTGA GTCGGACCCGTT
A

GAM281 278 LOC2844 3 17976 XP_209216.1 5 187 GGCCACAGCTCA TG CT A 3 B c
b
54 GGCTGGGCTGTG CAC CA CCAGCCTGGGC
GTGCCAGC GTG GT GGTCGGACTCG
GT CG A

GAM281 278 LOC2844 2 10621 XP_211470.1 5 658 CTCTGTCACCTA C CA 3 B c c
56 GGCTGCAGTGCA CACTGCACT CAGCCTGGG
GTGGCACA GTGACGTGA GTCGGATCC
C AC

GAM281 278 LOC2844 2 18777 XP_211470.1 3 256 CTCTGTTATCCA T CA 3 B c c
56 GGCTGGTGTGCA CACTGCAC CCAGCCTGGG
GTGATACA GTGACGTG GGTCGGACCT
T AT

GAM281 278 LOC2844 1 10211 XP_290826.1 3 308 GTCAAATGCCCA C-- G A---- 3 B c c

59 GGCAGATAGGGG ACT CACTCC GCCTGGGCA
TGGGTACC TGG GTGGGG CGGACCCGT
CCA - ATAGA

GAM281 278 LOC2844 1 19286 XP_209225.1 3 1168 CTCTGTCACCCA CT CA 3 B c c

71 GGCTGGGATGCA CACTGCA CCAGCCTGGG
GTGGCTTC GTGACGT GGTCGGACCC
AG AC

GAM281 278 LOC2844 1 12538 XP_302752.1 3 518 ATGCCCCCTCCA TG C - ----- 3 B c c

95 GGCTGAGACTGA CAC CA TC CAGCCT GGGCA
TGTGATAA GTG GT AG GTCGGA CCCGT
TA C A CCTCC

GAM281 278 LOC2845 1 14119 XP_211500.1 3 1747 CTCTGTCGCCCA CA A 3 B c c

12 GGCTGGAGCCCA CACTG CTCCAGCCTGGGC
GTGGCGAG GTGAC GAGGTCGGACCCG
CC C

GAM281 278 LOC2845 1 18865 XP_211502.1 5 908 CCCAATAGCCCA A 3 B b b

13 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCAGA GTGACGTGAGGTCGGACCCG
A

GAM281 278 LOC2845 1 4125 XP_209244.1 5 79 AGAGAAGGGCCA T A G A 3 B c c

14 AGGCCGGGTGCA CACTGCAC CC GCCT GGC
GTGGTTCA GTGACGTG GG CGGA CCG
- C A G

GAM281 278 LOC2845 1 19112 XP_211514.1 5 89 CCTTGCCCTTTG CT - --- 3 B c c

49 GGCTGGAGATGC CA GCA CTCCAGCCT GGGCAA
TTTGCCAG GT CGT GAGGTCGGG CCCGTT
TT A TTT

GAM281 278 LOC2845 1 9493 XP_211515.1 3 1303 CTCTGTCACCCA CA 3 B b b

51 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2845 1 3996 XP_209263.1 5 458 CTCTCTAACCCG C C CA 3 B c c

68 AGCTAGAGTGCA CACTGCACTC AGC TGGG
GTGACGCG GTGACGTGAG TCG GCCC
A A AA

GAM281 278 LOC2845 1 19533 XP_211522.1 3 7 CTCTGTCTCCCA G C CA 3 B c c

77 GACTGGAGTGAG CACT CACTCCAG CTGGG
TGGTGTGA GTGA GTGAGGTC GACCC
- A TC

GAM281 278 LOC2845 1 12803 XP_209278.3 5 73 TCTGTTGTCCAA C----- - 3 B c c

87 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM281 278 LOC2846 1 2771 XP_211543.1 3 26 GTGGGCTGCCCA T C G 3 B c c
06 GGATGCGGTGCG CAC GCACT CA CCTGGGCA
TGCTTCTG GTG CGTGG GT GGACCCGT
- C A
GAM281 278 LOC2846 1 12497 XP_211552.1 3 977 CTCGGTCACCTA CA 3 B c c
11 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGATGTGAGGTCGGATCC
AC
GAM281 278 LOC2846 1 18882 XP_211561.1 5 505 CTCTGTTGCCTA C C 3 B b b
28 GACTGGAGTGCA CA TGCACTCCAG CTGGGCAA
ATGGCGTG GT ACGTGAGGTC GATCCGTT
A A
GAM281 278 LOC2846 1 8272 XP_211562.1 3 2301 AGGTGTGGCCCA G CA--- A 3 B c
c
30 GGCAGGCTGAGT CACT CACTC GCCTGGGC
GGGTGGGC GTGG GTGAG CGGACCCG
- TCGGA G
GAM281 278 LOC2846 1 5249 XP_209310.1 3 233 ATTGCCAGTGGG -- G G-- 3 B c c
63 GTGGGCAGTGCA CACTGCACT CCA CCT GGCAA
GTGGGGTG GTGACGTGA GGT GGG CCGTT
CG G TGA
GAM281 278 LOC2846 3 501 XP_209319.1 5 101 TCTTATTGCCCA C C C 3 B c c
75 GACTAGAGTGCG CA TGCACTC AG CTGGGCAA
ATGGTGCG GT GCGTGAG TC GACCCGTT
A A A
GAM281 278 LOC2846 3 2389 XP_209319.1 5 560 CTCTGTCACCCA -- CA 3 B c c
75 GGCTGGAGTGTG CACTGCAC TCCAGCCTGGG
CAGTGGCG GTGACGTG AGGTCGGACCC
TG AC
GAM281 278 LOC2846 3 5250 XP_209319.1 5 560 CTGTCACCCAGG -- CA 3 B c c
75 CTGGAGTGTGCA CACTGCAC TCCAGCCTGGG
GTGGCGCG GTGACGTG AGGTCGGACCC
TG AC
GAM281 278 LOC2847 1 12803 XP_294994.1 5 866 TCTGTTGTCCAA C----- - 3 B c c
01 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM281 278 LOC2847 1 5153 XP_209332.1 3 524 CTCTGTTGCCCA A T 3 B b b
08 GGCTGGGTGCAG C CTGCAC CCAGCCTGGGCAA
CGGTGCGA G GACGTG GGTCGGACCCGTT
C -
GAM281 278 LOC2847 2 3182 XP_211602.1 3 472 CTTTGTTGCCCA 3 B b b
23 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGGCGTGAGGTCGGACCCGTT

GAM281 278 LOC2847 2 6498 XP_211602.1 3 61 CTCTGCCACCCA C CA 3 B c b
23 AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGCACG GTGACGTGAGGTCG ACCC
A AC
GAM281 278 LOC2847 1 10930 XP_211627.1 5 421 CTAAGTCACTGA C G CA 3 B c
c

54 GGCTGGAGTACA CACTG ACTCCAGCCT GG
GTGGCATG GTGAC TGAGGTCGGA TC
A G AC

GAM281 27805 LOC2848 3 853 XP_209371.1 3 1213 TTTGCCCAGGCT ---- 3 B b b
GGATGGAGTGCA CACTGCACTCCA GCCTGGGCAA
GTGGCGTG GTGACGTGAGGT CGGACCCGTT
AGGT

GAM281 27805 LOC2848 3 1544 XP_209371.1 3 1111 CTCTGCTGCTCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGTGCA GTGACGTGAGGTCGGACTCGT

GAM281 27805 LOC2848 3 8046 XP_209371.1 3 1213 CTCTTTTGCCCA ---- 3 B b b
GGCTGGATGGAG CACTGCACTCCA GCCTGGGCAA
TGCAGTGG GTGACGTGAGGT CGGACCCGTT
AGGT

GAM281 27839 LOC2848 1 19401 XP_211661.1 5 446 TCTTGTTGCCCG C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGGCCCGTT
A

GAM281 278 LOC2848 1 3582 XP_209383.1 3 138 CTCTGTCACCCA C A CA 3 B c c

53 GGCTGGAGCGTA CA TGC CTCCAGCCTGGG
ATGGCACA GT ATG GAGGTCGGACCC
A C AC

GAM281 27856 LOC2848 1 12736 XP_211668.2 3 619 TCTTGTCCCCCA C C CA 3 B c c
GACTGGAGTGCA CA TGCACTCCAG CTGGG
ATGGCACG GT ACGTGAGGTC GACCC
A A CC

GAM281 27856 LOC2848 1 12736 XP_302835.1 3 108 TCTTGTCCCCCA C C CA 3 B c c
GACTGGAGTGCA CA TGCACTCCAG CTGGG
ATGGCACG GT ACGTGAGGTC GACCC
A A CC

GAM281 27865 LOC2848 1 1645 XP_211672.1 3 70 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
ATGGCATG GT GCGTGAGGTCGGACCCGTT
A

GAM281 27874 LOC2848 2 3846 XP_209394.1 3 1070 GCTCTGTCGCCA C -- 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGG GCA
GTGGTGTG GTGAC TGAGGTCGGACC TGT
A GC

GAM281 27874 LOC2848 2 16244 XP_209394.1 3 616 GCTCTGCGCCCA G A 3 B b b
GGATGGAGTGCA CACTGCACTCCA CCTGGGC
GTGGCATG GTGACGTGAGGT GGACCCG
A C

GAM281 27834 LOC2849 1 14894 XP_211696.1 5 657 TTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC2849 2 4025 XP_211703.1 3 163 ACTCTGTCGCCA -- 3 B b b
50 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 LOC2849 2 17553 XP_211703.1 3 1526 CTCTGTCACCAA A - -- 3 B c b
50 GGCTGGAGTGCA C CTGCACTCCAGCCT GG GCA
GCGGTGTG G GACGTGAGGTCGGA CC TGT
C A AC
GAM281 278 LOC2850 1 3500 XP_211731.2 3 639 TGTGTGACCTTA C - - 3 B b b
02 GGCTGGAGTGCA CA TGCACTCCAGCCTG GG CA
ATGGCATG GT ACGTGAGGTCGGAT CC GT
A T A
GAM281 278 LOC2850 1 17523 XP_209440.1 3 2382 CTCTGTCACCCA C CA 3 B c c
26 GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGTGCG GTGACGTGAGGTC GACCC
A AC
GAM281 278 LOC2850 1 13688 XP_210798.1 3 74 TGCCGTCATCCA C -- CA 3 B c c
36 GGCTGGACAGTT CACTG AC TCCAGCCTGGG
CAGTGATT GTGAC TG AGGTCGGACCT
T AC AC
GAM281 278 LOC2850 1 2174 XP_211751.1 3 866 TTCTGTCACCCA A C CA 3 B c c
52 GGCTAGAGCGCA CACTGC CTC AGCCTGGG
GTGGCAAG GTGACG GAG TCGGACCC
C A AC
GAM281 278 LOC2850 1 20023 XP_211753.1 5 236 TGTCACCCAGGT C --- CA 3 B c c
58 GGCTGGAGTACA CACTG ACTCCAGCC TGGG
GTGGCCTG GTGAC TGAGGTCGG ACCC
A TGG AC
GAM281 278 LOC2850 1 5667 XP_209464.1 3 987 CTCTATCACCCA C CA 3 B c c
83 GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGTACG GTGACGTGA GTCGGACCC
A AC
GAM281 278 LOC2850 1 6092 XP_209465.1 3 42 TCTTGTTGCCCA C CA 3 B b b
88 GGCCAGAGTGCA CA TGCACTC GCCTGGGCAA
ATGGCGTG GT ACGTGAG CGGACCCGTT
A AC
GAM281 278 LOC2851 1 17113 XP_211773.1 3 843 GGGGATGAGCCA CA G- 3 B c
c
23 GGCTGGGGACAG CACTG CTCCAGCCTGG CA
TGGGGCTG GTGAC GGGGTCGGACC GT
A- GA
GAM281 278 LOC2851 2 5921 XP_211771.1 3 578 CTCTGTCACCCA CA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCCCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2851 2 11528 XP_211771.1 3 145 CTCTGTCACCCA CA 3 B b b
27 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC

```
                                                    AC
GAM281  278  LOC2851 2  4283  XP_211791.1  3  1871  TGCAGATTCCCA      T      CA       3  B  c  c
         66                    GGCTGGGTGCAG CACTGCAC CCAGCCTGGG
                              TGGCTCAC    GTGACGTG GGTCGGACCC
                                          -       TT
GAM281  278  LOC2851 2  19378 XP_211791.1  3  1871  ATGCAGATTCCC      T      CA       3  B  c  c

         66                    AGGCTGGGTGCA CACTGCAC CCAGCCTGGG
                              GTGGCTCA    GTGACGTG GGTCGGACCC
                                          -       TT
GAM281  278  LOC2851 1  7860  XP_209500.1  3  170   CTCTTTTGCCCA C-----  G      C        3  B  c  c
         76                    GACTGGAGTGAA     ACT CACTCCAG CTGGGCAA
                              GTAGCATG         TGA GTGAGGTC GACCCGTT
                                    GTACGA  A      A
GAM281  278  LOC2851 1  1745  XP_209509.1  3  678   CTCTGTTGCCCA                          3  B  b  b
         93                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
                              GTGGCGCA    GTGACGTGAGGTCGGACCCGTT

GAM281  278  LOC2852 1  13597 XP_209521.1  5  78    ATCTGTCACCCA     A       CA       3  B  c  c
         21                    GGCTGGAGCGCA CACTGC CTCCAGCCTGGG
                              GTGGTGTG    GTGACG GAGGTCGGACCC
                                        C         AC
GAM281  278  LOC2852 2  8001  XP_211813.1  3  723   CTCTGTCACCCA         C   CA       3  B  c  c
         31                    AGCTGGAGTGCA CACTGCACTCCAGC TGGG
                              GTGGTGCA    GTGACGTGAGGTCG ACCC
                                          A   AC
GAM281  278  LOC2852 2  8001  XP_211813.1  3  889   CTCTGTCACCCA         C   CA       3  B  c  c
         31                    AGCTGGAGTGCA CACTGCACTCCAGC TGGG
                              GTGGTGCA    GTGACGTGAGGTCG ACCC
                                          A   AC
GAM281  278  LOC2852 2  15366 XP_211813.1  3  1260  CACTGTCACCCA    G     C    CA       3  B  c
c
         31                    GTCTGGAGTGGA CACT CACTCCAG CTGGG
                              GTGGCATA    GTGA GTGAGGTC GACCC
                                        G       T    AC
GAM281  278  LOC2852 1  5012  XP_211818.1  3  654   GAGACCGTGTCC      T AG -          3  B  c  c
         56                    ATGGGGCGTGCA CACTGCAC CC  CC TGGGCA
                              GTGGAGGC    GTGACGTG GG  GG ACCTGT
                                        C  --  T
GAM281  278  LOC2852 1  15575 XP_211829.1  5  565   TCTTGTTACCCA  C          CA       3  B  c  c
         81                    GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
                              ATGGCACG    GT ACGTGAGGTCGGACCC
                                          A            AT
GAM281  278  LOC2852 1  9374  XP_209554.1  3  399   CTATGTCACTCA            CA       3  B  c  c
         99                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
                              GTGGCACA    GTGACGTGAGGTCGGACTC
                                          AC
GAM281  278  LOC2853 1  1027  XP_211844.1  3  477   CTCTGTCTCCCA     -       CA       3  B  c  c
         34                    GGCTGGAGTTGC CACTGCA CTCCAGCCTGGG
                              AGTGGTGC    GTGACGT GAGGTCGGACCC
```

T TC
GAM281 278 LOC2853 2 556 XP_211854.1 3 1258 CTCTGTTACCCA C CA 3 B c b
45 GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCGCG GTGACGTGAG TCGGACCC
A AT
GAM281 278 LOC2853 2 18883 XP_211854.1 3 869 CAGGGTTGCCCA G 3 B b b
45 GGGTGGAGTGCA CACTGCACTCCA CCTGGGCAA
GTGGCAGG GTGACGTGAGGT GGACCCGTT
G
GAM281 278 LOC2853 1 6117 XP_209581.1 3 515 CTCTGTCACCCA CA 3 B c c
66 GGCTGGGGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGGGGTCGGACCC
AC
GAM281 278 LOC2853 1 10352 XP_211861.3 3 251 CTTTGTCACCCA CA 3 B b b
69 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2853 1 19692 XP_211873.1 3 1012 CTCTCTCGCCAT TG A 3 B c c

89 GGTTGGAGTGCA CACTGCACTCCAGCC GGC
GTGGTGCG GTGACGTGAGGTTGG CCG
TA C
GAM281 278 LOC2853 2 9688 XP_211879.1 3 41 CTCTGTCTCCCA CA 3 B b b
92 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM281 278 LOC2853 2 17969 XP_211879.1 3 344 CTCTGTCGCCCA A 3 B b b
92 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2853 2 4655 XP_209593.1 3 1208 TCCTCTCGCCCA A 3 B b b
98 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTC GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2853 2 13286 XP_209593.1 3 906 CTCTGTCGCCCA C----- A 3 B c b
98 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGC
GTAGCGCG TGACGTGAGGTCGGACCCG
GCGCGA C
GAM281 278 LOC2854 1 4171 XP_209607.3 3 1518 TTCTGTCGCCCA A 3 B b b
29 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2854 1 13804 XP_211914.1 5 572 CACTGTCGCCCA A 3 B b b
88 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGC
GTGGTGCA GTGGCGTGAGGTCGGACCCG
C
GAM281 278 LOC2854 1 11239 XP_211917.1 3 164 CTCTGTCCCTCA C----- --- 3 B c c
91 GGCTGGAGTGCA ACTGCACTCCAGCCT GGGCA
GTAGCGTG TGACGTGAGGTCGGA CCTGT
GTGCGA CTC

GAM281 278 LOC2855 1 3519 XP_211923.1 5 176 TACTTTCATTCA CA 3 B c c
09 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACTT
AC
GAM281 278 LOC2855 2 6961 XP_209654.1 5 9 CTGTGTCGCCCA - A 3 B b b
40 GGCTGGAGTGCA CACT GCACTCCAGCCTGGGC
AGTGGCAT GTGA CGTGAGGTCGGACCCG
A C
GAM281 278 LOC2855 2 9543 XP_209654.1 5 1535 CTCTGTCACCCA CA 3 B b b
40 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2855 1 8718 XP_209660.1 3 436 CACTCTTGCCCA T C 3 B b b
60 GGCTGTAGTGCT CAC GCACT CAGCCTGGGCAA
GTGGCACG GTG CGTGA GTCGGACCCGTT
T T
GAM281 278 LOC2855 1 4455 XP_211941.1 5 1331 GCTCAGTTGCAT -- C----- A 3 B c c
77 CTGGAAGGTGCA CACTGCAC TCCAG CTGGGC
GTGTGCAC GTGACGTG AGGTC GACTCG
GA TACGTT -
GAM281 278 LOC2855 2 12804 XP_209671.1 3 721 CTCTGTCGCCAG - -- 3 B b b
89 GACTGGAGTGCA CACTGCACTCCAG CCTGG GCA
GTGACACG GTGACGTGAGGTC GGACC TGT
A GC
GAM281 278 LOC2855 2 17087 XP_209671.1 3 267 CTTGATCACCCA C CA 3 B c b
89 GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCGTG GTGACGTGAG TCGGACCC
A AC
GAM281 278 LOC2856 1 13843 XP_211959.1 5 850 CTCTGTTGCCCA C 3 B b b
26 GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGATACG GTGACGT AGGTCGGACCCGTT
A
GAM281 278 LOC2856 1 12452 XP_211965.1 5 243 GGTGTGTGGCCA T - -- G 3 B c c
33 GGCTGCAGAGCT CAC GCA CTC CAGCCTGG CA
GCGTGCCG GTG CGT GAG GTCGGACC GT
- C AC G
GAM281 278 LOC2856 1 4949 XP_209693.1 5 3929 TTCTGTCACCCA CA 3 B b b
38 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2856 1 19299 XP_209719.2 3 204 CTCTGTTGCTCA 3 B b b
79 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACTCGTT

GAM281 278 LOC2856 1 959 XP_211980.1 5 16 TTCTGTCGCCCA CA----- A 3 B c c
83 GGCTGGAGTGCA CTGCACTCCAGCCTGGGC
GGGGCATT GACGTGAGGTCGGACCCG
TTACGGG C
GAM281 278 LOC2856 1 17726 XP_209724.1 3 1089 CTCTGTTGCCCA C 3 B b b
89 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA

ATGGCATG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC2856 1 16940 XP_211981.1 5 24 CTCTGTTGCCCA 3 B b b
93 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2857 1 3414 XP_211992.1 3 45 CTGTGTTCAGGA C --- 3 B c c
13 TGTTGAAGTGCA CACTGCACT CAG CCTGGGCA
GTGTCAGA GTGACGTGA GTT GGACTTGT
A GTA

GAM281 278 LOC2857 1 18012 XP_211997.1 5 350 CTCTGTCAACCA --- 3 B b b
22 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGACTCT GTGACGTGAGGTCGGACC TGT
AAC

GAM281 278 LOC2857 1 11141 XP_209743.1 3 1367 TTCTGTCACCCA CA 3 B b b
44 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2857 2 7537 XP_209742.1 3 2182 ATCTGTCACCCA C----- CA 3 B c b

47 GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGTGCA TGACGTGAGGTCGGACCC
ACGTGA AC

GAM281 278 LOC2857 2 11528 XP_209742.1 3 2434 CTCTGTCACCCA CA 3 B b b
47 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC2857 1 13412 XP_209750.1 3 372 CACTCTTGCCCA - A 3 B b b
60 GGCTGGAGCGCA CACT GC CTCCAGCCTGGGCAA
AGTGGCGC GTGA CG GAGGTCGGACCCGTT
A C

GAM281 278 LOC2857 1 1304 XP_295177.1 5 220 AAATGTTGCCCA GCAC AG 3 B c
c
66 GGAAGGACAGGT CACT TCC CCTGGGCAA
GTG GTGG AGG GGACCCGTT
AC-- AA

GAM281 278 LOC2857 1 16810 XP_212013.1 5 229 CTATGGTCCACA C -- - - A 3 B c c
77 GGCTGGAGGGTG CA TGCAC TCCAGCCTG GG C
CATGGAAC GT ACGTG AGGTCGGAC CC G
- GG A T G

GAM281 278 LOC2858 1 559 XP_212055.1 3 719 CTCTGTCACCCA C CA 3 B c c
12 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGTG GT ACGTGAGGTCGGACCC
A AC

GAM281 278 LOC2858 1 12389 XP_212036.1 5 78 TCTTGTTGCCCA 3 B b b
13 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2858 2 1847 XP_209777.1 3 237 CTCTGTTGCCCA C G 3 B b b
22 GGATGGAATGCA CACTGCA TCCA CCTGGGCAA

GTGGCACA GTGACGT AGGT GGACCCGTT
A A
GAM281 278 LOC2858 2 9753 XP_209777.1 5 1360 CTGTGTCACCCA CA 3 B b b
22 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2858 1 986 XP_212043.1 5 165 CTCTGTCGCCAA CTG A 3 B c c
30 AGTTGGAGTGCA CACTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C
GAM281 278 LOC2858 3 4368 XP_212034.1 5 597 CTCTGTCGCCTA C A 3 B c b
43 GGCTGCAGTGCA CACTGCACT CAGCCTGGGC
GTGGCGGG GTGACGTGA GTCGGATCCG
C C
GAM281 278 LOC2858 3 14125 XP_212034.1 5 2338 CCTCATGTTCCA TCC ---- 3 B c
b
43 TGGGGCTGTGCA CACTGCAC AGCCT GGGCA
GTGCAATG GTGACGTG TCGGG CTTGT
--- GTAC
GAM281 278 LOC2858 3 17964 XP_212034.1 3 188 CTCTGTTGCCCA 3 B b b
43 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2858 1 18945 XP_212045.1 5 732 CTCTGTCACCCG CA 3 B c c
47 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGGCCC
AC
GAM281 278 LOC2858 1 10885 XP_212061.1 3 687 TTCTGTAACCCA CA 3 B b b
72 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCCTG GTGACGTGAGGTCGGACCC
AA
GAM281 278 LOC2858 1 15236 XP_209806.1 3 318 CTGTCACCCCCA CA CA 3 B c
c
96 GGCCAGAGTGCA CACTGCACTC GCCTGGG
GTGGTGCA GTGACGTGAG CGGACCC
AC CC
GAM281 278 LOC2859 2 6188 XP_209810.1 3 304 TGGAGAAATTCA T CA 3 B c c
14 GGCTGGGTGCAG CACTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA
GAM281 278 LOC2859 2 14560 XP_209810.1 3 304 ATGGAGAAATTC T CA 3 B c c
14 AGGCTGGGTGCA CACTGCAC CCAGCCTGGG
GTGGCTCA GTGACGTG GGTCGGACTT
- AA
GAM281 278 LOC2859 1 12799 XP_209822.1 3 327 CTGTCACCCCCA CA CA 3 B c
c
22 GGCCAGAGTGCA CACTGCACTC GCCTGGG
GTGGTGCG GTGACGTGAG CGGACCC
AC CC
GAM281 278 LOC2859 1 19536 XP_212104.1 3 41 CTATGTTGCCCA 3 B b b

23 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2859 1 1867 XP_209818.1 5 145 CTTTGTCACCCA T G CA 3 B c c
30 GGGTGGTGTGCA CACTGCAC CCA CCTGGG
GTGGAGCT GTGACGTG GGT GGACCC
T G AC
GAM281 278 LOC2859 1 12075 XP_212092.1 5 845 CTCTGTCACCCA CA 3 B b b
45 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2859 1 11558 XP_212103.1 3 296 CTCTGACATCCA C CA 3 B c c
46 AGCTGGGGTGCA CACTGCACTCCAGC TGGG
GTGGCGCG GTGACGTGGGGTCG ACCT
A AC
GAM281 278 LOC2859 1 15323 XP_209821.1 3 680 TGCTGTTGCCCA 3 B b b
52 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2859 1 2604 XP_209833.1 5 934 CTCTGTCACCCA C CA 3 B c c
61 GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCATG GTGACGT AGGTCGGACCC
A AC
GAM281 278 LOC2859 1 10956 XP_212107.1 3 211 GTGACTTGCCCA ------ A CAG 3 B c
c
68 GGGCAGAGGTTT CACT GC CTC CCTGGGCAA
TTGAAGTG GTGA TG GAG GGACCCGTT
AGTTTT - ACG
GAM281 278 LOC2859 1 5318 XP_212105.1 3 866 TCGTGTTGCCCC T 3 B b b
72 GGCTGGAGTGCA CACTGCACTCCAGCC GGGCAA
GTGGCGCT GTGACGTGAGGTCGG CCCGTT
C
GAM281 278 LOC2859 2 1397 XP_212117.1 5 4 TACTGTCATACA C----- T --- 3 B c b
79 GGCTGGCGTGCA ACTGCAC CCAGCCTG GGCA
GTAGTGGG TGACGTG GGTCGGAC CTGT
GGGTGA C ATA
GAM281 278 LOC2859 2 6388 XP_212117.1 5 548 CTCTGTCAGCCA C --- 3 B b b
79 GGCTGGAGTGCA CA TGCACTCCAGCCTGG GCA
ATGGCATG GT ACGTGAGGTCGGACC TGT
A GAC
GAM281 278 LOC2859 1 11742 XP_212111.1 3 936 TCTTGTTGCCCA CA ------ A 3 B c c

89 GGCAGGAGTACA CTGC ACTCC GCCTGGGCAA
ATGGCAGG GACG TGAGG CGGACCCGTT
G- GTAACA A
GAM281 278 LOC2859 1 17306 XP_212120.1 3 603 TGCTCTGTTGCC CC CTG 3 B c
c
99 AAGTTAAGTGCA CACTGCACT AGC GGCAA
GTGGTATG GTGACGTGA TTG CCGTT
A- AA-

GAM281 278 LOC2860 1 15231 XP_209866.1 3 1642 AATCGTCACCCA CC CA 3 B c c
29 CATTGGAGTGCA CACTGCACTCCAG TGGG
GTGGTACG GTGACGTGAGGTT ACCC
AC AC
GAM281 278 LOC2860 1 2244 XP_209868.1 5 640 TTTTGTTGCGCA C G 3 B b b
30 GGCTGGAGTGCA CA TGCACTCCAGCCTG GCAA
ATGGTGCA GT ACGTGAGGTCGGAC CGTT
A G
GAM281 278 LOC2860 1 7792 XP_209867.2 3 614 TCTTGTCAACCA GC GCA 3 B c c
32 GATTGGAGTGCA CACTGCACTCCA CTGG
GTGGTGCA GTGACGTGAGGT GACC
TA AAC
GAM281 278 LOC2860 1 11035 XP_209873.1 5 648 TTTTGTTGCCCA C 3 B b b
39 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC2860 1 9367 XP_212152.1 3 1054 CTCTGTTGTCCA 3 B b b
52 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACCTGTT

GAM281 278 LOC2860 1 9186 XP_212158.1 3 395 TGCTTCTGCCCA CA A ------ 3 B c c
58 GGCCTGGTCTGG CTGC CTCCA GCCTGGGCA
GGGCAGAG GACG GGGGT CGGACCCGT
GA - CTGGTC
GAM281 278 LOC2860 1 17965 NP_776192.1 5 66 CTCTGTTGCCCA C 3 B b b
75 GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGCGTG GTGAC TGAGGTCGGACCCGTT
A
GAM281 278 LOC2860 5 3810 XP_212163.1 3 451 CTCTGTCGCCCA A 3 B b b
78 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGAGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2860 5 13100 XP_212163.1 5 790 CTGTCTTGCCCA CA----- C 3 B c b

78 GGCTGGAGTTCA CTG ACTCCAGCCTGGGCAA
GGGGCTAT GAC TGAGGTCGGACCCGTT
TATCGGG T
GAM281 278 LOC2860 5 15083 XP_212163.1 3 760 CTCTGTCACCCA G CA 3 B c b

78 GGATGGAGTGCA CACTGCACTCCA CCTGGG
GTGTTGTG GTGACGTGAGGT GGACCC
A AC
GAM281 278 LOC2860 5 15589 XP_212163.1 5 1402 GCTCTGTTGCCA C G 3 B b b

78 GGCTGGAGTGCA CA TGCACTCCAGCCTGG CAA
CTGGGGCT GT ACGTGAGGTCGGACC GTT
C -
GAM281 278 LOC2860 5 16716 XP_212163.1 5 88 CTGGGCTGCCCA TG T AG 3 B c b

78 GGGGTGTGATGT CAC CAC CC CCTGGGCA
GGAGCTGG GTG GTG GG GGACCCGT
TA T --
GAM281 278 LOC2860 1 16409 XP_212166.3 5 142 GCCATGTGGAAC ----- TG-- A 3 B c c
90 TGCTGGAGTGCA CACTGCACTCCAGC C GGC
GTGGCATG GTGACGTGAGGTCG G CCG
TCAAG TGTA -
GAM281 278 LOC2861 1 11672 NP_848630.1 3 212 CTCCGTCTCCCA CA CA 3 B c c
03 GGCCAGAGTGCA CACTGCACTC GCCTGGG
GTGGCGCA GTGACGTGAG CGGACCC
AC TC
GAM281 278 LOC2861 1 11672 XP_209897.1 3 212 CTCCGTCTCCCA CA CA 3 B c c
03 GGCCAGAGTGCA CACTGCACTC GCCTGGG
GTGGCGCA GTGACGTGAG CGGACCC
AC TC
GAM281 278 LOC2861 1 7847 XP_212185.1 3 991 CTCTGCCACCCA CA 3 B b b
26 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2861 1 7113 XP_212194.1 5 446 TTTTGTCACCCA CA 3 B b b
32 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2861 2 3927 XP_209925.1 5 1001 CTCTGTTGACCA G G 3 B b b
66 GGCTGGAGTGAA CACT CACTCCAGCCTGG CAA
GTGGTGTG GTGA GTGAGGTCGGACC GTT
A A
GAM281 278 LOC2861 2 12946 XP_209925.1 3 672 ACTGCCATCTTC T C ----- 3 B c b
66 AAGCTGGGTGCA CACTGCAC CCAGC TG GGCA
GTGGCTCA GTGACGTG GGTCG AC CCGT
- A TTCTA
GAM281 278 LOC2861 1 8426 XP_212211.1 5 1936 GCTGTGTCACCA AC -- 3 B b b
70 GGCTGGAGCAGT CACTGC TCCAGCCTGG GCA
GGCACGAT GTGACG AGGTCGGACC TGT
-- AC
GAM281 278 LOC2861 1 12053 XP_212216.1 5 567 AAGATCCCCAGG T --- CA 3 B c c
84 GGACTGGGTGCA CACTGCAC CCAG CCTGGG
GTGGCTCA GTGACGTG GGTC GGACCC
- AGG CT
GAM281 278 LOC2861 2 3430 XP_212219.1 5 148 CTTTGTCACCCA C CA 3 B c b
86 GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC
GAM281 278 LOC2861 2 18020 XP_212219.1 3 390 CTCTATCACCCA CA 3 B b b
86 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGTGGCT GTGACGTGAGGTCGGACCC

AC
GAM281 278 LOC2862 1 2600 XP_209953.1 3 1535 CTCTGTTGCCCA C 3 B b b
06 GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGCACA GTGACGT AGGTCGGACCCGTT
A
GAM281 278 LOC2862 1 19893 XP_209941.1 3 913 CTCTGTCACCCA C CA 3 B c c
07 GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGCCACA GTGACGTGAGGTC GACCC
A AC
GAM281 278 LOC2862 3 2849 XP_212230.1 3 1658 CTCTGTCACCCA CA 3 B b b
08 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGTCACA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2862 3 4372 XP_212230.1 3 1457 CTCTGTCGCCCA C A 3 B b b
08 GGCTGGAGTTCA CACTG ACTCCAGCCTGGGC
GTGGCGCG GTGAC TGAGGTCGGACCCG
T C
GAM281 278 LOC2862 3 9724 XP_212230.1 3 2282 CTCTGTAGCCCA A 3 B b b
08 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGTGGCA GTGACGTGAGGTCGGACCCG
A
GAM281 278 LOC2862 1 19240 XP_212228.1 5 554 CTCTGTCAACCA C --- 3 B b b
15 GGCTGGAGTGCA CA TGCACTCCAGCCTGG GCA
CTGGCGCA GT ACGTGAGGTCGGACC TGT
C AAC
GAM281 278 LOC2862 1 6316 XP_212235.1 3 972 CTTGCACTGCCA A CT G 3 B c c

18 GGCTGGCTGTAG C CTGCA CCAGCCTGG CA
CGACTCTG G GATGT GGTCGGACC GT
C C- -
GAM281 278 LOC2862 1 7774 XP_212233.1 5 65 TGCCCCCTGCCA CA TC G 3 B c
c
21 GGCTGAGGGACA CACTG C CAGCCTGG CA
GTGACACA GTGAC G GTCGGACC GT
AG GA -
GAM281 278 LOC2862 1 6868 XP_212244.1 5 238 CTCTGTCGCTCA A A 3 B c c
45 GGCTGGAGAGCG CACTGC CTCCAGCCTGGGC
GTGGTGCA GTGGCG GAGGTCGGACTCG
A C
GAM281 278 LOC2862 1 11262 XP_209972.1 3 563 CGAGGGGCAGCA CT G G A 3 B c
c
58 CAGGGTGGTGCA CACTGCA CCA CCTG GC
GTGGGTGA GTGACGT GGT GGAC CG
-- G A A
GAM281 278 LOC2863 2 7808 XP_212274.3 3 1483 AAAAATCACACA T GGCA 3 B c
c
37 GGCTGGGTGCAG CACTGCAC CCAGCCTG
TGGCTCAT GTGACGTG GGTCGGAC
- ACAC
GAM281 278 LOC2863 2 14911 XP_212274.3 3 1483 GAAAAATCACAC T GGCA 3 B c
c

37 AGGCTGGGTGCA CACTGCAC CCAGCCTG
GTGGCTCA GTGACGTG GGTCGGAC
- ACAC
GAM281 278 LOC2863 1 15975 XP_212278.1 3 413 TGTTGTTGCCCA 3 B b b
41 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2863 1 15730 XP_212286.1 5 688 GCTCTGTCACCA A -- 3 B b b
54 GGCTGGAGGGCA CACTGC CTCCAGCCTGG GCA
GTGGCGCC GTGACG GAGGTCGGACC TGT
G AC
GAM281 278 LOC2863 1 7385 XP_212290.1 5 1101 CTCTGTCACCCA CA 3 B b b
56 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC2863 1 14974 XP_212285.1 5 14 CAATGTTGCCCA 3 B b b
57 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC2863 1 3785 XP_212291.1 3 157 TTCTGGTGTCCA - C-- C 3 B c c
71 GGCTGAAGTCCT CAC TG ACT CAGCCTGGGCA
CGTGTGAC GTG GC TGA GTCGGACCTGT
T TCC A
GAM281 278 LOC2863 4 2180 XP_212308.1 5 4010 ATAACCGGAGGC T GGCA 3 B c
b
95 AGGCTGGGTGCA CACTGCAC CCAGCCTG
GTGGCTCA GTGACGTG GGTCGGAC
- GGAG
GAM281 278 LOC2863 4 2722 XP_212308.1 5 5808 CCCTGTTGCCCA C CC 3 B b b

95 GGCTACAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCATG GT ACGTGA TCGGACCCGTT
A CA
GAM281 278 LOC2863 4 5359 XP_212308.1 3 232 AAAAATGTCTTA T T-- 3 B c b
95 TGGCTGGGTGCA CACTGCAC CCAGCC GGGCA
GTGGCTCA GTGACGTG GGTCGG TCTGT
- TAT
GAM281 278 LOC2863 4 16177 XP_212308.1 5 4010 TAACCGGAGGCA T GGCA 3 B c
b
95 GGCTGGGTGCAG CACTGCAC CCAGCCTG
TGGCTCAT GTGACGTG GGTCGGAC
- GGAG
GAM281 278 LOC2864 1 1038 XP_212310.1 5 501 TCTTGTTGCCCA C A C 3 B c c
01 GGCTAGAGGGCA CA TGC CTC AGCCTGGGCAA
ATGGTGCA GT ACG GAG TCGGACCCGTT
A G A
GAM281 278 LOC2864 1 2754 XP_212319.1 3 55 GTGCTGTTTCCT T -- 3 B b b
41 GGCTGGAGTGCA CACTGCACTCCAGCC GG GCA
GTGGCATG GTGACGTGAGGTCGG CC TGT
T TT

GAM281 278 LOC2864 1 9580 XP_210063.1 3 986 TGTTGTTGCCCA C 3 B b b
67 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC2865 1 3183 XP_212340.1 3 892 CTTTGTCGCCCA A 3 B b b
53 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC2865 1 9264 XP_210106.1 3 99 CTCTGTAGACCA A --- 3 B b b
58 GGCTGGAGCGCA CACTGC CTCCAGCCTGG GCA
GTGGCAGG GTGACG GAGGTCGGACC TGT
C AGA
GAM281 278 LOC2865 1 9264 XP_210108.1 3 99 CTCTGTAGACCA A --- 3 B b b
64 GGCTGGAGCGCA CACTGC CTCCAGCCTGG GCA
GTGGCAGG GTGACG GAGGTCGGACC TGT
C AGA
GAM281 278 LOC3385 1 13760 XP_294654.1 3 1173 GCTCCATCACCA GCA 3 B c
c
62 GGCTGGAGTGCA CACTGCACTCCAGCCTGG
GTGGTGCG GTGACGTGAGGTCGGACC
ACT
GAM281 278 LOC3385 2 7596 XP_294653.1 3 2270 TGACGCTGCCCA GC-- AG- 3 B c
b
65 GGAAAGGAGTTC CACT ACTCC CCTGGGCA
TGAGTGCT GTGA TGAGG GGACCCGT
GTCT AAA
GAM281 278 LOC3385 2 12867 XP_294653.1 3 1934 TTTTGTTGCCCA C 3 B b b
65 GGCTGGAGTTCA CACTG ACTCCAGCCTGGGCAA
GTGGCGTG GTGAC TGAGGTCGGACCCGTT
T
GAM281 278 LOC3385 1 4528 XP_290472.1 3 1085 CCCTGTCACCCA C C CA 3 B c
c
79 GGCTGGAATGCA CA TGCA TCCAGCCTGGG
ATGGCACG GT ACGT AGGTCGGACCC
A A AC
GAM281 278 LOC3385 1 7523 XP_294658.1 5 203 CACTTTGTTTCA T-- T-- - 3 B c c
85 GGCTGGTCTGTG CAC GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM281 278 LOC3386 1 18810 XP_294664.1 3 662 AGCCAGCATGCC TC T 3 B b b
09 TGGCTGTGTGCA CACTGCAC CAGCC GGGCA
GTGGCCAG GTGACGTG GTCGG TCCGT
T- -
GAM281 278 LOC3386 1 6626 XP_290494.1 3 2436 TCTTGTTGCCCA C 3 B b b
45 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGAGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC3387 1 12803 XP_211595.2 5 683 TCTGTTGTCCAA C----- - 3 B c c
09 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA

GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM281 278 LOC3387 2 14732 XP_294690.1 3 117 TTCTGATGCCCA 3 B b b
39 GGTTGGGGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCACA GTGACGTGGGGTTGGACCCGT

GAM281 278 LOC3387 2 15044 XP_294690.1 3 528 CTCTGTTGCCCA 3 B b b
39 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC3387 1 16493 XP_290570.1 3 878 GTCTGTCACCCA CA 3 B b b
73 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC3388 1 11507 XP_290216.1 3 337 TTTTATTGCCCA CT CCA 3 B c
c
19 GGCAGTGCTCTG CA GCACT GCCTGGGCAA
GGCAGGAA GT CGTGA CGGACCCGTT
CT ---
GAM281 278 LOC3388 1 12341 XP_294740.1 5 562 CTCTGTCACCAA C - -- 3 B c c
99 GGCTGGAGTGCA CA TGCACTCCAGCCT GG GCA
TTGGTGCA GT ACGTGAGGTCGGA CC TGT
T A AC
GAM281 278 LOC3389 2 4298 XP_294742.1 3 438 GCTCTGTCGCCA -- 3 B b b
23 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 LOC3389 2 8559 XP_294742.1 3 2044 TTCTGTCACTCA CA 3 B c b
23 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACTC
AC
GAM281 278 LOC3389 1 3348 XP_294757.1 3 1068 ACTGAAGTCCCA C - - - A 3 B c c
63 GGCTGGGGGTGT CA TG CACTCC AGCCTGGG C
CAATGGAC GT AC GTGGGG TCGGACCC G
A T G T A
GAM281 278 LOC3389 1 12479 XP_290663.1 3 299 CGCTGTTGCCCA C CC 3 B b b

91 GGCTCTAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCACG GT ACGTGA TCGGACCCGTT
A TC
GAM281 278 LOC3389 1 12479 XP_290659.1 3 299 CGCTGTTGCCCA C CC 3 B b b

99 GGCTCTAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCACG GT ACGTGA TCGGACCCGTT
A TC
GAM281 278 LOC3390 1 17484 XP_294802.2 3 894 TCTTATCGCCCA C A 3 B c c
77 GGCTGGGGTGCA CA TGCACTCCAGCCTGGGC
ATGGCGCA GT ACGTGGGGTCGGACCCG
A C
GAM281 278 LOC3390 1 9543 XP_290692.1 3 851 CTCTGTCACCCA CA 3 B b b

78 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC3391 1 14266 XP_290711.1 5 144 TTTGGCTGCCCA CT ACTCC 3 B c c
08 GGCTCGCCTTGA CA GC AGCCTGGGCA
CTCCAAAT GT CG TCGGACCCGT
TC C----
GAM281 278 LOC3391 1 15614 XP_294825.1 5 449 GCTCTGTTGCCA G 3 B b b
46 GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGTGCG GTGACGTGAGGTCGGACC GTT
-
GAM281 278 LOC3391 1 13344 XP_294827.1 3 708 GATTGCCAACGC - - CCT A 3 B c c
53 CTCTGGAGTGCT CA CT GCACTCCAG GGGC
GGCTGGGA GT GG CGTGAGGTC TCCG
C T --- C
GAM281 278 LOC3391 1 4196 XP_294832.1 3 2299 AAAGCTCGCCCA T - A 3 B b b
54 GGGCTGGGTGCA CACTGCAC CCAGCC TGGGC
GTGGCTCA GTGACGTG GGTCGG ACCCG
- G C
GAM281 278 LOC3391 1 16261 XP_290742.1 3 674 CTCTGTCACCCA C C CA 3 B c c
78 GGCTGGAGTACA CA TG ACTCCAGCCTGGG
ATGGCGTG GT AC TGAGGTCGGACCC
A A AC
GAM281 278 LOC3392 1 4056 XP_290756.1 3 357 CTCTGTGGCCCA C A 3 B b b
01 GGCTGAAGTGCA CACTGCACT CAGCCTGGGC
GTGGTGTG GTGACGTGA GTCGGACCCG
A G
GAM281 278 LOC3392 1 19537 XP_290762.2 5 411 CTCTGTTGCCCA --- 3 B b b
16 GGTTGGAGTACA CACTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA
GAM281 278 LOC3392 1 19537 XP_294900.2 5 411 CTCTGTTGCCCA --- 3 B b b
82 GGTTGGAGTACA CACTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA
GAM281 278 LOC3392 1 11314 XP_294899.2 5 1180 CTCTGTTGCCCA CA----- C 3 B c c
83 GGTTGGAGTACA CTG ACTCCAGCCTGGGCAA
GCAATGCC GAC TGAGGTTGGACCCGTT
CCGTAAC A
GAM281 278 LOC3392 1 12349 XP_294903.1 5 777 CCATGTTGCCCA TGCACT---- 3 B c c
98 GGCTGGTCTCAA CAC CCAGCCTGGGCAA
ACTTGTGA GTG GGTCGGACCCGTT
TTCAAACTCT
GAM281 278 LOC3393 1 2039 XP_290831.1 5 317 CCCCCTTGCCCA GCA-- --- 3 B c c

21 GGCCCTTGGGGG CACT CTCCA GCCTGGGCAA
AGGGGGTG GTGG GGGGT CGGACCCGTT
GGGAG TCC

GAM281 278 LOC3393 1 9544 XP_290838.1 3 2392 TCTTGTTGCCCA C C 3 B b b
24 GGCTGCAGTGCA CA TGCACT CAGCCTGGGCAA
ATGGCACA GT ACGTGA GTCGGACCCGTT
A C

GAM281 278 LOC3393 2 16940 XP_290830.1 3 372 CTCTGTTGCCCA 3 B b b
25 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC3393 2 17114 XP_290830.1 3 143 AGCCTTTCTCCA A CA 3 B c b
25 GGTGGGAGTGCA CACTGCACTCC GCCTGGG
GTGGCATG GTGACGTGAGG TGGACCT
G CT

GAM281 278 LOC3394 1 14072 XP_294926.1 3 2063 ATGGAATGCCTA CC - 3 B b b
00 GTGCTAAGTGCA CACTGCACT AGC CTGGGCA
GTGTCCTT GTGACGTGA TCG GATCCGT
A- T

GAM281 278 LOC3394 1 2027 XP_294944.1 5 627 CTCTGTTGCCCA CA----- 3 B c c
17 GGCTGGAGTGCA CTGCACTCCAGCCTGGGCAA
GGGGCGTA GACGTGAGGTCGGACCCGTT
ATGCGGG

GAM281 278 LOC3394 1 10679 XP_290902.1 3 308 TCTTGTCGCCCA C A 3 B b b
48 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCGCA GT ACGTGAGGTCGGACCCG
A C

GAM281 278 LOC3394 1 5488 XP_290911.1 3 1340 CTCTGTCGCCCA A 3 B b b
58 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACT GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC3394 1 13513 XP_290907.2 3 838 CTCTGTCGCCTA A 3 B b b
59 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGATCCG
C

GAM281 278 LOC3394 2 7386 XP_290919.1 3 1081 CTCTGTCGCGCA G G A 3 B c b

92 GGGTGGAGTGCG CACTGCACTCCA CCTG GC
GTGGCACG GTGGCGTGAGGT GGAC CG
G G C

GAM281 278 LOC3394 2 8590 XP_290919.1 3 1387 TCTTGTTGCCCA C 3 B b b
92 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
TTGGCGTG GT GCGTGAGGTCGGACCCGTT
T

GAM281 278 LOC3395 2 12075 XP_295005.1 3 1040 CTCTGTCACCCA CA 3 B b b
77 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3395 2 14733 XP_295005.1 3 1187 CTACGTGACCCA C----- - 3 B c b
77 GGCTGGAGTGTA ACTGCACTCCAGCCTGGG CA

GTAGCTAT TGATGTGAGGTCGGACCC GT
TATCGA A

GAM281 278 LOC3396 1 15295 XP_295014.1 3 1461 CTCTGTCACTTA CA 3 B c c
00 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGATTC
AC

GAM281 278 LOC3396 1 17076 XP_290981.1 3 1596 GCCCTGTTGCCA C G 3 B b b
59 GGCTGGAATGCA CACTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -

GAM281 278 LOC3396 1 1982 XP_295032.1 5 166 CTCTACCACCCA CA 3 B b b
85 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3396 1 15954 XP_295035.1 5 835 AGACAGGGTCTT CCT A 3 B c
c
94 GACTGGAGTGCA CACTGCACTCCAG GGGC
GTGGTGCG GTGACGTGAGGTC TCTG
AGT G

GAM281 278 LOC3397 1 11528 XP_295038.1 3 1272 CTCTGTCACCCA CA 3 B b b
11 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3397 2 16942 XP_295041.1 5 880 CTCTGTCGCCCA A 3 B b b
20 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC3397 2 18414 XP_295041.1 5 4000 TTCTGTCACCCA --- CA 3 B c b
20 GGCTGGAGTGCA CACT GCACTCCAGCCTGGG
AAGGTGCA GTGG CGTGAGGTCGGACCC
AAA AC

GAM281 278 LOC3398 1 13337 XP_295072.1 3 1492 GTCTGTCACCCA CA 3 B b b
03 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3398 2 1744 XP_291020.1 5 1637 CTCTGTCACCCA CA 3 B b b
09 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3398 2 17750 XP_291020.1 5 1174 CACTGTCACCTA CA 3 B c b
09 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTAAA GTGACGTGAGGTCGGATCC
AC

GAM281 278 LOC3398 2 7633 XP_291031.1 5 575 CTCTGTTGCCCA C 3 B b b
33 GCCTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCATT GTGACGTGAGGTC GACCCGTT
C

GAM281 278 LOC3398 2 10421 XP_291031.1 3 561 CTGTGATGCCGA G G 3 B b b
33 GGGTGGAGTGCA CACTGCACTCCA CCT GGCA

GTGGCACA GTGACGTGAGGT GGA CCGT
G G
GAM281 278 LOC3398 1 14645 NP_835467.1 5 48 TTCTGTCGCCCA A 3 B b b
34 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGC
GTGACGCG GTGATGTGAGGTCGGACCCG
C
GAM281 278 LOC3398 1 14645 XP_291033.1 5 48 TTCTGTCGCCCA A 3 B b b
34 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGC
GTGACGCG GTGATGTGAGGTCGGACCCG
C
GAM281 278 LOC3398 3 4026 XP_291050.1 3 183 CTGTGTTGCCCA C----- 3 B b b
72 GGCTGGAGTGCA ACTGCACTCCAGCCTGGGCAA
GTAGCTAT TGACGTGAGGTCGGACCCGTT
TATCGA
GAM281 278 LOC3398 3 5858 XP_291050.1 5 768 CTCAGTCGCTCA A 3 B b b
72 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACTCG
C
GAM281 278 LOC3398 3 9299 XP_291050.1 5 471 GTCTGTTGCCCA 3 B b b
72 GGTTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGGG GTGACGTGAGGTTGGACCCGTT

GAM281 278 LOC3398 1 1081 XP_295095.1 5 133 CTCTGTTGCCCA C 3 B b b
94 GGTTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCTTG GTGACGTGAG TTGGACCCGTT
A
GAM281 278 LOC3399 1 3425 XP_291065.1 3 1461 CTCTGTTGCCCA CA----- 3 B c c
07 GGCTGGAGTGCA CTGCACTCCAGCCTGGGCAA
GGGGCACG GACGTGAGGTCGGACCCGTT
GCACGGG
GAM281 278 LOC3399 1 10709 XP_291069.1 5 122 CTCTGTTGCCCA 3 B b b
09 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC3399 2 714 XP_295099.1 5 595 CAGAATCGCCCA - - T- A- A 3 B c c
14 GGCCAGGCTGTG CA CTGC AC CC GCCTGGGC
GCAGATGA GT GACG TG GG CGGACCCG
A G TC AC C
GAM281 278 LOC3399 2 18305 XP_295099.1 5 597 TCGCCCAGGCCA - - T- A- A 3 B c
c
14 GGCTGTGGCAGA CA CTGC AC CC GCCTGGGC
TGAGCCGT GT GACG TG GG CGGACCCG
A G TC AC C
GAM281 278 LOC3399 1 16942 XP_291095.1 3 714 CTCTGTCGCCCA A 3 B b b
70 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C
GAM281 278 LOC3400 1 3454 XP_291113.2 3 2922 AGCTGGCATGCT TC T 3 B c c
12 TGGCTGTGTGCA CACTGCAC CAGCC GGGCA
GTGGCCAG GTGACGTG GTCGG TTCGT

```
                                                T-    -
GAM281  278   LOC3400 1  12244  XP_295137.1  3  37    TCTTGTTGCCCA  C                  3  B  b  b
        37                          GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
                                  ATGCGCGA    GT ACGTGAGGTCGGACCCGTT
                                        A
GAM281  278   LOC3401 1  12803  XP_291150.1  5  683   TCTGTTGTCCAA C-----          -      3  B  c  c
        25                          GGCTGGAGTGTA      ACTGCACTCCAGCCT GGGCAA
                                  GTAGTGCT         TGATGTGAGGTCGGA CCTGTT
                                        TCGTGA           A
GAM281  278   LOC3401 1  10105  XP_291151.1  3  35    TCCATTGCTCAT       TCCA- C          3  B  c  c

        33                          GTCACTTGTGCA CACTGCAC    GC TGGGCAA
                                  GTGACTGA    GTGACGTG    TG ACTCGTT
                                        TTCAC  T
GAM281  278   LOC3401 1  11753  XP_291153.1  3  2141  CTCTGTCACTCA  C          CA       3  B  c  c

        38                          GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
                                  ATGACGTG    GT ACGTGAGGTCGGACTC
                                        A           AC
GAM281  278   LOC3401 1  10096  XP_291158.1  3  1441  GCTCTGTCACGA           - -        3  B  b  b
        56                          GGCTGGAGTGCA CACTGCACTCCAGCCT G GGCA
                                  GTGGCCCC    GTGACGTGAGGTCGGA C CTGT
                                        G A
GAM281  278   LOC3402 1  12803  XP_291203.1  5  683   TCTGTTGTCCAA C-----          -      3  B  c  c
        27                          GGCTGGAGTGTA      ACTGCACTCCAGCCT GGGCAA
                                  GTAGTGCT         TGATGTGAGGTCGGA CCTGTT
                                        TCGTGA           A
GAM281  278   LOC3402 1  2179   XP_295188.1  5  340   TCCAGCGGCCCA    CA  A     A       3  B  c
c
        38                          GGCGGGGGACAG CACTG  CTCC GCCTGGGC
                                  TGCCGTTC    GTGAC  GGGG CGGACCCG
                                        AG   -      G
GAM281  278   LOC3402 1  7647   XP_291211.1  3  41    CTCTGTCACCCA      T   C   CA       3  B  c  c
        49                          AGCTGGTGTGCA CACTGCAC CCAGC TGGG
                                  GTGGTGTG    GTGACGTG GGTCG ACCC
                                        T    A   AC
GAM281  278   LOC3402 2  11519  XP_295190.1  5  1303  CTCTATCACCCA    C     C   CA       3  B  c
c
        59                          AGCTGGAGTACA CACTG ACTCCAGC TGGG
                                  GTGGCACA    GTGAC TGAGGTCG ACCC
                                        A      A   AC
GAM281  278   LOC3402 2  18147  XP_295190.1  5  998   CTGTGTGGCCTA  C          A       3  B  c  c
        59                          GGTTGGAGTGCA CA TGCACTCCAGCCTGGGC
                                  ATGGCGCA    GT ACGTGAGGTTGGATCCG
                                        A           G
GAM281  278   LOC3402 1  15740  XP_291214.1  5  1350  TCTCTTGTCCAA C-----          -      3  B  c  c
        90                          GGCTGGAGTGTA      ACTGCACTCCAGCCT GGGCAA
                                  GTAGTGCT         TGATGTGAGGTCGGA CCTGTT
                                        TCGTGA           A
GAM281  278   LOC3403 1  18868  XP_291269.1  3  1383  TCTTGTTGCCCA  C                  3  B  b  b
```

90 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC3404 1 1309 XP_291274.1 5 647 TTTTGTTGCCCA C 3 B b b
08 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGATGCA GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC3404 1 1744 XP_295240.1 3 174 CTCTGTCACCCA CA 3 B b b
14 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3404 1 1744 XP_295252.1 5 244 CTCTGTCACCCA CA 3 B b b
50 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3408 1 6038 XP_295776.1 5 1004 TCTGCGGCCCGG A A - A 3 B c
c
15 GGCTGGAGCGCA C CTGC CTCCAGCCT GGGC
GCGGGAAG G GACG GAGGTCGGG CCCG
C C G G

GAM281 278 LOC3426 1 12875 XP_297028.1 3 611 CAGACTTGCCCA G C-- - -- 3 B c c
63 GCAGCATGAGTA CACT CACT CA GC CTGGGCAA
GTGAAGTG GTGA GTGA GT CG GACCCGTT
A TGA A AC

GAM281 278 LOC3429 1 13464 XP_292790.2 3 811 CTCTGTCACCCA CA 3 B b b
26 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC

GAM281 278 LOC3451 1 17910 XP_298539.1 3 246 TGATGAGTCTGT CA - A 3 B c c
19 GGCTGGAGACAG CACTG CTCCAGCC TGGGC
TGGGGTCT GTGAC GAGGTCGG GTCTG
A- T A

GAM281 278 LOC3452 1 523 NP_835236.1 3 952 CTCTTTCGCCCA A 3 B b b
75 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTATG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC3458 1 12611 XP_293993.2 5 33 AGGAGATGTCCA TG A C 3 B c c

78 GGCTGAAGGTGG CAC C CT CAGCCTGGGCA
TGATTTGA GTG G GA GTCGGACCTGT
GT - A

GAM281 278 LOC3465 1 18735 XP_294264.2 5 291 TCTGTATGCCCA -- AC - G 3 B c c

46 GGGTGAGAAGCC CACT GC TC CA CCTGGGCA
GAGTGGCT GTGA CG AG GT GGACCCGT
GC A- A G

GAM281 278 LOC3466 1 17927 XP_294357.2 3 372 GCTCTGTCTCCA C -- 3 B b b
53 GGCTGGAGTACA CACTG ACTCCAGCCTGG GCA
GTGGTGCG GTGAC TGAGGTCGGACC TGT
A TC

GAM281 278 LOC3476 2 9837 XP_300226.1 3 110 CATTGCCCTTCG CT - --- 3 B c c
48 GGCTGGAGATGC CA GCA CTCCAGCCT GGGCAA
TTTGCCGG GT CGT GAGGTCGGG CCCGTT
TT A CTT
GAM281 278 LOC3476 2 19153 XP_300226.1 3 1232 TGGTCTTGCCCA ---- CT C 3 B c
c
48 GCTGGGCTGCCT CACT GCA CCAGC TGGGCAA
CAGGTGTC GTGG CGT GGTCG ACCCGTT
ACTC CG -
GAM281 278 LOC3479 1 17689 XP_300565.1 5 189 TTTTATTGCCCA 3 B b b
18 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGATGTGAGGTCGGACCCGTT

GAM281 278 LOC3480 1 5985 XP_300620.1 3 979 CAGGCTCACCCA GC- CA 3 B c
c
71 GGCTGGGGTCTG CACT ACTCCAGCCTGGG
AGTGTCAC GTGA TGGGGTCGGACCC
GTC AC
GAM281 278 LOC3480 2 13716 XP_302653.1 3 1556 CCTTCTTCCCCA G - CA 3 B c b

75 GGCTGGGAGTGG CACT CACTCC AGCCTGGG
GTGAGACG GTGG GTGAGG TCGGACCC
- G CT
GAM281 278 LOC3480 2 14381 XP_302653.1 3 3385 GCTCTGTCACCA -- 3 B b b
75 GGCTGGAGTGCG CACTGCACTCCAGCCTGG GCA
GTGGCATA GTGGCGTGAGGTCGGACC TGT
AC
GAM281 278 LOC3480 1 16473 XP_300615.1 5 57 GAGACCGACGGC C CTG A 3 B c
c
94 CGCTGGAGTGCA CA TGCACTCCAGC GGC
CTGGCATG GT ACGTGAGGTCG CCG
C --- G
GAM281 278 LOC3481 1 12479 XP_300623.1 3 299 CGCTGTTGCCCA C CC 3 B b b

13 GGCTCTAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCACG GT ACGTGA TCGGACCCGTT
A TC
GAM281 278 LOC3481 1 13705 XP_300626.1 5 554 TCTTGTTGCCCA CA 3 B b b
15 GGCCCGAGTGCA CACTGCACTC GCCTGGGCAA
GTGGTGCG GTGACGTGAG CGGACCCGTT
CC
GAM281 278 LOC3481 1 4673 XP_302665.1 5 476 TAAGAGGCCCTG CCA - A 3 B c
c
25 GGCCGAGGTGCA CACTGCACT GCCT GGGC
GTGACCCT GTGACGTGG CGGG CCCG
AGC T G
GAM281 278 LOC3481 1 12479 XP_300635.1 3 299 CGCTGTTGCCCA C CC 3 B b b

37 GGCTCTAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCACG GT ACGTGA TCGGACCCGTT

A TC
GAM281 278 LOC3481 1 12479 XP_300636.1 3 299 CGCTGTTGCCCA C CC 3 B b b
42 GGCTCTAGTGCA CA TGCACT AGCCTGGGCAA
ATGGCACG GT ACGTGA TCGGACCCGTT
A TC
GAM281 278 LOC3482 1 15020 XP_302685.1 5 1375 AGGCTGCCGCGG A - - 3 B c c
12 GGCAGGGGTGCA CACTGCACTCC GCCT G GGCA
GTGGGTGT GTGACGTGGGG CGGG C CCGT
A G G
GAM281 278 LOC3482 1 15852 XP_300670.1 3 1531 CTCTGTTGCCCA C 3 B b b
35 GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGTACG GTGACGT AGGTCGGACCCGTT
A
GAM281 278 LOC3482 1 10989 XP_302704.1 3 341 AGAAACTGCGGC T A G- 3 B c c
61 AGGCCGGGTGCA CACTGCAC CC GCCTG GCA
GTGTCTCA GTGACGTG GG CGGAC CGT
- C GG
GAM281 278 LOC3482 1 7306 XP_300683.1 5 58 CTCTGTTGCCTG TG 3 B b b
62 GGCTGGAGTGCA CACTGCACTCCAGCC GGCAA
GTGCCACG GTGACGTGAGGTCGG CCGTT
GT
GAM281 278 LOC3483 1 16669 XP_302716.1 5 317 CTTTGTTGCCCA 3 B b b
14 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGGCGTGAGGTCGGACCCGTT
GAM281 278 LOC3483 1 19778 XP_300696.1 3 1763 AGTCTGTCACCA -- 3 B b b
26 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM281 278 LOC3483 1 8820 XP_030209.2 3 79 GCTCGTCACCCA --- CA 3 B c c
27 GGCTGGAGTGCA CAC TGCACTCCAGCCTGGG
ATTGTGCA GTG ACGTGAGGTCGGACCC
TTA AC
GAM281 278 LOC3483 1 2235 XP_302732.1 3 3437 GAGTCTTGAGGC CAGCC A 3 B c
c
69 CCATTGAGTGCA CACTGCACTC TGGGC
GTGTGAGA GTGACGTGAG ACCCG
TT--- G
GAM281 278 LOC3483 2 872 XP_302741.1 3 1206 CGCCGTTGCCCA 3 B b b
93 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT
GAM281 278 LOC3483 2 11192 XP_302741.1 3 744 CTAGGAGGCCCA G A 3 B c b
93 GGCTGGAGTGAG CACT CACTCCAGCCTGGGC
GTGGCACG GTGG GTGAGGTCGGACCCG
A G
GAM281 278 LOC3483 4 1569 XP_300729.1 5 150 CTCTGTCACCCA C CA 3 B c b
96 GGCTGGAATGCA CACTGCA TCCAGCCTGGG

GTGCAGTG GTGACGT AGGTCGGACCC
A AC

GAM281 278 LOC3483 4 4081 XP_300729.1 5 151 TCACCCAGGCTG ----- CA 3 B c b
96 GAATGCAGTGCA CACTGCAC TCCAGCCTGGG
GTGGCACA GTGACGTG AGGTCGGACCC
ACGTA AC

GAM281 278 LOC3483 4 9545 XP_300729.1 3 184 CTCTGTTGCCCA 3 B b b
96 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC3483 4 10270 XP_300729.1 3 1031 TCTTGTTATCCA C CA 3 B c b
96 GGCTGGGGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCG GT ACGTGGGGTCGGACCT
A AT

GAM281 278 LOC3484 2 7386 XP_300730.1 3 322 CTCTGTCGCGCA G G A 3 B c b
02 GGGTGGAGTGCG CACTGCACTCCA CCTG GC
GTGGCACG GTGGCGTGAGGT GGAC CG
G G C

GAM281 278 LOC3484 2 8590 XP_300730.1 3 628 TCTTGTTGCCCA C 3 B b b
02 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
TTGGCGTG GT GCGTGAGGTCGGACCCGTT
T

GAM281 278 LOC3484 1 19778 XP_300738.1 3 1763 AGTCTGTCACCA -- 3 B b b
45 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 LOC3484 1 15049 XP_302760.1 3 2633 CTCTGTCGCCCA A 3 B b b
55 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM281 278 LOC3484 2 4143 XP_300743.1 3 130 ACTCTGTCACCA -- 3 B b b
60 GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 LOC3484 2 13465 XP_300743.1 5 247 CTCTGTCACCCA C C CA 3 B c
b
60 GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCACC GT ACGTGAG TCGGACCC
A A AC

GAM281 278 LOC3484 1 17206 XP_209299.2 3 230 CTCTCTTACCCA C CA 3 B c c
74 AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGACATG GTGACGTGAGGTCG ACCC
A AT

GAM281 278 LOC3484 1 6119 XP_302789.1 5 27 CTCTGTCACCCA C CA 3 B c c
94 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCC GT ACGTGAGGTCGGACCC
A AC

GAM281 278 LOC3484 1 2771 XP_302799.1 3 26 GTGGGCTGCCCA T C G 3 B c c
99 GGATGCGGTGCG CAC GCACT CA CCTGGGCA
TGCTTCTG GTG CGTGG GT GGACCCGT

```
                                        -   C A
GAM281  278   LOC3485 1  19361 XP_300762.1  3  1203  CTTGCTCGCCCA        G     A       3  B  b  b
        03                                    GGGTGGAGTGCA CACTGCACTCCA CCTGGGC
                                            GTGGTGTG    GTGACGTGAGGT GGACCCG
                                                  G     C
GAM281  278   LOC3485 1  12803 XP_302806.1  5  745   TCTGTTGTCCAA C-----          -       3  B  c  c
        08                                    GGCTGGAGTGTA      ACTGCACTCCAGCCT GGGCAA
                                            GTAGTGCT         TGATGTGAGGTCGGA CCTGTT
                                                TCGTGA           A
GAM281  278   LOC3485 1  5488  XP_300778.1  3  1340  CTCTGTCGCCCA              A       3  B  b  b
        25                                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
                                            GTGGCACT    GTGACGTGAGGTCGGACCCG
                                                  C
GAM281  278   LOC3485 2  872   XP_302818.1  3  1206  CGCCGTTGCCCA                    3  B  b  b
        32                                    GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
                                            GTGGCATG    GTGGCGTGAGGTCGGACCCGTT

GAM281  278   LOC3485 2  11192 XP_302818.1  3  744   CTAGGAGGCCCA    G         A       3  B  c  b
        32                                    GGCTGGAGTGAG CACT CACTCCAGCCTGGGC
                                            GTGGCACG    GTGG GTGAGGTCGGACCCG
                                                  A          G
GAM281  278   LOC3485 1  1998  XP_302830.1  5  205   CGGGGCTGGGCA   TG  C     ---  A      3  B  c
c
        81                                    GGCTGGATGTGG CAC  CA TCCAGCCTG   GGC
                                            TGGTGTAC    GTG  GT AGGTCGGAC   TCG
                                                  GT  -       GGG   G
GAM281  278   LOC3486 1  10599 XP_300816.1  5  18    CTCTGTTGCTCA        C  C          3  B  c  c
        99                                    GTCTAGGGTGCA CACTGCACTC AG CTGGGCAA
                                            GTGACGTG    GTGACGTGGG TC GACTCGTT
                                                  A  T
GAM281  278   LOC3487 1  7387  XP_300808.1  5  298   CTCTGTCACCCA    C         CA       3  B  c  c
        02                                    GGCTGGAGTACA CACTG ACTCCAGCCTGGG
                                            GTGGCACG    GTGAC TGAGGTCGGACCC
                                                  A          AC
GAM281  278   LOC3487 1  2286  XP_300826.1  3  868   GAAGAGATATCC       CCA     CA       3  B  c
c
        38                                    AGGCCAGGTGCA CACTGCACT   GCCTGGG
                                            GTGGCTCA    GTGACGTGG   CGGACCT
                                                  AC-      AT
GAM281  278   LOC3487 1  810   XP_300843.1  3  447   GCTTGTTGCCCA                    3  B  b  b
        90                                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
                                            GTGGTGCA    GTGACGTGAGGTCGGACCCGTT

GAM281  278   LOC3487 1  7741  XP_302888.1  3  342   TGCTCTCGCCCA              A       3  B  b  b
        97                                    GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
                                            GTGGGTGG    GTGACGTGAGGTCGGACCCG
                                                  C
GAM281  278   LOC3487 1  19402 XP_300845.1  5  24    TCTTGTTGCCCA  C   C             3  B  b  b
        98                                    GGCTGGAATGCA CA TGCA TCCAGCCTGGGCAA
```

ATGGCGCG GT ACGT AGGTCGGACCCGTT
A A
GAM281 278 LOC3488 2 11688 XP_300853.1 5 284 CCCAGGCTGGAG -------- CA 3 B c b
25 TATAGTAGTGCA CACTGCAC TCCAGCCTGGG
GTGGTGTG GTGACGTG AGGTCGGACCC
ATGATATG --
GAM281 278 LOC3488 2 15126 XP_300853.1 5 279 CCCTGTTGCCCA --- 3 B b b
25 GGCTGGAGTATA CACTGC ACTCCAGCCTGGGCAA
GTAGTGCA GTGATG TGAGGTCGGACCCGTT
ATA
GAM281 278 LOC3488 1 12803 XP_300861.1 5 475 TCTGTTGTCCAA C----- - 3 B c c
42 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM281 278 LOC3488 1 3454 XP_302914.1 3 610 AGCTGGCATGCT TC T 3 B c c
99 TGGCTGTGTGCA CACTGCAC CAGCC GGGCA
GTGGCCAG GTGACGTG GTCGG TTCGT
T- -
GAM281 278 LOC3489 1 1305 XP_209688.1 3 240 GACGGGCACCCA T C CA 3 B c c
28 GGCTGCAGTGTG CAC GCACT CAGCCTGGG
TGAGGGGG GTG TGTGA GTCGGACCC
- C AC
GAM281 278 LOC3489 1 1900 XP_300434.1 3 607 AGAGTCTTGCTC CT 3 B b b
95 TGCTGGAGTGCG CACTGCACTCCAGC GGGCAA
GTGGTGCA GTGGCGTGAGGTCG CTCGTT
T-
GAM281 278 LOC3490 2 1746 XP_300250.1 5 533 CTCTGTCACCCA C CA 3 B c b
24 GACTGGAGTGCA CACTGCACTCCAG CTGGG
GTGGCATG GTGACGTGAGGTC GACCC
A AC
GAM281 278 LOC3490 2 4617 XP_300250.1 3 144 TCTTGTCACCCA CA 3 B b b
24 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM281 278 LOC3490 1 16022 XP_300932.1 3 177 CTCTGTCACCCA C CA 3 B c c
75 GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGGTACA GTGACGTGA GTCGGACCC
A AC
GAM281 278 LOC3490 2 6188 XP_300937.1 3 287 TGGAGAAATTCA T CA 3 B c c
96 GGCTGGGTGCAG CACTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA
GAM281 278 LOC3490 2 14560 XP_300937.1 3 287 ATGGAGAAATTC T CA 3 B c c
96 AGGCTGGGTGCA CACTGCAC CCAGCCTGGG
GTGGCTCA GTGACGTG GGTCGGACTT
- AA
GAM281 278 LOC3491 1 12803 XP_302960.1 5 184 TCTGTTGTCCAA C----- - 3 B c c
14 GGCTGGAGTGTA ACTGCACTCCAGCCT GGGCAA

GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM281 278 LOC3491 1 6676 XP_300958.1 5 25 CGCGGGCCCAGA A A -- A 3 B c c
36 GGCTGGAGGCAG C CTGC CTCCAGCCT GGGC
CGGGGAGC G GACG GAGGTCGGA CCCG
C - GA G

GAM281 278 LOC3491 4 3349 XP_300969.1 3 832 CCCTATTGCCCA C 3 B b b
70 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 LOC3491 4 9545 XP_300969.1 3 469 CTCTGTTGCCCA 3 B b b
70 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 LOC3491 4 11508 XP_300969.1 5 1053 CTCTGCCAGCCA C C --- 3 B c b

70 GACTGGAGTGCA CA TGCACTCCAG CTGG GCA
TTGGCGAG GT ACGTGAGGTC GACC CGT
T A GAC

GAM281 278 LOC3491 4 18074 XP_300969.1 5 147 TTCTGTGGCCCA A 3 B b b
70 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCTGT GTGACGTGAGGTCGGACCCG
G

GAM281 278 LOC3492 2 2323 XP_300251.1 5 412 GGGGCATGCCCA CA--- - CA 3 B c
c

51 GGCAGAGTGACA CTG CACTC GCCTGGGCA
GGAGAG GAC GTGAG CGGACCCGT
GAGAG A A-

GAM281 278 LOC3492 2 4454 XP_300251.1 3 444 CACTATCACCCA A C CA 3 B c c
51 GGCTAGAGGGCA CACTGC CTC AGCCTGGG
GTGGCACA GTGACG GAG TCGGACCC
G A AC

GAM281 278 LOC3493 1 10639 XP_088528.1 5 447 TCTGGTTGCCCA C 3 B b b
60 GGCTGGGGTACA CACTG ACTCCAGCCTGGGCAA
GTGGTGGA GTGAC TGGGGTCGGACCCGTT
A

GAM281 278 LOC3494 1 13466 XP_303044.1 5 14 CTCCGTTGCCCA C C 3 B b b
08 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGTGCG GT AC TGAGGTCGGACCCGTT
A A

GAM281 278 LOC3494 1 4112 XP_300513.1 3 1060 TTTTGCAGCCCA A 3 B b b
40 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
A

GAM281 278 LOC3501 1 18715 XP_303810.1 5 16 TCCCTCTGCCCA T A G 3 B c c
06 GGTGGGGGCCGT CAC GC CTCCA CCTGGGCA
GGCTGGAA GTG CG GGGGT GGACCCGT
C - -

GAM281 278 LOC3503 1 8276 XP_304054.1 5 113 AGCTGTGTCCAG CA------ C - 3 B c c

95 GGCTGGAGTCAG CTG ACTCCAGCC TGGGCA
AGCCTGCT GAC TGAGGTCGG ACCTGT
TCGTCCGA - G
GAM281 278 LOC5105 1 5678 NP_056995.1 3 405 GTGAACTGCTTA C A 3 B c c
8 GGTAGGAGTGCA CA TGCACTCC GCCTGGGCA
CTGCAGTT GT ACGTGAGG TGGATTCGT
C A
GAM281 278 LOC5112 1 1167 NP_057178.1 3 430 TAATCAGAAGCT T CTG A 3 B c
c
2 AAGCTGGGTGCA CACTGCAC CCAGC GGC
GTGGCTCA GTGACGTG GGTCG TCG
- AA- A
GAM281 278 LOC5119 2 3111 NP_057415.1 5 98 TCCTGTTACCCA CA CA 3 B c b
3 GGCTGGAGGACA CACTG CTCCAGCCTGGG
GTGATGTG GTGAC GAGGTCGGACCC
AG AT
GAM281 278 LOC5119 2 14721 NP_057415.1 3 733 TTCTGTTGTCCA G 3 B b b
3 GGATGGAGTGCA CACTGCACTCCA CCTGGGCAA
GTGGTTGA GTGACGTGAGGT GGACCTGTT
A
GAM281 278 LOC5125 1 14855 NP_057580.2 5 156 CTCTGTTACCCA CA 3 B b b
7 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AT
GAM281 278 LOC5133 1 8243 NP_057728.1 5 337 CTCTGTTGCCCA C C 3 B b b
4 GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA
ATGGCACA GT ACGTGAG TCGGACCCGTT
A A
GAM281 278 LOC5133 1 18703 NP_057730.1 3 665 CTCTGTTACCCA C CA 3 B c c
6 GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGAGTG GT ACGTGAGGTCGGACCC
A AT
GAM281 278 LOC5595 1 17853 NP_061976.1 5 0 GTCACCCAGGCT CA 3 B c c
4 GGAGTGTAGTGG CACTGCACTCCAGCCTGGG
CGCAATCT GTGATGTGAGGTCGGACCC
AC
GAM281 278 LOC5690 1 5945 NP_064528.1 3 518 CTTTGTCACCCA C CA 3 B c c
2 GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGTGCA GTGACGTGAG TCGGACCC
A AC
GAM281 278 LOC5710 1 16916 NP_065114.2 3 587 TCTTGTTGCCCA C 3 B b b
7 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 LOC5714 1 11036 NP_065155.2 3 736 TCTTGTTGCCCA --- 3 B b b
6 GGCTGGAGTGCA CACT GCACTCCAGCCTGGGCAA
ACGGTGCA GTGG CGTGAGGTCGGACCCGTT
CAA
GAM281 278 LOC5720 1 2349 XP_290488.1 5 223 GGGCCTCTCTGC CA----- GCC 3 B c
c

	9				CCGTGGAGTGCA CTGCACTCCA TGGGCA GGAGCGAA GACGTGAGGT GCCCGT AAGCGAG ---									
GAM281	278 0	LOC9011	1	10533	XP_029046.1	3	58	CCTTAGGGCCTA CCCTGGAGTGCT CACTGC ACTCCAG TGGGC GCAGTGTG GTGACG TGAGGTC ATCCG TCG CC G	---	CC	A	3	B	c c
GAM281	278 8	LOC9040	1	7704	XP_031517.1	5	1646	TCTTGTTACCCA GGCTGGAGTGCA CACTGCACTCCAGCCTGGG GTGGCGCG GTGACGTGAGGTCGGACCC AT		CA		3	B	b b
GAM281	278 5	LOC9048	2	6896	XP_032059.1	3	1341	CTCTGTCGCCCA GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC GTGATGCA GTGACGTGAGGTCGGACCCG C		A		3	B	b b
GAM281	278 5	LOC9048	2	18698	XP_032059.1	3	1183	CTCTGTCACCCA GGCTAGAGTGCA CACTGCACTC AGCCTGGG GTGGAGCG GTGACGTGAG TCGGACCC A AC		C	CA	3	B	c b
GAM281	278 9	LOC9099	1	15038	XP_035410.1	3	115	CTCTGTTGCCCA GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA GTGGCACG GTGAC TGAGGTCGGACCCGTT A		C		3	B	b b
GAM281	278 6	LOC9105	1	14660	NP_612377.1	3	786	CTCACTCTGGCG CTCTGGAGTGCA CACTGCACTCCA GCC GGG GTGGTGTG GTGACGTGAGGT CGG CTC CTCG T AC	----	T	CA	3	B	c c
GAM281	278 5	LOC9111	3	12591	XP_036218.1	3	758	GTCTTTCACCCA GGCTGGAGTGCT CAC GCACTCCAGCCTGGG GTGGCACG GTG CGTGAGGTCGGACCC T AC	T		CA	3	B	c b
GAM281	278 5	LOC9111	3	17831	XP_036218.1	3	2144	ACTTGTTGCCCA GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA ATGGTACA GT ACGTGAGGTCGGACCCGTT A	C			3	B	b b
GAM281	278 5	LOC9111	3	19989	XP_036218.1	3	285	TCTTGTCACCCA GGCTGGAGTGCA CA TGCACTCCAGCCTGGG ATGGCACG GT ACGTGAGGTCGGACCC A AC	C		CA	3	B	c b
GAM281	278 0	LOC9117	1	16178	XP_036612.1	5	209	CTTTGTCGCCCG GGCAGGAGTGCA CACTGCACTCC GCCTGGGC GTGGCTCA GTGACGTGAGG CGGGCCCG A C		A	A	3	B	c c
GAM281	278 0	LOC9125	1	8577	XP_037135.1	5	2207	CTCTGTCACCCA GGCTGGAGTTAT CACTG ACTCCAGCCTGGG AGTGACGT GTGAT TGAGGTCGGACCC AT AC	C-		CA	3	B	c c
GAM281	278	LOC9126	1	18355	XP_037268.1	5	267	GCAGGATGCCCA C----		AC	- -	3	B	c c

6 GGGCTCGGAAGC ACTGC TCC AGCC TGGGCA
AGTAAGGA TGACG AGG TCGG ACCCGT
AGGAA A- C G
GAM281 278 LOC9137 1 9077 XP_038063.5 3 1526 TCTTGTTGCCCA G 3 B b b
3 GGCTGGAGTGAA CACT CACTCCAGCCTGGGCAA
GTGGCGTG GTGA GTGAGGTCGGACCCGTT
A
GAM281 278 LOC9154 1 17238 XP_039115.1 5 1290 GCCCTGTGGCTG C TG G 3 B c
c
9 GGCTGGAGTGCA CA TGCACTCCAGCC G CA
ATGGCGCG GT ACGTGAGGTCGG C GT
A GT G
GAM281 278 LOC9166 1 8303 NP_612381.1 3 517 CTCTGTCGGCCA C C --- 3 B c c
1 GGCTGGAATGCA CA TGCA TCCAGCCTGG GCA
ATGGTGCC GT ACGT AGGTCGGACC TGT
A A GGC
GAM281 278 LOC9166 1 8075 NP_612382.1 3 339 CTCTGTGGCCCA A 3 B b b
3 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
G
GAM281 278 LOC9189 1 14589 XP_041340.1 3 205 CTCTGCCGCCCA A A 3 B b b
3 GGCGGGAGTGCA CACTGCACTCC GCCTGGGC
GTGGCAGT GTGACGTGAGG CGGACCCG
G C
GAM281 278 LOC9201 1 9327 XP_042234.2 3 3805 CTCTGTGGCCCA ACTCCA A 3 B
c c
7 GGCCGGCAGTGG CACTGC GCCTGGGC
CTGCCTCT GTGACG CGGACCCG
GC---- G
GAM281 278 LOC9214 1 4097 XP_043160.1 5 761 CCCTGCCGCCCA C A 3 B b b
8 GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGCACG GTGACGTGAG TCGGACCCG
A C
GAM281 278 LOC9236 1 1082 XP_044589.1 3 529 GGATGGTGATGT T TG 3 B b b
0 CGGCTGGGTGCA CACTGCAC CCAGCC GGCA
GTGGCTCA GTGACGTG GGTCGG CTGT
- --
GAM281 278 LOC9259 1 19339 NP_775739.1 3 3527 CTCTGTTGCCCG C C 3 B b b
7 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGCATG GT AC TGAGGTCGGGCCCGTT
A A
GAM281 278 LOC9265 1 10989 XP_046434.3 3 341 AGAAACTGCGGC T A G- 3 B c c
9 AGGCCGGGTGCA CACTGCAC CC GCCTG GCA
GTGTCTCA GTGACGTG GG CGGAC CGT
- C GG
GAM281 278 LOC9313 1 9953 XP_049396.1 5 1234 GCTCTGTCACCA A -- 3 B b b
2 GGCTGGAGGGCA CACTGC CTCCAGCCTGG GCA
GTGGTGCG GTGACG GAGGTCGGACC TGT

G AC
GAM281 278 LOC9443 1 18633 NP_660280.1 5 876 TTACAAAATTGC T TG 3 B b b
1 TGGCTGGGTGCA CACTGCAC CCAGCC GGCAA
GTGGCTTA GTGACGTG GGTCGG TCGTT
- --
GAM281 278 LSS 1 6091 NP_002331.2 3 1071 GTCTCATGCCCA CT T G 3 B c c
GGTGGGTGCTCT CA GCAC CCA CCTGGGCA
GGGCTGGA GT CGTG GGT GGACCCGT
CT - -
GAM281 278 LTB4R 1 1022 NP_000743.1 5 303 CTCTGTCATTCA --- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGTGCG GTGACGTGAGGTCGGAC CTGT
TTA
GAM281 278 LY75 1 17724 NP_002340.1 3 573 CTCTGTTGCCCA C C 3 B b b
GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGCGTG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 LYZ 1 7382 NP_000230.1 3 331 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM281 278 LZTS1 1 4518 NP_066300.1 3 1445 CTCTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC
GAM281 278 MAC30 1 5069 XP_031536.2 3 228 CTCTGTTGCCCA ----- 3 B b b
GGCTGGAGTAAA CACTGC ACTCCAGCCTGGGCAA
GGGCAGTG GTGACG TGAGGTCGGACCCGTT
GGAAA
GAM281 278 MADD 1 3262 NP_003673.2 3 559 AGCTACTGCCCA ACTCCAG 3 B c
c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569826.1 3 559 AGCTACTGCCCA ACTCCAG 3 B c
c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569827.1 3 559 AGCTACTGCCCA ACTCCAG 3 B c
c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569828.1 3 559 AGCTACTGCCCA ACTCCAG 3 B c
c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569829.1 3 559 AGCTACTGCCCA ACTCCAG 3 B c
c

GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569830.1 3 687 AGCTACTGCCCA ACTCCAG 3 B c c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569831.1 3 687 AGCTACTGCCCA ACTCCAG 3 B c c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MADD 1 3262 NP_569832.1 3 559 AGCTACTGCCCA ACTCCAG 3 B c c
GGGCCCGCAGTG CACTGC CCTGGGCA
TTGGCTGC GTGACG GGACCCGT
CCCG---
GAM281 278 MAIL 1 2338 NP_113607.1 3 872 CTCTGGCGCCCA C A 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGC
GTGGCATG GTGAC TGAGGTCGGACCCG
A C
GAM281 278 MAK 1 1989 NP_005897.1 3 644 CTCTTGTGTCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCACT GTGACGTGAGGTCGGACCTGT
GAM281 278 MAP2K1 1 5154 NP_002746.1 3 279 AAACCTGTGCCA CACTC - 3 B c c
GGCTGAATTACA CACTG CAGCCTGG GCA
GTGAAATT GTGAC GTCGGACC TGT
ATTAA G
GAM281 278 MAPA 1 5231 NP_660299.1 3 806 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGCTGCG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 MAPK8IP 1 14298 NP_203750.1 3 1043 CCCTGTGCTCAG GCA- - 3 B c c
3 GGCTGGAGAGAG CACT CTCCAGCC TGGGCA
GGTGGCGG GTGG GAGGTCGG ACTCGT
GAGA G
GAM281 278 MAPRE1 1 20000 NP_036457.1 3 1079 TGGGATCTGCCA C- ---- G 3 B c c
GGCTGGGGTGTT ACT GCACTCCAGCCTGG CA
TTCGGTAT TGG TGTGGGGTCGGACC GT
TA CTTT -
GAM281 278 MCLC 1 7270 NP_055942.1 3 316 CTCTGTCACCCA G CA 3 B c c
GGCTGGAGTGAG CACT CACTCCAGCCTGGG
GTGGTACA GTGG GTGAGGTCGGACCC
A AC
GAM281 278 MDM2 1 6671 NP_002383.1 3 355 CTCTGTTACCCA CA 3 B b b

GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM281 278 MDM2 1 6671 NP_006869.1 3 355 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM281 278 MDM2 1 6671 NP_006870.1 3 355 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM281 278 MDM2 1 6671 NP_006871.1 3 355 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM281 278 MDM2 1 6671 NP_006872.1 3 355 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM281 278 MDM2 1 6671 NP_006873.1 3 299 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT

GAM281 278 MDM4 1 7078 NP_002384.1 3 548 TTCTGTCTCCCA C CA 3 B c c
GGCTGAAGTGCA CACTGCACT CAGCCTGGG
GTGAGTCA GTGACGTGA GTCGGACCC
A TC

GAM281 278 MDS009 1 835 NP_064619.1 5 51 TGTTCGAGGACT T ---- - - 3 B c c
CGCGGGTGTGCA CACTGCAC CC AG CCT GGGCA
GTGCACCT GTGACGTG GG TC GGA CTTGT
T GCGC A G

GAM281 278 MEFV 2 5443 NP_000234.1 3 511 CTCTGTGGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
G

GAM281 278 MEFV 2 19829 NP_000234.1 3 823 TCTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 MESDC2 1 6523 XP_051854.1 3 73 GCTCTTTGCCCA G- C-- 3 B c c
GCTCCTGGGGTG CACT CACTCCAG CTGGGCAA
GGAGTGGT GTGA GTGGGGTC GACCCGTT
GG CTC

GAM281 278 MFAP4 1 9082 NP_002395.1 3 430 TAGTGTGCTAAG C-- CTG 3 B c c
CTGAGCAGTGCA CACTGCACT CAGC GGCA
GTGTGAAC GTGACGTGA GTCG TCGT
CGA AA-

GAM281 278 MFTC 1 16545 NP_110407.2 3 548 CTTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG

C

GAM281 278 MGAT2 1 9699 NP_079374.1 3 986 TCTTGTCGCTCA C A 3 B c c
GCCTGGAGTGCA CACTGCACTCCAG CTGGGC
GTGAGCTG GTGACGTGAGGTC GACTCG
C C

GAM281 278 MGC1020 1 5781 NP_659497.1 3 181 CTTTGTCACGCA C --- 3 B b b
0 GGCTAGAGTGCA CACTGCACTC AGCCTG GGCAA
GTGGCGCA GTGACGTGAG TCGGAC CTGTT
A GCA

GAM281 278 MGC1077 2 5386 NP_085044.2 5 225 CTAGAGATGCCC G CC 3 B b
b
2 ATCTGGAGTGAG CACT CACTCCAG TGGGCA
TGCAGGAC GTGA GTGAGGTC ACCCGT
- T-

GAM281 278 MGC1077 2 6519 NP_085044.2 5 225 AGATGCCCATCT G CC 3 B b b

2 GGAGTGAGTGCA CACT CACTCCAG TGGGCA
GGACCAGG GTGA GTGAGGTC ACCCGT
- T-

GAM281 278 MGC1081 1 2199 NP_085045.2 3 89 CTCTGTCGCCCA C C A 3 B c c
8 GGCTGGAGTACA CA TG ACTCCAGCCTGGGC
ATGGTGCG GT AC TGAGGTCGGACCCG
A A C

GAM281 278 MGC1110 1 17609 NP_115701.2 3 1315 CTGTGTTGCTCA 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACTCGTT

GAM281 278 MGC1226 2 4245 NP_116085.1 5 77 TCCTCCGCGGCG C G- A 3 B c b

2 GGTTTGGGTGCA CACTGCACTC AGCCTG GC
GTGGACCC GTGACGTGGG TTGGGC CG
T GG C

GAM281 278 MGC1226 2 12220 NP_116085.1 5 203 TGATGTTGCCCA C 3 B b b
2 GGCTAGAGTGCA CACTGCACTC AGCCTGGGCAA
GTGGCACA GTGACGTGAG TCGGACCCGTT
A

GAM281 278 MGC1251 1 18251 NP_291026.1 3 0 CCCCAGGTTGGA CA 3 B c c
8 GTGCAGTGGCGT CACTGCACTCCAGCCTGGG
GTCTTGGG GTGACGTGAGGTTGGACCC
C-

GAM281 278 MGC1276 1 10178 NP_116112.1 5 155 GCAGGTTGCCCA CA----- - AG 3 B c
c
0 GGAGGAGCTGCA CTGCA CTCC CCTGGGCAA
GCGCCAGC GACGT GAGG GGACCCGTT
CGACCGC C A-

GAM281 278 MGC1301 1 11562 NP_542387.1 3 458 CTCTGTTGCCCA CCA 3 B b
b
7 GGCAGTAGTGCA CACTGCACT GCCTGGGCAA
GTGGCGCG GTGACGTGA CGGACCCGTT
TGA

GAM281 278 MGC1302 1 13564 NP_689501.1 3 433 GTCTGTTTCCCA CA 3 B c c
4 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGATACA GTGATGTGAGGTCGGACCC
TT
GAM281 278 MGC1313 2 6646 NP_219363.1 3 766 TCTTGTTGCCCA CAC----- 3 B c b
8 GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCGCA ACGTGAGGTCGGACCCGTT
ACGCGATA
GAM281 278 MGC1313 2 9543 NP_219363.1 3 456 CTCTGTCACCCA CA 3 B b b
8 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 MGC1317 1 20116 NP_116101.1 3 289 CACTTCTGCCCA G CA-- 3 B c
c
0 GGCAGCAGGGTG CACT CACTC GCCTGGGCA
GGTGGGTA GTGG GTGGG CGGACCCGT
- ACGA
GAM281 278 MGC1320 1 9494 NP_113653.1 3 129 CTCTGTTGCCCA 3 B b b
4 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTATG GTGACGTGAGGTCGGACCCGTT
GAM281 278 MGC1428 1 3677 NP_542391.1 3 452 CTCTGTTGCCCA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGACGTG GTGACGTGAGGTCGGACCCGTT
GAM281 278 MGC1443 1 17347 NP_116286.1 5 825 CCCTGTCACCCA C CA 3 B c
c
6 GGCTGGGGTACG CACTG ACTCCAGCCTGGG
GTGGCATG GTGGC TGGGGTCGGACCC
A AC
GAM281 278 MGC1483 1 15044 NP_219480.1 3 381 CTCTGTTGCCCA 3 B b b
6 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT
GAM281 278 MGC1560 1 10968 NP_659474.1 5 287 CTCTGTTGCCCA C C 3 B b b
6 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
TTGGTGTG GT AC TGAGGTCGGACCCGTT
T A
GAM281 278 MGC1566 1 3620 NP_116145.1 3 25 CTAGGATGCCCA CA----- T - 3 B c c
8 GGGCTGGGTGCA CTGCAC CCAGCC TGGGCA
GCCAGCTG GACGTG GGTCGG ACCCGT
GTCGACC - G
GAM281 278 MGC1587 1 2894 NP_116309.1 5 81 CTCTGTCGCCCA G T A 3 B c c
3 GGCTGGCGTGAA CACT CAC CCAGCCTGGGC
GTGGCGCA GTGA GTG GGTCGGACCCG
A C C
GAM281 278 MGC1617 1 15168 NP_116155.1 3 268 TCCCAGTTCTGC G ------- CA 3 B c
c

9 GGCTGGAGTGGG CACT CACTCCAGCC TGGG
TGGGTGCA GTGG GTGAGGTCGG ACCC
- CGTCTTG T-
GAM281 278 MGC1842 1 15046 XP_037797.2 3 1420 CTCTGTTGCCCA C 3 B b b
GACTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCACG GTGACGTGAGGTC GACCCGTT
A
GAM281 278 MGC2167 1 16916 NP_443093.1 3 500 TCTTGTTGCCCA C 3 B b b
5 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 MGC2306 1 7160 NP_002041.2 3 225 GACCGCTGCCCA C ----- G 3 B c c

GGTGGGGTTTCC CA TGC ACTCCA CCTGGGCA
TGCATGGA GT ACG TGGGGT GGACCCGT
- TCCTT -
GAM281 278 MGC2474 2 7797 NP_076420.1 3 954 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 MGC2474 2 18665 NP_076420.1 3 1312 GCTCCTCACCCA C CA 3 B c
b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGTGTG GTGACGT AGGTCGGACCC
A AC
GAM281 278 MGC2477 3 5609 NP_077004.1 5 1480 CTCTGTTGCCCA C 3 B b b
GCTGGAGTGCAG CACTGCACTCCAGC TGGGCAA
TGGCGTGA GTGACGTGAGGTCG ACCCGTT
-
GAM281 278 MGC2477 3 8610 NP_077004.1 5 1291 TCTGTCGCCCAG - A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCC TGGGC
GTGGCGCG GTGACGTGAGGTCGG ACCCG
G C
GAM281 278 MGC2477 3 19729 NP_077004.1 5 1480 ACTCTGTTGCCC C 3 B b b
AGCTGGAGTGCA CACTGCACTCCAGC TGGGCAA
GTGGCGTG GTGACGTGAGGTCG ACCCGTT
-
GAM281 278 MGC2603 1 5845 NP_076942.1 3 419 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 MGC2691 1 15104 NP_659413.1 3 606 TGCCCTTCACCA --- GCCT--- 3 B c
c
4 TGAGAGGGTGCA CACTGCACTC CA GGGCA
GTGAGAAG GTGACGTGGG GT CCCGT
AGA ACCACTT
GAM281 278 MGC2718 1 3976 NP_076972.2 3 437 GAGCTGAGCCCA ACTC A 3 B c
c
GGCTGCGTAGTG CACTGC CAGCCTGGGC
ACCACAAG GTGATG GTCGGACCCG

C--- A

GAM281 278 MGC2734 2 18352 XP_300964.1 5 1668 TCTTGTTGCCCA - 3 B b b
5 GGGCTGGAGTGC CACTGCACTCCAGCC TGGGCAA
AGTGGCAT GTGACGTGAGGTCGG ACCCGTT
G

GAM281 278 MGC2734 2 19385 XP_300964.1 5 1668 CTTGTTGCCCAG - 3 B b b
5 GGCTGGAGTGCA CACTGCACTCCAGCC TGGGCAA
GTGGCATG GTGACGTGAGGTCGG ACCCGTT
G

GAM281 278 MGC2989 1 14858 NP_653219.1 3 606 CTCTGTCACCCA CA 3 B c c
1 GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGTGCA GTGGCGTGAGGTCGGACCC
AC

GAM281 278 MGC2989 1 16672 NP_659485.1 3 503 CTTTGTTGCCCA C 3 B b b
8 GACTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGGCATA GTGACGTGAGGTC GACCCGTT
A

GAM281 278 MGC3113 1 10136 NP_076940.1 3 713 CTCTGTTCCCCA A CA 3 B c c

GGCCGGAGTGCA CACTGCACTCC GCCTGGG
GTGGTACG GTGACGTGAGG CGGACCC
C CT

GAM281 278 MGC3207 2 5157 NP_115661.1 3 1437 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCC GTGACGTGAGGTCGGACCCG
C

GAM281 278 MGC3207 2 13812 NP_115661.1 3 788 ACTCGTTGCCCA CA----- 3 B c b

GGCTGGAGTGTA CTGCACTCCAGCCTGGGCAA
GAGGCGAG GATGTGAGGTCGGACCCGTT
GAGCGGA

GAM281 278 MGC3329 1 4477 NP_076991.2 3 1597 TCTTGTTGTCTA T 3 B b b
GGCTGGAGTGCC CAC GCACTCCAGCCTGGGCAA
GTGGTGCG GTG CGTGAGGTCGGATCTGTT
C

GAM281 278 MGC3348 1 11585 NP_694998.1 5 112 GCCCGGTGCCCA CA A------ 3 B c
c
6 GGCTGGGGCCGC CTGC CTCCAGCCTGGGCA
CAAGCAGC GACG GGGGTCGGACCCGT
C- AACCGCC

GAM281 278 MGC3363 1 12069 NP_689809.1 3 684 CTCTGTCACCCA CA 3 B c c
7 GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGTGTA GTGATGTGAGGTCGGACCC
AC

GAM281 278 MGC3388 1 8724 NP_659473.1 3 49 ATGCAATTTCCA T TCC ----- 3 B c c

7 GGCTGTGCTGTG CAC GCAC AGCCTGG GCA
GACTTCTT GTG CGTG TCGGACC CGT
T --- TTTAA

GAM281 278 MGC3403 1 9529 NP_694956.1 5 278 TTCAGCAGTCCA CTC A 3 B c
c

4 GGCTGATGCAGT CACTGCA CAGCCTGGGC
GGCTTCAA GTGACGT GTCGGACCTG
A-- A

GAM281 278 MGC3407 1 19817 NP_689688.1 3 189 TTCTGTCACCCA CA 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 MGC3413 2 8232 XP_291029.1 3 501 CTCTGTCACCCA CA 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM281 278 MGC3413 2 9087 XP_291029.1 3 335 CACTGTCACCCA CA 3 B b b
2 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM281 278 MGC3513 1 8535 NP_689640.1 5 174 CTCTCTCACCCA GC CA 3 B c
c
6 GGCTGGAGTAGA CACT ACTCCAGCCTGGG
GTGACAAT GTGA TGAGGTCGGACCC
GA AC

GAM281 278 MGC3544 2 6886 NP_694952.1 3 493 CTCTGTCGCCCA C A 3 B b b
0 GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGTGCA GTGACGT AGGTCGGACCCG
A C

GAM281 278 MGC3544 2 7378 NP_694952.1 3 184 CTCTGTCACCCA CA 3 B c b
0 GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGCGCA GTGGCGTGAGGTCGGACCC
AC

GAM281 278 MGC3546 1 7484 NP_694976.1 3 87 CCTTGTTGCCCA C 3 B b b
8 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 MGC3771 1 3231 NP_112232.1 5 748 CTCTTCTTCCCA C C CA 3 B c c

TGCTGGAGTGCA CA TGCACTCCAGC TGGG
ATGGCGCA GT ACGTGAGGTCG ACCC
A T TT

GAM281 278 MGC3932 1 13428 NP_689642.2 3 697 CTGGCTTGCCCA 3 B b b
0 GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGCTAG GTGGCGTGAGGTCGGACCCGTT

GAM281 278 MGC4015 1 10743 NP_689563.1 3 318 CTGTATTGCCCA TG 3 B b b
7 GGCTGGAGTGTG CAC CACTCCAGCCTGGGCAA
GTGGCACA GTG GTGAGGTCGGACCCGTT
GT

GAM281 278 MGC4016 1 7220 NP_714920.1 5 285 CTCTGTTGCCAA C G 3 B b b
8 GGCTGGAATGCA CACTGCA TCCAGCCT GGCAA
GTGGCGAG GTGACGT AGGTCGGA CCGTT
A A

GAM281 278 MGC4057 2 16218 NP_689989.1 3 904 TCTTGTCTCCCA C C CA 3 B c
c

9 GACTGGAGTGCA CA TGCACTCCAG CTGGG
ATGGCATG GT ACGTGAGGTC GACCC
A A TC
GAM281 278 MGC4057 2 19220 NP_689989.1 3 333 CTCTGTCACTCA CA 3 B c c
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTATA GTGACGTGAGGTCGGACTC
AC
GAM281 278 MGC4171 1 10555 NP_077283.1 5 256 TGCCCCTGCCCA G- TC-- 3 B c
c
GGCTGCCATGTG CACT CAC CAGCCTGGGCA
AGGGTGTG GTGG GTG GTCGGACCCGT
GA TACC
GAM281 278 MGC4248 2 3338 NP_115709.2 3 277 AATTGACTGCCA T G 3 B b b
GGCTGGGTGCAG CACTGCAC CCAGCCTGG CA
TGGCTCAC GTGACGTG GGTCGGACC GT
- -
GAM281 278 MGC4248 2 8539 NP_115709.2 3 277 AAATTGACTGCC T G 3 B b b
AGGCTGGGTGCA CACTGCAC CCAGCCTGG CA
GTGGCTCA GTGACGTG GGTCGGACC GT
- -
GAM281 278 MGC4312 1 12783 NP_775784.1 3 200 CTCTGTCACCCA C CA 3 B c c
2 GGTTGGAGTGCA CA TGCACTCCAGCCTGGG
TTGGTGTG GT ACGTGAGGTTGGACCC
T AC
GAM281 278 MGC4606 1 11069 NP_078792.1 3 36 CACTGCTCCTGC C CCT 3 B c
c
CTCTAGGGTGCA CACTGCACTC AG GGGCA
GTGTCCGT GTGACGTGGG TC TCCGT
A ---
GAM281 278 MGC5045 1 16867 NP_775733.1 3 89 ACTTCTTGCCCA C C 3 B b b
2 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGTGCG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 MGC5055 2 11296 NP_776163.1 3 459 ACTTTGCTCCCA C CA 3 B c b
9 GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCTAT GTGACGT AGGTCGGACCC
A TC
GAM281 278 MGC5055 2 15151 NP_776163.1 3 561 CTCTGTCGTCCA A 3 B b b
9 GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGACTCA GTGACGTGAGGTCGGACCTG
C
GAM281 278 MGC5149 1 13759 XP_051200.2 3 1953 ACTCTGTCACCA C -- 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGG GCA
GTGGCACG GTGACGTGAG TCGGACC TGT
A AC
GAM281 278 MGC9912 1 12221 NP_542395.1 3 351 GCTCTGTCGCCA C -- 3 B b b
GACTGGAGTGCA CACTGCACTCCAG CTGG GCA
GTGGCGCA GTGACGTGAGGTC GACC TGT

A GC
GAM281 278 MGRN1 1 16616 XP_048119.4 3 1594 TCTTGCTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCA
GTGGCTCA GTGACGTGAGGTCGGACCCGT

GAM281 278 MHC2TA 3 783 NP_000237.1 3 439 CACTGTTGCCCA T 3 B b b
GGCTGGCGTGCA CACTGCAC CCAGCCTGGGCAA
GTGGTGCG GTGACGTG GGTCGGACCCGTT
C
GAM281 278 MHC2TA 3 922 NP_000237.1 3 809 CAGATTGCAACA CAC G- 3 B c b

GGCTGGGCTTCA CACTG TCCAGCCTG GCAA
GTGGCAGC GTGAC GGGTCGGAC CGTT
TTC AA
GAM281 278 MHC2TA 3 2053 NP_000237.1 3 2660 CTCTTATGCCCA C 3 B b b
CGCTGGAGTGCA CACTGCACTCCAGC TGGGCA
GTGAGCCG GTGACGTGAGGTCG ACCCGT
C
GAM281 278 MIRAB13 1 11523 NP_203744.1 3 1732 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 MIRAB13 1 11523 XP_039236.6 3 2297 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 MKRN4 1 12075 NP_110384.1 3 373 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 MLANA 1 13029 NP_005502.1 3 611 TTTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGCG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 MLC1 1 19859 NP_055981.1 3 775 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAC GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM281 278 MLC1 1 19859 NP_055981.1 3 877 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAC GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM281 278 MLC1 1 19859 NP_631941.1 3 775 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAC GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM281 278 MLC1 1 19859 NP_631941.1 3 877 CTGTCATGCCCA T-- C 3 B c c
GCTTGGAGTGCC CAC GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C

GAM281 278 MLZE 1 9728 NP_113603.1 5 585 CGGAGTTGCCCA CA----- 3 B c c
GGCTGGAGTGCA CTGCACTCCAGCCTGGGCAA
GCGCATGG GACGTGAGGTCGGACCCGTT
GGTACGC
GAM281 278 MMPL1 1 4374 NP_004133.1 3 511 TTCTGTCCTCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGACATG GT ACGTGAGGTCGGACCT
A CC
GAM281 278 MO25 2 2695 NP_057373.1 3 377 ATCTTTGTTGGC CA--- TG 3 B c c
GATCTGAGTGCA CACTGCACTC GCC GGCAA
GTGTGGCA GTGACGTGAG CGG TTGTT
TCTAG --
GAM281 278 MO25 2 7980 NP_057373.1 5 281 GCCCCGTAGCAC A A G A 3 B c c
AGGCGGAGTGCA C CTGCACTCC GCCTG GC
GCGGAGGC G GACGTGAGG CGGAC CG
C - A A
GAM281 278 MOAP1 1 1744 NP_071434.2 3 300 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 moblak 1 19657 NP_570719.1 3 1259 CCGGCCTAACCA GCA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGG
GTGGTGGG GTGACGTGAGGTCGGACC
AAT
GAM281 278 MOCS3 1 12064 NP_055299.1 3 579 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGATGTGAGGTCGGACCCGTT

GAM281 278 MPL 2 11185 NP_005364.1 3 569 CTCTGTCACCCA C C CA 3 B c b
GGCTGCAGTGCA CA TGCACT CAGCCTGGG
ATGGCGCG GT ACGTGA GTCGGACCC
A C AC
GAM281 278 MPL 2 16608 NP_005364.1 3 750 TGCCTGTTGCCA C G 3 B b b
GACTGGAGTGCA CACTGCACTCCAG CTGG CAA
GTGGCACG GTGACGTGAGGTC GACC GTT
A -
GAM281 278 MRPL10 1 13874 NP_683685.1 5 70 CTGCCCCAGGCG C ----- 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCT GGGCA
GTGGCATG GTGACGTGAG TCGGG CCCGT
A CGGAC
GAM281 278 MRPL35 1 9545 NP_057706.2 3 1060 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 MRPL44 1 14596 NP_075066.1 3 259 CTCTGTCGCCCA C A 3 B b b
GGCTGGACTGCA CACTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
C C
GAM281 278 MRPL49 1 5438 NP_004918.1 3 324 CTCTGTTGCCCA G 3 B b b
GGGTGGAGTGCA CACTGCACTCCA CCTGGGCAA

GTGGCATG GTGACGTGAGGT GGACCCGTT
G
GAM281 278 MRPS27 1 4179 NP_055899.1 3 430 TTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 MSTP028 1 12951 NP_114160.1 3 1907 CTCTATTGGCCA G 3 B b b
GGCTGGAGTGTA CACTGCACTCCAGCCTGG CAA
GTGGCACC GTGATGTGAGGTCGGACC GTT
G
GAM281 278 MtFMT 1 12918 NP_640335.1 3 143 CTCTGTCACCCA CAC CA 3 B c c
GGCTGGAATCCA CACTG TCCAGCCTGGG
GTGGCACT GTGAC AGGTCGGACCC
CTA AC
GAM281 278 MTH2 1 15874 NP_060753.1 3 851 CTCTGTTGCCCA CC 3 B b b
CATTGGAGTGCA CACTGCACTCCAG TGGGCAA
GTGGCACG GTGACGTGAGGTT ACCCGTT
AC
GAM281 278 MTR 1 2028 NP_000245.1 3 813 CTCTGTCGCCCA CA----- A 3 B c c
GGCTGGAGTGCA CTGCACTCCAGCCTGGGC
GGGGCGCA GACGTGAGGTCGGACCCG
ACGCGGG C
GAM281 278 MU 1 2453 NP_071368.1 3 1094 CAGTCTAATTTG T ------ A 3 B c c
AGGCTGGGTGCA CACTGCAC CCAGCCT GGGC
GTGGCTCA GTGACGTG GGTCGGA TCTG
- GTTTAA A
GAM281 278 MYCL2 1 16868 NP_005368.1 3 1431 TCTTGTCGCCCA CT- A A 3 B c c
GGCTGGAGGTTA CA GC CTCCAGCCTGGGC
ATGGCATG GT TG GAGGTCGGACCCG
AAT - C
GAM281 278 MYLC2PL 1 3580 NP_612412.1 5 369 CTCTGTCGCCCA C A A 3 B c c
GGCTGGAGCGCA CA TGC CTCCAGCCTGGGC
ATGGCATG GT ACG GAGGTCGGACCCG
A C C
GAM281 278 MYO5C 1 4306 NP_061198.1 3 628 GCTCTATCGCCA GCA 3 B c c
GGCTGGAGTGTA CACTGCACTCCAGCCTGG
GTGGCATG GTGATGTGAGGTCGGACC
GCT
GAM281 278 NACT 1 19968 NP_808218.1 3 552 GCAACCTCCCAC - C- CA 3 B c c
TGCTGGAGTGCG CACT GCACTCCAGC TGGG
AGTGGGAA GTGA CGTGAGGTCG ACCC
G TC TC
GAM281 278 NALP12 1 3395 NP_150639.1 5 30 CTCTGTCACCAA CA----- - -- 3 B c c
GGCTGGAGTGCA CTGCACTCCAGCCT GG GCA
GGGGCACA GACGTGAGGTCGGA CC TGT
ACACGGG A AC
GAM281 278 Nanog 1 11523 NP_079141.1 3 282 CTCTGTCGCCCA A 3 B b b

GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 NCAG1 2 3766 NP_115536.1 3 3665 CTTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTCTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 NCAG1 2 3933 NP_115536.1 3 1953 TGTACCTGTTGG T A TG- 3 B c b

CGGCCGGGTGCA CACTGCAC CC GCC GGCA
GTGGCTCA GTGACGTG GG CGG TTGT
- C CGG

GAM281 278 NCOA6 2 12826 NP_054790.1 5 1279 CTCTGTCACCGA G CA 3 B c c

GGCTGGAGTGCA CACTGCACTCCAGCCT GG
GTGGCGCG GTGACGTGAGGTCGGA CC
G AC

GAM281 278 NCOA6 2 19446 NP_054790.1 5 884 CTCTGTCGCCCA C----- A 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGGC
GTCGTGCC TGACGTGAGGTCGGACCCG
CCGTGC C

GAM281 278 NCOA6IP 1 8841 NP_079107.5 3 280 TTTTACCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGCCATG GTGACGTGAGGTCGGACCCG
C

GAM281 278 NDP52 1 15337 NP_005822.1 3 1122 CTCTGTCACCCA C T CA 3 B c c

GGCTGGCGTGCA CA TGCAC CCAGCCTGGG
ATGGCGCA GT ACGTG GGTCGGACCC
A C AC

GAM281 278 NDRG3 1 15102 NP_114402.1 3 1152 CGCTGTTACCCA C CA 3 B c c

GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCGCA GT ACGTGAGGTCGGACCC
A AT

GAM281 278 NDRG4 1 6180 NP_065198.1 3 973 GAGCTCTGGCCA - TCC G 3 B c c

GGCTGTGCCAGT CACTG CAC AGCCTGG CA
GTGTCCCG GTGAC GTG TCGGACC GT
C --- G

GAM281 278 NDRG4 1 6180 NP_075061.1 3 973 GAGCTCTGGCCA - TCC G 3 B c c

GGCTGTGCCAGT CACTG CAC AGCCTGG CA
GTGTCCCG GTGAC GTG TCGGACC GT
C --- G

GAM281 278 NDUFC2 1 10192 NP_004540.1 3 1240 GCTCTGTCATCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GGCA
GTGGCGCA GTGACGTGAGGTCGGAC CTGT
TA

GAM281 278 NDUFS1 1 20168 NP_004997.3 3 62 TAATTAATGGAC C CC GG 3 B c
c

AACTGTAGTGCA CACTGCACT CAG TG CA
GTGATCCT GTGACGTGA GTC AC GT
T A- AG

GAM281 278 NEU3 1 12075 NP_006647.2 5 71 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM281 278 NF2 1 9169 NP_057502.1 5 480 CTTTGTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCGTG GT ACGTGAGGTCGGACCCG
A C

GAM281 278 NONO 1 17960 NP_031389.2 3 447 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGTA CACTGCACTCCAGCCTGGGC
GTGGCATG GTGATGTGAGGTCGGACCCG
C

GAM281 278 NOSIP 1 7311 NP_057037.1 5 53 TCTTGTTGCCTA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGCG GT ACGTGAGGTCGGATCCGTT
A

GAM281 278 NOTCH2 1 18893 NP_077719.2 5 208 TGGATCTGCCCA A ACT A 3 B c c
GGCGGCGGCGGC C CTGC CC GCCTGGGCA
GGCGGCGG G GGCG GG CGGACCCGT
C GC- -

GAM281 278 NP 1 13473 NP_000261.1 3 84 TCTTTGGCCCCT - C CT- A 3 B c c
TGCTGGAGTCAT CAC TG ACTCCAGC GGGC
GTGCCTCT GTG AC TGAGGTCG CCCG
T - TTC G

GAM281 278 NPCR 1 5959 NP_660361.1 5 744 CTCAGAGGTTTA -- A A 3 B c c
GGCTGGAGGCTT CACT GC CTCCAGCCTGGGC
GGTGAGAA GTGG CG GAGGTCGGATTTG
TT - G

GAM281 278 NPTXR 1 5189 NP_055108.2 3 3926 CACATGGGCCCA - C A 3 B c c
GGCTGAGTGTGA CACT GCACTC AGCCTGGGC
GTGAGCAT GTGA TGTGAG TCGGACCCG
G - G

GAM281 278 NPTXR 1 5189 NP_478058.1 3 3926 CACATGGGCCCA - C A 3 B c c
GGCTGAGTGTGA CACT GCACTC AGCCTGGGC
GTGAGCAT GTGA TGTGAG TCGGACCCG
G - G

GAM281 278 NQO1 1 14855 NP_000894.1 3 685 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AT

GAM281 278 NR2E1 1 13178 NP_003260.1 5 598 AGGAGCCTTGCA - A --- A 3 B c c
GGCTGGAGGGCG CA CTGC CTCCAGCCTG GGC
GCTGGAGA GT GGCG GAGGTCGGAC CCG
C G GTT A

GAM281 278 NRLN1 1 15825 NP_660277.1 5 22 GGCCAGTGCCCA -- CC 3 B b b
GGTTAGTGAGCA CACTGC ACT AGCCTGGGCA

GTGCCCGG GTGACG TGA TTGGACCCGT
AG --
GAM281 278 NT5C2 1 4030 NP_036361.1 5 35 CTCTGCTGCCCA C 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGCA
GTGATGTG GTGAC TGAGGTCGGACCCGT
A
GAM281 278 NUDT4 1 18879 NP_061967.2 3 1290 CTTTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCACA GT ACGTGAGGTCGGACCC
A AC
GAM281 278 NUP43 1 1900 NP_078923.2 3 606 AGAGTCTTGCTC CT 3 B b b
TGCTGGAGTGCG CACTGCACTCCAGC GGGCAA
GTGGTGCA GTGGCGTGAGGTCG CTCGTT
T-
GAM281 278 NXN 1 935 NP_071908.1 3 876 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
C
GAM281 278 OR51E2 1 4096 NP_110401.1 3 439 GCTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC
GAM281 278 ORC1L 1 17969 NP_004144.1 3 92 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM281 278 OSBPL2 1 7553 NP_055650.1 3 1126 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCATG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 OSBPL2 1 7553 NP_653081.1 3 1126 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCATG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 OTOA 1 18386 NP_733764.1 5 66 TGAGGATGTTCA C- - - 3 B c c
GGCTGGGGCTGC ACT GCA CTCCAGCCTGGGCA
TGGTTT TGG CGT GGGGTCGGACTTGT
TT T C
GAM281 278 P24B 1 2381 NP_031390.1 3 52 CCTCATGCCCCA CA------- AC - 3 B c c
GGCTGGAGCAGC CTGC TCCAGCCTGGG CA
TCTCCTAG GACG AGGTCGGACCC GT
GATCCTCTC -- C
GAM281 278 P2RX7 1 7388 NP_002553.2 3 1240 CACTGCACTCCA CA----- - T --- 3 B c c
GGCTGGGTGACA CTG CAC CCAGCCTGG GCA
GAGCGAGA GAC GTG GGTCGGACC CGT
AGAGCGA A - TCA
GAM281 278 P2RX7 1 7388 NP_803176.1 3 2481 CACTGCACTCCA CA----- - T --- 3 B c c
GGCTGGGTGACA CTG CAC CCAGCCTGG GCA
GAGCGAGA GAC GTG GGTCGGACC CGT
AGAGCGA A - TCA

GAM281 278 P2RXL1 1 4425 NP_005437.1 3 954 GCTCTGATCCCA G C CA 3 B c c
GGCTGGATGGAG CACT CA TCCAGCCTGGG
TGGCTGGA GTGA GT AGGTCGGACCC
G - TA
GAM281 278 P450RAI 1 18160 NP_063938.1 3 48 CAGCCCAGCCCA TG A-- A 3 B c c
-2 GGCAGCGGGGTG CAC CACTCC GCCTGGGC
GTGGTTGT GTG GTGGGG CGGACCCG
-- CGA A
GAM281 278 PAICS 1 16852 NP_006443.1 3 413 CACTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 PASK 1 2769 NP_055963.1 5 805 TCTTGTTGCTGA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCT GGCAA
GTGGCACC GTGACGTGAGGTCGGA TCGTT
G
GAM281 278 PCDHA9 2 10427 NP_054724.1 3 1915 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCC GTGACGTGAGGTCGGACCCGTT
GAM281 278 PCDHA9 2 16048 NP_054724.1 3 1315 TTCTGCCACCCA C CA 3 B c
b
GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM281 278 PCDHB11 1 10723 NP_061754.1 3 192 TTCTGTCGCCCT C T A 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCC GGGC
ATGGTGTG GT ACGTGAGGTCGG CCCG
A T C
GAM281 278 PCDHB16 1 4617 NP_066008.1 3 581 TCTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM281 278 PCDHB9 1 11523 NP_061992.2 3 527 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 PDCL 1 4627 NP_005379.2 3 1860 CTCTGTCACCCA T ------ CA 3 B c c
GGCTGGAGTACA CAC GC ACTCCAGCCTGGG
ATAGCGTG GTG CG TGAGGTCGGACCC
- ATAACA AC
GAM281 278 PDE6B 1 936 NP_000274.1 3 197 CTCTGTCACCCA T CA 3 B c c
GGCTGGAGTGCC CAC GCACTCCAGCCTGGG
GTGGCACG GTG CGTGAGGTCGGACCC
C AC
GAM281 278 PDGFC 3 905 NP_057289.1 3 45 AGCTCTTGCCCA C-- - 3 B b b
GAGCTGTGCAGT CACTGCACT CAGC CTGGGCAA
GCAGTGGC GTGACGTGA GTCG GACCCGTT

CGT A

GAM281 278 PDGFC 3 7486 NP_057289.1 3 45 GCAGCTCTTGCC C-- - 3 B b b
CAGAGCTGTGCA CACTGCACT CAGC CTGGGCAA
GTGCAGTG GTGACGTGA GTCG GACCCGTT
CGT A

GAM281 278 PDGFC 3 12574 NP_057289.1 3 45 TCTTGCCCAGAG C-- - 3 B b b
CTGTGCAGTGCA CACTGCACT CAGC CTGGGCAA
GTGGCTGA GTGACGTGA GTCG GACCCGTT
CGT A

GAM281 278 PDLIM2 1 14973 NP_789847.1 3 1201 CTCTATTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 PDZK1 1 4194 NP_002605.2 5 44 TTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 PDZRN1 1 5270 NP_699202.1 3 522 CACTCTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM281 278 PELI1 3 5491 NP_065702.2 5 2686 CTCTGTTGCCCA 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACT GTGACGTGAGGTTGGACCCGTT

GAM281 278 PELI1 3 7382 NP_065702.2 5 2122 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 PELI1 3 14861 NP_065702.2 5 1442 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM281 278 PEPP3 1 5136 NP_055750.1 3 1198 GCCCTGTTCCCC -- CCT----- A 3 B c
c
CTGGAATGTGCA CACTGCAC TCCAG GGGC
GTGGGCCA GTGACGTG AGGTC CCCG
TA CCCCTTGT -

GAM281 278 PER2 1 19703 NP_073728.1 3 1370 TCTTTTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM281 278 PFAS 1 16261 NP_036525.1 3 674 CTCTGTCACCCA C C CA 3 B c c
GGCTGGAGTACA CA TG ACTCCAGCCTGGG
ATGGCGTG GT AC TGAGGTCGGACCC
A A AC

GAM281 278 PHAX 1 12159 NP_115553.1 3 698 CCTGAACCCCCA C CA 3 B c c
GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCAGG GTGAC TGAGGTCGGACCC
A CC

GAM281 278 PHF1 1 5036 NP_002627.1 3 362 CCCTACTGCCCA GCAC--- 3 B c c
GGCTGGAATCCA CACT TCCAGCCTGGGCA
AGAGTGGG GTGA AGGTCGGACCCGT
GAACCTA
GAM281 278 PHF1 1 5036 NP_077084.1 3 138 CCCTACTGCCCA GCAC--- 3 B c c
GGCTGGAATCCA CACT TCCAGCCTGGGCA
AGAGTGGG GTGA AGGTCGGACCCGT
GAACCTA
GAM281 278 PIGR 1 11059 NP_002635.2 3 814 CACTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM281 278 PIK3C2B 1 10488 NP_002637.2 3 1447 GCCCTGTCGCCA -- 3 B b b
GGCTGGAGTGTA CACTGCACTCCAGCCTGG GCA
GTGGCATG GTGATGTGAGGTCGGACC TGT
GC
GAM281 278 PIK3CD 1 9545 NP_005017.2 3 822 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 PKNOX1 1 8826 NP_004562.2 3 1821 TCTTGTTGCCCA C A 3 B b b
GGCTGGAGGGCA CA TGC CTCCAGCCTGGGCAA
ATGGTGCA GT ACG GAGGTCGGACCCGTT
A G
GAM281 278 PMCHL1 1 16917 NP_114093.1 3 526 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 PMCHL2 1 16917 NP_114094.1 3 524 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 PMPCA 1 7640 NP_055975.1 3 246 TGAAGTGCCCAG A - 3 B b b
CGCTGGAGTGCA C CTGCACTCCAGC CTGGGCA
GCGTGCCA G GACGTGAGGTCG GACCCGT
C C
GAM281 278 PNMA2 2 8006 NP_009188.1 3 1714 CTCTATCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 PNMA2 2 17067 NP_009188.1 3 265 TCTCATCACCCA C CA 3 B c b
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGCACA GTGACGTGAG TCGGACCC
A AC
GAM281 278 POFUT1 1 11287 NP_056167.1 3 1737 CTCTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
TC
GAM281 278 POLE3 1 6151 NP_059139.2 3 1144 CTCTGTGGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC

GTGGCATG GTGACGTGAGGTCGGACCCG
G
GAM281 278 POLR2D 2 2798 NP_004796.1 3 520 AACTCTTGTCCA C-- --- 3 B c c
GGCTGGAGGAGT ACTGCACTCC AGCCTGGGCAA
GCAGTCGT TGACGTGAGG TCGGACCTGTT
TGC AGG
GAM281 278 POLR2D 2 5412 NP_004796.1 3 520 TCTTGTCCAGGC C----- --- 3 B c c
TGGAGGAGTGCA ACTGCACTCC AGCCTGGGCAA
GTCGTACA TGACGTGAGG TCGGACCTGTT
ACATGC AGG
GAM281 278 PON1 1 2152 NP_000437.3 3 1197 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 POU2AF1 1 20135 NP_006226.1 3 1375 CTCCATTGCCCA C C 3 B b b

GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
ATGGTGCG GT AC TGAGGTCGGACCCGTT
A A
GAM281 278 POU2F3 1 16114 NP_055167.1 3 1109 TGCTCCAGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
A
GAM281 278 POU3F1 1 7918 NP_002690.2 3 4 ACACACTGCCCG CC T 3 B b b
GCTCAGTGCAGT CACTGCACT AGCC GGGCA
GCCCCGCG GTGACGTGA TCGG CCCGT
C- -
GAM281 278 PP1628 1 10180 NP_079477.1 5 1282 ATTGCTCAGCCA - A TC ---- 3 B c c
GGCTGTGGAGCA CA CTGC C CAGCCTGG GCAA
GCTGAGGC GT GACG G GTCGGACC CGTT
C A GT GACT
GAM281 278 PP3111 1 10883 NP_071439.2 3 190 GAGCAGGCCCCA CT C- - A 3 B c
c

GGCTGGACCTGC CA GCA TCCAGCCTGGG C
CCTGTCCT GT CGT AGGTCGGACCC G
CC CC C G
GAM281 278 PP3856 1 10744 NP_660202.1 5 509 TCCAGGTGCCCT C------ C T 3 B c c
GGCTGGAGTCAG ACTG ACTCCAGCC GGGCA
TCCTCATC TGAC TGAGGTCGG CCCGT
CTACTCC - T
GAM281 278 PPAP2C 1 7299 NP_003703.1 3 35 GGACCCCGCCCA T - A- A 3 B c c
GGCAGGGAGCTG CAC GCA CTCC GCCTGGGC
CTGTGAGT GTG CGT GAGG CGGACCCG
T C GA C
GAM281 278 PPAP2C 1 7299 NP_803545.1 3 35 GGACCCCGCCCA T - A- A 3 B c c
GGCAGGGAGCTG CAC GCA CTCC GCCTGGGC
CTGTGAGT GTG CGT GAGG CGGACCCG
T C GA C
GAM281 278 PPAP2C 1 7299 NP_808211.1 3 35 GGACCCCGCCCA T - A- A 3 B c c
GGCAGGGAGCTG CAC GCA CTCC GCCTGGGC

CTGTGAGT GTG CGT GAGG CGGACCCG
T C GA C
GAM281 278 PPEF2 1 2954 NP_006230.2 3 368 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGGCGCG GT ACGTGAGGTCGGACCCGTT
T
GAM281 278 PPEF2 1 2954 NP_690910.1 3 1000 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGGCGCG GT ACGTGAGGTCGGACCCGTT
T
GAM281 278 PPEF2 1 2954 NP_690911.1 3 2213 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGGCGCG GT ACGTGAGGTCGGACCCGTT
T
GAM281 278 PPFIBP1 3 8231 NP_003613.2 3 2295 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 PPFIBP1 3 10708 NP_003613.2 3 1168 TTCTGTTGCCCA C 3 B b b
TGCTGGAGTGCA CACTGCACTCCAGC TGGGCAA
GTGGCGTG GTGACGTGAGGTCG ACCCGTT
T
GAM281 278 PPFIBP1 3 12217 NP_003613.2 3 861 CTCTGTCACCCA CT CA 3 B c b

GGTTGGAGTGCC CA GCACTCCAGCCTGGG
ATGGCATG GT CGTGAGGTTGGACCC
AC AC
GAM281 278 PPID 1 7378 NP_005029.1 3 247 CTCTGTCACCCA CA 3 B c c
GGCTGGAGTGCG CACTGCACTCCAGCCTGGG
GTGGCGCA GTGGCGTGAGGTCGGACCC
AC
GAM281 278 PPIL2 1 13122 NP_055152.1 3 392 CTCTGTTGCCCA CC 3 B b b
GGCTCCAGTGCA CACTGCACT AGCCTGGGCAA
GTGGTGTG GTGACGTGA TCGGACCCGTT
CC
GAM281 278 PPP1R12 2 3861 NP_002472.1 3 4497 CTCTCTCGCCCA A 3 B b b
B GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 PPP1R12 2 3861 NP_115288.1 3 4630 CTCTCTCGCCCA A 3 B b b
B GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 PPP1R12 2 13977 NP_002472.1 3 4662 CCATGTTGCCCA - G CT 3 B c
b
B GGCTGGTCTGAA CA CT CA CCAGCCTGGGCAA
GCTGCTGG GT GA GT GGTCGGACCCGTT
C A CT
GAM281 278 PPP1R12 2 13977 NP_115288.1 3 4795 CCATGTTGCCCA - G CT 3 B c
b

B GGCTGGTCTGAA CA CT CA CCAGCCTGGGCAA
GCTGCTGG GT GA GT GGTCGGACCCGTT
C A CT

GAM281 278 PRIM2A 1 10653 NP_000938.1 3 106 TCACTGTCACCA CC - -- 3 B c c
AGGCTTAGTGCA CACTGCACT AGCCT GG GCA
GTGACACA GTGACGTGA TCGGA CC TGT
T- A AC

GAM281 278 PRKR 1 4790 NP_002750.1 3 275 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGACACA GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 PRKWNK3 1 14862 NP_065973.1 3 639 CTCTGTCACCCA CA 3 B c c

GGTTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTTGGACCC
AC

GAM281 278 PRKY 1 6114 NP_002751.1 3 935 AAAATTTCATCT CC CA 3 B c c
AGGCTAGGTGCA CACTGCACT AGCCTGGG
GTGGCTTG GTGACGTGG TCGGATCT
A- AC

GAM281 278 PRND 2 1539 NP_036541.1 3 839 TCTTGTTGCCCA CAC----- 3 B c b
GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ACGGCATG ACGTGAGGTCGGACCCGTT
GTACGGCA

GAM281 278 PRND 2 4170 NP_036541.1 3 2764 TTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 PRO0297 1 10574 NP_054800.1 5 53 CTCTTTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 PRO0365 1 18148 NP_054845.1 5 883 GCTCTGTCGCCA C -- 3 B b b
GGCTGAAGTGCA CACTGCACT CAGCCTGG GCA
GTGGCGCA GTGACGTGA GTCGGACC TGT
A GC

GAM281 278 PRO0456 1 9064 NP_054846.1 3 540 GATTTTGAATTT T CA 3 B c c
AGGCTGGGTGCA CACTGCAC CCAGCCTGGG
GTGGCTCA GTGACGTG GGTCGGATTT
- AA

GAM281 278 PRO1048 1 12596 NP_060967.1 3 319 CTCTGCTGCCCA C 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGCA
GTGGCACA GTGAC TGAGGTCGGACCCGT
A

GAM281 278 PRO2730 1 2048 NP_079498.1 3 320 TGGTCAGGCCCA - G C A 3 B c c

GGCTGAGTGAGA CA CT CACTC AGCCTGGGC
TGAGCTGC GT GA GTGAG TCGGACCCG
A - - G

GAM281 278 PROM2 1 2147 NP_653308.1 3 786 CTCTGTCACCCA CA 3 B c c

GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGTGCA GTGATGTGAGGTCGGACCC
AC

GAM281 278 PSMD9 1 17758 NP_002804.2 3 752 CTTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGTCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 PSPH 1 15044 NP_004568.1 3 276 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 PSTPIP2 1 12057 NP_077748.2 3 1323 CTCTGTCCCCCA A C CA 3 B c c
GGCTGAAGTGCA C CTGCACT CAGCCTGGG
GCGGCATG G GACGTGA GTCGGACCC
C A CC

GAM281 278 PTGES 1 16070 NP_004869.1 3 528 CTCTGTTGCCCA G C 3 B b b
AGCTGGAGTGAA CACT CACTCCAGC TGGGCAA
GTGGTACA GTGA GTGAGGTCG ACCCGTT
A A

GAM281 278 PTGIS 2 10783 NP_000952.1 3 3269 GCTTATTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 PTGIS 2 17361 NP_000952.1 3 2840 CTCTGCTGCCCA C 3 B b b
GGCTAGAGTGCA CACTGCACTC AGCCTGGGCA
GTGGCGTG GTGACGTGAG TCGGACCCGT
A

GAM281 278 PTK2 1 10355 NP_005598.3 5 129 CCCAGGCTGCCA G G 3 B b b
GGCTGGAGTGGA CACT CACTCCAGCCTGG CA
GTGGCATG GTGA GTGAGGTCGGACC GT
G -

GAM281 278 PTPRT 1 12157 NP_008981.2 3 4538 TCCTGAATGCTA TG AC G 3 B c c
GGCTGGAAAGTG CAC C TCCAGCCTGG CA
GTGCCTGT GTG G AGGTCGGATC GT
GT AA -

GAM281 278 PTPRT 1 12157 NP_573400.1 3 4538 TCCTGAATGCTA TG AC G 3 B c c
GGCTGGAAAGTG CAC C TCCAGCCTGG CA
GTGCCTGT GTG G AGGTCGGATC GT
GT AA -

GAM281 278 PYGM 1 15938 NP_005600.1 5 741 GCTCCACTCCTT A ------ - A 3 B c c
GGCTGGAGGCAG CACTGC CTCCAGCC TGG GC
TGCTGAGG GTGACG GAGGTCGG ACC CG
- TTCCTC T -

GAM281 278 PYY 1 9133 NP_004151.1 3 175 CCCCGCCCCCTG T A --- A 3 B c c
GGCTGGAGGGCT CAC GC CTCCAGCCT GGGC
GTGTGTGG GTG CG GAGGTCGGG CCCG
T G TCC C

GAM281 278 QRSL1 1 14971 NP_060762.2 3 48 AAAATGACTTTT T CA 3 B c c
AGGCTGGGTGCA CACTGCAC CCAGCCTGGG
GTGGCTCA GTGACGTG GGTCGGATTT
- TC
GAM281 278 RAB11-F 1 13848 NP_116321.2 3 2596 CTCTGTTGCCCA 3 B b b
IP4 GGCTGGAGTGTA CACTGCACTCCAGCCTGGGCAA
GTGGTATG GTGATGTGAGGTCGGACCCGTT

GAM281 278 RAB21 1 7076 NP_055814.1 3 289 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
CTGGCTTG GT ACGTGAGGTCGGACCC
C AC
GAM281 278 RAB33B 1 7910 NP_112586.1 3 839 GCTCTGTCTCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGTC GTGACGTGAGGTCGGACC TGT
TC
GAM281 278 RAB36 2 808 NP_004905.1 3 1408 CCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTA GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 RAB36 2 1652 NP_004905.1 3 1726 CTCTGTCACCCA C CA 3 B c b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCACG GT ACGTGAGGTCGGACCC
A AC
GAM281 278 RAB39 1 3754 XP_084662.1 3 753 TTTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGGCA GTGACGTGAGGTCGGACCC
AC
GAM281 278 RAB4A 1 16568 NP_004569.2 5 27 GCGCCTGCGCGG - C - G 3 B c c
AGCTGGAGTCCG CA CTG ACTCCAGC CTG GCA
GCTGGGCC GT GGC TGAGGTCG GGC CGT
C C A G
GAM281 278 RABL2A 1 2648 NP_038198.1 3 578 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 RABL2B 1 2648 NP_009012.1 3 585 GCTCTGTCGCCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
GC
GAM281 278 RAI 1 8937 NP_006654.1 5 22 CAAGTGAGTCTC T A 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCC GGGC
GTGGTGCA GTGACGTGAGGTCGG TCTG
C A
GAM281 278 RAI17 1 7523 NP_065071.1 3 1485 CACTTTGTTTCA T-- T-- - 3 B c c
GGCTGGTCTGTG CAC GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM281 278 RAI17 1 7523 XP_166091.2 3 1485 CACTTTGTTTCA T-- T-- - 3 B c c
GGCTGGTCTGTG CAC GCAC CCAGCCTGGG CAA

CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM281 278 RAI3 1 12784 NP_003970.1 3 343 CTCTGTCACCCA C CA 3 B c c
GGCTTGAGTGCA CACTGCACTC AGCCTGGG
GTGGTGCG GTGACGTGAG TCGGACCC
T AC
GAM281 278 RAP140 1 16472 NP_056039.1 3 1919 CTCTGTCGCCCA C C A 3 B c c
AGCTGGAGTACA CACTG ACTCCAGC TGGGC
GTGGTGCA GTGAC TGAGGTCG ACCCG
A A C
GAM281 278 RARG 1 11090 NP_000957.1 5 41 CGGAGCCTCCCA A T CA 3 B c c
GGCTGGGGCAGT CACTGC C CCAGCCTGGG
GGGCATGG GTGACG G GGTCGGACCC
- - TC
GAM281 278 RASSF2 1 19336 NP_055552.1 3 3347 TTCTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGGG GTGACGTGAGGTCGGACCC
TT
GAM281 278 RASSF2 1 19336 NP_739579.1 3 3573 TTCTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGGG GTGACGTGAGGTCGGACCC
TT
GAM281 278 RASSF2 1 19336 NP_739580.1 3 3347 TTCTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGGG GTGACGTGAGGTCGGACCC
TT
GAM281 278 RBAK 1 12965 NP_066986.1 5 247 CGGCCTGGCCCA C TC--- A 3 B c c
GGCTGCCGCTGT CACTG AC CAGCCTGGGC
ACGGTGAG GTGGC TG GTCGGACCCG
A TCGCC G
GAM281 278 RBBP9 1 16100 NP_006597.2 3 1856 CTCTGTCTCCCA CA CA 3 B c c
GGCTGGAGGTCA CACTG CTCCAGCCTGGG
GTGGCACA GTGAC GAGGTCGGACCC
TG TC
GAM281 278 RCBTB1 1 13829 NP_060661.2 5 129 CTCTCTTGCCCA CAC C 3 B c
c
GACTGGAATACA CACTG TCCAG CTGGGCAA
GTGGTGTG GTGAC AGGTC GACCCGTT
ATA A
GAM281 278 RCD-8 1 13335 NP_055144.2 3 595 CTGCCTTGCCCA C AC- G - 3 B c c
GGGGTGGGATGG CA TGC TCCA CC TGGGCAA
CACTGAAG GT ACG GGGT GG ACCCGTT
C GTA G G
GAM281 278 RDH13 1 9713 NP_612421.1 5 227 ACTCTGTCGCCA C----- C -- 3 B c c
GGCTGGAATGCA ACTGCA TCCAGCCTGG GCA
GTAGGGCA TGACGT AGGTCGGACC TGT

ACGGGA A GC

GAM281 278 REC14 1 5212 NP_079510.1 5 14 TCCGACGTGCAG - C G A 3 B c c
CCTGGCAGTGCA CACTGCACT CCAG CTG GC
GTGAGCTG GTGACGTGA GGTC GAC TG
C C G C

GAM281 278 REGL 1 1455 NP_006499.1 3 167 TGTGCTCACCCA T--- - CA 3 B c c
GGCTGAGGGTGC CAC GCACTC CAGCCTGGG
CTTTGTGG GTG CGTGGG GTCGGACCC
TTTC A AC

GAM281 278 RGS16 1 13380 NP_002919.1 3 1254 CGGCAGAGCCCA GCA A 3 B c c
GGCTGGGGAAGT CACT CTCCAGCCTGGGC
GAACTACC GTGA GGGGTCGGACCCG
A-- A

GAM281 278 RGS3 1 3344 NP_570613.1 5 61 GTGCTCATGCCA C -- G 3 B c c
GGCTGACGGGTC CACTG ACTC CAGCCTGG CA
CAGTGCGG GTGAC TGGG GTCGGACC GT
C CA -

GAM281 278 RHD 2 4143 NP_057208.2 3 690 ACTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 RHD 2 4143 NP_057309.2 3 779 ACTCTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 RHD 2 13465 NP_057208.2 3 281 CTCTGTCACCCA C C CA 3 B c b
GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCACC GT ACGTGAG TCGGACCC
A A AC

GAM281 278 RHD 2 13465 NP_057309.2 3 370 CTCTGTCACCCA C C CA 3 B c b
GGCTAGAGTGCA CA TGCACTC AGCCTGGG
ATGGCACC GT ACGTGAG TCGGACCC
A A AC

GAM281 278 RHPN2 1 11803 NP_149094.2 3 890 CTGTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 RNF137 2 7446 NP_060543.4 3 163 TCTTTGCTACCA CT -- C -- 3 B c b
GGCTGAAGTCTG CA GC ACT CAGCCTGG GCAA
TCATGAAA GT TG TGA GTCGGACC CGTT
AC TC A AT

GAM281 278 RNF137 2 16940 NP_060543.4 3 829 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 RNF144 1 13909 NP_055561.1 3 145 TTCACAGTGTCA T AC G 3 B c c
GGCTGGACGCCG CAC GC TCCAGCCTGG CA
TGATTTCA GTG CG AGGTCGGACT GT
C C- -

GAM281 278 RNF8 1 13778 NP_003949.1 3 954 CTCTGTTGCCCA --- C 3 B b b
AGCTGGAGTACA CACTGC ACTCCAGC TGGGCAA
GTAGTGCA GTGATG TGAGGTCG ACCCGTT
ACA A
GAM281 278 RNPS1 1 1646 NP_006702.1 3 429 GGAGCTGCCCCA - CC - 3 B b b
GGCTTTAGTGCA CA CTGCACT AGCCTGGG CA
GCTGCCAA GT GACGTGA TCGGACCC GT
C TT C
GAM281 278 RNPS1 1 1646 NP_542161.1 3 429 GGAGCTGCCCCA - CC - 3 B b b
GGCTTTAGTGCA CA CTGCACT AGCCTGGG CA
GCTGCCAA GT GACGTGA TCGGACCC GT
C TT C
GAM281 278 RP2 1 6582 NP_008846.1 3 1766 TCTTGTTGCCCA C C 3 B b b
AGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
ATGGCGCG GT ACGTGAGGTCG ACCCGTT
A A
GAM281 278 RPH3AL 1 2614 NP_008918.1 3 641 CTTTGTTGCCCA 3 B b b
GGCTGGGGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGGGGTCGGACCCGTT

GAM281 278 RPP30 2 445 NP_006404.1 3 358 CTTTGTTGCTCA C 3 B b b
GGCTGGAGTACA CACTG ACTCCAGCCTGGGCAA
GTGGCATA GTGAC TGAGGTCGGACTCGTT
A
GAM281 278 RPP30 2 19325 NP_006404.1 3 1203 CTCTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCTCG GTGACGTGAGGTCGGACCC
CC
GAM281 278 RRP40 1 14169 NP_057126.1 5 100 GACGCGGAAGGC AGCCT A 3 B c
c
CCTGGGGGTGCA CACTGCACTCC GGGC
GTGGAGCG GTGACGTGGGG CCCG
GT--- G
GAM281 278 S100A15 1 19723 NP_789793.1 3 3404 CTCTGTCGCCCG T A 3 B c c
GGCTGGAGTGCT CAC GCACTCCAGCCTGGGC
GTGAGCTG GTG CGTGAGGTCGGGCCCG
T C
GAM281 278 SARM1 2 4282 NP_055892.1 3 3667 CTCTGTTGTCCA A 3 B b b
GGCTGGAGGGCA CACTGC CTCCAGCCTGGGCAA
GTGACATA GTGACG GAGGTCGGACCTGTT
G
GAM281 278 SARM1 2 7147 NP_055892.1 3 416 AGGCAATGCCCA C A --- A 3 B c b
GGCGGGCCTGGG CA TGC CT CC GCCTGGGCA
CACTGTAT GT ACG GG GG CGGACCCGT
C - TCC G
GAM281 278 SAS 1 17726 NP_005972.1 3 511 CTCTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCATG GT ACGTGAGGTCGGACCCGTT
A
GAM281 278 SBLF 1 14551 NP_006864.2 3 1609 CTCTGTTGCCCA C 3 B b b

GCCTGGAGTGCA CACTGCACTCCAG CTGGGCAA
GTGTGTCA GTGACGTGAGGTC GACCCGTT
C

GAM281 278 SCAMP-4 1 2153 NP_524558.1 3 873 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C

GAM281 278 SCAND2 1 7179 NP_071333.2 3 1783 TTCTATCACCCA G CA 3 B c c
GGCTGGAGTGGA CACT CACTCCAGCCTGGG
GTGGTATG GTGA GTGAGGTCGGACCC
G AC

GAM281 278 SCAP 1 9400 NP_036367.1 3 37 CCTCCTTGCCCA G -- A 3 B c c
GGCAGGAGGCTG CACT CA CTCC GCCTGGGCAA
GGGTGCTG GTGG GT GAGG CGGACCCGTT
G CG A

GAM281 278 SCARF1 1 5158 NP_003684.1 3 410 CTCTGTCCCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
CC

GAM281 278 SCML2 1 3898 NP_006080.1 3 1313 CTCTTGTGCCCA CAC----- 3 B c c
GGCTGGAGTGCA TGCACTCCAGCCTGGGCA
ATAGCTCG ACGTGAGGTCGGACCCGT
GCTCGATA

GAM281 278 SCN3B 2 4399 NP_060870.1 3 2013 CTCTGTCTCCCA C CA 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGTGCA GTGACGTGAG TCGGACCC
A TC

GAM281 278 SCN3B 2 16355 NP_060870.1 3 1054 CTCTGTCACCTA C CA 3 B c c
GGCTAGAGTGCA CACTGCACTC AGCCTGGG
GTGGTGTG GTGACGTGAG TCGGATCC
A AC

GAM281 278 SDS-RS1 1 14127 NP_612441.1 5 91 ATCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM281 278 SEDL 4 926 NP_055378.1 3 1000 TCCTGTTGTGCA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GCAA
GTGGCACA GTGACGTGAGGTCGGAC TGTT
G

GAM281 278 SEDL 4 11591 NP_055378.1 3 1346 CTCTGTTGTCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCAGT GT ACGTGAGGTCGGACCTGTT
A

GAM281 278 SEDL 4 15576 NP_055378.1 3 308 ACTCTGTTGCCA G 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG CAA
GTGGCGCA GTGACGTGAGGTCGGACC GTT
-

GAM281 278 SEDL 4 16937 NP_055378.1 3 638 TCCTGTTGTGCA C G 3 B b b
GGCTGTAGTGCA CACTGCACT CAGCCTG GCAA
GTGGCACG GTGACGTGA GTCGGAC TGTT

T G

GAM281 278 SELH 1 13030 NP_734467.1 5 160 CTTCGTTGCCCA CACTCC ----- 3 B c c

GTTTCCGCTCAG CACTG AGC CTGGGCAA
TGGTCGCG GTGAC TCG GACCCGTT
------ CCTTT

GAM281 278 SEMA3B 1 17810 NP_004627.1 3 378 AAGCTGTGAACA ---- CT GG 3 B c c

GGCTGGGCTGCT CACT GCA CCAGCCTG CA
GGAGGTGG GTGG CGT GGTCGGAC GT
AGGT CG AA

GAM281 278 SEMA3E 1 13353 NP_036563.1 3 5 TGCCCAGGCACA G ----- ------ 3 B c c

CGCTGGACTCCT CACT CAC TCCA GCCTGGGC
GTGGGGTG GTGG GTG AGGT CGGACCCG
G TCCTC CGCACA

A
T

GAM281 278 SEPN1 1 18255 NP_065184.1 3 1557 CTCTGTCACCCA CT CA 3 B c c

GGCTGGAGTGCT CA GCACTCCAGCCTGGG
ATGGCTCG GT CGTGAGGTCGGACCC
AT AC

GAM281 278 SERF1A 2 9219 NP_068802.1 3 243 ACTCTGTCACCA C -- 3 B b b

GACTGGAGTGCA CACTGCACTCCAG CTGG GCA
GTGGCGCC GTGACGTGAGGTC GACC TGT
A AC

GAM281 278 SERF1A 2 15849 NP_068802.1 3 410 CACTGTTGCCCA C 3 B b b

GGCTGGACTGCA CACTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
C

GAM281 278 SERF1B 2 9219 NP_075267.1 3 243 ACTCTGTCACCA C -- 3 B b b

GACTGGAGTGCA CACTGCACTCCAG CTGG GCA
GTGGCGCC GTGACGTGAGGTC GACC TGT
A AC

GAM281 278 SERF1B 2 15849 NP_075267.1 3 410 CACTGTTGCCCA C 3 B b b

GGCTGGACTGCA CACTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
C

GAM281 278 SERF2 1 16210 NP_005761.2 5 431 CTCTGTTACCCA C C CA 3 B c c

TGCTGGAGTACG CACTG ACTCCAGC TGGG
GTGGCGAG GTGGC TGAGGTCG ACCC
A T AT

GAM281 278 SERPINB 1 20173 NP_002631.1 3 89 ATTCCCTGTGAC CT C - 3 B c c
8

CTAGTTGGTGCA CACTGCA CCAGC TGGG CA
GTGGCTTG GTGACGT GGTTG ATCC GT
-- - A

GAM281 278 SERPINB 2 4363 NP_004146.1 3 511 CTCTGTCGCCCA A 3 B b b
9

GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC

GTGGCTCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 SERPINB 2 9152 NP_004146.1 3 2359 CTCTGTCACCCA CA 3 B c b
GGCTGGAGTGTA CACTGCACTCCAGCCTGGG
GTGGCATG GTGATGTGAGGTCGGACCC
AC
GAM281 278 SFXN2 1 3678 NP_849189.1 3 594 CTCTGTCGCCCA C A 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGCGCG GTGACGT AGGTCGGACCCG
A C
GAM281 278 SFXN2 1 3678 XP_058359.2 3 595 CTCTGTCGCCCA C A 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGCGCG GTGACGT AGGTCGGACCCG
A C
GAM281 278 SFXN5 1 11307 NP_653180.1 3 2319 GGGGTCTGCTCC - G CT 3 B c c
TGTGGCGGTGCA CACTGCACT CCA C GGGCA
GTGGCAAA GTGACGTGG GGT G CTCGT
C - TC
GAM281 278 SH3BP2 2 3836 NP_003014.2 3 1850 CCCTGTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGCCGTG GT ACGTGAGGTCGGACCCG
A C
GAM281 278 SH3BP2 2 9440 NP_003014.2 5 157 CTCAGTTGCCCA A C 3 B b b
GACTGGAGAGCA CACTGC CTCCAG CTGGGCAA
GTGGCCAA GTGACG GAGGTC GACCCGTT
A A
GAM281 278 SHFM3 1 2197 NP_071322.1 3 80 GACTTCTCTTGC CAGC TG 3 B c c
CTGGAGGGTGCA CACTGCACTC C GGCAA
GTGATAGC GTGACGTGGG G CCGTT
A--- GT
GAM281 278 SHOX 2 4375 NP_006874.1 3 0 GCCCAGGCTGGA C C A 3 B c c
GTATAATGGCAT CA TG ACTCCAGCCTGGGC
GTCTCGAC GT AT TGAGGTCGGACCCG
A A -
GAM281 278 SHOX 2 16527 NP_000442.1 3 1308 CTTTGTCGCCCA C----- A A 3 B c c
GGCTGGAGCGCA ACTGC CTCCAGCCTGGGC
GTCCCGCA TGACG GAGGTCGGACCCG
ACGCCC C C
GAM281 278 SIGLEC8 1 4513 NP_055257.1 3 516 CTCTGTCACCTA CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGGGCA GTGACGTGAGGTCGGATCC
AC
GAM281 278 SIL 1 12411 NP_003026.1 3 361 TCTTGTAGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCAGG GT ACGTGAGGTCGGACCCG
A A
GAM281 278 SIRPB1 1 14771 NP_006056.1 3 2041 ACCTTATTCCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG

ATGTCGTG GT ACGTGAGGTCGGACCC
A TT
GAM281 278 SLA2 1 19573 NP_115590.1 3 689 CCCTGTTGCCCA C C 3 B b b
TGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
ATGGCACG GT ACGTGAGGTCG ACCCGTT
A T
GAM281 278 SLA2 1 19573 NP_778252.1 3 792 CCCTGTTGCCCA C C 3 B b b
TGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
ATGGCACG GT ACGTGAGGTCG ACCCGTT
A T
GAM281 278 SLC12A8 1 5190 NP_078904.1 3 209 CCTTGTCACCCA C CA 3 B c c
GGCTGGAGTCCA CACTG ACTCCAGCCTGGG
GTGGCACA GTGAC TGAGGTCGGACCC
C AC
GAM281 278 SLC13A1 1 4370 NP_071889.2 3 1480 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGGG GTGACGTGAGGTCGGACCCG
C
GAM281 278 SLC13A3 1 7448 NP_073740.2 3 1089 CCGTGAGCCCGA TG AC - A 3 B c
c
GGCTGGAAGTGG CAC C TCCAGCCT GGGC
TGTCTGCC GTG G AGGTCGGA CCCG
GT A- G A
GAM281 278 SLC14A2 1 4514 NP_009094.2 5 33 CTCTGTCACCCA C C CA 3 B c c
GGCTGGAGTACA CA TG ACTCCAGCCTGGG
CTGGCACT GT AC TGAGGTCGGACCC
C A AC
GAM281 278 SLC15A1 1 18930 NP_005064.1 3 219 TCTTGTTGTCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCTGTT
A
GAM281 278 SLC16A4 1 611 NP_004687.1 3 183 CTCTTTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM281 278 SLC16A6 1 5302 NP_004685.1 5 45 CTCTGTCATTCA C----- CA --- 3 B c c
GGCAAGAGTGCA ACTGCACTC GCCTG GGCA
GTAGTGTG TGACGTGAG CGGAC CTGT
GTGTGA AA TTA
GAM281 278 SLC19A3 1 6713 NP_079519.1 3 1013 ACAGGAGTCAGA C G- A 3 B c
c
GGCTGGAGTGCA CA TGCACTCCAGCCT GGC
ATGGCGTG GT ACGTGAGGTCGGA CTG
A GA A
GAM281 278 SLC1A5 1 1277 NP_005619.1 3 177 GGGATGCCTGGC - C -- TG 3 B c c
TGCTGGAGTACA CAC TG ACTCCAGC C GGCA
TGTGTTCA GTG AC TGAGGTCG G CCGT
T A TC GT
GAM281 278 SLC21A2 1 18939 NP_005621.1 3 278 CCCAGATGCCCA CACTCC 3 B c
c

GGCTCACTTCAG CACTG AGCCTGGGCA
TGTTGAGT GTGAC TCGGACCCGT
TTCAC-

GAM281 278 SLC24A1 1 10966 NP_004718.1 3 687 TCTTGTTGCCCA C T 3 B b b
GGCTGGTGTGCA CA TGCAC CCAGCCTGGGCAA
ATGGCGTG GT ACGTG GGTCGGACCCGTT
A T

GAM281 278 SLC30A5 1 3692 NP_076960.1 3 153 CTCCATCGCCCA C A 3 B b b
GGCTGCAGTGCA CACTGCACT CAGCCTGGGC
GTGACACG GTGACGTGA GTCGGACCCG
C C

GAM281 278 SLC30A6 1 5362 NP_060434.2 3 507 CTCTGTCGCCCA C A 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGC
GTGGCATG GTGACGT AGGTCGGACCCG
A C

GAM281 278 SLC35E2 1 13336 XP_049733.6 3 1607 GTCTGTCACCCA C CA 3 B c c

GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC

GAM281 278 SLC39A1 1 9528 NP_055252.2 5 88 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCG CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGGCGTGAGGTCGGACCCGTT

GAM281 278 SLC39A3 1 20136 NP_653165.1 3 2288 GGGGTGCTCCTG G - T - 3 B c
c

GCCTGGAGTGGG CACT CACTCCAG CC GG GCA
TGGAGGCC GTGG GTGAGGTC GG CC CGT
- C T T

GAM281 278 SLC6A14 1 13830 NP_009162.1 3 1676 TTCTGTTGCCTG TG 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCC GGCAA
GTGGCATG GTGACGTGAGGTCGG CCGTT
GT

GAM281 278 SLC6A3 1 12941 NP_001035.1 3 1594 GTGGGCTCCAGG C -- - A 3 B c c

GACTGGAGTGTA CA TGCACTCCAG CCTGG GC
ATGCTCGG GT ATGTGAGGTC GGACC CG
A AG T G

GAM281 278 SMAC 2 1861 NP_620308.1 5 482 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGAG GTGACGTGAGGTCGGACCCG
C

GAM281 278 SMAC 2 18165 NP_620308.1 5 656 CTCTGTTGCCCA C 3 B b b
GGCTGAAGTGCA CACTGCACT CAGCCTGGGCAA
GTGGGGCG GTGACGTGA GTCGGACCCGTT
A

GAM281 278 SMCR5 1 8677 NP_658987.1 3 1706 AAAGTGTGTACA T A GG- 3 B c c

GGGCCGGGTGCA CACTGCAC CC GCCT GCA
GTGGCTCA GTGACGTG GG CGGG TGT

- C ACA

GAM281 278 SNAP23 1 19007 NP_003816.2 3 673 CTCTCTTGTCCA CAC----- 3 B c c
GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCGCG ACGTGAGGTCGGACCTGTT
GCGCGATA

GAM281 278 SNAP23 1 19007 NP_570710.1 3 673 CTCTCTTGTCCA CAC----- 3 B c c
GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCGCG ACGTGAGGTCGGACCTGTT
GCGCGATA

GAM281 278 SNARK 1 18622 NP_112214.1 3 602 TCTTGGTGCCCA C C 3 B b b
GGCTAGAGTGCA CA TGCACTC AGCCTGGGCA
ATGGCGCG GT ACGTGAG TCGGACCCGT
A A

GAM281 278 SNPH 1 15041 NP_055538.1 3 2430 GCCCTGGCCCAG - C- A 3 B c c
CTCTGGAGTGCA CAC TGCACTCCAG CTGGGC
TGTGTGTG GTG ACGTGAGGTC GACCCG
T TC G

GAM281 278 SNX15 1 7625 NP_037438.2 3 270 CTGTGTCGCCCA C A 3 B b b
GACTGGAGTGCA CACTGCACTCCAG CTGGGC
GTGGTGGG GTGACGTGAGGTC GACCCG
A C

GAM281 278 SNX15 1 7625 NP_680086.1 3 270 CTGTGTCGCCCA C A 3 B b b
GACTGGAGTGCA CACTGCACTCCAG CTGGGC
GTGGTGGG GTGACGTGAGGTC GACCCG
A C

GAM281 278 SNX22 1 13596 NP_079074.1 3 519 TCTTGTTGCCCA C 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGCACG GTGACGT AGGTCGGACCCGTT
A

GAM281 278 SNX27 1 16941 NP_112180.4 3 3109 CTCTGTCGCCCA A 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTTGGACCCG
C

GAM281 278 SPN 1 16209 NP_003114.1 3 185 CTTTGTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGCACGA GT ACGTGAGGTCGGACCCG
A C

GAM281 278 SPOP 1 5610 NP_003554.1 5 130 CTCTGTCACCCG CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGGCCC
AC

GAM281 278 SQV7L 1 7375 XP_047287.1 5 1345 CTCTGTTGCCCA C A 3 B b b
GGCAGGAGTACA CACTG ACTCC GCCTGGGCAA
GTGGCATT GTGAC TGAGG CGGACCCGTT
A A

GAM281 278 SRL 1 6681 XP_064152.3 3 585 CTCTGTCGGCCA --- 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTTGGACC TGT
GGC

GAM281 278 SRRM2 1 18975 NP_057417.2 5 1 GCGGCCCAGGCG - A A 3 B c c

GGGTGCGAGTGG CACT GCACTCC GCCTGGGC
CGCAGTCG GTGA CGTGGGG CGGACCCG
G - G

GAM281 278 SS18 1 17762 NP_005628.1 3 1674 TCTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM281 278 STAF65(1 2196 NP_055675.1 3 1380 CTCTGTCACCCA C CA 3 B c c
gamma) GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCA GT ACGTGAGGTCGGACCC
A AC

GAM281 278 STAM2 1 5301 NP_005834.3 3 360 CTCTGTCACCCA C----- CA 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGCATG TGACGTGAGGTCGGACCC
GTACGA AC

GAM281 278 STAU 1 3950 NP_004593.1 5 275 TCTTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM281 278 STE 1 3303 NP_005411.1 3 196 CTCTGTTGCCTA CA 3 B b b
GGCTGGAGGACA CACTG CTCCAGCCTGGGCAA
GTGGCACA GTGAC GAGGTCGGATCCGTT
AG

GAM281 278 STEAP2 1 9147 NP_694544.1 3 1987 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 STK10 1 2481 NP_005981.1 3 879 GCTGTACTGCCA T C - G 3 B c c
GGCTGCGATGCG CAC GCA TC CAGCCTGG CA
TGCTGGCC GTG CGT AG GTCGGACC GT
- - C -

GAM281 278 STOM 1 2907 NP_004090.3 3 495 TCTTGTTGCCCA CAC----- 3 B c c
GGCTGGAGTGCA TGCACTCCAGCCTGGGCAA
ATAGCATG ACGTGAGGTCGGACCCGTT
GTACGATA

GAM281 278 SYT11 1 9033 NP_689493.2 3 281 TCTTGTTGCCCG C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGTGAG GT ACGTGAGGTCGGGCCCGTT
A

GAM281 278 SYT13 1 15294 NP_065877.1 3 1526 CTTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TADA3L 1 9087 NP_597814.1 3 289 CACTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM281 278 TAF11 1 1997 NP_005634.1 3 391 CTCTATCACCTA A CA 3 B c c
GGCTGGAGTGCA C CTGCACTCCAGCCTGGG
GCGGCATG G GACGTGAGGTCGGATCC

C AC
GAM281 278 TAL1 2 3146 NP_003180.1 3 2548 CTATATTGCCCA C---- G CT- 3 B c c
GGCTGGTCTTGA ACT CA CCAGCCTGGGCAA
AGTCCTGG TGA GT GGTCGGACCCGTT
GGTCC A TCT
GAM281 278 TAL1 2 18260 NP_003180.1 3 2375 TTCTGTCACTCA C CA 3 B c c
GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGTGCC GTGAC TGAGGTCGGACTC
A AC
GAM281 278 TAPBP 3 11523 NP_003181.3 3 837 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM281 278 TAPBP 3 12247 NP_003181.3 3 230 CTCTTCCGCCCA C A 3 B b b
GGCTGCAGTGCA CACTGCACT CAGCCTGGGC
GTGGCATG GTGACGTGA GTCGGACCCG
C C
GAM281 278 TAPBP 3 16940 NP_003181.3 3 1142 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TAT 1 18942 NP_000344.1 3 779 CTCTGTCGCCCA C A 3 B b b
TGCTGGAGTGCA CACTGCACTCCAGC TGGGC
GTGGCGCG GTGACGTGAGGTCG ACCCG
T C
GAM281 278 TAZ 1 9257 NP_851831.1 3 96 CTGCTCTGCCCA C --- T G-- 3 B c c
GGAGGTGGCGTC ACTGC AC CCA CCTGGGCA
CAGCAGTC TGACG TG GGT GGACCCGT
C ACC C GGA
GAM281 278 TBC1D5 2 14859 NP_055559.1 5 590 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C
GAM281 278 TBC1D5 2 16449 NP_055559.1 5 920 CGCTCTTGTCCA C--- 3 B c b
GGCTGGAGTATA CACTG ACTCCAGCCTGGGCAA
ATGGTGCG GTGGT TGAGGTCGGACCTGTT
AATA
GAM281 278 TCF2 1 625 NP_006472.1 3 2022 CTCTGTCACCCG C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG GCCC
A AC
GAM281 278 TCL6 2 9387 NP_065578.2 5 1174 CCCTCTGTGCCA CA - 3 B b b
GGCCAGAGTGCA CACTGCACTC GCCTGG GCA
GTGGTGCA GTGACGTGAG CGGACC TGT
AC G
GAM281 278 TCL6 2 9387 NP_065579.2 5 1174 CCCTCTGTGCCA CA - 3 B b b
GGCCAGAGTGCA CACTGCACTC GCCTGG GCA
GTGGTGCA GTGACGTGAG CGGACC TGT
AC G
GAM281 278 TCL6 2 17450 NP_036600.2 5 645 CTCTGTCACTCA C CA 3 B c b

GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC

GAM281 278 TCL6 2 17450 NP_055233.1 5 645 CTCTGTCACTCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC

GAM281 278 TCL6 2 17450 NP_065575.1 5 645 CTCTGTCACTCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC

GAM281 278 TCL6 2 17450 NP_065577.2 5 645 CTCTGTCACTCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC

GAM281 278 TDGF1 1 8563 NP_003203.1 3 321 CTCTGTCACCCA C C CA 3 B c c
GGCTGGACTGCA CA TGCA TCCAGCCTGGG
ATGACGCG GT ACGT AGGTCGGACCC
A C AC

GAM281 278 TERA 1 17755 NP_067061.1 3 140 TCTTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AT

GAM281 278 TERF1 1 1745 NP_003209.1 3 419 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 TERF1 1 1745 NP_059523.1 3 419 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 TERF2 1 1744 NP_005643.1 3 141 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM281 278 TGIF2 1 6881 NP_068581.1 3 1452 CTCTGTCACCCG CA 3 B c c
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGGCCC
AC

GAM281 278 THEA 1 14452 NP_671517.1 3 631 GCAAGAGGCCAA T A- G A 3 B c c
GGCTGGAGAGGC CAC GC CTCCAGCCT GGC
GTGCCAGC GTG CG GAGGTCGGA CCG
- GA A G

GAM281 278 TIGD6 1 4933 NP_112215.1 3 909 TTATATTGCCTA C 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGGGCAA
GTGGTTAT GTGACGT AGGTCGGATCCGTT
A

GAM281 278 TIM50L 2 5989 XP_053074.2 3 614 CACTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGATGTG GT ACGTGAGGTCGGACCCGTT

T

GAM281 278 TIM50L 2 10157 XP_053074.2 3 1407 TCTTATTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCACG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 TK2 1 3160 NP_004605.1 3 696 TATGCTGCATTT CA TGG- 3 B c c
GGCTGGAGCCCG CACTG CTCCAGCC GCA
GTGTTCAG GTGGC GAGGTCGG CGT
CC TTTA

GAM281 278 TLR5 1 16229 NP_003259.2 5 97 CTCTGCCGCCCA C A 3 B b b
GGCTGGACTGCA CACTGCA TCCAGCCTGGGC
GTGACACA GTGACGT AGGTCGGACCCG
C C

GAM281 278 TMC1 1 2152 NP_619636.2 5 128 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TMEM14A 1 5271 NP_054770.1 5 75 CTCGGGGCTGCA - A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTG GGC
GTGGGACA GTGACGTGAGGTCGGAC TCG
G G

GAM281 278 TMPRSS3 1 6625 NP_076927.1 3 245 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM281 278 TMPRSS3 1 6625 NP_115777.1 3 245 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM281 278 TMPRSS3 1 6625 NP_115780.1 3 245 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM281 278 TNFAIP2 1 17621 NP_006282.2 3 1221 CTGTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCCTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TNFRSF1 1 4398 NP_003833.3 3 454 CTCTGTCTCCCA C CA 3 B c c
0B GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCA GT ACGTGAGGTCGGACCC
A TC

GAM281 278 TNFRSF1 1 4398 NP_671716.1 3 454 CTCTGTCTCCCA C CA 3 B c c
0B GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGTGCA GT ACGTGAGGTCGGACCC
A TC

GAM281 278 TNFRSF1 1 2200 NP_003830.1 3 503 GGCTCTGGCCCA C A 3 B b b
1A GGCTAGAGTGCA CACTGCACTC AGCCTGGGC
GTGGTGCG GTGACGTGAG TCGGACCCG
A G

GAM281 278 TNFRSF1 1 8120 NP_004186.1 3 288 GGAGGCTGTGTC - GCC 3 B c
c

8 CGTGGGTGTGCA CACTGCAC TCCA TGGGCA
GTGCCCAG GTGACGTG GGGT GCCTGT
T ---
GAM281 278 TNFRSF1 1 8120 NP_683699.1 3 35 GGAGGCTGTGTC - GCC 3 B c c

8 CGTGGGTGTGCA CACTGCAC TCCA TGGGCA
GTGCCCAG GTGACGTG GGGT GCCTGT
T ---
GAM281 278 TNFRSF1 1 8120 NP_683700.1 3 288 GGAGGCTGTGTC - GCC 3 B c
c

8 CGTGGGTGTGCA CACTGCAC TCCA TGGGCA
GTGCCCAG GTGACGTG GGGT GCCTGT
T ---
GAM281 278 TNFRSF9 1 13464 NP_001552.2 3 227 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC
GAM281 278 TNIP3 1 15713 NP_079149.2 3 706 AGATAAAGTCTT T TG - A 3 B c c
GGGCTGGGTGCA CACTGCAC CCAGCC GG C
GTGGCTCA GTGACGTG GGTCGG TC G
- GT T A
GAM281 278 TOLLIP 2 9557 NP_061882.2 3 1789 CTGCCTTCGCGT CT----- 3 B c c
TGCTGGGGTGCA CACTGCACTCCAGC GGGCA
GTGAGACT GTGACGTGGGGTCG TCCGT
TTGCGCT
GAM281 278 TOLLIP 2 13694 NP_061882.2 3 526 GGCCCCTGCCCA C C - 3 B c c
GGGCTTGGGTCT CACTG ACTC AGCC TGGGCA
GGTGAGCT GTGGT TGGG TCGG ACCCGT
C T G
GAM281 278 TOR1B 1 14221 NP_055321.1 3 180 CTCCGTCATCCA C CA 3 B c c
AGCTGGAGTGCA CACTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCT
A AC
GAM281 278 TP53 1 4654 NP_000537.2 3 833 CTTTGTTGCCCA G 3 B b b
GGCTGGAGTGGA CACT CACTCCAGCCTGGGCAA
GTGGCGTG GTGA GTGAGGTCGGACCCGTT
G
GAM281 278 TPMT 1 19670 NP_000358.1 3 426 TCTTGTTGCCCA CC 3 B b b
ACCTGGAGTGCA CACTGCACTCCAG TGGGCAA
GTGGTGCG GTGACGTGAGGTC ACCCGTT
CA
GAM281 278 TRAF2 1 778 NP_066961.2 3 301 AAGCTGCCCTTG TC-- CT 3 B c c
CTGTCCTGTGCA CACTGCAC CAGC GGGCA
GTGAAGGG GTGACGTG GTCG CCCGT
TCCT TT
GAM281 278 TRAF2 1 778 NP_663770.1 3 301 AAGCTGCCCTTG TC-- CT 3 B c c
CTGTCCTGTGCA CACTGCAC CAGC GGGCA
GTGAAGGG GTGACGTG GTCG CCCGT
TCCT TT
GAM281 278 TRAF5 1 7045 NP_004610.1 3 1091 CATTGTCACCCA C CA 3 B c c

GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC

GAM281 278 TRAF5 1 7045 NP_665702.1 3 1091 CATTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC

GAM281 278 TRAP150 1 4929 NP_005110.1 3 45 GATTCCTGCCCA C A--- AG 3 B c c

GGGGAGAGAGGC CA TGC CTCC CCTGGGCA
GCTGGGAA GT GCG GAGG GGACCCGT
C GAGA --

GAM281 278 TREX1 1 8479 NP_338598.1 5 1174 ATTTCTTGCCCA T CC 3 B c c
GGTTCCAGTGTG CAC GCACT AGCCTGGGCAA
TGTTCCAA GTG TGTGA TTGGACCCGTT
- CC

GAM281 278 TRIM16 1 4601 NP_006461.2 3 249 CACTGTTGCCCA A 3 B b b
GGCTGGAGAGCA CACTGC CTCCAGCCTGGGCAA
GTGGCGCG GTGACG GAGGTCGGACCCGTT
A

GAM281 278 TRIM5 1 5879 NP_149023.1 3 651 TCTTGTTCCCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGGCACG GT ACGTGAGGTCGGACCC
A CT

GAM281 278 TRIM6 1 13572 NP_477514.1 3 172 CTCTGTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
CTGGCGCA GT ACGTGAGGTCGGACCCG
C C

GAM281 278 TRPM6 1 18177 NP_060132.3 3 857 TCTTTTTACCCA C CA 3 B c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGATGCG GT ACGTGAGGTCGGACCC
A AT

GAM281 278 TRPV1 2 16980 NP_061197.3 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM281 278 TRPV1 2 16980 NP_542435.1 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM281 278 TRPV1 2 16980 NP_542436.1 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM281 278 TRPV1 2 16980 NP_542437.1 3 364 TCTTCTCACCCA C CA 3 B c b
GGCTGGAATGCA CACTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC

GAM281 278 TRPV1 2 19833 NP_061197.3 3 685 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA

GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TRPV1 2 19833 NP_542435.1 3 686 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TRPV1 2 19833 NP_542436.1 3 686 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TRPV1 2 19833 NP_542437.1 3 685 TCTTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM281 278 TSC1 1 15082 NP_000359.1 3 787 ATTGTGACCACA - T - - 3 B c c
GGCTGGTGTGTA CAC TGCAC CCAGCCTG GG CA
GGTGGTAA GTG ATGTG GGTCGGAC CC GT
G T A A
GAM281 278 TSPYL 1 15042 XP_166325.1 3 658 CTCTGTCGCCCA A 3 B b b
GGTTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTTGGACCCG
C
GAM281 278 TTC4 1 9587 NP_004614.1 3 189 AGCTGGACATAC C C--- GG 3 B c c
TGCTGGAGTCCA CACTG ACTCCAGC TG CA
GTGCTTTC GTGAC TGAGGTCG AC GT
C TCAT AG
GAM281 278 TTY7 1 1016 NP_114132.1 5 521 CCCCCATGCCCA G TC G 3 B c c
GGTGTGGTGAAG CACT CAC CA CCTGGGCA
TGAATCCC GTGA GTG GT GGACCCGT
A GT -
GAM281 278 TU12B1-TY 3 4256 NP_057659.1 3 3182 TCTTTTTGCCCA C A 3 B b b
GGCCGGAGTGCA CA TGCACTCC GCCTGGGCAA
ATGGCACG GT ACGTGAGG CGGACCCGTT
A C
GAM281 278 TU12B1-TY 3 15780 NP_057659.1 3 1305 TCTTATTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM281 278 TU12B1-TY 3 16036 NP_057659.1 3 2855 CTCTGTTGCCCA CC 3 B b b
TTCTGGAGTGCA CACTGCACTCCAG TGGGCAA
GTGGTGTG GTGACGTGAGGTC ACCCGTT
TT
GAM281 278 TUCAN 3 7106 NP_055774.1 3 2766 CTCTGTCATCTA CA 3 B c b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGATCT
AC
GAM281 278 TUCAN 3 9530 NP_055774.1 3 2457 CTCTGTTACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AT

GAM281 278 TUCAN 3 13395 NP_055774.1 3 3341 TGTGTGCCTATG T GC --- 3 B c b

AGATTGGGTGCA CACTGCAC CCA CT GGGCA
GTGTATCC GTGACGTG GGT GA TCCGT
- TA GTA

GAM281 278 TUFT1 1 6115 NP_064512.1 3 1286 CTCTGTCACCCA C----- CA 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGGG
GTAGCGCG TGACGTGAGGTCGGACCC
GCGCGA AC

GAM281 278 TXL-2 1 15381 NP_835231.1 5 95 AATTGCCCTGCA A --- 3 B b b
GGCTGGAGTGCA C CTGCACTCCAGCCT GGGCAA
GCGGCATG G GACGTGAGGTCGGA CCCGTT
C CGT

GAM281 278 TXNL2 1 9147 NP_006532.1 3 68 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 U1SNRNP 1 9590 NP_008951.1 5 122 GGGAGTCGCCCA A A 3 B c c

BP GGCTGGAGAGCG CACTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C

GAM281 278 U1SNRNP 1 9590 NP_851030.1 5 122 GGGAGTCGCCCA A A 3 B c c

BP GGCTGGAGAGCG CACTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C

GAM281 278 U1SNRNP 1 9590 NP_851034.1 5 122 GGGAGTCGCCCA A A 3 B c c

BP GGCTGGAGAGCG CACTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C

GAM281 278 UCK1 1 14148 NP_113620.1 3 761 CAGGTCTGTCCC A CA T 3 B c c
GGCTGGAGAACA C CTG CTCCAGCC GGGCA
GCGTCCAC G GAC GAGGTCGG CCTGT
C AA C

GAM281 278 UGDH 1 7909 NP_003350.1 3 153 CACTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM281 278 UGT1A1 1 10967 NP_000454.1 3 534 AATGAATGAATG C - TGGG 3 B c c

GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM281 278 UGT1A10 1 10967 NP_061948.1 3 535 AATGAATGAATG C - TGGG 3 B c c

GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM281 278 UGT1A4 1 10967 NP_009051.1 3 534 AATGAATGAATG C - TGGG 3 B c c

GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM281 278 UGT1A6 1 10967 NP_001063.1 3 533 AATGAATGAATG C - TGGG 3 B c c

GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM281 278 UGT1A8 1 10967 NP_061949.3 3 535 AATGAATGAATG C - TGGG 3 B c c

GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM281 278 UGT1A9 1 10967 NP_066307.1 3 534 AATGAATGAATG C - TGGG 3 B c c

GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT
C T TAA-

GAM281 278 UMPS 1 2144 NP_000364.1 3 391 CTCTGTTGCCCA G 3 B b b

GGATGGAGTGCA CACTGCACTCCA CCTGGGCAA
GTGGTGAG GTGACGTGAGGT GGACCCGTT
A

GAM281 278 UNC84B 1 13541 NP_056189.1 3 1393 TCTGGAGCATGA C GG- A 3 B c c

GGCTGGATGCAG CACTGCA TCCAGCCT GC
TGGTGGTG GTGACGT AGGTCGGA CG
- GTA A

GAM281 278 UNC84B 1 13541 XP_039332.1 3 1393 TCTGGAGCATGA C GG- A 3 B c c

GGCTGGATGCAG CACTGCA TCCAGCCT GC
TGGTGGTG GTGACGT AGGTCGGA CG
- GTA A

GAM281 278 URG4 1 6788 NP_060390.2 3 565 GACCCCTGCCCA C C CAG 3 B c c

GGAAGAGTTCAC CA TG ACTC CCTGGGCA
TGGTCGCT GT AC TGAG GGACCCGT
C T AA-

GAM281 278 USP22 1 11288 XP_042698.2 3 2025 GTTTGTTGCCCA G 3 B b b

GGCTGGAGTGAG CACT CACTCCAGCCTGGGCAA
TGGCACAG GTGA GTGAGGTCGGACCCGTT
-

GAM281 278 VDU1 1 3187 NP_055832.2 3 278 CTTTGTCACCCA T CA 3 B c c

GGCTGGAGTGCT CAC GCACTCCAGCCTGGG
GTGGTGTT GTG CGTGAGGTCGGACCC
T AC

GAM281 278 VENTX2 1 19331 NP_055283.1 3 305 CTCTGTCACCCA C CA 3 B c c

GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
ATGACGCA GT ACGTGAGGTCGGACCC

A AC
GAM281 278 VHL 2 3873 NP_000542.1 3 2569 CTCTGTTGCCCA CA----- 3 B c b
GGCTGGAGTGCA CTGCACTCCAGCCTGGGCAA
GAGGTGCG GACGTGAGGTCGGACCCGTT
GCGTGGA
GAM281 278 VHL 2 8786 NP_000542.1 3 989 TCTTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM281 278 VIPR2 1 7754 NP_003373.2 3 314 CTCTGTCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCCTG GTGACGTGAGGTCGGACCCG
C
GAM281 278 VPS33A 1 16690 NP_075067.2 3 232 CTCTGTCACCCA C C CA 3 B c c
GACTAGAGTGCA CACTGCACTC AG CTGGG
GTGGCACG GTGACGTGAG TC GACCC
A A AC
GAM281 278 VTI1A 1 2313 NP_660207.1 3 358 GCCCTGTCGCCT G T A 3 B c c
GGCTGGAGTGGA CACT CACTCCAGCC GGGC
GTGGCACA GTGA GTGAGGTCGG TCCG
G - C
GAM281 278 WBSCR1 1 11337 NP_071496.1 3 834 GGCTGGCCTCTC T T--- A 3 B c
c
TGGCTGGGTGCA CACTGCAC CCAGCC GGGC
GTGAATGG GTGACGTG GGTCGG TCCG
- TCTC G
GAM281 278 WBSCR1 1 11337 NP_114381.1 3 834 GGCTGGCCTCTC T T--- A 3 B c
c
TGGCTGGGTGCA CACTGCAC CCAGCC GGGC
GTGAATGG GTGACGTG GGTCGG TCCG
- TCTC G
GAM281 278 WBSCR18 1 2152 NP_115693.2 3 832 CTCTGTTGCCCA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT
GAM281 278 WHSC1 1 9245 NP_579889.1 3 3922 CCCTGTTGGCCA C----- G 3 B c c
GGCTGGAGTGCA ACTGCACTCCAGCCTGG CAA
GTAAGTGG TGACGTGAGGTCGGACC GTT
GGTGAA G
GAM281 278 WISP2 1 6412 NP_003872.1 3 109 GGTCCGTGCCCA CA--- CT --- 3 B c c
GGCCCTTGGCTG CTGCA CCA GCCTGGGCA
CAGGCAAC GACGT GGT CGGACCCGT
CAACG C- TCC
GAM281 278 XRCC2 3 9688 NP_005422.1 3 99 CTCTGTCTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM281 278 XRCC2 3 10148 NP_005422.1 3 278 TGTCTCCCAGGC --- CA 3 B c b

TGCTGGAGTGCA CACTGCACTCCA GCCTGGG
GTGGCACA GTGACGTGAGGT CGGACCC
CGT TC

GAM281 278 XRCC2 3 12605 NP_005422.1 3 278 CTCTGTCTCCCA --- CA 3 B c b
GGCTGCTGGAGT CACTGCACTCCA GCCTGGG
GCAGTGGC GTGACGTGAGGT CGGACCC
CGT TC

GAM281 278 YES1 1 16112 NP_005424.1 3 1378 CTCTGCCGCCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM281 278 ZAK 1 7294 NP_598407.1 3 2387 CTTTCCAGCATG GCCT 3 B b b
CCCTGGGGTGCA CACTGCACTCCA GGGCA
GTGGTCAG GTGACGTGGGGT CCCGT

GAM281 278 ZAP 1 3071 NP_064504.2 3 308 CTCCATCGTCCA A 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCTG
C

GAM281 278 ZBP1 1 16276 NP_110403.1 3 417 AAAACATAATCC T CC CA 3 B c c
CAACTGGGTGCA CACTGCAC CCAG TGGG
GTGGCTCA GTGACGTG GGTC ACCC
- A- TA

GAM281 278 ZFP30 1 9331 NP_055713.1 3 1854 CTCTTTCGCCCA T A 3 B b b
GGCTGGCGTGCA CACTGCAC CCAGCCTGGGC
GTGGCACA GTGACGTG GGTCGGACCCG
C C

GAM281 278 ZFP42 1 10587 NP_777560.1 3 643 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTCTA CACTG ACTCCAGCCTGGG
GTGTCGTG GTGAT TGAGGTCGGACCC
C AC

GAM281 278 ZFP64 1 15043 NP_060667.1 3 151 CTCTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCT GTGACGTGAGGTCGGACCC
TT

GAM281 278 ZFP64 1 15043 NP_071371.2 3 151 CTCTGTTTCCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGCT GTGACGTGAGGTCGGACCC
TT

GAM281 278 ZFYVE26 1 12160 XP_031077.1 3 3 CCCATGGCCCAG CT - --- A 3 B c c
GCTCCAGGAAGT CA GCACT CC AGCCTGGGC
GCCTTGGG GT CGTGA GG TCGGACCCG
TC A ACC G

GAM281 278 ZMYND17 1 456 NP_848546.1 3 219 CTCTGTTGCCCA A 3 B b b
GGCTGGAGTGCA C CTGCACTCCAGCCTGGGCAA
GCGGCATG G GACGTGAGGTCGGACCCGTT
C

GAM281 278 ZNF253 1 19746 NP_066385.1 3 292 TCTTGTCACCGA C G CA 3 B c c

GGCTGGAGTGCA CA TGCACTCCAGCCT GG

ATGACATG GT ACGTGAGGTCGGA CC
A G AC

GAM281 278 ZNF264 2 3319 NP_003408.1 3 2604 CTCTGTCACCCA T C CA 3 B c b
CGCTGGAGTGCT CAC GCACTCCAGC TGGG
GTGATGCG GTG CGTGAGGTCG ACCC
T C AC

GAM281 278 ZNF264 2 9147 NP_003408.1 3 2978 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM281 278 ZNF273 1 18868 XP_088082.1 3 843 TCTTGTTGCCCA C 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
ATGGCGTG GT ACGTGAGGTCGGACCCGTT
A

GAM281 278 ZNF289 1 13159 NP_115765.2 3 77 CCACAGTTCCCA CT - CA 3 B c c
GGCTGGGGATGC CA GCA CTCCAGCCTGGG
TTTGCCTT GT CGT GGGGTCGGACCC
TT A TT

GAM281 278 ZNF305 1 18505 NP_055539.1 3 2909 TCCTGTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
ATGGCACG GT ACGTGAGGTCGGACCCG
A C

GAM281 278 ZNF334 2 5064 NP_060572.2 5 42 TGTCACCCAGGC C --- CA 3 B c c
TGCTGGAGTACA CACTG ACTCCA GCCTGGG
GTGGCACA GTGAC TGAGGT CGGACCC
A CGT AC

GAM281 278 ZNF334 2 9628 NP_060572.2 5 42 CACTGTCACCCA C --- CA 3 B c c
GGCTGCTGGAGT CACTG ACTCCA GCCTGGG
ACAGTGGC GTGAC TGAGGT CGGACCC
A CGT AC

GAM281 278 ZNF339 1 1729 NP_067043.1 3 655 CTCTGTCACCCA C CA 3 B c c
GGCTGGAGTACA CACTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC

GAM281 278 ZNF345 1 1011 NP_003410.1 3 601 TCACTGTCACCA -- 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTCGGACC TGT
AC

GAM281 278 ZNF347 1 8447 NP_115973.1 3 126 AAATGCAATGAC T TGG---- 3 B c c
TGGCTGGGTGCA CACTGCAC CCAGCC GCA
GTGGCTCA GTGACGTG GGTCGG CGT
- TCAGTAA

GAM281 278 ZNF398 1 8530 NP_065832.1 5 255 CTCTGTCGCCCA C A A 3 B c c
GGCGGGAATGCA CACTGCA TCC GCCTGGGC
GTGGCGCA GTGACGT AGG CGGACCCG
A G C

GAM281 278 ZNF431 1 8477 XP_086098.2 3 1487 CTCTTTCGCCCA C A 3 B b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
TTGGCATG GT ACGTGAGGTCGGACCCG
T C

GAM281 278 ZNF432 1 5065 NP_055465.1 3 1769 TCTTGTTGCCCA CAC----- 3 B c c
GGTTGGAGTGTA TGCACTCCAGCCTGGGCAA
ATAGCACG ATGTGAGGTTGGACCCGTT
GCACGATA
GAM281 278 ZNF440 1 1744 NP_689570.1 3 1224 CTCTGTCACCCA CA 3 B b b
GGCTGGAGTGCA CACTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM281 278 ZNF70 1 17076 NP_068735.1 3 1596 GCCCTGTTGCCA C G 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM281 278 ZNF70 1 17076 NP_852101.1 3 1596 GCCCTGTTGCCA C G 3 B b b
GGCTGGAATGCA CACTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM391 326 5'OY11. 1 5923 NP_542942.1 5 516 CAGCTGATCCGG --- - -- C 3 C c c
1 ACTGGATGTGAC CAGA TCACATCCA TCCG TCA
CTTCTGCC GTCT AGTGTAGGT AGGC AGT
TCC C CT C
GAM391 326 APBB3 1 539 NP_573421.1 3 442 CAAGGCCATGGG AT -- CA 3 C c c
CATGGATGTGCT CAG CACATCCAT CCGT CC
GAACGAGG GTC GTGTAGGTA GGTA GG
-- CG CC
GAM391 326 APBB3 1 539 NP_573422.1 3 339 CAAGGCCATGGG AT -- CA 3 C c c
CATGGATGTGCT CAG CACATCCAT CCGT CC
GAACGAGG GTC GTGTAGGTA GGTA GG
-- CG CC
GAM391 326 APPBP2 1 1844 NP_006371.2 3 1503 AGTCTGTGGGTG AT CCG 3 C c
c
AATGGATGTGTG CAG CACATCCAT TCACC
TTGAATTT GTT GTGTAGGTA AGTGG
GT ---
GAM391 326 ASB1 1 11800 NP_057198.1 3 48 GATTCCAGTGAG ATCCA G 3 C c c
GGAGAAAGTGAT CAGATCAC TCC TCAC
CTGCAGGG GTCTAGTG AGG AGTG
AAAG- G
GAM391 326 ATP8B2 1 11976 XP_290875.1 5 828 TGCCAAGTTTGA A CAT C 3 C c
c
CGGTGAAGTGAT CAGATCAC TC CCGTCA
CTGTGAAC GTCTAGTG AG GGCAGT
A T-- T
GAM391 326 AXOT 1 3201 NP_073737.1 3 32 TCATATAAGACA CA C AC 3 C c c
GATGGATGATCT CAGATCA TCCATC GTC
GTGAACAT GTCTAGT AGGTAG CAG
-- A AA
GAM391 326 C14orf7 1 3928 XP_290629.1 5 13 CATTGAGGTCTC T T TC 3 C c c
8 GGTGGATGTGTC CAGA CACATCCA CCG ACC
TGCGCCGA GTCT GTGTAGGT GGC TGG

- - TC

GAM391 326 C1orf24 1 1181 NP_071366.1 3 603 GAAATGGAGGGT --- GT C 3 C c c
GGAAGGTGTGAT CAGATCACA TCCATCC CA
CTGTGGGA GTCTAGTGT AGGTGGG GT
GGA AG A

GAM391 326 C1orf24 1 1181 NP_443198.1 3 603 GAAATGGAGGGT --- GT C 3 C c c
GGAAGGTGTGAT CAGATCACA TCCATCC CA
CTGTGGGA GTCTAGTGT AGGTGGG GT
GGA AG A

GAM391 326 C21orf8 1 5611 NP_715632.1 3 180 ATCCATCTCTGA - A CG C 3 C c c
2 GATGGATGAGAA CAGAT C CATCCATC TCA
TCTGAGTC GTCTA G GTAGGTAG AGT
A A -- C

GAM391 326 C8orf6 2 6819 NP_663631.1 3 334 TTTTAGCATGAT A A C 3 C c c
GATGGATGGATG CAG TC CATCCATCCGTCA
GACTGGAG GTC AG GTAGGTAGGTAGT
- - A

GAM391 326 C8orf6 2 16546 NP_663631.1 3 335 AGCATGATGATG A A C 3 C c c
GATGGATGGACT CAG TC CATCCATCCGTCA
GGAGCTAG GTC AG GTAGGTAGGTAGT
- - A

GAM391 326 C9orf25 1 2377 NP_671735.1 3 704 AGGCTGAGGTTT T TC 3 C c c
GGGTGGTGTGAT CAGATCACA CCATCCG ACC
CTGTCCTA GTCTAGTGT GGTGGGT TGG
- T-

GAM391 326 CCR2 1 9391 NP_000638.1 3 421 TGGCAGGAGTTG ---- -- - C 3 C c c
GAAGTGTGTGAT CAGATCACA TCCA TCC GTCA
CTGTGGGC GTCTAGTGT AGGT AGG CGGT
GTGA TG A -

GAM391 326 CECR6 1 1794 NP_114096.1 3 1059 GTGGGTTTCCTG A- ------ 3 C c c
GATGGATGTGAA CAG TCACATCCATCCG TCAC
GTTGGGCC GTT AGTGTAGGTAGGT GGTG
GA CCTTTG

GAM391 326 CENTD2 1 12112 NP_056057.1 5 518 GTGGCAGCCCCG ------ 3 C c c
GGTGGGTGTGAT CAGATCACATCCATCC GTCAC
CTGTGGCT GTCTAGTGTGGGTGGG CGGTG
CCCCGA

GAM391 326 CGI-127 1 16833 NP_057145.1 3 1341 AATGAATGAATG TC - C 3 C c c
GATGGATGTTTT CAGA ACATCCATCCGT CA
GCATGCTC GTTT TGTAGGTAGGTA GT
-- A A

GAM391 326 CHERP 1 18403 NP_006378.2 3 331 CAGCCACGAAGG - G- AC 3 C c
c
GATGGATGTGCA CAGAT CACATCCATCC TC
TCTGCCCT GTCTA GTGTAGGTAGG AG
C GA CA

GAM391 326 CHRNB4 1 20038 NP_000741.1 3 40 GGTTGTGGGGTG GA A CG 3 C c
c
AGAGGATGTGAG CA TCACATCC TC TCACC
TGGCCGGG GT AGTGTAGG AG AGTGG

G- - --
GAM391 326 DAB2IP 1 8058 NP_115941.1 3 495 CCCCACCTGAAG AT G C 3 C c c
GGTGGATGTGCT CAG CACATCCATCC TCA
GGAGGGGT GTC GTGTAGGTGGG AGT
-- A C
GAM391 326 DDB1 1 4279 NP_001914.2 3 643 AAGAAGAAGGTG A A GT 3 C c c
GGAGGATGTGAA CAG TCACATCC TCC CACC
TTGTTAGT GTT AGTGTAGG AGG GTGG
A - --
GAM391 326 DKFZP43 1 13168 NP_056409.1 5 705 CAGGGGCTGACG A- ACA - - 3 C c
c
4O047 GATCGGGGAGAG CAG TC TCC ATCCGTCA CC
GCTGGGTG GTC AG GGG TAGGCAGT GG
GG AG- C C
GAM391 326 DKFZP43 1 7211 NP_055364.1 3 2928 CCTTGCTGATGA - TC C 3 C c c
4P211 GTAGGATGTGAT CAGATCACATCC A CGTCA
TTGGCTCT GTTTAGTGTAGG T GTAGT
A GA C
GAM391 326 E2F3 1 16925 NP_001940.1 3 360 CTGTGCCTGACG GA - - C 3 C c c
GATGGGCTGTAG CA TC ACA TCCATCCGTCA
AATGGGGT GT AG TGT GGGTAGGCAGT
A- A C C
GAM391 326 EPB41L4 2 5606 NP_060894.1 3 91 GTCTTGGCCTCA T AC 3 C c c
B GATGGATGGATG CAGA CACATCCATCCGTC
TGTTTGGA GTTT GTGTAGGTAGGTAG
- AC
GAM391 326 EPB41L4 2 16985 NP_060894.1 3 93 TGGCCTCAGATG T AC 3 C c c
B GATGGATGTGTT CAGA CACATCCATCCGTC
TGGACGAG GTTT GTGTAGGTAGGTAG
- AC
GAM391 326 EVC 2 672 NP_714928.1 3 3205 GGCTGTTATGGT - 3 C b b
GATGGATGGATG CAGATC ACATCCATCCGTCACC
TGGATTTG GTTTAG TGTAGGTAGGTAGTGG
G
GAM391 326 EVC 2 8983 NP_714928.1 3 3206 GTTATGGTGATG - 3 C b b
GATGGATGTGGA CAGATC ACATCCATCCGTCACC
TTTGGAAG GTTTAG TGTAGGTAGGTAGTGG
G
GAM391 326 FLJ1035 1 5633 NP_060537.2 3 194 TTGGTGGGGTAC A-- ---- G 3 C c c
0 AGTGGATGTGAA CAG TCACATCCAT CC TCACC
TACTGTAA GTC AGTGTAGGTG GG GGTGG
ATA ACAT -
GAM391 326 FLJ1070 1 3052 NP_060654.1 3 1662 CTACCCTGGTGG TCA GT 3 C c
c
2 GATGGATGGTTC CAGA CATCCATCC CACC
TGTAAATG GTCT GTAGGTAGG GTGG
TG- --
GAM391 326 FLJ1240 1 3246 NP_079381.1 3 1554 AGAATTTGAGGA A -- G C 3 C c c
9 ACTGGATGTGAC CAG TCACATCCA TCC TCA

TGTCATTG GTC AGTGTAGGT AGG AGT
- CA - T
GAM391 326 FLJ1426 1 17291 NP_079303.2 5 124 AGGATGTGACAT TC CC-- 3 C c c
0 CTGTGCTGTGAT CAGATCACA CAT GTCAC
CTGGATGA GTCTAGTGT GTG CAGTG
C- TCTA
GAM391 326 FLJ2027 1 518 NP_060207.1 3 1842 TTAGCAATGAGG -- A G C 3 C c c
5 AGGAAATGTGAT CAGATCACA TCC TCC TCA
CTGGCTGT GTCTAGTGT AGG AGG AGT
AA - - A
GAM391 326 FLJ3900 1 3674 NP_848616.1 5 52 GGAGGAGAGAAG TCCAT T 3 C c
c
5 TGCGGCTGTGAT CAGATCACA CCG CAC
CTGGGGAA GTCTAGTGT GGC GTG
C---- -
GAM391 326 FOXM1 1 11174 NP_068772.1 3 709 TTGGGGTGGGAG ATCA G- 3 C c
c
GATGGATGCAAC CAG CATCCATCC TCACC
TGAAGCAG GTC GTAGGTAGG GGTGG
AAC- AG
GAM391 326 FOXP1 1 4841 NP_116071.2 5 230 CAGCCATGAACG -- - C 3 C c c
GATGGATGTGAT CAG ATCACATCCATCCGT CA
GCCTGCTA GTC TAGTGTAGGTAGGCA GT
CG A A
GAM391 326 GALNACT 1 11066 NP_061060.3 3 348 CTAGGTGGAGCG AT - -- 3 C c
c
-2 GATGGAATGTGC CAG CACAT CCATCCGT CACC
TGGGCCAC GTC GTGTA GGTAGGCG GTGG
-- A AG
GAM391 326 GATA2 1 12989 NP_116027.2 3 1284 TATGCGGTGACG --- AT 3 C c c
GCGGGGTGTGGT CAG ATCACATCC CCGTCACC
GGCCTGTG GTC TGGTGTGGG GGCAGTGG
CGG GC
GAM391 326 GEMIN7 1 6579 NP_078983.1 5 75 CCCTGAGTGACG ACA CA 3 C c
c
GAAAGAGGTCTG CAGATC TC TCCGTCAC
GCGGCTTC GTCTGG AG AGGCAGTG
--- AA
GAM391 326 GRIN2B 1 14110 NP_000825.1 3 97 CGGAGGGTGACG A ---- AT 3 C c c
GGGGTGAACTTG C GATCA CATCC CCGTCACC
GTTCCCAT C TTGGT GTGGG GGCAGTGG
C TCAA --
GAM391 326 HEYL 1 11546 NP_055386.1 3 2234 TGGAAGGAAAGG CCATCC 3 C c
c
TGACTGTGTGAT CAGATCACAT GTCACC
CTGATTCT GTCTAGTGTG CAGTGG
T-----
GAM391 326 INMT 1 9915 NP_006765.3 3 1288 AGGTGTAAGGTA T --- GT- 3 C c c

CATGGATGTGCT CAGA CACATCCAT CC CACC
TTGGTCAA GTTT GTGTAGGTA GG GTGG
C CAT AAT

GAM391 326 JMJ 1 2359 NP_004964.2 3 521 CCGTGTGCCAGA TC-- C- - 3 C c c
TGAGCTTGTGAT CAGATCACA CATC GT CAC
CTGGGAAG GTCTAGTGT GTAG CG GTG
TCGA AC T

GAM391 326 KCNA5 1 3000 NP_002225.2 3 268 TGAGCGCTGTGA C CG 3 C c c
GATGGATGTATT CAGAT ACATCCATC TCAC
TGTAGCCA GTTTA TGTAGGTAG AGTG
- --

GAM391 326 KIAA027 1 13253 XP_048199.1 3 1898 TAATACTGATGT CA - C 3 C c c
6 GATGGATGCATT CAGAT CATCCATC CGTCA
TGTTTTGC GTTTA GTAGGTAG GTAGT
C- T C

GAM391 326 KIAA037 1 5037 XP_037759.2 3 2166 AAGGTGGCCATG - --- --- 3 C c c
6 GATGGATGGGCT CAGAT CA CATCCATCC GTCACC
GTATCTGT GTCTA GT GTAGGTAGG CGGTGG
T CGG TAC

GAM391 326 KIAA077 1 7493 NP_055505.1 3 3104 CTGGGGAAGTGG - A GT 3 C c c
3 GAGGGATGTGAT CAG ATCACATCC TCC CAC
GCTGGAGA GTC TAGTGTAGG AGG GTG
G G --

GAM391 326 KIAA093 1 11761 XP_166213.1 3 710 TTCTCTCATGTG - A T C 3 C c c
7 GATGGATGGACT CAGA TC CATCCATCCG CA
CTGGGGTT GTCT AG GTAGGTAGGT GT
C - - A

GAM391 326 KIAA146 1 16373 XP_166132.1 3 1668 CTAAAATGTGAA AT TCCG- 3 C c
c
2 CCGTTGGGTGAT CAGATCAC CCA TCAC
CTGTCCTT GTCTAGTG GGT AGTG
-- TGCCA

GAM391 326 KIAA195 1 13357 XP_057401.1 3 229 TGAAGCTCTGAA - CCG C 3 C c c
1 ATGCGATGTGAT CAGATCACATC CAT TCA
CTGTACCA GTCTAGTGTAG GTA AGT
C A-- C

GAM391 326 KIFC2 1 6714 NP_665697.1 3 504 CGGCTGGTGACT AT - ---- 3 C c c
GATGGATGGGTA CAG CAC ATCCATCC GTCACC
GTGGGCTG GTC GTG TGGGTAGG CAGTGG
GG A TAGT

GAM391 326 KREMEN1 1 7291 NP_114434.3 3 852 CGGGTGATGCTA AT- --- 3 C c c
GATGGATGTGTA CAG CACATCCATC CGTCACC
CCTGGTGG GTC GTGTAGGTAG GTAGTGG
CAT ATC

GAM391 326 LDB3 1 2117 XP_084376.6 3 1777 ATCAGGAAGGGA AT- CC A 3 C c c
CATGGATGTGCT CAG CACATCCAT GTC CC

CCTGCCAC GTC GTGTAGGTA CAG GG
CTC -- -

GAM391 326 LOC1250 1 19284 XP_058889.3 5 7 GTAGACGCCATG T ---- AC 3 C c c
61 ATGGATGTGTCT CAGA CACATCCATC CGTC
GGTGTGGG GTCT GTGTAGGTAG GCAG
- TACC AT

GAM391 326 LOC1392 1 11240 XP_208439.1 3 761 GAAGGACACGGT CACATC 3 C c
c
01 GATGGATGTACT CAGAT CATCCGTCACC
ATGTCTGA GTCTG GTAGGTAGTGG
TATCAT

GAM391 326 LOC1433 1 12539 XP_084485.1 3 1495 GGATGATGATAG AT C---- - 3 C c
c
10 CATGGATGTGCC CAG CACATCCAT CGTCA CC
TGAAATGC GTC GTGTAGGTA GTAGT GG
C- CGATA A

GAM391 326 LOC1456 1 10556 XP_085200.1 5 152 AATAAATGGTGT ATCACA 3 C c
c
60 GATGGATGGAAC CAG TCCATCCGTCAC
TAACTGGA GTC AGGTAGGTAGTG
AATCA-

GAM391 326 LOC1458 1 1993 XP_085246.1 3 525 ATAATTTGTGTC TC C T 3 C c c
20 GATGGATGTTCT CAGA ACATCCATC G CAC
GTGAAGGC GTCT TGTAGGTAG C GTG
-- - T

GAM391 326 LOC1462 1 11896 XP_096956.1 3 866 CCTCTTTGCTGA A TCC C 3 C c
c
43 CCTGGAGGTGAT CAGATCAC TCCA GTCA
CTGTGTAT GTCTAGTG AGGT CAGT
G C-- C

GAM391 326 LOC1465 1 18098 XP_085491.1 3 1764 TGGGGAGGTCTG A T- GT A 3 C c
c
17 GATGGATCTGTG CAGATC CATCCA CC C CC
TAGGAGTT GTCTAG GTAGGT GG G GG
- CT AG -

GAM391 326 LOC1487 1 17147 XP_086281.1 5 153 CAGGCTGGAGTG C----- T T T 3 C c
c
09 CGGTGGTGTGAT AGATCACA CCA CCG CAC
CTTGGCTC TCTAGTGT GGT GGC GTG
CTCGGT - - -

GAM391 326 LOC1501 1 7211 XP_086802.2 3 2930 CCTTGCTGATGA - TC C 3 C c c
74 GTAGGATGTGAT CAGATCACATCC A CGTCA
TTGGCTCT GTTTAGTGTAGG T GTAGT
A GA C

GAM391 326 LOC1502 1 7211 XP_059324.1 3 2929 CCTTGCTGATGA - TC C 3 C c c
13 GTAGGATGTGAT CAGATCACATCC A CGTCA
TTGGCTCT GTTTAGTGTAGG T GTAGT
A GA C

GAM391 326 LOC1510 1 6116 XP_098000.1 3 262 CTTAGCTGGGTG T T T 3 C b b
68 TGGTGGTGTGAT CAGATCACA CCA CCG CACC

CTGTAGTT GTCTAGTGT GGT GGT GTGG
- - -
GAM391 326 LOC1511 1 6464 XP_098006.1 5 1562 ACAACAGAGACG TC T AC 3 C c c
24 GATGGTGTTTCT CAGA ACA CCATCCGTC
GAGAGGAA GTCT TGT GGTAGGCAG
T- - AG
GAM391 326 LOC1518 1 9078 XP_098132.1 3 1733 GGCTGTGACGTC AT TC-- 3 C c c
77 ACTGGATGTGTC CAG CACATCCA CGTCAC
CTGATCTA GTC GTGTAGGT GCAGTG
CT CACT
GAM391 326 LOC1575 1 9551 XP_212210.1 5 876 TGGAGTGTGACG AT A - A 3 C c c
31 GAGGCATGGGGC CAG C CAT CC TCCGTCAC
CTGTGCTC GTC G GTA GG AGGCAGTG
CG G C -
GAM391 326 LOC1969 1 19127 XP_113795.1 5 173 CGTGTGGGGAGC -- -- G 3 C c c
88 TGGGTGTGTGAT CAGATCACAT CCA TCC TCAC
CTGGCCAG GTCTAGTGTG GGT AGG GGTG
TG CG -
GAM391 326 LOC1997 1 10043 XP_113998.1 5 90 TGTGACAGCGGG C----- A ----- 3 C c c
18 GATGGATGTGAC AG TCACATCCATCC GTCAC
CTTGCCCG TC AGTGTAGGTAGG CAGTG
GCCCGT C GGCGA
GAM391 326 LOC2002 1 12207 XP_117206.2 3 256 GGTTCTTGACCT A C- C 3 C c c
25 GGTGGATGTGGC CAG TCACATCCATC GTCA
TGCAGTCC GTC GGTGTAGGTGG CAGT
- TC T
GAM391 326 LOC2219 1 14906 XP_166555.2 5 597 AAAGGCGTGACG TCACA ---- 3 C c c
22 GAGAGCTGGGGC CAGA TCCA TCCGTCAC
TCTGAGAG GTCT GGGT AGGCAGTG
CG--- CGAG
GAM391 326 LOC2540 1 1936 XP_173023.1 3 781 CTCGGGGTGACG TC CCA 3 C c c
99 GAATGTTCTGGA CAGA ACAT TCCGTCACC
CCTTGATA GTCT TGTA AGGCAGTGG
-- ---
GAM391 326 LOC2830 1 19606 XP_210858.1 3 12 GGGCATAGAGTG A A - - 3 C c c
30 AGTGGATGTGAT CAG TC CATC CATCCG TCAC
GGGCTGTG GTC GG GTAG GTAGGT AGTG
- - T G
GAM391 326 LOC2830 1 7277 XP_210868.1 3 482 CTATTGGGATGG TC - A 3 C c c
49 AATGGATGTATT CAGA ACATCCAT CCGTC CC
TTGCATGT GTTT TGTAGGTA GGTAG GG
TA A -
GAM391 326 LOC2835 1 9689 XP_211079.1 5 10 AGCGTGGAGACG TCACA A 3 C c c

```
          30                          GATGGGAATTCT CAGA    TCCATCCGTC CC
                                     GCAGCCAC    GTCT    GGGTAGGCAG GG
                                               TAA--        A
GAM391    326    LOC2836 1  480    XP_211126.1  5  2007   CATACGTGCTGG       TCCA-   T        3  C  c
c
          24                          AAATGCTGTGAT CAGATCACA    TCCG CAC
                                     CTGCCCTG    GTCTAGTGT    AGGT GTG
                                                  CGTAA   C
GAM391    326    LOC2841 1  6945   XP_208171.1  5  219    GGTGGTGAACAG   GA        - -        3  C  c  c
          67                          GGTGGATGTGGC CA  TCACATCCATCC GT CACC
                                     GTGGCTCC    GT  GGTGTAGGTGGG CA GTGG
                                               GC         A  A
GAM391    326    LOC2843 1  3674   XP_209116.1  5  52     GGAGGAGAGAAG       TCCAT   T        3  C  c
c
          13                          TGCGGCTGTGAT CAGATCACA    CCG CAC
                                     CTGGGGAA    GTCTAGTGT    GGC GTG
                                                  C----   -
GAM391    326    LOC2845 1  19633  XP_211529.1  3  133    GTGTATGGATGA       A  ------    -     3  C  c  c
          91                          GGCTGGAGTGAT CAGATCAC TCCA     TCCGT CAC
                                     CTGGGACC    GTCTAGTG AGGT     AGGTA GTG
                                                  -   CGGAGT    T
GAM391    326    LOC2847 1  11856  XP_211633.1  5  1187   TGGGTTTGTGTG    --       TC  T        3  C  c  c

          91                          TGTGGATGTGGT CAGA  TCACATCCA  CG CAC
                                     TTCTGCCT    GTCT  GGTGTAGGT  GT GTG
                                                  TT        GT  -
GAM391    326    LOC2850 1  1586   XP_211742.1  3  903    AGAGGTAAGGGG C-     C  -    G        3  C  c
c
          43                          TGAGGATGTGAT   AGATCA ATC CATCC TCACC
                                     TGATTTCC      TTTAGT TAG GTAGG AGTGG
                                               CC     -  T    -
GAM391    326    LOC2851 1  9288   XP_211782.1  5  422    CAACACCTTGAT    A       TC    C        3  C  c  c
          51                          GTTGGATGTGAA CAG TCACATCCA  CGTCA
                                     CTGTGAGG    GTC AGTGTAGGT  GTAGT
                                                  A        T-     T
GAM391    326    LOC2854 1  14330  XP_209615.1  3  279    TCTTGTGGGTGA    A--       TCC         3  C  c
c
          52                          CCTGGATGTGAG CAG   TCACATCCA   GTCACC
                                     ACCTGGAG    GTC   AGTGTAGGT   CAGTGG
                                                  CAG        C--
GAM391    326    LOC2856 1  15156  XP_211985.1  5  388    TAGATGGGACGT    A  A     -   A        3  C  c  c

          87                          GATGGATGGAAT CAG TC CATCCATC CGTC CC
                                     TGAAGTTA    GTT AG GTAGGTAG GCAG GG
                                                  A  -       T    -
GAM391    326    LOC2859 1  8402   XP_212128.1  3  1332   TCAGTGGTGACG    A---  A  T   T        3  C  c
c
          96                          GTGGCTGAGAGC CAG    TC CA CCA CCGTCACC
                                     TCCTGGAT    GTC    AG GT GGT GGCAGTGG
                                                  CTCG  A  C   -
```

GAM391 326 LOC2862 1 1222 XP_209954.1 3 690 GGAGCCGTGGGG A T- G 3 C c c
20 CCTGGATGTGGA CAG TCACATCCA CC TCAC
CTGTGCAG GTC GGTGTAGGT GG GGTG
A CC -
GAM391 326 LOC2863 1 16638 XP_212294.1 5 853 AGACCCAGTCAC TCC C 3 C c c
72 ATTGGATGTGAT CAGATCACATCCA GT AC
CTGTATAA GTCTAGTGTAGGT CA TG
TA- C
GAM391 326 LOC3395 1 12947 XP_295008.1 5 621 ACAATTTGACAT A T C 3 C c c
68 GATGGATGGTGT CAG TCACA CCATCCGTCA
GGCTGGGA GTC GGTGT GGTAGGTAGT
- - A
GAM391 326 LOC3407 5 1668 XP_291690.2 5 156 TGGGTGGCCTGT - A- - -- 3 C c b
31 GATGGATGGGGG CAGA TC CATCCATC C GTCACC
CTCTGTGG GTCT GG GTAGGTAG G CGGTGG
C GG T TC
GAM391 326 LOC3407 5 6111 XP_291690.2 5 408 CGAGTGGCCTGT AT CAT 3 C c b
31 GATGGATGGCTG CAG CA CCATCCGTCAC
GCCTGTGG GTC GT GGTAGGTAGTG
CG C--
GAM391 326 LOC3407 5 9019 XP_291690.2 5 534 TGGGTGGCCTAT - A- C--- 3 C c b
31 GATGGATGGGGG CAGA TC CATCCATC GTCACC
CTCTGTGG GTCT GG GTAGGTAG CGGTGG
C GG TATC
GAM391 326 LOC3407 5 10106 XP_291690.2 5 229 TGGCCTGTGATG TC 3 C b b
31 GATGGATGTTCT CAGA ACATCCATCCGTCAC
GTGGTGAA GTCT TGTAGGTAGGTAGTG
--
GAM391 326 LOC3407 5 17313 XP_291690.2 5 30 CGAGTGGCCTGT TCA 3 C c b
31 GATGGATGGGTG CAGA CATCCATCCGTCAC
CTCTGTGG GTCT GTGGGTAGGTAGTG
C--
GAM391 326 LOC3484 1 13888 XP_302764.1 5 1425 CCATCTGCGTGA GA TCC 3 C c c
61 CCTGGATGTGAG CA TCACATCCA GTCAC
ATGTGGAG GT AGTGTAGGT CAGTG
AG C--
GAM391 326 LOC3494 3 5729 XP_303044.1 3 43 AATGGATGGATG - A AC 3 C c c
08 GATGGATGGATG CAG ATC CATCCATCCGTC
TTGGTGAA GTT TAG GTAGGTAGGTAG
G - GT
GAM391 326 LOC3494 3 6295 XP_303044.1 3 43 GACGAATGGATG - A AC 3 C c c
08 GATGGATGGATG CAG ATC CATCCATCCGTC
GATGTTGG GTT TAG GTAGGTAGGTAG
G - GT
GAM391 326 LOC3494 3 10334 XP_303044.1 3 46 GATGGATGGATG - A AC 3 C c c
08 GATGGATGTTGG CAG ATC CATCCATCCGTC

TGAAAATT GTT TAG GTAGGTAGGTAG
G - GT
GAM391 326 LOC3499 1 12995 XP_303713.1 5 40 GACCATCAAGTG CA GT 3 C c c
99 GGAAGATGTGAT CAGATCACATC TCC CAC
TTGTCTTG GTTTAGTGTAG AGG GTG
A- --
GAM391 326 LOC9024 1 7361 XP_030283.1 3 1105 CTTAGATGTGAT ATC- C 3 C c c
6 GATGGATGTACA CAG ACATCCATC GTCAC
ACTGCGTG GTC TGTAGGTAG TAGTG
AACA -
GAM391 326 LOC9071 1 16755 XP_033704.1 3 127 TCCCAGGCTGGG TCA G - 3 C c
c
9 GATGGATGCTCT CAGA CATCCATCC TCA CC
GACCACAG GTCT GTAGGTAGG GGT GG
C-- - C
GAM391 326 LOC9090 1 17746 XP_034809.1 3 1229 TGATGGAGGAAG A A--- C 3 C c
c
6 GATGGATTTGGT CAGATC CATCC TCCGTCA
TACCAGAT GTTTAG GTAGG AGGTAGT
- AAGG -
GAM391 326 MAPK8IP 1 6962 NP_203750.1 3 839 CTGGGTTGGGCT A-- C -- 3 C c c
3 GGTGGATGTGGG CAG TCACATCCATC GTC ACC
GCCTGGGA GTC GGTGTAGGTGG CGG TGG
CGG T GT
GAM391 326 MGC1077 1 3496 NP_085044.2 3 156 TTGAGGATAATA - ------ G C 3 C c c
2 AAGGTGTGTGAT CAGATCACAT CC ATCC TCA
CTGGTTTG GTCTAGTGTG GG TAGG AGT
T AAATAA - T
GAM391 326 MGC1087 1 17365 NP_115677.1 3 50 TGAGCAGGTGGG - - - GT 3 C c c
0 CGTGGATGTGGA CAG ATC ACATCCAT CC CACC
TACTGCCT GTC TAG TGTAGGTG GG GTGG
A G C --
GAM391 326 MGC1110 1 17225 NP_115701.2 3 1831 GATGTGATATGT G CC--- 3 C c
c
2 TATGGATGTGAT CA ATCACATCCAT GTCAC
GTGTTAGT GT TAGTGTAGGTA TAGTG
G TTGTA
GAM391 326 MGC1729 1 14020 NP_653227.1 5 283 GTGGCAGGTGCT T AT----- - 3 C c
c
9 CCAGGCTGTGAT CAGATCACA CC CC GTCAC
CTGCACCC GTCTAGTGT GG GG CGGTG
C ACCTCGT A
GAM391 326 MGC2306 1 12989 NP_002041.2 3 1284 TATGCGGTGACG --- AT 3 C c
c
GCGGGGTGTGGT CAG ATCACATCC CCGTCACC
GGCCTGTG GTC TGGTGTGGG GGCAGTGG
CGG GC

GAM391 326 MGC2508 1 11605 NP_077303.1 3 45 TCCACGGTGACG A T-- 3 C c c
GGTGGCTCTGTG CAG TCACA CCATCCGTCACC
GCTGGTAG GTC GGTGT GGTGGGCAGTGG
- CTC
GAM391 326 MTO1 1 17745 NP_598400.1 3 654 ATCCACAGTGTG CAC- T 3 C c c
GATGGATACTTA CAGAT ATCCATCCG CAC
TTTGGTGA GTTTA TAGGTAGGT GTG
TTCA -
GAM391 326 MYLK 1 11895 NP_444253.1 5 110 GACGGTGACCAT A- A --- 3 C c c
GGGGGATGTGAA CAG TCACATCC TCC GTCACC
GCTGGTTG GTC AGTGTAGG GGG CAGTGG
GA - TAC
GAM391 326 MYLK 1 11895 NP_444254.1 5 110 GACGGTGACCAT A- A --- 3 C c c
GGGGGATGTGAA CAG TCACATCC TCC GTCACC
GCTGGTTG GTC AGTGTAGG GGG CAGTGG
GA - TAC
GAM391 326 MYLK 1 11895 NP_444255.1 5 110 GACGGTGACCAT A- A --- 3 C c c
GGGGGATGTGAA CAG TCACATCC TCC GTCACC
GCTGGTTG GTC AGTGTAGG GGG CAGTGG
GA - TAC
GAM391 326 MYLK 1 11895 NP_444256.1 5 110 GACGGTGACCAT A- A --- 3 C c c
GGGGGATGTGAA CAG TCACATCC TCC GTCACC
GCTGGTTG GTC AGTGTAGG GGG CAGTGG
GA - TAC
GAM391 326 MYLK 1 11895 NP_444257.1 5 117 GACGGTGACCAT A- A --- 3 C c c
GGGGGATGTGAA CAG TCACATCC TCC GTCACC
GCTGGTTG GTC AGTGTAGG GGG CAGTGG
GA - TAC
GAM391 326 N33 1 6148 NP_006756.2 3 17 TGGACTTTGAGT CA - C 3 C c c
GGAAGATGTGAT CAGATCACATC TCCG TCA
TTGGACCA GTTTAGTGTAG AGGT AGT
A- G T
GAM391 326 NUP54 1 7998 NP_059122.2 5 22 AGAAAGGAGGCG ATCCA A 3 C c
c
GAACTCGGTGAT CAGATCAC TCCGTC CC
CTGACTGG GTCTAGTG AGGCGG GG
GCTCA A
GAM391 326 OTP 1 18727 NP_115485.1 3 1002 GTCATGTGACGA A CA - 3 C c c
GGAAGAGGTGAT CAGATCAC TC TC CGTCAC
CTGACCCA GTCTAGTG AG GG GCAGTG
G AA A
GAM391 326 PGRMC2 1 742 NP_006311.1 3 1092 AGTGGGTGTCAG T CCGT- 3 C c
c
TATGGATGTGTC CAGA CACATCCAT CACC
TGAATGTG GTCT GTGTAGGTA GTGG
- TGACT
GAM391 326 PREI3 1 13783 NP_056202.1 3 1932 AGGTAGTGACTG ATCCA- C 3 C c
c
AGATTTGGTGAT CAGATCAC TC GTCAC
CTGGCTGA GTCTAGTG AG CAGTG

GTTTAG T

GAM391 326 PRO2859 1 16593 NP_061013.1 5 478 CCAATGTGGAAC A CCG-- 3 C c c

AAATGGAGTGAT CAGATCAC TCCAT TCAC

CTGTTATC GTCTAGTG AGGTA GGTG

\- AACAA

GAM391 326 PRSS11 1 15793 NP_002766.1 3 68 CCGTGGATGACG - ACATC - 3 C c c

GATGAGGACTCT CAGA TC CATCCGTCA CC

GGGCTGCT GTCT AG GTAGGCAGT GG

C GA--- A

GAM391 326 SLC15A2 1 1490 NP_066568.2 3 495 AAGAATTGGTAT C C C 3 C c c

GTATGATGTGAT CAGATCACATC AT CGT ACC

CTGGTCCA GTCTAGTGTAG TA GTA TGG

\- T -

GAM391 326 SLC19A1 1 16419 NP_003047.1 3 903 AGGTGCGGGACC G CA----- T 3 C c c

ATCTGATGTGAT CA ATCACATC TCCG CACC

GTGAATAC GT TAGTGTAG GGGC GTGG

G TCTACCA -

GAM391 326 SLC20A1 1 9287 NP_005406.3 3 708 CTGGCAGTGTGG GA -- GT 3 C c c

GATGGATGAATG CA TCA CATCCATCC CAC

AAGTGGAA GT AGT GTAGGTAGG GTG

GA AA GT

GAM391 326 SLC24A1 1 17502 NP_004718.1 3 147 TAGGACCTCTGA C CC C 3 C c c

TATGAATGTGAT CAGATCACAT CAT GTCA

CTGAGACT GTCTAGTGTA GTA TAGT

A -- C

GAM391 326 SLC39A3 1 15092 NP_653165.1 3 25 TGTAGGGTGACG - A A---- 3 C c c

GAAAGTAGGAAG CAGAT CAC TCC TCCGTCACC

TGAATTTG GTTTA GTG AGG AGGCAGTGG

A A ATGAA

GAM391 326 SNRK 1 12233 NP_060189.2 3 1417 TCTGAGGTGACG CACA- CA 3 C c c

GACTGAGACGCA CAGAT TC TCCGTCACC

TCTGGTCC GTCTA AG AGGCAGTGG

CGCAG TC

GAM391 326 SOX11 1 14726 NP_003099.1 3 1950 CGGGGAGGGGCG AT ACA A 3 C c c

GATGGAGGGGCC CAG C TCCATCCGTC CC

TGGGTTGC GTC G AGGTAGGCGG GG

CG GG- -

GAM391 326 SPR 1 6469 NP_003115.1 3 374 CCTGTGGGTAGA A CA G - 3 C c c

GGAAAGAGTGAT CAGATCAC TC TCC TC ACC

CTGGTGTC GTCTAGTG AG AGG AG TGG

\- AA - A

GAM391 326 SPRY4 1 1887 NP_112226.2 3 1952 ACAGTTGTGACG C--- TC ---- 3 C c c

GATGTATGGATG AGA ACATCCA TCCGTCAC
TTCTTGAA TCT TGTAGGT AGGCAGTG
AAGT -- ATGT

GAM391 326 STAT3 1 10246 NP_003141.2 3 201 GAGAAATGAGTG AT CCG 3 C c c

AATGTGGGTGAT CAGATCAC CCAT TCAC
CTGCTTTT GTCTAGTG GGTG AGTG
-- TA-

GAM391 326 STAT3 1 10246 NP_644805.1 3 201 GAGAAATGAGTG AT CCG 3 C c c

AATGTGGGTGAT CAGATCAC CCAT TCAC
CTGCTTTT GTCTAGTG GGTG AGTG
-- TA-

GAM391 326 SURF6 1 10519 NP_006744.2 3 967 GCCCTGTGAAAG GA - CG 3 C c c

ATAGGATGTGAG CA TCACATCC ATC TCAC
GTGAGCAT GT AGTGTAGG TAG AGTG
GG A AA

GAM391 326 SYT3 1 3513 NP_115674.1 5 106 TAGTTGGTGCTG ATC T 3 C c c

GATGGATGTTTG CAG ACATCCATCCG CACC
TTGAATGA GTT TGTAGGTAGGT GTGG
GTT C

GAM391 326 TBC1D7 1 17570 NP_057579.1 3 71 AGCATTGTGTTC - TCCGT 3 C c c

TTGGCATGTGAT CAGATCACAT CCA CAC
CTGGGAAA GTCTAGTGTA GGT GTG
C TCTT-

GAM391 326 TCL6 1 4551 NP_065577.2 3 1275 GTGGGAAGGGGT ATCA C 3 C c c

GATGGATGATGA CAG CATC ATCCGTCACC
ACCTGGCA GTC GTAG TAGGTAGTGG
CAA- -

GAM391 326 TCL6 1 4551 NP_065578.2 3 1275 GTGGGAAGGGGT ATCA C 3 C c c

GATGGATGATGA CAG CATC ATCCGTCACC
ACCTGGCA GTC GTAG TAGGTAGTGG
CAA- -

GAM391 326 TNFRSF1 1 14661 NP_683760.1 3 303 ACTTCAAAGACG A C AC 3 C c c

9 GATGGGTTGAGC CAG TCA ATCCATCCGTC
TGGCAGCC GTC AGT TGGGTAGGCAG
G - AA

GAM391 326 TTTY14 1 2750 NP_114138.1 5 15 ATGGCTGTGACG GA --- 3 C c c

GATAAGGGGTGT CA TCACATCC ATCCGTCAC
GGGGTGCG GT GGTGTGGG TAGGCAGTG
GG GAA

GAM391 326 TTTY14 1 2750 XP_291361.1 5 136 ATGGCTGTGACG GA --- 3 C c c

GATAAGGGGTGT CA TCACATCC ATCCGTCAC
GGGGTGCG GT GGTGTGGG TAGGCAGTG
GG GAA

GAM633 340 ADCY7 1 8228 NM_001114.1 3 AGCAAAGCACTG C - TAT 3 C c c
TGCTGTGCTCAG CTGAGCAC AGC CA CTTTGCT
GACTCGTG TCG GT GAAACGA
- T CAC
GAM633 340 KIAA186 1 3886 XM_027658.5 3 AGCAAAGACAGC CA-- CATA 3 C c c
6 CAGCGTGCTCAG CTGAGCAC GC TCTTTGCT
GACTCGTG CG AGAAACGA
CGAC AC--
GAM633 340 KIAA187 1 6010 XM_056635.4 5 AGCAAAGACATT CCAGCC A 3 C c
c
9 CTGCTCAG CTGAGCA AT TCTTTGCT
GACTCGT TA AGAAACGA
CT---- C
GAM633 340 LOC1471 1 2676 3 AGCAAAGATGAC - CAGCCA 3 C c c
78 AGTGCTGCAG CTG AGCAC TATCTTTGCT
GAC TCGTG GTAGAAACGA
G ACA---
GAM633 340 LOC1576 1 20176 XM_291282.2 5 AGCAAAGGCTGC G CATA 3 C c
c
97 TGGTGTCAG CTGA CACCAGC TCTTTGCT
GACT GTGGTCG GGAAACGA
- TC--
GAM895 379 ABCA1 1 2647 NP_005493.2 3 1539 AAACAATGAATT ----- A -- 7 A c c
CTTCAACAGGGA AGCTG CC GTTGAAGAA CATT
AAACAGCT TCGAC GG CAACTTCTT GTAA
AAAAG A AA
GAM895 379 AD034 1 5799 NP_113668.2 3 565 GTCTTTAATGTT G TT 7 A c c
CTTTTTGGAGTT AGCT CCAG GAAGAACATT
AGGACCTC TTGA GGTT TTTCTTGTAA
- --
GAM895 379 AD034 1 5799 NP_694550.1 3 565 GTCTTTAATGTT G TT 7 A c c
CTTTTTGGAGTT AGCT CCAG GAAGAACATT
AGGACCTC TTGA GGTT TTTCTTGTAA
- --
GAM895 379 APTX 1 11308 NP_778242.1 5 225 ATAAGAAATGTT - CA A 7 A c c
CTCGACAGCAAG AGCT GC GTTGA GAACATTT
TTGAAAGC TTGA CG CAGCT CTTGTAAA
A A- -
GAM895 379 ARHGEF9 1 3229 NP_056000.1 3 603 TTATCAAATGTT CA- - 7 A c c
CCTTCAGCCCTG AGCTGC GTTGAAG AACATTT
CAGTTGCC TTGACG CGACTTC TTGTAAA
TCC C
GAM895 379 ARPC5 1 3112 NP_005708.1 3 956 GTCTTCAGTGTT AG 7 A c c
CTTCAGGGTAGT AGCTGCC TTGAAGAACATT
TGGGATCT TTGATGG GACTTCTTGTGA
--
GAM895 379 b5+b5R 1 14738 NP_057314.1 3 156 AAATCAAATGTT C A -- - 7 A c c
CCTTCAGTACAG AG TGCC GT TGAAG AACATTT
GTAACTTC TC ATGG CA ACTTC TTGTAAA

A A TG C

GAM895 379 BIRC5 1 19223 NP_001159.1 3 152 TCAAATTAGATG CT - GA 7 A c c
TTTCAACTGTGC AG GC CAGTTGAA ACATTT
TCCTGTTT TC CG GTCAACTT TGTAGA
CT T --

GAM895 379 BNC 1 19010 NP_001708.2 3 1448 GTGAAATGTATC C- - - 7 A c c
TTTCAACTGTTT AGCTG CAGTTGAA GA ACATTT
AGTTACCC TTGAT GTCAACTT CT TGTAAA
TT T A

GAM895 379 C13orf1 1 10373 NP_079389.1 3 159 TTTACAAATGTT T TTGA 7 A c c
8 CTGTTTTGGCTG AGC GCCAG AGAACATTT
CTATTGGT TCG CGGTT TCTTGTAAA
T TTG-

GAM895 379 CABYR 1 16855 NP_036321.2 5 149 CCAAAATGATTT - CCAG -- 7 A c c

CTTCAAAGCCCA AG CTG TTGAAGAA CATTT
GACTTG TC GAC AACTTCTT GTAAA
A CCGA TA

GAM895 379 CABYR 1 16855 NP_619585.1 5 57 CCAAAATGATTT - CCAG -- 7 A c c
CTTCAAAGCCCA AG CTG TTGAAGAA CATTT
GACTTG TC GAC AACTTCTT GTAAA
A CCGA TA

GAM895 379 CABYR 1 16855 NP_722452.1 5 149 CCAAAATGATTT - CCAG -- 7 A c c

CTTCAAAGCCCA AG CTG TTGAAGAA CATTT
GACTTG TC GAC AACTTCTT GTAAA
A CCGA TA

GAM895 379 CABYR 1 16855 NP_722453.1 5 149 CCAAAATGATTT - CCAG -- 7 A c c

CTTCAAAGCCCA AG CTG TTGAAGAA CATTT
GACTTG TC GAC AACTTCTT GTAAA
A CCGA TA

GAM895 379 CABYR 1 16855 NP_722454.1 5 149 CCAAAATGATTT - CCAG -- 7 A c c

CTTCAAAGCCCA AG CTG TTGAAGAA CATTT
GACTTG TC GAC AACTTCTT GTAAA
A CCGA TA

GAM895 379 CALM1 1 10029 NP_008819.1 3 2359 ATAAAGTGATTA ---- G G- - 7 A c c
GTTGAACTGGCA AGC TGCCAGTT AA AA CATTT
TCCTGCTT TCG ACGGTCAA TT TT GTGAA
TCCT G GA A

GAM895 379 CDYL 1 11324 NP_004815.2 3 1074 ACATTTAATGTT T--- GTTGA 7 A c
c

CTTGGCCTCTGC AGC GCCA AGAACATT
TTTTATGT TCG CGGT TCTTGTAA
TCTC -----

GAM895 379 CDYL 1 11324 NP_736607.1 3 1074 ACATTTAATGTT T--- GTTGA 7 A c
c

CTTGGCCTCTGC AGC GCCA AGAACATT
TTTTATGT TCG CGGT TCTTGTAA

TCTC -----
GAM895 379 CDYL 1 11324 NP_736608.1 3 1074 ACATTTAATGTT T--- GTTGA 7 A c c
CTTGGCCTCTGC AGC GCCA AGAACATT
TTTTATGT TCG CGGT TCTTGTAA
TCTC -----
GAM895 379 CGI-141 1 12491 NP_057156.1 3 121 GCTTGTAATGTT G A T 7 A c c
CTTTACAGGAGT AGCT CC GT GAAGAACATT
TTAAAACG TTGA GG CA TTTCTTGTAA
- A -
GAM895 379 CNTN3 1 19069 XP_039627.7 3 264 GATATAAATGTT GCC G 7 A c c
CTTAAACTATGA AGCT AGTT AAGAACATTT
GTTTAAGC TTGA TCAA TTCTTGTAAA
GTA A
GAM895 379 CPR8 2 1778 NP_065790.1 3 3523 ACTGGAAATGTT C AGA 7 A c c
CAACTGTAGTTT AGCTGC AGTTGA ACATTT
TATTAAGG TTGATG TCAACT TGTAAA
- ---
GAM895 379 CPR8 2 9187 NP_065790.1 3 3523 GACACTGGAAAT C AGA 7 A c c
GTTCAACTGTAG AGCTGC AGTTGA ACATTT
TTTTATTA TTGATG TCAACT TGTAAA
- ---
GAM895 379 CREBL2 1 14613 NP_001301.1 3 1494 AGTATATTTTGT GA TT 7 A c c
TCTGAACTGGCA AGCTGCCAGTT AGAACA
GTTTAAGA TTGACGGTCAA TCTTGT
G- TT
GAM895 379 DKFZp76 1 10303 NP_775734.1 3 3692 CAGTAAAGGTGT A----- TT - 7 A c c
1B107 TCCTTCCTGGCA GCTGCCAG GAAG AACATTT
GCGTATGC CGACGGTC CTTC TTGTGGA
CGTATG -- C
GAM895 379 EDARADD 1 18853 NP_542776.1 3 647 TGCCCAGTGGTG C AA- 7 A c c
CTTCAACTGGTA AG TGCCAGTTGAAG CATT
TCTATGAG TC ATGGTCAACTTC GTGA
T GTG
GAM895 379 EDARADD 1 18853 NP_665860.1 3 647 TGCCCAGTGGTG C AA- 7 A c c
CTTCAACTGGTA AG TGCCAGTTGAAG CATT
TCTATGAG TC ATGGTCAACTTC GTGA
T GTG
GAM895 379 EEF2K 1 3811 NP_037434.1 3 176 GAAAAATGTCTT T--- A 7 A c c
TGCTCCTTGGCA AGCTGCCAG TGAAGA CATTT
GCTACCAG TCGACGGTT GTTTCT GTAAA
CCTC -
GAM895 379 EXO70 1 16998 NP_056034.1 3 2109 GAGCGCCGTGTT CCA T 7 A c c
CTTCAGCCTCAG AGCTG GTTGAAGAACAT
CTGGAAGG TCGAC CGACTTCTTGTG
TC- C

GAM895 379 FABP7 1 14375 NP_001437.1 3 24 GCATAAAATGTT --- TTGAA 7 A c c
CCTGGTCGGGGC AGCT GCCAG GAACATTT
TTGGAAGA TCGG TGGTC CTTGTAAA
GGC -----
GAM895 379 FCGR3B 1 12304 NP_000561.1 5 21 ACTCCAGTGTGG GT AGA- 7 A c
c
CATCATGTGGCA AGCTGCCA TGA ACATT
GCTGCTCC TCGACGGT ACT TGTGA
GT ACGG
GAM895 379 FGFR2 1 7425 NP_000132.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075258.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075259.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075261.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075264.2 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075417.1 3 1239 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075418.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075419.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FGFR2 1 7425 NP_075420.1 3 1045 AGCAGAATGTGC TT- A 7 A c c
TTCTCTCTGGCA AGCTGCCAG GAAG ACATTT
GCTGGCCT TCGACGGTC CTTC TGTAAG
TCT G
GAM895 379 FHOD2 1 19209 XP_057927.2 3 687 CAGTACTGTGTT --- T 7 A c c
CTTCAGCTAGAG AGCTGCC AGTTGAAGAACAT
GCAGCTTT TCGACGG TCGACTTCTTGTG
AGA T
GAM895 379 FLJ1029 1 8638 NP_060520.2 5 254 ATTTAAAATGTT G AG----- 7 A c c

8 CTTCGGGGGAGA AGCT CC TTGAAGAACATTT
AGGGAGCT TCGA GG GGCTTCTTGTAAA
G AAGAGGG

GAM895 379 FLJ1274 1 19622 XP_290972.1 3 2343 TAGAGAATGTGG TG A- 7 A c c
7 CTTCAACTGGGC AGC CCAGTTGAAG ACATTT
TTATTAAA TCG GGTCAACTTC TGTAAG
-- GG

GAM895 379 FLJ2036 1 6214 NP_060252.1 3 135 AAAACCAATGTT G- - A 7 A c c
0 CTACAACTTGGA AGCT CCA GTTG AGAACATT
AAGTTTTC TTGA GGT CAAC TCTTGTAA
AA T A

GAM895 379 FLJ2067 1 14149 NP_060394.1 3 1869 TCAGTCTATGTT AGT T 7 A c c
1 CTTTAGGTAGCT AGCTGCC TGAAGAACAT
AGACACAA TCGATGG ATTTCTTGTA
--- T

GAM895 379 FLJ2071 1 17227 NP_060410.1 5 314 AAATGTTTTGTA T- ----- 7 A c c
9 ACTCAACTGGCC AGC GCCAGTTGA AGAACATTT
TGCTTCCT TCG CGGTCAACT TTTTGTAAA
TC CAATG

GAM895 379 FLJ2305 1 3463 NP_075058.1 3 805 TGATGAATGATT G TG - - 7 A c c
3 TTATTGGTGGCA AGCTGCCA T A AGAA CATTT
GCTGGGTG TCGACGGT G T TTTT GTAAG
- GT A A

GAM895 379 FOSB 1 13889 NP_006723.1 3 1291 ACCCCCAATATT - G C 7 A c c
TTTGGACTGGCA AG CTGCCAGTT AAGAA ATT
GACTCAAG TC GACGGTCAG TTTTT TAA
A G A

GAM895 379 FOXA1 1 19373 NP_004487.2 3 1349 GTGGAAAATGTT CAGT --- 7 A c
c
CTTGATCATTTG AGCTGC TGA AGAACATTT
CAGTTAAG TTGACG ACT TCTTGTAAA
TTT- AGT

GAM895 379 FOXD4 1 5668 XP_095746.6 5 576 CCCAGGACATGT G AA T 7 A c c
TCGACAATGGCA AGCTGCCA TTG GAACAT
GCTTTCTC TCGACGGT AAC CTTGTA
- AG C

GAM895 379 FPGT 1 17275 NP_003829.1 3 1309 TCATTAAATGTT C GAA 7 A c c
CAAAATTGTAGT AGCTGC AGTT GAACATTT
TTTAAAAA TTGATG TTAA CTTGTAAA
- AA-

GAM895 379 HIST2H2 1 7494 NP_003519.1 3 1141 AATGGAAATGTT G GTTGA 7 A c
c
BE CTTGGAGCTACT AGCT CCA AGAACATTT
TCCTCAAA TCGA GGT TCTTGTAAA
- -----

GAM895 379 HPCAL4 1 11696 NP_057341.1 3 2510 GCACTCAGTGTT TTGA 7 A c
c
CTGCCTCTGGCA AGCTGCCAG AGAACATT
GCTGTGCT TCGACGGTC TCTTGTGA
TCCG

GAM895 379 IRF5 1 4930 NP_002191.1 3 494 CATATCAGATGC GAA A 7 A c c
TCAAGGCTGGCA AGCTGCCAGTT GA CATTT
GCTACCCC TCGACGGTCGG CT GTAGA
AA- C
GAM895 379 IRF5 1 4930 NP_116032.1 3 494 CATATCAGATGC GAA A 7 A c c
TCAAGGCTGGCA AGCTGCCAGTT GA CATTT
GCTACCCC TCGACGGTCGG CT GTAGA
AA- C
GAM895 379 KCNAB1 1 13233 NP_003462.2 3 1041 AAGGCAAATGTT C C ---- 7 A c c
CATTGTTTAATT AG TGC AGTTGAA GAACATTT
AGCACTGG TC ACG TTAATTT CTTGTAAA
- A GTTA
GAM895 379 KCNAB1 1 13233 NP_751891.1 3 1041 AAGGCAAATGTT C C ---- 7 A c c
CATTGTTTAATT AG TGC AGTTGAA GAACATTT
AGCACTGG TC ACG TTAATTT CTTGTAAA
- A GTTA
GAM895 379 KCNAB1 1 13233 NP_751892.1 3 1041 AAGGCAAATGTT C C ---- 7 A c c
CATTGTTTAATT AG TGC AGTTGAA GAACATTT
AGCACTGG TC ACG TTAATTT CTTGTAAA
- A GTTA
GAM895 379 KDELR3 1 20033 NP_006846.1 3 76 ATTTTGAATGTT C TT A 7 A c c
CTCTTTGGCAAC AG TGCCAG GA GAACATTT
TTATCCAT TC ACGGTT CT CTTGTAAG
A T- -
GAM895 379 KDR 1 5354 NP_002244.1 3 654 AGGTTGCGTGTT TG - T 7 A c c
CTTCGAGTTGGG AGC CCAG TTGAAGAACAT
CTAAAGTA TCG GGTT AGCTTCTTGTG
-- G C
GAM895 379 KIAA023 1 14809 NP_055562.1 3 428 AGCCTGTGTGTT T- - T T 7 A c c
7 CTTCACCTGTGC AGC GC CAG TGAAGAACAT
CTGCTCCT TCG CG GTC ACTTCTTGTG
TC T C T
GAM895 379 KIAA159 1 13533 XP_050754.5 3 1031 AAGAAGAGTGTT -- GTT 7 A c c
4 CTTCTGGTAAAG AGCT GCCA GAAGAACATTT
CTAAAATT TCGA TGGT CTTCTTGTGAG
AA ---
GAM895 379 KIAA180 1 11408 NP_115810.1 3 354 GTATAGAATGTT G GTTGA 7 A c
c
5 CTTGGAAGCTCC AGCT CCA AGAACATTT
ATTGATTT TCGA GGT TCTTGTAAG
A -----
GAM895 379 KIAA189 1 15021 XP_058025.2 3 1718 ACAATGTTTCTT CT --- - 7 A c c
4 CTGCAACTGGCT AG GCCAGTT GAAGAA CATT
ACTCCTCT TC CGGTCAA CTTCTT GTAA
AT CGT T
GAM895 379 KIAA190 1 17616 XP_056282.1 3 3839 AGTCACCCATGT G A T 7 A c c
4 TCTCAACTGGAA AGCT CCAGTTGA GAACAT

GTTGGTCG TTGA GGTCAACT CTTGTA
A - C
GAM895 379 LCHN 1 13004 XP_098615.2 3 4800 TGGGAGGTAGTG C AAG 7 A c c

TTATAACTGGCA AG TGCCAGTTG AACATT
CTTTAATT TC ACGGTCAAT TTGTGA
- A--
GAM895 379 LGN 1 9501 NP_037428.2 3 253 CTGCTTGGGATG GTTG T 7 A c c
TGTTCTTTGGCA AGCTGCCA AAGAACAT
GCTTGTGA TCGACGGT TTCTTGTG
---- T
GAM895 379 LOC1267 1 11812 XP_059074.1 3 340 CCCCAGGAAATG GAAGA 7 A c
c
55 TGAAGACTGGCA AGCTGCCAGTT ACATTT
GCTTTCAA TCGACGGTCAG TGTAAA
AAG--
GAM895 379 LOC1346 1 6440 XP_059727.3 3 462 AGCTACGATGTT G T----- 7 A c c
37 CTTCCAGGGCAC AGCT CCAGT GAAGAACATT
TGGGGGCT TCGG GGTCA CTTCTTGTAG
G CGGGAC
GAM895 379 LOC1465 1 4472 XP_085492.1 3 133 AGCAGAAATGTT C C TTGAA 7 A c
c
20 CCTGCACTAGAC AG TGC AG GAACATTT
AATTAAAG TC ACG TC CTTGTAAA
- - -----
GAM895 379 LOC1486 1 12372 XP_097505.1 5 807 AGCAGAAATGGC G- A AA 7 A c
c
96 TCCAAAATGGCA AGCTGCCA TTG AG CATTT
GCTCATCA TCGACGGT AAC TC GTAAA
AA C G-
GAM895 379 LOC1515 1 19877 XP_098089.1 3 67 ATCGTAAATGTT CA GA- 7 A c c
84 CTGAAGACGAGC AGCTGC GTT AGAACATTT
AGCTGGAG TCGACG CAG TCTTGTAAA
AG AAG
GAM895 379 LOC1540 1 10300 XP_098468.1 5 1093 TTTTATAATGTT CA TG 7 A c c
84 CTTGTATAGCAG AGCTGC GT AAGAACATT
CTCGGTAC TCGACG TA TTCTTGTAA
A- TG
GAM895 379 LOC1584 1 1013 NP_640339.3 3 1047 CTTTTAAATGTT G TT A 7 A c c
27 CTCTCTGGGAGC AGCT CCAG GA GAACATTT
TTCATATA TCGA GGTC CT CTTGTAAA
G T- -
GAM895 379 LOC1999 1 13875 XP_114067.2 3 325 CTGGCCCATGGC T- AA T 7 A c
c
53 TTCCTACTGGCA AGCTGCCAGT GAAG CAT
GCTCCAGG TCGACGGTCA CTTC GTA
TC G- C
GAM895 379 LOC2031 1 1112 XP_300975.1 3 369 AATTGAAATGTT CCAGTTG 7 A c
c
07 CTTAATAGCTAA AGCTG AAGAACATTT

GTTTTAAA TCGAT TTCTTGTAAA
AA-----
GAM895 379 LOC2035 1 15970 XP_117550.1 3 1048 CAGAGAGATGTT T TTG- 7 A c c
04 CTTGTTTCTGGT AGC GCCAG AAGAACATTT
GTTGTCAC TTG TGGTC TTCTTGTAGA
- TTTG
GAM895 379 LOC2214 1 9114 XP_168060.2 3 229 ACGGCAATGCCT - G AA 7 A c c
24 TTGAACTTGGCA AGCTGCCA GTT AAG CATT
GCTCTGGC TCGACGGT CAA TTT GTAA
T G CC
GAM895 379 LOC2568 1 14032 XP_173004.1 3 0 AAATGTTCCTGA G TGAA-- 7 A c c
61 TTGCTGGAAGCT AGCT CCAGT GAACATTT
GCGGCTCA TCGA GGTCG CTTGTAAA
A TTAGTC
GAM895 379 LOC2831 1 10722 XP_210888.1 3 501 GTAGAAAAATGG G GAA 7 A c c
04 ATTGGGCTGGCA AGCTGCCAGTT AA CATTT
GCTCGAAG TCGACGGTCGG TT GTAAA
G AG-
GAM895 379 LOC2832 1 8821 NP_787089.1 5 356 CCAAGAAATGTT G GTTGA 7 A c c
41 CTATGGAAGTTT AGCT CCA AGAACATTT
ACGTTTTA TTGA GGT TCTTGTAAA
A A----
GAM895 379 LOC2832 1 18722 NP_775858.1 3 179 TGGGTTCTGCAT TTGAA T 7 A c c
48 GTGTTCCTGGCA AGCTGCCAG GAACAT
GCTGGGCC TCGACGGTC CTTGTG
----- T
GAM895 379 LOC2834 1 2908 XP_208665.1 3 182 GAAGTAAATGTT G G GA 7 A c c
25 CTGAGTGGAGTT AGCT CCA TT AGAACATTT
ACTAGAAT TTGA GGT AG TCTTGTAAA
- G --
GAM895 379 LOC2835 1 14912 XP_208746.1 3 2412 TGAGCTGTGCTT CAG - T 7 A c c
78 CTTCAAGTAGCT AGCTGC TTGAAGAA CAT
CAGTTCTT TCGATG AACTTCTT GTG
--- C T
GAM895 379 LOC2840 1 12876 XP_211303.1 3 715 TGTATGTTTTGT GA---- T 7 A c c
18 GCTGAACTGGCA AGCTGCCAGTT AGAACAT
GCTATCCC TCGACGGTCAA TTTTGTA
GTCGTG T
GAM895 379 LOC2844 1 6998 XP_210787.1 5 266 CAGTCAGATGTT CC TT 7 A c c
33 CTTCTCCTTCAG AGCTG AG GAAGAACATTT
CTTCGGCT TCGAC TC CTTCTTGTAGA
T- CT
GAM895 379 LOC2844 1 14287 XP_209210.1 3 234 ATCATAATGGTA T AGAA- 7 A c c

40 GATCCACTGGCA AGCTGCCAGT GA CATT
GCTTGCAC TCGACGGTCA CT GTAA
C AGATG
GAM895 379 LOC2845 1 11717 XP_211512.1 3 1444 TATTTGATGCTT CCAG - 7 A c
c
30 CTTCAAGTCAGC AGCTG TTGAAGAA CATT
TCTGACGT TCGAC AACTTCTT GTAG
TG-- C
GAM895 379 LOC2848 1 14102 XP_211657.1 5 316 CACCCCAATGTT C GA- 7 A c c
40 CTGGAGGCTGCG AGCTGC AGTT AGAACATT
GTTCTGCT TTGGCG TCGG TCTTGTAA
- AGG
GAM895 379 LOC2849 1 13512 XP_211703.1 5 374 ACATTTCCACTG TT A TT 7 A c c
50 TCTTCCCTGGCA AGCTGCCAG GAAGA CA
GCTGTGAT TCGACGGTC CTTCT GT
C- - CA
GAM895 379 LOC2851 1 13845 XP_211790.1 3 395 GGAGGAAATGTT G - 7 A b b
67 CATTCAGTGGTA AGCTGCCA TTGAA GAACATTT
GCTATTTC TCGATGGT GACTT CTTGTAAA
- A
GAM895 379 LOC2852 1 18929 XP_211818.1 3 1461 TGTTTTGTTCTA - A-- TT 7 A c c
56 GCCACACTGGCA AGCTGCCAGT TG AGAACA
GCTGTTAG TCGACGGTCA AC TCTTGT
C CGA TT
GAM895 379 LOC2855 1 17122 XP_209639.1 5 5 GCTGGTAATGAT T AAGA 7 A c c
00 GTATACCTGGCA AGCTGCCAG TG ACATT
GCTGACCG TCGACGGTC AT TGTAG
C A---
GAM895 379 LOC2855 1 14073 XP_211948.1 3 288 GGCATAAATGTT --- A - A- 7 A c c
95 CAATCTAACGGC AGCT GCC GTT GA GAACATTT
TTTGGTTG TTGG CGG CAA CT CTTGTAAA
TTT - T AA
GAM895 379 LOC2856 1 14073 XP_211976.2 3 291 GGCATAAATGTT --- A - A- 7 A c c
56 CAATCTAACGGC AGCT GCC GTT GA GAACATTT
TTTGGTTG TTGG CGG CAA CT CTTGTAAA
TTT - T AA
GAM895 379 LOC2859 1 1096 XP_212085.1 3 1052 GATGGATCTTTC ----- A- 7 A c c
54 TCAGGACTGGCA AGCTGCCAGTT GAAGA CATT
GTTACCCG TTGACGGTCAG TTTCT GTAG
GACTC AG
GAM895 379 LOC2861 1 3170 XP_212215.3 3 292 CATAAATATGTT G -- T T 7 A c c
77 CTTTACTGAGGG AGCT CC AGT GAAGAACAT
AGCTTAGA TCGA GG TCA TTTCTTGTA
G AG - T
GAM895 379 LOC2864 1 5918 XP_212310.1 5 1159 CAGCAATGTTTC -- -- 7 A b b
01 CTTCAACTCTGG AGCTGCCA GTTGAAG AACATT
CAGTTCCC TTGACGGT CAACTTC TTGTAA
CT CT

GAM895 379 LOC2864 1 17684 XP_210050.1 3 699 TGGAGGTATGTT AGT--- T 7 A c c
37 CTTCATGCAAGG AGCTGCC TGAAGAACAT
GCAGTTCC TTGACGG ACTTCTTGTA
GAACGT T
GAM895 379 LOC2865 1 3346 XP_210093.1 3 1677 TAATTTTAAGCA G AGA T 7 A c c
32 TGTTCAGTGGCA AGCTGCCA TTGA ACAT
GCTCCCCT TCGACGGT GACT TGTA
- --- C
GAM895 379 LOC3392 1 4240 XP_294904.1 5 424 AGGGAAAATGTT CCAGTT - 7 A c c
99 CATTCTTCATCA AGCTG GAA GAACATTT
GCTTTGCT TCGAC CTT CTTGTAAA
TACTT- A
GAM895 379 LOC3398 1 8112 XP_295080.1 5 2764 GGTTTGAGTGTT CCAGT 7 A c c
31 CTTCATCAGCTG AGCTG TGAAGAACATTT
ACCTTAAA TCGAC ACTTCTTGTGAG
T----
GAM895 379 LOC3403 1 3197 XP_294325.1 5 286 TATCAAAGTGTT C TT- 7 A c c
27 CTTCCTCCTGTC AGCTG CAG GAAGAACATTT
AGTTCAGT TTGAC GTC CTTCTTGTGAA
T CTC
GAM895 379 LOC3405 1 13494 XP_291321.1 5 327 AGAAAATGCAAG -- AGAA 7 A c c
27 TCAGGCCTGGCA AGCTGCCAG TTGA CATTT
GCTAGAGC TCGACGGTC GACT GTAAA
CG GAAC
GAM895 379 LOC3462 1 8351 XP_299387.1 5 24 TTAAGAGATGTT A- --- - 7 A c c
59 CTTACAGCTGGC GCT GCCAGTTG AAGAACATTT
CTGGGCAT CGG CGGTCGAC TTCTTGTAGA
TA GTC A
GAM895 379 LOC3483 1 9564 XP_302741.1 5 145 ACTAAAAATGTT CA GA--- 7 A c c
93 CTGTGAAAACAA AGCTGC GTT AGAACATTT
GCAGCTAG TCGACG CAA TCTTGTAAA
AA AAGTG
GAM895 379 LOC3484 1 18223 XP_300748.1 3 369 AAATGTTTTCTA - ----- 7 A c c
75 ACTCAACTGGCC AGCTG CCAGTTGA AGAACATTT
GGCTTCCT TCGGC GGTCAACT TTTTGTAAA
C CAATC
GAM895 379 LOC3485 1 9564 XP_302818.1 5 145 ACTAAAAATGTT CA GA--- 7 A c c
32 CTGTGAAAACAA AGCTGC GTT AGAACATTT
GCAGCTAG TCGACG CAA TCTTGTAAA
AA AAGTG
GAM895 379 LOC3489 1 14073 XP_302935.1 3 288 GGCATAAATGTT --- A - A- 7 A c c
89 CAATCTAACGGC AGCT GCC GTT GA GAACATTT
TTTGGTTG TTGG CGG CAA CT CTTGTAAA
TTT - T AA
GAM895 379 LOC3492 1 11021 XP_300471.1 3 83 AAAGAGTGAGTC - A- 7 A c c

54 TTCTGATTGGCA AGCTGCCAGTT GAAGA CATTT
GCTGTGGC TCGACGGTTAG CTTCT GTGAG
T GA
GAM895 379 LOC3493 1 11021 XP_300483.1 3 83 AAAGAGTGAGTC - A- 7 A c c
27 TTCTGATTGGCA AGCTGCCAGTT GAAGA CATTT
GCTGTGGC TCGACGGTTAG CTTCT GTGAG
T GA
GAM895 379 LOC9297 1 1682 XP_048529.2 3 1732 GTTAACAATGTT CCA A 7 A c c
3 CTCAGCCTCAGC AGCTG GTTGA GAACATT
TTCCTTAC TCGAC CGACT CTTGTAA
TC- -
GAM895 379 LSM6 1 8191 NP_009011.1 3 189 TTGTGAAATGTT - C T 7 A c c
CTTTCACTTGTA AGCT GC AGT GAAGAACATTT
AGTTTCAG TTGA TG TCA TTTCTTGTAAA
A T C
GAM895 379 MAGEA12 1 14575 NP_005358.1 3 230 TGTTCAAATGTT - A -- 7 A c c
CCTTTTAACGGA AGCTG CC GTTGAA GAACATTT
TGGTTGAA TTGGT GG CAATTT CTTGTAAA
A - TC
GAM895 379 MAGEA3 1 14575 NP_005353.1 3 230 TGTTCAAATGTT - A -- 7 A c c
CCTTTTAACGGA AGCTG CC GTTGAA GAACATTT
TGGTTGAA TTGGT GG CAATTT CTTGTAAA
A - TC
GAM895 379 MAGEA6 1 14575 NP_005354.1 3 230 TGTTCAAATGTT - A -- 7 A c c
CCTTTTAACGGA AGCTG CC GTTGAA GAACATTT
TGGTTGAA TTGGT GG CAATTT CTTGTAAA
A - TC
GAM895 379 MAGEA6 1 14575 NP_787064.1 3 230 TGTTCAAATGTT - A -- 7 A c c
CCTTTTAACGGA AGCTG CC GTTGAA GAACATTT
TGGTTGAA TTGGT GG CAATTT CTTGTAAA
A - TC
GAM895 379 MAGEA9 1 7705 NP_005356.1 3 245 TGTTCAAATGTT - GTT 7 A c c
CTTTTAATGGTC AGCTG CCA GAAGAACATTT
AGTTTAAT TTGAC GGT TTTCTTGTAAA
T AAT
GAM895 379 MDC1 1 4580 NP_055456.1 3 342 CATGCTCAGATG G AAGA 7 A c c
TCATAAGTGGCA AGCTGCCA TTG ACATTT
GCTATCTT TCGACGGT AAT TGTAGA
G AC--
GAM895 379 MECP2 1 534 NP_004983.1 3 946 GAAGAAAATGTT CCAGTT 7 A c c
CTTCCAGTTACT AGCTG GAAGAACATTT
TTCCAATT TTGAC CTTCTTGTAAA

GAM895 379 MGC1582 1 14513 NP_116271.1 3 408 GCCGTGTGTGTT - TT T 7 A c c
7 CTTCTCTGAGCA AGCTGC CAG GAAGAACAT
GCTCCTCC TCGACG GTC CTTCTTGTG

A T- T

GAM895 379 MGC4562 1 4552 NP_588616.1 3 148 ATGTAAAATGTT ----- A- A 7 A c c

CTCAGCCGGGCA AGCT GCC GTTGA GAACATTT

CGGTGGCT TCGG CGG CGACT CTTGTAAA

TGGCA GC -

GAM895 379 MYO5A 1 18843 NP_000250.1 3 313 AGAAAAATGTGT A----- - 7 A c c

CTTCAGCTGGCA GCTGCCAGTTGAAGA ACATTT

GCATTTAT CGACGGTCGACTTCT TGTAAA

TATTTA G

GAM895 379 MYOZ3 1 11685 NP_588612.1 3 761 TTAGAAAATGTT ---- T - 7 A c c

CCTTTTACTGAG AGCTGC CAGT GAAG AACATTT

ATGCAGTT TTGACG GTCA TTTC TTGTAAA

TAGA T C

GAM895 379 MYST2 1 3346 NP_008998.1 3 1435 TAATTTTAAGCA G AGA T 7 A c c

TGTTCAGTGGCA AGCTGCCA TTGA ACAT

GCTCCCCT TCGACGGT GACT TGTA

- --- C

GAM895 379 NDRG4 1 12095 NP_065198.1 3 1672 ATGTGTGGTGTT G GTT 7 A c c

CTTCTGGAGGTT AGCT CCA GAAGAACATT

GTCTCTTT TTGG GGT CTTCTTGTGG

A ---

GAM895 379 NDRG4 1 12095 NP_075061.1 3 1657 ATGTGTGGTGTT G GTT 7 A c c

CTTCTGGAGGTT AGCT CCA GAAGAACATT

GTCTCTTT TTGG GGT CTTCTTGTGG

A ---

GAM895 379 NPC2 1 10948 NP_006423.1 5 104 TTATCCGCGATG TT AA 7 A c c

CGTTTCCTGGCA AGCTGCCAG GAAG CATT

GCTACATT TCGACGGTC CTTT GTAG

-- GC

GAM895 379 NQO1 1 13009 NP_000894.1 3 276 TAGAAAAATGTT C AG 7 A c c

CTTTAAAGGCAT AG TGCC TTGAAGAACATTT

CTACACAA TC ACGG AATTTCTTGTAAA

T A-

GAM895 379 NT5E 1 17625 NP_002517.1 3 1408 CTTAAAAACAGT G AAGA 7 A c c

GTGCAAATGGCA AGCTGCCA TTG ACATT

GCTAGAGG TCGACGGT AAC TGTGA

A G---

GAM895 379 P5 1 17994 NP_005733.1 3 366 TGCTTGAATGTT T AG G 7 A c c

CTTGGAGGCTGT AGC GCC TT AAGAACATTT

TTCTTATG TTG CGG AG TTCTTGTAAG

T -- G

GAM895 379 PPP3CA 1 4752 NP_000935.1 3 106 CAGTTGGATGTT --- TTG- 7 A c c

CTTGCCTCTGAC AGCTGC CAG AAGAACATTT

AGTAGCTT TCGATG GTC TTCTTGTAGG

ACA TCCG

GAM895 379 PRKY 1 19311 NP_002751.1 3 1604 CCCCCAGATGTT TG TT 7 A c c

CTTCCCTGGGTG AGC CCAG GAAGAACATTT
TTGATGGC TTG GGTC CTTCTTGTAGA
TG C-
GAM895 379 PROS1 1 1078 NP_000304.1 3 645 AGCACAGGAATC TT C 7 A c c
TTCTTCTTGGCA AGCTGCCAG GAAGAA ATTT
GCTGCAGT TCGACGGTT CTTCTT TAAG
-- C
GAM895 379 PTGDR 1 1012 NP_000944.1 3 789 TTGCAAAATGTT CCAGTT 7 A c
c
CTTTCAGTTTTT AGCTG GAAGAACATTT
AGAACCTC TTGAC TTTCTTGTAAA

GAM895 379 PXF 1 17226 NP_002848.1 3 1619 GAAGGAAATGTT ---- AG A 7 A c c
CTCAAGGTCTCA AGCT GCC TTGA GAACATTT
GGCTATTT TCGG TGG AACT CTTGTAAA
ACTC -- -
GAM895 379 RAB5A 1 3629 NP_004153.2 3 477 CAGGCAAATGTT C TT -- 7 A c c
CATTTCTCCTGG AG TGCCAG GAA GAACATTT
TACCTGTA TC ATGGTC CTT CTTGTAAA
C CT TA
GAM895 379 RAP2A 1 8623 NP_066361.1 3 1755 CCCCCAAGTGTT ---- AA 7 A c c
TAATAACTGGCA AGCT GCCAGTTG GAACATTT
TTAAGCTT TCGA CGGTCAAT TTTGTGAA
ATTA AA
GAM895 379 RASSF2 1 16173 NP_055552.1 3 2826 AGGCTGGATGGA G - AA 7 A c
c
CTTCAACTTGGA AGCT CCA GTTGAAG CATTT
GTTGAGTT TTGA GGT CAACTTC GTAGG
- T AG
GAM895 379 RASSF2 1 16173 NP_739579.1 3 3052 AGGCTGGATGGA G - AA 7 A c
c
CTTCAACTTGGA AGCT CCA GTTGAAG CATTT
GTTGAGTT TTGA GGT CAACTTC GTAGG
- T AG
GAM895 379 RASSF2 1 16173 NP_739580.1 3 2826 AGGCTGGATGGA G - AA 7 A c
c
CTTCAACTTGGA AGCT CCA GTTGAAG CATTT
GTTGAGTT TTGA GGT CAACTTC GTAGG
- T AG
GAM895 379 SARS2 1 3298 NP_060297.1 3 122 GACATCTGTGTT C TT T 7 A c c
CTTCCTGTCAGC AGCTG CAG GAAGAACAT
TCCACGCC TCGAC GTC CTTCTTGTG
T -- T
GAM895 379 SEC23B 1 505 NP_006354.2 3 293 AATCAGAGGTAA GTT GA 7 A c c
TGTATTTTGGCA AGCTGCCA GAA ACATT
GCTTGTTT TCGACGGT TTT TGTAA
--- A-
GAM895 379 SEC23B 1 505 NP_116780.1 3 293 AATCAGAGGTAA GTT GA 7 A c c

TGTATTTTGGCA AGCTGCCA GAA ACATT
GCTTGTTT TCGACGGT TTT TGTAA
--- A-

GAM895 379 SEC23B 1 505 NP_116781.1 3 293 AATCAGAGGTAA GTT GA 7 A c c

TGTATTTTGGCA AGCTGCCA GAA ACATT
GCTTGTTT TCGACGGT TTT TGTAA
--- A-

GAM895 379 SFXN1 1 4597 NP_073591.2 3 676 ATTGTAAGTGTT AA 7 A c c
TACTGACTGGCA AGCTGCCAGTTG GAACATTT
GCTTTTAT TCGACGGTCAGT TTTGTGAA
CA

GAM895 379 Siat7c 1 3113 NP_694541.1 3 220 GCTCATGATGTT G TT 7 A c c
CTTTCTGGAGGT AGCT CCAG GAAGAACATT
TCAACACT TTGG GGTC TTTCTTGTAG
A --

GAM895 379 SKP1A 1 19958 NP_008861.2 3 1162 GAAGTAAATGTT G G GA 7 A c c

CTGAGTGGAGCT AGCT CCA TT AGAACATTT
ACTAGGAT TCGA GGT AG TCTTGTAAA
- G --

GAM895 379 SKP1A 1 19958 NP_733779.1 3 467 GAAGTAAATGTT G G GA 7 A c c
CTGAGTGGAGCT AGCT CCA TT AGAACATTT
ACTAGGAT TCGA GGT AG TCTTGTAAA
- G --

GAM895 379 SPATA2 1 17327 NP_006029.1 3 1625 TTTGCTGATGTT CC - 7 A c c
CTTCCAACTCAG AGCTG AGTTG AAGAACATT
TTGAGTGA TTGAC TCAAC TTCTTGTAG
-- C

GAM895 379 SRGAP1 1 6087 XP_051143.3 5 210 CAGCATGATGTT G TTG- 7 A c c

CTTGTCTTTGGA AGCT CCAG AAGAACATT
GCTTAGCC TCGA GGTT TTCTTGTAG
- TCTG

GAM895 379 STAT1 1 14937 NP_009330.1 3 478 TCTTTGCTTTAA GAAGA 7 A c c
GTGTAACTGGCA AGCTGCCAGTT ACATTT
GTTTTCCA TTGACGGTCAA TGTGAA

GAM895 379 SYT6 1 9597 XP_086135.1 3 1058 AGATTAAATGTT G AG- --- 7 A c c
CTTTTCCAAATG AGCT CC TTG AAGAACATTT
GGGAGTTT TTGA GG AAC TTCTTGTAAA
G GTA CTT

GAM895 379 TBC1D4 1 14754 NP_055647.1 3 1466 TGGGGTAATTTT G AG C 7 A c
c

CTTCAAAGGGAG AGCT CC TTGAAGAA ATT
TTTGTTAT TTGA GG AACTTCTT TAA
- GA T

GAM895 379 TCL6 2 779 NP_036600.2 5 1412 TCGTATATGAAA TTGAA 7 A c c
TGTTCCTTGGCA AGCTGCCAG GAACATTT
GCTGGACT TCGACGGTT CTTGTAAA

C----

GAM895 379 TCL6 2 779 NP_055233.1 5 1412 TCGTATATGAAA TTGAA 7 A c c
TGTTCCTTGGCA AGCTGCCAG GAACATTT
GCTGGACT TCGACGGTT CTTGTAAA

C----

GAM895 379 TCL6 2 779 NP_065575.1 5 1412 TCGTATATGAAA TTGAA 7 A c c
TGTTCCTTGGCA AGCTGCCAG GAACATTT
GCTGGACT TCGACGGTT CTTGTAAA

C----

GAM895 379 TCL6 2 779 NP_065577.2 5 1412 TCGTATATGAAA TTGAA 7 A c c
TGTTCCTTGGCA AGCTGCCAG GAACATTT
GCTGGACT TCGACGGTT CTTGTAAA

C----

GAM895 379 TCL6 2 5137 NP_036600.2 5 1413 ATATGAAATGTT TG- AA--- 7 A c c
CCTTGGCAGCTG AGC CCAGTTG GAACATTT
GACTGCTG TCG GGTCGAC CTTGTAAA
TCA GGTTC

GAM895 379 TCL6 2 5137 NP_055233.1 5 1413 ATATGAAATGTT TG- AA--- 7 A c c
CCTTGGCAGCTG AGC CCAGTTG GAACATTT
GACTGCTG TCG GGTCGAC CTTGTAAA
TCA GGTTC

GAM895 379 TCL6 2 5137 NP_065575.1 5 1413 ATATGAAATGTT TG- AA--- 7 A c c
CCTTGGCAGCTG AGC CCAGTTG GAACATTT
GACTGCTG TCG GGTCGAC CTTGTAAA
TCA GGTTC

GAM895 379 TCL6 2 5137 NP_065577.2 5 1413 ATATGAAATGTT TG- AA--- 7 A c c
CCTTGGCAGCTG AGC CCAGTTG GAACATTT
GACTGCTG TCG GGTCGAC CTTGTAAA
TCA GGTTC

GAM895 379 TPT 1 17162 NP_055132.1 3 32 CAACTCTTTCTG TT TT 7 A c c
TTCTTTCTGGCA AGCTGCCAG GAAGAACA
GCTATCTT TCGACGGTC TTTCTTGT
-- CT

GAM895 379 UNC5D 1 20188 NP_543148.1 3 430 GTCAGAGTTTTC C A- C 7 A c c
TACCAACTGGCA AG TGCCAGTTG AGAA ATTT
TCTGTGAT TC ACGGTCAAC TCTT TGAG
T CA T

GAM895 379 VENTX2 1 6385 NP_055283.1 3 1440 TGTTGTAAGTGT --- AA 7 A c c
TTACAACTGGCA AGC TGCCAGTTG GAACATTT
TGTGCTTT TCG ACGGTCAAC TTTGTGAA
TGT A-

GAM895 379 ZNF-kai 1 3272 NP_006768.1 3 317 AGTCTGAATGTT G ------ 7 A c c
so CTTTGAAAATAA AGCT CCAGTT GAAGAACATTT
CTGGAGTT TTGA GGTCAA TTTCTTGTAAG
- TAAAAG

GAM1032 303 ACP1 1 2659 NP_004291.1 3 492 TCCCCTCCGTAG A- T-- 6 A c c
GAGCTCACAGTC CTAGACTG AGCTCCT GAGG
TAGATTAG GATCTGAC TCGAGGA CTCC
AC TGC

GAM1032 303 ACP1 1 2659 NP_009030.1 3 492 TCCCCTCCGTAG A- T-- 6 A c c

GAGCTCACAGTC CTAGACTG AGCTCCT GAGG
TAGATTAG GATCTGAC TCGAGGA CTCC
AC TGC

GAM1032 303 ACP1 1 2659 NP_808222.1 3 785 TCCCCTCCGTAG A- T-- 6 A c c
GAGCTCACAGTC CTAGACTG AGCTCCT GAGG
TAGATTAG GATCTGAC TCGAGGA CTCC
AC TGC

GAM1032 303 ADCY1 1 5742 NP_066939.1 3 3002 ACACAACCAGAA GA GA 6 A c c
GGAGCTGAGTTT CTAGACT AGCTCCTT GG
GGCAACAA GGTTTGA TCGAGGAA CC
G- GA

GAM1032 303 ALS2 1 5747 NP_065970.1 5 45 GGTGCTGCCGGT T - TTGA 6 A c c
GGAGCTTCAGGT C AGAC TGAAGCTCC GG
CTTGATAG G TCTG ACTTCGAGG CC
T G TGG-

GAM1032 303 AMOT 1 4436 NP_573572.1 5 28 CCTTCCTTCCGA CTG -- 6 A c c
GGAGCTTTCTGG CTAGA AAGCTCCTTG AGGA
CTGCCTAA GGTCT TTCGAGGAGC TCCT
--- CT

GAM1032 303 ANKT 1 15792 NP_057443.1 3 818 CTTCACCTCAGT T -- - 6 A c c
GGAGCTTCTGAG C AGACT GAAGCTCC TTGAGG
TTTTATAC A TTTGA CTTCGAGG GACTCC
T GT T

GAM1032 303 ANKT 1 15792 NP_060924.4 3 817 CTTCACCTCAGT T -- - 6 A c c
GGAGCTTCTGAG C AGACT GAAGCTCC TTGAGG
TTTTATAC A TTTGA CTTCGAGG GACTCC
T GT T

GAM1032 303 APOL6 1 19543 NP_085144.1 3 1113 TCTTATTTCTGA T CT G 6 A c c
GGCCCTTCAGTC C AGACTGAAG CCTT AGGA
TCCTTTAT C TCTGACTTC GGAG TCTT
C CC -

GAM1032 303 BBS4 1 12747 NP_149017.2 3 632 TTTTGTTCTTGA AG - TG 6 A c c
GAGGGGTCAGTC CTAGACTGA CTC CT AGGA
TAGAAGCT GATCTGACT GGG GA TCTT
G- A GT

GAM1032 303 BG1 1 19594 NP_055977.3 3 85 CCTGAGCCCCAG CTC A 6 A c c
GTCTCTTCAGTC CTAGACTGAAG CTTG GG
TGGGCACA GGTCTGACTTC GGAC CC
TCT -

GAM1032 303 BPHL 1 4510 NP_004323.1 3 180 TGAAAACAGCCT A CCTT 6 A c c
CTAGCTTCAGGC CTAG CTGAAGCT GAGG
TGGGCACG GGTC GACTTCGA CTCC
G T---

GAM1032 303 C15orf1 1 10592 NP_060755.1 3 102 TGCTCTCCTCAA - ---- A T 6 A c c
2 GGGTATCAGACG CTA GACT GA GC CCTTGAGGA
GTCGTAGG GAT CTGG CT TG GGAACTCCT
G CAGA A -

GAM1032 303 C17orf2 1 6729 NP_085133.1 3 32 ATGAAGCCGACG A A- 6 A c c
8 AGGGGCTCAGTC CTAGACTGA GCTCCTTG GG

TAGGGGAA GATCTGACT CGGGGAGC CC
- AG

GAM1032 303 C1orf21 1 17052 NP_110433.1 3 5792 CCCCTGTGTCCT CT TTG 6 A c c

GGCATTTCAGTC CTAGACTGAAG CC AGGA
TAGACCTT GATCTGACTTT GG TCCT
AC ---

GAM1032 303 C20orf1 1 11258 NP_112181.1 3 197 ACCACAGTCCAA AC A A 6 A c c
29 GGAGCTCACCCT CTAG TGA GCTCCTTG GG
GGGCAACC GGTC ACT CGAGGAAC CT
CC - -

GAM1032 303 C20orf1 1 10164 NP_219489.1 3 2 TGCTCATCAAGG - TGAAG G 6 A c c

61 AGGTGCTGGACT CTAG AC CTCCTTGA GA
ACCCTTGC GGTC TG GAGGAACT CT
G ----- A

GAM1032 303 C21orf9 1 5545 NP_068760.1 3 163 AGAACTTTAACC C -- 6 A c c
7 GGAGCTTCATCT CTAGA TGAAGCTCC TTGAGG
AGTGATTG GATCT ACTTCGAGG AATTTC
- CC

GAM1032 303 CAMKK2 1 7725 NP_006540.3 3 517 CCGTGGTCTCAA A- AA--- 6 A c c

GGAGTCAGAGCA CTAG CTG GCTCCTTGAGG
GGGCTGGC GGTC GAC TGAGGAACTCT
GG GAGAC

GAM1032 303 CAMKK2 1 7725 NP_705719.2 3 615 CCGTGGTCTCAA A- AA--- 6 A c c

GGAGTCAGAGCA CTAG CTG GCTCCTTGAGG
GGGCTGGC GGTC GAC TGAGGAACTCT
GG GAGAC

GAM1032 303 CAMKK2 1 7725 NP_705720.1 3 615 CCGTGGTCTCAA A- AA--- 6 A c c

GGAGTCAGAGCA CTAG CTG GCTCCTTGAGG
GGGCTGGC GGTC GAC TGAGGAACTCT
GG GAGAC

GAM1032 303 CAMKK2 1 7725 NP_757365.1 3 517 CCGTGGTCTCAA A- AA--- 6 A c c

GGAGTCAGAGCA CTAG CTG GCTCCTTGAGG
GGGCTGGC GGTC GAC TGAGGAACTCT
GG GAGAC

GAM1032 303 CAMKK2 1 7725 NP_757380.1 3 616 CCGTGGTCTCAA A- AA--- 6 A c c

GGAGTCAGAGCA CTAG CTG GCTCCTTGAGG
GGGCTGGC GGTC GAC TGAGGAACTCT
GG GAGAC

GAM1032 303 CASP4 1 3772 NP_001216.1 3 61 AATCAACTTCAA AC --- 6 A c c
GGAGCACCTTCA CTAG TGAA GCTCCTTGAGG
TTAGTACA GATT ACTT CGAGGAACTTC
-- CCA

GAM1032 303 CASP4 1 3772 NP_150649.1 3 61 AATCAACTTCAA AC --- 6 A c c

GGAGCACCTTCA CTAG TGAA GCTCCTTGAGG
TTAGTACA GATT ACTT CGAGGAACTTC
-- CCA

GAM1032 303 CASP4 1 3772 NP_150650.1 3 61 AATCAACTTCAA AC --- 6 A c c
GGAGCACCTTCA CTAG TGAA GCTCCTTGAGG
TTAGTACA GATT ACTT CGAGGAACTTC
-- CCA

GAM1032 303 CD1D 1 16191 NP_001757.1 3 75 CCTCAGGTTCCC - - C----- 6 A c c
AAGACTTCAGTC CTAG ACTGAAG CT CTTGAGG
CTGGTCTG GGTC TGACTTC GA GGACTCC
C A ACCCTT

GAM1032 303 CDC25B 1 11047 NP_004349.1 3 289 TTGTGTCCTCCA T T- T 6 A c c
GGAGCTTCTTGT C AGAC GAAGCTCCT GAGGA
TTCCTTGT C TTTG CTTCGAGGA CTCCT
C TT C

GAM1032 303 CDC25B 1 11047 NP_068658.1 3 289 TTGTGTCCTCCA T T- T 6 A c c
GGAGCTTCTTGT C AGAC GAAGCTCCT GAGGA
TTCCTTGT C TTTG CTTCGAGGA CTCCT
C TT C

GAM1032 303 CDC25B 1 11047 NP_068659.1 3 289 TTGTGTCCTCCA T T- T 6 A c c
GGAGCTTCTTGT C AGAC GAAGCTCCT GAGGA
TTCCTTGT C TTTG CTTCGAGGA CTCCT
C TT C

GAM1032 303 CDC25B 1 11047 NP_068660.1 3 289 TTGTGTCCTCCA T T- T 6 A c c
GGAGCTTCTTGT C AGAC GAAGCTCCT GAGGA
TTCCTTGT C TTTG CTTCGAGGA CTCCT
C TT C

GAM1032 303 CFL2 1 16082 NP_068733.1 3 46 TCTGGATCTTAA T CT-- 6 A c c
GGAGCTTCCATT C AGA GAAGCTCCTTGAGG
TCTCCAGC C TCT CTTCGAGGAATTCT
C TTAC

GAM1032 303 CLCN1 1 7487 NP_000074.1 5 12 GCAGAGGCTTAA AC A G 6 A c c
GGAGCTACACTG CTAG TG AGCTCCTTGAG
GGGGAAGG GGTC AC TCGAGGAATTC
-- A G

GAM1032 303 CLN8 1 17822 NP_061764.2 3 3251 CACTTCTGTCGA - A- - 6 A c c
GGAGCTTCGGGG CT AG CTGAAGCTCCTTGA GGA
CTCAGAGA GA TC GGCTTCGAGGAGCT TCT
C GG G

GAM1032 303 CLONE24 1 7108 NP_056498.1 3 309 GGAATCCCCTAG - TGA 6 A c
c
945 GAGCCTTCAGTC CTAGACTGAAG CTCCT GGA
TGGGAGAA GGTCTGACTTC GAGGA CCT
C TCC

GAM1032 303 CLYBL 1 6231 NP_612124.2 3 1223 AGAAAACCCTTC G CC 6 A c c
AAAAGTTCAGTC CTAGACTGAA CT TTGAGG
TAGTCTGG GATCTGACTT GA AACTTC
- A-

GAM1032 303 COL19A1 1 3270 NP_001849.1 3 897 TTTGGTACTCTT --- CC 6 A c c
AAAGCTTCAGTG CTAG ACTGAAGCT TTGAGG

GCCTAGCA GATC TGACTTCGA AATTCT
CGG --
GAM1032 303 COL4A6 2 13214 NP_378667.1 3 508 CTCACTCTTCAA TGA ----- 6 A c c

GGAGGCCCACTG CTAGAC AG CTCCTTGAGGA
TGTCTAGG GATCTG TC GAGGAACTTCT
TG- ACCCG
GAM1032 303 COL4A6 2 15255 NP_001838.1 3 509 CTCACTCTTCAA T TG ----- 6 A c c

GGAGGCCCACTT C AGAC AAG CTCCTTGAGGA
GTGTCTTA A TCTG TTC GAGGAACTTCT
T TG ACCCG
GAM1032 303 CXYorf1 1 8588 XP_088704.2 3 2740 GACCAGCTTCAA A GAA 6 A c c

GGAGCGGAAGGC CTAG CT GCTCCTTGAGG
TGGCTTGA GGTC GA CGAGGAACTTC
G AGG
GAM1032 303 CYB5-M 1 17320 NP_085056.1 3 379 GACATTCTTAAC AA C- 6 A c c
AGGGCGGCAGTC CTAGACTG GCTC TTGAGGA
TAGTGTTG GATCTGAC CGGG AATTCTT
GG AC
GAM1032 303 DEPP 1 10673 NP_008952.1 3 996 CTCCTTCTCTGT - CTT 6 A c c
GAGCTGTCAGTC CTAGACTGA AGCTC GAGGA
TAGGTTAT GATCTGACT TCGAG CTCTT
G TGT
GAM1032 303 DIS3 1 16408 NP_055768.2 3 1037 CTCTGCCTTCAA G - 6 A b b
GGAGCTTGCAGT CTA ACTG AAGCTCCTTGAGG
ATAGTGAG GAT TGAC TTCGAGGAACTTC
A G
GAM1032 303 DISPB 1 17823 NP_277045.1 3 514 CCCTCTCTTTTG CT T 6 A c c
GGAGCTTCTCTG CTAGA GAAGCTCCT GAGGA
GGCAGAAT GGTCT CTTCGAGGG TTTCT
-- T
GAM1032 303 dJ383J4 1 9430 XP_294938.1 5 233 AGGTCTTCCTGG T C G 6 A c c
.3 GGGATTTCAGTC C AGACTGAAG TCCTT AGGA
TCCACATA C TCTGACTTT AGGGG TCCT
C - G
GAM1032 303 DKFZP43 1 3164 NP_056436.1 3 373 CTCAGCCCTCCT T CT TT 6 A c
c
4C171 GGCCCTTCAGTC C AGACTGAAG CC GAGG
TTGGTGCC G TCTGACTTC GG CTCC
T CC TC
GAM1032 303 DKFZp43 1 12853 XP_097012.2 3 753 GCCATCACTCAA A CT C - 6 A c
c
4O0320 GGACTTCTCTCC CT GA GAAG TCCTTGAG GA
AGGCCCCG GA CT CTTC AGGAACTC CT
C CT - A
GAM1032 303 DKFZp54 1 8359 NP_689592.1 3 642 CCCTGCCCTTGA AG -- TG 6 A c
c
7B1713 GGAGCTTCATTG CT AC TGAAGCTCCT AGG

TAGGGAGA GG TG ACTTCGAGGA TCC
GA TT GT
GAM1032 303 DKFZP56 1 7803 NP_056226.1 3 104 ATTCCAAGCTCG - A C G 6 A c c

6I1024 AGAGCTTCAGCC CT AG CTGAAGCTC TTGAG
TCAGGAAA GA TC GACTTCGAG AGCTC
C C - G
GAM1032 303 DKFZp58 1 5132 NP_112159.1 3 487 GTGTGTTCTTCA AG CCT 6 A c
c

6F1019 TAAGCTTCAGTG CT ACTGAAGCT TGAGGA
CAGGATTT GA TGACTTCGA ACTTCT
CG AT-
GAM1032 303 DKFZp68 1 11872 XP_300559.1 3 2422 ACTGTAGCCTTT - CCTT 6 A c
c

6G052 TAAGCTTCAGTC CT AGACTGAAGCT GAGG
TCAGCAGA GA TCTGACTTCGA TTCC
C ATT-
GAM1032 303 DMRT2 1 5107 NP_006548.1 3 849 CCTTGTCCTCAA CTC 6 A c c
GATTTTTAGTTT CTAGACTGAAG CTTGAGGA
GGCCCAAG GGTTTGATTTT GAACTCCT
TA-
GAM1032 303 DMRTC2 1 9542 NP_149041.1 3 897 AAGTGCCTTCAA C - 6 A b b
GGAGCTTACGTT CTAGA TG AAGCTCCTTGAGG
CTAGTTAG GATCT GC TTCGAGGAACTTC
T A
GAM1032 303 DNM2 1 19535 NP_004936.1 3 62 ACCCGCGGCGCA --- ---- A 6 A c c
GGAGCTTCAGTG CTAGACT GAAGCTCCT TG GG
GTCTGGGG GGTCTGG CTTCGAGGA GC CC
TGA CGCG G
GAM1032 303 DTX2 1 19806 NP_065943.1 5 234 CATTCCTCCTAA T TGA -- 6 A c c
GGAGCTGGTGTC C AGAC AGCTCCTT GAGGA
TTCATCCA C TCTG TCGAGGAA CTCCT
T TGG TC
GAM1032 303 E2F3 1 16241 NP_001940.1 3 1122 TAACAGCCCCAA GA- AA A 6 A c
c

GGAGCAGCAGGC CTA CTG GCTCCTTG GG
ATGGGTCC GGT GAC CGAGGAAC CC
ACG GA -
GAM1032 303 EDRF1 1 5132 NP_056423.2 3 487 GTGTGTTCTTCA AG CCT 6 A c c

TAAGCTTCAGTG CT ACTGAAGCT TGAGGA
CAGGATTT GA TGACTTCGA ACTTCT
CG AT-
GAM1032 303 ESR1 1 11698 NP_000116.1 3 2949 ATTTCTAAAATG - - TTG-- 6 A c c
GCAGCTTCAGTT CTAGA CTGAAGCT CC AGGA
CTAGAGAA GATCT GACTTCGA GG TCTT
T C TAAAA
GAM1032 303 FBXO10 1 1583 XP_291314.1 3 951 CTCGTTCCTCAA AGA GCT 6 A c
c

GGTTTAGCCGAG CT CTGAA CCTTGAGGA

ACACTGCC GA GATTT GGAACTCCT
GCC ---
GAM1032 303 FLJ1049 1 6405 NP_060584.2 3 1033 TGGGCTCCTCAA ACT CT 6 A c c
6 GGGACTTCCTGG CTAG GAAG CCTTGAGGA
AGAGTAGC GGTC CTTC GGAACTCCT
--- AG
GAM1032 303 FLJ1064 1 13957 NP_060637.1 3 914 AGTAGGTCTTGT - T T 6 A c c
8 GGGCATTCAGTC CTAGACTGAA GC CC TGAGG
TAGCCCAG GATCTGACTT CG GG GTTCT
A - T
GAM1032 303 FLJ1093 1 2710 NP_060747.1 3 87 TGGCCTCTGCAG AG T --- 6 A c c
2 GGAGCTTCGTAG CT AC GAAGCTCCTT GAGG
AGGTGAGG GA TG CTTCGAGGGA CTCC
GA - CGT
GAM1032 303 FLJ1150 1 1155 NP_078942.2 3 444 TTCTCCATTCAA C--- - - -- 6 A c c
6 GGAGCTTGTAGC TAGA CTG AAGCTCCTTGA GGA
TCTGAGCT GTCT GAT TTCGAGGAACT CCT
TCGA C G TA
GAM1032 303 FLJ1243 1 14060 NP_075565.1 3 794 ATTCTTCCCAAG A - A 6 A b b
9 GCAGCTTCAGCT CTAG CTGAAGCT CCTTG GGA
AGGAGTTT GATC GACTTCGA GGAAC CCT
- C -
GAM1032 303 FLJ1320 1 4441 NP_079037.2 3 2584 CCTTGCCTCAAG AC- - 6 A c c
4 TGAGCTTCAACC CTAG TGAAGCTC CTTGAGG
TTAGCCTC GATT ACTTCGAG GAACTCC
CCA T
GAM1032 303 FLJ1376 1 2505 NP_079288.1 3 1050 GCCACCTCCAGG T -- T 6 A c c
9 CTGGCTTCAGTC C AGACTGAAGCT CCT GAGG
TCCCATCC C TCTGACTTCGG GGA CTCC
C TC C
GAM1032 303 FLJ1415 1 5645 NP_079121.1 3 106 TGTTTTCTGCAA C- --- A- - 6 A c c
4 GGAGCTGCCAGC TAGA CTG AGCTCCTTG AGGA
CATCTAAC ATCT GAC TCGAGGAAC TCTT
CA ACC CG G
GAM1032 303 FLJ1416 1 2917 NP_078841.1 5 230 CAACGTCCTCAA A --- AA - 6 A c c
6 GGATGCCGTAGC CT GAC TG GC TCCTTGAGGA
CGTCAAGA GA CTG AT CG AGGAACTCCT
A CCG GC T
GAM1032 303 FLJ2001 1 2766 NP_060092.1 5 179 CCCGGCCCTCAA TGA -- 6 A c c
4 GGGACGCTGTCT CTAGAC AGC TCCTTGAGG
GGGGCCGG GGTCTG TCG GGGAACTCC
--- CA
GAM1032 303 FLJ2040 1 4190 NP_060275.1 5 124 CCGGCTCATCAA TGAAG G 6 A c c
1 GGAGGCCGTCTG CTAGAC CTCCTTGA GA
GGAAAAGA GGTCTG GAGGAACT CT
CCG-- A
GAM1032 303 FLJ2044 1 12035 NP_060294.1 3 999 CAAGCTCTTACA A- CT 6 A c c
5 GAGTTGACAGTC CTAGACTG AGCTC TGAGG

TAGTTTCA GATCTGAC TTGAG ATTCT
AG AC
GAM1032 303 FLJ2058 1 8842 NP_060361.1 3 258 CCATGAGACCTC A - CT 6 A c c
4 AGAGCTTCAGAT CT GA CTGAAGCTC TGAGG
CGAGGCCT GA CT GACTTCGAG ACTCC
G A --
GAM1032 303 FLJ2114 1 11110 NP_079136.1 3 449 TCGATAGTTACC G CC A 6 A c c
8 CAAAGTTCAGTC CTAGACTGAA CT TTG GG
TAGATGGC GATCTGACTT GA AAC CC
- -- -
GAM1032 303 FLJ2124 1 6131 NP_079123.1 3 183 CAGCCCTTAATT --- C-- 6 A c c
0 AGGGCTTCAGTG CTAG ACTGAAGCTC TTGAGG
ACTTAGAA GATT TGACTTCGGG AATTCC
CAG ATT
GAM1032 303 FLJ2180 1 7802 NP_078920.1 3 288 CTTCATCACCTT --- CCT 6 A c c
2 CAGGCTTCAGTG CTAG ACTGAAGCT TGAGG
TACTGGGT GGTC TGACTTCGG ACTTC
ATG ---
GAM1032 303 FLJ2263 1 2390 NP_079072.1 3 209 ATGAGGCCTCAA T CTCC 6 A c
c
9 TACTTTTCAGTC C AGACTGAAG TTGAGG
TTAATTGT A TCTGACTTT AACTCC
T TCAT
GAM1032 303 FLJ2595 1 3762 NP_775843.1 5 192 TTGACCCCTCAG AGA C 6 A c c
4 AGAGCTTCAGCC CT CTGAAGCTC TTGAGG
CAGACCTG GA GACTTCGAG GACTCC
CCC A
GAM1032 303 FLJ3056 1 12412 NP_659459.1 3 2326 GGCAGCCCCTGG GA - TG 6 A c
c
7 GTAGCTTCAGGA CTA CTGAAGCT CCT AGG
TGGGGCTG GGT GACTTCGA GGG TCC
AG T --
GAM1032 303 FLJ3065 1 1102 NP_653244.1 3 215 ATAATCCTATAT AG CT - 6 A c c
5 TGAGCTTCAGTG CT ACTGAAGCTC TG AGGA
GAGAATAA GA TGACTTCGAG AT TCCT
GG TT A
GAM1032 303 FLJ3211 1 13700 NP_694580.1 3 1785 CTAGGAACTCAA A AA G 6 A c
c
2 GGAGTCAGCCTA CTAG CTG GCTCCTTGAG
GACCCCAC GATC GAC TGAGGAACTC
C -- A
GAM1032 303 FLJ3572 1 9904 NP_775955.1 3 750 CTGCCTTCTCAA AA- 6 A c c
1 GGAGTCCACAGT CTAGACTG GCTCCTTGAGGA
CTGGAGGA GGTCTGAC TGAGGAACTCTT
ACC
GAM1032 303 FLJ3924 1 6728 NP_775935.1 3 397 CTAGAGCCTCAA A A- CT 6 A c c
9 GGTCTCCCAGTC CT GACTG AG CCTTGAGG
CAGAAACA GA CTGAC TC GGAACTCC

C CC T-
GAM1032 303 FLJ3963 1 8387 XP_290687.1 3 970 TTTCTTATTTCA GAC ---- 6 A c c
9 GGAGCTTCATAG CTA TGAAGCTCCT TGAGGA
GCATAGAC GAT ACTTCGAGGA ATTCTT
--- CTTT
GAM1032 303 FLJ9001 1 4414 NP_699196.1 3 28 GATTTGCCTCAA AG- CT- 6 A c c
3 GGCCTCTTCAGT CT ACTGAAG CCTTGAGG
ATAAGGAA GA TGACTTC GGAACTCC
ATA TCC
GAM1032 303 GAF1 1 6004 NP_056285.1 3 598 CCATGTCCTGAG TC- G 6 A c c
TCTGCTTCAGTC CTAGACTGAAGC CTT AGGA
TGGAGCTG GGTCTGACTTCG GAG TCCT
TCT -
GAM1032 303 GGA2 1 3682 NP_055859.1 3 2465 CACCACCCTGAA CT---- G 6 A c c
GGAGCTTCTTTT CTAGA GAAGCTCCTT AGG
CCTCTGGG GGTCT CTTCGAGGAA TCC
CCTTTT G
GAM1032 303 GGA2 1 3682 NP_619581.1 3 3553 CACCACCCTGAA CT---- G 6 A c c
GGAGCTTCTTTT CTAGA GAAGCTCCTT AGG
CCTCTGGG GGTCT CTTCGAGGAA TCC
CCTTTT G
GAM1032 303 GLCCI1 1 15598 XP_166529.2 3 1144 TGTCTTCCTCAA AAGCTC 6 A c
c
GCAGTTTAGGTG CTAGACTG CTTGAGGA
CATGATCT GATTTGAC GAACTCCT

GAM1032 303 GMEB2 1 1427 NP_036516.1 3 928 AGGTGTGTCCCT - T TG 6 A c c
AGGGCTTCAGTC CTAG ACTGAAGC CCT AGG
CTGGGGCA GGTC TGACTTCG GGA TCC
C - --
GAM1032 303 GNA11 1 10253 NP_002058.1 3 0 ACCTCAAGGAGT GAA---- 6 A c c
ACAACCTGGTCT CTAGACT GCTCCTTGAGG
GGCGCCCC GGTCTGG TGAGGAACTCC
TCCAACA
GAM1032 303 GNAT1 1 13082 NP_000163.2 3 47 AGTCGGGGACAA T AGG 6 A c
c
GGAGCTTCCGTC CTAGAC GAAGCTCCTTG
TGGCAAGG GGTCTG CTTCGAGGAAC
C AGG
GAM1032 303 GNAT1 1 13082 NP_653082.1 3 1182 AGTCGGGGACAA T AGG 6 A c
c
GGAGCTTCCGTC CTAGAC GAAGCTCCTTG
TGGCAAGG GGTCTG CTTCGAGGAAC
C AGG
GAM1032 303 GUCY2C 1 9622 NP_004954.1 3 245 CAGTTGTTCCAG ACT A 6 A c
c
GGAGCTTCTACC CTAG GAAGCTCCTTG GGA
TGGAAAAG GGTC CTTCGAGGGAC CTT
CAT -
GAM1032 303 H63 1 3048 NP_612432.2 3 2090 GCAACATTTCTT GAA CC 6 A c c

CAATTAGCAGTC CTAGACT GCT TTGAGGA
TAGACATT GATCTGA CGA AACTTCT
--- TT

GAM1032 303 H63 1 3048 NP_816929.1 3 2090 GCAACATTTCTT GAA CC 6 A c c
CAATTAGCAGTC CTAGACT GCT TTGAGGA
TAGACATT GATCTGA CGA AACTTCT
--- TT

GAM1032 303 HAS1 2 3709 NP_001514.1 3 155 GGGTCAGCCCAA CTC A 6 A c c
GATTCTTCAGTC CTAGACTGAAG CTTG GG
TGGACTAT GGTCTGACTTC GAAC CC
TTA -

GAM1032 303 HAS1 2 16698 NP_001514.1 3 43 ATGCCGCCTCAA AGA CT 6 A c c

GGGTCTTCAGGG CT CTGAAG CCTTGAGG
GAGGCCAG GA GACTTC GGAACTCC
GGG TG

GAM1032 303 HCNGP 1 18142 NP_037392.1 3 134 TGCCACCTGAGA T G- 6 A c c
GGAGCTTCTGTT CTAGAC GAAGCTCCTT AGG
TGGCATTC GGTTTG CTTCGAGGAG TCC
T AG

GAM1032 303 HES2 1 16768 XP_290879.1 3 796 CCGTGGCCTCAA - - - 6 A c c
GGAAGCTTGTGG CTAGA CTG AAGCT CCTTGAGG
CTTTGGAG GGTTT GGT TTCGA GGAACTCC
C G A

GAM1032 303 HIVEP1 1 6005 NP_002105.1 3 217 TTGTGCCTTTTA - T- 6 A c c
GGAGCTTTATGT CTAGAC TGAAGCTCCT GAGG
TTAGAAAC GATTTG ATTTCGAGGA TTCC
T TT

GAM1032 303 HLCS 1 4592 NP_000402.2 3 2300 CTGGGATCTCAA T -- 6 A c c
GGAGCTTTAAAG C AGACT GAAGCTCCTTGAGG
TCTTAATG A TCTGA TTTCGAGGAACTCT
T AA

GAM1032 303 HSPCAL3 1 1703 XP_084514.3 3 1004 CACTCCTGTCTT CCTT 6 A c
c

CTGGCTTCAGTC CTAGACTGAAGCT GAGGA
TGGAAGAT GGTCTGACTTCGG CTTCT
T---

GAM1032 303 IL18R1 1 17153 NP_003846.1 3 999 ATCCAACCTCTT T T TT 6 A c c
GGTGCTTCAGTT C AGACTGAAGC CC GAGG
TCCTCATC C TTTGACTTCG GG CTCC
C T TT

GAM1032 303 INA 1 2428 NP_116116.1 3 127 TAAAATGTCTTC T TC 6 A c c
AAGGCTTCAGTC C AGACTGAAGC CTTGAGGA
TCATATTT A TCTGACTTCG GAACTTCT
C --

GAM1032 303 INPP5D 1 8687 NP_005532.1 3 588 GCTCGGCCTTAA GA-- 6 A c c
GGAGCTGAAGAG CTAGACT AGCTCCTTGAGG
TCTGGGTA GGTCTGA TCGAGGAATTCC
GAAG

GAM1032 303 ITK 1 978 NP_005537.3 3 2068 AGATGATTTCTG GC- TT 6 A c c

GAACATTCAGTC CTAGACTGAA TCC GAGG
TAGAAAGA GATCTGACTT AGG CTTT
ACA T-

GAM1032 303 KCNIP2 1 16093 NP_775464.1 3 54 TTCTTTCCTCAA C-- A-- A - 6 A c c
GGAGACTCCAGC TAG CTG AG CTCCTTGAGGA
ACCTATGC ATC GAC TC GAGGAACTCCT
CGT CAC C A

GAM1032 303 KIAA032 1 5874 NP_055659.1 3 1471 CCCCTCCCGGAG AGA - --- 6 A c
c
9 GCAGCTTCAGGA CT CTGAAGCT CCTT GAGG
CAGGACAC GA GACTTCGA GGAG CTCC
CAG C GCC

GAM1032 303 KIAA037 1 17827 NP_055474.1 3 74 GGTATTCCTCAA CT A C-- 6 A c c
7 GCCCAGCATCCA CTAGA GA GCT CTTGAGGA
TCTGGTGA GGTCT CT CGA GAACTCCT
AC A CCC

GAM1032 303 KIAA045 1 8436 XP_027862.1 3 3477 TTCTTACCTCAA T AGCT 6 A c c
9 GGCTCTGTCTAG CTAGAC GA CCTTGAGG
CCATGTTA GATCTG CT GGAACTCC
T C---

GAM1032 303 KIAA069 1 10714 XP_051970.2 5 31 GAAAGTCTTCGA AGA C 6 A c c
4 GAAGCTTCAGAG CT CTGAAGCT CTTGAGGA
GAGGGAAG GA GACTTCGA GAGCTTCT
GGA A

GAM1032 303 KIAA127 1 12182 XP_045472.1 3 311 ATGTCCTCCAGA A CT-- -- 6 A c c
1 GGAGCTTCCTCC CT GA GAAGCTCCTT GAGGA
TCCAGGCC GA CT CTTCGAGGAG CTCCT
C CCTC AC

GAM1032 303 KIAA146 1 18401 XP_027396.4 3 69 CTAGGGTGCCTG AA TG 6 A c c
5 GGAGCAGCAGTC CTAGACTG GCTCCT AGG
TAGGGCTG GATCTGAC CGAGGG TCC
GA --

GAM1032 303 KIAA171 1 8259 XP_034823.5 3 48 CATTCTTCCCTT AAG TT 6 A c c
8 TGGAGACCAGTC CTAGACTG CTCC GAGG
TAGGGGTG GATCTGAC GAGG TTCC
CA- T-

GAM1032 303 KIAA187 1 16159 XP_056635.1 5 2668 CCCACCCTCATG AA- T 6 A c c
9 GAGCCTCCAGTC CTAGACTG GCTCC TGAGG
TAGCTGCC GATCTGAC CGAGG ACTCC
CTC T

GAM1032 303 KIF25 1 4138 NP_005346.2 5 194 ATGGACCTCAGG AGA- C- 6 A c c
TCAGCTTCAGCG CT CTGAAGCT CTTGAGG
TGAGAAGC GA GACTTCGA GGACTCC
GTGC CT

GAM1032 303 KIF25 1 4138 NP_085118.1 5 194 ATGGACCTCAGG AGA- C- 6 A c c
TCAGCTTCAGCG CT CTGAAGCT CTTGAGG

TGAGAAGC GA GACTTCGA GGACTCC
GTGC CT
GAM1032 303 KIR2DL1 1 7645 NP_055033.1 3 429 CTCCCCTCAGAC T - CC- 6 A c c
TAGCTTTCAGTC C AGACTGAA GCT TTGAGG
TTCTGTCA C TCTGACTT CGA GACTCC
T T TCA
GAM1032 303 KIR2DL2 1 7645 NP_055034.1 3 429 CTCCCCTCAGAC T - CC- 6 A c c
TAGCTTTCAGTC C AGACTGAA GCT TTGAGG
TTCTGTCA C TCTGACTT CGA GACTCC
T T TCA
GAM1032 303 LKAP 1 13514 NP_061954.1 3 690 GGGTTCCATTTA CTG T - 6 A c c
GGAGCTTTCTAG CTAGA AAGCTCCT GA GGA
AAAGTTGA GATCT TTCGAGGA TT CCT
--- T A
GAM1032 303 LNX 1 3987 NP_116011.1 5 155 GGTTTGCTTAAA --- G 6 A c c
GGAGCTTGGCTG CTAGACTG AAGCTCCTT AGG
GTTTGGGC GGTTTGGT TTCGAGGAA TTC
CGG A
GAM1032 303 LOC1214 1 10999 XP_062669.7 3 609 GTGATTCCTCAA CTGAAGC 6 A
c c
98 GGATCTAGAACC CTAGA TCCTTGAGGA
AGAAATAT GATCT AGGAACTCCT

GAM1032 303 LOC1328 1 17125 XP_059608.1 5 84 ACCTCTCCTCAA A GA -- 6 A c c
70 GGACTGCTAAGT CT GACT AGC TCCTTGAGGA
CAGGAAAT GG CTGA TCG AGGAACTCCT
A A- TC
GAM1032 303 LOC1431 1 11783 XP_096387.1 5 640 CCCCTTCCTCAA A G - 6 A c c
88 GGGTGTTTGGGT CT GACT AAGC TCCTTGAGGA
TAAGGCTG GA TTGG TTTG GGGAACTCCT
A G T
GAM1032 303 LOC1465 1 16407 NP_660314.1 3 134 GGCTTTCCTCAA T GA C-- 6 A c
c
42 GGATCCCTCAAG C AGACT AG TCCTTGAGGA
TTTCCAAC C TTTGA TC AGGAACTCCT
C AC CCT
GAM1032 303 LOC1476 1 4440 XP_097255.1 5 435 TTAGAAATCCTG T GCTC G 6 A c
c
22 AAGAATTCAGTC C AGACTGAA CTT AGGA
TTCGTCTA C TCTGACTT GAA TCCT
T AA-- G
GAM1032 303 LOC1477 1 4967 XP_097293.2 3 1419 CCCTGGGCTCCC CTCCT A 6 A
c c
91 ATCTCTTCAGTC CTAGACTGAAG TG GGA
TAGAGGCG GATCTGACTTC AC CCT
TCT-- -
GAM1032 303 LOC1492 1 5890 XP_086475.1 5 313 AGCCAGCCTCAA - AG- 6 A c c
71 GGAGACATCTGG CTAGACT GA CTCCTTGAGG
TTTAGGCC GATTTGG CT GAGGAACTCC
T ACA

GAM1032 303 LOC1493 1 19078 XP_086509.1 3 1299 CTCTTCTCTCAA - AA 6 A c c
72 GGAGCACAGTCC CTAG ACTG GCTCCTTGAGG
TGGGAAAG GGTC TGAC CGAGGAACTCT
C A-
GAM1032 303 LOC1493 1 6026 XP_097631.1 5 1040 ATATGTCTATTC GC T G 6 A c
c
86 CAGGATTCAGTC CTAGACTGAA TCCT GAG
TAGAAACT GATCTGACTT AGGA CTT
-- C A
GAM1032 303 LOC1501 1 11388 XP_097824.1 3 469 CTCAGGCTCCCA - CT- T A 6 A c
c
66 GGAGCTTCCACT CT AGA GAAGCTCCT G GGA
CTCAGACC GA TCT CTTCGAGGA C CCT
C CAC - -
GAM1032 303 LOC1502 1 18349 XP_097870.1 3 1230 TAGAGCGTCTCA AA TCC- 6 A c
c
25 GCATCGCCAGTC CTAGACTG GC TTGAGG
TAGACTGT GATCTGAC CG GACTCT
-- CTAC
GAM1032 303 LOC1509 1 3747 XP_097977.2 3 789 CCATCCGTCAGG - - TC - 6 A c c
46 TGGCGTTCAGTC CT AGACTGAA GC CTTGA GGA
TCAGAATA GA TCTGACTT CG GGACT CCT
C G GT G
GAM1032 303 LOC1511 1 17135 XP_098012.1 5 2543 GGTTTTCCTCAA A G C---- 6 A c
c
62 GGAACATTTTTG CTAG CT AAG TCCTTGAGGA
AGCTAGAA GATC GA TTT AGGAACTCCT
- G TTACA
GAM1032 303 LOC1516 1 13917 XP_087261.1 5 105 GCTTCTCCCGCA T A - A 6 A c c
47 GGAGCTTCGGGC C AG CTGAAGCTCCT TG GGA
TTCTCCTG C TC GGCTTCGAGGA GC CCT
T G C -
GAM1032 303 LOC1529 1 10090 XP_087561.1 5 19 CAGTCGACTTCA C CT 6 A c c
20 TGAGCTTCATTT CTAGA TGAAGCTC TGAGG
GGATTTCT GGTTT ACTTCGAG ACTTC
- T-
GAM1032 303 LOC1541 1 3687 XP_098488.2 3 11 TTCTCCAAGTCC A- ---- AG 6 A c c
84 TGAGCTTCAGAA CTAG CTGAAGCTC CTTG GA
CTAGGGAA GATC GACTTCGAG GAAC CT
AA TCCT CT
GAM1032 303 LOC1572 1 626 XP_098743.1 3 1184 CAAAATGCTCAA - AGC G 6 A c
c
73 GGAATTAGCTCT CTAGA CTGA TCCTTGAG
GGGAATAT GGTCT GATT AGGAACTC
C A-- G
GAM1032 303 LOC1573 1 15936 XP_098754.5 5 1668 CTGTCTGCTTCA - T T 6 A c c
81 GGAGCTTCGTAC CTAG AC GAAGCTCCT GAGG
TGGCTAAT GGTC TG CTTCGAGGA CTTC
A - -

GAM1032 303 LOC1576 1 17425 XP_088347.2 3 380 TCTTTCCTCTCC A CCTT- 6 A c c

27 AAAGCCTCAGTC CTAGACTGA GCT GAGGA
TAGCCTGC GATCTGACT CGA CTCCT
C AACCT

GAM1032 303 LOC1576 1 3788 XP_088353.1 5 2141 TAGAGCCTGCAA C--- - A- - 6 A c c

53 GGAGCTCCCGAG TAGACT G AGCTCCTTG AGG
TCTGAGGA GTCTGA C TCGAGGAAC TCC
AGGA G CC G

GAM1032 303 LOC1631 1 3542 XP_092058.1 3 412 CTGGCTCCTCAA T CT- AG 6 A c c

82 GGAGTCTCCCCT C AGA GA CTCCTTGAGGA
CTCCTGTA C TCT CT GAGGAACTCCT
C CCC CT

GAM1032 303 LOC1632 1 12269 XP_092087.3 3 46 AAATCCTTCAGC ----- CCTT 6 A c c

23 TGATTCTCAGTC CTAGACTGA AGCT GAGGA
TAGTAAAC GATCTGACT TCGA TTCCT
CTTAG C---

GAM1032 303 LOC1701 1 17459 XP_093106.2 5 110 CCCTAGGCTATA AG ------- TG 6 A c c

06 CAAGTCTCAGTC CTAGACTGA CT CCT AGG
TAGGGGAA GATCTGACT GA GGA TCC
CT ACATATC --

GAM1032 303 LOC2002 1 18830 XP_114166.1 3 317 GACACTCATCGA AG -- G 6 A c c

30 GGAGCTTCACTG CT AC TGAAGCTCCTTGA GA
TGCGGGAC GG TG ACTTCGAGGAGCT CT
CG TC A

GAM1032 303 LOC2012 1 8558 NP_775818.1 3 265 AGCCTTTTTGAA AAG ---- 6 A c c

92 GGGGACACAGTC CTAGACTG CTCCTT GAGG
TAGGAGGG GATCTGAC GGGGAA TTCC
ACA GTTT

GAM1032 303 LOC2018 2 5434 XP_114393.1 5 402 GCTAGCCCTCCT AAGC CTT 6 A c c

68 CCTGAAGCAGTC CTAGACTG TC GAGGA
TAGGAGCT GATCTGAC AG CTCCT
GA-- TC-

GAM1032 303 LOC2018 2 13599 XP_114393.1 3 661 CGCTTAAGCCCA A ----- T A 6 A c c

68 GGAGCTTAAGAC CTAG CTG AAGCTCCT G GG
CAGCCTGG GGTC GAC TTCGAGGA C CC
C CAGAA - -

GAM1032 303 LOC2219 1 15583 XP_166555.2 3 377 AGCTTTTCTGAA ACT G 6 A c c

22 GGAGCTTTCCTG CTAG GAAGCTCCTT AGGA
GCAGGGAC GGTC TTTCGAGGAA TCTT
C-- G

GAM1032 303 LOC2538 1 4330 XP_172854.1 3 124 GGCCAACCTCAA CT A- - 6 A c c

```
          05                          GGCAGTGCTCTC CTAGA  GA  GCT CCTTGAGG
                                     TGGTTTGC    GGTCT  CT  TGA GGAACTCC
                                              -- CG  C
GAM1032  303   LOC2834 1  5721  XP_211037.1  5  669   TTATTAATCATA  T    -     - GG      6  A  c  c
          42                          GGAGCTTGCAGT C AGACTG AAGCTCCT TGA
                                     CTCACTAG    A TCTGAC TTCGAGGA ACT
                                           C     G       T  AA
GAM1032  303   LOC2836 1  953   XP_211126.1  5  228   TCTGTGCTTCAA  AGA                6  A  c  c
          24                          GGAGCTTCAGAG CT  CTGAAGCTCCTTGAGG
                                     AGATTGCC    GA  GACTTCGAGGAACTTC
                                              GA-
GAM1032  303   LOC2837 1  12978 XP_208115.1  3  42    AACTGATATTAC        CTCC    G       6  A  c
c
          41                          TCAATTTCAGTC CTAGACTGAAG   TTGAG
                                     TGGACACT    GGTCTGACTTT   AACTC
                                              ----    A
GAM1032  303   LOC2837 1  8981  XP_208821.1  5  110   TGAGCTCCAGAA    CTG      GA        6  A  c
c
          53                          GGAGCTTTCTGG CTAGA  AAGCTCCTT  GGA
                                     GCCAGCTT    GGTCT  TTCGAGGAA  CCT
                                              ---       GA
GAM1032  303   LOC2838 1  15824 XP_208122.1  5  196   AGTCATCCTCAA    AC    C           6  A  c  c
          01                          GGATTTTATCCT CTAG  TGAAG TCCTTGAGGA
                                     GGAACATT    GGTC  ATTTT AGGAACTCCT
                                              CT    -
GAM1032  303   LOC2841 1  19059 XP_211362.1  3  723   GGAGTACCTCAA    A  AA  T          6  A  c
c
          73                          GGGCCCCGGCCT CTAG CTG  GC CCTTGAGG
                                     GGGTGGCG    GGTC GGC  CG GGAACTCC
                                              C  CC  -
GAM1032  303   LOC2841 1  15363 XP_209067.1  3  79    TGAGAACCTCAA    A  GAAG           6  A  c
c
          96                          GGAGGAGCTGGC CTAG CT   CTCCTTGAGG
                                     CTACCTGA    GGTC GA   GAGGAACTCC
                                              -  G---
GAM1032  303   LOC2842 1  17603 XP_211403.1  5  892   GACCCTGCTCAA    C  AG      G       6  A  c
c
          66                          GGAGGCTCATCT CTAGA TGA  CTCCTTGAG
                                     GGCCTCCT    GGTCT ACT  GAGGAACTC
                                              -  CG       G
GAM1032  303   LOC2842 1  6856  XP_211416.1  3  484   TTTCCTCAGGGA       AAGC---         6  A  c
c
          80                          TCCACCACAGTC CTAGACTG      TCCTTGAGGA
                                     TAGGCCAG    GATCTGAC      AGGGACTCCT
                                                 ACCACCT
GAM1032  303   LOC2845 1  843   XP_209254.1  5  547   TCGGCTCCTCAA  A   GAA  -          6  A  c  c
          42                          GGTGGTGGTTGA CT GACT   GCT CCTTGAGGA
                                     GGAGACAG    GA TTGG   TGG GGAACTCCT
```

```
                                        G   ---  T
GAM1032  303   LOC2845 1  8588  XP_209280.3  3  253   GACCAGCTTCAA    A  GAA            6  A  c
c
         95                          GGAGCGGAAGGC CTAG CT   GCTCCTTGAGG
                                    TGGCTTGA    GGTC GA   CGAGGAACTTC
                                             G  AGG
GAM1032  303   LOC2847 1  10782 XP_211622.1  3  227   ACTGCCCCTCTC  T        CTT          6  A  c
c
         51                          TGGGCTTCAGTT C AGACTGAAGCTC   GAGG
                                    TCCTCCTT    C TTTGACTTCGGG   CTCC
                                             C          TCT
GAM1032  303   LOC2848 1  12531 XP_211645.1  3  1374  TCGTTCCAAGGA  T      ---      A       6  A  c  c

         29                          GGCTCTTCAGTC C AGACTGAAG   CTCCTTG GGA
                                    TCACAGAT    A TCTGACTTC   GAGGAAC CTT
                                             C        TCG      -
GAM1032  303   LOC2848 1  7677  XP_211672.1  3  1322  CACCTTCTGCAA    ACT  A      -        6  A  c
c
         65                          GGAGCTCTGCTG CTAG   GA GCTCCTTG AGGA
                                    GGCCACCT    GGTC   CT CGAGGAAC TCTT
                                             GT-  -       G
GAM1032  303   LOC2849 1  8588  XP_209425.1  3  2203  GACCAGCTTCAA    A  GAA            6  A  c
c
         65                          GGAGCGGAAGGC CTAG CT   GCTCCTTGAGG
                                    TGGCTTGA    GGTC GA   CGAGGAACTTC
                                             G  AGG
GAM1032  303   LOC2849 1  7383  XP_211711.1  3  2035  GGAGCTCTCTAA   --   GA      -        6  A  c  c

         75                          GGAGCTAAGGTC CTA  GACT  AGCTCCTT GAGG
                                    CATGGGAA    GGT  CTGG  TCGAGGAA CTCT
                                             AC    AA       T
GAM1032  303   LOC2851 1  5205  XP_211773.1  3  1642  TGTCGGCTTCAA  T  A   AA            6  A  c
c
         23                          GGAGTCCAGCTT C AG CTG  GCTCCTTGAGG
                                    ATCTTCCT    A TC GAC  TGAGGAACTTC
                                             T  -   C-
GAM1032  303   LOC2854 1  5936  XP_209600.1  3  78    GCAATTCCTCAA     CTGAAGC           6  A  c
 c
         09                          GGATCTAGAACC CTAGA      TCCTTGAGGA
                                    AGAAATAC    GATCT      AGGAACTCCT
                                             -------
GAM1032  303   LOC2854 1  16068 XP_208320.1  3  369   CCTAAGCCCTAA  T  A   --      A       6  A  c  c

         42                          GGAGCTCCTCAG C AG CTGA  AGCTCCTTG GG
                                    CTTGAAAT    G TC GACT  TCGAGGAAT CC
                                             T  -   CC       C
GAM1032  303   LOC2856 1  4966  XP_211984.1  3  230   GCGTGGTCACGG    ACT       A        6  A  c
c
         92                          GGAGCTTCCTGG CTAG   GAAGCTCCTTG GG
                                    GCAAGCAA    GGTC   CTTCGAGGGGC CT
```

```
                                                  ---          A
GAM1032_303    LOC2857_1   4051   XP_212002.1   5  589    CAAACACCAGAA      TGA       GA          6  A  c
c
           35                                      GGAGCTGTCTGG CTAGAC   AGCTCCTT  GG
                                                  AAGGTTTG    GGTCTG   TCGAGGAA  CC
                                                        ---       GA
GAM1032_303    LOC2858_1   16977  XP_212053.1   3  2039   GTGAGTCTGTCA    A         TGA         6  A  c
c
           19                                      GGAGCTTCAGCC CTAG CTGAAGCTCCT   GGA
                                                  TAGCTGAT    GATC GACTTCGAGGA   TCT
                                                        C          CTG
GAM1032_303    LOC2859_1   3314   XP_209834.2   5  138    AGTGAACCTCAA   AGAC                  6  A  c
c
           36                                      GGGGTTTTACAG CT    TGAAGCTCCTTGAGG
                                                  GAGGAGCT    GA    ATTTTGGGGAACTCC
                                                        GGAC
GAM1032_303    LOC2861_1   7174   XP_209902.1   3  789    CGCTGCCAGCAA CT----     -        A-      6  A  c
c
           01                                      GGAGCTTGCAGT      AGACTG AAGCTCCTTG  GG
                                                  CTTGTAGC          TCTGAC TTCGAGGAAC  CC
                                                        CGATGT     G         GA
GAM1032_303    LOC2861_1   5795   XP_212196.1   5  155    CAGGGACCTCAA    GACTGA-                 6  A  c
 c
           35                                      GGAGCTATGAAC CTA      AGCTCCTTGAGG
                                                  ATAGAAAC    GAT       TCGAGGAACTCC
                                                        ACAAGTA
GAM1032_303    LOC2862_1   5769   XP_212233.1   5  1226   TCTTCTCCAGGG  -      ---- T  T        6  A  c  c
           21                                      CCTCATTCAGTC CT AGACTGAA    GC CCT GAGGA
                                                  TCAGACCA    GA TCTGACTT    CG GGA CTCTT
                                                        C       ACTC  -  C
GAM1032_303    LOC2863_1   14940  XP_212293.1   5  151    GACCCTGCAGGA    A G      -- -        6  A  c
c
           74                                      GGAGCTTGGACT CTAG CT AAGCTCCT  TG AGG
                                                  GGCCCCAG    GGTC GG TTCGAGGA  AC TCC
                                                        A  -       GG  G
GAM1032_303    LOC2865_1   2448   XP_208450.1   5  355    CCTTTCCATCAA  -  CT  A  -     -        6  A  c  c
           45                                      GGAGGCGTCCTT CT AGA  GA GC TCCTTGA GGA
                                                  CTCAGACA    GA TCT  CT CG AGGAACT CCT
                                                        C  TC  G  G      A
GAM1032_303    LOC3386_1   15446  XP_294664.1   3  458    GTGACCCTTCAA    A-    G             6  A  c  c
           09                                      GGAGTTCAGACC CTAG  CTGAA CTCCTTGAGG
                                                  TGGGGGCT    GGTC  GACTT GAGGAACTTC
                                                        CA    -
GAM1032_303    LOC3388_1   3752   XP_290601.1   3  352    AATGCACCTCAA    GA    AGC             6  A  c
c
           62                                      GGAATTAGAGTA CTA  CTGA   TCCTTGAGG
                                                  GCATGAAC    GAT  GATT   AGGAACTCC
                                                        GA   A--
GAM1032_303    LOC3390_1   10038  XP_294778.1   3  113    TCCTGCCCTCAA   A    -  CT           6  A  c  c
```

25 GGCACTTACAGT CT GACTG AAG CCTTGAGG
CCAGTTTC GA CTGAC TTC GGAACTCC
C A AC
GAM1032 303 LOC3390 1 17771 XP_294795.1 5 129 GTCCTTGTATAA - CT ---- 6 A c c
62 GGAGCTTTGCTC CTA GA GAAGCTCCTT GAGGA
TTGGAATT GGT CT TTTCGAGGAA TTCCT
T CG TATG
GAM1032 303 LOC3395 1 20113 XP_294983.1 5 663 ATTTGCCTTCTC T CTT 6 A c c
02 TGAGCTTCAGTT C AGACTGAAGCTC GAGG
TCCTTCTA C TTTGACTTCGAG CTTC
C TCT
GAM1032 303 LOC3395 1 9113 XP_293116.2 5 1 GGGCTGTAGGAG TG TGA 6 A c
c
81 CTTGTTTAGCCC CTAGAC AAGCTCCT GG
ACCTGCAT GATTTG TTCGAGGA TC
-- TG-
GAM1032 303 LOC3396 1 14951 XP_295028.1 5 1105 ATGGCAGTCGAA T - GG 6 A c
c
63 GGAGCTTCGTCT CTAGAC GAAGCTCCTT GA
GGCAGCAG GGTCTG CTTCGAGGAA CT
- G GA
GAM1032 303 LOC3400 1 3820 XP_295144.1 5 611 CTAGGCTGCTTC A CTT 6 A c c
64 TGAGCTTCAGCC CTAG CTGAAGCTC GAGG
TGGGAGCA GGTC GACTTCGAG CTTC
C T--
GAM1032 303 LOC3403 1 5378 XP_291236.1 3 147 GTCACACTTCAA --- AAG 6 A c c
23 GGAGGCAGCTCT CTAGA CTG CTCCTTGAGG
CTAGACAG GATCT GAC GAGGAACTTC
CTC G--
GAM1032 303 LOC3404 1 6280 XP_290420.1 3 1271 CCTAGTGGAGGA T --- G--- 6 A c
c
28 GGCTCTTCAGTC C AGACTGAAG CTCCTT AGG
TCCTGATT C TCTGACTTC GAGGAG TCC
C TCG GTGA
GAM1032 303 LOC3443 1 15185 XP_297561.1 5 16 ACCTCTCAAGGC T A --- 6 A c c
60 CCAGCTTCAGCC C AG CTGAAGCT CCTTGAGG
TCACCTTC A TC GACTTCGA GGAACTCT
C C CCC
GAM1032 303 LOC3445 1 676 XP_297716.1 5 892 GCCCAGCTGCAG A - A 6 A c c
63 GGAGCTTCTGGC CTAG CT GAAGCTCCTTG GG
CTGGGACC GGTC GG CTTCGAGGGAC TC
C T G
GAM1032 303 LOC3472 1 17210 XP_294563.2 3 1732 CTAAAAACCTTC AAGC C 6 A c
c
40 AAAGACCCAGTC CTAGACTG TC TTGAGG
TAGCCAAA GATCTGAC AG AACTTC
CC-- A
GAM1032 303 LOC3478 1 8070 XP_300546.1 3 116 TCTCTGTCTCAA GA AAG 6 A c
c

```
          53                    GGAGAGCAGGGT CTA  CTG   CTCCTTGAGG
                               AGGTGAAA    GAT  GAC   GAGGAACTCT
                                     GG   GA-
GAM1032  303   LOC3479 1  2888  XP_302624.1  5  814   TACCTGACTCAA     TGAA       G        6  A  c
c
          05                    GGAGTGTCTGGA CTAGAC    GCTCCTTGAG
                               GCACCTCC    GGTCTG    TGAGGAACTC
                                     ----         A
GAM1032  303   LOC3479 1  10678 XP_300275.1  5  344   CTTTTTCTTCAA    A--  AA           6  A  c  c
          21                    GGAGCACTAGCT CTAG   CTG  GCTCCTTGAGGA
                               GCTGGGGA    GGTC   GAT  CGAGGAACTTCT
                                     GTC   CA
GAM1032  303   LOC3483 2  6570  XP_300723.1  3  263   TCTCACCCTCAA   GAC  A             6  A  c  c

          78                    GGGGCTCACATG CTA   TGA GCTCCTTGAGG
                               GAGGACAA    GGT   ACT CGGGGAACTCC
                                     AC-   -
GAM1032  303   LOC3483 2  10330 XP_300723.1  3  830   GACTAACCTCAA T    GA  C-           6  A  c
c
          78                    GGATCCTGAGTC C AGACT  AG  TCCTTGAGG
                               TCCTTCAG    C TCTGA  TC  AGGAACTCC
                                     C    G-  CT
GAM1032  303   LOC3484 1  14041 XP_290909.1  3  554   CCACCCTCACAA     ---- A-     --       6  A  c  c
          54                    GGAGCTGCCATC CTAGAC    TG  AGCTCCT  TGAGG
                               CTGTTTGG    GGTTTG    AC  TCGAGGA  ACTCC
                                     TCCT  CG      AC
GAM1032  303   LOC3485 1  5434  XP_300769.1  5  400   GCTAGCCCTCCT      AAGC  CTT          6  A  c
 c
          04                    CCTGAAGCAGTC CTAGACTG    TC   GAGGA
                               TAGGAGCT    GATCTGAC    AG   CTCCT
                                     GA--  TC-
GAM1032  303   LOC3485 1  3393  XP_302813.1  5  556   TTCAGCCTTAAG  T       C-           6  A  c  c
          29                    GGTACTTCAGTC C AGACTGAAG  TCCTTGAGG
                               TTAACTGT    A TCTGACTTC  GGGAATTCC
                                     T       AT
GAM1032  303   LOC3487 1  5909  XP_300810.1  3  2245  CACTGCCCTCAA  T  A  G   T-           6  A  c
c
          01                    GGCTGCTTGAGG C AG CT AAGC  CCTTGAGG
                               CTCCCACG    C TC GA TTCG  GGAACTCC
                                     C  G  G   TC
GAM1032  303   LOC3487 1  1119  XP_302859.1  3  28    ATTCCTCCTCAA   G   AAGCT           6  A  c
c
          04                    GGCACCAGTGTG CTA ACTG    CCTTGAGGA
                               GAGGGCAT    GGT TGAC    GGAACTCCT
                                     G    CAC--
GAM1032  303   LOC3488 1  13599 XP_302903.1  3  655   CGCTTAAGCCCA    A  -----      T A      6  A  c
c
          43                    GGAGCTTAAGAC CTAG CTG    AAGCTCCT G GG
                               CAGCCTGG    GGTC GAC    TTCGAGGA C CC
                                     C   CAGAA       - -
```

GAM1032 303 LOC3489 1 3253 XP_300881.1 3 174 ACCTGGATTCTG -- C--- G 6 A c c
29 AGTTTTTCAGTC CTAGACTGAA GCTC TT AGG
TAGCCCAG GATCTGACTT TGAG AG TCC
TT TCTT G
GAM1032 303 LOC3490 1 5378 XP_300943.1 3 147 GTCACACTTCAA --- AAG 6 A c c
98 GGAGGCAGCTCT CTAGA CTG CTCCTTGAGG
CTAGACAG GATCT GAC GAGGAACTTC
CTC G--
GAM1032 303 LOC3493 1 9235 XP_301018.1 3 26 CTGGCTCCAGAA GA -- GA 6 A c
c
03 GGAGCTTTCCAG CTA CTG AAGCTCCTT GGA
GATAGCTT GAT GAC TTCGAGGAA CCT
AG CT GA
GAM1032 303 LOC3493 1 9235 XP_301025.1 3 26 CTGGCTCCAGAA GA -- GA 6 A c
c
15 GGAGCTTTCCAG CTA CTG AAGCTCCTT GGA
GATAGCTT GAT GAC TTCGAGGAA CCT
AG CT GA
GAM1032 303 LOC3493 1 15717 XP_301026.1 3 1 GCTCCAGAAGGA GA -- GA 6 A c
c
17 GCTTTCCAGGAT CTA CTG AAGCTCCTT GGA
AGCTTTGA GAT GAC TTCGAGGAA CCT
AG CT GA
GAM1032 303 LOC3493 1 15717 XP_301035.1 3 1 GCTCCAGAAGGA GA -- GA 6 A c
c
33 GCTTTCCAGGAT CTA CTG AAGCTCCTT GGA
AGCTTTGA GAT GAC TTCGAGGAA CCT
AG CT GA
GAM1032 303 LOC3493 1 8588 XP_301040.1 3 232 GACCAGCTTCAA A GAA 6 A c
c
38 GGAGCGGAAGGC CTAG CT GCTCCTTGAGG
TGGCTTGA GGTC GA CGAGGAACTTC
G AGG
GAM1032 303 LOC3504 1 10058 XP_304096.1 5 101 TTGAGCCTTTAG CT--- 6 A c c
48 GGAGCTTCTCTG CTAGA GAAGCTCCTTGAGG
TTTTGGGA GGTTT CTTCGAGGGATTTC
TGTCT
GAM1032 303 LOC3523 1 4515 XP_305612.1 5 58 ACCTGGCTTCCG GAC T 6 A c c
86 GGAGCTTCATAG CTA TGAAGCTCCT GAGG
ACCGATTG GAT ACTTCGAGGG CTTC
--- C
GAM1032 303 LOC3526 1 17140 XP_302538.1 3 346 CGAGACCTTGAA AG --- - 6 A c c
91 GGAGCTTTGCAA CT ACT GAAGCTCCTT GAGG
GTAGAGAA GA TGA TTTCGAGGAA TTCC
GA ACG G
GAM1032 303 LOC5133 1 8816 NP_057727.1 3 522 AGGCACGACCCT A C CT 6 A c
c
3 CAGATCTCAGTC CTAGACTGA G TC TGAGG

TAGTGAAG GATCTGACT C AG ACTCC
- T --
GAM1032 303 LOC9024 1 4074 XP_030283.1 5 806 TGCAGATTCTCA A CCT 6 A c c

6 TTAGCTTCAGCT CTAG CTGAAGCT TGAGGA
GGGTCATG GGTC GACTTCGA ACTCTT
- TT-
GAM1032 303 LOC9078 1 13538 XP_034110.1 3 100 CAGTCTTCTCAA T C AA 6 A c
c

5 GGAGCAATAATC C AGA TG GCTCCTTGAGGA
TTGGCTCA G TCT AT CGAGGAACTCTT
T A AA
GAM1032 303 LOC9197 1 16067 XP_041974.2 5 604 GGCCCTCCTCAA - - -- 6 A c c

4 GGTCAGCCTTCA CTAGA CTGAAG CT CCTTGAGGA
GATTTGGG GGTTT GACTTC GA GGAACTCCT
A C CT
GAM1032 303 LPIN2 1 1006 NP_055461.1 3 2076 TGGGCCTTCTTA G TC T- 6 A c c
GAGGGTTCAGTC CTAGACTGAA C CT GAGG
TAGGACCC GATCTGACTT G GA CTTC
G GA TT
GAM1032 303 LRIG1 1 2045 NP_056356.1 3 540 CATGCGCCGGAA AGA GA 6 A c
c

GGAGCTTCAGGT CT CTGAAGCTCCTT GG
GAGCACTG GA GACTTCGAGGAA CC
GTG GG
GAM1032 303 LSS 1 18091 NP_002331.2 3 322 GCACGGCCTCAA A GAA - 6 A c c
GGTAGTGAGGCT CTAG CT GCT CCTTGAGG
AGGAGGTT GATC GG TGA GGAACTCC
- AG- T
GAM1032 303 MBD2 1 13083 NP_056647.1 3 246 AAAGGTCTTCAA A GA 6 A c c
GGAGTTGGTCCA CT GACT AGCTCCTTGAGGA
GGTAGCAA GA CTGG TTGAGGAACTTCT
C --
GAM1032 303 MCAM 1 16374 NP_006491.1 3 254 CATCCCAAGCAA T AA A--- 6 A c
c

GGAGCCCCAGTC C AGACTG GCTCCTTG GGA
TCCCGAGC C TCTGAC CGAGGAAC CCT
C CC GAAC
GAM1032 303 MGC1020 1 18523 NP_659497.1 3 1398 TATGGAGTTCAG A- G 6 A c
c

0 GGAGCTTCAGGG CTAG CTGAAGCTCCTTGAG
TTGGCAAA GGTT GACTTCGAGGGACTT
GG G
GAM1032 303 MGC2574 1 16697 NP_077003.1 3 724 CCCTGCCCTCGA C---- C - 6 A c
c

GGAGCTTTCATT TAGA TGAA GCTCCTTGAGG
CTGATGGA GTCT ACTT CGAGGAGCTCC
AGGTA T T
GAM1032 303 MGC3464 1 14517 NP_689873.1 3 27 TGCAGACCTCAA ACT AG 6 A c
c

```
        8                       GGAGGCTCCCTA CTAG  GA  CTCCTTGAGG
                                GCAACAGC    GATC  CT  GAGGAACTCC
                                        C--  CG
GAM1032  303   MGC4544 1  11172 NP_689712.1  3  97   GCTTTGGCCCAG    -     CC  A       6  A  c
c
        1                       CCAGCTTCAGAT CTAGA CTGAAGCT  TTG GG
                                CTGGTCTT    GGTCT GACTTCGA  GAC CC
                                        A       CC  -
GAM1032  303   MKI67  1  7829  NP_002408.2  3  2018  TGGTAACTTCTC  T        CTT        6  A  c  c
                                TGAGCTTCAGTT C AGACTGAAGCTC  GAGG
                                TCCAAGTG    C TTTGACTTCGAG  CTTC
                                        C         TCT
GAM1032  303   MPO    1  14549 NP_000241.1  5  85   CCCCTCCCTCAA     TGAAG           6  A  c  c
                                GGAGGTCTGGCT CTAGAC    CTCCTTGAGG
                                TTATCCAT    GGTCTG    GAGGAACTCC
                                        -----
GAM1032  303   MS4A8B 1  7880  NP_113645.1  3  158   TCACCTTCATTC       GCTCC          6  A  c
c
                                TTCAATTCAGTC CTAGACTGAA    TTGAGGA
                                TAGGAAAC    GATCTGACTT    AACTTCT
                                        -----
GAM1032  303   MTR    1  12733 NP_000245.1  3  58   GATGATCCTCAA    AC  AAGC          6  A  c  c

                                GGAAATACAACC CTAG  TG   TCCTTGAGGA
                                TAGGGTGC    GATC  AC   AGGAACTCCT
                                        CA  ATAA
GAM1032  303   MTRF1L 1  16068 NP_061914.2  3  370   CCTAAGCCCTAA  T  A   --      A       6  A  c  c

                                GGAGCTCCTCAG C AG CTGA  AGCTCCTTG GG
                                CTTGAAAT    G TC GACT  TCGAGGAAT CC
                                        T  -   CC       C
GAM1032  303   Nanog  1  12978 NP_079141.1  3  42   AACTGATATTAC       CTCC    G       6  A  c  c
                                TCAATTTCAGTC CTAGACTGAAG   TTGAG
                                TGGACACT    GGTCTGACTTT   AACTC
                                        ----    A
GAM1032  303   NCOA6  1  10389 NP_054790.1  5  2049   AGATGCTTCCAA    -   --      -       6  A  c  c
                                GGAGCTACTTAG CTAGA CTGA  AGCTCCTTG AGG
                                TTTTAGGG    GATTT GATT  TCGAGGAAC TTC
                                        T   CA       C
GAM1032  303   NEDD4  1  6062  XP_046129.4  3  1341   CCTGATCCTCAA C    ----- -  C        6  A  c  c
                                GGAACTTGCAAA  TAGAC    TG AAG TCCTTGAGGA
                                TGTGTCTA     ATCTG    AC TTC AGGAACTCCT
                                        -    TGTAA  G   A
GAM1032  303   NEU3   1  12441 NP_006647.2  3  871   CTTTGCCCTCAA C---     A--           6  A  c  c
                                GGAGTTCACCAG    TAGACTG   AGCTCCTTGAGG
                                TTTATGGG        ATTTGAC   TTGAGGAACTCC
                                        GGGT      CAC
GAM1032  303   NOTCH3 1  8237  NP_000426.1  3  178   GGTCATCAGCCC  T       T  T A        6  A  c
c
                                AGGGCTTCAGTC C AGACTGAAGC CCT G GG
```

TTCCTTTA C TCTGACTTCG GGA C CC
T - - -
GAM1032 303 OR2H1 1 19602 NP_112145.1 3 1349 CTACTTCCTCAA A T- CT 6 A c c

GGTTCTTTCTGT CT GAC GAAG CCTTGAGGA
CCAGTTGC GA CTG TTTC GGAACTCCT
C TC TT
GAM1032 303 PIK3CG 1 6205 NP_002640.2 3 934 ATTACTTCTCAA - -- AGC 6 A c c
GGATTATTAGAA CTA GA CTGA TCCTTGAGGA
TCTTAGGT GAT CT GATT AGGAACTCTT
T AA ATT
GAM1032 303 PLP1 1 17932 NP_000524.2 3 813 TGTGGTTTCCAA GA GA A 6 A c c

GGAGCTGAGAAT CTA CT AGCTCCTTG GGA
AGAAGGAA GAT GA TCGAGGAAC CTT
AA G- -
GAM1032 303 PNMA2 1 15213 NP_009188.1 3 919 CCTGCCCTCAGA - G C 6 A c c
GAGGTTCCAGTC CTAGACTG AA CTC TTGAGG
TAGATGAG GATCTGAC TT GAG GACTCC
C G A
GAM1032 303 POFUT1 1 3733 NP_056167.1 3 2641 CTTTGTTCTCAA C - C 6 A c c
GGAATTTGCATT CTAGA TG AAG TCCTTGAGGA
CTAGAAAG GATCT AC TTT AGGAACTCTT
T G A
GAM1032 303 POLG 1 10516 NP_002684.1 3 48 ATTTGCTCCCGT A C T A 6 A c c
GGAGCTTCATCG CT GA TGAAGCTCC TG GGA
GGGTGGTG GG CT ACTTCGAGG GC CCT
G - T -
GAM1032 303 POLM 1 6542 NP_037416.1 3 505 TCGTGCCAGCAA TGAA- A- 6 A c
c

GGAGCCTACTGT CTAGAC GCTCCTTG GG
CTGGTGTG GGTCTG CGAGGAAC CC
TCATC GA
GAM1032 303 PPARGC1 1 9562 NP_037393.1 3 1386 CCATCCCTTAGG C----- C - 6 A c
c

TGAGCTTCAATC TAGA TGAAGCTC CTTGAGG
TAAGCATC ATCT ACTTCGAG GGATTCC
CTACGA A T
GAM1032 303 PPP1R13 1 10316 NP_056131.1 3 947 GGCCGCCACCAA A AA A- 6 A c
c
B GGAGCAGCAGCT CTAG CTG GCTCCTTG GG
GGGGCAGA GGTC GAC CGAGGAAC CC
- GA CA
GAM1032 303 PRKCM 1 3896 NP_002733.1 3 328 GTTTTTCTTACT C T- 6 A c c
GGAGCTTCATTT CTAGA TGAAGCTCC TGAGGA
TGGTAAGA GGTTT ACTTCGAGG ATTCTT
T TC
GAM1032 303 PRO0659 1 18366 NP_054857.2 5 331 CGAGGGCCTGGC A - TTG 6 A c
c

GGAGCTTCCAGC CTAG CTG AAGCTCC AGG

TGGGACCA GGTC GAC TTCGAGG TCC
- C CGG
GAM1032 303 Prostei 1 12567 NP_149093.1 3 249 AGGCCTTCCAAG --- 6 A c c
n GGGGTTTCAGTC CTAGACTGAAGCTCCTT GAGG
TGGACTTA GGTCTGACTTTGGGGGA TTCC
ACC
GAM1032 303 PSORS1C 1 11955 NP_054787.1 3 53 TGTTTCCCTCAA ACT- C 6 A c
c
1 GGACCTTTCTGC CTAG GAAG TCCTTGAGG
CTGGAAGT GGTC TTTC AGGAACTCC
CGTC C
GAM1032 303 PTP9Q22 1 4253 NP_689635.3 3 1087 CACTTGCCTCAA C- TC 6 A c
c
GGCTTTATATTT CTAGA TGAAGC CTTGAGG
GGCTGCTT GGTTT ATTTCG GAACTCC
AT --
GAM1032 303 PTP9Q22 1 4253 NP_818931.1 3 1087 CACTTGCCTCAA C- TC 6 A c
c
GGCTTTATATTT CTAGA TGAAGC CTTGAGG
GGCTGCTT GGTTT ATTTCG GAACTCC
AT --
GAM1032 303 PTPRO 1 1369 NP_109595.1 3 55 AGAGCTCTCCAC - - CTT 6 A c c
GAGTGTTCAGTC CTA GACTGAA GCTC GAGG
TTAGAACT GAT CTGACTT TGAG CTCT
T G CAC
GAM1032 303 PTPRO 1 1369 NP_109596.1 3 55 AGAGCTCTCCAC - - CTT 6 A c c
GAGTGTTCAGTC CTA GACTGAA GCTC GAGG
TTAGAACT GAT CTGACTT TGAG CTCT
T G CAC
GAM1032 303 PXN 1 16601 NP_002850.1 3 5 CTGCTTCCTCAA ACT CTC 6 A c c
GCTCTTCTGCTA CTAG GAAG CTTGAGGA
GTGCCCTG GATC CTTC GAACTCCT
GT- TC-
GAM1032 303 RANBP17 1 3335 NP_075048.1 3 648 GCATAAATCTGA G TC G 6 A c
c
AGTGGTTCAGTC CTAGACTGAA C CTT AGG
TAGAAGAA GATCTGACTT G GAA TCT
- GT G
GAM1032 303 RB1 1 12895 NP_000312.1 3 1382 GGGATATTTAAG A - G 6 A c c
GTAGCTTCAGCT CTAG CTGAAGCT CCTTGAG
AGCTTTTA GATC GACTTCGA GGAATTT
- T A
GAM1032 303 RFX5 1 16892 NP_000440.1 3 962 TTCTCCTCTAGG T C- - 6 A c c
GACTCTTCAGTC C AGACTGAAG TCCTT GAGGA
TCATTTAG A TCTGACTTC AGGGA CTCCT
C TC T
GAM1032 303 RGS11 1 1065 NP_003825.1 3 325 CTCCACCTTCTC A CT TT 6 A c c
TGGTCTTCAGTC CT GACTGAAG CC GAGGA
CAGCACTG GA CTGACTTC GG CTCTT
C T- T-

GAM1032 303 RINZF 1 7593 NP_076418.2 3 38 TATACTCCTCAA C A - 6 A c c
GGATGCTGCATT CTAGA TG AGC TCCTTGAGGA
TGGACCTA GGTTT AC TCG AGGAACTCCT
- G T
GAM1032 303 RNASE3L 1 16650 NP_037367.2 5 125 CCATATCATCAA C A- G 6 A c
c
GGAGCTGATAAT CTAGA TG AGCTCCTTGA GA
CTAGTGGA GATCT AT TCGAGGAACT CT
A AG A
GAM1032 303 RNF6 1 3285 NP_005968.1 5 352 CAGGAATCTCAG AGC- T 6 A c c
GATGAATCAGTC CTAGACTGA TCCT GAGG
TAGATCGA GATCTGACT AGGA CTCT
AAGT -
GAM1032 303 RXRA 1 11932 NP_002948.1 3 1584 GGTCTTGTCTTC AA CCTT 6 A c
c
CCAGCCGCAGTC CTAGACTG GCT GAGGA
TAGGAATG GATCTGAC CGA CTTCT
GC CC--
GAM1032 303 SBLF 1 8023 NP_006864.2 3 2321 TTCAGGACATCT T GCTC 6 A c c
CAAGATTCAGTC C AGACTGAA CTTGAGG
TTGACAAT G TCTGACTT GAACTCT
T A---
GAM1032 303 SCN2B 1 635 NP_004579.1 3 927 GCAGCTTTCTTT AG TT 6 A c c
GGGGCTTCAGTG CT ACTGAAGCTCC GAGGA
AGAACTCT GA TGACTTCGGGG TTCTT
G- T-
GAM1032 303 SERPINA 1 2046 NP_001076.1 3 167 CAGGGGCCCATG C- T A 6 A c
c
3 GACTCTTCAGTC CTAGACTGAAG TCC TG GG
TGGAGGGT GGTCTGACTTC AGG AC CC
TC T -
GAM1032 303 SF4 1 860 NP_066987.1 3 800 TCAGGACCTCAA C------- A A 6 A c c
GGGGCTCGGCTA TAG CTGA GCTCCTTGAGG
TGAGAAGG ATC GGCT CGGGGAACTCC
GGAAGAGT - -
GAM1032 303 SIAT1 1 11766 NP_003023.1 3 693 GTCTATCCTCAA AG A TC 6 A c c
GTTGCTACGGTT CT ACTG AGC CTTGAGGA
CAGTGAGA GA TGGC TCG GAACTCCT
CT A TT
GAM1032 303 SIAT1 1 11766 NP_775323.1 3 693 GTCTATCCTCAA AG A TC 6 A c c
GTTGCTACGGTT CT ACTG AGC CTTGAGGA
CAGTGAGA GA TGGC TCG GAACTCCT
CT A TT
GAM1032 303 SIAT1 1 11766 NP_775324.1 3 693 GTCTATCCTCAA AG A TC 6 A c c
GTTGCTACGGTT CT ACTG AGC CTTGAGGA
CAGTGAGA GA TGGC TCG GAACTCCT
CT A TT
GAM1032 303 SLC12A7 1 17066 NP_006589.1 3 542 TCTGTACCTCAA A GA CT 6 A c
c
GGCACTGAAGCT CTAG CT AG CCTTGAGG

GGAGGACT GGTC GA TC GGAACTCC
- AG AC
GAM1032 303 SLC35A4 1 5796 NP_542401.1 5 156 CCCGTTCCTCAA A -- GC 6 A c c

GGGATTCCTGGC CTAG CT GAA TCCTTGAGGA
TGGCTATG GGTC GG CTT GGGAACTCCT
- TC A-
GAM1032 303 SLC35E2 1 14041 XP_049733.6 3 2487 CCACCCTCACAA ---- A- -- 6 A c c

GGAGCTGCCATC CTAGAC TG AGCTCCT TGAGG
CTGTTTGG GGTTTG AC TCGAGGA ACTCC
TCCT CG AC
GAM1032 303 SMCR5 1 10482 NP_658987.1 3 906 CCTGGGCCCCTC T T TT 6 A c
c

TGGGCTTCAGTT C AGACTGAAGC CC GAGG
TCCCCACT C TTTGACTTCG GG CTCC
C - T-
GAM1032 303 SORCS2 1 6379 NP_065828.1 3 1892 AGTTGTCCTCAA AC AGCT 6 A c
c

GGTCATCCTGGA CTAG TGA CCTTGAGGA
GATGGGAT GGTC ACT GGAACTCCT
CT ----
GAM1032 303 SP7 1 20063 NP_690599.1 3 407 TCCCTCAGCCTC T CC---- 6 A c c
CAGGCTTCAGTC C AGACTGAAGCT TTGAGG
TTCCCAAC C TCTGACTTCGG GACTCC
T ACCTCC
GAM1032 303 SPON1 1 14025 NP_006099.1 3 285 ACATGTCCCTCT ACT TT 6 A c
c

GGAGCTTCCACC CTAG GAAGCTCC GAGG
TGGCCAGG GGTC CTTCGAGG CTCC
CAC T-
GAM1032 303 SUOX 1 15310 NP_000447.1 5 794 CAATCCCCTCAA C A- - --- 6 A c c
GGATCTGCATTC TAG CTGAA GC TCCTTGAGG
AGGCCTGC GTC GACTT CG AGGAACTCC
C CG A TCT
GAM1032 303 TACR3 1 15957 NP_001050.1 3 57 TGTGAGACCATC AA T T - 6 A c c
ATGGTGCCAGTC CTAGACTG GC CC TGA GG
TAGGACCC GATCTGAC CG GG ACT CC
-- T T A
GAM1032 303 TBX18 1 550 XP_291165.1 5 48 GGCTTCCAGCAG CT- A- 6 A c c
GGAGCTTCCCCT CTAGA GAAGCTCCTTG GGA
CTGGCGTC GGTCT CTTCGAGGGAC CCT
CCC GA
GAM1032 303 TK2 1 17771 NP_004605.1 3 962 GTCCTTGTATAA - CT ---- 6 A c c
GGAGCTTTGCTC CTA GA GAAGCTCCTT GAGGA
TTGGAATT GGT CT TTTCGAGGAA TTCCT
T CG TATG
GAM1032 303 TLR4 1 10745 NP_003257.1 3 171 TGCTAATCTCAA AG - 6 A c c
GGAGCTTCCAGT CT ACTG AAGCTCCTTGAGG
GCAGAGGG GA TGAC TTCGAGGAACTCT

```
                                        CG   C
GAM1032  303   TLR4   1  10745 NP_612564.1  3  171   TGCTAATCTCAA  AG   -          6  A  c  c
                                GGAGCTTCCAGT CT  ACTG AAGCTCCTTGAGG
                                GCAGAGGG   GA  TGAC TTCGAGGAACTCT
                                        CG   C
GAM1032  303   TLR4   1  10745 NP_612566.1  3  171   TGCTAATCTCAA  AG   -          6  A  c  c
                                GGAGCTTCCAGT CT  ACTG AAGCTCCTTGAGG
                                GCAGAGGG   GA  TGAC TTCGAGGAACTCT
                                        CG   C
GAM1032  303   TLR4   1  10745 NP_612567.1  3  171   TGCTAATCTCAA  AG   -          6  A  c  c
                                GGAGCTTCCAGT CT  ACTG AAGCTCCTTGAGG
                                GCAGAGGG   GA  TGAC TTCGAGGAACTCT
                                        CG   C
GAM1032  303   TNFRSF6 1  3084  NP_690611.1  3  276   TATCATCCTCAA   AC  AGC          6  A  c
c
                                GGACATTACTAG CTAG  TGA   TCCTTGAGGA
                                TGACTCAG    GATC  ATT   AGGAACTCCT
                                        --   AC-
GAM1032  303   TNFRSF6 1  3084  NP_690612.1  3  405   TATCATCCTCAA   AC  AGC          6  A  c
c
                                GGACATTACTAG CTAG  TGA   TCCTTGAGGA
                                TGACTCAG    GATC  ATT   AGGAACTCCT
                                        --   AC-
GAM1032  303   TNFRSF6 1  3084  NP_690613.1  3  322   TATCATCCTCAA   AC  AGC          6  A  c
c
                                GGACATTACTAG CTAG  TGA   TCCTTGAGGA
                                TGACTCAG    GATC  ATT   AGGAACTCCT
                                        --   AC-
GAM1032  303   TNFRSF6 1  3084  NP_690614.1  3  393   TATCATCCTCAA   AC  AGC          6  A  c
c
                                GGACATTACTAG CTAG  TGA   TCCTTGAGGA
                                TGACTCAG    GATC  ATT   AGGAACTCCT
                                        --   AC-
GAM1032  303   TNFRSF6 1  3084  NP_690615.1  3  393   TATCATCCTCAA   AC  AGC          6  A  c
c
                                GGACATTACTAG CTAG  TGA   TCCTTGAGGA
                                TGACTCAG    GATC  ATT   AGGAACTCCT
                                        --   AC-
GAM1032  303   TNFRSF6 1  3084  NP_690616.1  3  405   TATCATCCTCAA   AC  AGC          6  A  c
c
                                GGACATTACTAG CTAG  TGA   TCCTTGAGGA
                                TGACTCAG    GATC  ATT   AGGAACTCCT
                                        --   AC-
GAM1032  303   TOLLIP 1  13742 NP_061882.2  3  799   GTGTCCTCCCAG  T  CT-      A       6  A  c  c

                                GGAGCTTCTCTT C AGA   GAAGCTCCTTG GGA
                                CTCAACAG    A TCT   CTTCGAGGGAC CCT
                                        C   TCT        -
GAM1032  303   TYRP1  1  11984 NP_000541.1  5  36    GATTTTCCTCTA  T      TCCTT        6  A  c  c
```

CGTGCTTCAGTC C AGACTGAAGC GAGGA
TTCTCTAC C TCTGACTTCG CTCCT
T TGCAT

GAM1032 303 USP12L1 1 8209 XP_167944.1 3 2984 ACTTAACCTCTC T TCCTT 6 A c c

TGTGCTTCAGTC C AGACTGAAGC GAGG
TCCCTGTC C TCTGACTTCG CTCC
C TGTCT

GAM1032 303 VIPL 1 9897 NP_110432.1 3 482 CTGCCTACCTGA CT G 6 A c c
GGAGCTTTCTTT CTAGA GAAGCTCCTT AGG
GGAAACCA GGTTT TTTCGAGGAG TCC
C- -

GAM1032 303 WBP2 1 17972 NP_036610.2 3 718 TTCCTTCTAGAA ACT- ---- 6 A c c
GGAGCTTCCTGA CTAG GAAGCTCCTT GAGGA
CTGGAACC GGTC CTTCGAGGAA TTCCT
AGTC GATC

GAM1032 303 ZAK 1 5951 NP_598407.1 3 5130 TGTTGCCTGTGA CTG - 6 A c c
GGAGCTTTCTGG CTAGA AAGCTCCTTG AGG
CATGTGAT GGTCT TTCGAGGAGT TCC
--- G

GAM1338 360 15E1.2 1 13885 XP_290596.1 3 1201 CCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGA TGACGTGAGGTCGGACCC
ACT

GAM1338 360 7h3 1 16813 NP_149014.2 3 745 CCCTGAAGCGTC A - AA 3 C c c
AGGCTGGGGGCA ACTGC CTCCAGCCTGG GC
GTCTGGTA TGACG GGGGTCGGACT CG
- G AA

GAM1338 360 A1BG 2 10791 NP_570602.2 3 344 ACACTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGTTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 A1BG 2 19693 NP_570602.2 3 1396 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA

GAM1338 360 A2BP1 1 1212 NP_061193.2 5 560 AGCTTCTTGCCC A---- A CA- 3 C c c

AGGCAGAGAGAG CTGC CTC GCCTGGGCAA
CAGGAGCG GACG GAG CGGACCCGTT
GCGAG A AGA

GAM1338 360 AASS 1 18163 NP_005754.2 3 356 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTG TGACGTGAGGTCGGACCC
ACT

GAM1338 360 ABCA13 1 13800 NP_689914.2 3 1067 GCTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 ABCC11 1 18047 NP_149163.2 5 57 AGGAGATTGCCC CAG-- 3 C c c

AGGATCAAGGGT ACTGCACTC CCTGGGCAA
GCGGTGTT TGGCGTGGG GGACCCGTT
AACTA

GAM1338 360 ACADSB 1 14907 NP_001600.1 3 321 ACTCTGTCACCC C CAA 3 C c c

AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGCGC TGACGTGAG TCGGACCC
A ACT

GAM1338 360 AGO4 1 13702 NP_060099.2 3 1941 CCTGTTGCTCAT A----- C C--- 3 C c c

TAAGCTGAGTGC CTGCACTC AGC TGGGCAAC
AGACGTCC GACGTGAG TCG ACTCGTTG
CCTGCA - AATT

GAM1338 360 AHR 1 9011 NP_001612.1 3 1632 ACTCTGCCGCCC CC AA 3 C c c

AAACTGGAGTGC ACTGCACTCCAG TGGGC
AGTGGCAC TGACGTGAGGTC ACCCG
AA CC

GAM1338 360 AIM1 1 1383 XP_166300.1 3 713 AGACAGGATCTC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACTC
TAG

GAM1338 360 AKAP8 1 2643 NP_005849.1 3 209 GGCTTCTTGCCC G - CC-- 3 C c c

AGGTTTCAAAGC ACT CA CT AGCCTGGGCAA
TGAAGTAC TGA GT GA TTGGACCCGTT
A C AACT

GAM1338 360 ALDH1B1 1 19434 NP_000683.3 3 1072 ACTCTGTCGCCC AA 3 C b b

AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCCG
CT

GAM1338 360 ALOX15 1 18901 NP_001131.1 3 410 ACTTTGACACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACA

GAM1338 360 AMID 1 2328 NP_116186.1 3 693 GCCCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 ANKRD6 1 11653 NP_055757.1 3 1477 GCTCTGTCACCC C CAA 3 C c c

AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGCAT TGACGTGAGGTC GACCC
A ACT

GAM1338 360 AP1S3 1 15779 XP_291023.1 3 1017 ACTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 AP3S2 1 6113 NP_005820.1 3 656 GCTCTGTCACCC T CAA 3 C c c

AGGCTGGAGTGC AC GCACTCCAGCCTGGG
TGTGGTGC TG CGTGAGGTCGGACCC
T ACT

GAM1338 360 APAF1 2 803 NP_001151.1 3 629 TGCTTTGTTGCC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGCGC TGACGTGAGGTCGGACC GTTG
-

GAM1338 360 APAF1 2 803 NP_037361.1 3 629 TGCTTTGTTGCC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGCGC TGACGTGAGGTCGGACC GTTG
-

GAM1338 360 APAF1 2 1306 NP_001151.1 3 926 GCACTATCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 APAF1 2 1306 NP_037361.1 3 926 GCACTATCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 APM1 3 1962 NP_004788.1 3 811 ACTCTGTCACCC C CAA 3 C c b
AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGACAC TGAC TGAGGTCGGACCC
A ACT

GAM1338 360 APM1 3 2268 NP_004788.1 3 3331 GTTCTGTGGCCC C T AA 3 C c b

TGGCTGGAGTTC ACTG ACTCCAGCC GGGC
AGTGGTGT TGAC TGAGGTCGG CCCG
T T GT

GAM1338 360 APM1 3 13551 NP_004788.1 3 1807 CCCTCTGTTGCC C G 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGG CAAC
AGTGGCAT TGACGTGAG TCGGACC GTTG
A -

GAM1338 360 APOL2 1 16087 NP_112092.1 3 130 GCTCTATCGCCC G AA 3 C c c
AGGATGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGCTC TGACGTGAGGT GGACCCG
A CT

GAM1338 360 APOL2 1 16087 NP_663612.1 3 130 GCTCTATCGCCC G AA 3 C c c
AGGATGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGCTC TGACGTGAGGT GGACCCG
A CT

GAM1338 360 APPBP2 1 20094 NP_006371.2 3 3494 CTCTTGTTGCCC AC---- A - 3 C c
c

AGGCTGGGAGGG TGC CTCC AGCCTGGGCAAC
CAATGGCA ACG GAGG TCGGACCCGTTG
ACGGTA G G

GAM1338 360 APPL 1 12386 NP_036228.1 3 2973 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 AQP6 2 2103 NP_001643.1 3 613 GATCTGTTACCC C 3 C b b

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCAT TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 AQP6 2 2103 NP_445738.1 3 1779 GATCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCAT TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 AQP6 2 16104 NP_445738.1 5 751 GGACCTTGTCCC A-------- ACT - 3 C c b

AGGCTGGGCAGA CTGC CCAGCCTGGG CAA
GGTCAGGA GACG GGTCGGACCC GTT
AGGACTGGA --- T

GAM1338 360 AR 1 13404 NP_000035.2 5 1106 AGCCAAGCTCAA - G - AA 3 C c c
GGATGGAAGTGC ACTGCACT CCA CCT GGGC
AGTTAGGG TGACGTGA GGT GGA CTCG
A A A AA

GAM1338 360 ARHF 1 3172 NP_061907.1 3 1091 ATTCTGTCACTC C CAA 3 C c c
AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGCAT TGACGTGAG TCGGACTC
A ACT

GAM1338 360 ARHGAP1 1 8690 NP_004299.1 3 1136 CGCTCTGTCACC -- A 3 C b b

AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
AC C

GAM1338 360 ARHGAP1 1 7085 NP_055598.1 3 293 ACTCTGTCGTCC AA 3 C c c

1A AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCTG
CT

GAM1338 360 ARPP-19 1 18664 NP_006619.1 3 3490 TCACTCTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTGC TGACGTGAGGTCGGACCCGTT

GAM1338 360 ASB16 1 11661 NP_543139.4 3 142 ACTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 ASB6 1 1654 NP_060343.1 3 1441 GCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGATCC
ACT

GAM1338 360 ASB6 1 1654 NP_821066.1 3 2004 GCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGATCC
ACT

GAM1338 360 ASE-1 2 9101 NP_036231.1 3 450 GCTCTGTCGCCC AA 3 C c c
AGGTTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTTGGACCCG
CT

GAM1338 360 ASE-1 2 9988 NP_036231.1 3 742 CTGGTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 ATF7IP2 1 12397 NP_079273.1 3 540 GCTCTGTTGCCC C 3 C b b
AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGTCA TGAC TGAGGTCGGACCCGTTG
A
GAM1338 360 ATM 1 5585 NP_612150.1 3 121 CTCTGTCCGCCC T AA 3 C c c
AGGCTGGGTGCA ACTGCAC CCAGCCTGGGC
GTCACGGC TGACGTG GGTCGGACCCG
- CC
GAM1338 360 ATP1B2 1 19749 NP_001669.1 3 822 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 ATP1B4 1 15678 NP_036201.1 3 1877 CTGTTGTCACCC --- 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG CAAC
AGTGGTGT TGACGTGAGGTCGGACCC GTTG
ACT
GAM1338 360 ATP6V1A 1 19693 NP_001681.2 3 675 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA
GAM1338 360 ATP7A 1 19505 NP_000043.1 3 1059 GTTTTGCAGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
AC
GAM1338 360 AXL 1 5485 NP_001690.2 3 470 ACTGTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 AXL 1 5485 NP_068713.2 3 470 ACTGTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 BA108L7 1 4652 NP_112233.2 3 1054 ACTATTTTGCCC AC----- 3 C c c
.2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
GATGGTGC GCGTGAGGTCGGACCCGTT
CGTGGTA
GAM1338 360 BAG5 1 19878 NP_004864.1 3 1869 TCTCTGTTGCCC C 3 C b b
AGGCTGCAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGGTGC TGACGTGA GTCGGACCCGTTG
C
GAM1338 360 BAZ2A 1 16740 NP_038477.1 5 22 TTCTTATTGCCC AC----- C 3 C c c
AGGCTTGAGTGC TGCACTC AGCCTGGGCAA
AATGACCT ACGTGAG TCGGACCCGTT
TCCAGTA T
GAM1338 360 BCL10 1 17565 NP_003912.1 3 782 GCTCTATCGCCC AA 3 C b b

AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 BDKRB1 1 13940 NP_000701.2 5 91 GTCCGTCGGCCC C C AA 3 C c c

AGACTGAAGTGC ACTGCACT CAG CTGGGC
AGTGGCAC TGACGTGA GTC GACCCG
A A GC

GAM1338 360 BDP1 1 4304 NP_060899.1 3 152 GTTCTGTTGCCC CA 3 C b b
AGGCAAGAGTGC ACTGCACTC GCCTGGGCAAC
AGTGGTAT TGACGTGAG CGGACCCGTTG
AA

GAM1338 360 BENE 1 3688 NP_005425.1 3 472 GCTCTTCCTCCA - CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCT GGG
AGTGACGC TGACGTGAGGTCGGA CCT
A CCT

GAM1338 360 BHD 1 13142 NP_659434.2 3 911 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA

GAM1338 360 BNIP-S 1 17763 NP_612122.1 3 333 CGCTCTGTCGCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGC TGACGTGAGGTCGGACC TGT
GC C

GAM1338 360 BRIP1 1 721 NP_114432.1 3 207 GGTCTGTTGCCC C 3 C b b
AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
AGTGGTGT TGACGT AGGTCGGACCCGTTG
A

GAM1338 360 BTN3A1 1 17858 NP_008979.2 3 1055 TACTCTGTTGCT G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGTGC TGACGTGAGGTCGGATC GTTG
-

GAM1338 360 BXDC1 2 711 XP_166303.1 3 685 GTTCTGTCACCT G CAA 3 C c c
AGGGTGGAGTGC ACTGCACTCCA CCTGGG
AGTGGCAC TGACGTGAGGT GGATCC
G ACT

GAM1338 360 BXDC1 2 7070 XP_166303.1 3 1356 GCTCTGTCGCTC AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACTCG
CT

GAM1338 360 BY55 1 17712 NP_008984.1 5 45 TCACTGTCAACC CA --- A 3 C c c
AGGCCAGAGTGC ACTGCACTC GCCTGG GCA
AGTGAAGA TGACGTGAG CGGACC TGT
AC AAC C

GAM1338 360 C11orf1 1 13793 NP_065693.2 3 216 ACTCTGTTGCCC 3 C b b
7 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 C13orf1 1 2596 NP_065189.1 3 1685 ACCTTGTCACCC C CAA 3 C c c
AGGCTAGAGTGC ACTGCACTC AGCCTGGG

AGTGGCAC TGACGTGAG TCGGACCC
A ACT
GAM1338 360 C14orf1 1 19688 NP_060100.1 3 359 CTCTTGTTGCCC AC----- C 3 C c c
13 AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
AATGGCAT AC TGAGGTCGGACCCGTTG
TACGGTA A
GAM1338 360 C14orf1 1 11599 NP_660274.1 3 1619 GCTTTGTCACCT C CAA 3 C c c
43 AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGCGCG TGACGTGAGGTCG ATCC
A ACT
GAM1338 360 C14orf9 1 18182 NP_055643.1 3 967 GCTCTGTCACCC CAA 3 C c c
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 C1orf24 1 601 NP_443198.1 3 1461 GCTCTGTCGCCA G AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCT GGC
AGTGGTGT TGACGTGAGGTCGGA CCG
A CT
GAM1338 360 C1QTNF6 1 18746 NP_114116.2 3 542 GCTCTGTTGCCC C 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGTGC TGACGTGAG TCGGACCCGTTG
A
GAM1338 360 C20orf1 1 13924 NP_112181.1 3 1368 ACAGTTGCCTAC CCA- C- 3 C c
c
29 AGTATTCAGTGC ACTGCACT GC TGGGCAAC
AGTAACAT TGACGTGA TG ATCCGTTG
CTTA AC
GAM1338 360 C22orf1 1 14748 NP_003669.2 3 1824 GCTCTGTTGTCC 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCTGTTG

GAM1338 360 C4orf9 1 13142 XP_035572.1 3 369 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 C6orf33 1 7278 NP_588608.1 3 2344 ACTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGATGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 C6orf5 1 10778 NP_056339.2 3 1427 GCTCTGTCGTCC AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGCTGC TGACGTGAGGTCGGACCTG
CT
GAM1338 360 C6orf57 1 6442 NP_660310.1 3 500 TCTCTCTCACCC G CAA 3 C c c
AGGCTGGAGTGG ACT CACTCCAGCCTGGG
AGTGGCGC TGA GTGAGGTCGGACCC
G ACT
GAM1338 360 C7 1 11697 NP_000578.1 3 630 ACTTTGTTGCCC A 3 C b b
AGGCTGGAGCGC ACTGC CTCCAGCCTGGGCAAC

AGTGGGGT TGACG GAGGTCGGACCCGTTG
C
GAM1338 360 C9orf5 1 15709 NP_114401.1 3 1339 GGGTTCTTGGCC TG A C G 3 C c c
AGGCTGTAGGTG AC C CT CAGCCTGG CAA
GTGGCTCA TG G GA GTCGGACC GTT
GT - T G
GAM1338 360 C9orf9 2 13797 NP_061829.2 3 216 GCTCTGTCGCCC AA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
GGTGGCGC TGGCGTGAGGTCGGACCCG
CT
GAM1338 360 C9orf9 2 19273 NP_061829.2 3 855 ACTCTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 CAMLG 1 9364 NP_001736.1 3 790 CTCTTGTTGCCC AC----- C 3 C c c
AGGCTAGAGTGC TGCACTC AGCCTGGGCAAC
AATGGCGC ACGTGAG TCGGACCCGTTG
CGCGGTA A
GAM1338 360 CAPRI 1 12829 NP_008920.3 3 1973 ACTGTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AAATGGCT ACGTGAGGTCGGACCCGTTG
TCGGTAA
GAM1338 360 CARD6 1 13142 NP_115976.2 3 204 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 CASP2 1 18463 NP_001215.1 3 1633 GCTCTGTCGCCC A AA 3 C c c
AGGCTGGAGGGC ACTGC CTCCAGCCTGGGC
AGTGGCAC TGACG GAGGTCGGACCCG
G CT
GAM1338 360 CASP2 1 18463 NP_116764.1 3 1244 GCTCTGTCGCCC A AA 3 C c c
AGGCTGGAGGGC ACTGC CTCCAGCCTGGGC
AGTGGCAC TGACG GAGGTCGGACCCG
G CT
GAM1338 360 CASP2 1 18463 NP_116765.1 3 2058 GCTCTGTCGCCC A AA 3 C c c
AGGCTGGAGGGC ACTGC CTCCAGCCTGGGC
AGTGGCAC TGACG GAGGTCGGACCCG
G CT
GAM1338 360 CASP2 1 18463 NP_116766.1 3 2058 GCTCTGTCGCCC A AA 3 C c c
AGGCTGGAGGGC ACTGC CTCCAGCCTGGGC
AGTGGCAC TGACG GAGGTCGGACCCG
G CT
GAM1338 360 CASP8 1 9100 NP_001219.2 3 81 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC

AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 CASP8 1 9100 NP_203519.1 3 81 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 CASP8 1 9100 NP_203520.1 3 81 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 CASP8 1 9100 NP_203521.1 3 826 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 CBFA2T2 1 3868 NP_005084.1 3 1896 CTCTTGTCTCCC AC----- CA 3 C c
c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AC
AATCGCGC ACGTGAGGTCGGACCC TG
CGCGCTA TC
GAM1338 360 CBFA2T2 1 3868 NP_787060.1 3 1896 CTCTTGTCTCCC AC----- CA 3 C c
c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AC
AATCGCGC ACGTGAGGTCGGACCC TG
CGCGCTA TC
GAM1338 360 CCL16 1 10633 NP_004581.1 3 275 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 CCL22 1 11649 NP_002981.2 3 1274 ACTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 CCNF 1 14395 NP_001752.1 3 1292 CTCTTGTCTCCC T CA 3 C c c
CGGCTGGAGTGC ACTGCACTCCAGCC GGG AC
AGTGGCAT TGACGTGAGGTCGG CCC TG
C TC
GAM1338 360 CCRN4L 1 15829 NP_036250.2 3 102 GCTCTGTTGCCT C 3 C b b
AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGCCT TGAC TGAGGTCGGATCCGTTG
A
GAM1338 360 CD209 1 8229 NP_066978.1 3 1590 TGCTCTGTCGCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 CD24 1 18593 NP_037362.1 3 889 ACTTTGTCGCCC A AA 3 C c c
AGGCCGGAGTGC ACTGCACTCC GCCTGGGC
AGTGGTGC TGACGTGAGG CGGACCCG
C CT
GAM1338 360 CDC14B 1 7919 NP_201589.1 3 631 CTCTTGTTGTCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC

AGTGGCGC TGACGTGAGGTCGGACCTGTTG

GAM1338 360 CDC6 1 7495 NP_001245.1 3 413 ACCCTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA
GAM1338 360 CDCP1 1 20095 NP_073753.3 3 1771 ATTCTGTTGCCT 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGATCCGTTG

GAM1338 360 CDH1 2 3667 NP_004351.1 3 518 ATTCTATCGGCC GCAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGG
AGTGGTGC TGACGTGAGGTCGGACC
GGCT
GAM1338 360 CDH1 2 5919 NP_004351.1 3 824 GCTCCATCGCCC CT - AA 3 C c c
AGGCCTGGGATG ACTGCA CCAG CCTGGGC
CAGTGATG TGACGT GGTC GGACCCG
AG C CT
GAM1338 360 CDH17 1 5407 NP_004054.2 3 189 GCTCTGTCGCCC C AA 3 C c c
AGGCTGGAGTAC ACTG ACTCCAGCCTGGGC
AGTGGTGT TGAC TGAGGTCGGACCCG
A CT
GAM1338 360 CDK11 1 5408 XP_166324.1 3 3221 GCTCTGTCACCC C CAA 3 C c c

AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 CDKAL1 1 12153 NP_060244.1 3 442 CTCTTGTCCCCC --- CA 3 C b b

AGGCTGGAGTGG ACTGCAC TCCAGCCTGGG AC
TGCAGTGG TGACGTG AGGTCGGACCC TG
GTG CC
GAM1338 360 CEACAM8 1 436 NP_001807.2 3 352 GCTCTGTCGCCC AA 3 C b b

AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 CECR1 2 11209 NP_059120.2 3 387 CTCTTGTTGCCC AC----- C 3 C c c

AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
AATGGTGC AC TGAGGTCGGACCCGTTG
CGTGGTA A
GAM1338 360 CECR1 2 11209 NP_803124.1 3 387 CTCTTGTTGCCC AC----- C 3 C c c

AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
AATGGTGC AC TGAGGTCGGACCCGTTG
CGTGGTA A
GAM1338 360 CECR1 2 15125 NP_059120.2 3 1393 GCTCTGTTGCCC A----- G 3 C c c

AGGGTGGAGTGC CTGCACTCCA CCTGGGCAAC

AGCGGTGC GACGTGAGGT GGACCCGTTG
CGTGGC G
GAM1338 360 CECR1 2 15125 NP_803124.1 3 1393 GCTCTGTTGCCC A----- G 3 C c c

AGGGTGGAGTGC CTGCACTCCA CCTGGGCAAC
AGCGGTGC GACGTGAGGT GGACCCGTTG
CGTGGC G
GAM1338 360 CENPH 1 7835 NP_075060.1 3 262 GCTTTGTTGCCC A C 3 C b b
AGACTGGAGGGC ACTGC CTCCAG CTGGGCAAC
AGTGGCGC TGACG GAGGTC GACCCGTTG
G A
GAM1338 360 CENPJ 1 8802 NP_060921.2 5 121 GCTGAGCTGCCC AC ---- A 3 C c c

AGGCTTCACGGA ACTGC TCC AGCCTGGGCA
GCGGTGTT TGGCG AGG TCGGACCCGT
-- CACT C
GAM1338 360 CGI-150 1 19951 NP_057164.1 5 49 TGCTCTGTCATC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTGGCTC TGACGTGAGGTCGGAC CTGT
TA C
GAM1338 360 CHRAC1 1 18375 NP_059140.1 3 959 ACTCAGTTGCCC C 3 C b b
AGGCTGGATTGC ACTGCA TCCAGCCTGGGCAAC
GGTGGCGC TGGCGT AGGTCGGACCCGTTG
T
GAM1338 360 CHSY1 1 18370 NP_055733.2 3 638 ACTCTGTTACCC C C 3 C b b
AGGCTGGAATGC ACTGCA TCCAGCCTGGG AAC
AGTGGCGC TGACGT AGGTCGGACCC TTG
A A
GAM1338 360 CIAS1 1 7985 NP_004886.2 5 288 GCTGTGTCGCCT AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGATCCG
CT
GAM1338 360 CIP29 2 11639 NP_115740.3 3 163 TGCTCTGTTGCC C 3 C b b
CAGCTGGAGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGTGT TGACGTGAGGTCG ACCCGTTG
-
GAM1338 360 CIP29 2 20120 NP_115740.3 3 163 GCTCTGTTGCCC C 3 C b b
AGCTGGAGTGCA ACTGCACTCCAGC TGGGCAAC
GTGGTGTG TGACGTGAGGTCG ACCCGTTG
-
GAM1338 360 CLECSF1 2 1868 NP_072092.2 3 968 CTCTTGTTGCCC AC----- 3 C c b

2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AACGGCAC ACGTGAGGTCGGACCCGTTG
CACGGCA
GAM1338 360 CLECSF1 2 10233 NP_072092.2 3 319 ACTTTGTTACCC C 3 C b b
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCAC TGACGTGAGGTCGGACCC TTG
A
GAM1338 360 CMAR 2 6738 NP_005191.2 5 363 GCTGTGTTGCCA A----- G 3 C c c

AGGCTGGAGTGC CTGCACTCCAGCCT GGCAAC
AGGCCGCG GACGTGAGGTCGGA CCGTTG
GCGCCG A

GAM1338 360 CMAR 2 19999 NP_005191.2 5 231 GCGCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGCTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 CNN2 1 6909 NP_004359.1 3 735 TGGTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 CNP 1 5014 NP_149124.1 3 560 CTGCTATTTCCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGTGC TGACGTGAGGTCG ACCC
A TTT

GAM1338 360 COLEC12 1 13793 NP_110408.2 3 103 ACTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 CORO1C 1 1439 NP_055140.1 3 1013 AGCAGCTTGCCC C C C- 3 C c
c

AGCTCTTGAGTA ACTG ACTC AG CTGGGCAA
CAGTGGTG TGAC TGAG TC GACCCGTT
A T TC

GAM1338 360 COX15 1 18262 NP_510870.1 3 658 CTCTTGTTGCCC AC----- C 3 C c c

AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
AATGGCGT AC TGAGGTCGGACCCGTTG
TGCGGTA A

GAM1338 360 CPA4 1 10987 NP_057436.1 3 603 CTCTTGTTGCCC ACT----- 3 C c c
AGGCTGGAGTGT GCACTCCAGCCTGGGCAAC
GATGGGCT TGTGAGGTCGGACCCGTTG
TCGGGTAG

GAM1338 360 CPR8 1 9163 NP_065790.1 3 1690 GCTTTGTCAGCC --- 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCAA
AGTGACAC TGACGTGAGGTCGGACC TGTT
GAC

GAM1338 360 CPS1 1 4147 NP_001866.2 3 668 GTCACACTCTCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCT
CTC

GAM1338 360 CPSF2 2 6347 XP_029311.2 3 2044 CTCTTGTTGCCC AC----- C 3 C c c
AGACTGGAGTGC TGCACTCCAG CTGGGCAAC
AATGGCAC ACGTGAGGTC GACCCGTTG
CACGGTA A

GAM1338 360 CPSF2 2 6739 XP_029311.2 3 1219 ACAGAGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGA TGACGTGAGGTCGGACCC
ACT

GAM1338 360 CR1 1 13868 NP_000564.1 3 770 GCTCTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 CR1 1 13868 NP_000642.2 3 769 GCTCTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 CRLF3 1 9675 NP_057070.2 3 612 CTCTTGTCACTC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACTC
ACT
GAM1338 360 CRSP6 1 12005 NP_004259.3 3 434 ACTCTGTAGCCC C AA 3 C c c
AGTCTGGAGTGC ACTGCACTCCAG CTGGGC
AGTGGTGT TGACGTGAGGTC GACCCG
T AT
GAM1338 360 CRTAP 1 776 NP_006362.1 3 266 GCTCTCTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATGGCAC ACGTGAGGTCGGACCCGTT
CACGGTA
GAM1338 360 CRYZL1 1 2539 NP_660354.1 3 121 ATATTGTCCTAG A------ G -- - 3 C c c
ATGCTGGAGTGA CT CACTCCAGC CTGGG CAA
GATTATAT GA GTGAGGTCG GATCC GTT
TATATTA - TA T
GAM1338 360 CRYZL1 1 2539 NP_665857.1 3 121 ATATTGTCCTAG A------ G -- - 3 C c c
ATGCTGGAGTGA CT CACTCCAGC CTGGG CAA
GATTATAT GA GTGAGGTCG GATCC GTT
TATATTA - TA T
GAM1338 360 CSE-C 1 2336 NP_061851.1 5 2 GGAGTGCCCAGG G A 3 C b b
ATGGAGTGCAGT ACTGCACTCCA CCTGGGCA
GGCTATTC TGACGTGAGGT GGACCCGT
A G
GAM1338 360 CSE1L 1 3997 NP_803185.1 3 492 CTCTCATTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGAGCT TGACGTGAGGTCGGACCCGTT

GAM1338 360 CSNK2A2 1 15382 NP_001887.1 5 0 TGTCACCCAGGC CAA 3 C c c

TGGAGTGCAGTG ACTGCACTCCAGCCTGGG
GCGCAATC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 CTF1 1 6515 NP_001321.1 3 195 TCTCTGTCGCCC AA 3 C c c
AGGCTGGGGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGGGGTCGGACCCG
CT
GAM1338 360 CTSS 1 7946 NP_004070.3 3 1700 ACTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 CXCL16 1 11701 NP_071342.1 3 339 GCTCTGTCATCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCT
ACT

GAM1338 360 CXCL6 1 7236 NP_002984.1 3 51 ATAAAATTGCCC AC A ------ 3 C c c
AGTCTTCAGCGG ACTGC TCC GC CTGGGCAA
AGCAGTTT TGACG AGG CG GACCCGTT
-- - ACTTCT

GAM1338 360 CYCS 3 14950 NP_061820.1 3 1816 GCTGTGTCGCCA G AA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCT GGC
AGTGGTGC TGACGTGAGGTCGGA CCG
A CT

GAM1338 360 CYCS 3 15642 NP_061820.1 3 2206 CCCTTTTCGCCC C C AA 3 C c
c

AGGCTGAGTACA ACTG ACTC AGCCTGGGC
GTGGTGCA TGAC TGAG TCGGACCCG
A - CT

GAM1338 360 CYCS 3 19693 NP_061820.1 3 2619 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA

GAM1338 360 CYLC2 1 12632 NP_001331.1 3 730 GCTCTGTTGCCC C T 3 C b b
TGGCTGGAGTTC ACTG ACTCCAGCC GGGCAAC
AGTGACAT TGAC TGAGGTCGG CCCGTTG
T T

GAM1338 360 CYP1A2 3 6816 NP_000752.1 3 1084 CCTCTGTCTCCT C CA 3 C c b

AAGCTGGAGTGC ACTGCACTCCAGC TGGG AC
AGTGGCAT TGACGTGAGGTCG ATCC TG
A TC

GAM1338 360 CYP1A2 3 8688 NP_000752.1 3 787 TACTCTGTTGCC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGCGC TGACGTGAGGTCGGACC GTTG
-

GAM1338 360 CYP1A2 3 13973 NP_000752.1 3 417 AGTCTGTCACCC CAA 3 C c b

AGGTTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTTGGACCC
ACT

GAM1338 360 CYP2B6 2 3011 NP_000758.1 3 275 ACACTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 CYP2B6 2 4525 NP_000758.1 3 1242 GACATGTTGGCC A----- G - G 3 C c
b

AGGCTGGTGGTG CT CACT CCAGCCTGG CAAC
AGCTCCTG GA GTGG GGTCGGACC GTTG
GTCCTC - T G

GAM1338 360 CYP4F3 1 1417 NP_000887.1 3 1395 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC

GGTGGCAT TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 CYP51A1 1 10631 NP_000777.1 3 883 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 CYP8B1 1 5584 NP_004382.1 3 1005 ACTCTGTTGCCC C 3 C b b
AGGCTGCAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGGTGT TGACGTGA GTCGGACCCGTTG
C
GAM1338 360 DCX 1 6035 NP_000546.2 3 4961 CCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT
GAM1338 360 DCX 1 6035 NP_835364.1 3 4961 CCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT
GAM1338 360 DCX 1 6035 NP_835365.1 3 4961 CCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT
GAM1338 360 DCX 1 6035 NP_835366.1 3 4961 CCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT
GAM1338 360 DDX31 1 17894 NP_619526.1 3 189 CTTGATTGTCCC G T- 3 C c c
TGGATGGAGTGC ACTGCACTCCA CC GGGCAA
AGTCACCT TGACGTGAGGT GG CCTGTT
A TC
GAM1338 360 DES 1 5111 NP_001918.2 3 293 TGGATGGAGCCC AC A AA 3 C c c
AGGCGGGAGCGG ACTGC TCC GCCTGGGC
TGGCCCTG TGGCG AGG CGGACCCG
-- G AG
GAM1338 360 DFFB 2 7574 NP_004393.1 3 245 CTTTTGTTGCCC 3 C b b
AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGATGTGAGGTCGGACCCGTTG

GAM1338 360 DFFB 2 7848 NP_004393.1 3 888 ACTCTGTCGCTC AA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGATGC TGACGTGAGGTCGGACTCG
CT
GAM1338 360 DIAPH2 1 12586 NP_006720.1 3 4012 ACTCTGTCACCC C CAA 3 C c
c
AGGCTGCAGTGT ACTGCACT CAGCCTGGG
AGTGGTGC TGATGTGA GTCGGACCC
C ACT
GAM1338 360 DISC1 1 13620 NP_061132.1 3 3217 TCTCTGTCACCC C CAA 3 C c c

AAGTTGGAGTGC ACTGCACTCCAGC TGGG

AGTGGCCC TGACGTGAGGTTG ACCC
A ACT
GAM1338 360 DKFZP43 1 11474 NP_113664.1 3 2100 ACTCTGTTGCCC CA - 3 C b b
4B044 AAGGTAGAGTGC ACTGCACTC GCCT GGGCAAC
AGTGGCGT TGACGTGAG TGGA CCCGTTG
A- A
GAM1338 360 DKFZP43 1 1107 NP_115519.1 3 479 TCTTTGTTACCC C C 3 C b b
4B1727 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG AAC
AGTGGTGT TGAC TGAGGTCGGACCC TTG
A A
GAM1338 360 DKFZp43 1 7947 NP_060068.1 3 860 GCTCTGTCACCC C CAA 3 C c c
4C0923 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCGT TGAC TGAGGTCGGACCC
A ACT
GAM1338 360 DKFZP43 1 5299 XP_044196.3 3 1559 ACCCTGTTGCCC AC----- 3 C c c
4C212 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 DKFZP43 1 4843 NP_056410.2 3 809 CCTCTGTCGCCC C C AA 3 C c c
4D146 AGGCTAGAGTAT ACTG ACTC AGCCTGGGC
AGTGGTGT TGAT TGAG TCGGACCCG
A A CT
GAM1338 360 DKFZp43 1 18031 NP_060082.1 5 771 AGTCTGTTGCCC 3 C b b
4E2220 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 DKFZP43 1 14671 NP_110444.1 3 2410 ACTCTGTCACCT - CAA 3 C c c
4F0318 AGGCTGGAGTTG ACTGCA CTCCAGCCTGGG
CAGTGGTT TGACGT GAGGTCGGATCC
T ACT
GAM1338 360 DKFZp43 1 4173 NP_115624.1 3 1204 CTCTTGTTTCCC AC----- C 3 C c c
4F1719 AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGGTG ACGTGAGGTCGGACCC TTG
GTGGGTA T
GAM1338 360 DKFZp54 1 1994 NP_064546.1 3 257 GCTCCATTGCCC A----- C 3 C c c
7H025 AGGCTGGACTGC CTGCA TCCAGCCTGGGCAA
AGCAGCGT GACGT AGGTCGGACCCGTT
TGCGAC C
GAM1338 360 DKFZp54 1 3007 NP_694590.1 3 1543 GCACTGTCACCC CAA 3 C c c
7P234 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 DKFZP56 1 13202 NP_108648.1 3 921 GTTCTGTTGCCT CA 3 C b b

4D166 AGGCCAGAGTGC ACTGCACTC GCCTGGGCAAC
AGTGGCAT TGACGTGAG CGGATCCGTTG
AC
GAM1338 360 DKFZP56 1 519 NP_056416.1 5 1110 CTCTTGTCGCCC C AA 3 C c c

4G092 AGGCTGTAGTGC ACTGCACT CAGCCTGGGC
AGTGGTAC TGACGTGA GTCGGACCCG
T CT
GAM1338 360 DKFZP56 1 19815 XP_032397.1 3 258 ACTCTGTCACCT CAA 3 C c c

4I122 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT
GAM1338 360 DKFZP56 1 18946 NP_056274.1 3 522 CGCTCTGTCACC C -- A 3 C c c

4J0863 AGGCTTGAGTGC ACTGCACTC AGCCTGG GCA
AGTGGTGT TGACGTGAG TCGGACC TGT
T AC C
GAM1338 360 DKFZP56 1 1414 NP_114429.1 3 214 ACTCTGTTGCCC 3 C b b
4K0322 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 DKFZp56 1 811 NP_115497.2 3 695 GCTGTGTCACAC --- A 3 C c c
4K142 AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTGGCGT TGACGTGAGGTCGGAC CTGT
ACA G
GAM1338 360 DKFZP56 1 1963 NP_115496.1 3 225 GCTCTGTTGCCC C 3 C b b
4O0523 AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
AGTGGCGT TGACGT AGGTCGGACCCGTTG
A
GAM1338 360 DKFZP56 1 12834 NP_110443.1 5 179 TGCGTTTGTCCC CA- - - 3 C c c

6D1346 AGGCTCGGGGGC ACTG CTCC AGCCTGGG CAA
TCAGTGGG TGAC GGGG TCGGACCC GTT
TCG C T
GAM1338 360 DKFZP56 1 2402 NP_056226.1 3 713 TCTCTGTTGCCC AC----- C 3 C c
c
6I1024 AGGCTAGAGTGC TGCACTC AGCCTGGGCAAC
ACTGGTGG ACGTGAG TCGGACCCGTTG
GGTGGTC A
GAM1338 360 DKFZP58 1 5664 NP_056248.1 3 472 ACTCTGTCATCC CAA 3 C c c
6D0919 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCT
ACT
GAM1338 360 DKFZp66 1 13142 NP_808881.1 3 965 CTCTTGTTGCCC AC----- 3 C c c

7B1218 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 DKFZp66 2 9198 XP_117353.1 3 295 TCTCTGTCAGCC TG --- A 3 C c c

7E0512 AGGCTGGAGTGT AC CACTCCAGCCTGG GCA
GGTGGCAC TG GTGAGGTCGGACC TGT
GT GAC C
GAM1338 360 DKFZp66 2 17043 XP_117353.1 5 1636 GTCTTGTTTGCC AC - ----- G 3 C c
c
7E0512 AGGCTGAGGCTG TGCA CTC CAGCCTGG CAA
AGTTGCAT ACGT GAG GTCGGACC GTT
T- T TCGGA -
GAM1338 360 DKFZp76 1 5298 NP_775734.1 3 2764 GCTATGTCTCCC CA 3 C b b
1B107 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 DKFZp76 1 436 NP_689650.1 5 1004 GCTCTGTCGCCC AA 3 C b b
1B128 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 DKFZp76 1 12709 NP_061181.1 3 887 GATCTGTCGCCC AA 3 C b b

1H039 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTAGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 DKFZp76 1 969 NP_115656.1 5 1461 CTCTTGTCACCC CAA 3 C c c
1J139 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 DKFZp76 1 10882 XP_086327.6 3 1183 CACTCTGTTGCC C G 3 C b
b
1N1114 AGGCTGGAATGC ACTGCA TCCAGCCTGG CAAC
AGTGGCGT TGACGT AGGTCGGACC GTTG
A -
GAM1338 360 DKFZp76 1 11194 NP_060879.1 5 1530 CTCTTGTTGCCC C 3 C b b
1O0113 AGGCTTGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGATGC TGACGTGAG TCGGACCCGTTG
T
GAM1338 360 DKFZp76 1 1413 NP_690870.1 3 739 GCTCTGTCACCC CAA 3 C c c

1P1121 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 DKFZp76 1 11830 NP_848637.1 3 167 TCTCTGTGGCCC C AA 3 C c
c
2C2414 AGGCTGAAGTGC ACTGCACT CAGCCTGGGC
AGTGGTGT TGACGTGA GTCGGACCCG
A GT
GAM1338 360 DKFZp76 1 2137 XP_172976.2 3 1896 GCTCTGTCGCCC A----- AA 3 C c
c
2H185 AGGCTGGAGTGC CTGCACTCCAGCCTGGGC
AGAGGTGC GACGTGAGGTCGGACCCG
CGTGGA CT
GAM1338 360 DKFZp76 1 11659 NP_689624.1 3 254 GCTCTGTCACCC CAA 3 C c
c

2I137 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 DKFZp76 1 19272 NP_689597.1 3 704 TCAATGGTGCCC A 3 C b b
2I194 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
AGTGGCGT TGACGTGAGGTCGGACCCGT
G
GAM1338 360 DKFZp76 1 13546 NP_061189.2 3 780 GTTCTGTTGCCC AG 3 C b b

2L0311 AGGAGGGAGTGC ACTGCACTCC CCTGGGCAAC
AGTGGTGC TGACGTGAGG GGACCCGTTG
GA
GAM1338 360 DNAH11 1 18338 NP_003768.1 3 42 TTCCTCTAGCCT CT AA 3 C c c

CTGCTGGAGTGC ACTGCACTCCAGC GGGC
AGTGAGGA TGACGTGAGGTCG TCCG
TC AT
GAM1338 360 DRIM 1 2324 NP_055318.1 3 140 ACTCTGTCACCC A - CAA 3 C c c
AAGGCGGAGTGC ACTGCACTCC GCCT GGG
AGTGACGA TGACGTGAGG CGGA CCC
- A ACT
GAM1338 360 DRPLA 1 8154 NP_001931.1 5 183 ATTCAGCTGCCC G -- A-- A 3 C c c
AGGCAGAGGAGA ACT CA CTCC GCCTGGGCA
ATGGGGTC TGG GT GAGG CGGACCCGT
G AA AGA C
GAM1338 360 DSC3 1 2085 NP_001932.1 3 2047 GCTCTGACGCAC G AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTG GC
AGTGGCTC TGACGTGAGGTCGGAC CG
A CA
GAM1338 360 DSC3 1 2085 NP_077741.1 3 2261 GCTCTGACGCAC G AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTG GC
AGTGGCTC TGACGTGAGGTCGGAC CG
A CA
GAM1338 360 DSCR6 1 17339 NP_061835.1 3 545 CTCTTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGACAC TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 DUPLIN 1 2517 XP_208760.3 3 180 CTCTCTCACCCA C - CAA 3 C c c

GGCCTGAAGTGC ACTGCACT CAG CCTGGG
AGTGGCAT TGACGTGA GTC GGACCC
A C ACT
GAM1338 360 DUSP18 1 19123 NP_689724.2 3 650 GCTCTGTCACCC CC CAA 3 C c
c

ATCCTGGAGTGC ACTGCACTCCAG TGGG
AGTAGTGT TGACGTGAGGTC ACCC
CT ACT
GAM1338 360 DUSP19 2 710 NP_543152.1 3 2292 CTCTTATTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCGT TGACGTGAGGTCGGACCCGTT

GAM1338 360 DUSP19 2 969 NP_543152.1 3 637 CTCTTGTCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 DYRK1A 1 14469 NP_567824.1 5 62 CCGCCATCGTCC C T AA 3 C c
c
CGGCTGAAGTGC ACTGCACT CAGCC GGGC
AGTGGCAC TGACGTGA GTCGG CCTG
A C CT
GAM1338 360 EBAF 1 7720 NP_003231.2 3 508 ATGAAGGGCTTC A - AA 3 C c c
AGGCTGGGGGCA ACTGC CTCCAGCCTGG GC
GTGGACAG TGACG GGGGTCGGACT CG
- T GG
GAM1338 360 EEF2K 1 11618 NP_037434.1 3 344 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGACAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 EHD1 1 14949 NP_006786.2 3 329 CGGCCTTTGCTG -- - TG 3 C c c
TGGCTGGAGCTG ACTG CA CTCCAGCC GGCAA
GACAGTGC TGAC GT GAGGTCGG TCGTT
AG C TG
GAM1338 360 EHD2 1 6934 NP_055416.2 3 905 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGA TGACGTGAGGTCGGACCCG
CT
GAM1338 360 EIF2S3 1 11659 NP_001406.1 3 346 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 EIF5A2 1 1333 NP_065123.1 3 974 ACTCCATCAGCC GCAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGG
AGTGGTGC TGACGTGAGGTCGGACC
GACT
GAM1338 360 ELP3 1 6182 NP_060561.3 3 905 GCTGTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 EMR2 1 433 NP_038475.2 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 EMR2 1 433 NP_690880.1 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 EMR2 1 433 NP_690881.1 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT

GAM1338 360 EMR2 1 433 NP_690882.1 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 EMR2 1 433 NP_690883.1 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 EMR2 1 433 NP_690884.1 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 EMR2 1 433 NP_690885.1 5 150 ACTCTATCACCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACT
GAM1338 360 ENDOGL1 1 4223 NP_005098.1 3 153 GCCGTGTCATCC CAA 3 C c
c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
GGTGGTGG TGGCGTGAGGTCGGACCT
ACT
GAM1338 360 EREG 1 430 NP_001423.1 3 2042 GCTCTGTTGCCC 3 C b b
AGGTTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTTGGACCCGTTG

GAM1338 360 ET(B)R-LP-2 1 6465 NP_004758.2 3 512 GCTCTGTTGCCC AC----- C 3 C c c
AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
ATTTGCCT AC TGAGGTCGGACCCGTTG
TCCGTTT A
GAM1338 360 EVC 1 4148 NP_055371.1 3 2224 TCACTTTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCGT TGACGTGAGGTCGGACCCGTT

GAM1338 360 EVC 1 4148 NP_714928.1 3 2224 TCACTTTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCGT TGACGTGAGGTCGGACCCGTT

GAM1338 360 EVI5 2 16074 NP_005656.2 3 2216 CTCACTGCACTC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTG G GCA
AGTGGTAC TGACGTGAGGTCGGAC C CGT
T A C
GAM1338 360 EVI5 2 18007 NP_005656.2 3 515 AGTTTGTCACCC T CAA 3 C c b
AGGCTGGAGTGC AC GCACTCCAGCCTGGG
TGTGGTGT TG CGTGAGGTCGGACCC
T ACT
GAM1338 360 F11R 1 16292 NP_058642.1 3 2147 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 F11R 1 16292 NP_653085.1 3 2147 GCTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 F11R 1 16292 NP_653086.1 3 2149 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 F11R 1 16292 NP_653087.1 3 2149 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 F2RL3 1 13324 NP_003941.1 3 3004 GCGCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 F3 1 15547 NP_001984.1 3 424 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTAGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 F5 1 4594 NP_000121.1 5 45 CAAGCGCTGCCC A ---- -- A 3 C c c
AGGTCCTGGGGT CTGC ACTCCAG CCTGGGCA
GGTGGCAG GACG TGGGGTC GGACCCGT
- GTGG CT C

GAM1338 360 F8A 1 16334 NP_036283.2 3 50 TTCTTTTTGCCC AC C---- - 3 C c c
AGGCCTGGACTT TGCA TCCAG CCTGGGCAA
TTTGCATC ACGT AGGTC GGACCCGTT
CT TTTTC C

GAM1338 360 FAM13A1 1 17686 NP_055698.1 3 625 TGCATCTGCCCA - GCC A 3 C c c
CGATGGCAGTGC ACTGCACT CCA TGGGCA
AGTCATCA TGACGTGA GGT ACCCGT
C AGC C

GAM1338 360 FANCE 1 16751 NP_068741.1 3 279 GCTCTGTCATCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGATGC TGACGTGAGGTCGGACCT
ACT

GAM1338 360 FANCF 1 14445 NP_073562.1 3 737 GCTCTGTCACCC C CAA 3 C c c
AGTCTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGTGT TGACGTGAGGTC GACCC
T ACT

GAM1338 360 FBXL7 1 10986 NP_036436.1 3 967 TCCTCTTTTGCC T C G 3 C c c
AGGCTGGATGCT AC GCA TCCAGCCTGG CAA
GTCGTCTC TG CGT AGGTCGGACC GTT
T - -

GAM1338 360 FCAR 3 441 NP_579813.1 3 242 GCTCTTTCGCCA G AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCT GGC
AGTGGCAC TGACGTGAGGTCGGA CCG
A CT

GAM1338 360 FCAR 3 441 NP_579814.1 3 242 GCTCTTTCGCCA G AA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCT GGC
AGTGGCAC TGACGTGAGGTCGGA CCG
A CT

GAM1338 360 FCAR 3 10505 NP_001991.1 3 157 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGAGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FCAR 3 18209 NP_579803.1 3 157 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCAR 3 18209 NP_579805.1 3 157 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCAR 3 18209 NP_579806.1 3 157 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCAR 3 18209 NP_579807.1 3 157 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCAR 3 18209 NP_579808.1 3 281 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCAR 3 18209 NP_579811.1 3 157 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCAR 3 18209 NP_579812.1 3 157 GCTCTGTCACCC C CAA 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGAGC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 FCGR2A 1 10188 NP_067674.1 3 522 AATCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGC TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 FER1L4 1 1759 XP_300246.1 3 221 GCTCTGTCTCCC CA 3 C b b
AGGTTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTTGGACCC TG
TC

GAM1338 360 FER1L4 1 1759 XP_300246.1 3 370 GCTCTGTCTCCC CA 3 C b b
AGGTTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTTGGACCC TG
TC
GAM1338 360 FGD2 1 14487 NP_775829.1 3 549 ACTCTGTTTCCC AC----- C 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
ACAAACAT ACGTGAGGTCGGACCC TTG
TACAAAC T
GAM1338 360 FGF5 1 3375 NP_004455.1 3 2381 TGCTCTGTCACC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCAT TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 FGF5 1 3375 NP_149134.1 3 2712 TGCTCTGTCACC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCAT TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 FHL2 1 19820 NP_001441.2 5 448 GCTTTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 FISH 1 16564 NP_055446.1 5 208 GCTCTGTTGCTC C 3 C b b
AGGCTGGATTGC ACTGCA TCCAGCCTGGGCAAC
AGTGGCGT TGACGT AGGTCGGACTCGTTG
T
GAM1338 360 FKBP9 1 2718 NP_009201.1 3 805 CCGTTTGTCGCC -- 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCAA
AGTGGTGC TGACGTGAGGTCGGACC TGTT
GC
GAM1338 3600 FLJ0006 1 13800 XP_028154.1 5 29 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 3601 FLJ1010 2 9878 NP_078994.1 3 1313 TCAGGCTTGCCC T -- AG-- 3 C c b
AGGAAAGGGGCT AC GCAC TCC CCTGGGCAA
GTGCTGTC TG CGTG GGG GGACCCGTT
T TC GAAA
GAM1338 3601 FLJ1010 2 10153 NP_078994.1 3 252 GCTGTGTGGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
GT
GAM1338 3608 FLJ1029 1 468 NP_060520.2 3 183 GCTTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTAGCAC TGACGTGAGGTCGGACCCGTTG
GAM1338 3606 FLJ1034 1 7836 NP_060535.1 5 99 GCTCTGTCTCCC C CA 3 C c c
AGGCTGAAGTGC ACTGCACT CAGCCTGGG AC
AGTGGCAC TGACGTGA GTCGGACCC TG
A TC
GAM1338 360 FLJ1052 1 8795 NP_060594.2 3 1710 GAGTGGTTGCCC C- CCA 3 C c c

0 AGGCCTAGTTTC ACTG ACT GCCTGGGCAAC
AGTGGCAG TGAC TGA CGGACCCGTTG
TT TC-

GAM1338 360 FLJ1053 1 10633 NP_060599.1 3 805 ACTCTGTCACCC CAA 3 C c c
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ1056 1 16115 NP_060608.1 3 189 GTTCTGTCGCCC T AA 3 C c c
0 AGGCTGGCGTGC ACTGCAC CCAGCCTGGGC
AGTGGCGC TGACGTG GGTCGGACCCG
C CT

GAM1338 360 FLJ1056 1 7662 NP_060612.1 5 55 TCATGTCTGCCC - C AG A 3 C c c
9 AGGGGGACTGCG ACT GCA TCC CCTGGGCA
AGTTCCTG TGA CGT AGG GGACCCGT
G C G- C

GAM1338 360 FLJ1064 1 16789 NP_061896.1 5 68 CACTCTGCTGCC C A 3 C b b
0 TAGGCTGAGTGC ACTGCACTC AGCCTGGGCA
AGTGGTGT TGACGTGAG TCGGATCCGT
- C

GAM1338 360 FLJ1071 1 12092 NP_060659.1 3 359 TCACTGTTGCCC 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 FLJ1074 1 2269 NP_060671.2 3 1397 GAGCTGTTCCCA A------- AC - C 3 C c
c
3 GGGCTGGAGCAG CTGC TCCAGCC TGGG AAC
GTGTACCC GACG AGGTCGG ACCC TTG
CCCATGTG -- G -

GAM1338 360 FLJ1084 1 13800 NP_060711.1 3 351 GCTCTGTCACCC CAA 3 C c c
6 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ1084 1 18108 NP_060712.2 3 489 GCTCTGTCATGC --- A 3 C c c
7 AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
GGTGGTGC TGGCGTGAGGTCGGAC CTGT
GTA C

GAM1338 360 FLJ1090 1 13292 NP_060735.1 3 883 GCTCTGTCGCCC T C AA 3 C c
c
1 AGGCTGGAATGC AC GCA TCCAGCCTGGGC
TGTAGCAA TG CGT AGGTCGGACCCG
T A CT

GAM1338 360 FLJ1092 1 6574 NP_060743.1 3 2050 CGCTTGTTGCCC AC----- C 3 C c
c
2 AGGCTGGAATGC TGCA TCCAGCCTGGGCAAC
AATGGCGT ACGT AGGTCGGACCCGTTG
TGCGGTA A

GAM1338 360 FLJ1127 1 7307 NP_060845.1 5 53 CCGGGTCAAGGC CA T AA 3 C c
c
4 CCGGTCGAGTGC ACTGCACTC GCC GGGC
AGTACCAT TGACGTGAG TGG CCCG

C- - GA

GAM1338 360 FLJ1132 1 13280 NP_060860.1 3 97 CTCTCGTTGCCG G 3 C b b
3 AGGCTGGAGTGT ACTGCACTCCAGCCT GGCAAC
AGTAGTGT TGATGTGAGGTCGGA CCGTTG
G

GAM1338 360 FLJ1146 1 9552 NP_079239.2 3 144 TTCCTGTCACCC C CAA 3 C c c
7 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCGT TGAC TGAGGTCGGACCC
A ACT

GAM1338 360 FLJ1171 1 6034 NP_079122.1 3 1010 GCTCTGTCTCCC CA 3 C b b
0 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
TC

GAM1338 360 FLJ1171 1 4281 NP_078840.1 3 897 ACACCGTTGCCC A 3 C b b
5 AGGCTGGAGGGC ACTGC CTCCAGCCTGGGCAAC
AGTGACGT TGACG GAGGTCGGACCCGTTG
G

GAM1338 360 FLJ1178 1 11128 NP_079167.1 3 56 GGAAAGTTGCCC GC - AG- - 3 C c
c
3 AAGGAAGGGAAG ACT ACT CC CCT GGGCAAC
TTGAGTTC TGA TGA GG GGA CCCGTTG
GT A GAA A

GAM1338 360 FLJ1180 1 17222 NP_079250.1 3 1241 TCACTGTCACCC A CAA 3 C c
c
0 AGGCCGGAGTGC ACTGCACTCC GCCTGGG
AGTGGCAC TGACGTGAGG CGGACCC
C ACT

GAM1338 360 FLJ1236 1 14486 NP_115543.1 3 50 TCACCGTCCCCC T CA 3 C c c
3 AGGCTGGAGTGC AC GCACTCCAGCCTGGG AC
CGTGGCGT TG CGTGAGGTCGGACCC TG
C CC

GAM1338 360 FLJ1240 1 19506 NP_079381.1 3 1234 CTCTTGTTGATG GGG 3 C b
b
9 AGGCTGGAGTGC ACTGCACTCCAGCCT CAAC
AGTGGCGC TGACGTGAGGTCGGA GTTG
GTA

GAM1338 360 FLJ1257 1 14282 NP_075056.2 5 116 GCTCTGTCACCC C CAA 3 C c
c
2 AGGCTGGAGTAT ACTG ACTCCAGCCTGGG
AGTGGTGT TGAT TGAGGTCGGACCC
A ACT

GAM1338 360 FLJ1258 1 13509 NP_078896.2 5 37 GCTGTCTCACCC CAA 3 C c c
6 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ1264 1 1963 XP_291344.1 3 950 GCTCTGTTGCCC C 3 C b b
9 AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
AGTGGCGT TGACGT AGGTCGGACCCGTTG
A

GAM1338 360 FLJ1268 1 4553 NP_079193.2 3 211 TCACTCTTGCCC T 3 C b b

7 AGGCTGGGGTGT AC GCACTCCAGCCTGGGCAA
CGTGGCGT TG TGTGGGGTCGGACCCGTT
C

GAM1338 360 FLJ1278 1 8076 NP_115551.1 3 1019 GCTTTATCGCCC C AA 3 C c c
7 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGC
AGTGATGC TGAC TGAGGTCGGACCCG
A CT

GAM1338 360 FLJ1280 1 3651 NP_075054.1 3 1086 CACTGGCTGCCC ACTC A 3 C c
c
0 AGGCTGAATGGC ACTGC CAGCCTGGGCA
AGTGCCTG TGACG GTCGGACCCGT
GTAA C

GAM1338 360 FLJ1288 1 1302 NP_079221.1 3 240 GCTCTGTTGCCC C 3 C b b
8 AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGCAT TGACGTGAG TCGGACCCGTTG
A

GAM1338 360 FLJ1290 1 15276 NP_073590.1 3 1558 CTGTTGTTGCCC AC----- 3 C c c

3 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA

GAM1338 360 FLJ1296 1 3109 NP_078914.1 3 1534 GCTCTGTCGCCC AA 3 C b b
0 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 FLJ1297 1 14027 NP_079184.1 3 294 CTCTTGTTGCCC AC----- 3 C c c
3 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATAGCGC ACGTGAGGTCGGACCCGTTG
CGCGATA

GAM1338 360 FLJ1297 1 836 NP_079085.2 3 354 TCTCTGTCACCC CAA 3 C c c
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGCACA TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ1298 1 6642 XP_290685.1 3 1797 AAAACCAAGCCC A A AA 3 C c c

6 AGGCCGGGGGCG ACTGC CTCC GCCTGGGC
GTGGCTCA TGGCG GGGG CGGACCCG
- C AA

GAM1338 360 FLJ1307 1 6870 XP_117117.2 3 697 GCTCTGTCGGCC --- A 3 C c c
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCAT TGACGTGAGGTCGGACC TGT
GGC C

GAM1338 360 FLJ1311 1 7621 NP_078817.1 3 609 ACTCTGTCGCCC C AA 3 C c c
4 AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGCGT TGACGT AGGTCGGACCCG
A CT

GAM1338 360 FLJ1318 1 12816 NP_071346.1 3 413 GCTCTGTCACCC C CAA 3 C c
c
8 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTAGCAC TGACGTGAG TCGGACCC

A ACT

GAM1338 360 FLJ1318 1 11334 NP_079158.1 3 2176 AAACTTTGCTTC TG - T - 3 C c c
9 AGGCTGGGTAGT AC C AC CCAGCCTGG GCAA
GGTAGAGG TG G TG GGTCGGACT CGTT
GT A - T

GAM1338 360 FLJ1319 1 7946 NP_078890.1 3 402 ACTCTGTTGCCC 3 C b b
7 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 FLJ1326 1 1789 NP_079401.2 3 1173 ATTATTGCTCAC A---- A- - - 3 C c c
3 AGGCTGGGGAGG CTGC CTCCAGCCTG G GCAA
CAGAATGA GACG GGGGTCGGAC C CGTT
AGTAA GA A T

GAM1338 360 FLJ1345 1 5409 XP_038291.5 3 2587 ACTCTGTCGCCC C AA 3 C c c
6 AAGCTGGAGTGC ACTGCACTCCAGC TGGGC
AGTGGCAC TGACGTGAGGTCG ACCCG
A CT

GAM1338 360 FLJ1359 1 6935 NP_079116.2 5 97 CCCCGCAAAATC C ---- AA 3 C c c
0 AGGCTTGAGTGC ACTGCACTC AGCCTGG GC
AGTGGCGC TGACGTGAG TCGGACT CG
T AAAA CC

GAM1338 360 FLJ1376 1 4401 NP_079288.1 3 4075 TTAAAATTGCCC AC--- - G- 3 C c c
9 AGGGATGGTGGT TGCACT CCA CCTGGGCAA
GCACACTT ACGTGG GGT GGACCCGTT
TTCAC T AG

GAM1338 360 FLJ1391 1 8349 NP_073617.1 3 1667 TGGGATTGGCCC T- C AA 3 C c
c
0 AGCTTGGAGTGC AC GCACTCCAG CTGGGC
TTGTGTGG TG CGTGAGGTT GACCCG
TT C GT

GAM1338 360 FLJ1398 1 16972 NP_079046.1 5 244 ACTCTGTCACCT CAA 3 C c c
4 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGATCC
ACT

GAM1338 360 FLJ1432 1 14346 NP_079188.1 3 4478 CCAAGGTCCCTC ---- T- CA 3 C c
c
7 AGGCTGGTTGTG ACTG CAC CCAGCCTGGG AC
AAATCAGT TGAC GTG GGTCGGACTC TG
TAAA TT CC

GAM1338 360 FLJ1435 1 8244 NP_079008.1 3 316 GCTTTGTCGCCC AA 3 C b b
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAG TGACGTGAGGTCGGACCCG
CT

GAM1338 360 FLJ1444 1 16517 NP_116174.1 3 2235 ACTCTGTTACCC C C 3 C b b
2 AGGCTAGAGTGT ACTGCACTC AGCCTGGG AAC
AGTGGCAT TGATGTGAG TCGGACCC TTG
A A

GAM1338 360 FLJ1480 1 3409 NP_116231.1 3 436 CTCTGTCAACGC C ---- A 3 C c c
3 AGACTGGAGTGC ACTGCACTCCAG CTG GGCA

AGTGGCAC TGACGTGAGGTC GAC CTGT
A GCAA C
GAM1338 360 FLJ1495 1 13179 NP_116255.1 3 571 TTCTTGTTGCCG AC----- G 3 C c c
7 AGGCTGGAGTGC TGCACTCCAGCCT GGCAAC
AATGGCGC ACGTGAGGTCGGA CCGTTG
CGCGGTA G
GAM1338 360 FLJ2004 1 19070 NP_060108.1 3 131 GCTTTGTTTCCC C 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCAC TGACGTGAGGTCGGACCC TTG
T
GAM1338 360 FLJ2007 1 6780 NP_060126.1 3 2036 CTCTTGTTGCCC AC----- 3 C c c
9 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTAT ACGTGAGGTCGGACCCGTTG
TATGGTA
GAM1338 360 FLJ2009 1 13800 NP_060136.1 3 1357 GCTCTGTCACCC CAA 3 C c c
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 FLJ2013 1 15523 NP_060154.1 3 460 GCTCTGTCGCCC C AA 3 C c c
6 AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGTGC TGACGT AGGTCGGACCCG
A CT
GAM1338 360 FLJ2014 1 11745 NP_060157.1 3 398 GCTGTGTTGCCC A----- C 3 C c c
7 AGGCTAGAGTGC CTGCACTC AGCCTGGGCAAC
AGCAGTGA GACGTGAG TCGGACCCGTTG
AGTGAC A
GAM1338 360 FLJ2024 1 19728 NP_060193.1 3 2298 CTCTTGTTGCCC AC----- 3 C c c
5 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGACAC ACGTGAGGTCGGACCCGTTG
CACAGTA
GAM1338 360 FLJ2030 1 5707 NP_060228.1 3 703 CTTGGGCTGCTG -- AG G A 3 C c
c
8 AGGGGCTAGTGC ACTGCACT CC CCT GGCA
AGTGGTCC TGACGTGA GG GGA TCGT
TC -- G C
GAM1338 360 FLJ2030 1 2478 NP_060229.1 3 488 GGGTCCTTGCCC - T GC--- 3 C c c
9 AGTCAGATGGTG ACTG CAC CCA CTGGGCAA
TGCCAGTC TGAC GTG GGT GACCCGTT
C T AGACT
GAM1338 360 FLJ2032 1 9740 NP_060235.1 3 459 AGCAGCTTGCCC A---- A- - C 3 C c c
0 AGCTAGGAGCAG CTGC CTCC AGC TGGGCAA
CAGCAACA GACG GAGG TCG ACCCGTT
ACAAC AC A -
GAM1338 360 FLJ2050 1 2719 NP_060315.1 3 121 GACTGTTGCACC A---- AC - - 3 C c c

2 AGGCTGAGAAAG CTGC TC CAGCCTGG GCAAC
CAGCAATA GACG AG GTCGGACC CGTTG
ATAAC AA A A

GAM1338 360 FLJ2051 1 969 NP_060323.1 3 675 CTCTTGTCACCC CAA 3 C c c
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ2067 2 10861 NP_060394.1 3 1538 GGTCTGTTGCCC 3 C b b
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 FLJ2067 2 13745 NP_060394.1 3 629 GGTTGTCACTTA C G---- 3 C c b
1 AGTTTGGAGTGC ACTGCACTCCAG CT GGCAAC
AGTGGCAT TGACGTGAGGTT GA CTGTTG
T ATTCA

GAM1338 360 FLJ2070 1 20156 NP_060402.1 3 423 GCTCTCTCGCCC AA 3 C b b
0 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 FLJ2081 1 18464 NP_060431.1 3 95 ACTCTTTCACCC CAA 3 C c c
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ2088 1 6236 NP_079475.1 5 234 AACTGCTTGCCC - C G 3 C c c
6 AGGGTGCAGTGT ACT GCACT CA CCTGGGCAA
GAGTGTGA TGA TGTGA GT GGACCCGTT
G C G

GAM1338 360 FLJ2130 1 11446 NP_075052.1 3 1026 GCACTGTCTCCC A----- C CA 3 C c
c
2 AGGCTGGACTGC CTGCA TCCAGCCTGGG AC
AGCAGCGC GACGT AGGTCGGACCC TG
CGCGAC C TC

GAM1338 360 FLJ2160 1 11662 NP_079038.1 3 481 GCTCTGTCACCC C CAA 3 C c
c
3 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAT TGAC TGAGGTCGGACCC
A ACT

GAM1338 360 FLJ2167 1 1926 NP_112160.1 5 801 CTTCTGTCACCT CAA 3 C c c
3 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
AGTGACAT TGATGTGAGGTCGGATCC
ACT

GAM1338 360 FLJ2184 1 5009 NP_078885.1 3 75 GGAGTGATGAAC AC GG A 3 C c
c
1 GGGCTGGAGCAG ACTGC TCCAGCCTG CA
TCTGAGGA TGACG AGGTCGGGC GT
-- AA A

GAM1338 360 FLJ2202 1 10676 NP_079225.2 3 2125 AAAATCTGTCTC -- - - A 3 C c c
9 AGGCTGGTAGTT ACTGC ACT CCAGCCTG GGCA
AGCAGTTG TGACG TGA GGTCGGAC CTGT
AT T T C

GAM1338 360 FLJ2216 1 2733 NP_078809.2 5 475 CACTCTTCACTC C CAA 3 C c c
7 AGGCTGCAGTGC ACTGCACT CAGCCTGGG
AGTGGCGC TGACGTGA GTCGGACTC
C ACT
GAM1338 360 FLJ2232 1 10803 NP_078932.2 3 527 TCTCTGTCACCC CAA 3 C c c
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 FLJ2253 1 3548 NP_078926.2 5 341 ACTCTGTTACCC A C 3 C b b
1 AGGCCGGAGTGC ACTGCACTCC GCCTGGG AAC
AGTGGCGC TGACGTGAGG CGGACCC TTG
C A
GAM1338 360 FLJ2296 1 9754 NP_071384.1 3 231 GCTCTTTCGCCC G AA 3 C c c
5 AGGATGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGTGC TGACGTGAGGT GGACCCG
A CT
GAM1338 360 FLJ2305 1 16973 NP_075058.1 3 211 GCTCTATTGCCC 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCTC TGACGTGAGGTCGGACCCGTT

GAM1338 360 FLJ2318 1 10010 NP_078892.1 3 367 CGTTCTGTCGCT C AA 3 C c c
6 TAGCTGGAGTGC ACTGCACTCCAGC TGGGC
GGTGGCGT TGGCGTGAGGTCG ATTCG
- CT
GAM1338 360 FLJ2326 1 13801 NP_079391.1 5 181 ACTCTGTCGCCC AA 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 FLJ2335 1 14440 NP_115613.1 3 240 GCTCTGTTGCTG G 3 C b b
6 AGGCTGGAGTGC ACTGCACTCCAGCCT GGCAAC
AGTGATGT TGACGTGAGGTCGGA TCGTTG
G
GAM1338 360 FLJ2339 3 431 NP_079060.1 3 196 ACTCTGTCACCC C CAA 3 C c b
2 AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGCGC TGACGTGAGGTC GACCC
A ACT
GAM1338 360 FLJ2339 3 4022 NP_079060.1 3 606 ACTCTGTCCCCC CA 3 C b b
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
CC
GAM1338 360 FLJ2339 3 11425 NP_079060.1 3 496 GCTCTGTCACTG G CAA 3 C c
b
2 AGGCTGGAGTGC ACTGCACTCCAGCCT GG
AGTGGCGC TGACGTGAGGTCGGA TC
G ACT
GAM1338 360 FLJ2341 1 4771 NP_115614.1 3 1322 CCTCTGTTGCCC 3 C b b
6 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 FLJ2355 1 436 NP_079156.1 3 424 GCTCTGTCGCCC AA 3 C b b

6 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 FLJ2356 1 12755 XP_041701.4 3 1723 CTCTTGTTGCCC AC----- C 3 C c c

3 AGGCTAGAGTGC TGCACTC AGCCTGGGCAAC
AATGGCAC ACGTGAG TCGGACCCGTTG
CACGGTA A

GAM1338 360 FLJ2579 1 18075 NP_689633.1 3 562 GCTCTGTCTCCC A CA 3 C c c

5 AGGCCGGAGTGC ACTGCACTCC GCCTGGG AC
AGTGGCAC TGACGTGAGG CGGACCC TG
C TC

GAM1338 360 FLJ3050 1 15050 NP_694555.1 5 67 ACCCTGTTGCCC CAC 3 C b b

7 AGGCTGGAATAC ACTG TCCAGCCTGGGCAAC
AGTGGCAC TGAC AGGTCGGACCCGTTG
ATA

GAM1338 360 FLJ3053 1 15898 NP_653325.1 3 190 CTCTTGTTGCCC C 3 C b b

2 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGTAT TGAC TGAGGTCGGACCCGTTG
A

GAM1338 360 FLJ3113 3 1817 NP_775928.1 3 690 CTCTTGTCACCC A CAA 3 C c c

9 AGGCAGGAGTGC ACTGCACTCC GCCTGGG
AGTGGCGT TGACGTGAGG CGGACCC
A ACT

GAM1338 360 FLJ3113 3 7279 NP_775928.1 5 144 CCTCTCTGGCCC C AA 3 C c c

9 AAGCTGGAGTGC ACTGCACTCCAGC TGGGC
AGTGGCAC TGACGTGAGGTCG ACCCG
A GT

GAM1338 360 FLJ3113 3 19693 NP_775928.1 3 396 CTCTTGTTGCCC AC----- 3 C c c

9 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA

GAM1338 360 FLJ3115 1 13799 NP_653201.1 3 274 GCTCTGTCACCC C CAA 3 C c

c

3 AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGCAC TGACGTGAGGTC GACCC
A ACT

GAM1338 360 FLJ3133 1 7114 NP_689682.1 3 267 CTCTTGTTGCCC AC----- C 3 C c c

8 ACGCTGGAGTGC TGCACTCCAGC TGGGCAAC
AATGGTGC ACGTGAGGTCG ACCCGTTG
CGTGGTA C

GAM1338 360 FLJ3139 1 7878 NP_694569.1 5 139 GCTTTGTTGCCC ACT----- 3 C c c

3 AGGCTGGAGTGC GCACTCCAGCCTGGGCAAC
CTTGGCGC CGTGAGGTCGGACCCGTTG
CGCGGTTC

GAM1338 360 FLJ3140 1 11498 NP_689877.1 3 350 GCTCTGTTGGCC G 3 C b b

1 AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGTTCG TGACGTGAGGTCGGACC GTTG
G

GAM1338 360 FLJ3182 1 17212 NP_694574.1 5 97 TAGGTGTTGCCC - CCAGCC 3 C c

c

1 AAATTCAGTGTC ACTG CACT TGGGCAAC
AGTGAAGT TGAC GTGA ACCCGTTG
T CTTAA-
GAM1338 360 FLJ3209 2 11067 NP_776156.1 3 1415 TCTTTGTTGCCC AC----- 3 C c c
6 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA
GAM1338 360 FLJ3209 2 20189 NP_776156.1 3 1112 GCTCTGTTGCCC AC----- 3 C c c
6 AGGCTGGAGTGT TGCACTCCAGCCTGGGCAAC
AATGGTGC ATGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 FLJ3213 3 5404 NP_689671.2 3 1439 CTCTTGTTGCCC AC----- C 3 C c b
0 AGGCTAGAGTGC TGCACTC AGCCTGGGCAAC
AATGGCAT ACGTGAG TCGGACCCGTTG
TACGGTA A
GAM1338 360 FLJ3213 3 9100 NP_689671.2 3 518 GCTCTGTCGCCC AA 3 C b b
0 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 FLJ3213 3 17307 NP_689671.2 3 1142 TCTCTGTTGCCT TG 3 C b b
0 GGGCTGGAGTGC ACTGCACTCCAGCC GGCAAC
AGTGGCCC TGACGTGAGGTCGG CCGTTG
GT
GAM1338 360 FLJ3220 1 14825 NP_689710.1 3 40 ACTCTGTCGCCC A AA 3 C c c
6 AGGCTGGAGGGC ACTGC CTCCAGCCTGGGC
AGTGGCGT TGACG GAGGTCGGACCCG
G CT
GAM1338 360 FLJ3249 1 2883 NP_653208.1 3 743 GCTCTGTCACCC C CAA 3 C c c
9 AGTCTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGCAA TGACGTGAGGTC GACCC
T ACT
GAM1338 360 FLJ3273 1 7308 NP_689632.1 3 732 CAGCCGCTGCCC T - AG A 3 C c
c
1 AGGGGAGTGGCT AC GC ACTCC CCTGGGCA
GTGGGGAG TG CG TGAGG GGACCCGT
T G -- C
GAM1338 360 FLJ3280 1 7824 NP_694584.1 3 642 ACTCTGTCACCC CAA 3 C c c
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGA TGACGTGAGGTCGGACCC
ACT
GAM1338 360 FLJ3289 1 3716 NP_653268.1 3 703 ACTCTGTTGTCC A----- 3 C c c
4 AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGCGATAT GACGTGAGGTCGGACCTGTTG
TATAGC
GAM1338 360 FLJ3293 1 4748 NP_690873.1 3 603 GCTCTGTCACCC CAA 3 C c c
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGCTGT TGACGTGAGGTCGGACCC

ACT
GAM1338 360 FLJ3331 1 17978 NP_694961.1 3 206 GTCCTGAGGGTT - -------- AA 3 C c c
8 AGGCTGGAGTGA ACTG CACTCCAGCCT GGGC
CAGTTTCC TGAC GTGAGGTCGGA CCTG
A TTGGGAGT --
GAM1338 360 FLJ3350 1 2450 NP_689530.1 3 740 ACACTGTTGCCC 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGACGC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 FLJ3365 1 6177 NP_775912.1 3 325 GCTCTGTTGCCC AC----- 3 C c c
5 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
ACTGGCTT ACGTGAGGTCGGACCCGTTG
TTCGGTC
GAM1338 360 FLJ3481 2 434 NP_689516.1 3 206 AGTCTGCCACCC C CAA 3 C c c
7 AGGCTGGAGTCC ACTG ACTCCAGCCTGGG
AGTGGCGT TGAC TGAGGTCGGACCC
C ACC
GAM1338 360 FLJ3481 2 10174 NP_689516.1 5 270 CCCGCTGGTCCC T C - AA 3 C c
c
7 AGGCTGGATTGC AC GCA TCCAGCCTGGG C
CGTGGCAC TG CGT AGGTCGGACCC G
C T T GT
GAM1338 360 FLJ3492 1 14214 NP_689483.1 5 151 ACTTTGACCCCC CAA 3 C c c
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
CCA
GAM1338 360 FLJ3496 1 6348 XP_114353.1 3 1547 CTCTTGTTGCCC AC----- 3 C c c
9 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA
GAM1338 360 FLJ3510 1 6840 NP_689890.1 5 160 GCTCTGTCGTCC T AA 3 C c c
5 AGGCTGGAGTGC AC GCACTCCAGCCTGGGC
CGTGGCGT TG CGTGAGGTCGGACCTG
C CT
GAM1338 360 FLJ3568 2 3105 NP_787096.1 3 1070 ACTCTGTCACCC C CAA 3 C c
b
1 AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGCAC TGACGTGAGGTC GACCC
A ACT
GAM1338 360 FLJ3568 2 10703 NP_787096.1 3 1369 ACTCTGTTGCCC CAC 3 C b
b
1 AGGCTGGACTAC ACTG TCCAGCCTGGGCAAC
AGTGGCAC TGAC AGGTCGGACCCGTTG
ATC
GAM1338 360 FLJ3584 1 12720 XP_290755.1 3 1061 ACTTTGTCACCC C CAA 3 C c
c
8 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGCAT TGACGTGAG TCGGACCC
A ACT

GAM1338 360 FLJ3644 1 10632 NP_694965.1 3 230 ACTCTGTCACCC CAA 3 C c c
5 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
AGTGGTGC TGATGTGAGGTCGGACCC
ACT
GAM1338 360 FLJ3704 1 6414 NP_787085.1 3 764 TCTCTGTCGCCC C AA 3 C c c
5 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGC
AGTGGTGC TGAC TGAGGTCGGACCCG
A CT
GAM1338 360 FLJ3707 1 3106 NP_694588.1 5 42 ACTCTGTCACCC CAA 3 C c c
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 FLJ3726 1 9900 NP_787088.1 3 1282 TACTCCTTGCCT A--- C-- 3 C c c
6 AGGCTGGAGTTT CTG ACTCCAGCCTGGGCAA
ACAGAGAC GAC TGAGGTCGGATCCGTT
CAGA ATT
GAM1338 360 FLJ3730 1 11542 NP_694941.1 3 251 TTAGGGTTTTTC CA T C 3 C c c
0 AGGCTGGGCACA ACTG C CCAGCCTGGG AAC
GTGACTCA TGAC G GGTCGGACTT TTG
AC - T
GAM1338 360 FLJ3743 1 18178 NP_848612.1 3 197 GCTCTGTTACCC C 3 C b b
3 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG AAC
AGTGGTGC TGATGTGAGGTCGGACCC TTG
A
GAM1338 360 FLJ3754 1 435 NP_775938.1 3 743 GCTCTGTTGCCC 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 FLJ3797 1 13645 XP_290514.1 3 1354 ACGAGCAGCTCC C- - AA 3 C c
c
0 AGGCTGGAGTTC ACTG ACTCCAGCCTGG GC
TGGTTCTT TGGT TGAGGTCGGACC CG
CT T AC
GAM1338 360 FLJ3810 1 6516 NP_694993.2 3 741 CGCTCTGTTGCC A G 3 C b b
1 AGGCTGGAGGGC ACTGC CTCCAGCCTGG CAAC
AGTGGCAC TGACG GAGGTCGGACC GTTG
G -
GAM1338 360 FLJ3814 3 2644 XP_091919.5 5 25 CCTCTATTGCCC 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTGT TGACGTGAGGTCGGACCCGTT

GAM1338 360 FLJ3814 3 11661 XP_091919.5 3 1431 ACTCTGTTGCCC 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 FLJ3814 3 12581 XP_091919.5 3 258 ACTCTGTCTCCC CA 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGAGT TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 FLJ3828 2 17962 NP_689814.1 3 1965 GCTCTGTCGCCC AA 3 C b b

1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTAC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 FLJ3828 2 19457 NP_689814.1 3 109 ACTCTGTTGCCC T 3 C b b
1 TGGCTGGAGTGC ACTGCACTCCAGCC GGGCAAC
AGTAGAGT TGACGTGAGGTCGG CCCGTTG
T

GAM1338 360 FLJ3860 1 3109 NP_689867.1 3 287 GCTCTGTCGCCC AA 3 C b b
7 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 FLJ3879 1 18182 NP_848615.1 3 1161 GCTCTGTCACCC CAA 3 C c c

2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ3881 2 3017 NP_665872.1 3 213 AGTCTCTTACCC C CAA 3 C c c
9 AGGCTAGGGTGC ACTGCACTC AGCCTGGG
AGTGGTGT TGACGTGGG TCGGACCC
A ATT

GAM1338 360 FLJ3881 2 3726 NP_665872.1 3 1040 GCTCTGTCACTC C CAA 3 C c
c

9 ATGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCGT TGACGTGAGGTCG ACTC
T ACT

GAM1338 360 FLJ3899 2 5383 NP_776188.1 3 730 ACTGTGTCACCC CAA 3 C c c
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ3899 2 7191 NP_776188.1 3 1036 TCTCTGTCACCT CAA 3 C c c
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT

GAM1338 360 FLJ3941 1 17781 NP_775952.1 3 341 GGTCTTTCACCC CAA 3 C c c
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGCTGT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ3959 3 7948 NP_776164.1 3 1103 GCTCTGTCACCC CAA 3 C c c
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 FLJ3959 3 16019 NP_776164.1 3 626 TTGCTGTCTCCC A T CA 3 C c c

9 CGGCTGGAGCGC ACTGC CTCCAGCC GGG AC
AGTGGCAC TGACG GAGGTCGG CCC TG
C C TC

GAM1338 360 FLJ3959 3 16634 NP_776164.1 3 808 GCTCTGTCGCCC C AA 3 C c c

9 AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTTGTGA TGACGT AGGTCGGACCCG

A CT
GAM1338 360 FLJ3963 2 7663 XP_290687.1 3 1661 GCACCAAGAACA ------ - - AA 3 C c c
9 ATGCTGGAGTGC ACTGCACTCCAGC CT GG GC
AGTGGCGT TGACGTGAGGTCG GA CC CG
TAACAA A A --
GAM1338 360 FLJ3963 2 13371 XP_290687.1 3 681 GCTCTGTCGTCC AA 3 C c c
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCTG
CT
GAM1338 360 FLJ3982 2 8171 NP_775971.1 3 1941 TCACTGTTATCC A----- GC 3 C c c
1 AGGCTGGAGTGC CTGCACTCCAGCCTGG AAC
AGAGGCAC GACGTGAGGTCGGACC TTG
CACGGA TA
GAM1338 360 FLJ3982 2 14284 NP_775971.1 3 611 GCTCTGTCACCT C CAA 3 C c
c
1 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGTGC TGACGTGAG TCGGATCC
A ACT
GAM1338 360 FLJ9023 1 18854 NP_775852.1 3 73 ACTTTGTCGCCC AA 3 C b b
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 FLJ9058 1 3767 NP_699176.1 3 751 CCTCTCCTGCCC A C -- A 3 C c c
6 AGGGGCTAGAGA ACTGC CTC AGCCT GGGCA
GCAGTCTC TGACG GAG TCGGG CCCGT
A A GA C
GAM1338 360 FLJ9072 1 16986 NP_787115.1 3 524 GCTCTGTCGCCC AA 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGCCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 FNBP1 1 8560 XP_052666.3 3 1011 GCTCTATTGTTC C 3 C b b
AGACTGGAGTGC ACTGCACTCCAG CTGGGCAA
AGTGGCAT TGACGTGAGGTC GACTTGTT
A
GAM1338 360 FSHPRH1 1 13800 NP_006724.1 5 14 GCTCTGTCACCC CAA 3 C c
c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 FSTL1 1 3666 NP_009016.1 3 253 AATGGTGCTCTG - A -- A 3 C c c
GGGCTGGAGGCT ACT GC CTCCAGCCT GGGCA
AGTAAGGA TGA CG GAGGTCGGG CTCGT
T - GT G
GAM1338 360 FUT1 2 3102 NP_000139.1 3 612 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG
GAM1338 360 FUT1 2 7472 NP_000139.1 3 934 GCTCTGTAGCCC CA AA 3 C c b
AGGCCAGAGTGC ACTGCACTC GCCTGGGC

AGTGGCGC TGACGTGAG CGGACCCG
AC AT
GAM1338 360 G1P3 1 14496 NP_002029.3 3 135 ACTATATTGTCC C 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAA
AGTGGCTA TGACGTGAG TCGGACCTGTT
A
GAM1338 360 G1P3 1 14496 NP_075010.1 3 135 ACTATATTGTCC C 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAA
AGTGGCTA TGACGTGAG TCGGACCTGTT
A
GAM1338 360 G1P3 1 14496 NP_075011.1 3 135 ACTATATTGTCC C 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAA
AGTGGCTA TGACGTGAG TCGGACCTGTT
A
GAM1338 360 G2A 1 8834 NP_037477.1 3 1256 GCTCTGTTGCCT CA TG 3 C c c
GGGCTGGAGAAC ACTG CTCCAGCC GGCAAC
AGTGGCAC TGAC GAGGTCGG CCGTTG
AA GT
GAM1338 360 G6PC 1 8902 NP_000142.1 3 1428 CACCTATCACCC G CAA 3 C c c
AGGCTGGAGTGG ACT CACTCCAGCCTGGG
AGTGGCAC TGA GTGAGGTCGGACCC
G ACT
GAM1338 360 GAL3ST-4 1 13405 NP_078913.3 3 251 GCTCTGTCCCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
CC
GAM1338 360 GBP4 1 12569 NP_443173.2 3 1417 GCTTTGACACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGCAC TGACGTGAGGTCGGACCC
ACA
GAM1338 360 GGA2 1 520 NP_055859.1 3 1711 ACTCTGTCACTC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
GGTGGTAT TGGCGTGAGGTCGGACTC
ACT
GAM1338 360 GGA2 1 520 NP_619581.1 3 2799 ACTCTGTCACTC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
GGTGGTAT TGGCGTGAGGTCGGACTC
ACT
GAM1338 360 GLP1R 1 13842 NP_002053.2 3 1213 TAGTGATGTTGT CAG TG 3 C c c
TTGGGAGAGTGC ACTGCACTC CC GGCAAC
AGTAGTAA TGACGTGAG GG TTGTTG
A-- GT
GAM1338 360 GM2A 1 2518 NP_000396.1 3 760 CGCTTTGTCACC -- 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCAA
AGTGGTGC TGACGTGAGGTCGGACC TGTT
AC
GAM1338 360 GNE 1 7151 NP_005467.1 3 616 GGCATGAACCCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCTC TGACGTGAGGTCGGACCC
CAA

GAM1338 360 GNPNAT1 2 10643 XP_085119.1 3 2180 TCGCTGTTGCCC A----- A C 3 C c c

AGGCTAGAGCGC CTGC CTC AGCCTGGGCAAC
AGGGGCAC GACG GAG TCGGACCCGTTG
CACGGG C A

GAM1338 360 GNPNAT1 2 19027 XP_085119.1 3 2470 ACTCCATCACCC C CAA 3 C c c

AGGCTGGAGTCC ACTG ACTCCAGCCTGGG
AGTGGTGT TGAC TGAGGTCGGACCC
C ACT

GAM1338 360 GNRPX 1 17848 NP_060519.1 3 146 ACTGTGTTGCCC C 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGTGC TGACGTGAG TCGGACCCGTTG
A

GAM1338 360 GOLGA3 1 9100 NP_005886.2 3 600 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT

GAM1338 360 GP5 1 18832 NP_004479.1 3 595 GCTCTGTGGCCC T AA 3 C c c
AGGCTGGCGTGC ACTGCAC CCAGCCTGGGC
AGTGGGCC TGACGTG GGTCGGACCCG
C GT

GAM1338 360 GPP34R 1 16162 NP_060648.2 3 870 TTGCTCTTGCCC C A 3 C b b
AGGCAGGAGTAC ACTG ACTCC GCCTGGGCAA
AGTAGTGC TGAC TGAGG CGGACCCGTT
A A

GAM1338 360 GPR114 1 13684 NP_722579.1 3 911 TTGAATTTGCCC A TG - ----- 3 C c c

AGGTAGGCGTGA C CACTC CA GCCTGGGCAA
GAGTGTGG G GTGAG GT TGGACCCGTT
- GT A GCGGA

GAM1338 360 GPR26 1 9581 NP_703143.1 3 1151 CTCTTATTGCCC AC----- C 3 C c c
AGGCTAGAGTGC TGCACTC AGCCTGGGCAA
AATGGTGC ACGTGAG TCGGACCCGTT
CGTGGTA A

GAM1338 360 GPR4 2 15917 NP_005273.1 3 284 GCCCAGGCTGGA AA 3 C b b
GTGCAGTAGTGC ACTGCACTCCAGCCTGGGC
AGTCGTGG TGACGTGAGGTCGGACCCG
--

GAM1338 360 GPR4 2 16936 NP_005273.1 3 280 ACTGTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTAGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 GPR56 1 6235 NP_005673.2 5 24 GCTCTGTCACAC --- A 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTGGTGT TGACGTGAGGTCGGAC CTGT
ACA C

GAM1338 360 GPR66 1 4149 NP_006047.2 3 529 ACTCTGTCGCCC C AA 3 C c c
AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCGC TGACGTGAG TCGGACCCG
A CT
GAM1338 360 GPR81 1 9012 NP_115943.1 3 374 ACTCTGTGTCCC - A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG CA
AGTGGCAC TGACGTGAGGTCGGACCC GT
T G
GAM1338 360 GR6 1 11621 NP_031380.1 5 286 GCTCTGTCACCC C CAA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCAT TGACGT AGGTCGGACCC
A ACT
GAM1338 360 GRAF 1 18118 NP_055886.1 3 2800 ACTCTGTGGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
GT
GAM1338 360 GREB1 2 2321 NP_055483.2 3 1721 CTCTTGCTGCCC AC----- A 3 C c c

AGGCTGGAGTGC TGCACTCCAGCCTGGGCA
AATGGTGC ACGTGAGGTCGGACCCGT
CGTGGTA C
GAM1338 360 GREB1 2 18182 NP_055483.2 3 1091 GCTCTGTCACCC CAA 3 C c
c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 GRID1 1 12320 XP_043613.8 3 2299 GGGGAGGTGCCC --- T G A 3 C c
c
AGGTGGGTGGAC ACTG CAC CCA CCTGGGCA
CAGTACTC TGAC GTG GGT GGACCCGT
CAG - - G
GAM1338 360 GRINL1A 1 17379 NP_056347.1 3 712 GCTCTGTCGCCC AA 3 C b b

AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAG TGACGTGAGGTCGGACCCG
CT
GAM1338 360 GRM6 1 5942 NP_000834.1 3 2443 GCTCAATTTCTT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATTC
TTT
GAM1338 360 GRWD 1 6811 NP_113673.2 3 372 GGTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTAGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 GSDM 2 3037 NP_835465.1 3 295 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCTT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 GSDM 2 13197 XP_209009.1 3 293 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG

AGTGGCTT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 GTF2IRD 1 3107 NP_115579.3 3 142 GCTCTGTCGCCC AA 3 C c c
2 AGGTTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTTGGACCCG
CT
GAM1338 360 GTF2IRD 1 3107 NP_775808.1 3 142 GCTCTGTCGCCC AA 3 C c c
2 AGGTTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTTGGACCCG
CT
GAM1338 360 GTPBG3 2 7742 NP_116009.1 3 466 TGTCTATTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTGC TGACGTGAGGTCGGACCCGTT

GAM1338 360 GTPBG3 2 15596 NP_116009.1 3 630 GCTCTGTCACCC C CAA 3 C c
b
AGGCTGGAGTTC ACTG ACTCCAGCCTGGG
AGTGGTGC TGAC TGAGGTCGGACCC
T ACT
GAM1338 360 GYG 1 10290 NP_004121.2 3 442 TTAGAATTGCCC G --- - 3 C b b
AGTGCTGCCAGA ACT CACTC CAGC CTGGGCAA
GTGAGTGA TGA GTGAG GTCG GACCCGTT
- ACC T
GAM1338 360 H-plk 1 8288 NP_056936.1 5 982 TGCTGTGTCACC G -- A 3 C c c
AGGATGGAGTGC ACTGCACTCCA CCTGG GCA
AGTGGCAT TGACGTGAGGT GGACC TGT
A AC G
GAM1338 360 H63 1 2008 NP_612432.2 3 464 GTCTTGTTTCCC AC----- C 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGCAC ACGTGAGGTCGGACCC TTG
CACGGTA T
GAM1338 360 H63 1 2008 NP_816929.1 3 464 GTCTTGTTTCCC AC----- C 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGCAC ACGTGAGGTCGGACCC TTG
CACGGTA T
GAM1338 360 HAVCR2 1 16518 NP_116171.2 3 496 GCTCTGTTGCCC AC----- 3 C c
c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 HE9 1 13755 NP_741997.1 3 209 GCTCTGTTGCCC AC----- C 3 C c c
AGCCTGGAGTGC TGCACTCCAG CTGGGCAAC
AATGGCAC ACGTGAGGTC GACCCGTTG
CACGGTA C
GAM1338 360 HECA 1 6145 NP_057301.1 3 1529 CTCTTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 HEMK 1 12517 NP_057257.1 3 1819 GGATGTTGCACC CAGC - 3 C c
c

AGAAGAGAGTGC ACTGCACTC CTGG GCAAC
AGTGTTGG TGACGTGAG GACC CGTTG
AGAA A

GAM1338 360 HEPH 1 4303 NP_055614.1 5 130 GCTGGCGGACTC -- CAA 3 C c c
AGGCTGGGGTCT ACTGC ACTCCAGCCTGGG
GCAGTGCA TGACG TGGGGTCGGACTC
TC AGG

GAM1338 360 HLCS 1 10628 NP_000402.2 5 179 GTTCTGTCGTCC AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCTG
CT

GAM1338 360 HMG20A 1 19141 NP_060670.1 3 1221 GCTGTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGCTA TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 HPRN 1 11574 NP_071938.1 3 220 CTGGCTCTGCCC G G A 3 C c c

AGGTGGGGTGGG ACT CACTCCA CCTGGGCA
GTGGCCCA TGG GTGGGGT GGACCCGT
G - C

GAM1338 360 HRH4 3 5920 NP_067637.2 3 1416 GCTCTGTCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGCAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 HRH4 3 12079 NP_067637.2 3 1949 GCTCTGTTGCCC A C 3 C b b
ACGCAGGAGTGC ACTGCACTCC GC TGGGCAAC
AGTGGCAT TGACGTGAGG CG ACCCGTTG
A C

GAM1338 360 HRH4 3 14595 NP_067637.2 3 1171 GCTCTGTCTCCC A CA 3 C c b
AGGCTGGAGCGT ACTGC CTCCAGCCTGGG AC
AGTAATGC TGATG GAGGTCGGACCC TG
C TC

GAM1338 360 HSD3B7 1 16293 NP_079469.2 3 209 GCTCTGTCACCC C CAA 3 C c
c

AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGTGT TGACGTGAGGTC GACCC
A ACT

GAM1338 360 HSMPP8 1 19749 XP_167894.1 3 329 CTCTTGTTGCCC AC----- 3 C c c

AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA

GAM1338 360 HSPC065 2 7511 NP_054876.2 3 2125 TCTCTGTCCCCA --- A 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCT GGGCA
AGTGGTGC TGACGTGAGGTCGGA CCTGT
ACC C

GAM1338 360 HSPC065 2 10877 NP_054876.2 3 2292 GCTCTGTCCCCC C CA 3 C c
c

ATGCTGGAGTGC ACTGCACTCCAGC TGGG AC
AGTGGCAT TGACGTGAGGTCG ACCC TG

T CC
GAM1338 360 HTR1D 1 14604 NP_000855.1 3 290 TGCCCTCTCGCC ------- A 3 C c c
AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCA
AGTGGCAC TGATGTGAGGTCGGA CCCGT
CCGCTCT -
GAM1338 360 HTR1E 1 9063 NP_000856.1 5 137 TCTCAGTCGCCC A----- AA 3 C c c
AGGCTGGAGTGC CTGCACTCCAGCCTGGGC
AGCAGCAC GACGTGAGGTCGGACCCG
CACGAC CT
GAM1338 360 HUNK 1 1413 NP_055401.1 3 2962 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 HUS1 1 11161 NP_004498.1 3 1023 ATTCTGTCACCC C CAA 3 C c c
AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGCCAC TGACGTGAGGTC GACCC
A ACT
GAM1338 360 HYAL4 1 19431 NP_036401.1 5 82 ACTCTGTTGCCC 3 C b b
AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGATGTGAGGTCGGACCCGTTG
GAM1338 360 ICAM1 1 18182 NP_000192.1 3 1134 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 ICK 1 3106 NP_055735.1 3 1469 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 ICK 1 3106 NP_057597.2 3 1469 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 IGF1 1 8230 NP_000609.1 3 5347 GCACTGTCCCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
CC
GAM1338 360 IL11 1 17785 NP_000632.1 3 699 GCTCTGTTGCCT 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGAGGC TGACGTGAGGTCGGATCCGTTG
GAM1338 360 IL16 1 11272 NP_757366.1 5 98 ACTCTGTTGCCC --- 3 C b b
AGGCTGGAGTTC ACTGC ACTCCAGCCTGGGCAAC
AGCGGTGC TGGCG TGAGGTCGGACCCGTTG
ACT
GAM1338 360 IL21R 1 2012 NP_068570.1 3 1361 CTCTCGTCGCCC C AA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGTGC TGACGT AGGTCGGACCCG
A CT

GAM1338 360 IL21R 1 2012 NP_851564.1 3 1361 CTCTCGTCGCCC C AA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGTGC TGACGT AGGTCGGACCCG
A CT
GAM1338 360 IL21R 1 2012 NP_851565.1 3 1361 CTCTCGTCGCCC C AA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGTGC TGACGT AGGTCGGACCCG
A CT
GAM1338 360 IL28RA 1 17486 NP_734464.1 3 2267 TTCTTTTTGCCT 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTAC TGACGTGAGGTCGGATCCGTT

GAM1338 360 IL28RA 1 17486 NP_775087.1 3 2267 TTCTTTTTGCCT 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTAC TGACGTGAGGTCGGATCCGTT

GAM1338 360 IL28RA 1 17486 NP_775088.1 3 2964 TTCTTTTTGCCT 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTAC TGACGTGAGGTCGGATCCGTT

GAM1338 360 IMPACT 1 19846 NP_060909.1 3 2006 GCTCTGTCACCT CAA 3 C c
c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGATCC
ACT
GAM1338 360 IMPDH1 1 15608 NP_000874.1 5 178 AGCGGGGAGCCC CA A AA 3 C c
c
AGGCGGAGCCCA ACTG CTCC GCCTGGGC
GTCGACTC TGAC GAGG CGGACCCG
CC - AG
GAM1338 360 INHBE 1 9633 NP_113667.1 3 663 CGCTCTGTCACC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGACAC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 INMT 1 3109 NP_006765.3 3 621 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 IRF4 1 16311 NP_002451.1 3 101 GCTCTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGACAC TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 IRTA1 1 18021 NP_112572.1 3 78 TGTCCAAAGTCC CCA - AA 3 C c c
CAGGCCCAGTGC ACTGCACT GCCTGGG C
AGTCCTTG TGACGTGA CGGACCC G
CC- T AA
GAM1338 360 IRX5 1 5486 NP_005844.1 5 297 TTGCCCCGTAGG A----- -- ---- 3 C c c
AAGCTGGAGTGC CTGCACTCCAGC CT GGGCA
GGGCCTCG GGCGTGAGGTCG GG CCCGT
GCTCCG AA ATGC

A
T

GAM1338 360 ITPR2 1 2513 NP_002214.1 3 273 GGCTTGCCCAAA A--- A-- --- 3 C c c
AGGCTGGAGAGG CTGC CTCCAGCCT GGGCAA
GCAGGGAG GACG GAGGTCGGA CCCGTT
GAGG GGA AAA
GAM1338 360 JAK3 1 6262 NP_000206.1 3 400 CGCTCGTTACCC G C 3 C b b
AGGGTGGAGTGC ACTGCACTCCA CCTGGG AAC
AGTGGTAG TGACGTGAGGT GGACCC TTG
G A
GAM1338 360 JM11 1 15361 NP_296375.1 3 1439 TGCTCTGTCACC A----- -- A 3 C c c
AGGCTGGAGTGC CTGCACTCCAGCCTGG GCA
AGCGGCGC GACGTGAGGTCGGACC TGT
CGCGGC AC C
GAM1338 360 JRK 1 1529 NP_003715.1 3 1241 ACTCTGTTGACC G G 3 C b b
AGGCTGGAGTGA ACT CACTCCAGCCTGG CAAC
AGTGGTGT TGA GTGAGGTCGGACC GTTG
A A
GAM1338 360 KCNE3 1 6918 NP_005463.1 3 962 CCTATGTCACCC TC CAA 3 C c
c
AGGCTGTGGTGC ACTGCAC CAGCCTGGG
AGTAAGCC TGACGTG GTCGGACCC
GT ACT
GAM1338 360 KCNJ11 1 9100 NP_000516.2 5 52 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 KCNJ16 1 10579 NP_061128.1 3 624 TGCTACTTGCCC -- CCA 3 C b b

AGGTAGTGATCA ACTG CACT GCCTGGGCAA
GTGAGAGT TGAC GTGA TGGACCCGTT
TA ---
GAM1338 360 KCNJ16 1 10579 NP_733937.1 3 624 TGCTACTTGCCC -- CCA 3 C b b

AGGTAGTGATCA ACTG CACT GCCTGGGCAA
GTGAGAGT TGAC GTGA TGGACCCGTT
TA ---
GAM1338 360 KCNJ16 1 10579 NP_733938.1 3 624 TGCTACTTGCCC -- CCA 3 C b b

AGGTAGTGATCA ACTG CACT GCCTGGGCAA
GTGAGAGT TGAC GTGA TGGACCCGTT
TA ---
GAM1338 360 KENAE 1 18180 NP_789786.1 3 210 GCTCTGTCACCC CAA 3 C c c

AGGTTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTTGGACCC
ACT
GAM1338 360 KIAA006 1 13142 NP_055691.1 3 626 CTCTTGTTGCCC AC----- 3 C c c

```
          3                    AGGCTGGAGTGC      TGCACTCCAGCCTGGGCAAC
                               AATGGCAC          ACGTGAGGTCGGACCCGTTG
                                     CACGGTA
GAM1338  360   KIAA008 1  14875 NP_055584.1  3  2189  ATTCTGTCACCC            CAA       3  C  c  c

          7                    AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                               AGTGGCGT    TGACGTGAGGTCGGACCC
                                           ACT
GAM1338  360   KIAA011 1  1353  XP_290939.1  3  247   CTGTTGTCTCCC            ---       3  C  b  b
          7                    AGGCTGGAGTGC ACTGCACTCCAGCCTGGG  CAAC
                               AGTGGCGT    TGACGTGAGGTCGGACCC  GTTG
                                           TCT
GAM1338  360   KIAA018 1  2720  XP_050495.4  3  2249  AGAGGTCTGCCC    A T  G     A       3  C  c
c
          2                    AGGGTGGGAGCA ACTGC C CCA CCTGGGCA
                               GTGTCACT    TGACG G GGT GGACCCGT
                                     A -  G      C
GAM1338  360   KIAA018 1  6841  NP_066545.1  3  1107  GTTCTGTCACCC            CAA       3  C  c  c
          6                    AGGCTGGGGTGC ACTGCACTCCAGCCTGGG
                               AGTGGCGT    TGACGTGGGGTCGGACCC
                                           ACT
GAM1338  360   KIAA020 1  17371 NP_055688.1  3  1257  ACTCTGTCACCC      C      CAA       3  C  c
c
          5                    AGGCTGTAGTGC ACTGCACT CAGCCTGGG
                               AGTGGCAT    TGACGTGA GTCGGACCC
                                        T       ACT
GAM1338  360   KIAA023 1  4878  NP_055562.1  3  5051  CCCCTGATGCCC A------    T       A    3  C  c
c
          7                    AGGCTGGGTGCA      CTGCAC CCAGCCTGGGCA
                               GGCTCTCA          GACGTG GGTCGGACCCGT
                                     ACTCTCG     -         A
GAM1338  360   KIAA029 1  19689 XP_042833.2  3  3372  AGCTGGAGGCCC    A-        AA       3  C  c
c
          5                    GGGCTGGAGGGG ACTGC  CTCCAGCCTGGGC
                               CAGTGTTG    TGACG  GAGGTCGGGCCCG
                                        GG          GA
GAM1338  360   KIAA043 1  14441 NP_055616.1  5  676   GCTCTGTCACCC        C    CAA       3  C  c
c
          5                    AGTTTGGAGTGC ACTGCACTCCAG CTGGG
                               AGTGGTGC    TGACGTGAGGTT GACCC
                                           T    ACT
GAM1338  360   KIAA044 1  20115 XP_044155.1  5  2279  TCACTGTCTCCT            CA        3  C  b  b
          6                    AGGCTGGAGTGC ACTGCACTCCAGCCTGGG  AC
                               AGTGGTGT    TGACGTGAGGTCGGATCC  TG
                                           TC
GAM1338  360   KIAA045 1  3442  XP_027862.1  3  3703  GCTTTGTTGCCC  TG                3  C  b  b
          9                    AGGCTGGAGTGT AC  CACTCCAGCCTGGGCAAC
                               GGTGGGGC    TG  GTGAGGTCGGACCCGTTG
                                     GT
GAM1338  360   KIAA046 2  1413  NP_055666.1  3  701   GCTCTGTCACCC            CAA       3  C  c  c
```

9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 KIAA046 2 14283 NP_055666.1 3 349 GCTCTGTCACCC CAA 3 C c c
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 KIAA047 1 7946 NP_055679.1 3 1230 ACTCTGTTGCCC 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 KIAA049 1 6597 XP_034717.1 5 925 GCTCTCTTACCC C CAA 3 C c c
3 AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGACAT TGACGTGAGGTCG ACCC
A ATT
GAM1338 360 KIAA051 1 11210 NP_055547.1 3 3673 CTCTTGTTGCCC 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGACAC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 KIAA052 1 19044 XP_171054.1 3 364 ATGCTGTTGCCC 3 C b b
7 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGTCCC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 KIAA055 1 19623 NP_055605.1 3 2300 GCTCTGTTGCCC AC----- C 3 C c
c
5 ATGCTGGAGTGC TGCACTCCAGC TGGGCAAC
ATTGGCAC ACGTGAGGTCG ACCCGTTG
CACGGTT T
GAM1338 360 KIAA056 1 12972 XP_038150.2 3 319 ACTCTGTTGCCC A----- 3 C c c
1 GGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGCGGCGT GACGTGAGGTCGGGCCCGTTG
TGCGGC
GAM1338 360 KIAA056 1 10458 NP_055519.1 3 2048 GCTCTGTTGCCT 3 C b b
2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGATCCGTTG
GAM1338 360 KIAA056 1 19679 NP_055649.1 5 603 CTCTTGTTGCCC C 3 C b b
3 AGGCTGAAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGTTGT TGACGTGA GTCGGACCCGTTG
A
GAM1338 360 KIAA068 1 2671 NP_055667.1 3 31 CTGGCACCGAGA ---- - AA 3 C c c
2 GGGCTGGAGTGC ACTGCACTCCAGCCT GG GC
AGTGGCGT TGACGTGAGGTCGGG CC CG
AGAG A GT
GAM1338 360 KIAA083 1 16264 NP_055739.1 3 1917 GCTCAGCTGCCC TG A 3 C c
c
1 AGGCTGGAGTGT AC CACTCCAGCCTGGGCA
GGTGGCGC TG GTGAGGTCGGACCCGT
GT C

GAM1338 360 KIAA084 2 901 XP_049237.1 3 1171 ATTCTGTTGCCC C 3 C b b
1 AAGTTGGAGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGCAT TGACGTGAGGTTG ACCCGTTG
A
GAM1338 360 KIAA084 2 1519 XP_049237.1 3 1520 TGGCTGTTTCCC C C 3 C b b
1 AGGCTGAAGTGC ACTGCACT CAGCCTGGG AAC
AGTGGCAT TGACGTGA GTCGGACCC TTG
A T
GAM1338 360 KIAA086 1 10629 NP_055893.2 3 954 GCTCTGTCGCCC AA 3 C b b
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 KIAA092 2 864 NP_055712.1 3 2516 GTTCTGTTGCCT TG 3 C b b
4 GGGCTGGAGTGC ACTGCACTCCAGCC GGCAAC
AGTGGCGT TGACGTGAGGTCGG CCGTTG
GT
GAM1338 360 KIAA092 2 19935 NP_055712.1 3 1716 GCTATGTTGCCC C 3 C b b
4 AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGCTA TGACGTGAG TCGGACCCGTTG
A
GAM1338 360 KIAA093 1 10957 XP_052620.6 3 1213 ACTCTGTCGCCC AA 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGTCAA TGACGTGAGGTCGGACCCG
CT
GAM1338 360 KIAA100 2 8660 XP_290584.1 3 314 CTCTTGTCACCC C CAA 3 C c c
2 CAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTAGCAC TGACGTGAGGTCG ACCC
- CAC
GAM1338 360 KIAA100 2 12518 XP_290584.1 5 0 CGCCTAGGCTGG T A AA 3 C c c
2 AGCGCCGTGGTA AC GC CTCCAGCCTGGGC
CAGTCTTG TG CG GAGGTCGGATCCG
C C C-
GAM1338 360 KIAA104 1 5138 XP_051091.3 3 2455 GCTCTGTCACCC C CAA 3 C c
c
0 AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCAC TGACGT AGGTCGGACCC
A ACT
GAM1338 360 KIAA104 1 11112 NP_055762.1 3 967 GCCCTGTTGCCC 3 C b b
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 KIAA105 1 1530 NP_055771.1 5 226 GCTCTGTCACTC C CAA 3 C c c

2 AGGCTGCAGTGC ACTGCACT CAGCCTGGG
AGTGGCAT TGACGTGA GTCGGACTC
C ACT
GAM1338 360 KIAA105 1 7973 XP_043493.5 3 3277 ACTCTGTTGCCC 3 C b b
4 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGG TGACGTGAGGTCGGACCCGTTG

GAM1338 360 KIAA112 1 8868 NP_061872.1 3 1958 GCTCCATTGCCC CAC 3 C b b
8 AGGCTGGATTAC ACTG TCCAGCCTGGGCAA
AGTGGCGC TGAC AGGTCGGACCCGTT
ATT
GAM1338 360 KIAA114 1 13800 XP_044014.1 3 3994 GCTCTGTCACCC CAA 3 C c c
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 KIAA115 1 5405 XP_030864.2 3 2953 ACTCTGTCACCC CAA 3 C c c
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 KIAA117 1 7575 XP_045907.2 3 1244 CTCTTGTTGCCC AC----- C 3 C c c
0 AAGCTGGAGTGC TGCACTCCAGC TGGGCAAC
AATGGCAC ACGTGAGGTCG ACCCGTTG
CACGGTA A
GAM1338 360 KIAA118 1 9213 NP_065761.1 3 154 CGCTCTGTCGCC -- A 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGT TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 KIAA119 1 1683 XP_041843.1 3 1645 CACACTGTCGCC -- A 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGC TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 KIAA119 5 5522 NP_065765.1 3 992 ACTCTGTTGCCT G- 3 C b b
8 AGGCTGGAGTGA ACT CACTCCAGCCTGGGCAAC
AAGTGGCG TGA GTGAGGTCGGATCCGTTG
AA
GAM1338 360 KIAA119 5 8170 NP_065765.1 3 722 CTCTGTTGCCCC - 3 C b b
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG CAAC
AGTGGTGT TGACGTGAGGTCGGACCC GTTG
C
GAM1338 360 KIAA119 5 17224 NP_065765.1 3 3709 CTCACTGTTGCC G 3 C b b
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGCAC TGACGTGAGGTCGGACC GTTG
-
GAM1338 360 KIAA119 5 17617 NP_065765.1 3 420 CTCTTGTTGCCC 3 C b b
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 KIAA119 5 17786 NP_065765.1 3 1271 GAGTCCTTGCCC 3 C b b
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCGC TGACGTGAGGTCGGACCCGTT
GAM1338 360 KIAA120 1 10878 XP_027307.2 3 1885 TCCCTGTTGCCC AC----- C 3 C c
c
9 AAGTTGGAGTGC TGCACTCCAGC TGGGCAAC

AATCTTGG ACGTGAGGTTG ACCCGTTG
GGTTCTA A

GAM1338 3600 KIAA121 1 1409 XP_172801.1 3 104 GCTCTGTTACCC GC C 3 C b b
AGATTGGAGTGC ACTGCACTCCA CTGGG AAC
AGTGGCGC TGACGTGAGGT GACCC TTG
TA A

GAM1338 3607 KIAA125 3 3109 XP_031577.2 3 1694 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 3607 KIAA125 3 13137 XP_031577.2 3 3565 CTCTTGTTGCCC AC----- C 3 C c b
AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
AATGGCGC AC TGAGGTCGGACCCGTTG
CGCGGTA A

GAM1338 3607 KIAA125 3 14928 XP_031577.2 3 1025 GCTCTCTCACCC - CAA 3 C c b
AGGCTGGAGTGT ACT GCACTCCAGCCTGGG
AAGTGACA TGA TGTGAGGTCGGACCC
A ACT

GAM1338 3608 KIAA126 1 6348 XP_291055.1 3 897 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA

GAM1338 3607 KIAA128 1 13685 NP_065799.1 3 1242 CCCCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGGAT TGACGTGAGGTCGGACCCGTTG

GAM1338 3603 KIAA139 1 6495 XP_050793.2 3 1498 GCTCTGTTGCCC A----- 3 C c c
AGGCTGGAGTGT CTGCACTCCAGCCTGGGCAAC
AGAGACAC GATGTGAGGTCGGACCCGTTG
CACAGA

GAM1338 3605 KIAA146 1 13306 XP_027396.4 3 570 TGGTCTGTCGCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
GC C

GAM1338 3603 KIAA149 1 11663 XP_034415.1 3 2965 ACTCTGTTGCCC C C 3 C b b
AGTCTGGAGTTC ACTG ACTCCAG CTGGGCAAC
AGTGGCGC TGAC TGAGGTC GACCCGTTG
T T

GAM1338 3608 KIAA151 1 17375 XP_170889.1 3 94 ACTCTGTCGCCC G AA 3 C c c
AGGGTGGAGTGC ACTGCACTCCA CCTGGGC
GGTGGCAC TGGCGTGAGGT GGACCCG
G CT

GAM1338 3600 KIAA153 2 6360 XP_042661.5 3 817 TTTGCTCTTACC C CAA 3 C c c
CAGGCTGAGTGC ACTGCACTC AGCCTGGG
AGTGGCAG TGACGTGAG TCGGACCC
- ATT

GAM1338 360 KIAA153 2 12345 XP_042661.5 3 817 TTGCTCTTACCC C CAA 3 C c c

0 AGGCTGAGTGCA ACTGCACTC AGCCTGGG
GTGGCAGA TGACGTGAG TCGGACCC
- ATT

GAM1338 360 KIAA155 1 14408 XP_054472.2 3 1628 ACTTTGTCCCCC CA 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGTAC TGACGTGAGGTCGGACCC TG
CC

GAM1338 360 KIAA157 1 13037 XP_027744.1 3 881 ACTGTCTTGCCC 3 C b b
1 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCCT TGACGTGAGGTCGGACCCGTT

GAM1338 360 KIAA161 2 8578 NP_066002.1 3 1687 TGCTCTGTCACC A -- A 3 C c b
5 AGGCCGGAGTGC ACTGCACTCC GCCTGG GCA
AGTGGTGT TGACGTGAGG CGGACC TGT
C AC C

GAM1338 360 KIAA161 2 12534 NP_066002.1 3 1380 CTCTTGTTGCCT 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGATCCGTTG

GAM1338 360 KIAA167 2 6490 XP_037809.1 3 4093 GCTCTGTTGGCC C G 3 C b b
1 AGGCTGGAATGC ACTGCA TCCAGCCTGG CAAC
AGTGGCAC TGACGT AGGTCGGACC GTTG
A G

GAM1338 360 KIAA167 2 17814 XP_037809.1 3 1741 ACTCTGTTGCTC G C 3 C b b
1 AAGCTGGAGTGG ACT CACTCCAGC TGGGCAAC
AGTGGCAC TGA GTGAGGTCG ACTCGTTG
G A

GAM1338 360 KIAA171 2 8796 NP_085136.1 3 740 CTGTTGTTGCCC AC----- 3 C c c
2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATAGCAC ACGTGAGGTCGGACCCGTTG
CACGATA

GAM1338 360 KIAA171 2 8796 XP_041497.2 3 740 CTGTTGTTGCCC AC----- 3 C c c
2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATAGCAC ACGTGAGGTCGGACCCGTTG
CACGATA

GAM1338 360 KIAA171 2 12038 NP_085136.1 3 1317 ACTCTATTGCCC AC----- 3 C c c
2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
ACTGGCGT ACGTGAGGTCGGACCCGTT
TGCGGTC

GAM1338 360 KIAA171 2 12038 XP_041497.2 3 1486 ACTCTATTGCCC AC----- 3 C c c
2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
ACTGGCGT ACGTGAGGTCGGACCCGTT
TGCGGTC

GAM1338 360 KIAA172 1 12049 XP_040280.2 5 24 CCATCCTTGCCC T- --- A C 3 C c c
4 AGCCGGTGTGGT AC GCACT CC GC TGGGCAA
GCTTGTGT TG CGTGG GG CG ACCCGTT
TT TGT C -

GAM1338 360 KIAA173 2 12203 NP_219494.1 3 1427 CTCTTGTTGCCC AC------ C A 3 C c
c
7 AGGCGGAGTACA TG ACTCC GCCTGGGCAAC

ATGGTGGG AC TGAGG CGGACCCGTTG
GGGTGGTA A -

GAM1338 360 KIAA173 2 19235 NP_219494.1 3 2533 CATCGGTTGCCC ACTC - 3 C c c
7 AAGGCTGTAAGT ACTGC CAGCCT GGGCAAC
AGTGATGG TGATG GTCGGA CCCGTTG
AAT- A

GAM1338 360 KIAA178 1 18884 NP_115820.1 3 341 GCTGTGTCACCT CAA 3 C c c
4 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGATCC
ACT

GAM1338 360 KIAA182 1 9237 XP_041566.2 3 991 TCGGGGCTGACC CA- G A 3 C c c
2 AGGCTGGGGGTC ACTG CTCCAGCCTGG CA
CAGTGAAA TGAC GGGGTCGGACC GT
CTG A C

GAM1338 360 KIAA182 2 2385 XP_290834.1 3 1305 CCCTTGTCACCC C CAA 3 C c b
7 AGGCTGTAGTGC ACTGCACT CAGCCTGGG
GGTGGCGC TGGCGTGA GTCGGACCC
T ACT

GAM1338 360 KIAA182 2 19431 XP_290834.1 3 937 ACTCTGTTGCCC 3 C b b
7 AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGATGTGAGGTCGGACCCGTTG

GAM1338 360 KIAA182 1 12386 XP_030378.2 3 209 GCTCTGTTGCCC 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 KIAA183 1 17519 XP_114087.2 3 1677 TCTCTGCCAGCC --- A 3 C b b
6 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCAT TGACGTGAGGTCGGACC CGT
GAC C

GAM1338 360 KIAA189 1 19465 NP_056212.1 3 1231 TGAGATGGTGAC CT GG A 3 C c c
2 AGGCTGGCCTGC ACTGCA CCAGCCTG CA
AGTCAGCA TGACGT GGTCGGAC GT
CC A- G

GAM1338 360 KIAA192 1 18258 XP_057040.1 5 321 CTCTTGTTGCCC AC----- 3 C c c
2 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAT ACGTGAGGTCGGACCCGTTG
TACGGTA

GAM1338 360 KIAA192 2 7825 NP_694971.2 3 596 GCTCTGTCGCCC G AA 3 C c c
4 AGGATGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGCGC TGACGTGAGGT GGACCCG
A CT

GAM1338 360 KIAA192 2 12570 NP_694971.2 3 406 GTTCTGTCACCT C CAA 3 C c c
4 AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGTGC TGACGT AGGTCGGATCC

A ACT
GAM1338 360 KIAA197 3 4023 XP_058720.4 3 213 ACTCTGTCGCCC AA 3 C c c
1 AGGCTGGGGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGGGGTCGGACCCG
CT
GAM1338 360 KIAA197 3 13441 XP_058720.4 3 263 GCTCCGCTTCCC CAA 3 C c c
1 AGGCTGGGGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGGGGTCGGACCC
TTC
GAM1338 360 KIAA197 3 19552 XP_058720.4 3 561 TCTCTGTCATCC C CAA 3 C c c
1 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGCAC TGACGTGAG TCGGACCT
A ACT
GAM1338 360 KIAA198 1 18263 XP_113870.1 5 201 CTCTTGTTGCCC C 3 C b b
7 AGGTTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGCAC TGACGTGAG TTGGACCCGTTG
A
GAM1338 360 KIAA202 1 11722 XP_059415.2 3 1062 CTCTGGTTGCCC 3 C b b
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 KLF12 1 7570 NP_009180.3 3 949 GTGGGGCTGCCC C CCA A 3 C c
c
AGGCAAAGTCAG ACTG ACT GCCTGGGCA
TGAACATG TGAC TGA CGGACCCGT
- AA- C
GAM1338 360 KLRD1 1 8689 NP_002253.1 3 396 CTCACACTGCCC CA A 3 C c c
AGGCTGGAGCAT ACTG CTCCAGCCTGGGCA
AGTGGCAA TGAT GAGGTCGGACCCGT
AC C
GAM1338 360 KLRD1 1 8689 NP_031360.1 3 396 CTCACACTGCCC CA A 3 C c c
AGGCTGGAGCAT ACTG CTCCAGCCTGGGCA
AGTGGCAA TGAT GAGGTCGGACCCGT
AC C
GAM1338 360 KMO 1 5730 NP_003670.1 3 715 ACTCTGTTGACC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGTGA TGACGTGAGGTCGGACC GTTG
A
GAM1338 360 KSR 1 15951 XP_290793.1 5 1147 GCTCTATCACCC C CAA 3 C c c
AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTAGTGC TGACGTGA GTCGGACCC
A ACT
GAM1338 360 LAMP3 1 970 NP_055213.1 3 564 CTCTTGTCACCC C CAA 3 C c c
AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAC TGAC TGAGGTCGGACCC
A ACT
GAM1338 360 LCN7 1 3972 NP_071447.1 3 399 GCTCCGTTGCCC 3 C b b
AGGTTGGAGTGC ACTGCACTCCAGCCTGGGCAAC

AGTGGCCC TGACGTGAGGTTGGACCCGTTG

GAM1338 360 LCX 1 7409 XP_167612.2 3 44 CCCTCTTAATGC CC CT A 3 C c c
CTTTGCTAGTGC ACTGCACT AGC GGGCA
AGTGTATT TGACGTGA TCG TCCGT
-- TT A
GAM1338 360 LGP1 1 20143 NP_115873.1 5 31 ACTCTGTTGCCC C 3 C b b
AAGCTGGGGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGCAC TGACGTGGGGTCG ACCCGTTG
A
GAM1338 360 LIN-28 1 6030 NP_078950.1 3 2143 GCTGTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGAGCT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LNK 1 9510 NP_005466.1 3 1682 CTCTTGTCAACC --- 3 C b b
GGGCTGGAGTGC ACTGCACTCCAGCCTGG GCAA
AGTGGTGC TGACGTGAGGTCGGGCC TGTT
AAC
GAM1338 360 LOC1126 1 4875 XP_053145.1 3 168 GCCCTGTCACCC CAA 3 C c c

87 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1134 3 14262 NP_612437.2 3 851 ATTCTGTCACCC CAA 3 C c b

44 GGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGGCCC
ACT
GAM1338 360 LOC1134 3 15369 NP_612437.2 3 590 ACTCTGTCACAC --- A 3 C c b
44 AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTACAAT TGACGTGAGGTCGGAC CTGT
ACA C
GAM1338 360 LOC1134 3 15847 NP_612437.2 3 1176 GCTGTATTGCCC 3 C b b
44 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCGC TGACGTGAGGTCGGACCCGTT

GAM1338 360 LOC1151 1 8312 XP_055276.1 5 256 GCTCTATGGCCC C AA 3 C c c

23 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGC
AGTGACAC TGAC TGAGGTCGGACCCG
A GT
GAM1338 360 LOC1151 1 11459 XP_055292.1 3 372 AGGGTGTTGCCC G C-- C 3 C c
c
29 ATGCTTTTGGGT ACT CACTC AGC TGGGCAAC
GGGTCCCA TGG GTGGG TCG ACCCGTTG
- TTT T
GAM1338 360 LOC1156 1 6386 NP_663299.1 3 656 CGCTCTGTCGCC T AA 3 C c c

48 TGGCTGGAGTGC ACTGCACTCCAGCC GGGC
AGTGGTGT TGACGTGAGGTCGG TCCG

- CT

GAM1338 360 LOC1164 1 1487 XP_058095.1 5 1240 TCAATGGTGTCC A 3 C b b
11 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
AGTGGCGT TGACGTGAGGTCGGACCTGT
G

GAM1338 360 LOC1184 1 11022 XP_060981.3 3 217 GCTCTGTTGCCC A----- 3 C b b
90 AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGCGGCAT GACGTGAGGTCGGACCCGTTG
TACGGC

GAM1338 360 LOC1188 1 7879 NP_849154.1 3 580 TTACTCTCGCCC C AA 3 C c c
12 AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCAT TGACGTGAG TCGGACCCG
A CT

GAM1338 360 LOC1188 1 7879 XP_058346.2 3 580 TTACTCTCGCCC C AA 3 C c c
12 AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCAT TGACGTGAG TCGGACCCG
A CT

GAM1338 360 LOC1205 1 14215 XP_058475.1 3 678 ACTCTGTCGCGC C - AA 3 C c
c
26 CAGCTGGAGTGC ACTGCACTCCAGC TGG GC
AGTGCCAT TGACGTGAGGTCG ACC CG
- G CT

GAM1338 360 LOC1219 1 17591 XP_062872.2 5 584 GCTCTGTCACCC T CAA 3 C c
c
52 GGGCTGGAGTGC AC GCACTCCAGCCTGGG
TGTGGCTT TG CGTGAGGTCGGGCCC
T ACT

GAM1338 360 LOC1242 1 14470 XP_058785.3 5 255 CAACTTCAGTCC T A AA 3 C c
c
21 GGGCTGGAGGCC AC GC CTCCAGCCTGGGC
GTGCACAA TG CG GAGGTCGGGCCTG
C - AC

GAM1338 360 LOC1248 1 1585 XP_058857.1 3 60 ACTATGTTGCCC GCACT 3 C c
c
71 AGGCTGGTCTCA ACT CCAGCCTGGGCAAC
AGTTCCTG TGA GGTCGGACCCGTTG
ACTCT

GAM1338 360 LOC1250 1 9098 XP_058889.3 3 406 ACTCTGTCACCC CAA 3 C c c
61 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC1266 1 8179 XP_060121.4 3 193 GCTGTGTTGCCC AC----- 3 C c c
69 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA

GAM1338 360 LOC1272 1 2617 XP_059122.1 3 141 ACTTTGTTGCCC - AGC 3 C b b

53 AGAGGATGTGCA ACTGCAC TCC CTGGGCAAC
GTTGTCAT TGACGTG AGG GACCCGTTG
T A--

GAM1338 360 LOC1278 1 5401 XP_059184.1 5 111 TTGGTGTTGCCC A CA- 3 C c c
41 AGGCAGAGAGGG ACTGC CTC GCCTGGGCAAC
CAGTGTGG TGACG GAG CGGACCCGTTG
G AGA
GAM1338 360 LOC1283 1 2302 XP_059243.2 3 560 CTGTTGTTGCCC AC----- 3 C c c
87 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 LOC1322 1 13281 XP_059583.1 5 82 ACTTTGCTTCCC --- 3 C b b
41 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCAA
AGTGGTGC TGACGTGAGGTCGGACC CGTT
CTT
GAM1338 360 LOC1352 2 11660 XP_072402.4 3 1276 TCTTGCTCTCCC CAA 3 C c
b
93 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
TCT
GAM1338 360 LOC1352 2 15178 XP_072402.4 3 563 GCTCTGTTGCCC C 3 C b b
93 AGGCTGAAGTGT ACTGCACT CAGCCTGGGCAAC
AGTGGCAC TGATGTGA GTCGGACCCGTTG
A
GAM1338 360 LOC1357 1 14442 NP_612639.1 3 38 GCTCCGTCACCC CAA 3 C c c
63 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAA TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1358 1 7348 XP_059804.4 3 736 CTCTTGTTGCCC AC----- C 3 C c c
18 AGCCTGGAGTGC TGCACTCCAG CTGGGCAAC
AATAGCGT ACGTGAGGTC GACCCGTTG
TGCGATA C
GAM1338 360 LOC1378 1 18258 XP_059929.3 3 682 CTCTTGTTGCCC AC----- 3 C c c
86 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAT ACGTGAGGTCGGACCCGTTG
TACGGTA
GAM1338 360 LOC1394 1 17958 XP_066687.2 5 63 GCTCTGTTGCCC C 3 C b b
22 AGACTGGAGTGC ACTGCACTCCAG CTGGGCAAC
AGTGGTGT TGACGTGAGGTC GACCCGTTG
A
GAM1338 360 LOC1432 1 13142 NP_620167.1 5 53 CTCTTGTTGCCC AC----- 3 C c c
41 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 LOC1444 2 8561 XP_084852.6 3 1128 GGTCTGTTGCCT A 3 C b b
04 AGGCGGGAGTGC ACTGCACTCC GCCTGGGCAAC
AGTGGCAT TGACGTGAGG CGGATCCGTTG
G
GAM1338 360 LOC1444 2 11669 XP_084852.6 3 1293 GATCTGTTACCC C 3 C b b

```
          04                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
                                     AGTGACAC    TGACGTGAGGTCGGACCC TTG
                                                  A
GAM1338  360   LOC1444 2  16400  XP_096611.2  3  1901   AAGAATGGCTTC     -       - AA      3  C  c  c

          81                          AGGCTGGGGCTG ACTGCA CTCCAGCCTGG GC
                                     CAGTCACC    TGACGT GGGGTCGGACT CG
                                                  C        T  GT
GAM1338  360   LOC1444 2  17022  XP_096611.2  3  208    ACTCTGTCACTC            CAA       3  C  c  c

          81                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGTAT    TGACGTGAGGTCGGACTC
                                                  ACT
GAM1338  360   LOC1447 1  15441  XP_084949.1  5  56     ACTCTGTTGCCT    C               3  C  b  b
          42                          AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
                                     AGTGGCAA    TGAC TGAGGTCGGATCCGTTG
                                                  A
GAM1338  360   LOC1447 1  19847  XP_084963.2  5  180    GCTTTGTCACCC    C        CAA       3  C  c
c
          66                          AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
                                     AGTGGCGT    TGAC TGAGGTCGGACCC
                                                  A          ACT
GAM1338  360   LOC1447 2  14978  XP_084964.1  5  251    ATTCTGTTGCCC AC-----              3  C  c  c
          76                          AGGCTGGAGTGC       TGCACTCCAGCCTGGGCAAC
                                     AATGGCAT          ACGTGAGGTCGGACCCGTTG
                                           TACGGTA
GAM1338  360   LOC1447 2  16958  XP_084964.1  5  133    ACTCCATCACTC    C        CAA       3  C  c
c
          76                          AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
                                     AGTGCTGA    TGAC TGAGGTCGGACTC
                                                  A          ACT
GAM1338  360   LOC1448 1  12382  XP_084972.1  5  232    GCTCTGTCGCCC             AA       3  C  b  b

          17                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                     AGTGGTGC    TGACGTGAGGTCGGACCCG
                                                  CT
GAM1338  360   LOC1448 1  10644  XP_096698.1  3  381    GCTCTGTTGCCC A-----              3  C  b  b
          71                          AGGCTGGAGTGC      CTGCACTCCAGCCTGGGCAAC
                                     AGGGACAC          GACGTGAGGTCGGACCCGTTG
                                           CACAGG
GAM1338  360   LOC1452 1  15408  XP_085072.1  5  636    ACTCTTTTGCCC    GCA              3  C  b  b

          68                          AGGCTGGAGCGA ACT   CTCCAGCCTGGGCAA
                                     AGTGACGA    TGA   GAGGTCGGACCCGTT
                                                  AGC
GAM1338  360   LOC1454 1  8486   XP_085120.1  5  319    ACTGTGTCATGC    G        ---   A      3  C  c  c
          53                          AGGCTGGAGTGA ACT CACTCCAGCCTG   GGCA
                                     AGTCGTGT    TGA GTGAGGTCGGAC   CTGT
                                                  A          GTA    G
GAM1338  360   LOC1457 1  418    XP_085211.1  3  988    CGCTCTGTCACC    C        --  A      3  C  c  c
```

25 AGGCTGGAGTAC ACTG ACTCCAGCCTGG GCA
AGTGATGA TGAC TGAGGTCGGACC TGT
A AC C
GAM1338 360 LOC1457 2 3109 XP_085227.1 5 212 GCTCTGTCGCCC AA 3 C b b
57 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1457 2 13797 XP_085227.1 5 94 GCTCTGTCGCCC AA 3 C c b
57 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
GGTGGCGC TGGCGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1458 1 16182 XP_085254.1 5 944 ACACTAGTGCTT -- CT A 3 C c c

42 CCGCTGGAGTTT ACTGC ACTCCAGC GGGCA
GCAGTTTT TGACG TGAGGTCG TTCGT
TT CC G
GAM1338 360 LOC1461 1 15157 NP_778229.1 5 198 CTCTTGTTGCCC 3 C b b
77 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTAGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1462 4 3109 XP_085387.1 3 1706 GCTCTGTCGCCC AA 3 C b b

29 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1462 4 5010 XP_085387.1 3 4033 GCTCTGTTGCCT C 3 C b b
29 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGTGC TGAC TGAGGTCGGATCCGTTG
A
GAM1338 360 LOC1462 4 8345 XP_085387.1 3 3209 ACTCTGTCGCCC C AA 3 C c
b
29 AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCAC TGACGTGAG TCGGACCCG
A CT
GAM1338 360 LOC1462 4 13931 XP_085387.1 3 2309 TTCTTGTTGCCT AC----- 3 C c b

29 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGA ACGTGAGGTCGGATCCGTTG
AGCGGTA
GAM1338 360 LOC1463 2 6781 XP_085430.1 5 387 CACTCCGTTGCC T G 3 C b b
46 AGGCTGGAGTGC AC GCACTCCAGCCTGG CAAC
TGTGGCGC TG CGTGAGGTCGGACC GTTG
T -
GAM1338 360 LOC1463 2 16312 XP_085430.1 5 735 CACTCGTTGCCC 3 C b b
46 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1464 2 8579 XP_096998.2 5 536 CGCTCTGTCACC -- A 3 C b b
29 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGT TGACGTGAGGTCGGACC TGT

AC C
GAM1338 360 LOC1464 2 13213 XP_096998.2 5 54 GCCCAATCTGCC T -- G A 3 C c b

29 AGGCTGGACTGT AC GCAC TCCAGCCTGG CA
GCTGTTCC TG CGTG AGGTCGGACC GT
T TC - C
GAM1338 360 LOC1466 1 3109 XP_085514.2 5 1113 GCTCTGTCGCCC AA 3 C b b

03 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1467 1 13452 XP_085588.1 5 889 CTCTTGTTGCCC 3 C b b
84 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGTAC TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1468 1 11661 XP_097107.1 3 676 ACTCTGTTGCCC 3 C b b
39 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1468 1 2386 NP_660316.1 3 1176 GTGCTGCTGCCC A 3 C b b
94 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
AGTGGCAC TGACGTGAGGTCGGACCCGT
C
GAM1338 360 LOC1468 1 8862 XP_097120.1 5 549 ACTCTGTCACCC CAA 3 C c c
95 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1469 1 12152 XP_097121.1 3 1203 TTGTCAAAAATC ------ 3 C b b
01 AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCAA
AGTGGCAT TGACGTGAGGTCGGAC CTGTT
TAAAAA
GAM1338 360 LOC1469 2 14280 XP_085634.2 3 661 ACTCTGTCGCCC AA 3 C b b
09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1469 2 20010 XP_085634.2 3 994 GCTCTGTCGCCC AA 3 C b b

09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGG TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1470 1 6735 XP_054031.5 5 603 CTCTTGTTGCCC AC----- C 3 C c c

71 AGGCTGAAGTGC TGCACT CAGCCTGGGCAAC
AATGTTGT ACGTGA GTCGGACCCGTTG
TGTTGTA A
GAM1338 360 LOC1470 1 18093 XP_097182.1 5 17 GCTCTGTCCGCC --- A 3 C c c
80 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
GCC C
GAM1338 360 LOC1471 1 546 XP_085722.2 3 251 GCACTGTTGCCC 3 C b b

66 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1473 1 15088 XP_097225.1 5 1444 TGGCTTCAGCCC C T - AA 3 C c
c
43 AGGCGTGGTGTC ACTG AC CCA GCCTGGGC
AGTTTCCT TGAC TG GGT CGGACCCG
- T G AC
GAM1338 360 LOC1474 1 12382 XP_084000.1 3 142 GCTCTGTCGCCC AA 3 C b b

07 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1476 1 10349 XP_097255.1 3 528 TCTCTGTCCCCT C CA 3 C c c

22 AGGCTGCAGTGC ACTGCACT CAGCCTGGG AC
AGTGGCGC TGACGTGA GTCGGATCC TG
C CC
GAM1338 360 LOC1478 2 15453 XP_085924.2 3 145 CTCTTGTTGTCC AC----- C 3 C c
b
41 AGTCTGGAGTGC TGCACTCCAG CTGGGCAAC
AATGGCAC ACGTGAGGTC GACCTGTTG
CACGGTA T
GAM1338 360 LOC1478 2 18175 XP_085924.2 3 457 ACTCTGTCGCCC AA 3 C b b
41 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1479 1 438 XP_085974.1 3 578 ACTCTGTCACCC CAA 3 C c c
47 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1481 1 13130 NP_653293.1 3 2097 GCTCTGTCACCC --- CAA 3 C c
c
37 AGGCTGGAGTGC ACT GCACTCCAGCCTGGG
CATAGTGT TGA CGTGAGGTCGGACCC
TAC ACT
GAM1338 360 LOC1481 1 7524 XP_047554.4 3 982 TGTCGCCCACCC C CAA 3 C c
c
98 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAC TGAC TGAGGTCGGACCC
A ACC
GAM1338 360 LOC1487 1 18164 XP_086286.4 3 1372 ACTCTGTCGCCC AA 3 C b b

08 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTG TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1487 1 8427 XP_086281.1 5 142 TCTCTGGTACTC CAA 3 C c c
09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
GGTGGTGT TGGCGTGAGGTCGGACTC
ATG

GAM1338 360 LOC1491 1 9725 XP_097598.1 5 3316 CTCTTGTTGCCC C 3 C b b
49 AAGCTGGAGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGCGC TGACGTGAGGTCG ACCCGTTG
A
GAM1338 360 LOC1493 1 14762 NP_787072.1 3 370 ACCCCGTCGCAC G AA 3 C c
c
71 AGGCTGGAGTGC ACTGCACTCCAGCCTG GC
AGTGGCAA TGACGTGAGGTCGGAC CG
A CT
GAM1338 360 LOC1494 1 14821 XP_097645.1 5 1247 CTGCTGTTGCCC A----- - AC C 3 C c
c
64 AGCTGGACAGCT CT GC TCCAGC TGGGCAAC
AGAGTTAT GA CG AGGTCG ACCCGTTG
TATTGA T AC -
GAM1338 360 LOC1494 1 982 XP_086546.1 3 563 ACTCTGTTGCCC AC----- 3 C c c
66 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 LOC1494 1 2514 XP_086536.1 3 75 GCTCTGTCGTCG G AA 3 C c c
78 AGGCTGGAGTGT ACTGCACTCCAGCCT GGC
AGTGGTGC TGATGTGAGGTCGGA CTG
G CT
GAM1338 360 LOC1495 2 5777 XP_097661.1 3 1638 TCGCTGTTGCCC C 3 C b b
06 AGGCTGTAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGGTGC TGACGTGA GTCGGACCCGTTG
T
GAM1338 360 LOC1495 2 17503 XP_097661.1 3 3100 CTCTTGTCGGCC C --- 3 C b b

06 AGGCTAGAGTGC ACTGCACTC AGCCTGG GCAA
AGTGGCGC TGACGTGAG TCGGACC TGTT
A GGC
GAM1338 360 LOC1496 1 13800 XP_097706.1 3 612 GCTCTGTCACCC CAA 3 C c
c
92 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1497 1 19805 XP_097719.1 5 452 GTTCTGCTGCCC - C A 3 C c c
03 AAGCTGGAGTGG ACTGC ACTCCAGC TGGGCA
CAGTGGCA TGACG TGAGGTCG ACCCGT
G A C
GAM1338 360 LOC1500 1 18175 XP_097797.1 5 592 ACTCTGTCGCCC AA 3 C b b
54 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1502 1 1664 XP_097870.1 3 1703 GCTCTGTCGCTC AA 3 C c c
25 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACTCG
CT
GAM1338 360 LOC1503 1 19150 XP_086884.2 5 21 CGCTGCGCCTCC AC- ---- A 3 C c
c

56 AGGCTGGACCAG ACTGC TCCAGCCTGG GCA
CAGTTCCA TGACG AGGTCGGACC CGT
ACC TCCG C
GAM1338 360 LOC1504 1 2430 XP_086906.1 3 530 GCTCTGTTGTCC C 3 C b b
07 AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGTGT TGACGTGAG TCGGACCTGTTG
A
GAM1338 360 LOC1505 1 8861 XP_097917.1 5 1615 GCTCTGTTGCCC 3 C b b
87 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1510 1 5519 XP_097998.1 3 1066 TCTCTGTCACCC CAA 3 C c c

57 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1511 1 13932 XP_098006.1 5 1300 TGGCTGGTTCCC A -- C--- C 3 C c
c
24 AGGCTGCGCTGG CTG CACT CAGCCTGGG AAC
TGTTCAGC GAC GTGG GTCGGACCC TTG
C TT TCGC -
GAM1338 360 LOC1511 1 12600 XP_098019.1 3 457 AAAATGTACACC T --- A 3 C c c
96 AGGCTGGGTGCG ACTGCAC CCAGCCTGG GCA
GTGGCTCA TGGCGTG GGTCGGACC TGT
- ACA A
GAM1338 360 LOC1512 1 11934 XP_098021.1 3 367 CACGCTGTCACC -- A 3 C b b
01 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC1514 2 7086 XP_098063.1 5 738 GCTCTGTCATCC CAA 3 C c c
75 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCT
ACT
GAM1338 360 LOC1514 2 15680 XP_098063.1 5 99 GCTCTGTGGCCC AA 3 C c c
75 AGGCTGGAGTGT ACTGCACTCCAGCCTGGGC
AGTGGCGT TGATGTGAGGTCGGACCCG
GT
GAM1338 360 LOC1516 3 896 NP_612144.1 3 890 ACTCTGTCACCC C CAA 3 C c b

36 AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGTGT TGACGT AGGTCGGACCC
A ACT
GAM1338 360 LOC1516 3 2479 NP_612144.1 3 2150 ACTGTGTCCCCC CA 3 C b b

36 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
CC
GAM1338 360 LOC1516 3 19982 NP_612144.1 3 221 GCTCTGTCGCTC C AA 3 C c
b
36 GCGCTGGAGTGC ACTGCACTCCAGC TGGGC

AGTGGCAT TGACGTGAGGTCG GCTCG
C CT
GAM1338 360 LOC1519 1 2865 XP_087354.5 5 420 TGACTGTTGCCC C C 3 C b b
79 AAGCTGGAATGC ACTGCA TCCAGC TGGGCAAC
AGTGGCAC TGACGT AGGTCG ACCCGTTG
A A
GAM1338 360 LOC1522 2 1714 XP_098182.1 3 1353 GCTCTGTAGCCC AC AA 3 C c
c
45 AGGCTGGAGTGC TGCACTCCAGCCTGGGC
A ACGTGAGGTCGGACCCG
-- AT
GAM1338 360 LOC1522 2 19257 XP_098182.1 3 1273 GCTCTGTCGCCC ---- AA 3 C c
c
45 AGGCTGGAGTGA ACTGCAC TCCAGCCTGGGC
GTGCAGTG TGACGTG AGGTCGGACCCG
AGTG CT
GAM1338 360 LOC1524 1 13905 XP_098231.1 3 523 GATCTGTTGCCC 3 C b b
45 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGAGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1526 1 13870 XP_011108.2 3 708 TCTCTGTTGCCC 3 C b b
20 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1527 2 1141 XP_098257.1 5 422 GCTCTGTCGCCC C AA 3 C c c

19 AGCCTGGAGTGC ACTGCACTCCAG CTGGGC
AGTGGCAC TGACGTGAGGTC GACCCG
C CT
GAM1338 360 LOC1527 2 7621 XP_098257.1 5 115 ACTCTGTCGCCC C AA 3 C c c

19 AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGCGT TGACGT AGGTCGGACCCG
A CT
GAM1338 360 LOC1527 1 3556 XP_087525.1 5 421 GGTCTGTTACCC C 3 C b b
94 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCAT TGACGTGAGGTCGGACCC TTG
A
GAM1338 360 LOC1528 1 8155 XP_098266.2 3 1699 CTTTCTCGCACA - G AA 3 C c c

04 GGCTTGGAGTGC ACTGCACTCCA GCCTG GC
AGTGGTGC TGACGTGAGGT CGGAC CG
T A CT
GAM1338 360 LOC1530 1 19370 XP_098307.1 3 804 CTGATATCACCC CAA 3 C c c

77 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1538 4 6031 XP_087779.2 3 41 GCTCTGTCACCC A CAA 3 C c b

```
          11                      AGGCAGGAGTGC ACTGCACTCC GCCTGGG
                                  AGTGGCAC    TGACGTGAGG CGGACCC
                                           A      ACT
GAM1338  360   LOC1538 4  10119  XP_087779.2  3  961   AACCTGGTGCCC     -  G      A       3  C  b  b

          11                      AGGTGGAGGTGC ACTGCAC TCCA CCTGGGCA
                                  AGTGGGGG    TGACGTG AGGT GGACCCGT
                                           G   -      G
GAM1338  360   LOC1538 4  14281  XP_087779.2  3  1383  ACTCTGTTGCCC         C           3  C  b  b
          11                      AGACTGGAGTGC ACTGCACTCCAG CTGGGCAAC
                                  AGTGGTGT    TGACGTGAGGTC GACCCGTTG
                                           A
GAM1338  360   LOC1538 4  15030  XP_087779.2  3  1086  ACTCTGTCGCCC         C    AA       3  C  c
b
          11                      AGACTGGAGTGC ACTGCACTCCAG CTGGGC
                                  AGTAGCGC    TGACGTGAGGTC GACCCG
                                           A     CT
GAM1338  360   LOC1538 1  3293   XP_087798.1  5  127   ATTCTTTTGCCC                    3  C  b  b
          83                      AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
                                  AGTGGCAC    TGACGTGAGGTCGGACCCGTT

GAM1338  360   LOC1539 1  7292   XP_087801.1  5  187   ACTCTGTAGCCC         C    AA       3  C  c  c
          10                      AGTCTGGAGTGC ACTGCACTCCAG CTGGGC
                                  AGTGGTAC    TGACGTGAGGTC GACCCG
                                           T     AT
GAM1338  360   LOC1542 1  14848  XP_098505.1  5  117   CGCTCTGTCGCC           --  A       3  C  c  c
          82                      AGGTTGGAGTGC ACTGCACTCCAGCCTGG  GCA
                                  AGTGGCGT    TGACGTGAGGTTGGACC  TGT
                                              GC   C
GAM1338  360   LOC1548 1  3008   XP_098618.3  5  2826  CCTTTGTCAGCC AC-----          ---      3  C  c  c

          22                      AGGCTGGAGTGC       TGCACTCCAGCCTGG   GCAA
                                  AATGTGCA          ACGTGAGGTCGGACC   TGTT
                                         ACGTGTA            GAC
GAM1338  360   LOC1548 4  3038   XP_098626.1  5  109   ACTCTGTTGCCC         C           3  C  b  b
          77                      AGTCTGGAGTGC ACTGCACTCCAG CTGGGCAAC
                                  AGTGGCGC    TGACGTGAGGTC GACCCGTTG
                                           T
GAM1338  360   LOC1548 4  14342  XP_098626.1  3  982   ATTCTGTCTCGC        CA   ---  A       3  C  c
b
          77                      AGGCCAGAGTGC ACTGCACTC  GCCTG   GGCA
                                  AGTGGTGT    TGACGTGAG  CGGAC   CTGT
                                           AC    GCT   C
GAM1338  360   LOC1548 4  14885  XP_098626.1  3  3541  TCCTCTGTTGCC  T  C       G        3  C  c
b
          77                      AGGCTGGAATGC AC GCA TCCAGCCTGG CAAC
                                  CGTGGCGC    TG CGT AGGTCGGACC GTTG
                                           C  A       -
GAM1338  360   LOC1548 4  15947  XP_098626.1  3  1269  GCTCTGTCGCCC         G    AA       3  C  c
b
```

77 AGGGTGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGCGT TGACGTGAGGT GGACCCG
G CT
GAM1338 360 LOC1550 1 13906 XP_088142.4 3 57 GTGCTCCGGCCC C A-- AA 3 C c
c
66 AGGCGGGGGAGT ACTG ACTCC GCCTGGGC
CAGTGCCC TGAC TGAGG CGGACCCG
- GGG GC
GAM1338 360 LOC1580 1 12285 XP_088442.1 5 3579 CTCTTGTCACCC CAA 3 C c
c
14 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
AGTGGTGT TGATGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1582 1 8757 XP_098903.4 3 1266 GCTCTTTCGCCC C A AA 3 C c
c
28 AGGCCGGACTGC ACTGCA TCC GCCTGGGC
AGTGGCAG TGACGT AGG CGGACCCG
C C CT
GAM1338 360 LOC1583 1 18175 XP_098919.1 5 370 ACTCTGTCGCCC AA 3 C b b
10 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1584 1 1414 XP_098936.1 5 139 ACTCTGTTGCCC 3 C b b
02 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1584 1 7071 XP_098942.1 3 642 ACTCTGTCACTC CAA 3 C c c
36 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACTC
ACT
GAM1338 360 LOC1584 2 436 XP_098955.1 3 892 GCTCTGTCGCCC AA 3 C b b
76 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1584 2 1355 XP_098955.1 3 1218 GCTCTGTTGCCC C CT 3 C b
b
76 CAGCTTGAGTGC ACTGCACTC AGC GGGCAAC
AGTGGCGT TGACGTGAG TCG CCCGTTG
T AC
GAM1338 360 LOC1586 1 19124 XP_045161.1 3 425 TCTCTGTTGCCC AC----- 3 C c c

68 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 LOC1608 1 14437 XP_090573.3 5 536 ACTCCGTAGCCC AA 3 C b b

97 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
AT
GAM1338 360 LOC1624 2 1761 NP_835227.1 3 822 TCTCTGTTGCCC 3 C b b

27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1624 2 1761 XP_091549.3 3 816 TCTCTGTTGCCC 3 C b b
27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1624 2 12386 NP_835227.1 3 487 GCTCTGTTGCCC 3 C b b
27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1624 2 12386 XP_091549.3 3 487 GCTCTGTTGCCC 3 C b b
27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC1629 1 4276 XP_091886.7 3 255 CTCTCTGTCGCC C -- A 3 C c c
62 AGGCTGGAATGC ACTGCA TCCAGCCTGG GCA
AGTGCAGT TGACGT AGGTCGGACC TGT
A GC C
GAM1338 360 LOC1629 1 3050 XP_091890.6 3 379 GCTCTGTCGCCC C AA 3 C c c

67 ACGTTGGAGTGC ACTGCACTCCAGC TGGGC
AGTGATGT TGACGTGAGGTTG ACCCG
C CT
GAM1338 360 LOC1632 2 1413 NP_775802.1 3 1667 GCTCTGTCACCC CAA 3 C c
b
27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1632 2 9582 NP_775802.1 3 3357 CTCTTGTTGCCC C 3 C b b
27 AAGCTGGAGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGTGC TGACGTGAGGTCG ACCCGTTG
A
GAM1338 360 LOC1632 1 12968 XP_290865.1 3 506 TGCTTGTCATCC C C --- 3 C c c
33 AAGCTGGAGTAC ACTG ACTCCAGC TGG GCAA
AGTGCCAT TGAC TGAGGTCG ACC TGTT
A A TAC
GAM1338 360 LOC1674 1 10263 XP_094496.2 3 170 GTAGAATTGAGC ACT-- GG 3 C c
c
54 AGGCTGGCAATG ACTGC CCAGCCTG CAA
GCAGTTTT TGACG GGTCGGAC GTT
GTAAC GA
GAM1338 360 LOC1684 1 7426 XP_095114.2 3 695 ACTCTGTAACCC CAA 3 C c c
51 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCCT TGACGTGAGGTCGGACCC
AAT
GAM1338 360 LOC1962 1 8574 XP_113683.1 3 810 CACTCTGTCGCC -- A 3 C b b
64 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGT TGACGTGAGGTCGGACC TGT
GC C

GAM1338 360 LOC1963 1 6623 XP_113696.1 3 398 AGCCAGTGTTGC A---- A- TG 3 C c c
37 TGGCTGGAGAGG CTGC CTCCAGCC GGCAAC
CAGCAACA GACG GAGGTCGG TCGTTG
ACAAC GA --
GAM1338 360 LOC1965 1 12661 XP_116933.1 3 273 CCAGCACTGCCC GCA --- A 3 C c c
40 AGGTGGCTGGAG ACT CTCCAGCC TGGGCA
CGAGTCAC TGA GAGGTCGG ACCCGT
GC- TGG C
GAM1338 360 LOC1973 2 3887 XP_113872.2 3 2113 AATCTGTCACCC CAA 3 C c b
58 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC1973 2 5402 XP_113872.2 3 1711 CTCTTGTCGCCC AA 3 C b b
58 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC1998 2 5955 XP_117153.1 3 66 ACTTTGTCGCCC C AA 3 C c c
99 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGC
AGTGGTGC TGAC TGAGGTCGGACCCG
A CT
GAM1338 360 LOC1998 2 17148 XP_117153.1 5 183 ACTCTGTGTCTC C - A 3 C c c
99 AGGCTGGAGTAC ACTG ACTCCAGCCTG GGCA
AGTGGTGC TGAC TGAGGTCGGAC CTGT
A T G
GAM1338 360 LOC1999 1 11637 XP_114052.1 3 1224 GCTGTGTTGTCC 3 C b b
06 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCTGTTG
GAM1338 360 LOC2001 2 5066 XP_211599.1 3 1 CTGTCGTCCAGG AA 3 C c c
69 CTGGAGTGCAGT ACTGCACTCCAGCCTGGGC
ACGCAATC TGACGTGAGGTCGGACCTG
CT
GAM1338 360 LOC2001 2 6517 XP_117200.1 5 523 TTTCTGTCGTCC AA 3 C c c
69 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTAGCGC TGACGTGAGGTCGGACCTG
CT
GAM1338 360 LOC2008 2 15491 XP_117289.1 3 648 CTCTTGTTGTCC AC----- 3 C c c
60 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCTGTTG
CGCGGTA
GAM1338 360 LOC2008 2 18182 XP_117289.1 3 1712 GCTCTGTCACCC CAA 3 C c c
60 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2008 2 3376 NP_789785.1 3 934 ACTCTTGTTGCC A 3 C b b
95 CAGGCGGAGTGC ACTGCACTCC GCCTGGGCAAC

AGTGGAAC TGACGTGAGG CGGACCCGTTG

-

GAM1338 360 LOC2008 2 17681 NP_789785.1 3 934 CTCTTGTTGCCC A 3 C b b
95 AGGCGGAGTGCA ACTGCACTCC GCCTGGGCAAC
GTGGAACA TGACGTGAGG CGGACCCGTTG

-

GAM1338 360 LOC2009 1 873 XP_114317.3 3 321 GTTCTGTCACCC CAA 3 C c c
16 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGACTC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2011 2 13530 XP_290750.1 3 823 ACTCTGTGGCCC AA 3 C b b

64 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
GT

GAM1338 360 LOC2011 2 18118 NP_849158.1 3 823 ACTCTGTGGCCC AA 3 C b b

64 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
GT

GAM1338 360 LOC2012 1 19674 NP_775818.1 3 676 GCTCTGTCACTC C CAA 3 C c
c

92 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAC TGAC TGAGGTCGGACTC
A ACT

GAM1338 360 LOC2015 1 9102 XP_114343.2 3 1574 GCTCTGTTGCCC 3 C b b
62 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2017 1 18941 XP_114370.1 3 1954 ACTCTATTGCTC TG 3 C b b
25 AGGCTGGAGTGT AC CACTCCAGCCTGGGCAA
GGTGGCAG TG GTGAGGTCGGACTCGTT
GT

GAM1338 360 LOC2024 1 436 XP_117397.1 5 31 GCTCTGTCGCCC AA 3 C b b
00 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 LOC2024 1 15206 XP_114481.4 3 52 ACTCTGTTGCCC 3 C b b
04 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGG TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2024 1 1278 XP_114493.1 5 2041 TGCTCTGTCACC -- A 3 C b b
60 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGAGG TGACGTGAGGTCGGACC TGT
AC C

GAM1338 360 LOC2029 2 6782 XP_117486.2 3 2743 AGCTCTGTCACC -- A 3 C b b
34 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGC TGACGTGAGGTCGGACC TGT
AC C

GAM1338 360 LOC2029 2 9097 XP_117486.2 3 1522 ACTCTGTCACCC C CAA 3 C c
b

```
          34                          AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
                                     AGTGGCAT    TGAC TGAGGTCGGACCC
                                              A          ACT
GAM1338  360   LOC2030 1  8849  XP_114621.2  5  610   TGACCGTTGCCC AC---    ---    CC        3  C  c
c
          76                          ACCTGGAGGTGT    TGCAC  TCCAG  TGGGCAAC
                                     GCATGCCA       ACGTG  AGGTC  ACCCGTTG
                                            ACCGT    TGG    C-
GAM1338  360   LOC2035 2  2923  XP_114719.1  3  2892  CCCTTCTTGCCC AC-----              3  C  c  b

          47                          AGGCTGGAGTGC      TGCACTCCAGCCTGGGCAA
                                     AAGGGCGC         ACGTGAGGTCGGACCCGTT
                                            CGCGGGA
GAM1338  360   LOC2035 2  10631 XP_114719.1  3  1378  GCTCTGTTGCCC                    3  C  b  b
          47                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                     AGTGGTGC    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2192 1  12080 XP_166599.2  3  1202  TCTTGCTCGCCC        G     AA       3  C  c
c
          93                          AGGGTGGAGTGC ACTGCACTCCA CCTGGGC
                                     AGTGGTGT    TGACGTGAGGT GGACCCG
                                                  G      CT
GAM1338  360   LOC2197 2  3320  XP_167596.1  5  1057  ACTCTGTCATCC            CAA       3  C  c  c

          31                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGCAA    TGACGTGAGGTCGGACCT
                                                  ACT
GAM1338  360   LOC2197 2  10264 XP_167596.1  5  1214  GTCATGTTGCCC A------  CACT          3  C
c  c
          31                          AGGCTGGTCTCA      CTG   CCAGCCTGGGCAAC
                                     GGAGTCAC         GAC   GGTCGGACCCGTTG
                                            CACTGAG   TCT-
GAM1338  360   LOC2197 1  3675  XP_167601.1  3  868   GCTCTGTTGCCC                   3  C  b  b
          35                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                     AGTCGCAC    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2198 1  7138  XP_167782.1  3  1071  CTCTGTTGCCCC            -        3  C  b  b
          94                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG CAAC
                                     AGTGGCGT    TGACGTGAGGTCGGACCC GTTG
                                                  C
GAM1338  360   LOC2200 3  1413  NP_660352.1  3  542   GCTCTGTCACCC            CAA       3  C  c  c

          74                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGCAC    TGACGTGAGGTCGGACCC
                                                  ACT
GAM1338  360   LOC2200 3  2086  NP_660352.1  3  212   ACTCTGTCACAC           ---   A     3  C  c  c
          74                          AGGCTGGAGTGC ACTGCACTCCAGCCTG   GGCA
                                     AGTGGCAC    TGACGTGAGGTCGGAC   CTGT
                                                  ACA   C
GAM1338  360   LOC2200 3  4396  NP_660352.1  3  382   CACTCGTCACCC        C   CAA       3  C  c
c
```

74 CAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGTGC TGACGTGAGGTCG ACCC
- CAC
GAM1338 360 LOC2213 1 15454 XP_168093.1 5 7 CCGGGCTGTCCC A C - A 3 C c c

62 AGGCTGAGGCGG ACTGC CTC AGCCTGGG CA
TTGCTCCC TGGCG GAG TCGGACCC GT
- - T C
GAM1338 360 LOC2216 1 10616 XP_168131.1 5 810 GCTCTGTTGCCA G 3 C b b
63 AGGCTGGAGTGC ACTGCACTCCAGCCT GGCAAC
AGTGGAAC TGACGTGAGGTCGGA CCGTTG
A
GAM1338 360 LOC2219 1 3294 XP_168340.1 3 920 GGAGAATCGCTT CT AA 3 C c
c
46 GAGCTGGAGTGC ACTGCACTCCAGC GGGC
AGTGGTGC TGACGTGAGGTCG TTCG
AG CT
GAM1338 360 LOC2219 1 5581 XP_168342.1 3 56 ACTCTGTCTCCC C CA 3 C c c
64 AGGCTGGACTGC ACTGCA TCCAGCCTGGG AC
AGTGGTGC TGACGT AGGTCGGACCC TG
C TC
GAM1338 360 LOC2220 1 902 XP_166594.2 5 743 CTCTGTTGTCCA - 3 C b b
57 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC2221 1 563 XP_212100.1 5 75 ACGCAGGCTGCC C T G A 3 C c c

59 AGGCTGGCGTAC ACTG AC CCAGCCTGG CA
AGTGGCGC TGAC TG GGTCGGACC GT
A C - C
GAM1338 360 LOC2536 1 19268 XP_172985.2 5 300 GCTCTGTCTCCC CA 3 C b b
12 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
GGTGGCAC TGGCGTGAGGTCGGACCC TG
TC
GAM1338 360 LOC2538 1 7275 XP_172854.1 3 1253 ACTCTGTTGCCC 3 C b b
05 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGATGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2548 1 14560 XP_171170.1 3 279 ATGGAGAAATTC T CAA 3 C c
c
75 AGGCTGGGTGCA ACTGCAC CCAGCCTGGG
GTGGCTCA TGACGTG GGTCGGACTT
- AAA
GAM1338 360 LOC2550 2 11416 XP_173187.1 3 219 AGCACGGGGCCC C AA 3 C c
c
31 AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCGT TGACGTGAG TCGGACCCG
A GG
GAM1338 360 LOC2550 2 19099 XP_173187.1 5 310 AAGGCTTTGCAA - - CCTGG 3 C c
c

```
          31                          ACTGTGAAGTGC ACTGCACT C CAG     GCAA
                                     AGTGCCTA     TGACGTGA G GTC     CGTT
                                                    A T   AAA--
GAM1338  360    LOC2551 1   2303   XP_172941.1  3  612   CTCTCGTTGCCC AC-----                3  C  c  c
          77                          AGGCTGGAGTGC       TGCACTCCAGCCTGGGCAAC
                                     AATGGCGC           ACGTGAGGTCGGACCCGTTG
                                          CGCGGTA
GAM1338  360    LOC2554 1   9251   XP_173150.1  5  384   ACAAAGCCCTTC    C       ---    AA      3  C  c  c

          58                          AGGCTGGAGTAT ACTG ACTCCAGCCT   GGGC
                                     AGTGGCAT     TGAT TGAGGTCGGA   CCCG
                                               A         CTT    AA
GAM1338  360    LOC2554 1   18594  XP_172581.2  3  2633   CCTTTGTCACCC        A      CAA        3  C  c
c
          88                          AGGCCGGAGTGC ACTGCACTCC GCCTGGG
                                     AGTGGCAT     TGACGTGAGG CGGACCC
                                                    C       ACT
GAM1338  360    LOC2559 1   902    XP_171083.2  5  863    CTCTGTTGTCCA            -           3  C  b  b
          75                          AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
                                     AGTAGTGC     TGATGTGAGGTCGGA CCTGTTG
                                                    A
GAM1338  360    LOC2564 1   9741   XP_171149.1  3  1402   GGGAGGTTGCCC    - CT    - C-          3  C  c
c
          01                          ATTGTTTGGTTG ACTG CA  CCAG C  TGGGCAAC
                                     CCAGTCAT     TGAC GT  GGTT G  ACCCGTTG
                                               C  T-    T TT
GAM1338  360    LOC2566 1   3106   XP_172864.1  3  860    ACTCTGTCACCC              CAA        3  C  c  c
          14                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGCGC     TGACGTGAGGTCGGACCC
                                                    ACT
GAM1338  360    LOC2829 1   1691   XP_210837.1  3  861    GCTCTGTCTCCT     A         CA         3  C  c  c
          72                          AGGCTGGAGCGC ACTGC CTCCAGCCTGGG  AC
                                     AGTGGTGC     TGACG GAGGTCGGATCC  TG
                                               C          TC
GAM1338  360    LOC2829 2   10460  XP_210845.1  5  33     ACTTTGTCACCC    C         CAA        3  C  c
b
          87                          AGGCTGGAGTAT ACTG ACTCCAGCCTGGG
                                     AGTGGCAC     TGAT TGAGGTCGGACCC
                                               A          ACT
GAM1338  360    LOC2829 2   12386  XP_210845.1  3  527    GCTCTGTTGCCC                      3  C  b  b
          87                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                     AGTGGTGT     TGACGTGAGGTCGGACCCGTTG

GAM1338  360    LOC2829 1   5482   XP_208473.1  3  986    GCCCTGTTGCCC     A                3  C  b  b
          97                          AGGCTGGAGAGC ACTGC CTCCAGCCTGGGCAAC
                                     AGTGGTGC     TGACG GAGGTCGGACCCGTTG
                                               A
GAM1338  360    LOC2830 1   18916  XP_210875.1  3  1387   AGTTTGTCACCC              CAA        3  C  c
c
          61                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
```

AGTGGCAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2830 1 6936 XP_208509.1 3 177 ATTGTGTTCCCC C C 3 C b b
87 AGGCTGAAGTGC ACTGCACT CAGCCTGGG AAC
AGTGGCAT TGACGTGA GTCGGACCC TTG
A C
GAM1338 360 LOC2830 1 6866 XP_210885.1 5 1720 GCTCTGTCGCCC C AA 3 C c
c
89 AGGCTCGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCAT TGACGTGAG TCGGACCCG
C CT
GAM1338 360 LOC2831 1 1505 XP_210895.1 3 711 ACTCTCTTGCCC 3 C b b
19 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTAT TGACGTGAGGTCGGACCCGTT

GAM1338 360 LOC2831 1 469 XP_208525.3 3 379 TCTCTGTCACCC C CAA 3 C c c

30 AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCGT TGACGT AGGTCGGACCC
A ACT
GAM1338 360 LOC2831 1 15581 XP_210911.1 3 453 CACCCTGTTGCC C G 3 C b b

40 AGGCTGGAATGC ACTGCA TCCAGCCTGG CAAC
AGTGGCGC TGACGT AGGTCGGACC GTTG
A -
GAM1338 360 LOC2831 1 14843 XP_210920.1 3 2296 CACTCTGTCACC -- A 3 C b b
43 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC2831 1 17431 XP_210917.2 5 316 CCTCTGTCATCC CAA 3 C c c

52 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCT
ACT
GAM1338 360 LOC2831 1 19643 XP_208535.1 3 648 GCTCTGTTGCCC 3 C b b
70 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGA TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2831 1 13142 XP_210903.1 3 984 CTCTTGTTGCCC AC----- 3 C c c

77 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 LOC2832 1 15736 XP_208555.2 3 1675 GTACTGTTGTCC A 3 C b b
15 AGGCTGGAGCGC ACTGC CTCCAGCCTGGGCAAC
AGTTGATT TGACG GAGGTCGGACCTGTTG
C
GAM1338 360 LOC2832 1 10625 NP_787089.1 5 62 GCTCTGTCGCCC AA 3 C c c
41 AGGTTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTTGGACCCG

CT
GAM1338 360 LOC2832 1 13142 XP_210961.1 3 2047 CTCTTGTTGCCC AC----- 3 C c c
78 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCCGTTG
CACGGTA
GAM1338 360 LOC2832 1 438 XP_210962.1 3 345 ACTCTGTCACCC CAA 3 C c c
93 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2833 1 2314 XP_210973.1 3 15 TGCTCCGTTGCC AC----- C 3 C c c
23 TAGCTGGAGTGC TGCACTCCAGC TGGGCAAC
ACGATCTC ACGTGAGGTCG ATCCGTTG
CTCTAGC -
GAM1338 360 LOC2833 2 9238 XP_210981.1 3 1636 GCTCTGTCACCC A CAA 3 C c b
35 AGGCCGGAGTGC ACTGCACTCC GCCTGGG
AGTGGTGC TGACGTGAGG CGGACCC
C ACT
GAM1338 360 LOC2833 2 10626 XP_210981.1 3 1368 GCTCTGTTGCCC 3 C b b
35 AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGATGTGAGGTCGGACCCGTTG
GAM1338 360 LOC2833 1 8862 XP_208647.1 3 807 ACTCTGTCACCC CAA 3 C c c
77 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2833 1 7011 XP_211007.1 3 1633 GCTCTTACGCCC G C AA 3 C c c
87 AGGCTGGAATGA ACT CA TCCAGCCTGGGC
AGTGGCAT TGA GT AGGTCGGACCCG
A A CA
GAM1338 360 LOC2833 1 11655 XP_211021.1 5 133 ACTCTGTTGCCC C 3 C b b
94 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGCAC TGAC TGAGGTCGGACCCGTTG
A
GAM1338 360 LOC2833 1 13838 XP_211020.1 3 527 CACTCTGTTGCT G 3 C b b
95 AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGCAC TGACGTGAGGTCGGATC GTTG
-
GAM1338 360 LOC2834 1 6836 XP_211032.1 5 1942 CGCTGTATTGCC C G 3 C b b
32 AGACTGGAGTGC ACTGCACTCCAG CTGG CAA
AGTGGCGT TGACGTGAGGTC GACC GTT
A -
GAM1338 360 LOC2834 1 16416 XP_211034.1 5 1756 TTGCCATCTCAG C -- ---- 3 C c c
34 TTGCTGCAGTGC ACTGCACT CAGC CTG GGCAA
AGTGAATT TGACGTGA GTCG GAC CCGTT
C TT TCTA

GAM1338 360 LOC2834 1 5582 XP_211043.1 3 164 GCTCTGTCGCCC C AA 3 C c c

41 AGGCTGCAGTGC ACTGCACT CAGCCTGGGC
GGTGGTGC TGGCGTGA GTCGGACCCG
C CT

GAM1338 360 LOC2834 1 4817 XP_211037.1 5 973 ACACCTCTTGCC --- -- G 3 C b b

42 AGGCTGCAGAGC ACTGCA CTC CAGCCTGG CAA
TATGCAGT TGACGT GAG GTCGGACC GTT
ATC AC -

GAM1338 360 LOC2834 1 9159 XP_211044.1 5 305 ACTGTGTCATGC --- A 3 C c c

45 AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTGGCAT TGACGTGAGGTCGGAC CTGT
GTA G

GAM1338 360 LOC2834 1 3497 XP_208679.1 5 652 GCCATGTTGCCC A----- G CT- 3 C c
c

52 AGGCTGGTCTTG CT CA CCAGCCTGGGCAAC
AGAACTCC GA GT GGTCGGACCCGTTG
CCTCAA - TCT

GAM1338 360 LOC2834 1 12385 XP_211049.1 5 127 ACTCTGTCACCC CAA 3 C c c

54 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2834 1 3857 XP_211050.1 3 1034 AAAACCTTTGTC A T G 3 C c c

67 AGGCTGGGCGCG ACTGC C CCAGCCTGG CAA
GTGGCTCA TGGCG G GGTCGGACT GTT
C - -

GAM1338 360 LOC2834 1 12806 XP_211056.1 3 1713 GTTCTCTTGCCC 3 C b b

75 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCAC TGACGTGAGGTCGGACCCGTT

GAM1338 360 LOC2835 1 18182 XP_211075.1 3 1819 GCTCTGTCACCC CAA 3 C c
c

07 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2835 1 6317 XP_210264.2 3 714 CACCTTGTTCCC T TCC C 3 C c
c

14 AGGCTGTGCCGT AC GCAC AGCCTGGG AAC
CTTCTCCT TG CGTG TCGGACCC TTG
C --- -

GAM1338 360 LOC2835 1 13197 XP_211083.1 3 3278 ACTCTGTCACCC CAA 3 C c
c

34 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCTT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2835 1 10790 XP_211110.1 3 612 GCTCTGTCCCCC T CA 3 C c
c

51 AGGCTGGCGTGC ACTGCAC CCAGCCTGGG AC
AGTAGCAT TGACGTG GGTCGGACCC TG

```
                                                C        CC
GAM1338  360    LOC2835 2  8540   XP_211095.1   5  884    ACTCTGTTGCCC    C  TC              3  C  b  b

          75                          AGGCTGAGGTAC ACTG AC  CAGCCTGGGCAAC
                                     AGTGGCGT    TGAC TG  GTCGGACCCGTTG
                                               A  GA
GAM1338  360    LOC2835 2  13153  XP_211095.1   5  421    ACTCTGTTGCCC AC-----      C           3  C  c
b
          75                          AGGCTAGAGTGC       TGCACTC AGCCTGGGCAAC
                                     ACTAATAC          ACGTGAG TCGGACCCGTTG
                                             CATAATC      A
GAM1338  360    LOC2835 1  14938  NP_787093.1   3  910    GCTCTGTTGCCC                    3  C  b  b
          88                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                     GGTGGACT    TGGCGTGAGGTCGGACCCGTTG

GAM1338  360    LOC2836 2  1137   XP_211126.1   5  3888   GCTCTGTTGCCC    C               3  C  b  b
          24                          AGGCTGGAGTCC ACTG ACTCCAGCCTGGGCAAC
                                     AGTGGCAT    TGAC TGAGGTCGGACCCGTTG
                                               C
GAM1338  360    LOC2836 2  13972  XP_211126.1   5  750    ACTCTCACACCC            CAA       3  C  c  b

          24                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTCTCAA    TGACGTGAGGTCGGACCC
                                                  ACA
GAM1338  360    LOC2836 2  3786   XP_211134.1   5  1237   GCTCTGTCGCCC       C       AA        3  C  c
b
          37                          AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
                                     AGTGGTAT    TGACGTGAG TCGGACCCG
                                               A       CT
GAM1338  360    LOC2836 2  12382  XP_211134.1   5  360    GCTCTGTCGCCC            AA        3  C  b  b

          37                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                     AGTGGTGC    TGACGTGAGGTCGGACCCG
                                                  CT
GAM1338  360    LOC2836 1  435    XP_208764.1   3  226    GCTCTGTTGCCC                   3  C  b  b
          41                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                     AGTGGCAT    TGACGTGAGGTCGGACCCGTTG

GAM1338  360    LOC2836 1  11655  XP_211152.1   5  18     ACTCTGTTGCCC    C               3  C  b  b
          72                          AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
                                     AGTGGCAC    TGAC TGAGGTCGGACCCGTTG
                                               A
GAM1338  360    LOC2836 1  16069  XP_208788.1   3  334    AAGAAATTTGTC       T       G         3  C  b  b
          93                          AGGCTGGGTGCA ACTGCAC CCAGCCTGG CAA
                                     GTGGCTCA    TGACGTG GGTCGGACT GTT
                                               -       -
GAM1338  360    LOC2837 2  777    XP_211170.3   3  3386   TGCTCTGTCACC            --  A       3  C  c  c
          01                          AGGCTGGAGTGC ACTGCACTCCAGCCTGG  GCA
                                     GGTGGCAT    TGGCGTGAGGTCGGACC  TGT
                                                  AC  C
```

GAM1338 360 LOC2837 2 6491 XP_211170.3 3 1558 GCCTTCTTCCCC G - CAA 3 C c c

01 AGGCTGGGAGTG ACT CACTCC AGCCTGGG
GGTGAGAC TGG GTGAGG TCGGACCC
- G CTT

GAM1338 360 LOC2837 1 3109 XP_208115.1 3 289 GCTCTGTCGCCC AA 3 C b b

41 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 LOC2837 1 3888 XP_208835.1 3 298 GCGCTGTTGCCC AC----- CC 3 C c c

67 AGGCTCTAGTGC TGCACT AGCCTGGGCAAC
AATGGCAC ACGTGA TCGGACCCGTTG
CACGGTA TC

GAM1338 360 LOC2837 1 15679 XP_211199.1 5 1256 GCTCTGTCGCCC AA 3 C b b

78 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGG TGACGTGAGGTCGGACCCG
CT

GAM1338 360 LOC2838 1 11237 XP_208122.1 3 1460 CTAGTGTTGCCC 3 C b b

01 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2838 1 16635 XP_208850.1 3 948 ACTCTGTCATCC CAA 3 C c c

02 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCT
ACT

GAM1338 360 LOC2838 1 3834 XP_211218.1 3 255 ACTCTGTCACCC T CAA 3 C c c

18 CGGCTGGAGTGC ACTGCACTCCAGCC GGG
AGTGGTGT TGACGTGAGGTCGG CCC
C ACT

GAM1338 360 LOC2838 1 2515 NP_848611.1 5 91 CTGGAGTTGCCC GCA - -- 3 C c c

49 AGGCCCTGTGAG ACT CTC CA GCCTGGGCAAC
CAAGTGGC TGA GAG GT CGGACCCGTTG
AC- T CC

GAM1338 360 LOC2838 1 2515 XP_208870.1 5 91 CTGGAGTTGCCC GCA - -- 3 C c c

49 AGGCCCTGTGAG ACT CTC CA GCCTGGGCAAC
CAAGTGGC TGA GAG GT CGGACCCGTTG
AC- T CC

GAM1338 360 LOC2838 1 12708 XP_211229.1 3 678 ACTCTGTCACCG G CAA 3 C c c

51 AGGTTGGAGTGC ACTGCACTCCAGCCT GG
AGTGGTAT TGACGTGAGGTTGGA CC
G ACT

GAM1338 360 LOC2838 1 11601 XP_211233.1 3 694 GAAAGACTGAAG GGG A 3 C c c

```
          56                        AGGCTGGAGTGC ACTGCACTCCAGCCT  CA
                                   AGTGGCGC    TGACGTGAGGTCGGA  GT
                                               GAA  C
GAM1338  360   LOC2838 2  8996  NP_787095.1  3  1033  GCTCTGTCGACC A-----          ---  A  3  C  c
c
          61                        AGGCTGGAGTGC     CTGCACTCCAGCCTGG  GCA
                                   AGGGGCAC         GACGTGAGGTCGGACC  TGT
                                         CACGGG           AGC  C
GAM1338  360   LOC2838 2  10879 NP_787095.1  3  712   CCTCTGTCGTCC            AA       3  C  c  c
          61                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                   AGTGGCAC    TGACGTGAGGTCGGACCTG
                                               CT
GAM1338  360   LOC2838 1  14614 XP_208875.1  3  1505  CGCTTGTTGCCC AC-----              3  C  c
c
          63                        AGGCTGGAGTGC      TGCACTCCAGCCTGGGCAAC
                                   AATGGCGC          ACGTGAGGTCGGACCCGTTG
                                         CGCGGTA
GAM1338  360   LOC2838 1  9775  XP_211248.2  5  723   GCTCTGTCTCCC            CA       3  C  b  b
          87                        GGGCTGGAGTGC ACTGCACTCCAGCCTGGG  AC
                                   AGTGGCGC    TGACGTGAGGTCGGGCCC  TG
                                               TC
GAM1338  360   LOC2838 2  2692  XP_211249.1  3  1550  GCTCTGCTGCCC     C        A       3  C  b  b

          88                        AGGCTGGAATGC ACTGCA TCCAGCCTGGGCA
                                   AGTGGTGC    TGACGT AGGTCGGACCCGT
                                               A          C
GAM1338  360   LOC2838 2  5011  XP_211249.1  3  1413  GGTCCCAGCTCC    CA       - AA       3  C  c
b
          88                        AGGCTGGAGCCA ACTG  CTCCAGCCTGG GC
                                   GTGAAGGG    TGAC  GAGGTCGGACC CG
                                         C-         T  AC
GAM1338  360   LOC2838 1  13686 XP_208899.1  3  783   ATTCTGTCACCC        A     CAA       3  C  c
c
          89                        AGGCCGGAGTGC ACTGCACTCC GCCTGGG
                                   AGTGGTGT    TGACGTGAGG CGGACCC
                                               C      ACT
GAM1338  360   LOC2839 2  3604  XP_208909.1  5  2715  ACTCTGTTGCCC                    3  C  b  b
          28                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                   AGTGTCAC    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2839 2  13293 XP_208909.1  5  2419  GTTCTGCTGCCC             A       3  C  b  b
          28                        AGGTTGGAGTGC ACTGCACTCCAGCCTGGGCA
                                   AGTGGCAC    TGACGTGAGGTTGGACCCGT
                                               C
GAM1338  360   LOC2839 1  10232 XP_208905.2  5  919   GCTCCGTCACCC            CAA       3  C  c
c
          29                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                   AGTGGCGC    TGACGTGAGGTCGGACCC
                                               ACT
GAM1338  360   LOC2839 1  1384  XP_208145.2  3  1457  CTAGTGTCACCC            CAA       3  C  c  c
```

64 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGATCC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2840 1 795 XP_211298.1 3 16 ACTCTTGTTGCC AC----- C 3 C c c
16 TAGCTGGAGTGC TGCACTCCAGC TGGGCAAC
AATGGCGC ACGTGAGGTCG ATCCGTTG
CGCGGTA -
GAM1338 360 LOC2840 1 3858 XP_208961.1 3 353 GCTCTGTAACTC CAA 3 C c c
17 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACTC
AAT
GAM1338 360 LOC2840 1 19482 XP_211302.1 3 2840 GCTCTGTTGCCC C T 3 C b b

19 TGGCTGGAGTAC ACTG ACTCCAGCC GGGCAAC
AGTGGCAT TGAC TGAGGTCGG CCCGTTG
A T
GAM1338 360 LOC2840 2 429 XP_208983.3 3 1472 GCTCTGTTGCCC C 3 C b b
23 AGACTGGAGTGC ACTGCACTCCAG CTGGGCAAC
AGTGGCGT TGACGTGAGGTC GACCCGTTG
A
GAM1338 360 LOC2840 2 5520 XP_208983.3 3 1017 ACTGTGTCGCCC AA 3 C b b

23 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2840 1 17222 XP_208152.1 3 1241 TCACTGTCACCC A CAA 3 C c
c
48 AGGCCGGAGTGC ACTGCACTCC GCCTGGG
AGTGGCAC TGACGTGAGG CGGACCC
C ACT
GAM1338 360 LOC2840 1 17713 XP_208992.1 3 181 CCTCTGTTGTCC C C 3 C b b
63 AAGCTAGAGTGC ACTGCACTC AGC TGGGCAAC
AGTGATAC TGACGTGAG TCG ACCTGTTG
A A
GAM1338 360 LOC2840 2 5751 XP_211321.1 3 982 ACTCAGTCGCCC AA 3 C b b
74 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2840 2 18547 XP_211321.1 3 57 GCCCTGTTGCCC C 3 C b b
74 AGGCTGAAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGGTGC TGACGTGA GTCGGACCCGTTG
A
GAM1338 360 LOC2840 1 18527 XP_211323.1 3 1 CTGTCACCCAGG C CAA 3 C c
c
82 CTGAAGTGCAGT ACTGCACT CAGCCTGGG
GCAGGACC TGACGTGA GTCGGACCC
A ACT
GAM1338 360 LOC2840 3 16884 XP_211324.1 3 844 ACTCTGTCACCC T CAA 3 C c
c
95 TGGCTGGAGTGC ACTGCACTCCAGCC GGG

GGTGGCGA TGGCGTGAGGTCGG CCC
T ACT

GAM1338 360 LOC2840 3 18259 XP_211324.1 3 1042 GCTCTTTCGCCC C A AA 3 C c c
95 AGGCCGGACTGC ACTGCA TCC GCCTGGGC
AGTGGCGC TGACGT AGG CGGACCCG
C C CT

GAM1338 360 LOC2840 3 19595 XP_211324.1 3 142 GCTCTGTCATTC --- A 3 C c c
95 AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTGGTGC TGACGTGAGGTCGGAC CTGT
TTA C

GAM1338 360 LOC2840 1 18178 XP_209008.3 3 197 GCTCTGTTACCC C 3 C b b
98 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG AAC
AGTGGTGC TGATGTGAGGTCGGACCC TTG
A

GAM1338 360 LOC2841 1 11656 XP_209015.1 3 1540 GTCCAGTGCTCC T A - A 3 C c c
00 AGGCTGGGGGCC AC GC CTCCAGCCTGG GCA
GTGGATCC TG CG GGGGTCGGACC CGT
C - T G

GAM1338 360 LOC2841 1 4581 XP_209019.1 5 410 ACTCTGTTGCCC --- 3 C b b
01 AGGTTGGAGTAC ACTGC ACTCCAGCCTGGGCAAC
AGCAGTGC TGACG TGAGGTTGGACCCGTTG
ACA

GAM1338 360 LOC2841 3 6349 XP_211327.3 3 606 CTTTTGTTGCCC AC----- 3 C c c
02 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AACGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGCA

GAM1338 360 LOC2841 3 8270 XP_211327.3 3 801 CCTCTGTGGCCC A C AA 3 C c c
02 AGGCTGAAGAGC ACTGC CT CAGCCTGGGC
AGTAGTGT TGACG GA GTCGGACCCG
A A GT

GAM1338 360 LOC2841 3 17111 XP_211327.3 5 861 GCTTTGTCACCC CAA 3 C c c
02 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2841 1 11347 XP_209024.1 3 57 GCTTTGTCGCCC T AA 3 C c c
17 TGGCTGGAGTGC ACTGCACTCCAGCC GGGC
AGTTGCGC TGACGTGAGGTCGG CCCG
T CT

GAM1338 360 LOC2841 1 17271 XP_211342.1 3 0 TCGCCCAGGCTG AA 3 C b b
28 GAGTGCAGTGGT ACTGCACTCCAGCCTGGGC
AGATCAGG TGACGTGAGGTCGGACCCG
CT

GAM1338 360 LOC2841 1 5319 XP_209032.1 3 539 TGACTGTTGCCC AC----- 3 C c c
35 AGGCTGGAGTGT TGCACTCCAGCCTGGGCAAC
AATGGCGC ATGTGAGGTCGGACCCGTTG
CGCGGTA

GAM1338 360 LOC2841 2 8524 XP_209059.1 5 421 CTCTCGTTGCCA AC----- G 3 C c c

83 AGGCTGGAGTGC TGCACTCCAGCCT GGCAAC
AATGGCAC ACGTGAGGTCGGA CCGTTG
CACGGTA A

GAM1338 360 LOC2841 2 11460 XP_209059.1 5 921 TATCGATAGCCC C A AA 3 C c c

83 AGGCAGGAGTAC ACTG ACTCC GCCTGGGC
AGTGGCAC TGAC TGAGG CGGACCCG
A A AT

GAM1338 360 LOC2841 1 18182 XP_209060.2 3 1161 GCTCTGTCACCC CAA 3 C c c

86 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2842 1 5521 XP_211419.1 3 1828 ACTCTGTCTCCC CA 3 C b b

86 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
TC

GAM1338 360 LOC2842 1 7635 XP_209105.1 3 145 CTCTTGTTACCC A C 3 C b b

89 AGGCAGGAGTGC ACTGCACTCC GCCTGGG AAC
AGTGGCGT TGACGTGAGG CGGACCC TTG
A A

GAM1338 360 LOC2843 1 16163 XP_211426.1 3 314 CTCTTATTGCCC 3 C b b

04 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGACGA TGACGTGAGGTCGGACCCGTT

GAM1338 360 LOC2843 2 5320 XP_209162.1 3 1765 ACTCTCTCGCCC AA 3 C b b

17 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT

GAM1338 360 LOC2843 2 11486 XP_209162.1 3 812 ATTCTGTCACAC T C --- A 3 C c b

17 AGTCTGGAGTGC AC GCACTCCAG CTG GGCA
TGTGGTGC TG CGTGAGGTC GAC CTGT
T T ACA C

GAM1338 360 LOC2843 1 11657 XP_209143.1 3 1032 GTTCTGTCGTCC AA 3 C c c

25 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
GGTGGCGT TGGCGTGAGGTCGGACCTG
CT

GAM1338 360 LOC2843 1 10666 XP_211435.1 3 529 CACTTGTCACCC CAA 3 C c c

62 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCTC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2843 1 3968 XP_211439.1 5 345 GTTTTGTTGCCC A----- CACT 3 C c c

73 AGGCTGGTCTCC CTG CCAGCCTGGGCAAC
AGCTTCTA GAC GGTCGGACCCGTTG

ATCTTC CTCT
GAM1338 360 LOC2843 1 13618 XP_209154.1 3 930 GCTCTGTCATCC CAA 3 C c c

75 AGGTTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTTGGACCT
ACT
GAM1338 360 LOC2843 2 3410 XP_209157.1 3 663 CTCTTATTGCCC AC----- 3 C c c
76 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATGGTGC ACGTGAGGTCGGACCCGTT
CGTGGTA
GAM1338 360 LOC2843 2 9328 XP_209157.1 3 1219 GCTCTGTCGCCC C C AA 3 C c
c
76 AAGCTGAAGTGC ACTGCACT CAGC TGGGC
AGTGGTGC TGACGTGA GTCG ACCCG
A A CT
GAM1338 360 LOC2843 1 2198 XP_209163.1 3 383 GCTCTATTGCCC C 3 C b b
79 AGTCTGGAGTGC ACTGCACTCCAG CTGGGCAA
AGTGGCAT TGACGTGAGGTC GACCCGTT
T
GAM1338 360 LOC2843 1 2360 XP_211452.1 3 1674 GCTGTGTTGTCC AC----- 3 C c c

96 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGT ACGTGAGGTCGGACCTGTTG
TGTGGTA
GAM1338 360 LOC2844 1 10732 XP_211443.1 5 366 GCTCTGTTGCCC T 3 C b b
08 AGGCTGGTGTGT ACTGCAC CCAGCCTGGGCAAC
AGTGATCT TGATGTG GGTCGGACCCGTTG
T
GAM1338 360 LOC2844 1 7072 XP_211449.1 3 637 GGTGGTTGCTGA G G- 3 C c c
10 AGGCTGGAGTGG ACT CACTCCAGCCT GGCAAC
GTGTGGCA TGG GTGAGGTCGGA TCGTTG
- AG
GAM1338 360 LOC2844 3 2985 XP_209200.1 3 54 GCTTAGCCGTCC C AA 3 C c b
21 AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTAGTGC TGACGTGAG TCGGACCTG
A CC
GAM1338 360 LOC2844 3 3295 XP_209200.1 5 1327 GCTATGTTGCCC AC------ CT 3 C c
b
21 AGGCTGGTTGCA TGCA CCAGCCTGGGCAAC
AACTTCTG ACGT GGTCGGACCCGTTG
GTCTTCAA T-
GAM1338 360 LOC2844 3 3295 XP_209200.1 5 1371 GCTATGTTGCCC AC------ CT 3 C c
b
21 AGGCTGGTTGCA TGCA CCAGCCTGGGCAAC
AACTTCTG ACGT GGTCGGACCCGTTG
GTCTTCAA T-
GAM1338 360 LOC2844 3 15524 XP_209200.1 5 1198 GCTCTGTTGCCC 3 C b b
21 GGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGGCCCGTTG

GAM1338 360 LOC2844 2 932 XP_209198.1 3 475 ATGCTGCTGCCC A 3 C b b
26 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
AGTGGTGC TGACGTGAGGTCGGACCCGT
C
GAM1338 360 LOC2844 2 19419 XP_209198.1 3 310 GCTCTGTCGCCC AA 3 C b b
26 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGACAT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2844 1 6140 XP_290862.1 3 85 ACTCTGCTGCCC C A 3 C c c
36 GGGCTAGAGTGC ACTGCACTC AGCCTGGGCA
AGTGGTGG TGACGTGAG TCGGGCCCGT
A C
GAM1338 360 LOC2844 1 12050 XP_209210.1 3 761 CCCTCTGTCACC -- A 3 C b b
40 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC2844 1 18896 XP_209216.1 5 1115 ACTCTGTTGCCC C 3 C b b
54 AGGCTGAAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGGTGT TGACGTGA GTCGGACCCGTTG
A
GAM1338 360 LOC2844 2 6643 XP_211470.1 3 255 GCTCTGTTATCC T GC 3 C c c
56 AGGCTGGTGTGC ACTGCAC CCAGCCTGG AAC
AGTGATAC TGACGTG GGTCGGACC TTG
T TA
GAM1338 360 LOC2844 2 10594 XP_211470.1 5 657 GCTCTGTCACCT C CAA 3 C c
c
56 AGGCTGCAGTGC ACTGCACT CAGCCTGGG
AGTGGCAC TGACGTGA GTCGGATCC
C ACT
GAM1338 360 LOC2844 1 4926 XP_209225.1 3 1167 ACTCTGTCACCC CT CAA 3 C c
c
71 AGGCTGGGATGC ACTGCA CCAGCCTGGG
AGTGGCTT TGACGT GGTCGGACCC
AG ACT
GAM1338 360 LOC2844 1 17171 XP_211478.1 5 3281 GGCCTGAAGCCT CA-- AA 3 C c
c
75 AGGCTGGAGGGT ACTG CTCCAGCCTGGGC
TCAGTCGG TGAC GAGGTCGGATCCG
TTGG AA
GAM1338 360 LOC2845 1 16234 XP_211500.1 3 1746 TCTCTGTCGCCC CA AA 3 C c
c
12 AGGCTGGAGCCC ACTG CTCCAGCCTGGGC
AGTGGCGA TGAC GAGGTCGGACCCG
CC CT
GAM1338 360 LOC2845 1 19066 XP_211502.1 5 907 GCCCAATAGCCC AA 3 C b b
13 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAG TGACGTGAGGTCGGACCCG
AT

GAM1338 360 LOC2845 1 2846 XP_211513.1 5 339 GCTCTGTCTCCC A----- CA 3 C c c

31 AGGCTGGAGTGC CTGCACTCCAGCCTGGG AC
AGGCTTGG GACGTGAGGTCGGACCC TG
GGTTCG TC

GAM1338 360 LOC2845 1 17959 XP_211515.1 3 1302 ACTCTGTCACCC CAA 3 C c
c

51 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2845 1 11682 XP_211522.1 3 6 ACTCTGTCTCCC G C CA 3 C c c

77 AGACTGGAGTGA ACT CACTCCAG CTGGG AC
GTGGTGTG TGA GTGAGGTC GACCC TG
- A TC

GAM1338 360 LOC2845 1 902 XP_209278.3 5 72 CTCTGTTGTCCA - 3 C b b
87 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A

GAM1338 360 LOC2846 1 11652 XP_211552.1 3 976 GCTCGGTCACCT CAA 3 C c
c

11 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
AGTGGCGC TGATGTGAGGTCGGATCC
ACT

GAM1338 360 LOC2846 1 20050 XP_211561.1 5 504 ACTCTGTTGCCT AC----- C 3 C c
c

28 AGACTGGAGTGC TGCACTCCAG CTGGGCAAC
AATGGCGT ACGTGAGGTC GATCCGTTG
TGCGGTA A

GAM1338 360 LOC2846 1 19894 XP_211583.1 3 659 AACAGTAGGTCC - C AA 3 C c
c

68 AGGCTGGATGCT ACT GCA TCCAGCCTGGGC
GGTATGAT TGG CGT AGGTCGGACCTG
T - GA

GAM1338 360 LOC2846 1 8487 XP_209319.1 5 556 GCTCTGTCACCC -- CAA 3 C c c

75 AGGCTGGAGTGT ACTGCAC TCCAGCCTGGG
GCAGTGGC TGACGTG AGGTCGGACCC
TG ACT

GAM1338 360 LOC2847 1 902 XP_294994.1 5 865 CTCTGTTGTCCA - 3 C b b
01 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A

GAM1338 360 LOC2847 1 12721 XP_209332.1 3 522 GCTCTGTTGCCC A------ T 3 C c c

08 AGGCTGGGTGCA CTGCAC CCAGCCTGGGCAAC
GCGGTGCG GACGTG GGTCGGACCCGTTG
GCGTGGC -

GAM1338 360 LOC2847 2 6492 XP_211602.1 3 59 ACTCTGCCACCC C CAA 3 C c b

23 AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGCAC TGACGTGAGGTCG ACCC
A ACC
GAM1338 360 LOC2847 2 17106 XP_211602.1 3 471 GCTTTGTTGCCC 3 C b b
23 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGTGC TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2848 3 11447 XP_209371.1 3 1212 TTTTGCCCAGGC ---- 3 C b b
05 TGGATGGAGTGC ACTGCACTCCA GCCTGGGCAA
AGTGGCGT TGACGTGAGGT CGGACCCGTT
AGGT
GAM1338 360 LOC2848 3 17164 XP_209371.1 3 1212 GCTCTTTTGCCC ---- 3 C b b
05 AGGCTGGATGGA ACTGCACTCCA GCCTGGGCAA
GTGCAGTG TGACGTGAGGT CGGACCCGTT
AGGT
GAM1338 360 LOC2848 3 18781 XP_209371.1 3 1110 ACTCTGCTGCTC A 3 C b b
05 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
AGTGGTGC TGACGTGAGGTCGGACTCGT
C
GAM1338 360 LOC2848 1 4527 XP_211661.1 5 445 CTCTTGTTGCCC AC----- 3 C c c
39 GGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGGCCCGTTG
CGCGGTA
GAM1338 360 LOC2848 1 1299 XP_211672.1 3 69 ACTCTGTTGCCC AC----- 3 C c c
65 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
GATGGCAT GCGTGAGGTCGGACCCGTTG
TACGGTA
GAM1338 360 LOC2848 2 2751 XP_209394.1 3 615 TGCTCTGCGCCC G AA 3 C c c

74 AGGATGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGCAT TGACGTGAGGT GGACCCG
A CG
GAM1338 360 LOC2848 2 14015 XP_209394.1 3 1070 CGCTCTGTCGCC C -- A 3 C c
c
74 AGGCTGGAGTAC ACTG ACTCCAGCCTGG GCA
AGTGGTGT TGAC TGAGGTCGGACC TGT
A GC C
GAM1338 360 LOC2849 1 17477 XP_211696.1 5 656 GTTTTGTCGCCC AA 3 C b b
34 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2849 1 5006 XP_211705.1 3 413 GCTCCGTCGCCC CT AA 3 C c
c
47 AGGCTGGCATGC ACTGCA CCAGCCTGGGC
AGTTGCGC TGACGT GGTCGGACCCG
AC CT
GAM1338 360 LOC2849 1 6753 XP_211703.1 3 163 CACTCTGTCGCC -- A 3 C b b
50 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGT TGACGTGAGGTCGGACC TGT
GC C

GAM1338 360 LOC2849 1 8699 XP_211715.1 5 635 ACTGTCTTGCCC A--- A T ---- 3 C c c

60 AGGTAAGCTGGG CTGC C CCAGC CTGGGCAA
GCAGAGCC GACG G GGTCG GACCCGTT
CCGA - - AATG

GAM1338 360 LOC2850 1 14276 XP_209440.1 3 2381 GCTCTGTCACCC C CAA 3 C c
c

26 AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGTGC TGACGTGAGGTC GACCC
A ACT

GAM1338 360 LOC2850 1 5725 XP_211740.1 5 1119 ACTCTCTTGCCC A--- A T ---- 3 C c
c

32 AGGTAAGCTGGG CTGC C CCAGC CTGGGCAA
GCAGAGCC GACG G GGTCG GACCCGTT
CCGA - - AATG

GAM1338 360 LOC2850 1 18085 XP_209464.1 3 986 GCTCTATCACCC C CAA 3 C c
c

83 AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGTAC TGACGTGA GTCGGACCC
A ACT

GAM1338 360 LOC2850 1 20100 XP_209465.1 3 41 CTCTTGTTGCCC AC----- CA 3 C c
c

88 AGGCCAGAGTGC TGCACTC GCCTGGGCAAC
AATGGCGT ACGTGAG CGGACCCGTTG
TGCGGTA AC

GAM1338 360 LOC2851 1 4218 XP_211773.1 3 842 TGGGGATGAGCC CA G- A 3 C c
c

23 AGGCTGGGGACA ACTG CTCCAGCCTGG CA
GTGGGGCT TGAC GGGGTCGGACC GT
A- GA A

GAM1338 360 LOC2851 2 3106 XP_211771.1 3 144 ACTCTGTCACCC CAA 3 C c c
27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2851 2 19204 XP_211771.1 3 577 GCTCTGTCACCC CAA 3 C c
c

27 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCCC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2851 1 19378 XP_211791.1 3 1870 ATGCAGATTCCC T CAA 3 C c
c

66 AGGCTGGGTGCA ACTGCAC CCAGCCTGGG
GTGGCTCA TGACGTG GGTCGGACCC
- TTA

GAM1338 360 LOC2851 1 12167 XP_209500.1 3 170 GCTCTTTTGCCC G C 3 C b b
76 AGACTGGAGTGA ACT CACTCCAG CTGGGCAA
AGTAGCAT TGA GTGAGGTC GACCCGTT
A A

GAM1338 360 LOC2851 1 13870 XP_209509.1 3 677 TCTCTGTTGCCC 3 C b b
93 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC

AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC2852 1 15365 XP_209521.1 5 77 AATCTGTCACCC A CAA 3 C c c

21 AGGCTGGAGCGC ACTGC CTCCAGCCTGGG
AGTGGTGT TGACG GAGGTCGGACCC
C ACT

GAM1338 360 LOC2852 2 11238 XP_211813.1 3 722 GCTCTGTCACCC C CAA 3 C c
c

31 AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGTGC TGACGTGAGGTCG ACCC
A ACT

GAM1338 360 LOC2852 2 13069 XP_211813.1 3 888 ACTCTGTCACCC C CAA 3 C c
c

31 AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGTGC TGACGTGAGGTCG ACCC
A ACT

GAM1338 360 LOC2852 1 7766 XP_211829.1 5 564 CTCTTGTTACCC AC----- C 3 C c c

81 AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGCAC ACGTGAGGTCGGACCC TTG
CACGGTA A

GAM1338 360 LOC2852 1 15961 XP_209554.1 3 398 GCTATGTCACTC CAA 3 C c c

99 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACTC
ACT

GAM1338 360 LOC2853 1 17006 XP_211844.1 3 475 ACTCTGTCTCCC - CA 3 C b b
34 AGGCTGGAGTTG ACTGCA CTCCAGCCTGGG AC
CAGTGGTG TGACGT GAGGTCGGACCC TG
T TC

GAM1338 360 LOC2853 2 11821 XP_211854.1 3 868 ACAGGGTTGCCC G 3 C b b
45 AGGGTGGAGTGC ACTGCACTCCA CCTGGGCAAC
AGTGGCAG TGACGTGAGGT GGACCCGTTG
G

GAM1338 360 LOC2853 2 13276 XP_211854.1 3 1257 ACTCTGTTACCC C C 3 C b b

45 AGGCTAGAGTGC ACTGCACTC AGCCTGGG AAC
AGTGGCGC TGACGTGAG TCGGACCC TTG
A A

GAM1338 360 LOC2853 1 4019 XP_209581.1 3 514 GCTCTGTCACCC CAA 3 C c c

66 AGGCTGGGGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGGGGTCGGACCC
ACT

GAM1338 360 LOC2853 1 19816 XP_211861.3 3 250 ACTTTGTCACCC CAA 3 C c c

69 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC2853 1 7025 XP_211873.1 3 1011 TCTCTCTCGCCA TG AA 3 C c c
89 TGGTTGGAGTGC ACTGCACTCCAGCC GGC
AGTGGTGC TGACGTGAGGTTGG CCG
TA CT
GAM1338 360 LOC2853 2 436 XP_211879.1 3 343 GCTCTGTCGCCC AA 3 C b b
92 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2853 2 6034 XP_211879.1 3 40 GCTCTGTCTCCC CA 3 C b b
92 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 LOC2853 2 3701 XP_209593.1 3 1207 CTCCTCTCGCCC AA 3 C b b
98 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2853 2 4020 XP_209593.1 3 906 ACTCTGTCGCCC AA 3 C b b
98 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTAGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2854 1 4870 XP_209607.3 3 1517 CTTCTGTCGCCC AA 3 C b b
29 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2854 1 11093 XP_211914.1 5 571 TCACTGTCGCCC AA 3 C c c
88 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
GGTGGTGC TGGCGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2854 1 8951 XP_211917.1 3 164 GCTCTGTCCCTC --- A 3 C c c
91 AGGCTGGAGTGC ACTGCACTCCAGCCT GGGCA
AGTAGCGT TGACGTGAGGTCGGA CCTGT
CTC C
GAM1338 360 LOC2855 1 11997 XP_211923.1 5 175 CTACTTTCATTC CAA 3 C c c
09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACTT
ACT
GAM1338 360 LOC2855 2 5384 XP_209654.1 5 7 ACTGTGTCGCCC - AA 3 C c c
40 AGGCTGGAGTGC ACT GCACTCCAGCCTGGGC
AAGTGGCA TGA CGTGAGGTCGGACCCG
A CT
GAM1338 360 LOC2855 2 19426 XP_209654.1 5 1534 GCTCTGTCACCC CAA 3 C c c
40 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2855 1 7821 XP_209660.1 3 435 TCACTCTTGCCC T C 3 C b b
60 AGGCTGTAGTGC AC GCACT CAGCCTGGGCAA
TGTGGCAC TG CGTGA GTCGGACCCGTT
T T

GAM1338 360 LOC2855 2 3782 XP_209671.1 3 266 ACTTGATCACCC C CAA 3 C c c
89 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGCGT TGACGTGAG TCGGACCC
A ACT
GAM1338 360 LOC2855 2 14069 XP_209671.1 3 720 GCTCTGTCGCCA - -- A 3 C c c
89 GGACTGGAGTGC ACTGCACTCCAG CCTGG GCA
AGTGACAC TGACGTGAGGTC GGACC TGT
A GC C
GAM1338 360 LOC2856 1 16288 XP_211959.1 5 849 ACTCTGTTGCCC C 3 C b b
26 AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
AGTGATAC TGACGT AGGTCGGACCCGTTG
A
GAM1338 360 LOC2856 1 13619 XP_209693.1 5 3928 GTTCTGTCACCC CAA 3 C c c
38 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2856 1 16507 XP_209717.1 5 0 AGTTGCCTGAGG CCAG- - 3 C c c
78 ACAGCAGTGCAG ACTGCACT CCT GGGCAAC
TTGACATG TGACGTGA GGA TCCGTTG
CGACA G
GAM1338 360 LOC2856 1 15031 XP_209719.2 3 203 ACTCTGTTGCTC 3 C b b
79 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACTCGTTG
GAM1338 360 LOC2856 1 5151 XP_211980.1 5 14 GTTCTGTCGCCC A----- AA 3 C c c
83 AGGCTGGAGTGC CTGCACTCCAGCCTGGGC
AGGGGCAT GACGTGAGGTCGGACCCG
TACGGG CT
GAM1338 360 LOC2856 1 10580 XP_211985.1 3 580 ACAGGCCATGCT T GC A 3 C c c
87 CAGATGGAGTGC AC GCACTCCA CTGGGCA
TGTCTGGA TG CGTGAGGT GACTCGT
T A- A
GAM1338 360 LOC2856 1 4452 XP_209724.1 3 1088 TCTCTGTTGCCC AC----- 3 C c c
89 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAT ACGTGAGGTCGGACCCGTTG
TACGGTA
GAM1338 360 LOC2856 1 7946 XP_211981.1 5 23 ACTCTGTTGCCC 3 C b b
93 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 LOC2857 1 6411 XP_211992.1 3 44 GCTGTGTTCAGG C --- A 3 C c c
13 ATGTTGAAGTGC ACTGCACT CAG CCTGGGCA
AGTGTCAG TGACGTGA GTT GGACTTGT
A GTA G
GAM1338 360 LOC2857 1 19494 XP_211997.1 5 349 CCTCTGTCAACC --- A 3 C c c

22 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGACTC TGACGTGAGGTCGGACC TGT
AAC C
GAM1338 360 LOC2857 1 11603 XP_209743.1 3 1366 GTTCTGTCACCC CAA 3 C c
c
44 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2857 2 9553 XP_209742.1 3 2182 CATCTGTCACCC CAA 3 C c c
47 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2857 2 13800 XP_209742.1 3 2433 GCTCTGTCACCC CAA 3 C c
c
47 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2857 1 13064 XP_209750.1 3 371 CCACTCTTGCCC - A 3 C b b
60 AGGCTGGAGCGC ACT GC CTCCAGCCTGGGCAA
AAGTGGCG TGA CG GAGGTCGGACCCGTT
A C
GAM1338 360 LOC2858 1 17617 XP_212036.1 5 77 CTCTTGTTGCCC 3 C b b
13 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 LOC2858 2 6011 XP_209777.1 5 1359 ACTGTGTCACCC CAA 3 C c
b
22 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2858 2 6178 XP_209777.1 3 236 ACTCTGTTGCCC C G 3 C b b
22 AGGATGGAATGC ACTGCA TCCA CCTGGGCAAC
AGTGGCAC TGACGT AGGT GGACCCGTTG
A A
GAM1338 360 LOC2858 2 1414 XP_212034.1 3 187 ACTCTGTTGCCC 3 C b b
43 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAT TGACGTGAGGTCGGACCCGTTG
GAM1338 360 LOC2858 2 11782 XP_212034.1 5 596 GCTCTGTCGCCT C AA 3 C c
b
43 AGGCTGCAGTGC ACTGCACT CAGCCTGGGC
AGTGGCGG TGACGTGA GTCGGATCCG
C CT
GAM1338 360 LOC2858 1 7212 XP_212045.1 5 731 GCTCTGTCACCC CAA 3 C c c
47 GGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGGCCC
ACT
GAM1338 360 LOC2858 1 7986 XP_212061.1 3 686 GTTCTGTAACCC CAA 3 C c c

```
          72                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                   AGTGGCCT    TGACGTGAGGTCGGACCC
                                               AAT
GAM1338  360   LOC2858 1  4795  XP_209806.1  3  317   TCTGTCACCCCC       CA     CAA       3  C  c
c
          96                        AGGCCAGAGTGC ACTGCACTC  GCCTGGG
                                   AGTGGTGC    TGACGTGAG  CGGACCC
                                               AC      CCA
GAM1338  360   LOC2858 1  10004 XP_209807.1  3  355   ATGGAATTGCCC    ----  CCA  C        3  C  c
c
          99                        AGCCAGTCACAG ACTGC    ACT   GC TGGGCAA
                                   CAGTAGCT    TGACG    TGA   CG ACCCGTT
                                               ACAC   C--  -
GAM1338  360   LOC2859 1  14560 XP_209810.1  3  302   ATGGAGAAATTC      T       CAA       3  C  c
c
          14                        AGGCTGGGTGCA ACTGCAC CCAGCCTGGG
                                   GTGGCTCA    TGACGTG GGTCGGACTT
                                               -       AAA
GAM1338  360   LOC2859 1  4795  XP_209822.1  3  326   TCTGTCACCCCC       CA     CAA       3  C  c
c
          22                        AGGCCAGAGTGC ACTGCACTC  GCCTGGG
                                   AGTGGTGC    TGACGTGAG  CGGACCC
                                               AC      CCA
GAM1338  360   LOC2859 1  16934 XP_212104.1  3  40    ACTATGTTGCCC                    3  C  b  b
          23                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                   AGTGGTGC    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2859 1  12385 XP_212092.1  5  844   ACTCTGTCACCC            CAA       3  C  c  c

          45                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                   AGTGGTGC    TGACGTGAGGTCGGACCC
                                               ACT
GAM1338  360   LOC2859 1  11638 XP_212089.1  3  1361  TTGCCTCTATCA A--    ---      ------    3  C  c  c

          50                        GGGCTGGAGTGG   CTGCAC   TCCAGCCT    GGGCA
                                   TGCAGCCC      GACGTG   AGGTCGGG    TCCGT
                                         CCC     GTG      ACTATC

                                         A
                                         T

GAM1338  360   LOC2859 1  2758  XP_209821.1  3  679   ATGCTGTTGCCC                    3  C  b  b
          52                        AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                   AGTGGTGC    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2859 1  11621 XP_209833.1  5  933   GCTCTGTCACCC     C       CAA       3  C  c
c
          61                        AGGCTGGAATGC ACTGCA TCCAGCCTGGG
                                   AGTGGCAT    TGACGT AGGTCGGACCC
                                               A       ACT
```

GAM1338 360 LOC2859 1 8156 XP_212105.1 3 865 CTCGTGTTGCCC T 3 C b b
72 CGGCTGGAGTGC ACTGCACTCCAGCC GGGCAAC
AGTGGCGC TGACGTGAGGTCGG CCCGTTG
C
GAM1338 360 LOC2859 1 13228 XP_212117.1 5 4 CTACTGTCATAC T --- A 3 C c c
79 AGGCTGGCGTGC ACTGCAC CCAGCCTG GGCA
AGTAGTGG TGACGTG GGTCGGAC CTGT
C ATA C
GAM1338 360 LOC2859 1 19067 XP_212111.1 3 935 CTCTTGTTGCCC A ------ A 3 C c c
89 AGGCAGGAGTAC CTGC ACTCC GCCTGGGCAAC
AATGGCAG GACG TGAGG CGGACCCGTTG
- GTAACA A
GAM1338 360 LOC2859 1 18120 XP_212120.1 3 602 TTGCTCTGTTGC CC CTG 3 C c
c
99 CAAGTTAAGTGC ACTGCACT AGC GGCAAC
AGTGGTAT TGACGTGA TTG CCGTTG
A- AA-
GAM1338 360 LOC2860 1 10050 XP_209868.1 5 639 CTTTTGTTGCGC AC----- G 3 C c
c
30 AGGCTGGAGTGC TGCACTCCAGCCTG GCAAC
AATGGTGC ACGTGAGGTCGGAC CGTTG
CGTGGTA G
GAM1338 360 LOC2860 1 1208 XP_209867.2 3 613 CTCTTGTCAACC GC --- 3 C c c
32 AGATTGGAGTGC ACTGCACTCCA CTGG GCAA
AGTGGTGC TGACGTGAGGT GACC TGTT
TA AAC
GAM1338 360 LOC2860 1 17647 XP_209873.1 5 647 CTTTTGTTGCCC AC----- 3 C c c
39 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 LOC2860 1 14748 XP_212152.1 3 1053 GCTCTGTTGTCC 3 C b b
52 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCTGTTG

GAM1338 360 LOC2860 1 1410 NP_776192.1 5 65 ACTCTGTTGCCC C 3 C b b
75 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGCGT TGAC TGAGGTCGGACCCGTTG
A
GAM1338 360 LOC2860 1 3388 XP_209892.1 3 367 TTTTGAGACCTA - CAA 3 C c c
77 GGGCTGGAGTGC ACTGCACTCCAGCC TGGG
AGTTGAGC TGACGTGAGGTCGG ATCC
G AGA
GAM1338 360 LOC2860 4 8139 XP_212163.1 3 759 TCTCTGTCACCC G CAA 3 C c
b
78 AGGATGGAGTGC ACTGCACTCCA CCTGGG
AGTGTTGT TGACGTGAGGT GGACCC
A ACT
GAM1338 360 LOC2860 4 9300 XP_212163.1 5 1401 CGCTCTGTTGCC AC----- G 3 C c
b

78 AGGCTGGAGTGC TGCACTCCAGCCTGG CAAC
ACTGGGGC ACGTGAGGTCGGACC GTTG
CGGGGTC -
GAM1338 360 LOC2860 4 12045 XP_212163.1 3 450 GCTCTGTCGCCC AA 3 C b b

78 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGAGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC2860 4 13798 XP_212163.1 5 789 GCTGTCTTGCCC A----- C 3 C c b

78 AGGCTGGAGTTC CTG ACTCCAGCCTGGGCAA
AGGGGCTA GAC TGAGGTCGGACCCGTT
ATCGGG T
GAM1338 360 LOC2861 1 15670 NP_848630.1 3 211 TCTCCGTCTCCC CA CA 3 C c
c
03 AGGCCAGAGTGC ACTGCACTC GCCTGGG AC
AGTGGCGC TGACGTGAG CGGACCC TG
AC TC
GAM1338 360 LOC2861 1 15670 XP_209897.1 3 211 TCTCCGTCTCCC CA CA 3 C c
c
03 AGGCCAGAGTGC ACTGCACTC GCCTGGG AC
AGTGGCGC TGACGTGAG CGGACCC TG
AC TC
GAM1338 360 LOC2861 1 663 XP_212184.3 3 97 CACTGTTTGCCC A---- C--- AG 3 C c c

21 AGGGGATGACTG CTGCA TCC CCTGGGCAA
CAGGAGGC GACGT AGG GGACCCGTT
CGGAG CAGT --
GAM1338 360 LOC2861 1 8950 XP_212185.1 3 989 GCTCTGCCACCC CAA 3 C c c

26 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACC
GAM1338 360 LOC2861 1 2266 XP_212194.1 5 445 GTTTTGTCACCC CAA 3 C c c
32 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC2861 1 1529 XP_209925.1 5 1000 ACTCTGTTGACC G G 3 C b b

66 AGGCTGGAGTGA ACT CACTCCAGCCTGG CAAC
AGTGGTGT TGA GTGAGGTCGGACC GTTG
A A
GAM1338 360 LOC2861 1 14196 XP_212211.1 5 1934 TGCTGTGTCACC AC -- A 3 C c
c
70 AGGCTGGAGCAG ACTGC TCCAGCCTGG GCA
TGGCACGA TGACG AGGTCGGACC TGT
-- AC G
GAM1338 360 LOC2861 2 13117 XP_212219.1 5 147 ACTTTGTCACCC C CAA 3 C c
c
86 AGGCTGGAATGC ACTGCA TCCAGCCTGGG

```
                                    AGTGGCAC    TGACGT AGGTCGGACCC
                                          A         ACT
GAM1338  360   LOC2861 2  15317  XP_212219.1  3  389   ACTCTATCACCC            CAA       3  C  c  c

         86                         AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                    AGTGTGGC    TGACGTGAGGTCGGACCC
                                                ACT
GAM1338  360   LOC2862 1  19418  XP_209953.1  3  1534  GCTCTGTTGCCC     C              3  C  b  b
         06                         AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
                                    AGTGGCAC    TGACGT AGGTCGGACCCGTTG
                                          A
GAM1338  360   LOC2862 1  16987  XP_209941.1  3  912   ACTCTGTCACCC        C   CAA       3  C  c
c
         07                         AGACTGGAGTGC ACTGCACTCCAG CTGGG
                                    AGTGCCAC    TGACGTGAGGTC GACCC
                                              A    ACT
GAM1338  360   LOC2862 3  12039  XP_212230.1  3  1456  GCTCTGTCGCCC    C         AA       3  C  c
b
         08                         AGGCTGGAGTTC ACTG ACTCCAGCCTGGGC
                                    AGTGGCGC    TGAC TGAGGTCGGACCCG
                                          T          CT
GAM1338  360   LOC2862 3  14347  XP_212230.1  3  1657  ACTCTGTCACCC            CAA       3  C  c
b
         08                         AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                    AGTGTCAC    TGACGTGAGGTCGGACCC
                                                ACT
GAM1338  360   LOC2862 3  16222  XP_212230.1  3  2281  GCTCTGTAGCCC            AA        3  C  b
b
         08                         AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                    AGTGTGGC    TGACGTGAGGTCGGACCCG
                                                AT
GAM1338  360   LOC2862 1  13388  XP_209956.1  3  767   CTGGCCATGCCC    C T    -    A       3  C  c
c
         23                         AGGGCTGGTGTT ACTG AC CCAGCC TGGGCA
                                    GGTTGAGG    TGGT TG GGTCGG ACCCGT
                                          - T    G     A
GAM1338  360   LOC2862 1  18995  XP_212244.1  5  237   GCTCTGTCGCTC    A         AA       3  C  c  c

         45                         AGGCTGGAGAGC ACTGC CTCCAGCCTGGGC
                                    GGTGGTGC    TGGCG GAGGTCGGACTCG
                                          A          CT
GAM1338  360   LOC2863 1  14403  XP_212278.1  3  412   CTGTTGTTGCCC                    3  C  b  b
         41                         AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                    AGTGGCGT    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2863 1  20172  XP_212286.1  5  688   TGCTCTGTCACC    A       --  A       3  C  c  c
         54                         AGGCTGGAGGGC ACTGC CTCCAGCCTGG  GCA
                                    AGTGGCGC    TGACG GAGGTCGGACC  TGT
                                          G          AC   C
GAM1338  360   LOC2863 2  3910   XP_212290.1  5  628   CTTGCTGAAAAC A---  --         -----     3  C  c  c
```

```
          56                      AGGCTGGGGTGT   CT GCACTCCAGCCTG   GGCAA
                                  TGAGACAC      GA TGTGGGGTCGGAC   TCGTT
                                        CACA GT         AAAAG
GAM1338  360   LOC2863 2  13800 XP_212290.1  5 1100  GCTCTGTCACCC           CAA       3 C c
c
          56                      AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                  AGTGGCGC   TGACGTGAGGTCGGACCC
                                             ACT
GAM1338  360   LOC2863 1  13894 XP_212285.1  5 13   TCAATGTTGCCC                  3 C b b
          57                      AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                  AGTGGCGT   TGACGTGAGGTCGGACCCGTTG

GAM1338  360   LOC2863 1  18548 XP_212308.1  5 5807  ACCCTGTTGCCC AC-----    CC          3 C c
 c
          95                      AGGCTACAGTGC      TGCACT AGCCTGGGCAAC
                                  AATGGCAT         ACGTGA TCGGACCCGTTG
                                        TACGGTA     CA
GAM1338  360   LOC2864 1  16900 XP_210036.1  3 1358  CTTCAGTCCCTC  -  T----      CA     3 C c
c
          04                      AGGCTGGCAGCT ACT GCAC   CCAGCCTGGG AC
                                  GTGCTGGT   TGG CGTG   GGTCGGACTC TG
                                        T   TCGAC       CC
GAM1338  360   LOC2864 1  643   XP_212319.1  3 54   AGTGCTGTTTCC          T --  A      3 C c c
          41                      TGGCTGGAGTGC ACTGCACTCCAGCC GG GCA
                                  AGTGGCAT   TGACGTGAGGTCGG CC TGT
                                             T TT  C
GAM1338  360   LOC2864 1  12807 XP_210063.1  3 985   CTGTTGTTGCCC AC-----            3 C c c

          67                      AGGCTGGAGTGC      TGCACTCCAGCCTGGGCAAC
                                  AATGGCGC         ACGTGAGGTCGGACCCGTTG
                                        CGCGGTA
GAM1338  360   LOC2865 1  17107 XP_212340.1  3 891   ACTTTGTCGCCC           AA       3 C b b
          53                      AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                  AGTGGTGT   TGACGTGAGGTCGGACCCG
                                             CT
GAM1338  360   LOC2865 1  14505 XP_210106.1  3 98   GCTCTGTAGACC    A      ---  A     3 C c c
          58                      AGGCTGGAGCGC ACTGC CTCCAGCCTGG  GCA
                                  AGTGGCAG   TGACG GAGGTCGGACC  TGT
                                        C        AGA  C
GAM1338  360   LOC2865 1  14505 XP_210108.1  3 98   GCTCTGTAGACC    A      ---  A     3 C c c
          64                      AGGCTGGAGCGC ACTGC CTCCAGCCTGG  GCA
                                  AGTGGCAG   TGACG GAGGTCGGACC  TGT
                                        C        AGA  C
GAM1338  360   LOC3385 1  17586 XP_294654.1  3 1173  CGCTCCATCACC           GCAA       3 C c
c
          62                      AGGCTGGAGTGC ACTGCACTCCAGCCTGG
                                  AGTGGTGC   TGACGTGAGGTCGGACC
                                             ACTA
GAM1338  360   LOC3385 1  12519 XP_294653.1  3 1933  CTTTTGTTGCCC   C              3 C b b
          65                      AGGCTGGAGTTC ACTG ACTCCAGCCTGGGCAAC
```

AGTGGCGT TGAC TGAGGTCGGACCCGTTG
T
GAM1338 360 LOC3386 1 6141 XP_290494.1 3 2435 CTCTTGTTGCCC AC----- 3 C c c

45 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGAGC ACGTGAGGTCGGACCCGTTG
CGAGGTA
GAM1338 360 LOC3387 1 902 XP_211595.2 5 682 CTCTGTTGTCCA - 3 C b b
09 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC3387 2 11661 XP_294690.1 3 527 ACTCTGTTGCCC 3 C b b
39 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3387 2 17520 XP_294690.1 3 116 ATTCTGATGCCC A 3 C b b
39 AGGTTGGGGTGC ACTGCACTCCAGCCTGGGCA
AGTGGCAC TGACGTGGGGTTGGACCCGT
A
GAM1338 360 LOC3387 1 17388 XP_290570.1 3 877 GGTCTGTCACCC CAA 3 C c
c
73 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3388 1 11448 XP_290588.1 3 261 GTCGCCTGTCAA C TG- A 3 C c
c
17 CGGCTAGAGTGC ACTGCACTC AGCC GGCA
AGTAGCGT TGACGTGAG TCGG CTGT
A CAA C
GAM1338 360 LOC3389 2 3243 XP_294742.1 3 2043 ATTCTGTCACTC CAA 3 C c b

23 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACTC
ACT
GAM1338 360 LOC3389 2 14847 XP_294742.1 3 438 CGCTCTGTCGCC -- A 3 C b b
23 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 LOC3389 1 3888 XP_290663.1 3 298 GCGCTGTTGCCC AC----- CC 3 C c
c
91 AGGCTCTAGTGC TGCACT AGCCTGGGCAAC
AATGGCAC ACGTGA TCGGACCCGTTG
CACGGTA TC
GAM1338 360 LOC3389 1 3888 XP_290659.1 3 298 GCGCTGTTGCCC AC----- CC 3 C c
c
99 AGGCTCTAGTGC TGCACT AGCCTGGGCAAC
AATGGCAC ACGTGA TCGGACCCGTTG
CACGGTA TC
GAM1338 360 LOC3390 1 11283 XP_294781.1 3 1 GCTCCCTTGGGC - ---- AA 3 C c c
44 TGGAGCTGCAGT ACTGCA CTCCAGCCT GGGC

ACCGTACC TGACGT GAGGTCGGG CTCG
C TTCC --
GAM1338 360 LOC3390 1 19426 XP_290692.1 3 850 GCTCTGTCACCC CAA 3 C c
c
78 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3391 1 822 XP_294825.1 5 448 CGCTCTGTTGCC G 3 C b b
46 AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGTGC TGACGTGAGGTCGGACC GTTG
-
GAM1338 360 LOC3391 1 4453 XP_294848.1 3 446 CTGGACTGTTGT CC CCTG 3 C c
c
92 CACCTTCAGTGC ACTGCACT AG GGCAAC
AGTCACTG TGACGTGA TC CTGTTG
CT CA--
GAM1338 360 LOC3392 1 11830 XP_290756.1 3 356 TCTCTGTGGCCC C AA 3 C c
c
01 AGGCTGAAGTGC ACTGCACT CAGCCTGGGC
AGTGGTGT TGACGTGA GTCGGACCCG
A GT
GAM1338 360 LOC3392 1 4581 XP_290762.2 5 410 ACTCTGTTGCCC --- 3 C b b
16 AGGTTGGAGTAC ACTGC ACTCCAGCCTGGGCAAC
AGCAGTGC TGACG TGAGGTTGGACCCGTTG
ACA
GAM1338 360 LOC3392 1 4581 XP_294900.2 5 410 ACTCTGTTGCCC --- 3 C b b
82 AGGTTGGAGTAC ACTGC ACTCCAGCCTGGGCAAC
AGCAGTGC TGACG TGAGGTTGGACCCGTTG
ACA
GAM1338 360 LOC3392 1 15442 XP_294899.2 5 1179 ACTCTGTTGCCC A----- C 3 C c
c
83 AGGTTGGAGTAC CTG ACTCCAGCCTGGGCAAC
AGCAATGC GAC TGAGGTTGGACCCGTTG
CGTAAC A
GAM1338 360 LOC3393 1 11623 XP_290838.1 3 2391 TTCTTGTTGCCC AC----- C 3 C c
c
24 AGGCTGCAGTGC TGCACT CAGCCTGGGCAAC
AATGGCAC ACGTGA GTCGGACCCGTTG
CACGGTA C
GAM1338 360 LOC3393 1 7946 XP_290830.1 3 371 ACTCTGTTGCCC 3 C b b
25 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3394 2 14822 XP_294926.1 3 785 ACTCTGTTGCCC CA C 3 C c c

00 AAGCTGGAGAAC ACTG CTCCAGC TGGGCAAC
AGTGGCAC TGAC GAGGTCG ACCCGTTG
AA A
GAM1338 360 LOC3394 2 17314 XP_294926.1 3 2063 CATGGAATGCCT CC - A 3 C c
c

00 AGTGCTAAGTGC ACTGCACT AGC CTGGGCA
AGTGTCCT TGACGTGA TCG GATCCGT
A- T A

GAM1338 360 LOC3394 1 4497 XP_294944.1 5 625 ACTCTGTTGCCC A----- 3 C b b
17 AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGGGGCGT GACGTGAGGTCGGACCCGTTG
TGCGGG

GAM1338 360 LOC3394 1 436 XP_290911.1 3 1339 GCTCTGTCGCCC AA 3 C b b
58 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 LOC3394 1 13345 XP_290907.2 3 837 TCTCTGTCGCCT AA 3 C c c
59 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGATCCG
CT

GAM1338 360 LOC3394 2 13601 XP_290919.1 3 1080 GCTCTGTCGCGC G G AA 3 C c
c
92 AGGGTGGAGTGC ACTGCACTCCA CCTG GC
GGTGGCAC TGGCGTGAGGT GGAC CG
G G CT

GAM1338 360 LOC3394 2 19744 XP_290919.1 3 1386 CTCTTGTTGCCC ACT----- 3 C c
c
92 AGGCTGGAGTGC GCACTCCAGCCTGGGCAAC
GTTGGCGT CGTGAGGTCGGACCCGTTG
TGCGGTTG

GAM1338 360 LOC3395 2 9239 XP_295005.1 3 1187 GCTACGTGACCC - A 3 C b b
77 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG CA
AGTAGCTA TGATGTGAGGTCGGACCC GT
A G

GAM1338 360 LOC3395 2 18182 XP_295005.1 3 1039 GCTCTGTCACCC CAA 3 C c
b
77 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 LOC3396 1 15466 XP_295014.1 3 1460 GCTCTGTCACTT CAA 3 C c
c
00 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGATTC
ACT

GAM1338 360 LOC3396 1 18371 XP_290981.1 3 1595 TGCCCTGTTGCC C G 3 C b
b
59 AGGCTGGAATGC ACTGCA TCCAGCCTGG CAAC
AGTGGCGT TGACGT AGGTCGGACC GTTG
A -

GAM1338 360 LOC3396 1 7793 XP_295032.1 5 165 GCTCTACCACCC CAA 3 C c c

85 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGACCC
ACC

GAM1338 360 LOC3397 1 3106 XP_295038.1 3 1271 ACTCTGTCACCC CAA 3 C c c

11 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3397 1 7943 XP_295041.1 5 879 ACTCTGTCGCCC AA 3 C b b
20 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3398 1 2943 XP_295072.1 3 1491 AGTCTGTCACCC CAA 3 C c c
03 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3398 2 8744 XP_291020.1 5 1173 TCACTGTCACCT CAA 3 C c c
09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAA TGACGTGAGGTCGGATCC
ACT
GAM1338 360 LOC3398 2 9098 XP_291020.1 5 1636 ACTCTGTCACCC CAA 3 C c c
09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3398 2 8180 XP_291031.1 5 574 ACTCTGTTGCCC C 3 C b b
33 AGCCTGGAGTGC ACTGCACTCCAG CTGGGCAAC
AGTGGCAT TGACGTGAGGTC GACCCGTTG
C
GAM1338 360 LOC3398 2 10061 XP_291031.1 3 560 ACTGTGATGCCG G G A 3 C c
b
33 AGGGTGGAGTGC ACTGCACTCCA CCT GGCA
AGTGGCAC TGACGTGAGGT GGA CCGT
G G A
GAM1338 360 LOC3398 1 2474 NP_835467.1 5 47 ATTCTGTCGCCC AA 3 C c c
34 AGGCTGGAGTGT ACTGCACTCCAGCCTGGGC
AGTGACGC TGATGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3398 1 2474 XP_291033.1 5 47 ATTCTGTCGCCC AA 3 C c c
34 AGGCTGGAGTGT ACTGCACTCCAGCCTGGGC
AGTGACGC TGATGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3398 3 6179 XP_291050.1 5 470 GGTCTGTTGCCC 3 C b b
72 AGGTTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGG TGACGTGAGGTTGGACCCGTTG
GAM1338 360 LOC3398 3 10908 XP_291050.1 5 767 CCTCAGTCGCTC AA 3 C c b
72 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACTCG
CT
GAM1338 360 LOC3398 3 15990 XP_291050.1 3 183 GCTGTGTTGCCC 3 C b b
72 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTAGCTA TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3398 1 11426 XP_295095.1 5 132 GCTCTGTTGCCC C 3 C b b
94 AGGTTAGAGTGC ACTGCACTC AGCCTGGGCAAC
AGTGGCTT TGACGTGAG TTGGACCCGTTG
A
GAM1338 360 LOC3398 1 11602 XP_291059.1 3 959 ACAATAAGGTCC A C AA 3 C c
c
96 AGGCTGAGGTAG ACTGC CTC AGCCTGGGC
TCTCAGAT TGATG GAG TCGGACCTG
- - GA
GAM1338 360 LOC3399 1 1531 XP_291065.1 3 1459 ACTCTGTTGCCC A----- 3 C b b
07 AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGGGGCAC GACGTGAGGTCGGACCCGTTG
CACGGG
GAM1338 360 LOC3399 1 9102 XP_291069.1 5 121 GCTCTGTTGCCC 3 C b b
09 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3399 1 11079 XP_295107.1 5 630 ACATGGTGGCCA ---- C - AA 3 C c
c
42 CAGCTGGAGTGA ACTGC ACTCCAGC TG GGC
CCGCAGTG TGACG TGAGGTCG AC CCG
CCAG - A GT
GAM1338 360 LOC3399 1 8858 XP_291095.1 3 713 GCTCTGTCGCCC AA 3 C b b
70 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3400 1 664 XP_295137.1 3 36 CTCTTGTTGCCC AC----- 3 C c c
37 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGCGCG ACGTGAGGTCGGACCCGTTG
GCGCGTA
GAM1338 360 LOC3401 1 902 XP_291150.1 5 682 CTCTGTTGTCCA - 3 C b b
25 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC3401 1 8575 XP_291158.1 3 1441 CGCTCTGTCACG - - A 3 C c c
56 AGGCTGGAGTGC ACTGCACTCCAGCCT G GGCA
AGTGGCCC TGACGTGAGGTCGGA C CTGT
G A C
GAM1338 360 LOC3402 1 902 XP_291203.1 5 682 CTCTGTTGTCCA - 3 C b b
27 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC3402 1 15164 XP_291214.1 5 1350 CTCTCTTGTCCA - 3 C b b
90 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAA
AGTAGTGC TGATGTGAGGTCGGA CCTGTT
A
GAM1338 360 LOC3403 1 3427 XP_291269.1 3 1382 GTCTTGTTGCCC AC----- 3 C c c

90 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC

AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA
GAM1338 360 LOC3404 1 564 XP_291274.1 5 646 CTTTTGTTGCCC AC----- 3 C c c
08 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGATGC ACGTGAGGTCGGACCCGTTG
CGTAGTA
GAM1338 360 LOC3404 1 11659 XP_295240.1 3 173 GCTCTGTCACCC CAA 3 C c
c
14 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3404 1 4971 XP_295252.1 5 243 TCTCTGTCACCC CAA 3 C c c
50 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3429 1 1413 XP_292790.2 3 810 GCTCTGTCACCC CAA 3 C c c

26 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3452 1 14511 NP_835236.1 3 951 ACTCTTTCGCCC AA 3 C b b
75 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTAT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3466 2 4277 XP_294357.2 3 533 ACCACGTTGCCC A----- CACT 3 C c
c
53 AGGCTGGTCTCC CTG CCAGCCTGGGCAAC
AGCTCCTG GAC GGTCGGACCCGTTG
GTCCTC CTCT
GAM1338 360 LOC3466 2 14945 XP_294357.2 3 372 TGCTCTGTCTCC C -- A 3 C c c
53 AGGCTGGAGTAC ACTG ACTCCAGCCTGG GCA
AGTGGTGC TGAC TGAGGTCGGACC TGT
A TC C
GAM1338 360 LOC3479 1 983 XP_300565.1 5 188 CTTTTATTGCCC 3 C b b
18 AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAA
AGTGGCGC TGATGTGAGGTCGGACCCGTT

GAM1338 360 LOC3480 2 777 XP_302653.1 3 3385 TGCTCTGTCACC -- A 3 C c c
75 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
GGTGGCAT TGGCGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC3480 2 6491 XP_302653.1 3 1555 GCCTTCTTCCCC G - CAA 3 C c
c
75 AGGCTGGGAGTG ACT CACTCC AGCCTGGG
GGTGAGAC TGG GTGAGG TCGGACCC
- G CTT
GAM1338 360 LOC3481 1 3888 XP_300623.1 3 298 GCGCTGTTGCCC AC----- CC 3 C c
c
13 AGGCTCTAGTGC TGCACT AGCCTGGGCAAC
AATGGCAC ACGTGA TCGGACCCGTTG

CACGGTA TC
GAM1338 360 LOC3481 1 12601 XP_300626.1 5 553 CTCTTGTTGCCC CA 3 C b b
15 AGGCCCGAGTGC ACTGCACTC GCCTGGGCAAC
AGTGGTGC TGACGTGAG CGGACCCGTTG
CC
GAM1338 360 LOC3481 1 3888 XP_300635.1 3 298 GCGCTGTTGCCC AC----- CC 3 C c
c
37 AGGCTCTAGTGC TGCACT AGCCTGGGCAAC
AATGGCAC ACGTGA TCGGACCCGTTG
CACGGTA TC
GAM1338 360 LOC3481 1 3888 XP_300636.1 3 298 GCGCTGTTGCCC AC----- CC 3 C c
c
42 AGGCTCTAGTGC TGCACT AGCCTGGGCAAC
AATGGCAC ACGTGA TCGGACCCGTTG
CACGGTA TC
GAM1338 360 LOC3481 1 8803 XP_208864.1 3 1753 ACTCTGTTGCCC ACT----- 3 C c
c
61 AGGCTGGAGTGC GCACTCCAGCCTGGGCAAC
CTCTTCAT CGTGAGGTCGGACCCGTTG
TACTTCTC
GAM1338 360 LOC3482 1 11248 XP_300670.1 3 1530 ACTCTGTTGCCC C 3 C b b
35 AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
AGTGGTAC TGACGT AGGTCGGACCCGTTG
A
GAM1338 360 LOC3482 1 7914 XP_300683.1 5 57 GCTCTGTTGCCT TG 3 C b b
62 GGGCTGGAGTGC ACTGCACTCCAGCC GGCAAC
AGTGCCAC TGACGTGAGGTCGG CCGTTG
GT
GAM1338 360 LOC3483 1 9161 XP_302716.1 5 316 ACTTTGTTGCCC 3 C b b
14 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGCGT TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3483 1 1995 XP_300696.1 3 1763 CAGTCTGTCACC -- A 3 C b b
26 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCAT TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC3483 2 16960 XP_302741.1 3 1205 TCGCCGTTGCCC 3 C b b
93 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGCAT TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3483 2 20185 XP_302741.1 3 742 CCTAGGAGGCCC G AA 3 C c
b
93 AGGCTGGAGTGA ACT CACTCCAGCCTGGGC
GGTGGCAC TGG GTGAGGTCGGACCCG
A GA
GAM1338 360 LOC3483 2 1615 XP_300729.1 5 149 GCTCTGTCACCC C CAA 3 C c
b
96 AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGCAGT TGACGT AGGTCGGACCC
A ACT

GAM1338 360 LOC3483 2 10631 XP_300729.1 3 183 GCTCTGTTGCCC 3 C b b
96 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3484 2 13601 XP_300730.1 3 321 GCTCTGTCGCGC G G AA 3 C c
c
02 AGGGTGGAGTGC ACTGCACTCCA CCTG GC
GGTGGCAC TGGCGTGAGGT GGAC CG
G G CT
GAM1338 360 LOC3484 2 19744 XP_300730.1 3 627 CTCTTGTTGCCC ACT----- 3 C c
c
02 AGGCTGGAGTGC GCACTCCAGCCTGGGCAAC
GTTGGCGT CGTGAGGTCGGACCCGTTG
TGCGGTTG
GAM1338 360 LOC3484 1 1995 XP_300738.1 3 1763 CAGTCTGTCACC -- A 3 C b b
45 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCAT TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC3484 1 9100 XP_302760.1 3 2632 GCTCTGTCGCCC AA 3 C b b

55 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3484 1 8756 XP_300743.1 3 130 CACTCTGTCACC -- A 3 C b b
60 AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGCCGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 LOC3484 1 6597 XP_209299.2 3 229 GCTCTCTTACCC C CAA 3 C c
c
74 AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGACAT TGACGTGAGGTCG ACCC
A ATT
GAM1338 360 LOC3485 1 12080 XP_300762.1 3 1202 TCTTGCTCGCCC G AA 3 C c
c
03 AGGGTGGAGTGC ACTGCACTCCA CCTGGGC
AGTGGTGT TGACGTGAGGT GGACCCG
G CT
GAM1338 360 LOC3485 1 902 XP_302806.1 5 744 CTCTGTTGTCCA - 3 C b b
08 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC3485 1 436 XP_300778.1 3 1339 GCTCTGTCGCCC AA 3 C b b
25 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3485 2 16960 XP_302818.1 3 1205 TCGCCGTTGCCC 3 C b b
32 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGCAT TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3485 2 20185 XP_302818.1 3 742 CCTAGGAGGCCC G AA 3 C c
b

32 AGGCTGGAGTGA ACT CACTCCAGCCTGGGC
GGTGGCAC TGG GTGAGGTCGGACCCG
A GA
GAM1338 360 LOC3487 1 3103 XP_300808.1 5 297 ACTCTGTCACCC C CAA 3 C c
c
02 AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAC TGAC TGAGGTCGGACCC
A ACT
GAM1338 360 LOC3487 1 11124 XP_300843.1 3 446 TGCTTGTTGCCC 3 C b b
90 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3487 1 4796 XP_302888.1 3 341 TTGCTCTCGCCC AA 3 C b b
97 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGGTG TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC3487 1 5915 XP_300845.1 5 23 TTCTTGTTGCCC AC----- C 3 C c c
98 AGGCTGGAATGC TGCA TCCAGCCTGGGCAAC
AATGGCGC ACGT AGGTCGGACCCGTTG
CGCGGTA A
GAM1338 360 LOC3488 2 2639 XP_300853.1 5 283 GCCCAGGCTGGA -------- AA 3 C c
b
25 GTATAGTAGTGC ACTGCAC TCCAGCCTGGGC
AGTGGTGT TGACGTG AGGTCGGACCCG
ATGATATG --
GAM1338 360 LOC3488 2 10307 XP_300853.1 5 279 GCCCTGTTGCCC --- 3 C b b
25 AGGCTGGAGTAT ACTGC ACTCCAGCCTGGGCAAC
AGTAGTGC TGATG TGAGGTCGGACCCGTTG
ATA
GAM1338 360 LOC3488 1 902 XP_300861.1 5 474 CTCTGTTGTCCA - 3 C b b
42 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC3489 1 9379 XP_300434.1 3 606 CAGAGTCTTGCT CT 3 C b b
95 CTGCTGGAGTGC ACTGCACTCCAGC GGGCAA
GGTGGTGC TGGCGTGAGGTCG CTCGTT
T-
GAM1338 360 LOC3490 2 4753 XP_300250.1 3 143 CTCTTGTCACCC CAA 3 C c c
24 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 LOC3490 2 11653 XP_300250.1 5 532 GCTCTGTCACCC C CAA 3 C c
c
24 AGACTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGCAT TGACGTGAGGTC GACCC
A ACT
GAM1338 360 LOC3490 1 9465 XP_300932.1 3 176 ACTCTGTCACCC C CAA 3 C c
c
75 AGGCTGAAGTGC ACTGCACT CAGCCTGGG
AGTGGTAC TGACGTGA GTCGGACCC

A ACT
GAM1338 360 LOC3490 1 14560 XP_300937.1 3 285 ATGGAGAAATTC T CAA 3 C c
c
96 AGGCTGGGTGCA ACTGCAC CCAGCCTGGG
GTGGCTCA TGACGTG GGTCGGACTT
- AAA
GAM1338 360 LOC3491 1 902 XP_302960.1 5 183 CTCTGTTGTCCA - 3 C b b
14 AGGCTGGAGTGT ACTGCACTCCAGCCT GGGCAAC
AGTAGTGC TGATGTGAGGTCGGA CCTGTTG
A
GAM1338 360 LOC3491 3 4197 XP_300969.1 3 831 ACCCTATTGCCC AC----- 3 C c b
70 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATGGCGT ACGTGAGGTCGGACCCGTT
TGCGGTA
GAM1338 360 LOC3491 3 13839 XP_300969.1 5 146 CTTCTGTGGCCC AA 3 C b b
70 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCTG TGACGTGAGGTCGGACCCG
GT
GAM1338 360 LOC3491 3 19429 XP_300969.1 3 468 ACTCTGTTGCCC 3 C b b
70 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 LOC3493 1 13307 XP_088528.1 5 446 CTCTGGTTGCCC C 3 C b b
60 AGGCTGGGGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGTGG TGAC TGGGGTCGGACCCGTTG
A
GAM1338 360 LOC3494 1 12395 XP_303044.1 5 13 ACTCCGTTGCCC AC----- C 3 C c
c
08 AGGCTGGAGTAC TG ACTCCAGCCTGGGCAAC
AATGGTGC AC TGAGGTCGGACCCGTTG
CGTGGTA A
GAM1338 360 LOC3494 1 19505 XP_300513.1 3 1058 GTTTTGCAGCCC AA 3 C b b

40 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
AC
GAM1338 360 LOC3496 1 17346 XP_303409.1 5 173 GCATGTGTGCCC A CAG A 3 C c
c
13 AGGACCGGGGCA ACTGC CTC CCTGGGCA
GTCACCCA TGACG GGG GGACCCGT
- CCA G
GAM1338 360 LOC3501 1 20158 XP_303810.1 5 16 TTCCCTCTGCCC T A G A 3 C c
c
06 AGGTGGGGGCCG AC GC CTCCA CCTGGGCA
TGGCTGGA TG CG GGGGT GGACCCGT
C - - C
GAM1338 360 LOC5119 2 6812 NP_057415.1 5 97 CTCCTGTTACCC CA C 3 C c b
3 AGGCTGGAGGAC ACTG CTCCAGCCTGGG AAC
AGTGATGT TGAC GAGGTCGGACCC TTG
AG A

GAM1338 360 LOC5119 2 6858 NP_057415.1 3 732 GTTCTGTTGTCC G 3 C b b
3 AGGATGGAGTGC ACTGCACTCCA CCTGGGCAAC
AGTGGTTG TGACGTGAGGT GGACCTGTTG
A
GAM1338 360 LOC5125 1 18183 NP_057580.2 5 155 GCTCTGTTACCC C 3 C b b
7 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGT TGACGTGAGGTCGGACCC TTG
A
GAM1338 360 LOC5133 1 7944 NP_057728.1 5 336 ACTCTGTTGCCC AC----- C 3 C c
c
4 AGGCTAGAGTGC TGCACTC AGCCTGGGCAAC
AATGGCAC ACGTGAG TCGGACCCGTTG
CACGGTA A
GAM1338 360 LOC5133 1 18609 NP_057730.1 3 664 ACTCTGTTACCC AC----- C 3 C c
c
6 AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGAGT ACGTGAGGTCGGACCC TTG
TGAGGTA A
GAM1338 360 LOC5595 1 17853 NP_061976.1 5 0 GTCACCCAGGCT CAA 3 C c c
4 GGAGTGTAGTGG ACTGCACTCCAGCCTGGG
CGCAATCT TGATGTGAGGTCGGACCC
ACT
GAM1338 360 LOC5690 1 8077 NP_064528.1 3 517 ACTTTGTCACCC C CAA 3 C c
c
2 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGTGC TGACGTGAG TCGGACCC
A ACT
GAM1338 360 LOC5710 2 12670 NP_065114.2 5 83 TGTTGTTTGCCC A----- CT C 3 C c
c
7 AGCCTGGGCTGC CTGCA CCAG CTGGGCAA
AGAAAGCA GACGT GGTC GACCCGTT
ACGAAA CG C
GAM1338 360 LOC5710 2 19749 NP_065114.2 3 586 CTCTTGTTGCCC AC----- 3 C c c
7 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 LOC5714 1 17648 NP_065155.2 3 734 CTCTTGTTGCCC AC----- 3 C c c
6 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AACGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGCA
GAM1338 360 LOC9040 1 2729 XP_031517.1 5 1645 CTCTTGTTACCC C 3 C b b
8 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCGC TGACGTGAGGTCGGACCC TTG
A
GAM1338 360 LOC9048 2 10103 XP_032059.1 3 1182 TCTCTGTCACCC C CAA 3 C c
b
5 AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGAGC TGACGTGAG TCGGACCC

A ACT
GAM1338 360 LOC9048 2 15525 XP_032059.1 3 1340 GCTCTGTCGCCC AA 3 C b b
5 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGATGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 LOC9099 1 11655 XP_035410.1 3 114 ACTCTGTTGCCC C 3 C b b
9 AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC
AGTGGCAC TGAC TGAGGTCGGACCCGTTG
A
GAM1338 360 LOC9111 2 17070 XP_036218.1 3 2143 CACTTGTTGCCC AC----- 3 C c c
5 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTAC ACGTGAGGTCGGACCCGTTG
CATGGTA
GAM1338 360 LOC9111 2 18042 XP_036218.1 3 757 GGTCTTTCACCC T CAA 3 C c c
5 AGGCTGGAGTGC AC GCACTCCAGCCTGGG
TGTGGCAC TG CGTGAGGTCGGACCC
T ACT
GAM1338 360 LOC9117 1 3969 XP_036612.1 5 208 ACTTTGTCGCCC A AA 3 C c c
0 GGGCAGGAGTGC ACTGCACTCC GCCTGGGC
AGTGGCTC TGACGTGAGG CGGGCCCG
A CT
GAM1338 360 LOC9126 1 9160 XP_037268.1 5 267 TGCAGGATGCCC AC - - A 3 C c c
6 AGGGCTCGGAAG ACTGC TCC AGCC TGGGCA
CAGTAAGG TGACG AGG TCGG ACCCGT
A- C G A
GAM1338 360 LOC9137 1 5516 XP_038063.5 3 1525 CTCTTGTTGCCC G 3 C b b
3 AGGCTGGAGTGA ACT CACTCCAGCCTGGGCAAC
AGTGGCGT TGA GTGAGGTCGGACCCGTTG
A
GAM1338 360 LOC9166 1 13779 NP_612382.1 3 338 ACTCTGTGGCCC AA 3 C b b
3 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
GT
GAM1338 360 LOC9189 1 9129 XP_041340.1 3 203 GCTCTGCCGCCC A AA 3 C c c
3 AGGCGGGAGTGC ACTGCACTCC GCCTGGGC
AGTGGCAG TGACGTGAGG CGGACCCG
G CC
GAM1338 360 LOC9214 1 16536 XP_043160.1 5 759 GCCCTGCCGCCC C AA 3 C c c
8 AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGCAC TGACGTGAG TCGGACCCG
A CC
GAM1338 360 LOC9259 1 19028 NP_775739.1 3 3526 GCTCTGTTGCCC AC----- C 3 C c c

```
          7                          GGGCTGGAGTAC       TG ACTCCAGCCTGGGCAAC
                                     AATGGCAT          AC TGAGGTCGGGCCCGTTG
                                           TACGGTA  A
GAM1338  360   LOC9313 1   14290  XP_049396.1  5  1234   CGCTCTGTCACC     A        --  A       3  C  c  c

          2                          AGGCTGGAGGGC ACTGC CTCCAGCCTGG  GCA
                                     AGTGGTGC    TGACG GAGGTCGGACC  TGT
                                           G         AC   C
GAM1338  360   LTB4R  1   19595  NP_000743.1  5  302    GCTCTGTCATTC           ---   A      3  C  c  c
                                     AGGCTGGAGTGC ACTGCACTCCAGCCTG   GGCA
                                     AGTGGTGC    TGACGTGAGGTCGGAC   CTGT
                                           TTA    C
GAM1338  360   LY75   1   4451   NP_002340.1  3  572    TCTCTGTTGCCC AC-----  C              3  C  c  c
                                     AGGCTGGAGTAC       TG ACTCCAGCCTGGGCAAC
                                     AATGGCGT          AC TGAGGTCGGACCCGTTG
                                           TGCGGTA  A
GAM1338  360   LYZ    1   3109   NP_000230.1  3  330    GCTCTGTCGCCC              AA        3  C  b  b
                                     AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                     AGTGGCGC    TGACGTGAGGTCGGACCCG
                                           CT
GAM1338  360   LZTS1  1   13405  NP_066300.1  3  1444   GCTCTGTCCCCC             CA        3  C  b  b
                                     AGGCTGGAGTGC ACTGCACTCCAGCCTGGG  AC
                                     AGTGGCAT    TGACGTGAGGTCGGACCC  TG
                                           CC
GAM1338  360   MAC30  1   13959  XP_031536.2  3  226    ACTCTGTTGCCC     -----              3  C  b  b
                                     AGGCTGGAGTAA ACTGC    ACTCCAGCCTGGGCAAC
                                     AGGGCAGT    TGACG    TGAGGTCGGACCCGTTG
                                           GGAAA
GAM1338  360   MAK    1   11208  NP_005897.1  3  644    ACTCTTGTGTCC              A        3  C  b  b
                                     AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
                                     AGTGGCAC    TGACGTGAGGTCGGACCTGT
                                           G
GAM1338  360   MAML1  1   5648   NP_055572.1  3  885    TGTATGTTGCCC  TG A   A  -          3  C  c  c

                                     ATGGTGGGAGCG AC  C CTCC GCC TGGGCAAC
                                     TGGTCACT    TG  G GAGG TGG ACCCGTTG
                                           GT C    G   T
GAM1338  360   MAPRE1 1   6409   NP_036457.1  3  1079   TTGGGATCTGCC   ----         G  A     3  C  c
c
                                     AGGCTGGGGTGT ACT    GCACTCCAGCCTGG CA
                                     TTTCGGTA    TGG    TGTGGGGTCGGACC GT
                                           CTTT           -  C
GAM1338  360   MCLC   1   4526   NP_055942.1  3  315    GCTCTGTCACCC   G          CAA       3  C  c  c
                                     AGGCTGGAGTGA ACT CACTCCAGCCTGGG
                                     GGTGGTAC    TGG GTGAGGTCGGACCC
                                           A           ACT
GAM1338  360   MCM10  1   4821   NP_060988.2  3  954    ACTATGTCACCC           T  CAA       3  C  c  c

                                     TGGCTGGAGTGC ACTGCACTCCAGCC GGG
                                     AGTAGTGC    TGACGTGAGGTCGG CCC
```

T ACT

GAM1338 360 MDM2 1 6085 NP_002383.1 3 354 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGGTG TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 MDM2 1 6085 NP_006869.1 3 354 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGGTG TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 MDM2 1 6085 NP_006870.1 3 354 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGGTG TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 MDM2 1 6085 NP_006871.1 3 354 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGGTG TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 MDM2 1 6085 NP_006872.1 3 354 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGGTG TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 MDM2 1 6085 NP_006873.1 3 298 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGGTG TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 MDM4 1 19527 NP_002384.1 3 547 GTTCTGTCTCCC C CA 3 C c c
AGGCTGAAGTGC ACTGCACT CAGCCTGGG AC
AGTGAGTC TGACGTGA GTCGGACCC TG
A TC

GAM1338 360 MEFV 2 12284 NP_000234.1 3 822 CTCTTGTCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 MEFV 2 17376 NP_000234.1 3 510 GCTCTGTGGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
GT

GAM1338 360 MESDC2 1 17209 XP_051854.1 3 73 AGCTCTTTGCCC G- C-- 3 C c c
AGCTCCTGGGGT ACT CACTCCAG CTGGGCAA
GGGAGTGG TGA GTGGGGTC GACCCGTT
GG CTC

GAM1338 360 MFTC 1 10459 NP_110407.2 3 547 GCTTTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT

GAM1338 360 MGAT2 1 18270 NP_079374.1 3 985 CTCTTGTCGCTC C AA 3 C c c
AGCCTGGAGTGC ACTGCACTCCAG CTGGGC
AGTGAGCT TGACGTGAGGTC GACTCG
C CT

GAM1338 360 MGC1020 1 13048 NP_659497.1 3 180 GCTTTGTCACGC C --- 3 C b b

```
          0                          AGGCTAGAGTGC ACTGCACTC AGCCTG   GGCAA
                                     AGTGGCGC     TGACGTGAG TCGGAC   CTGTT
                                                  A      GCA
GAM1338   360    MGC1110 1   14977  NP_115701.2   3  1314   CCTGTGTTGCTC                    3   C   b   b
          2                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                     AGTGGTGT     TGACGTGAGGTCGGACTCGTTG

GAM1338   360    MGC1111 1   5608   NP_115686.2   3  366    GCGGCTTGTCCC   TG -  --       -       3   C   c
c
          5                          AGGCTGCTGGGC AC  CA CTC  CAGCCTGGG CAA
                                     TGTGGTCT     TG  GT GGG  GTCGGACCC GTT
                                                  GT  C   TC       T
GAM1338   360    MGC1226 1   6361   NP_116085.1   5  202    GTGATGTTGCCC        C           3   C   b   b
          2                          AGGCTAGAGTGC ACTGCACTC AGCCTGGGCAAC
                                     AGTGGCAC     TGACGTGAG TCGGACCCGTTG
                                                  A
GAM1338   360    MGC1251 1   18251  NP_291026.1   3  0      CCCCAGGTTGGA             CAA        3   C   c   c

          8                          GTGCAGTGGCGT ACTGCACTCCAGCCTGGG
                                     GTCTTGGG     TGACGTGAGGTTGGACCC
                                                  C--
GAM1338   360    MGC1276 1   5586   NP_116112.1   5  153    TGCAGGTTGCCC A-----   -   AG          3   C   c
c
          0                          AGGAGGAGCTGC      CTGCA CTCC  CCTGGGCAAC
                                     AGCGCCAG          GACGT GAGG  GGACCCGTTG
                                               GACCGC     C    A-
GAM1338   360    MGC1301 1   18970  NP_542387.1   3  457    GCTCTGTTGCCC        CCA             3   C   b
b
          7                          AGGCAGTAGTGC ACTGCACT   GCCTGGGCAAC
                                     AGTGGCGC     TGACGTGA   CGGACCCGTTG
                                                  TGA
GAM1338   360    MGC1302 1   15630  NP_689501.1   3  432    AGTCTGTTTCCC             C          3   C   b   b
          4                          AGGCTGGAGTGT ACTGCACTCCAGCCTGGG AAC
                                     AGTGATAC     TGATGTGAGGTCGGACCC TTG
                                                  T
GAM1338   360    MGC1313 2   14027  NP_219363.1   3  766    CTCTTGTTGCCC AC-----                3   C   c
c
          8                          AGGCTGGAGTGC       TGCACTCCAGCCTGGGCAAC
                                     AATAGCGC           ACGTGAGGTCGGACCCGTTG
                                               CGCGATA
GAM1338   360    MGC1313 2   19426  NP_219363.1   3  455    GCTCTGTCACCC             CAA        3   C   c
c
          8                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGTGT     TGACGTGAGGTCGGACCC
                                                  ACT
GAM1338   360    MGC1317 1   12394  NP_116101.1   3  288    GCACTTCTGCCC   G    CA--       A       3   C   c
 c
          0                          AGGCAGCAGGGT ACT CACTC    GCCTGGGCA
                                     GGGTGGGT     TGG GTGGG    CGGACCCGT
                                                  -    ACGA       C
```

```
GAM1338  360    MGC1320 1   17963  NP_113653.1  3  128   GCTCTGTTGCCC                    3  C  b  b
         4                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                    AGTGGTAT     TGACGTGAGGTCGGACCCGTTG

GAM1338  360    MGC1428 1   1959   NP_542391.1  3  451   GCTCTGTTGCCC                    3  C  b  b
         9                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                    AGTGACGT     TGACGTGAGGTCGGACCCGTTG

GAM1338  360    MGC1483 1   9102   NP_219480.1  3  380   GCTCTGTTGCCC                    3  C  b  b
         6                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                    AGTGGCGC     TGACGTGAGGTCGGACCCGTTG

GAM1338  360    MGC1560 1   6622   NP_659474.1  5  286   GCTCTGTTGCCC AC-----  C          3  C  c
c
         6                          AGGCTGGAGTAC       TG ACTCCAGCCTGGGCAAC
                                    ATTGGTGT           AC TGAGGTCGGACCCGTTG
                                           TGTGGTT  A
GAM1338  360    MGC1566 1   15177  NP_116145.1  3  24    CCTAGGATGCCC A-----     T    -    A    3  C  c
c
         8                          AGGGCTGGGTGC       CTGCAC CCAGCC TGGGCA
                                    AGCCAGCT           GACGTG GGTCGG ACCCGT
                                           TCGACC      -    G    A
GAM1338  360    MGC1570 1   6734   NP_116146.1  3  161   TAGGAAGTTGTG         AGC   -        3  C  c
c
         5                          TCAGAGGAGTGC ACTGCACTCC   CTGG GCAAC
                                    AGTCATCT     TGACGTGAGG   GACT TGTTG
                                                 A--   G
GAM1338  360    MGC1587 1   9079   NP_116309.1  5  80    TCTCTGTCGCCC   G  T        AA       3  C  c
c
         3                          AGGCTGGCGTGA ACT CAC CCAGCCTGGGC
                                    AGTGGCGC     TGA GTG GGTCGGACCCG
                                              A  C          CT
GAM1338  360    MGC1783 1   18441  NP_777586.1  5  118   TGTCAGCCTACC        -  C--    AA      3  C  c
c
         9                          AGCTCGGAGTGC ACTGCACTCC AGC   TGGGC
                                    AGTTCCTG     TGACGTGAGG TCG   ATCCG
                                                 C  ACC     AC
GAM1338  360    MGC1791 1   1588   NP_653222.2  3  0     GCCCAGGCCGGA    C    A      AA       3  C  c
c
         9                          GTACAGTGGCAT ACTG ACTCC GCCTGGGC
                                    GTCTCAGC     TGAC TGAGG CGGACCCG
                                              A    C       --
GAM1338  360    MGC1842 1   11658  XP_037797.2  3  1419  ACTCTGTTGCCC         C            3  C  b  b

                                    AGACTGGAGTGC ACTGCACTCCAG CTGGGCAAC
                                    AGTGGCAC     TGACGTGAGGTC GACCCGTTG
                                                 A
GAM1338  360    MGC2167 1   19749  NP_443093.1  3  499   CTCTTGTTGCCC AC-----                3  C  c
c
         5                          AGGCTGGAGTGC       TGCACTCCAGCCTGGGCAAC
```

AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 MGC2474 2 18119 NP_076420.1 3 1311 TGCTCCTCACCC C CAA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGTGT TGACGT AGGTCGGACCC
A ACT
GAM1338 360 MGC2474 2 19749 NP_076420.1 3 953 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGACCCGTTG
CGTGGTA
GAM1338 360 MGC2477 3 3973 NP_077004.1 5 1479 CACTCTGTTGCC C 3 C b b
CAGCTGGAGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGCGT TGACGTGAGGTCG ACCCGTTG
-
GAM1338 360 MGC2477 3 12048 NP_077004.1 5 1289 CTCTGTCGCCCA - AA 3 C c b
GGGCTGGAGTGC ACTGCACTCCAGCC TGGGC
AGTGGCGC TGACGTGAGGTCGG ACCCG
G CT
GAM1338 360 MGC2477 3 19729 NP_077004.1 5 1479 ACTCTGTTGCCC C 3 C b b
AGCTGGAGTGCA ACTGCACTCCAGC TGGGCAAC
GTGGCGTG TGACGTGAGGTCG ACCCGTTG
-
GAM1338 360 MGC2603 1 17763 NP_076942.1 3 419 CGCTCTGTCGCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGC TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 MGC2648 1 9741 NP_689840.1 3 1404 GGGAGGTTGCCC - CT - C- 3 C c c
4 ATTGTTTGGTTG ACTG CA CCAG C TGGGCAAC
CCAGTCAT TGAC GT GGTT G ACCCGTTG
C T- T TT
GAM1338 360 MGC2698 1 14418 NP_689976.1 3 665 TTTGTACTCACC TG ----- 3 C c c
9 AGGCTGGAGTGT AC CACTCCAGCCTGG GCAA
GGTAGCAC TG GTGAGGTCGGACC TGTT
GT ACTCA
GAM1338 360 MGC2734 2 7706 XP_300964.1 5 1667 TTCTTGTTGCCC - 3 C b b
5 AGGGCTGGAGTG ACTGCACTCCAGCC TGGGCAAC
CAGTGGCA TGACGTGAGGTCGG ACCCGTTG
G
GAM1338 360 MGC2734 2 18352 XP_300964.1 5 1667 TCTTGTTGCCCA - 3 C b b
5 GGGCTGGAGTGC ACTGCACTCCAGCC TGGGCAAC
AGTGGCAT TGACGTGAGGTCGG ACCCGTTG
G
GAM1338 360 MGC2989 1 18179 NP_653219.1 3 605 ACTCTGTCACCC CAA 3 C c c

```
          1                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     GGTGGTGC     TGGCGTGAGGTCGGACCC
                                                  ACT
GAM1338   360    MGC2989 1   9164   NP_659485.1   3  502    GCTTTGTTGCCC          C            3   C   b   b
          8                          AGACTGGAGTGC ACTGCACTCCAG CTGGGCAAC
                                     AGTGGCAT     TGACGTGAGGTC GACCCGTTG
                                                  A
GAM1338   360    MGC3113 1   15946  NP_076940.1   3  712    ACTCTGTTCCCC         A     C         3   C   b   b

                                     AGGCCGGAGTGC ACTGCACTCC GCCTGGG AAC
                                     AGTGGTAC     TGACGTGAGG CGGACCC TTG
                                                  C      C
GAM1338   360    MGC3195 1   15735  NP_114111.2   5  185    CCGGGACGCGCC     --         - AA       3   C   c
c
                                     GGGCTGGAGTGG ACTGC  ACTCCAGCCTGG GC
                                     GCGGTTAT     TGGCG  TGAGGTCGGGCC CG
                                                  GG          G  CA
GAM1338   360    MGC3207 2   12382  NP_115661.1   3  1436   GCTCTGTCGCCC             AA         3   C   b
b
                                     AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                     AGTGGTGC     TGACGTGAGGTCGGACCCG
                                                  CT
GAM1338   360    MGC3207 2   14723  NP_115661.1   3  786    CACTCGTTGCCC A-----                  3   C   c   b

                                     AGGCTGGAGTGT      CTGCACTCCAGCCTGGGCAAC
                                     AGAGGCGA          GATGTGAGGTCGGACCCGTTG
                                           AGCGGA
GAM1338   360    MGC3329 1   4873   NP_076991.2   3  1596   CTCTTGTTGTCT  T                  3   C   b   b
                                     AGGCTGGAGTGC AC GCACTCCAGCCTGGGCAAC
                                     CGTGGTGC     TG CGTGAGGTCGGATCTGTTG
                                                  C
GAM1338   360    MGC3363 1   12383  NP_689809.1   3  683    ACTCTGTCACCC             CAA        3   C   c
c
          7                          AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
                                     AGTGGTGT     TGATGTGAGGTCGGACCC
                                                  ACT
GAM1338   360    MGC3403 1   9789   NP_694956.1   5  276    ATTCAGCAGTCC     CTC       AA         3   C   c
c
          4                          AGGCTGATGCAG ACTGCA   CAGCCTGGGC
                                     TGGCTTCA     TGACGT   GTCGGACCTG
                                                  A--        AC
GAM1338   360    MGC3407 1   19879  NP_689688.1   3  188    ATTCTGTCACCC             CAA        3   C   c
c
          9                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGTGC     TGACGTGAGGTCGGACCC
                                                  ACT
GAM1338   360    MGC3413 2   8862   XP_291029.1   3  500    ACTCTGTCACCC             CAA        3   C   c   c

          2                          AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                     AGTGGCAT     TGACGTGAGGTCGGACCC
```

ACT
GAM1338 360 MGC3413 2 9188 XP_291029.1 3 334 TCACTGTCACCC CAA 3 C c c

2 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 MGC3544 2 13796 NP_694952.1 3 183 ACTCTGTCACCC CAA 3 C c
c
0 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
GGTGGCGC TGGCGTGAGGTCGGACCC
ACT
GAM1338 360 MGC3544 2 15523 NP_694952.1 3 492 GCTCTGTCGCCC C AA 3 C c
c
0 AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGTGC TGACGT AGGTCGGACCCG
A CT
GAM1338 360 MGC3546 1 15490 NP_694976.1 3 86 CCCTTGTTGCCC AC----- 3 C c c

8 AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA
GAM1338 360 MGC3932 1 2691 NP_689642.2 3 696 TCTGGCTTGCCC 3 C b b
0 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
GGTGGCTA TGGCGTGAGGTCGGACCCGTT

GAM1338 360 MGC4015 2 865 NP_689563.1 3 464 TCTATGTTGCCC A------ CACT 3 C c
b
7 AGGCTGGTCTCA CTG CCAGCCTGGGCAAC
GGCTCCTG GAC GGTCGGACCCGTTG
GTCCTCG TCT-
GAM1338 360 MGC4015 2 13547 NP_689563.1 3 317 GCTGTATTGCCC TG 3 C b
b
7 AGGCTGGAGTGT AC CACTCCAGCCTGGGCAA
GGTGGCAC TG GTGAGGTCGGACCCGTT
GT
GAM1338 360 MGC4016 1 3717 NP_714920.1 5 284 ACTCTGTTGCCA C G 3 C b b

8 AGGCTGGAATGC ACTGCA TCCAGCCT GGCAAC
AGTGGCGA TGACGT AGGTCGGA CCGTTG
A A
GAM1338 360 MGC4057 1 516 NP_689989.1 3 332 GCTCTGTCACTC CAA 3 C c c
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTAT TGACGTGAGGTCGGACTC
ACT
GAM1338 360 MGC4248 1 8539 NP_115709.2 3 275 AAATTGACTGCC T G A 3 C c c

AGGCTGGGTGCA ACTGCAC CCAGCCTGG CA
GTGGCTCA TGACGTG GGTCGGACC GT
- - C
GAM1338 360 MGC5045 1 8458 NP_775733.1 3 88 CACTTCTTGCCC AC----- C 3 C c c

2 AGGCTGGAGTAC TG ACTCCAGCCTGGGCAA
AATGGTGC AC TGAGGTCGGACCCGTT
CGTGGTA A

GAM1338 360 MGC5055 2 5794 NP_776163.1 3 457 CACTTTGCTCCC C -- 3 C b b
9 AGGCTGGAATGC ACTGCA TCCAGCCTGG GCAA
AGTGGCTA TGACGT AGGTCGGACC CGTT
A CT

GAM1338 360 MGC5055 2 7831 NP_776163.1 3 560 GCTCTGTCGTCC AA 3 C c b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGACTC TGACGTGAGGTCGGACCTG
CT

GAM1338 360 MGC5149 1 17590 XP_051200.2 3 1953 CACTCTGTCACC C -- A 3 C c
c
AGGCTAGAGTGC ACTGCACTC AGCCTGG GCA
AGTGGCAC TGACGTGAG TCGGACC TGT
A AC C

GAM1338 360 MGC9912 1 11391 NP_542395.1 3 351 TGCTCTGTCGCC C -- A 3 C c
c
AGACTGGAGTGC ACTGCACTCCAG CTGG GCA
AGTGGCGC TGACGTGAGGTC GACC TGT
A GC C

GAM1338 360 MGRN1 1 13807 XP_048119.4 3 1593 CTCTTGCTGCCC A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCA
AGTGGCTC TGACGTGAGGTCGGACCCGT
C

GAM1338 360 MHC2TA 3 4816 NP_000237.1 3 809 CCAGATTGCAAC A - ----- G- 3 C c b
AGGCTGGGCTTC CTGC ACT CCAGCCTG GCAA
AGTGGCAG GACG TGA GGTCGGAC CGTT
- G CTTCG AA

GAM1338 360 MHC2TA 3 6437 NP_000237.1 3 438 TCACTGTTGCCC T 3 C b b
AGGCTGGCGTGC ACTGCAC CCAGCCTGGGCAAC
AGTGGTGC TGACGTG GGTCGGACCCGTTG
C

GAM1338 360 MHC2TA 3 9987 NP_000237.1 3 2660 ACTCTTATGCCC C A 3 C b b
ACGCTGGAGTGC ACTGCACTCCAGC TGGGCA
AGTGAGCC TGACGTGAGGTCG ACCCGT
C A

GAM1338 360 MIRAB13 1 3109 NP_203744.1 3 1731 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 MIRAB13 1 3109 XP_039236.6 3 2296 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 MKRN4 1 12385 NP_110384.1 3 372 ACTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 MLANA 1 17276 NP_005502.1 3 610 CTTTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTA

GAM1338 360 MLZE 1 11404 NP_113603.1 5 583 ACGGAGTTGCCC A----- 3 C b b
AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGCGCATG GACGTGAGGTCGGACCCGTTG
GTACGC

GAM1338 360 MMAB 1 11037 NP_443077.1 3 340 TAAAAGTTGGAA - --- GGG 3 C c c

AGGCTGGAGCCG AC TGCAC TCCAGCCT CAAC
TGTGTGTG TG GTGTG AGGTCGGA GTTG
T CCG AAG

GAM1338 360 MO25 1 6709 NP_057373.1 3 377 CATCTTTGTTGG CA--- TG 3 C c c
CGATCTGAGTGC ACTGCACTC GCC GGCAA
AGTGTGGC TGACGTGAG CGG TTGTT
TCTAG --

GAM1338 360 MOAP1 1 11659 NP_071434.2 3 299 GCTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 moblak 1 2270 NP_570719.1 3 1259 CCCGGCCTAACC GCAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGG
AGTGGTGG TGACGTGAGGTCGGACC
AATC

GAM1338 360 MOCS3 1 6108 NP_055299.1 3 578 TCTCTGTTGCCC 3 C b b
AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGATGTGAGGTCGGACCCGTTG

GAM1338 360 MPL 1 11909 NP_005364.1 3 749 TTGCCTGTTGCC C G 3 C b b
AGACTGGAGTGC ACTGCACTCCAG CTGG CAAC
AGTGGCAC TGACGTGAGGTC GACC GTTG
A -

GAM1338 360 MRPL10 1 3339 NP_683685.1 5 69 CCTGCCCCAGGC C ----- A 3 C c c
GGGCTAGAGTGC ACTGCACTC AGCCT GGGCA
AGTGGCAT TGACGTGAG TCGGG CCCGT
A CGGAC C

GAM1338 360 MRPL35 1 10631 NP_057706.2 3 1059 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 MRPL44 1 6410 NP_075066.1 3 258 ACTCTGTCGCCC C AA 3 C c c
AGGCTGGACTGC ACTGCA TCCAGCCTGGGC
AGTGGTGC TGACGT AGGTCGGACCCG
C CT

GAM1338 360 MRPL49 1 13534 NP_004918.1 3 323 ACTCTGTTGCCC G 3 C b b
AGGGTGGAGTGC ACTGCACTCCA CCTGGGCAAC
AGTGGCAT TGACGTGAGGT GGACCCGTTG
G
GAM1338 360 MRPS27 1 13372 NP_055899.1 3 429 ATTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 MSL3L1 1 1303 NP_006791.2 3 157 TTTGAGTTGCCC CTCCAGCC 3 C
c c
ACATACTGCAGT ACTGCA TGGGCAAC
TATTCTGT TGACGT ACCCGTTG
CATAC---
GAM1338 360 MSL3L1 1 1303 NP_523353.1 3 157 TTTGAGTTGCCC CTCCAGCC 3 C
c c
ACATACTGCAGT ACTGCA TGGGCAAC
TATTCTGT TGACGT ACCCGTTG
CATAC---
GAM1338 360 MSL3L1 1 1303 NP_523354.1 3 157 TTTGAGTTGCCC CTCCAGCC 3 C
c c
ACATACTGCAGT ACTGCA TGGGCAAC
TATTCTGT TGACGT ACCCGTTG
CATAC---
GAM1338 360 MSTP028 1 11359 NP_114160.1 3 1906 GCTCTATTGGCC G 3 C b b
AGGCTGGAGTGT ACTGCACTCCAGCCTGG CAA
AGTGGCAC TGATGTGAGGTCGGACC GTT
G
GAM1338 360 MTH2 1 12462 NP_060753.1 3 850 GCTCTGTTGCCC CC 3 C b b
ACATTGGAGTGC ACTGCACTCCAG TGGGCAAC
AGTGGCAC TGACGTGAGGTT ACCCGTTG
AC
GAM1338 360 MTR 1 13325 NP_000245.1 3 811 GCTCTGTCGCCC A----- AA 3 C c c
AGGCTGGAGTGC CTGCACTCCAGCCTGGGC
AGGGGCGC GACGTGAGGTCGGACCCG
CGCGGG CT
GAM1338 360 MYO1D 1 2339 XP_050041.4 3 1791 GTTGCCTGTCAA A----- A ----- 3 C c c
AGGCTGGAGGGC CTGC CTCCAGCCT GGGCAA
AGGAGGAG GACG GAGGTCGGA TCCGTT
GAGGAG G AACTG
C
G
GAM1338 360 MYO5C 1 14846 NP_061198.1 3 628 CGCTCTATCGCC GCAA 3 C c
c
AGGCTGGAGTGT ACTGCACTCCAGCCTGG
AGTGGCAT TGATGTGAGGTCGGACC

GCTA
GAM1338 360 Nanog 1 3109 NP_079141.1 3 281 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 NCAG1 1 11436 NP_115536.1 3 3664 ACTTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTCT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 NCOA6 2 5484 NP_054790.1 5 884 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTCGTGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 NCOA6 2 6181 NP_054790.1 5 1278 GCTCTGTCACCG G CAA 3 C c
b
AGGCTGGAGTGC ACTGCACTCCAGCCT GG
AGTGGCGC TGACGTGAGGTCGGA CC
G ACT
GAM1338 360 NCOA6IP 2 3026 NP_079107.5 3 279 CTTTTACCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGCCAT TGACGTGAGGTCGGACCCG
CC
GAM1338 360 NCOA6IP 2 13249 NP_079107.5 3 443 ACCATGTTGCCC AC------ C T 3 C c
b
AGGCTGGTGTCA TG AC CCAGCCTGGGCAAC
AACTCCTG AC TG GGTCGGACCCGTTG
GTCCTCAA - T
GAM1338 360 NDRG3 1 20109 NP_114402.1 3 1151 TCGCTGTTACCC AC----- C 3 C c
c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGCGC ACGTGAGGTCGGACCC TTG
CGCGGTA A
GAM1338 360 NDUFC2 1 15362 NP_004540.1 3 1240 TGCTCTGTCATC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTG GGCA
AGTGGCGC TGACGTGAGGTCGGAC CTGT
TA C
GAM1338 360 NDUFS1 1 6109 NP_004997.3 3 1241 TCGCTTGAGCCC CA --- AA 3 C c
c
AGGCAGTTGGAG ACTG CTCCA GCCTGGGC
ACCAGTCT TGAC GAGGT CGGACCCG
CA TGA AG
GAM1338 360 NEU3 1 18182 NP_006647.2 5 70 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 NOL3 1 18676 NP_003937.1 3 190 GGCTGTTTGCCC G CAG--- 3 C c
c
AGGAACTTAGGG ACT CACTC CCTGGGCAA
TGGGTACC TGG GTGGG GGACCCGTT
- ATTCAA

GAM1338 360 NONO 1 1412 NP_031389.2 3 446 ACTCTGTCGCCC AA 3 C c c
AGGCTGGAGTGT ACTGCACTCCAGCCTGGGC
AGTGGCAT TGATGTGAGGTCGGACCCG
CT
GAM1338 360 NOSIP 1 8269 NP_057037.1 5 52 CTCTTGTTGCCT AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGC ACGTGAGGTCGGATCCGTTG
CGTGGTA
GAM1338 360 NOX5 1 7634 NP_078781.2 5 206 TCCATTGCGCCC CT AA 3 C c c
AGGCTGGTATGC ACTGCA CCAGCCTGGGC
AGTCATGT TGACGT GGTCGGACCCG
AT CG
GAM1338 360 NPTXR 1 17176 NP_055108.2 3 3925 TCACATGGGCCC - C AA 3 C c
c
AGGCTGAGTGTG ACT GCACTC AGCCTGGGC
AGTGAGCA TGA TGTGAG TCGGACCCG
G - GG
GAM1338 360 NPTXR 1 17176 NP_478058.1 3 3925 TCACATGGGCCC - C AA 3 C c
c
AGGCTGAGTGTG ACT GCACTC AGCCTGGGC
AGTGAGCA TGA TGTGAG TCGGACCCG
G - GG
GAM1338 360 NQO1 1 18183 NP_000894.1 3 684 GCTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGT TGACGTGAGGTCGGACCC TTG
A
GAM1338 360 NRLN1 1 15192 NP_660277.1 5 22 AGGCCAGTGCCC -- CC A 3 C c c
AGGTTAGTGAGC ACTGC ACT AGCCTGGGCA
AGTGCCCG TGACG TGA TTGGACCCGT
AG -- G
GAM1338 360 NT5C2 1 15388 NP_036361.1 5 34 GCTCTGCTGCCC C A 3 C b b
AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCA
AGTGATGT TGAC TGAGGTCGGACCCGT
A C
GAM1338 360 NUP43 1 9379 NP_078923.2 3 605 CAGAGTCTTGCT CT 3 C b b
CTGCTGGAGTGC ACTGCACTCCAGC GGGCAA
GGTGGTGC TGGCGTGAGGTCG CTCGTT
T-
GAM1338 360 NXN 1 436 NP_071908.1 3 875 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 OIP106 1 10262 NP_055780.1 5 17 GATAGGGTTCCC G CTC C 3 C c
c
AGGCTGCCTGGA ACT CA CAGCCTGGG AAC
GTTACATA TGA GT GTCGGACCC TTG
G CC- -
GAM1338 360 OR51E2 1 8690 NP_110401.1 3 439 CGCTCTGTCACC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA

AGTGGCGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 ORC1L 1 436 NP_004144.1 3 91 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 OSBPL2 1 18258 NP_055650.1 3 1125 CTCTTGTTGCCC AC----- 3 C c c

AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAT ACGTGAGGTCGGACCCGTTG
TACGGTA
GAM1338 360 OSBPL2 1 18258 NP_653081.1 3 1125 CTCTTGTTGCCC AC----- 3 C c c

AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAT ACGTGAGGTCGGACCCGTTG
TACGGTA
GAM1338 360 OTOA 1 9822 NP_733764.1 5 65 CTGAGGATGTTC - - A 3 C c c
AGGCTGGGGCTG ACT GCA CTCCAGCCTGGGCA
CTGGTTT TGG CGT GGGGTCGGACTTGT
T C A
GAM1338 360 P2RY11 1 6710 NP_002557.2 3 153 CAGCTGCAGCCC AC A AA 3 C c
c

AGGCAGGAGCAG ACTGC TCC GCCTGGGC
TCGCCTTT TGACG AGG CGGACCCG
-- A AC
GAM1338 360 PAICS 1 11127 NP_006443.1 3 412 TCACTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 PANK3 1 18008 NP_078870.1 3 1441 TCCCCTTGCCTG G CC- 3 C c
c

AATCTGGAGTGG ACT CACTCCAG TGGGCAA
GGTTGAGC TGG GTGAGGTC GTCCGTT
G TAA
GAM1338 360 PASK 1 3230 NP_055963.1 5 804 CTCTTGTTGCTG G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCT GGCAAC
AGTGGCAC TGACGTGAGGTCGGA TCGTTG
G
GAM1338 360 PCDHA9 2 10631 NP_054724.1 3 1914 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 PCDHA9 2 11879 NP_054724.1 3 1313 TTTCTGCCACCC C CAA 3 C c
b

AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAT TGAC TGAGGTCGGACCC
A ACC
GAM1338 360 PCDHB16 1 4753 NP_066008.1 3 580 CTCTTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG

AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 PCDHB9 1 3109 NP_061992.2 3 526 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 PDE6B 1 18070 NP_000274.1 3 196 GCTCTGTCACCC T CAA 3 C c c

AGGCTGGAGTGC AC GCACTCCAGCCTGGG
CGTGGCAC TG CGTGAGGTCGGACCC
C ACT
GAM1338 360 PDGFC 2 3930 NP_057289.1 3 44 CAGCTCTTGCCC C-- - 3 C b b
AGAGCTGTGCAG ACTGCACT CAGC CTGGGCAA
TGCAGTGG TGACGTGA GTCG GACCCGTT
CGT A
GAM1338 360 PDGFC 2 19767 NP_057289.1 3 44 CTCTTGCCCAGA C-- - 3 C b b
GCTGTGCAGTGC ACTGCACT CAGC CTGGGCAA
AGTGGCTG TGACGTGA GTCG GACCCGTT
CGT A
GAM1338 360 PDLIM2 1 4874 NP_789847.1 3 1200 GCTCTATTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGTAC TGACGTGAGGTCGGACCCGTT

GAM1338 360 PDZK1 1 11598 NP_002605.2 5 43 ATTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 PDZRN1 1 17567 NP_699202.1 3 521 TCACTCTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 PELI1 3 430 NP_065702.2 5 2685 GCTCTGTTGCCC 3 C b b
AGGTTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTTGGACCCGTTG

GAM1338 360 PELI1 3 13801 NP_065702.2 5 2121 ACTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 PELI1 3 18182 NP_065702.2 5 1441 GCTCTGTCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 PER2 1 6602 NP_073728.1 3 1369 TTCTTTTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCGC TGACGTGAGGTCGGACCCGTT

GAM1338 360 PEX10 1 7262 NP_002608.1 3 470 CTGGCGGGTTGC CCA CT 3 C c
c

```
                                TTCAGCCAGTGC ACTGCACT   GC  GGGCAAC
                                AGTGAGAA    TGACGTGA   CG  TTCGTTG
                                      C--  AC
GAM1338  360   PEX10  1  7262  NP_722540.1  3 470   CTGGCGGGTTGC       CCA  CT          3  C  c
c
                                TTCAGCCAGTGC ACTGCACT   GC  GGGCAAC
                                AGTGAGAA    TGACGTGA   CG  TTCGTTG
                                      C--  AC
GAM1338  360   PHAX   1  12387 NP_115553.1  3 697   ACCTGAACCCCC    C         CAA       3  C  c  c

                                AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
                                AGTGGCAG    TGAC TGAGGTCGGACCC
                                      A          CCA
GAM1338  360   PIGR   1  8350  NP_002635.2  3 813   TCACTGTCGCCC              AA        3  C  b  b
                                AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
                                AGTGGCGC    TGACGTGAGGTCGGACCCG
                                      CT
GAM1338  360   PIK3C2B 1  15277 NP_002637.2  3 1447  CGCCCTGTCGCC           --  A      3  C  c  c
                                AGGCTGGAGTGT ACTGCACTCCAGCCTGG  GCA
                                AGTGGCAT    TGATGTGAGGTCGGACC  TGT
                                      GC  C
GAM1338  360   PIK3CD  1  4771  NP_005017.2  3 821   CCTCTGTTGCCC                    3  C  b  b
                                AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
                                AGTGGTGC    TGACGTGAGGTCGGACCCGTTG

GAM1338  360   PKNOX1  1  11464 NP_004562.2  3 1820  CTCTTGTTGCCC AC-----  A            3  C  c
c
                                AGGCTGGAGGGC       TGC CTCCAGCCTGGGCAAC
                                AATGGTGC          ACG GAGGTCGGACCCGTTG
                                      CGTGGTA   G
GAM1338  360   PMCHL1  2  982   NP_114093.1  3 525   ACTCTGTTGCCC AC-----              3  C  c  c
                                AGGCTGGAGTGC       TGCACTCCAGCCTGGGCAAC
                                AATGGCAC          ACGTGAGGTCGGACCCGTTG
                                      CACGGTA
GAM1338  360   PMCHL1  2  12367 NP_114093.1  3 1087  AAAGACCTTTGT       CAG  G          3  C  c
c
                                CAAGGAGAGTGC ACTGCACTC   CCT GGCAA
                                AGTCAACC    TGACGTGAG   GGA CTGTT
                                      A--  A
GAM1338  360   PMCHL2  2  982   NP_114094.1  3 523   ACTCTGTTGCCC AC-----              3  C  c  c
                                AGGCTGGAGTGC       TGCACTCCAGCCTGGGCAAC
                                AATGGCAC          ACGTGAGGTCGGACCCGTTG
                                      CACGGTA
GAM1338  360   PMCHL2  2  12367 NP_114094.1  3 1085  AAAGACCTTTGT       CAG  G          3  C  c
c
                                CAAGGAGAGTGC ACTGCACTC   CCT GGCAA
                                AGTCAACC    TGACGTGAG   GGA CTGTT
                                      A--  A
GAM1338  360   PMPCA  1  7152  NP_055975.1  3 245   GTGAAGTGCCCA A-----       -    A   3  C  c  c
                                GCGCTGGAGTGC       CTGCACTCCAGC CTGGGCA
```

AGCGTGCC GACGTGAGGTCG GACCCGT
CCGTGC C G
GAM1338 360 PNMA2 2 11189 NP_009188.1 3 264 CTCTCATCACCC C CAA 3 C c c
AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGCAC TGACGTGAG TCGGACCC
A ACT
GAM1338 360 PNMA2 2 11236 NP_009188.1 3 1713 GCTCTATCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 POFUT1 1 1760 NP_056167.1 3 1736 GCTCTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
TC
GAM1338 360 POLE3 1 5665 NP_059139.2 3 1143 ACTCTGTGGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAT TGACGTGAGGTCGGACCCG
GT
GAM1338 360 POLR2D 2 850 NP_004796.1 3 520 TAACTCTTGTCC --- 3 C b b
AGGCTGGAGGAG ACTGCACTCC AGCCTGGGCAA
TGCAGTCG TGACGTGAGG TCGGACCTGTT
AGG
GAM1338 360 POLR2D 2 11282 NP_004796.1 3 520 CTCTTGTCCAGG --- 3 C b b
CTGGAGGAGTGC ACTGCACTCC AGCCTGGGCAA
AGTCGTAC TGACGTGAGG TCGGACCTGTT
AGG
GAM1338 360 PON1 1 19429 NP_000437.3 3 1196 ACTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG
GAM1338 360 POU2AF1 1 4674 NP_006226.1 3 1374 ACTCCATTGCCC AC----- C 3 C c c
AGGCTGGAGTAC TG ACTCCAGCCTGGGCAA
AATGGTGC AC TGAGGTCGGACCCGTT
CGTGGTA A
GAM1338 360 POU2F3 1 7036 NP_055167.1 3 1108 TTGCTCCAGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAT TGACGTGAGGTCGGACCCG
AC
GAM1338 360 POU3F1 1 7918 NP_002690.2 3 4 ACACACTGCCCG CC T A 3 C c c
GCTCAGTGCAGT ACTGCACT AGCC GGGCA
GCCCCGCG TGACGTGA TCGG CCCGT
C- - C
GAM1338 360 PP3856 1 6293 NP_660202.1 5 508 TTCCAGGTGCCC C T A 3 C c c
TGGCTGGAGTCA ACTG ACTCCAGCC GGGCA
GTCCTCAT TGAC TGAGGTCGG CCCGT
- T G
GAM1338 360 PPEF2 1 568 NP_006230.2 3 367 CTCTTGTTGCCC AC----- 3 C c c

AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
ATTGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTT
GAM1338 360 PPEF2 1 568 NP_690910.1 3 999 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
ATTGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTT
GAM1338 360 PPEF2 1 568 NP_690911.1 3 2212 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
ATTGGCGC ACGTGAGGTCGGACCCGTTG
CGCGGTT
GAM1338 360 PPFIA4 1 10102 XP_046751.3 3 1518 TGTTTCTTGGAT -- AG GG 3 C c
c
AGGGGCCAGTGC ACTGCACT CC CCTG CAA
AGTGCCAT TGACGTGA GG GGAT GTT
CC -- AG
GAM1338 360 PPFIBP1 2 5523 NP_003613.2 3 1167 ATTCTGTTGCCC C 3 C b b
ATGCTGGAGTGC ACTGCACTCCAGC TGGGCAAC
AGTGGCGT TGACGTGAGGTCG ACCCGTTG
T
GAM1338 360 PPFIBP1 2 8861 NP_003613.2 3 2294 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 PPID 1 3110 NP_005029.1 3 246 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
GGTGGCGC TGGCGTGAGGTCGGACCC
ACT
GAM1338 360 PPIL2 1 18677 NP_055152.1 3 391 GCTCTGTTGCCC CC 3 C b b
AGGCTCCAGTGC ACTGCACT AGCCTGGGCAAC
AGTGGTGT TGACGTGA TCGGACCCGTTG
CC
GAM1338 360 PPP1R12 2 14820 NP_002472.1 3 4496 ACTCTCTCGCCC AA 3 C b
b
B AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 PPP1R12 2 14820 NP_115288.1 3 4629 ACTCTCTCGCCC AA 3 C b
b
B AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 PPP1R12 2 17555 NP_002472.1 3 4661 GCCATGTTGCCC A----- G CT 3 C c
b
B AGGCTGGTCTGA CT CA CCAGCCTGGGCAAC
AGCTGCTG GA GT GGTCGGACCCGTTG
GTCGTC A CT
GAM1338 360 PPP1R12 2 17555 NP_115288.1 3 4794 GCCATGTTGCCC A----- G CT 3 C c
b
B AGGCTGGTCTGA CT CA CCAGCCTGGGCAAC

AGCTGCTG GA GT GGTCGGACCCGTTG
GTCGTC A CT
GAM1338 360 PRIM2A 1 12707 NP_000938.1 3 105 TTCACTGTCACC CC - -- A 3 C c c

AAGGCTTAGTGC ACTGCACT AGCCT GG GCA
AGTGACAC TGACGTGA TCGGA CC TGT
T- A AC C
GAM1338 360 PRKR 1 17566 NP_002750.1 3 274 GCTCTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGACAC ACGTGAGGTCGGACCCGTTG
CACAGTA
GAM1338 360 PRKWNK3 1 5524 NP_065973.1 3 638 TCTCTGTCACCC CAA 3 C c
c

AGGTTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTTGGACCC
ACT
GAM1338 360 PRND 2 5776 NP_036541.1 3 837 CTCTTGTTGCCC AC----- 3 C c b
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AACGGCAT ACGTGAGGTCGGACCCGTTG
TACGGCA
GAM1338 360 PRND 2 7084 NP_036541.1 3 2763 ATTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 PRO0297 1 1504 NP_054800.1 5 52 GCTCTTTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 PRO0365 1 7958 NP_054845.1 5 883 CGCTCTGTCGCC C -- A 3 C c c

AGGCTGAAGTGC ACTGCACT CAGCCTGG GCA
AGTGGCGC TGACGTGA GTCGGACC TGT
A GC C
GAM1338 360 PRO1048 1 2738 NP_060967.1 3 318 ACTCTGCTGCCC C A 3 C b b
AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCA
AGTGGCAC TGAC TGAGGTCGGACCCGT
A C
GAM1338 360 PROM2 2 6958 NP_653308.1 3 950 GCCATGTTGCCC ACT---- - 3 C c c

AGGCTGGAAGTG GCACT CCAGCCTGGGCAAC
TCTATGTT TGTGA GGTCGGACCCGTTG
TTGTATC A
GAM1338 360 PROM2 2 19427 NP_653308.1 3 785 GCTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
AGTGGTGC TGATGTGAGGTCGGACCC
ACT
GAM1338 360 PSMD9 1 11654 NP_002804.2 3 751 GCTTTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGTCGT TGACGTGAGGTCGGACCC

ACT

GAM1338 360 PSPH 1 9102 NP_004568.1 3 275 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 PSTPIP2 1 14086 NP_077748.2 3 1321 TCTCTGTCCCCC A----- C CA 3 C c c
AGGCTGAAGTGC CTGCACT CAGCCTGGG AC
AGCGGCAT GACGTGA GTCGGACCC TG
TACGGC A CC

GAM1338 360 PTGES 1 11575 NP_004869.1 3 527 GCTCTGTTGCCC G C 3 C b b
AAGCTGGAGTGA ACT CACTCCAGC TGGGCAAC
AGTGGTAC TGA GTGAGGTCG ACCCGTTG
A A

GAM1338 360 PTGIS 2 11917 NP_000952.1 3 2839 GCTCTGCTGCCC C A 3 C b b
AGGCTAGAGTGC ACTGCACTC AGCCTGGGCA
AGTGGCGT TGACGTGAG TCGGACCCGT
A C

GAM1338 360 PTGIS 2 13582 NP_000952.1 3 3268 CGCTTATTGCCC AC----- 3 C c b
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATGGCAC ACGTGAGGTCGGACCCGTT
CACGGTA

GAM1338 360 PTK2 1 17374 NP_005598.3 5 128 ACCCAGGCTGCC G G A 3 C c c
AGGCTGGAGTGG ACT CACTCCAGCCTGG CA
AGTGGCAT TGA GTGAGGTCGGACC GT
G - C

GAM1338 360 PYGM 1 4024 NP_005600.1 5 740 AGCTCCACTCCT A ------ - AA 3 C c c
TGGCTGGAGGCA ACTGC CTCCAGCC TGG GC
GTGCTGAG TGACG GAGGTCGG ACC CG
- TTCCTC T A-

GAM1338 360 RAB11-F IP4 1 5406 NP_116321.2 3 2595 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGT ACTGCACTCCAGCCTGGGCAAC
AGTGGTAT TGATGTGAGGTCGGACCCGTTG

GAM1338 360 RAB31 1 536 NP_006859.1 3 19 GTGCTGTTGCCC CACT - -- 3 C c c
AAGGGCGTGGTC ACTG CCA GCCT GGGCAAC
CACGGTAC TGGC GGT CGGG CCCGTTG
ACCT G AA

GAM1338 360 RAB33B 1 15333 NP_112586.1 3 839 CGCTCTGTCTCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGT TGACGTGAGGTCGGACC TGT
TC C

GAM1338 360 RAB36 1 15649 NP_004905.1 3 1407 CCCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA

GAM1338 360 RAB39 1 2158 XP_084662.1 3 752 GTTTTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGGGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 RABL2A 1 14847 NP_038198.1 3 578 CGCTCTGTCGCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 RABL2B 1 14847 NP_009012.1 3 585 CGCTCTGTCGCC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGCGC TGACGTGAGGTCGGACC TGT
GC C
GAM1338 360 RAI 1 17223 NP_006654.1 5 21 ACAAGTGAGTCT T AA 3 C c c
CGGCTGGAGTGC ACTGCACTCCAGCC GGGC
AGTGGTGC TGACGTGAGGTCGG TCTG
C AG
GAM1338 360 RAI3 1 16116 NP_003970.1 3 342 GCTCTGTCACCC C CAA 3 C c c
AGGCTTGAGTGC ACTGCACTC AGCCTGGG
AGTGGTGC TGACGTGAG TCGGACCC
T ACT
GAM1338 360 RAP140 1 9663 NP_056039.1 3 1918 GCTCTGTCGCCC C C AA 3 C c
c
AAGCTGGAGTAC ACTG ACTCCAGC TGGGC
AGTGGTGC TGAC TGAGGTCG ACCCG
A A CT
GAM1338 360 RARG 1 18678 NP_000957.1 5 39 ACGGAGCCTCCC A T CAA 3 C c
c
AGGCTGGGGCAG ACTGC C CCAGCCTGGG
TGGGCATG TGACG G GGTCGGACCC
- - TCC
GAM1338 360 RASSF2 1 7664 NP_055552.1 3 3346 GTTCTGTTTCCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGG TGACGTGAGGTCGGACCC TTG
T
GAM1338 360 RASSF2 1 7664 NP_739579.1 3 3572 GTTCTGTTTCCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGG TGACGTGAGGTCGGACCC TTG
T
GAM1338 360 RASSF2 1 7664 NP_739580.1 3 3346 GTTCTGTTTCCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGG TGACGTGAGGTCGGACCC TTG
T
GAM1338 360 RBBP9 1 2397 NP_006597.2 3 1855 GCTCTGTCTCCC CA CA 3 C c
c
AGGCTGGAGGTC ACTG CTCCAGCCTGGG AC
AGTGGCAC TGAC GAGGTCGGACCC TG
TG TC
GAM1338 360 RCBTB1 1 3049 NP_060661.2 5 128 GCTCTCTTGCCC CAC C 3 C c
c
AGACTGGAATAC ACTG TCCAG CTGGGCAA
AGTGGTGT TGAC AGGTC GACCCGTT
ATA A
GAM1338 360 RDH13 1 11485 NP_612421.1 5 227 CACTCTGTCGCC C -- A 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGG GCA

AGTAGGGC TGACGT AGGTCGGACC TGT
A GC C
GAM1338 360 RERE 1 8833 NP_036234.2 3 901 TCTTCCATTTTG A----- AGC G 3 C c c

CACAGGGAGTGC CTGCACTCC CTG GCAA
AGGAGGTG GACGTGAGG GAC CGTT
GTGGAG --- A
GAM1338 360 RGS3 1 3826 NP_570613.1 5 60 GGTGCTCATGCC C -- G A 3 C c c
AGGCTGACGGGT ACTG ACTC CAGCCTGG CA
CCAGTGCG TGAC TGGG GTCGGACC GT
C CA - A
GAM1338 360 RHD 1 8756 NP_057208.2 3 690 CACTCTGTCACC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGCCGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 RHD 1 8756 NP_057309.2 3 779 CACTCTGTCACC -- A 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGCCGC TGACGTGAGGTCGGACC TGT
AC C
GAM1338 360 RHPN2 1 5481 NP_149094.2 3 889 GCTGTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 RNAC 1 18459 NP_005763.2 3 220 TTGCCATTGCCC CA AG 3 C c c

AGGAGGGGCCCA ACTG CTCC CCTGGGCAA
GTCACCAT TGAC GGGG GGACCCGTT
CC A-
GAM1338 360 RNF137 1 8861 NP_060543.4 3 828 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 RNF8 1 14570 NP_003949.1 3 954 ACTCTGTTGCCC C C 3 C b b
AAGCTGGAGTAC ACTG ACTCCAGC TGGGCAAC
AGTAGTGC TGAC TGAGGTCG ACCCGTTG
A A
GAM1338 360 RP2 1 6575 NP_008846.1 3 1765 CTCTTGTTGCCC AC----- C 3 C c c
AAGCTGGAGTGC TGCACTCCAGC TGGGCAAC
AATGGCGC ACGTGAGGTCG ACCCGTTG
CGCGGTA A
GAM1338 360 RPH3AL 1 467 NP_008918.1 3 640 GCTTTGTTGCCC 3 C b b
AGGCTGGGGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGGGGTCGGACCCGTTG

GAM1338 360 RPP30 2 3259 NP_006404.1 3 1202 GCTCTGTCCCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCTC TGACGTGAGGTCGGACCC TG
CC
GAM1338 360 RPP30 2 13376 NP_006404.1 3 357 TCTTTGTTGCTC C 3 C b b
AGGCTGGAGTAC ACTG ACTCCAGCCTGGGCAAC

AGTGGCAT TGAC TGAGGTCGGACTCGTTG
A
GAM1338 360 S100A15 1 18561 NP_789793.1 3 3403 ACTCTGTCGCCC T AA 3 C c c
GGGCTGGAGTGC AC GCACTCCAGCCTGGGC
TGTGAGCT TG CGTGAGGTCGGGCCCG
T CT
GAM1338 360 SARM1 1 16324 NP_055892.1 3 3666 GCTCTGTTGTCC A 3 C b b
AGGCTGGAGGGC ACTGC CTCCAGCCTGGGCAAC
AGTGACAT TGACG GAGGTCGGACCTGTTG
G
GAM1338 360 SAS 1 1301 NP_005972.1 3 510 GCTCTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAT ACGTGAGGTCGGACCCGTTG
TACGGTA
GAM1338 360 SBLF 1 14250 NP_006864.2 3 1608 ACTCTGTTGCCC C 3 C b b
AGCCTGGAGTGC ACTGCACTCCAG CTGGGCAAC
AGTGTGTC TGACGTGAGGTC GACCCGTTG
C
GAM1338 360 SCAMP-4 1 19434 NP_524558.1 3 872 ACTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGT TGACGTGAGGTCGGACCCG
CT
GAM1338 360 SCAND2 1 16790 NP_071333.2 3 1782 ATTCTATCACCC G CAA 3 C c c
AGGCTGGAGTGG ACT CACTCCAGCCTGGG
AGTGGTAT TGA GTGAGGTCGGACCC
G ACT
GAM1338 360 SCARF1 2 9540 NP_003684.1 3 158 GCCAGTTGGCCC ACT- - --- - 3 C c b
AGGCCCCTGGCA GCACT CCA GCCTGGGC AAC
GTGCTCCC CGTGA GGT CGGACCCG TTG
CCCT C CCC G
GAM1338 360 SCARF1 2 12384 NP_003684.1 3 409 CCTCTGTCCCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
CC
GAM1338 360 SCMH1 1 9755 NP_036368.1 3 877 GGCAGGTTTTCC C C 3 C b b
AGGCTGGAGTCG ACTG ACTCCAGCCTGGG AAC
GTTCCACC TGGC TGAGGTCGGACCT TTG
- T
GAM1338 360 SCML2 1 9058 NP_006080.1 3 1313 ACTCTTGTGCCC AC----- A 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCA
AATAGCTC ACGTGAGGTCGGACCCGT
CTCGATA G
GAM1338 360 SCN3B 2 1471 NP_060870.1 3 1053 ACTCTGTCACCT C CAA 3 C c c

AGGCTAGAGTGC ACTGCACTC AGCCTGGG
AGTGGTGT TGACGTGAG TCGGATCC
A ACT

GAM1338 360 SCN3B 2 9932 NP_060870.1 3 2012 ACTCTGTCTCCC C CA 3 C c c
AGGCTAGAGTGC ACTGCACTC AGCCTGGG AC
AGTGGTGC TGACGTGAG TCGGACCC TG
A TC

GAM1338 360 SDS-RS1 2 2100 NP_612441.1 5 90 GATCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 SDS-RS1 2 6910 NP_612441.1 5 11 TGGTTCCCTGGC A----- A --- C 3 C c
c

AGGCTGGAGGGC CTGC CTCCAGCCTG GG AAC
AGGAGCTG GACG GAGGTCGGAC CC TTG
GTCGAG G GGT C

GAM1338 360 SDS3 1 8869 XP_045014.1 3 493 CACTATTTGCCC A---- A C -- 3 C c c
AGAAGCTTGGGG CTGC CTC AGC CTGGGCAA
CAGAGGTC GACG GGG TCG GACCCGTT
CTGGA - T AA

GAM1338 360 SEDL 4 7261 NP_055378.1 3 999 CTCCTGTTGTGC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTG GCAAC
AGTGGCAC TGACGTGAGGTCGGAC TGTTG
G

GAM1338 360 SEDL 4 13400 NP_055378.1 3 637 CTCCTGTTGTGC C G 3 C b b
AGGCTGTAGTGC ACTGCACT CAGCCTG GCAAC
AGTGGCAC TGACGTGA GTCGGAC TGTTG
T G

GAM1338 360 SEDL 4 13872 NP_055378.1 3 1345 GCTCTGTTGTCC AC----- 3 C c b
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAG ACGTGAGGTCGGACCTGTTG
GACGGTA

GAM1338 360 SEDL 4 16842 NP_055378.1 3 307 CACTCTGTTGCC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTGGCGC TGACGTGAGGTCGGACC GTTG
-

GAM1338 360 SERF1A 2 11123 NP_068802.1 3 243 CACTCTGTCACC C -- A 3 C c b
AGACTGGAGTGC ACTGCACTCCAG CTGG GCA
AGTGGCGC TGACGTGAGGTC GACC TGT
A AC C

GAM1338 360 SERF1A 2 14767 NP_068802.1 3 409 GCACTGTTGCCC C 3 C b b
AGGCTGGACTGC ACTGCA TCCAGCCTGGGCAAC
AGTGGCGT TGACGT AGGTCGGACCCGTTG
C

GAM1338 360 SERF1B 2 11123 NP_075267.1 3 243 CACTCTGTCACC C -- A 3 C c b
AGACTGGAGTGC ACTGCACTCCAG CTGG GCA
AGTGGCGC TGACGTGAGGTC GACC TGT
A AC C

GAM1338 360 SERF1B 2 14767 NP_075267.1 3 409 GCACTGTTGCCC C 3 C b b
AGGCTGGACTGC ACTGCA TCCAGCCTGGGCAAC

AGTGGCGT TGACGT AGGTCGGACCCGTTG
C

GAM1338 360 SERF2 1 13138 NP_005761.2 5 430 GCTCTGTTACCC C C C 3 C c c
ATGCTGGAGTAC ACTG ACTCCAGC TGGG AAC
GGTGGCGA TGGC TGAGGTCG ACCC TTG
A T A

GAM1338 360 SERPINB 2 437 NP_004146.1 3 2358 ACTCTGTCACCC CAA 3 C c b
9 AGGCTGGAGTGT ACTGCACTCCAGCCTGGG
AGTGGCAT TGATGTGAGGTCGGACCC
ACT

GAM1338 360 SERPINB 2 4057 NP_004146.1 3 510 TCTCTGTCGCCC AA 3 C b b
9 AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCTC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 SFXN2 1 1960 NP_849189.1 3 593 GCTCTGTCGCCC C AA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGCGC TGACGT AGGTCGGACCCG
A CT

GAM1338 360 SFXN2 1 1960 XP_058359.2 3 594 GCTCTGTCGCCC C AA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGCGC TGACGT AGGTCGGACCCG
A CT

GAM1338 360 SFXN4 1 6466 NP_849198.1 3 169 GAGATCGTTCCC G ---- T C 3 C c c
AGGCTGGCGTCT ACT C AC CCAGCCTGGG AAC
CTGGGGTT TGG G TG GGTCGGACCC TTG
G TCTC C -

GAM1338 360 SFXN4 1 6466 XP_058406.1 3 169 GAGATCGTTCCC G ---- T C 3 C c c
AGGCTGGCGTCT ACT C AC CCAGCCTGGG AAC
CTGGGGTT TGG G TG GGTCGGACCC TTG
G TCTC C -

GAM1338 360 SH3BP2 1 18716 NP_003014.2 5 156 GCTCAGTTGCCC A C 3 C b b
AGACTGGAGAGC ACTGC CTCCAG CTGGGCAAC
AGTGGCCA TGACG GAGGTC GACCCGTTG
A A

GAM1338 360 SHOX 1 3808 NP_000442.1 3 1308 GCTTTGTCGCCC A AA 3 C c c
AGGCTGGAGCGC ACTGC CTCCAGCCTGGGC
AGTCCCGC TGACG GAGGTCGGACCCG
C CT

GAM1338 360 SIGLEC8 1 3441 NP_055257.1 3 515 GCTCTGTCACCT CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGGGC TGACGTGAGGTCGGATCC
ACT

GAM1338 360 SLA2 1 15357 NP_115590.1 3 688 GCCCTGTTGCCC AC----- C 3 C c c
ATGCTGGAGTGC TGCACTCCAGC TGGGCAAC
AATGGCAC ACGTGAGGTCG ACCCGTTG
CACGGTA T

GAM1338 360 SLA2 1 15357 NP_778252.1 3 791 GCCCTGTTGCCC AC----- C 3 C c c
ATGCTGGAGTGC TGCACTCCAGC TGGGCAAC
AATGGCAC ACGTGAGGTCG ACCCGTTG

CACGGTA T
GAM1338 360 SLC11A2 1 16731 NP_000608.1 3 286 AAGTAGTTGCCC CA CCA -- 3 C c c
AAGGGCCAGCTC ACTG CT GCCT GGGCAAC
AGTTTATC TGAC GA CGGG CCCGTTG
TC C-- AA
GAM1338 360 SLC12A8 1 18425 NP_078904.1 3 208 GCCTTGTCACCC C CAA 3 C c c
AGGCTGGAGTCC ACTG ACTCCAGCCTGGG
AGTGGCAC TGAC TGAGGTCGGACCC
C ACT
GAM1338 360 SLC13A1 1 15679 NP_071889.2 3 1479 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGG TGACGTGAGGTCGGACCCG
CT
GAM1338 360 SLC15A1 1 20019 NP_005064.1 3 218 CTCTTGTTGTCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCAC ACGTGAGGTCGGACCTGTTG
CACGGTA
GAM1338 360 SLC16A4 1 20157 NP_004687.1 3 182 GCTCTTTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 SLC16A6 1 517 NP_004685.1 5 45 GCTCTGTCATTC CA --- A 3 C c c
AGGCAAGAGTGC ACTGCACTC GCCTG GGCA
AGTAGTGT TGACGTGAG CGGAC CTGT
AA TTA C
GAM1338 360 SLC24A1 1 7931 NP_004718.1 3 686 CTCTTGTTGCCC AC----- T 3 C c c
AGGCTGGTGTGC TGCAC CCAGCCTGGGCAAC
AATGGCGT ACGTG GGTCGGACCCGTTG
TGCGGTA T
GAM1338 360 SLC25A1 1 1937 NP_036272.2 3 794 GGGGAATGGCCC CT A AA 3 C c c
0 AGGCGGGCTGCG ACTGCA CC GCCTGGGC
GTTCCTCC TGGCGT GG CGGACCCG
CG - GT
GAM1338 360 SLC30A5 1 1341 NP_076960.1 3 152 GCTCCATCGCCC C AA 3 C c c
AGGCTGCAGTGC ACTGCACT CAGCCTGGGC
AGTGACAC TGACGTGA GTCGGACCCG
C CT
GAM1338 360 SLC30A6 1 11622 NP_060434.2 3 506 ACTCTGTCGCCC C AA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGGC
AGTGGCAT TGACGT AGGTCGGACCCG
A CT
GAM1338 360 SLC35E2 1 12300 XP_049733.6 3 1606 TGTCTGTCACCC C CAA 3 C c c

AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAT TGAC TGAGGTCGGACCC
A ACT

GAM1338 360 SLC39A1 1 19430 NP_055252.2 5 87 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
GGTGGTGC TGGCGTGAGGTCGGACCCGTTG

GAM1338 360 SLC6A14 1 16741 NP_009162.1 3 1675 GTTCTGTTGCCT TG 3 C b b

GGGCTGGAGTGC ACTGCACTCCAGCC GGCAAC
AGTGGCAT TGACGTGAGGTCGG CCGTTG
GT

GAM1338 360 SMAC 2 1245 NP_620308.1 5 481 CCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGA TGACGTGAGGTCGGACCCG
CT

GAM1338 360 SMAC 2 15275 NP_620308.1 5 655 GCTCTGTTGCCC C 3 C b b
AGGCTGAAGTGC ACTGCACT CAGCCTGGGCAAC
AGTGGGGC TGACGTGA GTCGGACCCGTTG
A

GAM1338 360 SNAP23 1 14270 NP_003816.2 3 673 GCTCTCTTGTCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATAGCGC ACGTGAGGTCGGACCTGTT
CGCGATA

GAM1338 360 SNAP23 1 14270 NP_570710.1 3 673 GCTCTCTTGTCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATAGCGC ACGTGAGGTCGGACCTGTT
CGCGATA

GAM1338 360 SNPH 1 1354 NP_055538.1 3 2430 GGCCCTGGCCCA - C- AA 3 C c c

GCTCTGGAGTGC AC TGCACTCCAG CTGGGC
ATGTGTGT TG ACGTGAGGTC GACCCG
T TC GT

GAM1338 360 SNX15 1 2728 NP_037438.2 3 269 GCTGTGTCGCCC C AA 3 C c c
AGACTGGAGTGC ACTGCACTCCAG CTGGGC
AGTGGTGG TGACGTGAGGTC GACCCG
A CT

GAM1338 360 SNX15 1 2728 NP_680086.1 3 269 GCTGTGTCGCCC C AA 3 C c c
AGACTGGAGTGC ACTGCACTCCAG CTGGGC
AGTGGTGG TGACGTGAGGTC GACCCG
A CT

GAM1338 360 SNX22 1 11205 NP_079074.1 3 518 CTCTTGTTGCCC C 3 C b b
AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAAC
AGTGGCAC TGACGT AGGTCGGACCCGTTG
A

GAM1338 360 SNX27 1 8857 NP_112180.4 3 3108 GCTCTGTCGCCC AA 3 C c c
AGGTTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCAC TGACGTGAGGTTGGACCCG
CT

GAM1338 360 SPOP 1 7212 NP_003554.1 5 129 GCTCTGTCACCC CAA 3 C c c

GGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGGCCC
ACT

GAM1338 360 SQV7L 1 15016 XP_047287.1 5 1344 GCTCTGTTGCCC C A 3 C b b
AGGCAGGAGTAC ACTG ACTCC GCCTGGGCAAC
AGTGGCAT TGAC TGAGG CGGACCCGTTG
A A

GAM1338 360 SRISNF2 1 9707 NP_055921.1 3 67 AGCAGGTTGCCC AC C--- 3 C c c

L ACCAAGCTGGAA ACTGC TCCAGC TGGGCAAC
GGCAGTGA TGACG AGGTCG ACCCGTTG
GA AACC

GAM1338 360 SRL 2 7583 XP_064152.3 5 1366 TCATTGTTGCCC AC -- AG----- 3 C c c
AGGAAGAGACGG TGCA CTCC CCTGGGCAAC
AGGATGCA ACGT GAGG GGACCCGTTG
-- AG CAGAGAA

GAM1338 360 SRL 2 9910 XP_064152.3 3 584 GCTCTGTCGGCC --- A 3 C c c
AGGTTGGAGTGC ACTGCACTCCAGCCTGG GCA
AGTGGTGC TGACGTGAGGTTGGACC TGT
GGC C

GAM1338 360 SRRM2 1 18975 NP_057417.2 5 0 GCGGCCCAGGCG - A AA 3 C c c

GGGTGCGAGTGG ACT GCACTCC GCCTGGGC
CGCAGTCG TGA CGTGGGG CGGACCCG
G - GC

GAM1338 360 SS18 1 10975 NP_005628.1 3 1673 CTCTTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT

GAM1338 360 STAM2 1 5920 NP_005834.3 3 360 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGCAT TGACGTGAGGTCGGACCC
ACT

GAM1338 360 STARD4 1 14279 NP_631903.1 3 245 ACTCTGTTGCCC A C 3 C b b
ATGCTGGAGGGC ACTGC CTCCAGC TGGGCAAC
AGTGGTAT TGACG GAGGTCG ACCCGTTG
G T

GAM1338 360 STAU 1 9365 NP_004593.1 5 274 CTCTTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGT TGACGTGAGGTCGGACCCG
CT

GAM1338 360 STE 1 13898 NP_005411.1 3 195 ACTCTGTTGCCT CA 3 C b b
AGGCTGGAGGAC ACTG CTCCAGCCTGGGCAAC
AGTGGCAC TGAC GAGGTCGGATCCGTTG
AG

GAM1338 360 STEAP2 1 1413 NP_694544.1 3 1986 GCTCTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 STOM 1 4144 NP_004090.3 3 495 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATAGCAT ACGTGAGGTCGGACCCGTTG
TACGATA
GAM1338 360 STXBP6 1 11916 NP_054897.4 5 275 TGTGTGGAGTTT C GCC C 3 C c
c
TCCATGAAGTGC ACTGCACT CA TGGG AAC
AGTCCCAA TGACGTGA GT ACCT TTG
A --- T
GAM1338 360 SYT11 1 1690 NP_689493.2 3 280 CTCTTGTTGCCC AC----- 3 C c c
GGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGTGA ACGTGAGGTCGGGCCCGTTG
AGTGGTA
GAM1338 360 SYT13 1 19065 NP_065877.1 3 1525 TCTTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TADA3L 1 10415 NP_597814.1 3 288 GCACTGTCACCC CAA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 TAL1 2 7347 NP_003180.1 3 2548 GCTATATTGCCC G CT- 3 C c c
AGGCTGGTCTTG ACT CA CCAGCCTGGGCAA
AAGTCCTG TGA GT GGTCGGACCCGTT
A TCT
GAM1338 360 TAL1 2 19155 NP_003180.1 3 2374 GTTCTGTCACTC C CAA 3 C c c
AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGTGC TGAC TGAGGTCGGACTC
A ACT
GAM1338 360 TAPBP 3 3109 NP_003181.3 3 836 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 TAPBP 3 6086 NP_003181.3 3 229 ACTCTTCCGCCC C AA 3 C c b
AGGCTGCAGTGC ACTGCACT CAGCCTGGGC
AGTGGCAT TGACGTGA GTCGGACCCG
C CC
GAM1338 360 TAPBP 3 8861 NP_003181.3 3 1141 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCAC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TAT 1 20161 NP_000344.1 3 778 GCTCTGTCGCCC C AA 3 C c c
ATGCTGGAGTGC ACTGCACTCCAGC TGGGC
AGTGGCGC TGACGTGAGGTCG ACCCG
T CT
GAM1338 360 TAZ 1 14872 NP_851831.1 3 96 CCTGCTCTGCCC --- T G-- A 3 C c c
AGGAGGTGGCGT ACTGC AC CCA CCTGGGCA
CCAGCAGT TGACG TG GGT GGACCCGT
ACC C GGA C

GAM1338 360 TBC1D5 1 12382 NP_055559.1 5 589 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGTGC TGACGTGAGGTCGGACCCG
CT
GAM1338 360 TCAP 1 19403 NP_003664.1 3 121 TGTAGTTTGCCC A---- - A - 3 C c c
AGAGTTGGGGGC CT GC CTCCAGC CTGGGCAA
TAGGGGAG GA CG GGGGTTG GACCCGTT
GAGGG T - A
GAM1338 360 TCF2 1 401 NP_006472.1 3 2021 CCTCTGTCACCC C CAA 3 C c c
GAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGTGC TGACGTGAGGTCG GCCC
A ACT
GAM1338 360 TCIRG1 1 7780 NP_006010.2 5 12 CTAGTCCCGGGC ---- - AA 3 C c c
TGGCGGGAGTGC ACTGCACTCC AGCCTGGG C
AGTTCTGA TGACGTGAGG TCGGGCCC G
GCGG T AT
GAM1338 360 TCL6 2 6911 NP_065578.2 5 1173 TCCCTCTGTGCC CA - A 3 C c c
AGGCCAGAGTGC ACTGCACTC GCCTGG GCA
AGTGGTGC TGACGTGAG CGGACC TGT
AC G C
GAM1338 360 TCL6 2 6911 NP_065579.2 5 1173 TCCCTCTGTGCC CA - A 3 C c c
AGGCCAGAGTGC ACTGCACTC GCCTGG GCA
AGTGGTGC TGACGTGAG CGGACC TGT
AC G C
GAM1338 360 TCL6 2 12973 NP_036600.2 5 644 GCTCTGTCACTC C CAA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCGC TGACGT AGGTCGGACTC
A ACT
GAM1338 360 TCL6 2 12973 NP_055233.1 5 644 GCTCTGTCACTC C CAA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCGC TGACGT AGGTCGGACTC
A ACT
GAM1338 360 TCL6 2 12973 NP_065575.1 5 644 GCTCTGTCACTC C CAA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCGC TGACGT AGGTCGGACTC
A ACT
GAM1338 360 TCL6 2 12973 NP_065577.2 5 644 GCTCTGTCACTC C CAA 3 C c c
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCGC TGACGT AGGTCGGACTC
A ACT
GAM1338 360 TERA 1 971 NP_067061.1 3 139 CTCTTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCGT TGACGTGAGGTCGGACCC TTG
A
GAM1338 360 TERF1 1 13870 NP_003209.1 3 418 TCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TERF1 1 13870 NP_059523.1 3 418 TCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC

AGTGGCGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TERF2 1 11659 NP_005643.1 3 140 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGT TGACGTGAGGTCGGACCC
ACT
GAM1338 360 TGIF2 1 7274 NP_068581.1 3 1451 GCTCTGTCACCC CAA 3 C c c
GGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGC TGACGTGAGGTCGGGCCC
ACT
GAM1338 360 TIGD6 1 17302 NP_112215.1 3 908 GTTATATTGCCT C 3 C b b
AGGCTGGAATGC ACTGCA TCCAGCCTGGGCAA
AGTGGTTA TGACGT AGGTCGGATCCGTT
A
GAM1338 360 TIM50L 2 7201 XP_053074.2 3 613 TCACTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
ATTGATGT ACGTGAGGTCGGACCCGTTG
TGTAGTT
GAM1338 360 TIM50L 2 7571 XP_053074.2 3 1406 CTCTTATTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAA
AATGGCAC ACGTGAGGTCGGACCCGTT
CACGGTA
GAM1338 360 TLR5 1 16358 NP_003259.2 5 95 ACTCTGCCGCCC C AA 3 C c c
AGGCTGGACTGC ACTGCA TCCAGCCTGGGC
AGTGACAC TGACGT AGGTCGGACCCG
C CC
GAM1338 360 TMC1 1 19429 NP_619636.2 5 127 ACTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TMEM14A 1 7622 NP_054770.1 5 74 GCTCGGGGCTGC - AA 3 C c c

AGGCTGGAGTGC ACTGCACTCCAGCCTG GGC
AGTGGGAC TGACGTGAGGTCGGAC TCG
G GG
GAM1338 360 TMPRSS3 1 15133 NP_076927.1 3 244 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGA TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TMPRSS3 1 15133 NP_115777.1 3 244 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGA TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TMPRSS3 1 15133 NP_115780.1 3 244 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCGA TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TNFAIP2 1 14228 NP_006282.2 3 1220 GCTGTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGCCT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TNFRSF1 1 9933 NP_003833.3 3 453 ACTCTGTCTCCC AC----- CA 3 C c c
0B AGGCTGGAGTGC TGCACTCCAGCCTGGG AC
AATGGTGC ACGTGAGGTCGGACCC TG
CGTGGTA TC
GAM1338 360 TNFRSF1 1 9933 NP_671716.1 3 453 ACTCTGTCTCCC AC----- CA 3 C c c
0B AGGCTGGAGTGC TGCACTCCAGCCTGGG AC
AATGGTGC ACGTGAGGTCGGACCC TG
CGTGGTA TC
GAM1338 360 TNFRSF1 1 11190 NP_003830.1 3 502 TGGCTCTGGCCC C AA 3 C c c
1A AGGCTAGAGTGC ACTGCACTC AGCCTGGGC
AGTGGTGC TGACGTGAG TCGGACCCG
A GT
GAM1338 360 TNFRSF9 1 438 NP_001552.2 3 226 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 TOR1B 1 2429 NP_055321.1 3 179 ACTCCGTCATCC C CAA 3 C c c
AAGCTGGAGTGC ACTGCACTCCAGC TGGG
AGTGGTGC TGACGTGAGGTCG ACCT
A ACT
GAM1338 360 TP53 1 2118 NP_000537.2 3 832 GCTTTGTTGCCC G 3 C b b
AGGCTGGAGTGG ACT CACTCCAGCCTGGGCAAC
AGTGGCGT TGA GTGAGGTCGGACCCGTTG
G
GAM1338 360 TPMT 1 10218 NP_000358.1 3 425 TTCTTGTTGCCC CC 3 C b b
AACCTGGAGTGC ACTGCACTCCAG TGGGCAAC
AGTGGTGC TGACGTGAGGTC ACCCGTTG
CA
GAM1338 360 TRAF5 1 10175 NP_004610.1 3 1090 TCATTGTCACCC C CAA 3 C c c
AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAT TGAC TGAGGTCGGACCC
A ACT
GAM1338 360 TRAF5 1 10175 NP_665702.1 3 1090 TCATTGTCACCC C CAA 3 C c c
AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAT TGAC TGAGGTCGGACCC
A ACT
GAM1338 360 TRIM16 1 13321 NP_006461.2 3 248 GCACTGTTGCCC A 3 C b b
AGGCTGGAGAGC ACTGC CTCCAGCCTGGGCAAC
AGTGGCGC TGACG GAGGTCGGACCCGTTG
A
GAM1338 360 TRIM5 1 9916 NP_149023.1 3 650 CTCTTGTTCCCC AC----- C 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGG AAC
AATGGCAC ACGTGAGGTCGGACCC TTG

CACGGTA C

GAM1338 360 TRPV1 2 1587 NP_061197.3 3 363 CTCTTCTCACCC C CAA 3 C c b
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCAC TGACGT AGGTCGGACCC
A ACT

GAM1338 360 TRPV1 2 1587 NP_542435.1 3 363 CTCTTCTCACCC C CAA 3 C c b
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCAC TGACGT AGGTCGGACCC
A ACT

GAM1338 360 TRPV1 2 1587 NP_542436.1 3 363 CTCTTCTCACCC C CAA 3 C c b
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCAC TGACGT AGGTCGGACCC
A ACT

GAM1338 360 TRPV1 2 1587 NP_542437.1 3 363 CTCTTCTCACCC C CAA 3 C c b
AGGCTGGAATGC ACTGCA TCCAGCCTGGG
AGTGGCAC TGACGT AGGTCGGACCC
A ACT

GAM1338 360 TRPV1 2 15897 NP_061197.3 3 684 CTCTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TRPV1 2 15897 NP_542435.1 3 685 CTCTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TRPV1 2 15897 NP_542436.1 3 685 CTCTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TRPV1 2 15897 NP_542437.1 3 684 CTCTTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGT TGACGTGAGGTCGGACCCGTTG

GAM1338 360 TSPYL 1 9101 XP_166325.1 3 657 GCTCTGTCGCCC AA 3 C c c
AGGTTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTTGGACCCG
CT

GAM1338 360 TTY7 1 16664 NP_114132.1 5 521 TCCCCCATGCCC G TC G A 3 C c
c
AGGTGTGGTGAA ACT CAC CA CCTGGGCA
GTGAATCC TGA GTG GT GGACCCGT
A GT - A

GAM1338 360 TU12B1-TY 3 7327 NP_057659.1 3 3181 CTCTTTTTGCCC AC----- A 3 C c b
AGGCCGGAGTGC TGCACTCC GCCTGGGCAA
AATGGCAC ACGTGAGG CGGACCCGTT
CACGGTA C

GAM1338 360 TU12B1-TY 3 12270 NP_057659.1 3 1304 CTCTTATTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAA
AGTGGCAC TGACGTGAGGTCGGACCCGTT

GAM1338 360 TU12B1-3 17849 NP_057659.1 3 2854 GCTCTGTTGCCC CC 3 C b b

TY ATTCTGGAGTGC ACTGCACTCCAG TGGGCAAC
AGTGGTGT TGACGTGAGGTC ACCCGTTG
TT

GAM1338 360 TUB 1 10826 NP_003311.2 3 45 TTGGGGTTGCCC A------- AC C 3 C c c
AGCCTGGAGCGG CTGC TCCAG CTGGGCAAC
AGCTTGCC GGCG AGGTC GACCCGTTG
CCGTTCGA -- C

GAM1338 360 TUB 1 10826 NP_813977.1 3 45 TTGGGGTTGCCC A------- AC C 3 C c c
AGCCTGGAGCGG CTGC TCCAG CTGGGCAAC
AGCTTGCC GGCG AGGTC GACCCGTTG
CCGTTCGA -- C

GAM1338 360 TUCAN 2 2265 NP_055774.1 3 2765 GCTCTGTCATCT CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGTGT TGACGTGAGGTCGGATCT
ACT

GAM1338 360 TUCAN 2 10630 NP_055774.1 3 2456 ACTCTGTTACCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGTGC TGACGTGAGGTCGGACCC TTG
A

GAM1338 360 TUFT1 1 19342 NP_064512.1 3 1286 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTAGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 TXL-2 1 7572 NP_835231.1 5 95 AAATTGCCCTGC A----- --- 3 C c c
AGGCTGGAGTGC CTGCACTCCAGCCT GGGCAA
AGCGGCAT GACGTGAGGTCGGA CCCGTT
TACGGC CGT

GAM1338 360 TXNL2 1 1413 NP_006532.1 3 67 GCTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 U1SNRNP 1 18791 NP_008951.1 5 121 AGGGAGTCGCCC A AA 3 C c
c

BP AGGCTGGAGAGC ACTGC CTCCAGCCTGGGC
GGTGGCGC TGGCG GAGGTCGGACCCG
A CT

GAM1338 360 U1SNRNP 1 18791 NP_851030.1 5 121 AGGGAGTCGCCC A AA 3 C c
c

BP AGGCTGGAGAGC ACTGC CTCCAGCCTGGGC
GGTGGCGC TGGCG GAGGTCGGACCCG
A CT

GAM1338 360 U1SNRNP 1 18791 NP_851034.1 5 121 AGGGAGTCGCCC A AA 3 C c
c

BP AGGCTGGAGAGC ACTGC CTCCAGCCTGGGC
GGTGGCGC TGGCG GAGGTCGGACCCG
A CT

GAM1338 360 UBCE7IP 1 2287 NP_055763.1 3 1216 TCTCTGTTGCCC A C C 3 C c c

5 AAGCTTGAGGGC ACTGC CTC AGC TGGGCAAC
AGTGGTGC TGACG GAG TCG ACCCGTTG
G T A

GAM1338 360 UBE2L3 1 11811 NP_003338.1 3 520 GCACTGTTGCCC C A - 3 C c c
AGTGTGGGAGTT ACTG ACTCC GC CTGGGCAAC
GGTTTAAA TGGT TGAGG TG GACCCGTTG
- G T

GAM1338 360 UGDH 1 12092 NP_003350.1 3 152 TCACTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 UMPS 1 19428 NP_000364.1 3 390 ACTCTGTTGCCC G 3 C b b
AGGATGGAGTGC ACTGCACTCCA CCTGGGCAAC
AGTGGTGA TGACGTGAGGT GGACCCGTTG
A

GAM1338 360 USP22 1 20055 XP_042698.2 3 2024 AGTTTGTTGCCC G 3 C b b
AGGCTGGAGTGA ACT CACTCCAGCCTGGGCAAC
GTGGCACA TGA GTGAGGTCGGACCCGTTG
-

GAM1338 360 VDU1 1 794 NP_055832.2 3 277 GCTTTGTCACCC T CAA 3 C c c
AGGCTGGAGTGC AC GCACTCCAGCCTGGG
TGTGGTGT TG CGTGAGGTCGGACCC
T ACT

GAM1338 360 VHL 2 969 NP_000542.1 3 988 CTCTTGTCACCC CAA 3 C c b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCGC TGACGTGAGGTCGGACCC
ACT

GAM1338 360 VHL 2 19946 NP_000542.1 3 2567 CCTCTGTTGCCC A----- 3 C b b
AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGAGGTGC GACGTGAGGTCGGACCCGTTG
CGTGGA

GAM1338 360 VIPR2 1 861 NP_003373.2 3 313 GCTCTGTCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCCT TGACGTGAGGTCGGACCCG
CT

GAM1338 360 VTI1A 1 1472 NP_660207.1 3 357 TGCCCTGTCGCC G T AA 3 C c c
TGGCTGGAGTGG ACT CACTCCAGCC GGGC
AGTGGCAC TGA GTGAGGTCGG TCCG
G - CT

GAM1338 360 WBSCR18 1 10631 NP_115693.2 3 831 GCTCTGTTGCCC 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGCAAC
AGTGGTGC TGACGTGAGGTCGGACCCGTTG

GAM1338 360 WHSC1 1 12602 NP_579889.1 3 3922 ACCCTGTTGGCC G 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGG CAAC
AGTAAGTG TGACGTGAGGTCGGACC GTTG
G

GAM1338 360 XRCC2 3 6034 NP_005422.1 3 98 GCTCTGTCTCCC CA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG

TC
GAM1338 360 XRCC2 3 16920 NP_005422.1 3 274 ACTCTGTCTCCC --- CA 3 C b b
AGGCTGCTGGAG ACTGCACTCCA GCCTGGG AC
TGCAGTGG TGACGTGAGGT CGGACCC TG
CGT TC
GAM1338 360 XRCC2 3 19967 NP_005422.1 3 274 CTGTCTCCCAGG --- CA 3 C b b
CTGCTGGAGTGC ACTGCACTCCA GCCTGGG AC
AGTGGCAC TGACGTGAGGT CGGACCC TG
CGT TC
GAM1338 360 YES1 1 18699 NP_005424.1 3 1376 GCTCTGCCGCCC AA 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCCG
CC
GAM1338 360 ZAP 1 19083 NP_064504.2 3 307 ACTCCATCGTCC AA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGGC
AGTGGCGC TGACGTGAGGTCGGACCTG
CT
GAM1338 360 ZFP30 1 432 NP_055713.1 3 1853 GCTCTTTCGCCC T AA 3 C c c
AGGCTGGCGTGC ACTGCAC CCAGCCTGGGC
AGTGGCAC TGACGTG GGTCGGACCCG
C CT
GAM1338 360 ZFP42 1 6576 NP_777560.1 3 642 GCTCTGTCACCC C CAA 3 C c c
AGGCTGGAGTCT ACTG ACTCCAGCCTGGG
AGTGTCGT TGAT TGAGGTCGGACCC
C ACT
GAM1338 360 ZFP64 1 13869 NP_060667.1 3 150 GCTCTGTTTCCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCGC TGACGTGAGGTCGGACCC TTG
T
GAM1338 360 ZFP64 1 13869 NP_071371.2 3 150 GCTCTGTTTCCC C 3 C b b
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG AAC
AGTGGCGC TGACGTGAGGTCGGACCC TTG
T
GAM1338 360 ZMYND17 1 11022 NP_848546.1 3 217 GCTCTGTTGCCC A----- 3 C b
b
AGGCTGGAGTGC CTGCACTCCAGCCTGGGCAAC
AGCGGCAT GACGTGAGGTCGGACCCGTTG
TACGGC
GAM1338 360 ZNF264 1 438 NP_003408.1 3 2977 ACTCTGTCACCC CAA 3 C c c
AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
ACT
GAM1338 360 ZNF273 1 19693 XP_088082.1 3 842 CTCTTGTTGCCC AC----- 3 C c c
AGGCTGGAGTGC TGCACTCCAGCCTGGGCAAC
AATGGCGT ACGTGAGGTCGGACCCGTTG
TGCGGTA
GAM1338 360 ZNF339 1 9097 NP_067043.1 3 654 ACTCTGTCACCC C CAA 3 C c c

AGGCTGGAGTAC ACTG ACTCCAGCCTGGG
AGTGGCAT TGAC TGAGGTCGGACCC

```
                                                A          ACT
GAM1338  360   ZNF345 1  11758 NP_003410.1  3 601   CTCACTGTCACC           --  A      3  C  b  b
                                 AGGCTGGAGTGC ACTGCACTCCAGCCTGG  GCA
                                 AGTGGTGC    TGACGTGAGGTCGGACC  TGT
                                                   AC   C
GAM1338  360   ZNF398 1  9774  NP_065832.1  5 254   GCTCTGTCGCCC     C  A     AA       3  C  c  c

                                 AGGCGGGAATGC ACTGCA TCC GCCTGGGC
                                 AGTGGCGC    TGACGT AGG CGGACCCG
                                                A  G      CT
GAM1338  360   ZNF432 1  7826  NP_055465.1  3 1769  CTCTTGTTGCCC AC-----                3  C  c  c
                                 AGGTTGGAGTGT      TGCACTCCAGCCTGGGCAAC
                                 AATAGCAC          ATGTGAGGTTGGACCCGTTG
                                       CACGATA
GAM1338  360   ZNF440 1  11659 NP_689570.1  3 1223  GCTCTGTCACCC            CAA       3  C  c  c

                                 AGGCTGGAGTGC ACTGCACTCCAGCCTGGG
                                 AGTGGCGT    TGACGTGAGGTCGGACCC
                                                   ACT
GAM1338  360   ZNF70  1  18371 NP_068735.1  3 1595  TGCCCTGTTGCC     C       G        3  C  b  b
                                 AGGCTGGAATGC ACTGCA TCCAGCCTGG CAAC
                                 AGTGGCGT    TGACGT AGGTCGGACC GTTG
                                                A       -
GAM1338  360   ZNF70  1  18371 NP_852101.1  3 1595  TGCCCTGTTGCC     C       G        3  C  b  b
                                 AGGCTGGAATGC ACTGCA TCCAGCCTGG CAAC
                                 AGTGGCGT    TGACGT AGGTCGGACC GTTG
                                                A       -
GAM2033  305   AGS3   1  749   XP_054763.1  5 33    CGGGGCAGGTTA    C ATTC            3  C  c  c
                                 GAGTCCCGATCT TCAAG TC   CTCTAACCT
                                 TGGCCAGG    GGTTC AG   GAGATTGGA
                                                T  CCCT
GAM2033  305   AK5    1  8265  NP_036225.2  5 559   GAGAGGAGGCTC    C-      TAA       3  C  c  c
                                 GAGGAATGAACC TCAAG  TCATTCCTC   CCTC
                                 TTGGTCTG    GGTTC  AGTAAGGAG   GGAG
                                                CA       CTC
GAM2033  305   ALS2CR3 1  735   NP_055864.1  3 396   GAACCCAGGTTA  AAG     C          3  C  c
c
                                 GAAGGATGGGAA TC   CTCATTC TCTAACCT
                                 GAGAAAAG    AG   GGGTAGG AGATTGGA
                                                AA-      A
GAM2033  305   ANGPT1 1  19390 NP_001137.2  5 124   GCAGATAGGGTA  A -  A     A        3  C  c
c
                                 GAGGAAAGGGTC TC AG CTC TTCCTCTA CCT
                                 TAGAATAT    AG TC GGG AAGGAGAT GGA
                                                A  T  A      G
GAM2033  305   ANGPT1 1  19390 NP_647451.1  5 124   GCAGATAGGGTA  A -  A     A        3  C  c
c
                                 GAGGAAAGGGTC TC AG CTC TTCCTCTA CCT
                                 TAGAATAT    AG TC GGG AAGGAGAT GGA
                                                A  T  A      G
```

GAM2033 305 ANKFY1 1 1403 NP_057460.2 3 3116 AACGTCTTGGGA AT AA 3 C c c
AAGGGGAGAGCT TCAAGCTC TCCTCT CCT
TGACCTCC AGTTCGAG AGGGGA GGG
-- AA
GAM2033 305 AQP6 1 1506 NP_001643.1 3 986 AGAGGTGGGATA - A- ---- 3 C c c
GAGGAAGGGAGG TCAAGC TC TTCCTCTA ACCTC
TTTGAGCC AGTTTG AG AAGGAGAT TGGAG
G GG AGGG
GAM2033 305 AQP6 1 1506 NP_445738.1 3 2152 AGAGGTGGGATA - A- ---- 3 C c c
GAGGAAGGGAGG TCAAGC TC TTCCTCTA ACCTC
TTTGAGCC AGTTTG AG AAGGAGAT TGGAG
G GG AGGG
GAM2033 305 B7-H4 1 13436 NP_078902.1 3 713 AATTGAGGCCTT - - TAA- 3 C c c
GAGGAATGAAGC TCAA GCT CATTCCTC CCTC
TTTGAAGG AGTT CGA GTAAGGAG GGAG
T A TTCC
GAM2033 305 BCAS1 1 8961 NP_003648.1 3 290 AGGGAGGGAATA A T A-- 3 C c c
GAGGAATGTGTT TC AGC CATTCCTCTA CCTC
CGGGTTAA GG TTG GTAAGGAGAT GGAG
C T AAG
GAM2033 305 BIVM 1 19466 NP_060163.2 5 462 CCCGACAGGCCA - C AA 3 C c c
GAGGAATCAGTT TC AAGCT ATTCCTCT CCT
TAGACTTG AG TTTGA TAAGGAGA GGA
A C CC
GAM2033 305 C13orf1 1 5972 NP_060655.1 3 2033 TGGCTGAGGTTA T TTCCT 3 C c c
7 GTGTGCTTGGAG TCAAGC CA CTAACCTC
GCTGCAGG GGTTCG GT GATTGGAG
T -----
GAM2033 305 C20orf1 1 2658 XP_086728.2 3 2442 AGGAGGGGGTTA - TC C 3 C c c
10 GAGAGTCTGTTT TCAAG C ATTC TCTAACCTC
TGATTGAT AGTTT G TGAG AGATTGGGG
T TC -
GAM2033 305 C2orf7 1 7328 NP_115695.1 3 131 TGGAGCCAGGTA A- A 3 C c c
GAGGAAAAGGGT TCAAGCTC TTCCTCTA CCT
TTGGGCGT GGTTTGGG AAGGAGAT GGA
AA -
GAM2033 305 C6orf69 1 2839 NP_775833.1 3 1874 TATTTGAGGTTA CT TCC 3 C c c
GGTGTGGCCTTG TCAAG CAT TCTAACCTC
ACCTTACC AGTTC GTG GGATTGGAG
CG T--
GAM2033 305 C6orf76 1 6766 NP_079083.1 3 70 CCCAGGGGGTTA AA- A 3 C c c
GAGGAGGGGTGA TC GCTC TTCCTCTAACCTC
AGATTGGG AG TGGG GAGGAGATTGGGG
AAG -
GAM2033 305 C8orf6 1 2293 NP_663631.1 5 632 TCAGGGCATTAG A - -- 3 C c c
AGAGAATGAGCC TCA GCTCATTC CTCTAA CCT
TGGTGGGT GGT CGAGTAAG GAGATT GGG

C A AC
GAM2033 305 CBL 1 1024 NP_005179.1 3 43 GCTGCAGGTTTA A- --- - 3 C c c
GAGGACCAGTGA TC AGCTCAT TCCTCTAA CCT
GTTGGGAG AG TTGAGTG AGGAGATT GGA
GG ACC T
GAM2033 305 CBX8 1 14537 NP_065700.1 3 54 CAGGGGAGAGAG -- - AA 3 C c c
TGAGCGTGAGCT TCAAGCTCAT TC CTCT CCTC
TGGCATAG GGTTCGAGTG AG GAGA GGGG
CG T GA
GAM2033 305 CCKAR 1 7362 NP_000721.1 5 79 CTTCGGTCATTA AA --- T 3 C c c
GAGGAATGAGCC TC GCTCATTCCTCTA ACC
GGGAGTGA GG CGAGTAAGGAGAT TGG
GC TAC C
GAM2033 305 CD8B1 1 16062 NP_004922.1 3 491 CCAGGTGCAGGT T---- - CT 3 C c c
TGGGAATGAGGC CAAGC TCATTCCT AACCT
TTGCTGAG GTTCG AGTAAGGG TTGGA
GAGTC G --
GAM2033 305 CD8B1 1 16062 NP_742097.1 3 441 CCAGGTGCAGGT T---- - CT 3 C c c
TGGGAATGAGGC CAAGC TCATTCCT AACCT
TTGCTGAG GTTCG AGTAAGGG TTGGA
GAGTC G --
GAM2033 305 CDH3 1 19023 NP_001784.2 3 193 CCTTTCAGGATG ----- A 3 C c c
GAGGAATGTGGG TCAAGCT CATTCCTCTA CCT
CAGTTTGA AGTTTGA GTAAGGAGGT GGA
CGGGT A
GAM2033 305 CDH6 1 19553 NP_004923.1 5 231 TAAGGAAGGAAG A - AA 3 C c c
GAGGAATGAGGC TC AGC TCATTCCTCT CCT
TGGATACG AG TCG AGTAAGGAGG GGA
G G AA
GAM2033 305 CG012 1 7096 XP_096710.1 5 415 AGGAGGTGGAGG A ---- A 3 C c c
TTGAAATGAGCT TCA GCTCATT CCTCTA CCTC
GAGATCAT AGT CGAGTAA GGAGGT GGAG
- AGTT -
GAM2033 305 CGI-19 1 12830 NP_057032.2 5 142 GAAGGAGCGTTC AGC T - 3 C c c
GAGGAATGGATG TCA TCATTCCTC AAC CTC
AGGTCGGG AGT GGTAAGGAG TTG GAG
A-- C C
GAM2033 305 CGI-37 1 13579 NP_057185.1 3 748 CACTTGAGGTTA ATTCCT 3 C c
c
GGAGTTTGAGAC TCAAGCTC CTAACCTC
CAGCCTGG AGTTTGAG GATTGGAG

GAM2033 305 CLDN14 1 13780 NP_652763.1 5 49 TCAGGGCGCAGG - - AA--- 3 C c c
AGGGAATGAGCT TCA AGCTCATTCC TCT CCT
GTGGATTT GGT TCGAGTAAGG AGG GGA
G G ACGCG

GAM2033 305 CNTN5 1 14059 NP_055176.1 3 101 AGAACCAGGATC TC TAA-- 3 C c c

CTGAGATGAGCT TCAAGCTCAT CTC CCT
TGAGCTTT AGTTCGAGTA GAG GGA
-- TCCTA

GAM2033 305 CNTN5 1 14059 NP_780775.1 3 101 AGAACCAGGATC TC TAA-- 3 C c c

CTGAGATGAGCT TCAAGCTCAT CTC CCT
TGAGCTTT AGTTCGAGTA GAG GGA
-- TCCTA

GAM2033 305 DBT 1 4072 NP_001909.1 3 379 CACCTGAGGTTA CATTCC 3 C c c

GAAGTTTGAGAC TCAAGCT TCTAACCTC
CAGCCTGG AGTTTGA AGATTGGAG

GAM2033 305 DCAMKL1 1 17620 NP_004725.1 3 768 GAATTGGGTTTG A - TCT 3 C c c

TGGCAAAGAGCT TCAAGCTC TT CC AACCT
TGACCCAG AGTTCGAG AA GG TTGGG
A C TGT

GAM2033 305 DKFZp43 1 12168 NP_115624.1 3 434 TAATTCAGGAGG ATTCC A 3 C c c

4F1719 TAGAATGGAGCT TCAAGCTC TCTA CCTC
TGAGATCA AGTTCGAG AGAT GGAG
GTA-- -

GAM2033 305 DKFZp43 1 5311 XP_290829.1 3 2605 AGAGGTGGGAGG T---- A 3 C c c

4H247 ATGCCTTGAGCT TCAAGCTCA TCCTCT ACCTC
TGAGAGGT AGTTCGAGT AGGAGG TGGAG
TCCGT G

GAM2033 305 DKFZP56 1 4512 NP_115504.1 5 110 TCCAAGGATTAG AT- C - 3 C c c

6M114 GTGATCGGAGCT TCAAGCTC TC TCTAA CCT
TGAAAAGA AGTTCGAG AG GGATT GGA
GCT T A

GAM2033 305 DPCR1 1 18332 NP_543146.1 3 173 TTGAAACTGGTT AG T T 3 C c c

GGGGAATGAGGT TCA CTCATTCC CTAACC
GATAAGCA AGT GAGTAAGG GGTTGG
G- - T

GAM2033 305 EHD3 1 11360 NP_055415.1 3 50 CGGGCAGTGTTA AAG- A - 3 C c c

GAGGAGGAGATG TC CTC TTCCTCTAAC CT
GGAGCGGT AG GAG GAGGAGATTG GA
GGTA - T

GAM2033 305 ERBB3 1 2087 NP_001973.1 3 501 AGAAAGAGGTTA GC - CT 3 C c c

GGAGTAGATATT TCAA TC ATTCCT AACCTC
GATTACTA AGTT AG TGAGGA TTGGAG
AT A --

GAM2033 305 ERdj5 1 7721 NP_061854.1 5 234 AAAAGGAAGTAT A CC ----- 3 C c c

TAGAAATGAGCT TCA GCTCATT TCTAA CCT
GAAGACCA AGT CGAGTAA AGATT GGA
- -- ATGAA

GAM2033 305 ESRRB 1 8932 NP_004443.2 5 130 CCTGGGGTGGAA C A-- 3 C c c
GAGAAATGAGCT TCAAGCTCATT CTCT ACCTC
TGGCTTGC GGTTCGAGTAA GAGA TGGGG
A AGG

GAM2033 305 FBXL7 1 3073 NP_036436.1 3 1918 ATGGAGAGGTTA AG CCT 3 C c c

GTGTGATGAGGT TCA CTCATT CTAACCTC
GGTGTCTG GGT GAGTAG GATTGGAG
G- TGT

GAM2033 305 FLJ1061 1 12018 NP_060625.1 5 197 GACATGCGGGAG AA - AA 3 C c c
8 AGAGAATGAGCC TC GCTCATTC CTCT CCT
AGAGGGAC AG CGAGTAAG GAGA GGG
AC A --

GAM2033 305 FLJ1091 1 976 NP_060741.1 5 92 TCTGTCCAGGTT A T 3 C b b
6 GAGGAATGGGCT TCA GCTCATTCCTC AACCT
GAACGTGT AGT CGGGTAAGGAG TTGGA
- -

GAM2033 305 FLJ1099 1 12447 NP_061917.2 5 296 ACAAGGTAGTAG C A--- 3 C c c
6 GAGGAATGACTT TCAAG TCATTCCTCT ACCT
GGTGTATC GGTTC AGTAAGGAGG TGGA
- ATGA

GAM2033 305 FLJ1156 1 7659 NP_078933.2 3 599 AAATTAAGGCTT A CTC - 3 C c c
5 AAAGAATGAGCA TCA GCTCATTC TAA CCT
TGGCCACA GGT CGAGTAAG ATT GGA
A AA- C

GAM2033 305 FLJ1349 1 8459 NP_078899.1 5 503 TGTGTGGGCCCA TT - AA- 3 C c c

1 GATGGTTGAGCT TCAAGCTCA CC TCT CCT
TGAGCAGG AGTTCGAGT GG AGA GGG
T- T CCC

GAM2033 305 FLJ1416 1 3447 XP_042704.1 3 386 GGGTGAAGTTGG A - C 3 C c c
7 CAGGGGAGAGCT TCAAGCTC TTCCT CTAAC TC
TGACACTT AGTTCGAG GGGGA GGTTG AG
A C A

GAM2033 305 FLJ1426 1 18009 NP_079303.2 5 277 GGCAGGAATGAC - CTAA-- 3 C c c
0 AGGAGATGAGCT TCAAGCTCAT TCCT CCT
TGAGGGAC AGTTCGAGTA AGGA GGA
G CAGTAA

GAM2033 305 FLJ1444 1 7173 NP_116174.1 3 278 CCCCAGGGTTGC A -- 3 C b b
2 TGAGGAAGAGCT TCAAGCTC TTCCTC TAACCT
TGATGATC AGTTCGAG AAGGAG GTTGGG
- TC

GAM2033 305 FLJ1487 1 13495 NP_116243.1 3 369 CTTGGGGTTATT -- TC 3 C c c
1 GGAGCCTGAGCT TCAAGCTCA TTCC TAACCTC
TGACCTCA AGTTCGAGT GAGG ATTGGGG

```
                                                CC    TT
GAM2033  305   FLJ2013 1   12404  NP_060155.1  3  1225   AGGAGGTGGAGG   A     ----     A        3  C  c
c
          9                          CTGCAATGAGCT TCA GCTCATT    CCTCTA CCTC
                                     GAGATAGT    AGT CGAGTAA    GGAGGT GGAG
                                                 -     CGTC     -
GAM2033  305   FLJ2023 1   17612  NP_061881.2  3  1913   ATCTAGAAGGTA       ATT    TA          3  C  c
c
          2                          TGGGGTAGAGCT TCAAGCTC   CCTC  ACCT
                                     TGACAGGG    AGTTCGAG   GGGG  TGGA
                                                 AT-    TA
GAM2033  305   FLJ2062 1   9074   NP_060377.1  3  430    TTGTGACCAGGG        T  TCTA          3  C  c
c
          5                          TCTGGATGAGCT TCAAGCTCAT CC    ACCT
                                     TGAATTTG    AGTTCGAGTA GG    TGGG
                                                 -  TC--
GAM2033  305   FLJ2330 1   19596  XP_291315.1  3  1423   GAGGAAATGAGA     CT       AA-----       3  C  c
c
          9                          GAGGAATGCTCT TCAAG  CATTCCTCT      CCTC
                                     TGAAAGGT    AGTTC  GTAAGGAGA      GGAG
                                                 TC        GAGTAAA
GAM2033  305   FLJ3195 1   18405  NP_653327.1  3  28     AAGGAGAAGCAG    - -      - AAC-       3  C  c  c
          1                          CAGGAATGATGC TCAA GC TCATTCCT CT    CTC
                                     TTTGATAC    AGTT CG AGTAAGGA GA    GAG
                                                 T  T       C  CGAA
GAM2033  305   GALNACT 1   14291  NP_061060.3  3  649    GAAAATAGGTTA     T   TCC-           3  C  c
c
          -2                         GAATCTATGGCT TCAAGC CAT    TCTAACCT
                                     TGATTAAA    AGTTCG GTA    AGATTGGA
                                                 -   TCTA
GAM2033  305   GATA5   1   18782  NP_536721.1  3  458    CCAAGCAGGGGA   AAG        AA          3  C  c
 c
                                     GAGGAATGAGGG TC   CTCATTCCTCT  CCT
                                     GAGCAGCT    AG   GAGTAAGGAGA  GGA
                                                 GG-          GG
GAM2033  305   GMFB    1   7743   NP_004115.1  3  2036   AGATTGAGGTTA   AA   CAT              3  C  c
c
                                     GAGGATCAGTAG TC  GCT   TCCTCTAACCTC
                                     GACATTTT    AG  TGA   AGGAGATTGGAG
                                                 GA   CT-
GAM2033  305   GNB1    1   18436  NP_002065.1  5  324    CTAAGATCGGAA         C   AA  T        3  C  c  c
                                     GATGAGTGAGCT TCAAGCTCATTC TCT  CC
                                     TGACCAGT    AGTTCGAGTGAG AGA  GG
                                                 T   A-  C
GAM2033  305   GRIN2B  1   13520  NP_000825.1  3  1352   GCAGACAGTTAA        C   -   CT       3  C  c
c
                                     GAGAAATGAGCT TCAAGCTCATT CTCT AAC
                                     TGACATTT    AGTTCGAGTAA GAGA TTG
                                                 A    A   AC
```

GAM2033 305 GTF2E1 1 994 NP_005504.1 3 149 TGCAAAGATTGA ATTCC A T 3 C c c

TGGTAGAGAGCT TCAAGCTC TCTA CC
TGACTTTT AGTTCGAG AGAT GG
----- - T

GAM2033 305 HCFC1 1 18043 NP_005325.1 3 1115 TATAGGGTCGAG AT --- A- 3 C c c

CCTAGGGGAGCT TCAAGCTC TCCT CT ACCT
TGAGGGAG AGTTCGAG GGGA GA TGGG
-- TCC GC

GAM2033 305 HK2 1 11683 NP_000180.2 3 178 ATTGTAGAGCTT TT T C 3 C c c

GGTGGCTGAGCT TCAAGCTCA CC CTAA CTC
TGGCCCTA GGTTCGAGT GG GGTT GAG
C- T C

GAM2033 305 HOXC4 1 19800 NP_055435.2 5 254 GAATGCAGGAGC - - AA 3 C c c

AGGAGTTGAGCT TCAAGCTCA TTCCT CT CCT
TGGGAGCT GGTTCGAGT GAGGA GA GGA
T C --

GAM2033 305 HOXC6 1 19800 NP_710160.1 5 91 GAATGCAGGAGC - - AA 3 C c c

AGGAGTTGAGCT TCAAGCTCA TTCCT CT CCT
TGGGAGCT GGTTCGAGT GAGGA GA GGA
T C --

GAM2033 305 HRK 1 11032 NP_003797.1 3 128 TTTCCAGAGGGG ATTC AA 3 C c c

GAGCCCAGAGCT TCAAGCTC CTCT CCTC
TGAAAGGC AGTTCGAG GAGG GGAG
ACCC G-

GAM2033 305 HSPA9B 1 9911 NP_004125.3 3 575 ATTAAAACAAGG A - CTA 3 C c c

TAGGAATGAGGC TC AGC TCATTCCT ACCT
TAGACCTT AG TCG AGTAAGGA TGGA
A G ---

GAM2033 305 INHBA 1 18996 NP_002183.1 3 373 CCCCTTGAGGTT TCCTCT 3 C c c

CCCTTGTGAGCT TCAAGCTCAT AACCTC
TGAATCAA AGTTCGAGTG TTGGAG
TTCCC-

GAM2033 305 KCNA7 1 8004 NP_114092.2 3 2585 AAAGGGCATTTA A CA- --- 3 C c c

GAGGAAGAAGGC TCA GCT TTCCTCTAA CCT
TGAAATCA AGT CGG AAGGAGATT GGG
- AAG TAC

GAM2033 305 KIAA071 1 10051 NP_055682.1 3 2870 ATTTGAGATGCA AAC- 3 C c c

1 GAGGAATGAGCT TCAAGCTCATTCCTCT CTC
TGAGCCTT AGTTCGAGTAAGGAGA GAG
CGTA

GAM2033 305 KIAA123 1 17086 XP_087386.3 3 989 TGGATGTGGTTA A T 3 C c c

7 GAGGGATGGGCT TCA GCTCATTCCTCTAACC
GAATAGGC AGT CGGGTAGGGAGATTGG

```
                                                -           T
GAM2033  305   KIAA124 1  3069  XP_039676.1  3  2449  ATGCCAAGGGGA   A     CC   AA          3  C  c
c
          0                          GAACAATGAGCT TCA GCTCATT  TCT  CCT
                                     GAAATTGT    AGT CGAGTAA  AGA  GGA
                                                 -     CA   GG
GAM2033  305   KIAA139 1  18176 XP_046685.4  3  1054  CAGCTGCAGTGG      A    CT   T        3  C  c
c
          9                          TTGGGAGGAGCT TCAAGCTC TTCCT  AACC
                                     TGACCAGT    AGTTCGAG GAGGG  TTGG
                                                 -    --   T
GAM2033  305   KIAA151 1  1300  NP_056308.2  3  771   GAGGGCAAGGCA      TTC   AA          3  C  c
c
          8                          AGAGCTTGAGCT TCAAGCTCA   CTCT  CCT
                                     TGAGCCTA    AGTTCGAGT   GAGA  GGA
                                                 TC-    AC
GAM2033  305   KIAA170 1  17708 NP_085139.1  3  1337  TAGTGAAAAGGT  -      TC   TA          3  C  c
c
          6                          GAGTTATGAGCT TC AAGCTCAT  CTC  ACCT
                                     TAGATTAC    AG TTCGAGTA  GAG  TGGA
                                                 A       TT  --
GAM2033  305   KIAA172 1  6209  XP_043492.2  3  1222  AAAGATAAGGTA    C-       CTA         3  C  c  c

          8                          CAGGAATGAACC TCAAG  TCATTCCT   ACCT
                                     TTGGTTTA    GGTTC  AGTAAGGA   TGGA
                                                 CA       CA-
GAM2033  305   LAMC2   1  15830 NP_061486.1  3  438   AAGAGGGGGTTA    G  CA-  -           3  C  c
c
                                     GAGAGAAGGCAG TCAA CT   TTC CTCTAACCTC
                                     GTTGAGAC    AGTT GA   AAG GAGATTGGGG
                                                 G  CGG   A
GAM2033  305   LOC1162 1  878   XP_300752.1  3  1364  CACCTGAGGTTA       ATTCCT           3  C  c
c
          28                         GGAGTTTGAGAC TCAAGCTC     CTAACCTC
                                     CAGCCTGG    AGTTTGAG     GATTGGAG
                                                 ------
GAM2033  305   LOC1300 1  9829  NP_612477.3  3  536   TGTTTTGGGTTA    - C   -           3  C  c  c
          26                         GAGAGAGTAAGA TCAAG CT ATTC CTCTAACCT
                                     TTTGAGAA    AGTTT GA TGAG GAGATTGGG
                                                 A A   A
GAM2033  305   LOC1433 1  8460  XP_084501.1  3  1120  CTGGGCCTCAGA       --    AA--        3  C  c  c

          81                         GGGCCATGAGCT TCAAGCTCAT  TCCTCT   CCT
                                     TGGCCAGG    GGTTCGAGTA  GGGAGA   GGG
                                                 CC     CTCC
GAM2033  305   LOC1460 1  7781  XP_096919.1  3  185   GGAGGGACTGGA    G       AA----       3  C  c
c
          13                         GAGGAATGAGAT TCAA CTCATTCCTCT     CCTC
                                     TGGCCAAA    GGTT GAGTAAGGAGA     GGAG
                                                 A         GGTCAG
```

GAM2033 305 LOC1465 1 15848 XP_085517.1 5 205 CAGGGGTCAGGT TT TA--- 3 C c c
99 GAGGCTTGAGCT TCAAGCTCA CCTC ACCTC
TGAGGAGT AGTTCGAGT GGAG TGGGG
TC TGGAC
GAM2033 305 LOC1503 1 6767 XP_086858.1 5 2205 TTAAGAGAGGCA TTCC AA 3 C c c
11 GAATCTTGAGCT TCAAGCTCA TCT CCTC
TGAGGCAC AGTTCGAGT AGA GGAG
TCTA C-
GAM2033 305 LOC1503 1 9075 XP_086907.1 3 485 TCGTCCAGGTTA T C-- 3 C b b
97 GAGTGCAATGGC TCAAGC CATT CTCTAACCT
TTGATCTC AGTTCG GTAA GAGATTGGA
- CGT
GAM2033 305 LOC1516 1 18792 NP_612144.1 3 577 TCACTGGGGTTA AA TT 3 C c c
36 GAGGTGGGTCCG TC GCTCA CCTCTAACCTC
AAATAATC AG TGGGT GGAGATTGGGG
CC --
GAM2033 305 LOC1527 2 11273 XP_087525.1 5 223 TGTCTGGGGTGA A TCTA 3 C c c
94 ATGGAATGAGCT TC AGCTCATTCC ACCTC
GGAGCTTG AG TCGAGTAAGG TGGGG
G TAAG
GAM2033 305 LOC1527 2 13308 XP_087525.1 5 225 GGGTGAATGGAA A TCTA 3 C c c
94 TGAGCTGGAGCT TC AGCTCATTCC ACCT
TGAACAAA AG TCGAGTAAGG TGGG
G TAAG
GAM2033 305 LOC1534 1 482 XP_098373.1 3 262 TACCATAAGAGG AAG TCT 3 C c c
42 TTGGAATGAGAG TC CTCATTCC AACCTC
GATGACTG AG GAGTAAGG TTGGAG
GA- ---
GAM2033 305 LOC1542 1 16834 XP_098497.1 3 810 GGCTAGGAGTTA AG A - 3 C c c
22 GAGGAAGAGAGT TCA CTC TTCCTCTAAC CT
GACTCAAA AGT GAG AAGGAGATTG GG
GA - A
GAM2033 305 LOC2200 1 3435 XP_166257.1 5 1344 GGGGCAGGGTTA AAG -- 3 C c c
38 GAGGGTTGTGAG TC CTCAT TCCTCTAACCT
GGGAAGAG AG GAGTG GGGAGATTGGG
GG- TT
GAM2033 305 LOC2207 1 4991 XP_167548.3 5 1211 GTCTGGCAGGTG AG A 3 C c c
39 GGGGAATGAGAT TCA CTCATTCCTCTA CCT
GAGAAAGT AGT GAGTAAGGGGGT GGA
A- -
GAM2033 305 LOC2218 1 12817 XP_166513.1 3 1232 TGCTAGGGGTTA TTCC 3 C c c

89 GGCTTTTGAGCT TCAAGCTCA TCTAACCTC
TGAACGCC AGTTCGAGT GGATTGGGG
TTTC
GAM2033 305 LOC2548 1 647 XP_173188.1 3 415 ATGCATAGGTTA T ------ C 3 C c c
26 GAGAAATGGAGA CAAGCT CATT CTCTAACCT
GAGGCTTG GTTCGG GTAA GAGATTGGA
- AGAGAG A
GAM2033 305 LOC2830 1 10331 XP_210872.1 3 1344 GCAGGAGGGTTA AA C - 3 C c
c
50 GAGTGAGTAGTA TC GCT ATTC CTCTAACCT
AGAGATGC AG TGA TGAG GAGATTGGG
AA - T
GAM2033 305 LOC2833 1 6632 XP_208656.1 3 310 GAAGAAATGAAA TCAT AA 3 C c
c
86 GGAAGAGGAGCT TCAAGC TCCTCT CCT
TGAGAGTC AGTTCG AGGAGA GGA
---- A-
GAM2033 305 LOC2834 1 5737 XP_211028.1 5 43 AGGTTGGGAAAT A ------ 3 C c c
03 GAGGAATGAGCC TCA GCTCATTCCTC TAACCT
TGACACCC AGT CGAGTAAGGAG GTTGGA
C TAAAGG
GAM2033 305 LOC2834 1 10804 XP_208679.1 3 39 TTCCAGAGGTTA TCATTCC 3 C c
c
52 GAAAACTTGCTT TCAAGC TCTAACCTC
GAAGTTCC AGTTCG AGATTGGAG
TTCAAA-
GAM2033 305 LOC2835 1 1881 NP_787093.1 3 1833 TGTTTGGGTAGA -- -- A 3 C c c
88 TCGGAATGAGTT TCAA GCTCATTCC TCTA CCT
GTTGAGCT AGTT TGAGTAAGG AGAT GGG
GT CT -
GAM2033 305 LOC2838 1 11219 XP_211218.1 5 323 TGTAAGTGTGTA CCT - - 3 C c c
18 GTTTGATGAGCT TCAAGCTCATT CTA AC CT
TGGACAAA GGTTCGAGTAG GAT TG GA
TTT G T
GAM2033 305 LOC2841 1 3307 XP_209024.1 5 203 GGAAGGTTGAGG - ---- T 3 C c c
17 CTGAAATGAGCT TCA AGCTCATT CCTC AACCT
GTGATCAT AGT TCGAGTAA GGAG TTGGA
G AGTC -
GAM2033 305 LOC2845 1 13346 XP_208210.1 3 354 GTGAGGGGCTGA CTC AA--- 3 C c
c
15 GAGGAATACTTG TCAAG ATTCCTCT CCTC
AAACAACA AGTTC TAAGGAGA GGAG
A-- GTCGG
GAM2033 305 LOC2851 1 18981 XP_211773.1 3 1688 CTGTTGAGTCGA G AAC 3 C c
c
23 GAGGAATGAGAT TCAA CTCATTCCTCT CTC
TGGGGTCA GGTT GAGTAAGGAGA GAG
A GCT
GAM2033 305 LOC2853 1 9690 XP_211880.1 3 766 TATTATTTGTTA C CT 3 C c c

```
          99                          GAGGAGTGACTT TCAAG TCATTCCTCTAAC
                                     GATTTGAA    AGTTC AGTGAGGAGATTG
                                              -          TT
GAM2033  305   LOC2857 1  11051  XP_212002.1  5  66    AAGGGGAGGTTA      CAT  T          3  C  c
c
          35                          GGGAGGTTTGAA TCAAGCT  TCC CTAACCTC
                                     GAGTGAGA    AGTTTGG  AGG GATTGGAG
                                               ---  -
GAM2033  305   LOC2858 1  16704  XP_212027.1  5  386   AGGGTTGGGTTA  A    TT           3  C  c  c

          05                          GAGGTGAGCTGG TC AGCTCA  CCTCTAACCT
                                     GGCCGGAG    GG TCGAGT  GGAGATTGGG
                                              G    --
GAM2033  305   LOC2859 1  19398  XP_212089.1  5  183   GCTGGGGAGGTA  A  TCA     A         3  C  c
 c
          50                          GAGGAAAGTGCT TC AGC  TTCCTCTA CCTC
                                     AGAGTACA    AG TCG  AAGGAGAT GGAG
                                              A  TGA     -
GAM2033  305   LOC2861 1  12741  XP_212216.1  3  578   AACAGGGGCTTA    G  CA      -        3  C  c
c
          84                          GAGGAAAGTTGA TCAA CT  TTCCTCTAA CCTC
                                     AGATTATA    AGTT GA  AAGGAGATT GGGG
                                              -  --       C
GAM2033  305   LOC2861 1  17366  XP_209940.1  3  333   GGGAGGCAGAGG  A    ----   AA       3  C  c
c
          97                          TTGCAATGAGCT TCA GCTCATT   CCTCT  CCTC
                                     GAGATCGC    AGT CGAGTAA   GGAGA  GGAG
                                              -     CGTT    C-
GAM2033  305   LOC2862 1  9029   XP_209949.1  3  500   CCTCTGTGGGGT T----   -      TA       3  C  c  c

          11                          GAGGAATGGGTC     CAAG CTCATTCCTC  ACCTC
                                     TTGTGAAA        GTTC GGGTAAGGAG  TGGGG
                                              AAAGT   T       --
GAM2033  305   LOC2864 1  14291  XP_208421.1  3  645   GAAAATAGGTTA     T  TCC-          3  C  c
c
          38                          GAATCTATGGCT TCAAGC CAT   TCTAACCT
                                     TGATTAAA    AGTTCG GTA   AGATTGGA
                                              -  TCTA
GAM2033  305   LOC3392 1  19779  XP_290271.2  3  808   AGAATGAGGTTA     - T  C          3  C  c  c
          12                          GAAGACTGCAGC TCAAGCT CA TC TCTAACCTC
                                     TTGGAGTC    GGTTCGA GT AG AGATTGGAG
                                               C  C  A
GAM2033  305   LOC3394 1  16199  XP_170914.2  3  1154  ATGCCAGGGTTA  AG  ATT           3  C  c
 c
          14                          GAGGCTAGAGAG TCA  CTC  CCTCTAACCT
                                     TGGAAGTC    GGT  GAG  GGAGATTGGG
                                              GA  ATC
GAM2033  305   LOC3398 1  1411   XP_295084.1  3  556   TACCTGAGGTTA      ATTCCT          3  C  c
c
          46                          GGAGTTTGAGAC TCAAGCTC     CTAACCTC
```

```
                                  CAGCCTGA    AGTTTGAG    GATTGGAG
                                              ------
GAM2033  305   LOC3398 1  3018  XP_295089.1  5  140   CTGGAGTGGGTA  A   A     A        3  C  c  c

         65                       GAGGAAAGGGCT TC AGCTC TTCCTCTA CCT
                                  AGGGTGAC    GG TCGGG AAGGAGAT GGG
                                        A   A      -
GAM2033  305   LOC3398 1  3796  XP_295095.1  5  139   TTGCCCAGGTTA     T   C--          3  C  c  c
         94                       GAGTGCAGTGGC TCAAGC CATT   CTCTAACCT
                                  TTGATCAT    AGTTCG GTGA   GAGATTGGA
                                            -   CGT
GAM2033  305   LOC3399 1  1577  XP_295115.1  5  1248  AGAGGAGGGCCA        CC   AA--       3  C  c
c
         75                       AGAAAATGAGCT TCAAGCTCATT  TCT    CCTC
                                  TGGTTTCC    GGTTCGAGTAA  AGA    GGAG
                                              A-   ACCG
GAM2033  305   LOC3482 1  562   XP_302702.1  5  820   GAAATGGTGAGG        ----    TA  T     3  C  c  c
         59                       GCACAGTGAGCT TCAAGCTCAT    TCCTC  ACC
                                  TGAAGGCT    AGTTCGAGTG    GGGAG  TGG
                                              ACAC    --   T
GAM2033  305   LOC3484 1  878   XP_057659.1  3  1389  CACCTGAGGTTA       ATTCCT           3  C  c
c
         42                       GGAGTTTGAGAC TCAAGCTC     CTAACCTC
                                  CAGCCTGG    AGTTTGAG     GATTGGAG
                                              ------
GAM2033  305   LOC3490 1  16834 XP_302946.1  3  810   GGCTAGGAGTTA    AG   A       -        3  C  c
c
         59                       GAGGAAGAGAGT TCA  CTC TTCCTCTAAC CT
                                  GACTCAAA    AGT  GAG AAGGAGATTG GG
                                        GA   -        A
GAM2033  305   LOC8346 1  17323 NP_112592.1  5  275   GGGCTGAGGTTA    A   ATT-  -          3  C  c
c
         8                        GAAGGTGCAGAG TCA GCTC    CCT CTAACCTC
                                  CGTGGAAG    GGT CGAG    GGA GATTGGAG
                                        G    ACGT   A
GAM2033  305   LOC8454 1  19084 NP_115898.2  3  2293   AAGTTAGAGTGA        -----  -     CT    3  C  c
c
         9                        GGGAAATGAGCT TCAAGCTCAT     TC CTCTAAC
                                  TGGCTTCT    GGTTCGAGTA     AG GAGATTG
                                              AAGGG  T      AA
GAM2033  305   LOC9011 1  19624 XP_029046.1  5  660   TAATAGTGCAGG    --        CTAA        3  C  c
c
         0                        AAGGGATGAGCT TCA  AGCTCATTCCT    CCT
                                  TTTGATTT    AGT  TCGAGTAGGGA    GGA
                                        TT         A---
GAM2033  305   LOC9156 1  12984 XP_039231.1  3  896   TGAGGCATGAGG       T----    TAA       3  C  c
c
         5                        ATTGCTTGAGCT TCAAGCTCA    TCCTC   CCTC
                                  TGGAAGGT    GGTTCGAGT    AGGAG   GGAG
                                              TCGTT    TAC
```

GAM2033 305 LOC9223 1 11714 XP_043739.2 3 322 CATCACAGGCTA TC A 3 C c c

5 GAGAGGTGAGCT TCAAGCTCAT CTCTA CCT
TGGAAAAG GGTTCGAGTG GAGAT GGA
GA C

GAM2033 305 LOH11CR 1 9708 NP_055437.1 3 469 TAGGAGGAGTTA G CA - 3 C c
c

2A GAGGGAAGTTGA TCAA CT TTCCTCTAAC CT
AAGCCAAC AGTT GA AGGGAGATTG GG
- -- A

GAM2033 305 LRP15 1 18470 NP_443185.1 5 545 GTTGGAGTAGAT -- TAAC- 3 C c c

GAGGAATGGGCT TCA AGCTCATTCCTC CTC
CGTGATTA AGT TCGGGTAAGGAG GAG
GC TAGAT

GAM2033 305 MGC1076 1 4067 NP_077321.1 3 801 AAAGGAAAGGAG - --- AA- 3 C c
c

5 ACAGAATGAGCT TCAA GCTCATTC CTCT CCT
TTGGTTAT GGTT CGAGTAAG GAGG GGA
T ACA AAA

GAM2033 305 MGC1301 1 878 NP_542387.1 3 605 CACCTGAGGTTA ATTCCT 3 C c
c

7 GGAGTTTGAGAC TCAAGCTC CTAACCTC
CAGCCTGG AGTTTGAG GATTGGAG

GAM2033 305 MGC3966 1 12535 NP_689607.1 5 124 GAGGAGGAGTTA AAG A - 3 C c
c

2 GAGGAGGAGGAG TC CTC TTCCTCTAAC CT
GAGGAGGA AG GAG GAGGAGATTG GG
GAG - A

GAM2033 305 MGC4633 1 20034 XP_290712.1 5 102 TGACTGAGGTTA AA - A T 3 C c
c

6 GGGAGGACGCCC TC GC TC TTCC CTAACCTC
GAGACCCC AG CG AG GAGG GATTGGAG
CC C - -

GAM2033 305 MGC4668 1 3484 NP_776169.1 3 557 ATATTCAGGTTT T---- - CT 3 C c c

0 CAGGAATGAGCC CAAG CTCATTCCT AACCT
TTGTAATA GTTC GAGTAAGGA TTGGA
ATAAT C CT

GAM2033 305 MOV10 1 13490 NP_066014.1 3 3 AGCCAGAGTGGA - AC 3 C c c
GGAATGAGCTCT TCA AGCTCATTCCTCTA CT
GAGACACA AGT TCGAGTAAGGAGGT GA
C GA

GAM2033 305 MRPS15 1 14750 NP_112570.2 5 76 CCGCGGGGGTTA A TCATT-- 3 C c
c

GAGGTCACCATG TCA GC CCTCTAACCTC
CTGAGGGT AGT CG GGAGATTGGGG
- TACCACT

GAM2033 305 NDST2 1 17608 NP_003626.1 3 261 TTGGGAGGTGGG AAG A- 3 C c
c

GAGGAATGAGAG TC CTCATTCCTCT ACCTC
GGTCCAGG GG GAGTAAGGAGG TGGAG
GA- GG

GAM2033 305 NEK3 1 3534 NP_002489.1 3 229 GGAGAAGGTATA A T - 3 C c c
GTGGAATGAGTG TCA GCTCATTCC CTA ACCT
TGAGCATC AGT TGAGTAAGG GAT TGGA
G T A

GAM2033 305 NEK3 1 3534 NP_689933.1 3 229 GGAGAAGGTATA A T - 3 C c c
GTGGAATGAGTG TCA GCTCATTCC CTA ACCT
TGAGCATC AGT TGAGTAAGG GAT TGGA
G T A

GAM2033 305 NHLH1 1 2657 NP_005589.1 3 479 AGGCTGGGGTTA TC- ---- 3 C c c
GAGTGGGGAGTG AAGCTCATTCC TCTAACCTC
GGCTTCTT TTCGGGTGAGG AGATTGGGG
TTC GGTG

GAM2033 305 NYD-SP1 1 12731 NP_112173.1 3 1042 TCTCCTAGGTTA A T -- 3 C c c

5 GAGAGGGGTGGC TCA GC CATTCCTCT AACCT
CTGGGGTG GGT CG GTGGGGAGA TTGGA
C - GA

GAM2033 305 OPRL1 1 6428 NP_000904.1 5 51 GGCCCTGGGTTA A TTC 3 C c c
GAGTCTGGGCGT TCA GCTCA CTCTAACCT
GGACGCGC GGT CGGGT GAGATTGGG
G CT-

GAM2033 305 OS4 1 16829 NP_005721.2 3 1169 TCCTGGGGTGAG ---- A- 3 C c c
GGGGAATGAGTG TCAAG CTCATTCCTCT ACCTC
TTCTTGAC AGTTC GAGTAAGGGGG TGGGG
TTGT AG

GAM2033 305 P2RY6 1 999 NP_004145.1 3 1049 AGGCCAAGGAAG TC AA 3 C c c

GAGGAATGCTTG TCAAGC ATTCCTCT CCT
AGCCCAAG AGTTCG TAAGGAGG GGA
-- AA

GAM2033 305 PCDH10 1 12871 NP_065866.1 5 51 AGAGACAGGTTA CA-- 3 C c c
GAGGGAAAGAGG TCAAGCT TTCCTCTAACCT
CTTGGGAA GGTTCGG AGGGAGATTGGA
AGAA

GAM2033 305 PCDH10 1 12871 NP_116586.1 5 51 AGAGACAGGTTA CA-- 3 C c c
GAGGGAAAGAGG TCAAGCT TTCCTCTAACCT
CTTGGGAA GGTTCGG AGGGAGATTGGA
AGAA

GAM2033 305 PJA2 1 8114 NP_055634.1 3 726 GCTCAGGGCTTG A CCT - 3 C c c
GTACAATGAGCT TCA GCTCATT CTAA CCT
GAATTAGA AGT CGAGTAA GGTT GGG
- CAT C

GAM2033 305 PMP2 1 3068 NP_002668.1 3 1563 GGCAAGGTAGGA CC-- A 3 C c c

ACAAGATGAGCT TCAAGCTCATT TCT ACCT
TGAAATAT AGTTCGAGTAG AGG TGGA
AACA A

GAM2033 305 POU2AF1 1 17878 NP_006226.1 3 951 AGGAGGAAGGCT C TAA--- 3 C c c

GAGGAATGACTT TCAAG TCATTCCTC CCTC
GGCTCCAG GGTTC AGTAAGGAG GGAG
- TCGGAA

GAM2033 305 PPP1R10 1 17303 NP_002705.2 3 1072 GGTCTTGGGTTA CT C--- 3 C c c

GAGCCAAAATGG TCAAG CATT CTCTAACCT
ATTTGAGG AGTTT GTAA GAGATTGGG
AG AACC

GAM2033 305 PPP1R12 1 18058 NP_002472.1 3 7301 GAAGAGAGGTTA A- CC 3 C c c

B GGTAAAGAGAGT TCAAGCTC TT TCTAACCTC
TTGGAGGA GGTTTGAG AA GGATTGGAG
AG AT

GAM2033 305 PPP1R12 1 18058 NP_115288.1 3 7434 GAAGAGAGGTTA A- CC 3 C c c

B GGTAAAGAGAGT TCAAGCTC TT TCTAACCTC
TTGGAGGA GGTTTGAG AA GGATTGGAG
AG AT

GAM2033 305 RAB13 1 5259 NP_002861.1 3 206 AGGGAGAAGGGA GC AA 3 C c c

GAGGAATGAATT TCAA TCATTCCTCT CCT
GAGGAAGT AGTT AGTAAGGAGA GGA
A- G-

GAM2033 305 RAB7L1 1 9099 NP_003920.1 3 1739 ACCTGGGAGTTA A ---- - 3 C c c

GAGGTTGCAGTG TCA GCTCATT CCTCTAAC CTC
AGCTGAGA AGT CGAGTGA GGAGATTG GGG
- CGTT A

GAM2033 305 RBT1 1 11335 NP_037500.2 5 194 TTTTAAGGCTTA A -- - 3 C c c

GAGGAACTTGAG TC AGCTCA TTCCTCTAA CCT
TTAGGATC GG TTGAGT AAGGAGATT GGA
A TC C

GAM2033 305 RHOBTB2 1 4604 NP_055993.1 3 1475 AGGGCGGGGCTG G ---- A 3 C c c

GAGGAATGTGGG TCAA CT CATTCCTCTA CCTC
GGATTGAA AGTT GG GTAAGGAGGT GGGG
A GGGT C

GAM2033 305 ROR1 1 5888 NP_005003.1 5 223 GGGAGCAGGTTA TC-- A--- 3 C c c

GAGGGACAAAGA AAGCTC TTCCTCTAACCT
GCTTTGCA TTCGAG AGGGAGATTGGA
ACGT AAAC

GAM2033 305 RTN2 1 8997 NP_005610.1 3 386 TGGGGCCCAGGG --- AA- 3 C c c

GAGGCCTGAGCT TCAAGCTCA TTCCTCT CCTC
TGGATTTA GGTTCGAGT GAGGGGA GGGG
CCG CCC

GAM2033 305 SF3B1 1 13074 NP_036565.1 3 126 GAACTGGTCATA A A -- T 3 C c c

GAGGAAGAGCTA TC AGCTC TTCCTCTA ACC
GAAATCCA AG TCGAG AAGGAGAT TGG
A - AC T

GAM2033 305 SFTPA2 1 11609 NP_008857.1 3 1208 CACTGAAGCTTA - --- C 3 C c c
GAGGAGTGAAAT TCAAG C TCATTCCTCTAA CT
GTTTTGAG AGTTT G AGTGAGGAGATT GA
T TAA C
GAM2033 305 SGSH 1 2077 NP_000190.1 3 657 AGCAGGCTCCCT TC TAA--- 3 C c
c
GAGTGATGAGCT TCAAGCTCAT CTC CCT
TGAACCTG AGTTCGAGTA GAG GGA
GT TCCCTC
GAM2033 305 SLC26A7 2 1641 NP_439897.1 3 998 TTTCTTTTGTTA AT CT 3 C c c
GAGGAGAGCTTG TCAAGCTC TCCTCTAAC
ATGTGATT AGTTCGAG AGGAGATTG
-- TT
GAM2033 305 SLC26A7 2 16968 NP_439897.1 3 998 TTTTTCTTTTGT AT CT 3 C c c
TAGAGGAGAGCT TCAAGCTC TCCTCTAAC
TGATGTGA AGTTCGAG AGGAGATTG
-- TT
GAM2033 305 SLC2A6 1 10370 NP_060055.1 3 727 GGGAGGTGGAGG A ---- A 3 C c
c
CTGCAATGAGCT TCA GCTCATT CCTCTA CCTC
GAGATCAT AGT CGAGTAA GGAGGT GGAG
- CGTC -
GAM2033 305 SMYD2 1 8651 NP_064582.1 3 177 ACTTTGAGGTTA CTC CT- 3 C c
c
GTCTGAATCTTG TCAAG ATTC CTAACCTC
AACTTTAA AGTTC TAAG GATTGGAG
--- TCT
GAM2033 305 SURF5 1 16437 NP_852468.1 3 1791 GCCTGCAGGTTA A A- C- 3 C c
c
GAAAGAGGCGAG TCA GCTC TTC TCTAACCT
CGTGGATT GGT CGAG GAG AGATTGGA
G CG AA
GAM2033 305 SURF6 1 16547 NP_006744.2 3 983 TAGGATGTGAGG TC TA 3 C c
c
TGAGCATGAGCT TCAAGCTCAT CTC ACCTC
TGAGCTGA AGTTCGAGTA GAG TGGAG
C- --
GAM2033 305 TDP1 1 12885 NP_060789.2 5 123 CACTTGAGGTTA ATTCCT 3 C c
c
GGAGTTTGAGAT TCAAGCTC CTAACCTC
CAGCCCGG AGTTTGAG GATTGGAG

GAM2033 305 TEP1 1 10717 NP_009041.2 3 374 TCTTGCCAGGAG AG AA 3 C c c
GAGGAATGAGAG TCA CTCATTCCTCT CCT
TGATGTTG AGT GAGTAAGGAGG GGA
GA A-
GAM2033 305 TGFA 1 16678 NP_003227.1 3 1973 TTTGCAGAGGCG A - CTAA 3 C c
c
TAGGAATGAGGC TC AGC TCATTCCT CCTC
TGGACAGA AG TCG AGTAAGGA GGAG

G G TGC-

GAM2033 305 TGFB3 1 16004 NP_003230.1 3 230 TGGGTTTGGTTA A CA T 3 C c c

GAGGAAGGCTGA TCA GCT TTCCTCTAACC
ACTCTTCA AGT CGG AAGGAGATTGG
- -- T

GAM2033 305 TLK2 1 19779 NP_006843.1 3 816 AGAATGAGGTTA - T C 3 C c c
GAAGACTGCAGC TCAAGCT CA TC TCTAACCTC
TTGGAGTC GGTTCGA GT AG AGATTGGAG
C C A

GAM2033 305 TNFSF4 1 1426 NP_003317.1 3 1629 TAGGTAAGGTAA - C- A 3 C c c
GAGGAATCAAGT TCA AGCT ATTCCTCT ACCT
TCTGAGTG AGT TTGA TAAGGAGA TGGA
C AC A

GAM2033 305 TP53INP 1 15816 NP_150601.1 3 3979 CTGGGGAGGTTA ----- TCC 3 C c
c

1 GATGTGTGTTTC TCAAGCT CAT TCTAACCTC
AGGCTTGG GGTTCGG GTG AGATTGGAG
ACTTT TGT

GAM2033 305 TRA16 1 1186 NP_795361.1 3 248 GCACCAGGTTGC A TC-- 3 C c c
TCTGGAAGAGCT TCAAGCTC TTCC TAACCT
TGAGGATG AGTTCGAG AAGG GTTGGA
- TCTC

GAM2033 305 TRIM9 1 1798 NP_055978.2 3 457 GGGGGAGGTAGG A -- A 3 C c c
GAAGAATGAGCT TCA GCTCATTC CTCTA CCTC
GAATTTGT AGT CGAGTAAG GGGAT GGAG
- AA -

GAM2033 305 TSN 1 7612 NP_004613.1 3 2230 TCAAGCAGGTTA AG - C- 3 C c c
GAGAAAATAGAG TCA CTC ATT CTCTAACCT
ATGAATTA AGT GAG TAA GAGATTGGA
A- A AA

GAM2033 305 WBSCR1 1 12817 NP_071496.1 3 1232 TGCTAGGGGTTA TTCC 3 C c
c

GGCTTTTGAGCT TCAAGCTCA TCTAACCTC
TGAACGCC AGTTCGAGT GGATTGGGG
TTTC

GAM2033 305 WBSCR1 1 12817 NP_114381.1 3 1232 TGCTAGGGGTTA TTCC 3 C c
c

GGCTTTTGAGCT TCAAGCTCA TCTAACCTC
TGAACGCC AGTTCGAGT GGATTGGGG
TTTC

GAM2071 371 15E1.2 1 13885 XP_290596.1 3 1201 CCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGA TGACGTGAGGTCGGACCCACTG

GAM2071 371 A1BG 1 10791 NP_570602.2 3 344 ACACTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGTTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 AASS 1 18163 NP_005754.2 3 356 GCTCTGTCACCC 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTG TGACGTGAGGTCGGACCCACTG

GAM2071 371 ABCA13 1 13800 NP_689914.2 3 1067 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 ABLIM1 1 13022 NP_002304.2 3 2384 GAATTATCACCC A------- TCCA 3 B c c
AGACATGTGCAG CTGCAC GTCTGGGTGA
ATGAAATG GACGTG CAGACCCACT
GTAAAGTA TA--
GAM2071 371 ABLIM1 1 13022 NP_006710.2 3 2384 GAATTATCACCC A------- TCCA 3 B c c
AGACATGTGCAG CTGCAC GTCTGGGTGA
ATGAAATG GACGTG CAGACCCACT
GTAAAGTA TA--
GAM2071 371 ABLIM1 1 13022 NP_006711.2 3 2384 GAATTATCACCC A------- TCCA 3 B c c
AGACATGTGCAG CTGCAC GTCTGGGTGA
ATGAAATG GACGTG CAGACCCACT
GTAAAGTA TA--
GAM2071 371 ACADSB 1 14907 NP_001600.1 3 321 ACTCTGTCACCC C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCGC TGACGTGAG TCGGACCCACTG
A
GAM2071 371 ADAMTS4 1 1318 NP_005090.1 3 669 GCTCTGTCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAC ACGTGAGGTCGGACCCGCTG
CACGGTA
GAM2071 371 ADCY5 1 19656 XP_171048.2 3 289 AGATGTTCACTC AC--- -- 3 B c c
AGACTGGGGGAT TGCA CTCCAGTCTGGGTGA
GCAATGTG ACGT GGGGTCAGACTCACT
GTGTA AG
GAM2071 371 ADCY6 1 14908 NP_056085.1 5 64 ACTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGC ACGTGAGGTCGGACCCACTG
CGCGGTA
GAM2071 371 AGMAT 1 2112 NP_079034.2 3 435 TGCTTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAT ACGTGAGGTCGGACCCACTG
TACGGTA
GAM2071 371 AHR 1 9011 NP_001612.1 3 1632 ACTCTGCCGCCC C A 3 B c c
AAACTGGAGTGC ACTGCACTCCAGT TGGGTG
AGTGGCAC TGACGTGAGGTCA ACCCGC
A C
GAM2071 371 AIM1 1 1383 XP_166300.1 3 713 AGACAGGATCTC TGA 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG
AGTGGCAC TGACGTGAGGTCGGACTC

TAG

GAM2071 371 ALDH1B1 1 19434 NP_000683.3 3 1072 ACTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 ALOX15 1 18901 NP_001131.1 3 410 ACTTTGACACCC A 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGTGC TGACGTGAGGTCGGACCCAC
A

GAM2071 371 AMID 1 2328 NP_116186.1 3 693 GCCCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 AMOTL1 1 18210 NP_570899.1 3 1150 AGGAATTCACCC A-- C ---- 3 B c c
AGGCAGCCTGGA CTG ACTCCA GTCTGGGTGA
GTCAGCCA GAC TGAGGT CGGACCCACT
ACC - CCGA

GAM2071 371 ANKRD6 1 11653 NP_055757.1 3 1477 GCTCTGTCACCC 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCAGACCCACTG

GAM2071 371 AP1S3 1 15779 XP_291023.1 3 1017 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 AP3S2 1 6113 NP_005820.1 3 656 GCTCTGTCACCC T 3 B b b
AGGCTGGAGTGC AC GCACTCCAGTCTGGGTGAC
TGTGGTGC TG CGTGAGGTCGGACCCACTG
T

GAM2071 371 APAF1 2 803 NP_001151.1 3 629 TGCTTTGTTGCC G TG 3 B c b
AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCGC TGACGTGAGGTCGGAC C TG
- GT

GAM2071 371 APAF1 2 803 NP_037361.1 3 629 TGCTTTGTTGCC G TG 3 B c b
AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCGC TGACGTGAGGTCGGAC C TG
- GT

GAM2071 371 APAF1 2 1306 NP_001151.1 3 926 GCACTATCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAT TGACGTGAGGTCGGACCCACT

GAM2071 371 APAF1 2 1306 NP_037361.1 3 926 GCACTATCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAT TGACGTGAGGTCGGACCCACT

GAM2071 371 APM1 2 1962 NP_004788.1 3 811 ACTCTGTCACCC C 3 B b b
AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGACAC TGAC TGAGGTCGGACCCACTG
A

GAM2071 371 APM1 2 13551 NP_004788.1 3 1807 CCCTCTGTTGCC C G TG 3 B c b
AGGCTAGAGTGC ACTGCACTC AGTCTG G AC
AGTGGCAT TGACGTGAG TCGGAC C TG
A - GT
GAM2071 371 APOBEC3 1 5126 NP_660341.2 3 351 GCTCTGTCACCC AC----- 3 B c c
F AGACTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCTT ACGTGAGGTCAGACCCACTG
TTCGGTA
GAM2071 371 APOL2 1 16087 NP_112092.1 3 130 GCTCTATCGCCC GT 3 B b b
AGGATGGAGTGC ACTGCACTCCA CTGGGTGA
AGTGGCTC TGACGTGAGGT GACCCGCT
AG
GAM2071 371 APOL2 1 16087 NP_663612.1 3 130 GCTCTATCGCCC GT 3 B b b
AGGATGGAGTGC ACTGCACTCCA CTGGGTGA
AGTGGCTC TGACGTGAGGT GACCCGCT
AG
GAM2071 371 APPL 1 12386 NP_036228.1 3 2973 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 AQP6 1 2103 NP_001643.1 3 613 GATCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCATTG

GAM2071 371 AQP6 1 2103 NP_445738.1 3 1779 GATCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCATTG

GAM2071 371 ARF4L 1 16932 NP_001652.1 3 103 GACCTCTCAGTC A----- G 3 B c c
AGACTGGGGTGC CTGCACTCCAGTCTGG TGA
AGGACCTG GACGTGGGGTCAGACT ACT
GTCCAG G
GAM2071 371 ARHA 1 2467 NP_001655.1 3 610 ATATATCTACCC C C A 3 B c c
AGACTAGATGTA ACTGCA TC AGTCTGGGTG
GTATTTTG TGATGT AG TCAGACCCAT
- A C
GAM2071 371 ARHF 1 3172 NP_061907.1 3 1091 ATTCTGTCACTC C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAT TGACGTGAG TCGGACTCACTG
A
GAM2071 371 ARHGAP1 1 8690 NP_004299.1 3 1136 CGCTCTGTCACC G 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 ARHGAP1 1 7085 NP_055598.1 3 293 ACTCTGTCGTCC GT 3 B b b

1A AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC

AGTGGCGC TGACGTGAGGTCGGACC CTG
TG
GAM2071 371 ARPP-19 2 5121 NP_006619.1 3 1361 GCTCTGTCACCT CC CT 3 B c b
GAGCTCTAGTGC ACTGCACT AGT GGGTGAC
AGTAGTGC TGACGTGA TCG TCCACTG
TC AG
GAM2071 371 ARPP-19 2 18664 NP_006619.1 3 3490 TCACTCTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTGC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 ASB16 1 11661 NP_543139.4 3 142 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 ASB6 2 1654 NP_060343.1 3 1441 GCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGATCCACTG
GAM2071 371 ASB6 2 1654 NP_821066.1 3 2004 GCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGATCCACTG
GAM2071 371 ASB6 2 20186 NP_060343.1 3 1135 ACTCTGTCACCC AC----- 3 B c b
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCGGACCCACTG
CGTGGTA
GAM2071 371 ASB6 2 20186 NP_821066.1 3 1698 ACTCTGTCACCC AC----- 3 B c b
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCGGACCCACTG
CGTGGTA
GAM2071 371 ASE-1 2 9101 NP_036231.1 3 450 GCTCTGTCGCCC GT 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCGC TGACGTGAGGT GACCCGCTG
TG
GAM2071 371 ASE-1 2 9988 NP_036231.1 3 742 CTGGTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG
GAM2071 371 ATP1B4 1 15678 NP_036201.1 3 1877 CTGTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG
GAM2071 371 ATP2C1 1 4782 NP_055197.1 5 203 CTTTGTAGCCAT CAGTCT - 3 B c c
CAACCCGAGTGC ACTGCACTC GGGT GA
AGTTTCGA TGACGTGAG CCCA CT
------ A
GAM2071 371 ATP6V0D 1 7490 NP_689778.1 3 436 ACTCTGTCACCT CC 3 B b b

2 AGGCTACAGTGC ACTGCACT AGTCTGGGTGAC
AGTGGTGT TGACGTGA TCGGATCCACTG
CA

GAM2071 371 ATP7A 1 19505 NP_000043.1 3 1059 GTTTTGCAGCCC GA 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCAC TGACGTGAGGTCGGACCCG
AC

GAM2071 371 AXL 1 5485 NP_001690.2 3 470 ACTGTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 AXL 1 5485 NP_068713.2 3 470 ACTGTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 B4GALT5 1 10889 NP_004767.1 3 1487 GCTCTGTCGCCT TG TC 3 B c
c
AAGCTGGAGTGT AC CACTCCAG TGGGTGAC
GGTGGCAC TG GTGAGGTC ATCCGCTG
GT GA

GAM2071 371 BACH1 1 2969 NP_001177.1 3 973 TTGCTTACTTTT A- CT- 3 B c c
TACCAGGAGTGC ACTGCACTCC GT GGGTGA
AGTTCATT TGACGTGAGG CA TTCATT
AC TTT

GAM2071 371 BAG5 1 19878 NP_004864.1 3 1869 TCTCTGTTGCCC C TG 3 B c c
AGGCTGCAGTGC ACTGCACT CAGTCTGGG AC
AGTGGTGC TGACGTGA GTCGGACCC TG
C GT

GAM2071 371 BAIAP3 1 14634 NP_003924.2 3 610 GGGACGTCACCC C - - 3 B b b
AAGGCTGGTGGT ACTG ACT CCAGTCT GGGTGAC
CAGTGTGA TGAC TGG GGTCGGA CCCACTG
- T A

GAM2071 371 BCL10 1 17565 NP_003912.1 3 782 GCTCTATCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCGC TGACGTGAGGTCGGACCCGCT

GAM2071 371 BDKRB1 1 13940 NP_000701.2 5 89 GTCCGTCGGCCC C - 3 B b b
AGACTGAAGTGC ACTGCACT CAGTCTGGGT GAC
AGTGGCAC TGACGTGA GTCAGACCCG CTG
A G

GAM2071 371 BDP1 1 4304 NP_060899.1 3 152 GTTCTGTTGCCC CA TG 3 B c c
AGGCAAGAGTGC ACTGCACTC GTCTGGG AC
AGTGGTAT TGACGTGAG CGGACCC TG
AA GT

GAM2071 371 BENE 1 3688 NP_005425.1 3 473 GCTCTTCCTCCA - T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGG GA
AGTGACGC TGACGTGAGGTCGGA CCT CT
A C

GAM2071 371 BMP1 1 769 NP_006120.1 3 66 CCTTGGTCGCCT A--- G -- 3 B c c
AGACTGGATAGT CT CAC TCCAGTCTGGGTGAC

GGGGGTGG GG GTG AGGTCAGATCCGCTG
GGTG G AT

GAM2071 371 BNIP-S 1 17763 NP_612122.1 3 333 CGCTCTGTCGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC GCTG
-

GAM2071 371 BTN3A1 1 17858 NP_008979.2 3 1055 TACTCTGTTGCT G TG 3 B c c

AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGTGC TGACGTGAGGTCGGAT C TG
- GT

GAM2071 371 BXDC1 2 711 XP_166303.1 3 685 GTTCTGTCACCT G 3 B b b
AGGGTGGAGTGC ACTGCACTCCA TCTGGGTGAC
AGTGGCAC TGACGTGAGGT GGATCCACTG
G

GAM2071 371 BXDC1 2 7070 XP_166303.1 3 1356 GCTCTGTCGCTC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACTCGCTG

GAM2071 371 BY55 1 17712 NP_008984.1 5 45 TCACTGTCAACC CA G 3 B c c
AGGCCAGAGTGC ACTGCACTC GTCTGG TGAC
AGTGAAGA TGACGTGAG CGGACC ACTG
AC A

GAM2071 371 C11orf1 1 13793 NP_065693.2 3 216 ACTCTGTTGCCC TG 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 C11orf9 1 5710 NP_037411.1 3 167 CTGGAAGTCTTC T - C T 3 B c c
ACACTGGAGTTG AC GCA CTCCAGT TGGG GAC
CTGTTCCA TG CGT GAGGTCA ACTT CTG
T T C -

GAM2071 371 C13orf1 1 2596 NP_065189.1 3 1685 ACCTTGTCACCC C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAC TGACGTGAG TCGGACCCACTG
A

GAM2071 371 C14orf1 1 2950 NP_009107.1 3 1450 ACTCTGTCACCC C-- 3 B b b
AGGCTGGGAATT ACTGCA TCCAGTCTGGGTGAC
GCAGTGGC TGACGT GGGTCGGACCCACTG
TAA

GAM2071 371 C14orf1 1 11599 NP_660274.1 3 1619 GCTTTGTCACCT TC 3 B b b
43 AAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGCGCG TGACGTGAGGTC ATCCACTG
GA

GAM2071 371 C14orf9 1 18182 NP_055643.1 3 967 GCTCTGTCACCC 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 C1orf24 1 601 NP_443198.1 3 1461 GCTCTGTCGCCA G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGTGAC
AGTGGTGT TGACGTGAGGTCGGA CCGCTG

A

GAM2071 371 C1QTNF6 1 18746 NP_114116.2 3 542 GCTCTGTTGCCC C TG 3 B c c

AGGCTAGAGTGC ACTGCACTC AGTCTGGG AC

AGTGGTGC TGACGTGAG TCGGACCC TG

A GT

GAM2071 371 C21orf1 1 2886 XP_114191.2 3 2454 ACTCAGGTCCCC A------ G C T 3 B c c

08 AGACTGCAGTGA CT CACT CAGTCTGGG GAC

GCTGACCT GA GTGA GTCAGACCC CTG

TCCAGTC - C -

GAM2071 371 C22orf1 2 14748 NP_003669.2 3 1824 GCTCTGTTGTCC TG 3 B b b

9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

AGTGGCAC TGACGTGAGGTCGGACCT TG

GT

GAM2071 371 C22orf1 2 16921 NP_003669.2 3 814 AAAGTCACAAGG CA GG-- 3 B c b

9 GGGCCTGAGTGC ACTGCACTC GTCT GTGAC

AGTGGCTC TGACGTGAG CGGG CACTG

TC GGAA

GAM2071 371 C3F 1 15743 NP_005759.2 3 223 GCTTTGTCACCC C C 3 B b b

ACGCTGGAATGC ACTGCA TCCAGT TGGGTGAC

AGTGGCGG TGACGT AGGTCG ACCCACTG

A C

GAM2071 371 C5orf4 1 10925 NP_057432.1 3 45 ACACAGCTCCCC - A T 3 B b b

AGACTGGAGGCT ACT GC CTCCAGTCTGGG GA

GGTCAGAG TGG CG GAGGTCAGACCC CT

T - -

GAM2071 371 C5orf4 1 10925 NP_115761.1 3 1551 ACACAGCTCCCC - A T 3 B b b

AGACTGGAGGCT ACT GC CTCCAGTCTGGG GA

GGTCAGAG TGG CG GAGGTCAGACCC CT

T - -

GAM2071 371 C5orf7 1 7567 NP_057688.1 3 117 GGCCCTTCACCC TG CCAG 3 B c c

AGAGCCAGTGTG AC CACT TCTGGGTGA

GTCAGTAT TG GTGA AGACCCACT

GT CCG-

GAM2071 371 C6orf14 1 12169 NP_699175.1 3 804 GCTCTGTCACCC C T 3 B b b

1 AGCCTGGAATGT ACTGCA TCCAG CTGGGTGAC

AGTGGCAT TGATGT AGGTC GACCCACTG

A C

GAM2071 371 C6orf33 1 7278 NP_588608.1 3 2344 ACTCTGTCGCCC 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC

AGTGATGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 C6orf5 1 10778 NP_056339.2 3 1427 GCTCTGTCGTCC GT 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC

AGTGCTGC TGACGTGAGGTCGGACC CTG

TG

GAM2071 371 C6orf57 1 6442 NP_660310.1 3 500 TCTCTCTCACCC G 3 B b b

AGGCTGGAGTGG ACT CACTCCAGTCTGGGTGA
AGTGGCGC TGA GTGAGGTCGGACCCACT
G

GAM2071 371 C9orf9 2 13797 NP_061829.2 3 216 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGCGC TGGCGTGAGGTCGGACCCGCTG

GAM2071 371 C9orf9 2 19273 NP_061829.2 3 855 ACTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC CTG
T

GAM2071 371 CA5A 1 6692 NP_001730.1 5 20 ATCACCCTCTTC C ----- 3 B b b
AGACTGGAGTCA ACTG ACTCCAGTCT GGGTGA
GTGGGAAC TGAC TGAGGTCAGA CCCACT
- CTTCT

GAM2071 371 CASP8 1 9100 NP_001219.2 3 81 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 CASP8 1 9100 NP_203519.1 3 81 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 CASP8 1 9100 NP_203520.1 3 81 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 CASP8 1 9100 NP_203521.1 3 826 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 CBFA2T2 1 3868 NP_005084.1 3 1896 CTCTTGTCTCCC AC----- T 3 B c
c
AGGCTGGAGTGC TGCACTCCAGTCTGGG GAC
AATCGCGC ACGTGAGGTCGGACCC CTG
CGCGCTA T

GAM2071 371 CBFA2T2 1 3868 NP_787060.1 3 1896 CTCTTGTCTCCC AC----- T 3 B c
c
AGGCTGGAGTGC TGCACTCCAGTCTGGG GAC
AATCGCGC ACGTGAGGTCGGACCC CTG
CGCGCTA T

GAM2071 371 CCL16 1 10633 NP_004581.1 3 275 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 CCL22 2 11649 NP_002981.2 3 1274 ACTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 CCL22 2 16005 NP_002981.2 3 950 CTCTTGTCACCC AC----- C 3 B c b

ACGCTGGAGTGC TGCACTCCAGT TGGGTGAC
AATGGTGT ACGTGAGGTCG ACCCACTG
TGTGGTA C

GAM2071 371 CCNF 1 14395 NP_001752.1 3 1292 CTCTTGTCTCCC T T 3 B b b
CGGCTGGAGTGC ACTGCACTCCAGTC GGG GAC
AGTGGCAT TGACGTGAGGTCGG CCC CTG
C T

GAM2071 371 CCR5 1 17905 NP_000570.1 3 1210 ACAGTCTCACCC T A CC 3 B c c

AGACTCCAGGCT AC GC CT AGTCTGGGTGA
GTCTTTCA TG CG GA TCAGACCCACT
T - CC

GAM2071 371 CD209 1 8229 NP_066978.1 3 1590 TGCTCTGTCGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC GCTG
-

GAM2071 371 CD24 1 18593 NP_037362.1 3 889 ACTTTGTCGCCC A 3 B b b
AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGTGC TGACGTGAGG CGGACCCGCTG
C

GAM2071 371 CDC14B 1 7919 NP_201589.1 3 631 CTCTTGTTGTCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCT TG
GT

GAM2071 371 CDC2L2 1 8250 NP_296370.1 5 17 GCTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGA ACGTGAGGTCGGACCCACTG
AGTGGTA

GAM2071 371 CDCP1 1 20095 NP_073753.3 3 1771 ATTCTGTTGCCT TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGATCC TG
GT

GAM2071 371 CDH1 1 3667 NP_004351.1 3 518 ATTCTATCGGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGA
AGTGGTGC TGACGTGAGGTCGGACC GCT
G

GAM2071 371 CDK11 1 5408 XP_166324.1 3 3221 GCTCTGTCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGCAC TGACGTGAGGTC ACCCACTG
GA

GAM2071 371 CDKAL1 1 12153 NP_060244.1 3 442 CTCTTGTCCCCC --- T 3 B b b
AGGCTGGAGTGG ACTGCAC TCCAGTCTGGG GAC
TGCAGTGG TGACGTG AGGTCGGACCC CTG
GTG C

GAM2071 371 CEACAM8 1 436 NP_001807.2 3 352 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 CENPH 1 7835 NP_075060.1 3 262 GCTTTGTTGCCC A TG 3 B c c
AGACTGGAGGGC ACTGC CTCCAGTCTGGG AC

AGTGGCGC TGACG GAGGTCAGACCC TG
G GT
GAM2071 371 CGI-150 1 19951 NP_057164.1 5 49 TGCTCTGTCATC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCTC TGACGTGAGGTCGGACT ACTG
-
GAM2071 371 CIAS1 1 7985 NP_004886.2 5 288 GCTGTGTCGCCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGATCCGCTG

GAM2071 371 CIP29 1 11639 NP_115740.3 3 163 TGCTCTGTTGCC T TG 3 B b b
CAGCTGGAGTGC ACTGCACTCCAG CTGGG AC
AGTGGTGT TGACGTGAGGTC GACCC TG
- GT
GAM2071 371 CLECSF1 1 10233 NP_072092.2 3 319 ACTTTGTTACCC 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCATTG

GAM2071 371 CLNS1A 1 8322 NP_001284.1 3 80 GGTGCCTCTTCC G TC T 3 B c c

ACTCTGGAGTGA ACT CACTCCAG TGGG GA
AGTTAATG TGA GTGAGGTC ACCT CT
A TC T
GAM2071 371 CMAR 1 19999 NP_005191.2 5 231 GCGCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGCTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 CNN2 1 6909 NP_004359.1 3 735 TGGTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 CNNM3 1 3981 NP_060093.2 3 373 TGGGCTGAGCCA - GTCT A 3 B c
c
CCTTGTGAGTGC ACTGCACTC CA GGGTG
AGTTACTG TGACGTGAG GT TCCAC
T ---- C
GAM2071 371 CNP 1 5014 NP_149124.1 3 560 CTGCTATTTCCC TC T 3 B c c
AAGCTGGAGTGC ACTGCACTCCAG TGGG GA
AGTGGTGC TGACGTGAGGTC ACCC TT
GA T
GAM2071 371 COLEC12 1 13793 NP_110408.2 3 103 ACTCTGTTGCCC TG 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 COPS7A 1 5715 NP_057403.1 5 118 GCCCAAGTCCCC CC C T 3 B c
c
CACACTCAGTGC ACTGCACT AGT TGGG GAC
AGTGATGA TGACGTGA TCA ACCC CTG
C- C C

GAM2071 371 CPR8 1 9163 NP_065790.1 3 1690 GCTTTGTCAGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGACAC TGACGTGAGGTCGGACC ACTG
G
GAM2071 371 CPS1 1 4147 NP_001866.2 3 668 GTCACACTCTCC ----- 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG GTGAC
AGTGGCAC TGACGTGAGGTCGGACC CACTG
TCTCA
GAM2071 371 CPSF2 2 6347 XP_029311.2 3 2044 CTCTTGTTGCCC AC----- TG 3 B c
b
AGACTGGAGTGC TGCACTCCAGTCTGGG AC
AATGGCAC ACGTGAGGTCAGACCC TG
CACGGTA GT
GAM2071 371 CPSF2 2 6739 XP_029311.2 3 1219 ACAGAGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGA TGACGTGAGGTCGGACCCACTG

GAM2071 371 CR1 1 13868 NP_000564.1 3 770 GCTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGT TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 CR1 1 13868 NP_000642.2 3 769 GCTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGT TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 CRLF3 1 9675 NP_057070.2 3 612 CTCTTGTCACTC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACTCACTG

GAM2071 371 CRSP6 1 12005 NP_004259.3 3 434 ACTCTGTAGCCC T GA 3 B c c
AGTCTGGAGTGC ACTGCACTCCAG CTGGGT
AGTGGTGT TGACGTGAGGTC GACCCG
T AT
GAM2071 371 CSE-C 1 2336 NP_061851.1 5 2 GGAGTGCCCAGG GT A 3 B c c
ATGGAGTGCAGT ACTGCACTCCA CTGGGTG
GGCTATTC TGACGTGAGGT GACCCGT
AG G
GAM2071 371 CSE1L 1 3997 NP_803185.1 3 492 CTCTCATTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGAGCT TGACGTGAGGTCGGACCC T
GT
GAM2071 371 CSEN 1 14933 NP_038462.1 3 1448 GGGGCCTCACCC CAC AG 3 B c
c
AGAAGGAACCCG ACTG TCC TCTGGGTGA
GTCCCAGG TGGC AGG AGACCCACT
CCA A-
GAM2071 371 CSNK2A2 1 15382 NP_001887.1 5 0 TGTCACCCAGGC 3 B b b
TGGAGTGCAGTG ACTGCACTCCAGTCTGGGTGAC
GCGCAATC TGACGTGAGGTCGGACCCACTG

GAM2071 371 CST 1 3944 NP_004852.1 5 75 CTGTGTCATCCA A----- - 3 B c c
GAGCTGGAGTGC CTGCACTCCAG TCTGGGTGAC
AGCGGCAC GACGTGAGGTC AGACCTACTG
CACGGC G
GAM2071 371 CTEN 1 14087 NP_116254.3 3 766 TCACTGTCACCC CTC 3 B b b
AGGCTGAACTGC ACTGCA CAGTCTGGGTGAC
AGTGGTGT TGACGT GTCGGACCCACTG
CAA
GAM2071 371 CTSS 1 7946 NP_004070.3 3 1700 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 CXCL16 1 11701 NP_071342.1 3 339 GCTCTGTCATCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCTACTG

GAM2071 371 CXYorf1 1 6801 XP_088704.2 5 642 AGGGCCTGTCCC A----- - CT T 3 B c c
TACTGAGAGTGC CTGCACTC CAGT GGG GAC
AGGGAACT GACGTGAG GTCA TCC CTG
TCAAGG A -- -
GAM2071 371 CYCS 1 14950 NP_061820.1 3 1816 GCTGTGTCGCCA G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGTGAC
AGTGGTGC TGACGTGAGGTCGGA CCGCTG
A
GAM2071 371 CYP1A2 3 6816 NP_000752.1 3 1084 CCTCTGTCTCCT TC T 3 B c b
AAGCTGGAGTGC ACTGCACTCCAG TGGG GAC
AGTGGCAT TGACGTGAGGTC ATCC CTG
GA T
GAM2071 371 CYP1A2 3 8688 NP_000752.1 3 787 TACTCTGTTGCC G TG 3 B c b
AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCGC TGACGTGAGGTCGGAC C TG
- GT
GAM2071 371 CYP1A2 3 13973 NP_000752.1 3 417 AGTCTGTCACCC GT 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCGT TGACGTGAGGT GACCCACTG
TG
GAM2071 371 CYP2B6 2 3011 NP_000758.1 3 275 ACACTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 CYP2B6 2 9252 NP_000758.1 3 702 ACTCTGTCACCC C C GT 3 B c b
AGGTTCGAGTTC ACTG ACTC A CTGGGTGAC
AGTGGTGC TGAC TGAG T GACCCACTG
T C TG
GAM2071 371 CYP4F3 1 1417 NP_000887.1 3 1395 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
GGTGGCAT TGGCGTGAGGTCGGACCC TG
GT

GAM2071 371 CYP51A1 1 10631 NP_000777.1 3 883 GCTCTGTTGCCC TG 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 CYP8B1 1 5584 NP_004382.1 3 1005 ACTCTGTTGCCC C TG 3 B c c

AGGCTGCAGTGC ACTGCACT CAGTCTGGG AC
AGTGGTGT TGACGTGA GTCGGACCC TG
C GT

GAM2071 371 DBR1 1 1031 NP_057300.1 3 85 CTCTTGTCACCT AC----- 3 B c c
AGACTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCAGATCCACTG
TGCGGTA

GAM2071 371 DCAMKL1 1 4605 NP_004725.1 3 1147 TGGGGCACAAGG A GG-- A 3 B c c

GGACTGGAGGCA ACTGC CTCCAGTCT GTG
GTTGCTTT TGACG GAGGTCAGG CAC
- GGAA G

GAM2071 371 DCX 1 6035 NP_000546.2 3 4961 CCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 DCX 1 6035 NP_835364.1 3 4961 CCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 DCX 1 6035 NP_835365.1 3 4961 CCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 DCX 1 6035 NP_835366.1 3 4961 CCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 DDX31 1 17894 NP_619526.1 3 190 CTTGATTGTCCC G TG T 3 B c c

TGGATGGAGTGC ACTGCACTCCA TC GG GAC
AGTCACCT TGACGTGAGGT AG CC CTG
- GT -

GAM2071 371 DFFB 2 7574 NP_004393.1 3 245 CTTTTGTTGCCC TG 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGATGTGAGGTCGGACCC TG
GT

GAM2071 371 DFFB 2 7848 NP_004393.1 3 888 ACTCTGTCGCTC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGATGC TGACGTGAGGTCGGACTCGCTG

GAM2071 371 DIAPH2 1 12586 NP_006720.1 3 4012 ACTCTGTCACCC C 3 B b b
AGGCTGCAGTGT ACTGCACT CAGTCTGGGTGAC

AGTGGTGC TGATGTGA GTCGGACCCACTG
C
GAM2071 371 DISC1 4 5967 NP_061132.1 3 881 CACAATACAGTA CCA A 3 B c b
CTCAGGCAGTGC ACTGCACT GTCTGGGTG
AGTACTCA TGACGTGA CGGACTCAT
--- G
GAM2071 371 DISC1 4 6590 NP_061132.1 3 842 GTGCAGTACTCA - AGT A 3 B c b
GTAAGGCAGTGC ACTGCACT CC CTGGGTG
AGTACTCA TGACGTGA GG GACTCAT
C AAT G
GAM2071 371 DISC1 4 6590 NP_061132.1 3 1158 GTGCAGTACTCA - AGT A 3 B c b
GTAAGGCAGTGC ACTGCACT CC CTGGGTG
AGTACTCA TGACGTGA GG GACTCAT
C AAT G
GAM2071 371 DISC1 4 10777 NP_061132.1 3 1034 ATACAGTACTCA - AGT A 3 B c b

GTTAGGCAGTGC ACTGCACT CC CTGGGTG
AGTACTCA TGACGTGA GG GACTCAT
C ATT G
GAM2071 371 DISC1 4 13620 NP_061132.1 3 3217 TCTCTGTCACCC TC 3 B b b
AAGTTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGCCC TGACGTGAGGTT ACCCACTG
GA
GAM2071 371 DKFZP43 1 11474 NP_113664.1 3 2100 ACTCTGTTGCCC CAG - TG 3 B c
c
4B044 AAGGTAGAGTGC ACTGCACTC TCT GGG AC
AGTGGCGT TGACGTGAG GGA CCC TG
AT- A GT
GAM2071 371 DKFZp43 1 7947 NP_060068.1 3 860 GCTCTGTCACCC C 3 B b b
4C0923 AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCGT TGAC TGAGGTCGGACCCACTG
A
GAM2071 371 DKFZp43 1 18031 NP_060082.1 5 771 AGTCTGTTGCCC TG 3 B b b
4E2220 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 DKFZp43 1 3669 XP_097012.2 3 383 AGCACTTCACCC CACT -- 3 B c
c
4O0320 AGAGCCTGGCAC ACTG CCAG TCTGGGTGA
ACAGTAGG TGAC GGTC AGACCCACT
ACAC CG
GAM2071 371 DKFZp54 1 3007 NP_694590.1 3 1543 GCACTGTCACCC 3 B b b
7P234 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 DKFZP56 1 13202 NP_108648.1 3 921 GTTCTGTTGCCT CA TG 3 B c
c
4D166 AGGCCAGAGTGC ACTGCACTC GTCTGGG AC
AGTGGCAT TGACGTGAG CGGATCC TG
AC GT

GAM2071 371 DKFZP56 1 519 NP_056416.1 5 1110 CTCTTGTCGCCC C 3 B b b
4G092 AGGCTGTAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGTAC TGACGTGA GTCGGACCCGCTG
T
GAM2071 371 DKFZP56 1 19815 XP_032397.1 3 258 ACTCTGTCACCT 3 B b b
4I122 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 DKFZP56 1 18946 NP_056274.1 3 522 CGCTCTGTCACC C G 3 B b b

4J0863 AGGCTTGAGTGC ACTGCACTC AGTCTGG TGAC
AGTGGTGT TGACGTGAG TCGGACC ACTG
T -
GAM2071 371 DKFZP56 1 1414 NP_114429.1 3 214 ACTCTGTTGCCC TG 3 B b b
4K0322 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 DKFZp56 1 811 NP_115497.2 3 695 GCTGTGTCACAC G 3 B b b
4K142 AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
AGTGGCGT TGACGTGAGGTCGGAC CACTG
A
GAM2071 371 DKFZP56 1 9020 NP_056278.1 3 292 TTTGACCACTTG C - A 3 B c c
6K1924 TGACTGGAGTTC ACTG ACTCCAGTC TGGGTG
AGTGGCCC TGAC TGAGGTCAG GTTCAC
T T C
GAM2071 371 DKFZP56 1 1708 NP_115504.1 3 745 AACTCATTAGCA C - -- 3 B c c
6M114 GATATGTAGTGC ACTGCACT CA GTCTG GGTGA
AGTGATTT TGACGTGA GT TAGAC TTACT
T A GA
GAM2071 371 DKFZP58 2 4762 NP_056348.2 3 191 CAGACAGCACCC G ----- A 3 B c c

6B1621 AGAGTGAGCTGG ACT CACTCCAGT CTGGGTG
AGTGGGTC TGG GTGAGGTCG GACCCAC
- AGTGA G
GAM2071 371 DKFZP58 2 20110 NP_056348.2 3 191 AGCACCCAGAGT G ----- A 3 B c
c
6B1621 GAGCTGGAGTGG ACT CACTCCAGT CTGGGTG
GTCCCCAT TGG GTGAGGTCG GACCCAC
- AGTGA G
GAM2071 371 DKFZp58 1 14672 XP_098416.1 3 3008 ACTCTGTCACCC AC----- 3 B c
c
6C0721 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAA ACGTGAGGTCGGACCCACTG
AACGGTA
GAM2071 371 DKFZP58 1 5664 NP_056248.1 3 472 ACTCTGTCATCC 3 B b b
6D0919 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCTACTG

GAM2071 371 DKFZp66 1 4387 NP_808881.1 3 73 TGAACGTCACCC A TC---- -- 3 B c c

7B1218 AGAGACTGTAAT CTGCAC CAGTCT GGGTGAC
TTGTGTAG GATGTG GTCAGA CCCACTG
- TTTAAT GA
GAM2071 371 DKFZp66 1 9198 XP_117353.1 3 295 TCTCTGTCAGCC TG G 3 B c c
7E0512 AGGCTGGAGTGT AC CACTCCAGTCTGG TGAC
GGTGGCAC TG GTGAGGTCGGACC ACTG
GT G
GAM2071 371 DKFZp76 1 5298 NP_775734.1 3 2764 GCTATGTCTCCC T 3 B b b
1B107 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 DKFZp76 1 436 NP_689650.1 5 1004 GCTCTGTCGCCC 3 B b b
1B128 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 DKFZp76 1 12709 NP_061181.1 3 887 GATCTGTCGCCC 3 B b b
1H039 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 DKFZp76 1 969 NP_115656.1 5 1461 CTCTTGTCACCC 3 B b b
1J139 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 DKFZp76 1 11194 NP_060879.1 5 1530 CTCTTGTTGCCC C TG 3 B c
c
1O0113 AGGCTTGAGTGC ACTGCACTC AGTCTGGG AC
AGTGATGC TGACGTGAG TCGGACCC TG
T GT
GAM2071 371 DKFZp76 1 1413 NP_690870.1 3 739 GCTCTGTCACCC 3 B b b
1P1121 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 DKFZp76 1 11830 NP_848637.1 3 167 TCTCTGTGGCCC C G 3 B c c

2C2414 AGGCTGAAGTGC ACTGCACT CAGTCTGGGT AC
AGTGGTGT TGACGTGA GTCGGACCCG TG
A G
GAM2071 371 DKFZp76 1 2137 XP_172976.2 3 1896 GCTCTGTCGCCC A----- 3 B c c
2H185 AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGAGGTGC GACGTGAGGTCGGACCCGCTG
CGTGGA
GAM2071 371 DKFZp76 1 11659 NP_689624.1 3 254 GCTCTGTCACCC 3 B b b
2I137 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 DKFZp76 1 19272 NP_689597.1 3 704 TCAATGGTGCCC A 3 B c c
2I194 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGCGT TGACGTGAGGTCGGACCCGT
G
GAM2071 371 DKFZp76 1 13546 NP_061189.2 3 780 GTTCTGTTGCCC AG TG 3 B c
c

2L0311 AGGAGGGAGTGC ACTGCACTCC TCTGGG AC
AGTGGTGC TGACGTGAGG GGACCC TG
GA GT

GAM2071 371 DMWD 1 10543 XP_027569.1 3 609 CCGCTTTCCCCA A----- AG- T 3 B c c
GAGGAGGAGTGC CTGCACTCC TCTGGG GA
AGGCCTGC GACGTGAGG AGACCC CT
CGTCCG AGG -

GAM2071 371 DRIM 1 2324 NP_055318.1 3 140 ACTCTGTCACCC A - 3 B b b
AAGGCGGAGTGC ACTGCACTCC GTCT GGGTGAC
AGTGACGA TGACGTGAGG CGGA CCCACTG
- A

GAM2071 371 DSC3 1 2085 NP_001932.1 3 2047 GCTCTGACGCAC G A 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTG GTG
AGTGGCTC TGACGTGAGGTCGGAC CGC
A A

GAM2071 371 DSC3 1 2085 NP_077741.1 3 2261 GCTCTGACGCAC G A 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTG GTG
AGTGGCTC TGACGTGAGGTCGGAC CGC
A A

GAM2071 371 DSCR3 1 13453 NP_006043.1 3 612 AGTCTGTCACCC A- ---- 3 B c c
AGGCTGGAGTGA CTG CACTCCAGTCTGGGTGAC
TCTCAGCT GAC GTGAGGTCGGACCCACTG
TC TCTA

GAM2071 371 DSCR6 1 17339 NP_061835.1 3 545 CTCTTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGACAC TGACGTGAGGTCGGACCC CTG
T

GAM2071 371 DUPLIN 2 2517 XP_208760.3 3 180 CTCTCTCACCCA C - 3 B b b
GGCCTGAAGTGC ACTGCACT CAG TCTGGGTGA
AGTGGCAT TGACGTGA GTC GGACCCACT
A C

GAM2071 371 DUPLIN 2 13723 XP_208760.3 3 180 GCTCTCTCACCC C - 3 B b b
AGGCCTGAAGTG ACTGCACT CAG TCTGGGTGA
CAGTGGCA TGACGTGA GTC GGACCCACT
A C

GAM2071 371 DUSP18 1 19123 NP_689724.2 3 650 GCTCTGTCACCC TC 3 B b b
ATCCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTAGTGT TGACGTGAGGTC ACCCACTG
CT

GAM2071 371 DUSP19 2 710 NP_543152.1 3 2292 CTCTTATTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCGT TGACGTGAGGTCGGACCC T
GT

GAM2071 371 DUSP19 2 969 NP_543152.1 3 637 CTCTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 DYRK1A 1 14469 NP_567824.1 5 62 CCGCCATCGTCC C T - 3 B c c
CGGCTGAAGTGC ACTGCACT CAG CTGGG TGA

AGTGGCAC TGACGTGA GTC GGCCC GCT
A - T

GAM2071 371 EDG8 1 11935 NP_110387.1 3 951 GCTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGGCA ACGTGAGGTCGGACCCACTG
ACGGGTA

GAM2071 371 EEF2K 1 11618 NP_037434.1 3 344 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGACAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 EHD2 1 6934 NP_055416.2 3 905 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGA TGACGTGAGGTCGGACCCGCTG

GAM2071 371 EIF2S3 1 11659 NP_001406.1 3 346 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 EIF5A2 1 1333 NP_065123.1 3 974 ACTCCATCAGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGA
AGTGGTGC TGACGTGAGGTCGGACC ACT
G

GAM2071 371 ELP3 1 6182 NP_060561.3 3 905 GCTGTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 EMR2 1 433 NP_038475.2 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA

GAM2071 371 EMR2 1 433 NP_690880.1 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA

GAM2071 371 EMR2 1 433 NP_690881.1 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA

GAM2071 371 EMR2 1 433 NP_690882.1 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA

GAM2071 371 EMR2 1 433 NP_690883.1 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA

GAM2071 371 EMR2 1 433 NP_690884.1 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA

GAM2071 371 EMR2 1 433 NP_690885.1 5 150 ACTCTATCACCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGGCAC TGACGTGAGGTC ACCCACT
GA
GAM2071 371 ENDOGL1 1 4223 NP_005098.1 3 153 GCCGTGTCATCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGTGG TGGCGTGAGGTCGGACCTACTG

GAM2071 371 EPHB6 1 19635 NP_004436.1 5 214 AACGGGGTCCCC A- A---- T 3 B c
c
GGACTGGAGAAG CTGC CTCCAGTCTGGG GAC
ACGCGGGT GGCG GAGGTCAGGCCC CTG
TG CAGAA -
GAM2071 371 EPN2 1 4430 NP_055779.1 3 2378 AGGAAGTCACCC CACTC T 3 B c
c
AGCTGTTTCTCA ACTG CAG CTGGGTGAC
GTCCCAGA TGAC GTC GACCCACTG
TCTTT -
GAM2071 371 EPN2 1 4430 NP_683723.1 3 2378 AGGAAGTCACCC CACTC T 3 B c
c
AGCTGTTTCTCA ACTG CAG CTGGGTGAC
GTCCCAGA TGAC GTC GACCCACTG
TCTTT -
GAM2071 371 EREG 1 430 NP_001423.1 3 2042 GCTCTGTTGCCC GT TG 3 B c c
AGGTTGGAGTGC ACTGCACTCCA CTGGG AC
AGTGGCAC TGACGTGAGGT GACCC TG
TG GT
GAM2071 371 EVC 1 4148 NP_055371.1 3 2224 TCACTTTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCGT TGACGTGAGGTCGGACCC T
GT
GAM2071 371 EVC 1 4148 NP_714928.1 3 2224 TCACTTTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCGT TGACGTGAGGTCGGACCC T
GT
GAM2071 371 EVI5 2 16074 NP_005656.2 3 2216 CTCACTGCACTC A 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGTAC TGACGTGAGGTCGGACTCAC
G
GAM2071 371 EVI5 2 18007 NP_005656.2 3 515 AGTTTGTCACCC T 3 B b b
AGGCTGGAGTGC AC GCACTCCAGTCTGGGTGAC
TGTGGTGT TG CGTGAGGTCGGACCCACTG
T
GAM2071 371 F11R 1 16292 NP_058642.1 3 2147 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 F11R 1 16292 NP_653085.1 3 2147 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 F11R 1 16292 NP_653086.1 3 2149 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 F11R 1 16292 NP_653087.1 3 2149 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 F2RL2 1 5026 NP_004092.1 3 200 ACTTTATCACCC T 3 B b b
AGACTGGCGTGC ACTGCAC CCAGTCTGGGTGA
AGTGGCAC TGACGTG GGTCAGACCCACT
C
GAM2071 371 F2RL3 1 13324 NP_003941.1 3 3004 GCGCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 F3 1 15547 NP_001984.1 3 424 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTAGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 FAM13A1 1 17686 NP_055698.1 3 625 TGCATCTGCCCA - G - A 3 B c c

CGATGGCAGTGC ACTGCACT CCA TC TGGGTG
AGTCATCA TGACGTGA GGT AG ACCCGT
C - C C
GAM2071 371 FANCE 1 16751 NP_068741.1 3 279 GCTCTGTCATCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGATGC TGACGTGAGGTCGGACCTACTG

GAM2071 371 FANCF 1 14445 NP_073562.1 3 737 GCTCTGTCACCC T 3 B b b
AGTCTGGAGTGC ACTGCACTCCAG CTGGGTGAC
AGTGGTGT TGACGTGAGGTC GACCCACTG
T
GAM2071 371 FAT3 1 7945 XP_061871.5 3 1358 GCTCTGTCACCC AC----- C 3 B c c
AGGCTAGAGTGC TGCACTC AGTCTGGGTGAC
AATGGCAT ACGTGAG TCGGACCCACTG
TACGGTA A
GAM2071 371 FBLN1 1 2764 NP_006476.1 3 512 GCTCAGAAGTCA CC TCT 3 B c c

CCTCCTCAGTGC ACTGCACT AG GGGTGAC
AGTTAGCC TGACGTGA TC TCCACTG
C- C--
GAM2071 371 FBXW8 1 20011 NP_036306.1 3 1493 GTCACCTAGACT AC----- ----- 3 B c
c
AGACTGGAGTGC TGCACTCCAGTCT GGGTGA
AATGGCCT ACGTGAGGTCAGA TCCACT
TCCGGTA TCAGA

C

G

GAM2071 371 FBXW8 1 20011 NP_699179.2 3 1493 GTCACCTAGACT AC----- ----- 3 B c c

AGACTGGAGTGC TGCACTCCAGTCT GGGTGA
AATGGCCT ACGTGAGGTCAGA TCCACT
TCCGGTA TCAGA

C
G

GAM2071 371 FCAR 3 441 NP_579813.1 3 242 GCTCTTTCGCCA G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGTGA
AGTGGCAC TGACGTGAGGTCGGA CCGCT
A

GAM2071 371 FCAR 3 441 NP_579814.1 3 242 GCTCTTTCGCCA G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGTGA
AGTGGCAC TGACGTGAGGTCGGA CCGCT
A

GAM2071 371 FCAR 3 10505 NP_001991.1 3 157 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGAGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 FCAR 3 18209 NP_579803.1 3 157 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 FCAR 3 18209 NP_579805.1 3 157 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 FCAR 3 18209 NP_579806.1 3 157 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 FCAR 3 18209 NP_579807.1 3 157 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 FCAR 3 18209 NP_579808.1 3 281 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 FCAR 3 18209 NP_579811.1 3 157 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 FCAR 3 18209 NP_579812.1 3 157 GCTCTGTCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGAGC TGACGTGA GTCGGACCCACTG

A

GAM2071 371 FCGR2A 1 10188 NP_067674.1 3 522 AATCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCATTG

GAM2071 371 FER1L4 1 1759 XP_300246.1 3 221 GCTCTGTCTCCC GT T 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGG GAC
AGTGGCAC TGACGTGAGGT GACCC CTG
TG T

GAM2071 371 FER1L4 1 1759 XP_300246.1 3 370 GCTCTGTCTCCC GT T 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGG GAC
AGTGGCAC TGACGTGAGGT GACCC CTG
TG T

GAM2071 371 FEZ1 1 659 NP_072043.1 3 825 ATTCTATCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
AATGGCAC ACGTGAGGTCGGACCCGCT
CACGGTA

GAM2071 371 FGF5 1 3375 NP_004455.1 3 2381 TGCTCTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCAT TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 FGF5 1 3375 NP_149134.1 3 2712 TGCTCTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCAT TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 FHL2 1 19820 NP_001441.2 5 448 GCTTTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FKBP9 1 2718 NP_009201.1 3 805 CCGTTTGTCGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC GCTG
-

GAM2071 371 FLJ0006 1 13800 XP_028154.1 5 29 GCTCTGTCACCC 3 B b b
0 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ1010 1 10153 NP_078994.1 3 252 GCTGTGTGGCCC G 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCGC TGACGTGAGGTCGGACCCG TG
G

GAM2071 371 FLJ1023 1 14903 NP_060503.1 3 794 GCTCTGTCACCC AC----- 3 B c c
2 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
GATGGCGC GCGTGAGGTCGGACCCACTG
CGCGGTA

GAM2071 371 FLJ1029 1 468 NP_060520.2 3 183 GCTTTGTTGCCC TG 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTAGCAC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 FLJ1034 1 7836 NP_060535.1 5 99 GCTCTGTCTCCC C T 3 B b b

6 AGGCTGAAGTGC ACTGCACT CAGTCTGGG GAC
AGTGGCAC TGACGTGA GTCGGACCC CTG
A T

GAM2071 3715 FLJ1053 1 10633 NP_060599.1 3 805 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 3710 FLJ1064 1 16789 NP_061896.1 5 68 CACTCTGCTGCC C A 3 B c c
TAGGCTGAGTGC ACTGCACTC AGTCTGGGTG
AGTGGTGT TGACGTGAG TCGGATCCGT
- C

GAM2071 3713 FLJ1071 1 12092 NP_060659.1 3 359 TCACTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 3717 FLJ1073 1 2224 NP_060668.1 3 786 CTGCACCACCCA CAGTC- A 3 B c c
CCTCCAGAGTGC ACTGCACTC TGGGTG
AGTGCTGG TGACGTGAG ACCCAC
ACCTCC C

GAM2071 3716 FLJ1084 1 13800 NP_060711.1 3 351 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 3717 FLJ1084 1 18108 NP_060712.2 3 489 GCTCTGTCATGC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
GGTGGTGC TGGCGTGAGGTCGGAC TACTG
G

GAM2071 3718 FLJ1099 1 20020 NP_060764.2 3 122 GCTCTGTCACCC C A TC 3 B c c
AAGCAGGATTGC ACTGCA TCC G TGGGTGAC
AGTGAGCC TGACGT AGG C ACCCACTG
T A GA

GAM2071 3714 FLJ1127 1 7307 NP_060845.1 5 49 CCGGGTCAAGGC CAGT --- 3 B c c
CCGGTCGAGTGC ACTGCACTC CTGGGT GAC
AGTACCAT TGACGTGAG GGCCCG CTG
CT-- GAA

GAM2071 3713 FLJ1132 1 13280 NP_060860.1 3 97 CTCTCGTTGCCG G TG 3 B c c
AGGCTGGAGTGT ACTGCACTCCAGTCT GG AC
AGTAGTGT TGATGTGAGGTCGGA CC TG
G GT

GAM2071 3717 FLJ1146 1 9552 NP_079239.2 3 144 TTCCTGTCACCC C 3 B b b
AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCGT TGAC TGAGGTCGGACCCACTG
A

GAM2071 3710 FLJ1171 1 6034 NP_079122.1 3 1010 GCTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC CTG
T

GAM2071 371 FLJ1180 1 17222 NP_079250.1 3 1241 TCACTGTCACCC A 3 B b b
0 AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCAC TGACGTGAGG CGGACCCACTG
C
GAM2071 371 FLJ1236 1 14486 NP_115543.1 3 50 TCACCGTCCCCC T T 3 B b b
3 AGGCTGGAGTGC AC GCACTCCAGTCTGGG GAC
CGTGGCGT TG CGTGAGGTCGGACCC CTG
C C
GAM2071 371 FLJ1257 1 14282 NP_075056.2 5 116 GCTCTGTCACCC C 3 B b b
2 AGGCTGGAGTAT ACTG ACTCCAGTCTGGGTGAC
AGTGGTGT TGAT TGAGGTCGGACCCACTG
A
GAM2071 371 FLJ1258 1 13509 NP_078896.2 5 37 GCTGTCTCACCC 3 B b b
6 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAC TGACGTGAGGTCGGACCCACT

GAM2071 371 FLJ1274 1 8373 XP_290972.1 3 2539 CTCTTGTCACCC AC----- 3 B c c
7 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGC ACGTGAGGTCGGACCCACTG
CGCGGTA
GAM2071 371 FLJ1288 1 1302 NP_079221.1 3 240 GCTCTGTTGCCC C TG 3 B c c
8 AGGCTAGAGTGC ACTGCACTC AGTCTGGG AC
AGTGGCAT TGACGTGAG TCGGACCC TG
A GT
GAM2071 371 FLJ1289 1 13646 NP_079226.1 3 1549 GTTGTGTCACCC C GT 3 B c c

1 AGGTTAGAGTGT ACTGCACTC A CTGGGTGAC
AGTGGCGC TGATGTGAG T GACCCACTG
A TG
GAM2071 371 FLJ1290 1 4783 NP_073590.1 3 224 CCAGCGTCTCCC C TCC- T 3 B c
c
3 AGACTTCTCGTA ACTG AC AGTCTGGG GAC
CAGTTAAT TGAC TG TCAGACCC CTG
A CTCT T
GAM2071 371 FLJ1296 1 3109 NP_078914.1 3 1534 GCTCTGTCGCCC 3 B b b
0 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FLJ1297 1 836 NP_079085.2 3 354 TCTCTGTCACCC 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGCACA TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ1307 1 6870 XP_117117.2 3 697 GCTCTGTCGGCC G 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCAT TGACGTGAGGTCGGACC GCTG
G
GAM2071 371 FLJ1308 1 3389 NP_079110.1 3 1858 CGCCCAGGCAGC CA------- A 3 B c
c
1 GGAATAGAGTGC ACTGCACTC GTCTGGGTG
AGTGCTTG TGACGTGAG CGGACCCGC

ATAAGGCGA -

GAM2071 3718 FLJ1318 1 12816 NP_071346.1 3 413 GCTCTGTCACCC C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTAGCAC TGACGTGAG TCGGACCCACTG
A

GAM2071 3717 FLJ1319 1 7946 NP_078890.1 3 402 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT

GAM2071 3716 FLJ1345 1 5409 XP_038291.5 3 2587 ACTCTGTCGCCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGCAC TGACGTGAGGTC ACCCGCTG
GA

GAM2071 3710 FLJ1359 1 6935 NP_079116.2 5 97 CCCCGCAAAATC C ---- A 3 B c c
AGGCTTGAGTGC ACTGCACTC AGTCTGG GTG
AGTGGCGC TGACGTGAG TCGGACT CGC
T AAAA C

GAM2071 3719 FLJ1363 1 1788 NP_078981.1 3 962 ATAGGCCAACCC CCA GA 3 B c c
AGACACAGTGCG ACTGCACT GTCTGGGT
GTACCAGA TGGCGTGA CAGACCCA
CA- AC

GAM2071 3714 FLJ1398 1 16972 NP_079046.1 5 244 ACTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGATCCACTG

GAM2071 3711 FLJ1435 1 8244 NP_079008.1 3 316 GCTTTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAG TGACGTGAGGTCGGACCCGCTG

GAM2071 3711 FLJ1464 1 18641 NP_116206.1 3 1412 GCCACTGCACTC A---- - T - A 3 B c c
CAGCTGGAGTGA CTG CACTCCAG CTGG GTG
CAGAGCCA GAC GTGAGGTC GACC CAC
ACCGA A - T G

GAM2071 3713 FLJ1480 1 3409 NP_116231.1 3 434 CTCTGTCAACGC G - 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTG GT GAC
AGTGGCAC TGACGTGAGGTCAGAC CA CTG
G A

GAM2071 3715 FLJ2004 1 19070 NP_060108.1 3 131 GCTTTGTTTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC TTG
T

GAM2071 3715 FLJ2009 1 13800 NP_060136.1 3 1357 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 3714 FLJ2034 1 8639 NP_060246.1 3 704 GCTCTGTCATCC C 3 B b b
AAACTGGAGTGC ACTGCACTCCAGT TGGGTGAC
AGTGGCAC TGACGTGAGGTCA ACCTACTG

A

GAM2071 371 FLJ2050 1 12154 NP_060319.1 3 2327 GCTCTGTCACCC AC----- 3 B c c

7 GGGCTGGAGTGT TGCACTCCAGTCTGGGTGAC
AACGTGGC ATGTGAGGTCGGGCCCACTG
CGGTGCA

GAM2071 371 FLJ2051 1 969 NP_060323.1 3 675 CTCTTGTCACCC 3 B b b

1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ2067 2 10861 NP_060394.1 3 1538 GGTCTGTTGCCC TG 3 B b b

1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 FLJ2067 2 13745 NP_060394.1 3 629 GGTTGTCACTTA T - 3 B c b

1 AGTTTGGAGTGC ACTGCACTCCAG CT GGGTGAC
AGTGGCAT TGACGTGAGGTT GA TTCACTG
T A

GAM2071 371 FLJ2070 1 20156 NP_060402.1 3 423 GCTCTCTCGCCC 3 B b b

0 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGTGC TGACGTGAGGTCGGACCCGCT

GAM2071 371 FLJ2081 1 18464 NP_060431.1 3 95 ACTCTTTCACCC 3 B b b

3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAC TGACGTGAGGTCGGACCCACT

GAM2071 371 FLJ2160 1 11662 NP_079038.1 3 481 GCTCTGTCACCC C 3 B b b

3 AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAT TGAC TGAGGTCGGACCCACTG
A

GAM2071 371 FLJ2167 1 1926 NP_112160.1 5 801 CTTCTGTCACCT 3 B b b

3 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGACAT TGATGTGAGGTCGGATCCACTG

GAM2071 371 FLJ2177 1 13303 NP_115585.1 3 784 CTTGTGTCACCC AC----- 3 B c c

7 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGC ACGTGAGGTCGGACCCACTG
CGCGGTA

GAM2071 371 FLJ2216 1 2733 NP_078809.2 5 475 CACTCTTCACTC C 3 B b b

7 AGGCTGCAGTGC ACTGCACT CAGTCTGGGTGA
AGTGGCGC TGACGTGA GTCGGACTCACT
C

GAM2071 371 FLJ2232 1 10803 NP_078932.2 3 527 TCTCTGTCACCC 3 B b b

9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ2253 1 3548 NP_078926.2 5 341 ACTCTGTTACCC A 3 B b b

1 AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCGC TGACGTGAGG CGGACCCATTG
C

GAM2071 371 FLJ2296 1 9754 NP_071384.1 3 231 GCTCTTTCGCCC GT 3 B b b
5 AGGATGGAGTGC ACTGCACTCCA CTGGGTGA
AGTGGTGC TGACGTGAGGT GACCCGCT
AG
GAM2071 371 FLJ2302 1 541 NP_079327.1 3 339 GGGTCAGTCTCC C C T 3 B c c
2 AAACTGGAGTTT ACTG ACTCCAGT TGGG GAC
GGTGGCTA TGGT TGAGGTCA ACCT CTG
T A -
GAM2071 371 FLJ2304 1 12648 NP_079450.1 3 111 GCTCCATCACCC CA TC 3 B c
c
0 AAGCCAGAGTGC ACTGCACTC G TGGGTGA
AGTGGTGA TGACGTGAG C ACCCACT
AC GA
GAM2071 371 FLJ2305 1 16973 NP_075058.1 3 211 GCTCTATTGCCC TG 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCTC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 FLJ2318 1 10010 NP_078892.1 3 367 CGTTCTGTCGCT T 3 B b b
6 TAGCTGGAGTGC ACTGCACTCCAG CTGGGTGAC
GGTGGCGT TGGCGTGAGGTC GATTCGCTG
-
GAM2071 371 FLJ2326 1 13801 NP_079391.1 5 181 ACTCTGTCGCCC 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FLJ2335 1 14440 NP_115613.1 3 240 GCTCTGTTGCTG G TG 3 B c c
6 AGGCTGGAGTGC ACTGCACTCCAGTCT GG AC
AGTGATGT TGACGTGAGGTCGGA TC TG
G GT
GAM2071 371 FLJ2339 3 431 NP_079060.1 3 196 ACTCTGTCACCC 3 B b b
2 AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCAGACCCACTG

GAM2071 371 FLJ2339 3 4022 NP_079060.1 3 606 ACTCTGTCCCCC T 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGC TGACGTGAGGTCGGACCC CTG
C
GAM2071 371 FLJ2339 3 11425 NP_079060.1 3 496 GCTCTGTCACTG G 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCT GGTGAC
AGTGGCGC TGACGTGAGGTCGGA TCACTG
G
GAM2071 371 FLJ2341 1 4771 NP_115614.1 3 1322 CCTCTGTTGCCC TG 3 B b b
6 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 FLJ2355 2 436 NP_079156.1 3 424 GCTCTGTCGCCC 3 B b b
6 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FLJ2355 2 6906 NP_079156.1 3 721 GCTCTGTCACCC C- 3 B b b

6 AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
CGGTGGTG TGGC TGAGGTCGGACCCACTG
CA
GAM2071 371 FLJ2383 1 14133 NP_689963.1 3 763 TTAACATCACCC CACTCC 3 B c c
4 AGATTTCTTCAG ACTG AGTCTGGGTGA
TTATAAAT TGAC TTAGACCCACT
TTCT--
GAM2071 371 FLJ2541 1 8998 NP_659455.2 5 106 GCTCTGTCACCC ACT----- 3 B c c
6 AGGCTGGAGTGC GCACTCCAGTCTGGGTGAC
CATGGCAT CGTGAGGTCGGACCCACTG
TACGGTAC
GAM2071 371 FLJ2579 1 18075 NP_689633.1 3 562 GCTCTGTCTCCC A T 3 B b b
5 AGGCCGGAGTGC ACTGCACTCC GTCTGGG GAC
AGTGGCAC TGACGTGAGG CGGACCC CTG
C T
GAM2071 371 FLJ3113 2 1817 NP_775928.1 3 690 CTCTTGTCACCC A 3 B b b
9 AGGCAGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCGT TGACGTGAGG CGGACCCACTG
A
GAM2071 371 FLJ3113 2 7279 NP_775928.1 5 144 CCTCTCTGGCCC TC GA 3 B c b
9 AAGCTGGAGTGC ACTGCACTCCAG TGGGT
AGTGGCAC TGACGTGAGGTC ACCCG
GA GT
GAM2071 371 FLJ3115 1 13799 NP_653201.1 3 274 GCTCTGTCACCC 3 B b b
3 AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCAGACCCACTG
GAM2071 371 FLJ3140 1 11498 NP_689877.1 3 350 GCTCTGTTGGCC G 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGTTCG TGACGTGAGGTCGGACC GTTG
G
GAM2071 371 FLJ3195 1 12975 NP_694575.1 3 1478 ACTCTGTCACCC A----- 3 B c c
8 AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGCAGTTG GACGTGAGGTCGGACCCACTG
GTTGAC
GAM2071 371 FLJ3197 1 10814 NP_653270.1 3 95 TTCTGGATCACG CCA G 3 B c c
8 TGGGCCCAGTGC ACTGCACT GTCTG GTGA
AGTTCAAA TGACGTGA CGGGT CACT
CC- G
GAM2071 371 FLJ3213 2 9100 NP_689671.2 3 518 GCTCTGTCGCCC 3 B b b
0 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG
GAM2071 371 FLJ3213 2 17307 NP_689671.2 3 1142 TCTCTGTTGCCT TG TG 3 B c b
0 GGGCTGGAGTGC ACTGCACTCCAGTC GG AC
AGTGGCCC TGACGTGAGGTCGG CC TG

GT GT

GAM2071 371 FLJ3249 1 2883 NP_653208.1 3 743 GCTCTGTCACCC T 3 B b b
9 AGTCTGGAGTGC ACTGCACTCCAG CTGGGTGAC
AGTGGCAA TGACGTGAGGTC GACCCACTG
T

GAM2071 371 FLJ3280 1 7824 NP_694584.1 3 642 ACTCTGTCACCC 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGA TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ3286 1 19864 NP_653214.1 3 1247 CTCTTGTCACCC AC----- C 3 B c
c
5 AGGCTGGAGTAC TG ACTCCAGTCTGGGTGAC
AATGATGC AC TGAGGTCGGACCCACTG
CGTAGTA A

GAM2071 371 FLJ3289 1 3716 NP_653268.1 3 703 ACTCTGTTGTCC A----- TG 3 B c c
4 AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGCGATAT GACGTGAGGTCGGACCT TG
TATAGC GT

GAM2071 371 FLJ3293 1 4748 NP_690873.1 3 603 GCTCTGTCACCC 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGCTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ3350 1 2450 NP_689530.1 3 740 ACACTGTTGCCC TG 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGACGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 FLJ3491 1 13154 NP_694995.1 3 1245 TGTGATTCACCC - TC - 3 B b b
7 AGATCTGTTGTG ACTG CAC CAG TCTGGGTGA
CCAGTTAG TGAC GTG GTC AGACCCACT
C TT T

GAM2071 371 FLJ3492 1 14214 NP_689483.1 5 151 ACTTTGACCCCC TGA 3 B c c
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
CCA

GAM2071 371 FLJ3510 1 6840 NP_689890.1 5 160 GCTCTGTCGTCC T GT 3 B c c
5 AGGCTGGAGTGC AC GCACTCCAGTCTGG GAC
CGTGGCGT TG CGTGAGGTCGGACC CTG
C TG

GAM2071 371 FLJ3528 1 7525 NP_689915.1 3 70 ATCACCTTACCA CCAG ------- 3 B c c
3 TCAGAGCAGTGC ACTGCACT TCTG GGTGA
AGTGCTCT TGACGTGA AGAC CCACT
CG-- TACCATT

GAM2071 371 FLJ3548 1 7675 NP_776181.1 3 521 ATTCTGTCACTC C TC 3 B c c
7 AAGCTGTAGTGC ACTGCACT CAG TGGGTGAC
AGTGGTGC TGACGTGA GTC ACTCACTG
T GA

GAM2071 371 FLJ3568 1 3105 NP_787096.1 3 1070 ACTCTGTCACCC 3 B b b
1 AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCAGACCCACTG

GAM2071 371 FLJ3584 1 12720 XP_290755.1 3 1061 ACTTTGTCACCC C 3 B b b
8 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAT TGACGTGAG TCGGACCCACTG
A
GAM2071 371 FLJ3603 1 17613 XP_290874.1 5 18 CTCCACACACCC G AG- A 3 B c c
2 AGAGAAGGAGTG ACT CACTCC TCTGGGTG
GGGTGGGG TGG GTGAGG AGACCCAC
G AAG A
GAM2071 371 FLJ3644 1 10632 NP_694965.1 3 230 ACTCTGTCACCC 3 B b b
5 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGATGTGAGGTCGGACCCACTG
GAM2071 371 FLJ3707 1 3106 NP_694588.1 5 42 ACTCTGTCACCC 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG
GAM2071 371 FLJ3743 1 18178 NP_848612.1 3 197 GCTCTGTTACCC 3 B b b
3 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGATGTGAGGTCGGACCCATTG
GAM2071 371 FLJ3754 1 435 NP_775938.1 3 743 GCTCTGTTGCCC TG 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 FLJ3794 1 7849 NP_848629.1 3 1269 ATACTTTTATAT - TGG 3 B c c
0 GATTGGCAGTGC ACTGCACT CCAGTC GTGA
AGTAAGTT TGACGTGA GGTTAG TATT
C TA-
GAM2071 371 FLJ3814 4 2644 XP_091919.5 5 25 CCTCTATTGCCC TG 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTGT TGACGTGAGGTCGGACCC T
GT
GAM2071 371 FLJ3814 4 6194 XP_091919.5 3 902 TACCCGTCACCC ACT GTC 3 B c
b
9 AAGTGGTAGTAG ACTGC CCA TGGGTGAC
TCTCTTAT TGATG GGT ACCCACTG
AT- GA-
GAM2071 371 FLJ3814 4 11661 XP_091919.5 3 1431 ACTCTGTTGCCC TG 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 FLJ3814 4 12581 XP_091919.5 3 258 ACTCTGTCTCCC T 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGAGT TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 FLJ3828 2 17962 NP_689814.1 3 1965 GCTCTGTCGCCC 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FLJ3828 2 19457 NP_689814.1 3 109 ACTCTGTTGCCC T TG 3 B c b
1 TGGCTGGAGTGC ACTGCACTCCAGTC GGG AC
AGTAGAGT TGACGTGAGGTCGG CCC TG
T GT
GAM2071 371 FLJ3860 2 3109 NP_689867.1 3 287 GCTCTGTCGCCC 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FLJ3860 2 18917 NP_689867.1 3 543 TCTCTGTCACCC AC----- 3 B c b
7 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGC ACGTGAGGTCGGACCCACTG
CGCGGTA
GAM2071 371 FLJ3870 1 6867 NP_776193.1 3 629 GCTTCTCTCCTC - CT- T 3 B c c
5 CTGCTGGAGTGC ACTG CACTCCAGT GGG GA
CAGTCCCT TGAC GTGAGGTCG TCC CT
C TCC T
GAM2071 371 FLJ3879 1 18182 NP_848615.1 3 1161 GCTCTGTCACCC 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ3881 1 3726 NP_665872.1 3 1040 GCTCTGTCACTC C 3 B b b
9 ATGCTGGAGTGC ACTGCACTCCAGT TGGGTGAC
AGTGGCGT TGACGTGAGGTCG ACTCACTG
T
GAM2071 371 FLJ3899 2 5383 NP_776188.1 3 730 ACTGTGTCACCC 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ3899 2 7191 NP_776188.1 3 1036 TCTCTGTCACCT 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 FLJ3941 1 17781 NP_775952.1 3 341 GGTCTTTCACCC 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGCTGT TGACGTGAGGTCGGACCCACT

GAM2071 371 FLJ3942 1 5369 NP_775880.1 5 423 ACTCTGTCACCC AC----- A 3 B c c
6 AGGCTGGAGAGC TGC CTCCAGTCTGGGTGAC
AATTGCAC ACG GAGGTCGGACCCACTG
CACGTTA A
GAM2071 371 FLJ3959 1 7948 NP_776164.1 3 1103 GCTCTGTCACCC 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 FLJ3963 2 7663 XP_290687.1 3 1661 GCACCAAGAACA ------ G A 3 B c b
9 ATGCTGGAGTGC ACTGCACTCCAGT CT GGTG
AGTGGCGT TGACGTGAGGTCG GA CCAC
TAACAA A G
GAM2071 371 FLJ3963 2 13371 XP_290687.1 3 681 GCTCTGTCGTCC GT 3 B b b

9 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTGGCGC TGACGTGAGGTCGGACC CTG
TG

GAM2071 371 FLJ3982 2 8171 NP_775971.1 3 1941 TCACTGTTATCC A----- 3 B c b
1 AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGAGGCAC GACGTGAGGTCGGACCTATTG
CACGGA

GAM2071 371 FLJ3982 2 14284 NP_775971.1 3 611 GCTCTGTCACCT C 3 B b b
1 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGTGC TGACGTGAG TCGGATCCACTG
A

GAM2071 371 FLJ9023 1 18854 NP_775852.1 3 73 ACTTTGTCGCCC 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FLJ9072 1 16986 NP_787115.1 3 524 GCTCTGTCGCCC 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGCCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 FNBP1 1 8560 XP_052666.3 3 1011 GCTCTATTGTTC TG 3 B c c
AGACTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCAT TGACGTGAGGTCAGACTT T
GT

GAM2071 371 FSHPRH1 1 13800 NP_006724.1 5 14 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 FUT1 2 3102 NP_000139.1 3 612 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 FUT1 2 7472 NP_000139.1 3 934 GCTCTGTAGCCC CA GA 3 B c b
AGGCCAGAGTGC ACTGCACTC GTCTGGGT
AGTGGCGC TGACGTGAG CGGACCCG
AC AT

GAM2071 371 G1P3 1 14496 NP_002029.3 3 135 ACTATATTGTCC C TG 3 B c c
AGGCTAGAGTGC ACTGCACTC AGTCTGGG A
AGTGGCTA TGACGTGAG TCGGACCT T
A GT

GAM2071 371 G1P3 1 14496 NP_075010.1 3 135 ACTATATTGTCC C TG 3 B c c
AGGCTAGAGTGC ACTGCACTC AGTCTGGG A
AGTGGCTA TGACGTGAG TCGGACCT T
A GT

GAM2071 371 G1P3 1 14496 NP_075011.1 3 135 ACTATATTGTCC C TG 3 B c c
AGGCTAGAGTGC ACTGCACTC AGTCTGGG A
AGTGGCTA TGACGTGAG TCGGACCT T
A GT

GAM2071 371 G6PC 1 8902 NP_000142.1 3 1428 CACCTATCACCC G 3 B b b
AGGCTGGAGTGG ACT CACTCCAGTCTGGGTGA
AGTGGCAC TGA GTGAGGTCGGACCCACT

G
GAM2071 371 GAL3ST-4 1 13405 NP_078913.3 3 251 GCTCTGTCCCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAT TGACGTGAGGTCGGACCC CTG
C
GAM2071 371 GBP4 1 12569 NP_443173.2 3 1417 GCTTTGACACCC A 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTAGCAC TGACGTGAGGTCGGACCCAC
A
GAM2071 371 GDEP 1 14396 NP_477516.1 3 163 CCTGTCAGTCCT TGC C -- 3 B c c

ATACTGGAGTCC AC ACTCCAGT TGGG TGAC
TGTTAATA TG TGAGGTCA ATCC ACTG
TCC T TG
GAM2071 371 GGA2 1 520 NP_055859.1 3 1711 ACTCTGTCACTC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGTAT TGGCGTGAGGTCGGACTCACTG

GAM2071 371 GGA2 1 520 NP_619581.1 3 2799 ACTCTGTCACTC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGTAT TGGCGTGAGGTCGGACTCACTG

GAM2071 371 GM2A 2 2518 NP_000396.1 3 761 CGCTTTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 GM2A 2 17118 NP_000396.1 3 1146 TAAGGGTGGCAG C GG G 3 B c b

GGACTGGAGTCA ACTG ACTCCAGTCT GT AC
GTTGGAGA TGAC TGAGGTCAGG CG TG
- GA G
GAM2071 371 GNE 1 7151 NP_005467.1 3 616 GGCATGAACCCC TGA 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG
AGTGGCTC TGACGTGAGGTCGGACCC
CAA
GAM2071 371 GNG4 1 11336 NP_004476.1 3 607 GCTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCGGACCCACTG
TGCGGTA
GAM2071 371 GNPNAT1 1 19027 XP_085119.1 3 2470 ACTCCATCACCC C 3 B b b

AGGCTGGAGTCC ACTG ACTCCAGTCTGGGTGA
AGTGGTGT TGAC TGAGGTCGGACCCACT
C
GAM2071 371 GNRPX 1 17848 NP_060519.1 3 146 ACTGTGTTGCCC C TG 3 B c c

AGGCTAGAGTGC ACTGCACTC AGTCTGGG AC
AGTGGTGC TGACGTGAG TCGGACCC TG
A GT
GAM2071 371 GOLGA3 1 9100 NP_005886.2 3 600 GCTCTGTCGCCC 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 GPR128 1 6503 NP_116176.1 5 221 TATTTCTCACCC TG C- G- 3 B c c

AGGAGTGGATTT AC CA TCCA TCTGGGTGA
GTGGTTTG TG GT AGGT GGACCCACT
GT TT GA

GAM2071 371 GPR4 2 15917 NP_005273.1 3 284 GCCCAGGCTGGA GA 3 B c b
GTGCAGTAGTGC ACTGCACTCCAGTCTGGGT
AGTCGTGG TGACGTGAGGTCGGACCCG
--

GAM2071 371 GPR4 2 16936 NP_005273.1 3 280 ACTGTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTAGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 GPR56 1 6235 NP_005673.2 5 24 GCTCTGTCACAC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
AGTGGTGT TGACGTGAGGTCGGAC CACTG
A

GAM2071 371 GPR66 1 4149 NP_006047.2 3 529 ACTCTGTCGCCC C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCGC TGACGTGAG TCGGACCCGCTG
A

GAM2071 371 GPR81 1 9012 NP_115943.1 3 374 ACTCTGTGTCCC TGA 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG
AGTGGCAC TGACGTGAGGTCGGACCC
TGT

GAM2071 371 GR6 1 11621 NP_031380.1 5 286 GCTCTGTCACCC C 3 B b b
AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC
AGTGGCAT TGACGT AGGTCGGACCCACTG
A

GAM2071 371 GRAF 1 18118 NP_055886.1 3 2800 ACTCTGTGGCCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCGC TGACGTGAGGTCGGACCCG TG
G

GAM2071 371 GREB1 1 18182 NP_055483.2 3 1091 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 GRINL1A 1 17379 NP_056347.1 3 712 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAG TGACGTGAGGTCGGACCCGCTG

GAM2071 371 GRM6 1 5942 NP_000834.1 3 2443 GCTCAATTTCTT ---- 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG TGA
AGTGGCAC TGACGTGAGGTCGGATTC ACT
TTTA

GAM2071 371 GRWD 1 6811 NP_113673.2 3 372 GGTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC

AGTAGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 GSDM 2 3037 NP_835465.1 3 295 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCTT TGACGTGAGGTCGGACCCACTG

GAM2071 371 GSDM 2 13197 XP_209009.1 3 293 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCTT TGACGTGAGGTCGGACCCACTG

GAM2071 371 GTF2IRD 1 3107 NP_115579.3 3 142 GCTCTGTCGCCC GT 3 B b b
2 AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCGT TGACGTGAGGT GACCCGCTG
TG
GAM2071 371 GTF2IRD 1 3107 NP_775808.1 3 142 GCTCTGTCGCCC GT 3 B b b
2 AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCGT TGACGTGAGGT GACCCGCTG
TG
GAM2071 371 GTPBG3 2 7742 NP_116009.1 3 466 TGTCTATTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTGC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 GTPBG3 2 15596 NP_116009.1 3 630 GCTCTGTCACCC C 3 B b b
AGGCTGGAGTTC ACTG ACTCCAGTCTGGGTGAC
AGTGGTGC TGAC TGAGGTCGGACCCACTG
T
GAM2071 371 H-plk 1 8288 NP_056936.1 5 982 TGCTGTGTCACC G G 3 B b b
AGGATGGAGTGC ACTGCACTCCA TCT GGTGAC
AGTGGCAT TGACGTGAGGT AGG CCACTG
- A
GAM2071 371 H2AV 1 11005 NP_619541.1 3 584 TTCTTGTCACCC AC----- 3 B c c
AGACTGGAGTGC TGCACTCCAGTCTGGGTGAC
GATGGCAC GCGTGAGGTCAGACCCACTG
CACGGTA
GAM2071 371 HECA 1 6145 NP_057301.1 3 1529 CTCTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 HEMK 1 12517 NP_057257.1 3 1819 GGATGTTGCACC CAG - TG 3 B c
c
AGAAGAGAGTGC ACTGCACTC TCTGG G AC
AGTGTTGG TGACGTGAG AGACC C TG
AGA A GT
GAM2071 371 HIP1R 1 4431 XP_290592.1 3 704 GCGCTGCCTTCA G TCT 3 B c c
CTCCTGGAGTGA ACT CACTCCAG GGGTGA
GTTTCCAT TGA GTGAGGTC CTCACT
- ---
GAM2071 371 HLCS 1 10628 NP_000402.2 5 179 GTTCTGTCGTCC GT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTGGTGT TGACGTGAGGTCGGACC CTG

TG
GAM2071 371 HMG20A 1 19141 NP_060670.1 3 1221 GCTGTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
GGTGGCTA TGGCGTGAGGTCGGACCC TG
GT
GAM2071 371 HRH4 2 5920 NP_067637.2 3 1416 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 HRH4 2 12079 NP_067637.2 3 1949 GCTCTGTTGCCC A C TG 3 B c b
ACGCAGGAGTGC ACTGCACTCC GT TGGG AC
AGTGGCAT TGACGTGAGG CG ACCC TG
A C GT
GAM2071 371 HS3ST4 1 2420 XP_056254.4 3 105 CTGCAGCTTCAC -- CT 3 B c c
TTGCTGGAGTGC ACT GCACTCCAGT GGGTGA
CAAGTAGA TGA CGTGAGGTCG TTCACT
AC --
GAM2071 371 HSA2508 1 588 NP_060871.1 3 1359 CTTCACTCACCC CACTC-- 3 B c c
39 AGCAGGTCAGTT ACTG CAGTCTGGGTGA
TTCTGTGC GTCT GGACGACCCACT
TTTGACT
GAM2071 371 HSD3B7 1 16293 NP_079469.2 3 209 GCTCTGTCACCC 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCAGACCCACTG

GAM2071 371 HSNOV1 1 1150 NP_059985.2 3 599 TATACAAGCATT CTG A 3 B c c

AAACTGGAGTGC ACTGCACTCCAGT GGTG
AGTAAACC TGACGTGAGGTCA TTAC
AA- G
GAM2071 371 HSPC065 2 7511 NP_054876.2 3 2125 TCTCTGTCCCCA - T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGG GAC
AGTGGTGC TGACGTGAGGTCGGA CCC CTG
A -
GAM2071 371 HSPC065 2 10877 NP_054876.2 3 2292 GCTCTGTCCCCC C T 3 B b b
ATGCTGGAGTGC ACTGCACTCCAGT TGGG GAC
AGTGGCAT TGACGTGAGGTCG ACCC CTG
T C
GAM2071 371 HTR1D 1 14604 NP_000855.1 3 290 TGCCCTCTCGCC G 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGG TGA
AGTGGCAC TGATGTGAGGTCGGACC GCT
-
GAM2071 371 HTR1E 1 9063 NP_000856.1 5 137 TCTCAGTCGCCC A----- 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGCAGCAC GACGTGAGGTCGGACCCGCTG
CACGAC

GAM2071 371 HUNK 1 1413 NP_055401.1 3 2962 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 HUS1 1 11161 NP_004498.1 3 1023 ATTCTGTCACCC 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGCCAC TGACGTGAGGTCAGACCCACTG

GAM2071 371 HYAL4 1 19431 NP_036401.1 5 82 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGATGTGAGGTCGGACCC TG
GT
GAM2071 371 HYPC 1 10529 NP_036404.1 3 205 GTCCCCTACTCC CC TG T 3 B c
c
CTGGACTAGTGC ACTGCACT AGTC GG GA
AGTCCTTG TGACGTGA TCAG CC CT
-- GT -
GAM2071 371 ICAM1 1 18182 NP_000192.1 3 1134 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 ICK 1 3106 NP_055735.1 3 1469 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 ICK 1 3106 NP_057597.2 3 1469 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 IGF1 1 8230 NP_000609.1 3 5347 GCACTGTCCCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAT TGACGTGAGGTCGGACCC CTG
C
GAM2071 371 IL11 2 6919 NP_000632.1 3 599 GGTCGGTCACCC A A ------- 3 B c b
AGACAGCTCTGT CTGC CTCCA GTCTGGGTGAC
GGAGGCAG GACG GAGGT CAGACCCACTG
- - GTCTCGA
GAM2071 371 IL11 2 17785 NP_000632.1 3 699 GCTCTGTTGCCT TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGAGGC TGACGTGAGGTCGGATCC TG
GT
GAM2071 371 IL20RA 1 9137 NP_055247.2 3 278 TAAATGTTTGCC A------ T GT 3 B c c
AGACTGGGTGCA CTGCAC CCAGTCTGG GAC
GAATTTAT GACGTG GGTCAGACC TTG
TATTTAA - GT
GAM2071 371 IL28RA 1 17486 NP_734464.1 3 2267 TTCTTTTTGCCT TG 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTAC TGACGTGAGGTCGGATCC T
GT
GAM2071 371 IL28RA 1 17486 NP_775087.1 3 2267 TTCTTTTTGCCT TG 3 B c c

AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTAC TGACGTGAGGTCGGATCC T
GT

GAM2071 371 IL28RA 1 17486 NP_775088.1 3 2964 TTCTTTTTGCCT TG 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTAC TGACGTGAGGTCGGATCC T
GT

GAM2071 371 IMPACT 1 19846 NP_060909.1 3 2006 GCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGATCCACTG

GAM2071 371 INHBE 1 9633 NP_113667.1 3 663 CGCTCTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGACAC TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 INMT 2 1421 NP_006765.3 3 444 GCTCTGTCACCC AC----- C 3 B c b
AGGCTAGAGTGC TGCACTC AGTCTGGGTGAC
AATGGCAC ACGTGAG TCGGACCCACTG
CACGGTA A

GAM2071 371 INMT 2 3109 NP_006765.3 3 621 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 IPO13 1 6877 NP_055467.1 5 252 GAGAGCTCACCC T A 3 B c c
AGGCGGGGGTGT AC GCACTCC GTCTGGGTGA
TGTGGGTA TG TGTGGGG CGGACCCACT
T G

GAM2071 371 IRF4 1 16311 NP_002451.1 3 101 GCTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGACAC TGACGTGAGGTCGGACCC CTG
T

GAM2071 371 ITGAL 1 17682 NP_002200.1 3 417 GCACACTCCCCT C CT- T 3 B c c
GCACTGGAGTCC ACTG ACTCCAGT GGG GA
AGTCTCTT TGAC TGAGGTCA CCC CT
C CGT -

GAM2071 371 ITGAX 1 11336 NP_000878.1 3 395 GCTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCGGACCCACTG
TGCGGTA

GAM2071 371 JAK3 1 6262 NP_000206.1 3 400 CGCTCGTTACCC G 3 B b b
AGGGTGGAGTGC ACTGCACTCCA TCTGGGTGAC
AGTGGTAG TGACGTGAGGT GGACCCATTG
G

GAM2071 371 JM11 1 15361 NP_296375.1 3 1439 TGCTCTGTCACC A----- G 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCTGG TGAC
AGCGGCGC GACGTGAGGTCGGACC ACTG
CGCGGC -

GAM2071 371 JRK 1 1529 NP_003715.1 3 1241 ACTCTGTTGACC G GT 3 B c c
AGGCTGGAGTGA ACT CACTCCAGTCTGG GAC
AGTGGTGT TGA GTGAGGTCGGACC TTG

A AG
GAM2071 371 KCNA5 1 18957 NP_002225.2 3 31 GGAGATTCAGGC ACT GG 3 B c c
AGACTGGTGGCA ACTGC CCAGTCTG TGA
GTGGAGTA TGACG GGTCAGAC ACT
GT- GG
GAM2071 371 KCNE3 1 6918 NP_005463.1 3 962 CCTATGTCACCC TC 3 B b b
AGGCTGTGGTGC ACTGCAC CAGTCTGGGTGAC
AGTAAGCC TGACGTG GTCGGACCCACTG
GT
GAM2071 371 KCNJ11 1 9100 NP_000516.2 5 52 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 KENAE 1 18180 NP_789786.1 3 210 GCTCTGTCACCC GT 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGTGT TGACGTGAGGT GACCCACTG
TG
GAM2071 371 KIAA005 1 16223 NP_055697.1 3 464 TTTGAGTCCTCA T GTC 3 B c c
3 TCCATGGAGTGC AC GCACTCCA TGGGTGA
TGTGTTTG TG CGTGAGGT ACCTACT
T ---
GAM2071 371 KIAA008 1 14875 NP_055584.1 3 2189 ATTCTGTCACCC 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 KIAA011 1 1353 XP_290939.1 3 247 CTGTTGTCTCCC T 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGT TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 KIAA018 1 6841 NP_066545.1 3 1107 GTTCTGTCACCC 3 B b b
6 AGGCTGGGGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGGGGTCGGACCCACTG

GAM2071 371 KIAA020 1 17371 NP_055688.1 3 1257 ACTCTGTCACCC C 3 B b b
5 AGGCTGTAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGCAT TGACGTGA GTCGGACCCACTG
T
GAM2071 371 KIAA035 1 12671 XP_290667.1 3 2510 CCCACCTCACCC ACTCC - 3 B c c
0 AGGTCTCAGCGG ACTGC AG TCTGGGTGA
CAGTGGGC TGACG TC GGACCCACT
GCGAC T
GAM2071 371 KIAA043 1 14441 NP_055616.1 5 676 GCTCTGTCACCC T 3 B b b
5 AGTTTGGAGTGC ACTGCACTCCAG CTGGGTGAC
AGTGGTGC TGACGTGAGGTT GACCCACTG
T
GAM2071 371 KIAA044 1 20115 XP_044155.1 5 2279 TCACTGTCTCCT T 3 B b b
6 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC

AGTGGTGT TGACGTGAGGTCGGATCC CTG
T
GAM2071 371 KIAA045 1 3442 XP_027862.1 3 3703 GCTTTGTTGCCC TG TG 3 B c c
9 AGGCTGGAGTGT AC CACTCCAGTCTGGG AC
GGTGGGGC TG GTGAGGTCGGACCC TG
GT GT
GAM2071 371 KIAA046 2 1413 NP_055666.1 3 701 GCTCTGTCACCC 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 KIAA046 2 14283 NP_055666.1 3 349 GCTCTGTCACCC 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 KIAA047 1 16265 NP_055672.1 5 287 AATTCCCACCAC - CT - A 3 B c c
1 AGACTGGCTTGT AC TGCA CCAGTCTG GGTG
ACGTCCTC TG ATGT GGTCAGAC CCAC
C TC A C
GAM2071 371 KIAA047 1 7946 NP_055679.1 3 1230 ACTCTGTTGCCC TG 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA047 1 11512 NP_055685.1 3 2195 GCTCTGTCACCC CAC 3 B b
b
8 AGACTGGAACAC ACTG TCCAGTCTGGGTGAC
AGTGGCAC TGAC AGGTCAGACCCACTG
ACA
GAM2071 371 KIAA049 1 6597 XP_034717.1 5 925 GCTCTCTTACCC TC 3 B b b
3 AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGACAT TGACGTGAGGTC ACCCATT
GA
GAM2071 371 KIAA049 1 5452 XP_031397.1 3 2801 GCCCTGTCACCC AC----- 3 B c c
5 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCGGACCCACTG
CGTGGTA
GAM2071 371 KIAA051 3 7613 NP_055547.1 5 89 GCTGTATTTCCC A----- T 3 B c b
3 AGGCTGGAGTGC CTGCACTCCAGTCTGGG GA
AGAGGCAC GACGTGAGGTCGGACCC TT
CACGGA T
GAM2071 371 KIAA051 3 11210 NP_055547.1 3 3673 CTCTTGTTGCCC TG 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGACAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA051 3 12742 NP_055547.1 3 4832 GGGTGTCTCTAG -- T T 3 B c b
3 CCTGCAGAGTGC ACTGCACTC CAG CTGGG GAC
AGTGAGTG TGACGTGAG GTC GATCT CTG
AC C -
GAM2071 371 KIAA052 1 19044 XP_171054.1 3 364 ATGCTGTTGCCC TG 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

AGTGTCCC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA053 1 483 XP_047659.6 3 1244 ATTCTGTCACCC C C 3 B b b
2 AGGCTAGAGTAC ACTG ACTC AGTCTGGGTGAC
AGTGGGAA TGAC TGAG TCGGACCCACTG
A A
GAM2071 371 KIAA055 1 16200 XP_085507.1 3 2605 ACTTCATTACCC AC----- 3 B c c
7 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
AAGGCACG ACGTGAGGTCGGACCCATT
GCACGGA
GAM2071 371 KIAA056 2 11513 XP_038150.2 3 1670 CCACGATCACCC A-- ---- A T 3 B c
c
1 AGCAGGAGTCGT CTGC ACTCC G CTGGGTGA
GGCAGAAC GACG TGAGG C GACCCACT
CAA GTGC A -
GAM2071 371 KIAA056 2 12972 XP_038150.2 3 319 ACTCTGTTGCCC A----- TG 3 B c c
1 GGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGCGGCGT GACGTGAGGTCGGGCCC TG
TGCGGC GT
GAM2071 371 KIAA056 1 10458 NP_055519.1 3 2048 GCTCTGTTGCCT TG 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGATCC TG
GT
GAM2071 371 KIAA056 1 19679 NP_055649.1 5 603 CTCTTGTTGCCC C TG 3 B c c
3 AGGCTGAAGTGC ACTGCACT CAGTCTGGG AC
AGTGTTGT TGACGTGA GTCGGACCC TG
A GT
GAM2071 371 KIAA060 1 11045 NP_055509.1 5 68 ACTCTTTCACCC A----- A 3 B c c
5 AGACTGGAGGGC CTGC CTCCAGTCTGGGTGA
AGCGGCGA GACG GAGGTCAGACCCACT
AGCGGC G
GAM2071 371 KIAA068 1 2671 NP_055667.1 3 30 CTGGCACCGAGA G--- A 3 B c c
2 GGGCTGGAGTGC ACTGCACTCCAGTCT GGTG
AGTGGCGT TGACGTGAGGTCGGG CCAC
AGAG G
GAM2071 371 KIAA083 1 16264 NP_055739.1 3 1917 GCTCAGCTGCCC TG A 3 B c
c
1 AGGCTGGAGTGT AC CACTCCAGTCTGGGTG
GGTGGCGC TG GTGAGGTCGGACCCGT
GT C
GAM2071 371 KIAA084 2 901 XP_049237.1 3 1171 ATTCTGTTGCCC TC TG 3 B c c
1 AAGTTGGAGTGC ACTGCACTCCAG TGGG AC
AGTGGCAT TGACGTGAGGTT ACCC TG
GA GT
GAM2071 371 KIAA084 2 1519 XP_049237.1 3 1520 TGGCTGTTTCCC C T 3 B c c
1 AGGCTGAAGTGC ACTGCACT CAGTCTGGG GAC
AGTGGCAT TGACGTGA GTCGGACCC TTG
A T
GAM2071 371 KIAA086 1 10629 NP_055893.2 3 954 GCTCTGTCGCCC 3 B b b

1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 KIAA092 2 864 NP_055712.1 3 2516 GTTCTGTTGCCT TG TG 3 B c c
4 GGGCTGGAGTGC ACTGCACTCCAGTC GG AC
AGTGGCGT TGACGTGAGGTCGG CC TG
GT GT
GAM2071 371 KIAA092 2 19935 NP_055712.1 3 1716 GCTATGTTGCCC C TG 3 B c c

4 AGGCTAGAGTGC ACTGCACTC AGTCTGGG AC
AGTGGCTA TGACGTGAG TCGGACCC TG
A GT
GAM2071 371 KIAA093 1 8504 XP_041191.2 3 161 GCTCAGTCGCTC AC----- 3 B c c
1 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGG ACGTGAGGTCGGACTCGCTG
GGTGGTA
GAM2071 371 KIAA093 1 10957 XP_052620.6 3 1213 ACTCTGTCGCCC 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGTCAA TGACGTGAGGTCGGACCCGCTG

GAM2071 371 KIAA093 1 7974 XP_166213.1 3 1848 TGCCTGTCACCC - - GT--- 3 B c c
7 AGTTCTGTGGAT ACT GCAC TCCA CTGGGTGAC
GTGCTGGT TGG CGTG AGGT GACCCACTG
T T GTCTT
GAM2071 371 KIAA100 1 8660 XP_290584.1 3 314 CTCTTGTCACCC CT 3 B b b
2 CAGCTGGAGTGC ACTGCACTCCAGT GGGTGAC
AGTAGCAC TGACGTGAGGTCG CCCACTG
AC
GAM2071 371 KIAA104 2 5080 XP_051091.3 3 1175 AGATAGTCAAGC CCAG A 3 B c
b
0 ATTTAGAAGTGC ACTGCACT TCTGGGTG
AGTGAACT TGACGTGA AGATTTAC
---- G
GAM2071 371 KIAA104 2 5138 XP_051091.3 3 2455 GCTCTGTCACCC C 3 B b b
0 AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC
AGTGGCAC TGACGT AGGTCGGACCCACTG
A
GAM2071 371 KIAA104 1 11112 NP_055762.1 3 967 GCCCTGTTGCCC TG 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA104 1 18400 NP_056096.1 3 82 TTGCTTCAGCCC C TCT- - 3 B c c

3 TTCCCTGAGTGC ACTGCACTC AG GGG TGA
AGTCCCCC TGACGTGAG TC CCC ACT
- CCTT G
GAM2071 371 KIAA104 1 9634 XP_048592.1 3 1482 GTTATTCAAAAG G ----- 3 B c c
5 GGAGTGGAGTGC ACTGCACTCCA TCT GGGTGAC
AGTCATGC TGACGTGAGGT AGG CTTATTG
G GAAAA

GAM2071 371 KIAA105 1 1530 NP_055771.1 5 226 GCTCTGTCACTC C 3 B b b
2 AGGCTGCAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGCAT TGACGTGA GTCGGACTCACTG
C
GAM2071 371 KIAA105 1 7973 XP_043493.5 3 3277 ACTCTGTTGCCC TG 3 B b b
4 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGG TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA112 1 6077 XP_050325.1 3 2308 CGATTCCTCGCC A----- - T G 3 B c c
6 AGCTGGGAGTGC CTGCACTCC AG CTGG TGA
AGAAGTCT GACGTGAGG TC GACC GCT
TCTGAA G - -
GAM2071 371 KIAA114 1 13800 XP_044014.1 3 3994 GCTCTGTCACCC 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG
GAM2071 371 KIAA115 1 5405 XP_030864.2 3 2953 ACTCTGTCACCC 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACCCACTG
GAM2071 371 KIAA118 1 9213 NP_065761.1 3 154 CGCTCTGTCGCC G 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGT TGACGTGAGGTCGGACC GCTG
-
GAM2071 371 KIAA119 1 1683 XP_041843.1 3 1645 CACACTGTCGCC G 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC GCTG
-
GAM2071 371 KIAA119 6 5522 NP_065765.1 3 992 ACTCTGTTGCCT G- TG 3 B c b
8 AGGCTGGAGTGA ACT CACTCCAGTCTGGG AC
AAGTGGCG TGA GTGAGGTCGGATCC TG
AA GT
GAM2071 371 KIAA119 6 8170 NP_065765.1 3 723 CTCTGTTGCCCC - TG 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGG G AC
AGTGGTGT TGACGTGAGGTCGGACC C TG
C GT
GAM2071 371 KIAA119 6 17224 NP_065765.1 3 3709 CTCACTGTTGCC ----- 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GTGA
AGTGGCAC TGACGTGAGGTCGGACC CACT
GTTGT
GAM2071 371 KIAA119 6 17617 NP_065765.1 3 420 CTCTTGTTGCCC TG 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA119 6 17786 NP_065765.1 3 1271 GAGTCCTTGCCC TG 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCGC TGACGTGAGGTCGGACCC T
GT

GAM2071 371 KIAA119 6 19094 NP_065765.1 3 1757 AGCTCTCACACA GCA - G 3 B c b
8 TGACTGGAGAGA ACT CTCCAGTC TG GTGA
AGTGAGAA TGA GAGGTCAG AC CACT
AGA T A
GAM2071 371 KIAA121 1 1409 XP_172801.1 3 104 GCTCTGTTACCC 3 B b b
0 AGATTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTTAGACCCATTG

GAM2071 371 KIAA125 2 3109 XP_031577.2 3 1694 GCTCTGTCGCCC 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 KIAA125 2 14928 XP_031577.2 3 1025 GCTCTCTCACCC - 3 B b b
7 AGGCTGGAGTGT ACT GCACTCCAGTCTGGGTGA
AAGTGACA TGA TGTGAGGTCGGACCCACT
A
GAM2071 371 KIAA127 1 15059 XP_046600.7 5 835 CTAAAATCATCC TG - C- 3 B c c
2 AGACTGTTGGTG AC C ACT CAGTCTGGGTGA
GTGGTGCT TG G TGG GTCAGACCTACT
GT G TT
GAM2071 371 KIAA128 1 13685 NP_065799.1 3 1242 CCCCTGTTGCCC TG 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGGAT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA139 1 6495 XP_050793.2 3 1498 GCTCTGTTGCCC A----- TG 3 B c c
3 AGGCTGGAGTGT CTGCACTCCAGTCTGGG AC
AGAGACAC GATGTGAGGTCGGACCC TG
CACAGA GT
GAM2071 371 KIAA140 1 15873 NP_065868.1 3 435 CCAAGGCACTCA CC- T A 3 B c c
7 GCCTTCTAGTGC ACTGCACT AG CTGGGTG
AGTAGCAT TGACGTGA TC GACTCAC
TCT C G
GAM2071 371 KIAA145 1 13974 XP_040100.3 3 2059 GCTCTGTCGCCC AC----- 3 B c c
6 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
ACTGGCGC ACGTGAGGTCGGACCCGCTG
CGCGGTC
GAM2071 371 KIAA146 1 13306 XP_027396.4 3 570 TGGTCTGTCGCC G 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC GCTG
-
GAM2071 371 KIAA150 1 16911 XP_290952.1 3 78 TGCTCGTCACCC AC----- 3 B c c
8 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATTGTGC ACGTGAGGTCGGACCCACTG
CGTGTTA
GAM2071 371 KIAA151 1 17375 XP_170889.1 3 94 ACTCTGTCGCCC G 3 B b b

8 AGGGTGGAGTGC ACTGCACTCCA TCTGGGTGAC
GGTGGCAC TGGCGTGAGGT GGACCCGCTG
G

GAM2071 3710 KIAA153 2 6360 XP_042661.5 3 817 TTTGCTCTTACC C 3 B b b
CAGGCTGAGTGC ACTGCACTC AGTCTGGGTGA
AGTGGCAG TGACGTGAG TCGGACCCATT
-

GAM2071 3710 KIAA153 2 12872 XP_042661.5 3 1177 TGCTCTGTCGCC AC----- G 3 B c b
AGGCTGGAGTGC TGCACTCCAGTCTGG TGAC
AATGGCGT ACGTGAGGTCGGACC GCTG
TGCGGTA -

GAM2071 3713 KIAA155 1 3650 XP_166320.1 3 3395 GCATTTTACCAT AC----- - 3 B c c
AGATTGGAGTGC TGCACTCCAGTCTG GGTGA
ATCCTTAG ACGTGAGGTTAGAT CCATT
GATTCCT A

GAM2071 3714 KIAA155 1 15297 XP_290768.1 3 1332 GCAGAGTGACCC A C G 3 B c c
AGACTGCAGGCA ACTGC CT CAGTCTGGGT AC
GTAACTGA TGACG GA GTCAGACCCA TG
- C G

GAM2071 3719 KIAA155 1 14408 XP_054472.2 3 1628 ACTTTGTCCCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGTAC TGACGTGAGGTCGGACCC CTG
C

GAM2071 3711 KIAA157 1 13037 XP_027744.1 3 881 ACTGTCTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCCT TGACGTGAGGTCGGACCC T
GT

GAM2071 3715 KIAA161 2 8578 NP_066002.1 3 1687 TGCTCTGTCACC A G 3 B b b
AGGCCGGAGTGC ACTGCACTCC GTCTGG TGAC
AGTGGTGT TGACGTGAGG CGGACC ACTG
C -

GAM2071 3715 KIAA161 2 12534 NP_066002.1 3 1380 CTCTTGTTGCCT TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGATCC TG
GT

GAM2071 3711 KIAA167 1 17814 XP_037809.1 3 1741 ACTCTGTTGCTC G TC TG 3 B c c
AAGCTGGAGTGG ACT CACTCCAG TGGG AC
AGTGGCAC TGA GTGAGGTC ACTC TG
G GA GT

GAM2071 3717 KIAA172 1 14415 XP_034262.4 3 779 CTCTTGTCTCCC C T 3 B b b
AGACTGGACTGC ACTGCA TCCAGTCTGGG GAC
AGTGGCAC TGACGT AGGTCAGACCC CTG
C T

GAM2071 3714 KIAA178 1 18884 NP_115820.1 3 341 GCTGTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGATCCACTG

GAM2071 371 KIAA182 2 2385 XP_290834.1 3 1305 CCCTTGTCACCC C 3 B b b
7 AGGCTGTAGTGC ACTGCACT CAGTCTGGGTGAC
GGTGGCGC TGGCGTGA GTCGGACCCACTG
T
GAM2071 371 KIAA182 2 19431 XP_290834.1 3 937 ACTCTGTTGCCC TG 3 B b b
7 AGGCTGGAGTGT ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGATGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA182 1 12386 XP_030378.2 3 209 GCTCTGTTGCCC TG 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KIAA183 1 17519 XP_114087.2 3 1677 TCTCTGCCAGCC G A 3 B c c
6 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TG
AGTGGCAT TGACGTGAGGTCGGACC AC
G C
GAM2071 371 KIAA185 1 19842 XP_045184.1 3 1928 GCCCAGGAACCC CAC GA 3 B c
c
3 AGACTGGACTTC ACTG TCCAGTCTGGGT
AGTCTCCC TGAC AGGTCAGACCCA
TTC AG
GAM2071 371 KIAA192 1 7825 NP_694971.2 3 596 GCTCTGTCGCCC GT 3 B b b
4 AGGATGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCGC TGACGTGAGGT GACCCGCTG
AG
GAM2071 371 KIAA195 1 12956 XP_057401.1 3 254 ACCAGGTCACCC G C-- ---- 3 B c c
1 AGCTATGCTGCA ACT CACT CAGT CTGGGTGAC
AAGTGGGT TGG GTGA GTCG GACCCACTG
- AAC TATC
GAM2071 371 KIAA197 1 19552 XP_058720.4 3 561 TCTCTGTCATCC C 3 B b b
1 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAC TGACGTGAG TCGGACCTACTG
A
GAM2071 371 KIAA198 1 18263 XP_113870.1 5 201 CTCTTGTTGCCC C GT TG 3 B c
c
7 AGGTTAGAGTGC ACTGCACTC A CTGGG AC
AGTGGCAC TGACGTGAG T GACCC TG
A TG GT
GAM2071 371 KIAA202 1 11722 XP_059415.2 3 1062 CTCTGGTTGCCC TG 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 KLF5 1 17531 NP_001721.2 3 1096 GTAATTTTATCT CC C 3 B c c
AAATTACAGTGC ACTGCACT AGT TGGGTGA
AGTTTAGT TGACGTGA TTA ATCTATT
CA A
GAM2071 371 KLK10 1 6691 NP_002767.2 3 288 CGGTCATCACCC A C- T 3 B c c
AGCCTCTGAGAG ACTGC CTC AG CTGGGTGA
CAGTTACT TGACG GAG TC GACCCACT

A TC C
GAM2071 371 KLK10 1 6691 NP_665895.1 3 288 CGGTCATCACCC A C- T 3 B c c
AGCCTCTGAGAG ACTGC CTC AG CTGGGTGA
CAGTTACT TGACG GAG TC GACCCACT
A TC C
GAM2071 371 KMO 1 5730 NP_003670.1 3 715 ACTCTGTTGACC GT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTGGTGA TGACGTGAGGTCGGACC TTG
AG
GAM2071 371 KSR 1 15951 XP_290793.1 5 1147 GCTCTATCACCC C 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGA
AGTAGTGC TGACGTGA GTCGGACCCACT
A
GAM2071 371 LAMP3 1 970 NP_055213.1 3 564 CTCTTGTCACCC C 3 B b b
AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAC TGAC TGAGGTCGGACCCACTG
A
GAM2071 371 LANO 1 4507 NP_060684.1 3 1649 GAATAAGTCTCT CAGTC T 3 B c
c
CATAATGAGTGC ACTGCACTC TGGG GAC
AGTGTCAG TGACGTGAG ACTC CTG
TAAT- T
GAM2071 371 LCN7 1 3972 NP_071447.1 3 399 GCTCCGTTGCCC GT TG 3 B c c
AGGTTGGAGTGC ACTGCACTCCA CTGGG AC
AGTGGCCC TGACGTGAGGT GACCC TG
TG GT
GAM2071 371 LEF1 1 11499 NP_057353.1 3 931 GATGCGTTCAGC CT GG 3 B c c
AGACTGGTTTGC ACTGCA CCAGTCTG TGA
AGTGAATT TGACGT GGTCAGAC ACT
TT G-
GAM2071 371 LHFP 1 8128 NP_005771.1 3 561 GGATTATCGCAC C -- G 3 B c c
AGACTGGGAGGT ACTG ACT CCAGTCTG GTGA
TTAGTGGT TGAT TGG GGTCAGAC CGCT
T AG A
GAM2071 371 LIN-28 1 6030 NP_078950.1 3 2143 GCTGTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGAGCT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LNK 1 9510 NP_005466.1 3 1682 CTCTTGTCAACC G 3 B b b
GGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGGCC ACTG
A
GAM2071 371 LOC1126 1 4875 XP_053145.1 3 168 GCCCTGTCACCC 3 B b b
87 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1128 1 16516 NP_612422.2 3 418 ACTCTGTCACCC AC----- 3 B c c

17 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAT ACGTGAGGTCGGACCCACTG

TACGGTA

GAM2071 371 LOC1134 3 14262 NP_612437.2 3 851 ATTCTGTCACCC 3 B b b
44 GGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGGCCCACTG

GAM2071 371 LOC1134 3 15369 NP_612437.2 3 590 ACTCTGTCACAC G 3 B b b
44 AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
AGTACAAT TGACGTGAGGTCGGAC CACTG
A

GAM2071 371 LOC1134 3 15847 NP_612437.2 3 1176 GCTGTATTGCCC TG 3 B b b

44 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCGC TGACGTGAGGTCGGACCC T
GT

GAM2071 371 LOC1156 1 6386 NP_663299.1 3 656 CGCTCTGTCGCC T TG 3 B c c

48 TGGCTGGAGTGC ACTGCACTCCAG C GGTGAC
AGTGGTGT TGACGTGAGGTC G CCGCTG
- GT

GAM2071 371 LOC1164 2 1487 XP_058095.1 5 1240 TCAATGGTGTCC GT A 3 B c c

11 AGGCTGGAGTGC ACTGCACTCCAGTCTGG G
AGTGGCGT TGACGTGAGGTCGGACC T
TG G

GAM2071 371 LOC1164 2 13193 XP_058095.1 5 547 CATGAGTTCCCC A----- C T 3 B c
c
11 CAACTGGAGTGC CTGCACTCCAGT TGGG GA
AGACAAGA GACGTGAGGTCA ACCC CT
AGAACA - C

GAM2071 371 LOC1184 1 11022 XP_060981.3 3 217 GCTCTGTTGCCC A----- TG 3 B c
c
90 AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGCGGCAT GACGTGAGGTCGGACCC TG
TACGGC GT

GAM2071 371 LOC1188 1 7879 NP_849154.1 3 580 TTACTCTCGCCC C 3 B b b
12 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGA
AGTGGCAT TGACGTGAG TCGGACCCGCT
A

GAM2071 371 LOC1188 1 7879 XP_058346.2 3 580 TTACTCTCGCCC C 3 B b b
12 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGA
AGTGGCAT TGACGTGAG TCGGACCCGCT
A

GAM2071 371 LOC1205 1 14215 XP_058475.1 3 678 ACTCTGTCGCGC T - 3 B b b
26 CAGCTGGAGTGC ACTGCACTCCAG CTGG GTGAC
AGTGCCAT TGACGTGAGGTC GACC CGCTG
- G

GAM2071 371 LOC1214 1 1850 XP_062669.7 3 1788 AAACACTCATCA CCAG- G 3 B c
c
98 GAAATTAAGTGC ACTGCACT TCTGG TGA
AGTCTAGT TGACGTGA AGACT ACT

ATTAA -

GAM2071 371 LOC1219 1 17591 XP_062872.2 5 584 GCTCTGTCACCC T 3 B b b
52 GGGCTGGAGTGC AC GCACTCCAGTCTGGGTGAC
TGTGGCTT TG CGTGAGGTCGGGCCCACTG
T

GAM2071 371 LOC1250 1 9098 XP_058889.3 3 406 ACTCTGTCACCC 3 B b b
61 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1276 1 14354 XP_059166.1 3 123 GTGTGTTCAGCC --- G 3 B b b
02 AGACTGGGCAGG ACTGCACT CCAGTCTGG TGA
TGCAGTCT TGACGTGG GGTCAGACC ACT
ACG G

GAM2071 371 LOC1308 1 16452 XP_065904.1 3 931 GCACTGTCGCCT AC----- 3 B c c

13 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AACAGTGT ACGTGAGGTCGGATCCGCTG
TGTGACA

GAM2071 371 LOC1319 1 5289 XP_067689.1 3 276 GTTAGTTCACCC A---- A - T- 3 B c c

63 AGTTCTGTGGGG CTGC CTC CAG CTGGGTGA
CAGGAAAG GACG GGG GTC GACCCACT
GAAAG - T TT

GAM2071 371 LOC1322 1 13281 XP_059583.1 5 82 ACTTTGCTTCCC TGA 3 B c c
41 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG
AGTGGTGC TGACGTGAGGTCGGACCC
TTC

GAM2071 371 LOC1344 1 11536 XP_068858.3 5 1554 TGGATTTCACCC A----- - AG 3 B c
c
66 AGGAGGAGTGGC CTGC ACTCC TCTGGGTGA
AGCAACTG GACG TGAGG GGACCCACT
GTCAAC G A-

GAM2071 371 LOC1352 1 11660 XP_072402.4 3 1276 TCTTGCTCTCCC T 3 B b b
93 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GA
AGTGGTGT TGACGTGAGGTCGGACCC CT
T

GAM2071 371 LOC1357 1 14442 NP_612639.1 3 38 GCTCCGTCACCC 3 B b b
63 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAA TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1394 1 17958 XP_066687.2 5 63 GCTCTGTTGCCC TG 3 B b b
22 AGACTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCAGACCC TG
GT

GAM2071 371 LOC1442 1 11361 XP_084786.1 5 398 GCTCTTTCGCCC AC----- 3 B c c

48 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
AATGGTGT ACGTGAGGTCGGACCCGCT
TGTGGTA

GAM2071 371 LOC1444 2 8561 XP_084852.6 3 1128 GGTCTGTTGCCT A TG 3 B c b

04 AGGCGGGAGTGC ACTGCACTCC GTCTGGG AC
AGTGGCAT TGACGTGAGG CGGATCC TG
G GT

GAM2071 371 LOC1444 2 11669 XP_084852.6 3 1293 GATCTGTTACCC 3 B b b
04 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGACAC TGACGTGAGGTCGGACCCATTG

GAM2071 371 LOC1444 1 17022 XP_096611.2 3 208 ACTCTGTCACTC 3 B b b
81 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACTCACTG

GAM2071 371 LOC1447 1 19847 XP_084963.2 5 180 GCTTTGTCACCC C 3 B b b
66 AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCGT TGAC TGAGGTCGGACCCACTG
A

GAM2071 371 LOC1448 1 12382 XP_084972.1 5 232 GCTCTGTCGCCC 3 B b b
17 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1448 1 10644 XP_096698.1 3 381 GCTCTGTTGCCC A----- TG 3 B c
c
71 AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGGGACAC GACGTGAGGTCGGACCC TG
CACAGG GT

GAM2071 371 LOC1454 1 8486 XP_085120.1 5 319 ACTGTGTCATGC G G 3 B c c
53 AGGCTGGAGTGA ACT CACTCCAGTCTG GTGAC
AGTCGTGT TGA GTGAGGTCGGAC TACTG
A G

GAM2071 371 LOC1456 1 2964 XP_085202.1 5 1172 GCTTGTCATGGG A----- GG- 3 B c
c
76 AGACTGGAGTGC CTGCACTCCAGTCT GTGAC
AGATTCTT GACGTGAGGTCAGA TACTG
TTCTTA GGG

GAM2071 371 LOC1457 2 3109 XP_085227.1 5 212 GCTCTGTCGCCC 3 B b b
57 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1457 2 13797 XP_085227.1 5 94 GCTCTGTCGCCC 3 B b b
57 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGCGC TGGCGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1457 1 6743 XP_085231.2 5 1118 GCTCTGTCACCC AC----- 3 B c c

83 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCGGACCCACTG
CGTGGTA

GAM2071 371 LOC1458 1 987 XP_096873.1 5 59 GCTCTGTCACCC AC----- 3 B c c
13 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAT ACGTGAGGTCGGACCCACTG
TACGGTA

GAM2071 371 LOC1459 1 1945 XP_085290.3 5 554 ACTCTGTCACCC AC----- G - 3 B c c
88 AAGATGGAGTGC TGCACTCCA TCT GGGTGAC
AATGGCAC ACGTGAGGT AGA CCCACTG
CACGGTA - A
GAM2071 371 LOC1461 1 15157 NP_778229.1 5 198 CTCTTGTTGCCC TG 3 B b b
77 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTAGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1462 2 3109 XP_085387.1 3 1706 GCTCTGTCGCCC 3 B b b
29 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1462 2 8345 XP_085387.1 3 3209 ACTCTGTCGCCC C 3 B b b
29 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAC TGACGTGAG TCGGACCCGCTG
A
GAM2071 371 LOC1463 1 4132 XP_085421.2 3 727 GGGTCTCACCTG C- 3 B b b
36 TCGCTGGAGTGC ACTGCACTCCAGT TGGGTGA
AGTGGTGT TGACGTGAGGTCG GTCCACT
CT
GAM2071 371 LOC1463 2 6781 XP_085430.1 5 387 CACTCCGTTGCC T G TG 3 B c b
46 AGGCTGGAGTGC AC GCACTCCAGTCTG G AC
TGTGGCGC TG CGTGAGGTCGGAC C TG
T - GT
GAM2071 371 LOC1463 2 16312 XP_085430.1 5 735 CACTCGTTGCCC TG 3 B b b
46 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1464 1 8579 XP_096998.2 5 536 CGCTCTGTCACC G 3 B b b
29 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGT TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 LOC1464 1 5238 XP_085461.6 5 100 CACTTGTCACCC AC----- 3 B c c
43 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGT ACGTGAGGTCGGACCCACTG
TGTGGTA
GAM2071 371 LOC1466 1 3109 XP_085514.2 5 1113 GCTCTGTCGCCC 3 B b b
03 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1467 1 13452 XP_085588.1 5 889 CTCTTGTTGCCC TG 3 B b b
84 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
GGTGGTAC TGGCGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1468 1 11661 XP_097107.1 3 676 ACTCTGTTGCCC TG 3 B b b
39 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC1468 1 2386 NP_660316.1 3 1176 GTGCTGCTGCCC A 3 B c c
94 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGCAC TGACGTGAGGTCGGACCCGT
C
GAM2071 371 LOC1468 1 8862 XP_097120.1 5 549 ACTCTGTCACCC 3 B b b
95 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1469 1 12152 XP_097121.1 3 1203 TTGTCAAAAATC G--- 3 B b b
01 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCAT TGACGTGAGGTCGGACT ACTG
AAAA
GAM2071 371 LOC1469 2 14280 XP_085634.2 3 661 ACTCTGTCGCCC 3 B b b
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1469 2 20010 XP_085634.2 3 994 GCTCTGTCGCCC 3 B b b
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGG TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1470 1 18093 XP_097182.1 5 17 GCTCTGTCCGCC GT 3 B b b
80 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTGGCGC TGACGTGAGGTCGGACC CTG
GC
GAM2071 371 LOC1471 1 546 XP_085722.2 3 251 GCACTGTTGCCC TG 3 B b b
66 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1473 1 14957 XP_097225.1 5 828 CCTCTGTCACCC TG A C 3 B c
c
43 AGGCTAGAGGGT AC C CTC AGTCTGGGTGAC
GGTGATAT TG G GAG TCGGACCCACTG
GT G A
GAM2071 371 LOC1474 1 12382 XP_084000.1 3 142 GCTCTGTCGCCC 3 B b b
07 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1476 1 10349 XP_097255.1 3 528 TCTCTGTCCCCT C T 3 B c c
22 AGGCTGCAGTGC ACTGCACT CAGTCTGGG GAC
AGTGGCGC TGACGTGA GTCGGATCC CTG
C C
GAM2071 371 LOC1478 2 11085 XP_085903.1 3 280 GCTCTGTCACCC G C 3 B b b

17 AGGCTGTAGTGG ACT CACT CAGTCTGGGTGAC
AGTGGTGT TGA GTGA GTCGGACCCACTG
G T
GAM2071 371 LOC1478 2 14003 XP_085903.1 3 444 CCTCTGTCGCCC AC----- 3 B c b

17 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGC ACGTGAGGTCGGACCCGCTG

CGCGGTA

GAM2071 371 LOC1478 1 18175 XP_085924.2 3 457 ACTCTGTCGCCC 3 B b b
41 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1479 1 438 XP_085974.1 3 578 ACTCTGTCACCC 3 B b b
47 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1481 1 13130 NP_653293.1 3 2097 GCTCTGTCACCC --- 3 B b b
37 AGGCTGGAGTGC ACT GCACTCCAGTCTGGGTGAC
CATAGTGT TGA CGTGAGGTCGGACCCACTG
TAC

GAM2071 371 LOC1487 1 18164 XP_086286.4 3 1372 ACTCTGTCGCCC 3 B b b
08 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTG TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1487 1 8427 XP_086281.1 5 142 TCTCTGGTACTC A 3 B c c
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
GGTGGTGT TGGCGTGAGGTCGGACTCAT
G

GAM2071 371 LOC1491 1 16592 XP_097594.1 5 500 GCTAAACAGCCA AC - G A 3 B c
c
34 AGACTGGAGCAG ACTGC TCCAGTCT GG TG
TCTCTCAC TGACG AGGTCAGA CC AC
-- A G A

GAM2071 371 LOC1491 1 9725 XP_097598.1 5 3316 CTCTTGTTGCCC TC TG 3 B c
c
49 AAGCTGGAGTGC ACTGCACTCCAG TGGG AC
AGTGGCGC TGACGTGAGGTC ACCC TG
GA GT

GAM2071 371 LOC1493 1 14762 NP_787072.1 3 370 ACCCCGTCGCAC G 3 B b b
71 AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
AGTGGCAA TGACGTGAGGTCGGAC CGCTG
A

GAM2071 371 LOC1494 1 2514 XP_086536.1 3 75 GCTCTGTCGTCG G GT 3 B c c
78 AGGCTGGAGTGT ACTGCACTCCAGTCT G GAC
AGTGGTGC TGATGTGAGGTCGGA C CTG
G TG

GAM2071 371 LOC1495 2 5777 XP_097661.1 3 1638 TCGCTGTTGCCC C TG 3 B c
c
06 AGGCTGTAGTGC ACTGCACT CAGTCTGGG AC
AGTGGTGC TGACGTGA GTCGGACCC TG
T GT

GAM2071 371 LOC1495 2 17503 XP_097661.1 3 3100 CTCTTGTCGGCC C G 3 B c c

06 AGGCTAGAGTGC ACTGCACTC AGTCTGG TGAC
AGTGGCGC TGACGTGAG TCGGACC GCTG
A G

GAM2071 371 LOC1496 1 13800 XP_097706.1 3 612 GCTCTGTCACCC 3 B b b

92 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1497 1 19805 XP_097719.1 5 452 GTTCTGCTGCCC - TC A 3 B c c

03 AAGCTGGAGTGG ACTGC ACTCCAG TGGGTG
CAGTGGCA TGACG TGAGGTC ACCCGT
G GA C

GAM2071 371 LOC1500 1 18175 XP_097797.1 5 592 ACTCTGTCGCCC 3 B b b
54 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1502 1 1664 XP_097870.1 3 1703 GCTCTGTCGCTC 3 B b b
25 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACTCGCTG

GAM2071 371 LOC1504 1 2430 XP_086906.1 3 530 GCTCTGTTGTCC C TG 3 B c c
07 AGGCTAGAGTGC ACTGCACTC AGTCTGGG AC
AGTGGTGT TGACGTGAG TCGGACCT TG
A GT

GAM2071 371 LOC1505 2 8861 XP_097917.1 5 1615 GCTCTGTTGCCC TG 3 B b b
87 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC1505 2 15619 XP_097917.1 3 1206 GTGTTCGCATCA - TC - 3 B c b

87 ACTTGGAAGTGC ACTGCACT CCAG TGG GTGA
AGTAATTG TGACGTGA GGTT ACT CGCT
A CA A

GAM2071 371 LOC1510 1 5519 XP_097998.1 3 1066 TCTCTGTCACCC 3 B b b
57 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1512 2 3299 XP_098021.1 3 1784 ATTCTGTCACCC AC----- C 3 B c
b
01 AGGCTGGAGTCC TG ACTCCAGTCTGGGTGAC
AATGGGGC AC TGAGGTCGGACCCACTG
CGGGGTA C

GAM2071 371 LOC1512 2 11934 XP_098021.1 3 367 CACGCTGTCACC G 3 B b b
01 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 LOC1514 2 7086 XP_098063.1 5 738 GCTCTGTCATCC 3 B b b
75 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCTACTG

GAM2071 371 LOC1514 2 15680 XP_098063.1 5 99 GCTCTGTGGCCC G 3 B b b
75 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGT AC
AGTGGCGT TGATGTGAGGTCGGACCCG TG
G

GAM2071 371 LOC1516 3 896 NP_612144.1 3 890 ACTCTGTCACCC C 3 B b b
36 AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC
AGTGGTGT TGACGT AGGTCGGACCCACTG
A
GAM2071 371 LOC1516 3 2479 NP_612144.1 3 2150 ACTGTGTCCCCC T 3 B b b
36 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC CTG
C
GAM2071 371 LOC1516 3 19982 NP_612144.1 3 221 GCTCTGTCGCTC C 3 B c b
36 GCGCTGGAGTGC ACTGCACTCCAGT TGGGTGAC
AGTGGCAT TGACGTGAGGTCG GCTCGCTG
C
GAM2071 371 LOC1522 1 19257 XP_098182.1 3 1273 GCTCTGTCGCCC ---- 3 B b b
45 AGGCTGGAGTGA ACTGCAC TCCAGTCTGGGTGAC
GTGCAGTG TGACGTG AGGTCGGACCCGCTG
AGTG
GAM2071 371 LOC1524 1 13905 XP_098231.1 3 523 GATCTGTTGCCC TG 3 B b b
45 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGAGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1526 1 13870 XP_011108.2 3 708 TCTCTGTTGCCC TG 3 B b b
20 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1527 1 1141 XP_098257.1 5 422 GCTCTGTCGCCC T 3 B b b
19 AGCCTGGAGTGC ACTGCACTCCAG CTGGGTGAC
AGTGGCAC TGACGTGAGGTC GACCCGCTG
C
GAM2071 371 LOC1527 1 3556 XP_087525.1 5 421 GGTCTGTTACCC 3 B b b
94 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCATTG

GAM2071 371 LOC1528 1 8155 XP_098266.2 3 1699 CTTTCTCGCACA - G 3 B b b
04 GGCTTGGAGTGC ACTGCACTCCA GTCTG GTGA
AGTGGTGC TGACGTGAGGT CGGAC CGCT
T A
GAM2071 371 LOC1530 1 19370 XP_098307.1 3 804 CTGATATCACCC 3 B b b
77 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCGC TGACGTGAGGTCGGACCCACT

GAM2071 371 LOC1538 3 6031 XP_087779.2 3 41 GCTCTGTCACCC A 3 B b b
11 AGGCAGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCAC TGACGTGAGG CGGACCCACTG
A
GAM2071 371 LOC1538 3 14281 XP_087779.2 3 1383 ACTCTGTTGCCC TG 3 B b b

11 AGACTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCAGACCC TG
GT
GAM2071 371 LOC1538 3 15030 XP_087779.2 3 1086 ACTCTGTCGCCC 3 B b b

11 AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCGC TGACGTGAGGTCAGACCCGCTG

GAM2071 371 LOC1538 1 3293 XP_087798.1 5 127 ATTCTTTTGCCC TG 3 B b b
83 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCAC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 LOC1539 1 7292 XP_087801.1 5 187 ACTCTGTAGCCC T GA 3 B c c
10 AGTCTGGAGTGC ACTGCACTCCAG CTGGGT
AGTGGTAC TGACGTGAGGTC GACCCG
T AT
GAM2071 371 LOC1542 1 14848 XP_098505.1 5 117 CGCTCTGTCGCC GT G 3 B b
b
82 AGGTTGGAGTGC ACTGCACTCCA CTGG TGAC
AGTGGCGT TGACGTGAGGT GACC GCTG
TG -
GAM2071 371 LOC1548 1 3008 XP_098618.3 5 2826 CCTTTGTCAGCC AC----- G 3 B c
c
22 AGGCTGGAGTGC TGCACTCCAGTCTGG TGAC
AATGTGCA ACGTGAGGTCGGACC ACTG
ACGTGTA G
GAM2071 371 LOC1548 3 3038 XP_098626.1 5 109 ACTCTGTTGCCC T TG 3 B c b
77 AGTCTGGAGTGC ACTGCACTCCAG CTGGG AC
AGTGGCGC TGACGTGAGGTC GACCC TG
T GT
GAM2071 371 LOC1548 3 14342 XP_098626.1 3 982 ATTCTGTCTCGC CA - T 3 B c b

77 AGGCCAGAGTGC ACTGCACTC GTCTG GG GAC
AGTGGTGT TGACGTGAG CGGAC CT CTG
AC G -
GAM2071 371 LOC1548 3 15947 XP_098626.1 3 1269 GCTCTGTCGCCC G 3 B b b

77 AGGGTGGAGTGC ACTGCACTCCA TCTGGGTGAC
AGTGGCGT TGACGTGAGGT GGACCCGCTG
G
GAM2071 371 LOC1580 1 12285 XP_088442.1 5 3579 CTCTTGTCACCC 3 B b b
14 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGATGTGAGGTCGGACCCACTG

GAM2071 371 LOC1583 1 18175 XP_098919.1 5 370 ACTCTGTCGCCC 3 B b b
10 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1584 1 1414 XP_098936.1 5 139 ACTCTGTTGCCC TG 3 B b b
02 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1584 1 7071 XP_098942.1 3 642 ACTCTGTCACTC 3 B b b
36 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACTCACTG

GAM2071 371 LOC1584 1 436 XP_098955.1 3 892 GCTCTGTCGCCC 3 B b b
76 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1585 1 9685 XP_088606.1 5 1037 TGCTCTATCACC AG G 3 B b
b
63 AGGTGGGAGTGC ACTGCACTCC TCTGG TGA
AGTGGCAC TGACGTGAGG GGACC ACT
GT -
GAM2071 371 LOC1608 1 14437 XP_090573.3 5 536 ACTCCGTAGCCC G 3 B b b
97 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCAC TGACGTGAGGTCGGACCCG TG
A
GAM2071 371 LOC1620 1 17143 XP_091339.2 5 164 CTACAGTCACCC CA- C T 3 B c
c
83 AGCTTAGAGCTC ACTG CTC AG CTGGGTGAC
CAGTCCCC TGAC GAG TT GACCCACTG
CTC A C
GAM2071 371 LOC1624 2 1761 NP_835227.1 3 822 TCTCTGTTGCCC TG 3 B b b
27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1624 2 1761 XP_091549.3 3 816 TCTCTGTTGCCC TG 3 B b b
27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1624 2 12386 NP_835227.1 3 487 GCTCTGTTGCCC TG 3 B b b

27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1624 2 12386 XP_091549.3 3 487 GCTCTGTTGCCC TG 3 B b b
27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC1629 1 3050 XP_091890.6 3 379 GCTCTGTCGCCC TC 3 B b b
67 ACGTTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGATGT TGACGTGAGGTT ACCCGCTG
GC
GAM2071 371 LOC1632 2 1413 NP_775802.1 3 1667 GCTCTGTCACCC 3 B b b
27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1632 2 9582 NP_775802.1 3 3357 CTCTTGTTGCCC TC TG 3 B c
b
27 AAGCTGGAGTGC ACTGCACTCCAG TGGG AC
AGTGGTGC TGACGTGAGGTC ACCC TG
GA GT
GAM2071 371 LOC1684 1 7426 XP_095114.2 3 695 ACTCTGTAACCC GA 3 B c c

51 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCCT TGACGTGAGGTCGGACCCA
AT
GAM2071 371 LOC1704 1 7616 XP_096330.1 5 65 GCAGCCTCATAA T GG 3 B c c
09 GGGCTGGAGTGC AC GCACTCCAGTCT GTGA
TGTGGTGC TG CGTGAGGTCGGG TACT
T AA
GAM2071 371 LOC1962 1 8574 XP_113683.1 3 810 CACTCTGTCGCC G 3 B b b
64 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGT TGACGTGAGGTCGGACC GCTG
-
GAM2071 371 LOC1969 1 7905 XP_116971.3 5 200 GAGACATCACCC C AGT--- 3 B c
c
93 AGTAGGAGGGAG ACTG ACTCC CTGGGTGA
TACGGTCT TGGC TGAGG GACCCACT
A GAGGAT
GAM2071 371 LOC1973 1 18551 NP_660337.1 5 104 TTGGACTCACCC A------ CCA 3 B c
c
36 AGATCTAGTGCA CTGCACT GTCTGGGTGA
GGGACACA GACGTGA TAGACCCACT
ACACAGG TC-
GAM2071 371 LOC1973 2 3887 XP_113872.2 3 2113 AATCTGTCACCC 3 B b b
58 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC1973 2 5402 XP_113872.2 3 1711 CTCTTGTCGCCC 3 B b b
58 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC1999 1 11637 XP_114052.1 3 1224 GCTGTGTTGTCC TG 3 B b b

06 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCT TG
GT
GAM2071 371 LOC2001 2 5066 XP_211599.1 3 1 CTGTCGTCCAGG GT 3 B b b
69 CTGGAGTGCAGT ACTGCACTCCAGTCTGG GAC
ACGCAATC TGACGTGAGGTCGGACC CTG
TG
GAM2071 371 LOC2001 2 6517 XP_117200.1 5 523 TTTCTGTCGTCC GT 3 B b b
69 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTAGCGC TGACGTGAGGTCGGACC CTG
TG
GAM2071 371 LOC2008 1 18182 XP_117289.1 3 1712 GCTCTGTCACCC 3 B b b
60 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2008 1 3376 NP_789785.1 3 934 ACTCTTGTTGCC A TG 3 B c c
95 CAGGCGGAGTGC ACTGCACTCC GTCTGGG AC
AGTGGAAC TGACGTGAGG CGGACCC TG
- GT

GAM2071_371 LOC2009_1 873 XP_114317.3 3 321 GTTCTGTCACCC 3 B b b
16 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGACTC TGACGTGAGGTCGGACCCACTG

GAM2071_371 LOC2011_2 13530 XP_290750.1 3 823 ACTCTGTGGCCC G 3 B b b
64 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCAC TGACGTGAGGTCGGACCCG TG
G
GAM2071_371 LOC2011_2 18118 NP_849158.1 3 823 ACTCTGTGGCCC G 3 B b b
64 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCGC TGACGTGAGGTCGGACCCG TG
G
GAM2071_371 LOC2012_1 14592 NP_775818.1 3 961 CATCTGTCACCC A----- T 3 B c c
92 AGGCTGGTGTGC CTGCAC CCAGTCTGGGTGAC
AGGGGTGC GACGTG GGTCGGACCCACTG
CGTGGG T
GAM2071_371 LOC2015_1 4316 XP_113972.1 3 6 GCTCTGTCACCC GC TC 3 B c c
10 AGGCTGTCGTAA ACT AC CAGTCTGGGTGAC
GTGGCAAT TGA TG GTCGGACCCACTG
A- CT
GAM2071_371 LOC2015_1 9102 XP_114343.2 3 1574 GCTCTGTTGCCC TG 3 B b b
62 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071_371 LOC2017_1 18941 XP_114370.1 3 1954 ACTCTATTGCTC TG TG 3 B c
c
25 AGGCTGGAGTGT AC CACTCCAGTCTGGG A
GGTGGCAG TG GTGAGGTCGGACTC T
GT GT
GAM2071_371 LOC2024_1 436 XP_117397.1 5 31 GCTCTGTCGCCC 3 B b b
00 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071_371 LOC2024_1 15206 XP_114481.4 3 52 ACTCTGTTGCCC TG 3 B b b
04 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGG TGACGTGAGGTCGGACCC TG
GT
GAM2071_371 LOC2024_1 1278 XP_114493.1 5 2041 TGCTCTGTCACC G 3 B b b
60 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGAGG TGACGTGAGGTCGGACC ACTG
-
GAM2071_371 LOC2029_2 6782 XP_117486.2 3 2743 AGCTCTGTCACC G 3 B b b
34 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC ACTG
-
GAM2071_371 LOC2029_2 9097 XP_117486.2 3 1522 ACTCTGTCACCC C 3 B b b
34 AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAT TGAC TGAGGTCGGACCCACTG
A
GAM2071_371 LOC2034_1 11590 NP_660348.1 3 529 GCTCTGTCACCC AC----- C 3 B c
c

27 AGACTGGAGTAC TG ACTCCAGTCTGGGTGAC
AATGACAC AC TGAGGTCAGACCCACTG
CACAGTA A
GAM2071 371 LOC2035 1 10631 XP_114719.1 3 1378 GCTCTGTTGCCC TG 3 B b b

47 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2192 1 12080 XP_166599.2 3 1202 TCTTGCTCGCCC G 3 B b b
93 AGGGTGGAGTGC ACTGCACTCCA TCTGGGTGA
AGTGGTGT TGACGTGAGGT GGACCCGCT
G
GAM2071 371 LOC2197 1 3320 XP_167596.1 5 1057 ACTCTGTCATCC 3 B b b
31 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAA TGACGTGAGGTCGGACCTACTG

GAM2071 371 LOC2197 1 3675 XP_167601.1 3 868 GCTCTGTTGCCC TG 3 B b b
35 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTCGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2198 1 7138 XP_167782.1 3 1072 CTCTGTTGCCCC - TG 3 B b b
94 AGGCTGGAGTGC ACTGCACTCCAGTCTGG G AC
AGTGGCGT TGACGTGAGGTCGGACC C TG
C GT
GAM2071 371 LOC2200 3 1413 NP_660352.1 3 542 GCTCTGTCACCC 3 B b b
74 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2200 3 2086 NP_660352.1 3 212 ACTCTGTCACAC G 3 B b b
74 AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
AGTGGCAC TGACGTGAGGTCGGAC CACTG
A
GAM2071 371 LOC2200 3 4396 NP_660352.1 3 382 CACTCGTCACCC CT 3 B b b
74 CAGCTGGAGTGC ACTGCACTCCAGT GGGTGAC
AGTGGTGC TGACGTGAGGTCG CCCACTG
AC
GAM2071 371 LOC2205 1 6273 NP_665808.1 5 748 TCTCTGTCATCT C TG 3 B c c
94 GGGCTGCAGTGC ACTGCACT CAGTC GGTGAC
AGTGGTGT TGACGTGA GTCGG CTACTG
C GT
GAM2071 371 LOC2216 1 10616 XP_168131.1 5 810 GCTCTGTTGCCA G TG 3 B c
c
63 AGGCTGGAGTGC ACTGCACTCCAGTCT GG AC
AGTGGAAC TGACGTGAGGTCGGA CC TG
A GT
GAM2071 371 LOC2216 1 1313 XP_168089.1 5 413 CACCCAACACCC TCCAG A 3 B c
c
83 AGAATCTGTGCA ACTGCAC TCTGGGTG
GTTATTTG TGACGTG AGACCCAC
TCTA- A

GAM2071 371 LOC2218 1 6429 XP_168226.1 5 1116 TGCTCTGTCGCC CA CTG 3 B c c
14 AAGCCAGAGTGC ACTGCACTC GT GGTGAC
AGTGGTGT TGACGTGAG CG CCGCTG
AC AA-
GAM2071 371 LOC2219 1 3294 XP_168340.1 3 920 GGAGAATCGCTT CT 3 B c c
46 GAGCTGGAGTGC ACTGCACTCCAGT GGGTGA
AGTGGTGC TGACGTGAGGTCG TTCGCT
AG
GAM2071 371 LOC2220 1 902 XP_166594.2 5 743 CTCTGTTGTCCA - TG 3 B c c
57 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT
GAM2071 371 LOC2220 1 6331 XP_166556.1 3 654 CTCTTGTCGCCC AC----- 3 B c c
68 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCGGACCCGCTG
TGCGGTA
GAM2071 371 LOC2529 1 8882 XP_170858.2 3 279 ACTCTGTCGCCC AC----- 3 B c c
83 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATACTGC ACGTGAGGTCGGACCCGCTG
CGTCATA
GAM2071 371 LOC2532 1 14534 XP_170765.2 3 757 CTGGCACTCAGG GC --- A 3 B c c
16 CAACTGGAGTAA ACT ACTCCAGT CTGGGTG
GTGCTCCC TGA TGAGGTCA GACTCAC
A- ACG G
GAM2071 371 LOC2536 1 19268 XP_172985.2 5 300 GCTCTGTCTCCC T 3 B b b
12 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
GGTGGCAC TGGCGTGAGGTCGGACCC CTG
T
GAM2071 371 LOC2538 1 7275 XP_172854.1 3 1253 ACTCTGTTGCCC TG 3 B b b
05 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGATGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2550 1 11416 XP_173187.1 3 219 AGCACGGGGCCC C GA 3 B c c
31 AGGCTAGAGTGC ACTGCACTC AGTCTGGGT
AGTGGCGT TGACGTGAG TCGGACCCG
A GG
GAM2071 371 LOC2554 1 18594 XP_172581.2 3 2633 CCTTTGTCACCC A 3 B b b
88 AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCAT TGACGTGAGG CGGACCCACTG
C
GAM2071 371 LOC2559 1 902 XP_171083.2 5 863 CTCTGTTGTCCA - TG 3 B c c
75 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT
GAM2071 371 LOC2566 1 3106 XP_172864.1 3 860 ACTCTGTCACCC 3 B b b
14 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2829 1 8939 XP_212606.1 5 164 CCTCTGTCGCCA T G- 3 B c c
05 AAGTTGGAGTGC ACTGCACTCCAG CT GGTGAC
AGTGGCGC TGACGTGAGGTT GA CCGCTG
- AA
GAM2071 371 LOC2829 1 8939 XP_212647.1 5 164 CCTCTGTCGCCA T G- 3 B c c
43 AAGTTGGAGTGC ACTGCACTCCAG CT GGTGAC
AGTGGCGC TGACGTGAGGTT GA CCGCTG
- AA
GAM2071 371 LOC2829 2 10460 XP_210845.1 5 33 ACTTTGTCACCC C 3 B b b
87 AGGCTGGAGTAT ACTG ACTCCAGTCTGGGTGAC
AGTGGCAC TGAT TGAGGTCGGACCCACTG
A
GAM2071 371 LOC2829 2 12386 XP_210845.1 3 527 GCTCTGTTGCCC TG 3 B b b
87 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2830 1 654 XP_210859.1 3 172 CTTGTGTCACCC A----- T 3 B c c
31 AGGCTGGCGTGC CTGCAC CCAGTCTGGGTGAC
AGGGCCCT GACGTG GGTCGGACCCACTG
TCCCGG C
GAM2071 371 LOC2830 1 18916 XP_210875.1 3 1387 AGTTTGTCACCC 3 B b b
61 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2830 1 18641 XP_208501.1 3 1414 GCCACTGCACTC A---- - T - A 3 B c
c
67 CAGCTGGAGTGA CTG CACTCCAG CTGG GTG
CAGAGCCA GAC GTGAGGTC GACC CAC
ACCGA A - T G
GAM2071 371 LOC2830 1 6936 XP_208509.1 3 177 ATTGTGTTCCCC C TG 3 B c c
87 AGGCTGAAGTGC ACTGCACT CAGTCTGGG AC
AGTGGCAT TGACGTGA GTCGGACCC TG
A CT
GAM2071 371 LOC2830 1 6866 XP_210885.1 5 1720 GCTCTGTCGCCC C 3 B b b
89 AGGCTCGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAT TGACGTGAG TCGGACCCGCTG
C
GAM2071 371 LOC2831 1 1505 XP_210895.1 3 711 ACTCTCTTGCCC TG 3 B b b
19 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTAT TGACGTGAGGTCGGACCC T
GT
GAM2071 371 LOC2831 1 469 XP_208525.3 3 379 TCTCTGTCACCC C 3 B b b
30 AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC
AGTGGCGT TGACGT AGGTCGGACCCACTG
A
GAM2071 371 LOC2831 1 14843 XP_210920.1 3 2296 CACTCTGTCACC G 3 B b b
43 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 LOC2831 1 17431 XP_210917.2 5 316 CCTCTGTCATCC 3 B b b
52 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCTACTG

GAM2071 371 LOC2831 1 19643 XP_208535.1 3 648 GCTCTGTTGCCC TG 3 B b b
70 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGA TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2831 2 4762 XP_210929.1 5 197 CAGACAGCACCC G ----- A 3 B c c

99 AGAGTGAGCTGG ACT CACTCCAGT CTGGGTG
AGTGGGTC TGG GTGAGGTCG GACCCAC
- AGTGA G
GAM2071 371 LOC2831 2 20110 XP_210929.1 5 197 AGCACCCAGAGT G ----- A 3 B c
c
99 GAGCTGGAGTGG ACT CACTCCAGT CTGGGTG
GTCCCCAT TGG GTGAGGTCG GACCCAC
- AGTGA G
GAM2071 371 LOC2832 1 14997 XP_208555.2 3 1990 CCTATGTCACCG CC G 3 B c
c
15 AGGCTACAGTGC ACTGCACT AGTCT GGTGAC
AGTGGTTC TGACGTGA TCGGA CCACTG
CA G
GAM2071 371 LOC2832 1 10625 NP_787089.1 5 62 GCTCTGTCGCCC GT 3 B b b
41 AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGTGC TGACGTGAGGT GACCCGCTG
TG
GAM2071 371 LOC2832 1 438 XP_210962.1 3 345 ACTCTGTCACCC 3 B b b
93 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2833 1 6052 XP_210978.1 5 937 GCTCTGTCGCCC AC----- 3 B c c
29 AGACTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCAGACCCGCTG
CGTGGTA
GAM2071 371 LOC2833 2 9238 XP_210981.1 3 1636 GCTCTGTCACCC A 3 B b b
35 AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGTGC TGACGTGAGG CGGACCCACTG
C
GAM2071 371 LOC2833 2 10626 XP_210981.1 3 1368 GCTCTGTTGCCC TG 3 B b b

35 AGGCTGGAGTGT ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGATGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2833 1 8862 XP_208647.1 3 807 ACTCTGTCACCC 3 B b b
77 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2833 1 13838 XP_211020.1 3 527 CACTCTGTTGCT G TG 3 B c c

95 AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCAC TGACGTGAGGTCGGAT C TG
- GT
GAM2071 371 LOC2834 1 6836 XP_211032.1 5 1942 CGCTGTATTGCC GTGA 3 B c c
32 AGACTGGAGTGC ACTGCACTCCAGTCTGG
AGTGGCGT TGACGTGAGGTCAGACC
GTTA
GAM2071 371 LOC2834 1 16416 XP_211034.1 5 1756 TTGCCATCTCAG C -- - A 3 B c c
34 TTGCTGCAGTGC ACTGCACT CAGT CTG GGTG
AGTGAATT TGACGTGA GTCG GAC CTAC
C TT T C
GAM2071 371 LOC2834 1 9159 XP_211044.1 5 305 ACTGTGTCATGC G 3 B b b
45 AGGCTGGAGTGC ACTGCACTCCAGTCTG GTGAC
AGTGGCAT TGACGTGAGGTCGGAC TACTG
G
GAM2071 371 LOC2834 1 17791 XP_208679.1 5 488 GGTCTGACACCT TG A 3 B c c
52 GGGCTGGAGTGC ACTGCACTCCAGTC GGTG
AGTGGTGC TGACGTGAGGTCGG CCAC
GT A
GAM2071 371 LOC2834 1 12385 XP_211049.1 5 127 ACTCTGTCACCC 3 B b b
54 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG
GAM2071 371 LOC2834 2 8583 XP_211056.1 3 2564 TCTGTTTCCCCC C- --- T 3 B c b
75 AGACTCCTGGAG ACTG ACTCCA GTCTGGG GA
TTCTAGTC TGAT TGAGGT CAGACCC CT
CT CCT C
GAM2071 371 LOC2834 2 12806 XP_211056.1 3 1713 GTTCTCTTGCCC TG 3 B b b
75 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCAC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 LOC2835 1 18182 XP_211075.1 3 1819 GCTCTGTCACCC 3 B b b
07 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG
GAM2071 371 LOC2835 1 13197 XP_211083.1 3 3278 ACTCTGTCACCC 3 B b b
34 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCTT TGACGTGAGGTCGGACCCACTG
GAM2071 371 LOC2835 1 6104 XP_211100.1 5 198 GAGCTCTCACCC G CCA - 3 B c c
65 AGAGCGTCAGTG ACT CACT G TCTGGGTGA
AGTTGGTG TGA GTGA C AGACCCACT
- CTG G
GAM2071 371 LOC2835 1 3904 XP_294741.1 5 479 ACTCTGTCACCC AC----- TC 3 B c c

85 AAGCTGGAGTGC TGCACTCCAG TGGGTGAC
ACTGGCAT ACGTGAGGTC ACCCACTG
TACGGTC GA
GAM2071 371 LOC2835 1 14938 NP_787093.1 3 910 GCTCTGTTGCCC TG 3 B b b

88 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
GGTGGACT TGGCGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2836 1 13972 XP_211126.1 5 750 ACTCTCACACCC A 3 B b b
24 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTCTCAA TGACGTGAGGTCGGACCCAC
A
GAM2071 371 LOC2836 2 3786 XP_211134.1 5 1237 GCTCTGTCGCCC C 3 B b b
37 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGTAT TGACGTGAG TCGGACCCGCTG
A
GAM2071 371 LOC2836 2 12382 XP_211134.1 5 360 GCTCTGTCGCCC 3 B b b
37 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2836 1 435 XP_208764.1 3 226 GCTCTGTTGCCC TG 3 B b b
41 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2836 1 11292 XP_208773.1 5 11 CTTTTGTCACCC ACT----- 3 B c c
64 AGGCTGGAGTGC GCACTCCAGTCTGGGTGAC
CATGGCAC CGTGAGGTCGGACCCACTG
CACGGTAC
GAM2071 371 LOC2836 1 18582 XP_211157.1 5 114 TCACTCCATGAA A----- ----- - 3 B c c
79 TGACTGGAGTGT CTGCACTCCAGTC TGG GTG
AGGGGCAG GATGTGAGGTCAG ACC CAC
GACGGG TAAGT T

A
T

GAM2071 371 LOC2836 1 5544 NP_787094.1 3 1228 ATTTTGTCACCG AC----- G 3 B c
c
87 AGGCTGGAGTGC TGCACTCCAGTCT GGTGAC
AATGGCCC ACGTGAGGTCGGA CCACTG
CCCGGTA G
GAM2071 371 LOC2837 2 777 XP_211170.3 3 3386 TGCTCTGTCACC G 3 B b b
01 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
GGTGGCAT TGGCGTGAGGTCGGACC ACTG
-
GAM2071 371 LOC2837 2 7650 XP_211170.3 5 528 TTCCTCGCACCC CA - G A 3 B c
b
01 AGATGGTAGCCA ACTG CT CCA TCTGGGTG
GTCTTCCA TGAC GA GGT AGACCCAC
C- T - G

GAM2071 371 LOC2837 1 16154 XP_208804.3 3 978 CCAGGCTCACCC GC- 3 B c c

06 AGGCTGGGGTCT ACT ACTCCAGTCTGGGTGA
GAGTGTCA TGA TGGGGTCGGACCCACT
GTC

GAM2071 371 LOC2837 1 3109 XP_208115.1 3 289 GCTCTGTCGCCC 3 B b b
41 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2837 1 15679 XP_211199.1 5 1256 GCTCTGTCGCCC 3 B b b
78 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGG TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2838 1 11237 XP_208122.1 3 1460 CTAGTGTTGCCC TG 3 B b b

01 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC2838 1 16635 XP_208850.1 3 948 ACTCTGTCATCC 3 B b b
02 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCTACTG

GAM2071 371 LOC2838 1 3834 XP_211218.1 3 255 ACTCTGTCACCC T 3 B b b
18 CGGCTGGAGTGC ACTGCACTCCAGTC GGGTGAC
AGTGGTGT TGACGTGAGGTCGG CCCACTG
C

GAM2071 371 LOC2838 1 12708 XP_211229.1 3 678 ACTCTGTCACCG GT G 3 B b
b
51 AGGTTGGAGTGC ACTGCACTCCA CT GGTGAC
AGTGGTAT TGACGTGAGGT GA CCACTG
TG G

GAM2071 371 LOC2838 2 8996 NP_787095.1 3 1033 GCTCTGTCGACC A----- G 3 B c
b
61 AGGCTGGAGTGC CTGCACTCCAGTCTGG TGAC
AGGGGCAC GACGTGAGGTCGGACC GCTG
CACGGG A

GAM2071 371 LOC2838 2 10879 NP_787095.1 3 712 CCTCTGTCGTCC GT 3 B b b
61 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTGGCAC TGACGTGAGGTCGGACC CTG
TG

GAM2071 371 LOC2838 1 9775 XP_211248.2 5 723 GCTCTGTCTCCC T 3 B b b
87 GGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGC TGACGTGAGGTCGGGCCC CTG
T

GAM2071 371 LOC2838 1 13686 XP_208899.1 3 783 ATTCTGTCACCC A 3 B b b
89 AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGTGT TGACGTGAGG CGGACCCACTG
C

GAM2071 371 LOC2839 3 3604 XP_208909.1 5 2715 ACTCTGTTGCCC TG 3 B b b
28 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

AGTGTCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2839 3 9603 XP_208909.1 5 810 CTCTTGTCACCT CA 3 B b b
28 AGGCCAGAGTGC ACTGCACTC GTCTGGGTGAC
AGTGTCAT TGACGTGAG CGGATCCACTG
AC
GAM2071 371 LOC2839 3 13293 XP_208909.1 5 2419 GTTCTGCTGCCC GT A 3 B c
b
28 AGGTTGGAGTGC ACTGCACTCCA CTGGGTG
AGTGGCAC TGACGTGAGGT GACCCGT
TG C
GAM2071 371 LOC2839 1 10232 XP_208905.2 5 919 GCTCCGTCACCC 3 B b b
29 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2839 1 15305 NP_787097.1 3 1068 GCTCTGTCACTT GT TG 3 B c
c
32 GGGTTGGAGTGC ACTGCACTCCA C GGTGAC
AGTTGCAG TGACGTGAGGT G TCACTG
TG GT
GAM2071 371 LOC2839 1 1384 XP_208145.2 3 1457 CTAGTGTCACCC 3 B b b
64 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGATCC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2840 1 6195 XP_208958.2 3 1484 ACACTGTCGCCC AC----- TC 3 B c
c
01 AATCTGGAGTGC TGCACTCCAG TGGGTGAC
ACTGGCGC ACGTGAGGTC ACCCGCTG
CGCGGTC TA
GAM2071 371 LOC2840 1 3858 XP_208961.1 3 353 GCTCTGTAACTC GA 3 B c c
17 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCGC TGACGTGAGGTCGGACTCA
AT
GAM2071 371 LOC2840 2 429 XP_208983.3 3 1472 GCTCTGTTGCCC TG 3 B b b
23 AGACTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCAGACCC TG
GT
GAM2071 371 LOC2840 2 5520 XP_208983.3 3 1017 ACTGTGTCGCCC 3 B b b
23 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2840 1 17222 XP_208152.1 3 1241 TCACTGTCACCC A 3 B b b
48 AGGCCGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCAC TGACGTGAGG CGGACCCACTG
C
GAM2071 371 LOC2840 1 17713 XP_208992.1 3 181 CCTCTGTTGTCC C TC TG 3 B c
c
63 AAGCTAGAGTGC ACTGCACTC AG TGGG AC
AGTGATAC TGACGTGAG TC ACCT TG
A GA GT

GAM2071 371 LOC2840 2 5751 XP_211321.1 3 982 ACTCAGTCGCCC 3 B b b
74 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2840 2 18547 XP_211321.1 3 57 GCCCTGTTGCCC C TG 3 B c b
74 AGGCTGAAGTGC ACTGCACT CAGTCTGGG AC
AGTGGTGC TGACGTGA GTCGGACCC TG
A GT

GAM2071 371 LOC2840 1 18527 XP_211323.1 3 1 CTGTCACCCAGG C 3 B b b
82 CTGAAGTGCAGT ACTGCACT CAGTCTGGGTGAC
GCAGGACC TGACGTGA GTCGGACCCACTG
A

GAM2071 371 LOC2840 2 16884 XP_211324.1 3 844 ACTCTGTCACCC T 3 B b b
95 TGGCTGGAGTGC ACTGCACTCCAGTC GGGTGAC
GGTGGCGA TGGCGTGAGGTCGG CCCACTG
T

GAM2071 371 LOC2840 2 19595 XP_211324.1 3 142 GCTCTGTCATTC 3 B b b
95 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACTTACTG

GAM2071 371 LOC2840 1 18178 XP_209008.3 3 197 GCTCTGTTACCC 3 B b b
98 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGATGTGAGGTCGGACCCATTG

GAM2071 371 LOC2841 1 17111 XP_211327.3 5 861 GCTTTGTCACCC 3 B b b
02 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2841 1 11925 XP_209004.1 3 252 GCCTGCCCAACC --- - G A 3 B c c
06 AGACTGGTAGTC ACTGC ACT CCAGTCTGG TG
CTGCAGTC TGACG TGA GGTCAGACC AC
TCC T A C

GAM2071 371 LOC2841 1 1709 XP_211338.2 5 329 TGGGGCTCCCAC AC----- - T 3 B c c
16 AGGCTGGAGTGC TGCACTCCAGTCTG GG GA
AATGGTGT ACGTGAGGTCGGAC CC CT
TGTGGTA A -

GAM2071 371 LOC2841 1 11347 XP_209024.1 3 57 GCTTTGTCGCCC T 3 B b b
17 TGGCTGGAGTGC ACTGCACTCCAGTC GGGTGAC
AGTTGCGC TGACGTGAGGTCGG CCCGCTG
T

GAM2071 371 LOC2841 2 17271 XP_211342.1 3 0 TCGCCCAGGCTG 3 B b b
28 GAGTGCAGTGGT ACTGCACTCCAGTCTGGGTGA
AGATCAGG TGACGTGAGGTCGGACCCGCT

GAM2071 371 LOC2841 2 17792 XP_211342.1 3 460 GCCCTGTCGCCC ACT----- 3 B c b
28 AGGCTGGAGTGC GCACTCCAGTCTGGGTGAC

CATGGCGC CGTGAGGTCGGACCCGCTG
CGCGGTAC
GAM2071 371 LOC2841 1 8678 XP_211353.1 5 368 CGCTCTGTCGCC AC----- G 3 B c
c
45 AGGCTGGAGTGC TGCACTCCAGTCTGG TGAC
AATGGCGC ACGTGAGGTCGGACC GCTG
CGCGGTA -
GAM2071 371 LOC2841 1 12420 XP_209051.1 3 1094 CTGTTGTCGCCT AC----- 3 B c
c
71 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGATGC ACGTGAGGTCGGATCCGCTG
CGTAGTA
GAM2071 371 LOC2841 1 18182 XP_209060.2 3 1161 GCTCTGTCACCC 3 B b b
86 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2841 1 7923 XP_211377.1 5 62 CTCTTGTCGCCC AC----- 3 B c c
91 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AACGGTAT ACGTGAGGTCGGACCCGCTG
TATGGCA
GAM2071 371 LOC2842 1 5421 XP_211411.1 5 1561 CATCTGTCACCC AC----- 3 B c c

67 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAT ACGTGAGGTCGGACCCACTG
TACGGTA
GAM2071 371 LOC2842 1 12113 XP_211412.1 5 1026 ACTTTGTCACCC AC----- 3 B c c

76 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCGGACCCACTG
TGCGGTA
GAM2071 371 LOC2842 1 5521 XP_211419.1 3 1828 ACTCTGTCTCCC T 3 B b b
86 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGTGC TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 LOC2842 1 7635 XP_209105.1 3 145 CTCTTGTTACCC A 3 B b b
89 AGGCAGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCGT TGACGTGAGG CGGACCCATTG
A
GAM2071 371 LOC2843 1 16163 XP_211426.1 3 314 CTCTTATTGCCC TG 3 B b b
04 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGACGA TGACGTGAGGTCGGACCC T
GT
GAM2071 371 LOC2843 2 12588 XP_211425.1 5 1681 ACTCTGTCACCC T C 3 B b b

05 ATGCTGGTGTGC ACTGCAC CCAGT TGGGTGAC
AGTGGCGT TGACGTG GGTCG ACCCACTG
T T
GAM2071 371 LOC2843 2 15706 XP_211425.1 5 1273 ACTCTGCCACCC C A 3 B b b

05 AGACTGAAGTGC ACTGCACT CAGTCTGGGTG

AGTGGTGC TGACGTGA GTCAGACCCAC
A C
GAM2071 371 LOC2843 2 5320 XP_209162.1 3 1765 ACTCTCTCGCCC 3 B b b
17 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCGT TGACGTGAGGTCGGACCCGCT

GAM2071 371 LOC2843 2 11486 XP_209162.1 3 812 ATTCTGTCACAC T T G 3 B c b
17 AGTCTGGAGTGC AC GCACTCCAG CTG GTGAC
TGTGGTGC TG CGTGAGGTC GAC CACTG
T T A
GAM2071 371 LOC2843 1 11129 XP_211432.1 5 1 TCTTCCCGAGGC T -- G T 3 B c c
21 CCTGGAGTGCCG AC GCACTCCA GTCT GG GA
TGCGTGTG TG CGTGAGGT CGGA CC CT
C CC G -
GAM2071 371 LOC2843 1 11657 XP_209143.1 3 1032 GTTCTGTCGTCC GT 3 B b b

25 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
GGTGGCGT TGGCGTGAGGTCGGACC CTG
TG
GAM2071 371 LOC2843 1 10666 XP_211435.1 3 529 CACTTGTCACCC 3 B b b
62 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCTC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2843 1 13618 XP_209154.1 3 930 GCTCTGTCATCC GT 3 B b b
75 AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCAT TGACGTGAGGT GACCTACTG
TG
GAM2071 371 LOC2843 1 9328 XP_209157.1 3 1219 GCTCTGTCGCCC C TC 3 B c
c
76 AAGCTGAAGTGC ACTGCACT CAG TGGGTGAC
AGTGGTGC TGACGTGA GTC ACCCGCTG
A GA
GAM2071 371 LOC2843 1 2198 XP_209163.1 3 383 GCTCTATTGCCC T TG 3 B c c
79 AGTCTGGAGTGC ACTGCACTCCAG CTGGG A
AGTGGCAT TGACGTGAGGTC GACCC T
T GT
GAM2071 371 LOC2844 1 3894 XP_209183.2 3 907 GCTCTGTCACCC C C 3 B b b
05 AGGCTGTAGTAC ACTG ACT CAGTCTGGGTGAC
AGTGGTGC TGAC TGA GTCGGACCCACTG
A T
GAM2071 371 LOC2844 2 2985 XP_209200.1 3 54 GCTTAGCCGTCC C GT A 3 B c b

21 AGGCTAGAGTGC ACTGCACTC AGTCTGG G
AGTAGTGC TGACGTGAG TCGGACC C
A TG C
GAM2071 371 LOC2844 2 15524 XP_209200.1 5 1198 GCTCTGTTGCCC TG 3 B b b

21 GGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGGCCC TG
GT

GAM2071 371 LOC2844 2 932 XP_209198.1 3 475 ATGCTGCTGCCC A 3 B c b
26 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGTGC TGACGTGAGGTCGGACCCGT
C
GAM2071 371 LOC2844 2 19419 XP_209198.1 3 310 GCTCTGTCGCCC 3 B b b
26 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGACAT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2844 1 6140 XP_290862.1 3 85 ACTCTGCTGCCC C A 3 B c c
36 GGGCTAGAGTGC ACTGCACTC AGTCTGGGTG
AGTGGTGG TGACGTGAG TCGGGCCCGT
A C
GAM2071 371 LOC2844 1 12050 XP_209210.1 3 761 CCCTCTGTCACC G 3 B b b
40 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 LOC2844 2 3963 XP_209216.1 5 679 GCACTGTCACCC AC----- 3 B c c
54 GGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCTC ACGTGAGGTCGGGCCCACTG
CTCGGTA
GAM2071 371 LOC2844 2 18896 XP_209216.1 5 1115 ACTCTGTTGCCC C TG 3 B c
c
54 AGGCTGAAGTGC ACTGCACT CAGTCTGGG AC
AGTGGTGT TGACGTGA GTCGGACCC TG
A GT
GAM2071 371 LOC2844 1 10594 XP_211470.1 5 657 GCTCTGTCACCT C 3 B b b
56 AGGCTGCAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGCAC TGACGTGA GTCGGATCCACTG
C
GAM2071 371 LOC2844 1 1740 XP_290826.1 3 569 CATAAAAGACCC - CC GA 3 B c
c
59 AGACTCAGCTGC ACTGCA CT AGTCTGGGT
AGTGAGGA TGACGT GA TCAGACCCA
C C- GA
GAM2071 371 LOC2844 1 4926 XP_209225.1 3 1167 ACTCTGTCACCC CT 3 B b b
71 AGGCTGGGATGC ACTGCA CCAGTCTGGGTGAC
AGTGGCTT TGACGT GGTCGGACCCACTG
AG
GAM2071 371 LOC2844 1 10824 XP_209231.1 3 487 CACCCTGGCTTC C------- T A 3 B c
c
86 CATCATGAGTGC ACTGCACTC AGTC GGGTG
AGTGTCAT TGACGTGAG TCGG CCCAC
TACTACCT T -
GAM2071 371 LOC2845 1 19066 XP_211502.1 5 907 GCCCAATAGCCC GA 3 B c c

13 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCAG TGACGTGAGGTCGGACCCG
AT
GAM2071 371 LOC2845 1 2846 XP_211513.1 5 339 GCTCTGTCTCCC A----- T 3 B c c
31 AGGCTGGAGTGC CTGCACTCCAGTCTGGG GAC

AGGCTTGG GACGTGAGGTCGGACCC CTG
GGTTCG T

GAM2071 371 LOC2845 1 17959 XP_211515.1 3 1302 ACTCTGTCACCC 3 B b b
51 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2845 1 11682 XP_211522.1 3 6 ACTCTGTCTCCC G T 3 B b b
77 AGACTGGAGTGA ACT CACTCCAGTCTGGG GAC
GTGGTGTG TGA GTGAGGTCAGACCC CTG
- T

GAM2071 371 LOC2845 1 902 XP_209278.3 5 72 CTCTGTTGTCCA - TG 3 B c c
87 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT

GAM2071 371 LOC2846 1 11652 XP_211552.1 3 976 GCTCGGTCACCT 3 B b b
11 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGATGTGAGGTCGGATCCACTG

GAM2071 371 LOC2846 1 8487 XP_209319.1 5 556 GCTCTGTCACCC -- 3 B b b
75 AGGCTGGAGTGT ACTGCAC TCCAGTCTGGGTGAC
GCAGTGGC TGACGTG AGGTCGGACCCACTG
TG

GAM2071 371 LOC2847 1 902 XP_294994.1 5 865 CTCTGTTGTCCA - TG 3 B c c
01 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT

GAM2071 371 LOC2847 2 6492 XP_211602.1 3 59 ACTCTGCCACCC TC A 3 B c b
23 AAGCTGGAGTGC ACTGCACTCCAG TGGGTG
AGTGGCAC TGACGTGAGGTC ACCCAC
GA C

GAM2071 371 LOC2847 2 17106 XP_211602.1 3 471 GCTTTGTTGCCC TG 3 B b b
23 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
GGTGGTGC TGGCGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC2848 2 11447 XP_209371.1 3 1212 TTTTGCCCAGGC ---- TG 3 B c
c
05 TGGATGGAGTGC ACTGCACTCCA GTCTGGG A
AGTGGCGT TGACGTGAGGT CGGACCC T
AGGT GT

GAM2071 371 LOC2848 2 18781 XP_209371.1 3 1110 ACTCTGCTGCTC A 3 B c c
05 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGTGC TGACGTGAGGTCGGACTCGT
C

GAM2071 371 LOC2848 1 15141 XP_211663.1 3 907 GTACTTAAAGCA GTC A 3 B c
c
45 CCTGTGGAGTGC ACTGCACTCCA TGGGTG
GGTCGCTC TGGCGTGAGGT GTCCAC
--- G

GAM2071 371 LOC2848 1 3436 XP_211668.2 3 618 CTCTTGTCCCCC AC----- T 3 B c c

```
          56                      AGACTGGAGTGC      TGCACTCCAGTCTGGG GAC
                                  AATGGCAC          ACGTGAGGTCAGACCC CTG
                                        CACGGTA             C
GAM2071  371   LOC2848 1  3436  XP_302835.1  3  107   CTCTTGTCCCCC AC-----          T      3  B  c  c

          56                      AGACTGGAGTGC      TGCACTCCAGTCTGGG GAC
                                  AATGGCAC          ACGTGAGGTCAGACCC CTG
                                        CACGGTA             C
GAM2071  371   LOC2848 1  2751  XP_209394.1  3  615   TGCTCTGCGCCC         GT     A       3  B  c  c

          74                      AGGATGGAGTGC ACTGCACTCCA  CTGGGTG
                                  AGTGGCAT    TGACGTGAGGT  GACCCGC
                                              AG      G
GAM2071  371   LOC2849 1  17477 XP_211696.1  5  656   GTTTTGTCGCCC                    3  B  b  b
          34                      AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
                                  AGTGGCAT    TGACGTGAGGTCGGACCCGCTG

GAM2071  371   LOC2849 2  1362  XP_211703.1  3  1524  GCTCTGTCACCA A-----          G       3  B  c  b

          50                      AGGCTGGAGTGC      CTGCACTCCAGTCT GGTGAC
                                  AGCGGTGT          GACGTGAGGTCGGA CCACTG
                                        TGTGGC              A
GAM2071  371   LOC2849 2  6753  XP_211703.1  3  163   CACTCTGTCGCC             G         3  B  b  b
          50                      AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
                                  AGTGGCGT    TGACGTGAGGTCGGACC GCTG
                                                 -
GAM2071  371   LOC2849 1  6801  XP_209425.1  5  122   AGGGCCTGTCCC A-----      -   CT  T     3  B  c
c
          65                      TACTGAGAGTGC      CTGCACTC CAGT  GGG GAC
                                  AGGGAACT          GACGTGAG GTCA  TCC CTG
                                        TCAAGG        A   --  -
GAM2071  371   LOC2849 1  5711  XP_211714.1  3  925   TAAGTCACTCCC A  ---   - --      --     3  B  c  c
          76                      AGACTAGGGAAG  CTG   CACT CC  AGTCTGGG  TGAC
                                  TGACTCAG     GAC   GTGA GG  TCAGACCC  ACTG
                                        -  TCA    A  GA       TC
GAM2071  371   LOC2850 1  14276 XP_209440.1  3  2381  GCTCTGTCACCC                    3  B  b  b
          26                      AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
                                  AGTGGTGC    TGACGTGAGGTCAGACCCACTG

GAM2071  371   LOC2850 1  5968  XP_211751.1  3  865   ATTCTGTCACCC     A  C             3  B  b  b
          52                      AGGCTAGAGCGC ACTGC CTC AGTCTGGGTGAC
                                  AGTGGCAA    TGACG GAG TCGGACCCACTG
                                              C   A
GAM2071  371   LOC2850 1  10836 XP_211753.1  5  232   GCTCTGTCACCC    C      ---          3  B  b  b
          58                      AGGTGGCTGGAG ACTG ACTCCAGT   CTGGGTGAC
                                  TACAGTGG    TGAC TGAGGTCG   GACCCACTG
                                              A       GTG
GAM2071  371   LOC2850 1  18085 XP_209464.1  3  986   GCTCTATCACCC       C             3  B  b  b
          83                      AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGA
                                  AGTGGTAC    TGACGTGA GTCGGACCCACT
```

A

GAM2071 371 LOC2850 1 2931 XP_209471.1 5 587 AAAAGTTAATTT C TG -- 3 B c c
94 TGGGCTGAGTGC ACTGCACTC AGTC GG TGAC
AGTGGCTT TGACGTGAG TCGG TT ATTG
- GT TA

GAM2071 371 LOC2851 2 3106 XP_211771.1 3 144 ACTCTGTCACCC 3 B b b
27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2851 2 19204 XP_211771.1 3 577 GCTCTGTCACCC 3 B b b
27 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCCC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2851 1 12167 XP_209500.1 3 170 GCTCTTTTGCCC G TG 3 B c c

76 AGACTGGAGTGA ACT CACTCCAGTCTGGG A
AGTAGCAT TGA GTGAGGTCAGACCC T
A GT

GAM2071 371 LOC2851 1 13870 XP_209509.1 3 677 TCTCTGTTGCCC TG 3 B b b
93 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC2852 1 15365 XP_209521.1 5 77 AATCTGTCACCC A 3 B b b
21 AGGCTGGAGCGC ACTGC CTCCAGTCTGGGTGAC
AGTGGTGT TGACG GAGGTCGGACCCACTG
C

GAM2071 371 LOC2852 3 3632 XP_211813.1 3 1259 TCACTGTCACCC G T 3 B b b
31 AGTCTGGAGTGG ACT CACTCCAG CTGGGTGAC
AGTGGCAT TGA GTGAGGTC GACCCACTG
G T

GAM2071 371 LOC2852 3 11238 XP_211813.1 3 722 GCTCTGTCACCC TC 3 B b b
31 AAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGTGC TGACGTGAGGTC ACCCACTG
GA

GAM2071 371 LOC2852 3 13069 XP_211813.1 3 888 ACTCTGTCACCC TC 3 B b b
31 AAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGTGC TGACGTGAGGTC ACCCACTG
GA

GAM2071 371 LOC2852 1 7766 XP_211829.1 5 564 CTCTTGTTACCC AC----- 3 B c c
81 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAC ACGTGAGGTCGGACCCATTG
CACGGTA

GAM2071 371 LOC2852 1 15961 XP_209554.1 3 398 GCTATGTCACTC 3 B b b
99 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACTCACTG

GAM2071 371 LOC2853 2 11821 XP_211854.1 3 868 ACAGGGTTGCCC G TG 3 B c
b
45 AGGGTGGAGTGC ACTGCACTCCA TCTGGG AC
AGTGGCAG TGACGTGAGGT GGACCC TG

G GT
GAM2071 371 LOC2853 2 13276 XP_211854.1 3 1257 ACTCTGTTACCC C 3 B b b
45 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCGC TGACGTGAG TCGGACCCATTG
A
GAM2071 371 LOC2853 1 4019 XP_209581.1 3 514 GCTCTGTCACCC 3 B b b
66 AGGCTGGGGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGGGGTCGGACCCACTG

GAM2071 371 LOC2853 1 19816 XP_211861.3 3 250 ACTTTGTCACCC 3 B b b
69 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2853 1 5624 XP_211869.1 3 264 CCCAGGTCACCC A--- - CA-- C 3 B c
c
70 AACCAGCGAGTG CTGC ACTC GT TGGGTGAC
GCAGAACT GACG TGAG CA ACCCACTG
TCAA G CGAC -
GAM2071 371 LOC2853 1 7025 XP_211873.1 3 1011 TCTCTCTCGCCA GT TG 3 B c
c
89 TGGTTGGAGTGC ACTGCACTCCA C GGTGA
AGTGGTGC TGACGTGAGGT G CCGCT
TG TA
GAM2071 371 LOC2853 2 436 XP_211879.1 3 343 GCTCTGTCGCCC 3 B b b
92 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2853 2 6034 XP_211879.1 3 40 GCTCTGTCTCCC T 3 B b b
92 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 LOC2853 2 3701 XP_209593.1 3 1207 CTCCTCTCGCCC 3 B b b
98 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGTGT TGACGTGAGGTCGGACCCGCT

GAM2071 371 LOC2853 2 4020 XP_209593.1 3 906 ACTCTGTCGCCC 3 B b b
98 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2854 1 3267 XP_209596.1 3 4639 CTTAGACCACCC GC CC A 3 B c
c
00 AGACTAGTCAAG ACT ACT AGTCTGGGTG
TATCTTCT TGA TGA TCAGACCCAC
AC -- C
GAM2071 371 LOC2854 1 1914 XP_209600.1 3 817 TTCTGATTCAGT G - GG 3 B c c
09 AGACTGGAGGTG ACT CAC TCCAGTCTG TGA
AAGTCAGG TGA GTG AGGTCAGAT ACT
A G G-
GAM2071 371 LOC2854 1 4870 XP_209607.3 3 1517 CTTCTGTCGCCC 3 B b b
29 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC

AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2854 1 11093 XP_211914.1 5 571 TCACTGTCGCCC 3 B b b
88 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGTGC TGGCGTGAGGTCGGACCCGCTG

GAM2071 371 LOC2854 1 8951 XP_211917.1 3 164 GCTCTGTCCCTC T 3 B b b
91 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTAGCGT TGACGTGAGGTCGGACTC CTG
C
GAM2071 371 LOC2855 1 11997 XP_211923.1 5 175 CTACTTTCATTC 3 B b b
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAT TGACGTGAGGTCGGACTTACT

GAM2071 371 LOC2855 2 5384 XP_209654.1 5 7 ACTGTGTCGCCC - 3 B b b
40 AGGCTGGAGTGC ACT GCACTCCAGTCTGGGTGAC
AAGTGGCA TGA CGTGAGGTCGGACCCGCTG
A
GAM2071 371 LOC2855 2 19426 XP_209654.1 5 1534 GCTCTGTCACCC 3 B b b
40 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2855 2 3782 XP_209671.1 3 266 ACTTGATCACCC C 3 B b b
89 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGA
AGTGGCGT TGACGTGAG TCGGACCCACT
A
GAM2071 371 LOC2855 2 14069 XP_209671.1 3 720 GCTCTGTCGCCA G 3 B b b
89 GGACTGGAGTGC ACTGCACTCCAGTCT GGTGAC
AGTGACAC TGACGTGAGGTCAGG CCGCTG
A
GAM2071 371 LOC2855 1 9271 XP_211946.2 3 539 TCATAAGGTAGT C CT TG 3 B c
c
94 CCACTGAAGTGC ACTGCACT CAGT GGG AC
AGTCATCA TGACGTGA GTCA CCT TG
A -- GA
GAM2071 371 LOC2856 1 15956 XP_211952.1 3 305 CCATCAAGTGGA --- GG 3 B c c

08 CTGGGGCAGTGC ACTGCACT CCAGTCTG TGA
AGTAGCAC TGACGTGA GGTCAGGT ACT
CGG GA
GAM2071 371 LOC2856 1 13619 XP_209693.1 5 3928 GTTCTGTCACCC 3 B b b
38 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2856 1 3501 XP_209697.1 5 189 TAGTCATCACCC C--- T 3 B c c
41 AGCTGGGCTTCT ACTGCA TCCAG CTGGGTGA
GCAGTGTT TGACGT GGGTC GACCCACT
CTTC -
GAM2071 371 LOC2856 1 15031 XP_209719.2 3 203 ACTCTGTTGCTC TG 3 B b b
79 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

AGTGGCAC TGACGTGAGGTCGGACTC TG
GT
GAM2071 371 LOC2856 1 5151 XP_211980.1 5 14 GTTCTGTCGCCC A----- 3 B c c
83 AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGGGGCAT GACGTGAGGTCGGACCCGCTG
TACGGG
GAM2071 371 LOC2856 1 10580 XP_211985.1 3 580 ACAGGCCATGCT T G A 3 B c
c
87 CAGATGGAGTGC AC GCACTCCA TCTGGGTG
TGTCTGGA TG CGTGAGGT AGACTCGT
T - A
GAM2071 371 LOC2856 1 7946 XP_211981.1 5 23 ACTCTGTTGCCC TG 3 B b b
93 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2857 1 19494 XP_211997.1 5 349 CCTCTGTCAACC G 3 B b b
22 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGACTC TGACGTGAGGTCGGACC ACTG
A
GAM2071 371 LOC2857 1 11603 XP_209743.1 3 1366 GTTCTGTCACCC 3 B b b
44 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2857 2 9553 XP_209742.1 3 2182 CATCTGTCACCC 3 B b b
47 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2857 2 13800 XP_209742.1 3 2433 GCTCTGTCACCC 3 B b b
47 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2858 1 13275 XP_212055.1 3 718 ACTCTGTCACCC AC----- 3 B c c

12 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCGGACCCACTG
TGCGGTA
GAM2071 371 LOC2858 1 17617 XP_212036.1 5 77 CTCTTGTTGCCC TG 3 B b b
13 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2858 1 7849 XP_209789.1 3 1271 ATACTTTTATAT - TGG 3 B c c
21 GATTGGCAGTGC ACTGCACT CCAGTC GTGA
AGTAAGTT TGACGTGA GGTTAG TATT
C TA-
GAM2071 371 LOC2858 1 6011 XP_209777.1 5 1359 ACTGTGTCACCC 3 B b b
22 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC2858 1 8939 XP_212043.1 5 164 CCTCTGTCGCCA T G- 3 B c c
30 AAGTTGGAGTGC ACTGCACTCCAG CT GGTGAC

AGTGGCGC TGACGTGAGGTT GA CCGCTG
- AA

GAM2071 371 40 LOC2858 1 15519 XP_208353.1 3 27 TCTACTAGTCGC ---- -- GT 3 B c c
TGGCCCCAGTGC ACTGCACT CCAGT CTGG GA
AGTACCCC TGACGTGA GGTCG GATC CT
CCCC CT AT

GAM2071 371 43 LOC2858 2 1414 XP_212034.1 3 187 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAT TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 43 LOC2858 2 11782 XP_212034.1 5 596 GCTCTGTCGCCT C 3 B b b
AGGCTGCAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGCGG TGACGTGA GTCGGATCCGCTG
C

GAM2071 371 47 LOC2858 1 7212 XP_212045.1 5 731 GCTCTGTCACCC 3 B b b
GGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGGCCCACTG

GAM2071 371 72 LOC2858 1 7986 XP_212061.1 3 686 GTTCTGTAACCC GA 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCCT TGACGTGAGGTCGGACCCA
AT

GAM2071 371 96 LOC2858 1 4795 XP_209806.1 3 317 TCTGTCACCCCC CA -- 3 B b b
AGGCCAGAGTGC ACTGCACTC GTCT GGGTGAC
AGTGGTGC TGACGTGAG CGGA CCCACTG
AC CC

GAM2071 371 22 LOC2859 1 4795 XP_209822.1 3 326 TCTGTCACCCCC CA -- 3 B b b
AGGCCAGAGTGC ACTGCACTC GTCT GGGTGAC
AGTGGTGC TGACGTGAG CGGA CCCACTG
AC CC

GAM2071 371 23 LOC2859 1 16934 XP_212104.1 3 40 ACTATGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 30 LOC2859 1 3828 XP_209818.1 5 144 GCTTTGTCACCC T G 3 B b b
AGGGTGGTGTGC ACTGCAC CCA TCTGGGTGAC
AGTGGAGC TGACGTG GGT GGACCCACTG
T G

GAM2071 371 45 LOC2859 1 12385 XP_212092.1 5 844 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 52 LOC2859 1 2758 XP_209821.1 3 679 ATGCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 61 LOC2859 1 11621 XP_209833.1 5 933 GCTCTGTCACCC C 3 B b b
AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC
AGTGGCAT TGACGT AGGTCGGACCCACTG
A

GAM2071 371 LOC2859 1 8156 XP_212105.1 3 865 CTCGTGTTGCCC T TG 3 B c c
72 CGGCTGGAGTGC ACTGCACTCCAGTC GGG AC
AGTGGCGC TGACGTGAGGTCGG CCC TG
C GT
GAM2071 371 LOC2859 1 3889 XP_212117.1 5 547 ACTCTGTCAGCC AC----- G 3 B c
c
79 AGGCTGGAGTGC TGCACTCCAGTCTGG TGAC
AATGGCAT ACGTGAGGTCGGACC ACTG
TACGGTA G
GAM2071 371 LOC2860 1 14224 XP_209866.1 3 1641 CAATCGTCACCC C 3 B b b
29 ACATTGGAGTGC ACTGCACTCCAGT TGGGTGAC
AGTGGTAC TGACGTGAGGTTA ACCCACTG
C
GAM2071 371 LOC2860 1 1208 XP_209867.2 3 613 CTCTTGTCAACC G 3 B b b
32 AGATTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTTAGACC ACTG
A
GAM2071 371 LOC2860 1 14748 XP_212152.1 3 1053 GCTCTGTTGTCC TG 3 B b b
52 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCT TG
GT
GAM2071 371 LOC2860 1 3388 XP_209892.1 3 367 TTTTGAGACCTA - GA 3 B c c
77 GGGCTGGAGTGC ACTGCACTCCAGTC TGGGT
AGTTGAGC TGACGTGAGGTCGG ATCCA
G GA
GAM2071 371 LOC2860 2 8139 XP_212163.1 3 759 TCTCTGTCACCC GT 3 B b b
78 AGGATGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGTTGT TGACGTGAGGT GACCCACTG
AG
GAM2071 371 LOC2860 2 12045 XP_212163.1 3 450 GCTCTGTCGCCC 3 B b b
78 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGAGC TGACGTGAGGTCGGACCCGCTG
GAM2071 371 LOC2861 1 15670 NP_848630.1 3 211 TCTCCGTCTCCC CA T 3 B c c
03 AGGCCAGAGTGC ACTGCACTC GTCTGGG GAC
AGTGGCGC TGACGTGAG CGGACCC CTG
AC T
GAM2071 371 LOC2861 1 15670 XP_209897.1 3 211 TCTCCGTCTCCC CA T 3 B c c
03 AGGCCAGAGTGC ACTGCACTC GTCTGGG GAC
AGTGGCGC TGACGTGAG CGGACCC CTG
AC T
GAM2071 371 LOC2861 1 19438 XP_212184.3 3 894 CCCTTGTCACCC A CA C 3 B c
c
21 ACGCAGAGGCAG ACTGC CTC GT TGGGTGAC
TGTCATGA TGACG GAG CG ACCCACTG
- A- C
GAM2071 371 LOC2861 1 8950 XP_212185.1 3 989 GCTCTGCCACCC A 3 B b b

```
          26                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
                                     AGTGGTGC    TGACGTGAGGTCGGACCCAC
                                                 C
GAM2071  371   LOC2861 1  2266  XP_212194.1  5  445   GTTTTGTCACCC                    3  B  b  b
          32                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
                                     AGTGGTGT    TGACGTGAGGTCGGACCCACTG

GAM2071  371   LOC2861 1  1529  XP_209925.1  5  1000  ACTCTGTTGACC   G        GT        3  B  c  c

          66                          AGGCTGGAGTGA ACT CACTCCAGTCTGG  GAC
                                     AGTGGTGT    TGA GTGAGGTCGGACC  TTG
                                              A          AG
GAM2071  371   LOC2861 2  13117 XP_212219.1  5  147   ACTTTGTCACCC     C              3  B  b  b
          86                          AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC
                                     AGTGGCAC    TGACGT AGGTCGGACCCACTG
                                              A
GAM2071  371   LOC2861 2  15317 XP_212219.1  3  389   ACTCTATCACCC                    3  B  b  b
          86                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
                                     AGTGTGGC    TGACGTGAGGTCGGACCCACT

GAM2071  371   LOC2862 1  16987 XP_209941.1  3  912   ACTCTGTCACCC                    3  B  b  b
          07                          AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
                                     AGTGCCAC    TGACGTGAGGTCAGACCCACTG

GAM2071  371   LOC2862 2  14347 XP_212230.1  3  1657  ACTCTGTCACCC                    3  B  b  b
          08                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
                                     AGTGTCAC    TGACGTGAGGTCGGACCCACTG

GAM2071  371   LOC2862 2  16222 XP_212230.1  3  2281  GCTCTGTAGCCC             GA        3  B  c
b
          08                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
                                     AGTGTGGC    TGACGTGAGGTCGGACCCG
                                                 AT
GAM2071  371   LOC2862 1  14899 XP_212228.1  5  553   ACTCTGTCAACC AC-----          G       3  B  c
c
          15                          AGGCTGGAGTGC       TGCACTCCAGTCTGG TGAC
                                     ACTGGCGC          ACGTGAGGTCGGACC ACTG
                                           CGCGGTC            A
GAM2071  371   LOC2862 1  4711  XP_212244.1  5  1305  GACCTACCCAGG   G      ---      A      3  B  c  c

          45                          CCACTGGAGTGA ACT CACTCCAGT   CTGGGTG
                                     GTCTAGAG    TGA GTGAGGTCA   GACCCAT
                                              -       CCG      C
GAM2071  371   LOC2863 1  14403 XP_212278.1  3  412   CTGTTGTTGCCC             TG        3  B  b  b
          41                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGG  AC
                                     AGTGGCGT    TGACGTGAGGTCGGACCC  TG
                                                 GT
GAM2071  371   LOC2863 1  13800 XP_212290.1  5  1100  GCTCTGTCACCC                    3  B  b  b
          56                          AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
                                     AGTGGCGC    TGACGTGAGGTCGGACCCACTG
```

GAM2071 371 LOC2863 1 13894 XP_212285.1 5 13 TCAATGTTGCCC TG 3 B b b
57 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC2864 1 643 XP_212319.1 3 54 AGTGCTGTTTCC T TG T 3 B c c
41 TGGCTGGAGTGC ACTGCACTCCAG C GG GAC
AGTGGCAT TGACGTGAGGTC G CC TTG
- GT T
GAM2071 371 LOC2865 1 17107 XP_212340.1 3 891 ACTTTGTCGCCC 3 B b b
53 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC3385 1 17586 XP_294654.1 3 1173 CGCTCCATCACC G 3 B b b
62 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGA
AGTGGTGC TGACGTGAGGTCGGACC ACT
-
GAM2071 371 LOC3385 1 18756 XP_290472.1 3 1084 ACCCTGTCACCC AC----- C 3 B c
c
79 AGGCTGGAATGC TGCA TCCAGTCTGGGTGAC
AATGGCAC ACGT AGGTCGGACCCACTG
CACGGTA A
GAM2071 371 LOC3387 1 902 XP_211595.2 5 682 CTCTGTTGTCCA - TG 3 B c c
09 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT
GAM2071 371 LOC3387 1 11661 XP_294690.1 3 527 ACTCTGTTGCCC TG 3 B b b
39 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC3387 1 17388 XP_290570.1 3 877 GGTCTGTCACCC 3 B b b
73 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3388 1 11448 XP_290588.1 3 263 GTCGCCTGTCAA C ----- 3 B c c
17 CGGCTAGAGTGC ACTGCACTC AGTC TGGGTGAC
AGTAGCGT TGACGTGAG TCGG GTCCGCTG
A CAACT
GAM2071 371 LOC3388 1 8888 XP_294740.1 5 561 CCTCTGTCACCA AC----- G 3 B c c

99 AGGCTGGAGTGC TGCACTCCAGTCT GGTGAC
ATTGGTGC ACGTGAGGTCGGA CCACTG
CGTGGTT A
GAM2071 371 LOC3389 2 3243 XP_294742.1 3 2043 ATTCTGTCACTC 3 B b b
23 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACTCACTG

GAM2071 371 LOC3389 2 14847 XP_294742.1 3 438 CGCTCTGTCGCC G 3 B b b
23 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC GCTG

-

GAM2071 371 LOC3390 2 7937 XP_290692.1 3 1829 GCTCTGTCACCC CA GT 3 B c b

78 AGGTTGGAGCAC ACTG CTCCA CTGGGTGAC
AGTGGTGC TGAC GAGGT GACCCACTG
AC TG

GAM2071 371 LOC3390 2 19426 XP_290692.1 3 850 GCTCTGTCACCC 3 B b b

78 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3391 1 822 XP_294825.1 5 448 CGCTCTGTTGCC G TG 3 B c c

46 AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGTGC TGACGTGAGGTCGGAC C TG
- GT

GAM2071 371 LOC3391 1 16519 XP_290742.1 3 673 ACTCTGTCACCC AC----- C 3 B c c

78 AGGCTGGAGTAC TG ACTCCAGTCTGGGTGAC
AATGGCGT AC TGAGGTCGGACCCACTG
TGCGGTA A

GAM2071 371 LOC3392 1 11830 XP_290756.1 3 356 TCTCTGTGGCCC C G 3 B c c

01 AGGCTGAAGTGC ACTGCACT CAGTCTGGGT AC
AGTGGTGT TGACGTGA GTCGGACCCG TG
A G

GAM2071 371 LOC3392 1 3121 XP_294903.1 5 1140 AGCTCACCACCC C CAG A 3 B c c

98 AGAATGATGCAG ACTGCA TC TCTGGGTG
TCAGCCTC TGACGT AG AGACCCAC
- TA- C

GAM2071 371 LOC3393 1 10660 XP_290835.1 3 685 ATTTAGTCACCC CA AG 3 B b b

18 AGAGGAGCCAGT ACTG CTCC TCTGGGTGAC
AAGTGTTA TGAC GAGG AGACCCACTG
C- --

GAM2071 371 LOC3393 2 7946 XP_290830.1 3 371 ACTCTGTTGCCC TG 3 B b b

25 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC3393 2 13290 XP_290830.1 3 143 CAGCCTTTCTCC AG T 3 B c b

25 AGGTGGGAGTGC ACTGCACTCC TCTGGG GA
AGTGGCAT TGACGTGAGG GGACCT CT
GT -

GAM2071 371 LOC3394 1 4497 XP_294944.1 5 625 ACTCTGTTGCCC A----- TG 3 B c c

17 AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGGGGCGT GACGTGAGGTCGGACCC TG
TGCGGG GT

GAM2071 371 LOC3394 1 19680 XP_290902.1 3 307 CTCTTGTCGCCC AC----- 3 B c c

48 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC

AATGGCGC ACGTGAGGTCGGACCCGCTG
CGCGGTA
GAM2071 371 LOC3394 1 436 XP_290911.1 3 1339 GCTCTGTCGCCC 3 B b b
58 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC3394 1 13345 XP_290907.2 3 837 TCTCTGTCGCCT 3 B b b
59 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGATCCGCTG

GAM2071 371 LOC3394 1 13601 XP_290919.1 3 1080 GCTCTGTCGCGC G G 3 B c
c
92 AGGGTGGAGTGC ACTGCACTCCA TCTG GTGAC
GGTGGCAC TGGCGTGAGGT GGAC CGCTG
G G
GAM2071 371 LOC3395 1 15942 XP_295008.1 3 86 CCCTCCTTGTCC C---- TG 3 B c c

68 AGACTGGGCTAC ACTGCA TCCAGTCTGGG A
TTGCAGTT TGACGT GGGTCAGACCT T
TCATC GT
GAM2071 371 LOC3395 2 9239 XP_295005.1 3 1187 GCTACGTGACCC G 3 B b b
77 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGT AC
AGTAGCTA TGATGTGAGGTCGGACCCA TG
G
GAM2071 371 LOC3395 2 18182 XP_295005.1 3 1039 GCTCTGTCACCC 3 B b b
77 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3396 1 15466 XP_295014.1 3 1460 GCTCTGTCACTT 3 B b b
00 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGATTCACTG

GAM2071 371 LOC3396 1 15723 XP_295016.1 5 1507 GTTCTGTCACCC AC----- T 3 B c
c
22 AGGCTGGCGTGC TGCAC CCAGTCTGGGTGAC
AATAGTTC ACGTG GGTCGGACCCACTG
CTTGATA C
GAM2071 371 LOC3396 1 1438 XP_295028.1 5 676 CATGTGACACTC TG - A 3 B c c
63 AGGCTGGAGTGG AC C ACTCCAGTCTGGGTG
TGGTAAGG TG G TGAGGTCGGACTCAC
GT G A
GAM2071 371 LOC3396 1 7793 XP_295032.1 5 165 GCTCTACCACCC A 3 B b b
85 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGTGT TGACGTGAGGTCGGACCCAC
C
GAM2071 371 LOC3397 1 3106 XP_295038.1 3 1271 ACTCTGTCACCC 3 B b b
11 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3397 2 7943 XP_295041.1 5 879 ACTCTGTCGCCC 3 B b b

20 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC3397 2 17652 XP_295041.1 5 3998 ATTCTGTCACCC AC----- 3 B c b

20 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AAAGGTGC ACGTGAGGTCGGACCCACTG
CGTGGAA
GAM2071 371 LOC3398 1 2943 XP_295072.1 3 1491 AGTCTGTCACCC 3 B b b
03 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3398 2 8744 XP_291020.1 5 1173 TCACTGTCACCT 3 B b b
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAA TGACGTGAGGTCGGATCCACTG

GAM2071 371 LOC3398 2 9098 XP_291020.1 5 1636 ACTCTGTCACCC 3 B b b
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3398 2 10731 XP_295074.1 5 338 GCTCTGTCACCT A--- TG -- 3 B c
c
13 AGACTGGAATGT C CAC TCCAGTCTGGGTGAC
GTGGCATA G GTG AGGTCAGATCCACTG
ATAC GT TA
GAM2071 371 LOC3398 2 13432 XP_295074.1 5 646 GCTCTGTTACCC A----- C 3 B c c

13 AGACTGGAGTAC CTG ACTCCAGTCTGGGTGAC
AGGGATGC GAC TGAGGTCAGACCCATTG
CGTAGG A
GAM2071 371 LOC3398 2 8180 XP_291031.1 5 574 ACTCTGTTGCCC T TG 3 B c c
33 AGCCTGGAGTGC ACTGCACTCCAG CTGGG AC
AGTGGCAT TGACGTGAGGTC GACCC TG
C GT
GAM2071 371 LOC3398 2 10061 XP_291031.1 3 560 ACTGTGATGCCG G G A 3 B c
c
33 AGGGTGGAGTGC ACTGCACTCCA TCT GGTG
AGTGGCAC TGACGTGAGGT GGA CCGT
G G A
GAM2071 371 LOC3398 1 2474 NP_835467.1 5 47 ATTCTGTCGCCC 3 B b b
34 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGACGC TGATGTGAGGTCGGACCCGCTG

GAM2071 371 LOC3398 1 2474 XP_291033.1 5 47 ATTCTGTCGCCC 3 B b b
34 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGACGC TGATGTGAGGTCGGACCCGCTG

GAM2071 371 LOC3398 3 6179 XP_291050.1 5 470 GGTCTGTTGCCC GT TG 3 B c
b
72 AGGTTGGAGTGC ACTGCACTCCA CTGGG AC

AGTGGCGG TGACGTGAGGT GACCC TG
TG GT

GAM2071 371 LOC3398 3 10908 XP_291050.1 5 767 CCTCAGTCGCTC 3 B b b
72 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACTCGCTG

GAM2071 371 LOC3398 3 15990 XP_291050.1 3 183 GCTGTGTTGCCC TG 3 B b b
72 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTAGCTA TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC3398 1 11426 XP_295095.1 5 132 GCTCTGTTGCCC C GT TG 3 B c c
94 AGGTTAGAGTGC ACTGCACTC A CTGGG AC
AGTGGCTT TGACGTGAG T GACCC TG
A TG GT

GAM2071 371 LOC3399 1 1531 XP_291065.1 3 1459 ACTCTGTTGCCC A----- TG 3 B c c
07 AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGGGGCAC GACGTGAGGTCGGACCC TG
CACGGG GT

GAM2071 371 LOC3399 1 9102 XP_291069.1 5 121 GCTCTGTTGCCC TG 3 B b b
09 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 LOC3399 1 8858 XP_291095.1 3 713 GCTCTGTCGCCC 3 B b b
70 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC3401 1 902 XP_291150.1 5 682 CTCTGTTGTCCA - TG 3 B c c
25 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT

GAM2071 371 LOC3401 1 2442 XP_291153.1 3 2140 ACTCTGTCACTC AC----- 3 B c c
38 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGACGT ACGTGAGGTCGGACTCACTG
TGCAGTA

GAM2071 371 LOC3401 1 8575 XP_291158.1 3 1441 CGCTCTGTCACG GG 3 B b b
56 AGGCTGGAGTGC ACTGCACTCCAGTCT GTGAC
AGTGGCCC TGACGTGAGGTCGGA CACTG
G-

GAM2071 371 LOC3402 1 902 XP_291203.1 5 682 CTCTGTTGTCCA - TG 3 B c c
27 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT

GAM2071 371 LOC3402 1 8336 XP_291211.1 3 40 GCTCTGTCACCC T TC 3 B b b
49 AAGCTGGTGTGC ACTGCAC CCAG TGGGTGAC
AGTGGTGT TGACGTG GGTC ACCCACTG
T GA

GAM2071 371 LOC3402 1 15164 XP_291214.1 5 1350 CTCTCTTGTCCA - TG 3 B c c
90 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG A
AGTAGTGC TGATGTGAGGTCGGA CCT T
A GT
GAM2071 371 LOC3403 1 3251 XP_290401.1 5 235 TGGATTTCACCC A----- - AG 3 B c c
18 AGGAGGAGTGGC CTGC ACTCC TCTGGGTGA
GGCAACTG GGCG TGAGG GGACCCACT
GTCAAC G A-
GAM2071 371 LOC3404 1 11659 XP_295240.1 3 173 GCTCTGTCACCC 3 B b b
14 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG
GAM2071 371 LOC3404 1 4971 XP_295252.1 5 243 TCTCTGTCACCC 3 B b b
50 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG
GAM2071 371 LOC3429 1 1413 XP_292790.2 3 810 GCTCTGTCACCC 3 B b b
26 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG
GAM2071 371 LOC3448 1 11441 XP_293599.2 5 1371 CTGGTTCACATT CC T A 3 B c
c
05 CAGCTCCAGTGC ACTGCACT AG CTGGGTG
AGTTCAAG TGACGTGA TC GACTTAC
CC - A
GAM2071 371 LOC3452 1 14511 NP_835236.1 3 951 ACTCTTTCGCCC 3 B b b
75 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGTAT TGACGTGAGGTCGGACCCGCT
GAM2071 371 LOC3478 1 12975 XP_302604.1 3 889 ACTCTGTCACCC A----- 3 B c c
03 AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGCAGTTG GACGTGAGGTCGGACCCACTG
GTTGAC
GAM2071 371 LOC3479 1 983 XP_300565.1 5 188 CTTTTATTGCCC TG 3 B c c
18 AGGCTGGAGTGT ACTGCACTCCAGTCTGGG A
AGTGGCGC TGATGTGAGGTCGGACCC T
GT
GAM2071 371 LOC3480 1 3526 XP_300592.1 5 318 GCTCTGTCGCCC C C 3 B b b
24 AGACTAGAATGC ACTGCA TC AGTCTGGGTGAC
AGTGGTGC TGACGT AG TCAGACCCGCTG
A A
GAM2071 371 LOC3480 1 16154 XP_300620.1 3 978 CCAGGCTCACCC GC- 3 B c c
71 AGGCTGGGGTCT ACT ACTCCAGTCTGGGTGA
GAGTGTCA TGA TGGGGTCGGACCCACT
GTC
GAM2071 371 LOC3480 2 777 XP_302653.1 3 3385 TGCTCTGTCACC G 3 B b b
75 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
GGTGGCAT TGGCGTGAGGTCGGACC ACTG

-

GAM2071 371 LOC3480 2 7650 XP_302653.1 5 528 TTCCTCGCACCC CA - G A 3 B c b

75 AGATGGTAGCCA ACTG CT CCA TCTGGGTG

GTCTTCCA TGAC GA GGT AGACCCAC

C- T - G

GAM2071 371 LOC3481 1 12601 XP_300626.1 5 553 CTCTTGTTGCCC CA TG 3 B c c

15 AGGCCCGAGTGC ACTGCACTC GTCTGGG AC

AGTGGTGC TGACGTGAG CGGACCC TG

CC GT

GAM2071 371 LOC3482 1 19539 XP_302704.1 3 100 GCGTCCACACCC C T A A 3 B c c

61 AGACGGGTCCAG ACTG AC CC GTCTGGGTG

TCCAGCCC TGAC TG GG CAGACCCAC

C - - A

GAM2071 371 LOC3482 1 7914 XP_300683.1 5 57 GCTCTGTTGCCT TG TG 3 B c c

62 GGGCTGGAGTGC ACTGCACTCCAGTC GG AC

AGTGCCAC TGACGTGAGGTCGG CC TG

GT GT

GAM2071 371 LOC3483 1 9161 XP_302716.1 5 316 ACTTTGTTGCCC TG 3 B b b

14 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

GGTGGCGT TGGCGTGAGGTCGGACCC TG

GT

GAM2071 371 LOC3483 1 1995 XP_300696.1 3 1763 CAGTCTGTCACC G 3 B b b

26 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC

AGTGGCAT TGACGTGAGGTCGGACC ACTG

-

GAM2071 371 LOC3483 1 16911 XP_030209.2 3 79 TGCTCGTCACCC AC----- 3 B c c

27 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC

AATTGTGC ACGTGAGGTCGGACCCACTG

CGTGTTA

GAM2071 371 LOC3483 2 16960 XP_302741.1 3 1205 TCGCCGTTGCCC TG 3 B b b

93 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

GGTGGCAT TGGCGTGAGGTCGGACCC TG

GT

GAM2071 371 LOC3483 2 20185 XP_302741.1 3 742 CCTAGGAGGCCC G GA 3 B c b

93 AGGCTGGAGTGA ACT CACTCCAGTCTGGGT

GGTGGCAC TGG GTGAGGTCGGACCCG

A GA

GAM2071 371 LOC3483 3 1615 XP_300729.1 5 149 GCTCTGTCACCC C 3 B b b

96 AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGAC

AGTGCAGT TGACGT AGGTCGGACCCACTG

A

GAM2071 371 LOC3483 3 5596 XP_300729.1 3 1616 ACTCTGTCACCC CC TC 3 B c b

96 AAGCTATGGTGC ACTGCACT AG TGGGTGAC

AGTGGCAC TGACGTGG TC ACCCACTG
TA GA
GAM2071 371 LOC3483 3 10631 XP_300729.1 3 183 GCTCTGTTGCCC TG 3 B b b
96 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC3484 1 13601 XP_300730.1 3 321 GCTCTGTCGCGC G G 3 B c c
02 AGGGTGGAGTGC ACTGCACTCCA TCTG GTGAC
GGTGGCAC TGGCGTGAGGT GGAC CGCTG
G G
GAM2071 371 LOC3484 1 1995 XP_300738.1 3 1763 CAGTCTGTCACC G 3 B b b
45 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCAT TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 LOC3484 1 9100 XP_302760.1 3 2632 GCTCTGTCGCCC 3 B b b
55 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG
GAM2071 371 LOC3484 2 442 XP_300743.1 5 246 ACTCTGTCACCC AC----- C 3 B c b
60 AGGCTAGAGTGC TGCACTC AGTCTGGGTGAC
AATGGCAC ACGTGAG TCGGACCCACTG
CACGGTA A
GAM2071 371 LOC3484 2 8756 XP_300743.1 3 130 CACTCTGTCACC G 3 B b b
60 AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGCCGC TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 LOC3484 1 6597 XP_209299.2 3 229 GCTCTCTTACCC TC 3 B b b
74 AAGCTGGAGTGC ACTGCACTCCAG TGGGTGA
AGTGACAT TGACGTGAGGTC ACCCATT
GA
GAM2071 371 LOC3484 1 6743 XP_302789.1 5 26 GCTCTGTCACCC AC----- 3 B c c
94 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCGGACCCACTG
CGTGGTA
GAM2071 371 LOC3485 1 12080 XP_300762.1 3 1202 TCTTGCTCGCCC G 3 B b b
03 AGGGTGGAGTGC ACTGCACTCCA TCTGGGTGA
AGTGGTGT TGACGTGAGGT GGACCCGCT
G
GAM2071 371 LOC3485 1 902 XP_302806.1 5 744 CTCTGTTGTCCA - TG 3 B c c
08 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT
GAM2071 371 LOC3485 1 436 XP_300778.1 3 1339 GCTCTGTCGCCC 3 B b b
25 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG
GAM2071 371 LOC3485 2 16960 XP_302818.1 3 1205 TCGCCGTTGCCC TG 3 B b
b
32 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC

GGTGGCAT TGGCGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC3485 2 20185 XP_302818.1 3 742 CCTAGGAGGCCC G GA 3 B c
b
32 AGGCTGGAGTGA ACT CACTCCAGTCTGGGT
GGTGGCAC TGG GTGAGGTCGGACCCG
A GA
GAM2071 371 LOC3487 1 3103 XP_300808.1 5 297 ACTCTGTCACCC C 3 B b b
02 AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAC TGAC TGAGGTCGGACCCACTG
A
GAM2071 371 LOC3487 1 11124 XP_300843.1 3 446 TGCTTGTTGCCC TG 3 B b b
90 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC3487 1 4796 XP_302888.1 3 341 TTGCTCTCGCCC 3 B b b
97 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGGTG TGACGTGAGGTCGGACCCGCT

GAM2071 371 LOC3487 1 8736 XP_300845.1 3 1396 GCTCTGTCACCC A C 3 B c c
98 AAATTGGAGGGC ACTGC CTCCAGT TGGGTGAC
GGTGATGT TGGCG GAGGTTA ACCCACTG
G A
GAM2071 371 LOC3488 1 2639 XP_300853.1 5 283 GCCCAGGCTGGA -------- GA 3 B c
c
25 GTATAGTAGTGC ACTGCAC TCCAGTCTGGGT
AGTGGTGT TGACGTG AGGTCGGACCCG
ATGATATG --
GAM2071 371 LOC3488 1 902 XP_300861.1 5 474 CTCTGTTGTCCA - TG 3 B c c
42 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT
GAM2071 371 LOC3490 2 4753 XP_300250.1 3 143 CTCTTGTCACCC 3 B b b
24 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 LOC3490 2 11653 XP_300250.1 5 532 GCTCTGTCACCC 3 B b b
24 AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCAGACCCACTG

GAM2071 371 LOC3490 1 9465 XP_300932.1 3 176 ACTCTGTCACCC C 3 B b b
75 AGGCTGAAGTGC ACTGCACT CAGTCTGGGTGAC
AGTGGTAC TGACGTGA GTCGGACCCACTG
A
GAM2071 371 LOC3491 1 902 XP_302960.1 5 183 CTCTGTTGTCCA - TG 3 B c c
14 AGGCTGGAGTGT ACTGCACTCCAGTCT GGG AC
AGTAGTGC TGATGTGAGGTCGGA CCT TG
A GT
GAM2071 371 LOC3491 2 13839 XP_300969.1 5 146 CTTCTGTGGCCC G 3 B b b
70 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC

AGTGGCTG TGACGTGAGGTCGGACCCG TG
G
GAM2071 371 LOC3491 2 19429 XP_300969.1 3 468 ACTCTGTTGCCC TG 3 B b b
70 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 LOC3492 1 17649 XP_300251.1 3 443 TCACTATCACCC A C 3 B b b
51 AGGCTAGAGGGC ACTGC CTC AGTCTGGGTGA
AGTGGCAC TGACG GAG TCGGACCCACT
G A
GAM2071 371 LOC3492 1 15530 XP_301008.1 3 209 CCAAAGTCACCC A--- - C-- T 3 B c
c
82 AGCTGAACAGTG CTGC ACT CAG CTGGGTGAC
GTAGAGTT GATG TGA GTC GACCCACTG
TTGA G CAA -
GAM2071 371 LOC3493 1 15530 XP_301024.1 3 184 CCAAAGTCACCC A--- - C-- T 3 B c
c
13 AGCTGAACAGTG CTGC ACT CAG CTGGGTGAC
GTAGAGTT GATG TGA GTC GACCCACTG
TTGA G CAA -
GAM2071 371 LOC3493 1 988 XP_303030.1 3 5794 GAGGATCACCTG A---- - - 3 B c c
24 AGACTGGAGATG CTGCA CTCCAGTCT GGGTGA
TAGAGGCT GATGT GAGGTCAGA TCCACT
TCGGA A G
GAM2071 371 LOC3494 1 19505 XP_300513.1 3 1058 GTTTTGCAGCCC GA 3 B c c

40 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCAC TGACGTGAGGTCGGACCCG
AC
GAM2071 371 LOC3515 1 14926 XP_302099.1 5 143 AGAGTGTCACCC A C TC 3 B c
c
97 AACCTGCAGGCA ACTGC CT CAG TGGGTGAC
GTGTCATG TGACG GA GTC ACCCACTG
- C CA
GAM2071 371 LOC5119 1 6858 NP_057415.1 3 732 GTTCTGTTGTCC GT TG 3 B c c

3 AGGATGGAGTGC ACTGCACTCCA CTGGG AC
AGTGGTTG TGACGTGAGGT GACCT TG
AG GT
GAM2071 371 LOC5124 1 10914 NP_057568.1 5 1 GGGTTCCCAGAC - CTC T 3 B c
c
8 TGAATTGTCAGT ACTG CA CAGTCTGGG GAC
GAGCGGAG TGAC GT GTCAGACCC TTG
T TAA -
GAM2071 371 LOC5125 1 18183 NP_057580.2 5 155 GCTCTGTTACCC 3 B b b
7 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCATTG

GAM2071 371 LOC5133 1 18609 NP_057730.1 3 664 ACTCTGTTACCC AC----- 3 B c c
6 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC

AATGGAGT ACGTGAGGTCGGACCCATTG
TGAGGTA

GAM2071 371 LOC5595 1 17853 NP_061976.1 5 0 GTCACCCAGGCT 3 B b b
4 GGAGTGTAGTGG ACTGCACTCCAGTCTGGGTGAC
CGCAATCT TGATGTGAGGTCGGACCCACTG

GAM2071 371 LOC5690 1 8077 NP_064528.1 3 517 ACTTTGTCACCC C 3 B b b
2 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGTGC TGACGTGAG TCGGACCCACTG
A

GAM2071 371 LOC9040 1 2729 XP_031517.1 5 1645 CTCTTGTTACCC 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCATTG

GAM2071 371 LOC9048 2 10103 XP_032059.1 3 1182 TCTCTGTCACCC C 3 B b b
5 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGAGC TGACGTGAG TCGGACCCACTG
A

GAM2071 371 LOC9048 2 15525 XP_032059.1 3 1340 GCTCTGTCGCCC 3 B b b
5 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGATGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LOC9105 1 6693 NP_612377.1 3 784 TCTCACTCTGGC ---- T 3 B c c
6 GCTCTGGAGTGC ACTGCACTCCA GTC GGGTGA
AGTGGTGT TGACGTGAGGT CGG CTCACT
CTCG T

GAM2071 371 LOC9111 2 6053 XP_036218.1 3 284 CTCTTGTCACCC AC----- 3 B c b
5 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAC ACGTGAGGTCGGACCCACTG
CACGGTA

GAM2071 371 LOC9111 2 18042 XP_036218.1 3 757 GGTCTTTCACCC T 3 B b b
5 AGGCTGGAGTGC AC GCACTCCAGTCTGGGTGA
TGTGGCAC TG CGTGAGGTCGGACCCACT
T

GAM2071 371 LOC9117 1 3969 XP_036612.1 5 208 ACTTTGTCGCCC A 3 B b b
0 GGGCAGGAGTGC ACTGCACTCC GTCTGGGTGAC
AGTGGCTC TGACGTGAGG CGGGCCCGCTG
A

GAM2071 371 LOC9125 1 16739 XP_037135.1 5 2205 GCTCTGTCACCC C- 3 B b b
0 AGGCTGGAGTTA ACTG ACTCCAGTCTGGGTGAC
TAGTGACG TGAT TGAGGTCGGACCCACTG
AT

GAM2071 371 LOC9137 1 5516 XP_038063.5 3 1525 CTCTTGTTGCCC G TG 3 B c c
3 AGGCTGGAGTGA ACT CACTCCAGTCTGGG AC
AGTGGCGT TGA GTGAGGTCGGACCC TG
A GT

GAM2071 371 LOC9166 1 13779 NP_612382.1 3 338 ACTCTGTGGCCC G 3 B b b
3 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGTGC TGACGTGAGGTCGGACCCG TG

G
GAM2071 371 LOC9180 1 3586 NP_620130.1 3 24 ATTTTAGCACCC CT- G A 3 B c c
1 AGATGGCATTGC ACTGCA CCA TCTGGGTG
AGTGCCAG TGACGT GGT AGACCCAC
TAC - G
GAM2071 371 LOC9189 1 9129 XP_041340.1 3 203 GCTCTGCCGCCC A A 3 B c c
3 AGGCGGGAGTGC ACTGCACTCC GTCTGGGTG
AGTGGCAG TGACGTGAGG CGGACCCGC
G C
GAM2071 371 LOC9214 1 16536 XP_043160.1 5 759 GCCCTGCCGCCC C A 3 B c c

8 AGGCTAGAGTGC ACTGCACTC AGTCTGGGTG
AGTGGCAC TGACGTGAG TCGGACCCGC
A C
GAM2071 371 LOC9265 1 19539 XP_046434.3 3 100 GCGTCCACACCC C T A A 3 B c
c
9 AGACGGGTCCAG ACTG AC CC GTCTGGGTG
TCCAGCCC TGAC TG GG CAGACCCAC
C - - A
GAM2071 371 LPHN1 1 12633 NP_055736.1 3 483 CCGGCTGCACCC AC AG A 3 B c
c
AGAGGGAGCAGT ACTGC TCC TCTGGGTG
GAGGCAGG TGACG AGG AGACCCAC
-- G- G
GAM2071 371 LTB4R 1 19595 NP_000743.1 5 302 GCTCTGTCATTC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACTTACTG

GAM2071 371 LYPLA2 1 15519 NP_009191.1 3 27 TCTACTAGTCGC ---- -- GT 3 B c c
TGGCCCCAGTGC ACTGCACT CCAGT CTGG GA
AGTACCCC TGACGTGA GGTCG GATC CT
CCCC CT AT
GAM2071 371 LYZ 1 3109 NP_000230.1 3 330 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 LZTS1 1 13405 NP_066300.1 3 1444 GCTCTGTCCCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAT TGACGTGAGGTCGGACCC CTG
C
GAM2071 371 MAK 1 11208 NP_005897.1 3 644 ACTCTTGTGTCC GT A 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGG G
AGTGGCAC TGACGTGAGGTCGGACC T
TG G
GAM2071 371 MAPA 1 12475 NP_660299.1 3 805 ACTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGCTGC ACGTGAGGTCGGACCCACTG
CGTCGTA
GAM2071 371 MCLC 1 4526 NP_055942.1 3 315 GCTCTGTCACCC G 3 B b b
AGGCTGGAGTGA ACT CACTCCAGTCTGGGTGAC

GGTGGTAC TGG GTGAGGTCGGACCCACTG
A

GAM2071 371 MCM10 1 4821 NP_060988.2 3 954 ACTATGTCACCC T 3 B b b
TGGCTGGAGTGC ACTGCACTCCAGTC GGGTGAC
AGTAGTGC TGACGTGAGGTCGG CCCACTG
T

GAM2071 371 MDC1 1 3945 NP_055456.1 3 365 CTATCTTTAGCC CTC G 3 B c c
AGACTGTTGCAG ACTGCA CAGTCTGG TGA
TTATTGCT TGACGT GTCAGACC ATT
T-- G

GAM2071 371 MDGA1 1 1000 NP_705691.1 3 2237 TCTGAGTTAATT A TG G 3 B c c

GGACTGGAGCGC ACTGC CTCCAGTC G TGAC
AGTCGGAC TGACG GAGGTCAG T ATTG
C GT A

GAM2071 371 MDM2 1 6085 NP_002383.1 3 354 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGTG TGACGTGAGGTCGGACCCATTG

GAM2071 371 MDM2 1 6085 NP_006869.1 3 354 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGTG TGACGTGAGGTCGGACCCATTG

GAM2071 371 MDM2 1 6085 NP_006870.1 3 354 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGTG TGACGTGAGGTCGGACCCATTG

GAM2071 371 MDM2 1 6085 NP_006871.1 3 354 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGTG TGACGTGAGGTCGGACCCATTG

GAM2071 371 MDM2 1 6085 NP_006872.1 3 354 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGTG TGACGTGAGGTCGGACCCATTG

GAM2071 371 MDM2 1 6085 NP_006873.1 3 298 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGTG TGACGTGAGGTCGGACCCATTG

GAM2071 371 MDM4 1 19527 NP_002384.1 3 547 GTTCTGTCTCCC C T 3 B b b
AGGCTGAAGTGC ACTGCACT CAGTCTGGG GAC
AGTGAGTC TGACGTGA GTCGGACCC CTG
A T

GAM2071 371 MEFV 2 12284 NP_000234.1 3 822 CTCTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 MEFV 2 17376 NP_000234.1 3 510 GCTCTGTGGCCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCAC TGACGTGAGGTCGGACCCG TG

G
GAM2071 371 MFTC 1 10459 NP_110407.2 3 547 GCTTTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 MGAT2 1 18270 NP_079374.1 3 985 CTCTTGTCGCTC T 3 B b b
AGCCTGGAGTGC ACTGCACTCCAG CTGGGTGAC
AGTGAGCT TGACGTGAGGTC GACTCGCTG
C
GAM2071 371 MGC1020 2 1700 NP_659497.1 3 539 GCTCTTTCACCC A----- C A 3 B c
b
0 AGGCCGGACTGC CTGCA TCC GTCTGGGTGA
AGCGGCGC GACGT AGG CGGACCCACT
CGCGGC C C
GAM2071 371 MGC1020 2 13048 NP_659497.1 3 180 GCTTTGTCACGC C G 3 B b
b
0 AGGCTAGAGTGC ACTGCACTC AGTCTG GTGAC
AGTGGCGC TGACGTGAG TCGGAC CACTG
A G
GAM2071 371 MGC1110 1 14977 NP_115701.2 3 1314 CCTGTGTTGCTC TG 3 B b
b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACTC TG
GT
GAM2071 371 MGC1226 1 6361 NP_116085.1 5 202 GTGATGTTGCCC C TG 3 B c
c
2 AGGCTAGAGTGC ACTGCACTC AGTCTGGG AC
AGTGGCAC TGACGTGAG TCGGACCC TG
A GT
GAM2071 371 MGC1251 1 18251 NP_291026.1 3 0 CCCCAGGTTGGA GT TGA 3 B c
c
8 GTGCAGTGGCGT ACTGCACTCCA CTGGG
GTCTTGGG TGACGTGAGGT GACCC
TG C--
GAM2071 371 MGC1301 1 16983 NP_116076.1 3 8 ACACAGCGCCTC AGT -- A 3 B c
c
0 CAGTGGGAGTGC ACTGCACTCC CTGG GTG
AGTTGGAT TGACGTGAGG GACC CGC
GT- TC G
GAM2071 371 MGC1301 1 18970 NP_542387.1 3 457 GCTCTGTTGCCC CCA TG 3 B c
c
7 AGGCAGTAGTGC ACTGCACT GTCTGGG AC
AGTGGCGC TGACGTGA CGGACCC TG
TGA GT
GAM2071 371 MGC1302 1 15630 NP_689501.1 3 432 AGTCTGTTTCCC T 3 B b b
4 AGGCTGGAGTGT ACTGCACTCCAGTCTGGG GAC
AGTGATAC TGATGTGAGGTCGGACCC TTG
T
GAM2071 371 MGC1313 1 19426 NP_219363.1 3 455 GCTCTGTCACCC 3 B b b
8 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC

AGTGGTGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 MGC1320 1 17963 NP_113653.1 3 128 GCTCTGTTGCCC TG 3 B b b
b
4 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTAT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 MGC1428 1 1959 NP_542391.1 3 451 GCTCTGTTGCCC TG 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGACGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 MGC1443 1 5075 NP_116286.1 5 824 GCCCTGTCACCC C 3 B b b
6 AGGCTGGGGTAC ACTG ACTCCAGTCTGGGTGAC
GGTGGCAT TGGC TGGGGTCGGACCCACTG
A
GAM2071 371 MGC1483 1 9102 NP_219480.1 3 380 GCTCTGTTGCCC TG 3 B b b
6 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 MGC1570 1 6734 NP_116146.1 3 161 TAGGAAGTTGTG AG - TG 3 B c
c
5 TCAGAGGAGTGC ACTGCACTCC TCTGG G AC
AGTCATCT TGACGTGAGG AGACT T TG
-- G GT
GAM2071 371 MGC1783 1 18441 NP_777586.1 5 118 TGTCAGCCTACC - C-- - 3 B c c
9 AGCTCGGAGTGC ACTGCACTCC AGT TGGG TGAC
AGTTCCTG TGACGTGAGG TCG ATCC ACTG
C ACC G
GAM2071 371 MGC1842 1 11658 XP_037797.2 3 1419 ACTCTGTTGCCC TG 3 B b
b
AGACTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCAGACCC TG
GT
GAM2071 371 MGC2474 1 18119 NP_076420.1 3 1311 TGCTCCTCACCC C 3 B b b
AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGA
AGTGGTGT TGACGT AGGTCGGACCCACT
A
GAM2071 371 MGC2477 2 3973 NP_077004.1 5 1479 CACTCTGTTGCC T TG 3 B b
b
CAGCTGGAGTGC ACTGCACTCCAG CTGGG AC
AGTGGCGT TGACGTGAGGTC GACCC TG
- GT
GAM2071 371 MGC2477 2 12048 NP_077004.1 5 1289 CTCTGTCGCCCA - 3 B b b
GGGCTGGAGTGC ACTGCACTCCAGTC TGGGTGAC
AGTGGCGC TGACGTGAGGTCGG ACCCGCTG
G
GAM2071 371 MGC2603 1 17763 NP_076942.1 3 419 CGCTCTGTCGCC G 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC GCTG
-

GAM2071 371 MGC2698 1 14418 NP_689976.1 3 665 TTTGTACTCACC TG G 3 B c c
9 AGGCTGGAGTGT AC CACTCCAGTCTGG TGA
GGTAGCAC TG GTGAGGTCGGACC ACT
GT -

GAM2071 371 MGC2734 1 18352 XP_300964.1 5 1667 TCTTGTTGCCCA - TG 3 B b b
5 GGGCTGGAGTGC ACTGCACTCCAGTC TGGG AC
AGTGGCAT TGACGTGAGGTCGG ACCC TG
G GT

GAM2071 371 MGC2989 1 18179 NP_653219.1 3 605 ACTCTGTCACCC 3 B b b
1 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGTGC TGGCGTGAGGTCGGACCCACTG

GAM2071 371 MGC2989 1 9164 NP_659485.1 3 502 GCTTTGTTGCCC TG 3 B b b
8 AGACTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAT TGACGTGAGGTCAGACCC TG
GT

GAM2071 371 MGC3113 1 15946 NP_076940.1 3 712 ACTCTGTTCCCC A TG 3 B c c
AGGCCGGAGTGC ACTGCACTCC GTCTGGG AC
AGTGGTAC TGACGTGAGG CGGACCC TG
C CT

GAM2071 371 MGC3195 1 15735 NP_114111.2 5 185 CCGGGACGCGCC -- - A 3 B c c
GGGCTGGAGTGG ACTGC ACTCCAGTCTGG GTG
GCGGTTAT TGGCG TGAGGTCGGGCC CGC
GG G A

GAM2071 371 MGC3207 2 12382 NP_115661.1 3 1436 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 MGC3207 2 14723 NP_115661.1 3 786 CACTCGTTGCCC A----- TG 3 B c b
AGGCTGGAGTGT CTGCACTCCAGTCTGGG AC
AGAGGCGA GATGTGAGGTCGGACCC TG
AGCGGA GT

GAM2071 371 MGC3248 1 11953 NP_115875.1 3 1331 TATTTCTCTCTC CCAGTC T 3 B c c
CCATAACAGTGC ACTGCACT TGGG GA
AGTGATAG TGACGTGA ACCC CT
CAAT-- T

GAM2071 371 MGC3329 1 4873 NP_076991.2 3 1596 CTCTTGTTGTCT T TG 3 B c c
AGGCTGGAGTGC AC GCACTCCAGTCTGGG AC
CGTGGTGC TG CGTGAGGTCGGATCT TG
C GT

GAM2071 371 MGC3363 1 12383 NP_689809.1 3 683 ACTCTGTCACCC 3 B b b
7 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGATGTGAGGTCGGACCCACTG

GAM2071 371 MGC3407 1 19879 NP_689688.1 3 188 ATTCTGTCACCC 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 MGC3413 2 8862 XP_291029.1 3 500 ACTCTGTCACCC 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 MGC3413 2 9188 XP_291029.1 3 334 TCACTGTCACCC 3 B b b
2 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 MGC3513 1 8783 NP_689640.1 5 173 GCTCTCTCACCC GC 3 B b b
6 AGGCTGGAGTAG ACT ACTCCAGTCTGGGTGA
AGTGACAA TGA TGAGGTCGGACCCACT
GA

GAM2071 371 MGC3544 1 13796 NP_694952.1 3 183 ACTCTGTCACCC 3 B b b
0 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGCGC TGGCGTGAGGTCGGACCCACTG

GAM2071 371 MGC3546 1 19258 NP_694976.1 3 453 TGGAGGTTACAC CCAG G 3 B
c c
8 AGGGTAAAGTGC ACTGCACT TCTG GTGAC
AGTATGAT TGACGTGA GGAC CATTG
AATG A

GAM2071 371 MGC3932 2 1498 NP_689642.2 3 893 CTTGTGTCATCC TG A- 3 B c c
0 AGACTGGAGCAG AC C CTCCAGTCTGGGTGAC
TGGTGCAA TG G GAGGTCAGACCTACTG
GT AC

GAM2071 371 MGC3932 2 2691 NP_689642.2 3 696 TCTGGCTTGCCC TG 3 B c c
0 AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
GGTGGCTA TGGCGTGAGGTCGGACCC T
GT

GAM2071 371 MGC3955 1 1145 NP_689703.1 3 149 GCACTTTCACCC CTCCAG 3 B c
c
8 AGAACCAATGCG ACTGCA TCTGGGTGA
GTGTTTCT TGGCGT AGACCCACT
AACCA-

GAM2071 371 MGC4015 1 13547 NP_689563.1 3 317 GCTGTATTGCCC TG TG 3 B c
c
7 AGGCTGGAGTGT AC CACTCCAGTCTGGG A
GGTGGCAC TG GTGAGGTCGGACCC T
GT GT

GAM2071 371 MGC4057 2 516 NP_689989.1 3 332 GCTCTGTCACTC 3 B b b

9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTAT TGACGTGAGGTCGGACTCACTG

GAM2071 371 MGC4057 2 3759 NP_689989.1 3 903 CTCTTGTCTCCC AC----- T 3 B c
b
9 AGACTGGAGTGC TGCACTCCAGTCTGGG GAC
AATGGCAT ACGTGAGGTCAGACCC CTG
TACGGTA T
GAM2071 371 MGC4312 1 16117 NP_775784.1 3 199 GCTCTGTCACCC AC----- GT 3 B c
c
2 AGGTTGGAGTGC TGCACTCCA CTGGGTGAC
ATTGGTGT ACGTGAGGT GACCCACTG
TGTGGTT TG
GAM2071 371 MGC4415 1 8576 NP_113672.1 3 990 AGATTGGAACCC CTCC GA 3 B
c c
AGACTTGCAGTC ACTGCA AGTCTGGGT
CAGCGCTG TGACGT TCAGACCCA
---- AG
GAM2071 371 MGC4673 1 3645 NP_714925.1 3 1978 TGCCAGTTCCAC A------ G - T 3 B c
c
2 AGACTGGAGTGA CT CACTCCAGTCTG GG GAC
GAACTTAT GA GTGAGGTCAGAC CC TTG
TATTCAA - A -
GAM2071 371 MGC5033 1 8882 NP_848604.1 3 279 ACTCTGTCGCCC AC----- 3 B c c

7 AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATACTGC ACGTGAGGTCGGACCCGCTG
CGTCATA
GAM2071 371 MGC5055 1 7831 NP_776163.1 3 560 GCTCTGTCGTCC GT 3 B b b

9 AGGCTGGAGTGC ACTGCACTCCAGTCTGG GAC
AGTGACTC TGACGTGAGGTCGGACC CTG
TG
GAM2071 371 MGC5149 1 17590 XP_051200.2 3 1953 CACTCTGTCACC C G 3 B b
b
AGGCTAGAGTGC ACTGCACTC AGTCTGG TGAC
AGTGGCAC TGACGTGAG TCGGACC ACTG
A -
GAM2071 371 MGC9912 1 11391 NP_542395.1 3 351 TGCTCTGTCGCC G 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCAGACC GCTG
-
GAM2071 371 MGRN1 1 13807 XP_048119.4 3 1593 CTCTTGCTGCCC A 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGCTC TGACGTGAGGTCGGACCCGT
C
GAM2071 371 MHC2TA 1 9987 NP_000237.1 3 2660 ACTCTTATGCCC C A 3 B c c
ACGCTGGAGTGC ACTGCACTCCAGT TGGGTG
AGTGAGCC TGACGTGAGGTCG ACCCGT
C A

GAM2071 371 MIRAB13 1 3109 NP_203744.1 3 1731 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 MIRAB13 1 3109 XP_039236.6 3 2296 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 MIS12 1 3332 NP_076944.1 3 444 TTTCTGTCACCC C----- C GT 3 B c c
AGGTTAGAGTAG ACTG ACTC A CTGGGTGAC
ATTTCAGT TGAC TGAG T GACCCACTG
TTTAGA A TG

GAM2071 371 MKRN4 1 12385 NP_110384.1 3 372 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 MLZE 1 11404 NP_113603.1 5 583 ACGGAGTTGCCC A----- TG 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGCGCATG GACGTGAGGTCGGACCC TG
GTACGC GT

GAM2071 371 MOAP1 1 11659 NP_071434.2 3 299 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 moblak 2 2270 NP_570719.1 3 1259 CCCGGCCTAACC GTGA 3 B c b

AGGCTGGAGTGC ACTGCACTCCAGTCTGG
AGTGGTGG TGACGTGAGGTCGGACC
AATC

GAM2071 371 moblak 2 18353 NP_570719.1 3 996 CCACTGTCGCCC C 3 B b b
AGACTGGAGTCC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAC TGAC TGAGGTCAGACCCGCTG
C

GAM2071 371 MOCS3 1 6108 NP_055299.1 3 578 TCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGATGTGAGGTCGGACCC TG
GT

GAM2071 371 MPL 2 633 NP_005364.1 3 568 ACTCTGTCACCC AC----- C 3 B c b
AGGCTGCAGTGC TGCACT CAGTCTGGGTGAC
AATGGCGC ACGTGA GTCGGACCCACTG
CGCGGTA C

GAM2071 371 MPL 2 11909 NP_005364.1 3 749 TTGCCTGTTGCC G TG 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCAC TGACGTGAGGTCAGAC C TG
- GT

GAM2071 371 MRPL30 1 1858 NP_660213.1 3 656 GCTCTGTCACCC CAC TC 3 B c
c

AAGCTGGAATAC ACTG TCCAG TGGGTGAC
AGTGGCAT TGAC AGGTC ACCCACTG
ATA GA

GAM2071 371 MRPL35 1 10631 NP_057706.2 3 1059 GCTCTGTTGCCC TG 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 MRPL49 1 13534 NP_004918.1 3 323 ACTCTGTTGCCC G TG 3 B c c

AGGGTGGAGTGC ACTGCACTCCA TCTGGG AC
AGTGGCAT TGACGTGAGGT GGACCC TG
G GT

GAM2071 371 MRPS27 1 13372 NP_055899.1 3 429 ATTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 MSTP028 1 11359 NP_114160.1 3 1906 GCTCTATTGGCC G 3 B c c
AGGCTGGAGTGT ACTGCACTCCAGTCTGG TGA
AGTGGCAC TGATGTGAGGTCGGACC GTT
G

GAM2071 371 MtFMT 1 2529 NP_640335.1 3 142 ACTCTGTCACCC CAC 3 B c c
AGGCTGGAATCC ACTG TCCAGTCTGGGTGAC
AGTGGCAC TGAC AGGTCGGACCCACTG
CTA

GAM2071 371 MTH2 1 12462 NP_060753.1 3 850 GCTCTGTTGCCC C TG 3 B c c
ACATTGGAGTGC ACTGCACTCCAGT TGGG AC
AGTGGCAC TGACGTGAGGTTA ACCC TG
C GT

GAM2071 371 MTR 1 13325 NP_000245.1 3 811 GCTCTGTCGCCC A----- 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGAC
AGGGGCGC GACGTGAGGTCGGACCCGCTG
CGCGGG

GAM2071 371 MYO5C 1 14846 NP_061198.1 3 628 CGCTCTATCGCC G 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGG TGA
AGTGGCAT TGATGTGAGGTCGGACC GCT
-

GAM2071 371 NAGPA 1 8883 NP_057340.1 3 402 GGCCAGCACCCC G T- A 3 B c c

TGGCTGGAGTGG ACT CACTCCAGTC GGGTG
GTTAAAGG TGG GTGAGGTCGG CCCAC
- TC G

GAM2071 371 NALP12 1 12925 NP_150639.1 5 28 GCTCTGTCACCA A----- G 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCT GGTGAC
AGGGGCAC GACGTGAGGTCGGA CCACTG
CACGGG A

GAM2071 371 Nanog 1 3109 NP_079141.1 3 281 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 NCAG1 1 11436 NP_115536.1 3 3664 ACTTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTCT TGACGTGAGGTCGGACCC TG

GT
GAM2071 371 NCOA6 2 5484 NP_054790.1 5 884 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTCGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 NCOA6 2 6181 NP_054790.1 5 1278 GCTCTGTCACCG G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCT GGTGAC
AGTGGCGC TGACGTGAGGTCGGA CCACTG
G
GAM2071 371 NCOA6IP 1 3026 NP_079107.5 3 279 CTTTTACCGCCC A 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGCCAT TGACGTGAGGTCGGACCCGC
C
GAM2071 371 NDP52 1 13886 NP_005822.1 3 1121 TCTCTGTCACCC AC----- T 3 B c c

AGGCTGGCGTGC TGCAC CCAGTCTGGGTGAC
AATGGCGC ACGTG GGTCGGACCCACTG
CGCGGTA C
GAM2071 371 NDRG3 1 20109 NP_114402.1 3 1151 TCGCTGTTACCC AC----- 3 B c c

AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGC ACGTGAGGTCGGACCCATTG
CGCGGTA
GAM2071 371 NDUFC2 1 15362 NP_004540.1 3 1240 TGCTCTGTCATC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACT ACTG
-
GAM2071 371 NEU3 1 18182 NP_006647.2 5 70 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 NF2 1 557 NP_057502.1 5 479 CCTTTGTCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCGT ACGTGAGGTCGGACCCGCTG
TGCGGTA
GAM2071 371 NONO 1 1412 NP_031389.2 3 446 ACTCTGTCGCCC 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGATGTGAGGTCGGACCCGCTG

GAM2071 371 NQO1 1 18183 NP_000894.1 3 684 GCTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCATTG

GAM2071 371 NTSR2 1 4568 NP_036476.1 5 113 GGCAGCTCGCCC A CC 3 B c c
AGACTCCGGGCA ACTGC CT AGTCTGGGTGA
GTGAGAGG TGACG GG TCAGACCCGCT
- CC
GAM2071 371 NUDT4 1 20051 NP_061967.2 3 1289 GCTTTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAC ACGTGAGGTCGGACCCACTG

CACGGTA

GAM2071 371 NXN 1 436 NP_071908.1 3 875 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 OR51E2 1 8690 NP_110401.1 3 439 CGCTCTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 ORC1L 1 436 NP_004144.1 3 91 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 P15RS 1 1032 NP_060640.2 3 2471 GGCAGATCATGC C TC G 3 B c
c
ATCTTTGAGTGC ACTGCACTC AG TG GTGA
AGTTTGGT TGACGTGAG TT AC TACT
T CT G

GAM2071 371 PAICS 1 11127 NP_006443.1 3 412 TCACTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 PART1 2 7026 NP_057674.1 3 1326 CAAGGGTCACCC C C--- 3 B b b
AAATAGCTGAGT ACTGCACTC AGT TGGGTGAC
GCAGTCCT TGACGTGAG TCG ACCCACTG
- ATAA

GAM2071 371 PART1 2 19024 NP_057674.1 3 1326 AGGGTCACCCAA C C--- 3 B b b
ATAGCTGAGTGC ACTGCACTC AGT TGGGTGAC
AGTCCTTG TGACGTGAG TCG ACCCACTG
- ATAA

GAM2071 371 PASK 1 3230 NP_055963.1 5 804 CTCTTGTTGCTG G TG 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCT GG AC
AGTGGCAC TGACGTGAGGTCGGA TC TG
G GT

GAM2071 371 PCDHA9 1 10631 NP_054724.1 3 1914 GCTCTGTTGCCC TG 3 B b
b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 PCDHB11 1 7975 NP_061754.1 3 504 TCTTAGTCACCC CA C 3 B c c
AGACTAGAGGTC ACTG CTC AGTCTGGGTGAC
AGTGGCAG TGAC GAG TCAGACCCACTG
TG A

GAM2071 371 PCDHB16 1 4753 NP_066008.1 3 580 CTCTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 PCDHB9 1 3109 NP_061992.2 3 526 GCTCTGTCGCCC 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 PDCL 1 14559 NP_005379.2 3 1860 GCTCTGTCACCC AC----- C 3 B c c

AGGCTGGAGTAC TG ACTCCAGTCTGGGTGAC
AATAGCGT AC TGAGGTCGGACCCACTG
TGCGATA A
GAM2071 371 PDE6B 1 18070 NP_000274.1 3 196 GCTCTGTCACCC T 3 B b b
AGGCTGGAGTGC AC GCACTCCAGTCTGGGTGAC
CGTGGCAC TG CGTGAGGTCGGACCCACTG
C
GAM2071 371 PDGFC 1 19767 NP_057289.1 3 44 CTCTTGCCCAGA C-- - TG 3 B c c
GCTGTGCAGTGC ACTGCACT CAG TCTGGG A
AGTGGCTG TGACGTGA GTC AGACCC T
CGT G GT
GAM2071 371 PDLIM2 1 4874 NP_789847.1 3 1200 GCTCTATTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGTAC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 PDZK1 1 11598 NP_002605.2 5 43 ATTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 PDZRN1 1 17567 NP_699202.1 3 521 TCACTCTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAC TGACGTGAGGTCGGACCCACT

GAM2071 371 PEGASUS 1 13389 NP_071911.2 3 259 TTTGACATTGGA - G- A 3 B c
c
GAATTGGAGTGC ACTGCACTCCAGT CT GGTG
AGTCATAA TGACGTGAGGTTA GA TTAC
A GG A
GAM2071 371 PELI1 3 430 NP_065702.2 5 2685 GCTCTGTTGCCC GT TG 3 B c b
AGGTTGGAGTGC ACTGCACTCCA CTGGG AC
AGTGGCAC TGACGTGAGGT GACCC TG
TG GT
GAM2071 371 PELI1 3 13801 NP_065702.2 5 2121 ACTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 PELI1 3 18182 NP_065702.2 5 1441 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 PER2 1 6602 NP_073728.1 3 1369 TTCTTTTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCGC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 PFAS 1 16519 NP_036525.1 3 673 ACTCTGTCACCC AC----- C 3 B c c

AGGCTGGAGTAC TG ACTCCAGTCTGGGTGAC
AATGGCGT AC TGAGGTCGGACCCACTG
TGCGGTA A

GAM2071 371 PIGR 2 5370 NP_002635.2 3 1117 ACTGTGTCACCC C 3 B b b
AGACTGGAATGC ACTGCA TCCAGTCTGGGTGAC
AGTGACAC TGACGT AGGTCAGACCCACTG
A

GAM2071 371 PIGR 2 8350 NP_002635.2 3 813 TCACTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 PIK3C2B 1 15277 NP_002637.2 3 1447 CGCCCTGTCGCC G 3 B b b

AGGCTGGAGTGT ACTGCACTCCAGTCTGG TGAC
AGTGGCAT TGATGTGAGGTCGGACC GCTG
-

GAM2071 371 PIK3CD 1 4771 NP_005017.2 3 821 CCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 PILRB 1 15120 NP_038468.3 3 189 TCCCTGAATCAC GCA TG 3 B c c

CGACTGGAGGAG ACT CTCCAGTC GGTGA
AGTTACCT TGA GAGGTCAG CCACT
GAG --

GAM2071 371 PILRB 1 15120 NP_778212.2 3 214 TCCCTGAATCAC GCA TG 3 B c c

CGACTGGAGGAG ACT CTCCAGTC GGTGA
AGTTACCT TGA GAGGTCAG CCACT
GAG --

GAM2071 371 PILRB 1 15120 NP_839956.1 3 189 TCCCTGAATCAC GCA TG 3 B c c

CGACTGGAGGAG ACT CTCCAGTC GGTGA
AGTTACCT TGA GAGGTCAG CCACT
GAG --

GAM2071 371 PIP5K1C 1 1328 NP_036530.1 3 1128 GGGACTCAGCCC A-- A ---- - 3 B c
c

AGACTGCCCTGG CTGC CTC CAGTCTGGG TGA
GGCAGCTT GACG GGG GTCAGACCC ACT
TTC - TCCC G

GAM2071 371 PIP5K1C 1 1328 XP_047620.2 3 1128 GGGACTCAGCCC A-- A ---- - 3 B c
c

AGACTGCCCTGG CTGC CTC CAGTCTGGG TGA
GGCAGCTT GACG GGG GTCAGACCC ACT
TTC - TCCC G

GAM2071 371 PITPNB 1 19285 NP_036531.1 3 1567 TGCATCCCTCCC ---- CT T 3 B c c

CCACTGGAGTGA ACTG CACTCCAGT GGG GA
TTTCAGTG TGAC GTGAGGTCA CCC CT
TTTA C- -

GAM2071 371 PMM2 1 1676 NP_000294.1 3 998 AGGCCTTCACCC A A ------- 3 B c c
AGACTTTACCGC CTGC CTCC AGTCTGGGTGA
GGAGGCGG GGCG GAGG TCAGACCCACT
- - CGCCATT
GAM2071 371 PNMA2 2 11189 NP_009188.1 3 264 CTCTCATCACCC C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGA
AGTGGCAC TGACGTGAG TCGGACCCACT
A
GAM2071 371 PNMA2 2 11236 NP_009188.1 3 1713 GCTCTATCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGTGC TGACGTGAGGTCGGACCCACT

GAM2071 371 POFUT1 1 1760 NP_056167.1 3 1736 GCTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAT TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 POLE3 1 5665 NP_059139.2 3 1143 ACTCTGTGGCCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT AC
AGTGGCAT TGACGTGAGGTCGGACCCG TG
G
GAM2071 371 POLR2D 1 11282 NP_004796.1 3 520 CTCTTGTCCAGG --- TG 3 B c c

CTGGAGGAGTGC ACTGCACTCC AGTCTGGG A
AGTCGTAC TGACGTGAGG TCGGACCT T
AGG GT
GAM2071 371 PON1 2 1117 NP_000437.3 3 445 CAGTACTCACCC CACTC 3 B c b

AGGGACTCCAGT ACTG CAGTCTGGGTGA
TCACAGGC CTTG CAGGGACCCACT
ACCT-
GAM2071 371 PON1 2 19429 NP_000437.3 3 1196 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 POU2F3 1 7036 NP_055167.1 3 1108 TTGCTCCAGCCC GA 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGT
AGTGGCAT TGACGTGAGGTCGGACCCG
AC
GAM2071 371 PPFIBP1 2 5523 NP_003613.2 3 1167 ATTCTGTTGCCC C TG 3 B c b

ATGCTGGAGTGC ACTGCACTCCAGT TGGG AC
AGTGGCGT TGACGTGAGGTCG ACCC TG
T GT
GAM2071 371 PPFIBP1 2 8861 NP_003613.2 3 2294 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 PPID 1 3110 NP_005029.1 3 246 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
GGTGGCGC TGGCGTGAGGTCGGACCCACTG

GAM2071 371 PPIL2 1 18677 NP_055152.1 3 391 GCTCTGTTGCCC CC TG 3 B c c
AGGCTCCAGTGC ACTGCACT AGTCTGGG AC
AGTGGTGT TGACGTGA TCGGACCC TG
CC GT
GAM2071 371 PPP1R12 1 14820 NP_002472.1 3 4496 ACTCTCTCGCCC 3 B b b
B AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGTGT TGACGTGAGGTCGGACCCGCT

GAM2071 371 PPP1R12 1 14820 NP_115288.1 3 4629 ACTCTCTCGCCC 3 B b b
B AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGTGT TGACGTGAGGTCGGACCCGCT

GAM2071 371 PPP2R1B 1 8962 NP_002707.2 3 371 GGGTGTGGACCC G - GA 3 B c
c
AGACGTGGAGTG ACT CACTCCA GTCTGGGT
GAGTGATT TGA GTGAGGT CAGACCCA
G G GG
GAM2071 371 PRDX6 1 19006 NP_004896.1 3 407 CTCCTGTCACCC A-- - -- TC 3 B c c

ATTTTGAAGAGT CTGC ACTC CAG TGGGTGAC
GGCAGAAC GACG TGAG GTT ACCCACTG
CAA G AA TT
GAM2071 371 PRIM2A 1 12707 NP_000938.1 3 105 TTCACTGTCACC CC G 3 B c c
AAGGCTTAGTGC ACTGCACT AGTCT GGTGAC
AGTGACAC TGACGTGA TCGGA CCACTG
T- A
GAM2071 371 PRKWNK3 1 5524 NP_065973.1 3 638 TCTCTGTCACCC GT 3 B b b

AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGTGT TGACGTGAGGT GACCCACTG
TG
GAM2071 371 PRKY 1 1958 NP_002751.1 3 2032 CCTTCTGCACCC G AG- A 3 B c c

AGAGTAGGGGTG ACT CACTCC TCTGGGTG
GAGTATAC TGA GTGGGG AGACCCAC
G ATG G
GAM2071 371 PRND 1 7084 NP_036541.1 3 2763 ATTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 PRO0159 1 4857 NP_054837.1 5 438 TGCTGAGTCCTC C - T 3 B b b
AGCACTGAGTGC ACTGCACTC AGT CTGGG GAC
AGTGCGTG TGACGTGAG TCA GACTC CTG
- C -
GAM2071 371 PRO0297 1 1504 NP_054800.1 5 52 GCTCTTTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCAC TGACGTGAGGTCGGACCCACT

GAM2071 371 PRO0365 1 7958 NP_054845.1 5 883 CGCTCTGTCGCC C G 3 B b b

AGGCTGAAGTGC ACTGCACT CAGTCTGG TGAC
AGTGGCGC TGACGTGA GTCGGACC GCTG
A -

GAM2071 371 PROM2 1 19427 NP_653308.1 3 785 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGATGTGAGGTCGGACCCACTG

GAM2071 371 PSMD9 1 11654 NP_002804.2 3 751 GCTTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGTCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 PSME4 1 14216 XP_040158.1 3 605 TGCACTTCCCAC C-- - T 3 B c c
AGACTGGAGTTT ACTG ACTCCAGTCTG GG GA
TTGGTGCT TGGT TGAGGTCAGAC CC CT
TTT A -

GAM2071 371 PSPH 1 9102 NP_004568.1 3 275 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 PTDSS2 1 12204 NP_110410.1 3 440 TCCCTGTCACCC A- --- T GT- 3 B c
c
AGCCATGGTGTG CTG CAC CCA CTGGGTGAC
GTCCAGGC GAC GTG GGT GACCCACTG
CG CTG T ACC

GAM2071 371 PTGES 1 11575 NP_004869.1 3 527 GCTCTGTTGCCC G TC TG 3 B c
c
AAGCTGGAGTGA ACT CACTCCAG TGGG AC
AGTGGTAC TGA GTGAGGTC ACCC TG
A GA GT

GAM2071 371 PTGIS 1 11917 NP_000952.1 3 2839 GCTCTGCTGCCC C A 3 B c c
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTG
AGTGGCGT TGACGTGAG TCGGACCCGT
A C

GAM2071 371 RAB11-F 1 5406 NP_116321.2 3 2595 GCTCTGTTGCCC TG 3 B b b
IP4 AGGCTGGAGTGT ACTGCACTCCAGTCTGGG AC
AGTGGTAT TGATGTGAGGTCGGACCC TG
GT

GAM2071 371 RAB21 1 17172 NP_055814.1 3 288 GCTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
ACTGGCTT ACGTGAGGTCGGACCCACTG
TTCGGTC

GAM2071 371 RAB33B 1 15333 NP_112586.1 3 839 CGCTCTGTCTCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGT TGACGTGAGGTCGGACCT CTG
-

GAM2071 371 RAB36 1 12750 NP_004905.1 3 1725 TCTCTGTCACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAC ACGTGAGGTCGGACCCACTG
CACGGTA

GAM2071 371 RAB39 1 2158 XP_084662.1 3 752 GTTTTGTCACCC 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 RAB40C 1 8129 NP_066991.1 3 774 CATCTCGCCCAC A----- -- TC 3 B c c

CCTGGAGAGTGC CTGCAC TCCAG TGGGTGA
AGAGCTAT GACGTG AGGTC ACCCGCT
TATCGA AG CC
GAM2071 371 RABL2A 1 14847 NP_038198.1 3 578 CGCTCTGTCGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC GCTG
-
GAM2071 371 RABL2B 1 14847 NP_009012.1 3 585 CGCTCTGTCGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCGGACC GCTG
-
GAM2071 371 RAD52 1 4266 NP_002870.2 3 707 GCTGTGTTGCCC C T TG 3 B c c
TGACTGGAGTTC ACTG ACTCCAGTC GGG AC
AGTGGTGC TGAC TGAGGTCAG CCC TG
T T GT
GAM2071 371 RAD52 1 4266 NP_602294.1 3 1878 GCTGTGTTGCCC C T TG 3 B c c

TGACTGGAGTTC ACTG ACTCCAGTC GGG AC
AGTGGTGC TGAC TGAGGTCAG CCC TG
T T GT
GAM2071 371 RAD52 1 4266 NP_602295.1 3 1971 GCTGTGTTGCCC C T TG 3 B c c

TGACTGGAGTTC ACTG ACTCCAGTC GGG AC
AGTGGTGC TGAC TGAGGTCAG CCC TG
T T GT
GAM2071 371 RAD52 1 4266 NP_602296.1 3 1457 GCTGTGTTGCCC C T TG 3 B c c

TGACTGGAGTTC ACTG ACTCCAGTC GGG AC
AGTGGTGC TGAC TGAGGTCAG CCC TG
T T GT
GAM2071 371 RAI 1 17223 NP_006654.1 5 20 ACAAGTGAGTCT T TGA 3 B c c
CGGCTGGAGTGC ACTGCACTCCAG CTGGG
AGTGGTGC TGACGTGAGGTC GGCTC
- TGA
GAM2071 371 RAI3 1 16116 NP_003970.1 3 342 GCTCTGTCACCC C 3 B b b
AGGCTTGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGTGC TGACGTGAG TCGGACCCACTG
T
GAM2071 371 RASSF2 1 7664 NP_055552.1 3 3346 GTTCTGTTTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGTGG TGACGTGAGGTCGGACCC TTG
T
GAM2071 371 RASSF2 1 7664 NP_739579.1 3 3572 GTTCTGTTTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGTGG TGACGTGAGGTCGGACCC TTG

T
GAM2071 371 RASSF2 1 7664 NP_739580.1 3 3346 GTTCTGTTTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGTGG TGACGTGAGGTCGGACCC TTG
T
GAM2071 371 RCBTB1 1 3049 NP_060661.2 5 128 GCTCTCTTGCCC CAC TG 3 B c
c
AGACTGGAATAC ACTG TCCAGTCTGGG A
AGTGGTGT TGAC AGGTCAGACCC T
ATA GT
GAM2071 371 RGS11 1 7393 NP_003825.1 3 816 CACCAGTCCCCC A------ G T T 3 B c
c
AGACTGGGTGAA CT CAC CCAGTCTGGG GAC
GGTACAGC GA GTG GGTCAGACCC CTG
CGACATG A - C
GAM2071 371 RHD 2 442 NP_057208.2 3 280 ACTCTGTCACCC AC----- C 3 B c b
AGGCTAGAGTGC TGCACTC AGTCTGGGTGAC
AATGGCAC ACGTGAG TCGGACCCACTG
CACGGTA A
GAM2071 371 RHD 2 442 NP_057309.2 3 369 ACTCTGTCACCC AC----- C 3 B c b
AGGCTAGAGTGC TGCACTC AGTCTGGGTGAC
AATGGCAC ACGTGAG TCGGACCCACTG
CACGGTA A
GAM2071 371 RHD 2 8756 NP_057208.2 3 690 CACTCTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGCCGC TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 RHD 2 8756 NP_057309.2 3 779 CACTCTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGCCGC TGACGTGAGGTCGGACC ACTG
-
GAM2071 371 RHPN2 1 5481 NP_149094.2 3 889 GCTGTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 RNF137 1 8861 NP_060543.4 3 828 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 RNF19 1 14309 NP_056250.2 5 116 ACGGTGTCACCC CAC G 3 B c
c
AGGGTGGAATAC ACTG TCCA TCTGGGTGAC
AGTGGTGT TGAC AGGT GGACCCACTG
ATA G
GAM2071 371 RPP30 1 3259 NP_006404.1 3 1202 GCTCTGTCCCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCTC TGACGTGAGGTCGGACCC CTG
C
GAM2071 371 S100A15 1 18561 NP_789793.1 3 3403 ACTCTGTCGCCC T 3 B b b
GGGCTGGAGTGC AC GCACTCCAGTCTGGGTGAC

TGTGAGCT TG CGTGAGGTCGGGCCCGCTG
T

GAM2071 371 SBLF 1 14250 NP_006864.2 3 1608 ACTCTGTTGCCC T TG 3 B c c
AGCCTGGAGTGC ACTGCACTCCAG CTGGG AC
AGTGTGTC TGACGTGAGGTC GACCC TG
C GT

GAM2071 371 SCAMP-4 1 19434 NP_524558.1 3 872 ACTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 SCAND2 1 16790 NP_071333.2 3 1782 ATTCTATCACCC G 3 B b b
AGGCTGGAGTGG ACT CACTCCAGTCTGGGTGA
AGTGGTAT TGA GTGAGGTCGGACCCACT
G

GAM2071 371 SCARF1 1 12384 NP_003684.1 3 409 CCTCTGTCCCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGTGC TGACGTGAGGTCGGACCC CTG
C

GAM2071 371 SCN3B 2 1471 NP_060870.1 3 1053 ACTCTGTCACCT C 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGTGT TGACGTGAG TCGGATCCACTG
A

GAM2071 371 SCN3B 2 9932 NP_060870.1 3 2012 ACTCTGTCTCCC C T 3 B b b
AGGCTAGAGTGC ACTGCACTC AGTCTGGG GAC
AGTGGTGC TGACGTGAG TCGGACCC CTG
A T

GAM2071 371 SDF2 1 4852 NP_008854.2 3 204 AGTCACTCTCCC C C---- T 3 B c c
AGACTTGCGTGG ACTG ACTC AGTCTGGG GA
GTCAGTTC TGAC TGGG TCAGACCC CT
- TGCGT T

GAM2071 371 SDS-RS1 1 2100 NP_612441.1 5 90 GATCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 SECTM1 1 14404 NP_002995.1 3 150 TCTGTGTCACCC A- --- TC- 3 B c
c
ACTCCTGGGTGC CTGCAC TCCAG TGGGTGAC
GTGCAGAC GACGTG GGGTC ACCCACTG
CA CGT CTC

GAM2071 371 SEDL 3 7261 NP_055378.1 3 999 CTCCTGTTGTGC G TG 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCAC TGACGTGAGGTCGGAC T TG
G GT

GAM2071 371 SEDL 3 13400 NP_055378.1 3 637 CTCCTGTTGTGC C G TG 3 B c c
AGGCTGTAGTGC ACTGCACT CAGTCTG G AC
AGTGGCAC TGACGTGA GTCGGAC T TG
T G GT

GAM2071 371 SEDL 3 16842 NP_055378.1 3 307 CACTCTGTTGCC G TG 3 B c c
AGGCTGGAGTGC ACTGCACTCCAGTCTG G AC
AGTGGCGC TGACGTGAGGTCGGAC C TG

- GT

GAM2071 371 SEL1L 1 16250 NP_005056.3 3 1828 TCTTACATGTAG C GG---- 3 B c c
AGATTTGAGTGC ACTGCACTC AGTCT GTGA
AGTTGGTA TGACGTGAG TTAGA CATT
T GATGTA

GAM2071 371 SEPN1 1 1799 NP_065184.1 3 1556 GCTCTGTCACCC ACT----- 3 B c c

AGGCTGGAGTGC GCACTCCAGTCTGGGTGAC
TATGGCTC CGTGAGGTCGGACCCACTG
CTCGGTAT

GAM2071 371 SERF1A 1 11123 NP_068802.1 3 243 CACTCTGTCACC G 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCAGACC ACTG
-

GAM2071 371 SERF1B 1 11123 NP_075267.1 3 243 CACTCTGTCACC G 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGCGC TGACGTGAGGTCAGACC ACTG
-

GAM2071 371 SERPINB 2 437 NP_004146.1 3 2358 ACTCTGTCACCC 3 B b b
9 AGGCTGGAGTGT ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGATGTGAGGTCGGACCCACTG

GAM2071 371 SERPINB 2 4057 NP_004146.1 3 510 TCTCTGTCGCCC 3 B b b
9 AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCTC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 SH3BP2 2 12957 NP_003014.2 3 1849 ACCCTGTCGCCC AC----- 3 B c
c

AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGCCGT ACGTGAGGTCGGACCCGCTG
TGCCGTA

GAM2071 371 SH3BP2 2 18716 NP_003014.2 5 156 GCTCAGTTGCCC A TG 3 B c c

AGACTGGAGAGC ACTGC CTCCAGTCTGGG AC
AGTGGCCA TGACG GAGGTCAGACCC TG
A GT

GAM2071 371 SIGLEC8 1 3441 NP_055257.1 3 515 GCTCTGTCACCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGGGC TGACGTGAGGTCGGATCCACTG

GAM2071 371 SLC12A8 1 18425 NP_078904.1 3 208 GCCTTGTCACCC C 3 B b b
AGGCTGGAGTCC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAC TGAC TGAGGTCGGACCCACTG
C

GAM2071 371 SLC13A1 1 15679 NP_071889.2 3 1479 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGG TGACGTGAGGTCGGACCCGCTG

GAM2071 371 SLC14A2 1 18700 NP_009094.2 5 32 GCTCTGTCACCC AC----- C 3 B c
c

AGGCTGGAGTAC TG ACTCCAGTCTGGGTGAC
ACTGGCAC AC TGAGGTCGGACCCACTG
CACGGTC A

GAM2071 371 SLC16A4 1 20157 NP_004687.1 3 182 GCTCTTTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGA
AGTGGCGC TGACGTGAGGTCGGACCCGCT

GAM2071 371 SLC16A6 1 517 NP_004685.1 5 45 GCTCTGTCATTC CA 3 B c c
AGGCAAGAGTGC ACTGCACTC GTCTGGGTGAC
AGTAGTGT TGACGTGAG CGGACTTACTG
AA

GAM2071 371 SLC25A1 1 18982 NP_005975.1 3 83 CTTTGTCTCACA CC TGG 3 B c c

TGATTCCAGTGC ACTGCACT AGTC GTGA
AGTAGTGC TGACGTGA TTAG CACT
CC TA-

GAM2071 371 SLC30A5 1 1341 NP_076960.1 3 152 GCTCCATCGCCC C 3 B b b
AGGCTGCAGTGC ACTGCACT CAGTCTGGGTGA
AGTGACAC TGACGTGA GTCGGACCCGCT
C

GAM2071 371 SLC35B2 1 17255 NP_835361.1 3 200 CTTAAGTCACCC -- CC- TC 3 B c c

ATCTTCCAGTAA ACTGC ACT AG TGGGTGAC
GCAGTTTA TGACG TGA TC ACCCACTG
AA CCT T-

GAM2071 371 SLC35B2 1 17255 XP_300918.1 3 200 CTTAAGTCACCC -- CC- TC 3 B c c

ATCTTCCAGTAA ACTGC ACT AG TGGGTGAC
GCAGTTTA TGACG TGA TC ACCCACTG
AA CCT T-

GAM2071 371 SLC35E2 1 12300 XP_049733.6 3 1606 TGTCTGTCACCC C 3 B b b
AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAT TGAC TGAGGTCGGACCCACTG
A

GAM2071 371 SLC39A1 1 19430 NP_055252.2 5 87 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
GGTGGTGC TGGCGTGAGGTCGGACCC TG
GT

GAM2071 371 SLC4A4 1 13075 NP_003750.1 5 14 ACACATCACACA T - G 3 B c c
GAATTGGAGTGC AC GCACTCCAGT CTG GTGA
TGTCCTTC TG CGTGAGGTTA GAC CACT
T A A

GAM2071 371 SLC6A14 1 16741 NP_009162.1 3 1675 GTTCTGTTGCCT TG TG 3 B c c

GGGCTGGAGTGC ACTGCACTCCAGTC GG AC
AGTGGCAT TGACGTGAGGTCGG CC TG
GT GT

GAM2071 371 SMAC 2 1245 NP_620308.1 5 481 CCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGA TGACGTGAGGTCGGACCCGCTG

GAM2071 371 SMAC 2 15275 NP_620308.1 5 655 GCTCTGTTGCCC C TG 3 B c b
AGGCTGAAGTGC ACTGCACT CAGTCTGGG AC
AGTGGGGC TGACGTGA GTCGGACCC TG
A GT
GAM2071 371 SNAP25 1 8525 NP_003072.2 3 710 ATTAAGTTATAC CCA T - 3 B c c
CAGCAAAAGTGC ACTGCACT G CTGG GTGAC
AGTAGTGT TGACGTGA C GACC TATTG
AAA - A
GAM2071 371 SNAP25 1 8525 NP_570824.1 3 710 ATTAAGTTATAC CCA T - 3 B c c
CAGCAAAAGTGC ACTGCACT G CTGG GTGAC
AGTAGTGT TGACGTGA C GACC TATTG
AAA - A
GAM2071 371 SNPH 1 1354 NP_055538.1 3 2430 GGCCCTGGCCCA - T- GA 3 B c c

GCTCTGGAGTGC AC TGCACTCCAG CTGGGT
ATGTGTGT TG ACGTGAGGTC GACCCG
T TC GT
GAM2071 371 SNX15 1 2728 NP_037438.2 3 269 GCTGTGTCGCCC 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGG TGACGTGAGGTCAGACCCGCTG

GAM2071 371 SNX15 1 2728 NP_680086.1 3 269 GCTGTGTCGCCC 3 B b b
AGACTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGG TGACGTGAGGTCAGACCCGCTG

GAM2071 371 SNX27 2 1972 NP_112180.4 3 1879 ACTCTGTCGCCC TG C 3 B c b
AGACTGGAATGT AC CA TCCAGTCTGGGTGAC
GGTGGCAT TG GT AGGTCAGACCCGCTG
GT A
GAM2071 371 SNX27 2 8857 NP_112180.4 3 3108 GCTCTGTCGCCC GT 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCAC TGACGTGAGGT GACCCGCTG
TG
GAM2071 371 SOX8 1 12214 NP_055402.2 3 495 GTGTCTGTCCGC G CT - T-- 3 B c c

AGACTGGGATGA ACT CA CCAGTCTG GG GAC
GTCTACTC TGA GT GGTCAGAC CC CTG
- AG G TGT
GAM2071 371 SPN 1 19300 NP_003114.1 3 184 GCTTTGTCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGCACG ACGTGAGGTCGGACCCGCTG
GCACGTA
GAM2071 371 SPOP 1 7212 NP_003554.1 5 129 GCTCTGTCACCC 3 B b b
GGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGGCCCACTG

GAM2071 371 SRCRB4D 1 19630 NP_542782.1 3 148 GGAGAGAGCCTA CCA A 3 B c
c
CCTAGACAGTGC ACTGCACT GTCTGGGTG

AGTCCTGC TGACGTGA CAGATCCAT
--- C

GAM2071 371 SRL 1 9910 XP_064152.3 3 584 GCTCTGTCGGCC GT G 3 B c c
AGGTTGGAGTGC ACTGCACTCCA CTGG TGAC
AGTGGTGC TGACGTGAGGT GACC GCTG
TG G

GAM2071 371 SS18 1 10975 NP_005628.1 3 1673 CTCTTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 STAF65(1 6743 NP_055675.1 3 1379 GCTCTGTCACCC AC----- 3 B c c
gamma) AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGTGC ACGTGAGGTCGGACCCACTG
CGTGGTA

GAM2071 371 STAM2 1 5920 NP_005834.3 3 360 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 STAU 1 9365 NP_004593.1 5 274 CTCTTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 STEAP2 1 1413 NP_694544.1 3 1986 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 STXBP6 1 11916 NP_054897.4 5 275 TGTGTGGAGTTT C GTC T 3 B c
c
TCCATGAAGTGC ACTGCACT CA TGGG GAC
AGTCCCAA TGACGTGA GT ACCT TTG
A --- T

GAM2071 371 SYT12 1 3730 NP_808878.1 3 1566 CTGAGCTCACCC G CCA-- 3 B c
c
AGGCCAGCAGGT ACT CACT GTCTGGGTGA
GGGGTATC TGG GTGG CGGACCCACT
G ACGAC

GAM2071 371 SYT13 1 19065 NP_065877.1 3 1525 TCTTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT

GAM2071 371 TADA3L 1 10415 NP_597814.1 3 288 GCACTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAT TGACGTGAGGTCGGACCCACTG

GAM2071 371 TAF11 1 17432 NP_005634.1 3 390 GCTCTATCACCT A----- 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCTGGGTGA
AGCGGCAT GACGTGAGGTCGGATCCACT
TACGGC

GAM2071 371 TAPBP 3 3109 NP_003181.3 3 836 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC

AGTGGCGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 TAPBP 3 6086 NP_003181.3 3 229 ACTCTTCCGCCC C A 3 B c b
AGGCTGCAGTGC ACTGCACT CAGTCTGGGTG
AGTGGCAT TGACGTGA GTCGGACCCGC
C C
GAM2071 371 TAPBP 3 8861 NP_003181.3 3 1141 GCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCAC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TAT 1 20161 NP_000344.1 3 778 GCTCTGTCGCCC C 3 B b b
ATGCTGGAGTGC ACTGCACTCCAGT TGGGTGAC
AGTGGCGC TGACGTGAGGTCG ACCCGCTG
T
GAM2071 371 TBC1D5 1 12382 NP_055559.1 5 589 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCGCTG

GAM2071 371 TCF2 1 401 NP_006472.1 3 2021 CCTCTGTCACCC TC 3 B b b
GAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGTGC TGACGTGAGGTC GCCCACTG
GA
GAM2071 371 TDGF1 1 10005 NP_003203.1 3 320 ACTCTGTCACCC AC----- C 3 B c c

AGGCTGGACTGC TGCA TCCAGTCTGGGTGAC
AATGACGC ACGT AGGTCGGACCCACTG
CGCAGTA C
GAM2071 371 TERA 1 971 NP_067061.1 3 139 CTCTTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCATTG

GAM2071 371 TERF1 1 13870 NP_003209.1 3 418 TCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TERF1 1 13870 NP_059523.1 3 418 TCTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TERF2 1 11659 NP_005643.1 3 140 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 TGFBR3 1 4831 NP_003234.1 3 382 TGAGTTTTACCC C --- 3 B c c
AGACTCAAGGAG ACTG ACTCC AGTCTGGGTGA
TTGGTAAA TGGT TGAGG TCAGACCCATT
- AAC
GAM2071 371 TGIF2 1 7274 NP_068581.1 3 1451 GCTCTGTCACCC 3 B b b
GGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGGCCCACTG

GAM2071 371 TMC1 1 19429 NP_619636.2 5 127 ACTCTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TMEM14A 1 7622 NP_054770.1 5 73 GCTCGGGGCTGC - GA 3 B c
c
AGGCTGGAGTGC ACTGCACTCCAGTCTG GGT
AGTGGGAC TGACGTGAGGTCGGAC TCG
G GG
GAM2071 371 TMPRSS3 1 15133 NP_076927.1 3 244 GCTCTGTTGCCC TG 3 B b
b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGA TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TMPRSS3 1 15133 NP_115777.1 3 244 GCTCTGTTGCCC TG 3 B b
b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGA TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TMPRSS3 1 15133 NP_115780.1 3 244 GCTCTGTTGCCC TG 3 B b
b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCGA TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TNFAIP2 1 14228 NP_006282.2 3 1220 GCTGTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGCCT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TNFRSF1 2 9933 NP_003833.3 3 453 ACTCTGTCTCCC AC----- T 3 B c c
0B AGGCTGGAGTGC TGCACTCCAGTCTGGG GAC
AATGGTGC ACGTGAGGTCGGACCC CTG
CGTGGTA T
GAM2071 371 TNFRSF1 2 9933 NP_671716.1 3 453 ACTCTGTCTCCC AC----- T 3 B c c
0B AGGCTGGAGTGC TGCACTCCAGTCTGGG GAC
AATGGTGC ACGTGAGGTCGGACCC CTG
CGTGGTA T
GAM2071 371 TNFRSF1 2 14554 NP_003833.3 3 2020 ACTCTCTCGCCC AC----- 3 B c
c
0B AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
AACGGTAC ACGTGAGGTCGGACCCGCT
CATGGCA
GAM2071 371 TNFRSF1 2 14554 NP_671716.1 3 2020 ACTCTCTCGCCC AC----- 3 B c
c
0B AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
AACGGTAC ACGTGAGGTCGGACCCGCT
CATGGCA

GAM2071 371 TNFRSF1 1 11190 NP_003830.1 3 502 TGGCTCTGGCCC C GA 3 B c c
1A AGGCTAGAGTGC ACTGCACTC AGTCTGGGT
AGTGGTGC TGACGTGAG TCGGACCCG
A GT
GAM2071 371 TNFRSF9 1 438 NP_001552.2 3 226 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 TOMM20- 1 11702 NP_055580.1 3 1882 CCGTTTCCTTGG - -- T 3 B c c
PENDING GAACTGGAGTGC ACTGCACTCCAGT CT GGG GAC
AGTATGAG TGACGTGAGGTCA GG TCC TTG
A GT T
GAM2071 371 TOR1B 1 2429 NP_055321.1 3 179 ACTCCGTCATCC TC 3 B b b
AAGCTGGAGTGC ACTGCACTCCAG TGGGTGAC
AGTGGTGC TGACGTGAGGTC ACCTACTG
GA
GAM2071 371 TP53 1 2118 NP_000537.2 3 832 GCTTTGTTGCCC G TG 3 B c c
AGGCTGGAGTGG ACT CACTCCAGTCTGGG AC
AGTGGCGT TGA GTGAGGTCGGACCC TG
G GT
GAM2071 371 TPMT 1 10218 NP_000358.1 3 425 TTCTTGTTGCCC TC TG 3 B c c
AACCTGGAGTGC ACTGCACTCCAG TGGG AC
AGTGGTGC TGACGTGAGGTC ACCC TG
CA GT
GAM2071 371 TRAF5 1 10175 NP_004610.1 3 1090 TCATTGTCACCC C 3 B b b
AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAT TGAC TGAGGTCGGACCCACTG
A
GAM2071 371 TRAF5 1 10175 NP_665702.1 3 1090 TCATTGTCACCC C 3 B b b
AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAT TGAC TGAGGTCGGACCCACTG
A
GAM2071 371 TRIM6 1 13974 NP_477514.1 3 171 GCTCTGTCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
ACTGGCGC ACGTGAGGTCGGACCCGCTG
CGCGGTC
GAM2071 371 TRPM6 1 1713 NP_060132.3 3 856 CTCTTTTTACCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
AATGATGC ACGTGAGGTCGGACCCATT
CGTAGTA
GAM2071 371 TRPV1 2 1587 NP_061197.3 3 363 CTCTTCTCACCC C 3 B b b
AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGA
AGTGGCAC TGACGT AGGTCGGACCCACT
A
GAM2071 371 TRPV1 2 1587 NP_542435.1 3 363 CTCTTCTCACCC C 3 B b b
AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGA
AGTGGCAC TGACGT AGGTCGGACCCACT
A
GAM2071 371 TRPV1 2 1587 NP_542436.1 3 363 CTCTTCTCACCC C 3 B b b

AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGA
AGTGGCAC TGACGT AGGTCGGACCCACT
A
GAM2071 371 TRPV1 2 1587 NP_542437.1 3 363 CTCTTCTCACCC C 3 B b b
AGGCTGGAATGC ACTGCA TCCAGTCTGGGTGA
AGTGGCAC TGACGT AGGTCGGACCCACT
A
GAM2071 371 TRPV1 2 15897 NP_061197.3 3 684 CTCTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TRPV1 2 15897 NP_542435.1 3 685 CTCTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TRPV1 2 15897 NP_542436.1 3 685 CTCTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TRPV1 2 15897 NP_542437.1 3 684 CTCTTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGT TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 TSARG1 1 15069 NP_620712.2 3 260 ACTCTGTCACCC A----- GT 3 B c
c
AGGTTGGAGTGC CTGCACTCCA CTGGGTGAC
AGCAGGGG GACGTGAGGT GACCCACTG
GGGGAC TG
GAM2071 371 TSPYL 1 9101 XP_166325.1 3 657 GCTCTGTCGCCC GT 3 B b b
AGGTTGGAGTGC ACTGCACTCCA CTGGGTGAC
AGTGGCGC TGACGTGAGGT GACCCGCTG
TG
GAM2071 371 TU12B1- 2 12270 NP_057659.1 3 1304 CTCTTATTGCCC TG 3 B b b
TY AGGCTGGAGTGC ACTGCACTCCAGTCTGGG A
AGTGGCAC TGACGTGAGGTCGGACCC T
GT
GAM2071 371 TU12B1- 2 17849 NP_057659.1 3 2854 GCTCTGTTGCCC TC TG 3 B c
b
TY ATTCTGGAGTGC ACTGCACTCCAG TGGG AC
AGTGGTGT TGACGTGAGGTC ACCC TG
TT GT
GAM2071 371 TUCAN 2 2265 NP_055774.1 3 2765 GCTCTGTCATCT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGT TGACGTGAGGTCGGATCTACTG

GAM2071 371 TUCAN 2 10630 NP_055774.1 3 2456 ACTCTGTTACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGTGC TGACGTGAGGTCGGACCCATTG

GAM2071 371 TUFT1 1 19342 NP_064512.1 3 1286 ACTCTGTCACCC 3 B b b

AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTAGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 TXNL2 1 1413 NP_006532.1 3 67 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG

GAM2071 371 UBAP2 1 5122 NP_060919.2 3 156 AGTCTGCCTCCC - CT-- T---- 3 B c c
AGACTGGCTACT AC TGCA CCAGTCTGGG GAC
GTATGTAA TG ATGT GGTCAGACCC CTG
T CATC TCCGT
GAM2071 371 UBAP2 1 5122 NP_065918.1 3 156 AGTCTGCCTCCC - CT-- T---- 3 B c c
AGACTGGCTACT AC TGCA CCAGTCTGGG GAC
GTATGTAA TG ATGT GGTCAGACCC CTG
T CATC TCCGT
GAM2071 371 UBAP2 1 5122 NP_680476.1 3 2644 AGTCTGCCTCCC - CT-- T---- 3 B c c

AGACTGGCTACT AC TGCA CCAGTCTGGG GAC
GTATGTAA TG ATGT GGTCAGACCC CTG
T CATC TCCGT
GAM2071 371 UBF-fl 1 17229 NP_116217.1 3 506 ACTCTGTCACCC A------ C A 3 B c c
AGGCGGGAGTTA CTG ACTCC GTCTGGGTGAC
GGTGGCAT GAT TGAGG CGGACCCACTG
TACGGTG - G
GAM2071 371 UGDH 1 12092 NP_003350.1 3 152 TCACTGTTGCCC TG 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 UMPS 1 19428 NP_000364.1 3 390 ACTCTGTTGCCC GT TG 3 B c c

AGGATGGAGTGC ACTGCACTCCA CTGGG AC
AGTGGTGA TGACGTGAGGT GACCC TG
AG GT
GAM2071 371 UNG2 1 10716 NP_066970.1 3 21 CTCTCCCGTACC CAG - A 3 B c c
TCAGAAGAGTGC ACTGCACTC TCTG GGTG
AGTACTGG TGACGTGAG AGAC CCAT
A-- T G
GAM2071 371 USP22 1 20055 XP_042698.2 3 2024 AGTTTGTTGCCC G TG 3 B c c
AGGCTGGAGTGA ACT CACTCCAGTCTGGG AC
GTGGCACA TGA GTGAGGTCGGACCC TG
- GT
GAM2071 371 VDU1 1 794 NP_055832.2 3 277 GCTTTGTCACCC T 3 B b b
AGGCTGGAGTGC AC GCACTCCAGTCTGGGTGAC
TGTGGTGT TG CGTGAGGTCGGACCCACTG
T
GAM2071 371 VENTX2 1 13003 NP_055283.1 3 304 GCTCTGTCACCC AC----- 3 B c c

AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGACGC ACGTGAGGTCGGACCCACTG
CGCAGTA

GAM2071 371 VHL 2 969 NP_000542.1 3 988 CTCTTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGC TGACGTGAGGTCGGACCCACTG

GAM2071 371 VHL 2 19946 NP_000542.1 3 2567 CCTCTGTTGCCC A----- TG 3 B c b
AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGAGGTGC GACGTGAGGTCGGACCC TG
CGTGGA GT
GAM2071 371 VIPR2 1 861 NP_003373.2 3 313 GCTCTGTCGCCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCCT TGACGTGAGGTCGGACCCGCTG

GAM2071 371 VPS33A 1 4137 NP_075067.2 3 231 GCTCTGTCACCC C 3 B b b
AGACTAGAGTGC ACTGCACTC AGTCTGGGTGAC
AGTGGCAC TGACGTGAG TCAGACCCACTG
A
GAM2071 371 VTI1A 1 1472 NP_660207.1 3 357 TGCCCTGTCGCC G T TG 3 B c c
TGGCTGGAGTGG ACT CACTCCAG C GGTGAC
AGTGGCAC TGA GTGAGGTC G CCGCTG
G - GT
GAM2071 371 WBSCR18 1 10631 NP_115693.2 3 831 GCTCTGTTGCCC TG 3 B b
b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG AC
AGTGGTGC TGACGTGAGGTCGGACCC TG
GT
GAM2071 371 WHSC1 1 12602 NP_579889.1 3 3922 ACCCTGTTGGCC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTAAGTG TGACGTGAGGTCGGACC GTTG
G
GAM2071 371 WISP1 1 6051 NP_003873.1 3 1501 CCAGAGTCACCC GCAC ------ 3 B c
c
AGTTGGTGACTG ACT TCCAGTC TGGGTGAC
GGAAAGTT TGA GGGTCAG ACCCACTG
AA-- TGGTTG
GAM2071 371 XRCC2 2 6034 NP_005422.1 3 98 GCTCTGTCTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCAC TGACGTGAGGTCGGACCC CTG
T
GAM2071 371 XRCC2 2 19967 NP_005422.1 3 274 CTGTCTCCCAGG --- T 3 B b b
CTGCTGGAGTGC ACTGCACTCCAGT CTGGG GAC
AGTGGCAC TGACGTGAGGTCG GACCC CTG
TCG T
GAM2071 371 YES1 1 18699 NP_005424.1 3 1376 GCTCTGCCGCCC A 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTG
AGTGGCGC TGACGTGAGGTCGGACCCGC
C
GAM2071 371 ZAP 1 19083 NP_064504.2 3 307 ACTCCATCGTCC GT 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG GA
AGTGGCGC TGACGTGAGGTCGGACC CT
TG

GAM2071 371 ZFP42 1 6576 NP_777560.1 3 642 GCTCTGTCACCC C 3 B b b
AGGCTGGAGTCT ACTG ACTCCAGTCTGGGTGAC
AGTGTCGT TGAT TGAGGTCGGACCCACTG
C
GAM2071 371 ZFP64 1 13869 NP_060667.1 3 150 GCTCTGTTTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGC TGACGTGAGGTCGGACCC TTG
T
GAM2071 371 ZFP64 1 13869 NP_071371.2 3 150 GCTCTGTTTCCC T 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGG GAC
AGTGGCGC TGACGTGAGGTCGGACCC TTG
T
GAM2071 371 ZMYND17 1 11022 NP_848546.1 3 217 GCTCTGTTGCCC A----- TG 3 B c c
AGGCTGGAGTGC CTGCACTCCAGTCTGGG AC
AGCGGCAT GACGTGAGGTCGGACCC TG
TACGGC GT
GAM2071 371 ZNF253 1 12223 NP_066385.1 3 291 CTCTTGTCACCG AC----- G 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCT GGTGAC
AATGACAT ACGTGAGGTCGGA CCACTG
TACAGTA G
GAM2071 371 ZNF264 2 438 NP_003408.1 3 2977 ACTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCAC TGACGTGAGGTCGGACCCACTG
GAM2071 371 ZNF264 2 15406 NP_003408.1 3 2603 ACTCTGTCACCC T C 3 B b b
ACGCTGGAGTGC AC GCACTCCAGT TGGGTGAC
TGTGATGC TG CGTGAGGTCG ACCCACTG
T C
GAM2071 371 ZNF302 1 19157 NP_060913.1 3 1035 ATTTAGTCACCC CA AG 3 B b b
AGAGGAGCCAGT ACTG CTCC TCTGGGTGAC
AAATGTTA TGAC GAGG AGACCCACTG
C- --
GAM2071 371 ZNF302 1 19157 NP_061145.1 3 1072 ATTTAGTCACCC CA AG 3 B b b
AGAGGAGCCAGT ACTG CTCC TCTGGGTGAC
AAATGTTA TGAC GAGG AGACCCACTG
C- --
GAM2071 371 ZNF305 1 10363 NP_055539.1 3 2908 CTCCTGTCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGAC
AATGGCAC ACGTGAGGTCGGACCCGCTG
CACGGTA
GAM2071 371 ZNF334 1 7143 NP_060572.2 5 38 GCACTGTCACCC C --- 3 B b b
AGGCTGCTGGAG ACTG ACTCCAGT CTGGGTGAC
TACAGTGG TGAC TGAGGTCG GACCCACTG
A TCG
GAM2071 371 ZNF339 1 9097 NP_067043.1 3 654 ACTCTGTCACCC C 3 B b b

AGGCTGGAGTAC ACTG ACTCCAGTCTGGGTGAC
AGTGGCAT TGAC TGAGGTCGGACCCACTG
A

GAM2071 371 ZNF345 1 11758 NP_003410.1 3 601 CTCACTGTCACC G 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGG TGAC
AGTGGTGC TGACGTGAGGTCGGACC ACTG
-

GAM2071 371 ZNF431 1 9382 XP_086098.2 3 1486 ACTCTTTCGCCC AC----- 3 B c c
AGGCTGGAGTGC TGCACTCCAGTCTGGGTGA
ATTGGCAT ACGTGAGGTCGGACCCGCT
TACGGTT

GAM2071 371 ZNF440 1 11659 NP_689570.1 3 1223 GCTCTGTCACCC 3 B b b
AGGCTGGAGTGC ACTGCACTCCAGTCTGGGTGAC
AGTGGCGT TGACGTGAGGTCGGACCCACTG

GAM2071 371 ZNF450 1 13289 NP_055612.1 3 1087 ACTGTATCACCC CA 3 B b b
AGGCCAGAGTGT ACTGCACTC GTCTGGGTGA
AGTGGCAC TGATGTGAG CGGACCCACT
AC

GAM2071 371 ZNF74 1 2276 NP_003417.1 5 1267 TGGACTTCACCC G AG 3 B c c
AGGAGGAGTGGG ACT CACTCC TCTGGGTGA
GTCAACTA TGG GTGAGG GGACCCACT
G A-

GAM2071 371 ZSIG11 1 13057 NP_057010.1 3 34 ATGGCCTGCACC C TCT A 3 B c
c

CTCCTGCAGTGC ACTGCACT CAG GGGTG
AGTTGCTG TGACGTGA GTC CCCAC
C CT- G

GAM2608 245 ABCC3 1 19582 NP_003777.2 3 110 TTGATAGCAAAC AT CA- 6 A c c

ACTGGGGGCACC TAAGGTGC CTAGTG GTTA
TTAAGATT ATTCCACG GGTCAC CGAT
GG AAA

GAM2608 245 ABCC3 1 19582 NP_064421.1 3 1126 TTGATAGCAAAC AT CA- 6 A c
c

ACTGGGGGCACC TAAGGTGC CTAGTG GTTA
TTAAGATT ATTCCACG GGTCAC CGAT
GG AAA

GAM2608 245 ABCC3 1 19582 NP_064422.1 3 3365 TTGATAGCAAAC AT CA- 6 A c
c

ACTGGGGGCACC TAAGGTGC CTAGTG GTTA
TTAAGATT ATTCCACG GGTCAC CGAT
GG AAA

GAM2608 245 ATP7A 1 10811 NP_000043.1 3 2925 GTTCAGACTCAC - C - C 6 A c c
CTATGTGGCACC TAAGGTGC AT TAG TG AGTT
TTAAACTT ATTCCACG TG ATC AC TCAG
G T C -

GAM2608 245 BACE 1 13378 NP_036236.1 3 1807 CATTCCCACTGC - T T 6 A c c
ACTTGGTGCTGC TAAGGT GCATC AGTGCAGT
TTTGGCTG GTTTCG CGTGG TCACGTCA

```
                                        T   T     C
GAM2608  245  BACE   1  13378 NP_620427.1  3 1807  CATTCCCACTGC    -  T    T     6 A c c
                                ACTTGGTGCTGC TAAGGT GCATC AGTGCAGT
                                TTTGGCTG   GTTTCG CGTGG TCACGTCA
                                        T   T     C
GAM2608  245  BACE   1  13378 NP_620428.1  3 1807  CATTCCCACTGC    -  T    T     6 A c c
                                ACTTGGTGCTGC TAAGGT GCATC AGTGCAGT
                                TTTGGCTG   GTTTCG CGTGG TCACGTCA
                                        T   T     C
GAM2608  245  BACE   1  13378 NP_620429.1  3 1807  CATTCCCACTGC    -  T    T     6 A c c
                                ACTTGGTGCTGC TAAGGT GCATC AGTGCAGT
                                TTTGGCTG   GTTTCG CGTGG TCACGTCA
                                        T   T     C
GAM2608  245  BMF    1  14471 NP_277038.1  3 2318  TGGTCTGACTGC     CATC          6 A c c
                                ACTGTCTCCATC TAAGGTG   TAGTGCAGTTA
                                TTATGCAA   ATTCTAC   GTCACGTCAGT
                                        CTCT
GAM2608  245  CREBL2  1  10963 NP_001301.1  3 314   CGATGAAGATTG      TCT          6 A c c

                                TATTTTTGCACC TAAGGTGCA  AGTGCAGTT
                                TTAACTCC   ATTCCACGT  TTATGTTAG
                                        TT-
GAM2608  245  DJ465N2 1  7651  NP_064713.2  3 56   CATGAAAACTGC   GG   TCT-          6 A c
c
         4.2.1                    ACTTTATTGCAA TAA  TGCA   AGTGCAGTT
                                GTTAGTGT   ATT  ACGT   TCACGTCAA
                                        GA   TATT
GAM2608  245  DKFZP58 1  1283  NP_665803.1  3 1161  CTTCTTCAGCTG     AT   T        6 A c c

         6C1619                    TCTGGCCGCACC TAAGGTGC  CTAG GCAGTT
                                TTAAAAAC   ATTCCACG  GGTC TGTCGA
                                        CC   -
GAM2608  245  DMN    1  5539  NP_056101.4  3 841   TGCAGACTTGCG      TCT-   -      6 A c c
                                CTTCTCTGCACC TAAGGTGCA   AGTGCA GTT
                                TTATCCCT   ATTCCACGT   TCGCGT CAG
                                        CTCT    T
GAM2608  245  DMN    1  5539  NP_663780.1  3 841   TGCAGACTTGCG      TCT-   -      6 A c c
                                CTTCTCTGCACC TAAGGTGCA   AGTGCA GTT
                                TTATCCCT   ATTCCACGT   TCGCGT CAG
                                        CTCT    T
GAM2608  245  ELOVL1  1  11677 NP_073732.1  3 51   ACCTAAGTGCCT      - -- T  G     6 A c c
                                CAGGACTGCACC TAAGGTGCA TCT  AG GCA TTA
                                TTAGGGCA   ATTCCACGT AGG  TC CGT AAT
                                        C  AC  -  G
GAM2608  245  ESM1   1  4688  NP_008967.1  3 1198  CAGGACTGTTGT    T     ---        6 A c c
                                ACTAGATGTTCT TAAGG GCATCTAGT   GCAGTT
                                TAGGAAAT   ATTCT TGTAGATCA   TGTCAG
                                        -      TGT
GAM2608  245  FAM3C  1  8964  NP_055703.1  3 1407  AATTAATTCATG      CTA---  C      6 A c c
```

AATAAATGCACC TAAGGTGCAT GTG AGTTA
TTATATGT ATTCCACGTA TAC TTAAT
AATAAG -

GAM2608 245 FBXL3A 1 14877 NP_036290.1 3 25 TAAAACTGCATG A-- TA- 6 A c c
ATGAATAGCACC TAAGGTGC TC GTGCAGTT
TTAATTTC ATTCCACG AG TACGTCAA
ATA TAG

GAM2608 245 FLJ1089 1 16988 NP_060733.1 3 2436 ACATTGCTGTTC C -- T 6 A c c
8 ACTAGATTATCT TAAGGTG ATCTAGTG CAGT
TAACAAAT ATTCTAT TAGATCAC GTCG
- TT T

GAM2608 245 FLJ1481 1 4188 NP_116232.2 3 16 GGGAGGACCGCT T -- A 6 A c c
0 AACTGGTGCACC TAAGGTGCA CTAGT GC GTT
TTGTCCTT GTTCCACGT GGTCA CG CAG
- AT C

GAM2608 245 FLJ1490 1 9840 NP_116248.1 3 433 TTCTGTAACTGC CATCT 6 A c c

6 ATTTTTCACCTT TAAGGTG AGTGCAGTTA
AAAAGTTA ATTCCAC TTACGTCAAT
TTT--

GAM2608 245 FLJ3399 1 13443 NP_694958.1 3 782 TTTTGAAACTGC TGC C 6 A c c

0 ACTAAATTTTTC TAAGG AT TAGTGCAGTT
TTAACATT ATTCT TA ATCACGTCAA
TTT A

GAM2608 245 FLJ3982 1 12614 NP_775971.1 5 525 CTAAGAAACACC T CA 6 A c c
1 ATTTGATGCACC TAAGGTGCATC AGTG GTT
TTAGAGAA ATTCCACGTAG TTAC CAA
T CA

GAM2608 245 FLJ4028 1 4292 NP_775953.1 5 259 CAGAAGAGATGA CTAG A 6 A c
c
8 TGGCAATGCACC TAAGGTGCAT TGC GTTA
TTGCAGGT GTTCCACGTA ACG TAGT
---- G

GAM2608 245 FLJ4058 1 17085 XP_069189.2 3 1481 TTGACAAACTGC T -- 6 A c c
4 ACCATAGGTGTT TAAGG GCATCTA GTGCAGTT
TTTAGACT ATTTT TGTGGAT CACGTCAA
- AC

GAM2608 245 GLS 1 9171 NP_055720.2 3 1510 AAACTTTACATG - T T - T 6 A c c
CCTGATGGCACC TAAGGTGC ATC AG GCA GT
TTACTCCA ATTCCACG TAG TC CGT CA
G - - A T

GAM2608 245 GRIA1 1 16531 NP_000818.1 3 341 TGAGGAAACTGC CATC 6 A c c

ACTGTTTTATTT TAAGGTG TAGTGCAGTT
TAATTCAG ATTTTAT GTCACGTCAA
TTT-

GAM2608 245 HPSE 1 6950 NP_006656.1 3 555 AAAGAGAAACTA TC TGC 6 A c c
TCTATTTGCACC TAAGGTGCA TAG AGTT
TTAAAAGA ATTCCACGT ATC TCAA

TT TA-

GAM2608 245 ITPKB 1 3880 NP_002212.1 3 129 CTCCTGAACTGC CATC- 6 A c c
ACTACAAGACAC TAAGGTG TAGTGCAGTT
TTTGTAGA GTTTCAC ATCACGTCAA
AGAAC

GAM2608 245 KIAA032 1 16873 XP_034819.1 3 671 CCCACTCACTGC T A T 6 A c c
6 ACTGGGGTCCTT TAAGG GC TCTAGTGCAGT
GGGGTTTG GTTCC TG GGGTCACGTCA
- - C

GAM2608 245 KIAA182 1 13511 XP_040784.1 3 1394 GAGAATCACTGC C T 6 A c c
6 ACTAGATCACTT TAAGGTG ATCTAGTGCAGT
TGTGTTTT GTTTCAC TAGATCACGTCA
- C

GAM2608 245 KIAA185 1 2810 XP_045184.1 3 2828 GAGCTGACTGAG ------ G 6 A c c
3 GGAAGATGCACC TAAGGTGCATCT AGT CAGTT
TTGATCTC GTTCCACGTAGA TCA GTCGA
AGGGAG -

GAM2608 245 LAMP1 1 6326 NP_005552.2 3 544 ATTCTTTACTGC GC-- - T 6 A c c
ACTCAGATTTAA TAAGGT ATCT AGTGCAGT
GCCTTACA ATTCCG TAGA TCACGTCA
AATT C T

GAM2608 245 LAPTM4A 1 6126 NP_055528.1 3 330 CTTTTTAACTGC TGCATCT 6 A c
c
ACTTTCTTTATA TAAGG AGTGCAGTTA
TAATCGTT ATTTC TCACGTCAAT
TT-----

GAM2608 245 LHCGR 1 15507 NP_000224.1 3 35 ATCAGTAACTGC T -- -- 6 A c c
ATTATTGAATTG TAAGG GCA TC TAGTGCAGTTA
TTCTTAAA ATTCT TGT AG ATTACGTCAAT
- TA TT

GAM2608 245 LOC1149 1 14175 XP_054936.4 3 1343 AACTGCAAATTG ----- TAG- 6 A c
c
71 GTAAGCAGCACC TAAGGTGC ATC TGCAGTT
TTAATACC ATTCCACG TGG ACGTCAA
ACGAA TTAA

GAM2608 245 LOC1471 1 18650 XP_300674.1 3 2479 ACTGGGAACTGC GT--- A 6 A c
c
36 ACCAGATGCTCA TAAG GCATCT GTGCAGTT
GACTTGGT GTTC CGTAGA CACGTCAA
AGACT C

GAM2608 245 LOC1502 1 8823 XP_086820.1 3 1244 GCACACAACTGC GCATC 6 A c
c
79 ACTGAAGCCTTG TAAGGT TAGTGCAGTT
TTCCTCTC GTTCCG GTCACGTCAA
AA---

GAM2608 245 LOC1588 1 5453 XP_098999.1 3 121 GCCAGCTGGATT --- G 6 A c c
63 GGCCAGTGCACC TAAGGTGCAT CTAGT CAGTT
TTGTATTC GTTCCACGTG GGTTA GTCGA
ACC G

GAM2608 245 LOC2012 1 15360 XP_113947.1 5 561 ATGTTTAACTGC CA AGT 6 A c
c

```
          87                        AGACTTGCCTTA TAAGGTG  TCT   GCAGTTA
                                   AAACAAGA    ATTCCGT  AGA   CGTCAAT
                                               TC   ---
GAM2608  245   LOC2204 1  5591  XP_165391.2  5  191   GAGAAGGACTGC       --   -          6  A  c  c
          86                        ACTTAGAACTGC TAAGGTGCA  TCTA GTGCAGTT
                                   ATTTTGGC    GTTTTACGT  AGAT CACGTCAG
                                               CA    T
GAM2608  245   LOC2536 1  17912 XP_172986.2  5  386   GGAGGTAGGGGC       CTA  G          6  A  c
c
          09                        TGGGCATGCACC TAAGGTGCAT   GT CAGTT
                                   TTGGTTAA    GTTCCACGTA   CG GTCGG
                                               ---  G
GAM2608  245   LOC2538 1  7852  XP_172854.1  3  2100  CTTTAGAGCTGC    T-  AT--           6  A  c  c

          05                        ACTAGCCTGGCT TAAGG  GC    CTAGTGCAGTT
                                   TTCTTATT    ATTCT  CG    GATCACGTCGA
                                               TT  GTCC
GAM2608  245   LOC2831 1  8224  XP_208043.1  5  191   GAGAAGGACTGC       --   -          6  A  c  c
          16                        ACTTAGAACTGC TAAGGTGCA  TCTA GTGCAGTT
                                   ATTTTGGT    GTTTTACGT  AGAT CACGTCAG
                                               CA    T
GAM2608  245   LOC2838 1  16975 XP_211223.1  3  179   TAGGAGCGAGGT       TCTA    G          6  A  c
c
          30                        GCACATTGCACC TAAGGTGCA    GTGCA TT
                                   TTACATCC    ATTCCACGT    CACGT GA
                                               TA--    G
GAM2608  245   LOC2849 1  13549 NP_775918.1  3  598   TATGAGAAAGGC     G       AG         6  A  c
c
          96                        ACTAGATGACTT TAAGGT CATCTAGTGC  TT
                                   TAGGATTT    ATTTCA GTAGATCACG  AA
                                               -       GA
GAM2608  245   LOC2855 1  13348 XP_211948.1  3  810   CATCTTAACTGC T-----     C-   A         6  A  c  c

          95                        ACAGATACCATC      AAGGTG  ATCT GTGCAGTTA
                                   TTCTCGGC         TTCTAC  TAGA CACGTCAAT
                                               CGGCTC     CA   -
GAM2608  245   LOC2856 1  13348 XP_211976.2  3  818   CATCTTAACTGC T-----     C-   A         6  A  c  c

          56                        ACAGATACCATC      AAGGTG  ATCT GTGCAGTTA
                                   TTCTCGGC         TTCTAC  TAGA CACGTCAAT
                                               CGGCTC     CA   -
GAM2608  245   LOC2864 1  8964  XP_208425.1  3  1407  AATTAATTCATG       CTA---  C          6  A  c
c
          60                        AATAAATGCACC TAAGGTGCAT     GTG AGTTA
                                   TTATATGT    ATTCCACGTA     TAC TTAAT
                                               AATAAG   -
GAM2608  245   LOC3390 1  3940  XP_290661.1  3  2497  CTAGTTAACTGC     ---  AT  AG          6  A  c
c
          05                        AGCAGGAGCATG TAAGG   TGC  CT  TGCAGTTA
                                   TCCTTAAG    ATTCC   ACG  GA  ACGTCAAT
```

TGT AG CG
GAM2608 245 LOC3392 1 2561 XP_294889.1 5 555 GTTTCTCAGCGG T T A 6 A c c
63 CCTAGATGCCTC TAAGG GCATCTAG GC GTT
TTGGTCTG GTTCT CGTAGATC CG CGA
C - G
GAM2608 245 LOC3489 1 13348 XP_302935.1 3 810 CATCTTAACTGC T----- C- A 6 A c c
89 ACAGATACCATC AAGGTG ATCT GTGCAGTTA
TTCTCGGC TTCTAC TAGA CACGTCAAT
CGGCTC CA -
GAM2608 245 LOC3494 1 10811 XP_300513.1 3 2541 GTTCAGACTCAC - C - C 6 A c c
40 CTATGTGGCACC TAAGGTGC AT TAG TG AGTT
TTAAACTT ATTCCACG TG ATC AC TCAG
G T C -
GAM2608 245 LOC5597 1 17137 NP_061333.1 3 34 CTGCTCATCTGA AT -- TT 6 A c c
4 CCACTGGGCACC TAAGGTGC CTAGTG CAG
TTAGTGCC ATTCCACG GGTCAC GTC
-- CA TA
GAM2608 245 MAML2 1 11423 XP_045716.1 3 157 GAAAGTAACTGC -- T G 6 A c c
AGTGATGAACAT TAAGGTG CATC A TGCAGTTA
TTTGGTCC GTTTTAC GTAG T ACGTCAAT
AA - G
GAM2608 245 MAP3K8 1 17674 NP_005195.2 5 613 CCCTGACACTGC A T T 6 A c c
ACTGAGCACTTT TAAGGTGC TC AGTGCAGT
ATGAGCTT ATTTCACG AG TCACGTCA
- - C
GAM2608 245 MAP4K5 1 14765 NP_006566.2 3 99 AATACAAACTGC C - 6 A c c
ACTATGATTTGC TAAGGTG ATC TAGTGCAGTT
TTTAACTA ATTTCGT TAG ATCACGTCAA
T T
GAM2608 245 MASP1 1 16184 NP_001870.3 3 667 CTAGGAACATGC GG - - 6 A c c
ACTAGATGACAG TAA TG CATCTAGTGCA GTT
ATTGCGGG GTT AC GTAGATCACGT CAA
AG A A
GAM2608 245 MGC1056 1 2731 NP_116036.1 3 88 TCCGGGCCCACC AGT TT 6 A c
c
1 TGCGGGTGCACC TAAGGTGCATCT GCAG
TTAAATCG ATTCCACGTGGG CGTC
--- CA
GAM2608 245 MGC1302 1 9146 NP_689501.1 3 1067 TCTGACACTGAA TG- T 6 A c
c
4 TTTGGATGCACC TAAGGTGCATCTAG CAGT
TTGTTTTA GTTCCACGTAGGTT GTCA
TAA C
GAM2608 245 MMD 1 14690 NP_036461.1 3 118 AAAAATAACTGC GCATC 6 A c c
ACTGACTTTATA TAAGGT TAGTGCAGTTA

TCTTTTGA ATTTCA GTCACGTCAAT

GAM2608 245 MMP26 1 3864 NP_068573.1 3 86 AGAACTGAAAGC - A ---- 6 A c c
ACTAGAGCAGCC TAAGG TGC TCTAGTGC AGTT
TTGGGGAC GTTCC ACG AGATCACG TCAA
G - AAAG

GAM2608 245 MMP3 1 13663 NP_002413.1 3 213 ATGGGCTGCTGC T- - - 6 A c c
TTAGCTTGCACC TAAGGTGCA CTA GT GCAGTT
TTGTCACA GTTCCACGT GAT CG CGTCGG
TC T T

GAM2608 245 NEDD4 1 15072 XP_046129.4 3 549 TTTTGTAGACCT CT T TT 6 A c c
GCCTTATGCACC TAAGGTGCAT AG GCAG
TTACTGCC ATTCCACGTA TC CGTC
T- - CA

GAM2608 245 NR1I2 1 11884 NP_003880.2 3 1067 GGAGAAGAACCA CT- CA 6 A c
c
TTTACATGCACC TAAGGTGCAT AGTG GTT
TTATATTT ATTCCACGTA TTAC CAA
CAT --

GAM2608 245 NR1I2 1 11884 NP_071285.1 3 1067 GGAGAAGAACCA CT- CA 6 A c
c
TTTACATGCACC TAAGGTGCAT AGTG GTT
TTATATTT ATTCCACGTA TTAC CAA
CAT --

GAM2608 245 NR1I2 1 11884 NP_148934.1 3 1067 GGAGAAGAACCA CT- CA 6 A c
c
TTTACATGCACC TAAGGTGCAT AGTG GTT
TTATATTT ATTCCACGTA TTAC CAA
CAT --

GAM2608 245 NUDT4 1 18737 NP_061967.2 3 1006 GAGACTGAAGAT A GT 6 A c c
TGTTAGGGCACC TAAGGTGC TCTA GCAGTT
TTAGAATG ATTCCACG GGAT TGTTAG
- --

GAM2608 245 PACSIN1 1 4408 NP_065855.1 3 2044 GGTGGGAAGCTG TCTAG - 6 A c
c
GCAATCTGCACC TAAGGTGCA TGC AGTT
TTGGGGCC GTTCCACGT ACG TCGA
CTA-- G

GAM2608 245 PDE4D 1 15887 NP_006194.1 3 761 TAATTTATGAAT TCT C 6 A c c
TTTACTTGCACC TAAGGTGCA AGTG AGTT
TTATAGTT ATTCCACGT TCAT TTAA
--- T

GAM2608 245 PERQ1 1 13107 NP_072096.1 3 152 CTTGTTACAAAC TA CA 6 A c c
ACACGATGCACC TAAGGTGCATC GTG GTT
TTAACTCA ATTCCACGTAG CAC CAA
-- A-

GAM2608 245 PGRMC1 1 12615 NP_006658.1 3 586 TTTCTGGACTGC T TC 6 A c
c

ACTGTTGTCCTT TAAGG GCA TAGTGCAGTT
GCCCTCAC GTTCC TGT GTCACGTCAG
- T-

GAM2608 245 RAB5A 1 5501 NP_004153.2 3 676 ATTTTGAGAACT C GTGC 6 A c c

AATAAATGCACC TAAGGTGCAT TA AGTT
TTAATGGT ATTCCACGTA AT TCAA
A AA--

GAM2608 245 RNF18 1 8224 NP_065091.1 5 191 GAGAAGGACTGC -- - 6 A c c
ACTTAGAACTGC TAAGGTGCA TCTA GTGCAGTT
ATTTTGGT GTTTTACGT AGAT CACGTCAG
CA T

GAM2608 245 ROCK2 1 19439 NP_004841.1 3 1174 ACTAAGACAGAC AGT 6 A c c

TGTAGATGCATT TAAGGTGCATCT GCAGTT
TTAAATAT ATTTTACGTAGA TGTCAG

GAM2608 245 SH3BGRL 1 18614 NP_113657.1 3 400 TCTTTAAGCTGC T----- - T 6 A c c

2 CTGGATTGCACC AAGGTGCA TCTAG GCAGTT
TTTGAAAT TTCCACGT AGGTC CGTCGA
TAAAGT T -

GAM2608 245 SIM2 1 4214 NP_005060.1 3 929 GGAACACTGTCA - G - T 6 A c c
ATGGACTGCACC TAAGGTGCA TCTA TG CAGT
TTGTGAAG GTTCCACGT AGGT AC GTCA
C A T C

GAM2608 245 STK38L 1 8158 NP_055815.1 3 288 CTTTCTAACTGC GG C---- 6 A c c
ACTGCTTACATG TAA TGCAT TAGTGCAGTTA
CGTATTAA ATT GCGTA GTCACGTCAAT
AT CATTC

GAM2608 245 TFB2M 1 2805 NP_071761.1 5 78 TGTAGTAGCTGC TG 6 A c c
ACTAGGTGATTC TAAGG CATCTAGTGCAGTTA
TTGGAGCG GTTCT GTGGATCACGTCGAT
TA

GAM2608 245 TTID 1 10202 NP_006781.1 3 242 ATTTGTAACTGC CA AG 6 A c c
AGAAGACTATCT TAAGGTG TCT TGCAGTTA
TAAAATAC ATTCTAT AGA ACGTCAAT
C- AG

GAM2608 245 USH2A 1 4007 NP_009054.3 3 1140 ATTGAGACTGGC T - - 6 A c c
TGCTGATGCACC TAAGGTGCATC AGT GC AGTT
TTGGTAAT GTTCCACGTAG TCG CG TCAG
- T G

GAM2608 245 ZID 1 5650 NP_006617.1 3 1481 TAAAGAAGACTG T----- G 6 A c c
ACTAGATGCATC AAGGTGCATCTAGT CAGTT
TTTCTTTG TTCTACGTAGATCA GTCAG
GTTTCT -

GAM3027 242 1 16500 NP_444285.1 5 991 GAAGGGCTGGTT T-- G 3 A c c
TGAATTTTGGTG TAGCACCA TT AAATCGGTT
CTACTATC ATCGTGGT AA TTTGGTCGG
TTT G

GAM3027 242 AIM1L 1 7873 NP_060447.1 3 318 GGCTACGACCGG T AAA 3 A c c
GACCACGTGGTG TAGCACCAT TG TCGGTT
CTATGGGA ATCGTGGTG AC GGCCAG
C CAG
GAM3027 242 BACH2 1 1058 NP_068585.1 3 201 GTGATAGTTACC - ATC T 3 A c c
TTCACAATGGTG TAGCACCATT TGAA GGT
CTACCCCT ATCGTGGTAA ACTT CCA
C --- T
GAM3027 242 C14orf1 1 9141 NP_061059.1 3 137 GCCGAAACCGAT TTGAA- 3 A c c

16 GTGTCTATGGTG TAGCACCAT ATCGGTT
CTGCACCT GTCGTGGTA TAGCCAA
TCTGTG
GAM3027 242 C5orf13 1 11415 NP_004763.1 3 568 GACCTGAGACAC GAA T 3 A c c

TGATGAATGGTG TAGCACCATTT ATCGGT
CTATTTTG ATCGTGGTAAG TAGTCA
--- C
GAM3027 242 C5orf5 1 11857 NP_057687.1 3 533 ATCAAACTGAGA C C -- 3 A c c
TTTCAAGTCGTA TAG AC ATTTGAAATC GGTT
CTATGGAA ATC TG TGAACTTTAG TCAA
A C AG
GAM3027 242 CCRL1 1 11537 NP_848540.1 5 101 CCCATTAAAGCA CA CG 3 A c c

TTTCAAAGAGTG TAGCAC TTTGAAAT GTT
CTAGATTC ATCGTG AAACTTTA CGA
AG --
GAM3027 242 COL4A5 1 18409 NP_000486.1 3 116 TTACTACTGCTG T AAT T 3 A c
c
CCGTCAATGGTG TAGCACCATT GA CGGT
CTACTATA ATCGTGGTAA CT GCCG
- --- T
GAM3027 242 COL4A5 1 18409 NP_203699.1 3 116 TTACTACTGCTG T AAT T 3 A c
c
CCGTCAATGGTG TAGCACCATT GA CGGT
CTACTATA ATCGTGGTAA CT GCCG
- --- T
GAM3027 242 COL4A5 1 18409 NP_203700.1 3 116 TTACTACTGCTG T AAT T 3 A c
c
CCGTCAATGGTG TAGCACCATT GA CGGT
CTACTATA ATCGTGGTAA CT GCCG
- --- T
GAM3027 242 COL5A2 1 17367 NP_000384.1 5 78 GAGCCCACAGCT TT A 3 A c c
GACTTCATGGTG TAGCACCA TGAA TCGGTT
CTACAATA ATCGTGGT ACTT AGTCGA
-- C
GAM3027 242 COL6A3 1 16712 NP_004360.1 3 176 GCTGCATGACCT - AATC 3 A c
c
ATCAGTATGGTG TAGCACCAT TTGA GGTTA
CTAATGTG ATCGTGGTA GACT CCAGT

```
                                                T   AT--
GAM3027  242   COL6A3  1  16712  NP_476505.1  3  176   GCTGCATGACCT      -   AATC        3  A  c
c
                                ATCAGTATGGTG TAGCACCAT TTGA   GGTTA
                                CTAATGTG    ATCGTGGTA GACT   CCAGT
                                            T   AT--
GAM3027  242   COL6A3  1  16712  NP_476506.1  3  176   GCTGCATGACCT      -   AATC        3  A  c
c
                                ATCAGTATGGTG TAGCACCAT TTGA   GGTTA
                                CTAATGTG    ATCGTGGTA GACT   CCAGT
                                            T   AT--
GAM3027  242   COL6A3  1  16712  NP_476507.1  3  176   GCTGCATGACCT      -   AATC        3  A  c
c
                                ATCAGTATGGTG TAGCACCAT TTGA   GGTTA
                                CTAATGTG    ATCGTGGTA GACT   CCAGT
                                            T   AT--
GAM3027  242   COL6A3  1  16712  NP_476508.1  3  176   GCTGCATGACCT      -   AATC        3  A  c
c
                                ATCAGTATGGTG TAGCACCAT TTGA   GGTTA
                                CTAATGTG    ATCGTGGTA GACT   CCAGT
                                            T   AT--
GAM3027  242   CSPG4   1  1254  NP_001888.1  3  670   GCAAGGAAGCTA      TTG   C         3  A  c  c

                                TTTAACATGGTG TAGCACCAT   AAAT GGTT
                                CTGAGCTA    GTCGTGGTA   TTTA TCGA
                                            CAA   -
GAM3027  242   CYCS    1  1967  NP_061820.1  3  1006  CAGCAGTGTTAA      TT  AATC        3  A  c
c
                                CCAGTCATGGTG TAGCACCA  TGA   GGTTA
                                CTAGATTG    ATCGTGGT  ACT   CCAAT
                                            --  GA--
GAM3027  242   DDX4    2  4569  NP_077726.1  3  211   TTGCAGTTACTG        AA    T       3  A  c  c
                                ATACAAATGGTG TAGCACCATTTG  ATCGGT
                                TTAACTGG    ATTGTGGTAAAC  TAGTCA
                                              A-    T
GAM3027  242   DDX4    2  14219 NP_061912.1  3  152   CCTACACTACTG        AA    T       3  A  c  c
                                ATACAAATGGTG TAGCACCATTTG  ATCGGT
                                TTAACTGG    ATTGTGGTAAAC  TAGTCA
                                              A-    T
GAM3027  242   DKFZp43 1  2186  NP_835224.1  3  314   ACTGATAATAAG      TG -------   T   3  A  c  c

          4O0515                  CTTTGAATGGTG TAGCACCATT  AA     ATCGGT
                                CTAATAAG    ATCGTGGTAA  TT     TAGTCA
                                            GT  CGAATAA    -
GAM3027  242   EBRP    1  13938 NP_115954.1  3  146   CTGAACAACCTG   C  -     C         3  A  c  c
                                TTTCAAATTGGT TAG ACCA TTTGAAAT GGTT
                                TTTAAGGC    ATT TGGT AAACTTTG CCAA
                                          T   T     T
GAM3027  242   ESDN    1  700   NP_563615.2  3  2266  GAGCTGAGCCTG T  ------      A -     3  A  c  c
                                ATTCAAATGGTT  AGC     ACCATTTGAA TC GGTT
```

TTTCTGCT TCG TGGTAAACTT AG CCGA
- TCTTTT - T
GAM3027 242 ESM1 1 11981 NP_008967.1 3 627 AACTGAGAGCAA - A ------ 3 A c c
TTTCAAAAGGCT TAGCA CC TTTGAAA TCGGTT
GCTGATGT GTCGT GG AAACTTT AGTCAA
C A AACGAG
GAM3027 242 FGD2 1 8607 NP_775829.1 3 436 TACCACCACCGA A A T 3 A c c
TTTAAATGGGCT TAGC CCATTTGAA TCGGT
GAGTTGGG GTCG GGTAAATTT AGCCA
- - C
GAM3027 242 FLJ1025 1 11858 NP_060509.1 5 0 CACCGATTTATG TTG T 3 A c c
1 GTGCTGACATCA TAGCACCAT AAATCGGT
GTGGCTCC GTCGTGGTA TTTAGCCA
--- C
GAM3027 242 FLJ1029 1 3351 NP_060518.1 3 1130 CCTTGTATAACT TT A 3 A c c
2 GAATTTATGGTG TAGCACCAT GAA TCGGTTA
CTATTTAA ATCGTGGTA TTT AGTCAAT
-- A
GAM3027 242 FLJ1040 1 2867 NP_061930.1 3 206 CCTCAGCAGAGC TTT AT 3 A c
c
4 CGCTTCCTGGTG TAGCACCA GAA CGGTT
CTACGCAG ATCGTGGT CTT GCCGA
C-- C-
GAM3027 242 FLJ2555 1 14472 NP_689558.2 3 384 TCTAAAACCCTT --- ATC 3 A c c
5 CATCCAATGGTG TAGCACCATT TGAA GGTT
CTAACCCC ATCGTGGTAA ACTT CCAA
CCT C--
GAM3027 242 FLJ3246 1 5290 NP_660090.1 3 197 CTTCCATCTCTT AAATC T 3 A c c

8 ACCCAAGTGGTG TAGCACCATTTG GGT
CTAAACAA ATCGTGGTGAAC CCA
----- T
GAM3027 242 FLJ3492 1 13523 NP_689483.1 5 80 GGTGGAAAGAGA AA GG 3 A c
c
2 TAGCAGGTGGTG TAGCACCATTTG ATC TT
CTAATTCA ATCGTGGTGGAC TAG AA
GA AG
GAM3027 242 FLJ3600 1 11041 NP_787101.1 3 428 TATGCCTGTACC TT AA T 3 A c
c
0 GATGGCATGGTG TAGCACCA TG ATCGGT
CTATATCC ATCGTGGT AC TAGCCA
-- GG T
GAM3027 242 FLJ3633 1 13204 XP_211925.1 3 1098 AACAGGAGCCGA C AA 3 A c
c
1 TGCCAAATGGTC TAG ACCATTTG ATCGGTT
TAGAGGCA ATC TGGTAAAC TAGCCGA
- CG
GAM3027 242 GALNT8 1 10446 NP_059113.1 3 19 AACAGCCAGTGT A--- C 3 A c c
CCTCAGATGGTG TAGCACCATTTGA AT GGTT
CTGGATCT GTCGTGGTAGACT TG CCGA

CCTG A
GAM3027 242 HBP1 1 16151 NP_036389.2 3 292 CTTGAAAATTGA TT A 3 A c c
TATCCTGTGGTG TAGCACCAT GA ATCGGTT
CTAAAGTA ATCGTGGTG CT TAGTTAA
TC A
GAM3027 242 HLF 1 18455 NP_002117.1 3 2550 AATTTATGGCCG - AAT 3 A c c
TATCAAATGGTA TAGC ACCATTTGA CGGTTA
GCTGAAAA GTCG TGGTAAACT GCCGGT
A AT-
GAM3027 242 ITGAD 1 7734 XP_113880.1 3 2084 ATGAGAGCTCAG GAA -- 3 A c c
ATGGAGATGGTG TAGCACCATTT ATC GGTT
CTAGAAGA ATCGTGGTAGA TAG TCGA
GG- AC
GAM3027 242 ITPR1 1 623 NP_002213.1 3 484 TAAATGGTTAAC C ATC 3 A c c
TTTCAAATGATG TAGCA CATTTGAA GGTTA
CTGCTGCC GTCGT GTAAACTT TCAAT
A ---
GAM3027 242 KCNH7 1 11768 NP_150375.2 5 48 GAAAGCGGGTGT --- A G 3 A c c
CTAGAAGTGGTG TAGCACCATTT GA ATC GTT
CTAATGGG ATCGTGGTGAA CT TGG CGA
GAT G G
GAM3027 242 KCNH7 1 11768 NP_775185.1 5 48 GAAAGCGGGTGT --- A G 3 A c c
CTAGAAGTGGTG TAGCACCATTT GA ATC GTT
CTAATGGG ATCGTGGTGAA CT TGG CGA
GAT G G
GAM3027 242 KIAA012 1 16707 NP_055607.1 3 4384 CAATAATGACTA CCA C 3 A c
c
5 TTTCAAAATTGC TAGCA TTTGAAAT GGTTA
TAAAAGAT ATCGT AAACTTTA TCAGT
TA- -
GAM3027 242 KIAA025 1 16077 XP_034905.1 3 823 AACTGTAACCGA C- TTGA 3 A c
c
6 TTGTATGACTGC TAGCA CAT AATCGGTTA
TGCACTTA GTCGT GTA TTAGCCAAT
CA TG--
GAM3027 242 KIAA139 1 18563 XP_046685.4 3 684 TGGAACTCCCGA A TT 3 A c c
9 TTTCAGGTGGGC TAGC CCATTTGAAATCGG
TAAAAGAG ATCG GGTGGACTTTAGCC
- CT
GAM3027 242 KIAA166 1 2583 XP_036936.1 3 262 TCTGAGAAGCCA CCA C 3 A c c
6 TTTCAAAGTTGC TAGCA TTTGAAAT GGTT
TGATAACT GTCGT AAACTTTA CCGA
TG- -
GAM3027 242 KIAA202 1 14473 XP_291326.1 3 5145 TTAGTAAGTTGC TTG T 3 A c c
2 TGATTTATGGTG TAGCACCAT AAATCGGT
CTAAAGAA ATCGTGGTA TTTAGTCG
--- T
GAM3027 242 KLF12 1 19711 NP_009180.3 3 3150 TATAGAGATTGA A A 3 A c c

TTTCAAGGGAGT TAGC CC TTTGAAATCGGTT
TACATTAT ATTG GG GAACTTTAGTTAG
A -
GAM3027 242 LEPRE1 1 12458 NP_071751.2 3 371 CTGCTCACAGCC TT- ATC 3 A c c
TTCTACATGGTG TAGCACCAT GAA GGTT
CTACTGCT ATCGTGGTA CTT CCGA
CAT ---
GAM3027 242 LOC1502 1 2583 XP_036942.1 3 262 TCTGAGAAGCCA CCA C 3 A c c
21 TTTCAAAGTTGC TAGCA TTTGAAAT GGTT
TGATAACT GTCGT AAACTTTA CCGA
TG- -
GAM3027 242 LOC1517 1 12738 XP_087279.6 5 1043 GGAAACCCTATT --- ATC 3 A c c
20 CAATAAATGGTG TAGCACCATT TGAA GGTT
CTGGGATA GTCGTGGTAA ACTT CCAA
ATA ATC
GAM3027 242 LOC1590 1 16816 XP_099021.1 3 652 TTTTAAAAATTA CA C 3 A c c
53 TTTCAAATGGAA TAG CCATTTGAAAT GGTT
CTGAAAGA GTC GGTAAACTTTA TTAA
AA -
GAM3027 242 LOC2220 1 17330 XP_167489.1 5 62 ACTAAAGAACCA - ATC 3 A c c
01 ATTCAAATGGAT TAGCA CCATTTGAA GGTT
GCTGAACA GTCGT GGTAAACTT CCAA
A AA-
GAM3027 242 LOC2831 1 5389 XP_208516.1 3 190 ACCCACAACATG GAAA - 3 A c c
20 AAAGAAATGGTG TAGCACCATTT TCG GTT
CTACCCAG ATCGTGGTAAA AGT CAA
GAA- A
GAM3027 242 LOC2833 1 8708 XP_208080.1 3 174 AAGTGCAAGAAT TTTGA 3 A c c
68 TGGTTGCTGGTG TAGCACCA AATCGGTT
CTACATGG ATCGTGGT TTGGTTAA
CG---
GAM3027 242 LOC2835 1 6585 XP_208708.1 3 306 ACGTCTTCGGCG TT A G 3 A c c
28 GATGTCATGGTG TAGCACCA TGA ATC GTT
CTGAACCA GTCGTGGT ACT TAG CGG
-- G G
GAM3027 242 LOC2835 1 4895 XP_211118.1 3 1135 CCTAGAAACTGA TTGAAA 3 A c c
70 GGGGCTATGGTG TAGCACCAT TCGGTT
CTAAGCAG ATCGTGGTA AGTCAA
TCGGGG
GAM3027 242 LOC2841 1 11041 XP_294862.1 3 992 TATGCCTGTACC TT AA T 3 A c c
24 GATGGCATGGTG TAGCACCA TG ATCGGT
CTATATCC ATCGTGGT AC TAGCCA

```
                                        -- GG     T
GAM3027  242   LOC2843 1  19882 XP_209154.1  3  1484  TGGAAATTCAAC      TTT    CG         3  A  c
c
         75                    TAATTTTTGGTG TAGCACCA  GAAAT  GTT
                              CTATTATT    ATCGTGGT  TTTTA  CAA
                                      ---    AT
GAM3027  242   LOC2844 1  8159  XP_210788.1  5  569   GCCGAAACCGAT      TTGAA-          3  A  c
c
         63                    GTGTCTATGGTG TAGCACCAT    ATCGGTT
                              CTGCATCT    GTCGTGGTA     TAGCCAA
                                      TCTGTG
GAM3027  242   LOC2847 1  10590 XP_209331.1  3  14    TGTACAATTGAA       GA  -          3  A  c  c
         09                    TTGGAAATGGTG TAGCACCATTT  AAT CGGTT
                              CTAGTCAG    ATCGTGGTAAA  TTA GTTAA
                                       GG  A
GAM3027  242   LOC2851 1  8965  XP_211790.1  3  1734  GTCAGTTGATTT       --    - GG       3  A  c  c
         67                    TCAACAATGGTG TAGCACCATT  TGAAA TC  TT
                              CTAAAACA    ATCGTGGTAA  ACTTT AG  GA
                                      CA    T  TT
GAM3027  242   LOC2856 1  9924  XP_209722.1  3  425   TTGACTGTATTC       ----   AT         3  A  c  c
         95                    ACATAAATGGTG TAGCACCATT   TGAA  CGGTTA
                              CTAAAACA    ATCGTGGTAA    ACTT  GTCAGT
                                      ATAC   AT
GAM3027  242   LOC2858 1  1968  XP_212038.1  5  199   CACCTTAAACTG T-----      TT          3  A  c  c
         27                    GTTTCTATGGTG     AGCACCAT  GAAATCGGTT
                              CTTCATCG         TCGTGGTA  CTTTGGTCAA
                                      GCTACT       T-
GAM3027  242   LOC2858 1  1968  XP_212604.1  5  199   CACCTTAAACTG T-----      TT          3  A  c  c
         27                    GTTTCTATGGTG     AGCACCAT  GAAATCGGTT
                              CTTCATCG         TCGTGGTA  CTTTGGTCAA
                                      GCTACT       T-
GAM3027  242   LOC2858 1  1968  XP_212645.1  5  199   CACCTTAAACTG T-----      TT          3  A  c  c
         27                    GTTTCTATGGTG     AGCACCAT  GAAATCGGTT
                              CTTCATCG         TCGTGGTA  CTTTGGTCAA
                                      GCTACT       T-
GAM3027  242   LOC2859 1  11415 XP_208364.1  3  556   GACCTGAGACAC       GAA    T        3  A  c
c
         39                    TGATGAATGGTG TAGCACCATTT  ATCGGT
                              CTATTTTG    ATCGTGGTAAG   TAGTCA
                                      ---     C
GAM3027  242   LOC2861 1  11415 XP_209928.1  3  455   GACCTGAGACAC       GAA    T        3  A  c
c
         73                    TGATGAATGGTG TAGCACCATTT  ATCGGT
                              CTATTTTG    ATCGTGGTAAG   TAGTCA
                                      ---     C
GAM3027  242   LOC3389 1  19734 XP_290624.1  3  96    CCAACCCTGCAT        AATC----        3  A  c
c
         21                    GGTCAAGTGGTG TAGCACCATTTGA      GGTT
                              CTAACCCA    ATCGTGGTGAACT      CCAA
                                       GGTACGTC
```

GAM3027 242 LOC3398 1 15901 XP_295087.1 3 456 ACCTATTGGCTA A C 3 A c c
56 TTGTGAATGGTG TAGCACCATTTG AAT GGTTA
CTGCTATG GTCGTGGTAAGT TTA TCGGT
G -
GAM3027 242 LOC3403 1 1433 XP_295225.1 5 241 AGGCCTGGATTC TG --- -- 3 A c c
62 TTTTGAGTGGTG TAGCACCATT AA ATC GGTT
CTACTGCC ATCGTGGTGA TT TAG CCGG
GT TCT GT
GAM3027 242 LOC3404 1 7731 XP_290420.1 3 1860 GCAGGCCTTTGT T TC--- 3 A c
c
28 TTTCCAATGGTG TAGCACCATT GAAA GGTT
CTATATTC ATCGTGGTAA CTTT CCGG
C TGTTT
GAM3027 242 LOC3405 1 16315 XP_291335.1 5 123 TTGTGCAGCCGA ACCA 3 A c
c
42 TTTCAAGGCTAA TAGC TTTGAAATCGGTT
GAGAGAAA ATCG GAACTTTAGCCGA

GAM3027 242 LOC3483 1 1132 XP_302741.1 3 1141 AAGGGTAACCGA G A--- 3 A c c
93 TTGGGGTAGGTG TA CACCATTTG AATCGGTTA
GTGGTAGT AT GTGGTGGAT TTAGCCAAT
G GGGG
GAM3027 242 LOC3485 1 1132 XP_302818.1 3 1141 AAGGGTAACCGA G A--- 3 A c c
32 TTGGGGTAGGTG TA CACCATTTG AATCGGTTA
GTGGTAGT AT GTGGTGGAT TTAGCCAAT
G GGGG
GAM3027 242 LOC3485 1 17835 XP_290964.1 5 283 GTAGATTCTGAT - TT 3 A c c
72 TTCCGAATGGTG TAGCACCATTTG AAATCGG
CTGCGGAA GTCGTGGTAAGC TTTAGTC
C TT
GAM3027 242 LOC3486 1 2583 XP_300791.1 3 262 TCTGAGAAGCCA CCA C 3 A c
c
01 TTTCAAAGTTGC TAGCA TTTGAAAT GGTT
TGATAACT GTCGT AAACTTTA CCGA
TG- -
GAM3027 242 LOC3496 1 9490 XP_303448.1 5 203 GAGACTGGAACA TT ----- 3 A c c
67 GTTTCCATGGTG TAGCACCAT GAAAT CGGTT
CTGGAGGA GTCGTGGTA CTTTG GTCAG
C- ACAAG
GAM3027 242 MEST 1 8219 NP_002393.2 3 1077 TGAAAGACCTAT AA- C 3 A c c
GAGCAAATGGTG TAGCACCATTTG AT GGTT
CTGAATAC GTCGTGGTAAAC TA CCAG
GAG T
GAM3027 242 MEST 1 8219 NP_803490.1 3 1077 TGAAAGACCTAT AA- C 3 A c c
GAGCAAATGGTG TAGCACCATTTG AT GGTT
CTGAATAC GTCGTGGTAAAC TA CCAG
GAG T
GAM3027 242 MEST 1 8219 NP_803491.1 3 1077 TGAAAGACCTAT AA- C 3 A c c

GAGCAAATGGTG TAGCACCATTTG AT GGTT
CTGAATAC GTCGTGGTAAAC TA CCAG
GAG T

GAM3027 242 METTL1 1 12414 NP_075421.1 3 628 TACCATAACCGA A TTTGAA 3 A c c

TGTGCTGGAGCT TAGC CCA ATCGGTTA
ACACGACT ATCG GGT TAGCCAAT
A CGTG--

GAM3027 242 MGC2201 1 4508 XP_035307.1 3 4481 ACTGAGGCTGCT T T- 3 A c c 4

TTTTAGTTGGTG TAGCACCA TTGAAA CGGTT
CTAACCTA ATCGTGGT GATTTT GTCGG
T TC

GAM3027 242 MGC2705 1 1363 NP_116090.2 3 560 TGTGACCTCATC TT TC--- 3 A c c

TTTCTCATGGTG TAGCACCAT GAAA GGTTA
CTATCCTG ATCGTGGTA CTTT CCAGT
CT CTACT

GAM3027 242 MORF4 1 7924 XP_165470.1 5 14 GTGGCAAATCAC A TC 3 A c c

TTATAAATGGTG TAGCACCATTTG AA GGTT
CTGAAGCA GTCGTGGTAAAT TT CTAA
A CA

GAM3027 242 NASP 1 16483 NP_002473.2 3 299 GTAGGCCTTTGT T TC--- 3 A c c

TTTCCAATGGTG TAGCACCATT GAAA GGTT
CTATATTC ATCGTGGTAA CTTT CCGG
C TGTTT

GAM3027 242 NASP 1 16483 NP_689511.2 3 299 GTAGGCCTTTGT T TC--- 3 A c c

TTTCCAATGGTG TAGCACCATT GAAA GGTT
CTATATTC ATCGTGGTAA CTTT CCGG
C TGTTT

GAM3027 242 NASP 1 16483 NP_751896.1 3 299 GTAGGCCTTTGT T TC--- 3 A c c

TTTCCAATGGTG TAGCACCATT GAAA GGTT
CTATATTC ATCGTGGTAA CTTT CCGG
C TGTTT

GAM3027 242 NAV3 1 9220 NP_055718.2 3 818 AAAGAAGGAACA TT CG 3 A c c

TTTCCTATGGTG TAGCACCAT GAAAT GTT
CTGTCTCA GTCGTGGTA CTTTA CAA
TC --

GAM3027 242 NCOA2 1 4666 NP_006531.1 5 79 GACCCGAGCCGA A---- TTT 3 A c c

TTTCTCTTGGAT TAGC CCA GAAATCGGTT
TTGGCTAC ATCG GGT CTTTAGCCGA
GTTTA TCT

GAM3027 242 NEK2 1 18583 NP_002488.1 3 77 TTAAAGACTGAT ----- - 3 A c c

ATTCAAATGCTG TAGCAC CATTTGAA ATCGGTT
TAGTGTTG GTTGTG GTAAACTT TAGTCAG
ATGTC A

GAM3027 242 PHC1 1 8708 NP_004417.1 3 174 AAGTGCAAGAAT TTTGA 3 A c c

TGGTTGCTGGTG TAGCACCA AATCGGTT
CTACATGG ATCGTGGT TTGGTTAA

```
                                                CG---
GAM3027  242   PNMA2  1  16185 NP_009188.1  3  2002  AAATGCAGCTAG    A      A -        3  A  c  c
                                ATTCAAATGGGC TAGC CCATTTGAA TC GGTT
                                TGATAACC    GTCG GGTAAACTT AG TCGA
                                             -       - A
GAM3027  242   PPP2R5C 1  14122 NP_002710.2  3  2216  GTACCAAACTGA   C  CA             3  A  c
c
                                TTTCAAAAGTAC TAG AC  TTTGAAATCGGTT
                                TACATTGA    ATC TG  AAACTTTAGTCAA
                                          A  A-
GAM3027  242   PPP2R5C 1  14122 NP_848701.1  3  2216  GTACCAAACTGA   C  CA             3  A  c
c
                                TTTCAAAAGTAC TAG AC  TTTGAAATCGGTT
                                TACATTGA    ATC TG  AAACTTTAGTCAA
                                          A  A-
GAM3027  242   PRO0132 1  18429 NP_054835.1  5  319   TCAGGCAACTGA   CAC              3  A  c
c
                                TTTCAAATGCCT TAG   CATTTGAAATCGGTT
                                ATGAAACC    ATC   GTAAACTTTAGTCAA
                                          C--
GAM3027  242   PRO2964 1  7172  NP_061017.1  5  114   TGAGATAAAACA    ----      AA  G      3  A  c  c

                                GATCAAATGGTT TAGC    ACCATTTGA  TC GTT
                                TAGGTTAA    ATTG    TGGTAAACT  AG CAA
                                           GATT       -- A
GAM3027  242   RAB30  1  1946  NP_055303.2  3  636   CAAGCTCCATAA      TTTG  TC         3  A  c
c
                                CTCCTTTTGGTG TAGCACCA    AAA  GGTTA
                                CTAATGAT    ATCGTGGT    TTT  TCAAT
                                          ----  CC
GAM3027  242   RFXAP  1  11150 NP_000529.1  3  531   AATGTTGATGGC       TT    C         3  A  c  c
                                TATTTTGTGGTG TAGCACCAT  GAAAT GGTTA
                                CTAACATG    ATCGTGGTG  TTTTA TCGGT
                                          --    -
GAM3027  242   RNASE6 1  3045  NP_005606.1  5  280   ACACTGAGACCA       GAAA -         3  A  c
c
                                GAAAAGATGGTG TAGCACCATTT    TC GGTT
                                CTATGCTT    ATCGTGGTAGA    AG CCAG
                                            AA--  A
GAM3027  242   RNASEL 1  12262 NP_066956.1  3  1460  TTGATTTGAACA      TTT    CG         3  A  c
c
                                AATTTTCTGGTG TAGCACCA   GAAAT  GTT
                                CTAAGTCT    ATCGTGGT   TTTTA  CAA
                                          C--    AA
GAM3027  242   RNGTT  1  16779 NP_003791.1  3  1961  GTAATTGTAACC    AC      TC         3  A  c
c
                                TTTCAAATGAGT TAGC  CATTTGAAA  GGTTA
                                TACGTGAA    ATTG  GTAAACTTT  CCAAT
                                          A-       --
GAM3027  242   SLC11A2 1  10424 NP_000608.1  3  1374  TGAGAACAGTAA       GAAA  G        3  A  c
 c
```

TGGAAAATGGTG TAGCACCATTT TC GTTA
TTGAAGGA GTTGTGGTAAA AG TAAT
---- G

GAM3027 242 SLC26A7 1 19030 NP_439897.1 3 2874 TTTGTGGCCAGA A- - - 3 A c c
TTTCAAATAGGG TAGC CC ATTTGAAATC GGTTA
AGTTAAGT ATTG GG TAAACTTTAG CCGGT
AG A A

GAM3027 242 SLC7A6 1 17897 NP_003974.1 3 1102 GACCCAAGCAAT TTTGAAATC 3 A c c
CCCAACCTGGTG TAGCACCA GGTT
CTAGGTCA ATCGTGGT CCAA

GAM3027 242 SNURF-S 1 3268 XP_085186.4 3 2307 CTTTCAAACTTG C A - 3 A c c
NRPN ATTCAAATGATG TAGCA CATTTGAA TCG GTT
TTAGTGAA ATTGT GTAAACTT AGT CAA
A - T

GAM3027 242 SS18 1 9679 NP_005628.1 3 294 TTTGGAACTGTG -- - 3 A c c
TTTCAAATGGAC TAGCA CCATTTGAAAT CGGTT
TGTTACAG ATTGT GGTAAACTTTG GTCAA
CA T

GAM3027 242 TCL1A 1 14577 NP_068801.1 3 453 CTGGACCAGTGG T A --- 3 A c c
TCTCACATGGTG TAGCACCAT TGA ATC GGTT
CTACGCCT ATCGTGGTA ACT TGG CCAG
C C TGA

GAM3027 242 TPK1 1 3731 NP_071890.2 3 1283 AAAGTAACTGTT TTT- T 3 A c c
TTCTTCTTGGTG TAGCACCA GAAA CGGTTA
CTATGACA ATCGTGGT CTTT GTCAAT
TCTT T

GAM3027 242 TRIM9 1 17715 NP_443210.1 3 435 TGACTGAATGTG G - ----- 3 A c c
TTTCAAATGGGT TA CACC ATTTGAAA TCGGTTA
GGTGGGGT GT GTGG TAAACTTT AGTCAGT
G G GTGTA

GAM3229 221 15E1.2 1 7550 XP_290596.1 3 1256 CTGGGCTCAAGT A TG 3 C c c
GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT

GAM3229 221 A1BG 1 4606 NP_570602.2 3 534 CTGGCCTTAAGT A TG 3 C c c
GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAATT
C GT

GAM3229 221 ABCB5 1 14539 XP_291215.1 3 849 CTGACCTCAGGT AGA TG 3 C c c
GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT

GAM3229 221 ACCN2 1 11565 NP_001086.2 3 1007 GTCTCTGAGAAC A TG-- - 3 C c c
CATTCTCCCACC TG GGTGGGAGAAT CTT GA
CCAAGTTC AC CCACCCTCTTA GAG CT
C CCAA T

GAM3229 221 ACCN2 1 11565 NP_064423.2 3 1007 GTCTCTGAGAAC A TG-- - 3 C c c

CATTCTCCCACC TG GGTGGGAGAAT CTT GA
CCAAGTTC AC CCACCCTCTTA GAG CT
C CCAA T

GAM3229 221 ADAMTS4 1 4409 NP_005090.1 3 889 CTGGGTTCCAGC TG T 3 C c c

AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCAGCCTC ACTCC CCTCTTAACGA CTT
GT C

GAM3229 221 ADCY6 1 16258 NP_056085.1 5 124 CCGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTCC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 AGL 1 14206 NP_000637.1 5 195 CTGGACTCAAGC T ------ AA 3 C c c
AACCCTCCCTCT GAGGT GGGAG TTGCTTGA
TTGGCCTC CTCCG CCCTC AACGAACT
- GTTTCT CC

GAM3229 221 AIM1 3 3982 XP_166300.1 3 774 CCAGGCTCAGGT A TG 3 C c b
GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GGACT
C GT

GAM3229 221 AIM1 3 4262 XP_166300.1 3 1422 CAATCTTCAAGC TGG-- A 3 C c b
AATCTTGGAATC TGAGG GAGA TTGCTTGAA
CTCAACTG ACTCC TTCT AACGAACTT
TAAGG -

GAM3229 221 AIM1 3 15456 XP_166300.1 3 911 CTGGGCTCAAGC A 3 C b b
AATTCACTCGCC TGAGGTGGG GAATTGCTTGA
TCGGCCTC GCTCCGCTC CTTAACGAACT
A

GAM3229 221 ALOX15 1 13880 NP_001131.1 3 473 CTGGGCTCAAAT A GC 3 C c c

GATCCTCCCACC TGAGGTGGGAG ATT TTGA
TCAGCCTC ACTCCACCCTC TAG AACT
C TA

GAM3229 221 AP1S3 1 7058 XP_291023.1 3 1077 CTGGGCTCAAGC A A 3 C b b
AATCCTCTCACC TG GGTGGGAG ATTGCTTGA
GCAGCCTC AC CCACTCTC TAACGAACT
G C

GAM3229 221 AP3S2 1 4992 NP_005820.1 3 716 CCGGGTTCAAGC TG T 3 C c c
ATTTCTCCTGTC TGAGG GGAGAA TGCTTGAA
TCAGCCTC ACTCT CCTCTT ACGAACTT
GT T

GAM3229 221 APAF1 2 2783 NP_001151.1 3 688 CTGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 APAF1 2 2783 NP_037361.1 3 688 CTGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT

GT

GAM3229 221 APAF1 2 15973 NP_001151.1 3 986 CTGGGTTCAAGC TG A 3 C c b

AATCCTCCTGCC TGAGG GGAG ATTGCTTGAA

TCAGCCTC ACTCC CCTC TAACGAACTT

GT C

GAM3229 221 APAF1 2 15973 NP_037361.1 3 986 CTGGGTTCAAGC TG A 3 C c b

AATCCTCCTGCC TGAGG GGAG ATTGCTTGAA

TCAGCCTC ACTCC CCTC TAACGAACTT

GT C

GAM3229 221 APM1 2 9383 NP_004788.1 3 3384 TCTACCATGAGC TG A 3 C c c

AATTCTCCTGCC TGAGG GGAGAATTGCTTG

TCAGCCTC ACTCC CCTCTTAACGAGT

GT A

GAM3229 221 APM1 2 12655 NP_004788.1 3 871 CTGGGTCCAAGC G G A 3 C c c

AATTATTGTGCC TGAGGTG GA AATTGCTTG

TCAGCCTC ACTCCGT TT TTAACGAAC

G A C

GAM3229 221 APOC3 1 20001 NP_000031.1 3 125 TTCTCAGTGCTC -- AATT - 3 C c c

TCCTACCCCACC TGAGGTGGG AG GC TTGA

TCATGCCT ACTCCACCC TC CG GACT

CA CTCT T

GAM3229 221 APTX 1 404 NP_778242.1 5 60 CTAGGCTCAAGC A 3 C b b

AATCCTTCCACC TGAGGTGGGAG ATTGCTTGA

TCAGTCTC ACTCCACCTTC TAACGAACT

C

GAM3229 221 APTX 1 404 NP_778243.1 5 100 CTAGGCTCAAGC A 3 C b b

AATCCTTCCACC TGAGGTGGGAG ATTGCTTGA

TCAGTCTC ACTCCACCTTC TAACGAACT

C

GAM3229 221 AQP6 1 3122 NP_001643.1 3 809 CTGACCTGAGGC - A GA 3 C c c

GATCTGCCCACC TGAGGTGGG AGA TTGCTT

TCGGCCTC GCTCCACCC TCT AGCGGA

G - GT

GAM3229 221 AQP6 1 3122 NP_445738.1 3 1975 CTGACCTGAGGC - A GA 3 C c c

GATCTGCCCACC TGAGGTGGG AGA TTGCTT

TCGGCCTC GCTCCACCC TCT AGCGGA

G - GT

GAM3229 221 ARCN1 2 2072 NP_001646.2 3 465 CTGGGTTCAAGC TG A 3 C c b

AAGTCTCCTGCC TGAGG GGAGA TTGCTTGAA

TCAGCCTC ACTCC CCTCT AACGAACTT

GT G

GAM3229 221 ARCN1 2 17074 NP_001646.2 3 599 CTGAGCTCAGGC AGA 3 C b b

AATCCGCCCACC TGAGGTGGG ATTGCTTGA

TCAGCCTC ACTCCACCC TAACGGACT

GCC

GAM3229 221 ARHGAP1 2 2783 NP_004299.1 3 1189 CTGGGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 ARHGAP1 2 7041 NP_004299.1 3 132 CCATCAGGCATG T----- -- AT- 3 C c b
CTCTCCCCCACC GAGGT GGGAGA TGCTTGA
TCTGTCCA CTCCA CCCTCT ACGGACT
ACCTGT CC CGT
GAM3229 221 ARHGEF7 1 13696 NP_663788.1 3 614 GTGTGTTCAGAG G ATT - 3 C c c
CTTGTCTCCACC TGAGGTGG AGA GCT TGAA
TCACGGCT ACTCCACC TCT CGA ACTT
- GTT G
GAM3229 221 ARPP-19 1 9396 NP_006619.1 3 3550 CTGGGTTCAAGC TG 3 C b b
AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 ASB6 1 10286 NP_060343.1 3 1195 CCAGGTTCAAGC TG 3 C b b
AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 ASB6 1 10286 NP_821066.1 3 1758 CCAGGTTCAAGC TG 3 C b b
AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 ATF7IP2 1 9615 NP_079273.1 3 588 CCTGGCTCAAGC G 3 C b b
AATTCTCCTATG TGA GTGGGAGAATTGCTTGA
TCAGCCTC ACT TATCCTCTTAACGAACT
G
GAM3229 221 ATP1B2 1 4784 NP_001669.1 3 882 CCAGGTTCAAGC 3 C b b
GATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGGTTC ACTCCGCCCTCTTAGCGAACTT
GAM3229 221 ATP6V0D 1 19565 NP_689778.1 3 912 CCAGATTCAAGC TG G A 3 C c c
2 AACTCTCTGCCT TGAGG G AGA TTGCTTGAA
CAGCCTCC ACTCC C TCT AACGAACTT
GT - C
GAM3229 221 ATP6V1A 1 9671 NP_001681.2 3 869 CAGACCTCAGGT AGA TG 3 C c c
GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT
GAM3229 221 ATP7A 1 9876 NP_000043.1 3 1119 CCGGATTCAAGG - G 3 C b b
AATTCTCCCTGC TGAGGT GGGAGAATT CTTGAA
CTCAGCCT ACTCCG CCCTCTTAA GAACTT
T G
GAM3229 221 AXL 1 3840 NP_001690.2 3 665 CTGACCTCAAGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GAACT

```
                                                G  - GT
GAM3229  221   AXL    1  3840  NP_068713.2  3  665   CTGACCTCAAGT       - A TG          3  C  c  c
                                GATCTGCCCACC TGAGGTGGG AGA T  CTTGA
                                TCAGCCTC    ACTCCACCC TCT A  GAACT
                                                G  - GT
GAM3229  221   B4GALT5 2  4737  NP_004767.1  3  1685  CTGGACTCAAGC T-----      AGA          3  C  c
b
                                AATCCGCCCACC     GAGGTGGG  ATTGCTTGA
                                TTGACTTC        TTCCACCC  TAACGAACT
                                      CTTCAG      GCC
GAM3229  221   B4GALT5 2  10951 NP_004767.1  3  1547  CTAGGCTCAAGC          T          3  C  b  b

                                CATTTTCCCACC TGAGGTGGGAGAAT GCTTGA
                                TCAGCCTC    ACTCCACCCTTTTA CGAACT
                                              C
GAM3229  221   BCAP31 1  3188  NP_005736.2  3  660   CTGACCTCAGGC       AGA            3  C  b  b

                                AATCCACCCACC TGAGGTGGG  ATTGCTTGA
                                TCAGCCTC    ACTCCACCC  TAACGGACT
                                              ACC
GAM3229  221   BCL10  1  7414  NP_003912.1  3  984   CTGGACTCAAGC  A    AGAA           3  C  c
c
                                AACCTACCCAGC TG GGTGGG   TTGCTTGA
                                GTGGCCTC    AC CCATCC   AACGAACT
                                      -     ----
GAM3229  221   BDKRB1 1  15600 NP_000701.2  5  150   CCAGGCTTAAAC          ------   A  3  C  c  c
                                GATTCTCCCACC TGAGGTGGGAGAATT    GCTTG
                                TCAGCCTC    ACTCCACCCTCTTAG    CGGAC
                                              CAAATT   C
GAM3229  221   BHD    2  2783  NP_659434.2  3  971   CTGGGTTCAAGC    TG             3  C  b  b
                                AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                TCAGCCTC    ACTCC  CCTCTTAACGAACTT
                                              GT
GAM3229  221   BHD    2  15210 NP_659434.2  3  1253  CTGAGTTCAAGC    TG   A          3  C  c  b
                                AGTCCTCCTGCT TGAGG  GGAG ATTGCTTGAA
                                TCAACATA    ACTTC  CCTC TGACGAACTT
                                              GT   C
GAM3229  221   BTN3A1 1  12851 NP_008979.2  3  1114  CTGGGTTCAAAC    TG      C          3  C  c
c
                                AATTCTCCTGCC TGAGG  GGAGAATTG TTGAA
                                TCAGCCTC    ACTCC  CCTCTTAAC AACTT
                                              GT       A
GAM3229  221   BXDC1  1  9229  XP_166303.1  3  1416  CCAGGTTCAAGC    TG     T          3  C  c  c
                                ATTCTTCTGCCT TGAGG  GGAGAAT GCTTGAA
                                CAGCCTCC    ACTCC  CTTCTTA CGAACTT
                                              GT     -
GAM3229  221   C1orf24 1  3152  NP_443198.1  3  1656  CTGATTTCAGGC       AGA            3  C  c  c
                                GATCCACCCACC TGAGGTGGG  ATTGCTTGAA
                                TCGACTTC    GCTCCACCC  TAGCGGACTT
                                              ACC
```

GAM3229 221 C1QTNF6 1 19016 NP_114116.2 3 493 CCCACATTCTAG GG- G T 3 C c c
AATTCTCCCAAC TGA TGGGAGAATT CT GAA
ATTATTTT ATT ACCCTCTTAA GA CTT
ACA - T
GAM3229 221 C20orf1 1 19165 XP_086728.2 3 3005 AACAGACTCAAG GAGAA G 3 C c c
10 GAGACAACCACC TGAGGTGG TT CTTGA
TCAACTGG ACTCCACC GA GAACT
AACA- G
GAM3229 221 C20orf1 2 4689 NP_689880.1 3 1174 CTGGATTCAAGT A TG 3 C c c
47 GATCCTCCCACC TGAGGTGGGAG AT CTTGAA
TCAGCCTC ACTCCACCCTC TA GAACTT
C GT
GAM3229 221 C20orf1 2 14837 NP_689880.1 3 1040 CTGAGCTCAAGT A TG 3 C c c
47 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 C20orf1 1 16804 NP_219489.1 3 1587 GGTTTATCAAGC T AA 3 C c c
61 AAAGCTTTTCTT TGAGG GGGAG TTGCTTGA
CATTTGAA ACTTC TTTTC AACGAACT
- GA
GAM3229 221 C20orf1 1 16804 NP_690857.1 3 857 GGTTTATCAAGC T AA 3 C c c
61 AAAGCTTTTCTT TGAGG GGGAG TTGCTTGA
CATTTGAA ACTTC TTTTC AACGAACT
- GA
GAM3229 221 C20orf1 1 18324 XP_290955.1 3 498 AACTCCTCAAGC - --- 3 C c c
77 AAAATTTCTGTT TGAGGTGGG AGAA TTGCTTGA
CATTTTAC ATTTTACTT TCTT AACGAACT
G TAA
GAM3229 221 C22orf1 1 12716 NP_003669.2 3 2021 CTGGGCTCGGGT A TG 3 C c c
9 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCGGCCTC GCTCCACCCTC TA GGGCT
C GT
GAM3229 221 C6orf14 1 3400 NP_699175.1 3 864 CTTGGCTTAAGT TG 3 C b b
1 GATTCTCCCACC TGAGGTGGGAGAAT CTTGA
TCAGCCTC ACTCCACCCTCTTA GAATT
GT
GAM3229 221 C6orf33 2 15159 NP_588608.1 3 2404 CCCAGCTCAAGC A 3 C b b
AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 C6orf33 2 19984 NP_588608.1 3 2539 CTGAACTCAAGT AGA TG 3 C c b
GATCCGCCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GAACT
GCC GT
GAM3229 221 C6orf57 1 16359 NP_660310.1 3 561 CCAGGTTCGGGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGGGCTT
GT

GAM3229 221 C6orf65 1 12905 NP_689944.1 3 840 TTAATGTTAAGC T--- - A- 3 C c c
AATTCCACCACA GAGGTG GG GAATTGCTTGA
CTTCTGAA CTTCAC CC CTTAACGAATT
AAGT A AC

GAM3229 221 C6orf9 1 8509 NP_071390.1 3 462 AGAGATTAAGAC A -- TG- 3 C c c
TATTCTCCCAGT TG GG TGGGAGAAT CTTGA
CCCACTAC AC CC ACCCTCTTA GAATT
- TG TCA

GAM3229 221 C8orf13 1 7963 XP_088377.1 3 165 CCTATTCAGTGG A -- TG T 3 C c c
TGCTCTCCCACC TG GGTGGGAGA AT CT GAA
CAGGGGCC AC CCACCCTCT TG GA CTT
- CG GT -

GAM3229 221 CAMLG 1 19721 NP_001736.1 3 986 CTGACCTCAGGT - A TG 3 C c c

GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT

GAM3229 221 CAPN5 1 8293 NP_004046.1 3 240 AGATTTCAAATA - A C 3 C c c
GTCCTCCCCACC TGAGGTGGG AG ATTG TTGAA
TCAACTGT ACTCCACCC TC TGAT AACTT
C C A

GAM3229 221 CAPRI 1 16875 NP_008920.3 3 2035 CCAGGTTCAAGC TG 3 C b b
AATTCTCTTGCC TGAGG GGAGAATTGCTTGAA
TCGGCCTC GCTCC TCTCTTAACGAACTT
GT

GAM3229 221 CASP10 2 9941 NP_001221.1 3 291 CCAGGCTCAAGC A T 3 C b b
TGTCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAGCCTC ACTCCACCCTC TG CGAACT
C T

GAM3229 221 CASP10 2 9941 NP_116758.1 3 946 CCAGGCTCAAGC A T 3 C b b
TGTCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAGCCTC ACTCCACCCTC TG CGAACT
C T

GAM3229 221 CASP10 2 9941 NP_116759.1 3 291 CCAGGCTCAAGC A T 3 C b b
TGTCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAGCCTC ACTCCACCCTC TG CGAACT
C T

GAM3229 221 CASP10 2 10169 NP_001221.1 3 425 CTGGGCTCAAGC A 3 C b b
GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCTTC ACTCCACCCTC TAGCGAACT
C

GAM3229 221 CASP10 2 10169 NP_116758.1 3 1080 CTGGGCTCAAGC A 3 C b b
GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCTTC ACTCCACCCTC TAGCGAACT
C

GAM3229 221 CASP10 2 10169 NP_116759.1 3 425 CTGGGCTCAAGC A 3 C b b
GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCTTC ACTCCACCCTC TAGCGAACT

C
GAM3229 221 CCL16 1 5788 NP_004581.1 3 350 CCAGGCTCAAGT A A TG 3 C c c
GATCCTCCCACC TG GGTGGGAG AT CTTGA
CCAGCCTC AC CCACCCTC TA GAACT
C C GT
GAM3229 221 CCL22 2 3458 NP_002981.2 3 1334 CTGGGTTCAAGC A 3 C b b
GATTCTCCCACC TG GGTGGGAGAATTGCTTGAA
CCAGCCTC AC CCACCCTCTTAGCGAACTT
C
GAM3229 221 CCL22 2 15508 NP_002981.2 3 1145 CTGTCCTCAGGT AGA 3 C c b

AATCCGCCCACC TGAGGTGGG ATTGCTTGA
TCAGCCTC ACTCCACCC TAATGGACT
GCC
GAM3229 221 CDCP1 2 10837 NP_073753.3 3 1965 CTGGGCTCAAGC TG A 3 C c
b

AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCGGCCTC GCTCC CCTC TAACGAACT
GT C
GAM3229 221 CDCP1 2 15862 NP_073753.3 3 1831 CTGGGCTCAAGC 3 C b b
AATTCTCCCACC TGAGGTGGGAGAATTGCTTGA
TCAGCCTC ACTCCACCCTCTTAACGAACT

GAM3229 221 CDH1 1 15318 NP_004351.1 3 882 TGGGGCTCAAGC TGA----- 3 C c c

AGTTCTCCCACC GGTGGGAGAATTGCTTGA
AGCCTCCT CCACCCTCTTGACGAACT
TCCTCCGA
GAM3229 221 CECR1 1 4587 NP_059120.2 3 447 CCGGGTTCAGGC G TG 3 C c c

AATTCTCTTGCA TGA G GGAGAATTGCTTGAA
TCAGCCTC ACT C TCTCTTAACGGACTT
A GT
GAM3229 221 CECR1 1 4587 NP_803124.1 3 447 CCGGGTTCAGGC G TG 3 C c c

AATTCTCTTGCA TGA G GGAGAATTGCTTGAA
TCAGCCTC ACT C TCTCTTAACGGACTT
A GT
GAM3229 221 CENPH 1 14468 NP_075060.1 3 322 CCGGGTTCAAGC T-- --- G 3 C c c

AGTTCTGCCTCA GAGGT GG AGAATTGCTTGAA
GCCTCCCA CTCCG CC TCTTGACGAACTT
ACC ACT G
GAM3229 221 CGI-43 1 3459 NP_056437.1 3 424 CTGAGCTCAAGC A 3 C b b
AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 CHEK1 1 1819 NP_001265.1 5 18 GCCGGAAAGCAT AT-- GA 3 C c c

TTGTCTCCCACC TGAGGTGGGAGA TGCTT

TCATCATA ACTCCACCCTCT ACGAA
GTTT AG
GAM3229 221 CIAS1 1 8694 NP_004886.2 5 348 CCGGGTTCAATC C 3 C b b
AATTCTCCTACC TGAGGTGGGAGAATTG TTGAA
TCAACTTC ACTCCATCCTCTTAAC AACTT
T
GAM3229 221 CIP29 1 8546 NP_115740.3 3 222 CCGGGTTCAAGC 3 C b b
AATTCTCCCATC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCTACCCTCTTAACGAACTT

GAM3229 221 CLECSF1 1 17166 NP_569708.1 5 132 CTGGCCTGAAGC AGA GA 3 C
c c
1 AATCCGCCCACC TGAGGTGGG ATTGCTT
TCAGCCTC ACTCCACCC TAACGAA
GCC GT
GAM3229 221 CLECSF1 1 2783 NP_072092.2 3 1029 CTGGGTTCAAGC TG 3 C b
b
2 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 CLECSF9 1 12935 NP_055173.1 5 36 TCTTTCAAGATT --- TG-- 3 C c c
CATTCTCCCTGA TGAGGT GGGAGAAT CTTGAA
ATCTTACC ATTCTA CCCTCTTA GAACTT
AGT CTTA
GAM3229 221 CMRF-35 1 3608 XP_046925.1 3 514 ATCAAGATCAAA - GC 3 C c c
H GATTCTCCCCAT TGAGGTGGG AGAATT TTGA
CTCACAGA ACTCTACCC TCTTAG AACT
C A-
GAM3229 221 CNTNAP2 1 17240 NP_054860.1 3 2386 GCAGGGATCAGT G TG T 3 C
c c
GGTTCTCCCATA TGA GTGGGAGAAT CT GA
TCACCATC ACT TACCCTCTTG GA CT
A GT -
GAM3229 221 COLEC12 1 5286 NP_110408.2 3 744 CTGGCCTCAAGC TG AA 3 C c
c
AACCCTCCTGCC TGAGG GGAG TTGCTTGA
TCAGTCTT ACTCC CCTC AACGAACT
GT CC
GAM3229 221 COQ7 1 5762 NP_057222.2 3 417 CTAGCCTCAAGC AGA 3 C b b
AATCCACCCACC TGAGGTGGG ATTGCTTGA
TCAGCCTT ACTCCACCC TAACGAACT
ACC
GAM3229 221 CPA4 1 2783 NP_057436.1 3 664 CTGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 cPLA2de 1 5366 NP_828848.1 3 2323 CTGAACTCAAGC TG A 3 C c c

lta AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT

GT C
GAM3229 221 cPLA2de 1 5366 XP_208820.2 3 1416 CTGAACTCAAGC TG A 3 C c c

lta AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 CPSF2 1 17815 XP_029311.2 3 1279 CAGGGTTCAAGT TG 3 C b b
GATTCTCCCACC TGAGGTGGGAGAAT CTTGAA
TCAGCCTC ACTCCACCCTCTTA GAACTT
GT
GAM3229 221 CRB3 1 2333 NP_777378.1 5 71 CTGGCCTCAAGC TG A 3 C c c
AATCCTCTTGCC TGAGG GGAG ATTGCTTGA
TCGGCCTC GCTCC TCTC TAACGAACT
GT C
GAM3229 221 CRLF3 1 18242 NP_057070.2 3 807 CTGACCTCAGGT A- T 3 C c c
GTTCCACCCACC TGAGGTGGG GAAT GCTTGA
TCAGCCTT ACTCCACCC CTTG TGGACT
AC -
GAM3229 221 CRTAP 1 7898 NP_006362.1 3 326 TTGGGTTCAAGC G TG G 3 C c
c
AATTCTGCTGCA TGA G G AGAATTGCTTGAA
TCAGCCTC ACT C C TCTTAACGAACTT
A GT G
GAM3229 221 CST 1 19277 NP_004852.1 5 127 TCAGGCTCAAGC A 3 C b b
AATCCTCCCGCC TGAGGTGGGAG ATTGCTTGA
TCAGCCTT ACTCCGCCCTC TAACGAACT
C
GAM3229 221 CTEN 1 12312 NP_116254.3 3 826 CCAGGTTCAAGC TG G 3 C c c
AATTATCCTGCC TGAGG GGA AATTGCTTGAA
TCAGGCTC ACTCC CCT TTAACGAACTT
GT A
GAM3229 221 CTSB 1 1677 NP_680090.1 5 178 GATGTAAGCGAT A--- A 3 C c c
CTGGTTCCCACC TGAGGTGGGAG ATTGCTTG
TCAGCCTC ACTCCACCCTT TAGCGAAT
GGTC G
GAM3229 221 CTSB 1 1677 NP_680092.1 5 178 GATGTAAGCGAT A--- A 3 C c c
CTGGTTCCCACC TGAGGTGGGAG ATTGCTTG
TCAGCCTC ACTCCACCCTT TAGCGAAT
GGTC G
GAM3229 221 CYP1A2 1 4564 NP_000752.1 3 477 GCAGGTTCAAGC A 3 C b b
AATCCTCCCACT TGAGGTGGGAG ATTGCTTGAA
TCAGCCTC ACTTCACCCTC TAACGAACTT
C
GAM3229 221 CYP2B6 2 5285 NP_000758.1 3 335 CGGGGATCAAGC TG A 3 C c c

AACTCTCCTGCC TGAGG GGAGA TTGCTTGA
TCAGCCTC ACTCC CCTCT AACGAACT
GT C
GAM3229 221 CYP2B6 2 11371 NP_000758.1 3 1271 CTGGCCTCAGGT AGA TG 3 C c
c

GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGTGTT ACTCCACCC TA GGACT
ACC GT

GAM3229 221 CYP2C18 1 7874 NP_000763.1 3 59 GCTGTCACCTGC GGT T-- 3 C c c

AATTCTCCCTTA TGA GGGAGAATTGC TGA
TCAGGGCC ACT CCCTCTTAACG ACT
ATT TCC

GAM3229 221 CYP51A1 1 18360 NP_000777.1 3 943 CCGGGTTCAAGC TG G 3 C b b

AATTCTCTGCCT TGAGG G AGAATTGCTTGAA
CAGCCTCC ACTCC C TCTTAACGAACTT
GT -

GAM3229 221 CYP8B1 2 5673 NP_004382.1 3 1065 CCGGGTTCAAGT TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGGCTT ACTCC CCTCTTAATGAACTT
GT

GAM3229 221 CYP8B1 2 15966 NP_004382.1 3 611 CTGGGTTTAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAATTT
GT

GAM3229 221 DBR1 1 6398 NP_057300.1 3 145 CCAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 DCX 1 8602 NP_000546.2 3 5171 TTGGCCTCAAAT - ATTGC 3 C c c
TATCTGCCCACC TGAGGTGGG AGA TTGA
TCGGCCTC GCTCCACCC TCT AACT
G ATTA-

GAM3229 221 DCX 1 8602 NP_835364.1 3 5171 TTGGCCTCAAAT - ATTGC 3 C c c
TATCTGCCCACC TGAGGTGGG AGA TTGA
TCGGCCTC GCTCCACCC TCT AACT
G ATTA-

GAM3229 221 DCX 1 8602 NP_835365.1 3 5171 TTGGCCTCAAAT - ATTGC 3 C c c
TATCTGCCCACC TGAGGTGGG AGA TTGA
TCGGCCTC GCTCCACCC TCT AACT
G ATTA-

GAM3229 221 DCX 1 8602 NP_835366.1 3 5171 TTGGCCTCAAAT - ATTGC 3 C c c
TATCTGCCCACC TGAGGTGGG AGA TTGA
TCGGCCTC GCTCCACCC TCT AACT
G ATTA-

GAM3229 221 DEPP 1 10348 NP_008952.1 3 1141 TTTCAGACAAGC ---- AG A 3 C c c

AATTACCCAGTT TGAGG TGGG AATTGCTTG
TCCTTATC ATTCC ACCC TTAACGAAC
TTTG A- A

GAM3229 221 DFFB 1 8629 NP_004393.1 3 397 CTGACCTCAGGT AGA TG 3 C c c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT

GCC GT
GAM3229 221 DHFR 1 19487 NP_000782.1 3 1121 GTGACCGCAAGC A A 3 C c c
GATTCACCCACC TGAGGTGGG GAATTGCTTG
TCAGCCTC ACTCCACCC CTTAGCGAAC
A G
GAM3229 221 DIRAS1 1 19599 NP_660156.1 3 2394 GCCCACCTCCAG ATT A 3 C c
c
GCCTCTCCCACC TGAGGTGGGAGA GCTTG
TCAGGCCC ACTCCACCCTCT CGGAC
C-- C
GAM3229 221 DISC1 1 14849 NP_061132.1 3 3416 GACCTCAGGCGA AGA-- 3 C c c

TCCACCCCCACC TGAGGTGGG ATTGCTTGA
TCGGCTTC GCTCCACCC TAGCGGACT
CCACC
GAM3229 221 DKFZP43 1 13291 NP_113664.1 3 2160 CCGGGTTCAAGC T GG------ 3 C c
c
4B044 AATTCTCATGCA GAGGT GAGAATTGCTTGAA
TCAGCCTC CTCCG CTCTTAACGAACTT
- ACTACGTA
GAM3229 221 DKFZp43 2 12561 NP_060068.1 3 1057 CTGGCCTCAAGC A 3 C b b

4C0923 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAGCGAACT
C
GAM3229 221 DKFZp43 2 15862 NP_060068.1 3 920 CTGGGCTCAAGC 3 C b b
4C0923 AATTCTCCCACC TGAGGTGGGAGAATTGCTTGA
TCAGCCTC ACTCCACCCTCTTAACGAACT

GAM3229 221 DKFZP43 1 1165 NP_110444.1 3 2471 CTGGGTTCAAGC TG 3 C b b

4F0318 AATTCTTCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CTTCTTAACGAACTT
GT
GAM3229 221 DKFZp43 1 10801 XP_051327.1 5 399 CTGAGTCGCACA A - CT 3 C c
c
4J0226 GTCTCTCCCACC TG GGTGGGAGA ATTG TGA
CGAATGCC GC CCACCCTCT TGAC GCT
- C AC
GAM3229 221 DKFZP56 1 15802 NP_056274.1 3 581 CCGGGTTCAAGC TG 3 C b
b
4J0863 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 DKFZP56 2 18357 NP_056226.1 3 906 CTGGCCTCAAGC A 3 C b b
6I1024 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCGACCTC GCTCCACCCTC TAGCGAACT
C
GAM3229 221 DKFZP56 2 19870 NP_056226.1 3 772 CTGGGCCCAAGC A 3 C b b

6I1024 AATTCTCCCACC TGAGGTGGGAGAATTGCTTG
TCAGCCTC ACTCCACCCTCTTAACGAAC
C
GAM3229 221 DKFZP58 1 15526 NP_054752.1 3 264 CTGGGCTCAAGT T----- TG 3 C c c
6A0522 GATTCTCCCACC GAGGTGGGAGAAT CTTGA
TTGACCTC TTCCACCCTCTTA GAACT
CTCCAG GT
GAM3229 221 DKFZp66 1 10537 NP_808881.1 3 1160 CTGACCTCAGGT AGA TG 3 C c c
7B1218 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 DKFZp66 1 18552 XP_117353.1 3 355 CCAGGTTCAAGC TG 3 C b b
7E0512 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 DKFZp68 1 6504 XP_300559.1 3 2345 TTTCATATTCAC TGCT 3 C c c
6G052 CATTCTTCCACC TGAGGTGGGAGAAT TGAA
TCATTGAA ACTCCACCTTCTTA ACTT
CC--
GAM3229 221 DKFZp76 1 13622 NP_061181.1 3 946 CCGGGTTCAAGC TG 3 C b b
1H039 AATTCTCCTGTC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCT CCTCTTAACGAACTT
GT
GAM3229 221 DKFZp76 1 10832 NP_690870.1 3 799 CCAAGTTCAGGC A TG 3 C c c
1P1121 AATTCTCCTGCC TG GG GGAGAATTGCTTGAA
CCAGCCTC AC CC CCTCTTAACGGACTT
C GT
GAM3229 221 DKFZp76 1 7031 NP_848637.1 3 226 CCAAGCTCAAGC T----- TG A 3 C c c
2C2414 AATCCTCCTGCC GAGG GGAG ATTGCTTGA
TCTGCCTC CTCC CCTC TAACGAACT
CTCCGT GT C
GAM3229 221 DKFZp76 1 4228 XP_172976.2 3 1956 CCCGGGTCAAGC TG 3 C b b
2H185 AATTCTCCTGCC TGAGG GGAGAATTGCTTGA
TCAGCTTC ACTCC CCTCTTAACGAACT
GT
GAM3229 221 DMPK 1 7032 NP_004400.3 5 251 AGGCCTCAACCC A TTGC- 3 C c c
CTTTCTCCCACC TG GGTGGGAGAA TTGA
CAGCCCCA AC CCACCCTCTT AACT
- TCCCC
GAM3229 221 DNAJA3 1 6370 NP_005138.2 3 873 AGTCAGGGGCTT - -- -- 3 C c c
GGTTCTCCCACT TG AGGTGGGAGAATT GCT TGA

TACACTGT AC TTCACCCTCTTGG CGG ACT
A TT GG
GAM3229 221 DUSP18 1 7626 NP_689724.2 3 847 CTGGCCTCAAGC G A 3 C b b
AATCCTCACGCC TGAGGTG GAG ATTGCTTGA
TCAGCCTC ACTCCGC CTC TAACGAACT
A C
GAM3229 221 DUSP19 1 6797 NP_543152.1 3 1486 CTGGGCTCAAGC A 3 C b b
AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGTCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 DUSP7 1 6796 XP_037430.6 3 198 GGCCCGCAGGCA A A- A 3 C c c
AGGTCTCCCACT TG GGTGGGAGA TTGCTTG
GCAGGGCT AC TCACCCTCT AACGGAC
G GG G
GAM3229 221 DYRK1A 1 15252 NP_567824.1 5 125 CTGGGCTTAAGC GA 3 C b b
AGTCTTCCCACC TGAGGTGGGA ATTGCTTGA
TCAGCCTC ACTCCACCCT TGACGAATT
TC
GAM3229 221 EIF5A2 1 14800 NP_065123.1 3 1034 CCGAGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 ELP3 1 11180 NP_060561.3 3 960 CCGGGTTCAAGC 3 C b b
GATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCGCCCTCTTAGCGAACTT
GAM3229 221 EVI5 1 10675 NP_005656.2 3 575 CCAGGTTCAAGC TG 3 C b b
AATTTTCCTGCT TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTTC CCTTTTAACGAACTT
GT
GAM3229 221 F3 1 17533 NP_001984.1 3 485 TCGGGTTCAAGC TG AG 3 C c c
AATTGTCTGCCT TGAGG GG AATTGCTTGAA
CAGCCTCC ACTCC CT TTAACGAACTT
GT G-
GAM3229 221 FABP2 1 15832 NP_000125.1 3 579 CTGGCCTCAAGC TG A 3 C c c
AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 FANCF 1 12811 NP_073562.1 3 798 CCAGGATCAAGC T-- - -- 3 C c c
AATTCTGACTCA GAGG TGGG AGAATTGCTTGA
GCCTCCCA CTCC ACTC TCTTAACGAACT
ACC G AG
GAM3229 221 FBXW8 2 3077 NP_036306.1 3 2621 TCATCTTCAAGC G AGAAT 3 C c
b
ACGCCAACTTCA TGAGGT GG TGCTTGAA
GGCAGTGT ACTTCA CC ACGAACTT
A GC---
GAM3229 221 FBXW8 2 3077 NP_699179.2 3 2621 TCATCTTCAAGC G AGAAT 3 C c
b

ACGCCAACTTCA TGAGGT GG TGCTTGAA
GGCAGTGT ACTTCA CC ACGAACTT
A GC---

GAM3229 221 FBXW8 2 14800 NP_036306.1 3 1557 CCGAGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 FBXW8 2 14800 NP_699179.2 3 1557 CCGAGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 FCAR 1 14078 NP_579813.1 3 302 CCAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTCC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 FCRH1 1 10358 NP_443170.1 3 846 TCAGGCTCAAGC AA 3 C b b
AAACCTCTCACC TGAGGTGGGAG TTGCTTGA
TCAGCCTG ACTCCACTCTC AACGAACT
CA

GAM3229 221 FGD2 1 7015 NP_775829.1 3 739 CCAGCCTCAAGC T----- A 3 C c c
GATGCTCCCACC GAGGTGGGAG ATTGCTTGA
TCCACCTC CTCCACCCTC TAGCGAACT
CTCCAC G

GAM3229 221 FHIT 1 894 NP_002003.1 3 160 TTCTTCAACCAG A -- C 3 C c c
TGATCCCCCACC TGAGGTGGG GA ATTG TTGAA
TCGGTCAC GCTCCACCC CT TGAC AACTT
C AG C

GAM3229 221 FISH 1 15859 NP_055446.1 5 269 CTGGGCTCAAGC A 3 C b b
AATCCTCCCACT TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTTCACCCTC TAACGAACT
C

GAM3229 221 FLJ0000 1 12711 NP_258260.1 3 317 GGTCTCTAGTAG T----- -- T 3 C c c
7 TTCTGGCCCACC GAGGTGGG AGAATTGCT GA
TCTTTCCC CTCCACCC TCTTGATGA CT
CCCTTT GG T

GAM3229 221 FLJ0006 1 717 XP_028154.1 5 89 CCGGGCTCACGC T T 3 C c c
0 CATTCTTCCACC TGAGGTGGGAGAAT GC TGA
TCAGCCTC ACTCCACCTTCTTA CG ACT
C C

GAM3229 221 FLJ1027 1 11366 NP_060515.1 3 829 ACCTTGTCCAAC - AA C A 3 C c c

6 CAGCTACCCACC TGAGGTGGG AG TTG TTG
TCAACTCC ACTCCACCC TC GAC AAC
A -- C C

GAM3229 221 FLJ1052 1 9307 NP_060594.2 3 1540 CTGGCCTCAAGC A 3 C b b
0 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C

GAM3229 221 FLJ1053 1 6398 NP_060599.1 3 865 CCAGGTTCAAGC TG 3 C b b
5 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 FLJ1070 1 4483 NP_060652.1 3 295 GGCCATTTCCAG A AATT T 3 C c
c
0 CCAGCTCCCACC TG GGTGGGAG GCT GAA
CATCTTTT AC CCACCCTC CGA CTT
- GAC- C
GAM3229 221 FLJ1084 3 3502 NP_060712.2 3 897 CTGGGATCAAGC T----- A 3 C c c
7 AATCCTTCCACC GAGGTGGGAG ATTGCTTGA
TTGCCCTC TTCCACCTTC TAACGAACT
CTCCCG C
GAM3229 221 FLJ1084 3 7550 NP_060712.2 3 772 CTGGGCTCAAGT A TG 3 C c c
7 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 FLJ1084 3 8121 NP_060712.2 3 550 TGGGCTTCAAGC G TG A 3 C c c
7 AATCCTCCTGTG TGA G GGAG ATTGCTTGAA
TCAGCCAC ACT T CCTC TAACGAACTT
G GT C
GAM3229 221 FLJ1123 1 9182 NP_060836.1 3 266 CTGGGCTCAAGT A TG 3 C c c
0 GATCCTTCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCTTC TA GAACT
C GT
GAM3229 221 FLJ1132 1 7842 NP_060860.1 3 157 CGGGTTCCAGCA TG - T 3 C c c
3 AATTCTCCTGCC TGAGG GGAGAATT GCT GAA
TCAGCCTC ACTCC CCTCTTAA CGA CTT
GT A C
GAM3229 221 FLJ1261 1 13971 NP_079058.1 3 871 CTGGACTCTAGT - A TG T 3 C c c
0 GATCTGCCCACC TGAGGTGGG AGA T CT GA
TCAACCTC ACTCCACCC TCT A GA CT
G - GT T
GAM3229 221 FLJ1274 1 3806 XP_290972.1 3 2733 CCGACCTCAGGT AGA TG 3 C c
c
7 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT
GAM3229 221 FLJ1290 2 15331 NP_073590.1 3 562 CCAGGTTCAAGC T----- AGAA 3 C c
c
3 AAAAGACCCACC GAGGTGGG TTGCTTGAA
TCTCTGCA CTCCACCC AACGAACTT
ACGTCT AGAA
GAM3229 221 FLJ1290 2 19721 NP_073590.1 3 1752 CTGACCTCAGGT - A TG 3 C c
c
3 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT

GAM3229 221 FLJ1297 2 3161 NP_079085.2 3 533 CTGAGCTCAGAT - A GC 3 C c b
5 GATCTGCCCACC TGAGGTGGG AGA TT TTGA
TCGGCCTC GCTCCACCC TCT AG GACT
G - TA
GAM3229 221 FLJ1297 2 6872 NP_079085.2 3 408 TGCCTCCCAAGC A A 3 C b b
5 AATCCTCCCACC TGAGGTGGGAG ATTGCTTG
TCAGCCTC ACTCCACCCTC TAACGAAC
C C
GAM3229 221 FLJ1298 1 7712 NP_079200.1 3 628 TCACCATCAAGC G GAGA 3 C c
c
5 AATCCATGTCAT TGA GTGG ATTGCTTGA
AGGGAAAC ACT TACC TAACGAACT
G ----
GAM3229 221 FLJ1307 2 6829 XP_117117.2 3 892 CTGACCTCAGGT A 3 C b b
2 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAATGGACT
C
GAM3229 221 FLJ1307 2 18493 XP_117117.2 3 757 ACAGGCTCAAGC TG 3 C b b
2 AATTCTCCTGCC TGAGG GGAGAATTGCTTGA
TCAGCCTC ACTCC CCTCTTAACGAACT
GT
GAM3229 221 FLJ1359 1 6224 NP_079116.2 5 157 CGGGGCTCAGGT TG 3 C c c
0 GATTTTCCCACC TGAGGTGGGAGAAT CTTGA
TCAGCTTT ACTCCACCCTTTTA GGACT
GT
GAM3229 221 FLJ1395 1 7938 NP_079035.1 3 210 TTCATTTCAGTC A TT- T 3 C c c
5 CTTTCCCCCACC TGAGGTGGG GAA GCT GAA
TCAGCGTC ACTCCACCC CTT TGA CTT
C TCC -
GAM3229 221 FLJ1405 1 8656 NP_078839.1 3 1907 TTTCTATCAAGC --- GAGAA 3 C c
c
4 AAGAATGCCACG TGAG GTGG TTGCTTGA
TACTCAGA ACTC CACC AACGAACT
ATG GTAAG
GAM3229 221 FLJ1435 2 7578 NP_079008.1 3 530 CTGAGCTCAAGC TG A 3 C c b
1 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 FLJ1435 2 8490 NP_079008.1 3 376 CTGGGCTCAAGC A 3 C b b
1 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCCG ACTCCACCCTC TAACGAACT
C
GAM3229 221 FLJ1480 1 18549 NP_116231.1 3 495 CCAGGCTCAAGC TG 3 C b b
3 AATTCTCCTGCC TGAGG GGAGAATTGCTTGA
TCAGCCTC ACTCC CCTCTTAACGAACT
GT
GAM3229 221 FLJ2003 1 14023 NP_060104.1 3 815 ACCAGATCAAGC - - 3 C c c
8 AATTCTATCTAT TG AGGTGGG AGAATTGCTTGA
TTACACTA AC TTTATCT TCTTAACGAACT
A A

GAM3229 221 FLJ2004 1 603 NP_060108.1 3 191 CTGGGTTCAGGC 3 C b b
5 AATTCTCCCACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCACCCTCTTAACGGACTT

GAM3229 221 FLJ2012 1 12250 NP_060146.1 3 89 AAAGACCTATCA GA GC 3 C c c
5 AAATGTCCCACC TGAGGTGGGA ATT TTGA
TTAAGCCC ATTCCACCCT TAA AACT
G- --
GAM3229 221 FLJ2020 1 18150 NP_060178.1 5 160 CCTCTCACAGTC A A - - 3 C c c
0 AGTCCTCCCACC TG GGTGGGAG ATTG CT TGA
CGAGTGAC GC CCACCCTC TGAC GA ACT
- C T C
GAM3229 221 FLJ2067 1 19922 NP_060394.1 3 1598 CCAGGCTCAAGC TG 3 C b b
1 AATTCTCCTGCC TGAGG GGAGAATTGCTTGA
TCAACCTT ACTCC CCTCTTAACGAACT
GT
GAM3229 221 FLJ2072 1 7073 NP_060423.2 3 529 GTGGCCTCAAGC A 3 C b b
9 AATCCTTCCACC TGAGGTGGGAG ATTGCTTGA
TCAGACTC ACTCCACCTTC TAACGAACT
C
GAM3229 221 FLJ2130 1 3479 NP_075052.1 3 1087 CTGGGTTCAAGC GT 3 C c c
2 AATTCTTCTGAC TGAG GGGAGAATTGCTTGAA
TCAGCCTC ACTC TCTTCTTAACGAACTT
AG
GAM3229 221 FLJ2234 1 15136 NP_073741.1 3 0 CTCAAGCAATTC GGA 3 C b b
7 GACATCTCAAGT TGAGGTG GAATTGCTTGA
GAGACATG ACTCTAC CTTAACGAACT
AG-
GAM3229 221 FLJ2252 1 19173 NP_079065.1 3 204 CCAGGTTCAAGC TG G 3 C c c
9 AATTATCCTGCC TGAGG GGA AATTGCTTGAA
TCAGCCTC ACTCC CCT TTAACGAACTT
GT A
GAM3229 221 FLJ2280 1 3918 NP_079071.1 3 411 CTGGGCTCAGGT TG 3 C c c
0 GATTCTCCCATC TGAGGTGGGAGAAT CTTGA
TCAGCCTC ACTCTACCCTCTTA GGACT
GT
GAM3229 221 FLJ2302 1 2778 NP_079212.1 3 389 CCGGGTTCAAGC TG 3 C b b
4 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TTAGCCTC ATTCC CCTCTTAACGAACTT
GT
GAM3229 221 FLJ2304 1 7588 NP_079450.1 3 293 CTGGGCTCAAGC T----- TG 3 C c c
0 AATTTTCCTGCC GAGG GGAGAATTGCTTGA
TTGGGCCT TTCC CCTTTTAACGAACT
TCCGGG GT
GAM3229 221 FLJ2304 1 11628 NP_078824.2 3 1495 TCCTGGCTCAAG A TG 3 C c c

7 TGATCTCCCACT TGAGGTGGGAGA T CTTGA
TCAGCCTC ACTTCACCCTCT A GAACT
- GT
GAM3229 221 FLJ2335 1 8065 NP_115613.1 3 300 CCAGGTTCAAGC 3 C b b
6 AATTCTCCCACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCACCCTCTTAACGAACTT

GAM3229 221 FLJ2341 1 15550 NP_115614.1 3 1382 CTGAGCTCAAGC TG G A 3 C c
c
6 AATCCTGCTGCC TGAGG G AG ATTGCTTGA
TCAGTTCT ACTCC C TC TAACGAACT
GT G C
GAM3229 221 FLJ2356 1 16466 XP_041701.4 3 1908 CTGACCTCAGGT A TG 3 C c c

3 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCGGCCTC GCTCCACCCTC TA GGACT
C GT
GAM3229 221 FLJ2528 1 1118 NP_689759.1 3 161 CTGGGCTCAAGT T----- A TG 3 C c
c
6 GATCCTCCCACC GAGGTGGGAG AT CTTGA
TCTGCCTC CTCCACCCTC TA GAACT
CTCCGT C GT
GAM3229 221 FLJ3065 1 11839 NP_689557.1 3 672 TAGATCATGGCT - T - 3 C c c
6 GTTCTTCCCACC TGAGGTGGGA GAAT GCT TGA
TCATCCCT ACTCCACCCT CTTG CGG ACT
T T T
GAM3229 221 FLJ3116 1 19706 NP_694567.1 3 1199 CCGGATTCAAGC TG 3 C b b

6 AATTCTTCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CTTCTTAACGAACTT
GT
GAM3229 221 FLJ3182 1 11267 NP_694574.1 3 339 GTCTACTGCTCA T----- ATT 3 C c c

1 GGCTCTCCCACT GAGGTGGGAGA GCTTGA
TCGTGGCA CTTCACCCTCT CGGACT
ACGGTG ---
GAM3229 221 FLJ3209 1 8326 NP_776156.1 3 1612 CCAACCTCAGGT AGA TG 3 C c
c
6 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT
GAM3229 221 FLJ3238 1 19381 NP_653209.1 3 155 GCTAAATCGGTT AATT- T 3 C c
c
4 CAGACTCCCACC TGAGGTGGGAG GCT GA
TCACCGTT ACTCCACCCTC TGG CT
AGACT -
GAM3229 221 FLJ3286 1 16336 NP_653214.1 3 1441 CTGACCTCAGGC - A 3 C b b
5 AATCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCAGCCTC ACTCCACCC TCT AACGGACT
G -

GAM3229 221 FLJ3289 1 18611 NP_653268.1 3 764 CTGGGCTCAAGG G A G 3 C c c
4 GATCCTGCCACC TGAGGTGG AG ATT CTTGA
TCAGCTAA ACTCCACC TC TAG GAACT
G C G
GAM3229 221 FLJ3365 1 2783 NP_775912.1 3 385 CTGGGTTCAAGC TG 3 C b b
5 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 FLJ3376 1 1133 NP_775881.1 3 1676 TGGGTATCAAGC G G- A 3 C c c
8 AAATCTGACCAC TGA GTGG AGA TTGCTTGA
ATCACCTC ACT CACC TCT AACGAACT
A AG A
GAM3229 221 FLJ3381 1 4586 NP_775781.1 3 934 CCGGGTTCAAGC TG 3 C b b
4 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCACCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 FLJ3386 1 2033 NP_775915.1 3 1165 GAATGGTCAAGC G GAA 3 C c c
0 AATCCCAACTTA TGAG TGGGA TTGCTTGA
TGATTACT ATTC ACCCT AACGAACT
A ---
GAM3229 221 FLJ3391 1 3095 NP_689620.1 3 879 ATGAGCTCAAGT A TG 3 C c c
8 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTA ACTCCACCCTC TA GAACT
C GT
GAM3229 221 FLJ3481 1 20002 NP_689516.1 3 266 CTGGGCTCAAGT A A 3 C b b
7 AATCCTCCCACC TG GGTGGGAG ATTGCTTGA
CCAGCCTC AC CCACCCTC TAATGAACT
C C
GAM3229 221 FLJ3548 1 7671 NP_776181.1 3 582 CCAGGTTCAAGA A TG 3 C c c
7 GATCCTCCCACC TGAGGTGGGAG AT CTTGAA
TCAGCTTC ACTCCACCCTC TA GAACTT
C GA
GAM3229 221 FLJ3568 2 14927 NP_787096.1 3 1429 CTGGGCTTAAGT A TG 3 C c b
1 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGTCTC ACTCCACCCTC TA GAATT
C GT
GAM3229 221 FLJ3568 2 20076 NP_787096.1 3 1130 CTAGGCTCAAGC A 3 C b b
1 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAACCTC ACTCCACCCTC TAGCGAACT
C
GAM3229 221 FLJ3574 1 19097 NP_671728.1 3 1056 GGTCAGGCCATT T----- ---- T 3 C c c
0 CTGTTGCCCACC GAGGTGGG AGAAT GCTTGA
TCGTGCTG CTCCACCC TCTTA CGGACT
GTCGTG GTTG C
GAM3229 221 FLJ3584 1 4410 XP_290755.1 3 1255 CTGAGCTCAAGC TG AGA 3 C c
c

8 AATCCACCTGCC TGAGG GG ATTGCTTGA
TCAGCCTA ACTCC CC TAACGAACT
GT ACC
GAM3229 221 FLJ3603 1 6274 XP_290874.1 3 923 TCCTGCCCTCAA AA TG 3 C c c
2 GTGGCTTCCACC TGAGGTGGGAG T CTTGA
TCAAGTGG ACTCCACCTTC G GAACT
-- GT
GAM3229 221 FLJ3707 1 7587 NP_694588.1 5 102 TGGGGTTCAAGC A 3 C b b
8 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGAA
TCAGCCTC ACTCCACCCTC TAGCGAACTT
C
GAM3229 221 FLJ3743 1 10075 NP_848612.1 3 257 CCGGGTTCAAGC TG 3 C b b
3 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 FLJ3814 1 11940 XP_091919.5 3 1626 CTGACCTCAGGT AGA TG 3 C c
c
9 GATACGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCA GT
GAM3229 221 FLJ3828 1 1314 NP_689814.1 3 2025 CTGGGTTCAAGC A TG G 3 C c
c
1 AATTGTCCTGCC TG GG GGA AATTGCTTGAA
CCAGCCTC AC CC CCT TTAACGAACTT
C GT G
GAM3229 221 FLJ3860 1 11533 NP_689867.1 3 738 CTGGCCTCAGGT - A TG 3 C c c
7 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT
GAM3229 221 FLJ3879 1 18663 NP_848615.1 3 1439 CAAGTGGCCAGG - T G A 3 C c
c
2 AATTCTCCTCCT TG AGG GGGAGAATT CTTG
GCACCGGG AC TCC TCCTCTTAA GGAC
G - - C
GAM3229 221 FLJ3881 2 1627 NP_665872.1 3 274 AGGCTCAAATGA A-- GC 3 C c b
9 TCTCCTCCCACC TGAGGTGGGAG ATT TTGA
TCAGCCTC ACTCCACCCTC TAG AACT
CTC TA
GAM3229 221 FLJ3881 2 9307 NP_665872.1 3 411 CTGGCCTCAAGC A 3 C b b
9 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 FLJ3899 1 12896 NP_776188.1 3 1096 CCGTGTTCAAGC 3 C b b
1 AATTCTCCTACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTA ACTCCATCCTCTTAACGAACTT
GAM3229 221 FLJ3905 1 5123 NP_775851.1 3 49 CTGGGCTCAAGC A 3 C b b
8 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAGCGAACT

C

GAM3229 221 FLJ3942 1 16679 NP_775880.1 5 485 TTGTCCTCAAGT A TG 3 C c c
6 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TTAGCCTC ATTCCACCCTC TA GAACT
C GT

GAM3229 221 FLJ3959 1 7239 NP_776164.1 3 686 CTGGGTTCAAGC TG 3 C b b
9 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGGCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 FLJ3963 1 2704 XP_290687.1 3 1831 GTTGGCCAGGCT - T A 3 C c c
9 GTTCTGCCCACC TGAGGTGGG AGAAT GCTTG
TCACCCTC ACTCCACCC TCTTG CGGAC
G T C

GAM3229 221 FLJ4013 1 3565 NP_775749.1 3 765 TAAATTTCAAGC G G- AT 3 C c c
7 ATCTGATCACAT TGA GTGG AGA TGCTTGAA
CACATGGT ACT CACT TCT ACGAACTT
A AG --

GAM3229 221 FLJ9011 1 1074 NP_699178.1 3 1510 TTCCCTTCAAGC G T--- AT 3 C c c
9 ATCTCCCTCATC T AGG GGGAGA TGCTTGAA
CTGGACTC G TCC CCCTCT ACGAACTT
G TACT --

GAM3229 221 FLJ9075 1 2556 NP_699197.1 5 213 TTGAGCTCAAGC TG AGA 3 C c
c
4 AATCCACCTGCC TGAGG GG ATTGCTTGA
TCAACCTC ACTCC CC TAACGAACT
GT ACC

GAM3229 221 FMR2 1 9034 NP_002016.1 3 5650 TGGAAACTCAGT T----- T 3 C c c
AATTCTCCCACC GAGGTGGGAGAATTGCT GA
TTCACATT TTCCACCCTCTTAATGA CT
TTACAC -

GAM3229 221 FSD1 1 12959 NP_077309.1 3 170 ACCCTGGCGGGC - ATT A 3 C c c
CCTCTCCCCACC TGAGGTGGG AGA GCTTG
TCACCTCT ACTCCACCC TCT CGGGC
C CC- G

GAM3229 221 FSTL3 1 13077 NP_005851.1 3 1381 TGGTCTTGGGCC ----- - TG 3 C c c
AGTTCTCCCACG TGAG GTGGGAGAATTG CT A
ACGGCTCA ACTC CACCCTCTTGAC GG T
GGCAG C GT

GAM3229 221 FTSJ2 1 14535 NP_803191.1 3 70 TTGACCTCAGGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT

GAM3229 221 FUT1 1 13673 NP_000139.1 3 1268 CTGGGCTCAAGC T----- A 3 C c c
AGTCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGCCTC TTCCACCCTC TGACGAACT
CTCCGG C

GAM3229 221 GAN 1 14322 NP_071324.1 3 1627 AAACATCACTTA A TGCT- 3 C c c

CGTTCTCCCACC TG GGTGGGAGAAT TGA
CATAGACA AC CCACCCTCTTG ACT
- CATTC

GAM3229 221 GBP4 1 655 NP_443173.2 3 1614 CTGAGCTCAAGC TG - A 3 C c c
AATCTGCCTGCT TGAGG GG AGA TTGCTTGA
TCAGCCTC ACTTC CC TCT AACGAACT
GT G -

GAM3229 221 GFAP 1 9652 NP_002046.1 3 592 CTGGGCTCAAGC - A 3 C b b
AGTCTACCCACC TGAGGTGGG AGA TTGCTTGA
TCAGCCTC ACTCCACCC TCT GACGAACT
A -

GAM3229 221 GLO1 1 14826 NP_006699.1 3 203 TGGTTTTCAAGC G A 3 C c c
AGTGCTTTATCT TGAGGTGG AG ATTGCTTGAA
CATGTCCT ACTCTATT TC TGACGAACTT
- G

GAM3229 221 GM2A 1 2783 NP_000396.1 3 820 CTGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 GNPNAT1 2 12484 XP_085119.1 3 2241 CTGGGCTCAAAT A GC 3 C c c

GATCCTTCCACC TGAGGTGGGAG ATT TTGA
TCAGCCTC ACTCCACCTTC TAG AACT
C TA

GAM3229 221 GNPNAT1 2 13881 XP_085119.1 3 2370 CTAGGCTCAAGT A TG 3 C c c

GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT

GAM3229 221 GPP34R 1 14018 NP_060648.2 3 1061 CTGGGCTCAAGC 3 C b b
AATTCTTCCACC TGAGGTGGGAGAATTGCTTGA
TCAGCCTC ACTCCACCTTCTTAACGAACT

GAM3229 221 GPR81 1 10075 NP_115943.1 3 434 CCGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 GPX6 2 7367 NP_056511.2 3 304 TATATCAAGCAA A -- 3 C b b
TAATCTCCCACC TG GGTGGGAGA ATTGCTTGA
CAAGGCTT AC CCACCCTCT TAACGAACT
- AA

GAM3229 221 GPX6 2 19324 NP_056511.2 3 304 AGTATATCAAGC A -- 3 C b b
AATAATCTCCCA TG GGTGGGAGA ATTGCTTGA
CCCAAGGC AC CCACCCTCT TAACGAACT
- AA

GAM3229 221 GR6 1 7906 NP_031380.1 5 345 CCCGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 GREB1 1 11197 NP_055483.2 3 1928 CTGGCCTCAGGT - A TG 3 C c c

GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCATCCTC ACTCCACCC TCT A GGACT
G - GT

GAM3229 221 GRID1 1 17543 XP_043613.8 3 2578 TCCTCTTCAAGC A G GAA 3 C c c

AGCAATCCAACC TG GGT GGA TTGCTTGAA
CAGAGCAG AC CCA CCT GACGAACTT
- A AAC

GAM3229 221 GRIN2A 1 13819 NP_000824.1 3 1277 AGTGAGACAAGC G T - A 3 C c c

AATTTCTCCCTT T AGG GGGAGAA TTGCTTG
CTGAGTTA A TCT CCCTCTT AACGAAC
G T T A

GAM3229 221 GRM6 1 12308 NP_000834.1 3 2500 CTGGGCTCAAGC A 3 C b b

AATCCTCCCGCT TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTTCGCCCTC TAACGAACT
C

GAM3229 221 GSDM 2 6398 XP_209009.1 3 353 CCAGGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 GSDM 2 10286 NP_835465.1 3 355 CCAGGTTCAAGC TG 3 C b b

AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT

GAM3229 221 HIC2 1 9438 NP_055909.1 3 3612 GGACCCTCACCA AG - CT 3 C c c

ACTTTCCCCACC TGAGGTGGG AA TTG TGA
TCAGGCAG ACTCCACCC TT AAC ACT
CT C C-

GAM3229 221 HIC2 1 9438 XP_036937.2 3 3612 GGACCCTCACCA AG - CT 3 C c c

ACTTTCCCCACC TGAGGTGGG AA TTG TGA
TCAGGCAG ACTCCACCC TT AAC ACT
CT C C-

GAM3229 221 HIG1 1 6969 NP_054775.1 5 77 GATTCTTCAAGC G GA A 3 C c c

AATCACTATGTC TGA GTGG GA TTGCTTGAA
AACAGACA ACT TATC CT AACGAACTT
G A- -

GAM3229 221 HLA-DOB 1 14561 NP_002111.1 3 184 TTCTGAGATCAT A AT T 3 C c c

GCATCTCCCACC TG GGTGGGAGA TGC TGA
CATCTGCC AC CCACCCTCT ACG ACT
- -- T

GAM3229 221 HOXB2 1 7506 NP_002136.1 3 82 TGGAAAAATCGA - ATT 3 C c c

GCCTCTCCCACC TGAGG TGGGAGA GCTTGA
CTCAGTCG ACTCC ACCCTCT CGAGCT
C C--

GAM3229 221 HS3ST5 1 8703 NP_705840.1 3 1012 TGGAAATCAAGT GAGAAT 3 C c c

ATAATAGCCACC TGAGGTGG TGCTTGA
TCAAAGAA ACTCCACC ATGAACT

GATAAT
GAM3229 221 HSD3B7 1 15973 NP_079469.2 3 269 CTGGGTTCAAGC TG A 3 C c c
AATCCTCCTGCC TGAGG GGAG ATTGCTTGAA
TCAGCCTC ACTCC CCTC TAACGAACTT
GT C
GAM3229 221 HSNOV1 1 10558 NP_059985.2 3 975 CTGAGCTAAAGC - A GA 3 C c c
GATCTGCCCACC TGAGGTGGG AGA TTGCTT
TCGGCCTC GCTCCACCC TCT AGCGAA
G - AT
GAM3229 221 HSPA5 1 12356 NP_005338.1 3 547 CTGGGCCCAAGT A TG A 3 C c c
GATCCTTCCACC TGAGGTGGGAG AT CTTG
TCAGTCTC ACTCCACCTTC TA GAAC
C GT C
GAM3229 221 HSPC063 2 5789 NP_054874.1 3 809 TGCTTCTCCAGC TT T 3 C c c
CTTTCTCCCATT TGAGGTGGGAGAA GCT GA
TCAGTAAG ACTTTACCCTCTT CGA CT
TC C
GAM3229 221 HSPC063 2 7180 NP_054874.1 3 307 CCAAATTCAAGC GG GAAT 3 C c c
ATTTCATCTCAA TGAGGTG A TGCTTGAA
GAGTTGTA ACTCTAC T ACGAACTT
TT ----
GAM3229 221 HSPC065 1 9903 NP_054876.2 3 2185 TGGGATTCAAGC 3 C b b
AATTCTCCCACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCACCCTCTTAACGAACTT
GAM3229 221 HSRNAFE 1 5540 NP_059991.1 3 416 CTTCCCCAAGGA AA- G A 3 C c c
V ACTGCTCCCACC TGAGGTGGGAG TT CTTG
TCAGCACG ACTCCACCCTC AA GAAC
GTC G C
GAM3229 221 HT009 1 10585 NP_060940.1 3 16 TCGTTCAGGTGC T-- -- 3 C c c
AATTCTTCTTGG TGAGG GGGAGAATTGC TTGAA
TCTCAGCT ACTCT TCTTCTTAACG GACTT
GGT TG
GAM3229 221 HTCD37 1 10478 NP_067045.1 3 97 TGGAGATTCAGC TG G T 3 C c c
AATTCTGTCTTC TGAGG G AGAATTGCT GAA
ATTGCTCC ACTTC T TCTTAACGA CTT
-- G -
GAM3229 221 HUS1 1 10277 NP_004498.1 3 1080 CTTGGCTCAAGG AAT - 3 C b b
CATCCTCCCACC TGAGGTGGGAG TGC TTGA
TCAGCTTC ACTCCACCCTC ACG AACT
CT- G
GAM3229 221 ICAM1 1 9491 NP_000192.1 3 1194 TTGGGCTCAAGT A TG 3 C c c
GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT

C GT
GAM3229 221 IGFBP5 1 512 NP_000590.1 5 204 TTGATTTCAACA T---- - T- C 3 C c c
TTTTCTCCCACC GAGG TGGGAGAA TG TTGAA
CTCTCGGC CTCC ACCCTCTT AC AACTT
CGGCT C TT -
GAM3229 221 IL11 1 10075 NP_000632.1 3 759 CCGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 IL12RB1 2 8116 NP_714912.1 3 366 CCAGACTCAAGT A TG 3 C c c
GATCCTTCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCTTC TA GAACT
C GT
GAM3229 221 IL12RB1 2 9835 NP_714912.1 3 209 CTGCCCTCAGGT AGA TG 3 C c
c
GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 IL19 2 11633 NP_037503.2 5 50 CTGACCTCAAGC T----- TG G 3 C c c
AATTGTCCTGCC GAGG GGA AATTGCTTGA
TCCTCAAC CTCC CCT TTAACGAACT
CAACTC GT G
GAM3229 221 IL19 2 14348 NP_037503.2 5 202 TTGGCCTCAAGG A G 3 C c c
GATCCTCCCACC TGAGGTGGGAG ATT CTTGA
TCGGCTTC GCTCCACCCTC TAG GAACT
C G
GAM3229 221 IL1A 1 13186 NP_000566.3 5 393 CCTTAATCAAGC T AA 3 C c c
AAACTTCCCTCT TGAGG GGGAG TTGCTTGA
TCAGAAAA ACTTC CCCTT AACGAACT
T CA
GAM3229 221 IL8 1 16050 NP_000575.1 3 75 GAAACTTCAAGC ---- - A 3 C c c
AAATCTACTTCA TGAGGTG GG AGA TTGCTTGAA
ACACTTCA ACTTCAC TC TCT AACGAACTT
AACT A A
GAM3229 221 KCNE3 1 19681 NP_005463.1 5 158 GCTTCTACCGAG A TT A 3 C c c
TCTTCCCCCACC TGAGGTGGG GAA GCTTG
TCAATCCC ACTCCACCC CTT TGAGC
C C- C
GAM3229 221 KDR 1 618 NP_002244.1 3 318 AGAGCTTCAAGC - AGA 3 C b b
AATGGCCCCATC TGAGG TGGG ATTGCTTGAA
CTCAAAGA ACTCC ACCC TAACGAACTT
T CGG
GAM3229 221 KENAE 1 3881 NP_789786.1 3 269 CCCGGTTCAGGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGGACTT
GT
GAM3229 221 KHSRP 1 10161 NP_003676.1 3 422 TAAAGCAATTCA - ------ GA 3 C c c
TTTTCTCCCACC TGAGG TGGGAGA ATTGCTT
CTCGGCCC GCTCC ACCCTCT TAACGAA

C TTTACT AT

GAM3229 221 KIAA018 1 8187 NP_066545.1 3 297 CTGGCCTCAAGC A 3 C b b
6 AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TTAGCTTC ATTCCACCCTC TGACGAACT
C

GAM3229 221 KIAA019 1 9437 NP_055581.2 3 50 CCTTCTTATTTA AATTG 3 C c c
3 AGACTTCCCACC TGAGGTGGGAG CTTGAA
TTACTAAA ATTCCACCCTT GAATTT
CA---

GAM3229 221 KIAA020 1 5448 NP_055688.1 3 1452 CTGACCTCAGGT - A TG 3 C c c
5 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCTTC GCTCCACCC TCT A GGACT
G - GT

GAM3229 221 KIAA028 1 18647 XP_166238.1 3 4612 TTTTCCATCCTG G T TT 3 C c c
0 TATTCTCCCACA TGA GTGGGAGAAT GC GA
TCACTACT ACT CACCCTCTTA TG CT
A - TC

GAM3229 221 KIAA039 1 9624 NP_055487.1 3 3144 CTGGGTTCAAGC T----- GG 3 C c
c
1 AATTCTCATGCC GAGGT GAGAATTGCTTGAA
TCTGCCTC CTCCG CTCTTAACGAACTT
CTCCGT TA

GAM3229 221 KIAA044 1 12906 XP_044155.1 5 2339 CAGGGCTCAGGT A TG 3 C c
c
6 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCAC ACTCCACCCTC TA GGACT
C GT

GAM3229 221 KIAA046 1 5867 NP_055666.1 3 761 CCAGGTTCACGC T T 3 C b b
9 CATTCTCCCGCC TGAGGTGGGAGAAT GC TGAA
TCAACCTC ACTCCGCCCTCTTA CG ACTT
C C

GAM3229 221 KIAA047 1 6356 NP_055685.1 3 2394 CTGAGCTCAAGC G 3 C b b
8 AGTTCTCCCACC T AGGTGGGAGAATTGCTTGA
TGGGCCTC G TCCACCCTCTTGACGAACT
G

GAM3229 221 KIAA049 1 13205 XP_034717.1 5 985 CTGGGCTCAAGC GA 3 C b b
3 AATCTTCCCACC TGAGGTGGGA ATTGCTTGA
TCAGCCTC ACTCCACCCT TAACGAACT
TC

GAM3229 221 KIAA051 1 10075 NP_055547.1 3 3733 CCGGGTTCAAGC TG 3 C b b
3 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 KIAA052 1 9370 XP_171054.1 3 424 CCAAGTTCAAGC TG 3 C b b
7 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 KIAA053 1 3516 XP_047659.6 3 125 TGGGGTTCAAGC A 3 C b b
2 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGAA
TCAACCCA ACTCCACCCTC TAACGAACTT
C
GAM3229 221 KIAA056 1 3797 NP_055519.1 3 2108 CCGGGTTCGAGC TG 3 C b b
2 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAGCTT
GT
GAM3229 221 KIAA060 1 1515 NP_055509.1 5 128 CCAGGTTCAAGC TG 3 C b b
5 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTT ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 KIAA082 1 15963 NP_056143.1 3 2556 CTGGGCTCAAGC TG A 3 C c
c
8 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCTTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 KIAA084 1 4565 XP_049237.1 3 1580 CTGGATTCAAAC GT G C 3 C c
c
1 AATTCTCATGTC TGAG G GAGAATTG TTGAA
TCAGCCTC ACTC T CTCTTAAC AACTT
TG A A
GAM3229 221 KIAA092 1 7195 NP_055712.1 3 1787 TTGGGTTCAAGC TG AGAA 3 C c
c
4 AACCCTGCCTCA TGAGG GG TTGCTTGAA
GCTAACCA ACTCC CC AACGAACTT
GT C---
GAM3229 221 KIAA093 1 12234 XP_052620.6 3 1272 CTGGGTTCAAGC T----- G 3 C c c
5 AATTCTCCAGCC GAGGT GGAGAATTGCTTGAA
TCTGCCTC CTCCG CCTCTTAACGAACTT
CTCCGT A
GAM3229 221 KIAA098 1 19897 NP_054742.1 3 854 CAGAGCCCAGTT - C A 3 C c c
2 AATTCTCCGCAC TGAGGTG GGAGAATTG TTG
CTCGGTTG GCTCCAC CCTCTTAAT GAC
G T C
GAM3229 221 KIAA101 1 845 XP_050742.5 3 827 CTGGGCTCAAGC T----- AA 3 C c c
0 AACCCTCCCGCC GAGGTGGGAG TTGCTTGA
TCCCTGCT CTCCGCCCTC AACGAACT
TCGTCC CC
GAM3229 221 KIAA104 1 11317 XP_051091.3 3 2515 CCGGGTTCAAGC TG A 3 C c
c
0 AGTTTCCTGCTT TGAGG GGAGA TTGCTTGAA
CAGACTTC ACTTC CCTTT GACGAACTT
GT -
GAM3229 221 KIAA104 1 10075 NP_055762.1 3 1027 CCGGGTTCAAGC TG 3 C b b
1 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT

GT

GAM3229 221 KIAA105 2 4043 XP_043493.5 3 3473 CTGACCTCAAGT AGA TG 3 C c b

4 GATCGGCCCACC TGAGGTGGG AT CTTGA

TCAGCCTC ACTCCACCC TA GAACT

GGC GT

GAM3229 221 KIAA105 2 15902 XP_043493.5 3 3337 CCAGGTTCAAGT TG 3 C b b

4 GATTCTCCCACC TGAGGTGGGAGAAT CTTGAA

TCAGCCTC ACTCCACCCTCTTA GAACTT

GT

GAM3229 221 KIAA114 1 10272 NP_065749.1 3 916 CTTGCTTCAAGG A G 3 C b b

5 GATCCTCCCACC TGAGGTGGGAG ATT CTTGAA

TCAGCCTC ACTCCACCCTC TAG GAACTT

C G

GAM3229 221 KIAA115 2 4896 XP_030864.2 3 3013 CTAGGCTCAAGC A 3 C b b

5 AATCCTCCCATC TGAGGTGGGAG ATTGCTTGA

TTAGCCTC ATTCTACCCTC TAACGAACT

C

GAM3229 221 KIAA115 2 9308 XP_030864.2 3 3158 TTGTGCTCAAGT TG 3 C b b

5 GATTCTCCCATC TGAGGTGGGAGAAT CTTGA

TCAGCCTC ACTCTACCCTCTTA GAACT

GT

GAM3229 221 KIAA119 4 1315 NP_065765.1 3 480 CTGGGTTCAAGC A TG 3 C c b

8 AATTCTCCTGCC TG GG GGAGAATTGCTTGAA

GCAGCCTC AC CC CCTCTTAACGAACTT

G GT

GAM3229 221 KIAA119 4 4779 NP_065765.1 3 4079 CCAGGTTCAAGC TG 3 C b b

8 AATTCTCCTGTT TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTTT CCTCTTAACGAACTT

GT

GAM3229 221 KIAA119 4 7372 NP_065765.1 3 3768 TCAGGTTCAAGC TG 3 C b b

8 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT

GT

GAM3229 221 KIAA119 4 12313 NP_065765.1 3 776 CTGGGTTCAAGC TG 3 C b b

8 AATTCTTCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTT ACTCC CTTCTTAACGAACTT

GT

GAM3229 221 KIAA120 1 13574 XP_031054.4 3 432 CAGGGTTCAAGC TG 3 C b b

0 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTT ACTCC CCTCTTAACGAACTT

GT

GAM3229 221 KIAA125 1 9371 XP_031577.2 3 1755 CCAGGTTTAAGC TG 3 C b b

7 AATTCTCCTGCT TGAGG GGAGAATTGCTTGAA

TCAACCTC ACTTC CCTCTTAACGAATTT

GT

GAM3229 221 KIAA131 1 1457 NP_065820.1 3 144 CTCCCGCTCCAG GAAT A 3 C c c

8 GCACATCCCACC TGAGGTGGGA TGCTTG

TTACCTCT ATTCCACCCT ACGGAC

AC-- C

GAM3229 221 KIAA139 1 14141 XP_032054.2 3 2557 CTGTGCTCAAGT AA TG 3 C c c

6 GACCCTCCCACC TGAGGTGGGAG T CTTGA

TCATTCTC ACTCCACCCTC A GAACT

CC GT

GAM3229 221 KIAA149 1 4891 XP_034415.1 3 3025 CCAGGTTCAAGC TG 3 C b b

3 AATTCTCCTGTC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCT CCTCTTAACGAACTT

GT

GAM3229 221 KIAA157 1 13416 XP_027744.1 3 941 CCGGGTTCAAGC TG----- TG 3 C c c

1 AATTCTCCTGCC AGG GGAGAATTGCTTGAA

TAAGCCTC TCC CCTCTTAACGAACTT

CTCCGAA GT

GAM3229 221 KIAA167 3 5639 XP_037809.1 3 1929 CTGGGCTCAAGC T G 3 C b b

1 AATTGTCCCTCC TGAGG GGGA AATTGCTTGA

TCAGCCTC ACTCC CCCT TTAACGAACT

T G

GAM3229 221 KIAA167 3 17241 XP_037809.1 3 1792 CTGGGCTCAAGT TG 3 C b b

1 GATTCTCCCACC TGAGGTGGGAGAAT CTTGA

TCAGCCTC ACTCCACCCTCTTA GAACT

GT

GAM3229 221 KIAA167 3 19751 XP_037809.1 3 4153 CTGGGCTCAAGC T----- A 3 C c b

1 AATCCTCTCATC GAGGTGGGAG ATTGCTTGA

TCCACCTC CTCTACTCTC TAACGAACT

CTCCAC C

GAM3229 221 KIAA172 2 7550 XP_034262.4 3 984 CTGGGCTCAAGT A TG 3 C c c

7 GATCCTCCCACC TGAGGTGGGAG AT CTTGA

TCAGCCTC ACTCCACCCTC TA GAACT

C GT

GAM3229 221 KIAA172 2 8253 XP_034262.4 3 840 CCAGACCCAAGT A TG A 3 C c c

7 GATCCTCCCACC TGAGGTGGGAG AT CTTG

TCAGCCTC ACTCCACCCTC TA GAAC

C GT C

GAM3229 221 KIAA176 1 2344 XP_047355.1 3 868 CAGAGTTCAAGC - AAT 3 C c c

5 ACATTCCTACCT TG AGGTGGGAG TGCTTGAA

GCAGGGCA AC TCCATCCTT ACGAACTT

G AC-

GAM3229 221 KIAA178 1 10075 NP_115820.1 3 401 CCGGGTTCAAGC TG 3 C b b

4 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT

GT

GAM3229 221 KIAA182 1 10075 XP_290834.1 3 1365 CCGGGTTCAAGC TG 3 C b b

7 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT

GT
GAM3229 221 KIAA182 1 15973 XP_030378.2 3 269 CTGGGTTCAAGC TG A 3 C c c
9 AATCCTCCTGCC TGAGG GGAG ATTGCTTGAA
TCAGCCTC ACTCC CCTC TAACGAACTT
GT C
GAM3229 221 KIAA192 1 7589 NP_694971.2 3 860 CAGGGCTCAAGC A 3 C b b
4 AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 KIAA197 1 7601 XP_058720.4 3 621 CCAGGTTCAAGC TG G 3 C c c
1 AATTCTCTGTCT TGAGG G AGAATTGCTTGAA
CAGCCTCC ACTCT C TCTTAACGAACTT
GT -
GAM3229 221 KIAA199 1 19071 XP_068710.3 3 4625 TCTCATTTAAGC T A 3 C c c
8 AATTTACTTCCT TGAGG GGG GAATTGCTTGAA
CATTCTGG ACTCC TTC TTTAACGAATTT
- A
GAM3229 221 KIAA202 1 7899 XP_086409.4 3 456 CCAATCCTTATC A - CT 3 C c c
5 AATTCTCACCAC TG GGTGG GAGAATTG TGA
CCCATAAA AC CCACC CTCTTAAC ATT
C A T-
GAM3229 221 KIAA202 3 17589 XP_059415.2 3 1122 CCGGGATCAAGC GAA 3 C b
b
8 AATCCCACTTCA TGAGGTGGGA TTGCTTGA
GCCTCTTG ACTTCACCCT AACGAACT

GAM3229 221 KIAA202 3 18073 XP_059415.2 3 1254 CTGGGTTCAAGC A 3 C b b
8 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGAA
TCGGCCTC GCTCCACCCTC TAACGAACTT
C
GAM3229 221 KIAA202 3 19988 XP_059415.2 3 950 CTGGCCTCAAGC T A 3 C b b
8 AATCCTCTCTCC TGAGG GGGAG ATTGCTTGA
TCAGCCTC ACTCC CTCTC TAACGAACT
T C
GAM3229 221 KMO 2 9048 NP_003670.1 3 884 CTGGCCTCATGT - A TG T 3 C c b
GATCTGCCCACC TGAGGTGGG AGA T C TGA
TCAGCCTC ACTCCACCC TCT A G ACT
G - GT T
GAM3229 221 KMO 2 15859 NP_003670.1 3 775 CTGGGCTCAAGC A 3 C b b
AATCCTCCCACT TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTTCACCCTC TAACGAACT
C
GAM3229 221 KRTHB2 1 12235 NP_149022.3 3 380 CACAAAGTCAGC A ATT T 3 C c
c
TCCTCTCCCACC TG GGTGGGAGA GCT GA
ACAGGCTC AC CCACCCTCT CGA CT
A CCT -
GAM3229 221 KSR 1 10075 XP_290793.1 5 1207 CCGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LAMP3 1 3841 NP_055213.1 3 758 TTGACCTCAGGT AGA TG 3 C c
c
GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 LAT1-3T 1 13820 NP_112488.1 3 1453 TGTTTATCAAGC G GG A 3 C c
c
M AATGCTCAGCTT T AGGT GAG ATTGCTTGA
GAAGAATA A TTCG CTC TAACGAACT
G A- G
GAM3229 221 LCN7 1 7234 NP_071447.1 3 458 CTGGGTTCAAGT AA TG 3 C c c
GACCCTCCCACC TGAGGTGGGAG T CTTGAA
TCAGCCTC ACTCCACCCTC A GAACTT
CC GT
GAM3229 221 LHX3 1 20146 NP_055379.1 3 695 CTCTCCAAGCTC T ---- -- A 3 C c c
AATTCTCTAAGC TGAGG GG GAGAATT GCTTG
CCCTCAGG ACTCC CC CTCTTAA CGAAC
- GAAT CT C
GAM3229 221 LIF 1 4988 NP_002300.1 3 2446 CTGGCTCTGAGT A ATT - 3 C c c
CGCTCTCCCACC TG GGTGGGAGA GCTT GA
CAGCCTGG AC CCACCCTCT TGAG CT
- CGC T
GAM3229 221 LNIR 1 6798 NP_112178.1 3 892 CTGGGCTCAAGC TG A 3 C c c
AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC1126 1 10726 XP_053145.1 3 362 CTGACCTCATGT AGA T 3 C c
c
87 AATCCACCCACC TGAGGTGGG ATTGC TGA
TCAGCCTC ACTCCACCC TAATG ACT
ACC T
GAM3229 221 LOC1150 1 15832 NP_612451.1 5 55 CTGGCCTCAAGC TG A 3 C c c
98 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC1152 1 12851 XP_055499.2 5 1814 CTGGGTTCAAAC TG C 3 C c
c
19 AATTCTCCTGCC TGAGG GGAGAATTG TTGAA
TCAGCCTC ACTCC CCTCTTAAC AACTT
GT A
GAM3229 221 LOC1175 1 3964 NP_476519.1 3 143 ACCAGGTCAAGC G GAGAA 3 C
c c
84 AAGATGCCATGT TGA GTGG TTGCTTGA
CACCCCTG ACT TACC AACGAACT
G GTAG-
GAM3229 221 LOC1188 1 16805 NP_849154.1 3 640 CCAGGTTCAAGC TG A 3 C c
c

```
          12                          AATTCCCCTGCC TGAGG  GG GAATTGCTTGAA
                                     TCAGCTTC    ACTCC  CC CTTAACGAACTT
                                               GT  C
GAM3229  221   LOC1188 1  16805 XP_058346.2  3  640   CCAGGTTCAAGC    TG  A            3  C  c
c
          12                          AATTCCCCTGCC TGAGG  GG GAATTGCTTGAA
                                     TCAGCTTC    ACTCC  CC CTTAACGAACTT
                                               GT  C
GAM3229  221   LOC1193 1  9142  NP_660290.1  3  180   TCGGGTTCCAGC    TG       T        3  C  c  c

          92                          AATTCTCCTGCC TGAGG  GGAGAATTGCT GAA
                                     TCAGCCTC    ACTCC  CCTCTTAACGA CTT
                                               GT        C
GAM3229  221   LOC1205 2  2073  XP_058475.1  3  149   TACAATTATCAA      GAGAA           3  C  c
c
          26                          GCAGAGACCACC TGAGGTGG    TTGCTTGA
                                     TCAGATTA    ACTCCACC    GACGAACT
                                               AGA--
GAM3229  221   LOC1205 2  10538 XP_058475.1  3  1004  CTGGCCTCAAAT       AGA  GC         3  C  c
 c
          26                          GATCCGCCCACC TGAGGTGGG   ATT  TTGA
                                     TCAACCTC    ACTCCACCC   TAG  AACT
                                               GCC   TA
GAM3229  221   LOC1218 2  1458  XP_071772.1  5  2045  GCTTCTTCAAGC      GAGAA           3  C  b
b
          38                          AAACCACCTCAC TGAGGTGG    TTGCTTGAA
                                     CACACTAT    ACTCCACC    AACGAACTT
                                               A----
GAM3229  221   LOC1218 2  14349 XP_071772.1  5  2044  GGCTGCTTCTTC      GAGAA           3  C  b
 b
          38                          AAGCAAACCACC TGAGGTGG    TTGCTTGAA
                                     TCACCACA    ACTCCACC    AACGAACTT
                                               A----
GAM3229  221   LOC1250 1  10075 XP_058889.3  3  466   CCGGGTTCAAGC    TG               3  C  b  b

          61                          AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                     TCAGCCTC    ACTCC  CCTCTTAACGAACTT
                                               GT
GAM3229  221   LOC1266 2  11629 XP_060121.4  3  394   CTGACCTCAAAT       AGA  GC         3  C  c
b
          69                          GATCCACCCACC TGAGGTGGG   ATT  TTGA
                                     TCAGTCTC    ACTCCACCC   TAG  AACT
                                               ACC   TA
GAM3229  221   LOC1266 2  13284 XP_060121.4  3  253   CTGGGTTCAAGC   - T              3  C  b  b
          69                          AGTTCTTCCCCA TGA GG GGGAGAATTGCTTGAA
                                     TCAGCCTC    ACT CC CCTTCTTGACGAACTT
                                               A  -
GAM3229  221   LOC1306 1  13129 XP_059464.2  5  135   CTGACCTCAAGT        A  TG          3  C  c  c

          39                          GATCCTCCCACC TGAGGTGGGAG AT  CTTGA
```

TCAGCCTC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 LOC1308 1 12421 XP_065904.1 3 823 CCGGGCTCAAGC A 3 C b b
13 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC1322 1 15759 XP_059583.1 3 39 CCTGGTTCAAGC T-- -- - 3 C c c
41 AATTCTGCCCCA GAGGT GGG AGAATTGCTTGAA
GCCTCCCA CTCCG CCC TCTTAACGAACTT
ACC AC G
GAM3229 221 LOC1352 1 12656 XP_072402.4 3 1336 CTGGACTCAAGC A 3 C b b
93 AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 LOC1358 1 19721 XP_059804.4 3 931 CTGACCTCAGGT - A TG 3 C c
c
18 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT
GAM3229 221 LOC1363 1 6455 XP_072455.2 3 1131 TCAGTCAAGGAC AA -- 3 C b b
45 AAACCTCCCACC TGAGGTGGGAG TTG CTTGA
TCACAGAC ACTCCACCCTC AAC GAACT
CA AG
GAM3229 221 LOC1378 1 9666 XP_059929.3 3 877 CGAACCTCAGGT AGA TG 3 C c
c
86 GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC1394 1 16130 XP_066687.2 5 123 CTGAGCTCAAGC A 3 C b b
22 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTT ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC1436 1 14289 XP_096471.1 5 296 GATCCTATCAGC A ATT T 3 C c
c
77 TTCTCTCCCACC TG GGTGGGAGA GCT GA
CAATTAGG AC CCACCCTCT CGA CT
- CTT -
GAM3229 221 LOC1444 1 19677 XP_084852.6 3 1185 CAGGGCTCAAGG A G 3 C b
b
04 GATCCTCCCACC TGAGGTGGGAG ATT CTTGA
TCAGCCTC ACTCCACCCTC TAG GAACT
C G
GAM3229 221 LOC1444 1 3550 XP_096611.2 3 268 TCAGGTTCAAGC GG 3 C b b
81 AATTCTCATGCT TGAGGT GAGAATTGCTTGAA
TCAGCCTC ACTTCG CTCTTAACGAACTT
TA
GAM3229 221 LOC1448 1 15802 XP_096698.1 3 417 CCGGGTTCAAGC TG 3 C b b
71 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 LOC1451 1 15484 XP_085049.1 3 29 AGACACTCACAC -- --- CT 3 C c c
88 AATTCTCAATCC TGAG GTGG GAGAATTG TGA
ACATTTCA ACTT CACC CTCTTAAC ACT
TA TAA AC
GAM3229 221 LOC1452 1 10524 XP_085072.1 5 831 CTAACCTCGGGT AGA TG 3 C c
c
68 GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTT ACTCCACCC TA GGGCT
ACC GT
GAM3229 221 LOC1453 1 12820 XP_096791.1 5 292 ATTTCATCTAGC GT- T 3 C c c
87 AATTCTCTTTGA TGAG GGGAGAATTGCT GA
CTTAGTCG ATTC TTCTCTTAACGA CT
AGT T
GAM3229 221 LOC1456 1 10802 XP_096816.1 3 1598 CCCCAATCTGCG - TT 3 C c c
01 GCTTCTCCCACC TGAGGTGGGAGAA TTGC GA
TCACTGGG ACTCCACCCTCTT GGCG CT
C T-
GAM3229 221 LOC1459 1 15535 XP_085290.3 5 614 CCAGGTTCAAGC TG G 3 C c
c
88 AATTATCCTGCC TGAGG GGA AATTGCTTGAA
TCAGCCAC ACTCC CCT TTAACGAACTT
GT A
GAM3229 221 LOC1462 1 15411 XP_085387.1 3 4225 CTGACCTCAGGT AGA TG 3 C c
c
29 GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC1463 1 5123 XP_085421.2 3 787 CTGGGCTCAAGC A 3 C b b
36 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAGCGAACT
C
GAM3229 221 LOC1463 1 3401 XP_085430.1 5 795 CTAGGTTCAAGC TG 3 C b b
46 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 LOC1464 1 9729 XP_085461.6 5 293 CTGACCTCAGGT - A TG 3 C c c
43 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GGACT
G - GT
GAM3229 221 LOC1467 1 19578 XP_097071.2 3 289 TTGTTTTTAGGC G G -- 3 C c c
13 AATTCTGGCTGG T AGGT GG AGAATTGCTTGAA
CCTGAGAA A TCCG TC TCTTAACGGATTT
G G GG
GAM3229 221 LOC1468 1 15412 XP_097109.2 3 1585 CCCACTCTCAGG AGAATT 3 C
c c
50 CCACTGCCCACC TGAGGTGGG GCTTGA

TCACTCAG ACTCCACCC CGGACT
GTCAC-
GAM3229 221 LOC1469 1 11082 XP_085634.2 3 721 CTGGGTTCAAGT TG 3 C b b
09 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTT ACTCC CCTCTTAATGAACTT
GT
GAM3229 221 LOC1470 1 11470 XP_097155.1 3 717 GTTCAGAGATCC AATT A 3 C c
c
04 AGGCCTCCCACC TGAGGTGGGAG GCTTG
TCAGACTC ACTCCACCCTC CGGAC
---- C
GAM3229 221 LOC1471 1 14800 XP_085722.2 3 311 CCGAGTTCAAGC TG 3 C b b

66 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC1473 1 7551 XP_097225.1 5 887 CTGGGTTCAAGT A TG 3 C c c
43 GATCCTCCCACC TGAGGTGGGAG AT CTTGAA
TCAGCTTC ACTCCACCCTC TA GAACTT
C GT
GAM3229 221 LOC1478 1 5287 XP_085903.1 3 504 CCGGGTTCAAGC TG 3 C b b
17 AATTCTTCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CTTCTTAACGAACTT
GT
GAM3229 221 LOC1479 1 4263 XP_085974.1 3 638 CCAGGCTCAAGT A TG 3 C c c

47 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 LOC1482 2 6399 XP_086095.1 3 1236 CCAGGTTCAAGC 3 C b b
03 AGTTCTCCTACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCATCCTCTTGACGAACTT

GAM3229 221 LOC1482 2 18261 XP_086095.1 3 1370 CTGACCTCAGGT A TG 3 C c
b
03 GATTCACCCACC TGAGGTGGG GAAT CTTGA
TCAGCTTC ACTCCACCC CTTA GGACT
A GT
GAM3229 221 LOC1487 1 6483 XP_086281.1 5 202 CTGAACTCAAGC T----- TG 3 C c c

09 AATTCTCCTGCC GAGG GGAGAATTGCTTGA
TTGGCCTC TTCC CCTCTTAACGAACT
CTCCGG GT
GAM3229 221 LOC1489 2 7157 XP_086361.1 5 2150 CCAGGCTCAAGC A 3 C b b
18 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCTCC ACTCCACCCTC TAGCGAACT
C
GAM3229 221 LOC1489 2 15411 XP_086361.1 5 1038 CTGACCTCAGGT AGA TG 3 C c
b
18 GATCCACCCACC TGAGGTGGG AT CTTGA

TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC1491 1 4780 XP_097598.1 5 3376 CTGGGTTCAAGC TG 3 C b b

49 AGTTCTCTTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC TCTCTTGACGAACTT
GT
GAM3229 221 LOC1493 1 4008 NP_787072.1 3 431 CCGGGCCCAGGT A A 3 C c c

71 AGTCCTCCCACC TGAGGTGGGAG ATTGCTTG
TCAGCCTC ACTCCACCCTC TGATGGAC
C C
GAM3229 221 LOC1494 2 10865 XP_086546.1 3 341 ATCAATGTTATT A T T - 3 C c c
66 CTCCCTCCCACC TG GG GGGAGAAT GC TTGA
ACTTCCCA AC CC CCCTCTTA TG AACT
- T T T
GAM3229 221 LOC1494 2 12245 XP_086546.1 3 340 CGAAATCAATGT A T T - 3 C c c
66 TATTCTCCCTCC TG GG GGGAGAAT GC TTGA
CACCACTT AC CC CCCTCTTA TG AACT
- T T T
GAM3229 221 LOC1496 1 10537 XP_086647.4 5 115 CTGACCTCAGGT AGA TG 3 C c
c
70 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC1496 1 619 XP_097706.1 3 672 CAGGATTCAAGC TG 3 C b b
92 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGTCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 LOC1498 1 7976 XP_097751.2 5 28 CCAGGTTCACGC T T 3 C c c
21 CATTCTCCCGCC TGAGGTGGGAGAAT GC TGAA
TCGGGAGC GCTCCGCCCTCTTA CG ACTT
C C
GAM3229 221 LOC1501 1 2705 XP_097824.1 5 536 CCAGGCTCAAGC GA T 3 C c c

66 CATCTTTCCACC TGAGGTGGGA AT GCTTGA
TCAGCCTG ACTCCACCTT TA CGAACT
TC C
GAM3229 221 LOC1504 1 7746 XP_086906.1 3 678 CTGGCCTCAAGC A 3 C b b
07 AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 LOC1505 1 6798 XP_097917.1 3 210 CTGGGCTCAAGC TG A 3 C c c

87 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC1509 1 13021 XP_097977.2 5 1666 TGGGGTCAGAGT ---- TG - 3 C c
c
46 GGTTCTCCCAGG TGAGG TGGGAGAAT CT TGA

GCCTTCAA ACTTC ACCCTCTTG GA ACT
CGGG GT G
GAM3229 221 LOC1511 1 2041 XP_098019.1 5 149 GGCAAGGTCATT GA GCT 3 C c
c
96 AAATTTGCCACC TGAGGTGG GAATT TGA
TCACACGT ACTCCACC TTTAA ACT
G- ATT
GAM3229 221 LOC1512 1 2056 XP_098021.1 3 1977 CTGGTTTCAAGC A 3 C b b
01 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGAA
TCGGCCTC GCTCCACCCTC TAGCGAACTT
C
GAM3229 221 LOC1516 1 15373 NP_612144.1 3 2211 CTGGGGCCAAGT A TG A 3 C c
c
36 GATCCTCCCACC TGAGGTGGGAG AT CTTG
TCAGCCTC ACTCCACCCTC TA GAAC
C GT C
GAM3229 221 LOC1516 1 12136 XP_098100.2 5 2142 TTGGGCTCAAGC TG A 3 C c
c
57 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC1524 1 10071 XP_098231.1 3 583 CTGGGTTCAAGC TG 3 C b b
45 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TTAGCCTC ATTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC1526 1 10075 XP_011108.2 3 767 CCGGGTTCAAGC TG 3 C b b
20 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC1527 1 10075 XP_098257.1 5 175 CCGGGTTCAAGC TG 3 C b b
19 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC1528 1 6723 XP_098266.2 3 1759 CTGGGCTCAAGC AA 3 C b b
04 GAGCCTCCCACC TGAGGTGGGAG TTGCTTGA
TCGGTCTT GCTCCACCCTC AGCGAACT
CG
GAM3229 221 LOC1531 1 4758 XP_098318.1 5 1579 GTGTCTATTCCT GA TT TT 3 C c
c
39 GCTTCCTCCACC TGAGGTGG GAA GC GAA
TCACCTTG ACTCCACC CTT CG CTT
TC -- TC
GAM3229 221 LOC1541 1 4758 XP_098488.2 5 1579 GTGTCTATTCCT GA TT TT 3 C c
c
84 GCTTCCTCCACC TGAGGTGG GAA GC GAA
TCACCTTG ACTCCACC CTT CG CTT

```
                                                TC  --  TC
GAM3229  221   LOC1542 1  18644  XP_098505.1  5  176   CCAGGTTCAAGC    TG              3  C  b  b

         82                          AATTCTTCTGCC TGAGG  GGAGAATTGCTTGAA
                                    TCAGCCTC    ACTCC  CTTCTTAACGAACTT
                                                GT
GAM3229  221   LOC1548 1  1820   XP_098618.3  5  2893  CTGGGCTCAAGC    TG              3  C  b  b

         22                          AATTCTTCTGCC TGAGG  GGAGAATTGCTTGA
                                    TCAGCCTC    ACTCC  CTTCTTAACGAACT
                                                GT
GAM3229  221   LOC1548 2  10615  XP_098626.1  5  303   CTGAGCTCAGGT      -  A TG         3  C  c
b
         77                          GATCTGCCCACC TGAGGTGGG AGA T  CTTGA
                                    TCGGCCTC    GCTCCACCC TCT A  GGACT
                                                G   - GT
GAM3229  221   LOC1548 2  14674  XP_098626.1  3  1042  CTGGGCTCAAGC    T    A          3  C  b
b
         77                          AATCCTCCCTCC TGAGG GGGAG ATTGCTTGA
                                    TCAGCCTC    ACTCC CCCTC TAACGAACT
                                                T    C
GAM3229  221   LOC1550 2  6455   XP_098647.1  5  898   TCAGTCAAGGAC       AA  --         3  C  b  b
         32                          AAACCTCCCACC TGAGGTGGGAG  TTG  CTTGA
                                    TCACAGAC    ACTCCACCCTC  AAC  GAACT
                                                CA   AG
GAM3229  221   LOC1550 2  16924  XP_098647.1  3  1434  CTGTTTCAAACT       AA  C-         3  C  c
b
         32                          AAAGCTCCCACC TGAGGTGGGAG  TTG  TTGAA
                                    TCGAACAT    GCTCCACCCTC  AAT  AACTT
                                                GA   CA
GAM3229  221   LOC1572 1  5282   XP_033876.1  5  733   CTACCGCAGGCA       AA-     A       3  C  c  c

         26                          AAGGTTCCCACC TGAGGTGGGAG   TTGCTTG
                                    TTACTACA    ATTCCACCCTT   AACGGAC
                                                GGA      G
GAM3229  221   LOC1580 1  16148  XP_088442.1  5  1774  GGATTTTTAAAG       -    GC         3  C  c  c

         14                          ATTCTTCCCACC TGAGGTGGGA GAATT  TTGAA
                                    TTAATTTT    ATTCCACCCT CTTAG  AATTT
                                                T    A-
GAM3229  221   LOC1582 1  19341  XP_098908.1  5  91    CAGTGTCAGCAT  G       AT--   T       3  C  c
c
         57                          GACTCTCCCACT T AGGTGGGAGA    TGCT GA
                                    TGGAAAGA    G TTCACCCTCT    ACGA CT
                                          G        CAGT   -
GAM3229  221   LOC1583 1  18514  XP_048539.1  5  799   CTACCGCAGGCG       AA-     A       3  C  c
c
         73                          AAGGTTCCCACC TGAGGTGGGAG   TTGCTTG
                                    TTACTACA    ATTCCACCCTT   AGCGGAC
                                                GGA      G
```

GAM3229 221 LOC1584 1 2018 XP_098936.1 5 199 CCTGCTTCAAGC T 3 C b b
02 TATTCTCCCACC TGAGGTGGGAGAAT GCTTGAA
TCATCCTC ACTCCACCCTCTTA CGAACTT
T
GAM3229 221 LOC1584 1 6246 XP_098955.1 3 1275 CTGGATTCAAGC TG 3 C b b
76 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC1585 1 9836 XP_088606.1 5 1103 CCGGGTCCAAGC TG A A 3 C c
c
63 AATTCCCCTGCC TGAGG GG GAATTGCTTG
TCAGTCTC ACTCC CC CTTAACGAAC
GT C C
GAM3229 221 LOC1588 1 1389 XP_099000.1 5 34 CTGGGTTCAAGC TG 3 C b b
65 AATTCTCCTGTC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCT CCTCTTAACGAACTT
GT
GAM3229 221 LOC1611 1 10075 XP_101622.1 3 1207 CCGGGTTCAAGC TG 3 C b
b
45 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC1629 1 18580 XP_091890.6 3 439 CCAGGTTCATGC TG T 3 C c c
67 AATTCTCCTGCC TGAGG GGAGAATTGC TGAA
TCAGTCTC ACTCC CCTCTTAACG ACTT
GT T
GAM3229 221 LOC1632 2 8466 NP_775802.1 3 1727 CTGGGTTCACGC TG T 3 C c
c
27 AATTCTCCTGCC TGAGG GGAGAATTGC TGAA
TCAGCCTC ACTCC CCTCTTAACG ACTT
GT C
GAM3229 221 LOC1632 2 19173 NP_775802.1 3 3417 CCAGGTTCAAGC TG G 3 C c
c
27 AATTATCCTGCC TGAGG GGA AATTGCTTGAA
TCAGCCTC ACTCC CCT TTAACGAACTT
GT A
GAM3229 221 LOC1635 1 2345 NP_659471.1 5 153 CTGGCTTCAAGC 3 C b b
90 GATTCTCCCACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCACCCTCTTAGCGAACTT
GAM3229 221 LOC1641 1 17694 XP_089415.1 3 48 TTTGCATGCTAA - --- T A 3 C c c
53 AATTCTCCCGGC TGAGGT GGGAGAATT GC TG
CTCATCCT ACTCCG CCCTCTTAA CG AC
G AAT T G
GAM3229 221 LOC1962 1 12821 XP_116897.1 3 837 CCTGTCCACTGC AAT T- A 3 C c
c
14 ACTCCTCCCACC TGAGGTGGGAG TGC TG
TCATTTTT ACTCCACCCTC ACG AC
CTC TC C

GAM3229 221 LOC1964 1 10525 NP_775813.1 3 406 CTGTTCCAGCAC - G T-- T 3 C c c
63 CCTTCTCCCAGC TG AG TGGGAGAA TGCT GAA
TGCATTCC AC TC ACCCTCTT ACGA CTT
G G CCC C
GAM3229 221 LOC1973 1 8630 XP_113872.2 3 2308 CTGACCTCAAGT AGA TG 3 C c c
58 GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GAACT
ACC GT
GAM3229 221 LOC1998 1 940 XP_117153.1 3 126 CCAGGTTCAAGT TG 3 C b b
99 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAATGAACTT
GT
GAM3229 221 LOC2008 2 6951 XP_117289.1 3 825 ATGTTAGTCAGG G ATT 3 C c b
60 CTGGTCTCCACC TGAGGTGG AGA GCTTGA
TCAGGTGA ACTCCACC TCT CGGACT
- GGT
GAM3229 221 LOC2008 2 18373 XP_117289.1 3 1772 TCAGGCTCAAGC A 3 C b b
60 AATCCTCCCGCC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCGCCCTC TAACGAACT
C
GAM3229 221 LOC2008 1 13587 NP_789785.1 3 994 CCAGGTTCAAGC TG 3 C b b
95 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGGCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2009 1 5449 XP_114317.3 3 462 CTGACCTCAAGT - A TG 3 C c c
16 GATCTACCCACC TGAGGTGGG AGA T CTTGA
TCGGCTTC GCTCCACCC TCT A GAACT
A - GT
GAM3229 221 LOC2012 1 11829 NP_775818.1 3 736 CTGAGCTCAAAG A GC 3 C c c
92 GATCCTCCCACC TGAGGTGGGAG ATT TTGA
TCAGCCTC ACTCCACCCTC TAG AACT
C GA
GAM3229 221 LOC2018 2 542 XP_114393.1 3 157 TTGGCCTCAAGC T ------ A 3 C c c
68 AATCCTTCCTCT GAGGT GGGAG ATTGCTTGA
TTGGCCTC CTCCG CCTTC TAACGAACT
- GTTTCT C
GAM3229 221 LOC2018 2 7507 XP_114393.1 3 21 CCTAGGCTAAGC A A 3 C c c
68 AATCCTCCCACC TGAGGTGGGAG ATTGCTTG
TTAGCCTC ATTCCACCCTC TAACGAAT
C C
GAM3229 221 LOC2024 1 4939 NP_660346.1 5 108 CTGGTCTCAAGC T----- T 3 C c c
59 CATTCTCCCACC GAGGTGGGAGAAT GCTTGA
TCTGTCCT CTCCACCCTCTTA CGAACT
TCCTGT C
GAM3229 221 LOC2029 1 6398 XP_117486.2 3 2802 CCAGGTTCAAGC TG 3 C b b

34 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2035 2 828 XP_114719.1 3 2953 CCGGGTTCAAGC TG 3 C b b
47 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCCC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 LOC2035 2 17521 XP_114719.1 3 1438 CCTGGGTTCAAG G TG 3 C b b
47 TGATTCTCCACC TGAGGTGG AGAAT CTTGAA
TCAGCCTC ACTCCACC TCTTA GAACTT
- GT
GAM3229 221 LOC2192 1 14079 XP_166599.2 3 1100 CTGGGCTCAAGC TG A 3 C c c
93 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCGGCTTC GCTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC2197 1 4505 XP_167596.1 5 1117 ATGGGCTCAAGC A 3 C b b
31 AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 LOC2200 1 9729 NP_660352.1 3 972 CTGACCTCAGGT - A TG 3 C c c
74 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GGACT
G - GT
GAM3229 221 LOC2209 1 4661 XP_167629.1 5 991 CCACATCAAAAC AGA C- 3 C c c
80 AGTGTGTCCACC TGAGGTGGG ATTG TTGA
TCAGTCAC ACTCCACCT TGAC AACT
GTG AA
GAM3229 221 LOC2214 1 14485 XP_168138.1 3 494 AAAAATTCAAGC T----- T 3 C c c
05 ACTTCTTCCCTC TGAGG GGGAGAA TGCTTGAA
CACCCTCA ACTCC CCTTCTT ACGAACTT
CACCTC C
GAM3229 221 LOC2216 1 4758 XP_168071.1 5 1572 GTGTCTATTCCT GA TT TT 3 C c c
01 GCTTCCTCCACC TGAGGTGG GAA GC GAA
TCACCTTG ACTCCACC CTT CG CTT
TC -- TC
GAM3229 221 LOC2216 1 4068 XP_168131.1 5 1005 CGGAGCTCAAGC T----- GA 3 C c c
63 AGTCTTCCCACC GAGGTGGGA ATTGCTTGA
TTGGCCTC TTCCACCCT TGACGAACT
CTCCGG TC
GAM3229 221 LOC2219 1 17132 XP_168340.1 3 980 CTGGGCTCAAGT A TG 3 C c c
46 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCTTC ACTCCACCCTC TA GAACT
C GT

GAM3229 221 LOC2219 1 3459 XP_165859.1 3 424 CTGAGCTCAAGC A 3 C b b
60 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC2220 2 8135 XP_166594.2 5 620 CCAGGCTCAAGC G G A 3 C c
c
57 AATCCTACCATG TGA GTGG AG ATTGCTTGA
TCAGCCTT ACT TACC TC TAACGAACT
G A C
GAM3229 221 LOC2220 2 9877 XP_166594.2 5 804 CCAGGCTGAAGC A GA 3 C c
c
57 GATCCTCCCACC TGAGGTGGGAG ATTGCTT
TCAACCTC ACTCCACCCTC TAGCGAA
C GT
GAM3229 221 LOC2222 1 18096 XP_168473.1 5 505 CTGGGCTCAAGC GT G 3 C c
c
24 AATTCTCATGTC TGAG G GAGAATTGCTTGA
TCAGCCTC ACTC T CTCTTAACGAACT
TG A
GAM3229 221 LOC2529 1 17884 XP_170858.2 3 339 CTGGGTTCAAGT TG 3 C b b
83 GATTCTCCCACC TGAGGTGGGAGAAT CTTGAA
TCAACCTC ACTCCACCCTCTTA GAACTT
GT
GAM3229 221 LOC2551 1 1329 XP_171131.1 5 90 GGTTTTTCAAGC T G ---- - 3 C c c
31 AAATTCTGATAC GAGGT GG AGAATT GCTTGAA
CAACCTCT CTCCA CC TCTTAA CGAACTT
T A ATAG A
GAM3229 221 LOC2553 1 10003 XP_171105.3 5 245 ACTGGCTCAAGC - A 3 C b b
38 AATCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCGGTCTC GCTCCACCC TCT AACGAACT
G -
GAM3229 221 LOC2554 1 5123 XP_173150.1 5 444 CTGGGCTCAAGC A 3 C b b
58 GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAGCGAACT
C
GAM3229 221 LOC2559 2 829 XP_171083.2 5 924 CCAGGCTGAAGT TG GA 3 C c
c
75 GATTCTCCCATC TGAGGTGGGAGAAT CTT
TCAACCTC ACTCTACCCTCTTA GAA
GT GT
GAM3229 221 LOC2559 2 8135 XP_171083.2 5 740 CCAGGCTCAAGC G G A 3 C c
c
75 AATCCTACCATG TGA GTGG AG ATTGCTTGA
TCAGCCTT ACT TACC TC TAACGAACT
G A C
GAM3229 221 LOC2566 1 14850 XP_172864.1 3 920 CCGGGTTCAAGC - A 3 C b b
14 AATCCTCCCTGC TGAGGT GGGAG ATTGCTTGAA
CTCAGCCT ACTCCG CCCTC TAACGAACTT
T C
GAM3229 221 LOC2829 1 9471 XP_212607.1 5 96 CTGGCTTCAAAC GG C 3 C c c

19 AATTCTCATGCC TGAGGT GAGAATTG TTGAA
TCAGCCTC ACTCCG CTCTTAAC AACTT
TA A
GAM3229 221 LOC2829 1 9471 XP_212649.1 5 96 CTGGCTTCAAAC GG C 3 C c c
56 AATTCTCATGCC TGAGGT GAGAATTG TTGAA
TCAGCCTC ACTCCG CTCTTAAC AACTT
TA A
GAM3229 221 LOC2829 1 3959 XP_210840.1 5 480 CCAAGTTCAAGT G 3 C b b
80 AATTCTCCAGCC TGAGGT GGAGAATTGCTTGAA
TCAGCCTC ACTCCG CCTCTTAATGAACTT
A
GAM3229 221 LOC2829 2 3573 XP_208473.1 3 1046 TTGGGGTCAAGC A T 3 C b b

97 CATCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAGCTTT ACTCCACCCTC TA CGAACT
C C
GAM3229 221 LOC2829 2 18319 XP_208473.1 3 680 CTGGGCTCAAGC T----- AGA 3 C c
b
97 AATCAGCCCACC GAGGTGGG ATTGCTTGA
TCTGCCTC CTCCACCC TAACGAACT
CTCCGT GAC
GAM3229 221 LOC2830 1 7798 XP_210859.1 3 1884 CTGGGTTGAAGC TG GA 3 C c
c
31 AATTCTTCTGCC TGAGG GGAGAATTGCTT
TCAGCCTC ACTCC CTTCTTAACGAA
GT GT
GAM3229 221 LOC2830 1 9872 XP_208495.1 5 1187 TCTCCATCAAGC A 3 C b b
46 AATATTTCCACT TGAGGTGGGAG ATTGCTTGA
TCAACTTC ACTTCACCTTT TAACGAACT
A
GAM3229 221 LOC2830 1 8704 XP_210875.1 3 1447 CTGGGCTCAAGC G A 3 C b b

61 AATCCTCACACC TGAGGTG GAG ATTGCTTGA
TCAGCCTC ACTCCAC CTC TAACGAACT
A C
GAM3229 221 LOC2830 1 2783 XP_210885.1 5 1780 CTGGGTTCAAGC TG 3 C b b

89 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2831 1 12579 XP_210890.2 3 1450 CCTCCCTATTAA GAATT 3 C c
c
12 GCTCATCCCACC TGAGGTGGGA GCTTGA
TCATGGAT ACTCCACCCT CGAATT
ACT--
GAM3229 221 LOC2831 1 1059 XP_210895.1 3 898 CTGGACTCAAGC T----- - A 3 C c c
19 AATCTGCCCACC GAGGTGGG AGA TTGCTTGA
TTGGCCTT TTCCACCC TCT AACGAACT
TTCCGG G -
GAM3229 221 LOC2831 1 18374 XP_208516.1 3 844 CAGCCTTCAAGC T A------- T 3 C c
c

```
          20                        ATTCCATTACGC  GAGGTGGG       GAAT GCTTGAA
                                   CCCATCTC     CTCTACCC       CTTA CGAACTT
                                          -       CGCATTAC    -
GAM3229  221   LOC2831 1  13623  XP_208525.3  3  447   CCGGGTTCAAGC     TG    A            3  C  c
c
          30                        AACTCTCCTGCC TGAGG  GGAGA TTGCTTGAA
                                   TCAGCCTC     ACTCC  CCTCT AACGAACTT
                                              GT    C
GAM3229  221   LOC2831 1  3801   XP_210903.1  3  1044  CCAGGCTCAAGC      GG             3  C  b
b
          77                        AATTCTTACGCC TGAGGTG  AGAATTGCTTGA
                                   TCAGCCTC     ACTCCGC  TCTTAACGAACT
                                                 AT
GAM3229  221   LOC2832 1  7550   XP_208555.2  3  2050  CTGGGCTCAAGT        A  TG          3  C  c
c
          15                        GATCCTCCCACC TGAGGTGGGAG AT  CTTGA
                                   TCAGCCTC     ACTCCACCCTC TA  GAACT
                                                 C  GT
GAM3229  221   LOC2832 1  3960   XP_210962.1  3  405   TCTGGCTCAAGC        A            3  C  b  b
          93                        AATCCTCTCACT TGAGGTGGGAG ATTGCTTGA
                                   TCAGCCTC     ACTTCACTCTC TAACGAACT
                                                 C
GAM3229  221   LOC2833 1  620    XP_210973.1  3  68    CTGGGTTCAAGC       A            3  C  b  b
          23                        GATTCACCCACC TGAGGTGGG GAATTGCTTGAA
                                   TCAGCCTC     ACTCCACCC CTTAGCGAACTT
                                                 A
GAM3229  221   LOC2833 1  6969   XP_208620.1  5  72    GATTCTTCAAGC   G   GA  A          3  C  c  c

          36                        AATCACTATGTC TGA GTGG  GA TTGCTTGAA
                                   AACAGACA     ACT TATC  CT AACGAACTT
                                              G   A-  -
GAM3229  221   LOC2833 1  19818  XP_211007.1  3  1694  CAAAATTCAAGC     TG             3  C  b  b

          87                        AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                   TCAGCCTC     ACTCC  CCTCTTAACGAACTT
                                                 GT
GAM3229  221   LOC2833 1  9191   XP_211021.1  5  328   CTAGCCTCAAGG       AGA  G          3  C  c
c
          94                        GATCCGCCCACC TGAGGTGGG   ATT CTTGA
                                   TCAGTCTC     ACTCCACCC   TAG GAACT
                                                 GCC  G
GAM3229  221   LOC2834 1  14686  XP_211053.1  5  1107  CTGGGCTCAAGA       G  TG          3  C  c
c
          84                        GATTGTCCCACC TGAGGTGGGA AAT  CTTGA
                                   TCAGCCTA     ACTCCACCCT TTA  GAACT
                                                 G  GA
GAM3229  221   LOC2834 1  4891   XP_211062.1  3  735   CCAGGTTCAAGC     TG             3  C  b  b
          87                        AATTCTCCTGTC TGAGG  GGAGAATTGCTTGAA
                                   TCAGCCTC     ACTCT  CCTCTTAACGAACTT
                                                 GT
```

GAM3229 221 LOC2835 2 17293 XP_211110.1 3 983 CTGGCCTCAAGC T----- A 3 C c b

51 AATCCTTCCATC GAGGTGGGAG ATTGCTTGA
TTGGCCTC TTCTACCTTC TAACGAACT
CTCCGG C

GAM3229 221 LOC2835 2 18515 XP_211110.1 3 672 CTAGGCTCAAGC A T 3 C b b

51 CATCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAGCCTC ACTCCACCCTC TA CGAACT
C C

GAM3229 221 LOC2835 1 6798 XP_211095.1 5 481 CTGGGCTCAAGC TG A 3 C c c

75 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C

GAM3229 221 LOC2835 1 1550 XP_208741.1 3 1521 CCAGGTTCAAGG G 3 C b b

90 GATTCTCCCACC TGAGGTGGGAGAATT CTTGAA
TCAGCCTC ACTCCACCCTCTTAG GAACTT
G

GAM3229 221 LOC2836 1 10286 XP_208764.1 3 286 CCAGGTTCAAGC TG 3 C b b

41 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT

GAM3229 221 LOC2836 1 3252 XP_211144.1 5 129 CTGACCTCCGGT - A TG T 3 C c
c

55 GATCTGCCCACC TGAGGTGGG AGA T CT GA
TCAGTCTC ACTCCACCC TCT A GG CT
G - GT C

GAM3229 221 LOC2837 1 19012 XP_211183.3 5 593 CTCAACATCTGA AT------ C 3 C c
c

28 TTGTTTTCCACC TGAGGTGGGAGA TG TTGA
TCAGCCTG ACTCCACCTTTT AC AACT
GTTAGTCT -

GAM3229 221 LOC2837 1 1069 XP_208835.1 3 358 CTGGGTTCAAGC TG 3 C b b

67 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC2838 1 12163 XP_208899.1 5 348 TCGGCTTCAAGC TG 3 C b b

89 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC2839 1 8866 XP_208909.1 5 2613 CTGACTTCAGGT AGA TG 3 C c
c

28 GATCCACCCACC TGAGGTGGG AT CTTGAA
TCGGCCTT GCTCCACCC TA GGACTT
ACC GT

GAM3229 221 LOC2840 1 14012 XP_208958.2 3 1544 CCGGGTTCAAGC 3 C b b

01 AATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGCCCC ACTCCGCCCTCTTAACGAACTT

GAM3229 221 LOC2840 1 2783 XP_211298.1 3 75 CTGGGTTCAAGC TG 3 C b b
16 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2840 1 17544 XP_211309.1 3 744 CTGGGCTCAAGC T----- A 3 C c c
41 AATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGTCTC TTCCACCCTC TAACGAACT
CTCTGG C
GAM3229 221 LOC2840 2 7960 XP_208992.1 3 81 CTGACCTCAAGC T----- - A 3 C c c
63 GATCTGCCCACC GAGGTGGG AGA TTGCTTGA
TCCGTCTC CTCCACCC TCT AGCGAACT
CTCTGC G -
GAM3229 221 LOC2840 2 9729 XP_208992.1 3 376 CTGACCTCAGGT - A TG 3 C c c
63 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GGACT
G - GT
GAM3229 221 LOC2840 1 1935 XP_211321.1 3 1042 CTGGGTTCAAGC TG 3 C b b
74 AATTTTCTTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC TCTTTTAACGAACTT
GT
GAM3229 221 LOC2840 3 3941 XP_211324.1 3 1372 CTGAGCTCAAGC T----- GA 3 C c
c
95 AGTCTTCCCACC GAGGTGGGA ATTGCTTGA
TTGGCCTC TTCCACCCT TGACGAACT
CTCCGG TC
GAM3229 221 LOC2840 3 6762 XP_211324.1 3 901 CCTGGCTCAAGT A TG 3 C c c
95 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTT ACTCCACCCTC TA GAACT
C GT
GAM3229 221 LOC2840 3 11871 XP_211324.1 3 205 GGGTTCACAAGC GG A 3 C c
c
95 AATTCTCATGCC TGAGGT GAGAATTGCTTG
TCAGCCTC ACTCCG CTCTTAACGAAC
TA A
GAM3229 221 LOC2840 1 10075 XP_209008.3 3 257 CCGGGTTCAAGC TG 3 C b b
98 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2841 1 2800 XP_209019.1 5 472 CTGGGTTTGAGC A TG 3 C c c
01 AATCCTCCCACC TGAGGTGGGAG ATTGCT AA
TCAGCCTC ACTCCACCCTC TAACGA TT
C GT
GAM3229 221 LOC2841 4 4684 XP_211327.3 3 215 CTGGGTTCAAGT A 3 C b b

02 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGAA
TCAGCCTC ACTCCACCCTC TAATGAACTT
C
GAM3229 221 LOC2841 4 6048 XP_211327.3 3 70 CTGTGCTCAAGC A T 3 C b b
02 CATCCTCCCACC TGAGGTGGGAG AT GCTTGA
TTAGCCTC ATTCCACCCTC TA CGAACT
C C
GAM3229 221 LOC2841 4 9397 XP_211327.3 5 104 CTGGGTTCAAGC 3 C b b
02 AATTCTCCTACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCATCCTCTTAACGAACTT

GAM3229 221 LOC2841 4 15652 XP_211327.3 3 869 CTGGGTTCAAGG A G 3 C b b

02 GATCCTCCCACC TGAGGTGGGAG ATT CTTGAA
TCAGCCTC ACTCCACCCTC TAG GAACTT
C G
GAM3229 221 LOC2841 1 3205 XP_209024.1 3 459 CTTTCCTCAAGC T----- A 3 C c c
17 AATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGCCTC TTCCACCCTC TAACGAACT
CTCCGG C
GAM3229 221 LOC2841 1 2340 XP_209032.1 3 599 CTGGGTTTCAGC TG T 3 C b b

35 AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCAGCCTC ACTCC CCTCTTAACGA CTT
GT -
GAM3229 221 LOC2841 2 4891 XP_209059.1 5 481 CCAGGTTCAAGC TG 3 C b b
83 AATTCTCCTGTC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCT CCTCTTAACGAACTT
GT
GAM3229 221 LOC2841 2 9729 XP_209059.1 5 616 CTGACCTCAGGT - A TG 3 C c b

83 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GGACT
G - GT
GAM3229 221 LOC2841 1 18663 XP_209060.2 3 1439 CAAGTGGCCAGG - T G A 3 C c
c
86 AATTCTCCTCCT TG AGG GGGAGAATT CTTG
GCACCGGG AC TCC TCCTCTTAA GGAC
G - - C
GAM3229 221 LOC2841 1 6160 XP_211377.1 5 123 CCAGGTTCAAGC 3 C b b
91 AATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCGCCCTCTTAACGAACTT

GAM3229 221 LOC2842 1 8657 XP_211408.1 3 41 CCAGGTTCAAGC TG G 3 C c c
60 AATTCTGCTGTC TGAGG G AGAATTGCTTGAA
TCAGCTTC ACTCT C TCTTAACGAACTT
GT G
GAM3229 221 LOC2842 1 10075 XP_211412.1 5 1086 CCGGGTTCAAGC TG 3 C b
b
76 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2842 1 13205 XP_211421.1 5 246 CTGGGCTCAAGC GA 3 C b b

94 AATCTTCCCACC TGAGGTGGGA ATTGCTTGA
TCAGCCTC ACTCCACCCT TAACGAACT
TC
GAM3229 221 LOC2843 1 4957 XP_211425.1 5 1334 CCATGTTCAAGC TG 3 C b b
05 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2843 1 16453 XP_209162.1 3 1885 GGCAGATCAAGC TG 3 C b
b
17 AATTCTCTTGCC TGAGG GGAGAATTGCTTGA
TCAGCCTC ACTCC TCTCTTAACGAACT
GT
GAM3229 221 LOC2843 1 12960 XP_211434.1 5 794 AAAGGATCAAGC T--- - - 3 C c c
37 AATCTCTTGCCA GAGGTGG GAGA ATTGCTTGA
CCTCCCAG CTCCACC TTCT TAACGAACT
GACC G C
GAM3229 221 LOC2843 1 11166 NP_778233.2 5 41 ACCTTCGTTGCA A - T- 3 C c c
61 ACTTCTCCCATC TG GGTGGGAGAA TTGC TGAA
CGAGTCAC GC CTACCCTCTT AACG GCTT
- C TT
GAM3229 221 LOC2843 1 941 XP_211435.1 3 589 CCAGGTTCAAGC TG 3 C b b
62 AATTCTCTTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC TCTCTTAACGAACTT
GT
GAM3229 221 LOC2844 2 2187 XP_209200.1 5 1402 CTGGCCTTCAGC A T 3 C b b
21 AATCCTCCCACC TGAGGTGGGAG ATTGCT GAA
TCAACCTC ACTCCACCCTC TAACGA CTT
C -
GAM3229 221 LOC2844 2 10044 XP_209200.1 3 114 CCGGGTTCAAGC 3 C b b
21 GATTCTCCCATC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCTACCCTCTTAGCGAACTT

GAM3229 221 LOC2844 4 7372 XP_209198.1 3 936 TCAGGTTCAAGC TG 3 C b b
26 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2844 4 9681 XP_209198.1 3 370 CTGGGTTCAAGC GGG 3 C b
b
26 AATTCTACCTCA TGAGGT AGAATTGCTTGAA
GTCTCCTG ACTCCA TCTTAACGAACTT

GAM3229 221 LOC2844 4 19721 XP_209198.1 3 645 CTGACCTCAGGT - A TG 3 C c
b
26 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT

GAM3229 221 LOC2844 4 20053 XP_209198.1 3 781 CCGACCTCAAGT A TG 3 C c b

26 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCACCCTC ACTCCACCCTC TA GAACT
C GT

GAM3229 221 LOC2844 1 19435 XP_290862.1 3 146 TGGGGTTCAAGT A TG 3 C c c

36 GATCCTCCCACC TGAGGTGGGAG AT CTTGAA
TCAGCCTC ACTCCACCCTC TA GAACTT
C GT

GAM3229 221 LOC2844 1 9887 XP_209216.1 5 1011 CTGACCTCAAGC GT - A 3 C c c

54 AATCTGCTCGTC TGAG GGG AGA TTGCTTGA
TTAGCCTC ATTC CTC TCT AACGAACT
TG G -

GAM3229 221 LOC2844 1 18780 XP_211470.1 3 315 CCGGTTTCAAGC TG 3 C b b

56 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC2844 1 6969 XP_209221.1 5 73 GATTCTTCAAGC G GA A 3 C c c

64 AATCACTATGTC TGA GTGG GA TTGCTTGAA
AACAGACA ACT TATC CT AACGAACTT
G A- -

GAM3229 221 LOC2844 2 6824 XP_209225.1 3 1366 CTGGCCTCAAGC A 3 C b b

71 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TTAGCCTC ATTCCACCCTC TAACGAACT
C

GAM3229 221 LOC2844 2 6873 XP_209225.1 3 1226 CCGGGCTCAAGT AA TG 3 C c b

71 GACCCTCCCACC TGAGGTGGGAG T CTTGA
TCAGCCTC ACTCCACCCTC A GAACT
CC GT

GAM3229 221 LOC2844 1 6825 XP_211478.1 5 1925 TCTCCCCCAATC ----- A CTT 3 C c c

75 TCCTCAGCCACC TGAGGTGG GAGA TTG GA
TCAAATCA ACTCCACC CTCT AAC CT
GACTC - CCC

GAM3229 221 LOC2845 1 13007 XP_211500.1 3 1940 CTGAGCTCAGGC - A 3 C b b

12 AGTCTACCCACC TGAGGTGGG AGA TTGCTTGA
TCAGCCTC ACTCCACCC TCT GACGGACT
A -

GAM3229 221 LOC2845 1 16576 XP_209244.1 3 124 CTAAGCTCAAGT A TG 3 C c c

14 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT

GAM3229 221 LOC2845 1 4506 XP_209263.1 5 517 CTGGGCTCAAGC GA 3 C b b

```
          68                        AGTCATCCCACC TGAGGTGGGA ATTGCTTGA
                                   TCAGCCTC    ACTCCACCCT TGACGAACT
                                               AC
GAM3229  221   LOC2845 1  9877  XP_209278.3  5  133   CCAGGCTGAAGC        A     GA        3  C  c
c
          87                        GATCCTCCCACC TGAGGTGGGAG ATTGCTT
                                   TCAACCTC    ACTCCACCCTC TAGCGAA
                                               C      GT
GAM3229  221   LOC2846 1  15653 XP_211562.1  3  1166  CAGGGGGTTCAC     GG     CT         3  C  c
 c
          30                        AATTCTCAGCTT TGAGGT  GAGAATTG  TGAA
                                   CATCTGAG    ACTTCG  CTCTTAAC  ACTT
                                               A-       --
GAM3229  221   LOC2847 1  8135  XP_294994.1  5  742   CCAGGCTCAAGC   G   G A            3  C  c
c
          01                        AATCCTACCATG TGA GTGG AG ATTGCTTGA
                                   TCAGCCTT    ACT TACC TC TAACGAACT
                                               G   A C
GAM3229  221   LOC2847 1  1735  XP_211602.1  3  119   CTAGGTTCAAGC  A TG               3  C  c  c
          23                        AATTCTCCTGCC TG GG  GGAGAATTGCTTGAA
                                   CCAGCCTC    AC CC  CCTCTTAACGAACTT
                                               C  GT
GAM3229  221   LOC2847 1  9999  XP_211620.1  3  191   CTGTGGAGCCAG       G  AA     A        3  C  c
c
          45                        GCAGCCTCCACC TGAGGTGG AG  TTGCTTG
                                   TCACAAGA    ACTCCACC TC  GACGGAC
                                               - C-      C
GAM3229  221   LOC2848 1  18808 XP_211658.1  3  106   CTGGGCTCAGGC T-----         T        3  C  c
c
          37                        GCTTCTCCCACC      GAGGTGGGAGAA TGCTTGA
                                   TTGGCCTC          TTCCACCCTCTT GCGGACT
                                               CTCCGG          C
GAM3229  221   LOC2848 2  10282 XP_211672.1  3  129   CCAGGTTCAAGC                    3  C  b  b
          65                        AATTCTCCTACC TGAGGTGGGAGAATTGCTTGAA
                                   TCAGCCTC    ACTCCATCCTCTTAACGAACTT

GAM3229  221   LOC2848 2  16817 XP_211672.1  3  1450  GCCACTTTCTGC  A      AAT  TT        3  C  c
 b
          65                        ATGGCTCCCACC TG GGTGGGAG  TGC  GAA
                                   GCAGCTGA    AC CCACCCTC  ACG  CTT
                                               G       GGT  T-
GAM3229  221   LOC2849 1  18766 XP_211696.1  5  851   CTGGTCTCAAGC       -  A           3  C  b  b
          34                        AATCTGCCCGCC TGAGGTGGG AGA TTGCTTGA
                                   TCGGCCTC    GCTCCGCCC TCT AACGAACT
                                               G  -
GAM3229  221   LOC2850 1  18439 XP_211730.1  5  495   TTTGCTCACAGC  A T        -         3  C  c  c
          01                        AATTCTCCTTCT TG GG GGGAGAATTGCT TGA
                                   ACAGAGGA    AC TC TCCTCTTAACGA ACT
                                               A T          C
GAM3229  221   LOC2850 2  3961  XP_209440.1  3  2441  CTGGGTTCAAGC     GG              3  C  b  b
```

26 AATTCTCATGCC TGAGGT GAGAATTGCTTGAA
TCAGTCCC ACTCCG CTCTTAACGAACTT
TA
GAM3229 221 LOC2850 2 6793 XP_209440.1 3 2575 CTGACTTCAAGT T----- - A TG 3 C c
b
26 GATCTGCCCACC GAGGTGGG AGA T CTTGAA
TCTGCCTC CTCCACCC TCT A GAACTT
CTCCGT G - GT
GAM3229 221 LOC2850 1 16976 XP_211739.1 3 71 CTGGCTTCAAGC T----- A 3 C c c
33 AATCCTTCCACT GAGGTGGGAG ATTGCTTGAA
TTGGCCTT TTTCACCTTC TAACGAACTT
TTCCGG C
GAM3229 221 LOC2850 1 9309 XP_211753.1 5 439 CTGGTTTCAAGC A 3 C b b
58 AATCCTCCTACC TGAGGTGGGAG ATTGCTTGAA
TCAGCTTC ACTCCATCCTC TAACGAACTT
C
GAM3229 221 LOC2850 1 2096 XP_209464.1 3 1046 CTGGCCTCAAAC A TGC 3 C c
c
83 TATCCTCCCACC TGAGGTGGGAG AT TTGA
TTAGCCTC ATTCCACCCTC TA AACT
C TCA
GAM3229 221 LOC2850 2 9680 XP_209465.1 3 229 CCGACCTCAGGT AGA TG 3 C c
b
88 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC2850 2 10075 XP_209465.1 3 101 CCGGGTTCAAGC TG 3 C b b
88 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2851 1 14792 XP_211777.1 5 389 CTGGACTCAAGC T----- - A 3 C c c
36 AATCTGCCCACC GAGGTGGG AGA TTGCTTGA
TTGCCTCC TTCCACCC TCT AACGAACT
CCTCCG G -
GAM3229 221 LOC2852 1 6398 XP_209521.1 5 137 CCAGGTTCAAGC TG 3 C b b
21 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2852 3 7578 XP_211813.1 3 782 CTGAGCTCAAGC TG A 3 C c b
31 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC2852 3 8476 XP_211813.1 3 1316 CTGGAGTCCAGC A T 3 C b b
31 AATCCTCCCACC TGAGGTGGGAG ATTGCT GA
TCAACCTC ACTCCACCCTC TAACGA CT
C C

GAM3229 221 LOC2852 3 16034 XP_211813.1 3 948 CCAGGCTCATGT A TG T 3 C c b
31 GATCCTCCCACC TGAGGTGGGAG AT C TGA
TCAGCCTC ACTCCACCCTC TA G ACT
C GT T
GAM3229 221 LOC2852 1 2404 XP_209554.1 3 458 CTGGGTTCAAAC GG C 3 C c c
99 AATTCTCATGCC TGAGGT GAGAATTG TTGAA
TCAGCCTC ACTCCG CTCTTAAC AACTT
TA A
GAM3229 221 LOC2853 1 16422 XP_211844.1 3 657 CTGGGCTCAAGC T----- A 3 C c c
34 AATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGCTTC TTCCACCCTC TAACGAACT
CTTCGG C
GAM3229 221 LOC2853 1 4229 XP_211853.1 5 42 CTGGGCTCAAGC T----- A 3 C c c
44 AATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TCCCAGTG CTCCACCCTC TAACGAACT
GTGACC C
GAM3229 221 LOC2853 1 2368 XP_211854.1 3 1069 CTGGGCTCAAGC T----- AGA 3 C c c
45 AATCCACCCACC GAGGTGGG ATTGCTTGA
TCTGCCTC CTCCACCC TAACGAACT
CTCCGT ACC
GAM3229 221 LOC2853 1 14046 XP_211870.1 5 1982 TACTTTTCAAGC GG GGA - 3 C c c
63 AAATTCAACAAA TGA TG GAATT GCTTGAA
TCAGTGTA ACT AC CTTAA CGAACTT
AA AA- A
GAM3229 221 LOC2853 1 10964 XP_209593.1 3 1267 CTGGGCTCAAGC A 3 C b b
98 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC2855 1 18955 XP_209654.1 5 650 AAAGGTTAAGAT - T - 3 C c c
40 GATTCTCCCTCC TG AGG GGGAGAATTG CTTGA
TGCAGCCT AC TCC CCCTCTTAGT GAATT
G T A
GAM3229 221 LOC2855 1 12848 XP_211947.1 3 1244 GTGCTTAAGAAT AATTG-- 3 C c c
87 GGGATTCCCACC TGAGGTGGGAG CTTGA
TCAGTTTA ACTCCACCCTT GAATT
AGGGTAA
GAM3229 221 LOC2855 2 6398 XP_209671.1 3 326 CCAGGTTCAAGC TG 3 C b b
89 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2855 2 11982 XP_209671.1 3 780 CCAGGTTCAAGC T 3 C b b
89 AATTCTCCTTCC TGAGG GGGAGAATTGCTTGAA
TCAGCCTC ACTCC TCCTCTTAACGAACTT

T
GAM3229 221 LOC2856 1 14142 XP_211959.1 5 909 CTGGGTTCAAGT AA 3 C b b
26 AACCCTCCCACC TGAGGTGGGAG TTGCTTGAA
TCAGCTTT ACTCCACCCTC AATGAACTT
CC
GAM3229 221 LOC2856 1 1800 XP_209693.1 5 3987 CCCAGTTCAAGC TG 3 C b b
38 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2856 1 14636 XP_211980.1 5 70 CTGAGCTCAAGC GG 3 C b b
83 AATTCTCATGCC TGAGGT GAGAATTGCTTGA
TCAGCCTC ACTCCG CTCTTAACGAACT
TA
GAM3229 221 LOC2857 1 19086 XP_211997.1 5 408 CCAGGCTCAAGT A TG 3 C c
c
22 GATCCTTCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCTTC TA GAACT
C GT
GAM3229 221 LOC2857 2 8764 XP_209743.1 3 1426 CTAGGCTCAAGC G 3 C b b
44 AATTCTCGTGCC TGAGGTG GAGAATTGCTTGA
TCAGCCTC ACTCCGT CTCTTAACGAACT
G
GAM3229 221 LOC2857 2 17380 XP_209743.1 3 1553 CTGACCTCAAGC T----- AG 3 C c
b
44 AATTTGCCCACC GAGGTGGG AATTGCTTGA
TCGTTCTC CTCCACCC TTAACGAACT
CTCTTG GT
GAM3229 221 LOC2857 2 6072 XP_209742.1 5 1479 GCCTCCCGGGCA - T A 3 C c c
47 CTTCTCCCCACC TGAGGTGGG AGAA TGCTTG
TCGGCCCC GCTCCACCC TCTT ACGGGC
C C C
GAM3229 221 LOC2857 2 13313 XP_209742.1 3 2242 CCAGGCTCAAGC G A 3 C c
c
47 AATCCTTGTGCC TGAGGTG GAG ATTGCTTGA
TCAGCCTC ACTCCGT TTC TAACGAACT
G C
GAM3229 221 LOC2857 1 4758 XP_212010.1 5 1579 GTGTCTATTCCT GA TT TT 3 C c
c
49 GCTTCCTCCACC TGAGGTGG GAA GC GAA
TCACCTTG ACTCCACC CTT CG CTT
TC -- TC
GAM3229 221 LOC2857 1 10409 XP_209750.1 3 432 CCGGTTTCAAGC G G 3 C c c
60 AGTTCTCCAGCA TGA GT GGAGAATTGCTTGAA
TCAGCCTC ACT CG CCTCTTGACGAACTT
A A
GAM3229 221 LOC2858 1 6398 XP_209777.1 3 296 CCAGGTTCAAGC TG 3 C b b
22 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA

TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2858 1 9471 XP_212057.1 5 96 CTGGCTTCAAAC GG C 3 C c c
35 AATTCTCATGCC TGAGGT GAGAATTG TTGAA
TCAGCCTC ACTCCG CTCTTAAC AACTT
TA A
GAM3229 221 LOC2858 1 10492 XP_212041.1 5 2553 GCCAGCCCACAG A TG A 3 C c
c
42 GGTTCCCCCACC TGAGGTGGG GAAT CTTG
TCAGAGTT ACTCCACCC CTTG GGAC
C -- A
GAM3229 221 LOC2858 1 10152 XP_212034.1 3 247 CCAGGTTTAAGC GG 3 C c c

43 AATTCTCATGCT TGAGGT GAGAATTGCTTGAA
TCAGCCTA ACTTCG CTCTTAACGAATTT
TA
GAM3229 221 LOC2858 1 10601 XP_212045.1 5 791 CCAGGTTCAAGC G A 3 C c c

47 AAGTCTTGTGCC TGAGGTG GAGA TTGCTTGAA
TCAGTTTA ACTCCGT TTCT AACGAACTT
G G
GAM3229 221 LOC2859 1 8542 XP_209822.1 3 385 CCGGGTCCCTGT TG TT- 3 C c
c
22 GATTTTCCCACC TGAGGTGGGAGAAT C GA
TCAGCCTC ACTCCACCCTTTTA G CT
GT TCC
GAM3229 221 LOC2859 1 7843 XP_212104.1 3 230 CTGGCCTCAAGC A 3 C b b
23 AATCCTCCTACC TGAGGTGGGAG ATTGCTTGA
TCGGCTTT GCTCCATCCTC TAACGAACT
C
GAM3229 221 LOC2859 2 6763 XP_209818.1 5 333 CTTGGCTCAAGT TG 3 C b b
30 GATTCTCCCACC TGAGGTGGGAGAAT CTTGA
TTAGCCTC ATTCCACCCTCTTA GAACT
GT
GAM3229 221 LOC2859 2 18902 XP_209818.1 5 204 CTGGGCTCAAGC A 3 C b b
30 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTA ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC2859 1 10240 XP_212099.1 5 2320 ATCTTTTCAAGC T---- G - 3 C c c

58 ATGTTCTACCAC GAGGTGG AGAAT TGCTTGAA
CTTGGAAG TTCCACC TCTTG ACGAACTT
GAAGG A T
GAM3229 221 LOC2859 1 12547 XP_209833.1 3 424 CTGATCTCAGGT AGA TG 3 C c
c
61 GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC2859 1 1953 XP_209842.1 3 2363 AATCCTCCTCAG - GAA 3 C c c

```
          69                    GCAGGTCCCACC TG AGGTGGGA   TTGCTTGA
                               TGCAGGCC    AC TCCACCCT   GACGGACT
                                     G      G--
GAM3229  221   LOC2859 1  9694  XP_212105.1  3  925   CCGGGTTCAAGC     GG              3  C  b  b

          72                    AATTCTCATGCC TGAGGT  GAGAATTGCTTGAA
                               TCAGCCTC    ACTCCG  CTCTTAACGAACTT
                                     TA
GAM3229  221   LOC2859 1  11099 XP_212120.1  3  789   CTGGCCTCAAGC  G      A          3  C  b  b

          99                    AATCCTCCCACC T AGGTGGGAG ATTGCTTGA
                               TGAGCCCC    A TCCACCCTC TAACGAACT
                                     G       C
GAM3229  221   LOC2860 1  3117  XP_209866.1  3  1700  CCAGGCTTAAGC    TG              3  C  b  b

          29                    AATTCTCCTGCC TGAGG  GGAGAATTGCTTGA
                               TCAGCCTC    ACTCC  CCTCTTAACGAATT
                                     GT
GAM3229  221   LOC2860 1  15856 XP_212158.1  3  510   ACTTCCTTCAGG     ---      G        3  C  c  c
          58                    GATTCTCCCTAA TGAGGT   GGGAGAATT CTTGAA
                               ATTTTAGC    ATTTTA   CCCTCTTAG GGACTT
                                     AAT       -
GAM3229  221   LOC2860 2  8047  XP_212163.1  5  1456  CCAGGTTCAGGC    TG              3  C  b  b

          78                    AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                               TCAGCCTC    ACTCC  CCTCTTAACGGACTT
                                     GT
GAM3229  221   LOC2860 2  13047 XP_212163.1  3  971   CTGGCCTCAAGC        A          3  C  b  b
          78                    AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
                               TCGGCCTC    GCTCCACCCTC TAACGAACT
                                     C
GAM3229  221   LOC2861 1  5123  NP_848630.1  3  259   CTGGGCTCAAGC        A          3  C  b  b
          03                    GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
                               TCAGCCTC    ACTCCACCCTC TAGCGAACT
                                     C
GAM3229  221   LOC2861 1  5123  XP_209897.1  3  259   CTGGGCTCAAGC        A          3  C  b  b
          03                    GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
                               TCAGCCTC    ACTCCACCCTC TAGCGAACT
                                     C
GAM3229  221   LOC2861 1  5503  XP_212219.1  5  207   CCAGGCTCAAGT        A  TG          3  C  c  c

          86                    GATCCTCCCACC TGAGGTGGGAG AT  CTTGA
                               TCAGTCTC    ACTCCACCCTC TA  GAACT
                                     C  GT
GAM3229  221   LOC2861 1  5905  XP_212217.1  3  192   CTGGACTCAAGT        A  TG          3  C  c  c
          91                    GATCCTCCCACC TGAGGTGGGAG AT  CTTGA
                               TCAGCCTC    ACTCCACCCTC TA  GAACT
                                     C  GT
GAM3229  221   LOC2862 1  15150 XP_209941.1  3  1107  CTGACGTCAAGC    -   A  A          3  C  b
b
```

07 AATCCCCCAGCC TGAGG TGGG GA TTGCTTGA
TCGGCCTC GCTCC ACCC CT AACGAACT
G C -
GAM3229 221 LOC2862 2 12103 XP_212230.1 3 1717 TTGGGTTCAAGC TG 3 C b b

08 AATTCTTCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CTTCTTAACGAACTT
GT
GAM3229 221 LOC2862 2 18679 XP_212230.1 3 1516 CCAGGTTCAAGC T-- --- G 3 C c
b
08 AATTCTGCCTCA GAGGT GG AGAATTGCTTGAA
GCCTCCCA CTCCG CC TCTTAACGAACTT
ACC ACT G
GAM3229 221 LOC2863 1 10661 XP_303033.1 5 113 CCTTTATCTCCA AGA C A 3 C c
c
34 ACAATATCCACC TGAGGTGGG ATTG TTG
TCACCAAA ACTCCACCT TAAC AAC
A-- - C
GAM3229 221 LOC2863 1 10075 XP_212278.1 3 472 CCGGGTTCAAGC TG 3 C b b

41 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC2863 1 13314 XP_212290.1 5 1160 CCGGGTTCACGG T - 3 C b b

56 CATTCTCCCGCC TGAGGTGGGAGAAT GCT TGAA
TCAGCCTC ACTCCGCCCTCTTA CGG ACTT
- C
GAM3229 221 LOC2863 1 16003 XP_212288.1 3 581 TGTGCTCAGGAA A ATTG- 3 C c
c
59 ACCTCACCCACC TGAGGTGGG GA CTTGA
TCAGCCCT ACTCCACCC CT GGACT
A CCAAA
GAM3229 221 LOC2864 1 1364 XP_212310.1 5 560 CCGGATTCAAGC TG 3 C b b
01 AGTTTTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTTTTGACGAACTT
GT
GAM3229 221 LOC2864 1 6220 XP_210047.1 3 867 CTGGCCTCAAGC A 3 C b b
35 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCATC ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC2864 1 15960 XP_210050.1 5 97 TTGGCCTCAAGC T ----- A 3 C c c
37 AATCCTCCTCCA GAGGT GGGAG ATTGCTTGA
GAGCCTCC CTCCG TCCTC TAACGAACT
C AGACC C
GAM3229 221 LOC2864 1 9998 XP_212319.1 3 113 CTGTGCTCAAGC TG 3 C b b
41 AATTCTCCTGCC TGAGG GGAGAATTGCTTGA
TCAGCTTC ACTCC CCTCTTAACGAACT
GT
GAM3229 221 LOC3385 1 16337 XP_290473.1 3 1051 CTGGCCTCAAGC G A 3 C c
c

75 AATGTTCCCATG TGA GTGGGAG ATTGCTTGA
TCAGCCTA ACT TACCCTT TAACGAACT
G G
GAM3229 221 LOC3386 1 5199 XP_294668.1 5 305 ATTGCCTCAGCC T----- A C 3 C c c

12 AAGTCTCCCACC GAGGTGGGAGA TTG TTGA
TCTCTGCT CTCCACCCTCT AAC GACT
TCGTCT G C
GAM3229 221 LOC3386 2 2827 XP_290494.1 3 2002 CCTGTTCCTTGT ---- TT- 3 C c c
45 AATTCTCCCACT TGAG GTGGGAGAATTGC GAA
GTTCTCAG ACTC CACCCTCTTAATG CTT
TTGT TTC
GAM3229 221 LOC3386 2 13444 XP_290494.1 3 2494 CCAGGTTCAAGT T---- - TG 3 C c
c
45 GATTCTCCCTGC GAGGT GGGAGAAT CTTGAA
CTCCGCCT CTCCG CCCTCTTA GAACTT
TCCGC T GT
GAM3229 221 LOC3387 2 8135 XP_211595.2 5 559 CCAGGCTCAAGC G G A 3 C c
c
09 AATCCTACCATG TGA GTGG AG ATTGCTTGA
TCAGCCTT ACT TACC TC TAACGAACT
G A C
GAM3229 221 LOC3387 2 9877 XP_211595.2 5 743 CCAGGCTGAAGC A GA 3 C c
c
09 GATCCTCCCACC TGAGGTGGGAG ATTGCTT
TCAACCTC ACTCCACCCTC TAGCGAA
C GT
GAM3229 221 LOC3387 1 9515 XP_290570.1 3 946 CCAGGTTCAAGC 3 C b b
73 GATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGTAGC ACTCCGCCCTCTTAGCGAACTT

GAM3229 221 LOC3387 1 14539 NP_848633.1 5 50 CTGACCTCAGGT AGA TG 3 C c
c
99 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT
GAM3229 221 LOC3388 1 19436 XP_290588.1 3 321 CTGAGCTCAAGC T AA 3 C b
b
17 AACCCTCCCTCC TGAGG GGGAG TTGCTTGA
TCAGCCTT ACTCC CCCTC AACGAACT
T CC
GAM3229 221 LOC3388 1 16899 XP_294731.1 3 291 TAACTTCACTGC TG - T- 3 C c c

64 AATTCTGTTTCC TGAGG GG AGAATTGC TGAA
CTCATTTG ACTCC TT TCTTAACG ACTT
CT G TC
GAM3229 221 LOC3388 1 8395 XP_294740.1 5 768 TTGACCTCAGGT AGA TG 3 C c
c
99 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT

ACC GT

GAM3229 221 LOC3389 1 8024 XP_290610.1 3 502 CCTCAGTAAAAG G ----- T 3 C c c
17 TCTTCTCCCAAC TGAG TGGGAGAA TTGCT GA
TCAGCCTG ACTC ACCCTCTT AATGA CT
A CTGAA -

GAM3229 221 LOC3389 1 1069 XP_290663.1 3 358 CTGGGTTCAAGC TG 3 C b b
91 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3389 1 1069 XP_290659.1 3 358 CTGGGTTCAAGC TG 3 C b b
99 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3390 1 9695 XP_294802.2 3 955 CTGGGTTCAAGA TG G 3 C c c
77 AATTCTCCTGCC TGAGG GGAGAATT CTTGAA
TTAGCCTC ATTCC CCTCTTAA GAACTT
GT A

GAM3229 221 LOC3390 1 9304 XP_290692.1 3 2021 CTGGCCTCAAGC 3 C b b
78 AATTCTCCCACT TGAGGTGGGAGAATTGCTTGA
TCAGCCTC ACTTCACCCTCTTAACGAACT

GAM3229 221 LOC3390 1 13820 XP_290239.1 5 1958 TGTTTATCAAGC G GG A 3 C c
c
91 AATGCTCAGCTT T AGGT GAG ATTGCTTGA
GAAGAATA A TTCG CTC TAACGAACT
G A- G

GAM3229 221 LOC3391 1 2752 XP_294825.1 5 507 CCGGGTTCAAGC T-- - -- 3 C c c
46 AATTCTGTCTCA GAGG TGGGA GAATTGCTTGAA
GCCTCCCG CTCC ACTCT CTTAACGAACTT
GCC G GT

GAM3229 221 LOC3391 1 19259 XP_290742.1 3 733 CTGGGTTCAAGC TG 3 C b b
78 AATTTTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTTTTAACGAACTT
GT

GAM3229 221 LOC3392 1 7031 XP_290756.1 3 415 CCAAGCTCAAGC T----- TG A 3 C c
c
01 AATCCTCCTGCC GAGG GGAG ATTGCTTGA
TCTGCCTC CTCC CCTC TAACGAACT
CTCCGT GT C

GAM3229 221 LOC3392 1 2800 XP_290762.2 5 472 CTGGGTTTGAGC A TG 3 C c c
16 AATCCTCCCACC TGAGGTGGGAG ATTGCT AA
TCAGCCTC ACTCCACCCTC TAACGA TT
C GT

GAM3229 221 LOC3392 1 2800 XP_294900.2 5 472 CTGGGTTTGAGC A TG 3 C c c
82 AATCCTCCCACC TGAGGTGGGAG ATTGCT AA
TCAGCCTC ACTCCACCCTC TAACGA TT

C GT
GAM3229 221 LOC3392 2 2800 XP_294899.2 5 1241 CTGGGTTTGAGC A TG 3 C c b
83 AATCCTCCCACC TGAGGTGGGAG ATTGCT AA
TCAGCCTC ACTCCACCCTC TAACGA TT
C GT
GAM3229 221 LOC3392 2 12131 XP_294899.2 5 1376 TGGGGTTCAAGC - A 3 C b b
83 AATCTGCCCACC TGAGGTGGG AGA TTGCTTGAA
TCAGCCTC ACTCCACCC TCT AACGAACTT
G -
GAM3229 221 LOC3393 2 9527 XP_290830.1 3 431 CCGGGCTCAAGT TG 3 C b b
25 GATTCTCCCGCC TGAGGTGGGAGAAT CTTGA
TCAGTCTC ACTCCGCCCTCTTA GAACT
GT
GAM3229 221 LOC3393 2 20083 XP_290830.1 5 37 CTGGGCTCAAGC - A 3 C b b
25 GATCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCAGTCTC ACTCCACCC TCT AGCGAACT
G -
GAM3229 221 LOC3394 1 17876 XP_294926.1 3 845 CTGGGCTCAAGT TT 3 C b b
00 GCTTCTCCCACC TGAGGTGGGAGAA GCTTGA
TCAGCCTC ACTCCACCCTCTT TGAACT
CG
GAM3229 221 LOC3394 2 537 XP_290907.2 3 897 CCGGGCTCAAGC TG A 3 C c c
59 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCTCC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC3394 2 4044 XP_290907.2 3 1032 CTGAACTCAGGC - ATT 3 C c c
59 TGTCTGCCCACC TGAGGTGGG AGA GCTTGA
TCAGCCTC ACTCCACCC TCT CGGACT
G GT-
GAM3229 221 LOC3394 2 1590 XP_290919.1 3 1446 CTTGGTTCAAGC TG 3 C b b
92 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC3394 2 3503 XP_290919.1 3 1140 CTGGGTGCAAGC TG G A 3 C c b
92 AATTATCCTGCC TGAGG GGA AATTGCTTG
TCAGCCTC ACTCC CCT TTAACGAAC
GT A G
GAM3229 221 LOC3395 1 18440 XP_295005.1 3 1245 ATGGCTTCAAGG - AA G 3 C c c
77 GAAACTCCCACC TGAGG TGGGAG TT CTTGAA
CTCAATAT ACTCC ACCCTC AG GAACTT
C AA G
GAM3229 221 LOC3396 1 18533 XP_295014.1 3 1520 CCAGGCTCAAGA A G 3 C b b
00 AATCCTCCCACC TGAGGTGGGAG ATT CTTGA

TCAGCCTC ACTCCACCCTC TAA GAACT
C A
GAM3229 221 LOC3396 1 19918 XP_293210.2 5 176 CTGGGGTCCAGC AGAAT T 3 C c c
35 GCTGCCCCCACC TGAGGTGGG TGCT GA
TCAACTCC ACTCCACCC GCGA CT
CCGTC C
GAM3229 221 LOC3396 1 19789 XP_295032.1 5 224 CTGGGCTCACAC A CT 3 C c c
85 AATCCTTCCACC TGAGGTGGGAG ATTG TGA
TCAGCATC ACTCCACCTTC TAAC ACT
C AC
GAM3229 221 LOC3396 2 7230 XP_295035.1 5 893 CTGGGTTCAAGC 3 C b b
94 AATTCTCCCACC TGAGGTGGGAGAATTGCTTGAA
TCAGCTGG ACTCCACCCTCTTAACGAACTT
GAM3229 221 LOC3396 2 12466 XP_295035.1 5 22 CTGACCTTAAGT AGA TG 3 C c b
94 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GAATT
ACC GT
GAM3229 221 LOC3397 1 9730 XP_295041.1 5 939 CTTCGTTCAAGC 3 C b b
20 GATTCTCCCACC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCACCCTCTTAGCGAACTT
GAM3229 221 LOC3397 1 7722 XP_295048.1 5 436 TAGTTATTAAGC AG GG -- 3 C c c
38 AATTGACTTTCA TG GTG AG AATTGCTTGA
CACCAACT AC CAC TC TTAACGAATT
CA TT AG
GAM3229 221 LOC3397 1 13172 XP_295053.1 3 33 CCCAGCTCAAGT A TG 3 C c c
51 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 LOC3398 1 10537 XP_295072.1 3 1686 CTGACCTCAGGT AGA TG 3 C c c
03 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC3398 1 11926 XP_295070.1 3 886 ACCACCCTCACC A -- CT 3 C c c
07 AATTCTCTCAAT TG GG TGGGAGAATTG TGA
CCCCATGA AC CC ACTCTCTTAAC ACT
C TA C-
GAM3229 221 LOC3398 1 17851 XP_291020.1 5 1831 CTGGCCTCAAGC AGAAT 3 C c c
09 ACTCCACCCACC TGAGGTGGG TGCTTGA
TCGGCCTC GCTCCACCC ACGAACT
ACCTC

GAM3229 221 LOC3398 1 10359 XP_295074.1 5 144 CTGGGCTCAAGC TG AGA 3 C c c

13 AATCCACCTGCT TGAGG GG ATTGCTTGA
TCAGCCTT ACTTC CC TAACGAACT
GT ACC

GAM3229 221 LOC3398 1 17042 XP_291031.1 5 90 CTGGGCTCGAGC 3 C b b

33 AATTCTCCCACC TGAGGTGGGAGAATTGCTTGA
TCAGCCTA ACTCCACCCTCTTAACGAGCT

GAM3229 221 LOC3399 1 8327 XP_291065.1 3 1656 CCGACCTCAGGT AGA TG 3 C c c

07 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
GCC GT

GAM3229 221 LOC3399 1 11400 XP_295107.1 5 2178 AGCTGCGTCAGA AGAA CT 3 C c c

42 CAACGACCCACC TGAGGTGGG TTG TGA
TCATCCCC ACTCCACCC AAC ACT
AGC- AG

GAM3229 221 LOC3401 2 8135 XP_291150.1 5 559 CCAGGCTCAAGC G G A 3 C c c

25 AATCCTACCATG TGA GTGG AG ATTGCTTGA
TCAGCCTT ACT TACC TC TAACGAACT
G A C

GAM3229 221 LOC3401 2 9877 XP_291150.1 5 743 CCAGGCTGAAGC A GA 3 C c c

25 GATCCTCCCACC TGAGGTGGGAG ATTGCTT
TCAACCTC ACTCCACCCTC TAGCGAA
C GT

GAM3229 221 LOC3401 1 2497 XP_291153.1 3 2335 CTGATCTCAAGT - A TG 3 C c c

38 GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GAACT
G - GT

GAM3229 221 LOC3401 1 1195 XP_291160.1 3 126 GTAACCTCAAGT A TG 3 C c c

70 GATGCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
G GT

GAM3229 221 LOC3402 1 8135 XP_291203.1 5 559 CCAGGCTCAAGC G G A 3 C c c

27 AATCCTACCATG TGA GTGG AG ATTGCTTGA
TCAGCCTT ACT TACC TC TAACGAACT
G A C

GAM3229 221 LOC3402 1 20021 XP_291211.1 3 100 CCAGGTTCAAGC TG 3 C b b

49 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCACCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3402 1 8135 XP_291214.1 5 1226 CCAGGCTCAAGC G G A 3 C c c

```
          90                          AATCCTACCATG TGA GTGG AG ATTGCTTGA
                                     TCAGCCTT    ACT TACC TC TAACGAACT
                                           G   A C
GAM3229  221   LOC3403 1  1655  XP_295212.1  5  198   ATTGGCTCCCAA       A  TT   A       3  C  c  c

          21                          GCTTCCCCCACC TGAGGTGGG GAA  GCTTG
                                     TCATATGT    ACTCCACCC CTT  CGAAC
                                           C  --   C
GAM3229  221   LOC3403 1  1473  XP_291269.1  3  1442  CCGGATTCAAGC    T              3  C  b  b
          90                          AATTCTCCTTCC TGAGG GGGAGAATTGCTTGAA
                                     TCAGCCTC    ACTCC TCCTCTTAACGAACTT
                                           T
GAM3229  221   LOC3404 2  7368  XP_295240.1  3  232   CTGGGTTCAAGC T-----    G           3  C  c  b

          14                          AGTTCTCGTGCC     GAGGTG GAGAATTGCTTGAA
                                     TCCCTGAG         CTCCGT CTCTTGACGAACTT
                                           GAGTCC    G
GAM3229  221   LOC3404 2  13658 XP_295240.1  3  359   CTGAGGTCAGGC       -  A          3  C  b  b
          14                          AATCTGCCCACC TGAGGTGGG AGA TTGCTTGA
                                     TCAGCCTC    ACTCCACCC TCT AACGGACT
                                           G  -
GAM3229  221   LOC3404 1  19097 XP_290428.1  3  1101  GGTCAGGCCATT T-----      ----   T      3  C  c
c
          94                          CTGTTGCCCACC     GAGGTGGG   AGAAT GCTTGA
                                     TCGTGCTG         CTCCACCC   TCTTA CGGACT
                                           GTCGTG      GTTG   C
GAM3229  221   LOC3405 1  9452  XP_295262.1  5  238   GAGAGGTTAAGC   G-   AG           3  C  c
c
          12                          AATTTGCCTAGG TGAG  TGGG  AATTGCTTGA
                                     TTCACACA    ACTT  ATCC  TTAACGAATT
                                           GG   GT
GAM3229  221   LOC3405 1  14406 XP_295268.1  5  284   CCGGGTTCAGGC    TG             3  C  b
b
          28                          AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                     TCAGCTTC    ACTCC  CCTCTTAACGGACTT
                                           GT
GAM3229  221   LOC3429 1  10075 XP_292790.2  3  870   CCGGGTTCAAGC    TG             3  C  b  b

          26                          AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                     TCAGCCTC    ACTCC  CCTCTTAACGAACTT
                                           GT
GAM3229  221   LOC3438 1  14285 XP_297895.1  5  91    CGGGCACTCTCA T-----      AGAA        3  C  c
c
          03                          GGCAACCCCACC     GAGGTGGG   TTGCTTGA
                                     TCCCCCTC         CTCCACCC   AACGGACT
                                           CTCCCC      C---
GAM3229  221   LOC3466 1  19528 XP_294357.2  3  431   CTGGGTTCAAGC    G              3  C  b  b
          53                          AATTCTCCAGCC TGAGGT GGAGAATTGCTTGAA
                                     TCAGCCTC    ACTCCG CCTCTTAACGAACTT
                                           A
```

GAM3229 221 LOC3478 1 16961 XP_302609.1 5 364 AAACAAGCTTAG G TT 3 C c c

48 GCTTCTCCCAAC TGAG TGGGAGAA GCTTGA
TTAACAAA ATTC ACCCTCTT CGGATT
A --

GAM3229 221 LOC3479 1 955 XP_300565.1 5 248 CCAGGTTCAAGC 3 C b b

18 GATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCGCCCTCTTAGCGAACTT

GAM3229 221 LOC3480 1 16020 XP_300615.1 5 113 CCAGGTTGAAGC TG GA 3 C c c

94 AATTCTCCTGCC TGAGG GGAGAATTGCTT
TCAGCCTT ACTCC CCTCTTAACGAA
GT GT

GAM3229 221 LOC3481 1 1069 XP_300623.1 3 358 CTGGGTTCAAGC TG 3 C b b

13 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3481 1 1069 XP_300635.1 3 358 CTGGGTTCAAGC TG 3 C b b

37 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3481 1 1069 XP_300636.1 3 358 CTGGGTTCAAGC TG 3 C b b

42 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3482 1 16390 XP_300670.1 3 1590 CCAGGTTCAAGC T - ---- 3 C c c

35 AGTTCTCTGCCC GAGG TGGG AGAATTGCTTGAA
CACCCTCC CTCC ACCC TCTTGACGAACTT
C C CGTC

GAM3229 221 LOC3482 1 19609 XP_300683.1 5 117 CTGGGCTCAAGC A A 3 C b b

62 AGTCCTCCCACC TG GGTGGGAG ATTGCTTGA
CCAGCCTC AC CCACCCTC TGACGAACT
C C

GAM3229 221 LOC3483 1 10183 XP_300723.1 3 1218 CTGAGCTCAAGC T----- A 3 C c c

78 GATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGCCTA TTCCACCCTC TAGCGAACT
ATCCGG C

GAM3229 221 LOC3483 1 10000 XP_302741.1 3 1265 CTAGGTTCAAGC TG 3 C b b

93 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTAC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 LOC3483 1 17091 XP_300729.1 5 33 CTGGCCTCAAGT A TG 3 C c c

96 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCGTC ACTCCACCCTC TA GAACT

C GT
GAM3229 221 LOC3484 2 1590 XP_300730.1 3 687 CTTGGTTCAAGC TG 3 C b b
02 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC3484 2 3503 XP_300730.1 3 381 CTGGGTGCAAGC TG G A 3 C c
b
02 AATTATCCTGCC TGAGG GGA AATTGCTTG
TCAGCCTC ACTCC CCT TTAACGAAC
GT A G
GAM3229 221 LOC3484 1 13205 XP_209299.2 3 289 CTGGGCTCAAGC GA 3 C b b
74 AATCTTCCCACC TGAGGTGGGA ATTGCTTGA
TCAGCCTC ACTCCACCCT TAACGAACT
TC
GAM3229 221 LOC3484 1 7579 XP_300352.1 3 1392 GCATCTCCAACA - AT C A 3 C c
c
88 TCTCTCCCCACC TGAGGTGGG AGA TG TTG
TCATGATT ACTCCACCC TCT AC AAC
C CT - C
GAM3229 221 LOC3485 1 14079 XP_300762.1 3 1100 CTGGGCTCAAGC TG A 3 C c
c
03 AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCGGCTTC GCTCC CCTC TAACGAACT
GT C
GAM3229 221 LOC3485 2 542 XP_300769.1 3 157 TTGGCCTCAAGC T ------ A 3 C c c
04 AATCCTTCCTCT GAGGT GGGAG ATTGCTTGA
TTGGCCTC CTCCG CCTTC TAACGAACT
- GTTTCT C
GAM3229 221 LOC3485 2 7507 XP_300769.1 3 21 CCTAGGCTAAGC A A 3 C c c
04 AATCCTCCCACC TGAGGTGGGAG ATTGCTTG
TTAGCCTC ATTCCACCCTC TAACGAAT
C C
GAM3229 221 LOC3485 2 8135 XP_302806.1 5 621 CCAGGCTCAAGC G G A 3 C c
c
08 AATCCTACCATG TGA GTGG AG ATTGCTTGA
TCAGCCTT ACT TACC TC TAACGAACT
G A C
GAM3229 221 LOC3485 2 9877 XP_302806.1 5 805 CCAGGCTGAAGC A GA 3 C c
c
08 GATCCTCCCACC TGAGGTGGGAG ATTGCTT
TCAACCTC ACTCCACCCTC TAGCGAA
C GT
GAM3229 221 LOC3485 1 10000 XP_302818.1 3 1265 CTAGGTTCAAGC TG 3 C b b
32 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTAC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC3485 1 10075 XP_300378.1 3 687 CCGGGTTCAAGC TG 3 C b b

67 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC3486 1 4582 XP_302853.1 3 393 ACCGGCTCAAGC A 3 C b b
87 AATCCTCCCATC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCTACCCTC TAACGAACT
C
GAM3229 221 LOC3487 1 18680 XP_300843.1 3 642 CTGGCCTCAAGC AGA 3 C c
c
90 AATCCACTCATC TGAGGTGGG ATTGCTTGA
TCGGCCTC GCTCTACTC TAACGAACT
ACC
GAM3229 221 LOC3487 1 750 XP_302888.1 3 405 CCGGGTTCAAGC TG 3 C b b
97 AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAACCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 LOC3488 1 9877 XP_300861.1 5 535 CCAGGCTGAAGC A GA 3 C c
c
42 GATCCTCCCACC TGAGGTGGGAG ATTGCTT
TCAACCTC ACTCCACCCTC TAGCGAA
C GT
GAM3229 221 LOC3488 2 542 XP_302903.1 3 151 TTGGCCTCAAGC T ------ A 3 C c c
43 AATCCTTCCTCT GAGGT GGGAG ATTGCTTGA
TTGGCCTC CTCCG CCTTC TAACGAACT
- GTTTCT C
GAM3229 221 LOC3488 2 7507 XP_302903.1 3 21 CCTAGGCTAAGC A A 3 C c c
43 AATCCTCCCACC TGAGGTGGGAG ATTGCTTG
TTAGCCTC ATTCCACCCTC TAACGAAT
C C
GAM3229 221 LOC3489 1 9882 XP_300875.1 5 308 ATTTTCTCAAGC GG 3 C c c
09 AATTTTTAAATT TGAGGT GAGAATTGCTTGA
TCATTCAT ACTTTA TTTTTAACGAACT
AA
GAM3229 221 LOC3489 1 15195 XP_300883.1 3 394 TTCCTTCACACC G T CT- 3 C c
c
38 AATTCTCCTCCT T AGG GGGAGAATTG TGAA
GAGACGGA A TCC TCCTCTTAAC ACTT
G - CAC
GAM3229 221 LOC3489 1 6161 XP_300434.1 3 665 CCAGGTTCAAGC TG 3 C b b
95 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGTCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC3490 1 8631 XP_300932.1 3 372 CTAACCTCAGGT AGA TG 3 C c
c
75 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT
GAM3229 221 LOC3491 1 3432 XP_173186.2 3 365 TCATCGAGCACC A AAT--- 3 C c
c
01 TTCGCTCCCACC TG GGTGGGAG TGCTTGA

CGGGGGAG GC CCACCCTC ACGAGCT
- GCTTCC
GAM3229 221 LOC3491 1 7284 XP_302978.1 3 914 ACACAACCAAGC A A A 3 C c c
69 AATCCTCGCTTT TGAGGTGGG GA TTGCTTG
ACAGATGA ATTTCGCTC CT AACGAAC
- - C
GAM3229 221 LOC3491 3 14615 XP_300969.1 3 891 CTGGGTTCAAGC G 3 C b b
70 AATTCTTGTGCC TGAGGTG GAGAATTGCTTGAA
TCAGCCTC ACTCCGT TTCTTAACGAACTT
G
GAM3229 221 LOC3491 3 20022 XP_300969.1 3 1429 CCAGGTTCAAGC G 3 C b b
70 AATTCTCGTGCC TGAGGTG GAGAATTGCTTGAA
TCAGCCTC ACTCCGT CTCTTAACGAACTT
G
GAM3229 221 LOC3491 3 20159 XP_300969.1 5 1242 TTGAGGTCAAGC AA 3 C b b
70 AACCCTCCCACC TGAGGTGGGAG TTGCTTGA
TCGGCCTG GCTCCACCCTC AACGAACT
CC
GAM3229 221 LOC3492 1 17381 XP_300988.1 3 1489 TGGATTTCAAGC - GG AAT 3 C c
c
36 ACTTTCACACTT TGAG GTG AG TGCTTGAA
AACAAAAT ATTC CAC TC ACGAACTT
A TT ---
GAM3229 221 LOC3492 1 2783 XP_300998.1 5 149 CTGGGTTCAAGC TG 3 C b b
61 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 LOC3493 1 6478 XP_088528.1 5 640 CCAGCCTCAGGT AGA TG 3 C c
c
60 GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACC GT
GAM3229 221 LOC3494 1 6220 XP_301084.1 3 867 CTGGCCTCAAGC A 3 C b b
30 AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCATC ACTCCACCCTC TAACGAACT
C
GAM3229 221 LOC3494 1 9876 XP_300513.1 3 1118 CCGGATTCAAGG - G 3 C b b
40 AATTCTCCCTGC TGAGGT GGGAGAATT CTTGAA
CTCAGCCT ACTCCG CCCTCTTAA GAACTT
T G
GAM3229 221 LOC5119 1 4293 NP_057415.1 3 924 CTGGACTCAAGC T----- A 3 C c c
3 AATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGCCTT TTCCACCCTC TAACGAACT
TTCCGG C
GAM3229 221 LOC5595 1 5283 NP_061976.1 5 60 TTGGGCTCAAGC A T 3 C b b
4 TATCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAGCCTC ACTCCACCCTC TA CGAACT
C T

GAM3229 221 LOC9040 1 16149 XP_031517.1 5 1705 CTGGGTTCAAGC TG A 3 C c c
8 AATCCTCCTGCC TGAGG GGAG ATTGCTTGAA
TTATCCTC ATTCC CCTC TAACGAACTT
GT C
GAM3229 221 LOC9048 1 2914 XP_032059.1 3 393 AGCGCTTCAGCA T----- AA- T 3 C c c
5 ACCGCTCCCACC GAGGTGGGAG TTGCT GAA
TCCTCCAG CTCCACCCTC AACGA CTT
GACCTC GCC -
GAM3229 221 LOC9125 1 18320 XP_037135.1 5 2266 CCAGTTTCAAGC GG 3 C b b
0 AATTCTCATGCC TGAGGT GAGAATTGCTTGAA
TCAGATTC ACTCCG CTCTTAACGAACTT
TA
GAM3229 221 LOC9259 1 4501 NP_775739.1 3 3586 CTGGGTTCAAGC TG T 3 C c c
7 ATTTCTCCTGCC TGAGG GGAGAA TGCTTGAA
TCAGCCTC ACTCC CCTCTT ACGAACTT
GT T
GAM3229 221 LOC9346 1 1098 XP_051528.1 3 26 CTAAAGTCAAGC T G- --- 3 C c c
3 AAATGTTCTAGC TGAGG GG AGAAT TGCTTGA
CCTTCAGG ACTTC CC TCTTG ACGAACT
- GA TAA
GAM3229 221 LRP4 1 16726 XP_035037.2 3 1998 ACTAATGGAAGC - GA 3 C c c
GATTCTCCCATG TGAG GTGGGAGAATTGCTT
CTCATGTG ACTC TACCCTCTTAGCGAA
G GG
GAM3229 221 LY6G6C 1 11181 NP_079537.1 3 163 GTCTCCTCATCC AAT CT 3 C c c
GTCCTTCCCACC TGAGGTGGGAG TG TGA
TCACACCC ACTCCACCCTT GC ACT
CCT CT
GAM3229 221 LZTS1 1 1073 NP_066300.1 3 1504 CTGGGCTCAAGC TG A 3 C c c
AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTT ACTCC CCTC TAACGAACT
GT C
GAM3229 221 MAC30 1 15124 XP_031536.2 3 432 CTAGGCTCAAGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGTCTC ACTCCACCC TCT A GAACT
G - GT
GAM3229 221 MANBAL 1 18033 NP_071360.1 5 332 CCCAGCTGGAGC TG GA 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCTT
TCAGCCTT ACTCC CCTCTTAACGAG
GT GT
GAM3229 221 MAP1LC3 1 18525 NP_073729.1 3 1044 GACAGCCATCAG AG G T 3 C c c
B AATTCTCCCACA TG GTGGGAGAATT CT GA
CCAAGTGC AC CACCCTCTTAA GA CT

CA - -
GAM3229 221 MAPA 1 17799 NP_660299.1 3 999 CTGACCTCAAGC - A 3 C b b
GATCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCGGCCTC GCTCCACCC TCT AGCGAACT
G -
GAM3229 221 MAPT 1 18784 NP_776088.1 3 1264 TCCCCTCCCCTC - T CTT- 3 C c c
ACTTCTCCCACC TG AGGTGGGAGAA TG GA
TGCAGAGC AC TCCACCCTCTT AC CT
G C TCCC
GAM3229 221 MARK2 1 8182 NP_004945.2 3 159 GGCCCTTCTCAG - TT T 3 C c c
TTTTCTCCCACA TGAG GTGGGAGAA GCT GA
TTCACCCC ACTT CACCCTCTT TGA CT
A T- -
GAM3229 221 MARK2 1 8182 NP_059672.1 3 159 GGCCCTTCTCAG - TT T 3 C c c
TTTTCTCCCACA TGAG GTGGGAGAA GCT GA
TTCACCCC ACTT CACCCTCTT TGA CT
A T- -
GAM3229 221 MCM10 1 6797 NP_060988.2 3 1015 CTGGGCTCAAGC A 3 C b b
AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGTCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 MEFV 1 5889 NP_000234.1 3 1018 CTGACCTCAGGT AGA TG 3 C c
c
GATGCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
ACG GT
GAM3229 221 MGC1020 1 5932 NP_659497.1 3 240 CCAGGCTCAAGT A TG 3 C c
c
0 GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCCC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 MGC1081 1 14416 NP_085045.2 3 148 CTGGGTTCAAGC TG G 3 C b
b
8 AATTCTCTGCCT TGAGG G AGAATTGCTTGAA
CAGCCTCC ACTCC C TCTTAACGAACTT
GT -
GAM3229 221 MGC1098 1 6559 NP_085053.1 3 261 CTTCGTTCAGCC - AATT T 3 C c
c
6 TCCCTCCCCACC TGAGGTGGG AG GCT GAA
TCACCCCA ACTCCACCC TC CGA CTT
C CCTC -
GAM3229 221 MGC1138 1 4993 NP_116322.1 3 564 CTGGGCTCAAGC T----- A 3 C c
c
6 AATCCTCCCACC GAGGTGGGAG ATTGCTTGA
TTGGCCTC TTCCACCCTC TAACGAACT
CTCCGG C
GAM3229 221 MGC1302 1 16302 NP_689501.1 3 492 CCAGGCTCAAAA A A GC 3 C c
c
4 GATGCTCCCACC TG GGTGGGAG ATT TTGA

ACAGCCTC AC CCACCCTC TAG AACT
A G AA
GAM3229 221 MGC1313 1 10825 NP_219363.1 3 826 CAGAGTTCAAGC T 3 C b b
8 AATTCTCCTTCC TGAGG GGGAGAATTGCTTGAA
TCAGCCTC ACTCC TCCTCTTAACGAACTT
T
GAM3229 221 MGC1428 1 13575 NP_542391.1 3 511 CTGGGCTCAAGT GA TG 3 C c
c
9 GATCATCCCACC TGAGGTGGGA AT CTTGA
TCAGCCTC ACTCCACCCT TA GAACT
AC GT
GAM3229 221 MGC1438 1 10978 NP_291022.1 3 294 GGTAGATTCAAA AGAATT - 3 C
c c
6 GCTCCACCCACC TGAGGTGGG GCTT GAA
TCATCCCA ACTCCACCC CGAA CTT
ACCT-- A
GAM3229 221 MGC1483 1 12819 NP_219480.1 3 440 CAGGGTTCGGGC TG 3 C c
c
6 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TTAGCCTC ATTCC CCTCTTAACGGGCTT
GT
GAM3229 221 MGC1560 1 9411 NP_659474.1 5 349 CCAGGCTCAAGC 3 C b b
6 AATTCTCCTACC TGAGGTGGGAGAATTGCTTGA
TCAGCCTC ACTCCATCCTCTTAACGAACT
GAM3229 221 MGC2167 1 1835 NP_443093.1 3 559 CCAGATTCAAGC TG 3 C b b
5 AATTCTCCTGTT TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTTT CCTCTTAACGAACTT
GT
GAM3229 221 MGC2452 1 6351 NP_116033.1 5 2195 GTTTGGTTCCAA AAT A 3 C c
c
GCACTTCCCACC TGAGGTGGGAG TGCTTG
TCAAACTC ACTCCACCCTT ACGAAC
C-- C
GAM3229 221 MGC2474 1 5948 NP_076420.1 3 1508 CTCGGTTCAAGC T----- A 3 C c
c
AATTCGCCCACC GAGGTGGG GAATTGCTTGAA
TTGGCCTC TTCCACCC CTTAACGAACTT
CTCCGG G
GAM3229 221 MGC2697 1 15483 NP_714915.1 3 131 TCCTGATCGAGA A TG 3 C c
c
9 GATTCACCCACC TGAGGTGGG GAAT CTTGA
TCGGCCTC GCTCCACCC CTTA GAGCT
A GA
GAM3229 221 MGC2734 2 8394 XP_300964.1 5 1727 CCAGGTTCAAGC T-- --- 3 C c c
5 AGTTCTTCCTCA GAGGT GGGAGAATTGCTTGAA
GCCTCCGG CTCCG CCTTCTTGACGAACTT
GGC ACT

GAM3229 221 MGC2734 2 10537 NP_787076.1 5 70 CTGACCTCAGGT AGA TG 3 C c c
5 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 MGC2734 2 10537 XP_300964.1 5 1861 CTGACCTCAGGT AGA TG 3 C c c
5 GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 MGC3113 2 2387 NP_076940.1 3 772 CTGGGCTCATGT A TG T 3 C c c
GATCCTCCCACC TGAGGTGGGAG AT C TGA
TCAGCCTC ACTCCACCCTC TA G ACT
C GT T
GAM3229 221 MGC3113 2 10712 NP_076940.1 3 913 CTGGGCTCAAGC TG GA 3 C c c
AATTCATCTGCC TGAGG G GAATTGCTTGA
TCAACCTC ACTCC C CTTAACGAACT
GT TA
GAM3229 221 MGC3351 1 18526 NP_689978.1 3 2197 GTTCAAGAGATC A---- TG 3 C c c
0 CATCCTCCCACC TGAGGTGGGAG AT CTTGAA
TCAGTCTC ACTCCACCCTC TA GAACTT
CTACC GA
GAM3229 221 MGC3363 1 10075 NP_689809.1 3 743 CCGGGTTCAAGC TG 3 C b b
7 AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 MGC3413 1 17411 XP_291029.1 3 694 CTGGGTTCAAGA T----- A G 3 C c c
2 AATCCTCCCACC GAGGTGGGAG ATT CTTGAA
TTGCCTCC TTCCACCCTC TAA GAACTT
CCTCCG C A
GAM3229 221 MGC3516 1 2119 NP_689765.1 3 63 CTGGGTTCAAGC AG G-- 3 C c c
3 AATTCTCTGGGG TG GT GGAGAATTGCTTGAA
CAGCAGTT AC CG TCTCTTAACGAACTT
GA GGG
GAM3229 221 MGC3530 1 14998 NP_787118.1 3 48 GGACAGGCCAGG GAATT A 3 C c c
8 CCTGATCCCACC TGAGGTGGGA GCTTG
TCACTTCC ACTCCACCCT CGGAC
AGTC- C
GAM3229 221 MGC3546 1 12471 NP_694976.1 3 280 CTGACCTCAGGT AGA TG 3 C c c
8 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTT GCTCCACCC TA GGACT
GCC GT

GAM3229 221 MGC4633 1 8629 XP_290712.1 3 124 CTGACCTCAGGT AGA TG 3 C c c
6 GATCCGCCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
GCC GT
GAM3229 221 MGC5033 1 17884 NP_848604.1 3 339 CTGGGTTCAAGT TG 3 C b b
7 GATTCTCCCACC TGAGGTGGGAGAAT CTTGAA
TCAACCTC ACTCCACCCTCTTA GAACTT
GT
GAM3229 221 MGC5149 1 940 XP_051200.2 3 2012 CCAGGTTCAAGT TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAATGAACTT
GT
GAM3229 221 MGC9726 1 18506 NP_796377.1 3 413 AGACCTTCCTCA AATTGCT 3 C c c
CCCGCTCCCACC TGAGGTGGGAG TGA
TCACACCC ACTCCACCCTC ACT
GCCC---
GAM3229 221 MHC2TA 2 12501 NP_000237.1 3 1574 CCTGGGCTAAGT A TG A 3 C c c
GATCCTCCCACC TGAGGTGGGAG AT CTTG
TCAGCCTC ACTCCACCCTC TA GAAT
C GT C
GAM3229 221 MHC2TA 2 14620 NP_000237.1 3 632 TTGACCTCGGGT AGA TG 3 C c c
GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGGCT
ACC GT
GAM3229 221 MICB 1 11538 NP_005922.1 3 754 CCAGGTTCAAGC G T 3 C b b
ACTTCTCGTACC TGAGGTG GAGAA TGCTTGAA
TCAGACTC ACTCCAT CTCTT ACGAACTT
G C
GAM3229 221 MIDORI 1 7016 NP_065829.1 3 257 CCCGGGCCTCAA T----- A A 3 C c c
GCAGTCCCCACC GAGGTGGG GA TTGCTTGA
TCCGAGTG CTCCACCC CT GACGAACT
GTGAGC - -
GAM3229 221 MIZF 1 6430 NP_056332.1 5 50 CTGGGCTCAAGC G AATT 3 C c c
CTTCCTCCCACC T AGGTGGGAG GCTTGA
TGAACCTC A TCCACCCTC CGAACT
G CTTC
GAM3229 221 MLANA 1 12846 NP_005502.1 3 670 CCAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TTAGCCTC ATTCC CCTCTTAACGAACTT
GT
GAM3229 221 MLZE 1 2064 NP_113603.1 5 643 CCGGGTTCAAGC TG G 3 C c c
AGTTCTCTGCCT TGAGG G AGAATTGCTTGAA
CAGCCTCC ACTCC C TCTTGACGAACTT
GT -

GAM3229 221 MMPL1 1 18579 NP_004133.1 3 720 TTGGGCTCAAGC G A 3 C c c
GATCCTCCCACC T AGGTGGGAG ATTGCTTGA
TGGGACTC G TCCACCCTC TAGCGAACT
G C
GAM3229 221 MRPL30 2 4263 NP_660213.1 3 716 CCAGGCTCAAGT A TG 3 C c b
GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTC ACTCCACCCTC TA GAACT
C GT
GAM3229 221 MRPL30 2 4509 NP_660213.1 3 855 CTGGGTTCAAGC A T 3 C b b
CATCCTCCCACC TGAGGTGGGAG AT GCTTGAA
TCAGCCTC ACTCCACCCTC TA CGAACTT
C C
GAM3229 221 MRPS27 1 10070 NP_055899.1 3 489 CCAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCGGCCTC GCTCC CCTCTTAACGAACTT
GT
GAM3229 221 MRS3/4 1 7253 NP_112489.2 3 86 TCTGTCTCCTGG A G T- 3 C c c
AATGCTCCCACC TGAGGTGGGAG ATT CT GA
TCAAGTGG ACTCCACCCTC TAA GG CT
G - TC
GAM3229 221 MtFMT 1 6398 NP_640335.1 3 202 CCAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 MTH2 1 18725 NP_060753.1 3 910 CTGGGTTCAAGC 3 C b b
AATTCTCCTACC TGAGGTGGGAGAATTGCTTGAA
TCAGCTTC ACTCCATCCTCTTAACGAACTT
GAM3229 221 MYLC2PL 1 13697 NP_612412.1 5 428 ACGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 MYO5C 1 12851 NP_061198.1 3 687 CTGGGTTCAAAC TG C 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTG TTGAA
TCAGCCTC ACTCC CCTCTTAAC AACTT
GT A
GAM3229 221 NAPA 1 5619 NP_003818.1 3 212 CTGGAGCTTAGG A - G 3 C c c
GATTCTCCCCAC TG GGTGGG AGAATT CTTGA
CCCAGCCC AC CCACCC TCTTAG GGATT
C C -
GAM3229 221 NCOA6 1 18704 NP_054790.1 5 1338 CTGGGCTCAAGC T----- AA 3 C c c
AACCCTCCCACC GAGGTGGGAG TTGCTTGA
TCCCATGC CTCCACCCTC AACGAACT
CGTACC CC
GAM3229 221 NCOA6IP 1 14417 NP_079107.5 3 338 CTGAGTTCAAGC TG A 3 C c c

AATCCTTCTGTC TGAGG GGAG ATTGCTTGAA
TCAGTCTC ACTCT CTTC TAACGAACTT
GT C

GAM3229 221 NDUFC2 1 2783 NP_004540.1 3 1299 CTGGGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 NEDD4 1 16923 XP_046129.4 3 2561 CATCTATCAAGC T GAGAA 3 C c c

AACACAGCCCCT TGAGG GG TTGCTTGA
TATCCCAG ATTCC CC AACGAACT
- GACAC

GAM3229 221 NEIL2 1 9514 NP_659480.1 3 621 TACAACTCAAGC T----- AAT 3 C c c
ATTCCTCCCACC GAGGTGGGAG TGCTTGA
TTGGTCTC TTCCACCCTC ACGAACT
CTCTGG CTT

GAM3229 221 NEUROD1 1 14176 NP_002491.1 3 709 CACAATTTGAGC GG - TG 3 C c c

AATTCATTTCAC TGAGGTG A GAATTGCT AA
TTTAAAGT ATTTCAC T CTTAACGA TT
TT A GT

GAM3229 221 NF2 2 8254 NP_057502.1 5 673 CCGACCTCAGGT - A TG 3 C c b
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
G - GT

GAM3229 221 NF2 2 11182 NP_057502.1 5 539 CCGGATTCAAGC 3 C b b
AATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCGCCCTCTTAACGAACTT

GAM3229 221 NQO1 1 19166 NP_000894.1 3 744 CCAGGTTCCAGC TG T 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCAGCCTC ACTCC CCTCTTAACGA CTT
GT C

GAM3229 221 NUP43 1 16948 NP_078923.2 3 664 CCGGGTTCAAGC TG 3 C b b
AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGTCTC ACTCC CCTCTTGACGAACTT
GT

GAM3229 221 OPRM1 1 17047 NP_000905.1 3 344 TTATTTTCAAGC GG- AA- 3 C c c

AAATATTTATGA TGAGGT GAG TTGCTTGAA
CCTCAACA ACTCCA TTT AACGAACTT
GTA ATA

GAM3229 221 OSBPL3 1 8465 NP_056365.1 3 2976 TGGGCTTCAAGC - AT- 3 C c c
ACTGTCTTCCAT TG AGGTGGGAGA TGCTTGAA
CTGCATCT AC TCTACCTTCT ACGAACTT
G GTC

GAM3229 221 OSBPL3 1 8465 NP_663160.1 3 2976 TGGGCTTCAAGC - AT- 3 C c c
ACTGTCTTCCAT TG AGGTGGGAGA TGCTTGAA
CTGCATCT AC TCTACCTTCT ACGAACTT

```
                                        G        GTC
GAM3229  221   OSBPL3  1  8465  NP_663161.1  3  2976  TGGGCTTCAAGC  -       AT-          3  C  c  c
                                ACTGTCTTCCAT TG AGGTGGGAGA  TGCTTGAA
                                CTGCATCT    AC TCTACCTTCT  ACGAACTT
                                        G        GTC
GAM3229  221   OSBPL3  1  8465  NP_663162.1  3  2976  TGGGCTTCAAGC  -       AT-          3  C  c  c
                                ACTGTCTTCCAT TG AGGTGGGAGA  TGCTTGAA
                                CTGCATCT    AC TCTACCTTCT  ACGAACTT
                                        G        GTC
GAM3229  221   OSBPL3  1  8465  NP_663163.1  3  4110  TGGGCTTCAAGC  -       AT-          3  C  c  c
                                ACTGTCTTCCAT TG AGGTGGGAGA  TGCTTGAA
                                CTGCATCT    AC TCTACCTTCT  ACGAACTT
                                        G        GTC
GAM3229  221   OSBPL3  1  8465  NP_663164.1  3  4110  TGGGCTTCAAGC  -       AT-          3  C  c  c
                                ACTGTCTTCCAT TG AGGTGGGAGA  TGCTTGAA
                                CTGCATCT    AC TCTACCTTCT  ACGAACTT
                                        G        GTC
GAM3229  221   OSBPL8  1  1446  NP_065892.1  3  3843  ATAAATTCAAGC  --   G  AAT          3  C  c
c
                                ACTACCACTGGT TGA  GGTGG AG  TGCTTGAA
                                CAGTTTTG    ACT  TCACC TC  ACGAACTT
                                        GG    A  ---
GAM3229  221   OSM    1  15290 NP_065391.1  3  208   GAGTCAGGCTGT        AATT---       3  C  c  c
                                TGCGCTCCCACC TGAGGTGGGAG     GCTTGA
                                TCAGCCCC    ACTCCACCCTC     CGGACT
                                        GCGTTGT
GAM3229  221   PAICS  2  963   NP_006443.1  3  604   CTGAACCCTAGT            TGA      3  C  c  b
                                AATTCTCCTATC TGAGGTGGGAGAATTGCT
                                TCAGCCTC    ACTCTATCCTCTTAATGA
                                        TCC
GAM3229  221   PAICS  2  12311 NP_006443.1  3  471   CTGGGCTCAAGC                  3  C  b  b
                                AGTTCTCCCACC TGAGGTGGGAGAATTGCTTGA
                                TCAGCCTC    ACTCCACCCTCTTGACGAACT

GAM3229  221   PCDHA9  1  2783  NP_054724.1  3  1373  CTGGGTTCAAGC    TG            3  C  b  b

                                AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                TCAGCCTC    ACTCC  CCTCTTAACGAACTT
                                        GT
GAM3229  221   PCDHB11 1  3153  NP_061754.1  3  251   TCGGGTTCAAGC   G TG            3  C  c
c
                                AATTCTCCTGCA TGA G  GGAGAATTGCTTGAA
                                TCAGCCTC    ACT C  CCTCTTAACGAACTT
                                        A GT
GAM3229  221   PCDHB16 1  5101  NP_066008.1  3  640   CTGGGCTCAACG       A  GC         3  C  c
c
                                GATCCTTCCACC TGAGGTGGGAG ATT  TTGA
                                TCAGCCTC    ACTCCACCTTC TAG  AACT
                                        C  GC
GAM3229  221   PCDHGA1 1  11054 NP_061735.1  3  1713  TCGCATAGTCAC  A     AA   T        3  C  c
 c
```

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA1 1 11054 NP_061736.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

0 GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA1 1 11054 NP_061737.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

1 GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA1 1 11054 NP_114481.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

1 GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA1 1 11054 NP_003726.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

2 GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA2 1 11054 NP_061738.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA3 1 11054 NP_061739.2 3 1713 TCGCATAGTCAC A AA T 3 C c
c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA4 1 11054 NP_061740.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA5 1 11054 NP_061741.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA6 1 11054 NP_061742.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA7 1 11054 NP_061743.1 3 1713 TCGCATAGTCAC A AA T 3 C c
c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA8 1 11054 NP_114477.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGA9 1 11054 NP_061744.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB1 1 11054 NP_061745.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB2 1 11054 NP_061746.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB3 1 11054 NP_061747.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB4 1 11054 NP_003727.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB5 1 11054 NP_061748.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB6 1 11054 NP_061749.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGB7 1 11054 NP_061750.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGC3 1 11054 NP_002579.2 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGC3 1 11054 NP_115779.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGC4 1 11054 NP_061751.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PCDHGC5 1 11054 NP_061752.1 3 1713 TCGCATAGTCAC A AA T 3 C c c

GTAGCTCCCACC TG GGTGGGAG TTGC TGA
CCACCCTC AC CCACCCTC GATG ACT
C -- C

GAM3229 221 PDCL 1 18230 NP_005379.2 3 1920 CTGGGTTCAAGC 3 C b b
AGTTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
TCAGCCTC ACTCCGCCCTCTTGACGAACTT

GAM3229 221 PDZRN1 1 19980 NP_699202.1 3 581 CTGGGTTCACGC T T 3 C b b

CATTCTCCCGCC TGAGGTGGGAGAAT GC TGAA
TCAGCCTC ACTCCGCCCTCTTA CG ACTT
C C

GAM3229 221 PEPP3 1 17981 NP_055750.1 3 943 ACTGTCTCCTCT AATT TT 3 C c c

GCTCCTCCCACC TGAGGTGGGAG GC GA
TCATCCCT ACTCCACCCTC CG CT
CT-- T-

GAM3229 221 PER1 1 4346 NP_002607.1 5 80 CCTCAGAGACTT ATTG--- - 3 C c c
AGATCTTCCACC TGAGGTGGGAGA CT TGA
TCACTCCC ACTCCACCTTCT GA ACT
AGATTCA G

GAM3229 221 PER2 1 10711 NP_073728.1 3 1565 CTGACCTCAAGC AGA 3 C c c
GATCCACCCACC TGAGGTGGG ATTGCTTGA
TCGGCCTC GCTCCACCC TAGCGAACT
ACC

GAM3229 221 PFAS 1 19259 NP_036525.1 3 733 CTGGGTTCAAGC TG 3 C b b
AATTTTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTTTTAACGAACTT
GT

GAM3229 221 PHTF2 1 18794 NP_065165.1 3 1072 ACTTATCTGGTG A - - T 3 C c c
CATTCTCCCCAC TG GGTGGG AGAAT TGCT GA
CCCACCCC AC CCACCC TCTTA GTGG CT
C C C T

GAM3229 221 PIK3AP1 1 4110 NP_689522.1 5 33 CTGAGCTCAAGC G A 3 C c c
AATCCTCCCGAC TGAG TGGGAG ATTGCTTGA

TCGGCTTC GCTC GCCCTC TAACGAACT
A C
GAM3229 221 PKNOX1 1 18518 NP_004562.2 3 1880 TTATGTTCAAGC T 3 C b b
AATTCTCCTTCC TGAGG GGGAGAATTGCTTGAA
TTAGCCTC ATTCC TCCTCTTAACGAACTT
T
GAM3229 221 PLA2G2D 1 12102 NP_036532.1 3 60 GCATGGAGCTCT A AT T 3 C c
c
GGCATCCCCACC TGAGGTGGG GA TGCT GA
TCAGTATC ACTCCACCC CT ACGG CT
- -- T
GAM3229 221 PLB 1 16989 NP_694566.1 3 269 ATTCTGACTCAA T--- -- GC 3 C c c
AATTCTCCTAAA GAGGT GGGAGAATT TTGA
CCTCCCTG CTCCA TCCTCTTAA AACT
GTCC AA --
GAM3229 221 PMCHL1 1 2034 NP_114093.1 3 585 CCGGGTTCAAGC TG A 3 C c
c
AATTTCCTGCCT TGAGG GGAGA TTGCTTGAA
CAGCCTCA ACTCC CCTTT AACGAACTT
GT -
GAM3229 221 PMCHL2 1 7283 NP_114094.1 3 583 CCGGGTTCAAGC TG A 3 C b
b
AATTCCCTGCCT TGAGG GG GAATTGCTTGAA
CAGCCTCA ACTCC CC CTTAACGAACTT
GT -
GAM3229 221 POLD3 1 11834 XP_166243.1 3 104 TGTAAGTTCATC G A CT 3 C c c
TAGATCTCCACC TGAGGTGG AGA TTG TGAA
TCACCTGT ACTCCACC TCT GAT ACTT
- A CT
GAM3229 221 POLR1B 1 14540 NP_061887.1 3 2605 CTGACCTCAAGT AGA TG 3 C c
c
GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GAACT
ACC GT
GAM3229 221 POLR1B 1 14540 NP_115588.1 3 1189 CTGACCTCAAGT AGA TG 3 C c
c
GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GAACT
ACC GT
GAM3229 221 PPFIBP1 2 7102 NP_003613.2 3 1386 CTGTCCTCAAGT A TG 3 C c b
GATCCTCCCACC TGAGGTGGGAG AT CTTGA
TCAGCCTT ACTCCACCCTC TA GAACT
C GT
GAM3229 221 PPFIBP1 2 15585 NP_003613.2 3 2354 CTGGGTTCACGC T T 3 C b b
CATTCTCCCACC TGAGGTGGGAGAAT GC TGAA
TCAGCTTC ACTCCACCCTCTTA CG ACTT
C C
GAM3229 221 PPID 1 8015 NP_005029.1 3 306 CCGGGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCTTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 PPIL2 1 6798 NP_055152.1 3 451 CTGGGCTCAAGC TG A 3 C c c
AATCCTCCTGCC TGAGG GGAG ATTGCTTGA
TCAGCCTC ACTCC CCTC TAACGAACT
GT C
GAM3229 221 PRICKLE 1 1859 XP_093799.2 3 734 GCCATCCTTAAG - AATT 3 C c c

2 TCTGCTCCCACC TGAGG TGGGAG GCTTGA
CTCAGTAG ACTCC ACCCTC TGAATT
C GTC-
GAM3229 221 PRM2 1 15684 NP_002753.1 3 89 TGAGGCCATAGC G A - A 3 C c c
AATTCCCCTACA TGA GTGGG GAATTGCT TG
TCAAATGC ACT CATCC CTTAACGA AC
A C T C
GAM3229 221 PRO0233 1 7103 NP_054840.1 3 311 GCTTTCTGGCCT TT-- T 3 C c c
TCTTTTCCCACC TGAGGTGGGAGAA GCT GAA
TTAGGCTT ATTCCACCCTTTT CGG CTT
CTTC T
GAM3229 221 PRO0297 1 16889 NP_054800.1 5 247 CTGGACTCAAGT AGA TG 3 C c
c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCCC GCTCCACCC TA GAACT
GCC GT
GAM3229 221 PSEN1 2 4484 NP_015557.1 3 654 GATGCCTTTGGC T T 3 C c c
AATTCTTCTTCT TGAGG GGGAGAATTGCT GA
CAAGCACT ACTCT TCTTCTTAACGG TT
- T
GAM3229 221 PSEN1 2 20121 NP_000012.1 3 655 ATTGCCTTTGGC T T 3 C c c
AATTCTTCTTCT TGAGG GGGAGAATTGCT GA
CAAGCACT ACTCT TCTTCTTAACGG TT
- T
GAM3229 221 PSK 1 14317 NP_057235.1 3 57 GCATTGAGCACT -- AT--- TG 3 C c c
TTATCTCCCACG TGAG GTGGGAGA TGCT A
ACTCAGTG ACTC CACCCTCT ACGA T
AG ATTTC GT
GAM3229 221 PSME3 1 5202 NP_005780.2 3 1480 TTTTAGTTGGGC A A TG 3 C c c

AGTGCTCCCACC TG GGTGGGAG ATTGCT A
CACCCTCC AC CCACCCTC TGACGG T
- G GT
GAM3229 221 PSME3 1 5202 NP_789839.1 3 1480 TTTTAGTTGGGC A A TG 3 C c c

AGTGCTCCCACC TG GGTGGGAG ATTGCT A
CACCCTCC AC CCACCCTC TGACGG T
- G GT
GAM3229 221 PSPH 1 9353 NP_004568.1 5 9 TTCTTCCAGCGA G -- T 3 C c c
TGGTCTCCCACT TGAG TGGGAGA ATTGCT GAA
CAGAGCTG ACTC ACCCTCT TAGCGA CTT

```
                                        -    GG    C
GAM3229  221   PTGES  1  11180 NP_004869.1  3  586   CCGGGTTCAAGC                    3  C  b  b
                                  GATTCTCCCGCC TGAGGTGGGAGAATTGCTTGAA
                                  TCAGCCTC    ACTCCGCCCTCTTAGCGAACTT

GAM3229  221   PTPN18 1  10017 NP_055184.2  3  1200  CCAACCTCAAGC    TG   A          3  C  c
c
                                  AATCCTCCTGCC TGAGG  GGAG ATTGCTTGA
                                  TCAGCCTC    ACTCC  CCTC TAACGAACT
                                        GT   C
GAM3229  221   PTPN21 1  18866 NP_008970.1  3  311   TATTTTCTAGAC      G    - T       3  C  c  c
                                  AATTCTCTATTT TGAGGTGG AGAATTG CT GAA
                                  TACTGAAG    ATTTTATC TCTTAAC GA CTT
                                        -     A  T
GAM3229  221   PVR    1  16119 NP_006496.2  3  565   TCAACGCCAAGT       A  T   A       3  C  c  c
                                  CATCCTCCCACC TGAGGTGGGAG AT GCTTG
                                  TCAGCCTC    ACTCCACCCTC TA TGAAC
                                        C  C    C
GAM3229  221   RA-GEF- 1  685   NP_057424.1  3  663   TCGTGTTCAAGC  AG     AA          3  C  c  c
          2                       AGCTCCCATGAC TG  GTGGGAG  TTGCTTGAA
                                  AACTTCCA    AC  TACCCTC  GACGAACTT
                                        AG      --
GAM3229  221   RAB11-F 1  4504  NP_116321.2  3  2785  CTGACCTCAAGT       A  TG          3  C  c  c

          IP4                      GATCCTCCCACC TGAGGTGGGAG AT  CTTGA
                                  TCAGCCTG    ACTCCACCCTC TA  GAACT
                                        C  GT
GAM3229  221   RAB33B 1  10964 NP_112586.1  3  510   CTGGGCTCAAGC       A           3  C  b  b
                                  AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
                                  TCAGCCTC    ACTCCACCCTC TAACGAACT
                                        C
GAM3229  221   RAI3   1  2965  NP_003970.1  3  402   CTGTGCTCAAGC T-----       A        3  C  c  c
                                  AATCCTCCCATC      GAGGTGGGAG ATTGCTTGA
                                  TCCATCTC         CTCTACCCTC TAACGAACT
                                        CTCTAC        C
GAM3229  221   RBBP9  1  14743 NP_006597.2  3  2049  CTGGCCTCAAGT       AGA  TG          3  C  c
c
                                  GATCCACCCACC TGAGGTGGG   AT  CTTGA
                                  TCAGCCGC    ACTCCACCC   TA  GAACT
                                        ACC  GT
GAM3229  221   RE2    1  2783  NP_722561.1  5  222   CTGGGTTCAAGC     TG              3  C  b  b
                                  AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                  TCAGCCTC    ACTCC  CCTCTTAACGAACTT
                                        GT
GAM3229  221   RHD    2  6398  NP_057208.2  3  749   CCAGGTTCAAGC     TG              3  C  b  b
                                  AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                  TCAGCCTC    ACTCC  CCTCTTAACGAACTT
                                        GT
GAM3229  221   RHD    2  6398  NP_057309.2  3  838   CCAGGTTCAAGC     TG              3  C  b  b
                                  AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
```

TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 RHD 2 17898 NP_057208.2 3 340 CTGGGTTCAAGC TG A 3 C c b
AAATCTCCTGCC TGAGG GGAGA TTGCTTGAA
TCAGCCTC ACTCC CCTCT AACGAACTT
GT A
GAM3229 221 RHD 2 17898 NP_057309.2 3 429 CTGGGTTCAAGC TG A 3 C c b
AAATCTCCTGCC TGAGG GGAGA TTGCTTGAA
TCAGCCTC ACTCC CCTCT AACGAACTT
GT A
GAM3229 221 RHPN2 1 14536 NP_149094.2 3 1085 CTGACCTCAAAT AGA GC 3 C c
c
GATCCACCCACC TGAGGTGGG ATT TTGA
TCAGCCTC ACTCCACCC TAG AACT
ACC TA
GAM3229 221 RI58 1 10523 NP_036552.1 3 1751 GCAAAGCAGGCC G TT- A 3 C c c
ATTTCTCCCACC T AGGTGGGAGAA GCTTG
TGAAAGTA A TCCACCCTCTT CGGAC
G TAC G
GAM3229 221 RNF135 1 15831 NP_115698.2 3 177 CTGGTCTCAAGC A 3 C b b
AGTCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TGACGAACT
C
GAM3229 221 RNF144 1 5448 NP_055561.1 3 3361 CTGACCTCAGGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCGGCTTC GCTCCACCC TCT A GGACT
G - GT
GAM3229 221 RNF19 1 15444 NP_056250.2 5 176 CTGGGCTCAAGC G AA 3 C b b
AACCCTGCCACC TGAGGTGG AG TTGCTTGA
TCAGCCTT ACTCCACC TC AACGAACT
G CC
GAM3229 221 RNF8 1 11343 NP_003949.1 3 1014 CCAGACTCAAGC A T 3 C b b
CATCCTCCCACC TGAGGTGGGAG AT GCTTGA
TCAACCTC ACTCCACCCTC TA CGAACT
C C
GAM3229 221 RP2 1 15091 NP_008846.1 3 1959 CTGACCTCAGGT AGA TG 3 C c
c
GATCCGTCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCT TA GGACT
GCC GT
GAM3229 221 RP4-622 1 6481 NP_061991.2 3 340 TTCCAGCTCAGA A AATT - 3 C c
c
L5 GCTCCTCCCACC TG GGTGGGAG GCT TGA
CCAACATA AC CCACCCTC CGA ACT
C CT-- G
GAM3229 221 RRM2B 1 9272 XP_042096.1 3 1519 ACCCCTTCAAGC A -- -- 3 C c c
AGTTGTTTCCCA TG GG TGGGAGA ATTGCTTGAA
TTCCCAAC AC CC ACCCTTT TGACGAACTT

- TT GT
GAM3229 221 S100A1 1 7600 NP_006262.1 5 63 ATCTGTCCAGAA AATTG- T 3 C c c
CCTGCTCCCACC TGAGGTGGGAG CT GA
TCAGGCCC ACTCCACCCTC GA CT
GTCCAA C
GAM3229 221 SC4MOL 1 3278 NP_006736.1 3 531 CCCAGTTCAAGC TG 3 C b b
AATTCTTCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CTTCTTAACGAACTT
GT
GAM3229 221 SCAMP-4 1 15109 NP_524558.1 3 932 CCGTGTTCAAGC TG 3 C b b
AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 SCML2 2 1648 NP_006080.1 3 1371 CCTGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCGAT ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 SCML2 2 12471 NP_006080.1 3 1481 CTGACCTCAGGT AGA TG 3 C c b
GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTT GCTCCACCC TA GGACT
GCC GT
GAM3229 221 SCN3B 3 856 NP_060870.1 3 2073 CCAGGTTTAAGC A 3 C b b
AATCCTCCCACC TGAGGTGGGAG ATTGCTTGAA
TCAGCCCC ACTCCACCCTC TAACGAATTT
C
GAM3229 221 SCN3B 3 12530 NP_060870.1 3 1113 TTGGGTTCAAGC GG 3 C b b
AATTCTCATGCC TGAGGT GAGAATTGCTTGAA
TCGGCCTC GCTCCG CTCTTAACGAACTT
TA
GAM3229 221 SCN3B 3 19668 NP_060870.1 3 2208 CTGGGCTCAAGC - G A 3 C b b
AATCTGCCAGCC TGAGG TGG AGA TTGCTTGA
TCAGCCTC ACTCC ACC TCT AACGAACT
G G -
GAM3229 221 SEDL 3 6019 NP_055378.1 3 1401 CTGACTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 SEDL 3 9526 NP_055378.1 3 697 CCGGGTTCAAGC T 3 C b b
AATTCTCCTTCT TGAGG GGGAGAATTGCTTGAA
TCAGCCTC ACTTC TCCTCTTAACGAACTT
T
GAM3229 221 SEDL 3 15920 NP_055378.1 3 1059 CTGGGTTCAAGC T 3 C b b
AATTCTCCTTCT TGAGG GGGAGAATTGCTTGAA
TCAGCCTC ACTTC TCCTCTTAACGAACTT
T

GAM3229 221 SEPN1 1 941 NP_065184.1 3 1616 CCAGGTTCAAGC TG 3 C b b
AATTCTCTTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC TCTCTTAACGAACTT
GT
GAM3229 221 SERF1A 1 4780 NP_068802.1 3 302 CTGGGTTCAAGC TG 3 C b b
AGTTCTCTTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC TCTCTTGACGAACTT
GT
GAM3229 221 SERF1B 1 4780 NP_075267.1 3 302 CTGGGTTCAAGC TG 3 C b b
AGTTCTCTTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC TCTCTTGACGAACTT
GT
GAM3229 221 SERF2 1 6225 NP_005761.2 5 490 CTGGATTCAAGC A 3 C b b
AATCCTCCCATC TGAGGTGGGAG ATTGCTTGAA
TCAGCCTC ACTCTACCCTC TAACGAACTT
C
GAM3229 221 SERPINB 2 3013 NP_004146.1 3 2553 CTGGCCTCAAGC AGA 3 C b
b
9 AATCCGCCTACC TGAGGTGGG ATTGCTTGA
TCAGCCTC ACTCCATCC TAACGAACT
GCC
GAM3229 221 SERPINB 2 10182 NP_004146.1 3 2418 CTGGATTCAAGC TG 3 C b
b
9 AATTCTCTTGCT TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTTC TCTCTTAACGAACTT
GT
GAM3229 221 SHOX 1 10964 NP_006874.1 3 375 CTGGGCTCAAGC A 3 C b b
AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAACGAACT
C
GAM3229 221 SIGLEC1 1 11214 NP_443116.1 3 365 CTGGGCTCAAGC T----- - A 3 C c
c
1 AATCTGCCCGCC GAGGTGGG AGA TTGCTTGA
TCTGCCTC CTCCGCCC TCT AACGAACT
CTCCGT G -
GAM3229 221 SIGLEC5 1 15567 NP_003821.1 3 226 CTGTCATCAAGC T-- -- - A 3 C c c
AATTCACTGCAT GAGG TG GG GAATTGCTTGA
CCCTCTGT CTCC AC TC CTTAACGAACT
TGT CT G A
GAM3229 221 SIGLEC8 1 6398 NP_055257.1 3 575 CCAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 SLA2 1 17394 NP_115590.1 3 748 CTGGATTCAAAC TG C 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTG TTGAA
TCAGCCTC ACTCC CCTCTTAAC AACTT
GT A
GAM3229 221 SLA2 1 17394 NP_778252.1 3 851 CTGGATTCAAAC TG C 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTG TTGAA
TCAGCCTC ACTCC CCTCTTAAC AACTT

```
                                                GT       A
GAM3229  221   SLC12A8 1  18490  NP_078904.1  3  268   CCGAGTTCAAGC     TG                3  C  b  b

                                      AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                      TCAGCTCT    ACTCC  CCTCTTAACGAACTT
                                                GT
GAM3229  221   SLC15A1 1  940    NP_005064.1  3  278   CCAGGTTCAAGT     TG                3  C  b  b
                                      AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                      TCAGCCTC    ACTCC  CCTCTTAATGAACTT
                                                GT
GAM3229  221   SLC16A6 1  3300   NP_004685.1  5  110   CTCAACTCAAGC         A            3  C  b  b
                                      AATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
                                      TCAGCCAC    ACTCCACCCTC TAACGAACT
                                                  C
GAM3229  221   SLC24A1 1  1284   NP_004718.1  3  746   CCCGGTTCAAGC     TG                3  C  b  b
                                      AATTCTCCTGCC TGAGG  GGAGAATTGCTTGAA
                                      TCAGCCTG    ACTCC  CCTCTTAACGAACTT
                                                GT
GAM3229  221   SLC2A10 1  7814   NP_110404.1  3  694   CTGAGCTCAAGT       AGA  TG          3  C  c
c
                                      GATCCACCCACC TGAGGTGGG   AT  CTTGA
                                      TCAGCCTC    ACTCCACCC   TA  GAACT
                                                ACC  GT
GAM3229  221   SLC35E2 2  13880  XP_049733.6  3  1666  CTGGGCTCAAAT        A  GC          3  C  c
c
                                      GATCCTCCCACC TGAGGTGGGAG ATT  TTGA
                                      TCAGCCTC    ACTCCACCCTC TAG  AACT
                                                  C  TA
GAM3229  221   SLC35E2 2  16129  XP_049733.6  3  1793  CTCGGCTCAAGC    GT    A           3  C  c
c
                                      AATCCTTCCTAC TGAG  GGGAG ATTGCTTGA
                                      TCAGCCTC    ACTC  CCTTC TAACGAACT
                                                AT    C
GAM3229  221   SLC36A1 1  989    NP_510968.1  3  379   TTAACAATTTTC        -------      C      3  C  c  c
                                      ATGTCCCCCACC TGAGGTGGG      AGAATTG TTGA
                                      TCATGTTT    ACTCCACCC      TTTTAAC AATT
                                                CCTGTAC      -
GAM3229  221   SLC39A1 1  17454  NP_055252.2  5  148   CCGGGCTCAGGT          TG          3  C  c  c

                                      GATTCTCCCGCC TGAGGTGGGAGAAT  CTTGA
                                      TCAGCACC    ACTCCGCCCTCTTA  GGACT
                                                  GT
GAM3229  221   SLC5A6  1  11338  NP_066918.1  3  623   TGTAGAGCAAGC         AT    A       3  C  c  c

                                      ACGTTTTCCACC TGAGGTGGGAGA  TGCTTG
                                      TCACTGTC    ACTCCACCTTTT  ACGAAC
                                                  GC     G
GAM3229  221   SLC6A12 1  9875   NP_003035.2  3  746   ACTGATCACAGA        --    GCT       3  C  c  c

                                      TTCTTTCCCACC TGAGGTGGGA  GAATT   TGA
```

TCACAATC ACTCCACCCT CTTAG ACT
TT AC-
GAM3229 221 SLC7A5 1 15377 NP_003477.3 3 2600 GTGTTTTCAAGC A AGAAT 3 C c
c
ACAACCCACCAC TG GGTGGG TGCTTGAA
AACAAGCA AC CCACCC ACGAACTT
A AAC--
GAM3229 221 SLC9A8 1 5218 XP_030524.2 3 1513 AAGCACATCTCC AT CTT 3 C c
c
ATCTCTTCCACC TGAGGTGGGAGA TG GA
TCAGGCAG ACTCCACCTTCT AC CT
CT CT-
GAM3229 221 SMARCF1 1 10764 NP_006006.3 3 98 GCCCTTTATTTA GAGAA T 3 C c
c
TGCAAAACCACC TGAGGTGG TTGC TGAA
TCAGAATC ACTCCACC AACG ATTT
AA--- T
GAM3229 221 SMARCF1 1 10764 NP_060920.4 3 1939 GCCCTTTATTTA GAGAA T 3 C
c c
TGCAAAACCACC TGAGGTGG TTGC TGAA
TCAGAATC ACTCCACC AACG ATTT
AA--- T
GAM3229 221 SMARCF1 1 10764 NP_624361.1 3 98 GCCCTTTATTTA GAGAA T 3 C c
c
TGCAAAACCACC TGAGGTGG TTGC TGAA
TCAGAATC ACTCCACC AACG ATTT
AA--- T
GAM3229 221 SNAP23 1 15734 NP_003816.2 3 733 CCTGGTTCAAGC T----- TG 3 C c
c
AATTCTCCTGCC GAGG GGAGAATTGCTTGAA
TTGCCTCC TTCC CCTCTTAACGAACTT
CCTCCG GT
GAM3229 221 SNAP23 1 15734 NP_570710.1 3 733 CCTGGTTCAAGC T----- TG 3 C c
c
AATTCTCCTGCC GAGG GGAGAATTGCTTGAA
TTGCCTCC TTCC CCTCTTAACGAACTT
CCTCCG GT
GAM3229 221 SNARK 1 9680 NP_112214.1 3 795 CCGACCTCAGGT AGA TG 3 C c
c
GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT
GAM3229 221 SNTB2 1 5203 NP_006741.1 3 57 ACTGTCACAAGA A G A 3 C c c
AATATTTCCACC TGAGGTGGGAG ATT CTTG
TCAAAA ACTCCACCTTT TAA GAAC
A A A
GAM3229 221 SNTB2 1 5203 NP_570896.1 3 665 ACTGTCACAAGA A G A 3 C c c
AATATTTCCACC TGAGGTGGGAG ATT CTTG
TCAAAA ACTCCACCTTT TAA GAAC
A A A

GAM3229 221 SNX15 1 17861 NP_037438.2 3 329 CCAGGTTCAAGC TG 3 C b b
AGTTCTCCTGTC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCT CCTCTTGACGAACTT
GT
GAM3229 221 SNX15 1 17861 NP_680086.1 3 329 CCAGGTTCAAGC TG 3 C b b
AGTTCTCCTGTC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCT CCTCTTGACGAACTT
GT
GAM3229 221 SNX22 1 10075 NP_079074.1 3 578 CCGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 SNX27 1 4464 NP_112180.4 3 3303 CTGACCTCAAGT - A 3 C b b
AATCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCGGCCTC GCTCCACCC TCT AATGAACT
G -
GAM3229 221 SP110 1 11431 NP_004500.2 3 40 TGTAAAGACTGA A AT GA 3 C c c
AGCATCCCCACC TGAGGTGGG GA TGCTT
TCAGGATT ACTCCACCC CT ACGAA
- -- GT
GAM3229 221 SP110 1 11431 NP_536349.1 3 40 TGTAAAGACTGA A AT GA 3 C c c
AGCATCCCCACC TGAGGTGGG GA TGCTT
TCAGGATT ACTCCACCC CT ACGAA
- -- GT
GAM3229 221 SPCX 1 6614 NP_775260.1 5 59 CTGGGTTCAAGC TG----- A 3 C c c
AATCCTCCCACC AGGTGGGAG ATTGCTTGAA
TGTGCCTC TCCACCCTC TAACGAACTT
CTCCGTG C
GAM3229 221 SS18 1 10286 NP_005628.1 3 1733 CCAGGTTCAAGC TG 3 C b b
AGTTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTGACGAACTT
GT
GAM3229 221 TAF11 2 5021 NP_005634.1 3 577 CTGGCTTCAAGC TG A 3 C c c
AGTCCTCCTGCC TGAGG GGAG ATTGCTTGAA
TCAGCCTC ACTCC CCTC TGACGAACTT
GT C
GAM3229 221 TAF11 2 16874 NP_005634.1 3 440 CTGGGCTTAAGT AA TG 3 C c c
GACCCTCCCACC TGAGGTGGGAG T CTTGA
TCAGTCTC ACTCCACCCTC A GAATT
CC GT
GAM3229 221 TAL1 2 3829 NP_003180.1 3 2575 CTGGCTTCAGGC T----- TG 3 C c b
AATTCTCCTGCC GAGG GGAGAATTGCTTGAA
TTTGCCTC TTCC CCTCTTAACGGACTT
CTCCGT GT
GAM3229 221 TAL1 2 5904 NP_003180.1 3 2433 CTGGGCTCAAGC A 3 C b b
AATCCTCTCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACTCTC TAACGAACT
C
GAM3229 221 TAPBP 2 9729 NP_003181.3 3 423 CTGACCTCAGGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA

TCAGCCTC ACTCCACCC TCT A GGACT
G - GT
GAM3229 221 TAPBP 2 12850 NP_003181.3 3 288 CTGGGTTCAAGC GGG 3 C c c

AATTCTGTGGCT TGAGGT AGAATTGCTTGAA
TCAGCCTC ACTTCG TCTTAACGAACTT
GTG
GAM3229 221 TEAD3 1 11870 NP_003205.1 3 1026 TGTTCCCTTAGG A TT 3 C c c
TTTTTCCCCACC TGAGGTGGG GAA GCTTGA
TCAATTTA ACTCCACCC CTT TGGATT
- TT
GAM3229 221 TES 1 16668 NP_056456.1 3 747 TTTATTTTGAGC TG TG 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT AA
TCAGCCTC ACTCC CCTCTTAACGA TT
GT GT
GAM3229 221 TES 1 16668 NP_690042.1 3 747 TTTATTTTGAGC TG TG 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT AA
TCAGCCTC ACTCC CCTCTTAACGA TT
GT GT
GAM3229 221 TGFBI 1 15372 NP_000349.1 3 370 CATGAATCAAGC G GAA 3 C c c

AATCCAGCCTCA TGAGGT GGA TTGCTTGA
TGGGAAGT ACTCCG CCT AACGAACT
A ---
GAM3229 221 TGIF2 1 18631 NP_068581.1 3 1507 CCGGGTTCAAGC TG AG 3 C c
c
AATTATTTGCCT TGAGG GG AATTGCTTGAA
CAGCCTCC ACTCC TT TTAACGAACTT
GT A-
GAM3229 221 TIM50L 1 5198 XP_053074.2 3 1466 CCGGGTTCAAGC A 3 C b b
AATGCTCCCGCC TGAGGTGGGAG ATTGCTTGAA
TCAACCTC ACTCCGCCCTC TAACGAACTT
G
GAM3229 221 TIMP3 1 10513 NP_000353.1 3 380 CACCCCTCTTGC A TT- TT 3 C c c

TTCTTCCCCACC TGAGGTGGG GAA GC GA
TCACCATC ACTCCACCC CTT CG CT
- CTT TT
GAM3229 221 TNFRSF1 2 2055 NP_003833.3 3 649 CTGGACTCAAGC - A 3 C b b
0B AGTCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCAGACTC ACTCCACCC TCT GACGAACT
G -
GAM3229 221 TNFRSF1 2 2055 NP_671716.1 3 649 CTGGACTCAAGC - A 3 C b b
0B AGTCTGCCCACC TGAGGTGGG AGA TTGCTTGA
TCAGACTC ACTCCACCC TCT GACGAACT
G -
GAM3229 221 TNFRSF1 2 2703 NP_003833.3 3 513 TCAGGCTCAAGC 3 C b b
0B GATTCTCCCACC TGAGGTGGGAGAATTGCTTGA
TCAGCCAT ACTCCACCCTCTTAGCGAACT

GAM3229 221 TNFRSF1 2 2703 NP_671716.1 3 513 TCAGGCTCAAGC 3 C b b
0B GATTCTCCCACC TGAGGTGGGAGAATTGCTTGA
TCAGCCAT ACTCCACCCTCTTAGCGAACT

GAM3229 221 TNFRSF1 1 18341 NP_003830.1 3 571 AGCAATCCAAGT A TG A 3 C c
c
1A GATCCTCCCACC TGAGGTGGGAG AT CTTG
TCAACCTT ACTCCACCCTC TA GAAC
C GT C
GAM3229 221 TP53I5 1 11115 XP_290532.2 5 1764 CGCTGCGGGCAG --- -- A 3 C c c
GGTTCTCCCAGC TGAGGT GGGAGAAT TGCTTG
ACCTCACT ACTCCA CCCTCTTG ACGGGC
CGA GG G
GAM3229 221 TPMT 1 8393 NP_000358.1 3 621 CTGACCTCAGGT - A TG 3 C c c
GATCTACCCACC TGAGGTGGG AGA T CTTGA
TCGGCCTC GCTCCACCC TCT A GGACT
A - GT
GAM3229 221 TPSG1 1 10281 NP_036599.1 5 10 AGGTATTCAAGT TG 3 C b b
GATTCTCCCATC TGAGGTGGGAGAAT CTTGAA
TCGGTCTC GCTCTACCCTCTTA GAACTT
GT
GAM3229 221 TRAM2 1 14318 NP_036420.1 3 2458 TTGCCATCAAGC TGG AA 3 C c
c
AACCCTCATTCT TGAGG GAG TTGCTTGA
CATGCCTG ACTCT CTC AACGAACT
TA- CC
GAM3229 221 TRIM16 1 14800 NP_006461.2 3 308 CCGAGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 TRIM5 1 11399 NP_149023.1 3 710 TCAGATTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 TRPV1 2 3431 NP_061197.3 3 423 CTGGATTCCAGC TG T 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCGGCTTC GCTCC CCTCTTAACGA CTT
GT C
GAM3229 221 TRPV1 2 3431 NP_542435.1 3 423 CTGGATTCCAGC TG T 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCGGCTTC GCTCC CCTCTTAACGA CTT
GT C
GAM3229 221 TRPV1 2 3431 NP_542436.1 3 423 CTGGATTCCAGC TG T 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCGGCTTC GCTCC CCTCTTAACGA CTT
GT C
GAM3229 221 TRPV1 2 3431 NP_542437.1 3 423 CTGGATTCCAGC TG T 3 C c c
AATTCTCCTGCC TGAGG GGAGAATTGCT GAA
TCGGCTTC GCTCC CCTCTTAACGA CTT
GT C

GAM3229 221 TRPV1 2 14539 NP_061197.3 3 561 CTGACCTCAGGT AGA TG 3 C c c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT

GAM3229 221 TRPV1 2 14539 NP_542435.1 3 561 CTGACCTCAGGT AGA TG 3 C c c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT

GAM3229 221 TRPV1 2 14539 NP_542436.1 3 561 CTGACCTCAGGT AGA TG 3 C c c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT

GAM3229 221 TRPV1 2 14539 NP_542437.1 3 561 CTGACCTCAGGT AGA TG 3 C c c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
GCC GT

GAM3229 221 TU12B1-TY 3 1925 NP_057659.1 3 2915 CCAGGTTCAAGC G 3 C b b

AATTTTCGTGCC TGAGGTG GAGAATTGCTTGAA
TCAGCCTC ACTCCGT CTTTTAACGAACTT
G

GAM3229 221 TU12B1-TY 3 3770 NP_057659.1 3 5262 CCTTCCTGCACG G T T A 3 C c b

CCATTCTCCACC TGAGGTGG AGAAT GC TG
TCAGTATC ACTCCACC TCTTA CG AC
- C C G

GAM3229 221 TU12B1-TY 3 11645 NP_057659.1 3 3050 CTAGCCTCAAGT - T 3 C b b

GTTCTGCCCACC TGAGGTGGG AGAAT GCTTGA
TCAGCCTT ACTCCACCC TCTTG TGAACT
G -

GAM3229 221 TUCAN 1 16766 NP_055774.1 3 2652 CTGGCCTCAAGT AGA TG 3 C c c

GATCCACCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GAACT
ACC GT

GAM3229 221 TUFT1 1 5345 NP_064512.1 3 1479 CTGACCTCAGGT AGA TG 3 C c c

GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCTTC GCTCCACCC TA GGACT
ACC GT

GAM3229 221 TUWD12 1 9384 NP_758440.1 3 273 AAGCATTCAAGC TG --- A 3 C c c

AACTCTGTATTT TGAGG GG AGA TTGCTTGAA
TCCTCATA ACTCC TT TCT AACGAACTT
TT ATG C

GAM3229 221 TXL-2 1 15613 NP_835231.1 3 522 TCTTTCCGTGTA GAATT A 3 C c c

AGCTATCCCACC TGAGGTGGGA GCTTG
TCAGCGGC ACTCCACCCT CGAAT
AT--- G

GAM3229 221 UBF-fl 1 12691 NP_116217.1 3 1039 CTGGGCTCAAGC - AT 3 C b b
ACTCTGCCCACC TGAGGTGGG AGA TGCTTGA
TCAGCCTC ACTCCACCC TCT ACGAACT
G C-

GAM3229 221 UMPS 1 14691 NP_000364.1 3 445 GACCTCCCAGGT A TG A 3 C c c

GATCCTCCCACC TGAGGTGGGAG AT CTTG
TCAGCTTC ACTCCACCCTC TA GGAC
C GT C

GAM3229 221 USP22 2 1601 XP_042698.2 3 2083 CTGGGTTCAAGC A G 3 C c c
AGTTCTCGTGCC TG GGTG GAGAATTGCTTGAA
GCAGCCTC AC CCGT CTCTTGACGAACTT
G G

GAM3229 221 USP22 2 14801 XP_042698.2 3 2205 CTGACCTCAGGC AGA 3 C c c

GATCCACCCACC TGAGGTGGG ATTGCTTGA
TCAGCGTC ACTCCACCC TAGCGGACT
ACC

GAM3229 221 VDU1 1 10537 NP_055832.2 3 471 CTGACCTCAGGT AGA TG 3 C c c

GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GGACT
ACC GT

GAM3229 221 VENTX2 1 19528 NP_055283.1 3 364 CTGGGTTCAAGC G 3 C b b
AATTCTCCAGCC TGAGGT GGAGAATTGCTTGAA
TCAGCCTC ACTCCG CCTCTTAACGAACTT
A

GAM3229 221 VHL 1 8629 NP_000542.1 3 1169 CTGACCTCAGGT AGA TG 3 C c c

GATCCGCCCACC TGAGGTGGG AT CTTGA
TCAGCCTC ACTCCACCC TA GGACT
GCC GT

GAM3229 221 VIK 1 3535 NP_612503.1 3 912 CTGGCCTCAAGC TG----- A 3 C c c
GATCCTCCCACC AGGTGGGAG ATTGCTTGA
TGTCCTCC TCCACCCTC TAGCGAACT
CCTCCTG C

GAM3229 221 VMP 1 5123 NP_542454.2 3 684 CTGGGCTCAAGC A 3 C b b
GATCCTCCCACC TGAGGTGGGAG ATTGCTTGA
TCAGCCTC ACTCCACCCTC TAGCGAACT
C

GAM3229 221 VNN1 1 16216 NP_004657.1 3 1474 AATCCTCAGAGC TG-- - 3 C c c
AATTCTCTGTAT TGAGG GGAGAATTGCT TGA
TCTCATAT ACTCT TCTCTTAACGA ACT
TATG G

GAM3229 221 VPS33A 1 12847 NP_075067.2 3 291 CTAGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT

```
                                                GT
GAM3229  221   WBP3   1  13231 NP_783863.2  3  4541  CTGCTTTCAAGC  A    AGAAT          3  C  c
c
                                ACCACACCCACC TG GGTGGG    TGCTTGAA
                                CAGATGAC    AC CCACCC    ACGAACTT
                                        -    ACACC
GAM3229  221   WBSCR23 1  4757  NP_079318.1  3  40   TCAGGTTCAAGC T-----   TG           3  C  c
c
                                AATTCTCCTGCC     GAGG  GGAGAATTGCTTGAA
                                TCCGCCTC         CTCC  CCTCTTAACGAACTT
                                      CTCCGC    GT
GAM3229  221   WDFY3  1  18416 NP_848700.1  5  35   CCAGGTTCAAGC   G TG             3  C  c  c

                                AATTCTCCTGCA TGA G  GGAGAATTGCTTGAA
                                TCAGCCTC    ACT C  CCTCTTAACGAACTT
                                         A GT
GAM3229  221   WFDC8  1  15411 NP_852611.1  3  225  CTGACCTCAGGT       AGA  TG         3  C  c
 c
                                GATCCACCCACC TGAGGTGGG   AT  CTTGA
                                TCAGCCTC    ACTCCACCC   TA  GGACT
                                          ACC  GT
GAM3229  221   WHSC1  2  5144  NP_579889.1  3  3986  CTTGGTTCCAGC    TG       T       3  C  c  c

                                AATTCTTCTGCC TGAGG  GGAGAATTGCT GAA
                                TCAGCCTC    ACTCC  CTTCTTAACGA CTT
                                          GT         C
GAM3229  221   WHSC1  2  18856 NP_015627.1  5  349  GCTGCACGTCAG      GA  AT          3  C  c
c
                                GTGTCCTCCACC TGAGGTGG  GA  TGCTTGA
                                TCAGTACT    ACTCCACC  CT  GTGGACT
                                          TC  --
GAM3229  221   WHSC1  2  18856 NP_055734.1  5  349  GCTGCACGTCAG      GA  AT          3  C  c
c
                                GTGTCCTCCACC TGAGGTGG  GA  TGCTTGA
                                TCAGTACT    ACTCCACC  CT  GTGGACT
                                          TC  --
GAM3229  221   WHSC1  2  18856 NP_579877.1  5  349  GCTGCACGTCAG      GA  AT          3  C  c
c
                                GTGTCCTCCACC TGAGGTGG  GA  TGCTTGA
                                TCAGTACT    ACTCCACC  CT  GTGGACT
                                          TC  --
GAM3229  221   WHSC1  2  18856 NP_579878.1  5  169  GCTGCACGTCAG      GA  AT          3  C  c
c
                                GTGTCCTCCACC TGAGGTGG  GA  TGCTTGA
                                TCAGTACT    ACTCCACC  CT  GTGGACT
                                          TC  --
GAM3229  221   WHSC1  2  18856 NP_579879.1  5  349  GCTGCACGTCAG      GA  AT          3  C  c
c
                                GTGTCCTCCACC TGAGGTGG  GA  TGCTTGA
                                TCAGTACT    ACTCCACC  CT  GTGGACT
```

TC --
GAM3229 221 WHSC1 2 18856 NP_579888.1 5 349 GCTGCACGTCAG GA AT 3 C c c
GTGTCCTCCACC TGAGGTGG GA TGCTTGA
TCAGTACT ACTCCACC CT GTGGACT
TC --
GAM3229 221 XPO5 1 18608 NP_065801.1 3 98 CTAGGCCCTTCT G AAT TT 3 C c c
TGCACTGCCACC TGAGGTGG AG TGC GAA
TCACTTTC ACTCCACC TC ACG CTT
G --- TT
GAM3229 221 XRCC2 2 10425 NP_005422.1 3 337 TTGGGTTCAAGT TG 3 C b b
GATTCTTCCACC TGAGGTGGGAGAAT CTTGAA
TCAGCCTC ACTCCACCTTCTTA GAACTT
GT
GAM3229 221 XRCC2 2 14540 NP_005422.1 3 472 CTGACCTCAAGT AGA TG 3 C c b
GATCCACCCACC TGAGGTGGG AT CTTGA
TCGGCCTC GCTCCACCC TA GAACT
ACC GT
GAM3229 221 ZAP 1 10075 NP_064504.2 3 367 CCGGGTTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT
GAM3229 221 ZFP42 1 20009 NP_777560.1 3 837 CTGACCTCCAGT - A TG T 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CT GA
TCGGCCTC GCTCCACCC TCT A GA CT
G - GT C
GAM3229 221 ZFP64 1 3840 NP_060667.1 3 330 CTGACCTCAAGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GAACT
G - GT
GAM3229 221 ZFP64 1 3840 NP_071371.2 3 330 CTGACCTCAAGT - A TG 3 C c c
GATCTGCCCACC TGAGGTGGG AGA T CTTGA
TCAGCCTC ACTCCACCC TCT A GAACT
G - GT
GAM3229 221 ZFP95 1 8365 NP_055384.1 3 93 ACAACTTCAAGC G G T 3 C c c
ATTTTTCCAGCG TGA GT GGAGAA TGCTTGAA
TTACCATC ATT CG CCTTTT ACGAACTT
G A T
GAM3229 221 ZFP95 1 8365 NP_659570.1 3 93 ACAACTTCAAGC G G T 3 C c c
ATTTTTCCAGCG TGA GT GGAGAA TGCTTGAA
TTACCATC ATT CG CCTTTT ACGAACTT
G A T
GAM3229 221 ZNF138 1 6482 XP_088081.1 3 1094 ATGCTTTTAACC GG C 3 C c c
AATTCTCAAATC TGAGGT GAGAATTG TTGAA
TTACTAAA ATTCTA CTCTTAAC AATTT
AA C
GAM3229 221 ZNF214 1 8097 NP_037381.1 5 202 GTACATCACGGC G ATT - 3 C c c

TTCTCTCCCACG TGA GTGGGAGA GCT TGA
TTAAGACT ATT CACCCTCT CGG ACT
G CTT C

GAM3229 221 ZNF264 1 1422 NP_003408.1 3 2663 CCGGGTTCAAGC TG GAG 3 C c c

AATTAACTGCCT TGAGG G AATTGCTTGAA
CAGCTTCC ACTCC C TTAACGAACTT
GT AA-

GAM3229 221 ZNF273 1 16389 XP_088082.1 3 902 CCAGATTCAAGC TG 3 C b b
AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGCCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 ZNF398 1 16846 NP_065832.1 5 314 CCTGGTTCAAGC GG 3 C b b
AATTCTCATGCC TGAGGT GAGAATTGCTTGAA
TCAGCCTC ACTCCG CTCTTAACGAACTT
TA

GAM3229 221 ZNF430 1 5502 NP_079465.1 3 407 AAGCTTTTAACC GG C 3 C c c
AATTCTCAAACC TGAGGT GAGAATTG TTGAA
TTACTAAA ATTCCA CTCTTAAC AATTT
AA C

GAM3229 221 ZNF431 1 16935 XP_086098.2 3 1546 CTGGTTTCAAGC TG A 3 C c c

AACTCTTCTGCC TGAGG GGAGA TTGCTTGAA
TCAGCATC ACTCC CTTCT AACGAACTT
GT C

GAM3229 221 ZNF440 2 8337 NP_689570.1 3 1420 TCCAGACCTCAT A CT 3 C c b
GATTTACCCACC TGAGGTGGG GAATTG TGA
TCGGCCTC GCTCCACCC TTTAGT ACT
A --

GAM3229 221 ZNF440 2 13052 NP_689570.1 3 1283 CAGGGTTCAAGC TG 3 C b b

AATTCTCCTGCC TGAGG GGAGAATTGCTTGAA
TCAGTCTC ACTCC CCTCTTAACGAACTT
GT

GAM3229 221 ZNF450 1 14177 NP_055612.1 3 1147 CTGGGCTCAAGC AA 3 C b b

AACCCTCCCACC TGAGGTGGGAG TTGCTTGA
TTAGCCTC ATTCCACCCTC AACGAACT
CC

GAM3229 221 ZNF74 1 15580 NP_003417.1 5 670 CCGGGTTCAAAC TGC 3 C c c
TATTCTCCCGCC TGAGGTGGGAGAAT TTGAA
TCAACCTC ACTCCGCCCTCTTA AACTT
TCA

GAM3298 259 15E1.2 1 7468 XP_290596.1 3 807 GGCTCACTCCTG CATAG T 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -

GAM3298 259 ABCC13 1 3706 NP_742021.1 3 1465 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 ACATE2 1 3706 NP_036464.1 3 374 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 ADCY1 1 14995 NP_066939.1 3 6275 GGCTCATGCCTG CATAG 6 A c c
TAAGCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCGA
GAM3298 259 ADCY7 1 17337 NP_001105.1 3 2266 AAAAATTACCTG CATAG 6 A c c
CAGGTATTTTCT AAAGTGCT TGCAGGTAG
TTTTATGA TTTTATGG ACGTCCATT

GAM3298 259 AGMAT 1 16781 NP_079034.2 3 516 GCCTCATGCCTG CATAG 6 A c c
TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 AK1 1 816 NP_000467.1 3 736 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 ALDH3A2 1 3706 NP_000373.1 3 839 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 ALDH9A1 1 3390 NP_000687.2 3 675 AATGTGAACTTG CA- T A 6 A c c
CCTAGTAAGCAC AAAGTGCT TAG GCAGGT
TTTGTCTC TTTCACGA ATC CGTTCA
ATG - A
GAM3298 259 ALTE 1 525 NP_004720.1 3 202 GGCTCCTGTCTA C----- T T 6 A c c
TAATCGCAGCAC AAAGTGCT ATAG GCAGG AG
TTTGGGAG TTTCACGA TATC TGTCC TC
CGCTAA - -
GAM3298 259 ANAPC7 1 16150 NP_057322.1 5 7 GGCTCATGCCTG CATAG 6 A c c
TAGTCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTG
GAM3298 259 APOL1 1 19832 NP_003652.2 3 632 GGCTCATGCCTG ATAG 6 A c c
TAATCCGAGCAC AAAGTGCTC TGCAGGTA
TTTGGGAG TTTCACGAG ATGTCCGT

CCTA
GAM3298 259 APOL1 1 19832 NP_663318.1 3 632 GGCTCATGCCTG ATAG 6 A c c
TAATCCGAGCAC AAAGTGCTC TGCAGGTA
TTTGGGAG TTTCACGAG ATGTCCGT
CCTA
GAM3298 259 AQP6 1 15019 NP_445738.1 5 809 AAGGGCTGCCAC CAT -- 6 A c c
TGCACTTAGCAC AAAGTGCT AGTGCA GGTAG
TTTCAGGC TTTCACGA TCACGT CCGTC
T-- CA
GAM3298 259 ASB1 1 4892 NP_057198.1 3 1954 GTTAGCTCCCTG T T T T 6 A c c
CACTCTGGCTCT AAAG GC CA AGTGCAGG AG
TTACTGGC TTTC CG GT TCACGTCC TC
T - C C
GAM3298 259 ASB13 1 17002 NP_078977.2 3 570 GTGTGGATGCTT A TGC 6 A c c
TTCCTGGAGCAC AAAGTGCTC TAG AGGTA
TTTCCAAG TTTCACGAG GTC TTCGT
- CTT
GAM3298 259 ASB9 1 4781 NP_076992.1 3 469 GCATATCTACTG CATA G 6 A c c
CATGCCAAGCAC AAAGTGCT GTGCAG TAG
TTTCTGCA TTTCACGA TACGTC ATC
ACCG -
GAM3298 259 ATF5 1 15319 NP_036200.2 3 128 GGCTTATGCTTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTTCGT
CCCTA
GAM3298 259 ATP1A2 1 3706 NP_000693.1 3 1243 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 BHMT2 1 6371 NP_060084.2 3 638 GACTCACACCTG CATAG A 6 A c c
CAATCCCAGCAC AAAGTGCT TGCAGGT
TTTGGGAG TTTCACGA ACGTCCA
CCCTA C
GAM3298 259 BPNT1 1 3706 NP_006076.2 3 57 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 BPNT1 1 3706 XP_035738.1 3 57 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 BTBD5 1 11724 NP_060128.1 3 1052 TCAAAATACCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA

GAM3298 259 BTN1A1 1 6923 NP_001723.1 3 1121 ACCTGTGTATTT TAGT 6 A c c

GCCCCTGAGCAC AAAGTGCTCA GCAGGTA
TTTCCTTT TTTCACGAGT CGTTTAT
CCC-

GAM3298 259 BTN3A1 1 2811 NP_008979.2 3 212 AGCTACAAGCAC - TA-- AG 6 A c
c

GCACTGAAGCAC AAAGTGCT CA GTGC GTAG
TTTACTGA TTTCACGA GT CACG CATC
A CACG AA

GAM3298 259 BTN3A2 1 16180 NP_008978.1 3 248 AGCTCATGCCTG CATAG 6 A c
c

TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGAAG TTTCACGA ATGTCCGT
TCCTA

GAM3298 259 C14orf1 1 11312 NP_689659.1 3 117 CAGACATACCTG T T T - 6 A c c
45 CAGCTTTGGCTC AAAG GC CA AG TGCAGGTA
TTTGGTAT TTTC CG GT TC ACGTCCAT
T - T G

GAM3298 259 C14orf5 1 14163 NP_660148.1 3 1795 CTATTCTTTATT C G C 6 A c c
2 TCAGTGTAGCAC AAAGTGCT ATA TG AGGTAG
TTTTAGAG TTTCACGA TGT AC TTTATT
- G -

GAM3298 259 C1orf34 1 840 XP_027172.1 3 4604 GGCTCATGCCTG CATAG 6 A c c

TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA

GAM3298 259 C20orf1 1 19207 NP_060366.1 3 238 ATGCAGAGCCTG A T T A 6 A c c
1 CACTCTGGCACT A AGTGC CA AGTGCAGGT
CGCTGAAG G TCACG GT TCACGTCCG
C - C A

GAM3298 259 C20orf1 1 7920 NP_112181.1 3 958 TGCTTGCTGTTA - AGT----- 6 A c c
29 GAGATGTAGCAC AAAGTGCT CAT GCAGGTA
TTTATCCT TTTCACGA GTA CGTTCGT
T GAGATTGT

GAM3298 259 C20orf1 1 9547 NP_542790.1 3 10 CAGCTGTGATGC - ---- A 6 A c c
64 ATTATTGAGCAC AAAGTGCTCA TAGTGCA GGT
TTTAGCTG TTTCACGAGT ATTACGT TCG
T AGTG A

GAM3298 259 C20orf1 1 16567 NP_291020.1 3 1026 TGGTTCTGCCTG CTCAT 6 A c
c
69 CACTTACTTTGT AAAGTG AGTGCAGGTAG
AATGCCAC TTTCAT TCACGTCCGTC

GAM3298 259 C6orf96 1 3433 NP_060379.1 3 107 GCCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTCGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 CABYR 1 5933 NP_036321.2 3 138 CACCGCCACCTG T TA A 6 A c c

CACCTGGGCCTT AAAG GCTCA GTGCAGGT
TTCCCCAA TTTC CGGGT CACGTCCA
- C- C
GAM3298 259 CABYR 1 5933 NP_722452.1 3 138 CACCGCCACCTG T TA A 6 A c c

CACCTGGGCCTT AAAG GCTCA GTGCAGGT
TTCCCCAA TTTC CGGGT CACGTCCA
- C- C
GAM3298 259 CAMK2D 1 879 NP_742125.1 3 973 TTTTGAAGGTAG CAT C G 6 A c
c

CTATACTAGCAC AAAGTGCT AGTG AG TA
TTTTGATC TTTCACGA TCAT TC AT
--- A G
GAM3298 259 CAMK2D 1 879 NP_742126.1 3 929 TTTTGAAGGTAG CAT C G 6 A c
c

CTATACTAGCAC AAAGTGCT AGTG AG TA
TTTTGATC TTTCACGA TCAT TC AT
--- A G
GAM3298 259 CD28 1 6352 NP_006130.1 3 863 GGCTCATGCTTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTTCGT
CCCTA
GAM3298 259 CD68 1 3706 NP_001242.1 3 171 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 CDAN1 1 12246 XP_085300.3 3 523 GGCTCATGCCTG CATAG 6 A c
c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 CFL2 1 16417 NP_068733.1 3 515 TATAACACTATG CA - A 6 A c c
CATTAAAAGCAC AAAGTGCT TAGTGCA GGT
TTTTTGTA TTTCACGA ATTACGT TCA
AA A C
GAM3298 259 CLDN15 1 16467 NP_612438.1 3 531 GGCTCATGCCTG CATAG 6 A c
c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGTAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 CNNM3 1 1930 NP_060093.2 3 447 CCAACCTATCGC CA - A 6 A c c
TGCTGGCAGCAC AAAGTGCT TAGT GC GGTAG
TTTTTGAG TTTCACGA GTCG CG CTATC
CG T -

GAM3298 259 COPA 1 815 NP_004362.1 3 308 GGCTCATACCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA
GAM3298 259 CRN 1 5868 NP_006578.2 3 1426 AGATACTACCTG TC-- --- 6 A c c
CAATTTTATACA AAAGTGC ATAG TGCAGGTAG
TGTATTTT TTTTATG TATT ACGTCCATC
TACA TTA
GAM3298 259 CRTAM 1 840 NP_062550.1 3 495 GGCTCATGCCTG CATAG 6 A c
c
TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 CT120 1 13728 NP_079068.1 3 188 AACTTGCCCTAT CATAG 6 A c c
TTGCAAAAGCAC AAAGTGCT TGCAGGTAG
TTTTGTAG TTTCACGA ACGTTTATC
AA---
GAM3298 259 CYCS 1 5995 NP_061820.1 3 3357 CGCTCATGCCTG CATAGT 6 A c
c
TGGTCCCAGCAC AAAGTGCT GCAGGTA
TTTGGGAG TTTCACGA TGTCCGT
CCCTGG
GAM3298 259 DDOST 1 3706 NP_005207.2 3 296 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 DDX51 2 5949 NP_778236.1 3 689 GGCAAATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 DDX51 2 6665 NP_778236.1 3 396 GGCTCATGCCTG CATAG 6 A c
c
TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 DDX54 1 8510 NP_076977.2 3 1544 TGCTGTCACCTG C----- A 6 A c c
CACTATCCAATT AAAGTGCT ATAGTGCAGGT
AGTATTTT TTTTATGA TATCACGTCCA
TTAACC C
GAM3298 259 DDX9 1 12897 NP_085077.1 5 10 TGCTGCTACCTG T ATAGT- 6 A c
c
CTTTCCAGAGCC AAAG GCTC GCAGGTAG
TTTCATCA TTTC CGAG CGTCCATC
- ACCTTT
GAM3298 259 DKFZp43 1 13379 XP_210937.1 3 2128 TGTGCCAGGTAC --- A- 6 A c c
4E1119 TGTTCTGAGCAC AAAGTGCTCA TAGTGC GGTA
TTTACAAA TTTCACGAGT GTCATG CCGT

CTT GA
GAM3298 259 DKFZP58 1 13787 XP_045876.1 3 552 CCTTCATGCCTG CATAG 6 A c c
6C1324 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 DKFZp76 1 3706 NP_689755.2 3 617 GGCTCATGCCTG CATAG 6 A c c
1G058 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 DKFZP76 1 3706 NP_113662.1 3 1184 GGCTCATGCCTG CATAG 6 A c c
1G1913 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 DKFZp76 1 13788 NP_060892.1 5 1219 TGAACATGCTGA TAG A- 6 A c c
1K1423 GCAGTTGAGCAC AAAGTGCTCA TGC GGTA
TTTTCCAT TTTCACGAGT ACG TCGT
TG- AG
GAM3298 259 EDG3 1 6456 NP_005217.1 5 2324 GTCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 EIF2C1 1 17274 NP_036331.1 3 722 TAATACTTAAGG A------ T --- 6 A c c
CACTATGGCACT AAGTGC CATAGTGC AGGTA
TAGCTTTG TTCACG GTATCACG TTCAT
GTTTCGA - GAA
GAM3298 259 EPB41L4 1 5651 NP_061987.2 3 1425 TTAATTGCTAGC TAG- A 6 A c c
B AAGGCTGAGCAC AAAGTGCTCA TGC GGTAG
TTTTCCAT TTTCACGAGT ACG TCGTT
CGGA A
GAM3298 259 ERAP140 1 7576 XP_059748.2 3 1346 GGCTCTTGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CCCTA
GAM3298 259 ERBB3 1 6353 NP_001973.1 3 673 GGCTCATGCCTG CATAG 6 A c c
TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 ET 1 1920 NP_077287.1 3 660 GGCTCATGCCTG CATAGT 6 A c c
TGGTCCCAGCAC AAAGTGCT GCAGGTA
TTTGGGAG TTTCACGA TGTCCGT
CCCTGG
GAM3298 259 EVA1 1 11961 NP_005788.1 3 1753 TAGTGTCTCCTT A- TGC T 6 A c c

CCTAAAGAGCAC AAAGTGCTC TAG AGG AG
TTTTGTAT TTTCACGAG ATC TCC TC
AA CT- -

GAM3298 259 F2RL3 1 12961 NP_003941.1 3 884 GGCTCACACCTG CATAG A 6 A c c

CAATCCCAGCAC AAAGTGCT TGCAGGT
TTTGGAAG TTTCACGA ACGTCCA
CCCTA C

GAM3298 259 FANCD2 1 9757 NP_149075.2 3 432 GGCTCATGCTTG CATAG 6 A c c

TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTTTGAG TTTCACGA ATGTTCGT
TCCTA

GAM3298 259 FBLP-1 1 3706 XP_290943.1 3 733 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FBXO27 1 3706 NP_849142.1 3 629 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FBXO27 1 3706 XP_059045.1 3 629 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FGFR2 1 3706 NP_075262.1 3 77 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FGFR2 1 3706 NP_075263.1 3 77 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FKBP14 2 3706 NP_060416.1 3 614 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FKBP14 2 17308 NP_060416.1 3 1228 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FKSG17 1 18744 NP_114420.1 3 272 TGGCTCATGCCT CAT TG- 6 A c c

GAATCTCAGCAC AAAGTGCT AG CAGGTA
TTTGGGAG TTTCACGA TC GTCCGT
C-- TAA

GAM3298 259 FLJ1005 1 841 NP_060455.1 3 1545 GGTTCATGCCTG CATAG 6 A c c
8 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FLJ1066 1 3983 NP_060643.1 3 263 CATGGCTGCCTG CATAG 6 A c c
5 TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTC
CCCTA

GAM3298 259 FLJ1085 1 16806 NP_060716.1 3 945 CAGATATTCCAC CATAG A 6 A c c
3 CTGTAATAGCAC AAAGTGCT TGCAGGT
TTTGGAAC TTTCACGA ATGTCCA
TA--- C

GAM3298 259 FLJ1101 1 1510 NP_060769.1 3 59 TAGTCCTACTGA AGTGCA 6 A c c
1 GAAAATGAGCAC AAAGTGCTCAT GGTAG
TTTGATCA TTTCACGAGTA TCATC
AAAGAG

GAM3298 259 FLJ1125 1 6479 NP_060840.1 3 1596 GGCTCACACCTG CAT A 6 A c c
9 TATTCCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TTATGTCCA
CCC C

GAM3298 259 FLJ1126 1 3706 NP_062553.1 3 957 GGCTCATGCCTG CATAG 6 A c c
7 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FLJ1199 1 17309 NP_079252.1 3 2091 GGCTCATGCCTG CATAG 6 A c c
6 TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTG

GAM3298 259 FLJ1213 1 18184 NP_079256.2 3 854 AAGGACTGCGAG C A AG 6 A c c
2 CACAGTCAGCAC AAAGTGCT AT GTGC GTAG
TTTGGCAG TTTCACGA TG CACG CGTC
C A AG

GAM3298 259 FLJ1227 1 19970 XP_290704.1 3 0 ACTGCCTGCTTG CA T 6 A c c
0 AAAGCACTTTCT AAAGTGCT TAG GCAGGTAG
GACCTACA TTTCACGA GTT CGTCCGTC
AA -

GAM3298 259 FLJ1259 1 2951 NP_079270.1 3 110 TCTGGGTACCAG - GCA 6 A c c
5 ACTACTGAGCAC AAAGTGCTCA TAGT GGTA
TTTCTGAC TTTCACGAGT ATCA CCAT

C GA-
GAM3298 259 FLJ1311 1 14687 NP_078817.1 3 500 GTCCCCTGCCTG CAT 6 A b b

4 CACTGGCACTTT AAAGTGCT AGTGCAGGTAG
GTCCAGTC TTTCACGG TCACGTCCGTC

GAM3298 259 FLJ1345 1 20122 XP_038291.5 3 1584 GGCTCATGCTTG CATAG 6 A c
c
6 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTTCGT
CCCTA
GAM3298 259 FLJ1362 1 16777 NP_079285.1 3 867 GGCTCATGCCTG CATAG 6 A c
c
1 TAATCGCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CGCTA
GAM3298 259 FLJ1408 1 13784 NP_079300.1 3 2254 GGCCCGAGGACC A CA A 6 A c
c
2 CACTGTGAGCAC A AGTGCTCATAGTG GGT
TCCACCCA C TCACGAGTGTCAC CCA
C -- G
GAM3298 259 FLJ1410 1 3706 NP_079302.1 3 843 GGCTCATGCCTG CATAG 6 A c
c
7 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ1439 1 7464 NP_116169.2 3 802 ATCATTTTCCTA CAT AG 6 A c c
9 CGGCGTTAGCAC AAAGTGCT AGTGC GTAG
TTTAAGCA TTTCACGA TTGCG CATC
--- G-
GAM3298 259 FLJ1464 1 816 NP_116207.1 3 303 GGCTCATGCCTG CATAG 6 A c
c
2 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ1488 1 17382 NP_116245.1 3 611 GGCTCATGCCTG CATAG 6 A c
c
8 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTCAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2005 1 841 NP_060114.1 3 258 GGTTCATGCCTG CATAG 6 A c c

9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2035 1 3706 NP_060251.1 3 1013 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 FLJ2045 1 16046 NP_060298.2 3 1222 GGCCCATGCCTG CATAG 6 A c c
2 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2046 1 3706 NP_060304.1 3 539 GGCTCATGCCTG CATAG 6 A c c
4 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2058 1 5838 XP_090970.4 5 386 GTTTGCAATATT CA T 6 A c c
2 TGTTTTAAGCAC AAAGTGCT TAG GCAGGTA
TTTGAAAC TTTCACGA ATT TGTTTAT
-- T
GAM3298 259 FLJ2070 1 3706 NP_060402.1 3 1026 GGCTCATGCCTG CATAG 6 A c c
0 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2114 1 20084 NP_073611.1 3 634 GGCACATGCCTG CATAG 6 A c c
4 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2136 1 18903 NP_079078.1 3 1286 GGCTCATGCCTG CATAG 6 A c c
9 TAAACCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCAA
GAM3298 259 FLJ2167 1 3706 NP_112160.1 3 36 GGCTCATGCCTG CATAG 6 A c c
3 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2187 1 3706 NP_075392.1 3 2325 GGCTCATGCCTG CATAG 6 A c c
0 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2304 1 6627 NP_079433.1 3 1032 AGCTTATACCTG CATAG 6 A c c
2 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
TCCTA
GAM3298 259 FLJ2312 1 730 NP_079039.1 3 678 GATTTGGGACCT C G C A 6 A c c
9 TCATATCAGCAC AAAGTGCT ATA TG AGGT
TTTGGACC TTTCACGA TAT AC TCCA
C - T G
GAM3298 259 FLJ2323 1 14990 NP_079219.1 3 622 GGCTCATGCCTG CATAG 6 A c c

5 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAT TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2336 1 17938 NP_075564.1 3 994 GGCTCATGCCTG CATAG 6 A c
c
0 TGATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA GTGTCCGT
CCCTA
GAM3298 259 FLJ2344 1 8160 NP_079101.1 3 91 GGCTCATGCCTG CATAG 6 A c
c
7 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2349 1 3706 NP_073598.1 3 352 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2349 1 3706 NP_073598.1 3 1029 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ2375 1 5102 NP_689495.1 3 696 ATACTACAATTG CAT -- 6 A c c
1 CACTTCCAGCAC AAAGTGCT AGTGCAG GTAG
TTTGAGAA TTTCACGA TCACGTT CATC
CCT AA
GAM3298 259 FLJ2383 1 8593 NP_689963.1 3 1131 GGCTCATGCCTG CATAG 6 A c
c
4 TAATGCCAGCAC AAAGTGCT TGCAGGTA
TTTGCCAA TTTCACGA ATGTCCGT
CCGTA
GAM3298 259 FLJ2517 1 8989 NP_653271.1 3 491 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTCGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3031 1 14675 NP_742148.1 3 15 TGGCTCATGCCT CATA 6 A c c
7 GTATCCCAGCAC AAAGTGCT GTGCAGGTA
TTTGGGAG TTTCACGA TATGTCCGT
CCC-
GAM3298 259 FLJ3089 1 3706 NP_689943.1 3 299 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3120 1 3706 NP_694568.1 3 892 GGCTCATGCCTG CATAG 6 A c
c
8 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT

CCCTA
GAM3298 259 FLJ3143 1 7468 NP_689709.1 3 1106 GGCTCACTCCTG CATAG T 6 A c c
4 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 FLJ3165 1 18701 NP_694572.1 3 181 AGATTAAACTCT T G - A 6 A c c
9 GATTTTGAGCAC AAAGTGCTCA AGT CAG GT
TTTGTGCT TTTCACGAGT TTA GTC CA
T - T A
GAM3298 259 FLJ3184 1 3706 NP_689700.1 3 188 GGCTCATGCCTG CATAG 6 A c c
2 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3188 1 9354 NP_689673.1 3 784 TGGCTCATGCCT CATAG 6 A c c
2 GTAATCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTA-
GAM3298 259 FLJ3202 1 840 NP_775853.2 3 5130 GGCTCATGCCTG CATAG 6 A c c
9 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 FLJ3283 1 16532 NP_689701.1 3 423 CTCCTACCACCC A CA--- 6 A c c
3 TTATTGGAGCAC AAAGTGCTC TAGTG GGTAG
TTTGTACT TTTCACGAG GTTAT CCATC
- TCCCA
GAM3298 259 FLJ3316 1 10382 NP_689896.1 3 24 AGAGTACTAATT C CA-- 6 A c c
7 CACTATGAACAC AAAGTG TCATAGTG GGTA
TTTTGTCA TTTCAC AGTATCAC TCAT
A TTAA
GAM3298 259 FLJ3350 1 17309 NP_689530.1 3 1211 GGCTCATGCCTG CATAG 6 A c c
5 TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 FLJ3491 1 3706 NP_694995.1 3 1592 GGCTCATGCCTG CATAG 6 A c c
7 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3722 1 3706 NP_787113.1 3 391 GGCTCATGCCTG CATAG 6 A c c
8 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3869 2 3706 NP_848608.1 3 1438 GGCTCATGCCTG CATAG 6 A c c

0 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3869 2 7398 NP_848608.1 3 448 GGATCACACCTG CATAG A 6 A c c
0 CAATCCCAGCAC AAAGTGCT TGCAGGT
TTTGGGAG TTTCACGA ACGTCCA
CCCTA C
GAM3298 259 FLJ3899 1 3706 NP_776188.1 3 184 GGCTCATGCCTG CATAG 6 A c c
1 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ3900 1 16046 NP_848616.1 3 1230 GGCCCATGCCTG CATAG 6 A c c
5 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FLJ9016 1 3706 NP_699169.1 3 442 GGCTCATGCCTG CATAG 6 A c c
5 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 FRSB 1 840 NP_005678.2 3 1090 GGCTCATGCCTG CATAG 6 A c c
TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 GALNT7 1 6665 NP_473451.2 3 900 GGCTCATGCCTG CATAG 6 A c c
TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 GBP4 1 7240 NP_443173.2 3 2518 ACTCATTGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CCCTA
GAM3298 259 GK001 1 11534 NP_064583.1 3 1083 AGGCCCATGTAT A----- ATA 6 A c c
CTGCACGAGCAC AAGTGCTC GTGCAGGTA
TTAGCTTG TTCACGAG CACGTCTAT
GTTCGA ---
GAM3298 259 GLO1 1 4209 NP_006699.1 3 1262 CCGTGCTTGTAC - A-- 6 A c c
TGCTAGAAGCAC AAAGTGCT C TAGTGCAGGTA
TTTATGTT TTTCACGA G GTCATGTTCGT
A ATC
GAM3298 259 GPR6 1 4712 NP_005275.1 3 360 TCCAATACTGCT C GC 6 A c c
TAATTATAGCAC AAAGTGCT ATAGT AGGTAG
TTTATTTT TTTCACGA TATTA TTCGTC

- A-
GAM3298 259 GPRK7 1 12104 NP_631948.1 3 1191 GGCTCATGCCTG CATAG 6 A c c
CAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ACGTCCGT
CCTTA
GAM3298 259 GRIPE 1 2629 XP_170749.4 5 421 TCTGGTCCTGCA - G- TA 6 A c c
GATGTGTAGCAC AAAGTGCT CATA TGCAGG
TTTGTAGT TTTCACGA GTGT ACGTCC
T AG TG
GAM3298 259 GTPBP5 1 17309 NP_056481.1 3 1435 GGCTCATGCCTG CATAG 6 A c c
TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 H2AFJ 1 11330 NP_060737.1 3 119 ATATCAGATATC C GTGC 6 A c c
TTTATATAGCAC AAAGTGCT ATA AGGTA
TTTTATGT TTTCACGA TAT TCTAT
- ATT-
GAM3298 259 HIG2 1 840 NP_037464.1 3 211 GGCTCATGCCTG CATAG 6 A c c
TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 HM13 1 3706 NP_848697.1 3 1227 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 HSPC043 1 16780 NP_067041.1 3 782 GCCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 IFIT4 1 3706 NP_001540.2 3 190 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 IL12RB2 1 5498 NP_001550.1 3 803 AGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 IL23R 1 15196 NP_653302.2 3 595 GGCTCATGCTTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGTAG TTTCACGA ATGTTCGT
CCCTA
GAM3298 259 INPP5B 1 19238 XP_300739.1 3 2842 GGCTTATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 IRAK4 1 16303 NP_057207.1 3 1103 GCTCATACCTGT CATAG- 6 A c c

AAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTAA

GAM3298 259 ITK 1 19655 NP_005537.3 3 1197 GAGTGCCTACTC A----- T G - 6 A c c
TGGCTTGAGCAC AAGTGCTCA AGT CAG GTAG
TTCTATAT TTCACGAGT TCG GTC CATC
TATATC - - T

GAM3298 259 KCNA7 1 11198 NP_114092.2 3 1905 GGCTCATGCCTG CATAG 6 A c c

TAACCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCCA

GAM3298 259 KIAA035 1 11293 XP_038655.4 3 805 ACTGGAAACCAG C A A 6 A c c
6 CACTGTCAGCAC AAAGTGCT ATAGTGC GGT
TTTGAGCC TTTCACGA TGTCACG CCA
C A A

GAM3298 259 KIAA039 1 18795 NP_055487.1 3 1721 GCTCATACCTGT CATAGT- 6 A c c
1 TAATTCCAGCAC AAAGTGCT GCAGGTA
TTTGGGAG TTTCACGA TGTCCAT
CCTTAAT

GAM3298 259 KIAA040 1 7576 NP_055517.1 3 3526 GGCTCTTGCCTG CATAG 6 A c c
8 TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CCCTA

GAM3298 259 KIAA044 1 1087 XP_044155.1 5 1289 GGCTCATGCCTG CATAG 6 A c c
6 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
TCCTA

GAM3298 259 KIAA051 1 3706 NP_055511.1 3 4779 GGCTCATGCCTG CATAG 6 A c c
4 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 KIAA062 1 5410 NP_055604.1 3 3399 CTCATGCCTGTA C-- A 6 A c c
8 TAATCCCAGCAC AAAGTGCT AT GTGCAGGTA
TTTGGGAG TTTCACGA TA TATGTCCGT
CCC A

GAM3298 259 KIAA083 2 840 NP_055739.1 5 198 GGCTCATGCCTG CATAG 6 A c c
1 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA

GAM3298 259 KIAA083 2 19561 NP_055739.1 3 789 TCCTGCCATCCA CA--- 6 A c c
1 CACTATGAGCAT AAAGTGCTCATAGTG GGTAG
TTTGAAAT TTTTACGAGTATCAC CCGTC
ACCTA
GAM3298 259 KIAA087 1 10203 NP_055755.1 3 2209 GGCTTATGCCTG CATAG 6 A c
c
2 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGAAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA088 1 3706 NP_056192.1 3 1907 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA091 1 12246 XP_044347.3 3 89 GGCTCATGCCTG CATAG 6 A c
c
3 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA095 1 6353 XP_039733.2 3 2684 GGCTCATGCCTG CATAG 6 A c
c
3 TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 KIAA098 1 4347 NP_054742.1 3 973 CTCACTGTTGCC A G 6 A c c
2 TGGCTGGAGCAC AAAGTGCTC TAGT CAGGTAG
TTTGGTTT TTTCACGAG GTCG GTCCGTT
- -
GAM3298 259 KIAA099 1 16161 NP_057165.2 3 109 CCTCAGCCAGTC - - A A 6 A c c
2 GCTATGCAGCAC AAAGTGCT CATAGTG C GGT
TTTCGGAC TTTCACGA GTATCGC G CCG
C T A A
GAM3298 259 KIAA119 1 12999 NP_056270.2 3 3058 AAACTTACTTGG C G- 6 A c c
4 GATTATTAGCAC AAAGTGCT ATAGT CAGGTAG
TTTCAAAC TTTCACGA TATTA GTTCATT
T GG
GAM3298 259 KIAA137 1 9122 XP_040708.2 3 702 GGCTTATGCCTG CATAG 6 A c
c
7 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGCAGG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA145 1 3706 XP_040100.3 3 707 GGCTCATGCCTG CATAG 6 A c
c
6 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA155 1 3706 XP_054472.2 3 3727 GGCTCATGCCTG CATAG 6 A c
c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT

CCCTA
GAM3298 259 KIAA159 1 11215 XP_045520.5 3 780 GGCTCCTGCCTA C----- T T 6 A c c

5 TAATCCCAGCAC AAAGTGCT ATAG GCAGG AG
TTTGGGAG TTTCACGA TATC CGTCC TC
CCCTAA - -
GAM3298 259 KIAA163 1 8338 NP_061176.2 3 91 GGCACATGCCTG CATAG 6 A c
c

0 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA172 1 20160 XP_040280.2 3 5080 GGCAGGTGCCTG CATAG 6 A c
c

4 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIAA172 1 10851 XP_034262.4 3 429 TGGTTCATGCCT CATAG 6 A c
c

7 GTAATCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTA-
GAM3298 259 KIAA173 1 6665 XP_290496.1 3 2698 GGCTCATGCCTG CATAG 6 A c
c

5 TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 KIAA177 1 7993 XP_086404.1 3 140 GGCTCATGCCTG CATAG 6 A c
c

1 TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 KIAA187 1 18994 XP_290737.1 3 1505 TGGCTCGTACCT CATAG 6 A c
c

1 GTAATCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCAT
CCTA-
GAM3298 259 KIAA195 1 6327 XP_166532.1 3 1157 TTTTGCTTCCTG T- - T T 6 A c c

0 CACTTTGAAGCT AAAG GCT CA AGTGCAGG AG
CCTTTACG TTTC CGA GT TCACGTCC TC
CT A T T
GAM3298 259 KIF11 1 3706 NP_004514.2 3 147 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 KIF3B 1 14234 NP_004789.1 3 2073 GACTCATGCCTG CATAG 6 A c
c

TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 KPNB3 2 7119 NP_002262.3 3 1797 TTTGCTGGGCAC --- A- 6 A c c

TATGCTAAGCAC AAAGTGCT CATAGTGC GGTAG
TTTGGGAG TTTCACGA GTATCACG TCGTT
ATC GG

GAM3298 259 KPNB3 2 18083 NP_002262.3 3 1797 GTGTTTGCTGGG --- A- 6 A c c
CACTATGCTAAG AAAGTGCT CATAGTGC GGTAG
CACTTTGG TTTCACGA GTATCACG TCGTT
ATC GG

GAM3298 259 KREMEN1 1 841 NP_114434.3 3 988 GGTTCATGCCTG CATAG 6 A c
c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 Link-GE 1 15182 NP_057423.1 3 61 CTTGGGCACCTG CAT - A 6 A c c
FII GCACTCAAGCAC AAAGTGCT AGTGC AGGT
TTTGCACG TTTCACGA TCACG TCCA
AC- G C

GAM3298 259 LOC1151 1 8061 XP_055292.1 3 1059 GGCTCAAGCCTG CAT A 6 A c
c

29 TACTCCCAGCAC AAAGTGCT AGTGCAGGT
TTTTGGAG TTTCACGA TCATGTCCG
CCC A

GAM3298 259 LOC1161 1 7468 NP_612467.1 3 63 GGCTCACTCCTG CATAG T 6 A c
c

43 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -

GAM3298 259 LOC1162 1 815 XP_300752.1 3 1316 GGCTCATACCTG CATAG 6 A c
c

28 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA

GAM3298 259 LOC1244 1 9305 XP_058804.4 3 2814 GGCACATGCCTG CATAG 6 A c
c

11 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA

GAM3298 259 LOC1305 2 5219 XP_059451.1 3 1849 TGTGCCAGGCAC --- A- 6 A c c
74 TATGCTAAGCAC AAAGTGCT CATAGTGC GGTA
TTTACATA TTTCACGA GTATCACG CCGT
ATC GA

GAM3298 259 LOC1305 2 10337 XP_059451.1 3 1849 GTATGTGCCAGG --- A- 6 A c c

74 CACTATGCTAAG AAAGTGCT CATAGTGC GGTA
CACTTTAC TTTCACGA GTATCACG CCGT
ATC GA

GAM3298 259 LOC1327 1 8048 XP_068002.4 3 246 GGCTCATGCCTG CATAG 6 A c
c

24 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
TCCTA

GAM3298 259 LOC1341 1 11885 NP_620164.1 3 256 GCCTCATGCCTG CATAG 6 A c c
47 TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 LOC1427 1 9354 XP_084337.1 3 1485 TGGCTCATGCCT CATAG 6 A c c
79 GTAATCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTA-
GAM3298 259 LOC1434 1 19260 NP_777562.1 3 1104 CCTGGCTCCCTG A CT T 6 A c c
58 CACTGTGCACGC A AGTG CATAGTGCAGG AG
TCCTCTTC C TCGC GTGTCACGTCC TC
C AC C
GAM3298 259 LOC1448 1 7468 XP_084972.1 3 437 GGCTCACTCCTG CATAG T 6 A c c
17 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC1448 1 7468 NP_612483.1 3 378 GGCTCACTCCTG CATAG T 6 A c c
45 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC1452 1 16046 XP_096740.1 3 2756 GGCCCATGCCTG CATAG 6 A c c
31 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1456 1 6352 XP_096829.1 3 658 GGCTCATGCTTG CATAG 6 A c c
63 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTTCGT
CCCTA
GAM3298 259 LOC1457 1 3706 XP_085227.1 3 626 GGCTCATGCCTG CATAG 6 A c c
57 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1458 1 14990 XP_085247.1 3 467 GGCTCATGCCTG CATAG 6 A c c
24 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAT TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1460 1 8603 XP_096919.1 3 275 AACCTGCCTCCC A----- - C- 6 A c c c
13 ACTACTGAGCAC AAGTGCTCA TAGTG AGGTAG
TTACCGAA TTCACGAGT ATCAC TCCGTC
AAGCCA C CC
GAM3298 259 LOC1469 1 11424 XP_097142.1 3 539 GTCTCACTCCTG CATAG T 6 A c c

58 TAATACCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCATA -
GAM3298 259 LOC1478 1 16695 XP_085924.2 3 1308 GGCTCATGCCTG CATAG 6 A c
c
41 TGATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA GTGTCCGT
TCCTA
GAM3298 259 LOC1494 1 7723 XP_097645.1 5 920 GGCTCTTGCCTG CATAG 6 A c
c
64 TAATCTTAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
TTCTA
GAM3298 259 LOC1499 1 3001 XP_086699.1 3 205 GAGGATGACCTG T T TA A 6 A c
c
10 CACCGTGTGCCT AAAG GC CA GTGCAGGT
TTAATGCA TTTC CG GT CACGTCCA
- T GC G
GAM3298 259 LOC1502 1 10727 XP_097870.1 3 3125 GGTTCACACCTG - TAG A 6 A c
c
25 TAATTGCAGCAC AAAGTGCT CA TGCAGGT
TTTGGGAG TTTCACGA GT ATGTCCA
C TA- C
GAM3298 259 LOC1502 1 3702 XP_086889.1 3 432 GGCTCATACCTG CATAG 6 A c
c
87 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCAT
CCCTA
GAM3298 259 LOC1502 1 12013 XP_097869.2 3 420 GGCTCATGCCTG CATAG 6 A c
c
99 TAACCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CTCCA
GAM3298 259 LOC1506 1 3706 XP_097931.1 3 656 GGCTCATGCCTG CATAG 6 A c
c
30 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1510 1 12510 XP_098000.1 3 143 GGCTCAAGCCTG C G A 6 A c
c
68 TAATGTCAGCAC AAAGTGCT ATA TGCAGGT
TTTAAAAG TTTCACGA TGT ATGTCCG
C A A
GAM3298 259 LOC1514 1 6221 XP_098060.1 3 859 GGCTCCTGCCTG CATAG 6 A c
c
38 TAATCGCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTC
CGCTA
GAM3298 259 LOC1533 1 16145 XP_098361.1 3 883 GGCTCATGCCTG CATAG 6 A c
c

38 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGGG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 LOC1535 2 3706 XP_087708.6 3 743 GGCTCATGCCTG CATAG 6 A c
c
61 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1535 2 4776 XP_087708.6 3 447 GGCTCATGCCTG CATA - 6 A c
c
61 TCATCCCAGCAC AAAGTGCT GTG CAGGTA
TTTGGGAG TTTCACGA TAC GTCCGT
CCC- T
GAM3298 259 LOC1536 1 8989 XP_098414.1 3 305 GGCTCATGCCTG CATAG 6 A c
c
82 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTCGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1537 1 6353 XP_098422.1 3 511 GGCTCATGCCTG CATAG 6 A c
c
27 TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 LOC1550 2 3706 XP_088117.1 3 468 GGCTCATGCCTG CATAG 6 A c
c
06 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1550 2 12246 XP_088117.1 3 783 GGCTCATGCCTG CATAG 6 A c
c
06 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1575 1 15279 XP_212210.1 5 1035 CCCTGAATCTCT G TA 6 A c
c
31 GCATATGAGCAT AAAGTGCTCATA TGCAGG
TTTTCTGG TTTTACGAGTAT ACGTCT
- CT
GAM3298 259 LOC1584 1 8220 XP_098939.1 3 1097 TGAGTGTGCCTG CATAG 6 A c
c
34 TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGAGGG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 LOC1590 1 816 XP_099018.1 3 803 GGCTCATGCCTG CATAG 6 A c
c
36 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1632 1 7144 XP_088769.6 3 201 AGCTCGCTCCTG CATAG T 6 A c
c

59 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC1653 1 3706 XP_092518.1 3 756 GGCTCATGCCTG CATAG 6 A c c
24 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1665 1 16780 XP_093920.5 3 543 GCCTCATGCCTG CATAG 6 A c c
22 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC1965 1 2952 XP_116933.1 5 464 ACTTTCAGCCTG A T A 6 A c c
40 CACTTGAGTATT A AGTGCTCA AGTGCAGGT
CCTTATGT C TTATGAGT TCACGTCCG
C - A
GAM3298 259 LOC1997 1 7468 XP_117123.2 3 830 GGCTCACTCCTG CATAG T 6 A c c
33 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC2000 2 3706 XP_114089.3 3 2186 GGCTCATGCCTG CATAG 6 A c c
08 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2000 2 6353 XP_114089.3 5 78 GGCTCATGCCTG CATAG 6 A c c
08 TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 LOC2014 1 9894 XP_113967.1 3 78 CGTTCTATTCTG CTCA - 6 A c c
75 CACTACAATCAT AAAGTG TAGTGCAGG TAG
TTTGACAA TTTTAC ATCACGTCT ATC
TAAC T
GAM3298 259 LOC2018 1 840 XP_114383.1 3 189 GGCTCATGCCTG CATAG 6 A c c
10 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 LOC2021 1 19238 XP_117365.1 5 546 GGCTTATGCCTG CATAG 6 A c c
34 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2207 2 5839 XP_167548.3 5 1788 CTCCCTGCCCTC CA --- 6 A b b
39 TGCACTAAGCAC AAAGTGCT TAGTGCA GGTAG
TTTCCAGG TTTCACGA ATCACGT CCGTC

```
                                                --      CTC
GAM3298  259    LOC2207 2  16984  XP_167548.3  5  1788   CCCTGCCCTCTG       CA     ---         6  A  b
b
          39                          CACTAAGCACTT AAAGTGCT  TAGTGCA   GGTAG
                                     TCCAGGCA    TTTCACGA  ATCACGT   CCGTC
                                                --      CTC
GAM3298  259    LOC2210 1  18581  XP_167640.1  3  573    AAACCAGGTATC       C  A   CA          6  A  c
c
          35                          CACACATAGCAC AAAGTGCT AT GTG  GGTA
                                     TTTTATTC    TTTCACGA TA CAC  CTAT
                                                - -  AC
GAM3298  259    LOC2216 1  10387  XP_168071.1  5  914    CAGTGTCTGCGT       A--  -    GT       6  A  c
c
          01                          CTAAGAGAGCAC AAAGTGCTC   TAG TGCAG  A
                                     TTTGTTGC    TTTCACGAG   ATC GCGTC  T
                                                 AGA  T    TG
GAM3298  259    LOC2219 1  3706   XP_168348.1  3  750    GGCTCATGCCTG       CATAG            6  A  c
c
          31                          TAATCCCAGCAC AAAGTGCT    TGCAGGTA
                                     TTTGGGAG    TTTCACGA    ATGTCCGT
                                                 CCCTA
GAM3298  259    LOC2219 1  15872  XP_168349.1  5  383    GGCTCTTGCCTG       CATAG            6  A  c
 c
          54                          TAATCCCAGCAC AAAGTGCT    TGCAGGTAG
                                     TTTGGGGA    TTTCACGA    ATGTCCGTT
                                                 CCCTA
GAM3298  259    LOC2220 1  14995  XP_168427.1  5  34     GGCTCATGCCTG       CATAG            6  A  c
c
          60                          TAAGCCCAGCAC AAAGTGCT    TGCAGGTA
                                     TTTGGGAG    TTTCACGA    ATGTCCGT
                                                 CCCGA
GAM3298  259    LOC2221 1  8175   XP_168431.1  5  730    GGCTGATGCCTG       CATAG            6  A  c
c
          60                          TAATCCCAGCAC AAAGTGCT    TGCAGGTA
                                     TTTGGGAG    TTTCACGA    ATGTCCGT
                                                 CCCTA
GAM3298  259    LOC2537 1  10198  XP_171023.1  3  1010   GATTACCTGTGC        --- A TG         6  A  c
c
          82                          AGTGCAGAGCAC AAAGTGCTC   AT G  CAGGTAG
                                     TTTAATGC    TTTCACGAG   TG C  GTCCATT
                                                 ACG  A GT
GAM3298  259    LOC2551 1  6353   XP_170826.1  3  110    GGCTCATGCCTG       CATAG            6  A  c
c
          85                          TAATCTCAGCAC AAAGTGCT    TGCAGGTA
                                     TTTGGGAG    TTTCACGA    ATGTCCGT
                                                 CTCTA
GAM3298  259    LOC2829 1  19337  XP_212579.1  3  441    GGCTCGTATCTG       CATAG            6  A  c
 c
          15                          TAATCCCAGCAC AAAGTGCT    TGCAGGTA
                                     TTTGAGAG    TTTCACGA    ATGTCTAT
```

CCCTA
GAM3298 259 LOC2829 1 19337 XP_212627.1 3 441 GGCTCGTATCTG CATAG 6 A c
c
51 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCTAT
CCCTA
GAM3298 259 LOC2829 1 7468 XP_208463.1 5 949 GGCTCACTCCTG CATAG T 6 A c
c
73 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC2830 1 3706 XP_208481.1 3 1109 GGCTCATGCCTG CATAG 6 A c
c
05 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2830 1 841 XP_210875.1 3 327 GGTTCATGCCTG CATAG 6 A c
c
61 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2831 1 14868 XP_210929.1 5 805 GGCTCACACCTG CATAG A 6 A c
c
99 CAATCCCAGCAC AAAGTGCT TGCAGGT
TTTGGGAG TTTCACGA ACGTCCA
CCCTA C
GAM3298 259 LOC2832 1 7329 XP_210945.1 3 306 GGCTCATGCCTG CATAG 6 A c
c
30 TGATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGTG TTTCACGA GTGTCCGT
CCCTA
GAM3298 259 LOC2832 1 19239 XP_210960.1 3 977 GGCTCATGCCTG CATAG 6 A c
c
89 CAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ACGTCCGT
CCCTA
GAM3298 259 LOC2834 2 3706 XP_208682.1 3 1438 GGCTCATGCCTG CATAG 6 A c
c
60 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2834 2 7398 XP_208682.1 3 448 GGATCACACCTG CATAG A 6 A c
c
60 CAATCCCAGCAC AAAGTGCT TGCAGGT
TTTGGGAG TTTCACGA ACGTCCA
CCCTA C
GAM3298 259 LOC2834 1 8626 XP_211056.1 3 726 GGCTCATGCCTG CATAG 6 A c
c
75 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGTG TTTCACGA ATGTCCGT

TCCTA
GAM3298 259 LOC2835 1 8580 XP_211070.1 3 1568 CTTTTCTACCTG A C--- T 6 A c c
08 CTCTATACTTGG A AGTGCT ATAG GCAGGTAG
CACTCAAT A TCACGG TATC CGTCCATC
C TTCA T
GAM3298 259 LOC2836 1 3706 XP_211152.1 3 376 GGCTCATGCCTG CATAG 6 A c
c
72 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2836 1 3706 XP_211167.1 3 5678 GGCTCATGCCTG CATAG 6 A c
c
90 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2836 1 16061 XP_208788.1 3 359 GGCTCATGCCTG CATAG 6 A c
c
93 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTTGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2837 1 11927 XP_208826.2 3 2899 GGCTCACTCCTG CATAG T 6 A
c c
60 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGAGG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC2838 1 5840 XP_208889.2 5 50 GTCACCTGGTTG A T T G 6 A c c
91 CACTATGGCCTC A AG GC CATAGTGCAG TAG
ATCTGTGG A TC CG GTATCACGTT GTC
C - - G
GAM3298 259 LOC2839 2 3706 XP_208906.1 3 783 GGCTCATGCCTG CATAG 6 A c
c
24 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2839 2 6479 XP_208906.1 3 370 GGCTCACACCTG CAT A 6 A c
c
24 TATTCCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TTATGTCCA
CCC C
GAM3298 259 LOC2839 1 3706 NP_835229.1 3 740 GGCTCATGCCTG CATAG 6 A c
c
85 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2839 1 3706 XP_208951.2 3 740 GGCTCATGCCTG CATAG 6 A c
c
85 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2840 1 3706 XP_211300.2 3 1563 GGCTCATGCCTG CATAG 6 A c c

14 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2840 1 3706 XP_208970.1 3 187 GGCTCATGCCTG CATAG 6 A c c

24 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2841 1 3706 XP_209047.2 3 499 GGCTCATGCCTG CATAG 6 A c c

61 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2843 1 16046 XP_209116.1 3 1230 GGCCCATGCCTG CATAG 6 A c c

13 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2843 1 3706 XP_209155.1 3 215 GGCTCATGCCTG CATAG 6 A c c

71 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2844 1 6665 XP_209187.1 3 253 GGCTCATGCCTG CATAG 6 A c c

17 TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA

GAM3298 259 LOC2844 1 17236 XP_211476.1 3 961 AGGGACCACCTG CATA A 6 A c c

61 CACCAGGCACTT AAAGTGCT GTGCAGGT
TTCTCCTC TTTCACGG CACGTCCA
AC-- C

GAM3298 259 LOC2844 1 8335 XP_211478.1 5 2698 TTTGCAAACCTG TCATA A 6 A c c

75 CACCTTGCACTT AAAGTGC GTGCAGGT
TTGGGTTC TTTCACG CACGTCCA
TTC-- A

GAM3298 259 LOC2844 1 3706 XP_209231.1 3 1318 GGCTCATGCCTG CATAG 6 A c c

86 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2845 1 12376 XP_209254.1 5 51 CAAAGCCTGCAG --- AG A 6 A c c

42 CGTGGCAAGCAC AAAGTGCT CAT TGCAGGT
TTTGCACA TTTCACGA GTG ACGTCCG
ACG CG A

GAM3298 259 LOC2845 1 1017 XP_211516.1 3 219 GGCACATGCCTG CATAG 6 A c
c
52 TGATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAT TTTCACGA GTGTCCGT
CCCTA
GAM3298 259 LOC2846 1 3703 XP_211567.1 3 546 GGCTCATGCTTG CATAG 6 A c
c
39 TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTTCGT
CTCTA
GAM3298 259 LOC2846 2 10343 XP_211569.1 3 1258 TGATCTGCCCTG A TA - 6 A c
c
47 CACTGAGCACTC A AGTGCTCA GTGCAGG TAG
AGTGGATA A TCACGAGT CACGTCC GTC
C -- C
GAM3298 259 LOC2846 2 15701 XP_211569.1 3 1258 CCTGATCTGCCC A TA - 6 A c
c
47 TGCACTGAGCAC A AGTGCTCA GTGCAGG TAG
TCAGTGGA A TCACGAGT CACGTCC GTC
C -- C
GAM3298 259 LOC2846 1 7468 XP_211581.1 5 1153 GGCTCACTCCTG CATAG T 6 A c
c
65 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC2847 1 3706 XP_211598.1 3 886 GGCTCATGCCTG CATAG 6 A c
c
07 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2847 1 18406 XP_211609.1 3 1913 CCCCTAAGCCTG A T A 6 A c
c
39 CACTCTGGGCGC A AGTGCTCA AGTGCAGGT
TCCTGCTG C TCGCGGGT TCACGTCCG
C C A
GAM3298 259 LOC2848 1 3706 XP_211671.1 3 274 GGCTCATGCCTG CATAG 6 A c
c
57 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2848 1 3706 XP_209386.1 3 1031 GGCTCATGCCTG CATAG 6 A c
c
58 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2849 2 3706 XP_211684.1 3 1620 GGCTCATGCCTG CATAG 6 A c
c
11 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2849 2 12485 XP_211684.1 3 2185 TGACCTATGCCT CATAG 6 A c c

11 GCAATCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ACGTCCGT
CCTA-

GAM3298 259 LOC2849 1 5498 XP_209413.1 3 371 AGCTCATGCCTG CATAG 6 A c c

12 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2849 1 13200 XP_211712.1 5 853 GGCACATGCCTG CATAG 6 A c c

72 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2849 1 17671 XP_211729.1 3 361 GCCTCATGCCTG CATAG 6 A c c

95 CAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ACGTCCGT
TCCTA

GAM3298 259 LOC2849 2 13613 XP_211726.1 3 407 ACAATCAACCTG TA A 6 A b b

98 CACTGAGCACTT AAAGTGCTCA GTGCAGGT
TGTGCGGG TTTCACGAGT CACGTCCA
-- A

GAM3298 259 LOC2849 2 14399 XP_211726.1 3 407 TTACAATCAACC TA A 6 A b b

98 TGCACTGAGCAC AAAGTGCTCA GTGCAGGT
TTTGTGCG TTTCACGAGT CACGTCCA
-- A

GAM3298 259 LOC2850 1 16577 XP_211730.1 5 283 AAATAGTACTTT CATA --- 6 A c c

01 TAGCATAAGCAC AAAGTGCT GTGC AGGTA
TTTCTGTG TTTCACGA TACG TTCAT
A--- ATT

GAM3298 259 LOC2850 1 3706 XP_211751.1 3 1221 GGCTCATGCCTG CATAG 6 A c c

52 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2850 1 3706 XP_211759.1 3 1482 GGCTCATGCCTG CATAG 6 A c c

82 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 LOC2853 1 4250 XP_211864.1 3 1123 GGCTCATGCCTG CATA - 6 A c c

76 TCATCCCAGCAC AAAGTGCT GTG CAGGTA
TTTGGGAA TTTCACGA TAC GTCCGT
CCC- T

GAM3298 259 LOC2853 1 3706 XP_211859.1 5 208 GGCTCATGCCTG CATAG 6 A c c

78 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2853 1 12631 XP_211868.1 3 348 TCCACCAACCTG CATA A 6 A c
c
79 CGCAGGCAGCAC AAAGTGCT GTGCAGGT
TTTTGGCC TTTCACGA CGCGTCCA
CGGA A
GAM3298 259 LOC2853 1 18417 XP_209593.1 3 357 CCCTGCCGCCTG C G A 6 A c
c
98 GGCTGTCAGCAC AAAGTGCT ATAGT CAGGT
TTTGGCAG TTTCACGA TGTCG GTCCG
C G C
GAM3298 259 LOC2854 1 19239 XP_209596.1 5 588 GGCTCATGCCTG CATAG 6 A c
c
00 CAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ACGTCCGT
CCCTA
GAM3298 259 LOC2855 1 4958 XP_209654.1 5 1987 GGCTCACTCCTG CATAG T 6 A c
c
40 TAATTCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCTTA -
GAM3298 259 LOC2856 1 2225 XP_209718.1 5 216 GCTCCACACCTG CAT- T A 6 A c
c
76 CCTCCATAGCAC AAAGTGCT AG GCAGGT
TTTGCCTG TTTCACGA TC CGTCCA
TACC - C
GAM3298 259 LOC2857 1 840 XP_211990.1 3 1564 GGCTCATGCCTG CATAG 6 A c
c
19 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 LOC2857 1 14868 XP_211997.1 3 1180 GGCTCACACCTG CATAG A 6 A
c c
22 CAATCCCAGCAC AAAGTGCT TGCAGGT
TTTGGGAG TTTCACGA ACGTCCA
CCCTA C
GAM3298 259 LOC2857 1 17940 XP_209742.1 3 986 GGCTCATGCCTG CATAG 6 A c
c
47 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGAAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2857 1 10387 XP_212010.1 5 914 CAGTGTCTGCGT A-- - GT 6 A c
c
49 CTAAGAGAGCAC AAAGTGCTC TAG TGCAG A
TTTGTTGC TTTCACGAG ATC GCGTC T
AGA T TG
GAM3298 259 LOC2857 1 3706 XP_212012.1 5 1586 GGCTCATGCCTG CATAG 6 A c
c

58 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2858 1 19337 XP_209790.1 3 441 GGCTCGTATCTG CATAG 6 A c
c
33 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCTAT
CCCTA
GAM3298 259 LOC2858 1 5474 XP_209770.1 3 1760 GGCTCATGCCTG CATAG 6 A c
c
54 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTTGAGG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2858 1 17309 XP_209775.1 3 1246 GGCTCATGCCTG CATAG 6 A c
c
59 TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 LOC2858 1 18034 XP_212058.1 3 16 TGGCTCACGCCT CAT A 6 A c
c
69 GTATTCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TTATGTCCG
CC- C
GAM3298 259 LOC2859 1 816 XP_212078.1 3 101 GGCTCATGCCTG CATAG 6 A c
c
12 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2859 2 3706 XP_212091.1 5 110 GGCTCATGCCTG CATAG 6 A c
c
20 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2859 2 15927 XP_212091.1 3 302 AGCTCCTGCCTG CAT G 6 A c
c
20 GATTCCCAGCAC AAAGTGCT AGT CAGGTAG
TTTGGGAG TTTCACGA TTA GTCCGTC
CCC G
GAM3298 259 LOC2859 1 11962 XP_208368.2 3 1148 GGCTCATGCCTG CATAG 6 A c
c
26 TGATCGCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA GTGTCCGT
CGCTA
GAM3298 259 LOC2859 1 16949 XP_212087.1 3 27 TACTCATGCCTG CATAG 6 A c
c
28 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2859 1 3706 XP_209820.1 3 952 GGCTCATGCCTG CATAG 6 A c
c

53 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2859 1 14995 XP_212088.1 3 874 GGCTCATGCCTG CATAG 6 A c
c
60 TAAGCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCGA
GAM3298 259 LOC2861 1 7202 XP_209910.2 3 15 GTGGCTCATGCC CATA 6 A c c

29 TGTATCCAGCAC AAAGTGCT GTGCAGGTA
TTTGGGAG TTTCACGA TATGTCCGT
CC--
GAM3298 259 LOC2861 1 7939 XP_209925.1 5 2256 GAGACTGCCGTG AT TG - 6 A c
c
66 TCCTCCGAGCAC AAAGTGCTC AG CA GGTAG
TTTGTTTT TTTCACGAG TC GT CCGTC
CC CT G
GAM3298 259 LOC2861 1 3702 XP_212216.1 5 594 GGCTCATACCTG CATAG 6 A c
c
84 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCAT
CCCTA
GAM3298 259 LOC2861 1 3706 XP_212219.1 3 691 GGCTCATGCCTG CATAG 6 A c
c
86 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2861 1 3706 XP_209940.1 3 133 GGCTCATGCCTG CATAG 6 A c
c
97 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2862 1 14873 XP_209955.1 3 131 TCCTGCTGCTGC CAT- -- 6 A c
c
22 ATTTTAAAGCAC AAAGTGCT AGTGCAG GTAG
TTTTATAG TTTCACGA TTACGTC CGTC
AATT GT
GAM3298 259 LOC2863 1 3706 XP_212274.3 3 1508 GGCTCATGCCTG CATAG 6 A c
c
37 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2863 1 10184 XP_212293.1 5 559 GACTCATGCCTG CATAG 6 A c
c
74 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC2864 1 7468 XP_212325.1 3 1298 GGCTCACTCCTG CATAG T 6 A c
c

70 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC3385 2 5498 XP_294651.1 3 396 AGCTCATGCCTG CATAG 6 A c c
49 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3385 2 8366 XP_294651.1 3 16 GGGCTCAAGCCT CAT A 6 A c c
49 GTATTCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TTATGTCCG
CC- A
GAM3298 259 LOC3385 1 5843 XP_294660.1 3 252 GGCTCACTCCTG CATAG T 6 A c c
94 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAA TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 LOC3389 1 3706 XP_294757.1 5 750 GGCTCATGCCTG CATAG 6 A c c
63 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3392 1 13707 XP_294901.1 5 2667 GGCTCACACCTG CAT - A 6 A c c
90 TCATTCCAGCAC AAAGTGCT AGTG CAGGT
TTTGAGAG TTTCACGA TTAC GTCCA
CC- T C
GAM3298 259 LOC3393 1 815 XP_294921.1 3 1156 GGCTCATACCTG CATAG 6 A c c
73 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA
GAM3298 259 LOC3394 1 19562 XP_294936.1 3 1058 TTCATGTACCTG TGC - 6 A c c
13 CACATGTGACCT AAAG TCATA GTGCAGGTA
TTGTGAAC TTTC AGTGT CACGTCCAT
C-- A
GAM3298 259 LOC3397 1 3706 XP_291005.1 3 2601 GGCTCATGCCTG CATAG 6 A c c
61 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3398 1 7576 XP_291038.1 3 677 GGCTCTTGCCTG CATAG 6 A c c
41 TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CCCTA
GAM3298 259 LOC3400 1 19238 XP_291125.2 3 182 GGCTTATGCCTG CATAG 6 A c c

38 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3400 1 16347 XP_295153.1 3 681 GGATCATGCCTG CATAG 6 A c
c
87 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3401 1 3706 XP_295183.1 3 1182 GGCTCATGCCTG CATAG 6 A c
c
84 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3402 1 3706 XP_295187.1 5 149 GGCTCATGCCTG CATAG 6 A c
c
08 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3402 1 16625 XP_295199.1 5 674 TGGCTCTACCTG TCATAG- 6 A c
c
69 CAGAAAGCTGCA AAAGTGC TGCAGGTAG
TTTTCCAA TTTTACG ACGTCCATC
TCGAAAG
GAM3298 259 LOC3403 1 4826 XP_295211.1 3 706 GGCTCATGCCTG CATAG 6 A c
c
20 TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTAGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 LOC3403 1 8160 XP_295225.1 3 267 GGCTCATGCCTG CATAG 6 A c
c
62 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3403 1 15241 XP_295235.1 3 36 GGCTCGTGCCTG CATA - 6 A c
c
94 TCATCCCAGCAC AAAGTGCT GTG CAGGTA
TTTGGGAG TTTCACGA TAC GTCCGT
CCC- T
GAM3298 259 LOC3405 1 1347 XP_291331.1 3 968 ATTTCTTGCCTG CATAG 6 A c
c
47 TAACCCTAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
TCCCA
GAM3298 259 LOC3434 1 5570 XP_295562.1 5 49 AGAACTCTCTGG A----- - GT 6 A c c
34 CACTATGGGCAC AAGTGCTCATAGTGC AG AG
TTGCACAT TTCACGGGTATCACG TC TC
TACACG G TC
GAM3298 259 LOC3462 1 18321 XP_294131.1 5 58 GCTTCCTACCTG CTCAT - 6 A c
c
32 CAGCTTCACTTT AAAGTG AG TGCAGGTAG

GCTCTAGT TTTCAC TC ACGTCCATC
T---- G
GAM3298 259 LOC3481 1 3706 XP_302651.1 5 1340 GGCTCATGCCTG CATAG 6 A c
c
02 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3484 1 815 XP_057659.1 3 1341 GGCTCATACCTG CATAG 6 A c
c
42 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA
GAM3298 259 LOC3484 1 3706 XP_302761.1 3 183 GGCTCATGCCTG CATAG 6 A c
c
56 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3485 1 3706 XP_300779.1 3 136 GGCTCATGCCTG CATAG 6 A c
c
27 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3487 1 3706 XP_300826.1 3 893 GGCTCATGCCTG CATAG 6 A c
c
38 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3490 1 18034 XP_302949.1 3 16 TGGCTCACGCCT CAT A 6 A c
c
63 GTATTCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TTATGTCCG
CC- C
GAM3298 259 LOC3490 1 16691 XP_302959.1 3 1120 GGCTCATGCCTG CATAG 6 A c
c
92 TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGAAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 LOC3491 1 17395 XP_302978.1 3 1280 GGCTTATGCCTG CATAG 6 A c
c
69 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGTG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3491 1 3706 XP_300969.1 3 2252 GGCTCATGCCTG CATAG 6 A c
c
70 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3492 1 19238 XP_301008.1 3 747 GGCTTATGCCTG CATAG 6 A c
c
82 TAATCCCAGCAC AAAGTGCT TGCAGGTA

TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3493 1 19238 XP_301024.1 3 722 GGCTTATGCCTG CATAG 6 A c c
13 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC3493 1 18956 XP_301029.1 3 228 GCTTCATGCCTG CATAG 6 A c c
23 TAATCCAAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
ACCTA
GAM3298 259 LOC5133 1 17893 NP_057727.1 3 958 GCTCATGCCTGT CATAG- 6 A c c
3 AATCTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTCTA
GAM3298 259 LOC5175 1 4777 NP_057566.1 3 225 GGCTCCTGCCTG CATAG 6 A c c
9 TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTC
CCCTA
GAM3298 259 LOC8586 1 6826 NP_149098.1 3 660 GGCTCATGCCTG CATAG 6 A c c
5 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTTCGGA TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC9105 1 12246 NP_612377.1 3 1707 GGCTCATGCCTG CATAG 6 A c c
6 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LOC9156 1 6049 XP_039231.1 3 728 GGCTCTTGCCTG CATAG 6 A c c
5 TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGATAG TTTCACGA ATGTCCGTT
CCCTA
GAM3298 259 LOC9361 1 10184 XP_052568.1 3 603 GACTCATGCCTG CATAG 6 A c c
3 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 LPHN3 1 3875 NP_056051.1 3 1999 AGTGGGCACCTG CTCA A 6 A c c
CACTACCACTTT AAAGTG TAGTGCAGGT
TTAGAGGA TTTCAC ATCACGTCCA
C--- C
GAM3298 259 MAP3K8 1 11824 NP_005195.2 5 610 TGCCCCTGACAC TA - A 6 A c c
TGCACTGAGCAC AAAGTGCTCA GTGCAG GT

TTTATGAG TTTCACGAGT CACGTC CA
-- A G
GAM3298 259 MATR3 1 19562 NP_061322.2 3 894 TTCATGTACCTG TGC - 6 A c c
CACATGTGACCT AAAG TCATA GTGCAGGTA
TTGTGAAC TTTC AGTGT CACGTCCAT
C-- A
GAM3298 259 MAWBP 2 4940 NP_071412.1 3 172 GGCTCATGCCTG CATAG 6 A c
c
TAATCGTAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
TGCTA
GAM3298 259 MAWBP 2 15240 NP_071412.1 3 1036 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGCAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 METAP1 1 12453 NP_055958.1 3 260 TTTTCTCATTTG T T A 6 A c c
CCCTTTGAGCAC AAAGTGCTCA AG GCAGGT
TTTTACTT TTTCACGAGT TC CGTTTA
T C C
GAM3298 259 MGAT3 2 16776 NP_835470.1 3 135 GCCTCGTGCCTG CATAG 6 A c
c
TGATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA GTGTCCGT
CCCTA
GAM3298 259 MGAT3 2 16780 XP_294343.2 3 135 GCCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MGC1076 1 3706 NP_077321.1 3 1579 GGCTCATGCCTG CATAG 6 A c
c
5 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MGC1077 1 3706 NP_078782.2 3 48 GGCTCATGCCTG CATAG 6 A c
c
1 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MGC1081 1 3706 NP_116060.1 5 34 GGCTCATGCCTG CATAG 6 A c
c
4 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MGC1305 1 11709 NP_116099.1 3 881 TTACGACTCCTG CATAG T 6 A c
c
3 TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAG TTTCACGA ATGTCC TC
CCCTA -

GAM3298 259 MGC1670 1 3706 NP_659479.1 3 632 GGCTCATGCCTG CATAG 6 A c c

3 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 MGC1779 1 15278 NP_689575.1 3 946 GGCTCACTACTG CATAG G 6 A c c

1 TAATTCCAGCAC AAAGTGCT TGCAG TAG
TTTGGGAG TTTCACGA ATGTC ATC
CCTTA -

GAM3298 259 MGC1798 1 3706 NP_705836.1 3 377 GGCTCATGCCTG CATAG 6 A c c

6 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 MGC2396 1 6794 NP_443084.1 3 15 GTCCTCATGCCT CATA 6 A c c

GTATCCCAGCAC AAAGTGCT GTGCAGGTA
TTTGGGAG TTTCACGA TATGTCCGT
CCC-

GAM3298 259 MGC2993 1 3706 NP_653198.1 3 55 GGCTCATGCCTG CATAG 6 A c c

7 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 MGC3005 1 6970 NP_653322.1 3 658 ATCATTCCTCCT A C T 6 A c c

2 CACTAGGAGCAC AAAGTGCTC TAGTG AGG AG
TTTGATGT TTTCACGAG ATCAC TCC TC
G - -

GAM3298 259 MGC3195 1 7576 NP_114111.2 3 677 GGCTCTTGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CCCTA

GAM3298 259 MGC3207 1 6665 NP_115661.1 3 1118 GGCTCATGCCTG CATAG 6 A c c

TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA

GAM3298 259 MGC3403 1 17939 NP_694956.1 3 1222 GGCTCGTGCCTG CATAG 6 A c c

4 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 MGC5083 1 17939 XP_171060.1 3 439 GGCTCGTGCCTG CATAG 6 A c c

6 TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 MGC5384 1 3706 NP_112234.1 3 352 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MICA 1 15857 NP_000238.1 3 56 TCCCTGCCTGGA AT- - G 6 A c c
TCTCACGAGCAC AAAGTGCTC AG T CAGGTAG
TTTCCCTC TTTCACGAG TC A GTCCGTC
CAC T G
GAM3298 259 MONDOA 1 16680 NP_055753.1 3 2529 GGCTCCTGCCTG ----- T T 6 A c
c
TGATCCTAGCAC AAAGTGC TCATAG GCAGG AG
TTTGGGAG TTTCACG AGTGTC CGTCC TC
ATCCT - -
GAM3298 259 MPRG 1 17939 NP_060175.2 3 2807 GGCTCGTGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MRE11A 1 9057 NP_005581.2 3 1275 GTTAGTGGCTGC C G C 6 A c
c
CTCATATAGCAC AAAGTGCT ATA TG AGGTAG
TTTTGAAG TTTCACGA TAT AC TCCGTC
- - -
GAM3298 259 MRE11A 1 9057 NP_005582.1 3 1275 GTTAGTGGCTGC C G C 6 A c
c
CTCATATAGCAC AAAGTGCT ATA TG AGGTAG
TTTTGAAG TTTCACGA TAT AC TCCGTC
- - -
GAM3298 259 MRPS18B 1 5843 NP_054765.1 3 64 GGCTCACTCCTG CATAG T 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGG AG
TTTGGGAA TTTCACGA ATGTCC TC
CCCTA -
GAM3298 259 MSH3 1 3706 NP_002430.1 3 500 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 MVP 1 6247 NP_059447.2 5 24 TGCAGCTACCTG A - CAT 6 A c c
CACTTCTAGATG A AGTG CT AGTGCAGGTAG
CTCCCCAG C TCGT GA TCACGTCCATC
C A TCT
GAM3298 259 NBR2 1 17309 NP_005812.1 3 365 GGCTCATGCCTG CATAG 6 A c
c
TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 NCOA3 1 13706 NP_006525.1 3 1306 AATTCCTCTACC CA GCA 6 A c
c
AGAACTAAGCAC AAAGTGCT TAGT GGTAG
TTTGTTAA TTTCACGA ATCA CCATC

-- AGA
GAM3298 259 NDP52 1 2868 NP_005822.1 3 647 TTTCTGGGTACC CA- TGC 6 A c c
TCTGGTTAGCAC AAAGTGCT TAG AGGTA
TTTCTACT TTTCACGA GTC TCCAT
TTG ---
GAM3298 259 NDUFC2 1 12246 NP_004540.1 3 838 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 NEDD4L 1 12224 NP_056092.2 3 1465 TGAGGGTACCTG TGC TA-- 6 A c c
CACAGTTTGATT AAAG TCA GTGCAGGTA
CTTTTCCA TTTC AGT CACGTCCAT
TT- TTGA
GAM3298 259 NFAT5 1 12246 NP_775322.1 3 232 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 NKTR 1 14143 NP_005376.2 3 676 TATAAATACCTG A- G ---- 6 A c c
CACTGTCTCTGA AAGT CTCA TAGTGCAGGTA
GGACTTAC TTCA GAGT GTCACGTCCAT
CA G CTCT
GAM3298 259 NMA 1 12002 NP_036474.1 3 76 TTGAGTTCTGCT ATA G G 6 A c c
GGACAGGAGCAC AAAGTGCTC GT CAG TAG
TTTATCTG TTTCACGAG CA GTC GTC
GA- G -
GAM3298 259 ODAG 1 13789 NP_066990.2 3 334 GGCTTATGCCTG - TAG 6 A c c
TAATTGCAGCAC AAAGTGCT CA TGCAGGTA
TTTTAGAG TTTCACGA GT ATGTCCGT
C TA-
GAM3298 259 OPTN 1 3706 NP_068815.2 3 173 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 PAFAH2 1 3706 NP_000428.2 3 925 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 PBXIP1 1 19722 NP_065385.2 3 160 TCACCAGCCCTG CT - TA 6 A c c
CACTGATGTCAC AAAGTG CAT AGTGCAGG
TTTATGTA TTTCAC GTA TCACGTCC
T- G CG
GAM3298 259 PCDH11Y 1 815 NP_116753.1 3 1025 GGCTCATACCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA

GAM3298 259 PCDH11Y 1 815 NP_116754.1 3 1025 GGCTCATACCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCCTA

GAM3298 259 PCDHA1 1 12657 NP_061723.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA1 1 12657 NP_113599.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA10 1 12657 NP_061724.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA10 1 12657 NP_114066.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA11 1 12657 NP_061725.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA12 1 12657 NP_061726.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA13 1 12657 NP_061727.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA2 1 12657 NP_061728.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA3 1 12657 NP_061729.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA4 1 12657 NP_061730.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA5 1 12657 NP_061731.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA6 1 12657 NP_061732.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA6 1 12657 NP_114037.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA7 1 12657 NP_061733.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA8 1 12657 NP_061734.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHA9 1 12657 NP_114063.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHAC1 1 12657 NP_061721.2 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PCDHAC2 1 12657 NP_061722.1 3 2270 AATTATAATGTA CATA 6 A c c

TCTGTACAGCAC AAAGTGCT GTGCAGGTA
TTTTTACA TTTCACGA CATGTCTAT

GAM3298 259 PEX26 1 16060 NP_060399.1 3 1879 GGCGCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 PIGM 1 1310 NP_660150.1 3 483 GGCCCTTGCCTG CATAG 6 A c c

TAGTCTCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CTCTG
GAM3298 259 PIGO 1 19803 NP_116023.2 3 290 GACTTGCACCTA C----- - A 6 A c c
TAATCCCAGCAC AAAGTGCT ATAG TGCAGGT
TTTGGGAG TTTCACGA TATC ACGTTCA
CCCTAA C G
GAM3298 259 PIGO 1 19803 NP_690577.1 3 290 GACTTGCACCTA C----- - A 6 A c c
TAATCCCAGCAC AAAGTGCT ATAG TGCAGGT
TTTGGGAG TTTCACGA TATC ACGTTCA
CCCTAA C G
GAM3298 259 PIK3R2 1 3706 NP_005018.1 3 674 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 PKHD1 1 12090 NP_619639.2 3 1964 TCAGTTTACCTG TGCT A 6 A c
c
CACATGCTTTCT AAAG CAT GTGCAGGTAG
TTCATTTC TTTC GTA CACGTCCATT
TTTC -
GAM3298 259 PLAC1 1 1845 NP_068568.1 3 106 CTCTTGTGACCC G CA A 6 A c c
TCATGTGAGCAC AAAGTGCTCATA TG GGT
TTTTGAGA TTTCACGAGTGT AC CCA
- TC G
GAM3298 259 PNPLA1 1 3706 NP_775947.1 3 420 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 POFUT1 2 6456 NP_758436.1 3 456 GTCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 POFUT1 2 8174 NP_056167.1 3 3491 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGCGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 POLH 1 11747 NP_006493.1 3 765 GGCTCATACCTG CATAG 6 A c
c
TAATGCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCAT
CCGTA

GAM3298 259 PORIMIN 1 5738 NP_443164.1 3 2003 TTTGAATACTTG CAT T- 6 A c c

TTTCTTTAGCAC AAAGTGCT AG GCAGGTA
TTTGAAGA TTTCACGA TC TGTTCAT
TT- TT

GAM3298 259 PP 1 5885 NP_066952.1 5 77 GCAGGACTCCGG A---- - A T 6 A c c
CACTATGAGCGG AAGT GCTCATAGTGC GG AG
CTTCAGCA TTCG CGAGTATCACG CC TC
ACGAC G G -

GAM3298 259 PPP1R3B 1 19238 NP_078883.1 3 987 GGCTTATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 PPP6C 1 17178 NP_002712.1 3 98 TACAATATACTT TAGTGC 6 A c c

TTTATTGAGCAC AAAGTGCTCA AGGTA
TTTGCTGC TTTCACGAGT TTCAT
TATTT-

GAM3298 259 PRKY 1 9486 NP_002751.1 3 3895 GTGTCATGCCTG CATAG 6 A c c

CAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ACGTCCGT
CCCTA

GAM3298 259 PRO0478 1 3706 NP_054848.1 3 344 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 PRO1496 1 16693 NP_061073.1 3 797 GGTTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGAAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 PRO1853 1 3706 NP_061077.1 3 324 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 PRO2859 1 3706 NP_061013.1 3 573 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 PRO2949 1 3706 NP_061014.1 3 489 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 PSEN1 1 8810 NP_000012.1 3 170 CTGACCACCTTG G C - A 6 A c c

CACTATTGGACT AAAGT CT ATAGTGCA GGT
TTGGAAGG TTTCA GG TATCACGT CCA
- T T C
GAM3298 259 PSEN1 1 8810 NP_015557.1 3 170 CTGACCACCTTG G C - A 6 A c c
CACTATTGGACT AAAGT CT ATAGTGCA GGT
TTGGAAGG TTTCA GG TATCACGT CCA
- T T C
GAM3298 259 PSK 1 17787 NP_057235.1 3 48 GCCCAAATCTAG TA --- A 6 A c c
AGCATTGAGCAC AAAGTGCTCA GTGC AGGT
TTTATCTC TTTCACGAGT TACG TCTA
-- AGA A
GAM3298 259 PTGIS 1 4543 NP_000952.1 3 1284 CCGGCTTGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTAG
TTTGGGAG TTTCACGA ATGTCCGTT
CCCTA
GAM3298 259 PTK6 1 3706 NP_005966.1 3 865 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 RAB4B 1 3706 NP_057238.2 5 437 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 RABEX5 1 6850 NP_055319.1 3 1330 GACAGCTACCTG TG- C 6 A c
c
CATTGTAGAACC AAAG CT ATAGTGCAGGTAG
TTTTCTTA TTTC GA TGTTACGTCCATC
CAA -
GAM3298 259 RAD51 1 16562 NP_002866.2 3 661 GTCTTGCGCCTG CAT A 6 A c c
TACTCCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TCATGTCCG
CCC C
GAM3298 259 RAD51 1 16562 NP_597994.1 3 661 GTCTTGCGCCTG CAT A 6 A c c
TACTCCCAGCAC AAAGTGCT AGTGCAGGT
TTTGGGAG TTTCACGA TCATGTCCG
CCC C
GAM3298 259 RDHL 1 3706 NP_005762.2 5 1283 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 RECQL5 1 2405 NP_004250.1 3 2236 GGCTCATACCTG CATAGT 6 A c
c
TTATACCAGCAC AAAGTGCT GCAGGTA
TTTGGGAG TTTCACGA TGTCCAT

CCATAT
GAM3298 259 SCR59 1 3706 NP_075559.1 3 732 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 SECTM1 1 18249 NP_002995.1 3 461 TACCTGTCCCTT -- ------ 6 A c c

GGCTATGAGCAG AAAGT GCTCATAGT GCAGGTA
GCTTTGGG TTTCG CGAGTATCG TGTCCAT
GA GTTCCC
GAM3298 259 SERF1A 1 4210 NP_068802.1 3 726 GGCTCATGCCTG TAG 6 A c c

TAATCTGAGCAC AAAGTGCTCA TGCAGGTA
TTTGGGAG TTTCACGAGT ATGTCCGT
CTA
GAM3298 259 SERF1B 1 4210 NP_075267.1 3 725 GGCTCATGCCTG TAG 6 A c c

TAATCTGAGCAC AAAGTGCTCA TGCAGGTA
TTTGGGAG TTTCACGAGT ATGTCCGT
CTA
GAM3298 259 SLC17A5 1 3707 NP_036566.1 3 801 GGCTCATGCCTG CATAG 6 A c c

TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 SLC26A4 1 3706 NP_000432.1 3 1671 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 SLC31A1 1 912 NP_001850.1 3 551 GGCCCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGGG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 SLC35E1 1 6353 NP_079157.2 3 1675 GGCTCATGCCTG CATAG 6 A c c

TAATCTCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CTCTA
GAM3298 259 SMARCD2 1 6099 NP_003068.2 3 499 TTTGGGTATTTG AG ----- 6 A c c

CACTATTTTGGG AA TGCTC ATAGTGCAGGTA
AGCAAGTT TT ACGAG TATCACGTTTAT
GA GGTTT
GAM3298 259 SNPH 1 4989 NP_055538.1 3 1040 ACTTCTGCTTTG CT - 6 A c c

CACTATGTTCAC AAAGTG CATAGTGCAG GTAG
TTTGGGGT TTTCAC GTATCACGTT CGTC
TT T
GAM3298 259 SNX11 1 19139 NP_037455.2 3 448 GTTTTTGCTGTA A T A-- 6 A c c

GCCCTAGAGCAC AAAGTGCTC TAG GC GGTAG
TTTGTTTG TTTCACGAG ATC CG TCGTT
- C ATG

GAM3298 259 SNX11 1 19139 NP_689450.1 3 448 GTTTTTGCTGTA A T A-- 6 A c c
GCCCTAGAGCAC AAAGTGCTC TAG GC GGTAG
TTTGTTTG TTTCACGAG ATC CG TCGTT
- C ATG

GAM3298 259 SNX22 1 8175 NP_079074.1 3 289 GGCTGATGCCTG CATAG 6 A c
c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 SNX25 1 11908 NP_114159.1 5 59 GCCAATACGTTC ATAGTGCA 6 A c
c

TACCGAGAGCAC AAAGTGCTC GGTAG
TTTGGAAT TTTCACGAG CCATC
AG------

GAM3298 259 SPTLC1 1 478 NP_847894.1 3 228 GGCTCATGCCTG CATAG 6 A c
c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTCAAAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 STAU 1 17501 NP_059347.1 5 372 GCTGTTTACCTG CT T 6 A c c
CATTTGTTCACT AAAGTG CA AGTGCAGGTAG
TTTGTTGA TTTCAC GT TTACGTCCATT
TT -

GAM3298 259 SYNJ2BP 1 666 NP_060843.1 3 762 GCTCATGCCTGT CATAG- 6 A c
c

AAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGTAG TTTCACGA ATGTCCGT
CCCTAA

GAM3298 259 TEM7 1 14878 NP_065138.2 3 2206 GGCTCGTGCCTG CAT 6 A c c
TACTCCCAGCAC AAAGTGCT AGTGCAGGTA
TTTGGGAG TTTCACGA TCATGTCCGT
CCC

GAM3298 259 TEX15 1 18387 NP_112561.1 3 583 TTAATTATATTG - AG AG 6 A c c
GCAATGAAGCAC AAAGTGCT CAT TGC GTA
TTTCAATG TTTCACGA GTA ACG TAT
A -- GT

GAM3298 259 TMG4 1 3706 NP_076986.1 3 84 GGCTCATGCCTG CATAG 6 A c c

TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 TNFRSF1 1 3706 NP_003835.2 3 136 GGCTCATGCCTG CATAG 6 A c
c

0A TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3298 259 TNFRSF1 1 20093 NP_003831.2 3 307 GGCTCATGCCTG CATAG 6 A c
c

0D TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGATAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 TOPK 1 4288 NP_060962.2 3 374 TAATGGATCTAC CAT CA 6 A c c
TGACATTAGCAC AAAGTGCT AGTG GGTAG
TTTGTACA TTTCACGA TTAC TCATC
--- AG
GAM3298 259 TRIM8 1 16708 NP_112174.1 3 861 ACAGCAACTTCC AG T 6 A c c
TGTAGTGAGCAC AAAGTGCTCAT TGCAGG AG
TTTGTATG TTTCACGAGTG ATGTCC TC
-- T
GAM3298 259 TRPM1 1 840 NP_002411.2 3 397 GGCTCATGCCTG CATAG 6 A c
c
TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 TXNL2 1 16694 NP_006532.1 3 790 GGCTCGTGCTTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTTCGT
CCCTA
GAM3298 259 UPK1B 1 3706 NP_008883.1 3 669 GGCTCATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 VHL 1 3706 NP_000542.1 3 3049 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 VPS4B 1 19238 NP_004860.2 3 643 GGCTTATGCCTG CATAG 6 A c
c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 WBSCR21 1 6665 NP_112585.2 3 868 GGCTCATGCCTG CATAG 6 A c
c
TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 WBSCR21 1 6665 NP_683710.1 3 61 GGCTCATGCCTG CATAG 6 A c
c
TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 WBSCR21 1 6665 NP_683711.1 3 61 GGCTCATGCCTG CATAG 6 A c
c
TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT

CCTTA
GAM3298 259 WBSCR21 1 6665 NP_683713.1 3 698 GGCTCATGCCTG CATAG 6 A c c
TAATTCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCTTA
GAM3298 259 WDR23 1 1087 NP_079506.3 3 1356 GGCTCATGCCTG CATAG 6 A c c
TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 WDR23 1 1087 NP_852002.1 3 1356 GGCTCATGCCTG CATAG 6 A c c
TAATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGGGAA TTTCACGA ATGTCCGT
TCCTA
GAM3298 259 WEE1 1 5763 NP_003381.1 3 491 ACTTGTATATCC A CA 6 A c c
CACTGGGAGCAC AAAGTGCTC TAGTG GGTA
TTTGTAGG TTTCACGAG GTCAC CTAT
G C-
GAM3298 259 XRCC2 1 2322 NP_005422.1 3 1907 GGCTCATGCCTG CATAG 6 A c c
TGATCCTAGCAC AAAGTGCT TGCAGGTA
TTTGCGAG TTTCACGA GTGTCCGT
TCCTA
GAM3298 259 ZFP30 1 1921 NP_055713.1 3 1373 GGCTCGTGCCTG CATAG 6 A c c
TAGTCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTG
GAM3298 259 ZNF174 1 7167 NP_003441.1 5 188 GCAAGCTACCTG ---- CATAG 6 A c c
CGACAGCTTGAA AAAGT GCT TGCAGGTAG
CTTTTCCT TTTCA CGA GCGTCCATC
AGTT CA---
GAM3298 259 ZNF197 1 12246 NP_008922.1 3 178 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGAGAG TTTCACGA ATGTCCGT
CCCTA
GAM3298 259 ZNF264 1 8644 NP_003408.1 3 1238 TCATCTTACCTG CATAG 6 A c c
TAATCCTAGCAC AAAGTGCT TGCAGGTAG
TTTGAGAC TTTCACGA ATGTCCATT
TCCTA
GAM3298 259 ZNF450 1 3706 NP_055612.1 3 2608 GGCTCATGCCTG CATAG 6 A c c
TAATCCCAGCAC AAAGTGCT TGCAGGTA
TTTGGGAG TTTCACGA ATGTCCGT
CCCTA

GAM3418 291 ADAM19 1 2787 NP_150377.1 3 3472 TGTGTCTGGGAT A----- AG A 3 A c c

CCAGGGCAATGT TCACATTGCC GGATT CCA
GAATTTTC AGTGTAACGG CCTAG GGT
CTTTTA GA -

GAM3418 291 B1 1 9166 NP_055266.1 3 528 TACTCTCTGGTA GC GA 3 A c c
AGACTTGAATGT ATCACATT CAGG TTACCA
GATTATTT TAGTGTAA GTTC AATGGT
-- AG

GAM3418 291 CDK4 2 5869 NP_000066.1 3 9 GATGAAGGTAAT A--- A G--- 3 A c c
CCGGAGTGGCAA TC CATTGCCA GGATTACC
TGGAGTGG AG GTAACGGT CCTAATGG
GGTG - GAGG

GAM3418 291 CDK4 2 12296 NP_000066.1 3 9 GAAGGTAATCCG A------ A G--- 3 A c c
GAGTGGCAATGG TC CATTGCCA GGATTACC
AGTGGCTG AG GTAACGGT CCTAATGG
GTCGGTG - GAGG

GAM3418 291 CPSF2 1 20174 XP_029311.2 5 34 CCGGCCGGTAGT A---- - T 3 A c c
CCCTGGCGCTGC TCA CA TGCCAGGGATTACC
TGACCCAG AGT GT GCGGTCCCTGATGG
GACCC C C

GAM3418 291 CYLD 1 18734 NP_056062.1 3 1692 ATGGGTGAATGA C GA--- 3 A c c

GCTTGTCAATGT ATCACATTG CAGG TTACC
GATTTTAA TAGTGTAAC GTTC AGTGG
T GAGTA

GAM3418 291 DKFZp54 1 3848 NP_775914.1 3 1290 ATGTTGAAAACT CCA CC 3 A c c

7G0215 AATCCCCAATGT ATCACATTG GGGATTA
GATTGTAT TAGTGTAAC CCCTAAT
--- CA

GAM3418 291 Ells1 1 11977 NP_690006.1 3 4394 AGCCTGTGGTCT A - - C 3 A c c
CCATGGCAATGG ATC CATTGCCA GG GATTAC
GTGTCCAT TGG GTAACGGT CC CTGGTG
- A T T

GAM3418 291 ESRRG 1 19845 NP_001429.1 3 1387 AGCTGCCATGGT G AGG 3 A c c

GGTTAGGAATGT ATCACATT CC GATTACCA
GATACATG TAGTGTAA GG TTGGTGGT
- A--

GAM3418 291 FLJ1117 1 12392 NP_060819.1 3 655 AGCAGGGTCCAT A G T- 3 A c c

5 TGCTGGCAATGG ATC CATTGCCAG GAT ACC
ATGGCCCA TAG GTAACGGTC TTA TGG
- G CC

GAM3418 291 FLJ1266 1 9523 NP_079428.1 3 74 AGGACCTTTGGA CAGG A 3 A c c

0 AATCAGCAATGT ATCACATTGC GATT CCA
GGTGATGG TGGTGTAACG CTAA GGT
A--- A

GAM3418 291 FLJ1314 1 3760 NP_068598.1 5 158 GTCATTTGTGAT TT- C 3 A c c
9 CCCTGGCTCTTG ATCACA GCCAGGGATTAC
TGATATGC TAGTGT CGGTCCCTAGTG
TCT T
GAM3418 291 FLJ1391 1 16332 NP_073607.2 3 182 GGATGTGGGTGT A----- TT T 3 A c
c
2 CCCTGGCTCTGT TCACA GCCAGGGAT ACC
GAGTCTTC AGTGT CGGTCCCTG TGG
CTTCTG CT -
GAM3418 291 FLJ1410 1 15222 NP_078965.1 3 1586 GCAATTGGTAAT A GCCA 3 A c
c
3 CCCCAAAATGGG ATC CATT GGGATTACCA
TGTATCTG TGG GTAA CCCTAATGGT
- AAC-
GAM3418 291 FLJ3103 1 10323 XP_037817.5 3 549 TATTGAAATTCT CC A CC 3 A c c
3 AACCCTCAATGT ATCACATTG AGGG TTA
GATGGTAT TAGTGTAAC TCCC AAT
-- - CT
GAM3418 291 GRIPE 1 1088 XP_170749.4 5 503 TCAAATTAAGGA GC A A 3 A c c
AGCTCTGAATGT ATCACATT CAGGG TT CC
GATTTGTG TAGTGTAA GTCTC AA GG
-- G -
GAM3418 291 GTF2E2 1 19529 NP_002086.1 3 194 GTAGAATGGGCT AGG TTA 3 A c
c
CATGGGCAATGT ATCACATTGCC GA CCA
GATGTTCC TAGTGTAACGG CT GGT
GTA CG-
GAM3418 291 HH114 1 11665 NP_115888.1 5 7 CACGAGGCTGGT CATT-- - 3 A c c
CCCTGGCCCAAC ATCA GCCAGGGATTA CC
ATGATACT TAGT CGGTCCCTGGT GG
ACAACC C
GAM3418 291 HTR7 1 751 NP_000863.1 3 881 AATGATGGGTTT GC G TT 3 A c c
TCCATGAAATGT ATCACATT CA GGA ACC
GATGCTTC TAGTGTAA GT CCT TGG
A- A TT
GAM3418 291 HTR7 1 751 NP_062873.1 3 912 AATGATGGGTTT GC G TT 3 A c c
TCCATGAAATGT ATCACATT CA GGA ACC
GATGCTTC TAGTGTAA GT CCT TGG
A- A TT
GAM3418 291 HTR7 1 751 NP_062874.1 3 960 AATGATGGGTTT GC G TT 3 A c c
TCCATGAAATGT ATCACATT CA GGA ACC
GATGCTTC TAGTGTAA GT CCT TGG
A- A TT
GAM3418 291 KIAA119 1 3870 XP_028968.3 3 408 AGGCTCAGGCAT -- TG TA 3 A c c
6 CCCTGGTGACCT ATCACA T CCAGGGAT CC
GTGGTTCT TGGTGT A GGTCCCTA GG
CC GT C-
GAM3418 291 KIAA120 1 16550 XP_049683.4 3 3014 TGCCTTGGTAAT A--- CC-- 3 A c
c

```
          3                          CCCTTAGATAAT    TCACATTG   AGGGATTACCA
                                     GTGGAAAC       GGTGTAAT   TCCCTAATGGT
                                           CAAA      AGAT
GAM3418  291   LIMK2  1  7977  NP_005560.1  3 322   CACCCAGGAACT   A       TTA        3  A  c  c
                                     CCCTGGCAGTGG ATC CATTGCCAGGGA  CC
                                     ATTGTGGG    TAG GTGACGGTCCCT  GG
                                           -         CAA
GAM3418  291   LIMK2  1  7977  NP_057952.1  3 322   CACCCAGGAACT   A       TTA        3  A  c  c
                                     CCCTGGCAGTGG ATC CATTGCCAGGGA  CC
                                     ATTGTGGG    TAG GTGACGGTCCCT  GG
                                           -         CAA
GAM3418  291   LOC1267 1  16572 XP_059074.1  3 610   ATGTTGAAACCT      CCA     CC       3  A  c
c
          55                         AATCCCCAATGT ATCACATTG  GGGATTA
                                     GATGGTAT    TAGTGTAAC  CCCTAAT
                                           ---      CC
GAM3418  291   LOC1296 1  3587  XP_059368.4  3 1402  TAGCATTAGGGT       C    TTA        3  A  c
c
          07                         TCTTTGCAATGT ATCACATTGC AGGGA  CC
                                     GGTATCTA    TGGTGTAACG TTTCT  GG
                                           -    TG-
GAM3418  291   LOC1456 1  8999  XP_096827.1  3 938   TTTATTGTGGAC      G  -  ATTA       3  A  c
c
          52                         CCCATGGAATGT ATCACATT CCA GGG   CCA
                                     GATTAAAT    TAGTGTAA GGT CCC   GGT
                                           -  A  CA--
GAM3418  291   LOC1457 1  8080  XP_085231.2  3 800   TAGGCCCATGGT      GC     T         3  A  c  c

          83                         GTTCCTGAATGT ATCACATT  CAGGGAT ACCA
                                     GATTGACA    TAGTGTAA  GTCCTTG TGGT
                                           --      -
GAM3418  291   LOC1525 1  10441 XP_087483.3  3 1653  AACATTTTTGGT       CCA            3  A  c  c

          19                         GGTCTTTAATGT ATCACATTG  GGGATTACCA
                                     GATGGACA    TAGTGTAAT  TTCTGGTGGT
                                           ---
GAM3418  291   LOC2832 1  13815 XP_210964.1  3 1221  CCCTAACAGGAA   A     GG   A        3  A  c
 c
          95                         ATTTGGCAATGG ATC CATTGCCA  GATT CC
                                     GGTCTGGG    TGG GTAACGGT  TTAA GG
                                           G      --  A
GAM3418  291   LOC2835 1  9453  XP_208702.1  5 1365  CCAAAGGGTAAT   A   CCA--          3  A  c
c
          05                         CCCCAAGACAAT ATC CATTG    GGGATTACC
                                     GGGTAAAA    TGG GTAAC    CCCTAATGG
                                           -    AGAAC
GAM3418  291   LOC2835 1  604   XP_294746.1  5 119   GCGGTTGAATTG   A    -  -  --       3  A  c  c
          96                         CCATGGCAATGC ATC CATTGCCA GG GATT  ACC
                                     GGTGGGCG    TGG GTAACGGT CC TTAA  TGG
                                           C      A G   GT
```

GAM3418 291 LOC2838 1 12884 XP_211215.1 5 150 AACCAAAGCGGT GGGAT 3 A c c
17 GCATGGCAATGT ATCACATTGCCA TACC
GATAGGGG TAGTGTAACGGT GTGG
AC---
GAM3418 291 LOC2839 1 2801 XP_208917.3 5 155 TGAGCGCTGGCA CC GA A 3 A c c
40 AGACCTCAATGT ATCACATTG AGG TT CCA
GATCAACA TAGTGTAAC TCC AA GGT
-- AG C
GAM3418 291 LOC2839 1 2801 XP_208940.2 3 470 TGAGCGCTGGCA CC GA A 3 A c c
80 AGACCTCAATGT ATCACATTG AGG TT CCA
GATCAACA TAGTGTAAC TCC AA GGT
-- AG C
GAM3418 291 LOC2845 1 11511 XP_209254.1 5 805 CTTCGTGGGTTT CA- TT 3 A c c
42 CCCTGGCAGGCT ATCA TTGCCAGGGA ACC
TGATGGCA TAGT GACGGTCCCT TGG
TCG T-
GAM3418 291 LOC2846 1 8747 XP_211569.1 3 1619 GTGCTTGAGGGT G GGA 3 A c c
47 GGCTGGGAATGT ATCACATT CCAG TTACC
GATATACA TAGTGTAA GGTC GGTGG
G ---
GAM3418 291 LOC2847 1 13651 XP_211601.1 5 609 AATCATCGTTTT A TT C 3 A c c
19 CCCTGGCAGGTG ATCAC TTGCCAGGGA AC
GTACAGCC TGGTG GACGGTCCCT TG
- TT C
GAM3418 291 LOC2849 1 6222 XP_211703.1 5 377 TTCCACTGTCTT - TT C 3 A c c
50 CCCTGGCAGCTG ATCACA TTGCCAGGGA AC
TGATGTGT TAGTGT GACGGTCCCT TG
C TC T
GAM3418 291 LOC2857 1 8604 XP_208349.1 3 1566 TGATAAATGGTG GC GA 3 A c c
86 AGATTTGAATGT ATCACATT CAGG TTACCA
GATAAGCA TAGTGTAA GTTT AGTGGT
-- AG
GAM3418 291 LOC3477 1 1860 XP_302601.1 5 424 TGCTTGGGTAAT A---- - CC 3 A c c
75 CCCTTTTAATGG TCAC ATTG AGGGATTACC
TGACTGAA AGTG TAAT TCCCTAATGG
AAGTC G TT
GAM3418 291 LOC3487 1 13922 XP_300399.1 3 456 TAATGGTGTCAC - - AT- 3 A c c
31 TGCTGGCAATGG ATCAC ATTGCCAG GG TACCA
TGATAATG TAGTG TAACGGTC TC GTGGT
G G ACT
GAM3418 291 LOC3492 1 17812 XP_300996.1 5 132 ACTTTGGAGGAA GCC A 3 A c c

```
          57                          TCTTTTGAATGT ATCACATT  AGGGATT CC
                                      GATGGATC    TAGTGTAA  TTTCTAA GG
                                                  GT-       -
GAM3418  291   LOC3492 1  17812 XP_301000.1  5  132   ACTTTGGAGGAA      GCC     A        3  A  c
c
          65                          TCTTTTGAATGT ATCACATT  AGGGATT CC
                                      GATGGATC    TAGTGTAA  TTTCTAA GG
                                                  GT-       -
GAM3418  291   MAPK14  1  5165  NP_001306.1  3  1540  TTGTAGGAATCC      GC --    A        3  A  c
c
                                      CTTTGAGAATGT ATCACATT  CA  GGGATT CC
                                      GATTCCTT    TAGTGTAA  GT  CCCTAA GG
                                                  GA  TT    -
GAM3418  291   MAPK14  1  5165  NP_620581.1  3  1540  TTGTAGGAATCC      GC --    A        3  A  c
c
                                      CTTTGAGAATGT ATCACATT  CA  GGGATT CC
                                      GATTCCTT    TAGTGTAA  GT  CCCTAA GG
                                                  GA  TT    -
GAM3418  291   MAPK14  1  5165  NP_620583.1  3  1621  TTGTAGGAATCC      GC --    A        3  A  c
c
                                      CTTTGAGAATGT ATCACATT  CA  GGGATT CC
                                      GATTCCTT    TAGTGTAA  GT  CCCTAA GG
                                                  GA  TT    -
GAM3418  291   MGC4586 1  5930  NP_689472.2  3  224   AGGAGGAGAGGT        GGGAT         3  A
c  c
          6                           GGATGGCAATGT ATCACATTGCCA    TACC
                                      GATTGGTG    TAGTGTAACGGT    GTGG
                                                    AG---
GAM3418  291   NEB    1  14890 NP_004534.1  3  124   CCTATGGTTTTT       C  G  TT-        3  A  c  c
                                      CTGTGTCAATGT ATCACATTG CA GGA  ACCA
                                      GATTTATG    TAGTGTAAC GT TCT  TGGT
                                                    T  G  TTT
GAM3418  291   NET-2  1  10940 NP_036470.1  3  516   CAATATTGGTGA      GCC  GA-         3  A  c
c
                                      CTACCTAAATGT ATCACATT  AGG  TTACCA
                                      GATTTTTG    TAGTGTAA  TCC  AGTGGT
                                                  A--  ATC
GAM3418  291   OGG1   1  20054 NP_058438.1  3  54    CTTGGAGGGCCT   ----       TTA      3  A  c  c
                                      CCTTGGCAATGC ATCA   CATTGCCAGGGA  CC
                                      ATTTGATG    TAGT    GTAACGGTTCCT  GG
                                                  TTAC        CCG
GAM3418  291   PCDH12  1  1606  NP_057664.1  5  973   GTAGGGGGTCTC   C--       ATT       3  A  c
c
                                      CCCTGGCAATTC ATCA  ATTGCCAGGG  ACC
                                      TTGATCGG    TAGT   TAACGGTCCC  TGG
                                                  TCT        CTC
GAM3418  291   POLS   1  19359 NP_008930.1  3  1552  AGTTCTAGATTG      GC      CC       3  A  c  c

                                      ATCTCTGAATGT ATCACATT  CAGGGATTA
                                      GATCGACG    TAGTGTAA  GTCTCTAGT
```

```
                                                --       TA
GAM3418  291   PP1665 1  1909  NP_110419.3  3 852   GAACCTAGGGCC       -    ATTA        3  A  c  c

                                    CTTGGCCAATGT ATCACATTG CCAGGG   CC
                                    GATTAAAG    TAGTGTAAC GGTTCC   GG
                                                C     CG--
GAM3418  291   PTPN11 1  13861 NP_002825.2  3 131   TTGGATTTGGAA       C  GA A        3  A  c
c
                                    GGCTTGCAATGT ATCACATTGC AGG  TT CCA
                                    GGTTGACT    TGGTGTAACG TTC  AA GGT
                                                - GG -
GAM3418  291   RAB17  1  16304 NP_071894.1  3 583   CCATGGTCTCCC         ---  TT       3  A  c  c
                                    GGCTGGCAATGT ATCACATTGCCA  GGGA  ACCA
                                    GGTGAAGC    TGGTGTAACGGT  CCCT  TGGT
                                                CGG   C-
GAM3418  291   SWAP70 1  18354 NP_055870.1  3 876   TTCCTGGTTGCC       G  ---  ATT        3  A  c
c
                                    CTTTTGGAATGT ATCACATT CCA  GGG  ACCA
                                    GATCCTGT    TAGTGTAA GGT  CCC  TGGT
                                                - TTT  GT-
GAM3418  291   SWAP70 1  18354 XP_049197.2  3 877   TTCCTGGTTGCC       G  ---  ATT        3  A  c
c
                                    CTTTTGGAATGT ATCACATT CCA  GGG  ACCA
                                    GATCCTGT    TAGTGTAA GGT  CCC  TGGT
                                                - TTT  GT-
GAM3418  291   WHSC1  1  13876 NP_055734.1  3 131   CAGCAAGGTAAT   A TT   ---          3  A  c  c

                                    CCTTGATGGCTG ATC CA  GCCA  GGGATTACC
                                    GATCTTTT    TAG GT  CGGT  TCCTAATGG
                                                - --   AGT
GAM3418  291   ZNF323 1  11866 NP_112161.2  3 561   TGCTATGGTCTC       G -  ATT        3  A  c  c

                                    CCCTAGGAATGT ATCACATT CC AGGG  ACCA
                                    GATAGATA    TAGTGTAA GG TCCC  TGGT
                                                - A   CTC
GAM3418  291   ZNF336 1  11914 NP_071927.1  3 2520  TTAAGGTGATTT       GCC--          3  A  c  c

                                    TTACAGAAATGT ATCACATT    AGGGATTACC
                                    GATTTTGC    TAGTGTAA    TTTTTAGTGG
                                                AGACA
GAM3431  356   A2BP1  1  7176  NP_665898.1  3 681   TTTAAACCATTC T-----          AAT      6  A  c  c
                                    CACCCGGCAGTA     AATACTGCCGGGT  GATGG
                                    TTCAGCTT        TTATGACGGCCCA  TTACC
                                            TTCGAC          CC-
GAM3431  356   A2BP1  1  7176  NP_665899.1  3 681   TTTAAACCATTC T-----          AAT      6  A  c  c
                                    CACCCGGCAGTA     AATACTGCCGGGT  GATGG
                                    TTCAGCTT        TTATGACGGCCCA  TTACC
                                            TTCGAC          CC-
GAM3431  356   A2BP1  1  7176  NP_665900.1  3 803   TTTAAACCATTC T-----          AAT      6  A  c  c
                                    CACCCGGCAGTA     AATACTGCCGGGT  GATGG
```

TTCAGCTT TTATGACGGCCCA TTACC
TTCGAC CC-
GAM3431 356 ABCC13 1 13374 NP_620054.1 3 790 TAGACAGTATTA CCGG 6 A c c
TTACATTCAGTA TAATACTG GTAATGATG
TTACAATG ATTATGAC CATTATTAT
TTA-
GAM3431 356 ARHE 1 4853 NP_005159.1 3 1595 TGCAGCATTATG G TA- 6 A c c
CTTTGGGCAGTA TAATACTGCC GG ATGATG
TTACAAAA ATTATGACGG TT TATTAC
G TCG
GAM3431 356 C3orf4 1 12739 NP_063948.1 3 459 TAGATAGCCAGT CG AA - 6 A c c
CAACCAGCAGTA TAATACTGC GGT TGA TGG
TTAGTGCT ATTATGACG CCA ACT ACC
A- -- G
GAM3431 356 CD59 1 18546 NP_000602.1 3 790 CTCTACTACATG GTA- A 6 A c c
TGACTGGCAGTA TAATACTGCCGG ATG TGG
TTAAGTGT ATTATGACGGTC TAC ATC
AGTG -
GAM3431 356 DKFZP43 1 13982 XP_166383.1 3 1116 TATGCATATTTT GG- TG- 6 A c c
4G1411 ATGGGGGCAGTA TAATACTGCC GTAA ATG
TTATTACA ATTATGACGG TATT TAC
GGG TTA
GAM3431 356 DKFZP56 1 3040 NP_113623.1 3 2147 TTCATTCATTAT C 6 A b b
4I0422 TACCTGACAGTA TAATACTG CGGGTAATGATGG
TTAAACTA ATTATGAC GTCCATTATTACT
A
GAM3431 356 FAT3 1 3238 XP_061871.5 3 368 GTTACAGCATCA C TAA 6 A c c
GTCCTTGCAGTA TAATACTGC GGG TGATG
TTAAAAAC ATTATGACG TCC ACTAC
T TG-
GAM3431 356 FLJ1319 1 14915 NP_078890.1 3 1645 CAGATTCATCAT GCC- 6 A c c
7 TATTCCTAAAGT TAATACT GGGTAATGATGG
ATTGCTGT GTTATGA CTTATTACTACT
AATC
GAM3431 356 FLJ3219 1 4685 NP_653290.2 3 180 GAAAAACATCAT CTG-- G 6 A c c
1 TACTGGAAACCT TAATA CCGG TAATGATG
ATTAAACA ATTAT GGTC ATTACTAC
CCAAA -
GAM3431 356 FLJ3391 1 9000 NP_689620.1 3 782 GCTAGCTATCAT A CCG 6 A c c
8 TACCAGTTAGAA TAAT CTG GGTAATGATGG
TTAACATT ATTA GAT CCATTACTATC
A TGA
GAM3431 356 FLJ4029 1 6666 XP_059377.5 3 957 AGCTGCTCACTA C A 6 A c c
8 TTATCTGCAGTA TAATACTGC GGGTAATG TGG
TTGATAAG GTTATGACG TCTATTAT ACT
- C

GAM3431 356 FOXP1 1 7666 NP_116071.2 3 976 GCCGATTCATTC -- - T -- 6 A c c
CACGCAGCAGTA TAATACTGC CG GG AATGA TGG
TTGGGGGT GTTATGACG GC CC TTACT GCC
AC A - TA
GAM3431 356 HSPC177 1 19777 NP_057494.2 3 570 TTTGATTCTATG CC T G 6 A c
c
GTTCCCTCAGTA TAATACTG GGG AAT ATGG
TTACATCT ATTATGAC CCC TTG TATC
T- - G
GAM3431 356 KIAA115 1 2654 XP_030864.2 3 5595 TCCCCTAATCAT - G 6 A c c
5 TACTTGGTAGTT TAATA CTGCCGGGTAATGAT
ATTAATCC ATTAT GATGGTTCATTACTA
T A
GAM3431 356 KIAA143 1 18507 XP_039698.3 3 34 AGGTTCCATCAC GGGTAA 6 A c
c
2 AAAGGGGCAGTA TAATACTGCC TGATGG
TTAATTAG ATTATGACGG ACTACC
GGAAAC
GAM3431 356 KIAA157 1 4405 NP_065978.1 3 195 GTGCCAATCCCA CG AT- - 6 A c c

6 TGCCATGCAGTA TAATACTGC GGTA GAT GG
TTATGTCC ATTATGACG CCGT CTA CC
TA ACC A
GAM3431 356 KIAA158 1 10648 NP_065983.1 5 89 CAGCAACATCAT T ----- 6 A c c
7 TACCGCTAGCGG TAA ACTGCCG GGTAATGATG
CAGTTTTG GTT TGACGGC CCATTACTAC
T GATCG
GAM3431 356 KIAA167 1 17033 XP_047672.4 3 1532 CCTATCCATCAT CT GGG 6 A c
c
3 TAAAAGGTTTAT TAATA GCC TAATGATGG
TATCAGTG ATTAT TGG ATTACTACC
T- AAA
GAM3431 356 KLHL3 1 2902 NP_059111.1 3 2794 CTCTCCATCTAC CGG--- AT 6 A c
c
AAAGTTGCAGTA TAATACTGC GTA GATGG
TTATGCAA ATTATGACG CAT CTACC
TTGAAA --
GAM3431 356 LOC1266 1 8765 XP_060121.4 3 2698 TGAGCTTCTGTC GCC - 6 A c
c
69 ATATGCCCAGTA TAATACT GGGTA ATGATGG
TTATGCTT ATTATGA CCCGT TACTGTC
--- A
GAM3431 356 LOC1448 1 552 XP_096696.1 5 377 CAACTCCATCAT A G - - 6 A c c
74 TCACACTGGAGG TAAT CT CCGG GT AATGATGG
ATTAGAGG ATTA GG GGTC CA TTACTACC
- A A C
GAM3431 356 LOC1505 1 6328 XP_097917.1 5 189 TTATACTGTTGA CC - 6 A c c
87 TTACTTTCAGTA TAATACTG GGGTAAT GATGG
TTAATATA ATTATGAC TTCATTA TTGTC
T- G

GAM3431 356 LOC2545 1 18418 XP_172961.1 5 1760 CTCGCCATTCAT ACT - 6 A c c
32 TACCCGGCTTGG TAAT GCCGGGTAATGA TGG
TTAATGCA ATTG CGGCCCATTACT ACC
GTT T
GAM3431 356 LOC2830 1 6480 XP_210869.1 5 830 TTCCCGTAATTA C-- G 6 A c c
53 CTTATTGCAGTA TAATACTGC GGGTAAT ATGG
TTGTGTTC GTTATGACG TTCATTA TGCC
TTA A
GAM3431 356 LOC2843 1 4230 XP_209162.1 3 2129 CCAAAACATCAT AC-- G 6 A c c
17 TATGTGGCACAT TAAT TGCCG GTAATGATG
GATTATAA ATTA ACGGT TATTACTAC
GTAC G
GAM3431 356 LOC2843 1 10520 XP_209143.1 3 152 TCATCAGGGCCA C-- AA--- 6 A c c
25 CCCCCTGCAGTA TAATACTGC GGGT TGATGG
TTGAGCAC GTTATGACG CCCA ACTACT
TCC CCGGG
GAM3431 356 LOC2850 1 19819 XP_211759.1 3 70 AAGGACGCCTTC AT T 6 A c c
82 TGCTTGGCAGTA TAATACTGCCGGGTA GA GG
TTAACTGG ATTATGACGGTTCGT CT CC
-- T
GAM3431 356 LOC2851 1 6394 XP_211784.1 3 1051 TTCATATTCTAT CCGGG 6 A c c
47 TATTGAACAGTA TAATACTG TAATGATGG
TTAATGCT ATTATGAC GTTATTATC
AA---
GAM3431 356 LOC2864 1 494 XP_210041.1 5 413 TACCACCATCAT A CC T 6 A c c
16 TCTTCACAGAAT TAAT CTG GGG AATGATGG
TACAAAAA ATTA GAC TTC TTACTACC
A AC -
GAM3431 356 LOC3399 1 6821 XP_295123.1 3 500 AAAATCCAGTTG - AATGA 6 A c c
87 ACCTGGACAGTA TAATACTG CCGGGT TGG
TTATATGT ATTATGAC GGTCCA ACC
A GTTG-
GAM3431 356 MGC2418 1 15915 NP_689565.1 3 235 AAGAATTTGCCA CGGGTAA 6 A c c
0 TCAGTAGCAGTA TAATACTGC TGATGG
TTAAGCAG ATTATGACG ACTACC
ATG----
GAM3431 356 MGC5055 1 4039 NP_776163.1 3 893 GTCACCCATCAT T C T 6 A c c
9 TCTTGCGTGTTG TAATAC GC GGG AATGATGG
TATGCTTT GTTGTG CG TTC TTACTACC
- - -
GAM3431 356 PIM2 1 2828 NP_006866.1 3 60 ATTACCAGTCAT CCGGG - 6 A c c
TAAAGTCCAGTA TAATACTG TAATGA TGG
TTACTAAG ATTATGAC ATTACT ACC

CTGAA G
GAM3431 356 PPARD 1 10291 NP_006229.1 3 364 CTGCCCCATCAT TA C - 6 A c c
TGCACCTGCAGG TAA CTGC GG GTAATGATGG
CTTAGGTC ATT GACG CC CGTTACTACC
CG T A
GAM3431 356 PSCD3 1 6586 NP_004218.1 3 441 CAAACGCATTCA -- - A 6 A c c
CTCGGGGCAGTA TAATACTGCC GGGT AATG TG
TTAACCGT ATTATGACGG CTCA TTAC GC
GG C -
GAM3431 356 RELN 1 615 NP_005036.2 3 266 GTAATATCAGTT G- - 6 A c c
ACAGTGGCAGTA TAATACTGCCG GTAA TGATG
TTGACAAT GTTATGACGGT CATT ACTAT
GA G
GAM3431 356 RELN 1 615 NP_774959.1 3 266 GTAATATCAGTT G- - 6 A c c
ACAGTGGCAGTA TAATACTGCCG GTAA TGATG
TTGACAAT GTTATGACGGT CATT ACTAT
GA G
GAM3431 356 RNGTT 1 19971 NP_003791.1 3 2137 CTGAACATAATA CG-- ATG 6 A c
c
CCATCTGCAGTA TAATACTGC GGTA ATG
TTATAAAA ATTATGACG CCAT TAC
TCTA AA-
GAM3431 356 RTKN2 1 8705 NP_660350.2 3 1900 GCCTTCCTTTAT CCGG T 6 A c
c
TACAAATCAGTA TAATACTG GTAATGA GG
TTAAAACT ATTATGAC CATTATT CC
TAAA T
GAM3431 356 SLC25A1 1 801 NP_003696.2 3 788 CATCTCCATCAT T -- G 6 A c c
2 TACTGGCTTAGT TAA ACT GCCGG TAATGATGG
TTTGCTTT GTT TGA CGGTC ATTACTACC
T TT -
GAM3431 356 SNX16 1 9454 NP_071416.2 3 1888 TTATAATGCATT CC T 6 A c c
TTACTCCCAGTA TAATACTG GGGTAA GATG
TTATGTTC ATTATGAC CTCATT TTAC
C- -
GAM3431 356 SNX16 1 9454 NP_690049.1 3 1888 TTATAATGCATT CC T 6 A c c
TTACTCCCAGTA TAATACTG GGGTAA GATG
TTATGTTC ATTATGAC CTCATT TTAC
C- -
GAM3431 356 SNX16 1 9454 NP_690050.1 3 1888 TTATAATGCATT CC T 6 A c c
TTACTCCCAGTA TAATACTG GGGTAA GATG
TTATGTTC ATTATGAC CTCATT TTAC
C- -
GAM3431 356 SRGAP2 1 5806 NP_055665.1 3 957 CCTAAGCCCCAT CCGG A 6 A c
c
CGTAGCACAGTA TAATACTG GT ATGATGG
TTACATGT ATTATGAC CG TGCTACC
A--- A
GAM3431 356 TBX4 1 19579 NP_060958.2 3 52 CCCCGGGACCGT CC G 6 A c c
GTTGCTCCAGTA TAATACTG GGGTAAT ATGG

TTAACCTC ATTATGAC CTCGTTG TGCC
-- -
GAM3431 356 ZNF183L 1 13659 NP_849192.1 3 165 TGCACTCCCATG C GT G 6 A c c
1 TTCACTGCAGTA TAATACTGC GG AAT ATGG
TTATTTGC ATTATGACG TC TTG TACC
- AC -
GAM3499 226 AGMAT 1 17623 NP_079034.2 3 289 ATAAAGGGGAAG - TTGG 3 A c c
TGAGGAGAATTT AAAGAA TTCTCCTT GCTT
CTTTCAAG TTTCTT AAGAGGAG TGAA
T ----
GAM3499 226 BTBD9 1 1931 NP_689946.1 5 184 AGGTCTCCCCGA - - CT 3 A c c
GAAGGAGAAGTT AAAGAATT CTCCTTTT GGG
CTTTAATT TTTCTTGA GAGGAAGA CCC
A G CT
GAM3499 226 C14orf1 1 9472 NP_061148.1 3 343 CAGGAGGCTGAG - G 3 A c c
17 GCAGGAGAATTC AAAGAATTCTCCT TTT GGCTT
TTTTAACC TTTCTTAAGAGGA GGA TCGGA
C G
GAM3499 226 C1orf24 1 18867 NP_443198.1 3 1316 TCCAAAAGATTA T- G 3 A c c
AAAGGAGTTGTT AAAGAAT CTCCTTTTGG CTT
CTTTTCTC TTTCTTG GAGGAAAATT GAA
TT A
GAM3499 226 CCND2 1 10931 NP_001750.1 3 4294 GCTTCTAAGCCA ATTC G 3 A c c
AAAGGATTCCTC AAAGA TCCTTTTGG CTT
TTTGTTTA TTTCT AGGAAAACC GAA
CCTT -
GAM3499 226 CDKN2B 1 7140 NP_004927.2 5 68 TTGGCCCAGCTG CC ---- 3 A c c
AAAACGGAATTC AAAGAATTCT TTT TGGGCT
TTTGCCGG TTTCTTAAGG AAA ACCCGG
CA GTCG
GAM3499 226 CDKN2B 1 7140 NP_511042.1 5 68 TTGGCCCAGCTG CC ---- 3 A c c
AAAACGGAATTC AAAGAATTCT TTT TGGGCT
TTTGCCGG TTTCTTAAGG AAA ACCCGG
CA GTCG
GAM3499 226 CGI-31 1 16300 NP_057043.1 3 528 TGTCGCTAGTCC AA TT 3 A c c
TAAGGAGAAACC AAAG TTCTCCTT GGGCT
TTTAACCA TTTC AAGAGGAA CCTGA
CA T-
GAM3499 226 CHD6 1 11177 NP_115597.3 3 224 CCTAGTCTAGGA A --- 3 A c c
GGCACAGAATTC A AGAATTCT CCTTTTGGGCT
TCATTCTG A TCTTAAGA GGAGGATCTGA
C CAC
GAM3499 226 CLCN6 1 10812 NP_001277.1 3 2246 CAGATAAGCCCA A - - CC 3 A c c
AAGACAGCAACT A AGAA TT CT TTTTGGGCTT
TCTCCACT C TCTT AA GA GAAACCCGAA
C C C CA

GAM3499 226 CLCN6 1 10812 NP_068503.1 3 2246 CAGATAAGCCCA A - - CC 3 A c c

AAGACAGCAACT A AGAA TT CT TTTTGGGCTT
TCTCCACT C TCTT AA GA GAAACCCGAA
C C C CA

GAM3499 226 CLCN6 1 10812 NP_068504.1 3 2246 CAGATAAGCCCA A - - CC 3 A c c

AAGACAGCAACT A AGAA TT CT TTTTGGGCTT
TCTCCACT C TCTT AA GA GAAACCCGAA
C C C CA

GAM3499 226 CLCN6 1 10812 NP_068505.1 3 2246 CAGATAAGCCCA A - - CC 3 A c c

AAGACAGCAACT A AGAA TT CT TTTTGGGCTT
TCTCCACT C TCTT AA GA GAAACCCGAA
C C C CA

GAM3499 226 CLDN1 1 19530 NP_066924.1 3 551 GCCTAATTTACC - ------ T 3 A c c
AAGGATGAATTC AAAGAATTC TCCTT TTGGGC
TTTCAATT TTTCTTAAG AGGAA AATCCG
T CCATTT -

GAM3499 226 CYP19A1 1 13808 NP_000094.2 3 626 CAAAAGTTTAAT C --- 3 A c c
CAGAGGAAATTC AAAGAATT TCCTT TTGGGCTT
TTTCCCAG TTTCTTAA AGGAG AATTTGAA
- ACT

GAM3499 226 CYP19A1 1 13808 NP_112503.1 3 626 CAAAAGTTTAAT C --- 3 A c c
CAGAGGAAATTC AAAGAATT TCCTT TTGGGCTT
TTTCCCAG TTTCTTAA AGGAG AATTTGAA
- ACT

GAM3499 226 DIAPH2 1 9117 NP_006720.1 3 2574 TCCAGAGGCTCT A T 3 A c c
AGAGGAGAATCT AAAGA TTCTCCTTT GGGCTT
TTCCTTGC TTTCT AAGAGGAGA CTCGGA
- T

GAM3499 226 DKFZp43 2 2462 NP_115623.1 3 1081 CCCACAAGCAGA -- TTTGG 3 A c b

4E0519 GTAGGAGAATAC AAAGA ATTCTCCT GCTT
TCTTTTCT TTTCT TAAGAGGA CGAA
CA TGAGA

GAM3499 226 DKFZp43 2 3588 NP_115623.1 3 1686 AGAGGTAGCCCA -- - 3 A b b

4E0519 AAAAGGGGAGTG AAAGA ATTCTCCTTTT GGGCT
ATCTTTCA TTTCT TGAGGGGAAAA CCCGA
AG A

GAM3499 226 DKFZP43 1 14688 NP_115525.1 3 25 TAAAGTTCTAGA T -- - 3 A c c

4G072 CTGGGTGAATTC AAAGAATTC CCT TTTGGG CTT
TTTCATGA TTTCTTAAG GGG AGATCT GAA
T TC T

GAM3499 226 DKFZP43 1 4289 NP_056483.1 3 59 GCTGCTGATAGG CCTT 3 A c c

4I092 TTCAAGGAATTC AAAGAATTCT TTGGGCTT
TTTAAACC TTTCTTAAGG AACTTGGA

GAM3499 226 DKFZP56 1 4069 XP_085525.3 3 2507 TGGGAGGCTGAA A- - G 3 A c c

```
          4M182                          GCAGGAGAATCA AAAG  ATTCTCCT TTT GGCTT
                                       CTTTAACC    TTTC  TAAGAGGA GAA TCGGA
                                                 AC       C   G
GAM3499  226    DKFZp76 1  964   XP_095568.5  3  1427  ATCTACTAAAGT        CCT   GG         3  A  c
c
          2C1112                         ACAAAGGAATTC AAAGAATTCT   TTTG  CTT
                                       TTTGGAAG    TTTCTTAAGG   AAAC  GAA
                                                 ---   AT
GAM3499  226    DKFZP76 1  10932 XP_040560.4  3  385   AATGGTTGAAGG        ---    G         3  A  c  c
          2N2316                         GAGAGAGAATTC AAAGAATTCTC   CTTTT GGCT
                                       TTTAAAAT    TTTCTTAAGAG   GGGAA TTGG
                                                 AGA    G
GAM3499  226    FLJ1289 1  18919 NP_073594.2  5  23    CCGGGAGCCCAC       CT  - TT          3  A  c
c
          2                              GGCGGTTAATTC AAAGAATT  CC T  TGGGCTT
                                       TTTTTACC    TTTCTTAA  GG G  ACCCGAG
                                                 TT  C GC
GAM3499  226    FLJ1345 1  12797 XP_038291.5  3  1885  TATTTCAGACAA        C-    GG         3  A  c  c

          6                              AATAGAGAATTC AAAGAATTCTC  TTTTG  CT
                                       TTTTAAAA    TTTCTTAAGAG  AAAAC  GA
                                                 AT    A-
GAM3499  226    FLJ2058 1  12014 XP_090970.4  5  1630  TGTGGTTCATCA        ---  TT          3  A  c  c
          2                              GGTGAGGAATTC AAAGAATTCT   CCT  TGGGCT
                                       TTTAATAA    TTTCTTAAGG   GGA  ACTTGG
                                                 AGT   CT
GAM3499  226    FLJ2344 1  18407 NP_079101.1  3  117   TGGGGAGCCAAG    A-      -  G         3  A  c  c

          7                              GCAGGAGAATCG AAAG  ATTCTCCT TTT GGCTT
                                       CTTTAGGC    TTTC  TAAGAGGA GGA CCGAG
                                                 GC       C   A
GAM3499  226    FLJ2353 1  18841 NP_079165.1  3  982   TGGAAGGCCAAA       C---     T  G       3  A  c  c

          7                              GGAATAAAATTC AAAGAATT    TCCTTT GG CTT
                                       TTTTATAT    TTTCTTAA    AGGAAA CC GAA
                                                 AATA     -  G
GAM3499  226    FLJ3068 1  16626 XP_166291.1  3  1920  CAGGAGGCTGAG    -       -  G         3  A  c  c
          1                              GCAGGAGAATTA AAAG AATTCTCCT TTT GGCTT
                                       CTTTAACC    TTTC TTAAGAGGA GGA TCGGA
                                                 A       C   G
GAM3499  226    FLJ3120 1  5760  NP_694568.1  3  1052  GGGAAGGCTGAG    A     -  G         3  A  c  c

          8                              GTAGGAGAATCT AAAGA TTCTCCT TTT GGCTT
                                       TTTGAATC    TTTCT AAGAGGA GGA TCGGA
                                                 -     T  G
GAM3499  226    FLJ3569 1  7369  NP_694972.2  3  24    AAGGTATAGCAG        CCTT  G-         3  A  c  c

          3                              CAGTTAGAATTC AAAGAATTCT    TTG  GCT
                                       TTTGCAAA    TTTCTTAAGA    GAC  CGA
                                                 TT--   GA
```

GAM3499 226 FLJ3675 1 7444 NP_776190.1 3 1688 TTGGGCCTCTCA A C --- 3 A c c
4 AAAGGAAATGCT AAAG ATT TCCTTTTG GGCTT
TTTGTTTA TTTC TAA AGGAAAAC CCGGG
G - TCT
GAM3499 226 FLJ3713 1 16721 NP_775958.1 3 494 TCAAACGTCCCA A ----- - T 3 A c c
1 AAAGGAGAAATG AAGAA TTCTCCTTTTGGG C
CTTTCTTA TTCTT AAGAGGAAAACCC G
A TCGTA T C
GAM3499 226 GP2 1 3890 NP_001493.1 3 367 CGGGAGGCCAAG A - -- G 3 A c c
GCAGGAGAATTG A AG AATTCTCCT TTTGG CTT
CTCGAACT G TC TTAAGAGGA GAACC GAG
C G CG G
GAM3499 226 GPR105 1 7994 NP_055694.1 3 1054 TTATGAGCTACC CTCC -- 3 A c
c
AAAACTAAATTC AAAGAATT TTTTGG GCTT
TTTCTCTG TTTCTTAA AAAACC CGAG
ATC- AT
GAM3499 226 GRIN3A 1 19610 NP_597702.1 3 2333 TTAAGGGAACCC TC CT 3 A c
c
AGAAGTGAATTC AAAGAATTC CTTTTGGG
TTTTGTAA TTTCTTAAG GAAGACCC
T- AA
GAM3499 226 HMG20A 1 17461 NP_060670.1 3 715 GATTGCTGCCCT -- T T 3 A c c
AAAGGAGAATGC AAAGA ATTCTCCTTT GGGC
TCTTTCCT TTTCT TAAGAGGAAA CCCG
CG T T
GAM3499 226 HNRPA0 1 10813 NP_006796.1 5 271 CCGGGCCTTGGA A - -- 3 A c c
GATGGAGAATTC A AGAATTCTCC TTTT GGGCTT
TCAGTTGT A TCTTAAGAGG AGAG TCCGGG
C T GT
GAM3499 226 KIAA051 1 18061 NP_055511.1 3 1519 TCCTGAAGCCCA A TC TT-- 3 A c
c
4 ACGATGGACCAT A AGAAT TCC TTGGGCTT
TCTCACCC A TCTTA AGG AACCCGAA
C CC TAGC
GAM3499 226 KIAA173 1 12467 XP_290496.1 3 1452 AAATAGTTCACG TTT-- 3 A c c
5 TTTGGAGAATTC AAAGAATTCTCC TGGGCT
TTTTGTAC TTTCTTAAGAGG ACTTGA
TTTGC
GAM3499 226 KIAA198 1 6965 NP_078853.1 5 323 ATTAAAAGGGTT CC 3 A c c
5 TAAGAAGAATTC AAAGAATTCT TTTTGGGCTT
TTTCTCAG TTTCTTAAGA AGAATTTGGG
--
GAM3499 226 KIAA202 1 18702 NP_742067.1 5 281 AATAACAGCCTG CT-- TT 3 A c c
4 AGGTTCCAATTC AAAGAATT CCTT GGGCT
TTTATCAT TTTCTTAA GGAG TCCGA
CCTT --
GAM3499 226 LGMN 1 10662 NP_005597.2 3 339 TAGCCCCTCTCA ATT ----- 3 A c c
AAAGGAGTCTTT AAAGA CTCCTTTT GGGCT

```
                                    ATTCTGAG    TTTCT  GAGGAAAA    CCCGA
                                            ---      CTCTC
GAM3499  226   LOC1152 1  2334  XP_055499.2  5  1384  TCGAGTGTGGTC    A-      TG        3  A  c
c
         19                          AAAGGAGAGAGT AAAGA  TTCTCCTTT  GGCT
                                    CTTTGTCA    TTTCT  GAGAGGAAA  CTGG
                                            GA       --
GAM3499  226   LOC1374 1  8695  XP_059909.1  3  46    CCACACGACAGC        CTTTT        3  A  c
c
         85                          CCTCGAGAATTC AAAGAATTCTC    GGGCT
                                    TTTCAAGT    TTTCTTAAGAG    CCCGA
                                            CT---
GAM3499  226   LOC1433 1  14117 XP_084501.1  3  616   GGACAGAGCCCA    AAT-    -         3  A  c
c
         81                          AAACGGGGGTAG AAAG   TCTCC TTTTGGGCTT
                                    ACTTTGTG    TTTC   GGGGG AAAACCCGAG
                                            AGAT    C
GAM3499  226   LOC1458 1  4635  XP_085255.1  3  527   ACTTTGAGACCC       CTCC     -        3  A  c
c
         44                          AGAAATAAATTC AAAGAATT   TTTTGGG CTT
                                    TTTCCTTT    TTTCTTAA    AAGACCC GAG
                                            ATA-      A
GAM3499  226   LOC1477 1  5469  XP_085862.1  5  1355  TGGGAGGCTGAG   G       -  G        3  A  c
c
         27                          GCAGGAGAATTG AAA AATTCTCCT TTT GGCTT
                                    TTTGACCT    TTT TTAAGAGGA GGA TCGGA
                                            G        C  G
GAM3499  226   LOC1493 1  7415  NP_787072.1  3  778   GGTAAGTTTTAG        CCT    G        3  A  c
c
         71                          TCAAAAGAATTC AAAGAATTCT   TTTGG CT
                                    TTTCTTGA    TTTCTTAAGA   AAACT GA
                                            ---     -
GAM3499  226   LOC1494 1  2383  NP_690048.1  3  1774  TTAAGCTAATAA        CCT-   --        3  A  c  c

         20                          ATATAAGAATTC AAAGAATTCT    TTTG  GGCTT
                                    TTTTGGAA    TTTCTTAAGA    AAAT  TCGAA
                                            ATAT    AA
GAM3499  226   LOC1496 1  5200  XP_097690.1  3  165   ATTTTGAGCAGC       TCTCCTTT          3  A  c
 c
         19                          ACAGTCCAATTC AAAGAAT       TGGGCT
                                    TTTAACTA    TTTCTTA       ACCTGA
                                            --------
GAM3499  226   LOC1501 1  1768  XP_086802.2  3  2816  AGTAGGTCCTGG       CTC    ---        3  A  c
c
         74                          AAAAGTAAATTC AAAGAATT   CTTTT   GGGCTT
                                    TTTATTTT    TTTCTTAA   GAAAA   CCTGGA
                                            AT-     GGT
GAM3499  226   LOC1502 1  11780 XP_086827.2  3  129   TTGCTAGCTCAG A-----         -        3  A  c  c
         12                          TGAGGGGAATTC      AAGAATTCTCCTT TTGGGCT
                                    TTCCAGAA         TTCTTAAGGGGAG GACTCGA
```

AAGACC T

GAM3499 226 LOC1502 1 1768 XP_059324.1 3 2816 AGTAGGTCCTGG CTC --- 3 A c c

13 AAAAGTAAATTC AAAGAATT CTTTT GGGCTT

TTTATTTT TTTCTTAA GAAAA CCTGGA

AT- GGT

GAM3499 226 LOC1550 1 3019 XP_088145.2 3 444 GGGGCTCAGATT --- T- 3 A c c

81 GGCACAGAATTC AAAGAATTCT CC TTTGGGCTT

TTTTGTGA TTTCTTAAGA GG AGACTCGGG

CAC TT

GAM3499 226 LOC1575 1 4290 XP_098783.1 5 1007 TTCAAGAGCCCA A CTCC 3 A c c

56 AAAACAGTTCTC A AGAATT TTTTGGGCTT

CTCCATGC C TCTTGA AAAACCCGAG

C CA--

GAM3499 226 LOC1972 1 19865 XP_113839.2 5 103 CCAGGAAGCCCG AA----- T 3 A c c

01 GCAGGAGAATTC AGAATTCTCCT TTGGGCTT

TGCCAGAT TCTTAAGAGGA GGCCCGAA

TAGACCG C

GAM3499 226 LOC2003 1 2412 XP_117226.1 3 370 AGCTTGTTCCCA C CT 3 A c c

39 AGAGGATAATTC AAAGAATT TCCTTTTGGG

TTTATACT TTTCTTAA AGGAGAACCC

T TT

GAM3499 226 LOC2015 1 8805 XP_113972.1 3 180 AGCTCTCTGCAA --- TT--- 3 A c c

10 GTGAGAGAATTC AAAGAATTCTC CTT GGGCT

TTTGGGAA TTTCTTAAGAG GAA CTCGA

AGT CGTCT

GAM3499 226 LOC2028 1 3019 XP_114560.1 3 440 GGGGCTCAGATT --- T- 3 A c c

02 GGCACAGAATTC AAAGAATTCT CC TTTGGGCTT

TTTTGTGA TTTCTTAAGA GG AGACTCGGG

CAC TT

GAM3499 226 LOC2568 1 18534 XP_173029.2 3 262 GATTATAGAGCA A CC G 3 A c c

95 CAGAAAGAATTC A AGAATTCT TTTTG GCTT

TCAAACTA A TCTTAAGA AAGAC CGAG

C -- A

GAM3499 226 LOC2830 1 10213 XP_302599.1 3 396 ATTGGAAGGTTC CTTT 3 A c c

38 ATTTGAGAATTC AAAGAATTCTC TGGGCTT

TTTCCTTC TTTCTTAAGAG ACTTGGA

TTT-

GAM3499 226 LOC2830 1 16956 XP_210878.1 5 138 AACAGACTCCTA - CT 3 A c c

70 AAAGGAGGGTTT AAAGAA TTCTCCTTTTGGG

CTTTCCTG TTTCTT GGGAGGAAAATCC

T TC

GAM3499 226 LOC2836 1 3498 XP_211144.1 3 832 GGGGAGGCTGAG - - G 3 A c c

55 GCAGGAGAATTG AAAG AATTCTCCT TTT GGCTT

CTTTGAAC TTTC TTAAGAGGA GGA TCGGA

G C G

GAM3499 226 LOC2836 1 11367 XP_211161.1 3 1334 TCACCTAGCTTG CTCCT - T 3 A c c

82 CCACAAAAATTC AAAGAATT TTTG GGC
TTTGGCGA TTTCTTAA AAAC CCG
----- A T

GAM3499 226 LOC2843 1 14189 XP_211433.1 5 348 ACTGTTCAGGGC A TTT G 3 A c c

60 CACGGAGAATTC A AGAATTCTCC TGG CTT
TCGAAGTC G TCTTAAGAGG ACC GGA
C C-- G

GAM3499 226 LOC2846 1 10960 XP_211571.1 5 302 TAATGGGAAGCC CTCC G 3 A c c

50 AGAACATAATTC AAAGAATT TTTTGG CTT
TTTTTCGA TTTCTTAA AAGACC GAA
TAC- -

GAM3499 226 LOC2848 1 2091 XP_211680.1 5 858 CGGGAGGCTGAG G - G 3 A c c

99 GCAGGAGAATTG AAA AATTCTCCT TTT GGCTT
TTTGAACC TTT TTAAGAGGA GGA TCGGA
G C G

GAM3499 226 LOC2849 1 15988 XP_211728.1 3 826 TTATTGCTGGCT C TT 3 A c c

99 CAAGGAAAATTC AAAGAATT TCCT TGGGCT
TTTGAAAT TTTCTTAA AGGA ACTCGG
A --

GAM3499 226 LOC3385 1 18841 XP_290466.1 3 1113 TGGAAGGCCAAA C--- T G 3 A c c

64 GGAATAAAATTC AAAGAATT TCCTTT GG CTT
TTTTATAT TTTCTTAA AGGAAA CC GAA
AATA - G

GAM3499 226 LOC3390 1 4465 XP_290697.2 5 2262 CAAGAGGCTGAG G - G 3 A c c

83 GCAGGAGAATTG AAA AATTCTCCT TTT GGCTT
TTTGAACC TTT TTAAGAGGA GGA TCGGA
G C G

GAM3499 226 LOC3470 1 15492 XP_299969.1 5 21 TGGGAAAGCCCA TTCT TT- 3 A c c

42 ACCTGGTTCTTT AAAGAA CC TTGGGCTT
AACAAGGC TTTCTT GG AACCCGAA
---- TCC

GAM3499 226 LOC3481 1 11763 XP_302672.1 3 220 GAAGCTCTCAAG TTTT---- 3 A c c

71 TGCGGAGAATTC AAAGAATTCTCC GGGCTT
TTTGCACA TTTCTTAAGAGG CTCGAA
CGTGAACT

GAM3499 226 LOC3490 1 8658 XP_300935.1 3 715 GGGGCTCAGATT -- -- 3 A c c

81 GGGACAGAATTC AAAGAATTC TCCT TTTGGGCTT
TTTTGTGA TTTCTTAAG AGGG AGACTCGGG
AC TT

GAM3499 226 LOC3490 1 3536 XP_300945.1 3 436 GGGGCTCAGATT --- T- 3 A c c

94 GGCACAGAATTC AAAGAATTCT CC TTTGGGCTT

TTTGTGAA TTTCTTAAGA GG AGACTCGGG
CAC TT
GAM3499 226 LOC3490 1 3536 XP_300940.1 3 436 GGGGCTCAGATT --- T- 3 A c c
97 GGCACAGAATTC AAAGAATTCT CC TTTGGGCTT
TTTGTGAA TTTCTTAAGA GG AGACTCGGG
CAC TT
GAM3499 226 LOC3491 1 3536 XP_300960.1 3 436 GGGGCTCAGATT --- T- 3 A c c
38 GGCACAGAATTC AAAGAATTCT CC TTTGGGCTT
TTTGTGAA TTTCTTAAGA GG AGACTCGGG
CAC TT
GAM3499 226 LOC9082 1 8249 NP_612373.1 5 511 TGCAGCAATCCA G TT - --- 3 A c c
6 AAAGGCAGTTTG AAA AA CT CCTTTTGG GCT
TTTGGGGT TTT TT GA GGAAAACC CGA
G T- C TAA
GAM3499 226 LOC9291 1 16021 NP_775740.1 3 1387 ATAACAAGTGAC - TTGG 3 A c
c
2 AAGGCAGAATTC AAAGAATTCT CCTT GCTT
TTTAAATC TTTCTTAAGA GGAA TGAA
C CAG-
GAM3499 226 LRRN1 1 7636 NP_065924.1 3 966 CTAGGCCCTAAA CT-- - 3 A c c
AGGTTTTAATTC AAAGAATT CCTTTT GGGCTT
TTTTTCTA TTTCTTAA GGAAAA CCCGGA
TTTT T
GAM3499 226 LZTFL1 1 4713 NP_065080.1 3 257 TTAGCTCACATG CTTT---- 3 A c c
CACTGAGAATTC AAAGAATTCTC TGGGCT
TTTACAGC TTTCTTAAGAG ACTCGA
TCACGTAC
GAM3499 226 MCF2 1 17926 NP_005360.2 3 481 AAACAATACAAA CTCCT 3 A c c
GCCCAGAAATTC AAAGAATT TTTGGGCTT
TTTTCGGG TTTCTTAA AGACCCGAA

GAM3499 226 MGC1483 1 6981 NP_219480.1 3 489 CGGGAGGCTGAG - - G 3 A c c
6 GCAGGAGAATCT AAAGA ATTCTCCT TTT GGCTT
CTTTCTTA TTTCT TAAGAGGA GGA TCGGA
C C G
GAM3499 226 MPP3 1 6425 NP_001923.2 3 107 CAAGCGCAGAGA A - --- G 3 A c c
GGGAGAGAATTC A AGAATTCTC CT TTTG GCTT
TCCACAAA C TCTTAAGAG GG AGAC CGAA
C A GAG G
GAM3499 226 MPPE1 1 13939 NP_075563.2 3 48 TATCAAAGCCCA AA CC- 3 A c c
AGAAATGGAACT AAAG TTCT TTTTGGGCTT
TTGGGCAG TTTC AAGG AGAACCCGAA
-- TAA
GAM3499 226 MYH11 1 6924 NP_002465.1 3 688 CTCACGTCAGGC CTTTT 3 A c
c
CTTTGAGAATTC AAAGAATTCTC GGGCTT

TTTCCCCC TTTCTTAAGAG TCCGGA
TT---
GAM3499 226 MYH11 1 6924 NP_074035.1 3 829 CTCACGTCAGGC CTTTT 3 A c c
CTTTGAGAATTC AAAGAATTCTC GGGCTT
TTTCCCCC TTTCTTAAGAG TCCGGA
TT---
GAM3499 226 NRIP1 1 11880 NP_003480.1 3 274 GTGAGTAGCCTA C C - 3 A c c
TGAATGAAATTC AAAGAATT TC TTT TGGGCT
TTTTATAA TTTCTTAA AG AAG ATCCGA
- T T
GAM3499 226 NRIP1 1 11880 XP_009699.1 3 275 GTGAGTAGCCTA C C - 3 A c c
TGAATGAAATTC AAAGAATT TC TTT TGGGCT
TTTTATAA TTTCTTAA AG AAG ATCCGA
- T T
GAM3499 226 ORC4L 1 5097 NP_002543.1 3 665 TACCATAGGTCA A --- G 3 A c c
AAAGGACTGGAA A AGAATTC TCCTTTTGG CT
TTTTCCTT C TTTTAAG AGGAAAACT GA
C GTC G
GAM3499 226 PCDHB7 1 9936 NP_061763.1 3 651 TTTCTGCCTAAT A -- T 3 A c c
TAAGGAGAAGTC AAAGA TTCTCCTT TTGGGC
TTTTATCA TTTCT AAGAGGAA AATCCG
G TT T
GAM3499 226 PRO0478 1 2029 NP_054848.1 3 288 CTGGCTGAATGG -- ---- G 3 A c c
TGAGGAGAATTT AAAGA ATTCTCCTT TT GGCT
TCTTTAAA TTTCT TAAGAGGAG AA TCGG
TT TGGT G
GAM3499 226 PTK2 1 9167 NP_005598.3 3 434 GGAAACCCAAGA --- CT 3 A c c
GGCTGAGAATTC AAAGAATTCT CCTTTTGGG
TTTTGTCT TTTCTTAAGA GGAGAACCC
GTC AA
GAM3499 226 PTK2 1 9167 NP_722560.1 3 434 GGAAACCCAAGA --- CT 3 A c c
GGCTGAGAATTC AAAGAATTCT CCTTTTGGG
TTTTGTCT TTTCTTAAGA GGAGAACCC
GTC AA
GAM3499 226 PTPRC 1 18645 NP_002829.2 3 319 GAGACAGAGAAA - GGG 3 A c c
GAGAGAGAATTC AAAGAATTCTC CTTTT CT
TTTCAAGT TTTCTTAAGAG GAGAA GA
A AGA
GAM3499 226 PTPRC 1 18645 NP_563578.1 3 319 GAGACAGAGAAA - GGG 3 A c c
GAGAGAGAATTC AAAGAATTCTC CTTTT CT
TTTCAAGT TTTCTTAAGAG GAGAA GA
A AGA
GAM3499 226 PTPRC 1 18645 NP_563579.1 3 319 GAGACAGAGAAA - GGG 3 A c c
GAGAGAGAATTC AAAGAATTCTC CTTTT CT
TTTCAAGT TTTCTTAAGAG GAGAA GA
A AGA

GAM3499 226 RAD18 1 3162 NP_064550.2 3 393 TCCAGCCTCACA TTC --- 3 A c c
AAAGGATTCTTT AAAGAA TCCTTTTG GGCT
CAACTTCT TTTCTT AGGAAAAC CCGA
--- ACT
GAM3499 226 SB52 1 6196 NP_612208.1 3 745 CTAGCAAGCCAC C TTTG- 3 A c c
TTCAGGAAATTC AAAGAATT TCCT GGCTT
TTTTGGAG TTTCTTAA AGGA CCGAA
- CTTCA
GAM3499 226 SEC15B 1 4566 XP_039570.3 3 1262 AAGCCTCCAGAA C--- -- 3 A c c
CTGTGAGAATTC AAAGAATTCTC TTTTGG GCTT
TTTTGTTT TTTCTTAAGAG AAGACC CGAA
TGTC TC
GAM3499 226 SLC35E2 1 8532 XP_049733.6 3 2178 CAGGAGGCTGAG G - G 3 A c
c
GCAGGAGAATTG AAA AATTCTCCT TTT GGCTT
TTTGAACC TTT TTAAGAGGA GGA TCGGA
G C G
GAM3499 226 SNX22 2 7099 NP_079074.1 3 777 GCTCGGCCCAAG A---- - -- 3 A c c
GCAGGAGAATCT AAGA ATTCTCCT TTTGGGCT
CTTGAAGC TTCT TAAGAGGA GAACCCGG
CGAAG C CG
GAM3499 226 SNX22 2 11732 NP_079074.1 3 451 CGGGAAGCTGAG --- - G 3 A c c
GTAGGAGAATCT AAAGA ATTCTCCT TTT GGCTT
CTCTTTTT TTTCT TAAGAGGA GGA TCGAA
CTC T G
GAM3499 226 SPRY3 1 428 NP_005831.1 3 3515 CAAGCCTCAAAT --- T T - 3 A c c
GGTGAATAATTC AAAGAAT TC CC TTTG GGCTT
TTTCCCTA TTTCTTA AG GG AAAC CCGAA
ATA T T T
GAM3499 226 TGIF2 1 7688 NP_068581.1 3 1041 CCCTGCAGCCTC TCCTT - 3 A c c
AGTTTTGAATTC AAAGAATTC TTG GGCT
TTTTAGCA TTTCTTAAG GAC CCGA
TTTT- T
GAM3499 226 TIX1 1 17199 NP_055850.1 3 6452 AAGCCTTGGGTA C ----- 3 A c c
GAATGGGAATTC AAAGAATTCTC TTTT GGGCTT
TTTACCCT TTTCTTAAGGG AAGA TCCGAA
T TGGGT
GAM3499 226 TLR3 1 13708 NP_003256.1 3 40 TATTCAATTAGC A --- TGG 3 A c c
AAAGGAGAAACT A AGAA TTCTCCTTT GCT
TTCTCAAT A TCTT AAGAGGAAA CGA
C TCA ---
GAM3499 226 TOP2A 1 14864 NP_001058.2 3 161 AAGTAAAGCCCA T CCTTT 3 A c
c
AGTGTTCTTTAG AAAGAAT CT TGGGCTT
CTTTTTAT TTTCTTG GA ACCCGAA
T -----
GAM3499 226 TP53BPL 1 1710 NP_005793.1 3 410 ATGTGTTATAAG A- TTTG 3 A c
c
CTAGGAGAATCC AAAG ATTCTCCT GGCTT

CTTTGGAC TTTC TAAGAGGA TCGAA
CC ----
GAM3499 226 VN1R1 1 14407 NP_065684.1 3 246 TCAAAAAGTTTA C 3 A c c
AAAAGGGAATTC AAAGAATTCTC TTTTGGGCTT
TTTAGAGA TTTCTTAAGGG AAAATTTGAA
A
GAM3499 226 WBSCR19 1 3019 NP_778234.2 3 445 GGGGCTCAGATT --- T- 3 A c c
GGCACAGAATTC AAAGAATTCT CC TTTGGGCTT
TTTTGTGA TTTCTTAAGA GG AGACTCGGG
CAC TT
GAM3499 226 ZNF214 1 6248 NP_037381.1 3 169 TTATTTGCTTCA AT - T 3 A c c
AAAGGAGATCTT AAAGA TCTCCTTTTGG GC
TAGAAAAA TTTCT AGAGGAAAACT CG
-- T T
GAM3499 226 ZNF333 1 15527 NP_115809.1 3 780 TGGGAGGCTGAG - G 3 A c c
GCAGGAGAATTC AAAGAATTCTCCT TTT GGCTT
TTTGAACC TTTCTTAAGAGGA GGA TCGGA
C G
GAM3499 226 ZNF36 1 10965 XP_168302.1 3 1273 TCTGTGGCAAAG CCTTTT 3 A c
c
CTCTTAGAATTC AAAGAATTCT GGGCTT
TTTGCAGT TTTCTTAAGA CTCGAA
TT----
GAM3770 241 ACTR1A 1 6045 NP_005727.1 3 1428 CTTCACACAGTA TTTGTAG 3 C c
c
TTCTCCCCCACG CGGCGTGGGGG ACT
CCGTCTAT GCCGCACCCCC TGA
TCTTA--
GAM3770 241 AMFR 1 6822 NP_001135.3 3 425 GCACAGTGTGAG TTG-- G 3 C c c
CCCGCCCCCACG CGGCGTGGGGGT TA ACT
TCGTGGGG GCTGCACCCCCG GT TGA
CCCGA G
GAM3770 241 AMFR 1 6822 NP_620408.1 3 1041 GCACAGTGTGAG TTG-- G 3 C c
c
CCCGCCCCCACG CGGCGTGGGGGT TA ACT
TCGTGGGG GCTGCACCCCCG GT TGA
CCCGA G
GAM3770 241 ARHGEF6 1 4040 NP_004831.1 3 1697 AACTTGAAGTTT --- G 3 C c c
GAAACCCCCAGC CGGCG TGGGGGTTT TAGACTT
TTGCTGAG GTCGT ACCCCCAAA GTTTGAA
TCG -
GAM3770 241 ATP8B2 1 17310 XP_290875.1 3 1900 CCACACAGTTTA C- ---- 3 C c c
CAAACCCAGTAT GGCGTGG GGGTTTGTAGACT
CATGTCTG CTGTACT CCCAAACATTTGA
GT ATGA
GAM3770 241 BZRAP1 1 7707 NP_004749.1 3 1165 AGATAGTTTGAC C - - 3 C c c
TGAACCCCCACC CGG GTGGGGGTTT GT AGACT
TTGACCTT GTT CACCCCCAAG CA TTTGA

```
                                        C       T G
GAM3770  241   C5orf4  1  7312  NP_057432.1  5  603   AAGTGTAGTCTA C---- CG  -          3  C  c  c
                                  CAAACCTCCTAT    GG  TGGG GGTTTGTAGACT
                                  ACCAGAAT        CC  ATCC CCAAACATCTGA
                                         TAAGA  AT   T
GAM3770  241   C5orf4  1  7312  NP_115761.1  3  709   AAGTGTAGTCTA C---- CG  -          3  C  c  c
                                  CAAACCTCCTAT    GG  TGGG GGTTTGTAGACT
                                  ACCAGAAT        CC  ATCC CCAAACATCTGA
                                         TAAGA  AT   T
GAM3770  241   CARD9   1  9215  NP_071747.2  3  487   AGCAGGTTTTGC  G       -   -      3  C  c  c
                                  GGAACCCCCATG CG CGTGGGGGTTT GTAGA CTT
                                  ACGCAGGC    GC GTACCCCCAAG CGTTT GGA
                                         A        G    T
GAM3770  241   CD1D    1  3178  NP_001757.1  5  135   CGCGCAGTCCGC        GT - TA        3  C  c  c

                                  GAGGTCCCCACG CGGCGTGGGG  TT G  GACT
                                  CCGGGCGA    GCCGCACCCC  GA C  CTGA
                                              TG  G GC
GAM3770  241   CDAN1   1  6457  XP_085300.3  5  902   CTGCAGCAGTCA   C      TT  A        3  C  c  c

                                  CCTACCCCCACC CGG GTGGGGGT  GT GACT
                                  TGTCCCAC    GTC CACCCCCA  CA CTGA
                                         -       TC  -
GAM3770  241   CDC42EP 1  19072 NP_006440.2  5  646   ATAATGCGGTGA       GG     AG         3  C  c
c
          3                       GCAGGCACCACG CGGCGTGG  GTTTGT  ACT
                                  CCGGCAGA    GCCGCACC  CGGACG  TGG
                                           A-      AG
GAM3770  241   CUL3    1  9467  NP_003581.1  3  2690  ATTATGTACTAT    ---        -  - T     3  C  c  c
                                  CAAACCCCCAAG CGGCG   TGGGGGTTTG TAG AC
                                  ATGCTGAT    GTCGT   ACCCCCAAAC ATC TG
                                           AGA        T  A  T
GAM3770  241   CYLN2   1  9937  NP_003379.2  3  51    CCCAGTCCACAC  G      G    TA---        3  C  c  c

                                  CAGAGCCCCACG C GCGTGGGG TTTG    GACT
                                  CGGCTGCC    G CGCACCCC AGAC    CTGA
                                         G       G    CACAC
GAM3770  241   CYLN2   1  9937  NP_115797.1  3  51    CCCAGTCCACAC  G      G    TA---        3  C  c  c

                                  CAGAGCCCCACG C GCGTGGGG TTTG    GACT
                                  CGGCTGCC    G CGCACCCC AGAC    CTGA
                                         G       G    CACAC
GAM3770  241   DKFZp43 1  4827  XP_038298.1  3  1464  GCCCCAGTCCCA   C       GTA-          3  C  c
c
          4E2321                    GAGACCCCCACC CGG GTGGGGGTTT   GACT
                                  TGGTGCCC    GTC CACCCCCAGA   CTGA
                                         -       GACC
GAM3770  241   DKFZP43 1  9323  NP_056307.1  5  411   ACACAGCCTGCA   C-      T--    A       3  C  c
c
          4H132                     CCCACCCCCACA CGG  GTGGGGGT   TGTAG CT
```

TCTGGGCC GTC CACCCCCA ACGTC GA
TA CCC C
GAM3770 241 DKFZP76 1 14838 NP_114428.1 3 896 CCTTCCGGTGCT G T T - 3 C c c
1D0211 CACACGCCCACG CGGCGTGGG GT TG AG ACT
CCGTGCCA GCCGCACCC CA AC TC TGG
G C - G
GAM3770 241 EDEM 1 4285 NP_055489.1 3 2264 TATGTTAAGTCA C- -- - A 3 C c c
CAAACCCACTTG CGG GT GG GGGTTTGT GACTT
ACTTCTGG GTC CA TC CCCAAACA CTGAA
TT GT A -
GAM3770 241 EDN3 1 6587 NP_000105.1 5 77 ATCGGCCGGCCT - T A 3 C c c
CGAACCCCCACA CGGC GTGGGGGTTTG AG CT
GCTGGAGG GTCG CACCCCCAAGC TC GG
A - C
GAM3770 241 ELMO1 1 16847 NP_055615.8 5 60 CACCCACGCCGC C- ----- - TGTA 3 C c c
CGCGGCCCCACG GGCGTGG GGGT T GACT
CTGGGCGA CGGGTCG CGGC C CGCC
AG CACCC G ----
GAM3770 241 ERdj5 1 5195 NP_061854.1 3 612 TGGCACAGTAAA -- AG 3 C c c
CAAACCCTGTTA CGGCGTG GGGGTTTGT ACT
TGCTGTAT GTCGTAT TCCCAAACA TGA
TG AA
GAM3770 241 FLJ1090 1 18342 NP_060735.1 3 22 GCCAGGTGTACT - TT- G 3 C c c
1 CTGCGCCCCACG CGGCGTGGGG GT GTA ACTT
CTGGAAAA GTCGCACCCC CG CAT TGGA
G TCT G
GAM3770 241 FLJ1094 1 17908 NP_060750.1 3 356 GCACAGAGCTCT GGG - 3 C c c
5 GCGGAGACCACG CGGCGTGG TTTGTAGA CTT
CCGACATC GCCGCACC AGGCGTCT GAG
AG- C
GAM3770 241 FLJ1278 1 18045 NP_071937.1 3 1397 GGATGAAGTCTA G GG TT 3 C c c
8 CCATTACCAGCT CGGC TGG GT GTAGACTT
GGGTCACC GTCG ACC TA CATCTGAA
- AT C-
GAM3770 241 FLJ1322 1 2074 NP_079075.1 3 71 CGGAGTTGAGCA GG-- A- 3 C c c
4 AACAACGCCACG CGGCGTGG GTTTGT GACTT
CCGCGTGC GCCGCACC CAAACG TTGAG
GCAA AG
GAM3770 241 FLJ2032 1 14004 NP_060235.1 5 163 GGGCCTACACTG ---- T- A 3 C c c
0 CCTCCTCCCACG CGGCGTGGG GGT TGTAG CTT
CCGTGCTT GCCGCACCC CCG ACATC GGG
TCCT TC C
GAM3770 241 FLJ2222 1 8328 NP_078924.1 3 80 GCCAGTCGTGCA C----- T-- - 3 C c c
2 CCCACCCCCACG GGCGTGGGGGT TGTA GACT
TCCACCCG CTGCACCCCCA ACGT CTGA
GCCCAC CCC G

GAM3770 241 FLJ2222 1 8328 NP_787098.2 3 257 GCCAGTCGTGCA C----- T-- - 3 C c c
2 CCCACCCCCACG GGCGTGGGGGT TGTA GACT
TCCACCCG CTGCACCCCCA ACGT CTGA
GCCCAC CCC G
GAM3770 241 FLJ2318 1 3020 NP_078892.1 3 967 TGCCTAGTGCTA G T - 3 C c c
6 CAAACCTTCCTG C GCG GGGGGTTTGTAG ACT
TGGGACTC G TGT CTTCCAAACATC TGA
G C G
GAM3770 241 FLJ2332 1 12687 NP_078930.1 3 1137 GAAAGTTTTTCA -- --- 3 C c c
3 TAAACCCCCACT CGGC GTGGGGGTTTGT AGACTT
TGTTGCTT GTTG CACCCCCAAATA TTTGAA
TT CTT
GAM3770 241 FLJ3209 1 12027 NP_776156.1 3 768 TCAGAGAGTCTA - GGGG 3 C c
c
6 CAGAACACGCAC CG GCGTG TTTGTAGACTT
GACGACAG GC CGCAC AGACATCTGAG
A A---
GAM3770 241 FLJ3238 1 18343 NP_653218.1 3 573 CCAGACAGTCTA C- GT-- -- 3 C c c

9 CAACTGCCCCCT GGC GGGGGT TTGTAGACT
CCAGCCCA CCG CCCCCG AACATCTGA
AC ACCT TC
GAM3770 241 FLJ3860 1 1795 NP_689867.1 3 1078 CCTGAGTCTCCA C----- G -- 3 C c c

7 CAGAGCCCCACG GGCGTGGGG TTTGT AGACTT
CCTGGCAT CCGCACCCC AGACA TCTGAG
TACGGT G CC
GAM3770 241 FRCP2 1 8098 NP_715637.1 3 1774 CCTTCCGGTCTA G- -- 3 C c c
CAAGAGCTCTCA CGGC TGGGGGT TTGTAGACT
AGGCTGGG GTCG ACTCTCG AACATCTGG
GA AG
GAM3770 241 GALNT2 1 6744 NP_004472.1 3 1874 GTGAATGGGCCA T AGA 3 C c
c
CGTGCCCCCACG CGGCGTGGGGGT TGT CT
CTGGATAC GTCGCACCCCCG GCA GG
T CCG
GAM3770 241 GDF10 1 15145 NP_004953.1 5 148 CGCAGTGGGCTA - - GG A 3 C c
c
CAAACTTTCGCA CG GC GTG GGTTTGTAG CT
GCGCGAGT GC CG CGC TCAAACATC GG
G A TT G
GAM3770 241 GLRA3 1 12548 NP_006520.1 5 309 AGCATCAGTCTA G GG -- 3 C c c

CACCAACACCAT C GCGTGG GTT TGTAGACT
GCGGGGTT G CGTACC CAA ACATCTGA
G A- CC
GAM3770 241 GNB4 1 19919 NP_067642.1 5 139 CGGCTGTGAGCT TT A 3 C c c
GCGCTCTCCACG CGGCGTGGGGG TGTAG CTT
CCGGCTCC GCCGCACCTCT GCGTC GAG
C- -

GAM3770 241 HIC2 1 3402 NP_055909.1 3 4048 GGAGCCTCAGTC GTTTG 3 C c c

TGACATTCCACG CGGCGTGGGG TAGACT
CCGGGGTG GCCGCACCTT GTCTGA
ACA--

GAM3770 241 HIC2 1 3402 XP_036937.2 3 4048 GGAGCCTCAGTC GTTTG 3 C c c

TGACATTCCACG CGGCGTGGGG TAGACT
CCGGGGTG GCCGCACCTT GTCTGA
ACA--

GAM3770 241 HMGB3 1 4089 NP_005333.1 3 913 CACAGCAGTGAA C AG 3 C c c

CAAACCCCCACT CGG GTGGGGGTTTGT ACT
CCGTTGTA GCC CACCCCCAAACA TGA
T AG

GAM3770 241 HS3ST4 1 1736 XP_056254.4 3 1218 GGGCTGTCTGCA ----- -- T 3 C c c
GAAACCCCCATC CGGC GTGGGGGTT TGTAGAC
AAGAGCTG GTCG TACCCCCAA ACGTCTG
AGAAC AG T

GAM3770 241 KIAA057 1 3719 XP_291018.1 3 4981 AGTCCCTCACCC ----- TA- 3 C c c
0 CCAACCCCCATG CGGCGTGGGGGTT TG GACT
CTGTTTGT GTCGTACCCCCAA AC CTGA
CCCCC TCC

GAM3770 241 KIAA103 1 12901 XP_038604.4 3 668 AGGGGACGGCTC TTTG - 3 C c
c
2 TGGTTCCCCACG CGGCGTGGGGG TAGA CT
CTGCCCCT GTCGCACCCCT GTCT GG
TG-- C

GAM3770 241 KIAA193 1 4111 NP_079113.1 5 97 TCCCCAGCTCTA G GG-- - 3 C c c
9 CAAACCAGGACA CGGC TG GGTTTGTAGA CT
GCTGAATC GTCG AC CCAAACATCT GA
- AGGA C

GAM3770 241 KIF5A 1 14793 NP_004975.1 5 117 CCCAAGAAGAGT GT TA 3 C c c
CCCAGCCCCACG CGGCGTGGGG TTG GACTT
CCGGCTAC GCCGCACCCC GAC CTGAG
-- C-

GAM3770 241 LOC1152 1 13877 XP_055499.2 3 1253 GTCTCCTGTCTT - T T 3 C c c
19 AGGCGTCCCACG CGGCGTGGGG GTTTG AGAC
CCGCGTGC GCCGCACCCT CGGAT TCTG
G - T

GAM3770 241 LOC1463 1 16441 NP_660313.1 3 125 CATGCATGTGGA -- AG T 3 C c
c
25 TAGACCCCCACG CGGC GTGGGGGTTTGT AC
GGCCGTGG GCCG CACCCCCAGATA TG
GG GG T

GAM3770 241 LOC1509 1 9952 XP_087049.1 3 2148 TGAACTCAGCTT G T A 3 C c c

35 CAAGACCCCACG CGGCGTGGGG TTTG AG CT
CTGCTGCA GTCGCACCCC GAAC TC GA
A T -

GAM3770 241 LOC1580 1 19866 XP_098861.2 3 949 TGTGCCTTGCCT TTT CT 3 C c c

62 CTGCCCTCCACG CGGCGTGGGGG GTAGA
CCGCCGCC GCCGCACCTCC CGTCT
--- CC

GAM3770 241 LOC1973 1 1678 NP_777577.1 3 396 GAGGAAACAAGC ----- AGA 3 C c c

22 CCCTGTCCCACG CGGCGTGGG GGTTTGT CTT
CCGTCTGC GCCGCACCC CCGAACA GAG
TGTCC AAG

GAM3770 241 LOC2024 1 3891 XP_114481.4 5 57 AGGGCCAGTGTA C GG G 3 C c c

04 CAAACCAGCACC CGG GTG GGTTTGTA ACT
TGCTAGGA GTC CAC CCAAACAT TGA
- GA G

GAM3770 241 LOC2214 1 11963 XP_166432.1 3 135 CGTTCAAGTCTA GTGGGG 3 C c c

42 CGAGCACAGCCG CGGC GTTTGTAGACTT
TGTTCTAA GCCG CGAGCATCTGAA
ACA---

GAM3770 241 LOC2535 1 6427 NP_694854.1 5 311 GAAGGCAAGCTC C TG T A 3 C c c

59 CAAACCCCTGCC CGG G GGGGTTTG AG CTT
TGGAAGAC GTC C CCCCAAAC TC GAA
- GT C -

GAM3770 241 LOC2557 1 746 NP_848606.1 3 63 CCCTCGAGAGCT GTTTG - 3 C c c

83 CTGTGCTCCACG CGGCGTGGGG TAGA CTT
CCGAGGAT GCCGCACCTC GTCT GAG
GT--- C

GAM3770 241 LOC2557 1 746 XP_170871.1 3 63 CCCTCGAGAGCT GTTTG - 3 C c c

83 CTGTGCTCCACG CGGCGTGGGG TAGA CTT
CCGAGGAT GCCGCACCTC GTCT GAG
GT--- C

GAM3770 241 LOC2830 1 14676 XP_208481.1 3 1045 TGAGTAAGTCTA G TT 3 C c c

05 CACTCTTAAGTC CGGC TGGGGGT GTAGACTT
GGTATGAA GCTG ATTCTCA CATCTGAA
A --

GAM3770 241 LOC2830 1 19707 XP_210866.1 3 670 TATTTGAGTGTA GTGG G 3 C c c

45 CAAACCCATGGC CGGC GGGTTTGTA ACTT
TGGGCTCA GTCG CCCAAACAT TGAG
GTA- G

GAM3770 241 LOC2830 1 12366 XP_210867.1 5 363 TTCCGAAGTCTA G GTTT-- 3 C c c

48 CCTAGTGCCCCA CGGC TGGGG GTAGACTT
GCCGAACC GCCG ACCCC CATCTGAA
- GTGATC

GAM3770 241 LOC2834 1 15833 XP_211049.1 5 1399 ACTCGAGTCCAT - - TG A 3 C c c

54 GGGACCCCCACG CG GCGTGGGGGT T T GACTT
CTCGTGAG GC CGCACCCCCA G A CTGAG
T G GT C

GAM3770 241 LOC2834 1 14118 XP_208695.1 5 21 ATCCACAGTCTA C---- - G 3 C c c

91 CAAAACCCCACA GGC GTGGGG TTTGTAGACT
GCTCCTGA TCG CACCCC AAACATCTGA
AGTCC A A

GAM3770 241 LOC2835 1 4485 XP_211081.1 3 1102 TGCTCAAGTCTA - - G T 3 C c c

26 CACACCTGTACA CG GC GTG GGGT TGTAGACTT
GCACGTTA GC CG CAT TCCA ACATCTGAA
A A G C

GAM3770 241 LOC2838 1 12309 XP_211241.1 5 672 GTTCAAGGGTCT ---- TTGT 3 C c c

75 TGTACCCCCACC CGGC GTGGGGGT AGACTT
TCAGCTGG GTCG CACCCCCA TCTGGG
ACTC TGT-

GAM3770 241 LOC2841 1 15952 XP_211336.1 5 455 ATAAAGACTAGA C -- G A 3 C c c

18 ACCACCCCCACT CGG GTGGGGGT TT TAG CTT
CTGCACTC GTC CACCCCCA AA ATC GAA
T CC G A

GAM3770 241 LOC2841 1 18185 XP_209031.1 3 343 TGTCGGGAGTCG GT GTA 3 C c c

30 GGAGTCTCCACG CGGCGTGGGG TT GACTT
CCGTGTGA GCCGCACCTC AG CTGAG
TG GG-

GAM3770 241 LOC2850 1 9957 XP_209463.1 3 188 CCTGCTCAAGCT GG TTG A 3 C c c

85 AAACGCACCACG CGGCGTGG GT TAG CTT
CCGGCTTT GCCGCACC CG ATC GAA
A- CAA -

GAM3770 241 LOC2855 1 10045 XP_209671.1 3 872 AGAGATGGGGTT GTA 3 C c c

89 GAAACCCCCATG CGGCGTGGGGGTTT GACTT
TTGGCCAG GTTGTACCCCCAAA TTGGG
G--

GAM3770 241 LOC2857 1 2857 XP_212000.1 3 236 CTCTGGTCATAA G G- - 3 C c c

27 GGAACCCCCACG CG CGTGGGGGTTT TA GACT
GTGCGTGG GT GCACCCCCAAG AT CTGG
G GA A

GAM3770 241 LOC2857 1 2909 XP_212014.1 3 610 ACCGGTCTACAT C------ C T--- 3 C c c

72 CGCACCCCCACC GG GTGGGGGT TGTAGACT
CCCACCCC CC CACCCCCA ACATCTGG
CCCCACC - CGCT

GAM3770 241 LOC2862 1 19388 XP_212231.1 5 223 TCGGGGTCGGGA -- GTA 3 C c c

14 GGCGTCCCCACG CGGCGTGGGG GTTT GACTT

CCGCCCGG GCCGCACCCC CGGA CTGGG
TG GGG
GAM3770 241 LOC2863 1 13537 XP_212298.1 5 14 ATTCCCAGTCTA C---- - G 3 C c c
81 CAAAACCCCACA GGC GTGGGG TTTGTAGACT
GCTCCTAG TCG CACCCC AAACATCTGA
GATCC A A
GAM3770 241 LOC3393 1 4480 XP_294925.1 5 568 CCACCGTCACAG - -- A T 3 C c c
92 GCCACCACCACG CGGCGTGG GG GTTTGT GAC
CCGTCAAT GCCGCACC CC CGGACA CTG
A AC - C
GAM3770 241 LOC3493 1 13537 XP_303025.1 5 14 ATTCCCAGTCTA C---- - G 3 C c c
12 CAAAACCCCACA GGC GTGGGG TTTGTAGACT
GCTCCTAG TCG CACCCC AAACATCTGA
GATCC A A
GAM3770 241 LOC3501 1 13364 XP_301527.1 5 26 TCAGTCTCACGA C --- - 3 C c c
54 CCTACCCCCACC CGG GTGGGGGT TTGT AGACT
CCGGACTG GCC CACCCCCA AGCA TCTGA
C TCC C
GAM3770 241 LOC3528 1 8614 XP_304742.1 3 203 GAAGTTTGAGGC G G ---- 3 C c c
56 CAAACCCCCAGC C GC TGGGGGTTTG TAGACTT
GGTCAGTG G CG ACCCCCAAAC GTTTGAA
G - CGGA
GAM3770 241 LOC6392 1 6921 NP_071380.1 5 428 CCATGGGGTCGC T A- 3 C c c
8 GCAGCTCCCACG CGGCGTGGGGGTT GT GACTT
CCG GCCGCACCCTCGA CG CTGGG
- CG
GAM3770 241 LOC9066 1 9653 XP_090790.7 3 123 TCCAGGAGTCAA ---- G A 3 C c c
8 CAAACCCCGGCT CGGC GT GGGGTTTGT GACTT
GAGGCTGA GTCG CG CCCCAAACA CTGAG
GAGT G A
GAM3770 241 MFI2 1 10773 NP_201573.1 3 86 CCAGGCTGGTCT C------ G T 3 C c c
CAAACCCCCAGC GGC TGGGGGTTTG AGACT
CTCAACTG CCG ACCCCCAAAC TCTGG
GTCAACT - -
GAM3770 241 MGC2734 1 1723 NP_149108.1 5 75 CGGGCATGAGCT GG G A 3 C c
c
GAGAGCACCACG CGGCGTGG GTTT TAG CTT
CCGAGGCC GCCGCACC CGAG GTC GAG
A- A -
GAM3770 241 MGC2793 1 13614 NP_659501.1 5 32 CTAGGAGGTCTA - GGGG 3 C c
c
CAAATAGCGACT CGG CGT GTTTGTAGACTT
GGGTAGCT GTC GCG TAAACATCTGGA
A A---
GAM3770 241 MGC2964 1 9449 NP_776171.1 5 78 CGGAAAGTCTCA C-- --- T-- T 3 C c
c
9 TCCACCCCCACA GGC GTGGGGGT TG AGACTT
TCGCCTCT CCG CACCCCCA AC TCTGAA
TCT CTA CCT -

GAM3770 241 MGC5576 1 11789 NP_076961.1 3 90 CTGAGTTCTGGA G TT -- - 3 C c c

CCTACCCCCACG C GCGTGGGGGT GT AGA CTT
TGGTGTAA G TGCACCCCCA CA TCT GAG
G TC GG T

GAM3770 241 MID1 1 2966 NP_150632.1 5 29 GCGCCGCGTCGA C A T 3 C c c

CAAACCCCCATC CGG GTGGGGGTTTGT GAC
CTGGGAAA GTC TACCCCCAAACA CTG
C G C

GAM3770 241 MRS3/4 1 4406 NP_112489.2 5 309 ATGCAGAGTCTA G --- T 3 C c c

CAGCCTGACCCA CGGC TGGG GGTT GTAGACTT
GCTGCCCG GTCG ACCC CCGA CATCTGAG
- AGT -

GAM3770 241 NCF4 1 11268 NP_000622.1 3 2 ACAGGGTCTACA - GG-- - 3 C c c

ACACGATGCCAT CGGC GTGG GT TTGTAGACTT
GGCTGACG GTCG TACC CA AACATCTGGG
G GTAG C

GAM3770 241 OTOP3 1 11275 XP_292588.2 5 448 CCGTGCTCTACC G -- CT 3 C c c

AAGATCCCCACG C GCGTGGGGGTTT GTAGA
CGGGGCCC G CGCACCCCTAGA CATCT
G AC CG

GAM3770 241 PGK1 1 495 NP_000282.1 3 959 ATCAAAAGTCTA - GG - 3 C c c

CATAACTAATAC CGGC GTG GGTT TGTAGACTT
AGCTGAGC GTCG CAT TCAA ACATCTGAA
A AA T

GAM3770 241 PITPN 1 423 NP_006215.1 3 761 CTCTGCAGTCTA C--- G G--- 3 C c c

CAAAATCGCCCC GGC TGGGG TTTGTAGACT
AGTCAACT CTG ACCCC AAACATCTGA
TCAA - GCTA

GAM3770 241 PTPRR 1 10961 NP_002840.1 5 283 CTGACTGCTCTG GTG CT 3 C c c

CAAACCCCAGCC CGGC GGGGTTTGTAGA
GAGGACCT GCCG CCCCAAACGTCT
A-- CG

GAM3770 241 RAD52 1 6948 NP_602294.1 3 761 AAGCAGCAGGTT GT TA 3 C c c

CGAGTCTCCACG CGGCGTGGGG TTG GACTT
CCGTCAGC GCCGCACCTC AGC TTGGA
TG --

GAM3770 241 RAD52 1 6948 NP_602295.1 3 834 AAGCAGCAGGTT GT TA 3 C c c

CGAGTCTCCACG CGGCGTGGGG TTG GACTT
CCGTCAGC GCCGCACCTC AGC TTGGA
TG --

GAM3770 241 RAD52 1 6948 NP_602296.1 3 320 AAGCAGCAGGTT GT TA 3 C c c

CGAGTCTCCACG CGGCGTGGGG TTG GACTT
CCGTCAGC GCCGCACCTC AGC TTGGA
TG --

GAM3770 241 RE2 1 1602 NP_031395.1 5 25 CCAGCATGCTCT GTTT CT 3 C c c

GCCCACCCCACG CGGCGTGGGG GTAGA
CCGAGGTG GCCGCACCCC CGTCT

ACC- CG
GAM3770 241 RE2 1 1602 NP_722561.1 5 279 CCAGCATGCTCT GTTT CT 3 C c c
GCCCACCCCACG CGGCGTGGGG GTAGA
CCGAGGTG GCCGCACCCC CGTCT
ACC- CG
GAM3770 241 RUNX3 1 16681 NP_004341.1 3 210 GAGGCATAGGTT C TT A 3 C c
c
ACCACCCCCACC CGG GTGGGGGT GTAG CT
CCGGCCCG GCC CACCCCCA CATT GA
C C- G
GAM3770 241 SDC3 1 5640 NP_055469.1 3 1334 GAGGTTTGGGGC -- ---- 3 C c c
CAGACCCCCACT CGGC GTGGGGGTTTG TAGACTT
AGCTGGGA GTCG CACCCCCAGAC GTTTGGA
AT CGGG
GAM3770 241 SIT 1 13417 NP_055265.1 3 329 GCTCCCTCATAG C----- TTGT 3 C c c
TCTACCCCCACG GGCGTGGGGGT AGACT
CCTCAGTG CCGCACCCCCA TCTGA
GTGACT ----
GAM3770 241 SLC2A6 1 10319 NP_060055.1 3 77 CTGTGTTGGCTA C G A 3 C c c
CAAACCTGCACC CGG GTG GGGTTTGTAG CT
CTGGGACC GTC CAC TCCAAACATC GG
C G -
GAM3770 241 SMN1 1 3206 NP_000335.1 5 123 CTTAAGAAGGGA G AGA 3 C c c
CGGGGCCCCACG CGGCGTGGGG TTTGT CTT
CTGCGCAC GTCGCACCCC GGGCA GAA
G GG-
GAM3770 241 SMN1 1 3206 NP_075012.1 5 123 CTTAAGAAGGGA G AGA 3 C c c
CGGGGCCCCACG CGGCGTGGGG TTTGT CTT
CTGCGCAC GTCGCACCCC GGGCA GAA
G GG-
GAM3770 241 SMN2 1 3206 NP_059107.1 5 123 CTTAAGAAGGGA G AGA 3 C c c
CGGGGCCCCACG CGGCGTGGGG TTTGT CTT
CTGCGCAC GTCGCACCCC GGGCA GAA
G GG-
GAM3770 241 SMN2 1 3206 NP_075013.1 5 123 CTTAAGAAGGGA G AGA 3 C c c
CGGGGCCCCACG CGGCGTGGGG TTTGT CTT
CTGCGCAC GTCGCACCCC GGGCA GAA
G GG-
GAM3770 241 SMN2 1 3206 NP_075014.1 5 123 CTTAAGAAGGGA G AGA 3 C c c
CGGGGCCCCACG CGGCGTGGGG TTTGT CTT
CTGCGCAC GTCGCACCCC GGGCA GAA
G GG-
GAM3770 241 SMN2 1 3206 NP_075015.1 5 123 CTTAAGAAGGGA G AGA 3 C c c
CGGGGCCCCACG CGGCGTGGGG TTTGT CTT
CTGCGCAC GTCGCACCCC GGGCA GAA
G GG-
GAM3770 241 STK29 1 19087 NP_003948.1 3 323 CAGGCCCCGTCC TT A T 3 C c c
ACCGCCTCCACG CGGCGTGGGGGT GT GAC
CCGCACCT GCCGCACCTCCG CA CTG

C- C C

GAM3770 241 SULF1 1 12171 NP_055985.1 3 1373 GACAAAGTCAAA GCG- A- 3 C c c

TAAACCCCCAAG CG TGGGGGTTTGT GACTT
GACGACAC GC ACCCCCAAATA CTGAA
AGGA AA

GAM3770 241 TCEA1 1 10324 NP_006747.1 3 1238 TTGCAAAGTCTA GTT 3 C c c

CATTTTATGCTG CGGCGTGGGG TGTAGACTT
AATCTGCA GTCGTATTTT ACATCTGAA

GAM3770 241 TK1 1 11195 NP_003249.1 3 311 TGGGGTGAGGGA G AGA 3 C c c

CAGAGCCCCACG CGGCGTGGGG TTTGT CTT
CTGTTGAC GTCGCACCCC AGACA GAG
G GG-

GAM3770 241 TOP1 1 17569 NP_003277.1 5 187 TTCGCCGTCTGC TT- T 3 C c c

GTCTCCCCCACG CGGCGTGGGGG TGTAGAC
CCGCCTCG GCCGCACCCCC GCGTCTG
TCT C

GAM3770 241 TSAP6 1 17391 NP_060704.1 3 1160 CCACCAAAGCTA GG- A 3 C c c

CAAACCTAAAAT CGGCGT GGGTTTGTAG CTT
GCTGCTGC GTCGTA TCCAAACATC GAA
AAA -

GAM3770 241 TULP4 1 5367 NP_064630.1 3 3656 GCAAAAAGTCTG C GTG----- 3 C c c

CAAACCCCAGGG GGC GGGGTTTGTAGACTT
TCAAGCCT CCG CCCCAAACGTCTGAA
T AACTGGGA

GAM3770 241 UBE4A 1 5235 NP_004779.1 3 1839 GCTTCCTAGTTA T A 3 C c c

ACAACCCCCATG CGGCGTGGGGGTT GT GACT
CTGCCTCC GTCGTACCCCCAA CA TTGA
- A

GAM3770 241 VIPR1 1 12543 NP_004615.2 3 316 GCAAAAAGTCTA C GG T 3 C c c

CATACTTTCATC CGG GTG GGT TGTAGACTT
CTGACTCT GTC TAC TCA ACATCTGAA
C TT T

GAM3770 241 ZBED4 1 2237 NP_055653.1 3 795 GTGGTCCCTGCT C----- -- -- 3 C c c

GAAACCCCCACG GGCGTGGGGGTTT GTA GACT
CCTCCGCT CCGCACCCCCAAA CGT CTGG
TCGCCT GT CC

GAM3770 241 ZFP36L2 1 14047 NP_008818.3 5 208 CGTCGTGGCTCA -- TA---- T 3 C c c

AGCCCGGCCACG CGGCGTGG GGGTTTG GAC
CCGCCCCA GCCGCACC CCCGAAC CTG
GG TCGGTG C

GAM3770 281 ABCD2 1 19013 NP_005155.1 5 311 AATGAGGGGCCT AAGAG 3 C c c

GGGAGGGAGGAG AAGTT CTCCCAGGCCT
CTTGGTGC TTCGA GAGGGTCCGGG
GGAGG

GAM3770 281 ABCF2 1 484 NP_009120.1 3 745 TTTCTCAGGCCT AA- C C 3 C c c
GTGATTCACAGA AAGTT GAG TC CAGGCCTG
CTTTAACA TTCAG CTT AG GTCCGGAC
ACA - T
GAM3770 281 AKAP2 1 7250 NP_009134.1 3 2040 TAAAACTGCCAA A A- CT 3 C c c
GGGAGCTCTAAC AAGTTA GAGCTCCC GGC
TTGAAGCC TTCAAT CTCGAGGG CCG
- AA TC
GAM3770 281 ALDH3A2 1 15493 NP_000373.1 3 1319 ACAAAGAGGCCT AA GC 3 C c
c
GGGATATTAGGA AAGTT GA TCCCAGGCCT
CTTTGGGG TTCAG TT AGGGTCCGGA
GA AT
GAM3770 281 ALDH6A1 1 7652 NP_005580.1 5 30 AGGGCGAGGCCT TAAG- C 3 C c
c
GGCAGCTGTAGT AAGT AGCT CCAGGCCT
GCTTCTGG TTCG TCGA GGTCCGGA
TGATG C
GAM3770 281 ALDH9A1 1 4064 NP_000687.2 5 317 CCGAGCAGGCCT TA-- TC-- 3 C c
c
GGCCGCGCTCTC AAGT AGAGC CCAGGCCTG
CCCGCTTC TTCG TCTCG GGTCCGGAC
CCCC CGCC
GAM3770 281 AMPD3 1 2981 NP_000471.1 3 237 CCTTGGGGATCT TAAG - 3 C c c
GGGAGCTGAGCA AAGT AGCTCCCAGG CCT
CTTGTCTA TTCA TCGAGGGTCT GGG
CGAG A
GAM3770 281 ARPP-21 1 4251 NP_057384.1 5 144 TGACAGGAGCTT AA- - 3 C c c
GGGAGCTCGGGA AAGTT GAGCTCCCAGGC CT
GCTTGGGA TTCGA CTCGAGGGTTCG GG
GGG A
GAM3770 281 ARSB 1 11835 NP_000037.1 3 278 GCCTTGGGACAG ----- -- - CT 3 C c c
CTGGGAACTTAA AAGTTAAG AGC TCCCA GGC
CTTGAAAT TTCAATTC TCG AGGGT CCG
AAGGG AC T --
GAM3770 281 BAIAP2 1 6156 NP_059345.1 3 384 CTGCAGGCACTG A------- TA - - 3 C c c
GGGAGCTCTGCT AGT AGAGCTCCC AG GCCTG
GGAATTGG TCG TCTCGAGGG TC CGGAC
GGTTAAGG -- G A
GAM3770 281 BCAP31 1 13375 NP_005736.2 3 256 CCTGCCAGGCCT A CC- 3 C c
c
GCACAGCCTTGG AAGTTAAG GCT CAGGCCTG
CTTCACGC TTCGGTTC CGA GTCCGGAC
- CAC
GAM3770 281 BCL7A 2 8131 NP_066273.1 3 1386 GTTCTGAGGCCT A---- TC- 3 C c c
GGTTTGCTCTTA AGTTAAGAGC CCAGGCCT

ATTAATAT TTAATTCTCG GGTCCGGA
TATAA TTT
GAM3770 281 BCL7A 2 16792 NP_066273.1 3 1386 TTCTGAGGCCTG A----- TC- 3 C c c
GTTTGCTCTTAA AGTTAAGAGC CCAGGCCT
TTAATATA TTAATTCTCG GGTCCGGA
ATATAA TTT
GAM3770 281 BIRC8 1 2524 NP_203127.2 5 213 CAGCTGGAGGCT AGA- G 3 C c c
GGGAGCGTTGTG AAGTTA GCTCCCAG CCT
GCTTCCTC TTCGGT CGAGGGTC GGA
GTTG -
GAM3770 281 BLAME 1 14865 NP_064510.1 5 27 TCCACTCGGCCT A - T 3 C c c
GGGAGGTTCTGG AAGTT AGAGC TCCCAGGCC
ATTTTGGC TTTAG TCTTG AGGGTCCGG
G G C
GAM3770 281 BRF2 1 4164 NP_060780.2 3 354 TCCTGCAGGCCT TA --- -- 3 C c c
GAGGGGGCTTCC AAGT AG AGCTCCC AGGCCTG
CTCTGCTT TTCG TC TCGGGGG TCCGGAC
TC CCT AG
GAM3770 281 BSN 1 11733 NP_003449.1 3 93 AGTCAGAGGCCT A-- A --- 3 C c c
GGGCGCAGCTCT AGTT AGAGCT CCCAGGCCT
GGACTCTG TCAG TCTCGA GGGTCCGGA
GTC G CGC
GAM3770 281 BTBD6 1 14701 NP_150374.1 3 97 GACACCATGAAA TCCCA 3 C c c
GGCTGCTCTTAA AAGTTAAGAGC GGCCT
CTTTGTCT TTCAATTCTCG TCGGA

GAM3770 281 C1orf25 1 8737 NP_112196.2 3 176 CTTAGCTGGTTT TA T 3 C c c
GGGAGCTTTGCT AAGT AGAGCTCCCAGGCC
TTCCAAGT TTCG TTTCGAGGGTTTGG
-- T
GAM3770 281 C20orf1 1 8221 NP_036393.1 3 135 TCAAACAGGCCT A- GCT 3 C c c
03 GGGTATCTGAGG AAGTT AGA CCCAGGCCTG
CTTGCTTG TTCGG TCT GGGTCCGGAC
AG AT-
GAM3770 281 C20orf1 1 9895 NP_543024.1 5 22 GGAGGAGTGGAG T ---- GG 3 C c c
52 TGGAGCTCTTGC AAG TAAGAGCTCC CA CCT
CTTGTTAC TTC GTTCTCGAGG GT GGA
C TGAG GA
GAM3770 281 C20orf1 1 13674 NP_543019.1 5 174 TCCCCAGTGTCT A - - 3 C c c
75 GGGAGCATCTGG AAGTTA GA GCTCCCAGGC CTG
CTTCCTCT TTCGGT CT CGAGGGTCTG GAC
- A T
GAM3770 281 C20orf1 2 12486 XP_045421.1 3 684 TTTCCAGAGGTG G CC G 3 C c c
94 TGTGGCTCTTAA AA TTAAGAGCT CA GCCT
GTTGACAT TT AATTCTCGG GT TGGA
G T- G

GAM3770 281 C20orf1 2 20123 XP_045421.1 3 858 AGTCTTAGGCCT TAAG TC 3 C c c
94 GGTGGCTGATCA AAGT AGC CCAGGCCTG
CTTGTGGG TTCA TCG GGTCCGGAT
CTAG GT
GAM3770 281 CCL1 1 11794 NP_002972.1 5 0 ACAGTGGTGAGC - GGC 3 C c c
TCTTAGCTTCAC AAGTTAAGAGCTC CCA CTG
CAGGCTCA TTCGATTCTCGAG GGT GAC
T ---
GAM3770 281 CCR1 1 17877 NP_001286.1 3 168 TAATGGTGGCCT A- - T T 3 C c c
GGGGCTTCTGAG AAGTT AGA GC CCCAGGCC
GCTTCTGG TTCGG TCT CG GGGTCCGG
AG T - T
GAM3770 281 CD1A 1 6426 NP_001754.1 5 158 GGGCAGCACACT T GA ------ 3 C c c
GGGAGCCATTTA AAGT AA GCTCCCAG GCCT
CTTTATGC TTCA TT CGAGGGTC CGGG
T AC ACACGA
GAM3770 281 CDC91L1 1 3448 NP_536724.1 3 203 TGGGGAAGAACT AA- GC 3 C c c
GGGAGCTCCCCA AAGTT GAGCTCCCAG CT
ACTTGGAC TTCAA CTCGAGGGTC GA
CCC AA
GAM3770 281 CDH5 1 10833 NP_001786.1 3 445 AGGCAAAGGCCT AGCTC 3 C c c
GGACAGCTTGAC AAGTTAAG CCAGGCCT
TTGTGGGG TTCAGTTC GGTCCGGA
GACA-
GAM3770 281 CDO1 1 4009 NP_001792.1 5 57 TGCCAGGGGCCT A- T ----- 3 C c c
GGGGGTGGGTCT AGT AAGAG CTCCCAGGCCT
CTTGCTGT TCG TTCTC GGGGGTCCGGG
TG - TGGGT
GAM3770 281 CLDN1 1 17449 NP_066924.1 5 93 AGCGAGCAGGGC A TCCC G 3 C c c
TCCCCGCCTTAA AAGTTAAG GC AG CCTG
CTTCCTCC TTCAATTC CG TC GGAC
- CCCC G
GAM3770 281 cPLA2de 1 17982 NP_828848.1 3 1031 TCTCCCAGGCCT A-- - - - 3 C c c
lta GGGTGGCCTCTG AGTTA AGAG CT CCCAGGCCTG
TAGCTGGT TCGAT TCTC GG GGGTCCGGAC
TGG G C T
GAM3770 281 cPLA2de 1 17982 XP_208820.2 3 125 TCTCCCAGGCCT A-- - - - 3 C c c
lta GGGTGGCCTCTG AGTTA AGAG CT CCCAGGCCTG
TAGCTGGT TCGAT TCTC GG GGGTCCGGAC
TGG G C T
GAM3770 281 CRP 1 11630 NP_000558.1 3 214 AGTGTCTGGTCT A---- - T 3 C c c
GGGAGCTCGTTA AGTTAA GAGCTCCCAGGCC
ACTATGCT TCAATT CTCGAGGGTCTGG
TCGTA G T
GAM3770 281 CRSP2 1 10521 NP_004220.2 3 2201 TCTAATAATCGG AGC G T 3 C c c

GTTGGGACTTAA AAGTTAAG TCCCAG CC
CTTTAAGG TTCAATTC AGGGTT GG
--- G C

GAM3770 281 DBC-1 1 17305 NP_066997.3 5 368 GTTGGGAGGCCT A ------ CT 3 C c c

GGGTCCTTTTCC AGTT AAGAG CCCAGGCCT
CCACGACT TCAG TTTTC GGGTCCGGA
- CACCCC CT

GAM3770 281 DGCR14 1 10110 NP_073210.1 3 112 GGGCCCAGGCCT AA G ----- 3 C c
c

GGGCCAGAAGCT GTTAA AGCT CCCAGGCCTG
GTTGACCA CAGTT TCGA GGGTCCGGAC
AC G AGACC

GAM3770 281 DKFZp43 1 8952 XP_209288.2 3 663 AAGGAGGGGTCT TTA- C 3 C c
c

4D177-I AGGAGCTCTGTC AAG AGAGCTCC AGGCCT
ike CCTTGTAA TTC TCTCGAGG TCTGGG
CCTG A

GAM3770 281 DKFZp76 1 10498 XP_294685.2 5 1758 GCTGTGAGGCCT A------ - A T 3 C c
c

1L1518 GGGGCCTTGCAC AGT TAAG GC CCCAGGCCT
TGGCTGGA TCA GTTC CG GGGTCCGGA
AGGTCGG C - -

GAM3770 281 Ells1 1 12892 NP_690006.1 3 3690 CATGAAGGAATA AGC CAG 3 C c
c

GGCAGGACTTAA AAGTTAAG TCC GCCTG
CTTGGGGT TTCAATTC AGG CGGAT
--- A--

GAM3770 281 ETV4 1 12526 NP_001977.1 3 628 AGGCCCAGGCCT TAA CT 3 C c
c

GGGTTTGTACTT AAGT GAG CCCAGGCCTG
CCACCTCC TTCA TTT GGGTCCGGAC
TG- --

GAM3770 281 FBXO2 1 4915 NP_036300.2 3 71 AGGTCGAGGGTA A ------ A- 3 C c c
GATAGGCCTTAA AAGTTAAG GCT CCC GGCCT
CTTAGTCC TTCAATTC CGG GGG CTGGA
- ATAGAT AG

GAM3770 281 FLJ1075 1 764 NP_060675.1 3 1138 AGGAGAGGGCCT T T 3 C b b
1 GGGGCTCTTGCT AAGT AAGAGC CCCAGGCCT
TCCCGAGA TTCG TTCTCG GGGTCCGGG
- -

GAM3770 281 FLJ1075 1 764 NP_060709.1 3 985 AGGAGAGGGCCT T T 3 C b b
1 GGGGCTCTTGCT AAGT AAGAGC CCCAGGCCT
TCCCGAGA TTCG TTCTCG GGGTCCGGG
- -

GAM3770 281 FLJ1212 1 6795 NP_079254.1 3 269 TAATGGTTTTGT T ---- T 3 C c c
1 TGGGGCTCTTAA AAGTTAAGAGC CCCAG GCC
CTTGCAAG TTCAATTCTCG GGGTT TGG
- GTTT T

GAM3770 281 FLJ1311 1 14164 NP_078817.1 3 463 TCCTTTGGGCCT --- T T 3 C c c

```
          4                          GGGGCTGTGCTT AAGTTAAG  AGC CCCAGGCC
                                     GGCTTGAA    TTCGGTTC  TCG GGGTCCGG
                                               GTG  -      G
GAM3770  281   FLJ1364 1  19731  NP_078860.1  3  660   GACATATATTAG    T     CCCA          3  C  c
c
          6                          GTCAGCTCTTAC AAGT AAGAGCT   GGCCTG
                                     TTTTGAAA    TTCA TTCTCGA   CTGGAT
                                               -     ----
GAM3770  281   FLJ2044 1  3014   NP_060294.1  3  1060  CAAGGTGAGGCC   TT      CC          3  C  c
c
          5                          TTGAGCTCTTTG AAG  AAGAGCTC  AGGCCT
                                     TTTTTATA    TTT  TTCTCGAG  TCCGGA
                                               GT       T-
GAM3770  281   FLJ2386 1  1191   NP_689875.1  3  838   GTCTGCCAGGCT    AAG       G         3  C  c
c
          7                          GGGAGCTGGAGC AAGTT  AGCTCCCAG CCTG
                                     TTGCTGAG    TTCGA  TCGAGGGTC GGAC
                                               GG-       -
GAM3770  281   FLJ3233 1  14094  NP_653166.1  3  1149  TGGCCCAGGCCT    TA A  -           3  C  c
c
          4                          GGCGGGCACTGC AAGT  AG GCTC CCAGGCCTG
                                     TTCCCGGC    TTCG  TC CGGG GGTCCGGAC
                                               -- A   C
GAM3770  281   FLJ3283 1  8952   NP_689701.1  3  1872  AAGGAGGGGTCT   TTA-      C          3  C  c
c
          3                          AGGAGCTCTGTC AAG   AGAGCTCC AGGCCT
                                     CCTTGTAA    TTC   TCTCGAGG TCTGGG
                                               CCTG      A
GAM3770  281   FLJ3707 1  924    NP_694588.1  5  515   GGCTCGGGGCCT A   - A --          3  C  c  c
          8                          GGGATGGCCTGT A GTTA AG GC  TCCCAGGCCT
                                     AATCAGCT    A TAAT TC CG  AGGGTCCGGG
                                               C   G  - GT
GAM3770  281   FREQ   1  12562  NP_055101.2  3  1914  AGGGCCAGGCCT A-  T   -- ---        3  C  c  c

                                     GGGTCTAGAATT  AGT AAGAG  CT   CCCAGGCCTG
                                     CTTGCTGC      TCG TTCTT  GA   GGGTCCGGAC
                                               CG  -    AA  TCT
GAM3770  281   GABRE  1  10097  NP_004952.1  3  0     ACTGGCTTGTTT      A  TCC    T       3  C  c  c

                                     GCCTTAACTTGT AAGTTAAG GC   CAGGCC
                                     AGTACCAG    TTCAATTC CG   GTTCGG
                                               - TTT     T
GAM3770  281   GABRE  1  10097  NP_068819.1  3  0     ACTGGCTTGTTT      A  TCC    T       3  C  c  c

                                     GCCTTAACTTGT AAGTTAAG GC   CAGGCC
                                     AGTACCAG    TTCAATTC CG   GTTCGG
                                               - TTT     T
GAM3770  281   GABRE  1  10097  NP_068822.1  3  0     ACTGGCTTGTTT      A  TCC    T       3  C  c  c

                                     GCCTTAACTTGT AAGTTAAG GC   CAGGCC
```

AGTACCAG TTCAATTC CG GTTCGG
- TTT T
GAM3770 281 GABRE 1 10097 NP_068830.1 3 0 ACTGGCTTGTTT A TCC T 3 C c c

GCCTTAACTTGT AAGTTAAG GC CAGGCC
AGTACCAG TTCAATTC CG GTTCGG
- TTT T
GAM3770 281 GATM 1 19758 NP_001473.1 3 25 ACTGACAGGCCT A--- A -- 3 C c c
GATGGAGCTTGT AGTTA GAGCTCC CAGGCCTG
GGCTGGCC TCGGT TTCGAGG GTCCGGAC
CCGG G TA
GAM3770 281 GDAP1L1 1 1628 NP_076939.3 3 26 TAGGCCAGGCCT A- A----- T 3 C c
c

GGGGCTTGGTGT AGTTA GAGC CCCAGGCCTG
CTGACTGT TCAGT TTCG GGGTCCGGAC
TG CTGTGG -
GAM3770 281 GNPNAT1 1 12686 XP_085119.1 3 2346 ATGTTGCCCAGG A----- CTC G 3 C
c c

CTGGTCTCTTAA AGTTAAGAG CCAG CCTG
CTCCTAGG TCAATTCTC GGTC GGAC
GGATCC T-- -
GAM3770 281 GPA33 1 11566 NP_005805.1 3 847 GGGGCAGGGCCT T ------ 3 C c c
GGGCCTCATGGC AAGT AAGAGCT CCCAGGCCT
TTTTGCTT TTCG TTTTCGG GGGTCCGGG
- TACTCC
GAM3770 281 GTR2 1 18842 NP_071440.1 3 91 GCTACAGGACAT TA - GG- 3 C c c
GGGAGCTGCTGC AAGT AG AGCTCCCA CCTG
TTGTGGGA TTCG TC TCGAGGGT GGAC
-- G ACA
GAM3770 281 HD 1 17396 NP_002102.2 3 1432 GGAGCTGGATTT TA - T 3 C c c
GGGAGCTCTGCT AAGT AGAGCTCCCAGG CC
TGCCGACT TTCG TCTCGAGGGTTT GG
-- A T
GAM3770 281 HEMK 1 18413 NP_057257.1 3 3794 CGCCAGGTTTCC C --- 3 C b b
TGGAGCTCTTGG AAGTTAAGAGCTCC AGG CCTG
CTTCAGCC TTCGGTTCTCGAGG TCC GGAC
- TTT
GAM3770 281 HERC3 1 13951 NP_055421.1 3 16 TTAGTTTGGCCT A CT T 3 C c c
GGGCTTCTCAGC AAGTT AGAG CCCAGGCC
TTGTCCAG TTCGA TCTT GGGTCCGG
C C- T
GAM3770 281 HFL-EDD 1 13232 NP_006544.1 5 74 GCTCACGGGCCT AGA T 3 C c
c
G1 GGGGCCATGGCT AAGTTA GC CCCAGGCCTG
TTCTTCTC TTCGGT CG GGGTCCGGGC
AC- -
GAM3770 281 hIAN2 1 19907 NP_078987.2 3 349 GAGGGCAGGCCT T CTCC 3 C c
c

GTATCTTTTACT AAGT AAGAG CAGGCCTG
TCTGTGTA TTCA TTTTC GTCCGGAC

```
                                        -    TAT-
GAM3770  281   HIP1R  1  16778 XP_290592.1  3  55    GGTGACAGGCCT A-----   A-   CT          3  C  c  c

                                GGGCCTCTGCAA      AGTT  AGAG  CCCAGGCCTG
                                CTGCCCTG          TCAA  TCTC  GGGTCCGGAC
                                      GTCCCG    CG    C-
GAM3770  281   HSD3B2 1  10226 NP_000189.1  3  285   CTGAACAATTGT        CTCCC    T        3  C  c
 c
                                GGTCTCTCTTAA AAGTTAAGAG    AGGCC
                                CTTGAGGT    TTCAATTCTC    TCTGG
                                      -----    T
GAM3770  281   HUMPPA 1  1054  XP_290730.2  3  73    TCCCTCAGGCCT     AAGA  -           3  C  c
c
                                GGGCGGTGCAGC AAGTT    GCT CCCAGGCCTG
                                TTCCAGAG    TTCGA    TGG GGGTCCGGAC
                                      CG--   C
GAM3770  281   ID4    1  2437  NP_001537.1  3  755   TTTTCTGTTTGG         TCC     T        3  C  c  c
                                CCTGGCTCTTAA AAGTTAAGAGC   CAGGCC
                                TTTGCTTT    TTTAATTCTCG   GTCCGG
                                      ---     T
GAM3770  281   IFITM2 1  3118  NP_006426.1  3  108   CCCCCAGAGGCC    TTA      CA          3  C  c  c

                                AGGAGCTCTGCC AAG   AGAGCTCC  GGCCT
                                CTTGACCT    TTC   TCTCGAGG  CCGGA
                                      CCG       A-
GAM3770  281   IL6R   1  10573 NP_000556.1  3  528   TTTTCTAGGCCT    T     ---           3  C  c  c
                                GGGGACGGCTTT AAGT AAGAGCT   CCCAGGCCTG
                                TACTTAAA    TTCA TTTTCGG   GGGTCCGGAT
                                      -      CAG
GAM3770  281   IL6R   1  10573 NP_852004.1  3  743   TTTTCTAGGCCT    T     ---           3  C  c  c
                                GGGGACGGCTTT AAGT AAGAGCT   CCCAGGCCTG
                                TACTTAAA    TTCA TTTTCGG   GGGTCCGGAT
                                      -      CAG
GAM3770  281   INHBB  1  14744 NP_002184.1  3  613   GCTTCAAGGCCT    TTA A     -          3  C  c  c
                                GGGGAGCCTGTC AAG   AG GCTCCC AGGCCT
                                CTTCCATG    TTC   TC CGAGGG TCCGGA
                                      CTG  -     G
GAM3770  281   KCNB2  1  6452  NP_004761.2  5  476   AGCGGGGTCTGT     AAG      --          3  C  c  c

                                GGGAGCTAGCTT AAGTT   AGCTCCCA  GGCCT
                                TGTCAGTG    TTCGA   TCGAGGGT  CTGGG
                                      ---       GT
GAM3770  281   KCND1  1  12525 NP_004970.3  3  978   GGGCTCCGGCCT     A  - -      T       3  C  c  c
                                GGGATGTTTCTG AAGTT AGAG C TCCCAGGCC
                                AACTTTGG    TTCAA TCTT G AGGGTCCGG
                                      G   T T       C
GAM3770  281   KDELR1 1  1055  NP_006792.1  3  183   ATCCAGGTCTTG     AA      --          3  C  c  c
                                GGGAGCTCAGGA AAGTT  GAGCTCCC  AGGCCTG
                                CTTGGGCT    TTCAG  CTCGAGGG  TCTGGAC
                                      GA       GT
```

GAM3770 281 KIAA019 1 19314 XP_038362.3 3 484 GACTAGGGGCCT A-- - - - 3 C c c
4 GGGTGGCCTCAT AGTTAA GAG CT CCCAGGCCT
TAACTCTA TCAATT CTC GG GGGTCCGGG
ATC A C T
GAM3770 281 KIAA025 1 19417 NP_055953.1 3 244 CAGTGTGGGCCT - CT T 3 C c c
2 GGGCTCTCTTGG AAGTT AAGAG CCCAGGCC
GCTTTATC TTCGG TTCTC GGGTCCGG
G TC G
GAM3770 281 KIAA065 1 10072 XP_051017.2 3 929 GTGAGGGCGCCT G AG - 3 C c
c
7 GGGAGCTGATGG AA TTA AGCTCCCAGGC CT
GTTAAGCC TT GGT TCGAGGGTCCG GG
G AG C
GAM3770 281 KIAA120 1 11915 XP_027307.2 3 1483 GGAAAGGGGCCT T TC 3 C c
c
9 GGGCTCTTCATT AAGT AAGAGC CCAGGCCT
TAAAGGTA TTTA TTCTCG GGTCCGGG
C --
GAM3770 281 KIAA152 1 17568 XP_036299.6 3 963 GGGCCCAGGCCT TAA CTC 3 C c
c
2 GGCCCTCCACAC AAGT GAG CCAGGCCTG
TTCATTCT TTCA CTC GGTCCGGAC
CAC CC-
GAM3770 281 KIAA181 1 6050 XP_046743.2 5 500 GGGAGGCGGCCT AAGA - T 3 C c
c
3 GGGGAGCCCCCA AAGTT GCTCCC AGGCC
ACTTATGC TTCAA CGAGGG TCCGG
CCCC G C
GAM3770 281 KLK12 1 12199 NP_665901.1 3 123 TCTTGTTGGCCT -- - C T 3 C c c
GGGAACTTCTTG AAGT TAAGA G TCCCAGGCC
GAACTTTA TTCA GTTCT C AGGGTCCGG
AG T A T
GAM3770 281 KLK12 1 12199 NP_665902.1 3 274 TCTTGTTGGCCT -- - C T 3 C c c
GGGAACTTCTTG AAGT TAAGA G TCCCAGGCC
GAACTTTA TTCA GTTCT C AGGGTCCGG
AG T A T
GAM3770 281 KRTHBP2 1 12132 XP_303553.1 3 139 TGGACAACAGCT AA---- GC 3 C c
c
GGGAGCTCAACA AAGTT GAGCTCCCAG CTG
TGGACTTG TTCAG CTCGAGGGTC GAC
GTACAA --
GAM3770 281 LCHN 1 19437 XP_098615.2 3 2222 GTCAGGGCTTCT AGCT -- 3 C c
c
GGGTTCCCTTAA AAGTTAAG CCCAG GCCT
CTTTGTGC TTCAATTC GGGTC CGGG
CCTT TT
GAM3770 281 LOC1227 1 12936 XP_058647.1 3 171 AGATCACTGCCT AG CT 3 C c
c
04 GGGAGGCTTGGC AAGTTAAG CTCCCAGGC

TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 LOC1248 1 15407 XP_064333.3 3 768 AGCCAGAGGCCT T - C- 3 C c c

42 GGGGACCTCCTT AAG TAAG AG TCCCAGGCCT
GCCTTCCC TTC GTTC TC GGGGTCCGGA
C C CA
GAM3770 281 LOC1378 1 4502 XP_059929.3 3 2171 GTTTCAAGGCCT A-- - -- 3 C c c

86 GGGAGTAATCTT AGTT AAGA GCTCCCAGGCCT
CAGCTCAC TCGA TTCT TGAGGGTCCGGA
CAC C AA
GAM3770 281 LOC1433 1 17009 XP_084485.1 3 1283 TGCTGGAGGCCT TA ---- 3 C c
c

10 GGGATGGAGTTC AAGT AGAGC TCCCAGGCCT
TGGGCTTA TTCG TCTTG AGGGTCCGGA
GG AGGT
GAM3770 281 LOC1436 1 11678 XP_096474.1 3 345 GGTCTGAGGCCT A---- TA G- 3 C c
c

80 GGGAGAGTCTCT AGT AGA CTCCCAGGCCT
ACTGTCTA TCA TCT GAGGGTCCGGA
ATCTG TC GA
GAM3770 281 LOC1442 1 16663 XP_084786.1 3 269 CACAGCAGGCCT TTA CC 3 C c
c

48 GTCAGTTCTCTC AAG AGAGCT CAGGCCTG
TTACCTTC TTC TCTTGA GTCCGGAC
TC- CT
GAM3770 281 LOC1444 1 6020 XP_084860.1 3 57 ATAAGTAGGCCT A A C 3 C c c

38 GGAGCCTCAGCT AAGTT AG GCTCC AGGCCTG
TCTGTAAA TTCGA TC CGAGG TCCGGAT
C - -
GAM3770 281 LOC1462 1 5022 XP_085387.1 3 2737 GGAACCTGGATA T ----- -- T 3 C c c

29 TTGAGCTCTTAC AAGT AAGAGCTC CCAGG CC
TTTTCTCC TTCA TTCTCGAG GGTCC GG
- TTATA AA -
GAM3770 281 LOC1463 1 17607 XP_096985.1 3 336 GCCACCAGGCCT A CC 3 C c
c

50 GCTGGTGTTTGG AAGTTAAG GCT CAGGCCTG
CTTCTCTA TTCGGTTT TGG GTCCGGAC
G TC
GAM3770 281 LOC1489 1 17967 XP_086361.1 5 2194 GACCACAGGCCT GCTC- 3 C c
c

18 GGCTAAATTTTG AAGTTAAGA CCAGGCCTG
ACTTTTTG TTCAGTTTT GGTCCGGAC
AAATC
GAM3770 281 LOC1501 1 6127 XP_097823.1 5 702 GGCTGGAGGCCT TAAGA-- 3 C c
c

57 GGGAGTCACAGG AAGT GCTCCCAGGCCT
TGCTTGGA TTCG TGAGGGTCCGGA
TGGACAC

GAM3770 281 LOC1511 1 14042 XP_098008.1 5 36 TGGCCTTCACCC CT ------- T 3 C c c

54 CGGGCCTCTTAA AAGTTAAGAG CCC AGGCC
CTTCAGGT TTCAATTCTC GGG TCCGG
C- CCCCACT T

GAM3770 281 LOC1516 1 13550 XP_087261.1 3 60 GGCAGCAGGAGG T- CAG 3 C c c

47 CGGAGCTCTTTT AAGT AAGAGCTCC GCCT
GCTTGGAT TTCG TTCTCGAGG CGGA
TT ---

GAM3770 281 LOC1527 1 6325 XP_098257.1 5 804 AGGCTGTGTCAT AG T ------ 3 C c c

19 GGGCGTCCTTAA AAGTTAAG C CCCA GGCCT
CTTTGGGA TTCAATTC G GGGT TCGGA
CT C ACTGTG

GAM3770 281 LOC1527 1 9283 XP_098264.1 5 332 CAGAGCCTGGAG A-- --- ---- - 3 C c c

90 CTGAGCTCTTGG AGTTA AGAGCTC CCAGGC CT
TGACTGGT TCAGT TCTCGAG GGTCCG GA
TGG GGT TCGA A

G
C

GAM3770 281 LOC1548 1 5835 XP_098618.3 5 1986 GCCCAAGGACCT A------- TA - 3 C c c

22 GGGAGCTCTGCT AGT AGAGCTCCCAGG CCT
CCCCACTC TCG TCTCGAGGGTCC GGA
CTCACCCC -- A

GAM3770 281 LOC1548 1 13099 XP_098623.1 5 951 GGCAATAGGCCT TAA GC- 3 C c c

60 GGGAAAGTCGCA AAGT GA TCCCAGGCCTG
CTTTCATC TTCA CT AGGGTCCGGAT
CG- GAA

GAM3770 281 LOC1550 1 2202 XP_098651.1 5 1243 TGCTCCTGGCCT A TC T 3 C c c

36 GGGCTCTGATTT AAGTTA GAGC CCAGGCC
CACTGTGT TTTAGT CTCG GGTCCGG
- -- T

GAM3770 281 LOC1703 1 17257 XP_096316.5 3 662 TCACACAGGCCT AA-- C--- 3 C c c

71 GGGGCAATCTCT GTTAAGAG TCCCAGGCCTG
TGACCTCA CAGTTCTC GGGGTCCGGAC
ACTC TAAC

GAM3770 281 LOC1964 1 19892 XP_031807.3 3 6 TGTGGTTTCTGG ---- -- T 3 C c c

84 GAGCTGGTTCTT AAGTTAAGA GCTCCCAG GCC
AATTTGGC TTTAATTCT CGAGGGTC TGG
TGGT TT T

GAM3770 281 LOC2212 1 18010 XP_166281.3 3 113 TTGCCAGGGACC TA CA - 3 C c c

18 AGGAGCTCTCAC AAGT AGAGCTCC GG CCT
TTTGCCTA TTCA TCTCGAGG CC GGG
C- A- A
GAM3770 281 LOC2540 1 3792 XP_173023.1 3 107 TACCTCAGGCCT AA-- 3 C c c
99 GGGGGCTCCCCC AAGTT GAGCTCCCAGGCCTG
GACTTGTT TTCAG CTCGGGGGTCCGGAC
CCCC
GAM3770 281 LOC2829 1 20085 XP_210833.1 3 591 GGTTTGTTTCTG ------- T 3 C c c
65 GGGAGCTCTTAA AAGTTAAGAGCTCCC AGGCC
TTTCTATT TTTAATTCTCGAGGG TTTGG
GTCTTTG -
GAM3770 281 LOC2838 1 9696 XP_211229.1 3 1100 GAAATTCCAGGT AGCTCCC 3 C
c c
51 CTTCTTGCTTAA AAGTTAAG AGGCCTG
CTTATATG TTCAATTC TCTGGAC
GTTCT--
GAM3770 281 LOC2839 1 13328 XP_211263.1 3 286 CTGGCCAGGCCT A A C-- 3 C c
c
21 GGCACAGCCCTG AAGTTA G GCT CCAGGCCTG
GCTTCCAC TTCGGT C CGA GGTCCGGAC
- C CAC
GAM3770 281 LOC2840 1 14562 XP_211325.1 3 754 TAAGCCAGGCCT G A G T 3 C c
c
84 GGGTGTCTGGAG AA TT AGA C CCCAGGCCTG
TTTGTGAA TT AG TCT G GGGTCCGGAC
G G - T
GAM3770 281 LOC2843 1 13309 XP_211438.1 3 1252 GGGCTTTGGCCT TAA - T 3 C c
c
36 GGGCAGCTTCCA AAGT GAGCT CCCAGGCC
CTTTCTGC TTCA TTCGA GGGTCCGG
CC- C T
GAM3770 281 LOC2845 1 4065 XP_211521.1 5 151 CGCTCCCCGCCT AA CT 3 C c
c
70 GGGAGCTCAGCT AAGTT GAGCTCCCAGGC
TTCCTCAG TTCGA CTCGAGGGTCCG
-- CC
GAM3770 281 LOC2847 1 9883 XP_209332.1 3 122 CTGGCCGGGCCT AAG -- 3 C c
c
08 GGGGTCGCTGTC AAGTT AGC TCCCAGGCCTG
AACTTGTT TTCAA TCG GGGGTCCGGGC
CTG CT
GAM3770 281 LOC2847 1 1836 XP_209343.1 5 585 CCTGAGCAGGCA - CAG 3 C c
c
36 AGGAGCTCTTGC AAGT TAAGAGCTCC GCCTG
ATTTGCTG TTTA GTTCTCGAGG CGGAC
C AA-
GAM3770 281 LOC2847 1 7838 XP_211622.1 3 896 GAGGAGGCACCT AAG -- 3 C c
c
51 GGGAGCTGAGCT AAGTT AGCTCCCAG GCCT
TAAGAGTT TTCGA TCGAGGGTC CGGA

```
                                        G--       CA
GAM3770  281   LOC2849 1  19759 XP_211723.1  3  44    TTTCCAAGGACT    AAGA     G         3  C  c
c
         97                      GGGAGCAAACTT AAGTT   GCTCCCAG CCT
                                GCAGGCTC    TTCAA    CGAGGGTC GGA
                                        A---      A
GAM3770  281   LOC2855 1  12902 XP_211943.1  5  735   CTATGGAGGCCT    AAG   -          3  C  c
c
         82                      GGCGGGCTAGCT AAGTT   AGCTC CCAGGCCT
                                TGGGTGTC    TTCGA   TCGGG GGTCCGGA
                                        ---    C
GAM3770  281   LOC2856 1  8952  XP_208333.1  3  299   AAGGAGGGGTCT   TTA-     C         3  C  c
c
         22                      AGGAGCTCTGTC AAG   AGAGCTCC AGGCCT
                                CCTTGTAA    TTC    TCTCGAGG TCTGGG
                                        CCTG      A
GAM3770  281   LOC2859 1  3942  XP_212090.1  5  147   AGCCAAAGGCCT A----     --  T        3  C  c  c
         51                      GGGGCTTCCTTG     AGTTAAG  AGC CCCAGGCCT
                                GCTCTTCT         TCGGTTC  TCG GGGTCCGGA
                                        TCTTC      CT  -
GAM3770  281   LOC2860 1  1673  XP_212158.1  3  346   CTCAGCCTTCTG         C-   C--      3  C  c  c
         58                      GCTAGCTCTTAG AAGTTAAGAGCT  CCAGG   CTG
                                CTTCCAGC    TTCGATTCTCGA  GGTCT   GAC
                                        TC    TCC
GAM3770  281   LOC2860 1  11859 XP_212163.1  5  1647  GCCACCAGGCCT   T-   CTC          3  C  c
c
         78                      GGCTCCTTTTCC AAGT  AAGAG   CCAGGCCTG
                                ACTTTCAT    TTCA  TTTTC   GGTCCGGAC
                                        CC    CTC
GAM3770  281   LOC2862 1  5166  XP_209953.1  3  14    TCGGGGCCTGCT A-----     A     ---      3  C  c  c
         06                      GGGAGCCCTTAA     AGTTAAG GCTCCCA   GGCCT
                                CTCCCCCA         TCAATTC CGAGGGT   CCGGG
                                        ACCCCC      C      CGT
GAM3770  281   LOC2864 1  18478 XP_208437.1  5  424   AGAACAGCACCT   ---      CC  C-       3  C  c
c
         93                      CAGAGCTCTTAA AAGT   TAAGAGCTC  AGG  CTG
                                ATGCTTAT    TTCG   ATTCTCGAG  TCC  GAC
                                        TAA       AC  AC
GAM3770  281   LOC3387 1  2578  XP_294696.2  5  20    GACACCTGGAAT     A      GG  T       3  C  c  c

         69                      GGGAGCTTGTAA AAGTTA GAGCTCCCA  CC
                                CTTTTACA    TTCAAT TTCGAGGGT  GG
                                        G       AA  T
GAM3770  281   LOC3391 1  19949 XP_294830.1  3  44    AACAGAGGGGAA   TT       AGG         3  C  c
c
         49                      GGGAGCTCTTTC AAG  AAGAGCTCCC   CCT
                                TTACATTT    TTC  TTCTCGAGGG   GGG
                                        T-        AA-
GAM3770  281   LOC3394 1  995   XP_294957.1  3  1821  CAAATCAGGCCT    AA-  CTCC          3  C  c
c
```

```
          42                          GCCTCCTGAATT AAGTT  GAG   CAGGCCTG
                                     TGTAAATA    TTTAA  CTC   GTCCGGAC
                                              GTC  C---
GAM3770  281   LOC3394 1  17748  XP_290919.1  3  361   GCAACCAGGCCT    AA  G  CC          3  C  c
 c
          92                          GAGGTCAGAATT AAGTT  GA CTC  AGGCCTG
                                     TGAACATA    TTTAA  CT GAG  TCCGGAC
                                              GA  G  --
GAM3770  281   LOC3395 1  18035  XP_294983.1  5  552   CAGGAGGGTGAT    A-       G-         3  C  c
c
          02                          GGGAGCTCTCCA AAGTT  AGAGCTCCCA  GCCT
                                     ATTTAGTT    TTTAA  TCTCGAGGGT  TGGG
                                              CC        AG
GAM3770  281   LOC3399 1  5687   XP_295115.1  5  291   GGGAAGGCCGCT    AAGA     --         3  C  c
c
          75                          GGGAGCATGAAC AAGTT   GCTCCCA  GGCCT
                                     TTCTGAGC    TTCAA   CGAGGGT  CCGGA
                                              GTA-      CG
GAM3770  281   LOC3403 1  3583   XP_295216.1  3  698   CCTTGGGGCCCT    A-  G     -        3  C  c  c
          19                          GGGAGATCTGGG AAGTT  AGA CTCCCAGG CCT
                                     ACTTCAGA    TTCAG  TCT GAGGGTCC GGG
                                              GG  A      C
GAM3770  281   LOC3485 2  12486  XP_211637.1  5  127   TTTCCAGAGGTG  G       CC  G         3  C  c
c
          49                          TGTGGCTCTTAA AA TTAAGAGCT  CA GCCT
                                     GTTGACAT    TT AATTCTCGG  GT TGGA
                                              G       T-  G
GAM3770  281   LOC3485 2  20123  XP_211637.1  5  301   AGTCTTAGGCCT    TAAG  TC           3  C  c
 c
          49                          GGTGGCTGATCA AAGT   AGC  CCAGGCCTG
                                     CTTGTGGG    TTCA   TCG  GGTCCGGAT
                                              CTAG  GT
GAM3770  281   LOC3488 1  14363  XP_300874.1  5  35    TTGCGTAGCCCT    T  A--      C        3  C  c  c

          97                          GGGAGCCACCTT AAGT AAG   GCTCCCAGG CTG
                                     GCTTCTGG    TTCG TTC   CGAGGGTCC GAT
                                              -  CAC       C
GAM3770  281   LOC3493 1  12158  XP_303037.1  3  275   CCAGCCAGGCCT A  TT-    ---- -        3  C  c
c
          64                          GGGCAGTGACCT  AG   AAGAG   CT CCCAGGCCTG
                                     CTTTCTCT    TC   TTCTC   GA GGGTCCGGAC
                                           - TCT    CAGT  C
GAM3770  281   LOC3496 1  19525  XP_303409.1  5  425   GGGGGTTGGCCT    TAA-  -      T       3  C  c
c
          13                          GGGAGCCTCCTC AAGT   GAG CTCCCAGGCC
                                     CGCTTCCC    TTCG   CTC GAGGGTCCGG
                                              CCTC  C       T
GAM3770  281   LOC9011 1  3656   XP_029046.1  5  455   ACCTAAGGTCTT       GC-  CC          3  C  c
c
          0                           AGAAAATCTTAA AAGTTAAGA   TC  AGGCCT
```

```
                                    CTTGAAAA    TTCAATTCT   AG  TCTGGA
                                                AAA  AT
GAM3770  281   LOC9017 1  8664  XP_029589.1  3  226   CCATCCAGGCCT     AA   TCC          3  C  c
c
         0                          GCTGTTCCAAAC AAGTT  GAGC   CAGGCCTG
                                    TTTTTCAG    TTCAA  CTTG   GTCCGGAC
                                              AC   TC-
GAM3770  281   LOC9166 1  2238  NP_612381.1  3  1006  TGAGGGCCCGCG   G        A---        3  C  c
c
         1                          GGGAGCTCTTAA AA TTAAGAGCTCCC    GGCCT
                                    GTTGGGCA    TT AATTCTCGAGGG    CCGGG
                                              G          GCGC
GAM3770  281   LOC9659 1  9043  XP_039922.1  5  2123  TGCCGGAGGCCT A---    A--    C         3  C  c
c
         7                          GGCAGCTCCGCT    AGTTA   GAGCT CCAGGCCT
                                    AACTCCAT        TCAAT   CTCGA GGTCCGGA
                                            TACC    CGC    C
GAM3770  281   LRRC8  1  11922 XP_026998.2  3  634   AAGGCCAGGCCT   TTAA     C          3  C  c
c
                                    GGAGCTTGCCTC AAG    GAGCTCC AGGCCTG
                                    TTCAGTAT    TTC    TTCGAGG TCCGGAC
                                              TCCG      -
GAM3770  281   MAPK8IP 1  11255 NP_203750.1  3  856   GATGTGGGGCCT     A----   C          3  C  c
c
         3                          GGGACTTCTCCA AAGTT    AGAG TCCCAGGCCT
                                    GAAGCTTA    TTCGA    TCTT AGGGTCCGGG
                                              AGACC    C
GAM3770  281   MDS018  1  7934  NP_068595.2  5  61    GAGCCCAGGCCT     AA--    C-         3  C  c  c

                                    GGCAGGCTCCCA AAGTT    GAGCT  CCAGGCCTG
                                    GAACTTGA    TTCAA    CTCGG  GGTCCGGAC
                                              GACC    AC
GAM3770  281   MFN1   1  8117  NP_060397.1  3  1279  AGGGGTGGGGCT          C  G  T       3  C  c  c

                                    GTGAGCTCTTAA AAGTTAAGAGCTC CAG CC
                                    TTTGTTTT    TTTAATTCTCGAG GTC GG
                                              T  G  G
GAM3770  281   MFN1   1  8117  NP_284941.1  3  293   AGGGGTGGGGCT          C  G  T       3  C  c  c
                                    GTGAGCTCTTAA AAGTTAAGAGCTC CAG CC
                                    TTTGTTTT    TTTAATTCTCGAG GTC GG
                                              T  G  G
GAM3770  281   MGC1113 1  7280  NP_113660.1  5  176   GGGGCTTCCCAT     AG      -----       3  C  c
c
         4                          GGGAGCTGATGG AAGTTA  AGCTCCCA    GGCCT
                                    CTTCGTGC    TTCGGT  TCGAGGGT    TCGGG
                                              AG       ACCCT
GAM3770  281   MGC2168 1  10713 NP_653236.1  3  132   TAGAGGGCTCCT    TA  A      ---         3  C  c
c
         8                          GGGAGCGCTCGC AAGT  AG GCTCCCAGG   CCT
                                    TTCTCCGT    TTCG  TC CGAGGGTCC   GGA
```

C- G TCG
GAM3770 281 MGC4238 1 7861 NP_115708.1 5 16 GGAAGGAGTCCT AGA --- 3 C c
c
GGGAGCATGGCT AAGTTA GCTCCCAGG CCT
TTCCCTGA TTCGGT CGAGGGTCC GGA
A-- TGA
GAM3770 281 MGC4671 1 9825 NP_714924.1 3 266 CTTTGCAGCTTT - CC C 3 C c c

9 GTTAGCTCTTAA AAGTT AAGAGCT CAGG CTG
ACTTCCAG TTCAA TTCTCGA GTTT GAC
A TT C
GAM3770 281 MONDOA 1 17392 NP_055753.1 3 1514 TCCTGCAGGCCT TA-- -- - 3 C c
c
GCGGGGATCTCT AAGT AGAG CTCC CAGGCCTG
CCCCACTT TTCA TCTC GGGG GTCCGGAC
CCCC TA C
GAM3770 281 MRPL52 1 12936 NP_848026.1 3 171 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 MRPL52 1 12936 NP_851312.1 3 452 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 MRPL52 1 12936 NP_851313.1 3 171 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 MRPL52 1 12936 NP_851821.1 3 171 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 MRPL52 1 12936 NP_851822.1 3 171 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 MRPL52 1 12936 NP_851823.1 3 171 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG
G- TC
GAM3770 281 MRPL52 1 12936 NP_851824.1 3 214 AGATCACTGCCT AG CT 3 C c
c
GGGAGGCTTGGC AAGTTAAG CTCCCAGGC
TTAGTACT TTCGGTTC GAGGGTCCG

G- TC
GAM3770 281 MSC 1 10452 NP_005089.1 5 81 GCTTCCCGGCCT - CT T 3 C c c
GGGTTTTTAGTC AAG TTAAGAG CCCAGGCC
TTCCTTGG TTC GATTTTT GGGTCCGG
T -- C
GAM3770 281 NID67 1 1378 NP_116565.1 5 37 GGTTCCAGGCCT A-- -- A- 3 C c c
GGGGGTCGCTTC AGTT AAG GCTCCCAGGCCTG
CAGCTGCC TCGA TTC TGGGGGTCCGGAC
CCG CC GC
GAM3770 281 NKX3-1 1 5499 NP_006158.2 3 1790 ACGCTGAGGCCT AAG---- - 3 C c
c
GGGAGTCTCTTG TTAAGAG CTCCCAGGCCT
AGCTCCAC AGTTCTC GAGGGTCCGGA
CACCTCG T
GAM3770 281 NMNAT2 1 1983 NP_055854.1 3 1410 CCTGCAGAGCCT A--- AAG-- - 3 C c
c
GGGAGCTGCAGG AGTT AGCTCCCAGGC CTG
AACTGTCT TCAA TCGAGGGTCCG GAC
TCTG GGACG A
GAM3770 281 NPC1L1 1 17761 NP_037521.1 3 752 AGTCTGAAGGCT A--- -- G 3 C c c
GGGAGCTCTTGG AGT TAAGAGCTCCCAG CCT
GGCTGGGC TCG GTTCTCGAGGGTC GGA
CGGG GG -
GAM3770 281 OSR1 1 8511 NP_005100.1 3 659 TCCAGAAAGGGT A CC G 3 C c c
TGCTAGCCTTAA AAGTTAAG GCT CAG CCT
CTTCAGCT TTCAATTC CGA GTT GGA
- TC G
GAM3770 281 PAK6 1 10797 NP_064553.1 3 907 TCTAACACTCCT AA-- CC 3 C c c
GGGAGCTCAGGA AAGTT GAGCTCCCAGG TG
GGCTTCTG TTCGG CTCGAGGGTCC AC
AGGA TC
GAM3770 281 PASK 1 20147 NP_055963.1 3 1237 GGAGCTGGGCCT A A --- T 3 C c c
GGGAACAGCCCT AAGTTA G GC TCCCAGGCC
GGCTTGGT TTCGGT C CG AGGGTCCGG
- C ACA G
GAM3770 281 PCOLN3 1 2932 NP_002759.1 3 6 CCTGCCAGGCCT G A CC- 3 C c
c
GCGTGGCCTTAG AA TTAAG GCT CAGGCCTG
GTTGTTCC TT GATTC CGG GTCCGGAC
G - TGC
GAM3770 281 PGF 1 11465 NP_002623.2 3 239 CCACAGACCCCT TAA C-- 3 C c c
GGGAGCTTCCGC AAGT GAGCTCCCAGG CTG
TTTGAAAG TTCG TTCGAGGGTCC GAC
CC- CCA
GAM3770 281 PPP1R12 1 19376 NP_002472.1 3 3293 ATGGGGCTCAGG AGCTCC 3 C
c c
B TCTGTCACTTAA AAGTTAAG CAGGCCTG
CTTAGAGT TTCAATTC GTCTGGAC

ACT---
GAM3770 281 PPP1R12 1 19376 NP_115288.1 3 3426 ATGGGGCTCAGG AGCTCC 3 C c c
B TCTGTCACTTAA AAGTTAAG CAGGCCTG
CTTAGAGT TTCAATTC GTCTGGAC
ACT---
GAM3770 281 PRSS7 1 4893 NP_002763.1 3 586 TGTCACAGGCCT GAGCTC 3 C c c
GGACTAAATTGA AAGTTAA CCAGGCCTG
TTTTACGT TTTAGTT GGTCCGGAC
AAATCA
GAM3770 281 PYGM 1 11354 NP_005600.1 5 724 CCCTTGAGGCTG A ------ A 3 C c c
GGGAGCTCCACT AGTTAA GAGCTCCC GGCCT
CCTTGGCT TCGGTT CTCGAGGG TCGGA
- CCTCAC G
GAM3770 281 RAB3IL1 1 7921 NP_037533.2 3 33 CGGCCCAGGCCT AA A- ---- 3 C c c
GAAGGGGAGCTC GTT AGAGCTCCC AGGCCTG
TGAGACAG CAG TCTCGAGGG TCCGGAC
GA AG GAAG
GAM3770 281 RASSF4 1 725 NP_114412.2 3 227 CGACCCAGGCCT AAGA - 3 C c c
GAGGGGCCAGGA AAGTT GCTCC CAGGCCTG
ACTTGCTG TTCAA CGGGG GTCCGGAC
GGAC A
GAM3770 281 RASSF4 1 725 NP_835281.1 3 720 CGACCCAGGCCT AAGA - 3 C c c
GAGGGGCCAGGA AAGTT GCTCC CAGGCCTG
ACTTGCTG TTCAA CGGGG GTCCGGAC
GGAC A
GAM3770 281 RFC1 1 12616 NP_002904.2 3 901 AACCAGGCTGGG --- G 3 C b b
TCAGGCTCTTAA AAGTTAAGAGCT CCCAG CCTG
TTTCACTA TTTAATTCTCGG GGGTC GGAC
ACT -
GAM3770 281 RNH 1 8721 NP_002930.2 5 869 TCCTGGCATCCT - G --- T 3 C c c
GGGAGGTCTCTG AAGTTA AGA CTCCCAG GCC
GCTTTGTG TTCGGT TCT GAGGGTC CGG
C G CTA T
GAM3770 281 RRM2 1 17167 NP_001025.1 3 215 GCCAGAAGGCCT AG C- 3 C c c
GGCTGGCTGTGA AAGTTA AGCT CCAGGCCT
CTTACCAT TTCAGT TCGG GGTCCGGA
G- TC
GAM3770 281 SEDL 1 1404 NP_055378.1 5 227 AAGACCATGTCT TAA C 3 C c c
GGGAGCTTCTAC AAGT GAGCTCCCAGGC TG
TTTGTAA TTCA TTCGAGGGTCTG AC
TC- T
GAM3770 281 SLC2A10 1 11011 NP_110404.1 3 1212 GGTCCAGGGCCT TA GC 3 C c c
GGGAAATTTCTA AAGT AGA TCCCAGGCCT

CTTATCCT TTCA TTT AGGGTCCGGG
TC AA
GAM3770 281 SMCR5 1 20071 NP_658987.1 3 899 ACTTCAAGGCCT TA CT- 3 C c c
GGGCCCCTCTGG AAGT AGAG CCCAGGCCT
GCTTCAGT TTCG TCTC GGGTCCGGA
GG CCC
GAM3770 281 SPINLW1 1 18980 NP_852479.1 5 275 GGGAAGAGGCCT AA--- A - - 3 C c c
GGGATGCTGCTA GTT AG AGC TCCCAGGCCT
AACATCCT CAA TC TCG AGGGTCCGGA
TCCTA A G T
GAM3770 281 SRL 1 10846 XP_064152.3 3 475 CCCCAGCCCTCG - TC - C 3 C c c
GCTGCCTCTTAA AAGTTAAGAG C CC AGG CTG
CTTTGGGT TTCAATTCTC G GG TCC GAC
C TC C C
GAM3770 281 SURF4 1 547 NP_149351.1 3 686 GGGTAACACCCT -- ------ 3 C c c
GGGAGTTTTAGT AAGTTA AGAGCTCCCAGG CCT
AGCTTGAG TTCGAT TTTTGAGGGTCC GGG
GA CACAAT
GAM3770 281 TMPRSS6 1 18491 NP_694564.2 3 7 GGTGTCAGGCCT T A TCC 3 C c c
GCTGCCCTTGCC AAG TAAG GC CAGGCCTG
TTGTCCTC TTC GTTC CG GTCCGGAC
C C TC-
GAM3770 281 TNFRSF1 1 4544 NP_001057.1 3 2045 GTGGACAGTCCT AA --- C 3 C c c
B GGGAGAACCTCA AAGTT GAG CTCCCAGG CTG
GGCTTCCT TTCGG CTC GAGGGTCC GAC
A- CAA T
GAM3770 281 TRPM2 1 16176 NP_003298.1 3 846 CATCTCAGGCCT T--- C- 3 C c c
GGCTGGCTCTTC AAGT AAGAGCT CCAGGCCTG
TGTGCTTT TTCG TTCTCGG GGTCCGGAC
TGTC TC
GAM3770 281 TXNL2 1 13570 NP_006532.1 3 574 GGTTCTAGGGCT AAG G 3 C c c
GGGAGCTGGGAT AAGTT AGCTCCCAG CCTG
TTGAACCA TTTAG TCGAGGGTC GGAT
GG- G
GAM3770 281 UBE2G1 1 14637 NP_003333.1 3 925 CACAGCTACAGG - CTCCC 3 C c c
CTTTCTACTTAA AAGTTAAG AG AGGCCTG
CTTCTGGG TTCAATTC TC TTCGGAC
A T----
GAM3770 281 UCHL1 1 5541 NP_004172.2 5 5 GGCACGAGGCCT A-- A-- - 3 C c c
GGGCGGCTCCGC AGTTA GAGCT CCCAGGCCT
TAGCTGTT TCGAT CTCGG GGGTCCGGA
TTG CGC C
GAM3770 281 UPLC1 1 10056 NP_060177.2 3 253 CGCTAGGGGCCT A---- - A 3 C c c
GGGAGCCCTGTG AGTTA AG GCTCCCAGGCCT

GCTGGATC TCGGT TC CGAGGGTCCGGG
CTAGG G C

GAM3770 281 VWF 1 11547 NP_000543.1 3 137 CCACAATAAAGG T CCA 3 C c c
CTGAGCTCTTAT AAG TAAGAGCTC GGCCT
CTTGCTGC TTC ATTCTCGAG TCGGA
T ---

GAM3770 281 YAP 1 18388 NP_060723.2 3 43 AGTCTGGAGACT T A GC 3 C c c
GGGAGCCTTCAC AAGT AAG GCTCCCAG CT
TTCGGCCT TTCA TTC CGAGGGTC GA
C - A-

GAM3770 281 YAP 1 18388 NP_620829.1 3 43 AGTCTGGAGACT T A GC 3 C c c
GGGAGCCTTCAC AAGT AAG GCTCCCAG CT
TTCGGCCT TTCA TTC CGAGGGTC GA
C - A-

GAM3770 281 YAP 1 18388 NP_620830.1 3 43 AGTCTGGAGACT T A GC 3 C c c
GGGAGCCTTCAC AAGT AAG GCTCCCAG CT
TTCGGCCT TTCA TTC CGAGGGTC GA
C - A-

GAM3770 281 YAP 1 18388 NP_620831.1 3 43 AGTCTGGAGACT T A GC 3 C c c
GGGAGCCTTCAC AAGT AAG GCTCCCAG CT
TTCGGCCT TTCA TTC CGAGGGTC GA
C - A-

GAM3770 281 YAP 1 18388 NP_620832.1 3 43 AGTCTGGAGACT T A GC 3 C c c
GGGAGCCTTCAC AAGT AAG GCTCCCAG CT
TTCGGCCT TTCA TTC CGAGGGTC GA
C - A-

GAM5227 299 3PAP 1 18356 NP_061934.2 3 842 TGAGGAGCGTCC -- T G 1 B c c
ATTCCTCTGGAG GAGAT CAGA GGAATGGA GCT
TCTCTCCT CTCTG GTCT CCTTACCT CGA
AG - G

GAM5227 299 A2M 1 1882 NP_000005.1 5 0 GCTACAATCCAT A GA 1 B c c
CTGGTCTCCTCC GAGATCAGATGGA TG GGC
AGCTCCTT CTCTGGTCTACCT AC TCG
A A-

GAM5227 299 ACAS2L 1 4172 NP_115890.2 3 297 ATTGCCATCTCC AT T C 1 B c c
ATTCCTCTGCCC GAG CAGA GGAATGGAGG
TCTTGAGC CTC GTCT CCTTACCTCT
CC - A

GAM5227 299 ACRV1 1 14126 NP_001603.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC

GAM5227 299 ACRV1 1 14126 NP_064454.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC

GAM5227 299 ACRV1 1 14126 NP_064492.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC

GAM5227 299 ACRV1 1 14126 NP_064493.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064494.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064495.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064496.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064497.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064498.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064499.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACRV1 1 14126 NP_064500.1 3 62 TAAAAAGCCTCC A --- 1 B c c
ATCACTCTATTT GAG TCAGATGGA ATGGAGGCT
GGCTCATT CTC GGTTTATCT TACCTCCGA
- CAC
GAM5227 299 ACTR1A 1 3042 NP_005727.1 3 747 CCAGGACCTCGC T TG- - 1 B c c

TTTCCATCTGTT GAGA CAGATGGAA GAGG CT
CTTGTTGC TTCT GTCTACCTT CTCC GG
T TCG A
GAM5227 299 AMOTL1 1 11813 NP_570899.1 3 2122 ACACTGGCCTCC G-- AT --- 1 B c
c

ATTCTGACATCT AG CAGATG GAATGGAGGCT
GGGCTGGG TC GTCTAC CTTACCTCCGG
GGG GG AGT
GAM5227 299 AMPD2 1 6548 NP_004028.3 3 109 CTGCATGTCTCC T T- 1 B c c
ATTCTTCTCTGT GAGA CAGA GGAATGGAGGC
CTCTGTCT CTCT GTCT TCTTACCTCTG
- CT
GAM5227 299 ANXA5 1 2768 NP_001145.1 3 177 AAAATAGTGGTG TGGAAT 1 B c
c

CTTCTTTCTGAT GAGATCAGA GGAGGC
CTCTAGTG CTCTAGTCT TCTTCG

T-----
GAM5227 299 APA1 1 11175 NP_067011.1 3 45 CCTGGAAGAGCA ATGGAG 1 B c c
ACTCTATCTGAT GAGATCAGATGGA GCT
CTCAAAAT CTCTAGTCTATCT CGA
CAA---
GAM5227 299 ARHGAP1 1 11478 NP_004299.1 3 1417 ACCTCGGCCCCA ATGGAA- A 1 B c c
GTGATGGCTGAT GAGATCAG TGG GGCT
CTCACTCC CTCTAGTC ACC CCGG
GGTAGTG -
GAM5227 299 ARHGAP1 1 440 NP_060757.4 3 52 AATAGAAGCTGG A GGA 1 B c c
2 ATTCCATCAGAT GAGATC GATGGAAT GGCT
TTCAAATG CTTTAG CTACCTTA TCGA
A GG-
GAM5227 299 ATP1A2 1 14999 NP_000693.1 3 995 CCAGCCTCTTCC TC T --- 1 B c c
ATTCCCTTTCTT GAGA AGA GGAATGGA GGCT
TTCATGCC CTTT TTT CCTTACCT CCGA
TC C TCT
GAM5227 299 B4GALT6 1 17518 NP_004766.1 3 705 TCCTTGCTTGCA - A G 1 B c c
ATCTCATCTGAT GAGATCAGATG GA TG AGGC
TTTGCTAG TTTTAGTCTAC CT AC TTCG
T A G
GAM5227 299 BAX 1 3053 NP_004315.1 3 115 CCTGGAGCCTCC A---- T AA- 1 B c c
ACTGCCTCTGGA GAG TCAGA GG TGGAGGCT
ATTGCTCA CTC GGTCT CC ACCTCCGA
GTTAA - GTC
GAM5227 299 BMP8 1 1565 NP_001711.2 3 1758 ATCTGCGCCTCC AT -- 1 B c c
ATTTTCTATCTG GAG CAGATGGA ATGGAGGC
CACTTTTT TTC GTCTATCT TACCTCCG
AC TT
GAM5227 299 BOP 1 6088 XP_097915.2 3 2590 CTTTCCTGTCTC G----- T AT 1 B c c
CTCTCCTCTGAT AGATCAGA GGA GGAGGC
CTGTTCTT TCTAGTCT CCT CCTCTG
TTCTTG - CT
GAM5227 299 BSCL2 1 15949 NP_116056.2 5 190 CCGCCATCCCCC T AAT--- - 1 B c c
GACCCCTCTGAT GAGATCAGA GG GGA GGC
CTCCGATC CTCTAGTCT CC CCT CCG
C CAGCCC A
GAM5227 299 C20orf4 1 16282 NP_060141.2 3 724 AAGCCCCATTCC A----- A 1 B c c
2 ATTCCTACAGAT GAGATC GATGGAATGG GGCT
CTCTCAGC CTCTAG TTACCTTACC CCGA
ACATCC -
GAM5227 299 C21orf9 1 13507 NP_694936.1 5 28 GGAGCCACCACT -- - A 1 B c c
0 TCCAGTTCTGAT GAGATCAGA TGGAA TGG GGCT
CTTCTCAT TTCTAGTCT ACCTT ACC CCGA
TG C A

GAM5227 299 C6orf15 1 4598 NP_689764.1 3 1395 CTGCCTGCCTCC T GGA 1 B c c

1 ATGGGATCTGTC GAGA CAGAT ATGGAGGC
TTTATATT TTCT GTCTA TACCTCCG
- GGG

GAM5227 299 CACNA1H 1 4280 NP_066921.1 3 210 CCACGAGCCTCC A - A 1 B c c

ATCCGTTCTGGT G GATCAGA TGGA TGGAGGCT
TCGGGTTT G TTGGTCT GCCT ACCTCCGA
C T -

GAM5227 299 CCL22 1 5881 NP_002981.2 3 126 TGCCAACTCTCT AT G C 1 B c c
GCATTCCCTGAT GAGATCAG GGAATG AGG
CTCCATCC CTCTAGTC CCTTAC TCT
-- G C

GAM5227 299 CD209 1 14170 NP_066978.1 3 947 ACAGTTCTGTCT A AA 1 B c c
CTACTACCTGAT GAGATCAG TGG TGGAGGC
CTCCTCCT CTCTAGTC ATC ATCTCTG
C --

GAM5227 299 CD34 1 8867 NP_001764.1 3 1219 TGGATCCTAGCC T ATG 1 B c c
TTATCCTCTGAT GAGATCAGA GGA GAGGCT
CTCCATGG CTCTAGTCT CCT TTCCGA
- A--

GAM5227 299 CDH16 1 18186 NP_004053.1 3 53 GCTTGGCCTCTG GA A- 1 B c c
GCTCCATCTGAG GA TCAGATGGA TGGAGGCT
TCCCCTGG CT AGTCTACCT GTCTCCGG
G- CG

GAM5227 299 CECR1 1 14307 NP_059120.2 3 269 TCAGAGTCTTCT T AT- 1 B c c
CCTCTCTCTGAT GAGATCAGA GGA GGAGGCT
CTCTGTGC CTCTAGTCT TCT CTTCTGA
C CCT

GAM5227 299 CECR1 1 14307 NP_803124.1 3 269 TCAGAGTCTTCT T AT- 1 B c c
CCTCTCTCTGAT GAGATCAGA GGA GGAGGCT
CTCTGTGC CTCTAGTCT TCT CTTCTGA
C CCT

GAM5227 299 CNNM4 1 14344 NP_064569.1 5 111 GGGCAACATCTC GGAA C 1 B c c

CAGCAATCTGAT GAGATCAGAT TGGAGG
CTCCTTCA CTCTAGTCTA ACCTCT
ACG- A

GAM5227 299 COL11A1 1 8352 NP_001845.2 3 461 ACGTGTCCCTGA A ---- G 1 B c c

ATTCCATCTGAC GAG TCAGATGGAAT GGA GC
TCTAATTT CTC AGTCTACCTTA CCT TG
- AGTC G

GAM5227 299 COL11A1 1 8352 NP_542196.1 3 461 ACGTGTCCCTGA A ---- G 1 B c c

ATTCCATCTGAC GAG TCAGATGGAAT GGA GC
TCTAATTT CTC AGTCTACCTTA CCT TG
- AGTC G

GAM5227 299 COL11A1 1 8352 NP_542197.1 3 461 ACGTGTCCCTGA A ---- G 1 B c c

ATTCCATCTGAC GAG TCAGATGGAAT GGA GC
TCTAATTT CTC AGTCTACCTTA CCT TG
- AGTC G
GAM5227 299 COLEC10 1 13201 NP_006429.1 3 156 TATGGAGCCTCC T - GA 1 B c c
ATCATCATGCTC GAGA CA GATG ATGGAGGCT
TTTTGTGA TTCT GT CTAC TACCTCCGA
C A --
GAM5227 299 CPD 1 3803 NP_001295.2 3 2957 ACCTGCTCCTCC TC - C 1 B c c
ATTTCCATTTAT GAGA AGATGGAA TGGAGG
TCTCAACA CTCT TTTACCTT ACCTCC
TA T T
GAM5227 299 CSNK1A1 1 8360 NP_001883.3 5 115 GCCCCAGCCTCC TCA - 1 B c c
ATCTTCGTCTCT GAGA GATGGA ATGGAGGCT
CAGGATGG CTCT CTGCTT TACCTCCGA
--- C
GAM5227 299 CTNND1 1 15067 NP_001322.1 3 31 ACCACTATCTCC AT C 1 B c c
GTTCCATCTGGG GAG CAGATGGAATGGAGG
CTTATATG TTC GTCTACCTTGCCTCT
GG A
GAM5227 299 CTSB 1 12008 NP_001899.1 3 689 AGGAGTTGTTTC A AA 1 B c c
TGACCCACTGAT GAGATCAG TGG TGGAGGC
CTCTACTA CTCTAGTC ACC GTCTTTG
- CA
GAM5227 299 CTSB 1 12008 NP_680090.1 3 689 AGGAGTTGTTTC A AA 1 B c c
TGACCCACTGAT GAGATCAG TGG TGGAGGC
CTCTACTA CTCTAGTC ACC GTCTTTG
- CA
GAM5227 299 CTSB 1 12008 NP_680091.1 3 689 AGGAGTTGTTTC A AA 1 B c c
TGACCCACTGAT GAGATCAG TGG TGGAGGC
CTCTACTA CTCTAGTC ACC GTCTTTG
- CA
GAM5227 299 CTSB 1 12008 NP_680092.1 3 689 AGGAGTTGTTTC A AA 1 B c c
TGACCCACTGAT GAGATCAG TGG TGGAGGC
CTCTACTA CTCTAGTC ACC GTCTTTG
- CA
GAM5227 299 CTSB 1 12008 NP_680093.1 3 689 AGGAGTTGTTTC A AA 1 B c c
TGACCCACTGAT GAGATCAG TGG TGGAGGC
CTCTACTA CTCTAGTC ACC GTCTTTG
- CA
GAM5227 299 CXADR 1 8611 NP_001329.1 3 23 GTATAAGCCTCC AT - --- 1 B c c
ATATGTCTCATC GAG CAGATG GA ATGGAGGCT
TGTGCTCT CTC GTCTAC CT TACCTCCGA
GT T GTA
GAM5227 299 DAG1 1 16633 NP_004384.1 3 1500 AGAACATCCGTC - A - C 1 B c c
CGTCCATCTGCA GAGAT CAGATGGA TGGA GG
TCTCTGTC CTCTA GTCTACCT GCCT CC
C - G T
GAM5227 299 DEFT1 1 863 NP_624312.1 3 194 ACCTTGTCCTCC TC AT - 1 B c c

ATTTCCTTTTCT GAGA AG GGAATGGAGG C
CATCCAAA CTCT TC CTTTACCTCC G
TT -- T

GAM5227 299 DGCR2 1 7719 NP_005128.1 3 686 CTTCACTGTGTC AT T G 1 B c c
TTTCCATCTGGG GAG CAGATGGAA GGA GC
CTCTGCAG CTC GTCTACCTT TCT TG
GG - G

GAM5227 299 DICER1 1 13841 NP_085124.2 3 709 CATGGATAGTCT TG A 1 B c c
TTAATCTCTGAT GAGATCAGA GA TGGAGGCT
CTTTTTGG TTCTAGTCT CT ATTTCTGA
-- A

GAM5227 299 DICER1 1 13841 NP_803187.1 3 709 CATGGATAGTCT TG A 1 B c c
TTAATCTCTGAT GAGATCAGA GA TGGAGGCT
CTTTTTGG TTCTAGTCT CT ATTTCTGA
-- A

GAM5227 299 DKFZP43 1 17734 NP_115507.2 5 388 CCTTCAGCCTCC GA -- --- 1 B c
c

4P0714 ATGCATCCAGTT GA TCAGA TGGA ATGGAGGCT
TTGAGTCA CT AGTTT ACCT TACCTCCGA
G- TG ACG

GAM5227 299 DKFZp54 1 18504 NP_061174.1 3 45 TCCACGTTTGAC A G- 1 B c c

7A023 ATTCCATCAGAT GAGATC GATGGAATG AGGC
TTCGTCCA CTTTAG CTACCTTAC TTTG
A AG

GAM5227 299 DKFZP58 1 1196 NP_056348.2 5 38 TTCAGAGCCTCC A GA AA 1 B c
c

6B1621 ACACCATGACCT GAG TCA TGG TGGAGGCT
CCAAGAAG CTC AGT ACC ACCTCCGA
C -- AC

GAM5227 299 DKFZp66 1 20018 NP_705833.1 3 253 TCTTGGAAAGGT GAT G 1 B c
c

7G2110 TCTATTCCTGAT GAGATCA GGAATGGAG CT
CTCCAGCT CTCTAGT CCTTATCTT GA
--- G

GAM5227 299 DKFZp76 1 3514 NP_775102.1 3 1955 TTGGGCCTTATC A AA -- 1 B c c

1H0421 AGCCCATCTGAT G GATCAGATGG TG GAGGCT
CCAGATCA C CTAGTCTACC AC TTCCGG
- CG TA

GAM5227 299 E2F3 1 16017 NP_001940.1 3 1934 TCTTCAGCCTCC AT AT A 1 B c c
ATCCCTGGCCTC GAG CAG GGA TGGAGGCT
CTCCCCTC CTC GTC CCT ACCTCCGA
CG -- -

GAM5227 299 EDF1 1 535 NP_003783.1 3 42 CGAAATCAGTGC ATGGAA - 1 B c c
GCTCCAGCTGAT GAGATCAG TGGAG GC
CTCGTTCC CTCTAGTC ACCTC CG
G----- G

GAM5227 299 EGFR 1 7441 NP_005219.2 3 764 TGTTTGTCTTCC A- ---- - 1 B c c
ATTCCATTGTTT GAG TCA GATGGAATGGAGG C
TGAAACTC CTC AGT TTACCTTACCTTC G

AA TTTG T

GAM5227 299 ELMO2 1 15621 NP_071369.4 5 47 AACAAGTTTGTC A A - 1 B c c
AATCCATCTGAA GAG TCAGATGGA TGG AGGCT
CTTCAGTT TTC AGTCTACCT ACT TTTGA
A A G

GAM5227 299 ELMO2 1 15621 NP_573403.1 5 47 AACAAGTTTGTC A A - 1 B c c
AATCCATCTGAA GAG TCAGATGGA TGG AGGCT
CTTCAGTT TTC AGTCTACCT ACT TTTGA
A A G

GAM5227 299 ENT4 1 8473 NP_694979.1 3 276 ACCTGCGTCTAC A - T - 1 B c c
CTTCCATCTGTG G GAT CAGATGGAA GG AGGC
TCCAGCGG C CTG GTCTACCTT CC TCTG
- T - A

GAM5227 299 FAD104 1 19708 NP_073600.2 3 2663 AATAAAGTGTTC ATGG - 1 B c c
TATTAACCTGAT GAGATCAG AATGGAG GCT
CTCTTTGC CTCTAGTC TTATCTT TGA
CAA- G

GAM5227 299 FAT3 1 7573 XP_061871.5 3 1215 GGCATACCTTTC T - C 1 B c c
AATTTCTCTGAT GAGATCAGA GGAAT GGAGG
CTCTATGG CTCTAGTCT CTTTA CTTTC
- A C

GAM5227 299 FBXW8 1 11502 NP_036306.1 3 2030 AGATACGCAGCC CAG- AG 1 B c c
ATTCCATATTCA GAGAT ATGGAATGG GC
TCTCCAAC CTCTA TACCTTACC CG
CTTA GA

GAM5227 299 FBXW8 1 11502 NP_699179.2 3 2030 AGATACGCAGCC CAG- AG 1 B c c
ATTCCATATTCA GAGAT ATGGAATGG GC
TCTCCAAC CTCTA TACCTTACC CG
CTTA GA

GAM5227 299 FLJ0002 1 10221 XP_036307.7 5 136 TTATTTGCCTCC A T A- 1 B c c
6 ATGGCCTTTGAA GAG TCAGA GG ATGGAGGC
CTTGCACA TTC AGTTT CC TACCTCCG
A - GG

GAM5227 299 FLJ0022 1 13481 XP_084552.3 3 1746 GGCACTTTTTCC A----- T - 1 B c c
5 AATTTGACTGAT GAGATCAG TGGAA GGAG GCT
CTCTAAAC CTCTAGTC ACCTT TTTC CGG
AGTTTA - A

GAM5227 299 FLJ1007 1 18487 NP_060458.2 3 1558 TAGAAGTCAGCT GAA 1 B c c
4 TTCACATCTGAT GAGATCAGATG TGGAGGCT
TTCTGTAT CTTTAGTCTAC ACTTTCGA

GAM5227 299 FLJ1009 1 10680 XP_043653.1 3 261 AAAGCAGTCTGT CA G 1 B c c
7 ATTCCATCATCT GAGAT GATGGAATG AGGCT
TCCTTTTT TTCTA CTACCTTAT TCTGA
-- G

GAM5227 299 FLJ1026 1 2454 NP_060512.2 5 36 CTTTCTGCAACC ATG AG 1 B c c

0 ATTCAGACTGAT GAGATCAG GAATGG GC
CTCGGGCT CTCTAGTC CTTACC CG
AGA AA
GAM5227 299 FLJ1042 1 1979 NP_060560.1 3 462 TGTAGCCACTTC AT A -- 1 B c c
0 AGTCCATCTGCC GAG CAGATGGA TGGA GGCT
CTCCAGAG CTC GTCTACCT ACTT CCGA
CC G CA
GAM5227 299 FLJ1250 1 8025 NP_079025.1 3 944 CTTTCTGTTCAC GA 1 B c c
5 ATTTCATCTGAT GAGATCAGATGGAATG GGC
TTTTAAAC TTTTAGTCTACTTTAC TTG
AC
GAM5227 299 FLJ1297 1 11304 NP_079085.2 3 591 GCCACTGCGTCC -- A G 1 B c c
5 GGTCCATCTGAC GAGA TCAGATGGA TGGA GC
TTCTCAAA CTCT AGTCTACCT GCCT CG
TC G G
GAM5227 299 FLJ1311 1 5150 NP_078817.1 3 1392 CATAAGGCCTCC ATCA 1 B c c
4 ATTCTGTCCGCT GAG GATGGAATGGAGGCT
CAGATTCT CTC CTGTCTTACCTCCGG
GC--
GAM5227 299 FLJ2025 1 9250 NP_060197.2 3 321 GCCTTCCACTTC C ----- - 1 B c c
4 CTTCCATCTCAT GAGAT AGATGGAA TGGA GGC
TTCTAAAC CTTTA TCTACCTT ACCT CCG
C CCTTC T
GAM5227 299 FLJ2351 1 10450 NP_078996.1 5 94 AGGAGAGCCTCC - C- A 1 B c c
0 ATCCTGTCTTCA GAG AT AGATGG ATGGAGGCT
TCCTCAAG CTC TA TCTGTC TACCTCCGA
C CT C
GAM5227 299 FLJ3171 1 8441 NP_689788.1 3 1175 GCTTGCTCCAAT T --- GC 1 B c c
3 TTTCCATCTGCT GAGA CAGATGGAA TGGAG
CTCTCTTC CTCT GTCTACCTT ACCTC
C TTA GT
GAM5227 299 FLJ3747 1 11160 NP_848652.1 3 682 CTGACGCCCTCC A T - 1 B c c
8 ATTTCTCTGGCT GAG TCAGA GGAATGGAGG C
CCGGCCCC CTC GGTCT CTTTACCTCC G
- - C
GAM5227 299 FLJ3860 1 8113 NP_694947.1 3 175 TAATGGCTGCCT AT AT 1 B c c
8 CCCTCTCCTGAT GAGATCAG GGA GGAGGC
CTCTTCAA CTCTAGTC TCT CCTCCG
C- C-
GAM5227 299 FLJ3869 1 5440 NP_848608.1 3 861 ATGAAGTCACCC A A- 1 B c c
0 ATTCCATTTGAC GAG TCAGATGGAATGG GGCT
TCTTTAGC CTC AGTTTACCTTACC CTGA
- CA
GAM5227 299 FLJ3911 1 19608 NP_689848.1 5 218 AAGGATGCCTCC TCAGAT 1 B c
c
6 ATTCCTGCTTCT GAGA GGAATGGAGGC
CACCT CTCT CCTTACCTCCG
TCGT--
GAM5227 299 FLJ3959 1 11751 NP_776164.1 3 669 ACTGCAGCCTCC AT T A 1 B c c

9 ATCCTCTGGGTT GAG CAGA GGA TGGAGGCT
CAAGCAAT CTT GTCT CCT ACCTCCGA
GG - -
GAM5227 299 FLJ3964 1 14874 NP_775896.2 3 891 GAGTCTGAAACC C ---- 1 B c c
7 ATTCCATTTCAT GAGAT AGATGGAATGG AGGCT
TTTGGTGA TTTTA TTTACCTTACC TCTGA
C AAAG
GAM5227 299 FRAT1 1 11515 NP_005470.2 3 1597 ATGTACAGAACA T GAGG 1 B c
c
CATTTCTCTGAT GAGATCAGA GGAATG CT
CTCCATAA CTCTAGTCT CTTTAC GA
- ACAA
GAM5227 299 FRAT1 1 11515 NP_852000.1 3 1147 ATGTACAGAACA T GAGG 1 B c
c
CATTTCTCTGAT GAGATCAGA GGAATG CT
CTCCATAA CTCTAGTCT CTTTAC GA
- ACAA
GAM5227 299 FYCO1 1 653 NP_078789.1 3 2190 GGGGCCTGGGAC GA G--- 1 B c
c
ATTCCATCTGAG GA TCAGATGGAATG AGGCT
GTCCTTCC CT AGTCTACCTTAC TCCGG
GG AGGG
GAM5227 299 FZD4 1 19026 NP_036325.2 3 2931 TTCACTGTCTCC CAG 1 B c c
ATTCCATAAATC GAGAT ATGGAATGGAGGC
TCTTCCTG CTCTA TACCTTACCTCTG
AA-
GAM5227 299 GCLM 1 4027 NP_002052.1 3 182 TATCTTGCCTCC TCA G - 1 B c c
ATATCAATCCAT GAGA GAT GA ATGGAGGC
TCTCATGA CTCT CTA CT TACCTCCG
TAC A A
GAM5227 299 GPR4 1 13775 NP_005273.1 3 323 ACTGCAGCCTCC AT AT AA 1 B c
c
ACCTCCTGGGCT GAG CAG GG TGGAGGCT
CTCCAGCG CTC GTC CC ACCTCCGA
GG CT --
GAM5227 299 GSPT1 1 10693 NP_002085.1 5 183 GCCCCTGCCTCC TCA T 1 B c
c
ATTTCTCGCTCT GAGA GA GGAATGGAGGC
CTGTCCAC CTCT CT CTTTACCTCCG
CG- -
GAM5227 299 H41 1 15147 NP_060018.1 3 81 ACCAACAGCCAT GA - 1 B b b
TCATCATCTGAT GAGATCAGATG ATGGA GGCT
CTCTGCTG CTCTAGTCTAC TACTT CCGA
-- A
GAM5227 299 HAS2 1 15347 NP_005319.1 5 420 CCGGTCGTCTCA ATG 1 B c c
AATTCATCTGAT GAGATCAGATGGA GAGGC
CTCTTATT CTCTAGTCTACTT CTCTG
AAA
GAM5227 299 HIF1AN 1 8091 NP_060372.1 3 1167 GCTAGAGCCTCC - GAT AA 1 B c
c

AGGCCCTATGAT GAG ATCA GG TGGAGGCT
GCTCCCTG CTC TAGT CC ACCTCCGA
G ATC GG

GAM5227 299 HN1L 1 6999 NP_653171.1 3 670 TCTGAAACCTCG -- AATG C 1 B c c
GCCTGATCTGAT GAGATCAGAT GG GAGG
CTCATGTT CTCTAGTCTA CC CTCC
GT GG-- A

GAM5227 299 HS3ST2 1 10566 NP_006034.1 3 80 AGATTTGCTCCC T AA AG 1 B c c

AGACCCTCTGAT GAGATCAGA GG TGG GC
CTCCCTCC CTCTAGTCT CC ACC CG
C AG CT

GAM5227 299 IHH 1 762 XP_050846.3 3 348 TGGGGAGGGCCC CA AG 1 B c c
ATTCCATCCATC GAGAT GATGGAATGG GCT
TTAGGCCC TTCTA CTACCTTACC CGG
C- --

GAM5227 299 IL1F8 1 2378 NP_055253.2 5 47 CTAGCCTCCTCA G----- AAT--- 1 B c c
CCACCATCTGAT AGATCAGATGG GGAGGCT
CTATCTTG TCTAGTCTACC CCTCCGA
GTTCTA ACCACT

GAM5227 299 IL1F8 1 2378 NP_775270.1 5 47 CTAGCCTCCTCA G----- AAT--- 1 B c c
CCACCATCTGAT AGATCAGATGG GGAGGCT
CTATCTTG TCTAGTCTACC CCTCCGA
GTTCTA ACCACT

GAM5227 299 IL1R1 1 7235 NP_000868.1 3 1784 ACTTGAGCCTCC AT TGG 1 B c c

ATTTCTGGCTTC GAG CAGA AATGGAGGCT
TAGTCTGG CTT GTCT TTACCTCCGA
CG ---

GAM5227 299 IL1RAP 1 19607 NP_002173.1 3 318 TTATATGTCTCC C-- T 1 B c c
ATTCTTTTTAAA GAGAT AGA GGAATGGAGGC
ATCTTAAC TTCTA TTT TCTTACCTCTG
AAA T

GAM5227 299 IMP-2 1 9919 NP_006539.2 3 898 TTCTCCATCTCC - T C 1 B c c
ATTCTTTTGAAT GAGAT CAGA GGAATGGAGG
TTCCTCAT CTTTA GTTT TCTTACCTCT
A - A

GAM5227 299 KIAA014 1 9212 NP_055476.1 3 2615 CCTGCTGGCCCC TGGAA A 1 B c c

0 AGGACTTCTGAT GAGATCAGA TGG GGCT
CTCAGTCC CTCTAGTCT ACC CCGG
TCAGG -

GAM5227 299 KIAA015 1 13266 NP_115558.2 3 168 GTGGGAGCCTCC T A A 1 B c c

7 ATCCGCTGCTCT GAGA CAG TGGA TGGAGGCT
TTACCTTT TTCT GTC GCCT ACCTCCGA
C - -

GAM5227 299 KIAA023 1 17412 XP_291106.1 3 527 GCGGTGGTCTCC CAGATG 1 B c c

2 ATTCAGCAAAAT GAGAT GAATGGAGGCT

CTCATGTA CTCTA CTTACCTCTGG
AAACGA
GAM5227 299 KIAA026 1 9788 XP_300768.1 3 2041 ACTGCTTCCTCA AG AT--- 1 B c c
8 CATCCATCTGAT G ATCAGATGGA GGAGGC
TGCACCAT C TAGTCTACCT CCTTCG
GT ACACT
GAM5227 299 KIAA029 1 19557 XP_042833.2 3 1079 TGTCCTGTCATC G AA - 1 B c c
5 TAGCCATCTGAT GA ATCAGATGG TGGA GGC
ATCTTCCT CT TAGTCTACC ATCT CTG
A G- A
GAM5227 299 KIAA036 1 10082 XP_041018.2 3 1876 CCATAAGCCTCC TC T ---- 1 B c c
7 ATCGTTTTCTCT GAGA AGA GGA ATGGAGGCT
TTTCTCCT CTCT TCT CTT TACCTCCGA
TT - TTGC
GAM5227 299 KIAA051 1 15950 NP_055511.1 3 4052 GATGTAGCCTCC T TGGAA- 1 B c c
4 AGGCACTTCTGC GAGA CAGA TGGAGGCT
TCTCTGGC CTCT GTCT ACCTCCGA
C TCACGG
GAM5227 299 KIAA072 1 19760 NP_067680.2 3 97 ACAGCATGCAGT T-- T AG 1 B c c
1 CTTCCATCTGCT GAGA CAGATGGAA GG GC
TTCTCTTC CTCT GTCTACCTT CT CG
TTC - GA
GAM5227 299 KIAA113 1 12332 XP_166110.3 3 1572 AAGCTTATTGCA A- G --- 1 B c c
6 TTCCACACTGAT GAGATCAG TGGAATG A GGCT
CTCTTGGC CTCTAGTC ACCTTAC T TCGA
AC G TAT
GAM5227 299 KIAA115 1 7957 XP_051093.2 3 4105 ACCTGTGTCCTC T A - 1 B c c
7 TACTTTTCTGAT GAGATCAGA GGA TGGAGG C
CTCCCACA CTCTAGTCT TTT ATCTCC G
- C T
GAM5227 299 KIAA144 1 6089 NP_065887.1 3 737 AGGAGGCCCTCC GAT - 1 B c c
6 ATTCCTGGTTTC GAGATCA GGAATGGAGG CT
TGTAGCTT CTTTGGT CCTTACCTCC GG
--- C
GAM5227 299 KIAA182 1 17711 XP_041566.2 3 2254 TCCCCAGCCTCC TCA AA 1 B c c
2 AACTCATCACCT GAGA GATGG TGGAGGCT
CTCAGGCC CTCT CTACT ACCTCCGA
CCA CA
GAM5227 299 KIAA185 1 9010 XP_049884.1 3 1861 GCCAGGATTCCT TC T- ----- 1 B c c
4 TTTCCATCTCCT GAGA AGATGGAA GGA GGC
CTCTTTCT CTCT TCTACCTT CCT CCG
CC TT TAGGA

GAM5227 299 KIAA187 1 15546 XP_056635.1 5 2676 CATGGAGCCTCC AT A A 1 B c c
9 AGTCTAGCTGCC GAG CAG TGGA TGGAGGCT
TCTTGTGC CTC GTC ATCT ACCTCCGA
C- G G
GAM5227 299 KLF12 1 5272 NP_009180.3 3 2902 GGAAGAGCCTCC G C 1 B b b
ATTTCATCTCAT GA AT AGATGGAATGGAGGCT
GTCCATTT CT TA TCTACTTTACCTCCGA
G C
GAM5227 299 LDLR 1 9706 NP_000518.1 3 814 CTACCCACTTCC GAT C 1 B c c
ATTCCCGTGGTC GAGATCA GGAATGGAGG
TCCTTGCA CTCTGGT CCTTACCTTC
GC- A
GAM5227 299 LHX9 1 7190 NP_064589.1 5 293 AGACCGATTTCC T A C 1 B c c
ACTCCATCTGTT GAGA CAGATGGA TGGAGG
TCTTCTCC CTTT GTCTACCT ACCTTT
- C A
GAM5227 299 LOC1151 1 9407 NP_660285.1 3 12 ATTGTCCCCTCC AGA C 1 B c c
31 ATTCTAGGATTT GAGATC TGGAATGGAGG
CATCGTCA CTTTAG ATCTTACCTCC
G-- C
GAM5227 299 LOC1433 1 1541 XP_084485.1 3 928 GCCATGTCCGTT --- --- 1 B c c
10 ATCTCATCTGAT GAGATCAGATGG AATGGA GGC
CTTTTGCT TTCTAGTCTACT TTGCCT CCG
CTA GTA
GAM5227 299 LOC1454 1 1961 XP_085120.1 3 1271 TAACTGGCCTCC C A----- 1 B c c
53 ATCTTGGGTCAT GAGAT AGATGG ATGGAGGCT
CTCATCTT TTCTA TCTACT TACCTCCGG
C GGGTTC
GAM5227 299 LOC1456 1 1398 XP_096816.1 3 1411 TTTGCCACCATC T ---- A 1 B c c
01 TCCTCCTCTGAT GAGATCAGA GGA ATGG GGC
CTCCTTTC CTCTAGTCT CCT TACC CCG
- CCTC A
GAM5227 299 LOC1457 1 17221 XP_085211.1 3 1025 ACTGCAGCCTCC AT AT AA 1 B c c
25 ACCTCCTGGGCT GAG CAG GG TGGAGGCT
CAAAGTGA CTC GTC CC ACCTCCGA
GG CT --
GAM5227 299 LOC1458 1 19334 XP_096884.1 3 53 ACATCTGTCTCC CAGAT 1 B c c
45 ATTCCTGCCATC GAGAT GGAATGGAGGC
TCTTCCTG CTCTA CCTTACCTCTG
CCGT-
GAM5227 299 LOC1462 1 10066 XP_085396.1 3 313 TGTCCTGCCTCC TCA A 1 B c c
72 ATGCTGTCCCTT GAGA GATGG ATGGAGGC
CTCAGCAC CTCT CTGTC TACCTCCG
TCC G

GAM5227 299 LOC1512 1 16533 XP_087136.1 3 468 GTGGTTGCCTCC T ATGGA 1 B c c

34 ATGCTGTTCTCA GAGA CAG ATGGAGGC
TCATAGTG CTCT GTC TACCTCCG
T G----

GAM5227 299 LOC1520 1 16522 XP_087376.2 5 24 GCTGAACAGCTT AT TG 1 B c c

78 TTCTTCCCTGAT GAGATCAG GGAA GAGGCT
CTCTCGGA CTCTAGTC CCTT TTTCGA
-- CT

GAM5227 299 LOC1535 1 10222 XP_098394.1 5 519 GAGGTCCTTCAG T A-- - 1 B c c

77 CCTCCATCTGTT GAGA CAGATGGA TGGAGG CT
CTCCCACC CTCT GTCTACCT ACTTCC GG
T CCG T

GAM5227 299 LOC1548 1 7900 XP_098621.1 3 735 TACTGAAGGCCT A AAT - 1 B c c

34 GCCCCAGCTGAT GAGATCAG TGG GG AGGCT
CTCGCTCG CTCTAGTC ACC CC TCCGG
G --- G

GAM5227 299 LOC1548 1 17668 XP_098626.1 3 3211 CTCTCTGCATCC ATC - G 1 B c c

77 ATTCCACTCTCC GAG AGA TGGAATGGA GC
ACTCTTGC CTC TCT ACCTTACCT CG
ACC C A

GAM5227 299 LOC1616 1 11973 XP_172921.1 5 311 GGCCCAGCCTCC TCA - 1 B c c

35 ATCTTCGTCTCT GAGA GATGGA ATGGAGGCT
CAGGACGG CTCT CTGCTT TACCTCCGA
--- C

GAM5227 299 LOC1645 1 1232 XP_104562.1 3 146 GGCCTAGCAGCC CA- - ----- 1 B c c

80 ATTCCACTCCAT GAGAT GA TGGAATGG AGGCT
GTCTCACT CTCTG CT ACCTTACC TCCGG
TAC C GACGA

GAM5227 299 LOC1996 1 17021 NP_660338.1 3 255 TTCCCAGAATCC AG -- GG 1 B c c

92 ATTCCATTTGTG G ATCA GATGGAATGGA CT
ATTCCATG C TAGT TTACCTTACCT GA
CT GT AA

GAM5227 299 LOC2005 1 5245 XP_114264.1 3 304 GGCTGTGATTCC T T ----- 1 B c c

74 ATTCCCTCTGCT GAGA CAGA GGAATGGA GGCT
TTCTTGAA CTTT GTCT CCTTACCT TCGG
C C TAGTG

GAM5227 299 LOC2006 1 15034 XP_117260.1 5 247 TCAAATGCCTCC CAG - 1 B c c

81 ATCTCCATACCA GAGAT ATGGA ATGGAGGC
TTTCAGTT CTTTA TACCT TACCTCCG
CCA C

GAM5227 299 LOC2011 1 2742 XP_117061.1 5 139 CCCAGAGCCTTG AT AATG-- 1 B c c

```
          94                    TTTGGCCCTGAT GAGATCAG  GG     GAGGCT
                               CTCTGACT    CTCTAGTC  CC     TTCCGA
                                        -- GGTTTG
GAM5227  299   LOC2222 1  13169 XP_168640.1  5 633   GCCACTTGTCTA        AA-  -----      1  B  c  c
          52                    CAACCATCTGAT GAGATCAGATGG  TGGA   GGC
                               CTTTGACA   TTCTAGTCTACC  ATCT   CCG
                                        AAC   GTTCA
GAM5227  299   LOC2541 1  2157  XP_171004.1  3 772   TTGGTAACCTCC   T  --       C      1  B  c  c
          28                    ATTCTAGTTCTG GAGA CAGA  TGGAATGGAGG
                               TCTCTGTG    CTCT GTCT  ATCTTACCTCC
                                        -  TG        A
GAM5227  299   LOC2545 1  3693  XP_172947.1  5 66    GTCCGCGCCTCC   TC  - G          1  B  c  c

          44                    ATTGCGCTCTCC GAGA  AGA TG AATGGAGGC
                               TCTTCACT    TTCT  TCT GC TTACCTCCG
                                        CC   C  G
GAM5227  299   LOC2545 1  13871 XP_170588.1  3 80    GTATCTGCCTCC   A   AT           1  B  c  c
          56                    ATTTTCCTGAGC GAG TCAG  GGAATGGAGGC
                               TCAAAAAG    CTC AGTC  TTTTACCTCCG
                                        G   C-
GAM5227  299   LOC2830 1  9893  XP_208026.2  5 125   TATTCCTCCTCC   A A        C      1  B  c  c
          18                    ATTCCATCGACT GAG TC GATGGAATGGAGG
                               CCCAGCAC    CTC AG CTACCTTACCTCC
                                        - -         T
GAM5227  299   LOC2831 2  10191 XP_210889.1  3 1119  CTAGAAGAGCCC       T AAT A-       1  B  c
c
          07                    ACCCTTTCTGAT GAGATCAGA GG   GG  GGCT
                               CTCCAAAA    CTCTAGTCT TC   CC  CCGA
                                        T  ---  AC
GAM5227  299   LOC2831 2  13094 XP_210889.1  3 274   TTAGTGCCTCTT   AT--      AT-        1  B  c
c
          07                    AGTCCATCTGTT GAG   CAGATGGA   GGAGGC
                               CCCTCTCC    CTC   GTCTACCT   TCTCCG
                                        CCTT       GAT
GAM5227  299   LOC2831 1  13811 XP_208532.1  3 520   TCCTTAGCCTCC     A TG--          1  B  c  c

          53                    ATTCAGCCTCAG GAGATC GA   GAATGGAGGCT
                               GTCTTTTG    TTCTGG CT   CTTACCTCCGA
                                        A  CCGA
GAM5227  299   LOC2833 1  19526 XP_210976.1  5 1436  GGACAGGACTTC   TC     T   -       1  B  c
c
          32                    CTTCCATCTTCT GAGA  AGATGGAA GGAGG CT
                               CCTGCTCA    CTCT  TCTACCTT CCTTC GG
                                        --      -   A
GAM5227  299   LOC2833 1  2089  NP_776254.1  3 282   TCGGGACCCTCT       TG      C      1  B  c  c

          85                    TCATTCTCTGAT GAGATCAGA  GAATGGAGG
                               CTCATCCT    CTCTAGTCT  CTTACTTCT
                                        --       C
GAM5227  299   LOC2834 1  5440  XP_208682.1  3 861   ATGAAGTCACCC   A        A-        1  B  c  c
```

```
          60                          ATTCCATTTGAC GAG TCAGATGGAATGG  GGCT
                                     TCTTTAGC    CTC AGTTTACCTTACC  CTGA
                                              -          CA
GAM5227  299   LOC2835 1  19940 XP_211083.1  3  4241  TCCCTTGCCTCC   A    TGGA-          1  B  c
 c
          34                          ATGCAATTCTGA GAG TCAGA    ATGGAGGC
                                     ACTTCAGA    TTC AGTCT    TACCTCCG
                                               A    TAACG
GAM5227  299   LOC2835 1  10476 XP_211110.1  3  2185  GCTTCAGCCTCC   TC-  - -          1  B  c  c

          51                          ATTCTCACTTTC GAGA   AGA TG GAATGGAGGCT
                                     CTTCTCAA    CTCT   TTT AC CTTACCTCCGA
                                               TCC   C  T
GAM5227  299   LOC2837 1  9445  XP_211186.1  5  696   CCCCAAGCCTCC   GA  A  T            1  B  c
c
          38                          ATTTCCTCAGAA GA  TC GA GGAATGGAGGCT
                                     GTCAAACA    CT  AG CT CTTTACCTCCGA
                                               GA  A  C
GAM5227  299   LOC2838 1  17351 XP_208846.1  5  157   CCAGAAATTTCT          AT    C       1  B  c  c
          06                          CCTCCATCTGAT GAGATCAGATGGA  GGAGG
                                     TTTGAACA    TTTTAGTCTACCT  CCTCT
                                               --    T
GAM5227  299   LOC2838 1  5876  NP_848611.1  3  301   GGAGAAGCCTCC    CA    A          1  B  c  c

          49                          ACTCCATTGTCT GAGAT  GATGGA TGGAGGCT
                                     CCTGGCCC    CTCTG  TTACCT ACCTCCGA
                                               --    C
GAM5227  299   LOC2839 1  6869  XP_208906.1  3  27    GCTAGATGGTCT       AT  ATG          1  B  c
c
          24                          CAATCTCCTGAT GAGATCAG  GGA   GAGGCT
                                     CTCGTGGT    CTCTAGTC  TCT   CTCTGG
                                               C-   AA-
GAM5227  299   LOC2839 1  1669  XP_208928.1  3  209   ACGCAGGCCTCC    C  A  GA           1  B  c
c
          49                          ATAACAATTATT GAGAT AG TG  ATGGAGGCT
                                     TCAGTGCA    CTTTA TT AC  TACCTCCGG
                                               - A  AA
GAM5227  299   LOC2840 1  15264 XP_211323.1  3  63    GGCTCAGCCTCC    - A   AA          1  B  c  c

          82                          AGATTAACTGGG GAGATC AG TGG  TGGAGGCT
                                     TCTCACTC    CTCTGG TC ATT  ACCTCCGA
                                               G  A   AG
GAM5227  299   LOC2841 1  12184 XP_211336.1  3  13    GTGCCCACATCT GA          ----       1  B  c  c
          18                          ATTCCATCTGGT   GATCAGATGGAATGGA   GGC
                                     CA          CTGGTCTACCTTATCT    CCG
                                               A-             ACAC
GAM5227  299   LOC2841 1  8059  XP_211365.1  5  116   CTTCCAGCCTCC   A   A  GAA          1  B  c
c
          78                          ACAGCTGACCTC GAG TCAG TG   TGGAGGCT
                                     CAAGTCGG    CTC AGTC AC   ACCTCCGA
```

C G ---
GAM5227 299 LOC2842 1 15205 XP_211415.1 5 715 CTATAATGCCCC GA----- A 1 B c c
81 ATTTCATCTGAT GATCAGATGGAATGG GGC
TGATGACC TTAGTCTACTTTACC CCG
CCAGTAG -
GAM5227 299 LOC2843 1 6963 XP_209143.1 3 221 TGCGGCCTGCCT G - - - 1 B c c
25 ATTCCATCTGAA GA AT CAGATGGAAT GG AGGCT
TGTCGCAT CT TA GTCTACCTTA CC TCCGG
G A T G
GAM5227 299 LOC2843 1 6814 XP_209154.1 3 1109 CCTGGATGGTCT TG G 1 B c c
75 CGATTTTCTGAT GAGATCAGA GAAT GAGGCT
CTTATGAT TTCTAGTCT TTTA CTCTGG
-- G
GAM5227 299 LOC2844 1 13078 XP_211453.1 5 319 GCAGTGGCCTCC AT AT- A 1 B c c
02 ATCCTCCCTGCT GAG CAG GGA TGGAGGCT
CAGCCACA CTC GTC CCT ACCTCCGG
-- CCT -
GAM5227 299 LOC2844 1 1608 XP_290826.1 5 105 GCGTGCACCCGC T -- AG 1 B c c
59 GTTCCATCTGTC GAGA CAGATGGAAT GG GC
TTCTGAGA TTCT GTCTACCTTG CC CG
- CG CA
GAM5227 299 LOC2846 1 9610 XP_211571.1 5 388 TGATTGAGTCTA A TGG 1 B c c
50 TTTTTCACTGAT GAGATCAG TGGAA AGGCT
CTCAGCAA CTCTAGTC ACTTT TCTGA
- TTA
GAM5227 299 LOC2851 1 13418 XP_209482.1 3 63 TCTCAGAAAGCC A ATG 1 B c c
17 TTTCTGACTGAT GAGATCAG TGGA GAGGCT
CTCAGCAT CTCTAGTC GTCT TTCCGA
A ---
GAM5227 299 LOC2851 1 7199 XP_211771.1 3 322 CCAGGATGGTCT AT GA G 1 B c c
27 CGATCTCCTGAT GAGATCAG G AT GAGGCT
CTCGTGAT CTCTAGTC C TA CTCTGG
-- TC G
GAM5227 299 LOC2851 1 16102 XP_211803.1 5 444 GACCTGCCCTCC TC---- - 1 B c c
94 ATTCTATCTACT GAGA AGATGGAATGGAGG C
CCCTCTCT CTCT TCTATCTTACCTCC G
CCCTCA C
GAM5227 299 LOC2852 1 567 XP_211836.1 3 624 CAGTCTACCTCC AT C 1 B c c
84 TATTCGTCTGAT GAGATCAGATGGA GGAGG
CTTGCTTA TTCTAGTCTGCTT CCTCC
AT A
GAM5227 299 LOC2855 1 1779 XP_211947.1 3 1751 AGAATATGGTCC -- GGC 1 B c c

```
          87                        ATTCCATCTGAG GAGA  TCAGATGGAATGGA
                                   TTTTCAAA    CTTT  AGTCTACCTTACCT
                                             TG           GGT
GAM5227  299   LOC2856 1  4976  XP_209720.1  3  577   CTGCCTCCCTCC  G  -    T----        1  B  c  c
          73                        TTTCCATCTTGG GA ATCA GATGGAA    GGAGGC
                                   TGTCTTCC    CT TGGT CTACCTT    CCTCCG
                                          G   T     TCCTC
GAM5227  299   LOC2857 1  3655  XP_209764.1  5  276   CTCCTTCCCTCC    ---      T   C      1  B  c  c
          99                        TTTCCATCTGGG GAGAT   CAGATGGAA GGAGG
                                   GGTCTCGG    CTCTG   GTCTACCTT CCTCC
                                             GGG       T   C
GAM5227  299   LOC2858 1  17117 XP_212028.1  3  1390  GGCCCCTCCTCC    CAGA       C        1  B
c  c
          06                        ATTCCAGCATTT GAGAT    TGGAATGGAGG
                                   CATCTGCC    CTTTA    ACCTTACCTCC
                                             CG--         T
GAM5227  299   LOC2858 2  4842  XP_212604.1  5  962   CAGTTAAGGCCT   A      ATG          1  B  c
c
          27                        CATCCATCTGAG GAG TCAGATGGA   GAGGCT
                                   CTCTGAAT    CTC AGTCTACCT   CTCCGG
                                             G       A--
GAM5227  299   LOC2858 2  13212 XP_212038.1  5  962   CAGTTAAGGCCC   A      A  A        1  B  c  c

          27                        CATCCATCTGAG GAG TCAGATGGA TGG GGCT
                                   CTCTGAAT    CTC AGTCTACCT ACC CCGG
                                             G       -  -
GAM5227  299   LOC2858 2  13212 XP_212645.1  5  962   CAGTTAAGGCCC   A      A  A        1  B  c  c

          27                        CATCCATCTGAG GAG TCAGATGGA TGG GGCT
                                   CTCTGAAT    CTC AGTCTACCT ACC CCGG
                                             G       -  -
GAM5227  299   LOC2859 1  5526  XP_209833.1  3  407   CCAGGCTGGTCT       A  GA           1  B  c  c

          61                        CCATCACCTGAT GAGATCAG TG  ATGGAGGCT
                                   CTCAGGTG    CTCTAGTC AC  TACCTCTGG
                                             C  --
GAM5227  299   LOC2860 1  17966 XP_212151.1  5  734   ATTGTAGCTGCC G-----  T        A       1  B  c
c
          45                        ATTCCATCTGTT      AGA CAGATGGAATGG GGCT
                                   CTAGGGAG          TCT GTCTACCTTACC TCGA
                                          GAGGGA   T          G
GAM5227  299   LOC2862 1  8321  XP_212230.1  3  1077  TTAGCAACCTTC   AT          C        1  B  c  c
          08                        ATTCCATCTGCC GAG  CAGATGGAATGGAGG
                                   TCCTTCAT    CTC  GTCTACCTTACTTCC
                                             C-           A
GAM5227  299   LOC2862 1  13323 XP_209977.1  5  1645  AAGTGCCTTCCG   AT      -  -        1  B  c  c

          55                        CTTCCATCTGCT GAG  CAGATGGAA TGGA GGC
                                   CCGCCCAG    CTC  GTCTACCTT GCCT CCG
                                             --       C   T
```

GAM5227 299 LOC2863 1 1632 XP_212286.1 5 444 GTGTTTTCCTCC -- A C 1 B c c
54 GTACCATCTGAC GAGA TCAGATGG ATGGAGG
GTTTCTGG CTTT AGTCTACC TGCCTCC
GC A T
GAM5227 299 LOC3386 1 10990 XP_294673.1 3 523 TCCAGGCCACCT AT AT- A 1 B c
c
53 TCTCCATCTGCT GAG CAGATGGA GG GGCT
CACTGAGG CTC GTCTACCT CC CCGG
-- CTT A
GAM5227 299 LOC3396 1 2642 XP_295029.1 5 343 CAGTAAGCATCC - A G 1 B c c
79 ATTCCATTGATA GAG ATCAG TGGAATGGA GCT
TTCGCTAA CTT TAGTT ACCTTACCT CGA
A - A
GAM5227 299 LOC3399 1 11160 XP_291101.1 3 682 CTGACGCCCTCC A T - 1 B c c
83 ATTTCTCTGGCT GAG TCAGA GGAATGGAGG C
CCGGCCCC CTC GGTCT CTTTACCTCC G
- - C
GAM5227 299 LOC3405 1 1223 XP_295260.1 5 91 CCAGGATGGTCT AT A G 1 B c c
04 CGATCCCCTGAT GAGATCAG GGA T GAGGCT
CTCGTGAT CTCTAGTC CCT A CTCTGG
C- - G
GAM5227 299 LOC3483 1 12324 XP_302744.1 3 418 TTTCCAGCCTCC C T AA 1 B c
c
99 AGCCTCTCATTT GAGAT AGA GG TGGAGGCT
CTGGGGCT CTTTA TCT CC ACCTCCGA
C - G-
GAM5227 299 LOC3484 1 6112 XP_302753.1 5 124 ATTGCAGCCTCC AT AT A 1 B c
c
28 ACTTCCTGGGCT GAG CAG GGA TGGAGGCT
CAAGCGAT CTC GTC CTT ACCTCCGA
GG -- C
GAM5227 299 LOC3484 1 9788 XP_046126.4 3 2038 ACTGCTTCCTCA AG AT--- 1 B c
c
77 CATCCATCTGAT G ATCAGATGGA GGAGGC
TGCACCAT C TAGTCTACCT CCTTCG
GT ACACT
GAM5227 299 LOC3489 1 8901 XP_209688.1 3 172 GCCCACAGCCCC G AAT A 1 B c
c
28 TGGTCATCTGAT GA ATCAGATGG GG GGCT
ATCAGAGC CT TAGTCTACT CC CCGA
A GGT -
GAM5227 299 LOC3492 1 8287 XP_300477.1 3 2389 TAAGGGGCCTCC ATC T A 1 B c
c
89 ATCCCTTTTACT GAG AGA GGA TGGAGGCT
CATTTGTA CTC TTT CCT ACCTCCGG
AT- C -
GAM5227 299 LOC3520 1 13440 XP_302245.1 5 34 CAGTGCCCTGGA - AT-- A 1 B c c
27 GTCCTATCTGAT GAGATCAGAT GGA GG GGC

CTCCGGGT CTCTAGTCTA CCT TC CCG
T GAGG -
GAM5227 299 LOC5692 1 14103 NP_064548.1 3 609 CCCACCGCCTCT GA- AT 1 B c c
0 TCTCCATCTGAG GA TCAGATGGA GGAGGC
AATCACGG CT AGTCTACCT TCTCCG
AAG CT
GAM5227 299 LOC9040 1 6783 XP_031517.1 3 741 CGCCCTGCCTCC G GAT -- 1 B c c
8 ATTTACCTTGTG GA ATCA GG AATGGAGGC
ATATCTTA CT TAGT CC TTACCTCCG
A GTT AT
GAM5227 299 LOC9052 1 13508 NP_835223.1 3 874 GAGCTGCCAGGC T-- A-- A 1 B c c
9 TCCTTTTCTGAT GAGATCAGA GGA TGG GGCT
CTCCCAGC CTCTAGTCT CCT ACC TCGA
TTT CGG G
GAM5227 299 LTA 1 16521 NP_000586.2 3 80 CATTCTGCCTCC CAGAT 1 B c c
ATTCTGACCATT GAGAT GGAATGGAGGC
TCAGGGGT CTTTA TCTTACCTCCG
CCAG-
GAM5227 299 LTB4R 1 19312 NP_000743.1 5 345 ACTGCAGCCTCC AT AT A 1 B c c
ACTTCCTGGGTT GAG CAG GGA TGGAGGCT
CACATGAT CTT GTC CTT ACCTCCGA
GG -- C
GAM5227 299 MAP4K2 1 12350 NP_004570.2 3 296 CCTGGGCCATCC AG C - 1 B c c
ATTCCATTTTGT G AT AGATGGAATGGA GGCT
TCCACATT C TG TTTACCTTACCT CCGG
CT T A
GAM5227 299 MCFP 1 906 NP_061331.1 5 44 TACCCCGCCTCC TCA- 1 B c c
ATTCCGTTGCTC GAGA GATGGAATGGAGGC
TCTCAGTC CTCT TTGCCTTACCTCCG
CTCG
GAM5227 299 MDS018 1 3171 NP_068595.2 3 1415 CCAGCAGCCTCC C T AA- 1 B c c
ACAGCCTTTATC GAGAT AGA GG TGGAGGCT
TCAACAGC CTCTA TTT CC ACCTCCGA
- - GAC
GAM5227 299 MGC1416 1 11439 NP_116281.1 5 400 ATCCCAGCCTCC AG T G -- 1 B c c
1 ATTCACCATGTG G A CA ATGG AATGGAGGCT
CTTCCGTG C T GT TACC TTACCTCCGA
CT C G AC
GAM5227 299 MGC1573 1 10025 NP_116269.2 3 112 GTTCTTAGTCTC - T 1 B c c
0 TTTCCATCTGTG GAGAT CAGATGGAA GGAGGCT
TCTTGGCT TTCTG GTCTACCTT TCTCTGA
T -
GAM5227 299 MGC1751 1 4222 NP_689684.1 5 341 GTTTATGCCTCC G C -- --- 1 B c c

```
          5                          ATTGCCCCAGTT  AGAT AGA  TGG   AATGGAGGC
                                     CTTATCTG     TCTA TCT  ACC   TTACCTCCG
                                           G   T  TG   CCG
GAM5227  299   MGC3020 1   3360  NP_076953.2  5  279   GCTCCACATCCT       ATG       C         1  B  c
c
                                     TCATTCACTGAT GAGATCAG   GAATGGAGG
                                     CTCTGGGA    CTCTAGTC   CTTACTTCC
                                              A--        T
GAM5227  299   MGC3113 1   1375  NP_076940.1  3  755   ACTGCAGCCTCC   AT   AT  AA           1  B  c
 c
                                     ACCTCCTGGGCT GAG  CAG  GG  TGGAGGCT
                                     CATGTGAT    CTC  GTC  CC  ACCTCCGA
                                           GG   CT  --
GAM5227  299   MGC3963 1   1566  NP_689762.1  5  17    AGAGCCGCCTCC      G    AT  A          1  B  c
c
          3                          ATGTGGTTTCGG GAGATCA ATGGA  GG GGCT
                                     AGTCGAGG    CTTTGGT TACCT  CC CCGA
                                              G    --  G
GAM5227  299   MI-ER1  1   2832  NP_065999.1  3  3028   CCCTAGACCTCC    T-   TG       -        1  B  c  c
                                     ATTCACTCTGTT GAGA  CAGA  GAATGGAGG CT
                                     TCTCTTCT    CTCT  GTCT  CTTACCTCC GA
                                           TT    CA        A
GAM5227  299   MLLT3   1   16801 NP_004520.1  3  1419   TTTGGTGTCATT    TC         A          1  B  c  c
                                     ATTCCATCTTCT GAGA  AGATGGAATGG GGC
                                     CCATAAGT    CTCT  TCTACCTTATT CTG
                                              --         A
GAM5227  299   MPL     1   8412  NP_005364.1  3  920    GCCAGGATGGTC        GGA  G           1  B  c  c
                                     TCGATATCTGAT GAGATCAGAT   AT GAGGCT
                                     CTCGTGAT    CTCTAGTCTA   TA CTCTGG
                                                 --- G
GAM5227  299   MPRG    1   19256 NP_060175.2  3  1199   CCTATCAGCTTT       A    TG  G         1  B  c
c
                                     GTTTCGCCTGAT GAGATCAG TGGAA  GAG CT
                                     CTCAAGTT    CTCTAGTC GCTTT  TTC GA
                                              C    GT   -
GAM5227  299   MXI1    1   10235 NP_005953.2  3  1171   TTTACCAGCTTT   G       AA           1  B  c  c
                                     TAACCATCTGAT GA ATCAGATGG  TGGAGGCT
                                     ATCTATAG    CT TAGTCTACC  ATTTTCGA
                                           A        A-
GAM5227  299   MXI1    1   10235 NP_569157.1  3  1166   TTTACCAGCTTT   G       AA           1  B  c  c
                                     TAACCATCTGAT GA ATCAGATGG  TGGAGGCT
                                     ATCTATAG    CT TAGTCTACC  ATTTTCGA
                                           A        A-
GAM5227  299   MYLK2   1   8353  NP_149109.1  3  859    GGGGCAGCCTCC    T    GGAA           1  B  c
c
                                     AGTCTGCTCTCA GAGA CAGAT    TGGAGGCT
                                     GCTTGTGC    CTCT GTCTG    ACCTCCGA
                                           C     ----
GAM5227  299   NCOR2   2   18576 NP_006303.1  3  145    GCCTGCGCCTCC  A  T      A           1  B  b
b
```

ATCCATCTGTCC G GA CAGATGGA TGGAGGC
GTCCAGAG C CT GTCTACCT ACCTCCG
- - -

GAM5227 299 NCOR2 2 19433 NP_006303.1 3 145 CGCCTGCGCCTC A T A 1 B b b

CATCCATCTGTC G GA CAGATGGA TGGAGGC
CGTCCAGA C CT GTCTACCT ACCTCCG
- - -

GAM5227 299 NDEL1 1 4770 NP_110435.1 3 586 TAAGCAGCTACC A AG A 1 B c c
ATTCCATGGACT GAG TC ATGGAATGG GGCT
TGCCTCCC TTC AG TACCTTACC TCGA
- G- A

GAM5227 299 NGB 1 16217 NP_067080.1 3 41 CCCGGCAGCCCC G---- - A A 1 B c c
CATCCATCTGTG AGAT CAGATGGA TGG GGCT
TCTGTCTG TCTG GTCTACCT ACC CCGA
GTCTG T - C

GAM5227 299 NME2 1 1264 NP_002503.1 3 78 ACACAGCTCTTC A A - 1 B c c
ATTCCATTGACT GAG TCAG TGGAATGGAG GCT
TAGAGGCA TTC AGTT ACCTTACTTC CGA
- - T

GAM5227 299 NSFL1C 1 15237 NP_061327.2 3 357 GGAGGAAACTTC TC T C 1 B c c

CTTCCATCTTCT GAGA AGATGGAA GGAGG
CTGCATAA CTCT TCTACCTT CCTTC
-- - A

GAM5227 299 P2RX1 1 8598 NP_002549.1 3 348 CCCGCTGCCTCC G----- - T 1 B c c
ATTTCTCTAGAT AGATC AGA GGAATGGAGGC
CTGTGCTC TCTAG TCT CTTTACCTCCG
CTCGTG A -

GAM5227 299 P53AIP1 1 17485 NP_071395.1 3 1296 GAGCAGTCTTCC C-- A - 1 B c c

ATTCCAACTTTA GAGAT AG TGGAATGGAGG CT
GTTTCTGC CTTTG TC ACCTTACCTTC GA
ATT A T

GAM5227 299 PCDHB12 1 7917 NP_061755.1 3 613 GACTTTGCTCCC T - AG 1 B c c

ATTCCATACTGT GAGA CAG ATGGAATGG GC
TTTTGTCA TTTT GTC TACCTTACC CG
T A CT

GAM5227 299 PCMF 1 11762 NP_064507.2 3 2 ATGAGCCTCCAC TC A AA 1 B c c
CACCTCCTCTTT GAGA AG TGG TGGAGGCT
GTGACATC TTCT TC ACC ACCTCCGA
CC C --

GAM5227 299 PCSK7 1 11321 NP_004707.2 3 284 GGTTTGGCCTCC TC - A 1 B c c
ATCCTCATCTCT GAGA AGATG G ATGGAGGCT
CTTGGGCC TTCT TCTAC C TACCTCCGG
C- T C

GAM5227 299 PDK4 1 2181 NP_002603.1 3 290 ATAAGCCTCAGT T TG-- 1 B c c
TTTCCATCTGTT GAGA CAGATGGAA GAGGCT
TTTGATAA TTTT GTCTACCTT CTCCGA

T TTGA

GAM5227 299 PEG10 1 10949 NP_055883.1 3 2236 GTGTCTGCCTCC --- GA- 1 B c c

ATATGCATCTGG GAGAT CAGATG ATGGAGGC

GCATTTCA CTTTA GTCTAC TACCTCCG

CGG GTA

GAM5227 299 PFKFB3 1 2796 NP_004557.1 3 36 CGTGTCGGTTCC C- --- 1 B c c

ATTCCATTTCCA GAGAT AGATGGAATGGA GGC

TTTCTGCA CTTTA TTTACCTTACCT CTG

CC TGG

GAM5227 299 PI4KII 1 11397 NP_060895.1 3 1932 GCCACAGCCTCC AGA AA 1 B c c

ACACCAGATCTC GAGATC TGG TGGAGGCT

CACATTGT CTCTAG ACC ACCTCCGA

--- AC

GAM5227 299 PLXNA2 1 6296 NP_079455.1 3 472 ATTTCTGTCTCC TC T 1 B c c

CTTCCATCTTTT GAGA AGATGGAA GGAGGC

CTCCCATT CTCT TCTACCTT CCTCTG

TT C

GAM5227 299 PODXL 1 15111 NP_005388.1 3 1879 CCTCACAGTCTG G AA G 1 B c c

TAGCCATCTGAT GA ATCAGATGG TG AGGCT

ATCCTAGG CT TAGTCTACC AT TCTGA

A G- G

GAM5227 299 POLE3 1 18239 NP_059139.2 3 1065 CTCCAAAGTGTG T --------- GC 1 B c c

AGTTCCTCTGAT GAGATCAGA GGAA TGGAG

CTCTTGAT CTCTAGTCT CCTT ACCTC

- GAGTGTGAA --

GAM5227 299 POU2F2 1 13248 NP_002689.1 3 177 GTGGCAGCCTCC CAGA - 1 B c c

ATCTCCAGCAAG GAGAT TGGA ATGGAGGCT

TCTCCTGG CTCTG ACCT TACCTCCGA

AACG C

GAM5227 299 PRKR 1 1023 NP_002750.1 5 312 ACTTTAGCAGTT A T G- 1 B c c

CTTCCATCTGAC GAG TCAGATGGAA GGA GCT

TCAGGTTT CTC AGTCTACCTT CTT CGA

- - GA

GAM5227 299 PRO2435 1 18921 NP_060997.1 5 0 GGTTTGCTTTCC GAAT 1 B c c

ATATCTGATCTT GAGATCAGATG GGAGGC

TAATCCAC TTCTAGTCTAT CTTTCG

AC--

GAM5227 299 PROM2 1 11956 NP_653308.1 3 828 ACTGCAGCCTCC AT AT AA 1 B c c

ACCTCCTGGGCT GAG CAG GG TGGAGGCT

CAAGCGAT CTC GTC CC ACCTCCGA

GG CT --

GAM5227 299 PSG7 1 3072 NP_002774.1 3 35 CTAGTTCCTCCA TC - C 1 B c c

ATTCCATCTTCT GAGA AGATGGAAT GGAGG

CCCATGGA CTCT TCTACCTTA CCTCC

```
                                        --      A   T
GAM5227  299   QSCN6  1  11516 NP_002817.2  3 545   TGGCCAGCCTCC   A A T  A-          1  B  c
c
                                AGCTCCTCAGAC GAG TC GA GGA  TGGAGGCT
                                CTCCTGGG    CTC AG CT CCT  ACCTCCGA
                                         C A -  CG
GAM5227  299   RAB17  1  18385 NP_071894.1  3 373   GTGGGAAGATGC        GAATG          1  B  c
c
                                CTTACGTCTGAT GAGATCAGATG    GAGGC
                                CTTGATGG    TTCTAGTCTGC    TTCCG
                                         A----
GAM5227  299   RAMP3  1  7834  NP_005847.1  3 624   CCTGCAGAGTCC G---  -   -       GG     1  B  c
c
                                ATTCCATCATGA    AG ATCA GATGGAATGGA  CT
                                TGCTGTGC       TC TAGT CTACCTTACCT  GA
                                      CGTG  G   A        GA
GAM5227  299   RELN   1  16254 NP_005036.2  3 68    GTGTTGCTCTCC    CA  T      -        1  B  c  c
                                ATTCTTTTAAAT GAGAT  GA GGAATGGAG GC
                                CTCGCACT    CTCTA  TT TCTTACCTC CG
                                         AA  T       T
GAM5227  299   RELN   1  16254 NP_774959.1  3 68    GTGTTGCTCTCC    CA  T      -        1  B  c  c
                                ATTCTTTTAAAT GAGAT  GA GGAATGGAG GC
                                CTCGCACT    CTCTA  TT TCTTACCTC CG
                                         AA  T       T
GAM5227  299   RETNLB 1  1728  NP_115968.1  5 46    GATCTAAGCTGC    TC      T  A         1  B  c  c
                                TTTCCATCTTTT GAGA  AGATGGAA GG GGCT
                                CTCCCAGC    CTCT  TCTACCTT TC TCGA
                                         TT      - G
GAM5227  299   RGS7   1  20171 NP_002915.2  3 193   CTCAATGCCTCC G--   --  A-           1  B  c  c
                                ATTCCAAACTGT   AGAT  CAG  TGGAATGGAGGC
                                TGTCTGCT      TCTG  GTC  ACCTTACCTCCG
                                      TCG   TT   AA
GAM5227  299   RNF24  1  16047 NP_009150.1  3 945   CCTCTCCCCCTC    TC      T    C        1  B  c  c

                                CTTCCATCTCTT GAGA  AGATGGAA GGAGG
                                CTCTCTCT    CTCT  TCTACCTT CCTCC
                                         TC      -   C
GAM5227  299   SCN4A  1  3212  NP_000325.1  3 1921  AGGCCTCCACTC    CA  T  A           1  B  c
c
                                CTTCCATCTCTT GAGAT  GA GGA TGGAGGCT
                                CCTTCAGA    CTCTA  CT CCT ACCTCCGG
                                         C-  T  C
GAM5227  299   SETDB2 1  9368  NP_114121.1  5 322   TTTCCAACCTCC    ---  A-       C     1  B  c  c
                                ATTTCAGCCTGT GAGAT   CAG  TGGAATGGAGG
                                CTGTCTCA    CTCTG   GTC  ACTTTACCTCC
                                         TCT  CG        A
GAM5227  299   SLC13A3 1  18351 NP_073740.2  3 2125  AAGAAAGCCATC G-----     T   T  -     1  B  c
c
                                TCTTCCTCTGAT      AGATCAGA GGAA GGA GGCT
                                CTGGGGTC         TCTAGTCT CCTT TCT CCGA
```

```
                                        CTGGGG      -   C   A
GAM5227  299   SLC17A7 1   4723  NP_064705.1  3  56    TCCAGGACCTCC     C  A        -        1  B  b  b
                                  ATTCCACTCATC GAGAT AG TGGAATGGAGG CT
                                  TCTGGCCT    CTCTA TC ACCTTACCTCC GG
                                        C -         A
GAM5227  299   SLC9A8  1   13104 XP_030524.2  3  853   TCTAGTCGCCTC         AAT          1  B  b  b
                                  CTGCCATCTGAT GAGATCAGATGG   GGAGGC
                                  CTCCCTCC    CTCTAGTCTACC   CCTCCG
                                        GT-
GAM5227  299   SS18    1   5489  NP_005628.1  3  108   AGAGATCCTTCC     C          C        1  B  c  c
                                  ATTCCATCTAGT GAGAT AGATGGAATGGAGG
                                  TTTTGGAA    TTTTG TCTACCTTACCTTC
                                        A           C
GAM5227  299   TCL6    1   13727 NP_055233.1  3  1883  GAGGAGCCCTCC  A  T   A        -        1  B  c  c
                                  ATTCCAATTGTC G GA CAG TGGAATGGAGG CT
                                  CACCCCTT    C CT GTT ACCTTACCTCC GA
                                        - -  A         C
GAM5227  299   TCL6    1   13727 NP_065575.1  3  1050  GAGGAGCCCTCC  A  T   A        -        1  B  c  c
                                  ATTCCAATTGTC G GA CAG TGGAATGGAGG CT
                                  CACCCCTT    C CT GTT ACCTTACCTCC GA
                                        - -  A         C
GAM5227  299   THEA    1   7538  NP_671517.1  3  7     CCCCCAGCCTCC   --- C  T  AA          1  B  c  c
                                  AGACCCTCTAAT GAG   AT AGA GG  TGGAGGCT
                                  GCCCTCAG    CTC   TA TCT CC  ACCTCCGA
                                        CCG  A   C  AG
GAM5227  299   TLE2    1   642   NP_003251.2  5  73    CTTGCCGCCTCC    ATCA     A           1  B  c  c
                                  ATATCATCAAGC GAG    GATGG ATGGAGGC
                                  TCTGGTGG    CTC    CTACT TACCTCCG
                                        GAA-     A
GAM5227  299   TMPRSS3 2   17983 NP_076927.1  3  165   GAAAGAGGCACC  AG       T  AG         1  B
c  c
                                  CTTCCATCTGAT G  ATCAGATGGAA GG  GCT
                                  TCCAGCAC    C  TAGTCTACCTT CC  CGG
                                        CT         - CA
GAM5227  299   TMPRSS3 2   17983 NP_115777.1  3  165   GAAAGAGGCACC  AG       T  AG         1  B
c  c
                                  CTTCCATCTGAT G  ATCAGATGGAA GG  GCT
                                  TCCAGCAC    C  TAGTCTACCTT CC  CGG
                                        CT         - CA
GAM5227  299   TMPRSS3 2   17983 NP_115780.1  3  165   GAAAGAGGCACC  AG       T  AG         1  B
c  c
                                  CTTCCATCTGAT G  ATCAGATGGAA GG  GCT
                                  TCCAGCAC    C  TAGTCTACCTT CC  CGG
                                        CT         - CA
GAM5227  299   TMPRSS3 2   19374 NP_076927.1  3  570   GCCTTTCCCACT         A---  ---       1  B  c  c

                                  GGTCCATCTGGT GAGATCAGATGGA   TGG  AGGC
                                  TTTCTCTC    TTTTGGTCTACCT   ACC  TCCG
                                        GGTC  CTT
GAM5227  299   TMPRSS3 2   19374 NP_115777.1  3  570   GCCTTTCCCACT         A---  ---       1  B  c  c
```

GGTCCATCTGGT GAGATCAGATGGA TGG AGGC
TTTCTCTC TTTTGGTCTACCT ACC TCCG
GGTC CTT
GAM5227 299 TMPRSS3 2 19374 NP_115780.1 3 570 GCCTTTCCCACT A--- --- 1 B c c

GGTCCATCTGGT GAGATCAGATGGA TGG AGGC
TTTCTCTC TTTTGGTCTACCT ACC TCCG
GGTC CTT
GAM5227 299 TNNC1 1 12996 NP_003271.1 3 56 TGCCCAGCCTCC GA A A- 1 B c c

AACTCCAGCTGA GA TCAG TGGA TGGAGGCT
GTCCTGGG CT AGTC ACCT ACCTCCGA
G- G CA
GAM5227 299 TRPS1 1 5417 NP_054831.1 3 3029 ATTAAAGCCTTT TCA 1 B b b
ATTCCATCTCTC GAGA GATGGAATGGAGGCT
AAGATATA CTCT CTACCTTATTTCCGA

GAM5227 299 TSTA3 1 19224 NP_003304.1 3 128 ACCTGGGCCTGC ATCA G 1 B c
c

ATTCCATCCGCT GAG GATGGAATG AGGCT
CTGCAGCC CTC CTACCTTAC TCCGG
GC-- G
GAM5227 299 VCIP135 1 16563 NP_079330.1 3 216 AGTACAGAGCAG AA AG 1 B c
c

TCACCATCTGAT GAGATCAGATGG TGG GCT
CTTCATCA TTCTAGTCTACC ACT CGA
-- GA
GAM5227 299 ZDHHC2 1 8860 NP_057437.1 3 364 TAGAAACTCCAT -- GC 1 B c c
TAATCATCTGAT GAGATCAGATGG AATGGAG
TTTCCGAA TTTTAGTCTACT TTACCTC
AA AA
GAM5227 299 ZNF297B 1 14345 NP_054726.1 3 835 ATTGTAGCCTCC AGA- GA 1 B c
c

ATACAGTGGGGT GAGATC TG ATGGAGGCT
CTTCTCTG TTCTGG AC TACCTCCGA
GGTG A-
GAM5346 319 AKAP11 1 11814 NP_652761.1 3 317 TTTTGAGAAACA T-- TG 3 B c c
CAGGCTTCTATG GAAGTT GAAGCCTGT TTC
ATTTCAGT CTTTAG CTTCGGACA AAG
TAT CA
GAM5346 319 AQP10 1 3157 NP_536354.2 3 80 GCCTGGGAACAA TT AGC 3 B c c

CAGTCATTCTTC GAAG TGA CTGTTGTTC
CTCTTTGT CTTC ACT GACAACAAG
TT ---
GAM5346 319 ARL6IP 1 422 NP_055976.1 3 664 AGGAATGTCTGA A ---- 3 B c c
CAGGCTTAAGCT GAAGTTTGA GCCTGTT GTTC
TTCGTCCC TTTCGAATT CGGACAG TAAG
- TCTG
GAM5346 319 ARNT2 1 12943 NP_055677.1 3 781 GAGCTGGGCTAA TTGA - 3 B c
c

CAGGCTGACACT GAAGT AGCCTGTT GTTCA
TCGGCAGG CTTCA TCGGACAA CGGGT
CAG- T

GAM5346 319 ATRX 1 13943 NP_612115.1 5 857 GCTTGTGGACAA TT A-- 3 B c c
CAGGTCAATCAT GAAG TGA GCCTGTTGTTCA
TTTCAAAA CTTT ACT TGGACAACAGGT
T- AAC

GAM5346 319 BTN2A2 1 2449 NP_008926.2 3 800 ATGGGGACACCA -- T 3 B b b
GTGGCTTCAAAC GAAGTTTGAAGCC TG TGTTC
TTCCTGAT CTTCAAACTTCGG AC ACAGG
TG C

GAM5346 319 BVES 1 7200 NP_009004.2 3 468 ATGAAAAAGCAG AG--- G- 3 B c c
GGAATCTCAAAC GAAGTTTGA CCTGTT TTCA
TTTAT TTTCAAACT GGACGA AAGT
CTAAG AA

GAM5346 319 C1orf17 1 9464 NP_055916.1 3 332 AAGGTTGAACAA AG A - 3 B c c
CATGGCTCAGAG GA TTTGA GCC TGTTGTTCA
TCTTGTTC CT AGACT CGG ACAACAAGT
G- - T

GAM5346 319 C1orf21 1 2690 NP_110433.1 3 381 TAGTGGTGAACT AAGC TT 3 B c
c

CAGATAACAAAC GAAGTTTG CTG GTTCA
TTCCCTTC CTTCAAAC GAC CAAGT
AATA T-

GAM5346 319 C1QDC1 1 6143 NP_115532.1 3 2168 TCTTCTGAACAA GAAG -- 3 B c
c

CTTAGGAGAAAC GAAGTTT CCT GTTGTTCA
TTTTGATC TTTCAAA GGA CAACAAGT
GA-- TT

GAM5346 319 C20orf3 1 9565 NP_060797.1 3 610 GAATCTGAACAA G ------ C 3 B c c
8 CAGTCTTCAGCC AAGTT TGAAG CTGTTGTTCA
CTAGACTT TTCAG ACTTC GACAACAAGT
- ATCCCG T

GAM5346 319 C21orf1 1 13650 NP_620418.1 5 199 CACTGGGAACAA GA----- 3 B c c
09 CAGGTTGCCTTA GAAGTTT AGCCTGTTGTTC
GAAGCTTT TTTCGAA TTGGACAACAAG
GATTCCG

GAM5346 319 C5orf6 1 4877 NP_057689.1 5 116 CTGGAAGAACAA A GAAG 3 B c c
CAGGGAAGACAT GA GTTT CCTGTTGTTC
CCATCATT CT CAGA GGACAACAAG
A AG--

GAM5346 319 CA8 1 2246 NP_004047.3 3 493 TAAGAACAGCAT AAG - -- 3 B c c
AGAGCTTCAAAA G TTTGAAGC CT GTTGTTC
TGCAAAGT C AAACTTCG GA CGACAAG
GTA A TA

GAM5346 319 CAMK2A 1 12760 NP_057065.2 3 3126 AACTTGAATGAA A CT T 3 B c
c

CACTGCTCAAAC GAAGTTTGA GC GT GTTCA
TTTCTGCT TTTCAAACT CG CA CAAGT
- T- -

GAM5346 319 CAMK2A 1 12760 NP_741960.1 3 3126 AACTTGAATGAA A CT T 3 B c c

CACTGCTCAAAC GAAGTTTGA GC GT GTTCA
TTTCTGCT TTTCAAACT CG CA CAAGT
- T- -

GAM5346 319 CARF 1 11378 NP_060102.1 3 92 TAGTATAAAACA --- T C 3 B c c

CAGGCTTTCACA GAAGTTTG AAGCCTGT GTT
AATTTTGT TTTTAAAC TTCGGACA CAA
ACT - A

GAM5346 319 CECR1 1 12603 NP_803124.1 5 37 CCCAGAGAGCAT T TGT 3 B c c

CTGGCTTCAATT GAAG TTGAAGCC TGTTC
TTCCTTTT CTTT AACTTCGG ACGAG
T TCT

GAM5346 319 CGI-141 1 6784 NP_057156.1 3 189 AAGCAGTGAAAA A TT G 3 B c c

CAGGCTTCTACT GA GT GAAGCCTGTT TTCA
CAAGTGAA CT CA CTTCGGACAA AAGT
- T- -

GAM5346 319 CHODL 1 3700 NP_079220.2 3 246 AAAGGATGCACC CC T- - 3 B c c

CAAACTTCAAAC GAAGTTTGAAG TG TGT TC
TTCAAGCA CTTCAAACTTC AC ACG AG
AA CC T

GAM5346 319 CHRNA3 1 15387 NP_000734.2 3 639 GATTATAAACAA GAAGC C 3 B c c

CAGAAACTTCTC GAAGTTT CTGTTGTT
AGTTTTGG CTTCAAA GACAACAA
----- A

GAM5346 319 CHST10 1 14727 NP_004845.1 3 1307 GGAGGAGGGAGC TT TT 3 B c c

CAGGCTTCGCTT GAAGT GAAGCCTG GTTC
CAAGGCGG CTTCG CTTCGGAC CGAG
-- --

GAM5346 319 CLOCK 1 6844 NP_004889.1 3 859 TTATTGATACAA GT-- -- - 3 B c c

CAGGATTTTCAA GAA TTGAAG CCTGTTGT TCA
GTTATTCA CTT AACTTT GGACAACA AGT
ATTG TA T

GAM5346 319 CNOT7 1 12054 NP_473367.1 3 298 CAGGTGAGAAAA TGA G 3 B c c

CAGGCTAATAAC GAAGTT AGCCTGTT TTC
TTCCATGA CTTCAA TCGGACAA AAG
TAA -

GAM5346 319 COL4A3B 1 13701 NP_005704.1 5 180 CGGCTGGAAGGG GTT G 3 B c c

P TAGGCTTCATTC GAA TGAAGCCTGTT TTC
ACCGCTCG CTT ACTTCGGATGG AAG
--- G

GAM5346 319 COL4A3B 1 13701 NP_112729.1 5 180 CGGCTGGAAGGG GTT G 3 B c c

P TAGGCTTCATTC GAA TGAAGCCTGTT TTC
ACCGCTCG CTT ACTTCGGATGG AAG

```
                                                  ---         G
GAM5346  319   COLEC12 1   1211   NP_110408.2  3  270   GTGTTGGGCAGG          TG-           3  B  c  c

                                  GTGGTTTCAAAC GAAGTTTGAAGCC  TTGTTCA
                                  TTCTGGCC    CTTCAAACTTTGG  GACGGGT
                                                TGG
GAM5346  319   COX5B   1   15248  NP_001853.2  5  20    GTCGCGGACGCA     ----      --  T       3  B  c  c
                                  ATGGCTTCAAGG GAAGT   TTGAAGCC  TGT GTTC
                                  TTACTTCG    CTTCA   AACTTCGG  ACG CAGG
                                               TTGG       TA  -
GAM5346  319   COX7A2L 1   14171  NP_004709.2  3  289   GAAGGCTGAACA  A  TG-      T          3  B  c
c
                                  CAGGCTTGTTAA GA GTT   AAGCCTGT GTTCA
                                  TGTCAGTC    CT TAA   TTCGGACA CAAGT
                                             G  TTG      -
GAM5346  319   CRSP3   1   19755  NP_004821.2  3  524   GTAGGAGCAAAC   GTT      -  -         3  B  c  c

                                  AAGGCTTCATAT GAA   TGAAGCCT GTT GTTC
                                  TCTTTTTA    CTT   ACTTCGGA CAA CGAG
                                             AT-       A  A
GAM5346  319   CRYL1   1   18424  NP_057058.1  5  70    CCCATTGAACAA     TTGA  C           3  B  c  c

                                  CAGCTGCTCATT GAAGT    AGC TGTTGTTCA
                                  TCCCCCAG    CTTTA    TCG ACAACAAGT
                                               CTCG   -
GAM5346  319   DDX11   1   13852  NP_004390.2  3  302   ATGGCTGAGAGC    TTT      TT          3  B  c
c
                                  CAGGCTTCCTTC GAAG   GAAGCCTG  GTTC
                                  CTGGTCTC    CTTC   CTTCGGAC  CGAG
                                               ---       --
GAM5346  319   DDX11   1   13852  NP_085911.1  3  302   ATGGCTGAGAGC    TTT      TT          3  B  c
c
                                  CAGGCTTCCTTC GAAG   GAAGCCTG  GTTC
                                  CTGGTCTC    CTTC   CTTCGGAC  CGAG
                                               ---       --
GAM5346  319   DDX11   1   13852  NP_085913.1  3  2442  ATGGCTGAGAGC    TTT      TT          3  B  c
c
                                  CAGGCTTCCTTC GAAG   GAAGCCTG  GTTC
                                  CTGGTCTC    CTTC   CTTCGGAC  CGAG
                                               ---       --
GAM5346  319   DDX56   1   13267  NP_061955.1  3  57    CATTGTGGAGCA    TT  -     T          3  B  c  c
                                  CAGGCTTACACC GAAG  TG AAGCCTGT GTTC
                                  CTTCGTGG    CTTC   AC TTCGGACA CGAG
                                               CC  A      -
GAM5346  319   DKFZp43 1   3872   XP_210937.1  3  1234  CCACCTGAACAA    T  AAG  T          3  B  c
c
          4E1119                    CTGGAGCAACCT GAAG TTG   CC GTTGTTCA
                                  TTAGTCTC    TTTC AAC   GG CAACAAGT
                                               C   GA-  T
GAM5346  319   DKFZP56 1   14703  NP_056438.1  3  2315  AAATGGAGGACA       AA   G          3  B  c
c
```

4D166 GAGGTGACAAAC GAAGTTTG GCCT TTGTTC
TTCAGTTT CTTCAAAC TGGA GACAGG
AG -
GAM5346 319 DKFZp76 1 15142 NP_115663.1 5 139 ACTGCCTGAATA G T 3 B c c
1O17121 CAGGCTTTAGGT GAA TTTGAAGCCTGT GTTCA
TCCCCTGG CTT GGATTTCGGACA TAAGT
- -
GAM5346 319 DMRT1 1 12585 NP_068770.1 3 55 CACTTGGAGTAA TTG-- 3 B c c
CAGGCTTATTCC GAAGT AAGCCTGTTGTTC
ACTTTCCA TTTCA TTCGGACAATGAG
CCTTA
GAM5346 319 EEF1D 1 10991 NP_001951.2 5 66 GGCGTCAGAAAA A T G 3 B c c
ATGGCTACAAAC GAAGTTTG AGCC GTT TTC
TTCCTAGC CTTCAAAC TCGG TAA AAG
A - A
GAM5346 319 EIF4EL3 1 14958 NP_004837.1 5 14 GAGGATGAACAA - G C 3 B c c
CAAGTTCGACGC GAAGT TTGAA C TGTTGTTCA
TTTGA TTTCG AGCTT G ACAACAAGT
C - A
GAM5346 319 FLJ1020 1 19088 NP_060494.1 3 180 ATAAATGAACAA GAAGCC 3 B c
c
4 CATAAAAACTTT GAAGTTT TGTTGTTCA
TGTTTTGA TTTCAAA ACAACAAGT
AAT---
GAM5346 319 FLJ1126 1 5853 NP_062553.1 3 518 CTGCATGAACAA AA- 3 B c c
7 CAGGTAAATAAA GAAGTTTG GCCTGTTGTTCA
TTTTAGAT TTTTAAAT TGGACAACAAGT
AAA
GAM5346 319 FLJ1172 1 11865 XP_044426.1 3 1606 TCAGTGGGGGCA AA - 3 B c c
4 GTCAGGCCAAAC GAAGTTTG GCCTG TTGTTC
TTCTCATT CTTCAAAC CGGAC GACGGG
-- T
GAM5346 319 FLJ1180 1 12794 NP_079100.1 5 236 TCTAGGGAACAA GT GCC 3 B c
c
6 CACAATTCGATT GAA TTGAA TGTTGTTC
CACCGTAT CTT AGCTT ACAACAAG
-- AAC
GAM5346 319 FLJ1229 1 7539 NP_079376.1 3 1047 GGGGTTAGGGCA GCCTG 3 B c
c
4 AAACATTCAAAC GAAGTTTGAA TTGTTC
TTCATCAG CTTCAAACTT AACGGG
ACAA-
GAM5346 319 FLJ1289 1 2301 NP_079226.1 3 1339 CTGGATGAACAA A T AA ------ 3 B c
c
1 CACACTTAGGCC GA GT TG GCCT GTTGTTCA
ACACTCAG CT CA AC CGGA CAACAAGT
- C -- TTCACA
GAM5346 319 FLJ1400 1 9178 NP_078953.2 3 1471 TCAAATAGCACA AG - C 3 B c c
1 CAGGAATCAAAC GAAGTTTGA CCTGT TGTT

TTTGGTAA TTTCAAACT GGACA ACGA
AA C T
GAM5346 319 FLJ1481 1 10584 NP_116234.1 3 1055 TCGCAGGACTGA GAA G TG 3 B c c
6 ATGAAGGCAAAC GAAGTTT GCCT T TTCA
TTCCCAAC CTTCAAA CGGA A AAGT
--- - GT
GAM5346 319 FLJ2020 1 2433 XP_098142.1 3 816 GTCCTTGCACAT A GT T 3 B c c
9 TGGGCTTCAAAC G AGTTTGAAGCCT TGT CA
TCCTCTTC C TCAAACTTCGGG ACA GT
C TT C
GAM5346 319 FLJ2030 1 6291 NP_060223.1 3 878 GCCCCAGAACAA ------ C 3 B c c
0 CAGTTTCACTTT GAAGTT TGAAGC TGTTGTTC
GTGGCTTT TTTCGG ACTTTG ACAACAAG
TGTTTC -
GAM5346 319 FLJ2127 1 15440 NP_079308.1 3 720 TTCTTAGCAACA AGC-- C 3 B c c
2 GAAAAATCAAAC GAAGTTTGA CTGTTGTT
TTCTGTTA CTTCAAACT GACAACGA
AAAAA T
GAM5346 319 FLJ2325 1 19128 NP_079003.1 5 21 TTTGATTGAACA -- -- T 3 B c c
9 CAGGCTTGACAG GAAG TTTG AAGCCTGT GTTCA
AATCTTCT CTTC AGAC TTCGGACA CAAGT
TA AG -
GAM5346 319 FLJ2386 1 11394 NP_689732.1 5 163 CAGCCGATGGAC A TGTT 3 B c c
1 TTGGCTTCAAGC GA GTTTGAAGCC GTTCA
TCAGATTT CT CGAACTTCGG CAGGT
- TT--
GAM5346 319 FLJ2535 1 16387 NP_653188.1 5 72 GATGAGCGCTTC A T--- 3 B c c
9 CAGGCTTCAGGC GA GTTTGAAGCCTG TGTTCA
TCAGAAGG CT CGGACTTCGGAC GCGAGT
- CTTC
GAM5346 319 FLJ3202 1 5186 NP_689893.1 3 2396 AACAACAACATA A--- C- C 3 B c c
8 GCCTAGTCAAAC GAAGTTTGA GC TGTTGTT
TTCTCAGG CTTCAAACT CG ACAACAA
GATC AT C
GAM5346 319 FLJ3294 1 9834 NP_653220.1 5 361 AGATAGTGAAAA TT - G 3 B c c
0 CAGGCTATTGCT GAAG TGA AGCCTGTT TTCA
CTTCCCAT CTTC GTT TCGGACAA AAGT
TC A -
GAM5346 319 FLJ3572 1 14579 NP_689823.1 5 47 AGGGAGGGATGG -- TG 3 B c c
8 CAGGCTTCAGCC GAAGT TTGAAGCCTGT TTC
ACTTCTCC CTTCA GACTTCGGACG AGG
CC GT
GAM5346 319 FLJ3580 1 3807 NP_694589.1 5 270 CTGCCTGGGAAA GTT G 3 B c c
1 CAGGCTTCATTC GAA TGAAGCCTGTT TTCA
AGCACAGC CTT ACTTCGGACAA GGGT
--- A

GAM5346 319 FLJ3657 1 11409 NP_775793.1 3 1627 ACCCTTGAACAA A GA -- 3 B c c 6
CACAGGTTAGAG G AGTTT AGCCTGT TGTTCA
CTGCATAT C TCGAG TTGGACA ACAAGT
G A- CA
GAM5346 319 FLJ3722 1 11241 NP_787113.1 3 752 GTCTTCGGACAA T -- 3 B c c 8
CAGGTAGTTCTA GAAGTT GAA GCCTGTTGTTC
ATTTCTTA CTTTAA CTT TGGACAACAGG
T GA
GAM5346 319 FLJ3730 1 12590 NP_848610.1 3 145 AGCTGTGAACAA GAA- --- 3 B c c 7
CCATGGGCATGA GAAGTTT GCCT GTTGTTCA
AGATTTCT CTTTAGA CGGG CAACAAGT
AGTA TAC
GAM5346 319 FLRT2 1 11704 NP_037363.1 3 2591 TGAACCTAGTAA TT ----- 3 B c c
CAGGCTTTATTT GAAG TGAAGCCTGTT GTTCA
TCACCTTG CTTT ATTTCGGACAA CAAGT
T- TGATC
GAM5346 319 G2 1 13665 XP_039515.8 3 1572 CTGATTAGAAGG - G G G 3 B c c
GGAGGTTCAAAC GA AGTTTGAA CCT TT TTC
TGTCAATG CT TCAAACTT GGA GG AAG
G - G G
GAM5346 319 GPR124 1 6815 NP_116166.6 3 1247 TGGGAAGAACAA AG AAG- 3 B c c
CAGGAAACCAAG GA TTTG CCTGTTGTTC
GTCTGACC CT GAAC GGACAACAAG
G- CAAA
GAM5346 319 GRSF1 1 17530 NP_002083.1 3 1088 TGGACAAAATGG TGA TG- 3 B c c
CTGGCTTCAAAA GAAGTT AGCC TTGTTCA
TATAGTCA CTTCGG TCGG AACAGGT
--- TAA
GAM5346 319 HMG20A 1 1619 NP_060670.1 3 1089 ATGTGAGGAAGA TTT G 3 B c c
CAGGCTTCCCTT GAAG GAAGCCTGTT TTC
CCTTCCCC CTTC CTTCGGACAG AGG
C-- A
GAM5346 319 IARS 1 8969 NP_002152.1 3 5 TGTTACCAACAA AAGC C 3 B c c
CAGCAGACTTCT GAAGTTTG CTGTTGTT
ACATGTAC CTTCAGAC GACAACAA
---- C
GAM5346 319 IARS 1 8969 NP_038203.1 3 5 TGTTACCAACAA AAGC C 3 B c c
CAGCAGACTTCT GAAGTTTG CTGTTGTT
ACATGTAC CTTCAGAC GACAACAA
---- C
GAM5346 319 IL23A 1 15401 NP_057668.1 5 0 AAAACAACAGGA A - ------ C 3 B c c
AGCAGCTTACAA GA GTTTG AAGC CTGTTGTT
ACTCGGTG CT CAAAC TTCG GACAACAA
- A ACGAAG A
GAM5346 319 ITPKB 1 8612 NP_002212.1 3 1009 GCAGGAAGAAGG TT G 3 B c c

CAGGCTTCTGGC GAAGT GAAGCCTGTT TTC
TTCCAGAG CTTCG CTTCGGACGG AAG
GT -
GAM5346 319 JMJD1 1 1010 NP_060903.2 3 44 TGAATTACAGGC -- ----- T 3 B c c
AGCTGTTCAAAC GA AGTTTGAA GCCTGT GTTCA
TCTTCAGG CT TCAAACTT CGGACA TAAGT
TC GTCGA T
GAM5346 319 KCNA3 1 9276 NP_002223.2 3 265 CATTGTAAACAA ---- C C 3 B c c
CAGACTTACGTT GAAGTTTGA AG CTGTTGTT
AAACTTCA CTTCAAATT TC GACAACAA
GCAT A A
GAM5346 319 KIAA021 1 15087 NP_055575.1 3 150 CAAGCGGGTCAT T GT - 3 B c c

8 AAGGCTTCAGCT GAAGTT GAAGCCT TG TTC
TCTGGGTG CTTCGA CTTCGGA AC GGG
- AT T
GAM5346 319 KIAA096 1 5013 XP_290942.1 3 481 AACTCTGAACAA TGAA T--- 3 B c
c
2 CCCACGGCAGCT GAAGTT GCC GTTGTTCA
TCTAGCCC CTTCGA CGG CAACAAGT
---- CACC
GAM5346 319 KIAA155 1 19516 XP_290768.1 3 1970 GCACACAGAAAA TTT A G 3 B c
c
4 CAGGCTCTGCCT GAAG GA GCCTGTT TTC
TCACATGT CTTC CT CGGACAA AAG
CGT - -
GAM5346 319 KIAA167 1 13140 XP_047672.4 3 273 GCTGGAAACCAA AAG G -- 3 B c
c
3 GAGGATCCAAAC GAAGTTTG CCT TTG TTC
TTCCTGCA CTTCAAAC GGA AAC AAG
CTA G CA
GAM5346 319 KIAA199 1 1079 XP_068710.3 3 2638 GGCTATAAAATA -- G C 3 B c c
8 AAGGCTTCAAAT GAAG TTTGAAGCCT TTGTT
TCTTCAAA CTTC AAACTTCGGA AATAA
TT - A
GAM5346 319 LOC1154 2 14698 XP_052510.3 5 251 CACTGCAACAAC AAG- C 3 B c
c
42 AGGAGTGCAAAC GAAGTTTG CCTGTTGTT
TTCTCTAC CTTCAAAC GGACAACAA
GTGA C
GAM5346 319 LOC1154 2 16018 XP_052510.3 5 251 ACACTGCAACAA AAG- C 3 B c
c
42 CAGGAGTGCAAA GAAGTTTG CCTGTTGTT
CTTCTCTA CTTCAAAC GGACAACAA
GTGA C
GAM5346 319 LOC1260 1 10991 XP_058967.6 5 66 GGCGTCAGAAAA A T G 3 B c c

37 ATGGCTACAAAC GAAGTTTG AGCC GTT TTC
TTCCTAGC CTTCAAAC TCGG TAA AAG
A - A

GAM5346 319 LOC1309 1 3929 XP_059490.3 3 1807 GAAACCGAAAAA TT - G 3 B c c
85 CAGGCTTGTGTC GAAG TG AAGCCTGTT TTC
CTTCCATT CTTC GT TTCGGACAA AAG
CT G A
GAM5346 319 LOC1448 1 780 XP_096699.1 5 1018 CACTAGAATACA - C-- T 3 B c c
66 TCAGCTTCAAAC GAA GTTTGAAGC TGT GTTC
ATTCACAA CTT CAAACTTCG ACA TAAG
A ACT -
GAM5346 319 LOC1456 1 16433 XP_035608.1 3 184 CAGAATATACAG AA --- - 3 B c c
44 AAAGCAACAAAC GAAGTTTG GC CTGT TGTTC
TTCGTAAA CTTCAAAC CG GACA ATAAG
AA AAA T
GAM5346 319 LOC1457 1 2737 XP_096860.1 5 423 ACCAAAGGAGCT C TT 3 B c c
86 CAGTTTTCAAAC GAAGTTTGAAG CTG GTTC
TTTAATGG TTTCAAACTTT GAC CGAG
T T-
GAM5346 319 LOC1459 1 11305 NP_612640.1 3 12 AGTCATGAACAA A GA- CC 3 B c
c
57 CACTGAGAAACG GA GTTT AG TGTTGTTCA
TCAAAGTG CT CAAA TC ACAACAAGT
G GAG --
GAM5346 319 LOC1489 1 8659 XP_086361.1 3 83 ACAAGAAAAATA - C- G 3 B c c
18 GTTTTTACAAAC GAAGTTTG AAG CTGTT TTC
TTCTAGTT CTTCAAAC TTT GATAA AAG
A TT A
GAM5346 319 LOC1491 1 11810 XP_097584.1 5 243 AGGAAAAGACAA CC C 3 B c
c
27 TACCCTTCAAAC GAAGTTTGAAG TGTTGTT
TTTGAGAG TTTCAAACTTC ATAACAG
CC A
GAM5346 319 LOC1493 1 16788 XP_086509.1 3 1402 AGAGGCCAAAAC G --- TT 3 B c
c
72 CAGGCTTCAGGT GAA TTTGAAGCCTG TTG C
TCGGGAAG CTT GGACTTCGGAC AAC G
- CAA CG
GAM5346 319 LOC1550 1 10054 XP_098650.3 5 67 ATGCTTGAACCC GA TT 3 B c c
60 CAGGCTTCAGAC AGTTTGAAGCCTG GTTCA
T TCAGACTTCGGAC CAAGT
-- CC
GAM5346 319 LOC1584 1 1358 XP_088580.1 3 127 CATTTTTGAGAA A ---- G 3 B c c
50 CAGGCTTTTGAT GA GTTT GAAGCCTGTT TTCA
AAACTCAC CT CAAA TTTCGGACAA GAGT
- TAGT -
GAM5346 319 LOC1963 1 3387 XP_113696.1 5 4 TTTGAGAAAAGC G TTG- 3 B c c
37 CAGGCTTCAGAG GAA TTTGAAGCCTG TTC
TTCCTGCT CTT AGACTTCGGAC AAG
G CGAA
GAM5346 319 LOC2000 1 11957 XP_114089.3 3 2123 CCAGCGGGGATA -- G 3 B c c

08 GAGGCTTCAAAA GAAGT TTGAAGCCT TTGTTC
GCTTTGAA TTTCG AACTTCGGA GATAGG
AA -
GAM5346 319 LOC2024 1 2543 XP_117401.1 5 862 TCTTTAGAACAG - TGT 3 B c c
51 TGGTTCTCAAAC GAAGTTTGA AGCC TGTTC
TTTAGTAC TTTCAAACT TTGG ACAAG
C TG-
GAM5346 319 LOC2204 1 17554 XP_071675.1 5 1344 CGAGTTGGGACT ---- GTT 3 B c
c
77 AGGGCTTCAATT GAAGT TTGAAGCCT GTTC
TCACTTCT CTTCA AACTTCGGG CAGG
CTTT AT-
GAM5346 319 LOC2547 1 17345 XP_171166.1 3 253 GGATTTGAACAA T A - 3 B c c
19 CATGGTTATAAT GAAG TTG AGCC TGTTGTTCA
TTTCAAAT CTTT AAT TTGG ACAACAAGT
T A T
GAM5346 319 LOC2831 1 18560 XP_210895.1 3 577 ATCGCAGACAGT - - C 3 B c c
19 CAGGCTTCAGGC GA AGTTTGAAGCCTG TTGTT
TGTCTGAC CT TCGGACTTCGGAC GACAG
G T A
GAM5346 319 LOC2833 1 884 XP_211007.1 3 1248 TCCCCTGAACAA - G CCT 3 B c
c
87 CCTCTTGGAACT GA AGTTT AAG GTTGTTCA
CTCCACAT CT TCAAG TTC CAACAAGT
C G TC-
GAM5346 319 LOC2835 1 763 XP_211072.1 3 159 CTTCTAGGACAG AGCC 3 B c c
16 CATTTCTCAAAC GAAGTTTGA TGTTGTTC
TTTAATGT TTTCAAACT ACGACAGG
CTTT
GAM5346 319 LOC2835 1 12590 XP_208705.1 3 145 AGCTGTGAACAA GAA- --- 3 B c
c
21 CCATGGGCATGA GAAGTTT GCCT GTTGTTCA
AGATTTCT CTTTAGA CGGG CAACAAGT
AGTA TAC
GAM5346 319 LOC2838 1 6494 XP_211248.2 5 225 ATCCCCAAACAG GT C 3 B c c
87 TAGGCTTCAGTT GAA TTGAAGCCTGTTGTT
CCCTGCCA CTT GACTTCGGATGACAA
-- A
GAM5346 319 LOC2839 1 1883 XP_208907.1 3 1308 TGCGTGGAGCTG T--- T 3 B c c
25 CAGGCTTCAGCT GAAG TTGAAGCCTGT GTTC
GCCTTCAA CTTC GACTTCGGACG CGAG
CGTC T
GAM5346 319 LOC2840 1 8913 XP_211302.1 3 2112 AGGATGGAGCAA - T 3 B c c
19 TGGTTCTCAAAC GAAGTTTGA AGCC GTTGTTC
TTCAGCCA CTTCAAACT TTGG TAACGAG
C -
GAM5346 319 LOC2841 1 1642 XP_209032.1 3 1323 TTGCTGGAACAA TGA CC 3 B c
c

```
          35                        CAACTGACTTCA GAAGTT  AG  TGTTGTTC
                                   TGATTTGC    CTTCAG  TC  ACAACAAG
                                             --- A-
GAM5346  319   LOC2842 1  1752  XP_211392.1  3  2911  TCTTCATGAATG          G TG          3  B  c  c

          21                        GAGGCTTCAGAT GAAGTTTGAAGCCT T  TTCA
                                   TTTTCTGA    TTTTAGACTTCGGA G  AAGT
                                             - GT
GAM5346  319   LOC2842 1  1292  XP_211402.1  5  1303  AAGATGAGCTGG       A  CC   -          3  B  c
c
          62                        CACTCTGCAAAC GAAGTTTG AG  TGTT GTTCA
                                   TTCTTTAA    CTTCAAAC TC  ACGG CGAGT
                                             G  TC   T
GAM5346  319   LOC2845 1  417   XP_211498.1  5  839   TCAGGTGATGAA    -  ----      GT       3  B  c  c
          06                        CAGGCTGAAATC GAAGT TTGA   AGCCTGTT  TCA
                                   AGTACTTC    CTTCA GACT   TCGGACAA  AGT
                                             T   AAAG       GT
GAM5346  319   LOC2845 1  15471 XP_209254.1  3  601   CACTGTGCAACA   G         T  C        3  B  c  c

          42                        CAGGCTTCAGAT GAA TTTGAAGCCTGT GTT
                                   TCATGTAT    CTT AGACTTCGGACA CAA
                                             -         -  C
GAM5346  319   LOC2845 1  9611  XP_211519.1  5  763   GGTTGAGAACAA  A-     AGC            3  B  c
c
          61                        CAGTCAAACCCT GA  GTTTGA   CTGTTGTTC
                                   CTTCTTCC    CT  CAAACT   GACAACAAG
                                             CC     ---
GAM5346  319   LOC2847 1  10156 XP_211622.1  3  638   CACAGAGCTGGA  A   TG       --         3  B  c
c
          51                        CAGGCTTTGAAC G AGTT  AAGCCTGTT  GTTC
                                   TCCTGGAT    C TCAA  TTCGGACAG  CGAG
                                             C   GT       GT
GAM5346  319   LOC2847 1  16414 XP_208248.1  5  648   AGTGGGTGAGGA  -          G  C        3  B  c
c
          96                        CAGGCTTCAGGC GA AGTTTGAAGCCTGTT TT
                                   TGTCTCTT    CT TCGGACTTCGGACAG AG
                                             G           G  T
GAM5346  319   LOC2848 1  7326  XP_211680.1  3  1697  ATCCAGAGCTAA   GT  GA      -          3  B  c
c
          99                        CAGGCTAAAGTT GAA  TT  AGCCTGTT GTTC
                                   TCCCATTC    CTT  AA  TCGGACAA CGAG
                                             TG  A-       T
GAM5346  319   LOC2849 1  15142 XP_209414.1  5  236   ACTGCCTGAATA   G         T          3  B  c  c
          25                        CAGGCTTTAGGT GAA TTTGAAGCCTGT GTTCA
                                   TCCCCTGG    CTT GGATTTCGGACA TAAGT
                                             -         -
GAM5346  319   LOC2851 1  3929  XP_209508.3  3  1807  GAAACCGAAAAA    TT -      G         3  B  c  c

          92                        CAGGCTTGTGTC GAAG  TG AAGCCTGTT TTC
                                   CTTCCATT    CTTC  GT TTCGGACAA AAG
```

```
                                        CT  G       A
GAM5346  319   LOC2855 1  5061  XP_211930.1  3  54    CATGAATGTACA      --   C  -        3  B  c  c
          35                          AGTTTAGCAAAC GAAGTTTG  AAGC TGT TGTTCA
                                     TTCCTCCT    CTTCAAAC  TTTG ACA GTAAGT
                                           GA   A  T
GAM5346  319   LOC2858 1  8268  XP_209777.1  5  1038  GCTTTAGAGCAG        C TG          3  B  c
c
          22                          TGGTCTTCAAAC GAAGTTTGAAG C  TTGTTC
                                     TTTGAAAG    TTTCAAACTTC G  GACGAG
                                           T GT
GAM5346  319   LOC2858 1  1533  XP_212054.1  3  495   AGGCTGAGGAAA  A    A     G-        3  B  c  c

          57                          CAGGCTCAAACT GA GTTTGA GCCTGTT  TTCA
                                     CAGCTGGT    CT CAAACT CGGACAA  GAGT
                                           -    -     AG
GAM5346  319   LOC3385 1  17259 XP_290465.1  5  1365  CTTTGCAAAGCA     TG     T  C       3  B  c
c
          58                          CAGGCTTAATTT GAAGTT  AAGCCTGT GTT
                                     CATTGCTG    CTTTAA  TTCGGACA CGA
                                           --      -  A
GAM5346  319   LOC3392 1  11810 XP_294874.2  5  243   AGGAAAAGACAA        CC     C       3  B  c
c
          32                          TACCCTTCAAAC GAAGTTTGAAG  TGTTGTT
                                     TTTGAGAG    TTTCAAACTTC  ATAACAG
                                           CC      A
GAM5346  319   LOC3398 1  6647  XP_291028.1  3  311   CAATGGAAGAAC       AGCC-   G        3  B  c
 c
          29                          AAGACATCAAAC GAAGTTTGA    TGTT TTC
                                     TTCGTGAA    CTTCAAACT    ACAA AAG
                                           ACAGA   G
GAM5346  319   LOC3400 1  15029 XP_295148.1  3  170   ATGAGGTTGGAC     ---      GT        3  B  c  c

          74                          AAGGCTTCACAG GAAGTT   TGAAGCCT  TGTTCA
                                     AATTTCTG    CTTTAA   ACTTCGGA  ACAGGT
                                           GAC      --
GAM5346  319   LOC3401 1  16181 XP_295157.1  3  434   CTACAGGAACAA     TTGA  --          3  B  c
c
          13                          CAGATGTTGAGT GAAGT   AGC  CTGTTGTTC
                                     ACTTCTAG    CTTCA   TTG  GACAACAAG
                                           TGAG   TA
GAM5346  319   LOC3436 1  11126 XP_293153.2  5  492   GCACTTTTGAAC       AGCC   --        3  B  c
c
          99                          TTGACATCAAAC GAAGTTTGA   TGTT  GTTCA
                                     TTTCTGAT    TTTCAAACT   ACAG  CAAGT
                                           ----   TT
GAM5346  319   LOC3461 1  11727 XP_294100.1  5  223   CAGTTTGGACAA  AG      - G          3  B  c
c
          78                          GGAGCTTCAAAA GA  TTTGAAGC CT TTGTTCA
                                     CTCGGCCA    CT  AAACTTCG GG AACAGGT
                                           CA      A  -
```

GAM5346 319 LOC3479 1 17961 XP_302628.1 3 314 ATTAGAAGAAAC CC- G- 3 B c c

26 ACACCTTCAAAC GAAGTTTGAAG TGTT TTC
TTCAACTT CTTCAAACTTC ACAA AAG
CAC AG

GAM5346 319 LOC3481 1 1883 XP_300648.1 3 402 TGCGTGGAGCTG T--- T 3 B c c

74 CAGGCTTCAGCT GAAG TTGAAGCCTGT GTTC
GCCTTCAA CTTC GACTTCGGACG CGAG
CGTC T

GAM5346 319 LOC3487 1 10026 XP_300845.1 3 814 GCCAGTGAATGA --- TG 3 B c c

98 CAGGCTTTGAGG GAAGTTT GAAGCCTGT TTCA
AGCTTCTC CTTCGAG TTTCGGACA AAGT
GAG GT

GAM5346 319 LOC3492 1 6413 XP_300476.1 5 449 TTTTAAGAACAA AA C- 3 B c c

88 CAGCCCTTCAGG G GTTTGAAG CTGTTGTTC
CGGCGAAA C CGGACTTC GACAACAAG
GG CC

GAM5346 319 LOC9327 1 4336 XP_050184.1 5 75 CTACCATCAGAA AA G G 3 B c c

3 AAGAGGCCAAAC GAAGTTTG GCCT TT TTC
TTCTATCA CTTCAAAC CGGA AA AAG
-- G -

GAM5346 319 MAGEC3 1 17747 NP_803251.1 5 318 GCTCCTGAACAA A T A 3 B c c

CAGGCCTCATGC GA GT TGA GCCTGTTGTTCA
CTCTCTTT CT CG ACT CGGACAACAAGT
C T C

GAM5346 319 MAP3K7I 1 1518 NP_055908.1 3 1080 CTGACAGAACAA AA - 3 B c c
P2 CAAGGTTAAGCT GAAGTTTG GCCT GTTGTTC
TCATCTGC CTTCGAAT TGGA CAACAAG
-- A

GAM5346 319 MAP3K7I 1 1518 NP_663317.1 3 1761 CTGACAGAACAA AA - 3 B c c
P2 CAAGGTTAAGCT GAAGTTTG GCCT GTTGTTC
TCATCTGC CTTCGAAT TGGA CAACAAG
-- A

GAM5346 319 MCM6 1 7000 NP_005906.2 3 204 TTCATACCAACA - T C 3 B c c
CAGGCTTCAGCA GAAGT TTGAAGCCTGT GTT
CTTCCTTT CTTCA GACTTCGGACA CAA
C - C

GAM5346 319 MECP2 1 17727 NP_004983.1 3 1564 CACCCTGAACAA TT --- C 3 B c c

CGAGCCTTTTCA GAAG TGAA GC TGTTGTTCA
CCCTTCTA CTTC ACTT CG GCAACAAGT
CC TTC A

GAM5346 319 MGC1319 1 14308 NP_116079.1 5 163 CATCCTGGACAA A GAAG 3 B c c

8 CAGGAGTGAAAC G AGTTT CCTGTTGTTCA
TCCGTCTC C TCAAA GGACAACAGGT
C GTGA

GAM5346 319 MGC1638 1 14308 NP_659476.1 3 681 CATCCTGGACAA A GAAG 3 B c c

5 CAGGAGTGAAAC G AGTTT CCTGTTGTTCA
TCCGTCTC C TCAAA GGACAACAGGT
C GTGA

GAM5346 319 MGC3476 1 1883 NP_775890.1 3 1136 TGCGTGGAGCTG T--- T 3 B c c

1 CAGGCTTCAGCT GAAG TTGAAGCCTGT GTTC
GCCTTCAA CTTC GACTTCGGACG CGAG
CGTC T

GAM5346 319 MGC4572 1 10845 NP_689777.1 5 20 AGTAACTTCATG A CCTGT 3 B c c

6 AATACTACAAAC GAAGTTTG AG TGTTCA
TTCCAGTC CTTCAAAC TC ATAAGT
A -----

GAM5346 319 MGC5528 1 600 NP_076999.1 3 25 CTTAAAGAACAA TTT C 3 B c c
CAGTCTTTTCTT GAAG GAAG CTGTTGTTC
CAGGACTC CTTC TTTC GACAACAAG
T-- T

GAM5346 319 MI-ER1 1 3518 NP_065999.1 3 1264 GTGAAGTTTGAA CCT G 3 B c c

AACTTTTCAAAC GAAGTTTGAAG GTT TTCA
TTTTCTAG TTTCAAACTTT CAA AAGT
T-- -

GAM5346 319 MME 1 4799 NP_000893.1 3 1656 CTCCCAGAACAA T- - CC 3 B c c
CAACTATCCTGA GAAGTT GA AG TGTTGTTC
CTTCTAAT CTTCAG CT TC ACAACAAG
TC A A-

GAM5346 319 MME 1 4799 NP_009218.1 3 1656 CTCCCAGAACAA T- - CC 3 B c c
CAACTATCCTGA GAAGTT GA AG TGTTGTTC
CTTCTAAT CTTCAG CT TC ACAACAAG
TC A A-

GAM5346 319 MME 1 4799 NP_009219.1 3 1656 CTCCCAGAACAA T- - CC 3 B c c
CAACTATCCTGA GAAGTT GA AG TGTTGTTC
CTTCTAAT CTTCAG CT TC ACAACAAG
TC A A-

GAM5346 319 MME 1 4799 NP_009220.1 3 1656 CTCCCAGAACAA T- - CC 3 B c c
CAACTATCCTGA GAAGTT GA AG TGTTGTTC
CTTCTAAT CTTCAG CT TC ACAACAAG
TC A A-

GAM5346 319 MYF5 1 4931 NP_005584.1 3 70 CACAGGACGAAG AG- G-- 3 B c c
AAGGCTTCAAAA GA TTTGAAGCCT TTGTTC
AGTCCCAA CT AAACTTCGGA AGCAGG
GAA AGA

GAM5346 319 NOTCH2 1 5941 NP_077719.2 3 2486 GGAGGACAACAC -- C- 3 B c c

TGCCTTTCAAAC GAAGTTTGAA GC TGTTGTTC
TTTTTACT TTTCAAACTT CG ACAACAGG
TC TC

GAM5346 319 NSE1 1 7984 NP_660158.1 3 1163 CCATTTTAGCAA GA-- C 3 B c c

CAGGCTAATAAA GAAGTTT AGCCTGTTGTT
ATTTCAAA CTTTAAA TCGGACAACGA
ATAA T

GAM5346 319 NYD-SP1 1 17669 NP_114162.1 5 0 GGGGGAGCCAGG AG TT 3 B c c

4 CTTCGGAATCAC GA TTTGAAGCCTG GTTC
TGAGAGAG CT AGGCTTCGGAC CGAG
A- --

GAM5346 319 OTX3 1 7260 NP_671725.1 3 1317 AGCACATAGGCT A - C 3 B c c
CAGGCTTCTGTA GAAGTTTGA GCCTGT TGTT
GGCTTCCT CTTCGGACT CGGATA ACGA
- C -

GAM5346 319 OTX3 1 7260 NP_757379.1 3 1317 AGCACATAGGCT A - C 3 B c c
CAGGCTTCTGTA GAAGTTTGA GCCTGT TGTT
GGCTTCCT CTTCGGACT CGGATA ACGA
- C -

GAM5346 319 PANK2 1 15989 NP_705903.1 3 430 CCAGGCTGGGCT TGTT 3 B c c

GTGGCTTCAAGC GAAGTTTGAAGCC GTTCA
TTTGGAAA TTTCGAACTTCGG CGGGT
TGT-

GAM5346 319 PSMD8 1 19154 NP_002803.1 5 24 TGAACGGGGCGG A -- 3 B c c
CAGGCTTCTCGA G AGTTTGA AGCCTGTTGTTC
GCTCCGGG C TCGAGCT TCGGACGGCGGG
C CT

GAM5346 319 PTBP1 1 18181 NP_002810.1 3 1007 CGCCTAGAAAAC - CT G 3 B c c

TTGCTCTCAAAC GAAGTTTGA AGC GTT TTC
TTCAGGGT CTTCAAACT TCG CAA AAG
C TT -

GAM5346 319 PTBP1 1 18181 NP_114367.1 3 1007 CGCCTAGAAAAC - CT G 3 B c c

TTGCTCTCAAAC GAAGTTTGA AGC GTT TTC
TTCAGGGT CTTCAAACT TCG CAA AAG
C TT -

GAM5346 319 PTBP1 1 18181 NP_114368.1 3 1006 CGCCTAGAAAAC - CT G 3 B c c

TTGCTCTCAAAC GAAGTTTGA AGC GTT TTC
TTCAGGGT CTTCAAACT TCG CAA AAG
C TT -

GAM5346 319 PTBP1 1 18181 NP_787041.1 3 1007 CGCCTAGAAAAC - CT G 3 B c c

TTGCTCTCAAAC GAAGTTTGA AGC GTT TTC
TTCAGGGT CTTCAAACT TCG CAA AAG
C TT -

GAM5346 319 PTGIS 1 9392 NP_000952.1 3 3878 CAGATGGAGAAA GA- G 3 B c c
CAGGCTCTGAGA GAAGTTT AGCCTGTT TTC
TTTCACAG CTTTAGA TCGGACAA GAG
GTC A

GAM5346 319 SH3YL1 1 16719 NP_056492.1 3 274 AGTTCTCTTGTG A CCTGT 3 B c c

AACACTTCAAAC GA GTTTGAAG TGTTCA
ATCGCTAA CT CAAACTTC ACAAGT
A -----

GAM5346 319 SIRPB2 1 17134 NP_061026.1 5 10 GTTTGAACAGAG AG T -- 3 B c c
CAGGCTTCTGAG GA TT GAAGCCTGT TGTTCA
GTCTCCAA CT AG CTTCGGACG ACAAGT
GG T AG

GAM5346 319 SIRPB2 1 17134 NP_543006.1 5 10 GTTTGAACAGAG AG T -- 3 B c c
CAGGCTTCTGAG GA TT GAAGCCTGT TGTTCA
GTCTCCAA CT AG CTTCGGACG ACAAGT
GG T AG

GAM5346 319 TERF2 1 2418 NP_005643.1 3 17 GCATGAACTGAA TT -- 3 B c c
CAGGCTTTCATT GAAGT GAAGCCTGTT GTTCA
TCCACAGA CTTTA TTTCGGACAA CAAGT
C- GT

GAM5346 319 TRAD 1 2049 NP_008995.1 3 981 TCCTATGAACAA - AA CT 3 B c c
CGTACCAACACT GAAGT TTG GC GTTGTTCA
TTCTGATT TTTCA AAC TG CAACAAGT
C CA --

GAM5346 319 USP24 1 17338 XP_165973.3 3 1672 AACGGACAGAGG AA---- G 3 B c
c
CGAGTGGCAAAC GAAGTTTG GCCT TTGTTC
TTCAGACG CTTCAAAC CGGA GACAGG
GGTGAG -

GAM5346 319 ZNF254 1 9378 NP_004867.1 3 254 CAGTGTGAACAA AA - 3 B b b
CGTGGCCAAGCT GAAGTTTG GCC TGTTGTTCA
TCGACAAT CTTCGAAC CGG GCAACAAGT
-- T

GAM5346 319 ZNF255 1 2601 NP_005765.1 5 1016 TAACACTGAACA AGTT G 3 B c
c
AAGGCTTCACTT GA TGAAGCCT TTGTTCA
GTCCTCAT CT ACTTCGGA AACAAGT
GTTC -

GAM5346 319 ZNF431 1 9162 XP_086098.2 3 476 ACTACTTTTGAC A CT C 3 B c c
AACGCCTCAAAC GAAGTTTGA GC GTTGTT
TTTTCTAA TTTCAAACT CG CAACAG
C -- T

GAM5385 218 ABLIM1 1 16103 NP_002304.2 3 4264 TAGAAGAAAGAG C CCGG 6 A c
c
AAACCTTCACTT TCA AGTGAA TCTCTTTC
TGGCATTT GGT TCACTT AGAGAAAG
T CCAA

GAM5385 218 ABLIM1 1 16103 NP_006710.2 3 4264 TAGAAGAAAGAG C CCGG 6 A c
c
AAACCTTCACTT TCA AGTGAA TCTCTTTC
TGGCATTT GGT TCACTT AGAGAAAG
T CCAA

GAM5385 218 ABLIM1 1 16103 NP_006711.2 3 4264 TAGAAGAAAGAG C CCGG 6 A c
c
AAACCTTCACTT TCA AGTGAA TCTCTTTC

TGGCATTT GGT TCACTT AGAGAAAG
T CCAA
GAM5385 218 ACAA2 1 10451 NP_006102.1 3 24 CCTGAGAGACCA ---- C T 6 A c c
GTGAGCTCACTG TCACAGTGA AC GGTCTCTT
TGACCCAT AGTGTCACT TG CCAGAGAG
CGAG A T
GAM5385 218 AD-020 1 16382 NP_064526.1 3 1821 AACAGGAAAGAG -- - CGG 6 A c
c
AGTTACACCTTG TCACA GTG AAC TCTCTTTC
TGGGTGTG GGTGT CAC TTG AGAGAAAG
TC A ---
GAM5385 218 ALOX15B 1 5527 NP_001132.1 3 442 GCTGCCAAAGAG A AA 6 A c
c
ACTGGGCGCAGT TCAC GTG CCGGTCTCTTT
GGCTCATG GGTG CGC GGTCAGAGAAA
A G-
GAM5385 218 AP1GBP1 1 14123 NP_009178.2 3 738 CAAAAGAAAGAG C ACC 6 A c
c
ACTTCATTTGGC TCA AGTGA GGTCTCTTTC
AGTTCTGA GGT TTACT TCAGAGAAAG
- ---
GAM5385 218 AP1GBP1 1 14123 NP_542117.1 3 738 CAAAAGAAAGAG C ACC 6 A c
c
ACTTCATTTGGC TCA AGTGA GGTCTCTTTC
AGTTCTGA GGT TTACT TCAGAGAAAG
- ---
GAM5385 218 AP1GBP1 1 14123 NP_542118.1 3 600 CAAAAGAAAGAG C ACC 6 A c
c
ACTTCATTTGGC TCA AGTGA GGTCTCTTTC
AGTTCTGA GGT TTACT TCAGAGAAAG
- ---
GAM5385 218 APTX 1 9973 NP_060162.1 5 424 GAAGAGAAAGAG A GAA - 6 A c c
ATCAGGCAACAG TCAC GT CC GGTCTCTTTC
TGATTCTA AGTG CA GG CTAGAGAAAG
A AC- A
GAM5385 218 APTX 1 9973 NP_778241.1 5 244 GAAGAGAAAGAG A GAA - 6 A c c
ATCAGGCAACAG TCAC GT CC GGTCTCTTTC
TGATTCTA AGTG CA GG CTAGAGAAAG
A AC- A
GAM5385 218 ARHE 1 5435 NP_005159.1 3 460 GTCCTCAAGGGG AA - 6 A c c
GAACTGGCACTG TCACAGTG CCGGT CTCTTT
TGACCTTA AGTGTCAC GGTCA GGGGGA
-- A
GAM5385 218 ARHGEF4 1 15522 NP_056135.2 3 859 CATAAGAGAGAG TGAAC 6 A
c c
ACCGAATTCTGT TCACAG CGGTCTCTTTC
GGCTCAGC GGTGTC GCCAGAGAGAG
TTAA-
GAM5385 218 ARHGEF4 1 15522 NP_127462.1 3 1510 CATAAGAGAGAG TGAAC 6 A
c c

ACCGAATTCTGT TCACAG CGGTCTCTTTC
GGCTCAGC GGTGTC GCCAGAGAGAG
TTAA-
GAM5385 218 ARL8 1 13890 NP_848930.1 3 32 TGCTTGAAAGAG T -- C---- 6 A c c
ACTGCTCTATTT CACAG TGAA CGGTCTCTTTC
ATTCTGTG GTGTC ATTT GTCAGAGAAAG
- TT ATCTC
GAM5385 218 ARL8 1 13890 XP_167671.1 3 32 TGCTTGAAAGAG T -- C---- 6 A c c
ACTGCTCTATTT CACAG TGAA CGGTCTCTTTC
ATTCTGTG GTGTC ATTT GTCAGAGAAAG
- TT ATCTC
GAM5385 218 ATRN 1 14810 NP_647537.1 3 315 TAGGAATGACAC -- C - 6 A c c
TCAGGTTCACTG TCACAGTGAACC GGT TC TTTC
TGGAAAAC GGTGTCACTTGG TCA AG AAGG
AC C T
GAM5385 218 BRRN1 1 8848 NP_056156.2 3 13 TGAGGCAAGGAG C 6 A c c
ATTGGTTCACTA TCA AGTGAACCGGTCTCTTT
TGGAGAAG GGT TCACTTGGTTAGAGGAA
A
GAM5385 218 C20orf1 1 1219 NP_689515.1 3 963 AATGAGACAGGA C TC T 6 A c c
58 AGCTGTTCACTG TCACAGTGAA CGG TCTT
TGAAACAG AGTGTCACTT GTC AGGA
- GA C
GAM5385 218 C20orf1 1 13482 XP_066058.2 3 512 CTTGACAAAGAG GTGAA G 6 A c
c
74 ACGGGGGTGTGA TCACA CC GTCTCTTT
ACTGGGCA AGTGT GG CAGAGAAA
GG--- G
GAM5385 218 C21orf9 1 4794 NP_660162.1 3 52 ACCGTGGAGAGG CCG 6 A c c
3 AGGCATTCACTG TCACAGTGAA GTCTCTTT
TGGGGTGT GGTGTCACTT CGGAGGAG
A--
GAM5385 218 CEACAM8 1 3579 NP_001807.2 3 499 TTTAGTAGAGAC -- G TT 6 A c
c
GGGGTTTCACTG TCACAGTGAA CC GTCTCT
TGGTCTCA GGTGTCACTT GG CAGAGA
TG G TG
GAM5385 218 CG012 1 19634 XP_096710.1 5 1420 TGACCAAAAGAG C T C- 6 A c c
ACCTTGTTTTCT TCA AG GAAC GGTCTCTTT
TTGAGAAG AGT TC TTTG CCAGAGAAA
T T TT
GAM5385 218 CISH 1 2516 NP_037456.4 3 846 ATCTGCATAGAG - T TT 6 A c c
CTGGTCTCACTG TCACAGTGA ACCGG CTCT
TGGCGCAG GGTGTCACT TGGTC GAGA
C - TA
GAM5385 218 CISH 1 2516 NP_659508.1 3 846 ATCTGCATAGAG - T TT 6 A c c
CTGGTCTCACTG TCACAGTGA ACCGG CTCT
TGGCGCAG GGTGTCACT TGGTC GAGA
C - TA

GAM5385 218 CLONE24 1 19577 NP_056498.1 3 378 CCAGAAGAAGAG GAACC 6 A c c
945 ACCTGCAACTGT TCACAGT GGTCTCTTT
GAGAGTCC AGTGTCA CCAGAGAAG
ACGT-
GAM5385 218 CSF1 1 13158 NP_000748.3 3 812 CTCATGAAGGAA AACC TC 6 A c c
GCCATTGCACTG TCACAGTG GG TCTTTC
TGAACACT AGTGTCAC CC AGGAAG
GTTA GA
GAM5385 218 CSF1 1 13158 NP_757350.1 3 812 CTCATGAAGGAA AACC TC 6 A c c
GCCATTGCACTG TCACAGTG GG TCTTTC
TGAACACT AGTGTCAC CC AGGAAG
GTTA GA
GAM5385 218 DDO 1 6520 NP_003640.1 3 41 GACAGCAAAGAG - GAAC 6 A c c
ACTGAGAGACTG TCA CAGT CGGTCTCTTT
TTGATCAA AGT GTCA GTCAGAGAAA
T GAGA
GAM5385 218 DDO 1 6520 NP_004023.1 3 41 GACAGCAAAGAG - GAAC 6 A c c
ACTGAGAGACTG TCA CAGT CGGTCTCTTT
TTGATCAA AGT GTCA GTCAGAGAAA
T GAGA
GAM5385 218 DISC1 1 8442 NP_061132.1 3 3956 CACACTGCCAGG ACC T 6 A c c
GGAGCCTCACTG TCACAGTGA GG CTCTTT
TGAAGTCT AGTGTCACT CC GAGGGG
--- -
GAM5385 218 DKFZP56 1 775 NP_056438.1 5 145 CAAACCAAAGAG A G C 6 A c c
4D166 ACCGTTCGTGGA TC CA TGAAC GGTCTCTTT
GTCTAATG AG GT GCTTG CCAGAGAAA
- - -
GAM5385 218 DKFZP58 1 12685 NP_054752.1 3 214 AGACAGGGAGAC T----- - G- 6 A c c
6A0522 AGGGTCTCACTG CACAGTGA ACC GTCTCTTT
TGTTGCCT GTGTCACT TGG CAGAGGGA
TCCGTT C GA
GAM5385 218 DNAJC5 1 5877 XP_028966.2 3 1948 TGACAAGAGGAG AACCG 6 A c c
AGATATGCACTG TCACAGTG GTCTCTTT
TGATATTA AGTGTCAC TAGAGAGG
GTA--
GAM5385 218 DOT1L 1 13923 NP_115871.1 3 138 CAAGGACGGACG AA--- G -- 6 A c c
GGAGCTCCACTG TCACAGTG CC GTC TCTTT
TGAATCGG AGTGTCAC GG CAG AGGAA
CTCGA G GC
GAM5385 218 DUSP16 2 10606 XP_039106.1 5 448 AAAGAGAAAGAG C CCG 6 A c c
ACATTCACTTGG TCA AGTGAA GTCTCTTTC

AGGGCTCT GGT TCACTT CAGAGAAAG
- A--
GAM5385 218 DUSP16 2 19356 XP_039106.1 5 445 AACGGGAAAGAG C CCG 6 A c c
AAAGAGACATTC TCA AGTGAA GTCTCTTTC
ACTTGGAG GGT TCACTT CAGAGAAAG
- A--
GAM5385 218 DYRK2 1 19011 NP_003574.1 3 907 TACAGAAAAGAG - CCG 6 A c c
ACATTTCAGCTG TCACAG TGAA GTCTCTTT
TGATTATG AGTGTC ACTT CAGAGAAA
G TA-
GAM5385 218 DYRK2 1 19011 NP_006473.1 3 907 TACAGAAAAGAG - CCG 6 A c c
ACATTTCAGCTG TCACAG TGAA GTCTCTTT
TGATTATG AGTGTC ACTT CAGAGAAA
G TA-
GAM5385 218 EGFL4 1 14183 XP_290821.1 3 1526 GGCTTCAGAGAG AACCGG 6 A c c
GGAGAAGCACTG TCACAGTG TCTCTTTC
TGAGGCCT AGTGTCAC AGAGGGAG
GA----
GAM5385 218 EPB49 1 11878 NP_001969.1 5 30 AGAGAGGGCCAG AA---- - T 6 A c c
GCAGTCGCACTG TCACAGTG CC GGTC CTTTC
TGAACAGA AGTGTCAC GG CCGG GAGAG
GCTGAC A -
GAM5385 218 ERG-1 1 13141 NP_071317.2 5 151 GTTGGGGAGAGA ACC - 6 A c c
GAACCCTCACTG TCACAGTGA GGT CTCTTTC
TGGGGAAT GGTGTCACT CCA GAGAGAG
C-- A
GAM5385 218 FBLN1 2 12051 NP_006478.1 3 392 CCGAAAGCCTAG AAC TT 6 A c c
AGACCGCCACTG TCACAGTG CGGTCTCT
TGATTCAC AGTGTCAC GCCAGAGA
C-- TC
GAM5385 218 FBLN1 2 16278 NP_006478.1 3 392 GAAAGCCTAGAG AAC TT 6 A c c
ACCGCCACTGTG TCACAGTG CGGTCTCT
ATTCACCT AGTGTCAC GCCAGAGA
C-- TC
GAM5385 218 FCGR1A 1 11092 NP_000557.1 3 776 CACTGCAAAGAG AG C G 6 A c c
ACGCTTCAAGTG TCAC TGAA CG TCTCTTT
GGGAGAAG GGTG ACTT GC AGAGAAA
A- C -
GAM5385 218 FGFR1 1 4651 NP_000595.1 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G

GAM5385 218 FGFR1 1 4651 NP_056934.2 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075593.1 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075594.1 5 659 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075595.1 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075596.1 5 648 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075597.1 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075598.1 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FGFR1 1 4651 NP_075599.1 5 649 TGAAAAGGAGGA AC- - 6 A c c
TCGAGCTCACTG TCACAGTGA CGGTC TCTTT
TGGAGTAT GGTGTCACT GCTAG AGGAA
CGA G
GAM5385 218 FLJ1042 1 14824 NP_060560.1 3 673 GGCCTCTGAAGG ACC 6 A c c
0 GATTCCTCACTG TCACAGTGA GGTCTCTTT
TGGGCAGC GGTGTCACT TTAGGGAAG
CC-
GAM5385 218 FLJ1070 1 11748 NP_060656.1 5 159 AAGTTGGATTGA CCG T TT 6 A c
c
6 GCATATTCACTG TCACAGTGAA G CTC TC
TGAAATTA AGTGTCACTT C GAG AG
ATA - TT
GAM5385 218 FLJ1091 1 13403 NP_060741.1 5 204 AGAAGAGGGAGA ACCGG- 6 A c
c
6 AGCACGTCACTG TCACAGTGA TCTCTTTC
TGGTTGTA GGTGTCACT AGAGGGAG
GCACGA
GAM5385 218 FLJ1180 1 1416 NP_079250.1 3 1048 GTGTTTAGAAGT ACCGG - 6 A c
c
0 AGGAAGTCACTG TCACAGTGA TCT CTTT

TGAGCAAT AGTGTCACT GGA GAAG
GAA-- T
GAM5385 218 FLJ2018 1 17813 NP_060170.1 3 579 TCTAGAGGAAGT CC - - 6 A c c
4 ATCTATTCACTG TCACAGTGAA GGT CT CTTT
TGAAAATC AGTGTCACTT CTA GA GGAG
AT T A
GAM5385 218 FLJ2046 1 17685 NP_060304.1 3 377 ACAAAGAAAGAG A AA 6 A c c
4 AAAGGGGCCGGG TCAC GTG CCGGTCTCTTTC
CGCGGTGG GGTG CGC GGCCGGGGAAAG
G G-
GAM5385 218 FLJ2249 1 4622 NP_079091.1 5 344 GAAGGAGGAGGC AA-- G 6 A c c
4 GGGGCTGCACTG TCACAGTG CC GTCTCTTTC
TGAGCCCG AGTGTCAC GG CGGAGGAGG
GTCG G
GAM5385 218 FLJ3211 1 10311 NP_694580.1 3 299 GTGAAAGGGTGA -- GT- 6 A c c
2 TGGATTTCACTG TCACAGTGAA CCG CTCTTTC
TGAATATG AGTGTCACTT GGT GGGAAAG
TA AGT
GAM5385 218 FLJ3211 1 6946 NP_689534.1 3 342 ATCAAGGCTTTA ACCG T 6 A c c
5 AGAGACTCACTG TCACAGTGA GTCTCTT
TGATGCCT AGTGTCACT CAGAGAA
---- T
GAM5385 218 FTSJ2 1 3879 NP_803191.1 3 1193 AGTACCACGGAA AA GG T 6 A c
c
GGAAGGGCACTG TCACAGTG CC TC CTTTC
TGAAGCAG AGTGTCAC GG AG GAAGG
G- A- -
GAM5385 218 G2 1 15665 XP_039515.8 3 769 TAACTGAAAGAG AC GA - 6 A c c
AATCGGTGCTAA TC AGT ACCGGT CTCTTTC
GAGCTTTT AG TCG TGGCTA GAGAAAG
AA -- A
GAM5385 218 GPT2 1 12001 NP_597700.1 3 1860 TTTTAAAAAGAG C AAC- 6 A c c
ACTGTATACACT TCA AGTG CGGTCTCTTT
TGATTTGC AGT TCAC GTCAGAGAAA
- ATAT
GAM5385 218 GRHPR 1 3593 NP_036335.1 5 36 ACTGCGGATGAG C- GA- T 6 A c
c
ACCGGTGCGACT TCA AGT ACCGGTCTC TTC
CATGAAGG AGT TCA TGGCCAGAG AGG
AC GCG T
GAM5385 218 GRID1 1 9369 XP_043613.8 3 2354 TAGAGAAAAGAG C C- 6 A c c
ACCATGTTTATT TCA AGTGAAC GGTCTCTTT
TGGGTAGG GGT TTATTTG CCAGAGAAA
- TA
GAM5385 218 H-plk 1 8719 NP_056936.1 5 783 ACTGGATGAGAT --- G T 6 A c c
GGTATCTCACTG TCACAGTGA ACCG TCTC TTC
TGGTTTTT GGTGTCACT TGGT AGAG AGG
CTA - T

GAM5385 218 HGC6.2 1 11193 NP_055171.1 3 477 GCTGTGAAAGAG TGAACCG 6 A c c
ATCTGTGACCTT TCACAG GTCTCTTTC
GCACCCTG AGTGTC TAGAGAAAG

GAM5385 218 HLA-G 1 17163 NP_002118.1 3 351 TGTTTAAAGTGT ACC CT-- 6 A c c
CACCCCTCACTG TCACAGTGA GGT CTTT
TGACTGAT AGTGTCACT CCA GAAA
CC- CTGT
GAM5385 218 IRF4 1 2090 NP_002451.1 3 2884 AACTAAAAAGAG A AAC 6 A c c
ACTGTGCCATGG TCAC GTG CGGTCTCTTT
TGAGAAAA AGTG TAC GTCAGAGAAA
G CGT
GAM5385 218 ITGAL 1 16142 NP_002200.1 5 88 GGATGAAGGATT ACC- TC 6 A c c
CCTGCATCACTG TCACAGTGA GG TCTTTC
TGA AGTGTCACT CC AGGAAG
ACGT TT
GAM5385 218 KIAA031 1 14991 NP_055636.1 3 1184 GGAGGAAGCTTA - ----- TC 6 A c c
7 TTAGGTTCACTG TCA CAGTGAACC GG TCTTTC
TTGAATGA AGT GTCACTTGG TC AGGAGG
T ATTAT GA
GAM5385 218 KIAA035 1 18577 NP_055645.1 3 405 GGAGGTAAAGGG -- GG 6 A c c
2 AGGTTTTCACTG TCACAGTGA ACC TCTCTTT
TGGGTGTT GGTGTCACT TGG AGGGAAA
TT --
GAM5385 218 KIAA051 1 1534 NP_055511.1 3 3271 AAGCAGGGATGG - C - 6 A c c
4 CCTGTTCCACTG TCACAGTG AAC GGTC TCTTT
TGATCTTA AGTGTCAC TTG CCGG AGGGA
C T T
GAM5385 218 KIAA072 1 4456 NP_067680.2 3 1482 AGCTGGAAAGAG A A- GG 6 A c c
1 AGAGAAGGGCCT TCAC GTGA CC TCTCTTTC
CACAGTGA AGTG CACT GG AGAGAGAG
A CC GA
GAM5385 218 KIAA087 1 10335 XP_290852.1 3 590 GCAGGGAAAGAG A GA - 6 A c c
6 ACCCGGTAATTG TC CAGT ACCGG TCTCTTTC
GAGGGTGA AG GTTA TGGCC AGAGAAAG
- A- C
GAM5385 218 KIAA097 1 10280 NP_055745.1 3 126 AGTCCCAGAAGT ACC CT- 6 A c c
2 AAACCCTCACTG TCACAGTGA GGT CTTT
TGAATCAG AGTGTCACT CCA GAAG
C-- AAT
GAM5385 218 KIAA175 1 14851 NP_203755.1 3 918 CTGGAGAAAGAG - AA --- 6 A c c
4 ACACACGGGGTG TCACAGT G CCG GTCTCTTTC

```
                                    ACTGTGGC    GGTGTCA T  GGC   CAGAGAAAG
                                              G GG   ACA
GAM5385  218   KIAA190 1   19375  XP_056282.1  3  1029   CCGCAGAAGGGC       A   GT-          6  A  c
c
         4                          AGCGGTGCACTG TCACAGTG ACCG   CTCTTT
                                    TGATGCCT    AGTGTCAC TGGC   GGGAAG
                                              G   GAC
GAM5385  218   KIDINS2 1   2942   XP_291015.1  3  154    GAGGTAAAAGAG     G  AACCG          6  A  c
c
         20                         ACATCTGCAGTG TCACA TG    GTCTCTTT
                                    TGACAGAA    AGTGT AC    CAGAGAAA
                                              G  GTCTA
GAM5385  218   LGALS3  1   506    NP_002297.1  3  77     TGTGTAAAGGTT        C-  TC          6  A  c  c
                                    TCATGTTCACTG TCACAGTGAAC  GG  TCTTT
                                    TGAGTGAA    AGTGTCACTTG  CT  GGAAA
                                                TA  TT
GAM5385  218   LMO4    1   3198   NP_006760.1  3  498    TAAAGGAAAGAG     TGAA  -          6  A  c  c
                                    ATGTGGCTTTTG TCACAG    CCG GTCTCTTTC
                                    TGATATTC    AGTGTT    GGT TAGAGAAAG
                                              TTC-  G
GAM5385  218   LOC1136 1   821    XP_054492.1  3  136    CAGCCTGAAGAA      GAACC          6  A  c
c
         12                         AAGAGGCCACTG TCACAGT    GGTCTCTTT
                                    TGACTACA    AGTGTCA    CCGGAGAAA
                                              -----
GAM5385  218   LOC1269 1   2569   XP_059091.2  3  675    CAAAGTTGAAGG       AACCG          6  A  c
c
         17                         GACAAGGCACTG TCACAGTG    GTCTCTTT
                                    TGAGGGGA    AGTGTCAC    CAGGGAAG
                                              GGAA-
GAM5385  218   LOC1272 1   14394  XP_072073.5  3  554    CGGTTGACTGAG      GA---       TT       6  A  c
c
         62                         ACCGGTCTGTGG TCACAGT    ACCGGTCTC  TC
                                    CTGTGGGC    GGTGTCG    TGGCCAGAG  AG
                                              GTGTC       TC
GAM5385  218   LOC1282 1   1443   XP_059223.4  5  1155   GGAGGAGAGTGG       AA-----  G        6  A  c
c
         39                         CGGCTGACACTG TCACAGTG      CCG TCTCTTTC
                                    TGAAGGAG    AGTGTCAC      GGT AGAGGAGG
                                              AGTCGGC  G
GAM5385  218   LOC1306 1   17789  XP_059463.2  3  63     CATATACAAGGG  -     CC  T          6  A  c  c
         33                         AGCCCTTCACTG TCA CAGTGAA  GG CTCTTT
                                    TTGATACA    AGT GTCACTT  CC GAGGGA
                                              T     -- C
GAM5385  218   LOC1355 1   18796  XP_059776.1  3  647    TTTGAAAGCAGG  A      C- GT  -        6  A  c
c
         21                         TCATGTTCACTG TC CAGTGAAC  G  CT CTTTC
                                    CGATGCTG    AG GTCACTTG  C  GA GAAAG
                                              C       TA TG  C
GAM5385  218   LOC1433 1   9647   XP_084501.1  3  1422   ACCTGGGGCGAG      GAA      - TT       6  A  c
 c
```

```
          81                          ACCGGGTGACTG TCACAGT   CCGGTCTC T  C
                                     TGGCAGTG    GGTGTCA   GGCCAGAG G  G
                                                 GTG       C GG
GAM5385  218   LOC1444 1  16762  NP_612482.1  3  493   ATCTTGTTAGAG        CC  T          6  A  c  c

          67                          AGCTTTTCACTG TCACAGTGAA  GG CTCTTT
                                     TGAGGAAG    AGTGTCACTT  TC GAGAGA
                                                 T-  -
GAM5385  218   LOC1446 1  18404  XP_096656.1  3  1167  GCTACCCAAGAG      GAA --      T       6  A  c
c
          78                          ACCATGGACTGT TCACAGT   CC  GGTCTCTT
                                     GGACTCTT    GGTGTCA   GG  CCAGAGAA
                                                 --- TA       C
GAM5385  218   LOC1459 1  16415  XP_096914.1  5  762   TCAGCCAGGTAA       ACCG            6  A  b
b
          80                          AGGGACTCACTG TCACAGTGA   GTCTCTTT
                                     TGATCGTG    AGTGTCACT   CAGGGAAA
                                                 ----
GAM5385  218   LOC1478 1  8092   XP_097313.2  3  934   GGGTGTGGAGTG       ACCGGT          6  A
c  c
          08                          AAAGAGTCACTG TCACAGTGA    CTCTTTC
                                     TGGTGGGG    GGTGTCACT    GAGAAAG
                                                 ------
GAM5385  218   LOC1484 1  14739  XP_086188.6  3  963   CTGTTCAAAGAG T   ----   CG--        6  A  c
c
          18                          ACATTTGTTCAA  CACAG   TGAAC   GTCTCTTT
                                     TCTCTGTG    GTGTC   ACTTG   CAGAGAAA
                                           -   TCTA    TTTA
GAM5385  218   LOC1488 1  7024   NP_660321.1  5  21    AGGAGCTGAGAA       AC   C   T       6  A  c
c
          23                          ACCGAGTCACTG TCACAGTGA  CGGT TCTT
                                     TGAAAAGA    AGTGTCACT  GCCA AGAG
                                                 GA   A   T
GAM5385  218   LOC1505 1  2809   XP_086942.1  3  582   CAGGGAAATGGG      - CC   C        6  A  c
c
          27                          CCTCTTCCACTG TCACAGTG AA  GGTCT TTTC
                                     TGATCTCC    AGTGTCAC TT  CCGGG AAAG
                                                 C  CT    T
GAM5385  218   LOC1527 1  6839   XP_098264.1  5  470   ATGCAGAAAGAG     TGAACCG          6  A
c  c
          90                          ATATTCTGTGAT TCACAG      GTCTCTTTC
                                     AGATATAT    AGTGTC      TAGAGAAAG
                                                 TTA----
GAM5385  218   LOC1531 1  7502   XP_098319.1  5  1840  CCTGGGGGAGGG       A -     TT       6  A  c
c
          46                          GCCTGGTCACTG TCACAGTGA CC GGTCTCT  C
                                     TGAACACA    AGTGTCACT GG CCGGGGA  G
                                                 - T      GG
GAM5385  218   LOC1583 1  5669   XP_048461.1  5  944   GCTTTGAAAGAG   A   A   --          6  A  c  c
          81                          AAACTGGCTCAC TCAC GTGA CCGG  TCTCTTTC
```

AGTGAGTG AGTG CACT GGTC AGAGAAAG
A C AA
GAM5385 218 LOC2001 1 5297 XP_211599.1 5 1455 GACTTCAAAGAG A GT- -- 6 A c c
69 ACCATGGTTCCG TC CA GAACC GGTCTCTTT
TTGGAGGC AG GT CTTGG CCAGAGAAA
- TGC TA
GAM5385 218 LOC2025 1 16316 XP_011448.4 3 42 GGACAGGAAGAG - T CC-- 6 A c c
51 ACCTTATTTCCT TCA CAG GAA GGTCTCTTTC
GATGGGAC GGT GTC CTT CCAGAGAAGG
A - TATT
GAM5385 218 LOC2032 1 6033 XP_116805.2 3 3615 AGAAAGGATACT - ----- T 6 A c c
49 GTCGGTTCACTG TCA CAGTGAACCG GTC CTTTC
TTGAGCAG AGT GTCACTTGGC TAG GAAAG
T TGTCA -
GAM5385 218 LOC2196 1 14755 XP_167572.1 5 427 GATGTGGAAGGA AA- GG 6 A c c
90 GGGGAAGCACTG TCACAGTG CC TCTCTTTC
TGACCTCC AGTGTCAC GG GGAGGAAG
GAA --
GAM5385 218 LOC2558 2 8949 XP_170628.1 3 506 CAGCCTGAAGAG ---- C 6 A c c
70 ACCAGTGAGCTC TCACAGTGA AC GGTCTCTTT
ACTGTGAC AGTGTCACT TG CCAGAGAAG
CGAG A
GAM5385 218 LOC2558 2 17784 XP_170628.1 3 506 CTGAAGAGACCA ---- C 6 A c c
70 GTGAGCTCACTG TCACAGTGA AC GGTCTCTTT
TGACCCAC AGTGTCACT TG CCAGAGAAG
CGAG A
GAM5385 218 LOC2831 1 6144 XP_210921.1 3 321 GGGTAGAAAGAG G ACC 6 A c c
67 ACTCTCGTGTGG TCACA TGA GGTCTCTTTC
AGGTTACA GGTGT GCT TCAGAGAAAG
- C--
GAM5385 218 LOC2832 1 4599 XP_210962.1 5 382 GGAAGAAAAGAG C - - - 6 A c c
93 ACCAGGTCTCAG TCA AG TGA ACC GGTCTCTTT
CTTGACTA AGT TC ACT TGG CCAGAGAAA
- G C A
GAM5385 218 LOC2834 1 1830 XP_208686.1 3 215 ACAACCCGGAAA ACC C 6 A c c
65 GAACCATCACTG TCACAGTGA GGT TCTTTC
TGAAGGGC AGTGTCACT CCA AGAAAG
A-- -
GAM5385 218 LOC2834 1 3455 XP_211053.1 5 28 CTCCTGAAAGAG AC- - G 6 A c c
84 ATGGATTCATTA TC AGTGAA CCG TCTCTTTC
AGGAAATT AG TTACTT GGT AGAGAAAG
GAA A -
GAM5385 218 LOC2836 1 1336 XP_208102.1 3 335 CAAAAGATAACA - C--- 6 A c c
61 TTGGTGTCACTG TCACAGTGA ACCGGT TCTTT
TGGTATTA GGTGTCACT TGGTTA AGAAA

```
                                                G     CAAT
GAM5385  218   LOC2840 1  1416  XP_208152.1  3  1048  GTGTTTAGAAGT       ACCGG  -        6  A  c
c
          48                                     AGGAAGTCACTG TCACAGTGA    TCT CTTT
                                                TGAGCAAT    AGTGTCACT    GGA GAAG
                                                       GAA--  T
GAM5385  218   LOC2841 1  6084  XP_209019.1  5  1676  TAGAGGAAAGAG   -   A C--  -        6  A  c  c

          01                                     AACCCTTGTACA TCA CAGTG AC   GGT CTCTTTC
                                                CTGTTGGT    GGT GTCAC TG   CCA GAGAAAG
                                                       T    A  TTC   A
GAM5385  218   LOC2841 1  17928 XP_209041.1  5  1196  ACCTTTCTGAGA       AACCG           6  A  c
c
          58                                     GAGGCACCACTG TCACAGTG    GTCTCTTTC
                                                TGACCTTC    AGTGTCAC    CGGAGAGAG
                                                       CA---
GAM5385  218   LOC2842 1  10396 XP_211400.1  5  1603  TTTTAAAAAGCA       ACCG   -        6  A  c
c
          63                                     GACATCTCACTG TCACAGTGA    GTCT CTTT
                                                TGGTCTAC    GGTGTCACT    CAGA GAAA
                                                       CTA-   C
GAM5385  218   LOC2845 1  5552  XP_211518.1  3  66    AGTCCAAAGGAC       - CG-  T        6  A  c  c
          55                                     AGTGTGTCACTG TCACAGTGA AC   GTC CTTT
                                                TGAACTGG    AGTGTCACT TG   CAG GAAA
                                                       G  TGA  -
GAM5385  218   LOC2847 1  6441  XP_211612.1  3  802   CCCACCTGGTAG       A  -   - TT      6  A  c  c

          37                                     ACACGGTCACTG TCACAGTGA CCG GTCT CT
                                                TGACAGGA    AGTGTCACT GGC CAGA GG
                                                       -  A   T  TC
GAM5385  218   LOC2847 1  10735 XP_209363.1  3  712   TTATTTAAAGAG   C   A  CG           6  A  c
c
          59                                     ACAGTACACTCT TCA AGTG AC  GTCTCTTT
                                                GAAAGAAC    AGT TCAC TG  CAGAGAAA
                                                       C   A  A-
GAM5385  218   LOC2848 1  13073 XP_211685.1  3  1661  AGTGGGAAAGAG   -  TGA  G          6  A  c
c
          98                                     AGGGACGGGTCT TCA CAG   ACC GTCTCTTTC
                                                GATGAGTT    AGT GTC   TGG CAGGGAGAG
                                                       A  ---  G
GAM5385  218   LOC3388 1  12400 XP_294723.1  5  6     GAGAAGGAAGAG   C  GA  -          6  A  c  c

          25                                     ACCAGGTGGGCT TCA AGT  ACC GGTCTCTTTC
                                                CTGAGACA    AGT TCG  TGG CCAGAGAAGG
                                                       C  GG  A
GAM5385  218   LOC3392 1  6084  XP_290762.2  5  1676  TAGAGGAAAGAG   -   A C--  -        6  A  c  c

          16                                     AACCCTTGTACA TCA CAGTG AC   GGT CTCTTTC
                                                CTGTTGGT    GGT GTCAC TG   CCA GAGAAAG
                                                       T    A  TTC   A
```

GAM5385 218 LOC3392 1 6084 XP_294900.2 5 1675 TAGAGGAAAGAG - A C-- - 6 A c c

82 AACCCTTGTACA TCA CAGTG AC GGT CTCTTTC
CTGTTGGT GGT GTCAC TG CCA GAGAAAG
T A TTC A

GAM5385 218 LOC3401 1 3108 XP_295181.1 5 896 AATCAGAGAGAG AC GT 6 A c
c

78 CTCGACTCACTG TCACAGTGA CG CTCTTTC
TGGGTCAG GGTGTCACT GC GAGAGAG
CA TC

GAM5385 218 LOC3410 2 2544 XP_295967.2 5 351 GCCCTGCGGGAG CC T TT 6 A c
c

36 GACCATTCACTG TCACAGTGAA GGTC CT C
TGAGAAAA AGTGTCACTT CCAG GA G
A- - GG

GAM5385 218 LOC3410 2 4152 XP_295967.2 5 431 CGGGACAAAGAG GA --- 6 A c c

36 ACTGTTGGTAAC TCACAGT ACC GGTCTCTTT
TGTGGATT GGTGTCA TGG TCAGAGAAA
A- TTG

GAM5385 218 LOC3416 1 8348 XP_292193.1 5 71 GAGAGATGAGAG TC--- CC 6 A c
c

40 AGGCCTTCACTG ACAGTGAA GGTCTCTTTC
TTCACC TGTCACTT CCGGAGAGAG
CCACT --

GAM5385 218 LOC3432 1 5095 XP_291488.1 5 325 GGGAGCCAAGGT CCG T 6 A c
c

65 GACACTTCACTG TCACAGTGAA GTC CTTT
TGAAGCCC AGTGTCACTT CAG GGAA
CA- T

GAM5385 218 LOC3485 1 18900 XP_302813.1 5 598 AGTTTGAAAGAG C T GG 6 A c
c

29 AGGGTTCCCTAT TCA AG GAACC TCTCTTTC
GAATAAGA AGT TC CTTGG AGAGAAAG
A C G-

GAM5385 218 LOC3487 1 2809 XP_211718.1 3 582 CAGGGAAATGGG - CC C 6 A c
c

34 CCTCTTCCACTG TCACAGTG AA GGTCT TTTC
TGATCTCC AGTGTCAC TT CCGGG AAAG
C CT T

GAM5385 218 LOC3510 1 18415 XP_304617.1 3 5 TGAAAAGAGACT GAA---- 6 A c c
12 GGCCGAAGAACT TCACAGT CCGGTCTCTTT
GTGAATAG AGTGTCA GGTCAGAGAAA
AGAAGCC

GAM5385 218 LOC3520 1 1884 XP_305365.1 5 248 GTGGAGGAGGAA A GG--- 6 A c
c

51 GGAGGATCACTG TCACAGTGA CC TCTCTTTC
TGGAAATC GGTGTCACT GG GGAGGAGG
A AGGAA

GAM5385 218 LOC5590 1 6986 NP_061157.2 3 99 CAGGGAGGAGCT A C -- 6 A c c

```
        8                       GCCTGTTCACTG TC CAGTGAAC GGT  CTCTTTC
                                GGATCAGC    AG GTCACTTG CCG  GAGGAGG
                                        G       T   TC
GAM5385  218   LOC9071 1  17254 XP_033704.1  3  224   AGCTGGAGAGGG        C  GT          6  A  c
c
        9                       TGCGTTTCACTG TCACAGTGAA CG  CTCTTTC
                                TGGGGTGT    GGTGTCACTT GC  GGGAGAG
                                        T  GT
GAM5385  218   LOC9194 2  7137  XP_041721.2  3  93    TTTGGGAAAGAG   C    ----- G         6  A  c  c
        7                       ACAGGAAAGATT TCA AGTGAA    CC GTCTCTTTC
                                CACTTGAA    AGT TCACTT    GG CAGAGAAAG
                                        -    AGAAA  A
GAM5385  218   LOC9194 2  13311 XP_041721.2  3  1158  TCCTGTCAAGAG   -   A  --     T      6  A  c  c

        7                       ACCTAGGTCTAC TCA CAGTG ACC  GGTCTCTT
                                TGATGGCA    GGT GTCAT TGG  CCAGAGAA
                                        A    C  AT      C
GAM5385  218   LOC9659 1  9062  XP_039922.1  3  513   ACCACAGAGGGG       AA -          6  A  c  c
        7                       ACCAGGGCACTG TCACAGTG  CC GGTCTCTTT
                                TGAGCCCT    AGTGTCAC  GG CCAGGGGAG
                                        G-  A
GAM5385  218   LOH11CR 1  14358 NP_055437.1  3  532   GACAGAGACTGC       A  -----    T     6  A  c
c
        2A                       AGGGGTCCACTG TCACAGTG ACC    GGTCTCT TC
                                TGAGAGGT    AGTGTCAC TGG    TCAGAGA AG
                                        C   GGACG      C
GAM5385  218   MEF2B  1  13472 NP_005910.1  5  46    AGAAAGTCACGG  A      CG   ----       6  A  c  c

                                ACAAGTTCACTG TC CAGTGAAC  GTCT   CTTTC
                                AGAGCGTC    AG GTCACTTG  CAGG   GAAAG
                                        A       AA   CACT
GAM5385  218   MGC1106 1  10669 NP_115688.1  3  892   TTGGGGAAAGAG     T  ACC----          6  A  c
 c
        1                       ACCTTTAAAATC TCACAG GA      GGTCTCTTTC
                                TTGTGGTG    GGTGTT CT      CCAGAGAAAG
                                        -  AAAATTT
GAM5385  218   MGC1821 1  8207  NP_689665.1  5  636   CGTAAAATAGAA        ACCG T          6  A  c
c
        6                       GAGCAGTCACTG TCACAGTGA   G CTCTTT
                                TGGAACTA    GGTGTCACT    C GAGAAG
                                        GA-- -
GAM5385  218   MGC3471 1  10134 NP_775936.1  5  127   ACTAGAAAAGAG   -  T-   CG          6  A  c
c
        3                       ACAGTTCTTCTG TCA CAG  GAAC  GTCTCTTT
                                CTGACAAC    AGT GTC  CTTG  CAGAGAAA
                                        C   TT   A-
GAM5385  218   NR2F2  1  11718 NP_066285.1  3  773   TTTAAGAAAGAG       GAACCGG          6  A  c
 c
                                AATGAACTGTGG TCACAGT      TCTCTTTC
                                AATTTATT    GGTGTCA      AGAGAAAG
```

```
                                                AGTA---
GAM5385  218   NY-REN- 1  974   XP_027116.6  3  1300  TACAGCCAAGGG       AC   -    T       6  A  c  c

          25                          CACTGCTCACTG TCACAGTGA  CGGT CTCTT
                                     TGGCCCGT    GGTGTCACT  GTCA GGGAA
                                                   C-   C    C
GAM5385  218   NY-REN- 1  4623  NP_542385.1  3  990   AACATGAAAGAG      TGAACC             6  A  c
c
          41                          ATCTTTGTGAAT TCACAG     GGTCTCTTTC
                                     AAATTCAA    AGTGTT     CTAGAGAAAG
                                                   T-----
GAM5385  218   OSBPL10 1  2040  NP_060254.2  3  890   TTGGGGAAAGAG      T   CCGG---          6  A  c
 c
                                     AAGAGAATTTCC TCACAG GAA      TCTCTTTC
                                     TGTGGATT    GGTGTC CTT      AGAGAAAG
                                                   -  TAAGAGA
GAM5385  218   PAX7   1  16405 NP_002575.1  5  516   GGAAAGAAAGAG    AG-  AAC             6  A  c
c
                                     ATCGCAGCAGGG TCAC   TG   CGGTCTCTTTC
                                     GTGAAGGG    AGTG   AC   GCTAGAGAAAG
                                                   GGG  GAC
GAM5385  218   PAX7   1  16405 NP_039236.1  5  516   GGAAAGAAAGAG    AG-  AAC             6  A  c
c
                                     ATCGCAGCAGGG TCAC   TG   CGGTCTCTTTC
                                     GTGAAGGG    AGTG   AC   GCTAGAGAAAG
                                                   GGG  GAC
GAM5385  218   PHGDH  1  14461 NP_006614.2  3  62    TTTTCTGAAGAA       AACC   C          6  A  c
c
                                     ACCCACCCACTG TCACAGTG    GGT TCTTT
                                     TGATCAAT    AGTGTCAC    CCA AGAAG
                                                   CCAC   A
GAM5385  218   PLEKHA4 1  6785  NP_065955.1  5  171   CTTAAGGAAGAG      TGAACC             6  A  c
 c
                                     ACCCTGTGAGTC TCACAG     GGTCTCTTTC
                                     TGACAATA    AGTGTC     CCAGAGAAGG
                                                   ------
GAM5385  218   PMCHL1 1  10293 NP_114093.1  3  1332  GAATGTAAAGAG   - -    CC-             6  A  c
c
                                     ACCACCTTCACT TCA CA GTGAA   GGTCTCTTT
                                     TGTTGAGA    AGT GT CACTT   CCAGAGAAA
                                                   T  T    CCA
GAM5385  218   PMCHL2 1  3755  NP_114094.1  3  1330  GAATGTAAAGAG   - -    CCG-            6  A  c
c
                                     ACGCCCTTCACA TCA CA GTGAA    GTCTCTTT
                                     TGTTGAGA    AGT GT CACTT    CAGAGAAA
                                                   T  A    CCCG
GAM5385  218   PTPN9  1  13095 NP_002824.1  3  957   AATTTGGGGAAC       AACC    C          6  A  c
c
                                     AGACCTCCACTG TCACAGTG    GGTCT TTTC
                                     TGATTCCA    AGTGTCAC    CCAGA AAGG
```

CT-- C

GAM5385 218 RASD1 1 9061 NP_057168.1 3 203 GGAAGGAAAGAG A --- AA G 6 A c c

AACGGGCCAAGA TC CAGT G CCG TCTCTTTC
CTGGGACT AG GTCA C GGC AGAGAAAG
G GAA CG A

GAM5385 218 RGS2 1 19470 NP_002914.1 3 302 ATGATGAAAGAG - A- CG- 6 A c c

ACAATGTAATAC TCA CAGTG AC GTCTCTTTC
TGTTGGTC GGT GTCAT TG CAGAGAAAG
T AA TAA

GAM5385 218 RGS6 1 19481 NP_004287.3 3 111 CCTTACGAGGAG A - 6 A b b

ACTTGGTCACTG TCACAGTGA CCG GTCTCTTT
TGAAGGAG AGTGTCACT GGT CAGAGGAG
- T

GAM5385 218 RIS 1 6292 NP_057647.1 3 254 GGCCGTAGAGGG AACCGG 6 A c c

AAACAGCCACTG TCACAGTG TCTCTTT
TGACAACC AGTGTCAC AGGGAGA
CGACAA

GAM5385 218 S100A15 1 5854 NP_789793.1 3 671 TGTGGAAGTGAG A- GG - 6 A c c

AAGGAGTCACTG TCACAGTGA CC TCTC TTTC
TGATGCTT AGTGTCACT GG AGAG GAAG
GA A- T

GAM5385 218 SCAMP3 1 12492 NP_005689.2 3 172 GACAGGCGTGTG CGG TT 6 A c c

GGGAGTTCACTG TCACAGTGAAC TCTCT
TGACCTAG AGTGTCACTTG AGGGG
--- TG

GAM5385 218 SCAMP3 1 12492 NP_443069.1 3 172 GACAGGCGTGTG CGG TT 6 A c c

GGGAGTTCACTG TCACAGTGAAC TCTCT
TGACCTAG AGTGTCACTTG AGGGG
--- TG

GAM5385 218 SEC61A1 1 9945 NP_037468.1 3 1959 CCAGCTTCCAGG AC T 6 A c c

GGACTGTCACTG TCACAGTGA CGGTCTCTT
TGGACGCC GGTGTCACT GTCAGGGGA
-- C

GAM5385 218 SEPX1 1 5607 NP_057416.1 3 195 CTTGGAAAAGAG - TG CC 6 A c c

ACTCATTTGCTG TCA CAG AA GGTCTCTTT
ATGGTTCA GGT GTC TT TCAGAGAAA
A GT AC

GAM5385 218 SERPINI 1 7346 NP_006208.1 3 2 AAGGAAGAGATT CC-- 6 A c c
2 TAGATTCACTGT TCACAGTGAA GGTCTCTTTC
GATGAAAA AGTGTCACTT TTAGAGAAGG
AGAT

GAM5385 218 SLC21A1 1 6067 NP_059131.1 5 125 AAGAGGAAAGAG AG- AC 6 A c c

4 AAGAGATCGCTC TCAC TGA CGGTCTCTTT
AGGGGTGA AGTG ACT GCTAGAGAAG
GGG C-
GAM5385 218 SLC37A3 1 18317 NP_115671.1 3 407 GACAAAGAATCC C--- TC 6 A c c
CTCTGTTCACTG TCACAGTGAAC GG TCTTT
TGGTGGGA GGTGTCACTTG CC AGAAA
TCTC TA
GAM5385 218 TBC1D4 1 20148 NP_055647.1 3 705 ATACATAAAGAG AA G--- 6 A c c
ACAGTAGGACAT TCACAGTG CC GTCTCTTT
TGTGGCTG GGTGTTAC GG CAGAGAAA
A- ATGA
GAM5385 218 TLP19 1 12082 NP_056997.1 3 146 ACACTGGAAGGA ACC - 6 A c c
GCGCTCTCACTG TCACAGTGA GGT CTCTTTC
TGGAAGAG GGTGTCACT TCG GAGGAAG
C-- C
GAM5385 218 TRIM43 1 17789 NP_620155.1 3 63 CATATACAAGGG - CC T 6 A c c
AGCCCTTCACTG TCA CAGTGAA GG CTCTTT
TTGATACA AGT GTCACTT CC GAGGGA
T -- C
GAM5385 218 TUB 1 20119 NP_003311.2 3 3679 AGCTGAATGAGT C- T T 6 A c c
CTGCTTTCACTG TCACAGTGAA CGG CTC TTC
TGACTGGG AGTGTCACTT GTC GAG AAG
TC T T
GAM5385 218 TUB 1 20119 NP_813977.1 3 3679 AGCTGAATGAGT C- T T 6 A c c
CTGCTTTCACTG TCACAGTGAA CGG CTC TTC
TGACTGGG AGTGTCACTT GTC GAG AAG
TC T T
GAM5385 218 UBL3 1 17405 NP_009037.1 3 2215 TAAGTGAAATAA - - CTC 6 A c c
ACTGGTTCACTA TC AC AGTGAACCGGT TTTC
GTAGAGAA AG TG TCACTTGGTCA AAAG
A A AAT
GAM5385 218 UPF2 1 17322 NP_056357.1 3 291 GTCAAGAAATGA C G - 6 A c c
GATGGTTCACTT TCA AGTGAACCG TCTC TTTC
GACTACTG AGT TCACTTGGT AGAG AAAG
- - T
GAM5385 218 UPF2 1 17322 NP_542166.1 3 291 GTCAAGAAATGA C G - 6 A c c
GATGGTTCACTT TCA AGTGAACCG TCTC TTTC
GACTACTG AGT TCACTTGGT AGAG AAAG
- - T
GAM5385 218 USP15 1 7999 NP_006304.1 3 43 GCCATAAAAGAG - T CCG 6 A c c
ACACTTTCCTGC TCA CAG GAA GTCTCTTT
TGGTGGTA GGT GTC CTT CAGAGAAA
C - TCA
GAM5385 218 XT3 1 9855 NP_064593.1 3 741 TGGAAAAGGAGT AA- GGT 6 A c c
CAGGAGCCACTG TCACAGTG CC CTCTTT
TGAGGTGA AGTGTCAC GG GAGGAA
CGA ACT
GAM5385 218 XT3 1 9855 NP_071800.1 3 741 TGGAAAAGGAGT AA- GGT 6 A c c

CAGGAGCCACTG TCACAGTG CC CTCTTT
TGAGGTGA AGTGTCAC GG GAGGAA
CGA ACT

GAM5385 218 ZNF272 1 19140 XP_030227.3 3 285 CCCATGAAAGAG T-- A ---- 6 A c c
ACCCAGTGGTTA CACAGTGA CC GGTCTCTTTC
CTGTGCAC GTGTCATT GG CCAGAGAAAG
CAC - TGAC

GAM5385 218 ZNF463 1 1764 NP_061025.3 5 564 TTACCAGTGAGG AAC C 6 A c c

AAACCGACACTG TCACAGTG CGGT TCTTT
TGAGCTCT AGTGTCAC GCCA AGGAG
A-- A

GAM7052 296 1 17475 NP_054819.1 3 829 GGGACCAGGAGT -- CC A- 3 C c c
AGCTGTCATTTG CATGT AAT CAGCTACTC GG
ATATGTAT GTATA TTA GTCGATGAG CC
GT CT GA

GAM7052 296 A1BG 3 1831 NP_570602.2 3 560 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGA ACAT AGGGTCGATGAGTCC
AGTACGG C

GAM7052 296 A1BG 3 4738 NP_570602.2 3 429 AGCCTCCCAAGT AA---- CA 3 C c c
AGCTGGGAGCCT CATGT TCCCAGCTACT GG
GGGCATGC GTACG AGGGTCGATGA CC
GGTCCG AC

GAM7052 296 A1BG 3 19222 NP_570602.2 3 210 CAGGGCTGAGTG TA - 3 C c c
GGCTGGGATCTC CATG ATCCCAGCT ACTCAG
GTGTCCTC GTGC TAGGGTCGG TGAGTC
TC G

GAM7052 296 A2BP1 1 11694 NP_061193.2 3 77 CGAGGCCTGAGT ATCC C 3 C c
c

ATTGCAATACAT CATGTA CAG TACTCAGG
GCAGTAGT GTACAT GTT ATGAGTCC
AAC- -

GAM7052 296 A2BP1 1 11694 NP_665898.1 3 77 CGAGGCCTGAGT ATCC C 3 C c
c

ATTGCAATACAT CATGTA CAG TACTCAGG
GCAGTAGT GTACAT GTT ATGAGTCC
AAC- -

GAM7052 296 A2BP1 1 11694 NP_665899.1 3 77 CGAGGCCTGAGT ATCC C 3 C c
c

ATTGCAATACAT CATGTA CAG TACTCAGG
GCAGTAGT GTACAT GTT ATGAGTCC
AAC- -

GAM7052 296 A2BP1 1 11694 NP_665900.1 3 199 CGAGGCCTGAGT ATCC C 3 C c
c

ATTGCAATACAT CATGTA CAG TACTCAGG
GCAGTAGT GTACAT GTT ATGAGTCC
AAC- -

GAM7052 296 ABCB5 1 15685 XP_291215.1 3 740 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGAGTAC TGTA TCCCAGCTACTCAGG
AGGCGTGC ACAT AGGGTCGATGAGTCC
CGTGCGG G

GAM7052 296 ABTB1 1 17325 NP_115937.1 5 377 GCTTCCTGCAGG - A A- - 3 C c c
AGGCGGGATTAC CAT GTAATCCC GCT CT CAGG
TATGACGA GTA CATTAGGG CGG GA GTCC
T - AG C

GAM7052 296 ADAMTS4 1 6395 NP_005090.1 3 755 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCTCCT ACATTAGGGTCGATGAGTCC
TCCTCGG

GAM7052 296 ADCY6 1 20175 NP_056085.1 5 149 CAGCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCC ACATTAGGGTCGATGAGTCC
CCCGCGG

GAM7052 296 AGTPBP1 1 16343 NP_056054.1 3 280 AAAAACCTGAGT CCCAGC 3 C c c

ATCATTGCATGA CATGTAAT TACTCAGG
ATTTTTAT GTACGTTA ATGAGTCC
CT----

GAM7052 296 AKR1A1 1 18726 NP_006057.1 5 358 AGCCTGCCCAGG C T ---- 3 C c c

TGCTGAGATTAC CATGTAATC CAGC ACT CAGG
ATGTATGA GTACATTAG GTCG TGG GTCC
A - ACCC

GAM7052 296 ALDH1B1 1 17862 NP_000683.3 3 1158 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGTACAT ATATTAGGGTCGATGAGTCC
TACATGG

GAM7052 296 ALOX15 1 11095 NP_001131.1 3 499 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCTCAT ACAT AGGGTCGATGAGTCC
TACTCGG C

GAM7052 296 AP1S3 1 809 XP_291023.1 3 1103 AGCCTCCTGAGT CA----- AT 3 C c c

AGCTGGGGCTAC TGTA CCCAGCTACTCAGG
AGGTGTGT ACAT GGGTCGATGAGTCC
TGTGTGG CG

GAM7052 296 AP3S2 1 6157 NP_005820.1 3 742 AGCCTCCCCAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG CC

GAM7052 296 APPBP2 1 14578 NP_006371.2 3 3581 AGCCTTCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCTCCT ACATTAGGGTCGATGAG CC

```
                                        TCCTCGG          -
GAM7052  296   APTX   1  2203  NP_060162.1  3  236   TCTGGTGAGGGT  T  -       AG      3  C  c  c
                                GGCTGGGATATA CA GTA ATCCCAGCTACTC
                                CCTGACCC    GT CAT TAGGGTCGGTGGG
                                        C  A         AG
GAM7052  296   APTX   1  2203  NP_778239.1  3  422   TCTGGTGAGGGT  T  -       AG      3  C  c  c
                                GGCTGGGATATA CA GTA ATCCCAGCTACTC
                                CCTGACCC    GT CAT TAGGGTCGGTGGG
                                        C  A         AG
GAM7052  296   APTX   1  2203  NP_778241.1  3  236   TCTGGTGAGGGT  T  -       AG      3  C  c  c
                                GGCTGGGATATA CA GTA ATCCCAGCTACTC
                                CCTGACCC    GT CAT TAGGGTCGGTGGG
                                        C  A         AG
GAM7052  296   APTX   1  2203  NP_778242.1  3  236   TCTGGTGAGGGT  T  -       AG      3  C  c  c
                                GGCTGGGATATA CA GTA ATCCCAGCTACTC
                                CCTGACCC    GT CAT TAGGGTCGGTGGG
                                        C  A         AG
GAM7052  296   APTX   1  2203  NP_778243.1  3  236   TCTGGTGAGGGT  T  -       AG      3  C  c  c
                                GGCTGGGATATA CA GTA ATCCCAGCTACTC
                                CCTGACCC    GT CAT TAGGGTCGGTGGG
                                        C  A         AG
GAM7052  296   AQP6   1  11163 NP_001643.1  3  699   AGCCTCCCAAGT CA-----          CA      3  C  c
c
                                AGCTGGGATTAC      TGTAATCCCAGCTACT  GG
                                AGGCGCCT          ACATTAGGGTCGATGA  CC
                                        TCCGCGG           AC
GAM7052  296   AQP6   1  11163 NP_445738.1  3  1865  AGCCTCCCAAGT CA-----          CA      3  C  c
c
                                AGCTGGGATTAC      TGTAATCCCAGCTACT  GG
                                AGGCGCCT          ACATTAGGGTCGATGA  CC
                                        TCCGCGG           AC
GAM7052  296   ARCN1  1  14158 NP_001646.2  3  490   CAGCCTCCGAGT CA-----  A       --      3  C  c
c
                                AGCTGGGACTAC      TGTA TCCCAGCTACTC  AGG
                                AGGTGCAC          ACAT AGGGTCGATGAG  TCC
                                        CACGTGG   C         CC
GAM7052  296   ARHF   1  13834 NP_061907.1  3  1177  AGCCTCCTGAGT     A              3  C  b  b
                                AGCTGGGACTAC CATGTA TCCCAGCTACTCAGG
                                ATGCGCAC    GTACAT AGGGTCGATGAGTCC
                                          C
GAM7052  296   ARHGAP1 2  13952 NP_004299.1  3  1349  GGCCTCCCAAAG    ----      T  CA      3  C  c
 c
                                TGCTGGGATTCC CATGT    AATCCCAGC ACT  GG
                                AGGCGTGA    GTGCG    TTAGGGTCG TGA  CC
                                          GACC       -  AA
GAM7052  296   ARHGAP1 2  15853 NP_004299.1  3  1215  AGCCTCCTGAGT CA-----  A             3  C  c
 c
                                AGCTGGGACTAT      TGTA TCCCAGCTACTCAGG
                                AGGTGCAT          ATAT AGGGTCGATGAGTCC
                                        TACGTGG   C
```

GAM7052 296 ARPP-19 1 4389 NP_006619.1 3 3576 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGTCC ACATTAGGGTCGATGA CC
CCTGCGG AC

GAM7052 296 ASB16 1 10273 NP_543139.4 3 228 AAACTTCCGAGT CA----- A A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTC GG
AGGCATGA ACAT AGGGTCGATGAG CC
AGTACGG C -

GAM7052 296 ASB6 2 9847 NP_060343.1 3 1527 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C

GAM7052 296 ASB6 2 9847 NP_821066.1 3 2090 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C

GAM7052 296 ASB6 2 13406 NP_060343.1 3 1221 AGCCTCCTGAGT CA----- C 3 C c c

AGCTGGCATTAT TGTAAT CCAGCTACTCAGG
AGGTGCCC ATATTA GGTCGATGAGTCC
CCCGTGG C

GAM7052 296 ASB6 2 13406 NP_821066.1 3 1784 AGCCTCCTGAGT CA----- C 3 C c c

AGCTGGCATTAT TGTAAT CCAGCTACTCAGG
AGGTGCCC ATATTA GGTCGATGAGTCC
CCCGTGG C

GAM7052 296 ASE-1 1 6396 NP_036231.1 3 536 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCCCCT ACAT AGGGTCGATGAGTCC
TCCCCGG C

GAM7052 296 ATP1B4 1 11229 NP_036201.1 3 1963 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCC
CACACGG

GAM7052 296 ATP6V0D 2 6393 NP_689778.1 3 937 AGCCTCCCGAGT CA----- A 3 C c c

2 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AAGCACCC ACATTAGGGTCGATGAG CC
CCCACGA C

GAM7052 296 ATP6V0D 2 14828 NP_689778.1 3 663 GGCCTCCCAAAG T CA 3 C c c

2 TGTTGGGATTAC CATGTAATCCCAGC ACT GG
ATGCATGA GTACATTAGGGTTG TGA CC
- AA

GAM7052 296 ATP6V1A 1 16885 NP_001681.2 3 761 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG

AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C
GAM7052 296 ATP7A 1 3639 NP_000043.1 3 1146 AGCCTCCTGAGT CA----- C 3 C c c

AGCTAGGATTAC TGTAATCC AGCTACTCAGG
AGGTGCCT ACATTAGG TCGATGAGTCC
TCCGTGG A
GAM7052 296 ATP8B2 1 11229 XP_290875.1 3 1101 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCC
CACACGG
GAM7052 296 AXL 1 9692 NP_001690.2 3 556 GGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGT ACATTAGGGTCGATGA CC
TGTGTGG AC
GAM7052 296 AXL 1 9692 NP_068713.2 3 556 GGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGT ACATTAGGGTCGATGA CC
TGTGTGG AC
GAM7052 296 B3GALT5 1 7881 NP_006048.1 3 608 AGGGCTGGATGT ---- -- 3 C c c
AGCTGGGATTGA CATG TAATCCCAGCTAC TCAG
GTCCATGT GTAC GTTAGGGTCGATG GGTC
CTGA TA
GAM7052 296 B3GALT5 1 7881 NP_149360.1 3 608 AGGGCTGGATGT ---- -- 3 C c c
AGCTGGGATTGA CATG TAATCCCAGCTAC TCAG
GTCCATGT GTAC GTTAGGGTCGATG GGTC
CTGA TA
GAM7052 296 B3GALT5 1 7881 NP_149361.1 3 608 AGGGCTGGATGT ---- -- 3 C c c
AGCTGGGATTGA CATG TAATCCCAGCTAC TCAG
GTCCATGT GTAC GTTAGGGTCGATG GGTC
CTGA TA
GAM7052 296 B3GALT5 1 7881 NP_149362.1 3 608 AGGGCTGGATGT ---- -- 3 C c c
AGCTGGGATTGA CATG TAATCCCAGCTAC TCAG
GTCCATGT GTAC GTTAGGGTCGATG GGTC
CTGA TA
GAM7052 296 B3GALT5 1 7881 NP_149363.1 3 608 AGGGCTGGATGT ---- -- 3 C c c
AGCTGGGATTGA CATG TAATCCCAGCTAC TCAG
GTCCATGT GTAC GTTAGGGTCGATG GGTC
CTGA TA
GAM7052 296 BAG5 1 19275 NP_004864.1 3 1955 AGCCACCTGAGT AA---- 3 C c c
AGCTGGGAGTAC CATGT TCCCAGCTACTCAGG
AGGCATGT GTACG AGGGTCGATGAGTCC
GACATG
GAM7052 296 BCAP31 1 13785 NP_005736.2 3 553 AGCCTCCTGAGC CA----- A 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCT CTCAGG
AGGCGCTG ACATTAGGGTCGA GAGTCC
GTCGCGG C
GAM7052 296 BCLG 1 10887 NP_110393.1 5 107 AGAGTCCTGAGT T AA --- C 3 C c c

ACCTCGTGGGAA CA GT TCCCA G TACTCAGG
CTTGGGCA GT CA AGGGT C ATGAGTCC
T -- GCT C

GAM7052 296 BCLG 1 10887 NP_620048.1 5 107 AGAGTCCTGAGT T AA --- C 3 C c c

ACCTCGTGGGAA CA GT TCCCA G TACTCAGG
CTTGGGCA GT CA AGGGT C ATGAGTCC
T -- GCT C

GAM7052 296 BM-002 1 9516 NP_057701.1 3 1770 AGCCTCACGAGT CA----- A --- 3 C c
c

AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCATGC ACAT AGGGTCGATGAG TCC
CGTACGG C CAC

GAM7052 296 BRCA1 1 19804 NP_009237.1 3 76 AGTCTCCCAAGT ----- CA 3 C c c

AGCTGGGACTAT CATGTAA TCCCAGCTACT GG
TTTGCATG GTACGTT AGGGTCGATGA CC
TTATC AC

GAM7052 296 BRIP1 1 16280 NP_114432.1 3 292 AGCCTTCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTGC ACAT AGGGTCGATGAGTCT
CGTGTGG C

GAM7052 296 BXDC1 1 10897 XP_166303.1 3 1441 AGCCTCCCGAGT CA----- A 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCC ACATTAGGGTCGATGAG CC
CCCACGG C

GAM7052 296 C19orf9 1 7215 XP_290171.1 5 45 GGCCTCCCAAAG ---- T CA 3 C c c

TGCTGGGATTAA CATGT AATCCCAGC ACT GG
AGGCGTGA GTGCG TTAGGGTCG TGA CC
GAAA - AA

GAM7052 296 C1QTNF6 1 13966 NP_114116.2 3 628 AGCCTCCCTAGT CA----- C 3 C c
c

GGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCGCCT ACATTAGGGTCGGTGA TCC
TCCGCGG -

GAM7052 296 C20orf1 1 16361 NP_219489.1 3 808 AGCCTCCTGAGC CA----- A 3 C c c

61 AGCTGGGATTAC TGTAATCCCAGCT CTCAGG
AGGCGCAC ACATTAGGGTCGA GAGTCC
CACGCGG C

GAM7052 296 C20orf1 1 16361 NP_690857.1 3 78 AGCCTCCTGAGC CA----- A 3 C c c
61 AGCTGGGATTAC TGTAATCCCAGCT CTCAGG
AGGCGCAC ACATTAGGGTCGA GAGTCC
CACGCGG C

GAM7052 296 C4orf9 1 4343 XP_035572.1 3 438 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGACATGT ACATTAGGGTCGATGAG CC
TGTACAG C

GAM7052 296 C6orf14 1 17672 NP_699175.1 3 352 AGCCTCCTCAGT CA----- C 3 C c c
1 AGCTGGGATTAC TGTAATCCCAGCTACT AGG

AGGCATGT ACATTAGGGTCGATGA TCC
TGTACGG C
GAM7052 296 C6orf57 1 5864 NP_660310.1 3 586 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGACACCC ACATTAGGGTCGATGAGTCC
CCCACAG
GAM7052 296 C8orf12 1 8627 NP_473358.1 5 389 GAAGCCTGGGTA CC C-- 3 C c c
AAATTGTATTAC CATGTAAT CAG TACTCAGG
ATGATCTT GTACATTA GTT ATGGGTCC
T- AAA
GAM7052 296 C9orf9 1 16870 NP_061829.2 3 940 AGCCTCCTGAGT CA----- C 3 C c c
AGCTGGAATTAC TGTAAT CCAGCTACTCAGG
AGGCGCCC ACATTA GGTCGATGAGTCC
CCCGCGG A
GAM7052 296 CACNG6 1 10214 NP_114103.2 3 292 ACCTGATGGGGT GTA ---- 3 C c
c
AGCTGGGGTGTG CAT ATCCCAGCTAC TCAGG
GGGTTGGG GTG TGGGGTCGATG AGTCC
--- GGGT
GAM7052 296 CACNG6 1 10214 NP_665813.1 3 292 ACCTGATGGGGT GTA ---- 3 C c
c
AGCTGGGGTGTG CAT ATCCCAGCTAC TCAGG
GGGTTGGG GTG TGGGGTCGATG AGTCC
--- GGGT
GAM7052 296 CACNG6 1 10214 NP_665814.1 3 292 ACCTGATGGGGT GTA ---- 3 C c
c
AGCTGGGGTGTG CAT ATCCCAGCTAC TCAGG
GGGTTGGG GTG TGGGGTCGATG AGTCC
--- GGGT
GAM7052 296 CAMLG 1 2107 NP_001736.1 3 876 AGCCTCCCAAGT CA----- CA 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC
CGTACGG AC
GAM7052 296 CAPRI 1 7042 NP_008920.3 3 2061 GGCCTCCCGAGT AA---- A 3 C c c
AGCTGGGACTGG CATGT TCCCAGCTACTC GG
AGGCGTGT GTGCG AGGGTCGATGAG CC
GAGGTC C
GAM7052 296 CARD6 1 2824 NP_115976.2 3 290 AGCCTCTCGAGT CA----- --- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCATGC ACATTAGGGTCGATGAG TCC
CGTACGG CTC
GAM7052 296 CBFA2T2 1 1249 NP_005084.1 3 1982 AGCCTTCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCT
CGTACGG
GAM7052 296 CBFA2T2 1 1249 NP_787060.1 3 1982 AGCCTTCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCT
CGTACGG
GAM7052 296 CCL16 1 12626 NP_004581.1 3 376 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCTTGC ACAT AGGGTCGATGAGTCC
CGTTCGG C
GAM7052 296 CCL22 2 6967 NP_002981.2 3 1036 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTTCCT ACATTAGGGTCGATGAGTCC
TCCTTGG
GAM7052 296 CCL22 2 13638 NP_002981.2 3 1360 AGCCTCCCAAGT CA----- CA 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGT ACATTAGGGTCGATGA CC
TGTGTGG AC
GAM7052 296 CCL28 1 5390 NP_062820.1 3 180 AGCCTTCCAAGT CA----- C--- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTGTGC ACATTAGGGTCGATGA TCC
CGTGTGG ACCT
GAM7052 296 CCNF 1 8016 NP_001752.1 3 1376 AGCCTCCTGGGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AAGCACCC ACATTAGGGTCGATGGGTCC
CCCACGA
GAM7052 296 CCNL2 1 8702 NP_112199.1 5 1131 CTGTGTTTGGCT C ---- -- T 3 C c c
TCCAGGAATTAC CATGTAAT CC AGCT AC CAG
ATGAACGA GTACATTA GG TCGG TG GTC
A ACCT TT T
GAM7052 296 CD24 1 12740 NP_037362.1 3 975 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCT ACATTAGGGTCGATGA CC
TCCACGG AC
GAM7052 296 CDC14B 1 8433 NP_201589.1 3 717 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCGTCT ATATTAGGGTCGATGAGTCC
TCTGCGG
GAM7052 296 CDC2L2 1 14683 NP_296370.1 5 103 CCCAATCCTAGT --- A C 3 C c c
AGCTGGGAGTAT CAT GTA TCCCAGCTACT AGG
CAGGTGAG GTG TAT AGGGTCGATGA TCC
GAC G -
GAM7052 296 CDC6 1 2823 NP_001245.1 3 499 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCC ACATTAGGGTCGATGAG CC
CCCGTGG C
GAM7052 296 CDH1 1 15641 NP_004351.1 3 604 AGCCTCCCAAGT AA---- CA 3 C c c

AGCTGGGACCAC CATGT TCCCAGCTACT GG
AGGCATGC GTACG AGGGTCGATGA CC

GACACC AC
GAM7052 296 CDH11 1 7516 NP_387513.1 3 212 TCAAACCTGAGT ATCCCAGC 3 C c c
ATCAGTACATGC CATGTA TACTCAGG
CTAGACCT GTACAT ATGAGTCC
GACT----
GAM7052 296 CEACAM8 1 9995 NP_001807.2 3 438 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCT ACAT AGGGTCGATGAGTCC
TCCGCGG C
GAM7052 296 CECR1 2 5536 NP_059120.2 3 947 AGTCTCCCGAAG T T CA 3 C c c
TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGACATGA GT CATTAGGGTCG TGA CC
- - AG
GAM7052 296 CECR1 2 5536 NP_803124.1 3 947 AGTCTCCCGAAG T T CA 3 C c c
TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGACATGA GT CATTAGGGTCG TGA CC
- - AG
GAM7052 296 CECR1 2 16723 NP_059120.2 3 1481 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 CECR1 2 16723 NP_803124.1 3 1481 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 CGI-14 1 17011 NP_057028.2 3 159 CCTGGAGGCGGT A- ----- 3 C c c
GGCTGGGATAAA CATGT ATCCCAGCTACT CAGG
CGTGCACC GTGCA TAGGGTCGGTGG GTCC
AA CGGAG
GAM7052 296 CGI-18 1 16885 NP_057031.1 5 100 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C
GAM7052 296 CHRAC1 1 8325 NP_059140.1 3 1045 ATCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTGT ACATTAGGGTCGATGAGTCC
TGTGCGG
GAM7052 296 CHRNB4 1 13754 NP_000741.1 3 516 AACCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGAAAGCC ACATTAGGGTCGATGA CC
CCGAAAG AC
GAM7052 296 CHSY1 1 9811 NP_055733.2 3 724 TGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACAC ACATTAGGGTCGATGAG CC
CACACGG C

GAM7052 296 CIAS1 1 12643 NP_004886.2 5 374 AACTTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCC ACATTAGGGTCGATGAGTCC
CCCGCGG

GAM7052 296 CIP29 1 11229 NP_115740.3 3 248 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCC
CACACGG

GAM7052 296 CLECSF1 1 10135 NP_072092.2 3 1054 AGCCTCCCAAGT CA----- CA 3 C c
c
2 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGTCAGGC ACATTAGGGTCGATGA CC
CGGACTG AC

GAM7052 296 CLN8 1 3696 NP_061764.2 3 1723 ACCCTTTCAAGT CA----- C--- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTACCT ACATTAGGGTCGATGA TCC
TCCATGG ACTT

GAM7052 296 cPLA2de 1 10898 NP_828848.1 3 2350 AGCCTCCCAAAG T T CA 3 C c
c
lta TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGGTGTGA GT CATTAGGGTCG TGA CC
- - AA

GAM7052 296 cPLA2de 1 10898 XP_208820.2 3 1443 AGCCTCCCAAAG T T CA 3 C c
c
lta TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGGTGTGA GT CATTAGGGTCG TGA CC
- - AA

GAM7052 296 CPSF2 1 16291 XP_029311.2 3 2132 AGCATCTCGAGT CA----- - 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCATGC ACATTAGGGTCGATGAG TCT
CGTACGG C

GAM7052 296 CRLF3 1 10228 NP_057070.2 3 698 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTCG ACATTAGGGTCGATGAGTCC
GCTGTGG

GAM7052 296 CRSP6 1 5118 NP_004259.3 3 520 AGCCTTCCGAGT AA---- A 3 C c c
AGCTGGGACCAC CATGT TCCCAGCTACTC GG
AGGCATGC GTACG AGGGTCGATGAG CC
GACACC -

GAM7052 296 CTEN 1 4888 NP_116254.3 3 852 AGGCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGAG CC
TGTACGG C

GAM7052 296 CYCS 2 6532 NP_061820.1 3 2705 AGCCTCTCAAGT CA----- C--- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AAGCATGC ACATTAGGGTCGATGA TCC

CGTACGA ACTC
GAM7052 296 CYCS 2 18745 NP_061820.1 3 2286 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTGC TGTAATCCCAGCTACTCAGG
AGGCACCC ACGTTAGGGTCGATGAGTCC
CCCACGG
GAM7052 296 CYLC2 1 13498 NP_001331.1 3 817 AGCCTCTCTGGT CA----- T 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTAC CAGG
AGGGAAGG ACATTAGGGTCGATG GTCT
GGAAGGG -
GAM7052 296 CYP24A1 1 5450 NP_000773.1 3 76 AAGCGGACTGAG C- A---- T 3 C c
c

TGCTGGGATCCA ATGT ATCCCAGC ACTCAG
AGGCATTC TACG TAGGGTCG TGAGTC
CT GAACC -
GAM7052 296 CYP2B6 2 14013 NP_000758.1 3 361 AGCCTCCCTAGT CA----- C 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCATGC ACATTAGGGTCGATGA TCC
CGTACGG -
GAM7052 296 CYP2B6 2 14638 NP_000758.1 3 1171 CAGCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGT ACATTAGGGTCGATGA CC
TGTACGG AC
GAM7052 296 CYP8B1 2 5688 NP_004382.1 3 637 AGCCTCCCCAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCT ACATTAGGGTCGATGA CC
TCCACGG CC
GAM7052 296 CYP8B1 2 14961 NP_004382.1 3 1091 AGGCTTCTGAGT CA----- 3 C c
c

AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGTGCGC ATATTAGGGTCGATGAGTCT
CGCGTGG
GAM7052 296 DCX 1 5712 NP_000546.2 3 5054 AGTCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGC ACATTAGGGTCGATGAG CC
CGTGCGG C
GAM7052 296 DCX 1 5712 NP_835364.1 3 5054 AGTCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGC ACATTAGGGTCGATGAG CC
CGTGCGG C
GAM7052 296 DCX 1 5712 NP_835365.1 3 5054 AGTCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGC ACATTAGGGTCGATGAG CC
CGTGCGG C
GAM7052 296 DCX 1 5712 NP_835366.1 3 5054 AGTCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGC ACATTAGGGTCGATGAG CC

CGTGCGG C
GAM7052 296 DFFB 2 12740 NP_004393.1 3 974 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCT ACATTAGGGTCGATGA CC
TCCACGG AC
GAM7052 296 DFFB 2 16722 NP_004393.1 3 288 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGAG CC
TGTACGG C
GAM7052 296 DKFZp43 1 8218 NP_060068.1 3 1083 AGCCTCCTGAGT CA----- 3 C c c

4C0923 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCGAGA ATATTAGGGTCGATGAGTCC
AGAGCGG
GAM7052 296 DKFZP43 1 2840 NP_056410.2 3 1041 GGCCTCCCCAAG ---- T CA 3 C c
c
4D146 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GATA - AC
GAM7052 296 DKFZP43 1 5215 NP_110444.1 3 2496 AGCCTCCTGAGT CA----- 3 C c
c
4F0318 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGATGTGC ACATTAGGGTCGATGAGTCC
CGTGTAG
GAM7052 296 DKFZp54 1 15974 NP_061174.1 3 185 TAGAAACTGAGT T- C 3 C c c
7A023 AGTTTGGATTTT CATG AATCC AGCTACTCAG
TATGGCTC GTAT TTAGG TTGATGAGTC
TT T
GAM7052 296 DKFZP56 1 11229 NP_056416.1 5 1196 AGCCTCCTGAGT CA----- 3 C c
c
4G092 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCC
CACACGG
GAM7052 296 DKFZP56 1 19558 NP_115496.1 3 311 AGCCTCCTGAGT CA----- C 3 C c
c
4O0523 ATCTGGGATTAC TGTAATCCCAG TACTCAGG
AGGCGTGC ACATTAGGGTC ATGAGTCC
CGTGCGG T
GAM7052 296 DKFZP56 1 9433 NP_056226.1 3 797 AGCCTCCTGAGT CA----- A 3 C c
c
6I1024 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AAGTGTGC ACAT AGGGTCGATGAGTCC
CGTGTGA C
GAM7052 296 DKFZP58 1 9678 NP_056248.1 3 559 AGCTCCCCAAGT AA---- CA 3 C c
c
6D0919 AGCTGGGACTAG CATGT TCCCAGCTACT GG
AGGCATGC GTACG AGGGTCGATGA CC
GAGATC AC
GAM7052 296 DKFZp58 1 3745 NP_689960.1 3 440 TATGCCCTGAGT TAA CCA 3 C c
c

```
          6I1420                      AGCGAGTCCATG CATG  TC  GCTACTCAGG
                                    TCACTCAG    GTAC  AG  CGATGAGTCC
                                          CTG  ---
GAM7052  296   DKFZP58 1  3746  NP_112584.1  3  3136  ACAGAGTGCTGG  T  A     A T        3  C  c
c
          6M1120                      AGCTGGGAATAC CA GTA TCCCAGCT C CAG
                                    TGACCCAG    GT CAT AGGGTCGA G GTC
                                          -  A      - -
GAM7052  296   DKFZp66 1  7365  NP_808881.1  3  1051  AGCTTCCCGAGT CA-----          A     3  C  c
c
          7B1218                      AGCTGGGATTAC      TGTAATCCCAGCTACTC GG
                                    AGGCGTGC         ACATTAGGGTCGATGAG CC
                                          CGTGCGG            C
GAM7052  296   DKFZp76 1  14917 NP_775734.1  3  259   TACACACTGAGT   T  CCCA           3  C  c
c
          1B107                       AGTATGTATTTC CATG AAT   GCTACTCAG
                                    ATGGATGA    GTAC TTA   TGATGAGTC
                                          T  TGTA
GAM7052  296   DKFZp76 1  3467  NP_689650.1  5  1089  AGCCTCTGGAGT CA-----          ---   3  C  c
c
          1B128                       AGCTGGGATTAC      TGTAATCCCAGCTACTC  AGG
                                    AGATGGGA         ACATTAGGGTCGATGAG  TCC
                                          AGGGTAG            GTC
GAM7052  296   DKFZp76 1  3638  NP_061181.1  3  972   AGCCTCCCAAGT CA-----          CA    3  C  c
c
          1H039                       AGCTGGGATTAC      TGTAATCCCAGCTACT  GG
                                    AGGTGCCC         ACATTAGGGTCGATGA  CC
                                          CCCGTGG            AC
GAM7052  296   DKFZp76 1  6533  NP_690870.1  3  825   AGCCTCCTGATT CA-----         C      3  C  c  c

          1P1121                      AGCTGGGATTAC      TGTAATCCCAGCTA TCAGG
                                    AGGCGTGT         ACATTAGGGTCGAT AGTCC
                                          TGTGCGG            T
GAM7052  296   DKFZp76 1  13279 NP_061189.2  3  859   TACCTCCTGAGT CA-----       C       3  C  c
c
          2L0311                      AACTGGGATTAC      TGTAATCCCAG TACTCAGG
                                    AGTCGTGT         ACATTAGGGTC ATGAGTCC
                                          TGTGCTG          A
GAM7052  296   DLAD   1  10031 NP_490649.1  5  6     TGCAGGCTGGGT   GTAATC           3  C  c
c
                                    AGCTGGTAGAAA CAT     CCAGCTACTCAG
                                    TGTTGTGG    GTA     GGTCGATGGGTC
                                          AAGAT-
GAM7052  296   DLST   1  9118  NP_001924.2  3  1173  ATTCCTTGGAGC   T      CTA  --       3  C  c  c
                                    CACTGGGATTCA CATG AATCCCAG   CTC  AGG
                                    TGGCTTTG    GTAC TTAGGGTC   GAG  TCC
                                          -       ACC   GT
GAM7052  296   DSC3   1  9847  NP_001932.1  3  2134  AGCCTCCTGAGT CA-----  A          3  C  c  c
                                    AGCTGGGACTAC      TGTA TCCCAGCTACTCAGG
                                    AGGCGCCC         ACAT AGGGTCGATGAGTCC
```

CCCGCGG C
GAM7052 296 DSC3 1 9847 NP_077741.1 3 2348 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 DYRK1A 1 17441 NP_567824.1 5 150 AGCCTCCCCAGT CA----- CA 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGTGTTAT ACATTAGGGTCGATGA CC
TATTGTG CC
GAM7052 296 EDEM 1 12749 NP_055489.1 3 496 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGAGC ACATTAGGGTCGATGAG CC
CGAGTGG C
GAM7052 296 EEF2K 1 13359 NP_037434.1 3 430 AGCCTCCCAAGT T CA 3 C b b
AGCTGGGATTAC CA GTAATCCCAGCTACT GG
TGGTGCAC GT CATTAGGGTCGATGA CC
- AC
GAM7052 296 EGR1 1 10941 NP_001955.1 3 1059 TACCTACTGAGT TGT - AG 3 C c
c
AGGCGGCGATTT CA AATC CC CTACTCAG
TTGTATGT GT TTAG GG GATGAGTC
TT- C CG
GAM7052 296 EHD2 1 10698 NP_055416.2 3 991 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTGC TGTA TCCCAGCTACTCAGG
AGGCACGC ACGT AGGGTCGATGAGTCC
CGCACGG C
GAM7052 296 ELP3 1 8011 NP_060561.3 3 986 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCC ACATTAGGGTCGATGAGTCC
CCCACGG
GAM7052 296 ESM1 1 1018 NP_008967.1 5 48 CGAGCCGGAGGC AA A- A 3 C c c
AGCTGGGAAACA CATGT TCCCAGCT CTC GG
TGAAGAGC GTACA AGGGTCGA GAG CC
A- CG G
GAM7052 296 ET(B)R- 1 9691 NP_004758.2 3 598 AGCCTCCTGAGT CA----- 3 C c c
LP-2 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG
GAM7052 296 F11R 1 9554 NP_058642.1 3 2233 AGTCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
GGGTGCGT GCATTAGGGTCGATGAGTCC
TGCGTGG
GAM7052 296 F11R 1 9554 NP_653085.1 3 2233 AGTCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
GGGTGCGT GCATTAGGGTCGATGAGTCC
TGCGTGG
GAM7052 296 F11R 1 9554 NP_653086.1 3 2235 AGTCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG

GGGTGCGT GCATTAGGGTCGATGAGTCC
TGCGTGG
GAM7052 296 F11R 1 9554 NP_653087.1 3 2235 AGTCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
GGGTGCGT GCATTAGGGTCGATGAGTCC
TGCGTGG
GAM7052 296 F2RL2 1 6476 NP_004092.1 3 266 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
ACCACCAT ACATTAGGGTCGATGA CC
TACCACC AC
GAM7052 296 F3 1 14740 NP_001984.1 3 510 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCGC ACATTAGGGTCGATGAG CC
CGCGTGG C
GAM7052 296 FABP2 1 17010 NP_000125.1 3 456 AGGCTTCTGAGT TAA C 3 C c c

AGCTAGGACTAT CATG TCC AGCTACTCAGG
GGGTACAT GTAT AGG TCGATGAGTCT
C-- A
GAM7052 296 FANCE 1 1495 NP_068741.1 3 365 AGCCTCCCAAGT A CA 3 C c c
AGCTGGGACTAC CATGTA TCCCAGCTACT GG
ATGCACAT GTACAT AGGGTCGATGA CC
C AC
GAM7052 296 FANCF 1 13765 NP_073562.1 3 820 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCAG ACATTAGGGTCGATGA CC
GACGTGG AC
GAM7052 296 FBXO32 1 4134 NP_478136.1 3 65 TGCTGACTGGAG AA AC 3 C c c

AGCTGGGAATAT CATGT TCCCAGCT TCAG
GGCATTTG GTATA AGGGTCGA GGTC
-- GA
GAM7052 296 FBXO32 1 4134 NP_680482.1 3 65 TGCTGACTGGAG AA AC 3 C c c

AGCTGGGAATAT CATGT TCCCAGCT TCAG
GGCATTTG GTATA AGGGTCGA GGTC
-- GA
GAM7052 296 FBXW8 1 8434 NP_036306.1 3 1583 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTCC ACATTAGGGTCGATGAGTCC
CCTGCGG
GAM7052 296 FBXW8 1 8434 NP_699179.2 3 1583 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTCC ACATTAGGGTCGATGAGTCC
CCTGCGG
GAM7052 296 FCGR2A 1 6966 NP_067674.1 3 606 CAGCCTCCCAGT ---- C-- 3 C c c
AGCTGGGATTAG CATGT AATCCCAGCTACT AGG
AGGCATGT GTACG TTAGGGTCGATGA TCC

GAGA CCC
GAM7052 296 FCRH1 1 6123 NP_443170.1 3 872 AGCCTGCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAG
AGGCACAT ACAT AGGGTCGATGAGTC
TACACGG C
GAM7052 296 FER1L4 1 20036 XP_300246.1 3 307 AGCCTCCCCAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGTGG ACATTAGGGTCGATGA CC
GGTGCGG CC
GAM7052 296 FER1L4 1 20036 XP_300246.1 3 456 AGCCTCCCCAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGTGG ACATTAGGGTCGATGA CC
GGTGCGG CC
GAM7052 296 FEZ1 1 4759 NP_072043.1 3 911 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTGC ACAT AGGGTCGATGAGTCC
CGTGTGG C
GAM7052 296 FGF5 2 14043 NP_004455.1 3 2465 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGACTCAT ACATTAGGGTCGATGA CC
TACTCAG AC
GAM7052 296 FGF5 2 14043 NP_149134.1 3 2796 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGACTCAT ACATTAGGGTCGATGA CC
TACTCAG AC
GAM7052 296 FGF5 2 17245 NP_004455.1 3 757 TAAACCTTTGGT GTA C- 3 C c c
GGCTGGGATATG CAT ATCCCAGCTACT AGG
ATGGGTTA GTA TAGGGTCGGTGG TCC
GTA TT
GAM7052 296 FGF5 2 17245 NP_149134.1 3 1088 TAAACCTTTGGT GTA C- 3 C c c
GGCTGGGATATG CAT ATCCCAGCTACT AGG
ATGGGTTA GTA TAGGGTCGGTGG TCC
GTA TT
GAM7052 296 FLJ1023 2 6964 NP_060503.1 5 93 AGTCTCTTGAGT CA----- C 3 C c c
2 AGCTGAGATTAC TGTAATC CAGCTACTCAGG
AGGTACGC ACATTAG GTCGATGAGTTC
CGCATGG A
GAM7052 296 FLJ1023 2 15854 NP_060503.1 3 880 AGCCTCACAAGT CA----- C--- 3 C c
c
2 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTGCCC ACATTAGGGTCGATGA TCC
CCCGTGG ACAC
GAM7052 296 FLJ1034 1 14573 NP_060535.1 5 185 AGCCTTCTGAGT CA----- A 3 C c c

6 AGCTGGGAGTAC TGTA TCCCAGCTACTCAGG

AGGCGCCC ACAT AGGGTCGATGAGTCT
CCCGCGG G
GAM7052 296 FLJ1056 1 9847 NP_060608.1 3 275 AGCCTCCTGAGT CA----- A 3 C c c
0 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 FLJ1061 1 3913 NP_061940.1 3 701 GGCCTCCCAAAG ---- T CA 3 C c c
3 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GATA - AA
GAM7052 296 FLJ1062 1 8748 NP_060627.1 3 1311 GACTCCCTGAGT TAA---- GC 3 C c
c
0 AATGGGAGTTCT CATG TCCCA TACTCAGG
TTCATGGC GTAC AGGGT ATGAGTCC
TTTCTTG A-
GAM7052 296 FLJ1064 1 9332 NP_061896.1 5 151 GGCCTACCGAGT CA----- A A 3 C c
c
0 AGCTGGGACTAC TGTA TCCCAGCTACTC GG
AGGCACGC ACAT AGGGTCGATGAG CC
CGCACGG C -
GAM7052 296 FLJ1084 2 16146 NP_060712.2 3 924 GCCCTCCCAAAG ---- T CA 3 C c c
7 TGTTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTTG TGA CC
GATA - AA
GAM7052 296 FLJ1084 2 19185 NP_060712.2 3 798 AGCCTCCTGAGT AA---- C 3 C c c
7 AGCTGAGACCAC CATGT TC CAGCTACTCAGG
AGGCGTGT GTGCG AG GTCGATGAGTCC
GACACC A
GAM7052 296 FLJ1090 1 1578 NP_060735.1 3 969 AGCCTTCTGAGT CA----- 3 C c c
1 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCAAGC ACATTAGGGTCGATGAGTCT
CGAACGG
GAM7052 296 FLJ1092 1 857 NP_060743.1 3 2275 AGCCACCCAAAG C T CA 3 C c c
2 TGCTGGAATTAC CATGTAAT CCAGC ACT GG
ATGGGTGA GTACATTA GGTCG TGA CC
A - AA
GAM7052 296 FLJ1146 1 18821 NP_079239.2 3 229 GGCCTCCTGAGT CA----- A 3 C c
c
7 AGCTGGGACTGC TGTA TCCCAGCTACTCAGG
AGTTGTAA ACGT AGGGTCGATGAGTCC
AATGTTG C
GAM7052 296 FLJ1182 1 11535 NP_079369.1 3 1119 TGCCTTGACTGT CCA -- 3 C c c
7 GGCGATGATTAC CATGTAATC GCTAC TCAGG
ATGAAAAC GTACATTAG CGGTG AGTTC
TAG TC

GAM7052 296 FLJ1236 1 8012 NP_115543.1 3 136 AGCCTCCCGAGT CA----- A 3 C c c

3 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCT ACATTAGGGTCGATGAG CC
TCCACGG C

GAM7052 296 FLJ1257 1 1348 NP_075056.2 3 1666 TGGAGCCCTGAT G GC C 3 C c
c

2 GAATGGGATTAG CAT TAATCCCA TA TCAGG
TGCTTTAT GTG ATTAGGGT GT AGTCC
- AA -

GAM7052 296 FLJ1264 1 10699 XP_291344.1 3 1036 AGCCTCCTGAGT CA----- A 3 C c
c

9 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACAC ACAT AGGGTCGATGAGTCC
CACACGG C

GAM7052 296 FLJ1274 1 2107 XP_290972.1 3 2625 AGCCTCCCAAGT CA----- CA 3 C c
c

7 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC
CGTACGG AC

GAM7052 296 FLJ1278 1 9691 NP_115551.1 3 1106 AGCCTCCTGAGT CA----- 3 C c c

7 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG

GAM7052 296 FLJ1290 1 17852 NP_073590.1 3 1643 AGCCTCCTGAGT CA----- C 3 C c
c

3 AGCTGTGATTAC TGTAATC CAGCTACTCAGG
AGGCATGC ACATTAG GTCGATGAGTCC
CGTACGG T

GAM7052 296 FLJ1297 1 13360 NP_079184.1 3 380 AGACTCCTAAGT CA----- C 3 C c c

3 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCACCT ACATTAGGGTCGATGA TCC
TCCACGG A

GAM7052 296 FLJ1307 1 16722 XP_117117.2 3 783 AGCCTCCCGAGT CA----- A 3 C c
c

2 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGAG CC
TGTACGG C

GAM7052 296 FLJ1317 1 10344 NP_076412.1 5 239 GGCCTCCCAAAG ---- T CA 3 C c
c

1 TGCTGGGATTAG CATGT AATCCCAGC ACT GG
AGGCGTGA GTGCG TTAGGGTCG TGA CC
GAGA - AA

GAM7052 296 FLJ1318 1 11689 NP_071346.1 3 498 AGCCTCCTGAGT CAT----- 3 C c c

8 AGCTGGGATTAT GTAATCCCAGCTACTCAGG
GGACAAAT TATTAGGGTCGATGAGTCC
TAAACAGG

GAM7052 296 FLJ1320 1 7003 NP_079037.2 3 2610 AGCCTCCTGAGT AA--- CA 3 C c
c

4 AGCCAGGACTAT CATGT TCC GCTACTCAGG
GGCATGTA GTACG AGG CGATGAGTCC
GTATC AC

GAM7052 296 FLJ1444 1 9691 NP_116174.1 3 2321 AGCCTCCTGAGT CA----- 3 C c c
2 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG

GAM7052 296 FLJ1480 1 7216 NP_116231.1 3 521 AGCCTCCTGAGT CA----- 3 C c c
3 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGTGCGA ATATTAGGGTCGATGAGTCC
AGCGTGG

GAM7052 296 FLJ2004 1 5969 NP_060108.1 3 217 AGCCTCCTGAGT CA----- 3 C c c
5 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAT ACATTAGGGTCGATGAGTCC
TACACGG

GAM7052 296 FLJ2007 1 17687 NP_060126.1 3 2119 CTCACCCTCAGT ---- C 3 C b b
9 AGCTGGGATTAT CATGT AATCCCAGCTACT AGG
TGGCATGC GTACG TTAGGGTCGATGA TCC
GTTA C

GAM7052 296 FLJ2013 1 9023 NP_060154.1 3 546 AGCCTCCTGAGT CA----- C 3 C c c
6 AGCTAGGATTAC TGTAATCC AGCTACTCAGG
AGGTGTGT ACATTAGG TCGATGAGTCC
TGTGTGG A

GAM7052 296 FLJ2024 1 12481 NP_060193.1 3 2384 AGCCTCCCGAGT CA----- A 3 C c
c
5 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCC ACATTAGGGTCGATGAG CC
CCCGCGG C

GAM7052 296 FLJ2027 1 14443 NP_060208.1 3 19 CAGCCTCCTGGT CA----- A T 3 C c
c
6 AGCTGGGACTAC TGTA TCCCAGCTAC CAGG
AGCTTCCT ACAT AGGGTCGATG GTCC
TCCTTCG C -

GAM7052 296 FLJ2050 2 3913 NP_060319.1 3 2554 GGCCTCCCAAAG ---- T CA 3 C c
c
7 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GATA - AA

GAM7052 296 FLJ2050 2 16723 NP_060319.1 3 2416 AGCCTCCTGAGT CA----- 3 C c c
7 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG

GAM7052 296 FLJ2051 1 9847 NP_060323.1 3 761 AGCCTCCTGAGT CA----- A 3 C c c
1 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C

GAM7052 296 FLJ2186 1 3914 NP_073596.1 3 683 GGCAGTGCTGAG TA-- A 3 C c c
5 GGCTGGGATGCT CATG ATCCCAGCT CTCAG

CTGTGACC GTGT TAGGGTCGG GAGTC
CTCG -
GAM7052 296 FLJ2253 1 7027 NP_078926.2 5 426 AGTCCCCCGAGT CA----- A 3 C c c
1 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGATGCCC ACATTAGGGTCGATGAG CC
CCCGTAG C
GAM7052 296 FLJ2259 1 8875 NP_078979.1 5 849 CCTGTGAGCCTT T ------ ACT 3 C c c
3 GACTGGGATTCA CATG AATCCCA GCT CAGG
TGATGTGG GTAC TTAGGGT CGA GTCC
- CAGTTC GT-
GAM7052 296 FLJ2267 1 19747 NP_060168.1 3 1001 TCCTCAGTTCCC - ---- C 3 C c c
9 AGCTGGGATTGC CAT GTAATCCCAGCT ACT AGG
TATGCACT GTA CGTTAGGGTCGA TGA TCC
T CCCT C
GAM7052 296 FLJ2267 1 19747 NP_115603.1 3 1176 TCCTCAGTTCCC - ---- C 3 C c c
9 AGCTGGGATTGC CAT GTAATCCCAGCT ACT AGG
TATGCACT GTA CGTTAGGGTCGA TGA TCC
T CCCT C
GAM7052 296 FLJ2279 1 9450 NP_071357.1 3 341 AGTCTCCTGAGC CA----- A 3 C c c
4 AGCTGGGATTAC TGTAATCCCAGCT CTCAGG
AGGCAAAC ACATTAGGGTCGA GAGTCC
CAAACGG C
GAM7052 296 FLJ2296 1 2108 NP_071384.1 3 317 AGCCTCCTGAGT CA----- 3 C c c
5 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
GGGCATGT GCATTAGGGTCGATGAGTCC
TGTACGG
GAM7052 296 FLJ2302 1 14741 NP_079212.1 3 415 AGCCTCCTGAGT CA----- C 3 C c
c
4 AGCTGGAATTAT TGTAAT CCAGCTACTCAGG
AGGCACAT ATATTA GGTCGATGAGTCC
TACACGG A
GAM7052 296 FLJ2315 1 6505 NP_079048.2 5 86 AGCCTCCCGAGT CA----- A 3 C c c
1 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGAATCT ACATTAGGGTCGATGAG CC
TCTAAGG C
GAM7052 296 FLJ2339 1 18508 NP_079060.1 3 817 AGCCTCTTGAGT CA----- 3 C c c
2 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGAACGC ACATTAGGGTCGATGAGTTC
CGCAAGG
GAM7052 296 FLJ2341 1 1770 NP_115614.1 3 1408 AGTTCTCCGAGT AA A 3 C b b
6 AGCTGGGACCAC CATGT TCCCAGCTACTC GG
ATGTGTAA GTACA AGGGTCGATGAG CC
CC -
GAM7052 296 FLJ2355 1 19274 NP_079156.1 3 809 AGCCTCCTGAGT CA----- 3 C c c
6 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTGT ACATTAGGGTCGATGAGTCC
TGTGCGG
GAM7052 296 FLJ2356 1 3638 XP_041701.4 3 1809 AGCCTCCCAAGT CA----- CA 3 C c
c

3 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC

GAM7052 296 FLJ2503 1 1524 NP_689779.1 3 659 CTATTTCTGGGA A A 3 C c c
3 AGCTGGGAGTAT CATGTA TCCCAGCT CTCAGG
GTGACATT GTGTAT AGGGTCGA GGGTCT
G A

GAM7052 296 FLJ2506 1 16676 NP_689717.2 3 353 ATCGGCCTGAGG -- TA 3 C b b
7 CTGGGACATTAC CATGTAA TCCCAGC CTCAGG
ATGAAATC GTACATT AGGGTCG GAGTCC
AC --

GAM7052 296 FLJ2542 1 12652 NP_689589.1 3 121 TGGACCTGGTGC T AA -- T 3 C c
c
9 AGCTGGGAAGCT CA GT TCCCAGCT AC CAGG
TGGGACTC GT CG AGGGTCGA TG GTCC
T A- CG -

GAM7052 296 FLJ2579 1 11825 NP_689633.1 3 654 AGCCTCCTGAGT AA---- C 3 C c c

5 AGCTAGGACTGT CATGT TCC AGCTACTCAGG
AGGCATGT GTACG AGG TCGATGAGTCC
GATGTC A

GAM7052 296 FLJ3050 1 6534 NP_694555.1 5 153 AGCCTCTCAAGT CA----- C--- 3 C c c

7 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGGCTTC ACATTAGGGTCGATGA TCC
CTTCGGG ACTC

GAM7052 296 FLJ3053 1 4754 NP_653325.1 3 276 TGCCTCCCAAGT CA----- CA 3 C c
c
2 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 FLJ3113 1 16723 NP_775928.1 3 483 AGCCTCCTGAGT CA----- 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG

GAM7052 296 FLJ3133 1 13983 NP_689682.1 3 353 GGCCTCCTGATT CA----- C 3 C c c

8 AGCTGGGATTAC TGTAATCCCAGCTA TCAGG
AGGCATGT ACATTAGGGTCGAT AGTCC
TGTACGG T

GAM7052 296 FLJ3139 1 4686 NP_694569.1 5 223 AGCCTCCTGAGT CA----- A 3 C c c
3 AGCTGGGACTAT TGTA TCCCAGCTACTCAGG
AGGCTCCC ATAT AGGGTCGATGAGTCC
CCCTCGG C

GAM7052 296 FLJ3195 1 18462 NP_694575.1 3 1685 GTCCTCCCAAAG ---- T CA 3 C c
c
8 TGCTGGGATTAA CATGT AATCCCAGC ACT GG
TGGCGTGA GTGCG TTAGGGTCG TGA CC
GTAA - AA

GAM7052 296 FLJ3209 2 1832 NP_776156.1 3 1502 AGCCCCCAGAGT CA----- A 3 C c
c

6 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGAG CC
TGTACGG A
GAM7052 296 FLJ3209 2 12527 NP_776156.1 3 1198 AGCCTCCCGAGT CA----- A 3 C c
c
6 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCT ACATTAGGGTCGATGAG CC
TCCGCGG C
GAM7052 296 FLJ3213 1 14068 NP_689671.2 3 1525 AGCCTCTTGAGT CA----- 3 C c c

0 GGCTGGGATTGC TGTAATCCCAGCTACTCAGG
AGGCGCCC ACGTTAGGGTCGGTGAGTTC
CCCGCGG
GAM7052 296 FLJ3280 1 702 NP_694584.1 3 729 AGCCTCCCAAGT CA----- CA 3 C c c

3 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACAT ACATTAGGGTCGATGA CC
TACACGG AC
GAM7052 296 FLJ3286 1 16885 NP_653214.1 3 1333 AGCCTCCCGAGT CA----- A 3 C c
c
5 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C
GAM7052 296 FLJ3365 1 19276 NP_775912.1 3 411 AGCCTCCTGAGT CA----- 3 C c c
5 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCGTGC ATATTAGGGTCGATGAGTCC
CGTGCGG
GAM7052 296 FLJ3381 1 13609 NP_775781.1 3 960 ACCCTCCCAAGT CA----- CA 3 C c
c
4 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC
GAM7052 296 FLJ3481 1 5119 NP_689516.1 5 354 AGCCTCCTGAGT CA----- A 3 C c c
7 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGAATTA ACAT AGGGTCGATGAGTCC
ATTAAGG C
GAM7052 296 FLJ3492 1 11941 NP_689483.1 5 235 AGCCGCCTGAGT CA----- AA 3 C c
c
2 AGCTGGGACCAC TGT TCCCAGCTACTCAGG
AGTTTCAG ACA AGGGTCGATGAGTCC
GACTTTG CC
GAM7052 296 FLJ3496 1 6275 XP_114353.1 3 1633 AGCCTCCTGAGT CA----- 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTATGT ACATTAGGGTCGATGAGTCC
TGTATGG
GAM7052 296 FLJ3510 1 6938 NP_689890.1 5 246 AGCCTCCTGAGT CA----- 3 C c c
5 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGACCAG ACATTAGGGTCGATGAGTCC
GACCAGG
GAM7052 296 FLJ3644 1 9024 NP_694965.1 3 316 GGCCTCCCGAGT CA----- A 3 C c c

5 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGTGC ACATTAGGGTCGATGAG CC
CGTGTGG C
GAM7052 296 FLJ3707 1 15855 NP_694588.1 5 128 AGCCTCCCAAGT CA----- CA 3 C c
c
8 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCAC ACATTAGGGTCGATGA CC
CACGTGG AC
GAM7052 296 FLJ3743 1 4384 NP_848612.1 3 283 AGCCTCCTGAGT AATC---- 3 C c c

3 AGCTGGCACTGT CATGT CCAGCTACTCAGG
AGGCATGT GTACG GGTCGATGAGTCC
GATGTCAC
GAM7052 296 FLJ3754 1 17646 NP_775938.1 3 829 AGCCTCCTGAGT CA----- T 3 C c c

3 AGCTGGGTTTAC TGTAA CCCAGCTACTCAGG
AGGTGCCT ACATT GGGTCGATGAGTCC
TCCGTGG T
GAM7052 296 FLJ3810 1 1941 NP_694993.2 3 826 AGCCTTCCGAGT CA----- A A 3 C c
c
1 AGCTGGGACTAC TGTA TCCCAGCTACTC GG
AGGCGCAT ACAT AGGGTCGATGAG CC
TACGCGG C -
GAM7052 296 FLJ3814 2 14014 XP_091919.5 3 344 AGCCTCCTGAGT CA----- C 3 C c c

9 AGCTGAGATTAC TGTAATC CAGCTACTCAGG
AGGTGTGT ACATTAG GTCGATGAGTCC
TGTGTGG A
GAM7052 296 FLJ3814 2 15374 XP_091919.5 3 1517 AACCTCCTGAGT CA----- A 3 C c
c
9 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCT ACAT AGGGTCGATGAGTCC
TCCACGG C
GAM7052 296 FLJ3828 1 7430 NP_689814.1 3 195 AGCTTCCTGAGT CA----- AA 3 C c c

1 AGCTGGGACAAC TGT TCCCAGCTACTCAGG
AGGTGTGA ACA AGGGTCGATGAGTCC
AGTGTGG AC
GAM7052 296 FLJ3860 1 8761 NP_689867.1 3 629 AGCCTCCTGAGT CA----- A 3 C c c
7 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCC ACAT AGGGTCGATGAGTCC
CCCACGG C
GAM7052 296 FLJ3871 1 10312 NP_689580.1 3 558 GGTTGGTTGAGT C---- TC- 3 C c c

6 AGCTGGTGTTTG ATGTAA CCAGCTACTCAG
CATCCTGG TACGTT GGTCGATGAGTT
GGTCC TGT
GAM7052 296 FLJ3872 1 7203 NP_776166.1 3 1176 GAGGACCTGGAG TAA AC 3 C c
c
3 AGCTGGGAGACC CATG TCCCAGCT TCAGG

ATGATGAG GTAC AGGGTCGA GGTCC
CAG GA
GAM7052 296 FLJ3881 1 5470 NP_665872.1 3 1126 AGCCTCCTGAGT CA----- 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTGC ACATTAGGGTCGATGAGTCC
CGTGCGG
GAM7052 296 FLJ3899 1 16971 NP_776188.1 3 1122 AGCCTACTGGGT CA----- A 3 C c
c
1 AGCTGGGACTAC TGTA TCCCAGCTACTCAG
AGGGGTGC ACAT AGGGTCGATGGGTC
CGTGGGG C
GAM7052 296 FLJ3905 1 4759 NP_775851.1 3 75 AGCCTCCTGAGT CA----- A 3 C c c
8 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTGC ACAT AGGGTCGATGAGTCC
CGTGTGG C
GAM7052 296 FLJ3907 1 6073 NP_689553.1 3 20 CAGTCTCCTGGT CA----- T 3 C c c
5 AGCTGGGATTAC TGTAATCCCAGCTAC CAGG
AGGCATGC ACATTAGGGTCGATG GTCC
CGTACGG -
GAM7052 296 FLJ3959 2 2431 NP_776164.1 3 1189 ATCCTTCGGAGT CA----- --- 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCAGGT ACATTAGGGTCGATGAG TCC
TGGACGG GCT
GAM7052 296 FLJ3959 2 3756 NP_776164.1 3 712 AGGCTCCTGAGT CA----- 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACGT ACATTAGGGTCGATGAGTCC
TGCACGG
GAM7052 296 FLJ3963 2 8837 XP_290687.1 3 767 AGCCTTCCGAGT CA----- A 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCC ACATTAGGGTCGATGAG CC
CCCGCGG -
GAM7052 296 FLJ3963 2 14740 XP_290687.1 3 1746 AGCCTCCCGAGT CA----- A 3 C c
c
9 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCGC ACATTAGGGTCGATGAG CC
CGCGTGG C
GAM7052 296 FLJ3982 1 648 NP_775971.1 3 696 AGATTCCTGAGT CA----- AA 3 C c c
1 AGCTGGGACCAC TGT TCCCAGCTACTCAGG
AGATTACT ACA AGGGTCGATGAGTCC
TCATTAG CC
GAM7052 296 FUT1 2 9847 NP_000139.1 3 1017 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 FUT1 2 16237 NP_000139.1 3 832 GGCCTCCCAAAG T T CA 3 C c c
TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGGCATGA GT CATTAGGGTCG TGA CC
- - AA
GAM7052 296 G2A 1 4759 NP_037477.1 3 1342 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG

AGGTGTGC ACAT AGGGTCGATGAGTCC
CGTGTGG C
GAM7052 296 GFAP 1 18063 NP_002046.1 3 617 AGCCTCCTGTGT CA----- T 3 C c c
AGCTGGGATTAT TGTAATCCCAGCTAC CAGG
AGATTGGA ATATTAGGGTCGATG GTCC
AGGTTAG T
GAM7052 296 GFER 1 1984 NP_005253.2 3 845 GGGGGCCAGAGT T A ----- A 3 C c c

AGCTGATGTAGG CA GTA TCC CAGCTACTC GG
AGTACTGG GT CAT AGG GTCGATGAG CC
- G ATGTA A
GAM7052 296 GGA2 1 15132 NP_055859.1 3 1749 AGCCTCTCGAGT CA----- A --- 3 C c
c

AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCGTGA ACAT AGGGTCGATGAG TCC
AGTGCGG C CTC
GAM7052 296 GGA2 1 15132 NP_619581.1 3 2837 AGCCTCTCGAGT CA----- A --- 3 C c
c

AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCGTGA ACAT AGGGTCGATGAG TCC
AGTGCGG C CTC
GAM7052 296 GHR 1 2927 NP_000154.1 3 1646 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACGC ACAT AGGGTCGATGAGTCC
CGCACGG C
GAM7052 296 GNE 1 10442 NP_005467.1 3 690 AGCCTCTTGAGT CA----- 3 C c c
GGCTGGGATTGC TGTAATCCCAGCTACTCAGG
GGGCACAT GCGTTAGGGTCGGTGAGTTC
TACACGG
GAM7052 296 GNG4 1 16886 NP_004476.1 3 693 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGATCAT TGT ATCCCAGCTACTCAGG
AGGCACGC ATA TAGGGTCGATGAGTCC
CGCACGG C
GAM7052 296 GNPNAT1 1 3158 XP_085119.1 3 2680 AGCCTCCAGAGT C----- C A 3 C c
c

ATCTGGGATTAC ATGTAATCCCAG TACTC GG
ATATGTCG TACATTAGGGTC ATGAG CC
GCTGTA T A
GAM7052 296 GOLGA3 1 11625 NP_005886.2 3 686 ATTCTCCCCAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG CC
GAM7052 296 GP5 1 3078 NP_004479.1 3 680 AGCGTTCTGAGT ---- 3 C b b
AGCTGGGATTAG CATGT AATCCCAGCTACTCAGG
AGGCGTGT GTGCG TTAGGGTCGATGAGTCT
GAGA
GAM7052 296 GPR56 1 3347 NP_005673.2 5 110 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGGTG ACATTAGGGTCGATGAG CC
GTGGTGG C
GAM7052 296 GR6 1 14557 NP_031380.1 5 370 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGAAAATC ACATTAGGGTCGATGAGTCC
CTAAAAG
GAM7052 296 GTF2E1 1 3032 NP_005504.1 3 391 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCT ACATTAGGGTCGATGAG CC
TCCGTGG C
GAM7052 296 GTPBG3 2 1434 NP_116009.1 3 716 AGCCTCTTGAGT CA----- A 3 C c
c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCAC ACAT AGGGTCGATGAGTTC
CACGCGG C
GAM7052 296 GTPBG3 2 16887 NP_116009.1 3 552 AGCCTCCTGAGT CA----- 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGT ACATTAGGGTCGATGAGTCC
TGTACGG
GAM7052 296 GYLTL1B 1 14235 NP_689525.1 5 551 TGGCAGGCTGGG GTA A 3 C c
c
GGCTGGGATGTG CAT ATCCCAGCT CTCAG
ATGGGTGT GTA TAGGGTCGG GGGTC
GTG -
GAM7052 296 H-plk 1 5790 NP_056936.1 5 1067 AGTCTCCTGAGT CA----- A 3 C c c
AGCTGGGATCAC TGT ATCCCAGCTACTCAGG
AGGGACCA ACA TAGGGTCGATGAGTCC
ACCAGGG C
GAM7052 296 H2AV 2 9267 NP_619541.1 3 669 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGCAC ACATTAGGGTCGATGA CC
CACGCGG AC
GAM7052 296 H2AV 2 17174 NP_619541.1 3 805 AGCCTTCCAAAG T T CA 3 C c c
TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGGCAGGA GT CATTAGGGTCG TGA CC
- - AA
GAM7052 296 H63 1 1187 NP_612432.2 3 550 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC
GAM7052 296 H63 1 1187 NP_816929.1 3 550 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC
GAM7052 296 HAVCR2 1 5471 NP_116171.2 3 582 AGCCTCCTGAGT CA----- 3 C c c

GGCTGGGATTAC TGTAATCCCAGCTACTCAGG

AGGCATGC ACATTAGGGTCGGTGAGTCC
CGTACGG
GAM7052 296 HBP17 1 8507 NP_005121.1 5 31 TTCACTCCCACT - CTACT 3 C c c
GCCTGGGATTGC CA TGTAATCCCAG CAG
ACTGGATC GT ACGTTAGGGTC GTC
C C----
GAM7052 296 HIF3A 1 4583 NP_690009.1 3 178 GGCCTCCCAAAG T T CA 3 C c c
TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGGTATGA GT CATTAGGGTCG TGA CC
- - AA
GAM7052 296 HRH4 1 10866 NP_067637.2 3 1502 AGCCACCTGAGC CA----- A 3 C c
c
AGCTGGGATTGC TGTAATCCCAGCT CTCAGG
AGGTGCAT ACGTTAGGGTCGA GAGTCC
TACGTGG C
GAM7052 296 HSD17B1 1 13157 NP_000404.1 5 6 GGCCTCCCAAAG ---- T CA 3 C c
c
TGCTGGGATTAG CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GAGA - AA
GAM7052 296 HSMPP8 1 5864 XP_167894.1 3 414 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGACACCC ACATTAGGGTCGATGAGTCC
CCCACAG
GAM7052 296 HSPC065 1 686 NP_054876.2 3 2378 AGCCTCCCCAGT CA----- CA 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGCCC ACATTAGGGTCGATGA CC
CCCGCGG CC
GAM7052 296 HTR1E 1 19389 NP_000856.1 5 222 CAGCTTCCTAGT CA----- C 3 C c c
AGCTGGGATTGC TGTAATCCCAGCTACT AGG
AGGCACTC ACGTTAGGGTCGATGA TCC
CTCACGG -
GAM7052 296 HUS1 1 16890 NP_004498.1 3 1106 AGCTTCCTGACT T A C 3 C c c
AGCTGGGACTAC CA GTA TCCCAGCTA TCAGG
TGGTGTGC GT CAT AGGGTCGAT AGTCC
- C C
GAM7052 296 IFNAR2 1 10469 NP_000865.2 3 1286 TCCCTCGCAAGT CA----- C--- 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCGCCT ACATTAGGGTCGATGA TCC
TCCGCGG ACGC
GAM7052 296 IGF1 1 8011 NP_000609.1 3 5433 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCC ACATTAGGGTCGATGAGTCC
CCCACGG
GAM7052 296 IL12RB1 1 12219 NP_714912.1 3 391 AGCCTCTGGAGT CA----- A --- 3 C c
c

AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGACATGC ACAT AGGGTCGATGAG TCC
CGTACAG C GTC

GAM7052 296 IL28RA 1 1187 NP_734464.1 3 2353 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 IL28RA 1 1187 NP_775087.1 3 2353 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 IL28RA 1 1187 NP_775088.1 3 3050 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 IMPACT 1 11567 NP_060909.1 3 2065 AGCCTGCCAAGT CA----- --- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT CAGG
AGACAGGC ACATTAGGGTCGATGA GTCC
CGGACAG ACC

GAM7052 296 INMT 1 16621 NP_006765.3 3 530 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGAGCTC ACAT AGGGTCGATGAGTCC
CTCGAGG C

GAM7052 296 IRF4 1 3531 NP_002451.1 3 188 AGCCTCCCTGGT CA----- T 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTAC CAGG
AGGTGTGA ACATTAGGGTCGATG GTCC
AGTGTGG -

GAM7052 296 JAK3 1 7364 NP_000206.1 3 489 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGTGC ACATTAGGGTCGATGAG CC
CGTGTGG C

GAM7052 296 JM11 1 19302 NP_296375.1 3 1516 ACCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACAC ACATTAGGGTCGATGAG CC
CACACGG C

GAM7052 296 KCNJ11 1 4460 NP_000516.2 5 138 AGCTTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCGC ACATTAGGGTCGATGAGTCC
CGCGTGG

GAM7052 296 KIAA008 2 16774 NP_055584.1 3 2275 AGCCCCCTGAGT CA----- 3 C c c

7 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCCT ACATTAGGGTCGATGAGTCC
TCCGTGG

GAM7052 296 KIAA008 2 18062 NP_055584.1 3 2408 GGCCTCCCAAAA TACTCA 3 C c c

```
          7                          TGCTGGGATTAC CATGTAATCCCAGC     GG
                                     ATGCATGA    GTACATTAGGGTCG     CC
                                                   TAAAAC
GAM7052  296   KIAA011 1  11163  XP_290939.1  3  333   AGCCTCCCAAGT CA-----          CA      3  C  c
c
          7                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                     AGGCGCCT           ACATTAGGGTCGATGA  CC
                                            TCCGCGG              AC
GAM7052  296   KIAA018 1  4041   NP_066545.1  3  1193  AGCCTCCCAAGT CA-----          CA      3  C  c
c
          6                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                     AGGCACAG           ACATTAGGGTCGATGA  CC
                                            GACACGG              AC
GAM7052  296   KIAA040 1  17968  NP_055472.1  5  126   AGCCTCCCTAGC   --  A      A  C        3  C  c  c

          6                          AGCTGGGACTAT CAT  GTA TCCCAGCT CT AGG
                                     TAGTGCAC    GTG  TAT AGGGTCGA GA TCC
                                               AT   C       C  -
GAM7052  296   KIAA045 1  7366   XP_027862.1  3  3789  AGCCTCCTGAGT CA-----                3  C  c  c
          9                          AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                     AGGTGTGT           ACATTAGGGTCGATGAGTCC
                                            TGTGTGG
GAM7052  296   KIAA047 1  12393  XP_290898.1  5  106   AGCCTCCTGAGT CA-----   A            3  C  c  c

          2                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGCTTGT           ACAT AGGGTCGATGAGTCC
                                            TGTTCGG    C
GAM7052  296   KIAA047 1  7779   NP_055679.1  3  1316  AGCCTCCAGAGT CA-----          A      3  C  c
c
          5                          AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                     AGGCGCCC           ACATTAGGGTCGATGAG CC
                                            CCCGCGG              A
GAM7052  296   KIAA049 1  4636   XP_031397.1  3  2887  AGCCTTCTGAGT CA-----                3  C  c  c
          5                          AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                     ACGCGTGT           ACATTAGGGTCGATGAGTCT
                                            TGTGCGC
GAM7052  296   KIAA051 2  5592   NP_055547.1  3  3759  AGCCTCCTGAGT CA-----   A            3  C  c
c
          3                          AGCTGGGATGAC       TGT ATCCCAGCTACTCAGG
                                     AGGTGCAC           ACA TAGGGTCGATGAGTCC
                                            CACGTGG    G
GAM7052  296   KIAA051 2  19867  NP_055547.1  5  175   AGCCTTCCGAGT CA-----          A      3  C  c
c
          3                          AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                     AGGCACCT           ACATTAGGGTCGATGAG CC
                                            TCCACGG              -
GAM7052  296   KIAA055 1  8953   NP_055605.1  3  2386  AACCTCCCTAGT CA-----          C      3  C  c  c

          5                          AGCTGGGATTAC       TGTAATCCCAGCTACT AGG
                                     AGGTGCAC           ACATTAGGGTCGATGA TCC
```

CACGTGG -
GAM7052 296 KIAA055 2 9434 XP_085507.1 3 596 ATCCTCCTGAGT CA----- 3 C c c
7 AGCTGGGGTTAC TGTAATCCCAGCTACTCAGG
AGGTGTGT ACATTGGGGTCGATGAGTCC
TGTGTGG
GAM7052 296 KIAA055 2 14583 XP_085507.1 3 2691 AGCCTCCTGAGT CA----- 3 C c c
7 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCGC ACATTAGGGTCGATGAGTCC
CGCGTGG
GAM7052 296 KIAA056 1 5466 NP_055519.1 3 2134 AGCCTCCCGAGT CA----- A 3 C c
c
2 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGT ACATTAGGGTCGATGAG CC
TGTGCGG C
GAM7052 296 KIAA056 1 697 NP_055649.1 5 689 GGCCTCCTGAGT CA----- 3 C c c
3 AGCTGGGGTTGC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACGTTGGGGTCGATGAGTCC
CGTGTGG
GAM7052 296 KIAA060 1 5865 NP_055509.1 5 154 AGCCTTCCGAGT CA----- A 3 C c c
5 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCC ACATTAGGGTCGATGAG CC
CCCGTGG -
GAM7052 296 KIAA064 1 6764 NP_079069.1 5 54 AGCCTCCTAAGT CA----- C 3 C c c
3 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGAAATG ACATTAGGGTCGATGA TCC
GTAAAGG A
GAM7052 296 KIAA066 1 19611 NP_055642.1 5 46 AGGCTCCTGAGT CA----- A 3 C c c
3 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGATTAC ACAT AGGGTCGATGAGTCC
CATTAGG C
GAM7052 296 KIAA083 1 10893 NP_055739.1 3 2003 AGCCTCCCGAGT CA----- A 3 C c
c
1 AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGGCACCT ATATTAGGGTCGATGAG CC
TCCACGG C
GAM7052 296 KIAA084 1 5866 XP_049237.1 3 1606 AGCCTCCTGAAT CA----- C 3 C c c
1 AGCTGGGATTAC TGTAATCCCAGCTA TCAGG
AGGCACCC ACATTAGGGTCGAT AGTCC
CCCACGG A
GAM7052 296 KIAA086 1 9847 NP_055893.2 3 1038 AGCCTCCTGAGT CA----- A 3 C c
c
1 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 KIAA093 1 8012 XP_041191.2 3 246 AGCCTCCCGAGT CA----- A 3 C c c

1 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCT ACATTAGGGTCGATGAG CC
TCCACGG C
GAM7052 296 KIAA096 1 2109 XP_290942.1 3 1609 AGCCTCCTGAGT CA----- C 3 C c
c
2 AGCTAGGATTAC TGTAATCC AGCTACTCAGG
AGGCATGT ACATTAGG TCGATGAGTCC
TGTACGG A
GAM7052 296 KIAA097 1 16232 NP_055745.1 3 791 CCGATTCTGAGT TA----- G 3 C c c

2 AGTGGGATGAAG CATG ATCCCA CTACTCAGG
TCTCATGC GTAC TAGGGT GATGAGTCT
TCTGAAG -
GAM7052 296 KIAA098 1 7266 XP_028867.2 3 1308 GAGGCTGCAGTG CA----- - - 3 C c c

1 AGCTGGGATTAC TGTAATCCCAGCT ACT CAG
ACCATTGC ACATTAGGGTCGA TGA GTC
CGTTACC G C
GAM7052 296 KIAA100 1 11806 XP_290584.1 5 82 CAGCCATTGAGT CA----- A 3 C c c
2 AGCTGGGATGAC TGT ATCCCAGCTACTCAG
AGGCACAT ACA TAGGGTCGATGAGTT
TACACGG G
GAM7052 296 KIAA104 1 18227 NP_055762.1 3 1188 AGCCTCCTAGAG CA----- T - 3 C c
c
1 TGCTGGGATTAC TGTAATCCCAGC ACTC AGG
AGACATGA ACATTAGGGTCG TGAG TCC
AGTACAG - A
GAM7052 296 KIAA105 1 3041 XP_043493.5 3 3363 AGCCTCCCAAGT AA---- CA 3 C c
c
4 AGCTGGGACCAC CATGT TCCCAGCTACT GG
ACGCATGC GTACG AGGGTCGATGA CC
CACACC AC
GAM7052 296 KIAA106 1 13719 XP_048786.4 3 1782 CAGTTTCACAGT A CAG 3 C c
c
1 AGCTGGGATGCA CATGTA TCCCAGCTACT
TGGATGAC GTACGT AGGGTCGATGA
- CAC
GAM7052 296 KIAA112 1 5120 NP_061872.1 3 2044 AGCCTCCTGAGT CA----- A 3 C c
c
8 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGT ACAT AGGGTCGATGAGTCC
TGTACGG C
GAM7052 296 KIAA118 1 2092 NP_065761.1 3 373 TGCCCCTCAAAG T C-- 3 C c c
5 TGCTGGGATTAC CATGTAATCCCAGC ACT AGG
GTGATCCA GTGCATTAGGGTCG TGA TCC
- AAC
GAM7052 296 KIAA119 1 12481 XP_041843.1 3 1730 AGCCTCCCGAGT CA----- A 3 C c
c
3 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCC ACATTAGGGTCGATGAG CC

CCCGCGG C
GAM7052 296 KIAA119 3 1359 NP_065765.1 3 3794 AGCCTCCTGAGT CA----- A 3 C c c
8 AGCTGGGACTAT TGTA TCCCAGCTACTCAGG
AGGCGCGT ATAT AGGGTCGATGAGTCC
TGCGCGG C
GAM7052 296 KIAA119 3 12377 NP_065765.1 3 4105 AGCCTCCTGAGT CA----- 3 C c c
8 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCGT ACATTAGGGTCGATGAGTCC
TGCGCGG
GAM7052 296 KIAA119 3 18274 NP_065765.1 3 802 AGCCTTCCAAGT CA----- C--- 3 C c c
8 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AAGTGCCC ACATTAGGGTCGATGA TCC
CCCGTGA ACCT
GAM7052 296 KIAA120 1 10959 XP_031054.4 3 458 AGCCTTCGGAGT CA----- --- 3 C c c
0 GGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGTGTGC ACATTAGGGTCGGTGAG TCC
CGTGTGG GCT
GAM7052 296 KIAA120 1 15011 XP_027307.2 3 1963 AGCCTCTTGAAT CA----- C 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTA TCAGG
AGGCGCCC ACATTAGGGTCGAT AGTTC
CCCGCGG A
GAM7052 296 KIAA125 2 7935 XP_031577.2 3 3652 GCCTTCCTGAGT CA----- A 3 C c c
7 AGTTGGGAATAC TGTA TCCCAGCTACTCAGG
AGGCATGC ACAT AGGGTTGATGAGTCC
CGTACGG A
GAM7052 296 KIAA125 2 12291 XP_031577.2 3 1781 AACCTCTAGAGT CA----- --- 3 C c c
7 AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCGCAT ACATTAGGGTCGATGAG TCC
TACGCGG ATC
GAM7052 296 KIAA126 1 16885 XP_291055.1 3 983 AGCCTCCCGAGT CA----- A 3 C c c
8 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C
GAM7052 296 KIAA127 1 13714 XP_300760.1 5 464 AGCCTCTGGAGT CA----- --- 3 C c c
3 AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCACGC ACATTAGGGTCGATGAG TCC
CGCACGG GTC
GAM7052 296 KIAA128 1 14633 NP_065799.1 3 1328 AACCTCCTGAGT CA----- A 3 C c c
7 AGCTGGGACTGC TGTA TCCCAGCTACTCAGG
AGGCACGC ACGT AGGGTCGATGAGTCC

CGCACGG C

GAM7052 296 KIAA144 1 3913 NP_065885.1 3 931 GGCCTCCCAAAG ---- T CA 3 C c c

3 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GATA - AA

GAM7052 296 KIAA145 1 6661 XP_040100.3 3 2145 AGCCTCCCAAGT T A CA 3 C c
c

6 AGCTGGGACTAC CA GTA TCCCAGCTACT GG
TGGCACCC GT CAT AGGGTCGATGA CC
- C AC

GAM7052 296 KIAA149 1 9995 XP_034415.1 3 3051 AGCCTCCTGAGT CA----- A 3 C c c

3 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCT ACAT AGGGTCGATGAGTCC
TCCGCGG C

GAM7052 296 KIAA151 1 14558 XP_170889.1 3 180 AGCCTCCTGAGT CA----- A 3 C c c

8 AGCTGGGATAAC TGT ATCCCAGCTACTCAGG
AGGTGTGG ACA TAGGGTCGATGAGTCC
GGTGTGG A

GAM7052 296 KIAA153 1 12327 XP_042661.5 3 1262 AGCGTCCTGAGT CA----- A 3 C c
c

0 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCGC ACAT AGGGTCGATGAGTCC
CGCGCGG C

GAM7052 296 KIAA157 1 9469 XP_027744.1 3 967 AGCCTCTCGAGT CA----- A --- 3 C c c

1 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCGTGC ACAT AGGGTCGATGAG TCC
CGTGCGG C CTC

GAM7052 296 KIAA161 2 15445 NP_066002.1 3 1465 AGCCTCCTGATT CA----- C 3 C c
c

5 AGCTGGGATTAC TGTAATCCCAGCTA TCAGG
AGGCATGC ACATTAGGGTCGAT AGTCC
CGTACGG T

GAM7052 296 KIAA161 2 18920 NP_066002.1 3 1772 AGCCTGCCAAGT CA----- --- 3 C c
c

5 AGCTGGGATTAC TGTAATCCCAGCTACT CAGG
AGGCATGC ACATTAGGGTCGATGA GTCC
CGTACGG ACC

GAM7052 296 KIAA161 1 1187 XP_166140.1 3 795 AGCCTCCCAAGT CA----- CA 3 C c
c

7 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 KIAA171 2 15686 NP_085136.1 3 1403 AGCCTCCTGAGT CA----- A 3 C c
c

2 AGCTGGGACTAT TGTA TCCCAGCTACTCAGG
AGGCCTGT ATAT AGGGTCGATGAGTCC

TGTCCGG C
GAM7052 296 KIAA171 2 15686 XP_041497.2 3 1572 AGCCTCCTGAGT CA----- A 3 C c c
2 AGCTGGGACTAT TGTA TCCCAGCTACTCAGG
AGGCCTGT ATAT AGGGTCGATGAGTCC
TGTCCGG C
GAM7052 296 KIAA171 2 16883 NP_085136.1 3 826 AGCCTCCTGAGT CA----- 3 C c c
2 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCATGC ATATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 KIAA171 2 16883 XP_041497.2 3 826 AGCCTCCTGAGT CA----- 3 C c c
2 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCATGC ATATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 KIAA173 1 3033 NP_219494.1 3 1512 GGCCTCCCAAGT CA----- CA 3 C c c
7 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCT ACATTAGGGTCGATGA CC
TCCGTGG AC
GAM7052 296 KIAA182 1 1496 XP_290834.1 3 1391 AGCCTCCCAAGT CA----- CA 3 C c c
7 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGTGT ACATTAGGGTCGATGA CC
TGTGCGG AC
GAM7052 296 KIAA182 1 2825 XP_030378.2 3 295 AGCCTCCTGAGT CA----- 3 C c c
9 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCCT ACATTAGGGTCGATGAGTCC
TCCGTGG
GAM7052 296 KIAA183 1 14962 XP_114087.2 3 1763 AGTCTCCTGAGT CA----- 3 C c c
6 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCC ACATTAGGGTCGATGAGTCC
CCCACGG
GAM7052 296 KIAA192 1 10834 XP_057040.1 5 407 AGCCTCCCAAGT CA----- CA 3 C c c
2 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGT ACATTAGGGTCGATGA CC
TGTACGG AC
GAM7052 296 KIAA194 1 17635 XP_086981.2 3 1596 AGAGTCCTCCAG TA ACTC 3 C c c
0 AGCTGGGATCCC CATG ATCCCAGCT AGG
ATGGGCGC GTAC TAGGGTCGA TCC
CC GACC
GAM7052 296 KIAA197 2 12858 XP_058720.4 3 781 GGCCACCCAAAG ---- T CA 3 C c c
1 TGTTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTTG TGA CC
GATA - AA
GAM7052 296 KIAA197 2 16885 XP_058720.4 3 646 AGCCTCCCGAGT CA----- A 3 C c c

1 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C
GAM7052 296 KIAA198 1 6990 XP_113870.1 5 287 TGCCTCCCGAGT CA----- A 3 C c c

7 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATCT ACATTAGGGTCGATGAG CC
TCTACGG C
GAM7052 296 KIAA202 1 17522 XP_059415.2 3 1145 AGCCTCTTGAAT AA---- C 3 C c c

8 AGCTGGGACTAG CATGT TCCCAGCTA TCAGG
AAGCATGC GTACG AGGGTCGAT AGTTC
AAGATC A
GAM7052 296 KLRC3 1 12994 NP_002252.1 3 51 GGCCTCCCAAGT T T CA 3 C c c
TGCTGGGATTAC CA GTAATCCCAGC ACT GG
TGACACAA GT CATTAGGGTCG TGA CC
- T AC
GAM7052 296 LAMP3 1 1656 NP_055213.1 3 650 AGCTTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACAC ACATTAGGGTCGATGAG CC
CACACGG C
GAM7052 296 LHFP 1 3333 NP_005771.1 3 810 ATTTCTCTGAGT - ATCCC 3 C c c
AGCTTCTGCTAT CAT GTA AGCTACTCAGG
GATATTCT GTA CGT TCGATGAGTCT
T CT---
GAM7052 296 LNIR 1 5115 NP_112178.1 3 918 AGCCTCCCTAGT G -- C 3 C c c
AGCTGGGACTTT CAT TAA TCCCAGCTACT AGG
AAGTGTAC GTG ATT AGGGTCGATGA TCC
A TC -
GAM7052 296 LNK 1 8674 NP_005466.1 3 1765 GACCTCTCAAGT CA----- C--- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AAGCACCA ACATTAGGGTCGATGA TCC
ACCACGA ACTC
GAM7052 296 LOC1126 1 11096 XP_053145.1 3 253 AGCCTCTGAAGT CA----- - 3 C c c

87 AGCTGGGATTAC TGTAATCCCAGCTACT CAGG
AGGCATGT ACATTAGGGTCGATGA GTCT
TGTACGG A
GAM7052 296 LOC1128 1 12527 NP_612422.2 3 487 AGCCTCCCGAGT CA----- A 3 C c
c

17 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCT ACATTAGGGTCGATGAG CC
TCCGCGG C
GAM7052 296 LOC1134 2 9691 NP_612437.2 3 1262 AGCCTCCTGAGT CA----- 3 C c c

44 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG
GAM7052 296 LOC1134 2 13633 NP_612437.2 3 937 AGCTTCCTAAGT CA----- C 3 C c
c

```
          44                          AGCTGGGATTAC       TGTAATCCCAGCTACT AGG
                                     AGGCGTGC          ACATTAGGGTCGATGA TCC
                                           CGTGCGG             A
GAM7052  296   LOC1156 2  3028  NP_663299.1  3  741   AGCCTCCTGAGT CA-----                3  C  c  c
          48                          AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                     AGGTGCCC          ACATTAGGGTCGATGAGTCC
                                           CCCGTGG
GAM7052  296   LOC1156 2  5621  NP_663299.1  3  879   TGGCCTCCTGGG CA-----         T        3  C  c
c
          48                          TGCTGGGATTAC       TGTAATCCCAGC ACTCAGG
                                     AGACGTGA          ACATTAGGGTCG TGGGTCC
                                           AGTGCAG           -
GAM7052  296   LOC1184 1  13356 XP_060981.3  3  304   AGCCTCCCTAGT CA-----           C      3  C  c
c
          90                          AGCTGGGATTAC       TGTAATCCCAGCTACT AGG
                                     AGGTGCAC          ACATTAGGGTCGATGA TCC
                                           CACGTGG             -
GAM7052  296   LOC1188 1  13816 NP_849154.1  3  666   AGCTTCCTGAGT CA-----  A             3  C  c
c
          12                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGAGCGC          ACAT AGGGTCGATGAGTCC
                                           CGCGAGG    C
GAM7052  296   LOC1188 1  13816 XP_058346.2  3  666   AGCTTCCTGAGT CA-----  A             3  C  c
c
          12                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGAGCGC          ACAT AGGGTCGATGAGTCC
                                           CGCGAGG    C
GAM7052  296   LOC1219 1  18973 XP_062872.2  5  670   AGCCTCCTGAGT CA-----  A             3  C  c
c
          52                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGCATGC          ACAT AGGGTCGATGAGTCC
                                           CGTACGG    C
GAM7052  296   LOC1250 1  13952 XP_058889.3  3  626   GGCCTCCCAAAG     ----       T  CA      3  C  c
c
          61                          TGCTGGGATTCC CATGT    AATCCCAGC ACT  GG
                                     AGGCGTGA    GTGCG    TTAGGGTCG TGA  CC
                                           GACC        -  AA
GAM7052  296   LOC1262 1  18559 XP_059009.2  5  126   GGCAGCTGGAGG     AA---      A  -      3  C  c
c
          57                          AGCTGGGACGGC CATGT     TCCCAGCT CTC AG
                                     GGCATGAG    GTACG     AGGGTCGA GAG TC
                                           GCGGC       G   G
GAM7052  296   LOC1283 1  10834 XP_059243.2  3  646   AGCCTCCCAAGT CA-----           CA      3  C  c
c
          87                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                     AGGCATGT          ACATTAGGGTCGATGA  CC
                                           TGTACGG             AC
GAM7052  296   LOC1290 1  10993 XP_059329.1  3  106   TTGTACCCAGAT    G--         C  A       3  C  c
c
          39                          AGCTGGGATTGG CAT   TAATCCCAGCTA TC GG
```

```
                                    AAGTGAGG    GTG   GTTAGGGTCGAT AG CC
                                          AAG         - A
GAM7052  296   LOC1306 1  19669  XP_059464.2  5  161   AGCCTCCCCGAG    ----       T   A      3  C  c  c

         39                          TGCTGGGATTAA CATGT    AATCCCAGC ACTC GG
                                    AGACGTGA    GTGCA    TTAGGGTCG TGAG CC
                                          GAAA       -   C
GAM7052  296   LOC1308 1  2257   XP_065904.1  3  1018  TGCCTCCTGAGT CA-----     C           3  C  c
c
         13                          AGCTGGAATTAC       TGTAAT CCAGCTACTCAGG
                                    AGGCATGT          ACATTA GGTCGATGAGTCC
                                          TGTACGG     A
GAM7052  296   LOC1352 1  18228  XP_072402.4  3  649   AGCCTACCAAGT CA-----          CA      3  C  c
c
         93                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                    AGGTGTGT          ACATTAGGGTCGATGA  CC
                                          TGTGTGG             A-
GAM7052  296   LOC1357 1  19515  NP_612639.1  3  124   AGCCTCCTGAGT CA-----     C           3  C  c
c
         63                          AGCTGGAATTAC       TGTAAT CCAGCTACTCAGG
                                    AGGAGGAT          ACATTA GGTCGATGAGTCC
                                          TAGGAGG     A
GAM7052  296   LOC1378 1  2107   XP_059929.3  3  768   AGCCTCCCAAGT CA-----          CA      3  C  c
c
         86                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                    AGGCATGC          ACATTAGGGTCGATGA  CC
                                          CGTACGG             AC
GAM7052  296   LOC1428 1  6899   XP_084355.1  3  545   AGCCTCCCCAGT CA-----          CA      3  C  c
c
         26                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                    AGGCGCCG          ACATTAGGGTCGATGA  CC
                                          GCCGCGG             CC
GAM7052  296   LOC1429 1  4637   XP_096364.1  3  1076  GAGCTTGCAGTG C-----          -  -     3  C  c  c

         48                          AGCTGGGATTGC      ATGTAATCCCAGCT ACT CAGG
                                    ATCACTGC          TACGTTAGGGTCGA TGA GTTC
                                          CGTCAC            G  C
GAM7052  296   LOC1432 1  16432  NP_620167.1  5  139   AGCCTTCCAAGT CA-----          C---    3  C  c
c
         41                          AGCTGGGATTAC       TGTAATCCCAGCTACT    AGG
                                    AGGAGTTA          ACATTAGGGTCGATGA    TCC
                                          ATTGAGG             ACCT
GAM7052  296   LOC1439 1  19303  XP_084664.1  3  12    AGCCTCCTGAGT CA   A -------          3  C  c
c
         16                          AGCTGTACTACA   TGTA TCC      CAGCTACTCAGG
                                    GGAATGCA      ACGT AGG      GTCGATGAGTCC
                                          --   A   ACATCAT
GAM7052  296   LOC1441 1  18030  NP_778228.1  3  506   AGGCCTCAGGGT   T       C    --        3  C  c  c

         00                          GTCTGGGATTGC CA GTAATCCCAG TACTC  AGG
```

```
                                    TGGGGAGG    GT CGTTAGGGTC GTGGG  TCC
                                                -       T    AC
GAM7052  296   LOC1442 1  12527  XP_084786.1  5  484   AGCCTCCCGAGT CA-----          A     3  C  c
c
         48                          AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                    AGGCGCCT          ACATTAGGGTCGATGAG CC
                                          TCCGCGG             C
GAM7052  296   LOC1447 1  13167  XP_084949.1  5  142   AGCCTTCTGAGT CA-----   A           3  C  c
c
         42                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                    AGGCACAT          ACAT AGGGTCGATGAGTCT
                                          TACACGG    C
GAM7052  296   LOC1452 1  10250  XP_085072.1  5  722   AGCCTCCCAAGT CA-----          CA     3  C  c
c
         68                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                    AGGTGCTC          ACATTAGGGTCGATGA  CC
                                          CTCGTGG             AC
GAM7052  296   LOC1454 1  6583   XP_085120.1  5  5     AGCCTCTGGAGT CA-----          ---    3  C  c  c
         53                          AGCTGGGATTAC       TGTAATCCCAGCTACTC   AGG
                                    AGGTGCGC          ACATTAGGGTCGATGAG   TCC
                                          CGCGTGG             GTC
GAM7052  296   LOC1456 1  20072  XP_096832.1  5  22    AGCCTCCCAAAG     ----       T  CA     3  C  c  c

         78                          TGCTGGGATTAT CATGT    AATCCCAGC ACT  GG
                                    AGGCATGA    GTACG    TTAGGGTCG TGA  CC
                                                GATA       -  AA
GAM7052  296   LOC1457 1  15280  XP_085227.1  5  297   AGCCTCCTGAGT CA-----               3  C  c  c

         57                          AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                    AGCTCTGG          ACATTAGGGTCGATGAGTCC
                                          GGTCTCG
GAM7052  296   LOC1461 1  2107   NP_778229.1  5  277   AGCCTCCCAAGT CA-----          CA     3  C  c
c
         77                          AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                    AGGCATGC          ACATTAGGGTCGATGA  CC
                                          CGTACGG             AC
GAM7052  296   LOC1463 1  10470  XP_085430.1  5  472   AGCCTCCGGAGT CA-----          A     3  C  c
c
         46                          AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                    AGGCATGC          ACATTAGGGTCGATGAG CC
                                          CGTACGG             G
GAM7052  296   LOC1464 1  8011   XP_096998.2  5  621   AGCCTCCTGAGT CA-----               3  C  c  c
         29                          AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                    AGGCACCC          ACATTAGGGTCGATGAGTCC
                                          CCCACGG
GAM7052  296   LOC1464 1  4286   XP_085461.6  5  184   AGTCTTCCGAGT CA-----          A     3  C  c  c

         43                          AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                    AGGCGTGT          ACATTAGGGTCGATGAG CC
                                          TGTGCGG             -
```

GAM7052 296 LOC1468 1 10012 XP_085603.1 5 56 AGCCTCCAGAGT CA----- A 3 C c c

20 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCT ACATTAGGGTCGATGAG CC
TCCACGG A

GAM7052 296 LOC1468 1 1234 NP_660316.1 3 1253 AGCCTCCCGAGT CA----- A 3 C c c

94 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACGC ACATTAGGGTCGATGAG CC
CGCACGG C

GAM7052 296 LOC1470 1 1525 XP_054031.5 5 689 GGCCTCCTGAGT CA----- 3 C c c

71 AGCTGGGATTGC TGTAATCCCAGCTACTCAGG
AGGTATGC ACGTTAGGGTCGATGAGTCC
CGTATGG

GAM7052 296 LOC1471 1 3032 XP_085722.2 3 337 AGCCTCCCGAGT CA----- A 3 C c c

66 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCT ACATTAGGGTCGATGAG CC
TCCGTGG C

GAM7052 296 LOC1477 1 8528 XP_097293.2 5 838 CGTAACCAGAGA G TA A 3 C c c

91 CGCTGGGATTAG CAT TAATCCCAGC CTC GG
TGGGTGGG GTG ATTAGGGTCG GAG CC
- CA A

GAM7052 296 LOC1478 2 16859 XP_085903.1 3 185 GGCCTCCCAAAG ---- T CA 3 C c c

17 TGTTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTTG TGA CC
GATA - AA

GAM7052 296 LOC1478 2 18468 XP_085903.1 3 944 AGCCTCCTGAGT CA----- C 3 C c c

17 AGCTTGGATTAC TGTAATCC AGCTACTCAGG
AGGCACAA ACATTAGG TCGATGAGTCC
AACACGG T

GAM7052 296 LOC1478 2 2989 XP_085924.2 3 231 AGCCTCCAAAGT CA----- CA 3 C c c

41 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC
CGTACGG AA

GAM7052 296 LOC1478 2 8527 XP_085924.2 3 546 AGCCTCCTGAGT CA----- A 3 C c c

41 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCT ACAT AGGGTCGATGAGTCC
TCCACGG C

GAM7052 296 LOC1481 1 16957 XP_047554.4 3 1067 AGCCTCCCAAGT CA----- CA 3 C c c

98 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACAA ACATTAGGGTCGATGA CC
AACACGG AC

GAM7052 296 LOC1482 1 2820 XP_086095.1 3 1262 AGCCTCCCGAGT CA----- A 3 C c c
03 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
GGGCATAT GCATTAGGGTCGATGAG CC
TATACGG C
GAM7052 296 LOC1494 1 19862 XP_086546.1 3 648 AGCCTCCTGAGT CA----- 3 C c c
66 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATCC ACATTAGGGTCGATGAGTCC
CCTACGG
GAM7052 296 LOC1494 1 4344 XP_086536.1 3 160 AGCCTCCTGAGT CA----- 3 C c c
78 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGACATGC ACATTAGGGTCGATGAGTCC
CGTACAG
GAM7052 296 LOC1495 2 12482 XP_097661.1 3 3183 AGCCTCCTGAGT CA----- 3 C c c
06 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCT ACATTAGGGTCGATGAGTCC
TCCGCGG
GAM7052 296 LOC1495 2 15681 XP_097661.1 3 1724 AGCCTCCCGAGT CA----- A 3 C c c
06 AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGTGCCC ACGTTAGGGTCGATGAG CC
CCCGTGG C
GAM7052 296 LOC1496 1 12440 XP_097706.1 3 698 AGTCTCCCAAGT CA----- CA 3 C c c
92 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGT ACATTAGGGTCGATGA CC
TGTGTGG AC
GAM7052 296 LOC1500 1 3913 XP_097797.1 5 812 GGCCTCCCAAAG ---- T CA 3 C c c
54 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GATA - AA
GAM7052 296 LOC1502 1 5964 XP_097870.1 3 1786 AGCCTCCCGAGT CA----- A 3 C c c
25 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACAC ACATTAGGGTCGATGAG CC
CACACGG C
GAM7052 296 LOC1502 1 9847 XP_086852.1 5 25 AGCCTCCTGAGT CA----- A 3 C c c
82 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 LOC1503 1 11386 XP_086907.1 3 564 AGTCTCCCGAGT CA----- A 3 C c c
97 AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGGCGCCC ATATTAGGGTCGATGAG CC
CCCGCGG C
GAM7052 296 LOC1505 1 9025 XP_097917.1 5 1701 AGCCTCCCAAGT CA----- CA 3 C c c

87 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGC ACATTAGGGTCGATGA CC
CGTGTGG AC
GAM7052 296 LOC1510 1 14936 XP_097998.1 3 1151 AGCCTCCCGAGT CA----- A 3 C c
c
57 AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGACACGT ATATTAGGGTCGATGAG CC
TGCACAG C
GAM7052 296 LOC1514 1 6688 XP_098063.1 5 184 AGCCTCCCGAGT CA----- A 3 C c
c
75 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGCCTGAA ACATTAGGGTCGATGAG CC
AAGTCCG C
GAM7052 296 LOC1516 1 7366 NP_612144.1 3 976 AGCCTCCTGAGT CA----- 3 C c c
36 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGT ACATTAGGGTCGATGAGTCC
TGTGTGG
GAM7052 296 LOC1526 1 11229 XP_011108.2 3 793 AGCCTCCTGAGT CA----- 3 C c c

20 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCC
CACACGG
GAM7052 296 LOC1526 1 5099 XP_087500.1 5 50 AGCCTCCCAAGT CA----- CA 3 C c
c
67 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGCGATTG ACATTAGGGTCGATGA CC
GTTAGCG AC
GAM7052 296 LOC1527 2 726 XP_098257.1 5 335 GGCCTCCCAGAG ----- T A 3 C c c
19 TGCTGGGATTTA CATGT AATCCCAGC ACTC GG
CAGGCATG GTACG TTAGGGTCG TGAG CC
GACAT - A
GAM7052 296 LOC1527 2 14742 XP_098257.1 5 201 AGCCTCCTGAGT CA----- 3 C c c

19 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCGT ACATTAGGGTCGATGAGTCC
TGCGTGG
GAM7052 296 LOC1528 1 2898 XP_098266.2 3 1785 GGTCTTCTGAGT CA----- A 3 C c
c
04 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGC ACAT AGGGTCGATGAGTCT
CGTACGG C
GAM7052 296 LOC1530 1 4990 XP_098307.1 3 888 TCAGCCTCGAGT CA----- A - 3 C c
c
77 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCGCAT ACAT AGGGTCGATGAG TCC
TACGCGG C C
GAM7052 296 LOC1542 1 19732 XP_098505.1 5 202 AGCCTCCTGAGT CA----- A 3 C c
c
82 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACAT ACAT AGGGTCGATGAGTCC

TACACGG C
GAM7052 296 LOC1547 1 16887 XP_098602.1 3 282 AGCCTCCTGAGT CA----- 3 C c c

39 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGT ACATTAGGGTCGATGAGTCC
TGTACGG
GAM7052 296 LOC1548 1 1649 XP_098618.3 5 2919 AGCCTCCTGAGT CA----- 3 C c c

22 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGGCGCT ACATTAGGGTCGATGAGTCC
TCGCGGG
GAM7052 296 LOC1548 1 17476 XP_088059.1 3 128 TGCAGAACTGTT C G ACT 3 C c
c
66 CAGTGGTATTAC CATGTAAT CCA CT CAG
ATGAAATG GTACATTA GGT GA GTC
T - CTT
GAM7052 296 LOC1548 3 2182 XP_098626.1 5 195 CAGCCTCCTGAG CA----- A A 3 C c
c
77 AGCTGGGACTAC TGTA TCCCAGCT CTCAGG
AGGCGCCT ACAT AGGGTCGA GAGTCC
TCCGCGG C -
GAM7052 296 LOC1548 3 14460 XP_098626.1 3 3626 AGGCTCCCAAGT CA----- CA 3 C c
c
77 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC
GAM7052 296 LOC1548 3 19863 XP_098626.1 3 1355 AGCCTCCCGAGT CA----- A 3 C c
c
77 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATCT ACATTAGGGTCGATGAG CC
TCTACGG C
GAM7052 296 LOC1575 1 1954 XP_212210.1 5 516 GCCTCACCCAGT G -- CA 3 C c
c
31 AGCTGGGAAATT CAT TAA TCCCAGCTACT GG
AGGTGGGG GTG ATT AGGGTCGATGA CC
G AA C-
GAM7052 296 LOC1578 1 6270 XP_098833.2 5 318 CGCCTCCCGAGT CA----- A 3 C c
c
58 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGAG CC
TGTACGG C
GAM7052 296 LOC1584 1 14740 XP_098942.1 3 728 AGCCTCCCGAGT CA----- A 3 C c
c
36 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCGC ACATTAGGGTCGATGAG CC
CGCGTGG C
GAM7052 296 LOC1584 1 12099 XP_098955.1 3 1300 AGCCTCCTGAGT G -- 3 C b b

76 AGCTGGGATCAT CAT TA ATCCCAGCTACTCAGG
AGATGCCT GTA AT TAGGGTCGATGAGTCC

G AC
GAM7052 296 LOC1585 1 17909 XP_088594.1 5 496 TGGAGCTGGAGA AA A - 3 C c c
27 AGCTGGGACACA CATGT TCCCAGCT CTC AG
TGGCACCA GTACA AGGGTCGA GAG TC
C- A G
GAM7052 296 LOC1586 1 14574 XP_045161.1 3 511 AGCCTCCTGAGT CA----- 3 C c c
68 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCAGAC ACATTAGGGTCGATGAGTCC
CAGACGG
GAM7052 296 LOC1588 1 4005 XP_099000.1 5 60 AGCCTCTCGAGT CA----- --- 3 C c c
65 AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCGCAT ACATTAGGGTCGATGAG TCC
TACGCGG CTC
GAM7052 296 LOC1608 1 15778 XP_090573.3 5 623 GGCCTTCCCAGT CA----- C--- 3 C c c
97 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCACAT ACATTAGGGTCGATGA TCC
TACACGG CCCT
GAM7052 296 LOC1629 1 15400 XP_091890.6 3 465 AGTCTCCTGAGT CA----- A 3 C c c
67 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCGT ACAT AGGGTCGATGAGTCC
TGCGTGG C
GAM7052 296 LOC1629 1 16333 XP_091914.2 3 94 GGCCTCCCAAAG ---- T CA 3 C c c
93 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
GGACGTGA GTGCA TTAGGGTCG TGA CC
GGTA - AA
GAM7052 296 LOC1632 2 12735 NP_775802.1 3 1753 AGCCTCCTAAGT CA----- C 3 C c c
27 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCACCC ACATTAGGGTCGATGA TCC
CCCACGG A
GAM7052 296 LOC1632 2 12740 NP_775802.1 3 3443 AGCCTCCCAAGT CA----- CA 3 C c c
27 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCT ACATTAGGGTCGATGA CC
TCCACGG AC
GAM7052 296 LOC1640 2 7689 XP_089356.1 3 911 AGCCTCCCGAGT CA----- A 3 C c c
91 AGCTGGGGTTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTGGGGTCGATGAG CC
CGTACGG C
GAM7052 296 LOC1640 2 8838 XP_089356.1 3 1048 GGCCTCCCAAAG ---- T CA 3 C c c
91 TGCTGGGATTAC CATGT AATCCCAGC ACT GG
CGGCATGA GTACG TTAGGGTCG TGA CC
GCCA - AA

GAM7052 296 LOC1684 1 17863 XP_095114.2 3 781 AGCTTCCCGAGT CA----- A 3 C c c

51 AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGGCACAC ATATTAGGGTCGATGAG CC
CACACGG C

GAM7052 296 LOC1696 1 11251 XP_095809.4 3 1205 AGCCTCCTGAAA CA----- AC 3 C c c

11 AGCTGGGATTAC TGTAATCCCAGCT TCAGG
AGGGCCCT ACATTAGGGTCGA AGTCC
TCCCGGG AA

GAM7052 296 LOC1962 1 2824 XP_113683.1 3 895 AGCCTCTCGAGT CA----- --- 3 C c c

64 AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCATGC ACATTAGGGTCGATGAG TCC
CGTACGG CTC

GAM7052 296 LOC1997 1 9306 XP_117119.1 5 228 AGCCTCCTGAGT CA----- C 3 C c c

25 ACCTGGGATTAC TGTAATCCCAG TACTCAGG
AGGTGCAC ACATTAGGGTC ATGAGTCC
CACGTGG C

GAM7052 296 LOC1998 1 1343 XP_114040.1 5 2253 TCATCCTGAAGT GTA --- - 3 C c c

58 AGCTGGATTGAT CAT ATC CCAGCTACT CAGG
AGAATGAC GTA TAG GGTCGATGA GTCC
AGA TTA A

GAM7052 296 LOC1998 1 9143 XP_117153.1 5 269 AGCCTCTCGAGT CA----- A --- 3 C c c

99 AGCTGGGAGTAC TGTA TCCCAGCTACTC AGG
AGATGCAC ACAT AGGGTCGATGAG TCC
CACGTAG G CTC

GAM7052 296 LOC2003 1 12277 XP_117226.1 3 1264 AGCCACCTGAGT CA----- A 3 C c c

39 AGCAGGGATTAC TGTAATCCC GCTACTCAGG
AGGTGTGT ACATTAGGG CGATGAGTCC
TGTGTGG A

GAM7052 296 LOC2004 1 11368 XP_117239.1 5 257 AGCCTCCTGAGT CA----- 3 C c c

91 AGTTGGGATTAC TGTAATCCCAGCTACTCAGG
AGATGCCC ACATTAGGGTTGATGAGTCC
CCCGTAG

GAM7052 296 LOC2011 1 3032 NP_849158.1 3 909 AGCCTCCCGAGT CA----- A 3 C c c

64 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCT ACATTAGGGTCGATGAG CC
TCCGTGG C

GAM7052 296 LOC2011 1 3032 XP_290750.1 3 909 AGCCTCCCGAGT CA----- A 3 C c c

64 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCT ACATTAGGGTCGATGAG CC
TCCGTGG C

GAM7052 296 LOC2012 1 9524 NP_775818.1 3 1024 AGCCTCCTGAGT CA----- 3 C c c

92 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTAT ACATTAGGGTCGATGAGTCC
TATGTGG

GAM7052 296 LOC2015 1 16775 XP_114343.2 3 1660 AGCCTCCTGAGT CA----- A 3 C c
c

62 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCCT ACAT AGGGTCGATGAGTCC
TCCGTGG C

GAM7052 296 LOC2024 1 9253 XP_117397.1 5 117 AGCCTCACGAGT CA----- A --- 3 C c
c

00 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCGCCT ACAT AGGGTCGATGAG TCC
TCCGCGG C CAC

GAM7052 296 LOC2029 1 18974 XP_117486.2 3 2828 AGCCTCCTGAGT AA---- 3 C c
c

34 AGCTGGGACTAT CATGT TCCCAGCTACTCAGG
AGGCATGT GTACG AGGGTCGATGAGTCC
GATATC

GAM7052 296 LOC2197 2 3064 XP_167596.1 5 1143 AGCCTCCTGGGT CA----- A 3 C c
c

31 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCTTGC ACAT AGGGTCGATGGGTCC
CGTTCGG C

GAM7052 296 LOC2197 2 5076 XP_167596.1 5 570 GGCCTCCTGAGT CA----- C 3 C c
c

31 ACCTGGGATTAT TGTAATCCCAG TACTCAGG
AGGCACAA ATATTAGGGTC ATGAGTCC
AACACGG C

GAM7052 296 LOC2197 1 3029 XP_167601.1 3 954 AGCTTCCCGAGT CA----- A 3 C c
c

35 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCT ACATTAGGGTCGATGAG CC
TCCGCGG C

GAM7052 296 LOC2200 2 12482 NP_660352.1 3 468 AGCCTCCTGAGT CA----- 3 C c c

74 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCT ACATTAGGGTCGATGAGTCC
TCCGCGG

GAM7052 296 LOC2200 2 14319 NP_660352.1 3 864 GGCCTCCCAAAG ---- T CA 3 C c
c

74 TGCTGGGATTAG CATGT AATCCCAGC ACT GG
AAGCGTGA GTGCG TTAGGGTCG TGA CC
AAGA - AA

GAM7052 296 LOC2215 1 8853 XP_168133.1 3 1262 AGCCTCCTGAGT CA----- A 3 C c
c

40 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGTTTCGT ACAT AGGGTCGATGAGTCC
TGCTTTG C

GAM7052 296 LOC2218 1 16581 XP_168226.1 5 1201 AGCTTCCTGAGT CA----- G 3 C c c
14 AGGTGGGATTAC TGTAATCCCA CTACTCAGG
AAGCATGC ACATTAGGGT GATGAGTCC
CGTACGA G
GAM7052 296 LOC2220 1 1573 XP_166556.1 3 741 AGTCTCCTGAGT CA----- 3 C c c
68 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCCC ACATTAGGGTCGATGAGTCC
CCCGTGG
GAM7052 296 LOC2221 1 11226 XP_212100.1 5 160 TGCCTCCTGAGT T 3 C b b
59 AGCTGGGATTAC CA GTAATCCCAGCTACTCAGG
TGGCACAC GT CATTAGGGTCGATGAGTCC
-
GAM7052 296 LOC2222 1 9925 XP_168473.1 5 531 AGCCTCCTGAGT CA----- 3 C c c
24 GGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGTGTGT ATATTAGGGTCGGTGAGTCC
TGTGTGG
GAM7052 296 LOC2536 1 11867 XP_172985.2 5 386 AGCTTCCTGAGT CA----- 3 C c c
12 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGAGCAT ACATTAGGGTCGATGAGTCC
TACGAGG
GAM7052 296 LOC2538 1 9847 XP_173230.1 5 20 AGCCTCCTGAGT CA----- A 3 C c c
42 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 LOC2539 2 2107 XP_171064.1 3 679 AGCCTCCCAAGT CA----- CA 3 C c c
81 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC
CGTACGG AC
GAM7052 296 LOC2539 2 3391 XP_171064.1 3 814 AGCCTCCTGAGT CA----- A 3 C c c
81 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCCC ACAT AGGGTCGATGAGTCC
CCCGTGG C
GAM7052 296 LOC2545 1 4317 XP_172961.1 5 14 AGCCTCCCAAGT TAA- CA 3 C c c
32 AGCTGGGACCAC CATG TCCCAGCTACT GG
CATGCCCA GTAC AGGGTCGATGA CC
CACC AC
GAM7052 296 LOC2829 1 14138 XP_212606.1 5 250 AGCCTCCTAAGT CA----- C 3 C c c
05 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AAGTGCCC ACATTAGGGTCGATGA TCC
CCCGTGA A
GAM7052 296 LOC2829 1 8853 XP_212603.1 3 1262 AGCCTCCTGAGT CA----- A 3 C c c
16 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG

AGTTTCGT ACAT AGGGTCGATGAGTCC
TGCTTTG C
GAM7052 296 LOC2829 1 14138 XP_212647.1 5 250 AGCCTCCTAAGT CA----- C 3 C c
c
43 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AAGTGCCC ACATTAGGGTCGATGA TCC
CCCGTGA A
GAM7052 296 LOC2829 1 8853 XP_212644.1 3 1262 AGCCTCCTGAGT CA----- A 3 C c
c
53 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGTTTCGT ACAT AGGGTCGATGAGTCC
TGCTTTG C
GAM7052 296 LOC2830 1 13809 XP_210847.1 5 91 CTCCTGAGCACC - GCTA--- 3 C c
c
12 CCATGGGATTAC CA TGTAATCCCA CTCAGG
GCTGTGTG GT GCATTAGGGT GAGTCC
C ACCCCAC
GAM7052 296 LOC2830 1 16357 XP_210885.1 5 1806 AGCCTCCTGAGT CA----- 3 C c
c
89 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGTGCAT ATATTAGGGTCGATGAGTCC
TACGTGG
GAM7052 296 LOC2831 1 3679 XP_210903.1 3 2017 TTTCTGCTGAGT CCCA- 3 C c
c
77 AGTATTTCATTG CATGTAAT GCTACTCAG
TATGGATG GTATGTTA TGATGAGTC
CTTTA
GAM7052 296 LOC2832 1 8183 XP_208555.2 3 2076 AGCCTCCTGAGT AA---- 3 C c c

15 AGCTGGGACTAG CATGT TCCCAGCTACTCAGG
AGGCATGT GTACG AGGGTCGATGAGTCC
GAGATC
GAM7052 296 LOC2832 1 1942 NP_787089.1 5 147 AGCTTCCTGAGT CA----- A 3 C c c

41 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTAC ACAT AGGGTCGATGAGTCC
CATGTGG C
GAM7052 296 LOC2832 1 10694 XP_210962.1 3 431 AGCCTCCTGAGT CA----- 3 C c c

93 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGA ACATTAGGGTCGATGAGTCC
AGTACGG
GAM7052 296 LOC2833 1 14245 XP_210981.1 3 1722 AGCCTCCTGAGT CA----- A 3 C c
c
35 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTAC ACAT AGGGTCGATGAGTCC
CATGTGG C
GAM7052 296 LOC2833 2 9023 XP_208647.1 3 893 AGCCTCCTGAGT CA----- C 3 C c
c
77 AGCTAGGATTAC TGTAATCC AGCTACTCAGG

AGGTGTGT ACATTAGG TCGATGAGTCC
TGTGTGG A
GAM7052 296 LOC2833 2 18130 XP_208647.1 3 1029 GGCCTCCCAAAG ---- T CA 3 C c
c
77 TGCTGGGATTTC CATGT AATCCCAGC ACT GG
AGGCGTGA GTGCG TTAGGGTCG TGA CC
GACT - AA
GAM7052 296 LOC2833 1 1113 XP_211007.1 3 1720 AGCCTCCCGAGT CA----- A 3 C c
c
87 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGAAGAT ACATTAGGGTCGATGAG CC
TAGAAGG C
GAM7052 296 LOC2834 1 16677 XP_211024.1 5 529 AGCCTCCCGAGT CA----- A 3 C c
c
00 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGAGGCT ACATTAGGGTCGATGAG CC
TCGGAGG C
GAM7052 296 LOC2834 1 9847 XP_211032.1 5 2027 AGCCTCCTGAGT CA----- A 3 C c
c
32 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 LOC2834 1 8011 XP_211049.1 5 213 AGCCTCCTGAGT CA----- 3 C c c
54 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCC ACATTAGGGTCGATGAGTCC
CCCACGG
GAM7052 296 LOC2834 1 10199 XP_211062.1 3 762 GCCTCCCTGAGT CA----- A 3 C c
c
87 GGCAGGGATTAC TGTAATCCC GCTACTCAGG
AGGAACCC ACATTAGGG CGGTGAGTCC
CCCAAGG A
GAM7052 296 LOC2835 2 1226 XP_211075.1 3 2813 CATTTGCTGTGT C-- --- T 3 C c c
07 AGCTGGGACAGT ATGTAA TCCCAGCTAC CAG
TACATTTC TACATT AGGGTCGATG GTC
CTT GAC T
GAM7052 296 LOC2835 2 4986 XP_211075.1 3 1905 AGCTTCCCAAGT CA----- CA 3 C c
c
07 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC
GAM7052 296 LOC2835 1 5965 XP_208097.1 3 505 AGCCTCCTGAGT CA----- 3 C c c
23 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCACAC ATATTAGGGTCGATGAGTCC
CACACGG
GAM7052 296 LOC2836 1 12482 XP_211126.1 5 3971 AGCCTCCTGAGT CA----- 3 C c
c
24 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCT ACATTAGGGTCGATGAGTCC
TCCGCGG
GAM7052 296 LOC2836 1 19555 XP_211134.1 5 1323 AGCCTCCTGAGT CA----- C 3 C c
c

37 ACCTGGGATTAC TGTAATCCCAG TACTCAGG
AGGCGCGC ACATTAGGGTC ATGAGTCC
CGCGCGG C
GAM7052 296 LOC2836 1 5466 XP_208764.1 3 312 AGCCTCCCGAGT CA----- A 3 C c
c
41 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGT ACATTAGGGTCGATGAG CC
TGTGCGG C
GAM7052 296 LOC2836 2 16035 XP_211144.1 5 155 AGTCTCCCAAAG ---- A CA 3 C c
c
55 GGCTGGGATTAA CATGT AATCCCAGCT CT GG
AGGCATGA GTACG TTAGGGTCGG GA CC
GAAA - AA
GAM7052 296 LOC2836 2 19485 XP_211144.1 5 18 CACCTCCTGAGT CA----- A 3 C c c
55 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGTTGTGC ACAT AGGGTCGATGAGTCC
CGTGTTG C
GAM7052 296 LOC2836 1 4911 XP_211167.1 3 1805 GCCTCCTGAAGT AATC---- - 3 C c
c
90 AGCTGGAACTAC CATGT CCAGCTACT CAGG
AGACATGC GTACA GGTCGATGA GTCC
GACATCAA A
GAM7052 296 LOC2837 1 12676 XP_211170.3 3 3470 AGCCTTCTGAGT CA----- A 3 C c
c
01 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACAC ACAT AGGGTCGATGAGTCT
CACACGG C
GAM7052 296 LOC2838 1 13947 XP_211236.1 5 1254 AGCCTCCTGAGT CA----- A 3 C c
c
57 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACGT ACAT AGGGTCGATGAGTCC
TGCACGG C
GAM7052 296 LOC2838 2 3638 NP_787095.1 3 798 AGCCTCCCAAGT CA----- CA 3 C c
c
61 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC
GAM7052 296 LOC2838 2 4775 NP_787095.1 3 1120 AGCCTCCAGAGT CA----- A 3 C c
c
61 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACGT ACATTAGGGTCGATGAG CC
TGCACGG A
GAM7052 296 LOC2838 1 12833 XP_208875.1 3 1592 GCCTTCCTGAGT CA----- 3 C c
c
63 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCAGCC ACATTAGGGTCGATGAGTCC
CCGACGG
GAM7052 296 LOC2838 2 765 XP_208899.1 3 869 AGCCTCCCGAGT CA----- A 3 C c c

89 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCAC ACATTAGGGTCGATGAG CC
CACGCGG C
GAM7052 296 LOC2838 2 5077 XP_208899.1 3 20 CAGCATCCTGGT CA----- A T 3 C c
c
89 AGCTGGGACTAC TGTA TCCCAGCTAC CAGG
AAGTGTGA ACAT AGGGTCGATG GTCC
AGTGTGA C -
GAM7052 296 LOC2839 3 5120 XP_208909.1 5 2801 AGCCTCCTGAGT CA----- A 3 C c
b
28 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGT ACAT AGGGTCGATGAGTCC
TGTACGG C
GAM7052 296 LOC2839 3 10829 XP_208909.1 5 896 AGCCTCCTAAGT CA----- C 3 C c
b
28 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCATGC ACATTAGGGTCGATGA TCC
CGTACGG A
GAM7052 296 LOC2839 3 10915 XP_208909.1 5 2505 ATTCTCCTGAGT T 3 C b b
28 AGCTGGGATTGC CA GTAATCCCAGCTACTCAGG
TGGTGCAC GT CGTTAGGGTCGATGAGTCC
-
GAM7052 296 LOC2840 1 15850 XP_208958.2 3 1570 AGCCCCCTGAGT CA----- 3 C c
c
01 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCAC ACATTAGGGTCGATGAGTCC
CACGTGG
GAM7052 296 LOC2840 1 15391 XP_208983.3 3 1103 ATCCTCCGGAGT CA----- A 3 C c
c
23 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCT ACATTAGGGTCGATGAG CC
TCCGCGG G
GAM7052 296 LOC2840 1 6628 XP_208992.1 3 266 AGCCTCCCTAGT CA----- C 3 C c
c
63 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGCCATGC ACATTAGGGTCGATGA TCC
CGTACCG -
GAM7052 296 LOC2840 1 7784 XP_211322.1 3 947 GCCCTTGGGAGT GTAAT --- 3 C c
c
80 AGCTGGGTGAAT CAT CCCAGCTACTC AGG
GGACGATG GTA GGGTCGATGAG TCC
AGT-- GGT
GAM7052 296 LOC2840 1 4384 XP_209008.3 3 283 AGCCTCCTGAGT AATC---- 3 C c
c
98 AGCTGGCACTGT CATGT CCAGCTACTCAGG
AGGCATGT GTACG GGTCGATGAGTCC
GATGTCAC
GAM7052 296 LOC2841 3 10012 XP_211327.3 5 130 AGCCTCCAGAGT CA----- A 3 C c
c
02 AGCTGGGATTAC TGTAATCCCAGCTACTC GG

AGGCACCT ACATTAGGGTCGATGAG CC
TCCACGG A
GAM7052 296 LOC2841 3 12703 XP_211327.3 3 96 AGCCTCCCAAGC A A CA 3 C c
c
02 AGCTGGGACTAC CATGTA TCCCAGCT CT GG
ATGTATGT GTACAT AGGGTCGA GA CC
C C AC
GAM7052 296 LOC2841 3 16386 XP_211327.3 5 947 AGCTTCCTGAGG CA----- A 3 C c
c
02 AGCTGGGATTAT TGTAATCCCAGCT CTCAGG
AGGTGCAT ATATTAGGGTCGA GAGTCC
TACGTGG G
GAM7052 296 LOC2841 1 8308 XP_211338.2 5 414 AGCCTCCTGAGT CA----- 3 C c c
16 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGATCCTG ACATTAGGGTCGATGAGTCC
GTCCTAG
GAM7052 296 LOC2841 1 7907 XP_209024.1 3 143 AGCCTGCTGAGT CA----- 3 C c c
17 AGCTGGGATTGC TGTAATCCCAGCTACTCAG
AGGTGTGT ACGTTAGGGTCGATGAGTC
TGTGTGG
GAM7052 296 LOC2841 1 12522 XP_209032.1 3 625 AGCCTCCTGAGT CA----- 3 C c c
35 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCC ACATTAGGGTCGATGAGTCC
CCCGCGG
GAM7052 296 LOC2841 1 15851 XP_211354.1 3 694 CTTGAACCTGTG TA ACT 3 C c
c
55 AGCTGGGATCGT CATG ATCCCAGCT CAGG
GCCACTGC GTGC TAGGGTCGA GTCC
-- GT-
GAM7052 296 LOC2841 1 6477 XP_209051.1 3 1181 AGCCTCCCTGGC CA----- A T 3 C c
c
71 AGCTGGGATTAC TGTAATCCCAGCT C CAGG
AGGTGCAC ACATTAGGGTCGA G GTCC
CACGTGG C -
GAM7052 296 LOC2841 2 8749 XP_209059.1 5 51 AGCCTCCCAAGT CA----- CA 3 C c
c
83 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTCC ACATTAGGGTCGATGA CC
CCTGTGG AC
GAM7052 296 LOC2841 2 10894 XP_209059.1 5 1007 AGCCTCCTGAGT CA----- 3 C c
c
83 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCT ACATTAGGGTCGATGAGTCC
TCCACGG
GAM7052 296 LOC2842 1 17615 XP_211408.1 3 67 AGCTTCCTGAGT AA---- 3 C c c
60 AGCTGGGAGGAC CATGT TCCCAGCTACTCAGG
AGGCATGC GTACG AGGGTCGATGAGTCC
GACAGG
GAM7052 296 LOC2842 1 7059 XP_211415.1 5 35 AGCGTCCTGAGT CA----- AA 3 C c
c

```
          81                          AGCTGGGACCAC      TGT  TCCCAGCTACTCAGG
                                     AGGTGCCC         ACA  AGGGTCGATGAGTCC
                                           CCCGTGG   CC
GAM7052  296   LOC2842 1  19098  XP_211419.1  3  1914  AGCCTCCCAAGT            CA        3  C  b
b
          86                          AGCTGGGATTAC CATGTAATCCCAGCTACT  GG
                                     ATGTGTGT    GTACATTAGGGTCGATGA  CC
                                                 AC
GAM7052  296   LOC2842 1  3340   XP_209105.1  3  231   AGCCTCCCAAGT      T       CA        3  C  c  c
          89                          AGCTGGGTTTAT CATGTAA CCCAGCTACT  GG
                                     ATGTGCCC    GTATATT GGGTCGATGA  CC
                                                 T        AC
GAM7052  296   LOC2843 2  16484  XP_211425.1  5  1360  AGCCTCCCAAGT CA-----          CA      3  C  c
 c
          05                          AGCTGGGATTAC      TGTAATCCCAGCTACT  GG
                                     AGGCATGG         ACATTAGGGTCGATGA  CC
                                           GGTACGG            AC
GAM7052  296   LOC2843 2  16775  XP_211425.1  5  1767  AGCCTCCTGAGT CA-----   A            3  C  c
c
          05                          AGCTGGGACTAC      TGTA TCCCAGCTACTCAGG
                                     AGGTGCCT         ACAT AGGGTCGATGAGTCC
                                           TCCGTGG   C
GAM7052  296   LOC2843 1  15828  XP_302720.1  5  60    AGCCTCCTGAGT CA-----       C         3  C  c
c
          11                          AACTGGGGTTAC      TGTAATCCCAG TACTCAGG
                                     AGGCGCGC         ACATTGGGGTC ATGAGTCC
                                           CGCGCGG         A
GAM7052  296   LOC2843 1  7004   XP_211437.1  3  521   AGCTTCCCGAGT CA-----          A      3  C  c
c
          56                          AGCTGGGATTAC      TGTAATCCCAGCTACTC GG
                                     AGATGTGA         ACATTAGGGTCGATGAG CC
                                           AGTGTAG            C
GAM7052  296   LOC2843 2  1466   XP_211435.1  3  614   AGCCTCCTGAGT CA-----                3  C  c  b
          62                          AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                     AACCGTGT         ACATTAGGGTCGATGAGTCC
                                           TGTGCCA
GAM7052  296   LOC2843 2  11728  XP_211435.1  3  746   AGTCTCCTAAAG          T  C-        3  C  b  b
          62                          TGCTGGGATTAC CATGTAATCCCAGC ACT  AGG
                                     ATGTGTGA    GTACATTAGGGTCG TGA  TCC
                                                 -  AA
GAM7052  296   LOC2843 1  15146  XP_211452.1  3  1760  AGCCTCCTGAGT CA-----     C           3  C  c
c
          96                          AGCTGAGATTAC      TGTAATC CAGCTACTCAGG
                                     AGGCACAC         ACATTAG GTCGATGAGTCC
                                           CACACGG      A
GAM7052  296   LOC2844 3  5116   XP_209198.1  3  808   ACCCTCCCAAAG     ----       T  CA      3  C  c  c

          26                          TGCTGGGATTAT CATGT    AATCCCAGC ACT  GG
                                     AGGCATGA    GTACG    TTAGGGTCG TGA  CC
                                           GATA       -  AA
```

GAM7052 296 LOC2844 3 5145 XP_209198.1 3 393 AGTCTCCTGAGT CA----- A 3 C c c

26 AGCTGGGATGAC TGT ATCCCAGCTACTCAGG
AGGCACGC ACA TAGGGTCGATGAGTCC
CGCACGG G

GAM7052 296 LOC2844 3 12481 XP_209198.1 3 962 AGCCTCCCGAGT CA----- A 3 C c
c

26 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCC ACATTAGGGTCGATGAG CC
CCCGCGG C

GAM7052 296 LOC2844 1 8011 XP_290862.1 3 172 AGCCTCCTGAGT CA----- 3 C c c

36 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCC ACATTAGGGTCGATGAGTCC
CCCACGG

GAM7052 296 LOC2844 2 13118 XP_209216.1 5 1201 AGCCTCCTGAGT CA----- T 3 C c
c

54 AGCTGGGCTTAC TGTAA CCCAGCTACTCAGG
AGGCACCC ACATT GGGTCGATGAGTCC
CCCACGG C

GAM7052 296 LOC2844 2 15855 XP_209216.1 5 765 AGCCTCCCAAGT CA----- CA 3 C c
c

54 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCAC ACATTAGGGTCGATGA CC
CACGTGG AC

GAM7052 296 LOC2845 1 5969 XP_211522.1 3 91 AGCCTCCTGAGT CA----- 3 C c c

77 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAT ACATTAGGGTCGATGAGTCC
TACACGG

GAM7052 296 LOC2845 1 5500 XP_209277.2 3 192 GGGCAGGCCTGA TA TA 3 C c
c

85 GGCTGGGATCCC CATG ATCCCAGC CTCAGG
GTGCTGCT GTGC TAGGGTCG GAGTCC
CC --

GAM7052 296 LOC2845 1 507 XP_211529.1 5 247 AGCCTCCCAAGT CA----- CA 3 C c
c

91 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGTTTCCA ACATTAGGGTCGATGA CC
ACCTTTG AC

GAM7052 296 LOC2846 1 11163 XP_211561.1 5 590 AGCCTCCCAAGT CA----- CA 3 C c
c

28 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGCCT ACATTAGGGTCGATGA CC
TCCGCGG AC

GAM7052 296 LOC2847 1 17993 XP_209332.1 3 608 AGCCTCCTGAGT CA----- AA 3 C c
c

08 AGCTGGGACCAC TGT TCCCAGCTACTCAGG
AGGCGAGT ACA AGGGTCGATGAGTCC
TGAGCGG CC

GAM7052 296 LOC2847 1 7366 XP_211602.1 3 145 AGCCTCCTGAGT CA----- 3 C c c

23 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG

AGGTGTGT ACATTAGGGTCGATGAGTCC
TGTGTGG
GAM7052 296 LOC2848 1 2369 XP_209371.1 3 1301 AGCCTCCTGAGT CA----- 3 C c c

05 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGACTCCA ACATTAGGGTCGATGAGTCC
ACCTCAG
GAM7052 296 LOC2848 2 14664 XP_211672.1 3 155 AGCCTCCTGAGT CA----- A 3 C c
c
65 AGCTGGGATCAC TGT ATCCCAGCTACTCAGG
AGGCACAC ACA TAGGGTCGATGAGTCC
CACACGG C
GAM7052 296 LOC2848 2 15707 XP_211672.1 3 1790 ATTGAACTTGAA CA- AC 3 C c
c
65 GCATCGGATTAC CATGTAATCC GCT TCAGG
ATGTTTGT GTACATTAGG CGA AGTTC
CTA --
GAM7052 296 LOC2848 1 18809 XP_209394.1 3 1156 AGCCTCCTGAGT CA----- A 3 C c
c
74 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGATGCAT ACAT AGGGTCGATGAGTCC
TACGTAG C
GAM7052 296 LOC2849 1 16887 XP_211696.1 5 742 AGCCTCCTGAGT CA----- 3 C c c

34 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGT ACATTAGGGTCGATGAGTCC
TGTACGG
GAM7052 296 LOC2849 2 7168 XP_211705.1 3 631 GTCCTCCCAAAG ---- T CA 3 C c c

47 TGCTGGGATTGA CATGT AATCCCAGC ACT GG
AGGCGTGA GTGCG TTAGGGTCG TGA CC
GAAG - AA
GAM7052 296 LOC2849 2 10834 XP_211705.1 3 496 AGCCTCCCAAGT CA----- CA 3 C c
c
47 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGT ACATTAGGGTCGATGA CC
TGTACGG AC
GAM7052 296 LOC2849 1 8376 XP_211703.1 3 1611 AGTCTACTGCGT CA----- T 3 C c
c
50 AGCTGGGATTAC TGTAATCCCAGCTAC CAG
AGGTGCCC ACATTAGGGTCGATG GTC
CCCGTGG C
GAM7052 296 LOC2849 1 7724 XP_211721.1 5 757 GGCCTCCCAAAG -- T CA 3 C c c

82 TGCTGGGATTAT CATGTA ATCCCAGC ACT GG
ACATGTGA GTACAT TAGGGTCG TGA CC
AT - AA
GAM7052 296 LOC2850 1 17393 XP_211753.1 5 324 AGCCTCCTGAGT CA----- A 3 C c
c
58 AGTTGGGACTAC TGTA TCCCAGCTACTCAGG

```
                                  AGGCATAT          ACAT AGGGTTGATGAGTCC
                                         TATACGG    C
GAM7052  296   LOC2851 1  3391  XP_211771.1  3  230   AGCCTCCTGAGT CA-----   A            3  C  c
c
         27                       AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                  AGGTGCCC          ACAT AGGGTCGATGAGTCC
                                         CCCGTGG    C
GAM7052  296   LOC2851 1  7526  XP_211791.1  3  606   GCTTTGAACTTG       CCCA   -         3  C  c
c
         66                       ATGTGGCATTAC CATGTAAT    GCTAC TCAGG
                                  ATGTTCTT    GTACATTA    CGGTG AGTTC
                                              ----    T
GAM7052  296   LOC2851 2  8008  XP_209509.1  3  1880  AGCCTCCTGAGT CA-----                3  C  c  c

         93                       GGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                  AGGCGCCC          ACATTAGGGTCGGTGAGTCC
                                         CCCGCGG
GAM7052  296   LOC2851 2  16072 XP_209509.1  3  763   AGCCTCCTGAGT CA-----   A            3  C  c
c
         93                       AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                  AGGTGTGT          ACAT AGGGTCGATGAGTCC
                                         TGTGTGG    C
GAM7052  296   LOC2852 1  13978 XP_211813.1  3  973   AGCCTCCTGAGT CA-----        C       3  C  c
c
         31                       AACTGGGATTAC       TGTAATCCCAG TACTCAGG
                                  AGAGCCCA          ACATTAGGGTC ATGAGTCC
                                         ACCCGAG     A
GAM7052  296   LOC2852 1  5734  XP_211829.1  5  668   AGCCTTCCGAGT CA-----          A     3  C  c
c
         81                       AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                  AGGCACCC          ACATTAGGGTCGATGAG CC
                                         CCCACGG          -
GAM7052  296   LOC2853 1  14034 XP_211850.1  3  1573  AGCCTCCTGAGT  T     C            3  C  b  b

         36                       AGCTAGGGTTAC CA GTAATCC AGCTACTCAGG
                                  CTGCCACC    GT CATTGGG TCGATGAGTCC
                                          C      A
GAM7052  296   LOC2853 2  2258  XP_209593.1  3  992   AGCCTCCTGAGT CA-----   AT           3  C  c
c
         98                       AGCTGGGGCTAC       TGTA  CCCAGCTACTCAGG
                                  AGGCGCCT          ACAT  GGGTCGATGAGTCC
                                         TCCGCGG    CG
GAM7052  296   LOC2853 2  14737 XP_209593.1  3  1293  AGCCTCCTGAGT CA-----   A            3  C  c
c
         98                       AGCTGGGATCAC       TGT ATCCCAGCTACTCAGG
                                  AGGTGTGT          ACA TAGGGTCGATGAGTCC
                                         TGTGTGG    C
GAM7052  296   LOC2854 1  1360  XP_209617.1  5  1859  AGCCTCCCAAGT CA-----          CA     3  C  c
c
         56                       AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
```

```
                                  AGGTGTGA          ACATTAGGGTCGATGA  CC
                                         AGTGTGG             AC
GAM7052  296   LOC2855 1  6609   XP_209643.1  3  96    AGCCTCCCAAGT CA-----          CA      3  C  c
c
         10                        AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                  AGGCGCGT          ACATTAGGGTCGATGA  CC
                                         TGCGCGG             AC
GAM7052  296   LOC2855 1  11163  XP_209671.1  3  352   AGCCTCCCAAGT CA-----          CA      3  C  c
c
         89                        AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                  AGGCGCCT          ACATTAGGGTCGATGA  CC
                                         TCCGCGG             AC
GAM7052  296   LOC2856 1  18681  XP_209718.1  3  56    TTGAGACTGAGT  T    CC  G           3  C  c
c
         76                        AGATGAATTATT CA GTAAT  CA CTACTCAG
                                  GAATGTGA     GT TATTA  GT GATGAGTC
                                           -    A-  A
GAM7052  296   LOC2856 1  11222  XP_211980.1  5  96    AGCCTCCAGAGT CA-----          A      3  C  c
c
         83                        AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                  AGGCATGC          ACATTAGGGTCGATGAG CC
                                         CGTACGG             A
GAM7052  296   LOC2857 1  4287   XP_211997.1  5  433   AGCCTCCCAAGT CA-----          CA      3  C  c
c
         22                        AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                  AGATGTGT          ACATTAGGGTCGATGA  CC
                                         TGTGTAG             AC
GAM7052  296   LOC2857 2  4189   XP_209742.1  3  1366  AGCCTCCTGAGT     AA----     C         3  C  c
c
         47                        AACTGGGACTGT CATGT      TCCCAG TACTCAGG
                                  AAACATGA     GTACA      AGGGTC ATGAGTCC
                                           AATGTC      A
GAM7052  296   LOC2857 2  5620   XP_209742.1  3  2267  AGCCTCCTGAGT CA-----    A           3  C  c
c
         47                        AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                  AGTTGTGC          ACAT AGGGTCGATGAGTCC
                                         CGTGTTG    C
GAM7052  296   LOC2858 1  15916  XP_212055.1  3  802   AGCCTCCTGAGT CA-----                3  C  c  c

         12                        AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                  AGACGCAC          ACATTAGGGTCGATGAGTCC
                                         CACGCAG
GAM7052  296   LOC2858 1  12894  XP_212036.1  5  163   AGCCTCATGAGT CA-----           G      3  C  c
c
         13                        AGCTGGGATTAC       TGTAATCCCAGCTACTCA
                                  AGGTATGT          ACATTAGGGTCGATGAGT
                                         TGTATGG             A
GAM7052  296   LOC2858 1  649    XP_209777.1  5  1445  AGCTTCCCAAGT CA-----          CA      3  C  c
c
         22                        AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
```

AGGCGTAC ACATTAGGGTCGATGA CC
CATGCGG AC
GAM7052 296 LOC2858 1 14138 XP_212043.1 5 250 AGCCTCCTAAGT CA----- C 3 C c
c
30 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AAGTGCCC ACATTAGGGTCGATGA TCC
CCCGTGA A
GAM7052 296 LOC2858 2 3009 XP_212034.1 5 2164 GCAAGCAAGCCT CCCA A 3 C c
c
43 GAGAGGCATTAC CATGTAAT GCT CTCAGG
ATGGGCTG GTACATTA CGG GAGTCC
---- A
GAM7052 296 LOC2858 2 12028 XP_212034.1 3 273 AGCCTACCAAGT CA----- CA 3 C c
c
43 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGAGTGC ACATTAGGGTCGATGA CC
CGTGAGG A-
GAM7052 296 LOC2858 1 3638 XP_209779.1 3 81 AGCCTCCCAAGT CA----- CA 3 C c
c
53 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC
GAM7052 296 LOC2858 2 13183 XP_209806.1 3 63 AGCCTCCCAAGT CA----- CA 3 C c
c
96 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGC ACATTAGGGTCGATGA CC
CGCACGG AC
GAM7052 296 LOC2858 2 19678 XP_209806.1 3 402 AGCCTCCCGAGT CA----- A 3 C c
c
96 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGTGG ACATTAGGGTCGATGAG CC
GGTGTGG C
GAM7052 296 LOC2859 2 13183 XP_209822.1 3 63 AGCCTCCCAAGT CA----- CA 3 C c
c
22 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGC ACATTAGGGTCGATGA CC
CGCACGG AC
GAM7052 296 LOC2859 2 19678 XP_209822.1 3 411 AGCCTCCCGAGT CA----- A 3 C c
c
22 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGTGG ACATTAGGGTCGATGAG CC
GGTGTGG C
GAM7052 296 LOC2859 1 5346 XP_209834.2 3 354 AAGGCTCTGAGT TAATCCC 3 C c
c
36 AGCTCATGCTTC CATG AGCTACTCAGG
CAGACTGA GTAC TCGATGAGTCT

GAM7052 296 LOC2859 1 18469 XP_212103.1 3 380 AGGCTCCTGAGT CA----- C 3 C c
c
46 AGCTAGGATTAC TGTAATCC AGCTACTCAGG

AGGCACAT ACATTAGG TCGATGAGTCC
TACACGG A
GAM7052 296 LOC2859 2 10251 XP_209821.1 3 902 GGTCTCCCAAAG ---- T CA 3 C c c
52 TGCTGGGATTAT CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GATA - AA
GAM7052 296 LOC2859 2 13737 XP_209821.1 3 765 AGCCTCCTGAGT CA----- 3 C c c
52 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AAGGGCAC ACATTAGGGTCGATGAGTCC
CACGGGA
GAM7052 296 LOC2859 1 4709 XP_209833.1 3 314 AGCCTCCAAAGT CA----- CA 3 C c c
61 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTTTGC ACATTAGGGTCGATGA CC
CGTTTGG AA
GAM7052 296 LOC2859 1 1250 XP_212105.1 3 951 AGCCTCCTGAGT CA----- 3 C c c
72 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCACGT ATATTAGGGTCGATGAGTCC
TGCACGG
GAM7052 296 LOC2859 1 9691 XP_212114.1 5 21 AGCCTCCTGAGT CA----- 3 C c c
81 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG
GAM7052 296 LOC2859 1 9996 XP_212111.1 3 1021 AGACTCCTGAGT CA----- 3 C c c
89 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGT ACATTAGGGTCGATGAGTCC
TGTACGG
GAM7052 296 LOC2859 1 14823 XP_212120.1 3 685 AGCCTTTCGAGT CA----- A --- 3 C c c
99 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGTGTGT ACAT AGGGTCGATGAG TCC
TGTGTGG C CTT
GAM7052 296 LOC2860 1 8761 XP_209868.1 5 725 AGCCTCCTGAGT CA----- A 3 C c c
30 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCC ACAT AGGGTCGATGAGTCC
CCCACGG C
GAM7052 296 LOC2860 1 4778 XP_209873.1 5 733 AGCCTCCTGAGT CA----- A 3 C c c
39 AGCTGGGACTGC TGTA TCCCAGCTACTCAGG
AGGCACCC ACGT AGGGTCGATGAGTCC
CCCACGG C
GAM7052 296 LOC2860 1 12351 XP_212152.1 3 1274 GGCCTCCTGAAG CA----- T - 3 C c c
52 TGTTGGGATTAC TGTAATCCCAGC ACT CAGG
AGGCGTGA ACATTAGGGTTG TGA GTCC
AGTGCGG - A

GAM7052 296 LOC2860 1 1551 XP_212156.1 3 324 ATATCTGGTTTA - CT-- T 3 C c c
59 TCTGGGTATTAC CATGTAAT CCCAG AC CAGG
ATGCGTTT GTACATTA GGGTC TG GTCT
T TATT -
GAM7052 296 LOC2860 1 16730 XP_209892.1 3 452 AGCCTCCTGAGT CA----- 3 C c c
77 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGATGTAT ACATTAGGGTCGATGAGTCC
TATGTAG
GAM7052 296 LOC2860 3 7215 XP_212163.1 3 998 GGCCTCCCAAAG ---- T CA 3 C c
c
78 TGCTGGGATTAA CATGT AATCCCAGC ACT GG
AGGCGTGA GTGCG TTAGGGTCG TGA CC
GAAA - AA
GAM7052 296 LOC2860 3 8761 XP_212163.1 5 1482 AGCCTCCTGAGT CA----- A 3 C c
c
78 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCC ACAT AGGGTCGATGAGTCC
CCCACGG C
GAM7052 296 LOC2860 3 18097 XP_212163.1 5 883 CTCAGCCTGAGT CA----- A 3 C c
c
78 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTGT ACAT AGGGTCGATGAGTCC
TGTGTGG C
GAM7052 296 LOC2861 1 20073 XP_212211.1 5 2152 GGCCTCCTGAAG CA----- T - 3 C c
c
70 TGCTGGGATTAC TGTAATCCCAGC ACT CAGG
AGGCATGA ACATTAGGGTCG TGA GTCC
AGTACGG - A
GAM7052 296 LOC2862 1 1985 XP_212228.1 5 639 TGCCTCCTGAGT CA----- 3 C c c
15 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCAT ACATTAGGGTCGATGAGTCC
TACGTGG
GAM7052 296 LOC2862 1 4345 XP_212235.1 3 191 AGCCTCCCGGGT CA----- A 3 C c
c
18 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGGG CC
TGTACGG C
GAM7052 296 LOC2862 2 7295 XP_212238.1 3 237 AGCGTCCTGAGT CA---- - 3 C c c
35 AGCTGGGGATTA TGTAATCCC AGCTACTCAGG
CAGGCGCC ACATTAGGG TCGATGAGTCC
CCGCGG G
GAM7052 296 LOC2862 2 8806 XP_212238.1 3 237 GCGTCCTGAGTA CA----- - 3 C c c
35 GCTGGGGATTAC TGTAATCCC AGCTACTCAGG
AGGCGCCC ACATTAGGG TCGATGAGTCC
CCCGCGG G
GAM7052 296 LOC2862 2 7295 XP_212241.1 3 242 AGCGTCCTGAGT CA---- - 3 C c c
37 AGCTGGGGATTA TGTAATCCC AGCTACTCAGG
CAGGCGCC ACATTAGGG TCGATGAGTCC

CCGCGG G
GAM7052 296 LOC2862 2 8806 XP_212241.1 3 242 GCGTCCTGAGTA CA----- - 3 C c c

37 GCTGGGGATTAC TGTAATCCC AGCTACTCAGG
AGGCGCCC ACATTAGGG TCGATGAGTCC
CCCGCGG G
GAM7052 296 LOC2862 1 10128 XP_212244.1 5 313 AGCCTCCTGAGT AA---- C 3 C c
c

45 AGCTAGGACTAT CATGT TCC AGCTACTCAGG
AGGCATGC GTACG AGG TCGATGAGTCC
GATATC A
GAM7052 296 LOC2863 1 2204 XP_212278.1 3 497 AGCCTCCCAAGT CA----- CA 3 C c
c

41 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGATCATG ACATTAGGGTCGATGA CC
GTACTAG AC
GAM7052 296 LOC2863 1 10895 XP_212286.1 5 773 AGCCTCCTGAGT CA----- A 3 C c
c

54 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGTGT ACAT AGGGTCGATGAGTCC
TGTGCGG C
GAM7052 296 LOC2863 1 15760 XP_212298.1 3 117 AGCCTCCTGAGT AA---- 3 C c c

81 AGCTGGGACTAG CATGT TCCCAGCTACTCAGG
AGGCGTGT GTGCG AGGGTCGATGAGTCC
GAGATC
GAM7052 296 LOC2863 1 15494 XP_212308.1 5 5894 AGCCTCCTGAGT AATC---- 3 C c
c

95 AGCTGGAACCAC CATGT CCAGCTACTCAGG
AGGCATGT GTACG GGTCGATGAGTCC
GACACCAA
GAM7052 296 LOC2864 1 6157 XP_212310.1 5 586 AGCCTCCCCAGT CA----- CA 3 C c
c

01 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG CC
GAM7052 296 LOC2864 1 16885 XP_210063.1 3 1071 AGCCTCCCGAGT CA----- A 3 C c
c

67 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C
GAM7052 296 LOC2865 1 12740 XP_212340.1 3 977 AGCCTCCCAAGT CA----- CA 3 C c
c

53 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCT ACATTAGGGTCGATGA CC
TCCACGG AC
GAM7052 296 LOC3385 2 4912 XP_294653.1 3 2016 AGCCTGTCAAGT CA----- --- 3 C c
c

65 AGCTGGGATTAC TGTAATCCCAGCTACT CAGG
AGGCGTGT ACATTAGGGTCGATGA GTCC

TGTGCGG ACT
GAM7052 296 LOC3385 2 13157 XP_294653.1 3 2154 GGCCTCCCAAAG ---- T CA 3 C c c
65 TGCTGGGATTAG CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GAGA - AA
GAM7052 296 LOC3385 1 10830 XP_290473.1 3 1077 AGCCTACCAAGT TAA CA 3 C c c
75 AGCTGGGACCAT CATG TCCCAGCTACT GG
GGGTGTGT GTAC AGGGTCGATGA CC
C-- A-
GAM7052 296 LOC3386 1 19998 XP_294671.1 5 4 AGCAGCCTGCAA -- ACT 3 C c c
38 GCTGGGAGCTTG CATGTAA TCCCAGCT CAGG
CATGGGTG GTACGTT AGGGTCGA GTCC
CG AC-
GAM7052 296 LOC3386 1 7837 XP_290494.1 3 2521 CGCCTCCCAAGT CA----- CA 3 C c c
45 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTACCT ACATTAGGGTCGATGA CC
TCCATGG AC
GAM7052 296 LOC3387 2 12023 XP_294688.1 3 73 TGCGTGCCTGTG A-- T T 3 C c c
31 TGCTGGGATCTA CATGT ATCCCAGC AC CAGG
GCGTGGCC GTGCG TAGGGTCG TG GTCC
ATC - T
GAM7052 296 LOC3387 2 17885 XP_294688.1 3 467 GCCCTGGAGAGT - A- T --- 3 C c c
31 CGCTGGGATGCA CAT GT ATCCCAGC ACTC AGG
CGGTGGGC GTG CA TAGGGTCG TGAG TCC
G CG C AGG
GAM7052 296 LOC3387 1 16372 XP_294690.1 3 191 AGCCTCCTGAGT CA----- A 3 C c c
39 AGCTGGGACTGC TGTA TCCCAGCTACTCAGG
AGAAGTGC ACGT AGGGTCGATGAGTCC
CGTGAAG C
GAM7052 296 LOC3387 1 18646 XP_290570.1 3 963 TCCCGCCTCAGT CA----- C 3 C c c
73 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTGCCC ACATTAGGGTCGATGA TCC
CCCGTGG C
GAM7052 296 LOC3388 1 9873 XP_294740.1 5 480 GCCTCCCTGAGT CA----- A 3 C c c
99 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACAC ACAT AGGGTCGATGAGTCC
CACACGG C
GAM7052 296 LOC3389 1 9896 XP_294742.1 3 2129 AGCCTCTGGAGT CA----- A --- 3 C c c
23 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGCGTGT ACAT AGGGTCGATGAG TCC
TGTGCGG C GTC

GAM7052 296 LOC3390 1 16281 XP_290692.1 3 1915 AGCCTCCCAAGT CA----- CA 3 C c
c
78 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCAGAC ACATTAGGGTCGATGA CC
CAGACGG AC
GAM7052 296 LOC3393 1 17237 XP_290838.1 3 2477 AGCCTCTTGAGT CA----- 3 C c
c
24 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTTC
CGTACGG
GAM7052 296 LOC3394 1 14659 XP_290902.1 3 393 AGCCTCCTGAGT CA----- 3 C c c
48 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATAC ACATTAGGGTCGATGAGTCC
CATACGG
GAM7052 296 LOC3394 1 2858 XP_290919.1 3 1472 AGCCTCTCGAGT CA----- --- 3 C c
c
92 AGCTGGGATTAT TGTAATCCCAGCTACTC AGG
AGGCGTCC ATATTAGGGTCGATGAG TCC
CCTGCGG CTC
GAM7052 296 LOC3395 1 19920 XP_290946.1 3 247 AGCTTCCTAAAG T T C- 3 C c c
45 TGCTGGGATTAC CA GTAATCCCAGC ACT AGG
TGGCATGA GT CATTAGGGTCG TGA TCC
- - AA
GAM7052 296 LOC3395 1 19920 XP_290949.1 3 247 AGCTTCCTAAAG T T C- 3 C c c
53 TGCTGGGATTAC CA GTAATCCCAGC ACT AGG
TGGCATGA GT CATTAGGGTCG TGA TCC
- - AA
GAM7052 296 LOC3396 1 10808 XP_295014.1 3 1546 AGCCTCCTGAGT G A-- 3 C c
c
00 AGCTGGGACCAT CAT TA TCCCAGCTACTCAGG
AGGTGTGA GTG AT AGGGTCGATGAGTCC
G ACC
GAM7052 296 LOC3396 1 1892 XP_295016.1 5 1593 AGCCTCCAGAGT CA----- A 3 C c
c
22 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACGC ACATTAGGGTCGATGAG CC
CGCACGG A
GAM7052 296 LOC3396 1 19261 XP_290981.1 3 1680 AGCCTCCTGAGT CA----- A 3 C c
c
59 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCGT ACAT AGGGTCGATGAGTCC
TGCGTGG C
GAM7052 296 LOC3398 1 1251 XP_291020.1 5 1258 AGCCTCCTGAGT CA----- 3 C c c
09 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACGC ACATTAGGGTCGATGAGTCC
CGCACGG

GAM7052 296 LOC3398 1 14207 XP_295079.1 5 75 AGCCTCCTGAGT CA----- A 3 C c c

32 AGCTGGGATAAC TGT ATCCCAGCTACTCAGG
AGACATGC ACA TAGGGTCGATGAGTCC
CGTACAG A

GAM7052 296 LOC3398 2 17916 XP_291031.1 3 646 AGCCTCCTGAAT CA----- C 3 C c c

33 AGCTGGGATTAC TGTAATCCCAGCTA TCAGG
AGGCACCT ACATTAGGGTCGAT AGTCC
TCCACGG A

GAM7052 296 LOC3398 2 18479 XP_291031.1 5 660 AGCCTCCTGAGT CAT----- 3 C c c

33 AGCTGGGATTAC GTAATCCCAGCTACTCAGG
CAGTGCAC CATTAGGGTCGATGAGTCC
CACGTGAC

GAM7052 296 LOC3399 1 9636 XP_291069.1 5 207 AGGCCCCTGAGT CA----- 3 C c c

09 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACGT ACATTAGGGTCGATGAGTCC
TGCACGG

GAM7052 296 LOC3400 1 13456 XP_295137.1 3 121 AGTCTGCCGAGT CA----- A 3 C c c

37 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG -

GAM7052 296 LOC3400 1 11211 XP_295146.1 3 40 AGCCTACAGAGT CA- A --- 3 C c c

65 AGCTGGGAATAC TGTA TCCCAGCTACTC AGG
AAGT ACAT AGGGTCGATGAG TCC
TGA A ACA

GAM7052 296 LOC3401 2 2492 XP_295156.1 3 375 AGCCTGCCAAAG T T ---- 3 C c c

09 TGCTGGGATTAC CA GTAATCCCAGC ACT CAGG
TGGCGTGA GT CATTAGGGTCG TGA GTCC
- - AACC

GAM7052 296 LOC3401 2 9847 XP_295156.1 3 246 AGCCTCCTGAGT CA----- A 3 C c c

09 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C

GAM7052 296 LOC3401 1 10831 XP_291153.1 3 2226 GGCCTCCTGAGT CA----- 3 C c c

38 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG

GAM7052 296 LOC3401 1 765 XP_291158.1 3 1523 AGCCTCCCGAGT CA----- A 3 C c c

56 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCAC ACATTAGGGTCGATGAG CC
CACGCGG C

GAM7052 296 LOC3402 1 12172 XP_295190.1 5 1083 AGCCTCCTGAGT CA----- 3 C c c

```
          59                          AGCTGGGATTGC       TGTAATCCCAGCTACTCAGG
                                     AGGTGCCC          ACGTTAGGGTCGATGAGTCC
                                           CCCGTGG
GAM7052  296   LOC3403 1  16887  XP_291269.1  3  1468  AGCCTCCTGAGT CA-----                3  C  c
c
          90                          AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                     AGGCATGT          ACATTAGGGTCGATGAGTCC
                                           TGTACGG
GAM7052  296   LOC3404 1  8761   XP_291274.1  5  732   AGCCTCCTGAGT CA-----  A             3  C  c
c
          08                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGCACCC          ACAT AGGGTCGATGAGTCC
                                           CCCACGG   C
GAM7052  296   LOC3405 1  9710   XP_295268.1  3  1087  CACATCTCCTAG     AA      A  C         3  C  c
c
          28                          AGCTGGGAATGT CATGT  TCCCAGCT CT AGG
                                     GTCCCTAA    GTGTA  AGGGTCGA GA TCC
                                           --      - -
GAM7052  296   LOC3405 1  13947  XP_291331.1  3  472   AGCCTCCTGAGT CA-----  A             3  C  c
c
          47                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGCACGT          ACAT AGGGTCGATGAGTCC
                                           TGCACGG   C
GAM7052  296   LOC3429 1  4809   XP_292790.2  3  896   AGCCTCACGAGT CA-----           ---    3  C  c  c

          26                          AGCTGGGATTAC       TGTAATCCCAGCTACTC   AGG
                                     AGGCATGC          ACATTAGGGTCGATGAG   TCC
                                           CGTACGG             CAC
GAM7052  296   LOC3448 1  10624  XP_293599.2  3  415   ACTGGCATTGTT     AA       - ----       3  C  c  c
          05                          AGCTGGGGACAT CATGT  TCCCAGCTA C    TCAG
                                     GGAAGTGG    GTACA  GGGGTCGAT G    GGTC
                                           --       T TTAC
GAM7052  296   LOC3452 1  9847   NP_835236.1  3  1037  AGCCTCCTGAGT CA-----  A             3  C  c
c
          75                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                     AGGCGCCC          ACAT AGGGTCGATGAGTCC
                                           CCCGCGG   C
GAM7052  296   LOC3478 1  19575  XP_302604.1  3  1096  TTCCTCCCAAAG     ----       T   CA      3  C  c
c
          03                          TGCTGGGATTAA CATGT    AATCCCAGC ACT  GG
                                     TGGCGTGA    GTGCG    TTAGGGTCG TGA  CC
                                           GTAA        -  AA
GAM7052  296   LOC3479 1  7074   XP_302624.1  5  453   AGACTCCCGAGT CA-----           A     3  C  c
c
          05                          AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                     AGGCACAT          ACATTAGGGTCGATGAG CC
                                           TACACGG             C
GAM7052  296   LOC3480 1  12676  XP_302653.1  3  3469  AGCCTTCTGAGT CA-----  A             3  C  c
c
          75                          AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
```

AGGCACAC ACAT AGGGTCGATGAGTCT
CACACGG C
GAM7052 296 LOC3480 2 16360 XP_300615.1 3 319 AGCCTCCCGAGT CA----- A 3 C c
c
94 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCAT ACATTAGGGTCGATGAG CC
TACGTGG C
GAM7052 296 LOC3480 2 16871 XP_300615.1 5 138 AGCCTTCCGAGT CA----- A A 3 C c
c
94 AGCTGGGACTAC TGTA TCCCAGCTACTC GG
AGTGCTTC ACAT AGGGTCGATGAG CC
CTTCGTG C -
GAM7052 296 LOC3482 1 17011 XP_302683.1 5 119 CCTGGAGGCGGT A- ----- 3 C c c

08 GGCTGGGATAAA CATGT ATCCCAGCTACT CAGG
CGTGCACC GTGCA TAGGGTCGGTGG GTCC
AA CGGAG
GAM7052 296 LOC3482 1 4503 XP_300670.1 3 1615 ACCCTCCCGAGT CA----- A 3 C c
c
35 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCC ACATTAGGGTCGATGAG CC
CCCGCGG C
GAM7052 296 LOC3482 1 5537 XP_300683.1 5 142 CAGCCTCTGAGT CA----- A 3 C c
c
62 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AAGTGCAT ACAT AGGGTCGATGAGTCT
TACGTGA C
GAM7052 296 LOC3483 2 2104 XP_300729.1 3 1118 CAGCCTGCCAAG CA----- C --- 3 C c
c
96 TAGCTGGATTAC TGTAATCC AGCTACT CAGG
AGGCACGT ACATTAGG TCGATGA GTCC
TGCACGG - ACC
GAM7052 296 LOC3483 2 10170 XP_300729.1 3 1118 AGCCTGCCAAGT CA------ C --- 3 C c
c
96 AGCTGGATTACA TGTAATCC AGCTACT CAGG
GGCACGTG ACATTAGG TCGATGA GTCC
GTGCACGG - ACC
GAM7052 296 LOC3484 1 2858 XP_300730.1 3 713 AGCCTCTCGAGT CA----- --- 3 C c c

02 AGCTGGGATTAT TGTAATCCCAGCTACTC AGG
AGGCGTCC ATATTAGGGTCGATGAG TCC
CCTGCGG CTC
GAM7052 296 LOC3484 3 1361 XP_302753.1 5 167 AGCTTCCTGAGT CA----- A 3 C c c

28 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCGC ACAT AGGGTCGATGAGTCC
CGCGTGG C
GAM7052 296 LOC3484 3 2400 XP_302753.1 5 3 GCCTCCTGAGTA CA------ A 3 C c c
28 GCTGGGACTACA TGTA TCCCAGCTACTCAGG
AGTGTGTA ACAT AGGGTCGATGAGTCC

ATGTGTGA C
GAM7052 296 LOC3484 3 7896 XP_302753.1 3 341 CTGCTGGCTCAA A AC--- 3 C c c

28 AGCTGGGACTAC CATGTA TCCCAGCT TCAG
ATGAAAGT GTACAT AGGGTCGA GGTC
C AACTC
GAM7052 296 LOC3484 1 13251 XP_300743.1 3 215 AGCCTCCCGAGT CA----- A 3 C c
c

60 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AAGTGCAC ACATTAGGGTCGATGAG CC
CACGTGA C
GAM7052 296 LOC3484 1 19920 XP_300758.1 3 245 AGCTTCCTAAAG T T C- 3 C c c

92 TGCTGGGATTAC CA GTAATCCCAGC ACT AGG
TGGCATGA GT CATTAGGGTCG TGA TCC
- - AA
GAM7052 296 LOC3485 1 5965 XP_300378.1 3 713 AGCCTCCTGAGT CA----- 3 C c c

67 AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCACAC ATATTAGGGTCGATGAGTCC
CACACGG
GAM7052 296 LOC3486 1 13715 XP_300816.1 5 211 GGTCCCCTGAAG CA----- T - 3 C c
c

99 TGCTGGGATTAC TGTAATCCCAGC ACT CAGG
AGGTGTGA ACATTAGGGTCG TGA GTCC
AGTGTGG - A
GAM7052 296 LOC3487 1 7313 XP_302888.1 3 431 AACCTCCTGAGT CA----- 3 C c c

97 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGAGTGT ACATTAGGGTCGATGAGTCC
TGTGAGG
GAM7052 296 LOC3487 2 3079 XP_300845.1 3 356 CTCAGCCTGAGT CA ----- 3 C c c

98 AGCTGGGATGGG TGTA ATCCCAGCTACTCAGG
ACTACAGA ACAT TAGGGTCGATGAGTCC
AG CAGGG
GAM7052 296 LOC3487 2 12640 XP_300845.1 3 1481 AGCCTCCTGAGT CA----- C 3 C c
c

98 AGCTGAGATTAC TGTAATC CAGCTACTCAGG
AGGTGCCC ACATTAG GTCGATGAGTCC
CCCGTGG A
GAM7052 296 LOC3488 2 473 XP_302910.1 5 197 CAGCCTCCTGAG CA----- C 3 C c c

88 TAGCTGGATTAC TGTAATCC AGCTACTCAGG
AGGGCCTG ACATTAGG TCGATGAGTCC
GTCCGGG -
GAM7052 296 LOC3488 2 5196 XP_302910.1 5 197 AGCCTCCTGAGT CA------ C 3 C c
c

88 AGCTGGATTACA TGTAATCC AGCTACTCAGG
GGGCCTGG ACATTAGG TCGATGAGTCC
GGTCCGGG -
GAM7052 296 LOC3489 1 1705 XP_302929.1 3 387 AGCCTCCCTAGT CA----- C 3 C c
c

```
          47                    AGCTGGGATTAC      TGTAATCCCAGCTACT AGG
                                AGGCGCGC          ACATTAGGGTCGATGA TCC
                                     CGCGCGG           -
GAM7052  296   LOC3490 1  17749  XP_300932.1  3  262   AGCCTCCTGAGT CA-----  AA            3  C  c
c
          75                    AGCTGGGACCAC      TGT  TCCCAGCTACTCAGG
                                AGGTATGC          ACA  AGGGTCGATGAGTCC
                                     CGTATGG   CC
GAM7052  296   LOC3491 3  5467   XP_300969.1  3  1455  AGCCTCCTGAGT CA-----              3  C  c  c

          70                    AGCTGGGATTAT      TGTAATCCCAGCTACTCAGG
                                AGGCGTGT          ATATTAGGGTCGATGAGTCC
                                     TGTGCGG
GAM7052  296   LOC3491 3  11095  XP_300969.1  5  1134  AGCCTCCTGAGT CA-----  A            3  C  c
c
          70                    AGCTGGGACTAC      TGTA TCCCAGCTACTCAGG
                                AGGCTCAT          ACAT AGGGTCGATGAGTCC
                                     TACTCGG   C
GAM7052  296   LOC3491 3  13113  XP_300969.1  3  554   AGTCTCCTGAGT CA-----  A            3  C  c
c
          70                    AGCTGGGATCAC      TGT ATCCCAGCTACTCAGG
                                AGGCATGC          ACA TAGGGTCGATGAGTCC
                                     CGTACGG   C
GAM7052  296   LOC3492 1  3623   XP_300251.1  3  529   AGCCTCTCAAGT CA-----          C---    3  C  c
c
          51                    AGCTGGGATTAC      TGTAATCCCAGCTACT   AGG
                                AGGCGCCC          ACATTAGGGTCGATGA   TCC
                                     CCCGCGG           ACTC
GAM7052  296   LOC3492 1  8011   XP_300998.1  5  175   AGCCTCCTGAGT CA-----              3  C  c  c
          61                    AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                AGGCACCC          ACATTAGGGTCGATGAGTCC
                                     CCCACGG
GAM7052  296   LOC3492 1  16887  XP_303013.1  3  5431  AGCCTCCTGAGT CA-----              3  C  c
c
          72                    AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                AGGCATGT          ACATTAGGGTCGATGAGTCC
                                     TGTACGG
GAM7052  296   LOC3492 1  16887  XP_303015.1  3  5422  AGCCTCCTGAGT CA-----              3  C  c
c
          79                    AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                AGGCATGT          ACATTAGGGTCGATGAGTCC
                                     TGTACGG
GAM7052  296   LOC3493 1  16887  XP_303022.1  3  5408  AGCCTCCTGAGT CA-----              3  C  c
c
          01                    AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                AGGCATGT          ACATTAGGGTCGATGAGTCC
                                     TGTACGG
GAM7052  296   LOC3493 1  5500   XP_301019.1  3  167   GGGCAGGCCTGA    TA      TA           3  C  c
c
          05                    GGCTGGGATCCC CATG  ATCCCAGC  CTCAGG
```

```
                                  GTGCTGCT    GTGC  TAGGGTCG  GAGTCC
                                        CC       --
GAM7052  296   LOC3493 1  16887  XP_303023.1  3  5435  AGCCTCCTGAGT CA-----                3  C  c
c
         06                        AGCTGGGATTAC       TGTAATCCCAGCTACTCAGG
                                  AGGCATGT          ACATTAGGGTCGATGAGTCC
                                        TGTACGG
GAM7052  296   LOC3493 1  16885  XP_088528.1  5  532   AGCCTCCCGAGT CA-----           A     3  C  c
c
         60                        AGCTGGGATTAC       TGTAATCCCAGCTACTC GG
                                  AGGCATGC          ACATTAGGGTCGATGAG CC
                                        CGTACGG             C
GAM7052  296   LOC3494 2  15314  XP_303044.1  3  137   TTTTTCTGAGTA       CC  GC-          3  C  c
c
         08                        TAATGTTATTAC CATGTAAT  CA   TACTCAGG
                                  ATGGTCCT    GTACATTA  GT   ATGAGTCT
                                        TT  AAT
GAM7052  296   LOC3494 2  19208  XP_303044.1  5  98    AGCCTCCTGAGT CA-----   A            3  C  c
c
         08                        AGCTGGGACTAC       TGTA TCCCAGCTACTCAGG
                                  AGATGTAG          ACAT AGGGTCGATGAGTCC
                                        GATGTAG    C
GAM7052  296   LOC3494 1  3639   XP_300513.1  3  1145  AGCCTCCTGAGT CA-----      C          3  C  c
c
         40                        AGCTAGGATTAC       TGTAATCC AGCTACTCAGG
                                  AGGTGCCT          ACATTAGG TCGATGAGTCC
                                        TCCGTGG       A
GAM7052  296   LOC5118 1  11729  NP_057387.1  3  371   TCAGCCTCTCGG   --       G    C       3  C  c  c

         6                         TGGTGGGATTAT CAT  GTAATCCCA CTACT AGG
                                  GAATGATT    GTA  TATTAGGGT GGTGG TCT
                                        AG       -    C
GAM7052  296   LOC5714 1  1187   NP_065155.2  3  821   AGCCTCCCAAGT CA-----          CA     3  C  c
c
         6                         AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                  AGGCACCC          ACATTAGGGTCGATGA  CC
                                        CCCACGG             AC
GAM7052  296   LOC9040 1  18503  XP_031517.1  5  1730  ATCCTCCCAAGT CA-----          CA     3  C  c
 c
         8                         AGCTGGGATTAC       TGTAATCCCAGCTACT  GG
                                  AGATGCCT          ACATTAGGGTCGATGA  CC
                                        TCCGTAG             AC
GAM7052  296   LOC9080 1  16793  NP_653168.1  3  19    CGGCTTCCTGGT     AA----       T       3  C  c  c

         6                         AGCTGGGACTAG CATGT     TCCCAGCTAC CAGG
                                  AGATGTGT    GTGTA     AGGGTCGATG GTCC
                                        GAGATC        -
GAM7052  296   LOC9105 2  4090   NP_612377.1  3  992   GCCTCACCAAAG  T        T  CA        3  C  c
c
         6                         TGTTGGGATTAC CA GTAATCCCAGC ACT  GG
```

TGGTGTGA GT CATTAGGGTTG TGA CC
- - AA
GAM7052 296 LOC9105 2 13610 NP_612377.1 3 873 CTGCCTCCGAGT CA----- A -- 3 C c
c
6 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGTGTGA ACAT AGGGTCGATGAG TCC
AGTGTGG C CC
GAM7052 296 LOC9111 2 4889 XP_036218.1 3 843 AGCTTCCTGAGT CA----- A 3 C c b

5 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCC ACAT AGGGTCGATGAGTCC
CCCACGG C
GAM7052 296 LOC9111 2 12496 XP_036218.1 3 370 AGCCTCCCGAGT T A 3 C b b

5 AGCTGGGATTAC CA GTAATCCCAGCTACTC GG
TGGTGCCC GT CATTAGGGTCGATGAG CC
- C
GAM7052 296 LOC9125 1 6792 XP_037135.1 5 2291 AGATTCCCGAGT CA----- A 3 C c
c
0 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGATGTGC ACATTAGGGTCGATGAG CC
CGTGTAG C
GAM7052 296 LOC9154 1 7060 XP_039115.1 5 1375 AGCCTCCTGAGT CA----- A 3 C c
c
9 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AAGCATGC ACAT AGGGTCGATGAGTCC
CGTACGA C
GAM7052 296 LOC9214 1 14963 XP_043160.1 5 844 GGCCTCTGGAGT CA----- A --- 3 C c
c
8 AGCTGGGACTAC TGTA TCCCAGCTACTC AGG
AGGTGCCC ACAT AGGGTCGATGAG TCC
CCCGTGG C GTC
GAM7052 296 LOC9259 1 9812 NP_775739.1 3 3612 AGCCTCCCAAGT CA----- CA 3 C c
c
7 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCAGCA ACATTAGGGTCGATGA CC
ACGACGG AC
GAM7052 296 LOC9334 1 7858 NP_612411.2 3 1892 AGCCTCCCAAGT CA----- CA 3 C c
c
9 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGTGCCTG ACATTAGGGTCGATGA CC
GTCCGTG AC
GAM7052 296 LSS 1 13480 NP_002331.2 3 660 GCTCGCCTGAGT TA--- GC 3 C c c
ATGGGGTGGTGT CATG ATCCCA TACTCAGG
CATGGAGC GTAC TGGGGT ATGAGTCC
TGTGG --
GAM7052 296 MAK 1 7895 NP_005897.1 3 729 AGCCTCCCGAGT ---- A 3 C c c
AGCTGGGATTAG CATGT AATCCCAGCTACTC GG
AGGCGTGT GTGCG TTAGGGTCGATGAG CC
GAGA C

GAM7052 296 MANBAL 1 12674 NP_071360.1 5 357 AGCCTTCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGTTGGTT ACAT AGGGTCGATGAGTCT
TTGGTTG C

GAM7052 296 MAPA 2 2128 NP_660299.1 3 1025 GGCCTCCTGAAG CA----- T - 3 C c c

TGCTGGGATTAC TGTAATCCCAGC ACT CAGG
AGGCGTGG ACATTAGGGTCG TGA GTCC
GGTGCGG - A

GAM7052 296 MAPA 2 9966 NP_660299.1 3 890 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGCACCCG ACATTAGGGTCGATGAGTCC
GCCCACG

GAM7052 296 MEF2A 1 12527 NP_005578.1 5 157 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCT ACATTAGGGTCGATGAG CC
TCCGCGG C

GAM7052 296 MEFV 2 3905 NP_000234.1 3 908 AGCCTCCGAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGCCC ACATTAGGGTCGATGA CC
CCCGCGG AG

GAM7052 296 MEFV 2 12378 NP_000234.1 3 596 AGCCTCCTGAGC CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCT CTCAGG
AGGTGCGT ACATTAGGGTCGA GAGTCC
TGCGTGG C

GAM7052 296 MFI2 1 19559 NP_201573.1 3 130 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGATGAC TGT ATCCCAGCTACTCAGG
AGGCGTGC ACA TAGGGTCGATGAGTCC
CGTGCGG G

GAM7052 296 MFTC 1 8527 NP_110407.2 3 633 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCT ACAT AGGGTCGATGAGTCC
TCCACGG C

GAM7052 296 MGC1110 1 8801 NP_115701.2 3 1672 GGCCTCCTAGAG CA----- T - 3 C c c

2 TGCTGGGATTAC TGTAATCCCAGC ACTC AGG
AGGTGTGA ACATTAGGGTCG TGAG TCC
AGTGTGG - A

GAM7052 296 MGC1251 1 16735 NP_291026.1 3 82 AGCCTCCCGAGT CA----- A 3 C c c

8 AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGGCGAGT ATATTAGGGTCGATGAG CC
TGAGCGG C

GAM7052 296 MGC1307 1 20118 NP_116078.2 3 501 TCTGCTTCCTAT A CTC 3 C c c

1 AGCTGGGATGAT CATGT ATCCCAGCTA AGG

ATGGGGGA GTATA TAGGGTCGAT TCC
G A--
GAM7052 296 MGC1320 1 10962 NP_113653.1 3 214 AGCCTCCCCAGT CA----- CA 3 C c
c
4 AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCA ACATTAGGGTCGATGA CC
ACCACGG CC
GAM7052 296 MGC1428 1 7116 NP_542391.1 3 537 AGCCTCCTGAGT CA----- A 3 C c
c
9 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTATGC ACAT AGGGTCGATGAGTCC
CGTATGG C
GAM7052 296 MGC2418 1 7412 NP_689565.1 5 299 AGCCTCTCCAGT CA----- C--- 3 C c
c
0 AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTGTGT ACATTAGGGTCGATGA TCC
TGTGTGG CCTC
GAM7052 296 MGC2734 1 7770 XP_300964.1 5 1751 AGCCTCCGGAGT CA----- A 3 C c
c
5 AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGC ACATTAGGGTCGATGAG CC
CGTGCGG G
GAM7052 296 MGC2964 1 2841 NP_776171.1 5 47 CAATTCCTGAGT T TC AG 3 C c
c
9 AGGGCCTTGCTT CA GTAA CC CTACTCAGG
GAGTTCTT GT CGTT GG GATGAGTCC
T CC --
GAM7052 296 MGC2989 1 6192 NP_653219.1 3 673 AGCCTCCTGAGT CA----- AA 3 C c
c
1 AGCTGGGAGGAC TGT TCCCAGCTACTCAGG
AGGCATAT ACA AGGGTCGATGAGTCC
TATACGG GG
GAM7052 296 MGC2989 1 8105 NP_659485.1 3 590 AGCCTCCTGATT AA---- C 3 C c
c
8 AGCTGGGACTAT CATGT TCCCAGCTA TCAGG
AGGCGTGT GTGCG AGGGTCGAT AGTCC
GATATC T
GAM7052 296 MGC3207 2 13361 NP_115661.1 3 1522 AGCCTCCCGAGT CA----- A 3 C c
c
AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGAGCCT ACGTTAGGGTCGATGAG CC
TCCGAGG C
GAM7052 296 MGC3207 2 16723 NP_115661.1 3 873 AGCCTCCTGAGT CA----- 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 MGC3333 1 9435 NP_689579.2 3 163 TGAACCAGAAGT ---- - - A 3 C c c
8 AGCTGGGCATTG CATG TAAT CCCAGCTACT C GG
GAGTCATG GTAC GTTA GGGTCGATGA G CC

```
                                        TGAG  C       A A
GAM7052  296   MGC3363 1  14742  NP_689809.1  3  769   AGCCTCCTGAGT CA-----              3  C  c
c
         7                          AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                    AGGTGCGT          ACATTAGGGTCGATGAGTCC
                                          TGCGTGG
GAM7052  296   MGC3413 2  7217   XP_291029.1  3  419   AGCCACCTGACT CA-----         C       3  C  c
c
         2                          AGCTGGGATTGC      TGTAATCCCAGCTA TCAGG
                                    AGCCTGCA          ACGTTAGGGTCGAT AGTCC
                                          ACGTCCG           C
GAM7052  296   MGC3413 2  18011  XP_291029.1  3  586   AGCCTCCCAAGT CA-----          CA      3  C  c
c
         2                          AGCTGGGATTAC      TGTAATCCCAGCTACT  GG
                                    AGGCGTGC          ACATTAGGGTCGATGA  CC
                                          CGTGCGG           AC
GAM7052  296   MGC3504 1  16147  NP_694940.1  5  329   CATCAACAGACT         AGCTA          3  C  c
c
         8                          GGGAGGGATTAC CATGTAATCCC    CTCAG
                                    GTGGGGTC    GTGCATTAGGG    GGGTC
                                          A----
GAM7052  296   MGC3546 1  17258  NP_694976.1  3  172   AGCCTCCGGAGT CA-----          A      3  C  c
c
         8                          AGCTGGGGTTAC      TGTAATCCCAGCTACTC GG
                                    AGGCACGG          ACATTGGGGTCGATGAG CC
                                          GGCACGG           G
GAM7052  296   MGC4016 1  6366   NP_714920.1  5  370   GGCCTCCTGAGT CA-----  AA          3  C  c
c
         8                          AGCTGGGACGAC      TGT  TCCCAGCTACTCAGG
                                    AGGCGTGC          ACA  AGGGTCGATGAGTCC
                                          CGTGCGG   GC
GAM7052  296   MGC4057 1  18904  NP_689989.1  3  995   AGCCTCCTGAGT CA-----  A          3  C  c
c
         9                          AGCTGGGACTAT      TGTA TCCCAGCTACTCAGG
                                    AGGTTGCT          ATAT AGGGTCGATGAGTCC
                                          TCGTTGG   C
GAM7052  296   MGC4312 1  19043  NP_775784.1  3  253   TGCCTCCTGAGT CA-----  A          3  C  c
c
         2                          AGCTGGGACTAC      TGTA TCCCAGCTACTCAGG
                                    AGGCGCAC          ACAT AGGGTCGATGAGTCC
                                          CACGCGG   C
GAM7052  296   MGC4633 3  4916   XP_290712.1  3  151   AGCCTCCCAAAG    ----     G   CA      3  C  c
c
         6                          TGGTGGGATTAT CATGT   AATCCCA CTACT  GG
                                    AGGCATGA    GTACG   TTAGGGT GGTGA  CC
                                          GATA      -    AA
GAM7052  296   MGC4633 3  5284   XP_290712.1  3  16    TTTATCCTGAGT CA------        C       3  C  c  c

         6                          ACTGGGATTACA      TGTAATCCCAG TACTCAGG
                                    GGCGCCCA          ACATTAGGGTC ATGAGTCC
```

ACCCGCGG -
GAM7052 296 MGC4633 3 10377 XP_290712.1 3 16 CTTTATCCTGAG CA----- C 3 C c c
6 TACTGGGATTAC TGTAATCCCAG TACTCAGG
AGGCGCCC ACATTAGGGTC ATGAGTCC
CCCGCGG -
GAM7052 296 MGC4673 1 5120 NP_714925.1 3 935 AGCCTCCTGAGT CA----- A 3 C c c
2 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGT ACAT AGGGTCGATGAGTCC
TGTACGG C
GAM7052 296 MGC5045 1 6275 NP_775733.1 3 174 AGCCTCCTGAGT CA----- 3 C c c
2 AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTATGT ACATTAGGGTCGATGAGTCC
TGTATGG
GAM7052 296 MGC5055 1 19560 NP_776163.1 3 647 AGCCTCCAGAGT G -- A 3 C c c
9 AGCTGGGATTTT CAT TA ATCCCAGCTACTC GG
AGGTGTGC GTG AT TAGGGTCGATGAG CC
G TT A
GAM7052 296 MGRN1 2 14616 XP_048119.4 3 1679 AGGCTCCTGAGT CA---- - 3 C c c
AGCTGGGGATTA TGTAATCCC AGCTACTCAGG
CAGGTGCC ACATTAGGG TCGATGAGTCC
CCGTGG G
GAM7052 296 MGRN1 2 16263 XP_048119.4 3 1679 GGCTCCTGAGTA CA----- - 3 C c c
GCTGGGGATTAC TGTAATCCC AGCTACTCAGG
AGGTGCCT ACATTAGGG TCGATGAGTCC
TCCGTGG G
GAM7052 296 MLANA 1 5470 NP_005502.1 3 696 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTGC ACATTAGGGTCGATGAGTCC
CGTGCGG
GAM7052 296 MLZE 1 18046 NP_113603.1 5 668 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCT ACATTAGGGTCGATGA CC
TCCGTGG AC
GAM7052 296 MMPL1 1 10936 NP_004133.1 3 608 TGGGACCTGAGT AA---- 3 C c c
AGCTGGGACCAC CATGT TCCCAGCTACTCAGG
AGGCATGC GTACG AGGGTCGATGAGTCC
GACACC
GAM7052 296 moblak 1 9025 NP_570719.1 3 1082 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGC ACATTAGGGTCGATGA CC
CGTGTGG AC
GAM7052 296 MOCS1 1 16709 NP_005933.1 3 56 ACCCAGGCCTGG GTA A T 3 C c c

AGCTGGGATGCA CAT ATCCCAGCT C CAGG
ATGTAGGC GTA TAGGGTCGA G GTCC
ACG - -
GAM7052 296 MOCS1 1 16709 NP_005934.2 3 824 ACCCAGGCCTGG GTA A T 3 C c
c
AGCTGGGATGCA CAT ATCCCAGCT C CAGG
ATGTAGGC GTA TAGGGTCGA G GTCC
ACG - -
GAM7052 296 MOCS1 1 16709 NP_620306.1 3 56 ACCCAGGCCTGG GTA A T 3 C c
c
AGCTGGGATGCA CAT ATCCCAGCT C CAGG
ATGTAGGC GTA TAGGGTCGA G GTCC
ACG - -
GAM7052 296 MOCS3 1 12388 NP_055299.1 3 664 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCAC ACATTAGGGTCGATGAGTCC
CACGCGG
GAM7052 296 MPL 1 19484 NP_005364.1 3 653 GGCCTCCCTAGT CA----- C 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCGCAC ACATTAGGGTCGATGA TCC
CACGCGG -
GAM7052 296 MRPL38 1 15457 NP_115867.1 5 47 GGCCTCCCAAAG ---- T CA 3 C c
c
TGCTGGGATTCC CATGT AATCCCAGC ACT GG
CGGCGTGA GTGCG TTAGGGTCG TGA CC
GCCC - AA
GAM7052 296 MRPL44 1 8317 NP_075066.1 3 344 AGCCTCCCTAGT CA----- C 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCACAC ACATTAGGGTCGATGA TCC
CACACGG -
GAM7052 296 MRPL49 1 13740 NP_004918.1 3 408 AGCCTCTTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCC ACATTAGGGTCGATGAGTTC
CCCGCGG
GAM7052 296 MSCP 1 12409 NP_061049.2 3 1207 GTGTGATGGGGG - G A- G 3 C c
c
AGTGGGTATTAC CATGTAAT CCCA CT CTCA
ATGCATTG GTACATTA GGGT GA GGGT
T - GG A
GAM7052 296 MSTP028 1 14617 NP_114160.1 3 1992 AGCCTCCCGAGT CA----- A 3 C c
c
AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGTACCC ACGTTAGGGTCGATGAG CC
CCCATGG C
GAM7052 296 MtFMT 1 11229 NP_640335.1 3 228 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCC

CACACGG
GAM7052 296 MTH2 1 4662 NP_060753.1 3 936 AGCTTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGGCACCC ATATTAGGGTCGATGAG CC
CCCACGG C
GAM7052 296 MYO5C 1 8527 NP_061198.1 3 713 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCT ACAT AGGGTCGATGAGTCC
TCCACGG C
GAM7052 296 NCAG1 1 9119 NP_115536.1 3 3750 AGCCTCCTGAAT CA----- C 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTA TCAGG
AGGTGCAC ACATTAGGGTCGAT AGTCC
CACGTGG A
GAM7052 296 NCOA6 1 8801 NP_054790.1 5 1106 GGCCTCCTAGAG CA----- T - 3 C c
c
TGCTGGGATTAC TGTAATCCCAGC ACTC AGG
AGGTGTGA ACATTAGGGTCG TGAG TCC
AGTGTGG - A
GAM7052 296 NCOA6IP 1 16997 NP_079107.5 3 364 AGTCTCCTCAGT G -- C 3 C c c
AGCTGGGGCTTT CAT TAA TCCCAGCTACT AGG
AGGTGGGC GTG ATT GGGGTCGATGA TCC
G TC C
GAM7052 296 NDP52 1 13638 NP_005822.1 3 1205 AGCCTCCCAAGT CA----- CA 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGT ACATTAGGGTCGATGA CC
TGTGTGG AC
GAM7052 296 NF2 1 1234 NP_057502.1 5 565 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACGC ACATTAGGGTCGATGAG CC
CGCACGG C
GAM7052 296 NHLH1 1 10682 NP_005589.1 3 593 GGGAATCTCAGT TAA C 3 C c c
AGCTGGGAATTA CATG TCCCAGCTACT AGG
TGGAAAAA GTAT AGGGTCGATGA TCT
TA- C
GAM7052 296 NID 1 10147 NP_002499.1 3 283 TATACACCCCTG CAGC 3 C c c
AGTGAGGATTAC CATGTAATCC TACTCAGG
ATGCCCAT GTACATTAGG GTGAGTCC
A---
GAM7052 296 NMT1 1 14612 NP_066565.1 3 571 CCCTTCTGAATC T A AC- 3 C c c
AGCTGGGATGAC CA GT ATCCCAGCT TCAGG
TGGCTTTG GT CA TAGGGTCGA AGTCT
- G CTA
GAM7052 296 NOSIP 1 4828 NP_057037.1 5 138 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGATGAC ACATTAGGGTCGATGAG CC

CAGTAGG C
GAM7052 296 NUDT4 1 13741 NP_061967.2 3 1375 AGCCTCCCGAGT CA----- A 3 C c c
AGTTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCT ACATTAGGGTTGATGAG CC
TCCGCGG C
GAM7052 296 NUFIP1 1 12644 NP_036477.1 3 1810 CAGTTTCTGAAA CCCA - --- 3 C c c
TGTAAGCATTAC CATGTAAT GCT AC TCAGG
ATGACTAT GTACATTA CGA TG AGTCT
---- A TAA
GAM7052 296 NUMA1 1 13914 NP_006176.1 5 204 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCGCAT ACATTAGGGTCGATGA CC
TACGCGG AC
GAM7052 296 NXN 1 10897 NP_071908.1 3 961 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCC ACATTAGGGTCGATGAG CC
CCCACGG C
GAM7052 296 ORAOV1 1 8157 NP_703152.1 3 1492 AGCCTCCCTAGT CA----- C 3 C c c
AGCTGGGATTAT TGTAATCCCAGCTACT AGG
AGGCGCCC ATATTAGGGTCGATGA TCC
CCCGCGG -
GAM7052 296 OSBPL2 1 13183 NP_055650.1 3 1211 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGC ACATTAGGGTCGATGA CC
CGCACGG AC
GAM7052 296 OSBPL2 1 13183 NP_653081.1 3 1211 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGC ACATTAGGGTCGATGA CC
CGCACGG AC
GAM7052 296 PASK 1 9616 NP_055963.1 5 890 AGCCTTCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGGATGT ACATTAGGGTCGATGAG CC
TGTAGGG -
GAM7052 296 PCDHA9 1 11228 NP_054724.1 3 1399 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAT TGTAATCCCAGCTACTCAGG
AGGCACAT ATATTAGGGTCGATGAGTCC
TACACGG
GAM7052 296 PDE6B 2 7445 NP_000274.1 3 414 AGCTTCCTGAAG CA----- T - 3 C c c
TGCTGGGATTAC TGTAATCCCAGC ACT CAGG
AGGCATGA ACATTAGGGTCG TGA GTCC
AGTACGG - A
GAM7052 296 PDE6B 2 9847 NP_000274.1 3 282 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG

AGGCGCCC ACAT AGGGTCGATGAGTCC
CCCGCGG C
GAM7052 296 PELI1 1 10821 NP_065702.2 5 2772 AACCTCCTTAGT CA----- C 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCATGT ACATTAGGGTCGATGA TCC
TGTACGG T
GAM7052 296 PER2 1 18316 NP_073728.1 3 1455 AGCCTCCTGAGT CA----- AA 3 C c
c
AGCTGGGACCAC TGT TCCCAGCTACTCAGG
AGGCGACT ACA AGGGTCGATGAGTCC
TCAGCGG CC
GAM7052 296 PHAX 1 14737 NP_115553.1 3 781 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGATCAC TGT ATCCCAGCTACTCAGG
AGGTGTGT ACA TAGGGTCGATGAGTCC
TGTGTGG C
GAM7052 296 PIK3C2B 1 16722 NP_002637.2 3 1532 AGCCTCCCGAGT CA----- A 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGT ACATTAGGGTCGATGAG CC
TGTACGG C
GAM7052 296 PIK3CD 1 9691 NP_005017.2 3 908 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG
GAM7052 296 PKNOX1 1 16723 NP_004562.2 3 1906 AGCCTCCTGAGT CA----- 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 PLCD3 1 11178 NP_588614.1 3 20 AGCGCTCCTGGT CA----- A T 3 C c
c
AGCTGGGACTAC TGTA TCCCAGCTAC CAGG
AGGCACAG ACAT AGGGTCGATG GTCC
GACACGG C -
GAM7052 296 PNMA2 1 10897 NP_009188.1 3 1798 AGCCTCCCGAGT CA----- A 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCC ACATTAGGGTCGATGAG CC
CCCACGG C
GAM7052 296 POLD3 1 19468 XP_166243.1 3 1418 GGATTGTGCTGA - CTAC 3 C c
c
CTTTGGGATTAA CATGT AATCCCAG TCAG
CATGAGCT GTACA TTAGGGTT AGTC
A TC--
GAM7052 296 POU2AF1 1 16360 NP_006226.1 3 1459 AGCCTCCCGAGT CA----- A 3 C c
c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCAT ACATTAGGGTCGATGAG CC
TACGTGG C
GAM7052 296 PP1665 1 15458 NP_110419.3 5 149 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGTTCCCA ACATTAGGGTCGATGA CC
ACCCTTG AC

GAM7052 296 PPEF2 1 16723 NP_006230.2 3 447 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG

GAM7052 296 PPEF2 1 16723 NP_690910.1 3 1079 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG

GAM7052 296 PPEF2 1 16723 NP_690911.1 3 2292 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG

GAM7052 296 PPFIBP1 1 9291 NP_003613.2 3 1075 AGCCTCCCAAAG ---- C CA 3 C c
c

TACTGGGATTAT CATGT AATCCCAG TACT GG
AGGCATGA GTACG TTAGGGTC ATGA CC
GATA - AA

GAM7052 296 PPID 1 10127 NP_005029.1 3 332 AGCTTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGT ACATTAGGGTCGATGA CC
TGCACGG AC

GAM7052 296 PPP1R16 1 4482 NP_056383.1 3 2685 AATTTACTGAGT AATCC 3 C c
c

B AGCTGCAACATG CATGT CAGCTACTCAG
CCAGCCTC GTACA GTCGATGAGTC
AC---

GAM7052 296 PRKR 2 14827 NP_002750.1 3 360 AGCCTCCTGAGT CA------ C 3 C c c

AGCTGGATTACA TGTAATCC AGCTACTCAGG
GGCATGTG ACATTAGG TCGATGAGTCC
GTGTACGG -

GAM7052 296 PRKR 2 15131 NP_002750.1 3 360 CAGCCTCCTGAG CA----- C 3 C c c

TAGCTGGATTAC TGTAATCC AGCTACTCAGG
AGGCATGT ACATTAGG TCGATGAGTCC
TGTACGG -

GAM7052 296 PRKWNK3 1 5689 NP_065973.1 3 727 AGCCTCCTGAGT CA----- A 3 C c
c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCCA ACAT AGGGTCGATGAGTCC
ACCGCGG C

GAM7052 296 PRND 1 14582 NP_036541.1 3 924 AGCCTTCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGTGT ACATTAGGGTCGATGAG CC
TGTGTGG -

GAM7052 296 PRO0971 1 7840 NP_061039.2 3 565 GAAATGCTGAAG C AGC - 3 C c
c

TATCGGCATTAC CATGTAAT CC TACT CAG
ATGTGTTT GTACATTA GG ATGA GTC
C CT- A

GAM7052 296 PSTPIP2 1 8011 NP_077748.2 3 1408 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACCC ACATTAGGGTCGATGAGTCC
CCCACGG

GAM7052 296 PTGES 1 12377 NP_004869.1 3 612 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCGT ACATTAGGGTCGATGAGTCC
TGCGCGG

GAM7052 296 PTGIS 1 8761 NP_000952.1 3 2925 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCACCC ACAT AGGGTCGATGAGTCC
CCCACGG C

GAM7052 296 PTPN18 1 17110 NP_055184.2 3 1110 AGCCTGCCGAGT CA----- A A 3 C c
c

AGCTGGGACTAC TGTA TCCCAGCTACTC GG
AGGTCTAA ACAT AGGGTCGATGAG CC
AATCTGG C -

GAM7052 296 PTPRT 1 18384 NP_008981.2 3 7066 GAGATCTTGTGG TA ACT 3 C c
c

AGCTGGGATCAT CATG ATCCCAGCT CAGG
GTTTGAAC GTAC TAGGGTCGA GTTC
-- GGT

GAM7052 296 PTPRT 1 18384 NP_573400.1 3 7066 GAGATCTTGTGG TA ACT 3 C c
c

AGCTGGGATCAT CATG ATCCCAGCT CAGG
GTTTGAAC GTAC TAGGGTCGA GTTC
-- GGT

GAM7052 296 RAB11-F 1 1607 NP_116321.2 3 2681 AACTGCCTGAGT CA----- A 3 C c
c

IP4 AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGC ACAT AGGGTCGATGAGTCC
CGTACGG C

GAM7052 296 RAB33B 1 19271 NP_112586.1 3 924 AGCCTCCCGAGT CA----- A 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGTGC ACATTAGGGTCGATGAG CC
CGTGCGG C

GAM7052 296 RAB34 1 8691 NP_114140.2 3 162 CCACAGAGGGGT TA AG 3 C c c

AGCTGGGATCAT CATG ATCCCAGCTACTC
GCTAGTCA GTAC TAGGGTCGATGGG
-- GA

GAM7052 296 RAB36 1 2107 NP_004905.1 3 1493 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC

CGTACGG AC
GAM7052 296 RAI 1 13915 NP_006654.1 5 114 GGCCTTCCGAGT CA----- A 3 C c c
AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGCGTGT ACGTTAGGGTCGATGAG CC
TGTGCGG -
GAM7052 296 RAP1GA1 1 16882 NP_002876.1 3 582 GAGGTCACTGAA C - AC 3 C c c
GACTGTGATTAC CATGTAATC CAG CT TCAG
ATGCACCT GTACATTAG GTC GA AGTC
T A --
GAM7052 296 RASSF2 1 9279 NP_055552.1 3 2655 CTGAGCCTATCT GTA ------ 3 C c c
GGCTGGGATGGT CAT ATCCCAGCTA CTCAG
GGAATTAA GTG TAGGGTCGGT GAGTC
G-- CTATCC
GAM7052 296 RASSF2 1 9279 NP_739579.1 3 2881 CTGAGCCTATCT GTA ------ 3 C c c
GGCTGGGATGGT CAT ATCCCAGCTA CTCAG
GGAATTAA GTG TAGGGTCGGT GAGTC
G-- CTATCC
GAM7052 296 RASSF2 1 9279 NP_739580.1 3 2655 CTGAGCCTATCT GTA ------ 3 C c c
GGCTGGGATGGT CAT ATCCCAGCTA CTCAG
GGAATTAA GTG TAGGGTCGGT GAGTC
G-- CTATCC
GAM7052 296 RBM8A 1 18273 NP_005096.1 3 404 ACTGTCCCTAGT CA----- C 3 C c c
AGTTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCACAT ACATTAGGGTTGATGA TCC
TACACGG -
GAM7052 296 RDH13 1 7857 NP_612421.1 5 312 GGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGGACTA ACAT AGGGTCGATGAGTCC
ATCAGGG C
GAM7052 296 RHD 2 8197 NP_057208.2 3 775 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AAGTGCGC ACATTAGGGTCGATGAG CC
CGCGTGA C
GAM7052 296 RHD 2 8197 NP_057309.2 3 864 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AAGTGCGC ACATTAGGGTCGATGAG CC
CGCGTGA C
GAM7052 296 RHD 2 13068 NP_057208.2 3 366 AGCCTCCAAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AA
GAM7052 296 RHD 2 13068 NP_057309.2 3 455 AGCCTCCAAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AA

GAM7052 296 RINZF 1 3551 NP_076418.2 3 218 CAAACAACCATG C TCA 3 C c c
TGGTTGGATTAC CATGTAATCC AGCTAC GG
ATGGAGTC GTACATTAGG TTGGTG CC
- TA-

GAM7052 296 RNF137 1 4953 NP_060543.4 3 1050 AGCCTCCCACAG ---- T CA 3 C c
c

TGCTGGGATTAG CATGT AATCCCAGC ACT GG
AGGCATGA GTACG TTAGGGTCG TGA CC
GAGA - CA

GAM7052 296 RNF144 1 1187 NP_055561.1 3 3252 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 RNF3 1 6218 NP_006306.2 3 1768 GGGTCTATGAGT ATCC G 3 C c
c

AGCTGTGTATGA CATGTA CAGCTACTCA
ATAAATAT GTATGT GTCGATGAGT
---- A

GAM7052 296 RP2 1 10728 NP_008846.1 3 1850 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGAATAC TGTA TCCCAGCTACTCAGG
AGCATGCG ACAT AGGGTCGATGAGTCC
GCGTACG A

GAM7052 296 RPH3AL 1 2060 NP_008918.1 3 725 AGCCTCCTGAGT CA----- G 3 C c
c

AGGTGGGATTAC TGTAATCCCA CTACTCAGG
AGATGCCC ACATTAGGGT GATGAGTCC
CCCGTAG G

GAM7052 296 RPP30 2 14044 NP_006404.1 3 1288 AGCCTCCTGAGT CA----- A 3 C c
b

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCGCTC ACAT AGGGTCGATGAGTCC
CTCGCGG C

GAM7052 296 RPP30 2 17179 NP_006404.1 3 588 GGCCTCCTAAAG T C- 3 C b b
TGCTGGGATTAC CATGTAATCCCAGC ACT AGG
ATGAGCCA GTACATTAGGGTCG TGA TCC
- AA

GAM7052 296 SAS 1 12782 NP_005972.1 3 596 AGTCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGTGC ACATTAGGGTCGATGA CC
CGTGTGG AC

GAM7052 296 SC4MOL 1 1187 NP_006736.1 3 557 AGCCTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC

GAM7052 296 SCAND2 1 13669 NP_071333.2 3 1868 AGCCTCCTGAGT T T 3 C b b

CGCTGGGATTAC CA GTAATCCCAGC ACTCAGG
TGAGATTG GT CATTAGGGTCG TGAGTCC
- C

GAM7052 296 SCN3B 1 6424 NP_060870.1 3 1139 GGCCTCTCCAGT CA----- C--- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTGTGC ACATTAGGGTCGATGA TCC
CGTGTGG CCTC

GAM7052 296 SDS-RS1 1 12439 NP_612441.1 5 176 AGCCTTCTGAGT CA----- C 3 C c c

AGCTGGAATTAC TGTAAT CCAGCTACTCAGG
AGGCTGTC ACATTA GGTCGATGAGTCT
CTGTCGG A

GAM7052 296 SEDL 1 16885 NP_055378.1 3 1085 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGC ACATTAGGGTCGATGAG CC
CGTACGG C

GAM7052 296 SEMA4G 1 6560 NP_060363.2 5 151 TTCTGACCTCTT T - C---- 3 C c c

AGCTGGGGATTC CATG AATCCC AGCTA TCAGG
CATGGCCA GTAC TTAGGG TCGAT AGTCT
C G TCTCC

GAM7052 296 SEPN1 1 16360 NP_065184.1 3 1642 AGCCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCAT ACATTAGGGTCGATGAG CC
TACGTGG C

GAM7052 296 SERF1A 2 12128 NP_068802.1 3 495 AGCTTCCTGAGT CA----- G 3 C c c

AGATGGGATTAC TGTAATCCCA CTACTCAGG
AGGCGCCT ACATTAGGGT GATGAGTCC
TCCGCGG A

GAM7052 296 SERF1A 2 13493 NP_068802.1 3 328 AGCCTCCTGGGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACGC ACATTAGGGTCGATGGGTCC
CGCACGG

GAM7052 296 SERF1B 2 12128 NP_075267.1 3 495 AGCTTCCTGAGT CA----- G 3 C c c

AGATGGGATTAC TGTAATCCCA CTACTCAGG
AGGCGCCT ACATTAGGGT GATGAGTCC
TCCGCGG A

GAM7052 296 SERF1B 2 13493 NP_075267.1 3 328 AGCCTCCTGGGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACGC ACATTAGGGTCGATGGGTCC
CGCACGG

GAM7052 296 SF3A3 1 5836 NP_006793.1 3 322 AACTTTACTAGT GT C C 3 C c c

AGCTGAGATTTA CAT AATC CAGCTACT AG
ATGGGCAC GTA TTAG GTCGATGA TC

```
                                        AT   A      -
GAM7052  296   SFXN2  1  16442 NP_849189.1  3  679   AGCCTCTCAAGT CA-----          C---    3  C  c  c

                                AGCTGGGATTAC      TGTAATCCCAGCTACT   AGG
                                AGGGCACC          ACATTAGGGTCGATGA   TCC
                                      CCACGGG             ACTC
GAM7052  296   SFXN2  1  16442 XP_058359.2  3  680   AGCCTCTCAAGT CA-----          C---    3  C  c  c

                                AGCTGGGATTAC      TGTAATCCCAGCTACT   AGG
                                AGGGCACC          ACATTAGGGTCGATGA   TCC
                                      CCACGGG             ACTC
GAM7052  296   SHC1   1  15883 NP_003020.1  3  126   GCCTTGTGTCAG     AA-      --- T       3  C  c  c
                                AGCTGGGAGTAG CATGT   TCCCAGCT   AC CAGG
                                CATGGACT    GTACG   AGGGTCGA   TG GTTC
                                      ATG       GAC  T
GAM7052  296   SHOX   2  2823  NP_006874.1  3  81    AGCCTCCCGAGT CA-----           A      3  C  c  c
                                AGCTGGGATTAC      TGTAATCCCAGCTACTC GG
                                AGGTGCCC          ACATTAGGGTCGATGAG CC
                                      CCCGTGG             C
GAM7052  296   SHOX   2  8761  NP_006874.1  3  401   AGCCTCCTGAGT CA-----  A              3  C  c  c
                                AGCTGGGACTAC      TGTA TCCCAGCTACTCAGG
                                AGGCACCC          ACAT AGGGTCGATGAGTCC
                                      CCCACGG   C
GAM7052  296   SIRPB1 1  16887 NP_006056.1  3  2126  AGCCTCCTGAGT CA-----                3  C  c  c

                                AGCTGGGATTAC      TGTAATCCCAGCTACTCAGG
                                AGGCATGT          ACATTAGGGTCGATGAGTCC
                                      TGTACGG
GAM7052  296   SLC12A8 1  17034 NP_078904.1  3  292   TCAGCTCTGAGT CA-----                3  C  c  c

                                AGCTGGGATTAT      TGTAATCCCAGCTACTCAGG
                                AGGCATGC          ATATTAGGGTCGATGAGTCT
                                      CGTACGG
GAM7052  296   SLC15A1 2  12924 NP_005064.1  3  304   AGCCTCCCGAGT     ----          A      3  C  c  c
                                GGCTGGGATTAG CATGT   AATCCCAGCTACTC GG
                                CGGCATGC    GTACG   TTAGGGTCGGTGAG CC
                                      GCGA          C
GAM7052  296   SLC15A1 2  15654 NP_005064.1  3  437   GGCCTGCCAAAG CA-----         T  ----    3  C  c
c
                                TGCTGGGATTAC      TGTAATCCCAGC ACT   CAGG
                                AGGCTTGA          ACATTAGGGTCG TGA   GTCC
                                      AGTTCGG           -  AACC
GAM7052  296   SLC19A3 1  1083  NP_079519.1  3  1097  AGCCTCCCAGGT    TAA        CA         3  C  c
 c
                                AGCTGGGACTAT CATG   TCCCAGCTACT  GG
                                GGGTGCAC    GTAT   AGGGTCGATGG  CC
                                      C--           AC
GAM7052  296   SLC2A10 1  17326 NP_110404.1  3  589   AGCCTCCTAAGT CA-----           C      3  C  c
c
                                AGCTGGGATTAC      TGTAATCCCAGCTACT AGG
```

AGGCGCGT ACATTAGGGTCGATGA TCC
TGCGCGG A
GAM7052 296 SLC30A5 1 5862 NP_076960.1 3 238 AGCCTCCTGAGT CA----- C 3 C c c
AGCTGGAATTAC TGTAAT CCAGCTACTCAGG
AGGCACCC ACATTA GGTCGATGAGTCC
CCCACGG A
GAM7052 296 SLC30A6 2 8012 NP_060434.2 3 592 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACCT ACATTAGGGTCGATGAG CC
TCCACGG C
GAM7052 296 SLC30A6 2 15429 NP_060434.2 3 728 AGCCTCCCAAAG G T CA 3 C c c
TGCTGGGATTAG CAT TAATCCCAGC ACT GG
GTGTGAGC GTG ATTAGGGTCG TGA CC
G - AA
GAM7052 296 SLC6A14 1 15390 NP_009162.1 3 1761 AGCCTCTTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCCC ACAT AGGGTCGATGAGTTC
CCCGTGG C
GAM7052 296 SLC9A5 1 2167 NP_004585.1 3 882 CATTGCTCTGGG TGT A 3 C c c
GGCTGGGATTCC CA AATCCCAGCT CTCAGG
TGGCTAAG GT TTAGGGTCGG GGGTCT
CC- -
GAM7052 296 SMAC 2 2683 NP_620308.1 5 741 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGAGCGT ACATTAGGGTCGATGAG CC
TGCGAGG C
GAM7052 296 SMAC 2 11548 NP_620308.1 5 566 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGCGCCC ACGTTAGGGTCGATGAG CC
CCCGCGG C
GAM7052 296 SNAP23 1 9468 NP_003816.2 3 758 TGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTGT ACATTAGGGTCGATGAGTCC
TGTGCGG
GAM7052 296 SNAP23 1 9468 NP_570710.1 3 758 TGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGTGT ACATTAGGGTCGATGAGTCC
TGTGCGG
GAM7052 296 SNARK 1 1482 NP_112214.1 3 687 AGCCTCCCTAGT CA----- C 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCGCCC ACATTAGGGTCGATGA TCC
CCCGCGG -
GAM7052 296 SNX22 1 3382 NP_079074.1 3 604 AGCCTCTCGAGT CA----- --- 3 C c c

GGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCATCC ACATTAGGGTCGGTGAG TCC
CCTACGG CTC
GAM7052 296 SNX27 2 2903 NP_112180.4 3 3194 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATAC ACATTAGGGTCGATGA CC
CATACGG AC
GAM7052 296 SNX27 2 4461 NP_112180.4 3 1964 ACCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGTGC ACAT AGGGTCGATGAGTCC
CGTGTGG C
GAM7052 296 SPOP 1 6561 NP_003554.1 5 215 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGGTGAA ACATTAGGGTCGATGAG CC
AAGTGGG C
GAM7052 296 SRF 2 1206 NP_003122.1 3 557 CAGCTCCTGAGT - AT-- 3 C c c
AGCTGGGCCTGT CA TGTA CCCAGCTACTCAGG
GCACTGGG GT ACGT GGGTCGATGAGTCC
C GTCC
GAM7052 296 SRF 2 2413 NP_003122.1 3 1794 CTCCTGGAGACT TAA -- - 3 C c c
AGCTGGGGCTTA CATG TCCCAGCTA CTC AGG
TGGGTGGC GTAT GGGGTCGAT GAG TCC
TC- CA G
GAM7052 296 SRL 1 17636 XP_064152.3 3 670 AGCCTCCTGAGT CA----- C 3 C c c
AGCTGAGATTAT TGTAATC CAGCTACTCAGG
AGGCCTAC ATATTAG GTCGATGAGTCC
CATCCGG A
GAM7052 296 STAF65(1 4663 NP_055675.1 3 1465 AGCCACCTGAGT CA----- 3 C c c
gamma) AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
ACGCACAT ACATTAGGGTCGATGAGTCC
TACACGC
GAM7052 296 STOM 1 18019 NP_004090.3 3 581 AGCCTCCCCAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCTCAT ACATTAGGGTCGATGA CC
TACTCGG CC
GAM7052 296 SYT11 1 1187 NP_689493.2 3 366 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC
GAM7052 296 SYT13 1 12639 NP_065877.1 3 1611 AGCCTCCTGGGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCCC ACATTAGGGTCGATGGGTCC
CCCGTGG
GAM7052 296 TAF7L 1 5620 NP_079161.1 3 355 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG

AGTTGTGC ACAT AGGGTCGATGAGTCC
CGTGTTG C

GAM7052 296 TAPBP 1 2176 NP_003181.3 3 314 AGCCTCCGGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACAT ACATTAGGGTCGATGAG CC
TACACGG G

GAM7052 296 TBX5 1 11145 NP_000183.2 5 463 AAACCAACCTTG A- ACTC 3 C c c

AGCTGGGAGGTA CATGTA TCCCAGCT AGG
CGTGCTCT GTGCAT AGGGTCGA TCC
GG GT--

GAM7052 296 TBX5 1 11145 NP_542448.1 5 463 AAACCAACCTTG A- ACTC 3 C c c

AGCTGGGAGGTA CATGTA TCCCAGCT AGG
CGTGCTCT GTGCAT AGGGTCGA TCC
GG GT--

GAM7052 296 TCL6 1 3638 NP_036600.2 5 730 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC

GAM7052 296 TCL6 1 3638 NP_055233.1 5 730 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC

GAM7052 296 TCL6 1 3638 NP_065575.1 5 730 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC

GAM7052 296 TCL6 1 3638 NP_065577.2 5 730 AGCCTCCCAAGT CA----- CA 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC

GAM7052 296 TERF1 1 18226 NP_003209.1 3 501 CAGCCTCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCT
CACACGG

GAM7052 296 TERF1 1 18226 NP_059523.1 3 501 CAGCCTCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCACAC ACATTAGGGTCGATGAGTCT
CACACGG

GAM7052 296 TGIF2 1 8013 NP_068581.1 3 1532 AGCCTCCCGAGT CA----- A 3 C c c
AGCTGGGATTAT TGTAATCCCAGCTACTC GG
AGGCACCC ATATTAGGGTCGATGAG CC
CCCACGG C

GAM7052 296 THRA 1 4481 NP_003241.2 3 102 GAGGTGCCTGAA AA AC 3 C c c
AGCTGGGAGCGT CATGT TCCCAGCT TCAGG
GGGCTCAG GTGCG AGGGTCGA AGTCC
-- A-

GAM7052 296 TLR5 1 8290 NP_003259.2 5 180 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGATTGAT ACATTAGGGTCGATGA CC
TAGTTAG AC

GAM7052 296 TMC1 1 13103 NP_619636.2 5 213 GGCCTCCTGAGT CA----- T 3 C c c
AGCTGGGATTTC TG AATCCCAGCTACTCAGG
AGGCCATG AC TTAGGGTCGATGAGTCC
GTACCGG T

GAM7052 296 TNFAIP2 1 8132 NP_006282.2 3 1426 AGCCTCCTAAAG ---- T C- 3 C c c
TGCTGGGATTAT CATGT AATCCCAGC ACT AGG
AGGCATGA GTACG TTAGGGTCG TGA TCC
GATA - AA

GAM7052 296 TNFRSF1 1 19950 NP_003833.3 3 2107 AGCCTCCGGAGT CA----- A 3 C c
c

0B AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGCACCC ACGTTAGGGTCGATGAG CC
CCCACGG G

GAM7052 296 TNFRSF1 1 19950 NP_671716.1 3 2107 AGCCTCCGGAGT CA----- A 3 C c
c

0B AGCTGGGATTGC TGTAATCCCAGCTACTC GG
AGGCACCC ACGTTAGGGTCGATGAG CC
CCCACGG G

GAM7052 296 TNFRSF1 1 7043 NP_003830.1 3 596 AACCTTCGGAGT CA----- A --- 3 C c
c

1A AGCTGGGATCAC TGT ATCCCAGCTACTC AGG
AGCTGCAG ACA TAGGGTCGATGAG TCC
GACGTCG C GCT

GAM7052 296 TOMM40 1 15424 NP_006105.1 3 217 GGGATTCTGAGT AA A 3 C c
c

AGCAGGGGCAGC CATGT TCCC GCTACTCAGG
ATGCCCAG GTACG GGGG CGATGAGTCT
AC A

GAM7052 296 TOR1B 1 11224 NP_055321.1 3 264 AGCCTCCCGAGT CA----- A 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCATGA ACATTAGGGTCGATGAG CC
AGTACGG C

GAM7052 296 TPMT 1 1523 NP_000358.1 3 511 GGCCTCCTGAGT CA----- 3 C c c
GGCTGGGATTGC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACGTTAGGGTCGGTGAGTCC
CGTGTGG

GAM7052 296 TPSG1 1 13903 NP_036599.1 5 36 GGTCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCAT ACAT AGGGTCGATGAGTCC
TACGTGG C

GAM7052 296 TRAF5 1 12522 NP_004610.1 3 1176 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCGCCC ACATTAGGGTCGATGAGTCC
CCCGCGG

GAM7052 296 TRAF5 1 12522 NP_665702.1 3 1176 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG

AGGCGCCC ACATTAGGGTCGATGAGTCC
CCCGCGG
GAM7052 296 TRIM16 2 3032 NP_006461.2 3 334 AGCCTCCCGAGT CA----- A 3 C c b

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCT ACATTAGGGTCGATGAG CC
TCCGTGG C
GAM7052 296 TRIM16 2 18408 NP_006461.2 3 469 GGCCTCCCAAAG T CA 3 C b b

TGCTGGGATTAC CATGTAATCCCAGC ACT GG
ATGCGTGA GTACATTAGGGTCG TGA CC
- AA
GAM7052 296 TRIM5 1 3638 NP_149023.1 3 736 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC
GAM7052 296 TRIM6 1 17246 NP_477514.1 3 257 AGCATCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACCC ACATTAGGGTCGATGA CC
CCCACGG AC
GAM7052 296 TRPV1 1 18293 NP_061197.3 3 449 GGCTTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGT ACATTAGGGTCGATGA CC
TGCACGG AC
GAM7052 296 TRPV1 1 18293 NP_542435.1 3 449 GGCTTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGT ACATTAGGGTCGATGA CC
TGCACGG AC
GAM7052 296 TRPV1 1 18293 NP_542436.1 3 449 GGCTTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGT ACATTAGGGTCGATGA CC
TGCACGG AC
GAM7052 296 TRPV1 1 18293 NP_542437.1 3 449 GGCTTCCCAAGT CA----- CA 3 C c
c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCACGT ACATTAGGGTCGATGA CC
TGCACGG AC
GAM7052 296 TSAP6 1 12675 NP_060704.1 5 84 AGCCTCCGGAGT CA----- A 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACGT ACATTAGGGTCGATGAG CC
TGCACGG G
GAM7052 296 TU12B1- 3 2107 NP_057659.1 3 1390 AGCCTCCCAAGT CA----- CA 3 C c
c
TY AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC

CGTACGG AC
GAM7052 296 TU12B1-3 2823 NP_057659.1 3 3267 AGCCTCCCGAGT CA----- A 3 C c c
TY AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTGCCC ACATTAGGGTCGATGAG CC
CCCGTGG C
GAM7052 296 TU12B1-3 8615 NP_057659.1 3 2941 AGCCTCCCGAGT T A A 3 C c c
TY AGCTGGGACTAC CA GTA TCCCAGCTACTC GG
TGGTACAT GT CAT AGGGTCGATGAG CC
- C C
GAM7052 296 TUCAN 1 16723 NP_055774.1 3 2541 AGCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGCATGC ACATTAGGGTCGATGAGTCC
CGTACGG
GAM7052 296 TXNL2 1 9280 NP_006532.1 3 153 AGCCTTCTGAGT AA---- 3 C c c
AGCTGGGACCAC CATGT TCCCAGCTACTCAGG
AGGCGTGC GTGCG AGGGTCGATGAGTCT
GACACC
GAM7052 296 UBF-fl 1 16551 NP_116217.1 3 592 AGCCTCCCGAGT -- A A 3 C c c
AGCAGGGATTAC CAT GTAATCCC GCTACTC GG
CGGTGTGC GTG CATTAGGG CGATGAG CC
GC A C
GAM7052 296 UPK1B 1 16344 NP_008883.1 3 495 TCTTTCTAGAGT ATCCC - 3 C c c
AGCTCCCATATA CATGTA AGCTACTC AGG
TGGAGATG GTATAT TCGATGAG TCT
ACCC- A
GAM7052 296 VDU1 1 9640 NP_055832.2 3 363 AGCCTCTCGAGT CA----- --- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTC AGG
AGGCACCT ACATTAGGGTCGATGAG TCC
TCCACGG CTC
GAM7052 296 VHL 2 17725 NP_000542.1 3 2651 CTCACCCTCCTG CA----- TAC 3 C c c
AGCTGGGATTAC TGTAATCCCAGC TCAGG
AGGCGCCT ACATTAGGGTCG AGTCC
TCCGCGG ---
GAM7052 296 VHL 2 19938 NP_000542.1 3 1061 ATCCTCCTGAGT CA----- 3 C c c
AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGCCT ACATTAGGGTCGATGAGTCC
TCCGTGG
GAM7052 296 VIPR2 1 8429 NP_003373.2 3 531 GGCCTCCCAAAG --- T CA 3 C c c
TGCTGGGATTAA CATGT AATCCCAGC ACT GG
GGCGTGAG GTGCG TTAGGGTCG TGA CC
GAA - AA
GAM7052 296 VPS33A 1 18973 NP_075067.2 3 317 AGCCTCCTGAGT CA----- A 3 C c c
AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGCATGC ACAT AGGGTCGATGAGTCC

CGTACGG C

GAM7052 296 WBSCR23 1 17673 NP_079318.1 3 67 CGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGCATGC ACATTAGGGTCGATGA CC
CGTACGG AC

GAM7052 296 ZFP30 1 2558 NP_055713.1 3 1939 AGACTTCCGAGT CA----- A 3 C c c

GGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCGCCC ACATTAGGGTCGGTGAG CC
CCCGCGG -

GAM7052 296 ZIC2 1 5098 NP_009060.2 3 749 TATTTTTCTGTT T CT 3 C c c

AGCTGGGTTTAC CATGTAA CCCAGCTA CAGG
ATGTGATG GTACATT GGGTCGAT GTCT
T T-

GAM7052 296 ZMYND17 1 13356 NP_848546.1 3 304 AGCCTCCCTAGT CA----- C 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGTGCAC ACATTAGGGTCGATGA TCC
CACGTGG -

GAM7052 296 ZNF137 1 11225 NP_003429.1 3 775 AGCTTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGTATGA ACATTAGGGTCGATGAG CC
AGTATGG C

GAM7052 296 ZNF253 1 3638 NP_066385.1 3 377 AGCCTCCCAAGT CA----- CA 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT GG
AGGTGCCC ACATTAGGGTCGATGA CC
CCCGTGG AC

GAM7052 296 ZNF264 1 9691 NP_003408.1 3 3063 AGCCTCCTGAGT CA----- 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTCAGG
AGGTGTGC ACATTAGGGTCGATGAGTCC
CGTGTGG

GAM7052 296 ZNF273 1 12971 XP_088082.1 3 928 AGCCTCCCTAGT CA----- C 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCATGT ACATTAGGGTCGATGA TCC
TGTACGG -

GAM7052 296 ZNF305 1 16268 NP_055539.1 3 2994 AGTCTCCCGAGT CA----- A 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACTC GG
AGGCACTT ACATTAGGGTCGATGAG CC
TTCACGG C

GAM7052 296 ZNF432 1 12735 NP_055465.1 3 1854 AGCCTCCTAAGT CA----- C 3 C c c

AGCTGGGATTAC TGTAATCCCAGCTACT AGG
AGGCACCC ACATTAGGGTCGATGA TCC
CCCACGG A

GAM7052 296 ZNF440 1 13692 NP_689570.1 3 1309 AGTCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTGC TGTA TCCCAGCTACTCAGG
AGGCATGC ACGT AGGGTCGATGAGTCC
CGTACGG C
GAM7052 296 ZNF70 1 19261 NP_068735.1 3 1680 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCGT ACAT AGGGTCGATGAGTCC
TGCGTGG C
GAM7052 296 ZNF70 1 19261 NP_852101.1 3 1680 AGCCTCCTGAGT CA----- A 3 C c c

AGCTGGGACTAC TGTA TCCCAGCTACTCAGG
AGGTGCGT ACAT AGGGTCGATGAGTCC
TGCGTGG C
GAM7080 399 A1BG 1 10195 NP_570602.2 3 993 CCACAGCAGAGC G A T 3 C c c
TGGACGCTGTGG TTTCCACAGCG CCA TTCT
AAATGGCT AAAGGTGTCGC GGT GAGA
A C C
GAM7080 399 ABCB9 1 10223 NP_062570.1 5 292 CCAACCAGCAGG G CA T 3 C c
c

ATGCGGCTGTGG TTTCCACAGC GC ATTCT
AAGGCGGT GAAGGTGTCG CG TAGGA
G -- C
GAM7080 399 ABCB9 1 10223 NP_062571.1 5 292 CCAACCAGCAGG G CA T 3 C c
c

ATGCGGCTGTGG TTTCCACAGC GC ATTCT
AAGGCGGT GAAGGTGTCG CG TAGGA
G -- C
GAM7080 399 ACTR10 1 11903 NP_060947.1 5 24 GCCGAGACTTGT ACA --- 3 C c c

TGGCCGCGGAGA TTTCC GCGGCCAAT TCTT
CTGCGACC AGAGG CGCCGGTTG AGAG
--- TTC
GAM7080 399 ADRA2B 1 7602 NP_000673.1 3 1504 CACCCAGAACAG G GG C 3 C c
c

TTGGAAGTGTGG TTTCCACA C CCAATT TTC
AAAGGAGG AAAGGTGT G GGTTGA AAG
- AA C
GAM7080 399 AP3S2 1 5422 NP_005820.1 3 1805 CAGAAGGTGGGC ---- AAT 3 C c c

CGCTTCCTGTGG TTTCCACA GCGGCC TCTTC
AAGAGGGA GAAGGTGT CGCCGG GGAAG
CCTT GT-
GAM7080 399 ARHGAP1 1 13878 NP_060757.4 3 766 TGAGTTATTGGT C ----- T- 3 C c
c

2 ATGACCCTGTGG TTTCCACAG GG CCAAT CTT
AAACACAC AAAGGTGTC CC GGTTA GAG
- AGTAT TT
GAM7080 399 ATRN 1 4659 NP_647537.1 3 1790 CCCATGAAGAAT CAGC C 3 C c
c

TGCCTGGAAAGA TTTCCA GGC AATTCTTC

TGTTTTCA AAAGGT CCG TTAAGAAG
---- -
GAM7080 399 BACH2 1 16479 NP_068585.1 3 2410 TCACCATGAGGT C C TT 3 C c
c
TTGCCTTTGTGG TTTCCACAG GGC AA CTT
AAAACTCG AAAGGTGTT CCG TT GAG
T - TG
GAM7080 399 BFSP2 1 3480 NP_003562.1 3 9 GGACAGGGAGGA G CAA 3 C c c
GAGCGGCTGTGG TTTCCACAGC GC TTCTTC
AGAAACTT AGAGGTGTCG CG AGGAGG
G AG-
GAM7080 399 BIN3 1 3365 NP_061158.1 3 938 CTAGGAGAGTAG GG-- A 3 C c c
GAAGAGCTGTGG TTTCCACAGC CC ATTCTTC
AGGACACA GGAGGTGTCG GG TGAGAGG
AGAA A
GAM7080 399 BMI1 1 9667 NP_005171.4 3 224 GTTATAAAGAAT C CG 3 C c c
TGGTTTCTTGGA TTTCCA AG GCCAATTCTT
AAGCAGGC AAAGGT TC TGGTTAAGAA
- TT
GAM7080 399 BSN 1 13114 NP_003449.1 3 57 TGAAGAGAGGTA ----- AA 3 C c c
TCATTGCTGTGG TTTCCACAGCG GCC TTCTTC
AAAAATCT AAAGGTGTCGT TGG GAGAAG
TACTA A-
GAM7080 399 C14orf1 1 16767 NP_064600.1 3 358 GGGAGAGCAGCT G AA----- 3 C c
c
32 GAGGCCGTGTGG TTTCCACA CGGCC TTCTTC
AAAATTAG AAAGGTGT GCCGG GAGAGG
- AGTCGAC
GAM7080 399 C14orf3 1 7617 XP_058661.2 5 51 GAGTGAGAACCT G -- 3 C c c
5 TGGCGGCTGTGG TTTCCACAGC GCCAA TTCTT
AGGCTGCC GGAGGTGTCG CGGTT AAGAG
G CC
GAM7080 399 C17orf3 1 8416 NP_003867.1 5 253 GTGTCTCCAAGA TT C AT 3 C c c
5 TGGCCGCTTGGG T CCA AGCGGCCA TCTT
GAAGGAGG A GGT TCGCCGGT AGAA
GG - --
GAM7080 399 C1orf38 1 9052 NP_004839.1 3 770 TGCAGACGGGGA C CA 3 C c c
GTAGCTTTGTGG TTTCCACAG GGC ATTCTTC
AAACTGAT AAAGGTGTT TCG TGAGGGG
- A-
GAM7080 399 C20orf1 1 14702 NP_060622.2 5 219 TCTAAAGAGAAT A GC 3 C c c
2 TGGTTATGGGGA TTTCC CA GGCCAATTCTT
AAATAACA AAAGG GT TTGGTTAAGAG
G A-
GAM7080 399 C9orf14 1 2384 XP_098859.2 3 265 TAAGAAGCTCTG G C T--- 3 C c c
TTGTCGATGTGG TTTCCACA CGGC AAT CTTC
AAAAATAT AAAGGTGT GCTG TTG GAAG
A - TCTC
GAM7080 399 CABIN1 1 4584 NP_036427.1 5 24 GGGACAGACTGG --- AT T 3 C c c
CCGTTGCTGTGG TTTCCACAGC GGCCA TCT

AGACGCCT AGAGGTGTCG CCGGT AGA
TTG C- C
GAM7080 399 CALB2 1 14269 NP_001731.1 3 567 TAAAATGGAAAG - - AA T 3 C c c
GTCCTGCTGTGG TTTCCACAGC GG CC TTCT
AAACTT AAAGGTGTCG CC GG AAGG
T T A- T
GAM7080 399 CALB2 1 14269 NP_009018.1 3 803 TAAAATGGAAAG - - AA T 3 C c c
GTCCTGCTGTGG TTTCCACAGC GG CC TTCT
AAACTT AAAGGTGTCG CC GG AAGG
T T A- T
GAM7080 399 CALB2 1 14269 NP_009019.1 3 710 TAAAATGGAAAG - - AA T 3 C c c
GTCCTGCTGTGG TTTCCACAGC GG CC TTCT
AAACTT AAAGGTGTCG CC GG AAGG
T T A- T
GAM7080 399 CAMK2G 1 8935 NP_001213.2 3 701 AGGGAAGAGAAT CA G 3 C c
c
TGGTGCTGCAGA TTTC CAGCG CCAATTCTT
AGTGTACC GAAG GTCGT GGTTAAGAG
AC -
GAM7080 399 CAMK2G 1 8935 NP_751909.1 3 701 AGGGAAGAGAAT CA G 3 C c
c
TGGTGCTGCAGA TTTC CAGCG CCAATTCTT
AGTGTACC GAAG GTCGT GGTTAAGAG
AC -
GAM7080 399 CAMK2G 1 8935 NP_751910.1 3 727 AGGGAAGAGAAT CA G 3 C c
c
TGGTGCTGCAGA TTTC CAGCG CCAATTCTT
AGTGTACC GAAG GTCGT GGTTAAGAG
AC -
GAM7080 399 CAMK2G 1 8935 NP_751911.1 3 701 AGGGAAGAGAAT CA G 3 C c
c
TGGTGCTGCAGA TTTC CAGCG CCAATTCTT
AGTGTACC GAAG GTCGT GGTTAAGAG
AC -
GAM7080 399 CAMK2G 1 8935 NP_751912.1 3 1066 AGGGAAGAGAAT CA G 3 C c
c
TGGTGCTGCAGA TTTC CAGCG CCAATTCTT
AGTGTACC GAAG GTCGT GGTTAAGAG
AC -
GAM7080 399 CAMK2G 1 8935 NP_751913.1 3 701 AGGGAAGAGAAT CA G 3 C c
c
TGGTGCTGCAGA TTTC CAGCG CCAATTCTT
AGTGTACC GAAG GTCGT GGTTAAGAG
AC -
GAM7080 399 CAST 1 6367 NP_775085.1 5 20 CGAGTGAAGAAT -- G C- 3 C c c
TCAGCAGCTAAG TTTCCAC AGC GC AATTCTTC
TGGAAGTT GAAGGTG TCG CG TTAAGAAG
AA A AC
GAM7080 399 CBX1 1 1246 NP_006798.1 3 306 AACTTGCAGAAT G G T 3 C c c
TGGGTGTGTGGG TTTCCACA CG CCAATTCT

AGAGCAAA GAGGGTGT GT GGTTAAGA
- G C
GAM7080 399 CDC14B 1 14202 NP_003662.1 3 371 CTTCAGAAGAAT - CGGC- 3 C c c
TGAGGATCTGAT TTTCCA CAG CAATTCTTC
GGAGGTTT GGAGGT GTC GTTAAGAAG
A TAGGA
GAM7080 399 CDC14B 1 14202 NP_201588.1 3 371 CTTCAGAAGAAT - CGGC- 3 C c c
TGAGGATCTGAT TTTCCA CAG CAATTCTTC
GGAGGTTT GGAGGT GTC GTTAAGAAG
A TAGGA
GAM7080 399 CDK11 1 15392 XP_166324.1 3 4214 TGAAGGAAGAAT C CGGCC 3 C c c
TCTATGGAAATT TTTCCA AG AATTCTTC
ACAAATCC AAAGGT TC TTAAGAAG
A -----
GAM7080 399 CPLX1 1 2150 NP_006642.1 5 167 TGACCCCTGGAG C CAA 3 C c c
GAGCCACTGTGG TTTCCACAG GGC TTCTTC
AAGCAGAG GAAGGTGTC CCG AGGAGG
A ---
GAM7080 399 DIO1 1 977 NP_000783.2 3 523 TATGGGAAGAAT -- - CC 3 C c c
TCCAGTTGTTAG TTTCC ACAGC GG AATTCTTC
GAAGAGAT GAAGG TGTTG CC TTAAGAAG
AT A --
GAM7080 399 DIO2 1 16860 NP_000784.2 3 2504 GAATTTCTGGAA GGCCAA 3 C c c
GAAAGGCTGTGG TTTCCACAGC TTCTTC
AAGGGCCA GAAGGTGTCG AAGAAG
GA----
GAM7080 399 DIO2 1 16860 NP_054644.1 3 2504 GAATTTCTGGAA GGCCAA 3 C c c
GAAAGGCTGTGG TTTCCACAGC TTCTTC
AAGGGCCA GAAGGTGTCG AAGAAG
GA----
GAM7080 399 DISC1 1 9394 NP_061132.1 3 3877 GCTAAGAACTCA C A--- 3 C c c
TGGCCACTGTGG TTTCCACAG GGCCA TTCTT
AAATCTTG AAAGGTGTC CCGGT AAGAA
A ACTC
GAM7080 399 DKFZP43 1 8194 XP_044196.3 3 1231 TGCCTGAAAAAT CAGC C 3 C c c
4C212 TGGCCATGGAGG TTTCCA GGCCAATT TTC
CACACCAA GGAGGT CCGGTTAA AAG
A--- A
GAM7080 399 DKFZP43 1 8462 NP_056458.1 3 497 CCATGAAGATGA --- GC AT 3 C c c
4F122 TCTTGGCTGTGG TTTCCACAGC G CA TCTTC
AGAGCCAG AGAGGTGTCG C GT AGAAG
GTT TA --

GAM7080 399 DKFZp56 1 18331 NP_064501.1 3 412 AACAAGAAATAA G AA---- 3 C c c

6D234 AAGGTGTTGTGG TTTCCACAGCG CC TTCTT
AAACTTAA AAAGGTGTTGT GG AAGAA
- AAAATA

GAM7080 399 DKFZp76 1 11577 XP_089143.5 3 938 AGTTTTAAGAAT A C GC 3 C c c

1A078 TGTTCCTTGGGG TTTCC CAG G CAATTCTT
AAAAATTT AAAGG GTT C GTTAAGAA
G C TT

GAM7080 399 DKFZp76 1 4006 NP_775102.1 3 1840 CAAGAGAATTGT GC--- 3 C c c

1H0421 AAAATGTTGTGG TTTCCACAGCG CAATTCTT
AAAATGAT AAAGGTGTTGT GTTAAGAG
AAAAT

GAM7080 399 DMP1 1 895 NP_004398.1 3 587 TAGCAGAAGAAT CA GG 3 C c c
TGGAGTTGGAAG TTTCCA GC CCAATTCTTC
GTTGCATA GAAGGT TG GGTTAAGAAG
-- A-

GAM7080 399 DNMT3A 1 6530 NP_715640.1 5 209 TCATTGCAGGAA GCCA 3 C c c

TGAATGCTGTGG TTTCCACAGCG ATTCTT
AAGAAAAC GAAGGTGTCGT TAAGGA
AAG-

GAM7080 399 DPYS 1 2493 NP_001376.1 3 250 TATTGTGATGGA G AA T 3 C c c
AAGGCTGTGTGG TTTCCACA CGGCC TTCT
AAATTCAT AAAGGTGT GTCGG AAGG
- A- T

GAM7080 399 EHF 1 8009 NP_036285.2 3 829 TGGAAAAAGGAG G G AA- 3 C c c
ACGGTGGTGTGG TTTCCACA C GCC TTCTT
AAATGGCT AAAGGTGT G TGG AGGAA
- G CAG

GAM7080 399 EHF 1 8009 NP_758433.1 3 829 TGGAAAAAGGAG G G AA- 3 C c c
ACGGTGGTGTGG TTTCCACA C GCC TTCTT
AAATGGCT AAAGGTGT G TGG AGGAA
- G CAG

GAM7080 399 ELYS 1 16818 NP_056261.1 5 101 CATGGCGGCGGA G AA T 3 C c c

ACGGCGCTGTGG TTTCCACAGCG CC TTCT
AAGTATGC GAAGGTGTCGC GG AAGG
- C- C

GAM7080 399 ENTH 1 9793 NP_055481.1 3 50 TGAATGAAGAAT C GGCC 3 C c c
TTTTAGCTGTGC TTT CACAGC AATTCTTC
AGATAGGT AGA GTGTCG TTAAGAAG
C ATTT

GAM7080 399 EPHA3 1 2129 NP_005224.2 3 48 TCTGGACGGAAG G A T 3 C c c
TGGTGGCTGTGG TTTCCACAGC GCCA TTCT
AAGGCGTA GAAGGTGTCG TGGT AAGG
G G C

GAM7080 399 ERBB2IP 1 13817 NP_061165.1 3 1100 CACAGTGATAGA GCCA 3 C c c

GAATTGCTGTGG TTTCCACAGCG ATTCTT
AGAGTTAT AGAGGTGTCGT TAAGAG

GAM7080 399 FLJ1094 1 11146 NP_060750.1 3 727 TGGTGGGGAAGG C- AA 3 C c c
5 GGCCATCTGTGG TTTCCACAG GGCC TTCTTC
AAGAAACA GAAGGTGTC CCGG AAGGGG
TA GG

GAM7080 399 FLJ1101 1 424 NP_060771.1 5 5 AAGTTGGAGGTA GC AAT- 3 C c c
6 GGGGCCTGTGGA TTTCCACA GGCC TCTTC
AACATGAA AAAGGTGT CCGG GGAGG
-- GGAT

GAM7080 399 FLJ1108 1 4825 NP_060788.1 5 90 ATAAACAAGAAT A GCGG-- 3 C c c
8 TGGAAGACATGA TTTCC CA CCAATTCTT
GGAAAGCT AAAGG GT GGTTAAGAA
A ACAGAA

GAM7080 399 FLJ1277 1 10912 NP_115550.2 3 1359 AATCGAAGGAAT ACA ----- 3 C c c
0 TGGCCCAATGGC TTTCC GC GGCCAATTCTT
GAGGAGAG AGAGG CG CCGGTTAAGGA
AG- GTAAC

GAM7080 399 FLJ1416 1 17295 NP_078841.1 3 1051 TGATAGCGAAGG GCG CA 3 C c c
6 ATAGCAATGTGG TTTCCACA GC ATTCTTC
AAAATTTG AAAGGTGT CG TAGGAAG
AA- A-

GAM7080 399 FLJ2074 1 7141 NP_061893.1 3 168 GAAGGGTGAGAG -- A--- 3 C c c
8 GCAGTGCTGTGG TTTCCACAGCG GCC ATTCTTC
AAGGGGCC GAAGGTGTCGT CGG TGGGAAG
GA AGAG

GAM7080 399 FLJ2159 1 8448 NP_079099.1 3 1253 GTTGTAGCTAGA CAAT 3 C b b
6 GAGCCGCTGTGG TTTCCACAGCGGC TCTT
AAAATATG AAAGGTGTCGCCG AGAG

GAM7080 399 FLJ2174 1 8081 NP_115583.1 3 651 GCTGTGTGAATT C -- TT 3 C c c
2 CAGGCCTTGTGG TTTCCACAG GGCC AATTC
AAAACACC AAAGGTGTT CCGG TTAAG
- AC TG

GAM7080 399 FLJ2305 1 1870 NP_078858.1 3 1112 ATTTTAAAGAAT ACAGC C 3 C c c
6 TGACCTAAGGAA TTTCC GG CAATTCTT
AGCTTATG AAAGG CC GTTAAGAA
AAT-- A

GAM7080 399 FLJ3254 1 4634 NP_689653.1 3 1155 CAGTGAAGGCAT GG AT--- 3 C c c
9 AATGGGCTGTGG TTTCCACAGC CCA TCTTC
AGACCTTC AGAGGTGTCG GGT GGAAG
-- AATAC

GAM7080 399 FLJ3292 1 9432 NP_653178.1 3 499 CAGCATGGGAAA CGG A- 3 C c c
6 ATGGGACTGTGG TTTCCACAG CCA TTCTT
AAATAAAG AAAGGTGTC GGT AAGGG
AG- AA
GAM7080 399 FLJ3633 1 18131 XP_211925.1 3 693 CGTGAGGAAGGC CG-- CAA 3 C c c
1 GCAGCTCTGTGG TTTCCACAG GC TTCTTC
AAAGGTCA AAAGGTGTC CG AAGGAG
TCGA CGG
GAM7080 399 FLJ3877 1 6074 NP_848623.1 5 10 AAGGAGCAGTGC -- - ATT 3 C c c
3 GCTAAGCTGTGG TTTCCACAGC GGC CA CTTC
AAAATTCC AAAGGTGTCG TCG GT GAGG
AA C GAC
GAM7080 399 FRAT2 1 9254 NP_036215.1 3 627 GAGGTGAAGAAT A- CC 3 C c c
TTTGCAGGTGGG TTTCCAC GCGG AATTCTTC
AGATTTGG GAGGGTG CGTT TTAAGAAG
GA --
GAM7080 399 GFRA1 1 2463 NP_005255.1 3 498 TCTTACCAAGAG C A 3 C c c
TGGGCTTTGTGG TTTCCACAG GGCC ATTCTT
AAACAGCT AAAGGTGTT TCGG TGAGAA
- G
GAM7080 399 GFRA1 1 2463 NP_665736.1 3 498 TCTTACCAAGAG C A 3 C c c
TGGGCTTTGTGG TTTCCACAG GGCC ATTCTT
AAACAGCT AAAGGTGTT TCGG TGAGAA
- G
GAM7080 399 GNAQ 1 11690 NP_002063.1 3 81 ACAAGAGGGACT ----- - AA 3 C c c
GTATTTCTGTGG TTTCCACAG CGG CC TTCTT
AAAACAAT AAAGGTGTC GTC GG GAGAA
TTTAT A --
GAM7080 399 GPS2 1 5146 NP_004480.1 5 1849 ACGGGAGCAATG -- CA- - 3 C c c
TTGCCGCTGTAC TTTCC ACAGCGGC ATT CTTC
GGAGAGTG AGAGG TGTCGCCG TAA GAGG
CA TTG C
GAM7080 399 GPS2 1 5146 NP_116329.1 5 606 ACGGGAGCAATG -- CA- - 3 C c c
TTGCCGCTGTAC TTTCC ACAGCGGC ATT CTTC
GGAGAGTG AGAGG TGTCGCCG TAA GAGG
CA TTG C
GAM7080 399 GRM4 1 9216 NP_000832.1 3 52 GGAGGAGGAGCC ----- CAA 3 C c c
GTGACCCTGTGG TTTCCACAG CGGC TTCTTC
AAGGTGCG GAAGGTGTC GCCG GAGGAG
CCAGT AG-
GAM7080 399 GRPR 1 12903 NP_005305.1 5 14 TAAATATCAGGA GCCAA 3 C c c
AAGACGCTGTGG TTTCCACAGCG TTCTT
GAAAATAG AAGGGTGTCGC AAGGA
AGA--
GAM7080 399 GSTM3 1 10695 NP_000840.2 5 55 CTGCTGAGGAAG GG-- AA 3 C c c

GATAGGCTGTGG TTTCCACAGC CC TTCTTC
AAATTAGG AAAGGTGTCG GG AAGGAG
GATA --
GAM7080 399 H2AV 1 9227 NP_619541.1 3 1256 CTTGAAGATAGA GC AAT--- 3 C c c

GGGGCCATGTGG TTTCCACA GGCC TCTTC
AAATCAAG AAAGGTGT CCGG AGAAG
A- GGAGAT
GAM7080 399 HDAC9 1 2779 NP_055522.1 3 1138 GGGTGAACAGGA C CAA 3 C c c

AATGCCTTGTGG TTTCCACAG GGC TTCTT
AAACAGGA AAAGGTGTT CCG AAGGA
- TA-
GAM7080 399 HERC3 1 4462 NP_055421.1 3 224 GGGGTGAAAAAT -- C C 3 C c c
TGGCCCTTGTAT TTTCC ACAG GGCCAATT TTC
GGGAGGTG GAGGG TGTT CCGGTTAA AAG
TA C A
GAM7080 399 HMG20A 1 15708 NP_060670.1 5 34 GGCTGAGGGAAT C C 3 C c c

TGTCCTCTGTGG TTTCCACAG GG CAATTCTT
AAGGGACT GAAGGTGTC CC GTTAAGGG
T T
GAM7080 399 HSPC052 1 19338 NP_054869.1 3 422 TTCAAGAAGTTA GC C -- 3 C c c

ATTGCTATGTGG TTTCCACA GGC AATT CTTC
AAAGAAGG AAAGGTGT TCG TTAA GAAG
A- - TT
GAM7080 399 HSPC132 1 9884 NP_057483.1 3 685 TTAAGATACTTG GG-- T-- 3 C c c

GAATAGCTGTGG TTTCCACAGC CCAA TCTT
AGGAAGAA GGAGGTGTCG GGTT AGAA
ATAA CAT
GAM7080 399 HTR2C 1 17294 NP_000859.1 3 6 AGCGAAAGGATT - G C 3 C c c
AGCAGTGTGTGG TTTCCACA GC GC AATTCTT
AAAGAACA AAAGGTGT TG CG TTAGGAA
G A A
GAM7080 399 ICA1 1 8564 NP_004959.1 3 68 TCAGCAAAGAGT ---- A 3 C c c
GGGCCGCTGTGT TTTCC ACAGCGGCC ATTCTT
TTGGAGAC AGAGG TGTCGCCGG TGAGAA
TTTG G
GAM7080 399 ICA1 1 8564 NP_071683.1 3 1147 TCAGCAAAGAGT ---- A 3 C c c
GGGCCGCTGTGT TTTCC ACAGCGGCC ATTCTT
TTGGAGAC AGAGG TGTCGCCGG TGAGAA
TTTG G
GAM7080 399 IL24 1 6880 NP_006841.1 5 221 ACCAAGAAGAAT C -- 3 C c c
TGAGGCTGCTTG TTTCCA AGCGGCC AATTCTTC
GGAGGAAG GAGGGT TCGTCGG TTAAGAAG
- AG
GAM7080 399 IL6ST 1 18250 NP_002175.2 5 100 CGCCAAGGGGTT - C 3 C c c
CGTGCGCTGTGG TTTCCACAGCG GC AATTCTT

AGACGCGG AGAGGTGTCGC TG TTGGGGA
G C
GAM7080 399 IL6ST 1 18250 NP_786943.1 5 100 CGCCAAGGGGTT - C 3 C c c
CGTGCGCTGTGG TTTCCACAGCG GC AATTCTT
AGACGCGG AGAGGTGTCGC TG TTGGGGA
G C
GAM7080 399 ITR 1 19486 NP_851320.1 3 260 ATTATTGAAGCG GC CC - 3 C c c
ATTTCTATGTGG TTTCCACA GG AATT CTTC
AAATAAAT AAAGGTGT TC TTAG GAAG
A- T- C
GAM7080 399 KCNQ2 1 18822 NP_004509.2 3 2949 TCACGAGGCTTG - - TT 3 C c c
GACCTGCTGTGG TTTCCACAGC GG CCAA CTT
AGGGTGCC GGAGGTGTCG CC GGTT GAG
T A CG
GAM7080 399 KCNQ2 1 18822 NP_004509.2 3 3266 TCACGAGGCTTG - - TT 3 C c c
GACCTGCTGTGG TTTCCACAGC GG CCAA CTT
AGGGTGCC GGAGGTGTCG CC GGTT GAG
T A CG
GAM7080 399 KIAA019 1 11451 XP_038362.3 3 869 GGGCCTGGGAAT TC GC 3 C c
c
4 TGGCCATGTGTT TT CACA GGCCAATTCTT
AATTTATT AA GTGT CCGGTTAAGGG
TT A-
GAM7080 399 KIAA029 1 7477 XP_042833.2 3 529 CACCCTGGGAAT - G 3 C c c
5 TGGCAGCATGTG TTTCCACA GC GCCAATTCTT
GAGGAACT GGAGGTGT CG CGGTTAAGGG
A A
GAM7080 399 KIAA029 1 17364 XP_084529.6 3 976 GGTTGCAGAGGC -- A- T 3 C c c
8 TGGCCGCTGCCT TTTCCA CAGCGGCCA TTCT
GGAAGTGT GAAGGT GTCGCCGGT GAGA
CC CG C
GAM7080 399 KIAA064 1 616 NP_056015.1 3 2218 AGGGAAGCAAGA GG A 3 C c c
8 GTAGGGTTGTGG TTTCCACAGC CC ATTCTT
AAAGACCA AAAGGTGTTG GG TGAGAA
-- A
GAM7080 399 KIAA071 1 10952 NP_055682.1 3 3034 CCTGTAAGAAAA GC A- 3 C c
c
1 TGAATGTTGTGG TTTCCACAGCG CA TTCTT
AAATTCTT AAAGGTGTTGT GT AAGAA
AA AA
GAM7080 399 KIAA096 1 3532 XP_166543.3 3 918 GCTGAGTGAGAA - G AA 3 C c c
0 GGCAGTTTGTGG TTTCCACAG C GCC TTCTT
AAATGGAA AAAGGTGTT G CGG AAGAG
T A --
GAM7080 399 KIAA103 2 1597 NP_055724.1 3 2704 TGAGCTGAGACT GG - T 3 C c c
6 TCGGGGCTGTGG TTTCCACAGC CC AA TCTT
AGACCAGC AGAGGTGTCG GG TT AGAG
G- C C

GAM7080 399 KIAA103 2 10200 NP_055724.1 3 3039 TGAGTTCAAGAA C- CAA 3 C c c
6 AGCTACCTGTGG TTTCCACAG GGC TTCTT
AAAATGGA AAAGGTGTC TCG AAGAA
CA A--
GAM7080 399 KIAA104 1 2608 NP_055743.1 3 1783 GTAAAGACTGGG G A T 3 C c c
6 ATGGTTGTGTGG TTTCCACA CGGCCA TTCT
AAAACTTT AAAGGTGT GTTGGT AGGG
- - T
GAM7080 399 KIAA106 1 3207 XP_042635.3 3 1106 ATTCTGGGGAGA C CAA 3 C c c
9 GCAGCCTTGTGG TTTCCACAG GGC TTCTTC
AAATTGAT AAAGGTGTT CCG GAGAGG
- AC-
GAM7080 399 KIAA111 1 3218 NP_055833.1 5 19 TTTAGAGAACTG G-- A 3 C c c
7 GTATAGCTGTGG TTTCCACAGC GCCA TTCTT
AGAGGGAG AGAGGTGTCG TGGT AAGAG
ATA C
GAM7080 399 KIAA145 1 11038 XP_038035.4 3 603 ACATGTAAGAAT A C 3 C c c
0 TGCTTGTTGGGA TTTCC CAGCGG CAATTCTT
AGAGTGCT GAAGG GTTGTT GTTAAGAA
- C
GAM7080 399 KIAA191 1 459 XP_290732.1 3 456 AGGGCTGGAGGA C CA 3 C c c
7 TCGCTCCTGTGG TTTCCACAG GGC ATTCTTC
AAAGGGAG AAAGGTGTC TCG TAGGAGG
C C-
GAM7080 399 KIAA202 1 15054 XP_290463.1 5 421 GTTCACGAAGTG C AATT 3 C c c
0 AGGCCGCTGTTG TTTC ACAGCGGCC CTTC
AAATTCGT AAAG TGTCGCCGG GAAG
T AGT-
GAM7080 399 LOC1151 1 15815 XP_055292.1 5 743 ATGAAATTGGGA G C 3 C c c
29 GTTGCTGTGTGG TTTCCACA CGGC AATTCTT
AAACTCAA AAAGGTGT GTCG TTGAGGG
- -
GAM7080 399 LOC1248 1 8762 XP_058863.4 5 100 CATCAAAGGAGA GG AAT 3 C c c
95 TTCGGGCTGTGG TTTCCACAGC CC TCTTC
AAGGCTCC GAAGGTGTCG GG AGAGG
-- CTT
GAM7080 399 LOC1443 1 15953 XP_096576.1 5 32 CTGGGAGGAGTG CG CA-- 3 C c c
19 TTTGCACTGTGG TTTCCACAG GC ATTCTTC
AAATTGGT AAAGGTGTC CG TGAGGAG
A- TTTG
GAM7080 399 LOC1467 1 965 XP_097071.2 3 118 GGAGGAAGAGTT GG - 3 C c c
13 TGGGGGCTGTGG TTTCCACAGC CCAA TTCTTC
AGGGAAGG GGAGGTGTCG GGTT GAGAAG
GG T

GAM7080 399 LOC1472 1 18084 XP_085742.1 5 139 AAAGAAGCTCGG -- AA--- 3 C c c

29 GCTGCCATGTGG TTTCCACA GCGGCC TTCTT
AAAAGAAT AAAGGTGT CGTCGG AAGAA
AC GCTCG

GAM7080 399 LOC1496 1 7399 XP_086669.2 3 47 ATCAAAGAACCA CAA-- 3 C c c

72 CAGCCGCTGTGG TTTCCACAGCGGC TTCTT
GAGGATTA GAGGGTGTCGCCG AAGAA
ACACC

GAM7080 399 LOC1500 2 499 XP_097792.1 3 144 CAAAAAGAATTG GC-- 3 C b b

51 CCCACGCTGTGG TTTCCACAGCG CAATTCTT
AAGATAAA GAAGGTGTCGC GTTAAGAA
ACCC

GAM7080 399 LOC1500 2 9570 XP_097792.1 3 144 AACAAAAAGAAT GC-- 3 C b b

51 TGCCCACGCTGT TTTCCACAGCG CAATTCTT
GGAAGATA GAAGGTGTCGC GTTAAGAA
ACCC

GAM7080 399 LOC1575 1 4249 XP_098783.1 3 356 AGGACCTGGAGG C CA 3 C c
c

56 GGTGCTCTGTGG TTTCCACAG GGC ATTCTTC
AAACTGCT AAAGGTGTC TCG TGGGGAG
- --

GAM7080 399 LOC1577 1 17175 XP_098819.1 5 470 ATCATCAGGGAT CAG 3 C c
c

37 TGGCCGATGGAG TTTCCA CGGCCAATTCTT
ATGAAATG AGAGGT GCCGGTTAGGGA
A--

GAM7080 399 LOC1608 1 19486 XP_090573.3 3 260 ATTATTGAAGCG GC CC - 3 C c
c

97 ATTTCTATGTGG TTTCCACA GG AATT CTTC
AAATAAAT AAAGGTGT TC TTAG GAAG
A- T- C

GAM7080 399 LOC1646 1 3527 XP_092894.3 3 189 CCTGGAGCTGTG -- ATT 3 C c c

33 GCCTGGCTGTGG TTTCCACAGC GGCCA CTTC
AGGGCCGG GGAGGTGTCG CCGGT GAGG
GT GTC

GAM7080 399 LOC1998 1 1893 XP_114040.1 5 1282 TGCAACAGGTCC AATT 3 C c
c

58 AGGCTGCTGTGG TTTCCACAGCGGCC CTT
AAGCTGCT GAAGGTGTCGTCGG GGA
ACCT

GAM7080 399 LOC1999 1 4186 XP_114056.3 3 122 ATTTTGAGATGG CGG AT- 3 C c
c

20 TGGAATCTGTGG TTTCCACAG CCA TCTT
AAACTTTC AAAGGTGTC GGT AGAG
TAA GGT

GAM7080 399 LOC2002 1 8763 XP_114166.1 3 11 GACGAAGGGGTG --- CAA 3 C c
c

30 CCTGAGCTGTGG TTTCCACAGC GGC TTCTTC

AGAGGGTG AGAGGTGTCG CCG GGGAAG
AGT TG-
GAM7080 399 LOC2548 1 8776 XP_173188.1 3 1047 GACTGGAGATTT CGG- T 3 C c c
26 GGAGATTTGTGG TTTCCACAG CCAA TCTTC
AAAAGTGA AAAGGTGTT GGTT AGAGG
TAGA T
GAM7080 399 LOC2554 1 6761 XP_173150.1 5 62 TAGAAACGTGGC ---- A-- T 3 C c c
58 TTTGGGCTGTGG TTTCCACAGC GGCCA TTCT
AAACGCTG AAAGGTGTCG TCGGT AAGA
GGTT GCA T
GAM7080 399 LOC2564 1 14202 XP_171149.1 3 984 CTTCAGAAGAAT - CGGC- 3 C c c
01 TGAGGATCTGAT TTTCCA CAG CAATTCTTC
GGAGGTTT GGAGGT GTC GTTAAGAAG
A TAGGA
GAM7080 399 LOC2830 1 17378 XP_208488.1 3 1253 AGAAGCAAGAAT A- C C 3 C c c
35 TGCTTTTGAAGG TTTCC CAG GGC AATTCTT
AAATGGAT AAAGG GTT TCG TTAAGAA
AA T -
GAM7080 399 LOC2831 1 5966 XP_210930.1 5 1067 TACCGGAAGAAG G GC- A 3 C c c
96 TGAAACGTGTGG TTTCCACA CG CA TTCTTC
AAAATGCC AAAGGTGT GC GT AAGAAG
- AAA G
GAM7080 399 LOC2833 1 10759 XP_210989.1 3 263 TGAGAGAACAAC C A--- 3 C c c
52 TGTCTGCTGTGG TTTCCACAGCGG CA TTCTT
AAAGTAAC AAAGGTGTCGTC GT AAGAG
T CAAC
GAM7080 399 LOC2833 1 8184 XP_211010.1 3 2183 AGGAGGAAGAAT CAC G- 3 C c c
92 TGGCAGGCTAAA TTTC AGC GCCAATTCTTC
GAAGATGA GAAG TCG CGGTTAAGAAG
AAA GA
GAM7080 399 LOC2834 1 11008 XP_211056.1 3 4769 TTGGCTAAGAAT T---- - 3 C c c
75 TGTGTCGTTGTG TTCCACAGCGGC CAATTCTT
GGGTGGGC GGGGTGTTGCTG GTTAAGAA
CGGGT T
GAM7080 399 LOC2834 1 9217 XP_211062.1 3 3884 GAATTCAAGAAT C GGC 3 C c c
87 TGAGGTTTGGGA TTTCCA AGC CAATTCTT
ACTTCTGC AAGGGT TTG GTTAAGAA
- GA-
GAM7080 399 LOC2835 1 10098 XP_211110.1 3 2694 TGGAGAAAGAAT ----- GC - 3 C c c
51 TGTGCCATGAAA TTTCCA CA GGC CAATTCTT
AATGGAAA AAAGGT GT CCG GTTAAGAA
AAAAA A- T

GAM7080 399 LOC2836 1 15253 XP_211159.2 3 542 GCAAGAAAGGAA C - AA 3 C c c
78 AGGATCCTGTGG TTTCCACAG GG CC TTCTT
AAGGGTCT GAAGGTGTC CT GG AGGAA
- A AA
GAM7080 399 LOC2841 1 19691 XP_211354.1 3 406 TTCCCAATTAGG GCGGCC 3 C c c
55 AATTCAATGTGG TTTCCACA AATTCTT
AAAACATA AAAGGTGT TTAAGGA
AAC---
GAM7080 399 LOC2844 1 6823 XP_211470.1 3 2219 CAGGTCAAGGAA CG- AA 3 C c c
56 GGCATCCTGTGG TTTCCACAG GCC TTCTT
AAGTAACA GAAGGTGTC CGG AAGGA
CTA --
GAM7080 399 LOC2846 1 984 XP_209289.1 3 724 GGCACAGGGGGT CG A- 3 C c c
13 CAGGCACTGTGG TTTCCACAG GCC ATTCTT
AAAGAAGG AAAGGTGTC CGG TGGGGG
A- AC
GAM7080 399 LOC2846 1 3202 XP_209326.1 5 230 TCTGTGAGACAT TT - AT 3 C c c
97 GGCTCGCTGTGG T CCACAGCG GCCA TCTT
GGAAGGCA A GGTGTCGC CGGT AGAG
GG T AC
GAM7080 399 LOC2848 1 6074 XP_209372.1 5 10 AAGGAGCAGTGC -- - ATT 3 C c c
08 GCTAAGCTGTGG TTTCCACAGC GGC CA CTTC
AAAATTCC AAAGGTGTCG TCG GT GAGG
AA C GAC
GAM7080 399 LOC2848 1 7599 XP_211654.1 5 1161 CCAAGGGAGGCT G TT 3 C c c
36 TGGCGGCTGTGG TTTCCACAGC GCCAA CTTC
AGGCGAGT GGAGGTGTCG CGGTT GAGG
G CG
GAM7080 399 LOC2850 1 3915 XP_209446.1 5 315 GGCTCCCAGGAA - AA T 3 C c c
35 GGGCCGCTGCTG TTTCCA CAGCGGCC TTCT
GAGATGGG AGAGGT GTCGCCGG AGGA
C GA C
GAM7080 399 LOC2852 1 7389 XP_208309.1 3 73 TGCAAAGCTGTT -- C T- 3 C c c
62 GCCATGCTGTGG TTTCCACAGC GGC AAT CTT
AAGCTCTG GAAGGTGTCG CCG TTG GAA
TA - TC
GAM7080 399 LOC2855 1 1910 NP_775933.1 3 146 TTGTCAAGCAAT GC C - 3 C c c
33 TTGTCCATGTGG TTTCCACA GGC AATT CTT
AAAGAATT AAAGGTGT CTG TTAA GAA
AC T C
GAM7080 399 LOC2856 1 15058 XP_211951.1 3 150 AAAAAGGAAGGG C--- AA 3 C c c

16 CCTCTCCTGTGG TTTCCACAG GGCC TTCTT
AAAGGGAA AAAGGTGTC CCGG AGGAA
CTCT GA
GAM7080 399 LOC2856 1 16233 XP_209717.1 5 457 ATGAGAGGGGTG C A- 3 C c c

78 AGGTCTCTGTGG TTTCCACAG GGCC ATTCTTC
AAGGACAG GAAGGTGTC CTGG TGGGGAG
T AG
GAM7080 399 LOC2858 1 10911 XP_209784.1 5 1044 GGGATGAAGAAT A GG ---- 3 C c
c

31 TGACTGGGAGCT TTTCC CAGC CCA ATTCTTC
GAGGAGGG GGAGG GTCG GGT TAAGAAG
A AG CAGT
GAM7080 399 LOC2858 1 10911 XP_212577.1 5 1044 GGGATGAAGAAT A GG ---- 3 C c
c

31 TGACTGGGAGCT TTTCC CAGC CCA ATTCTTC
GAGGAGGG GGAGG GTCG GGT TAAGAAG
A AG CAGT
GAM7080 399 LOC2858 1 10911 XP_212625.1 5 1044 GGGATGAAGAAT A GG ---- 3 C c
c

31 TGACTGGGAGCT TTTCC CAGC CCA ATTCTTC
GAGGAGGG GGAGG GTCG GGT TAAGAAG
A AG CAGT
GAM7080 399 LOC2859 1 20134 XP_212085.1 5 1077 TGAAAGAAGAAT GCGGCC 3 C
c c

54 TTGTGGAAGTTA TTTCCACA AATTCTTC
ATTTGTAA GAAGGTGT TTAAGAAG

GAM7080 399 LOC2859 1 12641 XP_212099.1 5 1445 TAGAGGGCATTT C-- - 3 C c c
58 CTGTCGCTGTGG TTTCCACAGCGGC AAT TCTTC
AAGTTGTT GAAGGTGTCGCTG TTA GGGAG
TCT C
GAM7080 399 LOC2860 1 2162 XP_212166.3 5 1019 GATACAAAGAAT G GGC- 3 C c
c

90 TGAAAAGTGTGG TTTCCACA C CAATTCTT
AGGATCTG GGAGGTGT G GTTAAGAA
- AAAA
GAM7080 399 LOC2864 1 4159 XP_210036.1 3 1331 AAACAAAGATTC C- CAAT 3 C c
c

04 TGCCAACTGTGG TTTCCACAG GGC TCTT
AAACTTCA AAAGGTGTC CCG AGAA
AA TCTT
GAM7080 399 LOC2864 1 7177 XP_210044.1 5 137 AAGACGAAGTTC GCG ATT 3 C c
c

30 TGGCAAATGTGG TTTCCACA GCCA CTTC
AAAACCTG AAAGGTGT CGGT GAAG
AAA CTT
GAM7080 399 LOC2864 1 1246 XP_212322.1 3 452 AACTTGCAGAAT G G T 3 C c c
48 TGGGTGTGTGGG TTTCCACA CG CCAATTCT
AGAGCAAA GAGGGTGT GT GGTTAAGA

```
                                                - G      C
GAM7080  399   LOC3388 1  19377  XP_290597.1  3  3613   TAGAGATGGAGA      AGCG   A          3  C
c  c
          41                          GAAATGGTGTGG TTTCCAC   GCCA TTCTT
                                     AAACATTT    AAAGGTG   TGGT AAGAG
                                                 ----   A
GAM7080  399   LOC3388 1  526   XP_294733.1  5  187    AACAAGAACCTG    CA      AA---         3  C  c  c

          52                          AGGCCGCTGGAG TTTC  CAGCGGCC    TTCTT
                                     AAAAGGAA    AAAG  GTCGCCGG    AAGAA
                                               AG       AGTCC
GAM7080  399   LOC3395 1  6991   XP_294623.1  3  295    TACTTCAAGAAG        GGCCAA          3  C  c
c
          43                          AAGAAGCTGTGG TTTCCACAGC     TTCTTC
                                     AAGCCCAG    GAAGGTGTCG     AAGAAG
                                                 AAG---
GAM7080  399   LOC3398 1  15682  XP_291059.1  3  1599   CAAGTCAAGAAT     C   GGC            3  C  c
c
          96                          TGAGGTTTGGGA TTTCCA AGC   CAATTCTT
                                     ACCTCCAC    AAGGGT TTG   GTTAAGAA
                                                 -   GA-
GAM7080  399   LOC3399 1  10378  XP_291065.1  3  870    GAAGGAGCATCC          CAA-----        3  C  c
c
          07                          GTGCTGCTGTGG TTTCCACAGCGGC       TTCTTC
                                     AAAATATC    AAAGGTGTCGTCG       AGGAAG
                                                   TGCCTACG
GAM7080  399   LOC3399 1  1546   XP_295115.1  5  164    CTCTCACAAGGA T-----          AA        3  C  c  c

          75                          AGGCCGCTGTGG      TTCCACAGCGGCC  TTCTT
                                     AGCGTGGA         GAGGTGTCGCCGG  AAGGA
                                           AGGTGC          --
GAM7080  399   LOC3402 1  11781  XP_295188.1  5  182    AGACAAGGGTGG      C      --          3  C  c  c
          38                          TGGCCGCTCTGG TTTCCA AGCGGCCA  ATTCTT
                                     AGGTGCCT    GGAGGT TCGCCGGT  TGGGAA
                                                 C       GG
GAM7080  399   LOC3402 1  11781  XP_295191.1  5  182    AGACAAGGGTGG      C      --          3  C  c  c
          41                          TGGCCGCTCTGG TTTCCA AGCGGCCA  ATTCTT
                                     AGGTGCCT    GGAGGT TCGCCGGT  TGGGAA
                                                 C       GG
GAM7080  399   LOC3404 1  14512  XP_291312.1  3  366    AGCACCAAGCGG        G   ATT         3  C  c
c
          93                          TGGTGGCTGTGG TTTCCACAGC GCCA   CTT
                                     AGGAAGCC    GGAGGTGTCG TGGT   GAA
                                                   G   GGC
GAM7080  399   LOC3478 1  15054  XP_166630.4  5  1339   GTTCACGAAGTG    C       AATT         3  C  c
c
          04                          AGGCCGCTGTTG TTTC ACAGCGGCC    CTTC
                                     AAATTCGT    AAAG TGTCGCCGG    GAAG
                                                 T       AGT-
GAM7080  399   LOC3481 1  17092  XP_211219.1  5  462    GACAGCCTGGAG        GG   -   T       3  C  c
c
```

55 CTTGGGCTGTGG TTTCCACAGC CCAA TTCT
AAGATTTC GAAGGTGTCG GGTT GAGG
-- C T
GAM7080 399 LOC3483 1 16073 XP_300723.1 3 443 GTTCAAAGAGAT C - 3 C c c
78 TGACTGCTGTGG TTTCCACAGCGG CAAT TCTT
AGACAGAT AGAGGTGTCGTC GTTA AGAA
A G
GAM7080 399 LOC3484 2 10426 XP_302764.1 5 1056 GAAGTCAAGAAT C GG 3 C c
c
61 TGGGGTTTGGAA TTTCCA AGC CCAATTCTT
ACCTTCGC AAAGGT TTG GGTTAAGAA
- G-
GAM7080 399 LOC3484 2 13532 XP_302764.1 3 969 TTGAAATGGAAT GCG T 3 C c
c
61 TGGCAATGTGGG TTTCCACA GCCAATTCT
AAATAAGA AAGGGTGT CGGTTAAGG
AA- T
GAM7080 399 LOC3520 1 16506 XP_305365.1 5 252 GAGGAGGAAGGA C - AA- 3 C c
c
51 GGATCACTGTGG TTTCCACAG GG CC TTCTTC
AAATCGTC AAAGGTGTC CT GG AAGGAG
A A AGG
GAM7080 399 LOC9078 1 6662 XP_034127.1 5 1883 TCAAGTAAGAAT AC- GG 3 C c
c
6 TGGGTTAAGGGA TTTCC AGC CCAATTCTT
AAAATAGA AAAGG TTG GGTTAAGAA
GAA --
GAM7080 399 LOC9090 1 8870 XP_034809.1 3 4039 AGCAGCTGAAGG CGG AA 3 C c
c
6 AGGAGTTTGTGG TTTCCACAG CC TTCTTC
AAAATTTA AAAGGTGTT GG AGGAAG
TGA --
GAM7080 399 LOC9194 1 9979 XP_041723.1 3 213 TGTAGAGCATTC -- CC T 3 C c c
8 CCTGCGATGTGG TTTCCACA GCGG AAT CTT
AAAATTCT AAAGGTGT CGTC TTA GAG
AG CC C
GAM7080 399 MAP3K12 1 6350 NP_006292.2 3 191 CTCTAGGGACAC G AT- 3 C c
c
TGGCAGCTGTGG TTTCCACAGC GCCA TCTT
AAATGAAT AAAGGTGTCG CGGT AGGG
A CAC
GAM7080 399 MAPKBP1 1 6124 XP_031706.7 5 214 AGTGGGAAGACA C CAAT 3 C c
c
GTGCCGCTGTTG TTTC ACAGCGGC TCTTC
AGACAAGA AGAG TGTCGCCG AGAAG
T TGAC
GAM7080 399 MGC2648 1 14202 NP_689840.1 3 984 CTTCAGAAGAAT - CGGC- 3 C c
c
4 TGAGGATCTGAT TTTCCA CAG CAATTCTTC
GGAGGTTT GGAGGT GTC GTTAAGAAG

```
                                        A  TAGGA
GAM7080  399   MGC5391 1  11363 NP_116129.2  3  92   GCTGAGGACTGC   -      --- A       3  C  c  c
                                ACGCCGCTGTGC TTTC CACAGCGGC  CA TTCTT
                                GGAAGCCC    AAGG GTGTCGCCG  GT AGGAG
                                        C       CAC  C
GAM7080  399   MGST1  1  18899 NP_064696.1  3  318   CTATAAAAGAAT   - CA  GC          3  C  c
c
                                TGCACGTATGAG TTTC CA  GCG  CAATTCTT
                                AAACCTAT    AAAG GT  TGC  GTTAAGAA
                                        A  A-  AC
GAM7080  399   MGST1  1  18899 NP_665707.1  3  318   CTATAAAAGAAT   - CA  GC          3  C  c
c
                                TGCACGTATGAG TTTC CA  GCG  CAATTCTT
                                AAACCTAT    AAAG GT  TGC  GTTAAGAA
                                        A  A-  AC
GAM7080  399   MGST1  1  18899 NP_665734.1  3  318   CTATAAAAGAAT   - CA  GC          3  C  c
c
                                TGCACGTATGAG TTTC CA  GCG  CAATTCTT
                                AAACCTAT    AAAG GT  TGC  GTTAAGAA
                                        A  A-  AC
GAM7080  399   MGST1  1  18899 NP_665735.1  3  318   CTATAAAAGAAT   - CA  GC          3  C  c
c
                                TGCACGTATGAG TTTC CA  GCG  CAATTCTT
                                AAACCTAT    AAAG GT  TGC  GTTAAGAA
                                        A  A-  AC
GAM7080  399   MKRN1  1  5996  NP_038474.1  3  1267  TGTTGGAAGAAT    --  C  CC         3  C  c  c

                                TCCTTGATTGGA TTTCCA  CAG GG  AATTCTTC
                                AATTGTAC    AAAGGT  GTT CC  TTAAGAAG
                                        TA  -  --
GAM7080  399   MMAB   1  4890  NP_443077.1  3  264   GTGGGAATGAAT    ACA  --     -      3  C  c  c
                                TGGCATTGCAGG TTTCC  GCG  GCCAATTC TTC
                                AAAGACAG    AAAGG  CGT  CGGTTAAG AAG
                                        A--  TA      T
GAM7080  399   MOCS2  1  18450 NP_004522.1  5  324   GAAATAAAAGCG       G  C  T        3  C  c  c

                                TTGCAGCTGTGG TTTCCACAGC GC AAT CTT
                                AAGGAGAT    GAAGGTGTCG CG TTG GAA
                                        A  -  C
GAM7080  399   NBS1   1  9084  NP_002476.1  5  37    CCCTGAGGAGCC      G  -  AA        3  C  c  c
                                GGACCGATGTGG TTTCCACA CGG CC  TTCTTC
                                AAACTGCT    AAAGGTGT GCC GG  GAGGAG
                                        A  A  CC
GAM7080  399   NEDD5  1  5197  NP_004395.1  3  1008  ATAGAAGATCTG       C  C--  AT       3  C  c
c
                                CCTCCCCTGTGG TTTCCACAG GG  CA  TCTTC
                                AAATTGGG    AAAGGTGTC CC  GT  AGAAG
                                        C  TCC  CT
GAM7080  399   NEIL2  1  18237 NP_659480.1  3  999   CAATTCAGGAAT       GG  A--        3  C  c  c
                                CAAGGGCTGTGG TTTCCACAGC  CC  ATTCTT
```

AGAAACTC AGAGGTGTCG GG TAAGGA
-- AAC

GAM7080 399 OGG1 1 9506 NP_002533.1 5 1244 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058212.1 5 1244 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058213.1 5 1244 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058214.1 5 288 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058434.1 5 295 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058436.1 5 295 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058437.1 5 295 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OGG1 1 9506 NP_058438.1 5 295 ACTACGGGGCGG C ATT 3 C c c

TGCCTGCTGTGG TTTCCACAGCGG CA CTTC
AAATGCCT AAAGGTGTCGTC GT GGGG
C GGC

GAM7080 399 OLIG2 1 1833 NP_005797.1 3 936 AGAATTAAAAGG --- ---- T 3 C c c
CAGTTGCTGTGG TTTCCACAGCG GCC AATTCT
AAACAGTT AAAGGTGTCGT CGG TTAAGA
TGA AAAA -

GAM7080 399 PCSCL 1 13407 XP_027668.7 3 1761 TTAAGAAAGAAT CAC G 3 C c c

TGGACGTTAGAA TTTC AGCG CCAATTCTT
GTTGTCAT GAAG TTGC GGTTAAGAA

A-- A
GAM7080 399 PEG10 1 7017 NP_055883.1 3 4578 GAATGGTATTGA CG TT 3 C c c

ATTGGTCTGTGG TTTCCACAG GCCAATTC
AAAATTGC AAAGGTGTC TGGTTAAG
-- TT
GAM7080 399 PIP5K1C 1 5961 NP_036530.1 3 1495 GCGCCCGGAAGG --- AA T 3 C c
c

CCCCTGCTGTGG TTTCCACAGC GGCC TTCT
AGAAGCCG AGAGGTGTCG CCGG AAGG
TCC -- C
GAM7080 399 PIP5K1C 1 5961 XP_047620.2 3 1495 GCGCCCGGAAGG --- AA T 3 C c
c

CCCCTGCTGTGG TTTCCACAGC GGCC TTCT
AGAAGCCG AGAGGTGTCG CCGG AAGG
TCC -- C
GAM7080 399 PLEKHE1 1 996 XP_166290.1 5 456 CAACTGGGATTT GG- T 3 C c c
GGGGAGCTGTGG TTTCCACAGC CCAA TCTT
AGGGTGCA GGAGGTGTCG GGTT AGGG
AGG T
GAM7080 399 PPEF1 2 3646 NP_689411.1 3 328 CCGTGGAAGAAT GC C--- 3 C c c
TTCGTGCCATGT TTTCCACA GGC AATTCTTC
GGAAACTT AAAGGTGT CCG TTAAGAAG
A- TGCT
GAM7080 399 PPEF1 2 10928 NP_689411.1 3 328 GTGGAAGAATTT GC C--- 3 C c c
CGTGCCATGTGG TTTCCACA GGC AATTCTTC
AAACTTTT AAAGGTGT CCG TTAAGAAG
A- TGCT
GAM7080 399 PPM1A 1 11868 NP_808820.1 5 358 TTCTTGAAAGAC - CAAT 3 C c c

AGCTGGCTGTGG TTTCCACAGC GGC TCTT
AGAGCCTT AGAGGTGTCG TCG AGAA
G AC--
GAM7080 399 PPP1R9A 1 3742 NP_060120.1 3 550 GACAGTGAGACC CCAAT 3 C c
c

ACCCCGCTGTGG TTTCCACAGCGG TCTT
AAACATGG AAAGGTGTCGCC AGAG
CCACC
GAM7080 399 ProSAPi 1 12114 NP_055541.1 3 954 GAGAACGGGCCC ------ AA 3 C c c

P2 AGGGTGCTGTGG TTTCCACAGC GGCC TTCTT
AGATCAAC AGAGGTGTCG CCGG AAGAG
TGGGAC GC
GAM7080 399 RAB35 1 18480 NP_006852.1 3 1625 GGCCTGGGAAGG G AA 3 C c
c

AGGGTGCTGTGG TTTCCACAGCG CC TTCTTC
AGGGGGCT GGAGGTGTCGT GG AGGAAG
G --
GAM7080 399 RAB6A 1 6689 NP_002860.2 5 6 CACGAGGGGCGG G AA-- 3 C c c
CGGCAGCTGTGG TTTCCACAGC GCC TTCTTC

AAGCTCAG GAAGGTGTCG CGG GGGGAG
A CGGC
GAM7080 399 REC8 1 18238 NP_005123.1 5 143 CTCGAGGACCGA - AAT- 3 C c c
GGCCTGCTGTGG TTTCCACAGC GGCC TCTTC
AGGACACC GGAGGTGTCG CCGG AGGAG
T AGCC
GAM7080 399 SCN3B 1 15263 NP_060870.1 3 2423 AGTTAGAAAAAT - AGC C 3 C c
c
TGGCCTCAGTGT TTTC CAC GGCCAATT TTC
GAAATTTT AAAG GTG CCGGTTAA AAG
T ACT A
GAM7080 399 SF4 1 5616 NP_066987.1 3 127 TGATAGAGAAAT - -- - - 3 C c c
TGGCCCGCTTTG TTT CCACA GCGG CCAATT CTT
TGGCAGAA AGA GGTGT CGCC GGTTAA GAG
C TT C A
GAM7080 399 SHAPY 1 7951 NP_620148.1 5 172 GGAGATGGAGTA ------- AT 3 C c c
ATTTTGCTGTGG TTTCCACAGCGG CCA TCTTC
AAAGACTT AAAGGTGTCGTT GGT AGAGG
TTAATGA --
GAM7080 399 SLC26A9 1 10994 NP_443166.1 3 2013 TGAGGGTTGCAG - ---- 3 C c c
AGCCCGCTGTGG TTTCCACAGCGG C CAATTCTT
AGGTAAGA GGAGGTGTCGCC G GTTGGGAG
C AGAC
GAM7080 399 SLC26A9 1 10994 NP_599152.1 3 1548 TGAGGGTTGCAG - ---- 3 C c c
AGCCCGCTGTGG TTTCCACAGCGG C CAATTCTT
AGGTAAGA GGAGGTGTCGCC G GTTGGGAG
C AGAC
GAM7080 399 SNPH 1 6584 NP_055538.1 3 3167 TTCACGAAGAAT GCGG -- 3 C c
c
TCAGGGGATGTG TTTCCACA CC AATTCTTC
GGAAGTGG AAGGGTGT GG TTAAGAAG
AGG- AC
GAM7080 399 SULT4A1 2 1964 NP_055166.1 3 1231 TGGTCAGGAGGG CA 3 C c
b
TCGCTGCTGTGG TTTCCACAGCGGC ATTCTTC
AAGGGGTC GAAGGTGTCGTCG TGGGAGG
C-
GAM7080 399 SULT4A1 2 1964 NP_795343.1 3 1430 TGGTCAGGAGGG CA 3 C c
b
TCGCTGCTGTGG TTTCCACAGCGGC ATTCTTC
AAGGGGTC GAAGGTGTCGTCG TGGGAGG
C-
GAM7080 399 SULT4A1 2 19791 NP_795343.1 3 110 AAACCAGGAAGA GG 3 C b
b
GTTGGGCTGTGG TTTCCACAGC CCAATTCTTC
AAGGACAT GAAGGTGTCG GGTTGAGAAG
--
GAM7080 399 TAZ 1 443 NP_851831.1 3 513 GGGCGGAGAACA - CAA 3 C c c
AGTCGGCTGTGG TTTCCACAGC GGC TTCTTC
AGATGCGG AGAGGTGTCG CTG AAGAGG

```
                                                G  AAC
GAM7080  399   TBC1D5  1  7853  NP_055559.1  3  481   ATACCAAGAAAG       C  CCAA-          3  C  c
c
                                 CTTCCTCTGTGG TTTCCACAG GG    TTCTT
                                 AAATCTGT    AAAGGTGTC CC    AAGAA
                                              T  TTCGA
GAM7080  399   TBCD   1  687   NP_005984.2  3  78    TGTTCCTGAGGG       G    AA          3  C  c  c
                                 AGGCCGGTGTGG TTTCCACA CGGCC  TTCTTC
                                 AAAGCCTT    AAAGGTGT GCCGG  AGGGAG
                                              G    --
GAM7080  399   TBL1X  1  13310 NP_005638.1  3  2808  CTGTAATCAAGA T-----      GC    A        3  C  c
c
                                 AATGGCCTGTGG      TTCCACA  GGCCA TTCTT
                                 AATGTTAT          AAGGTGT  CCGGT AAGAA
                                          TATTGT      --    A
GAM7080  399   TCF3   1  19748 NP_003191.1  3  458   TATCACTCAAGG         G  AA          3  C  c  c
                                 GGGATGCTGTGG TTTCCACAGCG CC  TTCTT
                                 AAACCTGG    AAAGGTGTCGT GG  GGGAA
                                              A  --
GAM7080  399   TGIF   1  14220 NP_733796.2  5  233   GGGACAGGGAAT    A  C             3  C  c  c
                                 TGGCCCTGGGAG TTTCC CAG GGCCAATTCTT
                                 AAAACGCG    AGAGG GTC CCGGTTAAGGG
                                              -  -
GAM7080  399   TH1L   1  11801 NP_057481.1  3  407   AGAACATTCCAG         CCAA   T        3  C  c  c

                                 AACCCGTTGTGG TTTCCACAGCGG    TTCT
                                 AAAAACCC    AAAGGTGTTGCC    AAGA
                                              C---   C
GAM7080  399   TLR4   1  14153 NP_612567.1  5  384   GTTTACAGAAGC        G   A-   T       3  C  c  c
                                 TGGTGGCTGTGG TTTCCACAGC GCCA  TTCT
                                 AGACAAAT    AGAGGTGTCG TGGT  AAGA
                                              G   CG   C
GAM7080  399   TNFSF15 1  1718  NP_005109.2  3  1050  AGGCAGAAGAAT    A  --  C           3  C  c  c

                                 TGCTTGAACTGG TTTCC CAG  CGG CAATTCTTC
                                 GGAGGCAG    GAGGG GTC  GTT GTTAAGAAG
                                              -  AA  C
GAM7080  399   TOR1B  1  15595 NP_055321.1  3  320   ATAGAATCTAAG        CGGC            3  C  c
c
                                 AGTTGATTGTGG TTTCCACAG    CAATTCTT
                                 AAAACACG    AAAGGTGTT    GTTGAGAA
                                              A---
GAM7080  399   TPM3   1  5328  NP_705935.1  3  498   GAGCCCAGGGAG         CCAA           3  C  c  c

                                 ACTCCGCTGTGG TTTCCACAGCGG    TTCTT
                                 GAAACCTC    AAGGGTGTCGCC    AGGGA
                                              TCAG
GAM7080  399   TREM5  1  10274 NP_777552.1  3  67    TTCCAGAAGAGA        GG  AA--         3  C  c
c
                                 CTCGGGCTGTGG TTTCCACAGC  CC    TTCTTC
```

AAGGAACA GAAGGTGTCG GG GAGAAG
-- CTCA
GAM7080 399 TRIM41 1 12798 NP_291027.2 3 1013 GGGAAAAGGGAA - AA 3 C c c

GGCGTGCTGTGG TTTCCACAGCG GCC TTCTT
AAATAAAA AAAGGTGTCGT CGG GGGAA
G AA
GAM7080 399 TXNRD1 1 10465 NP_003321.1 5 322 CGCTCTCGGAAT ACA T 3 C c
c

TGGCCGCGGAAA TTTCC GCGGCCAATTCT
CCGATCTG AAAGG CGCCGGTTAAGG
--- C
GAM7080 399 UBL1 1 4385 NP_003343.1 3 427 GTTTTTCAGAGA CGGC A 3 C c c
ACTGAACTGTGG TTTCCACAG CA TTCTT
AAAAATGA AAAGGTGTC GT AAGAG
AA-- C
GAM7080 399 ULK1 1 19009 NP_003556.1 3 867 GTGTTTAAGAAT A C 3 C c c
TGGTTTTGGGAG TTTCC CAG GGCCAATTCTT
GGCGAGGA GGAGG GTT TTGGTTAAGAA
- -
GAM7080 399 WIT-1 1 4885 NP_056939.1 5 411 GTCCCAGAGAAA G- CAA 3 C c c
AGCAGGCTGTGG TTTCCACAGC GC TTCTT
AAAACTGG AAAGGTGTCG CG AAGAG
GA AA-
GAM7080 399 ZNF10 1 7309 NP_056209.2 3 151 ACATTAGAGAAT A-- C 3 C c c
TGGTCCTGGAAG TTTCC CAG GGCCAATTCTT
GGAAAGAA AAGGG GTC CTGGTTAAGAG
AAG -
GAM7080 399 ZNF197 1 16525 NP_008922.1 3 749 TTAAAGATAGTG C-- AT- 3 C c c
TCCCTGCTGTGG TTTCCACAGCGG CA TCTT
AAAACCTG AAAGGTGTCGTC GT AGAA
CCT GAT
GAM7080 399 ZNF263 1 4318 NP_005732.2 3 684 CAGCCCAGGAAT ACAGCG 3 C c
c

TGGCAGAGGAAG TTTCC GCCAATTCTT
TAGGTGTC GAAGG CGGTTAAGGA
AGA---
GAM7553 354 1 5708 NP_061085.1 3 122 TTCCAACCTAAG TC ---- 6 A c c
ATAGTTAACTAC TAGGTAGTT CTGTT GTTGGG
CTGAGACC GTCCATCAA GATAG CAACCT
TT AATC
GAM7553 354 ADORA3 1 12859 NP_000668.1 5 767 AGATGCCCAACA - TTC 6 A c
c

ACAGCACTGCTC TAG GTAGT CTGTTGTTGGG
TGT GTC CGTCA GACAACAACCC
T C--
GAM7553 354 AP1S2 1 16481 NP_003907.3 3 366 ACTGTATTTGAC T G TG 6 A c c
AAAGGAAACTCT TAGG AGTTTCCT TTGT GG
TAAATTAT ATTC TCAAAGGA AACA TT
- - GT

GAM7553 354 ASB13 1 2982 NP_078977.2 3 1281 ACCCCGCCCACA G- GT T 6 A c c

ACAGGGAGTTAA TAG TA TTCCTGTTGT GGG
ACTGGAGG GTC AT AGGGACAACA CCC
AA TG -

GAM7553 354 BIG1 1 13008 NP_006412.1 3 818 AATATCCCTACT TC - T 6 A c c

GACAGTAACTAC TAGGTAGTT CTGTT GT GGG
CTGTCACA GTCCATCAA GACAG CA CCC
T- T T

GAM7553 354 BIKE 1 2961 NP_060063.1 3 666 GCCGTCTCAACA A TT 6 A c c

ACAGGCATCACC TAGGT GT CCTGTTGTTGGG
TGAATATC GTCCA TA GGACAACAACTC
C C-

GAM7553 354 BLAME 1 19073 NP_064510.1 3 846 TTGCCCCAGCCA T TT - 6 A c c

ACAGGACGTTCT TAGG AG TCCTGTTG TTGGG
TGCACAAC GTTC TT AGGACAAC GACCC
- GC C

GAM7553 354 BPESC1 1 5329 NP_068584.1 3 2139 TGCACACCAACT T-- TT 6 A c c

CCAGGAAACTCA TAGG AGTTTCCTG GTTGG
TTCTGGGC GTCT TCAAAGGAC CAACC
TAC CT

GAM7553 354 C14orf6 1 4755 NP_777639.1 3 27 TGCAGGCCAGTA AG 6 A c c
5 ACAGGAAGGGCC TAGGT TTTCCTGTTGTTGG
TGGGGAGA GTCCG GAAGGACAATGACC
G-

GAM7553 354 CALN1 1 19469 NP_113656.1 3 429 ACCCAAGGGTCA GT ---- 6 A c c

ACAGGAGACTCT TAG AGTTTCCTGTTG TTGGG
CTGCTGAG GTC TCAGAGGACAAC AACCC
TC TGGG

GAM7553 354 CASP7 1 3279 NP_001218.1 3 615 AGGGAGTTTAAT - T 6 A c c

ACAGGAAATTGA TAGGT AGTTTCCTGT GTTGGG
CTTACATA ATTCA TTAAAGGACA TAATTT
G -

GAM7553 354 CASP7 1 3279 NP_203124.1 3 615 AGGGAGTTTAAT - T 6 A c c

ACAGGAAATTGA TAGGT AGTTTCCTGT GTTGGG
CTTACATA ATTCA TTAAAGGACA TAATTT
G -

GAM7553 354 CASP7 1 3279 NP_203125.1 3 615 AGGGAGTTTAAT - T 6 A c c

ACAGGAAATTGA TAGGT AGTTTCCTGT GTTGGG
CTTACATA ATTCA TTAAAGGACA TAATTT
G -

GAM7553 354 CASP7 1 3279 NP_203126.1 3 731 AGGGAGTTTAAT - T 6 A c c

ACAGGAAATTGA TAGGT AGTTTCCTGT GTTGGG
CTTACATA ATTCA TTAAAGGACA TAATTT
G -

GAM7553 354 CAV1 1 16480 NP_001744.2 3 372 AAAGAACCAACA TCCT 6 A c c

ACCTCAACTGCC TAGGTAGTT GTTGTTGG
TACTCCAA ATCCGTCAA CAACAACC
CTC-

GAM7553 354 CCKBR 1 12352 NP_000722.2 3 140 TAACCCCAACGC AG--- - 6 A c c
ACAGGAAAAGGT TAGGT TTTCCTGT TGTTGGG
AGCTTACC ATTCG AAAGGACA GCAACCC
ATGGA C
GAM7553 354 CCKBR 1 12352 NP_795344.1 3 140 TAACCCCAACGC AG--- - 6 A c c
ACAGGAAAAGGT TAGGT TTTCCTGT TGTTGGG
AGCTTACC ATTCG AAAGGACA GCAACCC
ATGGA C
GAM7553 354 CLK2 1 8616 NP_001282.1 3 275 GATTTCCTCAAA TCC G 6 A c c
GACAACAACTAC TAGGTAGTT TGTT TTGGG
CTGCCCTA GTCCATCAA ACAG AACTC
CA- A
GAM7553 354 COBL 1 14286 NP_056013.2 3 403 CCACATACAGAT ------ - T 6 A c c
GGATGAAACTAC TAGGTAGTTTC CTGT TGT GG
TTACTGAT ATTCATCAAAG GACA ACA CC
TAGGTA T -
GAM7553 354 CORO1C 1 5674 NP_055140.1 3 661 GATGACTGTACA AG - 6 A c c
ACAGGAAGACTT TAGGT TTTCCTGTTGT TGG
GAAAAATC GTTCA GAAGGACAACA GTC
-- T
GAM7553 354 CXCL12 1 14753 NP_000600.1 3 1600 AGGAAGTCAAAG G - G 6 A c c
CAAGGAAACTAT TA GTAGTTTCCT GTT TTGG
GTAACATG AT TATCAAAGGA CGA AACT
G A -
GAM7553 354 CYP2B6 1 7396 NP_000758.1 3 910 TCTCCCCCAACA GTTTCCTG 6 A
c c
AAACCCATACCT TAGGTA TTGTTGGG
ATCAAGCT ATCCAT AACAACCC
ACCCAA--
GAM7553 354 DKFZP56 1 10761 NP_113623.1 3 956 TAAAATTTAATC T 6 A c c
4I0422 ACAGGAAACTAC TAGGTAGTTTCCTGT GTTGGG
TTATATCT ATTCATCAAAGGACA TAATTT
C
GAM7553 354 DNMT3A 1 17093 NP_072046.2 3 746 GGTGCCTACCAC TA - T 6 A c
c
ACAGGAAACCTT TAGG GTTTCCTGT TG TGGG
GAAGAAAA GTTC CAAAGGACA AC ATCC
-- C C
GAM7553 354 DNMT3A 1 17093 NP_715640.1 3 746 GGTGCCTACCAC TA - T 6 A c
c
ACAGGAAACCTT TAGG GTTTCCTGT TG TGGG
GAAGAAAA GTTC CAAAGGACA AC ATCC
-- C C
GAM7553 354 DNMT3A 1 17093 NP_783328.1 3 746 GGTGCCTACCAC TA - T 6 A c
c
ACAGGAAACCTT TAGG GTTTCCTGT TG TGGG
GAAGAAAA GTTC CAAAGGACA AC ATCC
-- C C
GAM7553 354 EML1 1 12454 NP_004425.1 5 289 AGGCCGTGCTTA AG T--- 6 A c c

ACAGGAAAGGAC TAGGT TTTCCTGTTG TGG
CTACCAAA ATCCA AAAGGACAAT GCC
GG TCGT

GAM7553 354 EMP1 1 3219 NP_001414.1 5 42 CAGTACACCAGC T- ---- G 6 A c c
AGAGGAAACTTA AGGT AGTTTCCT TTGTTGG
TAACCTCG TCCA TCAAAGGA GACGACC
GC ATAT -

GAM7553 354 FBXW5 1 3849 NP_839890.1 3 551 TGTCGCCCGACA GTTT 6 A c c

ACAGGTACCTGT TAGGTA CCTGTTGTTGGG
ACGTGAAC GTCCAT GGACAACAGCCC

GAM7553 354 FBXW5 1 3849 NP_839891.1 3 634 TGTCGCCCGACA GTTT 6 A c c

ACAGGTACCTGT TAGGTA CCTGTTGTTGGG
ACGTGAAC GTCCAT GGACAACAGCCC

GAM7553 354 FLJ1012 1 16520 NP_060471.1 3 805 AAACTGCCAACC A T 6 A c c
0 ACAGGAAACAGC TAGGT GTTTCCTGT GTTGG
CTGGCAAA GTCCG CAAAGGACA CAACC
A C

GAM7553 354 FLJ1114 1 16418 NP_060808.2 3 75 ATTTTCCCAACA A CTG 6 A c c
2 AGTAGAAACACT TAGGT GTTTC TTGTTGGG
TAAAATCA ATTCA CAAAG AACAACCC
- ATG

GAM7553 354 FLJ1258 1 9318 NP_078896.2 3 1066 TCTACCAAAAAT TG-- 6 A c c
6 ACAGGAAATTAT TAGGTAGTTTCCTGT TTGG
CTGGGCAT GTCTATTAAAGGACA AACC
TAAA

GAM7553 354 FLJ2015 2 9513 NP_060161.1 3 101 GTTAAAACAACA - TTCC G 6 A c c

6 ACAACACTATCC TAGG TAGT TGTTGTTG
TATAAACT ATCC ATCA ACAACAAC
T CA-- A

GAM7553 354 FLJ2015 2 15489 NP_060161.1 3 101 AAAACAACAACA - TTCC G 6 A c
c
6 ACACTATCCTAT TAGG TAGT TGTTGTTG
AAACTAGA ATCC ATCA ACAACAAC
T CA-- A

GAM7553 354 FLJ2029 1 9807 NP_060219.1 3 525 GGCCAGTAACAT TTCC---- 6 A c c

4 TGCCAATACTAC TAGGTAGT TGTTGTTGG
CTACCGGC ATCCATCA ACAATGACC
TAACCGTT

GAM7553 354 FLJ2058 1 9319 XP_090970.4 5 343 AGTGTGTGGTAG TCCTGT 6 A c
c
2 CCAACAAACTAC TAGGTAGTT TGTTGG
CTAGAAAC ATCCATCAA ACAACC

GAM7553 354 FLJ2158 1 7169 NP_115580.2 3 355 TTACCCTGGACA AGT -- 6 A c c

8 GCAGGAAACCTG TAGGT TTCCTGTTGTT GGG
TATATTCA GTCCA AAGGACGACAG CCC
--- GT

GAM7553 354 FLJ2262 1 10995 NP_078991.2 5 287 TGGGACACTAGA T - G 6 A c c
5 ACAGGAAGGCTC TAGG AGT TTCCTGTT TTGG
CTGGGCCT GTCC TCG AAGGACAA GATC
- G -

GAM7553 354 FLJ2337 1 2294 NP_079232.2 5 567 CTCGTCCTAGCA AGT 6 A c c
5 ACAGGAGACCTG TAGGT TTCCTGTTGTTGGG
ACAGATGC GTCCA GAGGACAACGATCC

GAM7553 354 FLJ2346 1 6368 NP_078851.1 3 239 TCCAGCCCCAGG ----- G 6 A c c
7 ACAGGAAACAGA TAGGTAGTT TCCTGTT TTGGG
ACTGCCTG GTCCGTCAA AGGACAG GACCC
GACAA -

GAM7553 354 FLJ2375 1 1290 NP_689888.1 3 531 AGATCCCCAACA TA CTG- 6 A c
c
4 AGACCGAGACCC TAGG GTTTC TTGTTGGG
TGGACGAG GTCC CAGAG AACAACCC
-- CCAG

GAM7553 354 FLJ3331 1 17788 NP_694961.1 3 912 CTGCTGTTGATA A TG 6 A c c
8 GCAGGAAACCAC TAGGT GTTTCCTGTTGT G
CTGCTGGG GTCCA CAAAGGACGATA T
C GT

GAM7553 354 FLJ3370 1 11952 NP_775946.1 3 1485 GCCCCACACACA T -- --- 6 A c c
8 ACAGGGTAAATT TAGG AGTT TCCTGTTGT TGGG
CCTACTCC ATCC TTAA GGGACAACA ACCC
- AT CAC

GAM7553 354 FLJ3703 1 13349 NP_689734.1 3 837 CCTCCCCACACA A---- TT - 6 A c c
4 ACAGGCTACGAA TAGGT GT CCTGTTGT TGGG
GAACCTGG GTCCA CA GGACAACA ACCC
AGAAG TC C

GAM7553 354 FUK 1 13518 NP_659496.1 3 35 CTTCTCTCTGCA AG T 6 A c c
ACAGGAGAAAAC TAGGT TTTCCTGTTGT GGG
CTGGAGCT GTCCA AGAGGACAACG CTC
AA T

GAM7553 354 FYCO1 1 1084 NP_078789.1 3 1253 TCTTCCCCAACA T---- - TC 6 A c c
ACAGATAGCTCA AGGT AGTT CTGTTGTTGGG
CCTTGGAC TCCA TCGA GACAACAACCC
CAGGT C TA

GAM7553 354 G6PT1 1 13519 NP_001458.1 3 265 GCCTTCAGACAA T - --- 6 A c c
ACAGGAAACTTC TAGG AGTTTCCTGTT GTT GGG
TGCAGTCA GTCT TCAAAGGACAA CAG TCC
- A ACT

GAM7553 354 GATA6 1 2438 NP_005248.1 3 983 AAAATTGCAACA TTCC G 6 A c c
ACACTTTACTAC TAGGTAGT TGTTGTTG
CTAACGGA ATCCATCA ACAACAAC
TTTC G

GAM7553 354 GATS 1 5950 NP_849153.1 3 1674 TGTAACCTAGGA --- G 6 A c c
GCAGGAAACTTC TAGGT AGTTTCCTGTT TTGGG
AGCTTAAC ATTCG TCAAAGGACGA GATCC
ACT G
GAM7553 354 GLG1 1 1019 NP_036333.1 3 34 CACCTTGACCAC T G T 6 A c c
CAAAGGAACTAC TAGGTAGTT CCT TTG TGG
CTATCCAG ATCCATCAA GGA AAC ACC
- - C
GAM7553 354 GMPR2 1 8654 NP_057660.1 5 103 TCCTCCCCAACA GTTTC - 6 A c
c
AACAGTACCTGG TAGGTA CTGTT GTTGGG
GATGGAGC GTCCAT GACAA CAACCC
----- A
GAM7553 354 GOR 1 7795 NP_758439.1 5 554 GCAGCCCCAACA GTTT --- 6 A c c
AGAACAGGTACC TAGGTA CCTGT TGTTGGG
TGAACGTG GTCCAT GGACA ACAACCC
---- AGA
GAM7553 354 GRIA1 1 8118 NP_000818.1 3 331 CTGGAACACTAA - GT 6 A c c
TGAGGAAACTGC TAG GTAGTTTCCT TGTTGG
ACTGTTTT GTC CGTCAAAGGA GTAATC
A --
GAM7553 354 HOXB8 1 19126 NP_076921.1 3 434 GTTCTCCCAACA C 6 A b b
ACATGAAACTGC TAGGTAGTTTC TGTTGTTGGG
CTATTCAC ATCCGTCAAAG ACAACAACCC
T
GAM7553 354 HPSE 1 15551 NP_006656.1 3 1218 TCACTGCCAACA T TT C- 6 A c c
ACAACGAGGTTC TAGG AG TC TGTTGTTGG
CTATAATT ATCC TT AG ACAACAACC
- GG CA
GAM7553 354 HSC3 1 9997 NP_660157.1 3 1133 GAATCACTCCAG T GT 6 A c c
ACAGGAAATTTT TAGG AGTTTCCTGTT TGGG
CTATTTTT ATCT TTAAAGGACAG ACCT
T --
GAM7553 354 HSD3B1 1 13457 NP_000853.1 3 199 ATTGGCCCAACA - TTT G- 6 A c
c
AGAAGGTTTCTG TAGG TAG CCT TTGTTGGG
TCCTAATC ATCC GTC GGA AACAACCC
T TTT AG
GAM7553 354 HSPC063 1 5807 NP_054874.1 3 433 TTTCCCCAGCAT CCTGT- 6 A c
c
TTCCAAAACTAC TAGGTAGTTT TGTTGGG
CTAGTCCC ATCCATCAAA ACGACCC
ACCTTT
GAM7553 354 HSPC065 1 1070 NP_054876.2 3 1977 CCGCAATTAACA A 6 A c c
ACAGGAAACAAT TAGGT GTTTCCTGTTGTTGG
CTGAACAG GTCTA CAAAGGACAACAATT
A
GAM7553 354 IARS 1 8969 NP_002152.1 3 3 TGTTACCAACAA T C 6 A c c
CAGCAGACTTCT TAGG AGTTT CTGTTGTTGG

ACATGTAC ATCT TCAGA GACAACAACC
- C

GAM7553 354 IARS 1 8969 NP_038203.1 3 3 TGTTACCAACAA T C 6 A c c
CAGCAGACTTCT TAGG AGTTT CTGTTGTTGG
ACATGTAC ATCT TCAGA GACAACAACC
- C

GAM7553 354 IL22RA2 1 8508 NP_443194.1 3 678 AAACTATCAACA - - - 6 A c c
ACAAGGAAGTCT TAG GTAG TTTCCT GTTGTTGG
GCTCTGTA GTC CGTC GAAGGA CAACAACT
T T A

GAM7553 354 IL22RA2 1 8508 NP_851826.1 3 678 AAACTATCAACA - - - 6 A c c
ACAAGGAAGTCT TAG GTAG TTTCCT GTTGTTGG
GCTCTGTA GTC CGTC GAAGGA CAACAACT
T T A

GAM7553 354 IL22RA2 1 8508 NP_851827.1 3 811 AAACTATCAACA - - - 6 A c c
ACAAGGAAGTCT TAG GTAG TTTCCT GTTGTTGG
GCTCTGTA GTC CGTC GAAGGA CAACAACT
T T A

GAM7553 354 KCNE3 2 682 NP_005463.1 3 846 CATTGCCAGGCA T-- --- - 6 A c c
ACAGGACTAAAC AGGTAGTT TCCTGTTGT TGG
TACCTCCA TCCATCAA AGGACAACG ACC
ACC ATC G

GAM7553 354 KCNE3 2 15160 NP_005463.1 3 846 TGCCAGGCAACA T----- --- - 6 A c c
GGACTAAACTAC AGGTAGTT TCCTGTTGT TGG
CTCCAAAG TCCATCAA AGGACAACG ACC
GAAACC ATC G

GAM7553 354 KIAA020 1 8043 NP_055688.1 3 4226 CAATCCCCAACA --- CT 6 A c c
5 ATTAGGAACTGG TAGG TAGTTTC GTTGTTGGG
ACCCTGGG GTCC GTCAAGG TAACAACCC
CAG AT

GAM7553 354 KIAA025 1 3428 NP_055557.1 3 277 AAGTTCCCTCCA --- T- TT 6 A c c
5 ACAGGAACTCTC TAGGT AG TTCCTGTTG GGG
TGACCTGT GTCCA TC AAGGACAAC CCC
GTC TC CT

GAM7553 354 KIAA049 1 5785 XP_031397.1 3 2059 CATGCCCCAACA GT - G 6 A c c

5 AGAGGAAGACTG TAG AGTTT CCT TTGTTGGG
TCTGGCTC GTC TCAGA GGA AACAACCC
TG A G

GAM7553 354 KIAA080 1 6556 XP_031357.4 3 312 AAACTCTGCCCA AG TT 6 A c c
2 ACAGGAGAGATC TAGGT TTTCCTGTTG GG
TAGTTTTC ATCTA AGAGGACAAC CC
G- --

GAM7553 354 KIAA192 1 6303 XP_085210.1 5 97 TGTGGCCCAACA T--- G 6 A c c
0 AGAGGAAGCTCT TAGG AGTTTCCT TTGTTGGG
CCCCTGAC GTCC TCGAAGGA AACAACCC
CCTC G

GAM7553 354 LCMT2 1 14172 NP_055608.2 3 556 ATAGTTTTAACA A 6 A c c
ACAGGAAACACT TAGGT GTTTCCTGTTGTTGGG
TGTAGGAC GTTCA CAAAGGACAACAATTT

-

GAM7553 354 LHFPL2 1 6663 XP_046054.1 3 2301 GAACCCCAAACC CCT TG- 6 A c c

ACTAAAAACTAC TAGGTAGTTT GT TTGGG
CTAAACAC ATCCATCAAA CA AACCC
AAT CCA

GAM7553 354 LOC1202 1 17035 NP_620143.1 3 163 GGAGGTTCTACA A-- T 6 A c c
24 ACAGGAAATCAG TAGGT GTTTCCTGTTGT GGG
GCCTACAG ATCCG TAAAGGACAACA CTT
GAC T

GAM7553 354 LOC1386 1 9140 XP_059987.2 3 211 AACAGAGAAGTA A GG 6 A c c

49 ACAGGAAACACC TAGGT GTTTCCTGTTGTT
TAACGCAA ATCCA CAAAGGACAATGA
- AG

GAM7553 354 LOC1444 1 2439 XP_084860.1 5 969 AGTTGTCTAACC CCT T 6 A c c

38 ACTGAAAACTAC TAGGTAGTTT GT GTTGGG
CTAGCCAG ATCCATCAAA CA CAATCT
AGT C

GAM7553 354 LOC1459 1 8430 XP_071845.2 5 35 AATCTCGCCCAA AG-- GT 6 A c c

21 ACAGGAAAGCAA TAGGT TTTCCTGTT TGGG
ACCTGAAA GTCCA AAAGGACAA ACCC
AACG --

GAM7553 354 LOC1491 1 14584 XP_097598.1 5 3028 TTTCTTCTCTCA T TT 6 A c c
49 ACAGGAACCTGC TAGGTAG TTCCTGTTG GGG
CTGAGGAC GTCCGTC AAGGACAAC CTC
C T-

GAM7553 354 LOC1507 1 5023 NP_787049.1 3 1793 GGATGCCATACA G TT - 6 A c c

59 ACAGGACTATGT TA GTAG TCCTGTTGT TGG
GATGGTTT GT TATC AGGACAACA ACC
G -- T

GAM7553 354 LOC1539 1 19972 XP_098450.1 5 71 AACGTCCACCAA A TT 6 A c c
59 CCAGGAAACACC TAGGT GTTTCCTG GTTGG
TGCCTCCA GTCCA CAAAGGAC CAACC
- --

GAM7553 354 LOC1550 1 19733 XP_098651.1 3 254 GGCTCCTAACTC A TT- 6 A c c

36 TCAGGAAACACT TAGGT GTTTCCTG GTTGGG
TGTCGGCT GTTCA CAAAGGAC CAATCC
- TCT

GAM7553 354 LOC2003 1 3065 XP_114226.1 3 615 GGATGCCATACA G TT - 6 A c c
99 ACAGGACTATGT TA GTAG TCCTGTTGT TGG
GATGATTT GT TATC AGGACAACA ACC
G -- T

GAM7553 354 LOC2015 1 9241 XP_113971.1 3 13 CCGAAGCCAACA --- TCCT 6 A c c

01 ACTAGCTGGTCC TAGG TAGTT GTTGTTGG

CTGTCG GTCC GTCGA CAACAACC
CTG T---
GAM7553 354 LOC2206 1 5260 XP_167540.4 3 98 GCTTCCTCAGCA AGT- 6 A c c
86 ACAGGAGCCGGA TAGGT TTCCTGTTGTTGGG
CCTACAAC ATCCA GAGGACAACGACTC
GGCC
GAM7553 354 LOC2214 1 2379 XP_168136.1 3 1168 TTGGTCCCAACA TA A- ---- 6 A c
c
95 AGGCCCAGGAAA GGT GTTTCCTG TTGTTGGG
CAGACCCT CCA CAAAGGAC AACAACCC
TC GA CCGG
GAM7553 354 LOC2219 1 19315 XP_166555.2 3 1743 ATATACCCAACA GG CT 6 A c
c
22 ACTGGAATTGTT TA TAGTTTC GTTGTTGGG
TACACATG AT GTTAAGG CAACAACCC
TT T-
GAM7553 354 LOC2219 1 13252 XP_166542.2 3 1106 AGTAGCCCAACA ---- TT - 6 A c c
38 ACAAGGCTGCTG TAGGT AGT CCT GTTGTTGGG
GGGGCCTG GTCCG TCG GGA CAACAACCC
GGGG TC A
GAM7553 354 LOC2539 1 11790 XP_170804.3 3 367 ACATACTCTCAC A T T 6 A c c
82 ACAGGAAACGAC TAGGT GTTTCCTGT GT GGG
CTGGAAGA GTCCA CAAAGGACA CA CTC
G - -
GAM7553 354 LOC2834 1 19068 XP_211062.1 3 2510 TGTCACCCCACA G -- T 6 A c c
87 ACAGGAGGGGTT TAG TAG TTTCCTGTTGT GGG
AGCTGTGC GTC ATT GGAGGACAACA CCC
G GG C
GAM7553 354 LOC2836 1 15683 XP_211164.1 5 1104 AGGGGTACCAAA GTA- G 6 A c
c
86 ACAGGAAGCCTC TAG GTTTCCTGTT TTGG
ACTAGGAA ATC CGAAGGACAA AACC
ACTC -
GAM7553 354 LOC2838 1 20068 XP_211243.1 5 0 GCCCAACAACTT - CCT 6 A c c
68 TGAACTGGCCTG TAGGT AGTTT GTTGTTGGG
GGGATTTC GTCCG TCAAG CAACAACCC
G TTT
GAM7553 354 LOC2839 1 12361 XP_208907.1 5 80 ATGCCAGCGCCA GT --- 6 A c c
25 ACAGGAGGCTGT TAG AGTTTCCTGTT GTTGG
CTGGACAC GTC TCGGAGGACAA CGACC
TG CCG
GAM7553 354 LOC2840 1 4066 XP_211322.1 5 139 TGGGGTCAAGGA - - G 6 A c c
80 ACAGGAAGCTGA TAGGT AGTTTCCTGT T TTGG
CCTGGATG GTCCA TCGAAGGACA G AACT
G A G
GAM7553 354 LOC2846 1 1014 XP_209323.1 5 259 GGCCGCTAGCGC --- - 6 A c c
93 ACAGGAAAATCC TAGGTAG TTTCCTGT TGTTGG
TACCTGAT GTCCATC AAAGGACA GCGATC

CTA C

GAM7553 354 LOC2849 1 5023 XP_209434.1 3 590 GGATGCCATACA G TT - 6 A c c
94 ACAGGACTATGT TA GTAG TCCTGTTGT TGG
GATGGTTT GT TATC AGGACAACA ACC
G -- T

GAM7553 354 LOC2851 1 14257 XP_211791.1 3 437 TGCATAACAATA -- -- G 6 A c c
66 ACAGGAATGACT TAGGT AGTT TCCTGTTGTTG
TTGCCTGC GTCCG TCAG AGGACAATAAC
TT TA A

GAM7553 354 LOC2854 1 5962 XP_209630.1 3 1455 TACTTCTCAACA G TCC 6 A c
c
84 ACATCAACTATG TA GTAGTT TGTTGTTGGG
TAAAATGA AT TATCAA ACAACAACTC
G CT-

GAM7553 354 LOC2857 1 15629 XP_212001.1 3 741 AGAAACCCAACA G- - 6 A c c
29 ATTGGGAGATTG TAG TAGTTTCCTG TTGTTGGG
AGCTGGGA GTC GTTAGAGGGT AACAACCC
GA T

GAM7553 354 LOC2858 1 5709 XP_209784.1 3 45 GGAGCCAGTGAG AG GT-- 6 A c
c
31 ACAGGAAAAACC TAGGT TTTCCTGTT TGG
TAGTAACG ATCCA AAAGGACAG ACC
A- AGTG

GAM7553 354 LOC2858 1 5709 XP_212577.1 3 45 GGAGCCAGTGAG AG GT-- 6 A c
c
31 ACAGGAAAAACC TAGGT TTTCCTGTT TGG
TAGTAACG ATCCA AAAGGACAG ACC
A- AGTG

GAM7553 354 LOC2858 1 5709 XP_212625.1 3 45 GGAGCCAGTGAG AG GT-- 6 A c
c
31 ACAGGAAAAACC TAGGT TTTCCTGTT TGG
TAGTAACG ATCCA AAAGGACAG ACC
A- AGTG

GAM7553 354 LOC3388 1 2464 XP_290601.1 3 939 GGCCTAACAACA G CC- 6 A c c

62 ACAAAAATACTT TAGGTA TTT TGTTGTTGGG
ACAGGTCA ATTCAT AAA ACAACAATCC
A ACA

GAM7553 354 LOC3388 1 5837 XP_294736.1 5 1094 CAAAACCCCACA T CT T 6 A c
c
66 ATGAGATACTAC TAGGTAGT TC GTTGT GGG
CTACACGG ATCCATCA AG TAACA CCC
T AG C

GAM7553 354 LOC3389 1 11382 XP_294744.1 5 287 TACTATCTAACA A TTC- 6 A c c

09 ACAGTCTTGCAC TAGGT GT CTGTTGTTGGG
CTAAAGAC ATCCA CG GACAACAATCT
- TTCT

GAM7553 354 LOC3389 1 10252 XP_294767.2 5 1074 GCCGCCGCAGTC TT ---- T 6 A c
c

```
          81                          CCCAGGCACTAC TAGGTAGT  CCTG    TTGT GG
                                     CTATGAAG    ATCCATCA  GGAC    GACG CC
                                               C-    CCCT    -
GAM7553  354   LOC3392 1  14173  XP_294901.1  5  4340  ATGACAATACCA      TT   TGTT          6  A  c
c
          90                          GCCCTGGACTAC TAGGTAG  TCC    GTTGG
                                     CTACCTGT    ATCCATC  AGG    CGACC
                                               --   TCC-
GAM7553  354   LOC3397 1  19316  XP_295067.1  3  261   TCAGTCTCCACA   G    ---      T       6  A  c  c
          89                          ACAGGACGAAGC TAG TAGTT   TCCTGTTGT GGG
                                     TGGCTGAG    GTC GTCGA   AGGACAACA CCT
                                               G    AGC       -
GAM7553  354   LOC3398 1  2461   XP_295079.1  5  396   CAACACCCAACA T-----   AG            6  A  c  c

          32                          ACAGGAAGAAAT      AGGT  TTTCCTGTTGTTGGG
                                     CTCAAAAT          TCTA  GAAGGACAACAACCC
                                               TAAAAC    AA
GAM7553  354   LOC3398 1  6271   XP_291050.1  5  924   TATTTCCTAACA    T-    -           6  A  c  c
          72                          ACAGAGAGATTC TAGG  AGTTTC CTGTTGTTGGG
                                     TCTTATGT    ATTC  TTAGAG GACAACAATCC
                                               TC     A
GAM7553  354   LOC3404 1  7795   XP_290424.2  5  540   GCAGCCCCAACA     GTTT    ---          6  A  c
c
          49                          AGAACAGGTACC TAGGTA   CCTGT   TGTTGGG
                                     TGAACGTG    GTCCAT    GGACA   ACAACCC
                                               ----     AGA
GAM7553  354   LOC3426 1  2579   XP_297028.1  3  531   ACTGTGTCAACA                    6  A  b  b
          63                          ACAGGAAACTAT TAGGTAGTTTCCTGTTGTTGG
                                     TTGTATTT    GTTTATCAAAGGACAACAACT

GAM7553  354   LOC3448 1  20037  XP_298385.1  3  481   CGCCGCTCATCA     AG       T          6  A  c
c
          86                          ACAGGAAAGCTT TAGGT  TTTCCTGTTG TGGG
                                     GGGAAAGA    GTTCG  AAAGGACAAC ACTC
                                               --        T
GAM7553  354   LOC3481 1  10252  XP_302662.1  5  1065  GCCGCCGCAGTC       TT   ----   T       6  A  c
c
          27                          CCCAGGCACTAC TAGGTAGT  CCTG    TTGT GG
                                     CTATGAAG    ATCCATCA  GGAC    GACG CC
                                               C-    CCCT    -
GAM7553  354   LOC3481 1  10252  XP_302666.1  5  1074  GCCGCCGCAGTC       TT   ----   T       6  A  c
c
          30                          CCCAGGCACTAC TAGGTAGT  CCTG    TTGT GG
                                     CTATGAAG    ATCCATCA  GGAC    GACG CC
                                               C-    CCCT    -
GAM7553  354   LOC3485 1  10979  XP_300243.1  3  653   ATCATCCCAACA    T    CTG--          6  A  c
c
          44                          AAATATGAAACT TAGG AGTTTC    TTGTTGGG
                                     TCTGTAAG    GTCT TCAAAG    AACAACCC
                                               -     TATAA
```

GAM7553 354 LOC3486 1 5260 XP_300790.1 3 98 GCTTCCTCAGCA AGT- 6 A c c
00 ACAGGAGCCGGA TAGGT TTCCTGTTGTTGGG
CCTACAAC ATCCA GAGGACAACGACTC
GGCC
GAM7553 354 LOC3491 1 3138 XP_291247.1 3 658 TCATCAGCAACA AG CC 6 A c
c
40 ACAAAACCTGAT TAGGT TTT TGTTGTTGG
ATTCCAAG GTCCA AAA ACAACGACT
-- CA
GAM7553 354 LOC3492 1 17133 XP_301010.1 3 57 CGGCCACACTTA T T- - 6 A c c
87 ACAGGAAGCTCC TAGG AGTTTCCTGTTG TG GG
TAGGCCTC ATCC TCGAAGGACAAT AC CC
- TC A
GAM7553 354 LOC3493 1 15332 XP_301020.1 3 58 CGCCCACGCTTA T T--- 6 A c c
09 ACAGGAAGCTCC TAGG AGTTTCCTGTTG TGGG
TAGGCCTC ATCC TCGAAGGACAAT ACCC
- TCGC
GAM7553 354 LOC8029 1 19304 NP_079474.2 5 304 AAGTCCCAGGAC G -- G 6 A c
c
8 GGTGGAAACTAG TAG TAGTTTCC TGTT TTGGG
CTAGTAGA ATC ATCAAAGG GCAG GACCC
G TG -
GAM7553 354 LOC8502 1 13738 NP_116326.1 5 351 CGCCCCCAGCAC - T 6 A b b
6 CACGGAAACTAC TAGGTAGTTTCC TG TGTTGGG
CTACATGC ATCCATCAAAGG AC ACGACCC
C C
GAM7553 354 LOC9090 1 15110 XP_034809.1 5 1650 GGCTAAACCGAT T- - T 6 A c c

6 ACAGGAAAGCTC TAGG AGTTT CCTGT GTTGG
TCTTAGAA ATTC TCGAA GGACA TAGCC
TC A -
GAM7553 354 MBNL2 1 5708 NP_005748.1 3 588 TTCCAACCTAAG TC ---- 6 A c c
ATAGTTAACTAC TAGGTAGTT CTGTT GTTGGG
CTGAGACC GTCCATCAA GATAG CAACCT
TT AATC
GAM7553 354 MBNL2 1 5708 NP_659002.1 3 235 TTCCAACCTAAG TC ---- 6 A c c
ATAGTTAACTAC TAGGTAGTT CTGTT GTTGGG
CTGAGACC GTCCATCAA GATAG CAACCT
TT AATC
GAM7553 354 MFAP1 1 18621 NP_005917.1 3 2 CTGCCAAGAAGC C G- 6 A c c
GGAAAACTACCT TAGGTAGTTT CTGTT TTGG
AGGTCCAA ATCCATCAAA GGCGA AACC
A AG
GAM7553 354 MGC1023 1 3443 NP_689928.1 5 509 TTGTCCTCAACA T C- 6 A c c
3 ACAGCAAAGCTT TAGG AGTTT CTGTTGTTGGG
CTTGGGAG GTTC TCGAA GACAACAACTC
T AC
GAM7553 354 MGC1138 3 5617 NP_116322.1 3 1553 TCAAAAACAACA TA CC G 6 A c
c
6 ACAACAACAAAA TAGG GTTT TGTTGTTG

```
                                ACCCTATT    ATCC  CAAA  ACAACAAC
                                        --   A-       A
GAM7553  354   MGC1138 3  11951  NP_116322.1  3  1554   ACAACAACAACA    TA   CC      G        6  A  c
 c
          6                      ACAAAAACCCTA TAGG  GTTT  TGTTGTTG
                                TTCCTTGC    ATCC  CAAA  ACAACAAC
                                        --   A-       A
GAM7553  354   MGC1138 3  13670  NP_116322.1  3  1554   AAAACAACAACA    TA   CC      G        6  A  c
 c
          6                      ACAACAAAAACC TAGG  GTTT  TGTTGTTG
                                CTATTCCT    ATCC  CAAA  ACAACAAC
                                        --   A-       A
GAM7553  354   MGC1311 1  11612  NP_115742.2  3  1104   TGCCAGCCAACA     GTTTCC             6  A
c  c
          4                      ACAAATGCCTGA TAGGTA     TGTTGTTGG
                                TCTTCCGG    GTCCGT     ACAACAACC
                                        AA----
GAM7553  354   MGC1325 1  18632  NP_116103.1  3  409    CCAGGGCGAGAG        C----  G   --       6  A  c
 c
          1                      TTGAAAAACTAC TAGGTAGTTT    CT TTGT  TGG
                                CTACAGGG    ATCCATCAAA    GA AGCG  ACC
                                        AAGTT  G    GG
GAM7553  354   MGC1618 1  10586  NP_115748.1  5  366    GCTGCCAGGATG        ----  T   G        6  A  c
c
          6                      GAAACTAACTAC TAGGTAGTT    TCC GTT TTGG
                                CTGAAGAG    GTCCATCAA    AGG TAG GACC
                                        TCAA   -   -
GAM7553  354   MGC2185 1  11923  NP_443094.2  3  272    CTTGGTTCAACA       T   C             6  A  c  c
          4                      ACAAGAACTTAC TAGGTAG TTC TGTTGTTGGG
                                TTAAAACA    ATTCATT AAG ACAACAACTT
                                        C   A
GAM7553  354   MGC2688 1  11130  NP_689552.2  3  587    CTGGGCCCACAG     A        GT          6  A  c
c
          5                      ACAGGAAATGAC TAGGT GTTTCCTGTT  TGGG
                                CTGACCTC    GTCCA TAAAGGACAG  ACCC
                                        G         AC
GAM7553  354   MGC3020 1  13408  NP_076953.2  3  377    ACCTACCCAACA     A-   CCTG           6  A  c
 c
                                AGAACCAACCTG TAGGT  GTTT    TTGTTGGG
                                AGCAGCTG    GTCCA  CAAG    AACAACCC
                                        AC    ----
GAM7553  354   MGC3040 1  11387  XP_039805.6  3  690    CCACTGCTAACA T-------     TT           6  A  c
c
                                ACAGGACTGCCT        AGGTAG  TCCTGTTGTTGG
                                TTCCCTGG           TCCGTC  AGGACAACAATC
                                        GGTCCCTT     --
GAM7553  354   MGC3476 1  10760  NP_775890.1  5  80     ATGCCAGCGTCA    GT         ---          6  A  c  c

          1                      ACAGGAGGCTGT TAG  AGTTTCCTGTT   GTTGG
                                CTGGACAC    GTC  TCGGAGGACAA   CGACC
```

TG CTG
GAM7553 354 MGC3504 1 17290 NP_694940.1 3 529 GCAAACCCAACA A CTG 6 A c c
8 AGATGAGACACT TAGGT GTTTC TTGTTGGG
TAAACCCA ATTCA CAGAG AACAACCC
- TAG
GAM7553 354 MTND4L 1 1170 NP_776060.1 3 146 ACCAAATCAACA AGTTTCC 6 A c c
ACAACCTATTTA TAGGT TGTTGTTGG
GCTGTTCC ATCCA ACAACAACT

GAM7553 354 MYEOV 1 1311 NP_620123.1 3 109 CCACTTAACAGA --- G-- 6 A c c
TGAGGAAACTGA TAGGT AGTTTCCT TTGTTGGG
GGCCTAGA ATCCG TCAAAGGA GACAATTC
GAG GTA
GAM7553 354 NPCR 1 2329 NP_660361.1 5 1291 GAACCCTTATAA G T- T- 6 A c c
CTTGGAAACTAA TAG TAGTTTCC GTTGT GGG
CTGAATGG GTC ATCAAAGG CAATA CCC
A TT TT
GAM7553 354 OIP5 1 14429 NP_009211.1 3 69 CTGTCTTCAACA TT 6 A c c
ACAGGTGCTGCT TAGGTAGT CCTGTTGTTGGG
TAGTCATT ATTCGTCG GGACAACAACTT
T-
GAM7553 354 P5326 1 5216 NP_113638.1 3 2 GTGCCAACAACG - C 6 A b b
TGGAACTGACCT TAGGT AGTTTC TGTTGTTGG
AAGGGGCC ATCCA TCAAGG GCAACAACC
G T
GAM7553 354 PCSK1 1 5073 NP_000430.3 3 894 TTTTCAGCAGTA A --- 6 A c c
ACAGGAAACCAC TAGGT GTTTCCTGT TGTTGGG
TTATCACA ATTCA CAAAGGACA ACGACTT
C ATG
GAM7553 354 PH-4 1 6158 NP_060202.2 3 457 TGGTCCCTGGCA AGTT TG 6 A c c
ACAGGAACCTGG TAGGT TCCTGTTGT GG
GCAGCTTA GTCCA AGGACAACG CC
---- GT
GAM7553 354 PIK4CB 1 19981 NP_002642.1 3 93 AGAAACCCCAAA A-- TTG 6 A c c
CCAGGAAACCCC TAGGT GTTTCCTG TTGGG
ACCTACCC ATCCA CAAAGGAC AACCC
CCC CA-
GAM7553 354 PLSCR2 1 12505 NP_065092.1 5 241 TACCCAGGACGT TC- T -- 6 A c c
CAGCATGACTAC TAGGTAGTT CTG TGT TGGG
CTAGTCCC ATCCATCAG GAC GCA ACCC
TAC T GG
GAM7553 354 PRO2730 1 10196 NP_079498.1 3 797 AACCATGGGTTA -- T---- 6 A c c
ACAGGAAAGGCT TAGGTAGT TTCCTGTTG TGG
ACCTAACT ATCCATCG AAGGACAAT ACC
GA TGGGT
GAM7553 354 PRPF4B 1 7882 NP_003904.2 3 2289 CCCAATTTAGCA CC--- -- 6 A c c

TATCTAGACTAC TAGGTAGTTT TGTT GTTGGG
CTATTTGA ATCCATCAGA ACGA TAACCC
TCTAT TT

GAM7553 354 RGS18 1 19908 NP_570138.1 3 583 TATAAGCCAGCA T T 6 A c c
ACAGGAACTTTT TAGG AGTT CCTGTTGTTGG
GTGAAGAC GTTT TCAA GGACAACGACC
- -

GAM7553 354 RP4-622 1 12523 NP_061991.2 3 841 ACATCCCCAACA A- TT -- 6 A c c
L5 ACAGCAGGGACC TAGGT GT C CTGTTGTTGGG
AACCTATG ATCCA CA G GACAACAACCC
AC GG AC

GAM7553 354 SF3A3 1 9859 NP_006793.1 3 863 TGCAGCCCAACA TA --- - - 6 A c c
AACAAGGGAACT GGT AGTTTCCT GTT GTTGGG
AGGACCGA CCA TCAAGGGA CAA CAACCC
AG GGA A A

GAM7553 354 SLC21A6 1 10610 NP_006437.2 5 92 TGAGCATCAACA A CC 6 A c c
ACAAAAACATTT TAGGT GTTT TGTTGTTGG
GTATGATA GTTTA CAAA ACAACAACT
- A-

GAM7553 354 SLC35E2 1 617 XP_049733.6 3 3927 AACTTTCCCCAT AG TGT 6 A c c
ACAGGAAAACTT TAGGT TTTCCTGT TGGG
GAAAATTA GTTCA AAAGGACA ACCC
-- T--

GAM7553 354 STAM 1 12483 NP_003464.1 3 216 GCCCCTGCAGAG ---- G T 6 A c c
GAATGAAACTAC TAGGTAGTT TCCT TTGT GGG
TTACAACA ATTCATCAA AGGA GACG CCC
AGTA - T

GAM7553 354 TACSTD2 1 2226 NP_002344.1 3 257 TTCGGTCCAACA GTA- 6 A c c
ACAGGAAACCTG TAG GTTTCCTGTTGTTGGG
ACTGGGGC GTC CAAAGGACAACAACCT
AGTC

GAM7553 354 TCN2 1 2859 NP_000346.2 3 89 GATGTCCCTGGA - T GTT 6 A c c
ACAGGAACTCGC TAGGT AGTT CCTGTT GGG
CTGACCCT GTCCG TCAA GGACAA CCC
C - GGT

GAM7553 354 TDGF1 1 2899 NP_003203.1 3 1040 ATGTCCCCAACA TCCTG 6 A c c
AGATTGCTTAAT TAGGTAGTT TTGTTGGG
AAATTGTG ATTCGTTAG AACAACCC

GAM7553 354 TDRD1 1 18304 NP_112568.1 5 210 TTTACCACCTCA - - TT 6 A c c
ACAGGAACATTG TAGGT AGT TTCCTGTTG GG
ACTTGTTT GTTCA TTA AAGGACAAC CC
G C T-

GAM7553 354 TNFSF8 1 2875 NP_001235.1 3 513 GGACTCTCTCAC T- T T 6 A c c
ACAGGAAACTTC TAGG AGTTTCCTGT GT GGG
CCTATACT ATCC TCAAAGGACA CA CTC
CT - -

GAM7553 354 TRAF6 1 13703 NP_004611.1 3 37 CCTCACTTGCTC TTCC G 6 A c c

AAAAACAACTAC TAGGTAGT TGTT TTGGG
CTGGAGAA GTCCATCA ACAA AACTC
---- A

GAM7553 354 TRAF6 1 13703 NP_665802.1 3 37 CCTCACTTGCTC TTCC G 6 A c c

AAAAACAACTAC TAGGTAGT TGTT TTGGG
CTGGAGAA GTCCATCA ACAA AACTC
---- A

GAM7553 354 UBE4A 1 1390 NP_004779.1 3 2624 TCTAACTGCTCA A- TT- 6 A c c
ACAGGAAATGAA TAGGT GTTTCCTGTTG GG
CCTAGAAA ATCCA TAAAGGACAAC TC
AG TCG

GAM7553 354 X123 1 17404 NP_004807.1 3 535 TCTTTAGGCAAA T G G 6 A c c
ACAGGAAACTTC TAGG AGTTTCCTGTT TTG
TTAAGTGA ATTC TCAAAGGACAA AAC
T - G

GAM7553 354 ZNF24 1 19115 NP_008896.1 3 290 TTACTTCTCCAA CCT - 6 A c c
ATAATGAACTAC TAGGTAGTTT GTTGTT GGG
CTGATTCA GTCCATCAAG TAATAA CCT
--- A

GAM7776 246 15E1.2 1 12868 XP_290596.1 3 1202 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGAC GTGACGTGAGGTCGGACCC
AC

GAM7776 246 A1BG 2 2534 NP_570602.2 3 345 CACTGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 A1BG 2 18868 NP_570602.2 3 1397 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 AASS 1 6339 NP_005754.2 3 356 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 ABCA13 1 7385 NP_689914.2 3 1068 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 ABCC11 1 7022 NP_149163.2 5 57 GGAGATTGCCCA CAG-- 3 C c c

GGATCAAGGGTG CATTGCACTC CCTGGGCAA
CGGTGTTG GTGGCGTGGG GGACCCGTT
AACTA

GAM7776 246 ABCD3 1 14444 NP_002849.1 3 579 TCCTTGTGTGTG T- GCCT 3 C c
c

TCTTGGAGTGCA CA TGCACTCCA GGGCA

TTTGACTC GT ACGTGAGGT TCTGT
TT ----
GAM7776 246 ACADSB 1 16689 NP_001600.1 3 322 CTCTGTCACCCA C CA 3 C c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCGCG GTGACGTGAG TCGGACCC
A AC
GAM7776 246 ACP5 1 6638 NP_001602.1 3 263 ACCTTTGCTGAG AGC- G 3 C c c
TTCCGGGGTGCA CATTGCACTCC CT GGCAA
ATGGGGGA GTAACGTGGGG GA TCGTT
CCTT G
GAM7776 246 ADAMTS4 2 1651 NP_005090.1 3 670 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCACA GTAACGTGAGGTCGGACCCG
C
GAM7776 246 ADAMTS4 2 13757 NP_005090.1 3 166 CCCTAATGCGCA TT CT- G 3 C c b
GGCTGGCCCTGC CA GCA CCAGCCTG GCA
CCTGGTTT GT CGT GGTCGGAC CGT
CC CCC G
GAM7776 246 ADCY6 2 15161 NP_056085.1 3 1225 GAGAGATGCCCA G ----- 3 C c b
GGTTGCACAGGA CATT CACTCC AGCCTGGGCA
GTGGGATG GTAG GTGAGG TTGGACCCGT
G ACACG
GAM7776 246 ADCY6 2 15161 NP_066193.1 3 1225 GAGAGATGCCCA G ----- 3 C c b
GGTTGCACAGGA CATT CACTCC AGCCTGGGCA
GTGGGATG GTAG GTGAGG TTGGACCCGT
G ACACG
GAM7776 246 ADCY6 2 16688 NP_056085.1 5 65 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 ADORA2A 1 19456 NP_000666.2 3 164 AAGGGAGCCCCA T A- - A 3 C c c
GGCTGGAGCAGC CAT GC CTCCAGCCTGGG C
ATGAGGCC GTA CG GAGGTCGGACCC G
- AC C A
GAM7776 246 AGMAT 1 9193 NP_079034.2 3 436 GCTTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 AHR 1 8217 NP_001612.1 3 1634 CTCTGCCGCCCA CC A 3 C c c
AACTGGAGTGCA CATTGCACTCCAG TGGGC
GTGGCACA GTGACGTGAGGTC ACCCG
AA C
GAM7776 246 AIM1 1 16864 XP_166300.1 3 715 GACAGGATCTCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACTC

TA
GAM7776 246 AKR1D1 1 8063 NP_005980.1 3 62 TCCCATGAGTGC CCAGC G 3 C c c
CAAGACGGTGCA CATTGCACT CT GGCA
ATGGGTAG GTAACGTGG GA CCGT
CA--- A
GAM7776 246 ALDH1B1 1 2153 NP_000683.3 3 1073 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 ALOX15 1 19939 NP_001131.1 3 412 CTTTGACACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCC GTGACGTGAGGTCGGACCC
AC
GAM7776 246 AMID 1 5895 NP_116186.1 3 694 CCCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 ANKRD6 1 1746 NP_055757.1 3 1478 CTCTGTCACCCA C CA 3 C c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCATG GTGACGTGAGGTC GACCC
A AC
GAM7776 246 AP3S2 1 19874 NP_005820.1 3 657 CTCTGTCACCCA T CA 3 C c c
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGTGCA GTG CGTGAGGTCGGACCC
T AC
GAM7776 246 APAF1 2 16578 NP_001151.1 3 630 GCTTTGTTGCCA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-
GAM7776 246 APAF1 2 16578 NP_037361.1 3 630 GCTTTGTTGCCA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-
GAM7776 246 APAF1 2 19360 NP_001151.1 3 927 CACTATCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 APAF1 2 19360 NP_037361.1 3 927 CACTATCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 APM1 2 5598 NP_004788.1 3 812 CTCTGTCACCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGACACG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 APM1 2 20035 NP_004788.1 3 3332 TTCTGTGGCCCT C T A 3 C c c
GGCTGGAGTTCA CATTG ACTCCAGCC GGGC
GTGGTGTG GTGAC TGAGGTCGG CCCG

T T G

GAM7776 246 APOBEC3 1 5622 NP_660341.2 3 352 CTCTGTCACCCA C CA 3 C c c

F GACTGGAGTGCA CATTGCACTCCAG CTGGG

ATGGCTTG GTAACGTGAGGTC GACCC

A AC

GAM7776 246 APOL1 1 9574 NP_003652.2 3 118 GCTCTGTCGCCA CTG A 3 C c c

AGTTGGAGTGCA CATTGCACTCCAGC GGC

ATGGTGCG GTAACGTGAGGTTG CCG

AA- C

GAM7776 246 APOL1 1 9574 NP_663318.1 3 118 GCTCTGTCGCCA CTG A 3 C c c

AGTTGGAGTGCA CATTGCACTCCAGC GGC

ATGGTGCG GTAACGTGAGGTTG CCG

AA- C

GAM7776 246 APOL2 1 8064 NP_112092.1 3 131 CTCTATCGCCCA G A 3 C c c

GGATGGAGTGCA CATTGCACTCCA CCTGGGC

GTGGCTCA GTGACGTGAGGT GGACCCG

A C

GAM7776 246 APOL2 1 8064 NP_663612.1 3 131 CTCTATCGCCCA G A 3 C c c

GGATGGAGTGCA CATTGCACTCCA CCTGGGC

GTGGCTCA GTGACGTGAGGT GGACCCG

A C

GAM7776 246 APPBP2 1 4095 NP_006371.2 3 3495 TCTTGTTGCCCA A - 3 C b b

GGCTGGGAGGGC CATTGC CTCC AGCCTGGGCAA

AATGGCAC GTAACG GAGG TCGGACCCGTT

G G

GAM7776 246 APPL 1 12068 NP_036228.1 3 2974 CTCTGTTGCCCA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 AQP2 1 18318 NP_000477.1 3 152 CGTGCGCGCCCA T CCA A 3 C c c

GGCCAGTGCTGT CAT GCACT GCCTGGGC

GAGCAGGC GTG CGTGA CGGACCCG

T C-- C

GAM7776 246 AQP6 3 3169 NP_001643.1 3 614 ATCTGTTACCCA CA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCATG GTGACGTGAGGTCGGACCC

AT

GAM7776 246 AQP6 3 3169 NP_445738.1 3 1780 ATCTGTTACCCA CA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCATG GTGACGTGAGGTCGGACCC

AT

GAM7776 246 AQP6 3 7869 NP_445738.1 5 1736 CAGGTCAGCTCA - A-- A 3 C c c

GGCTGGAGCAGG CAT TGC CTCCAGCCTGGGC

CATATGAG GTA ACG GAGGTCGGACTCG

T GAC A

GAM7776 246 AQP6 3 8069 NP_001643.1 5 55 CAGGTCAGCTCA - A-- A 3 C c c

GGCTGGAGCAGG CAT TGC CTCCAGCCTGGGC
TATATGAG GTA ATG GAGGTCGGACTCG
T GAC A

GAM7776 246 ARCN1 1 13747 NP_001646.2 3 406 CTTTGTAACCCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
ATGGCATG GTAACGT AGGTCGGACCC
A AA

GAM7776 246 ARFRP1 1 6901 NP_003215.1 3 335 CTCCAGTGCTCA T - ---- 3 C c c
GGCTGGCTTGGG CAT GCA CT CCAGCCTGGGCA
CTGCATGA GTA CGT GG GGTCGGACTCGT
- C GTTC

GAM7776 246 ARHGAP1 1 4096 NP_004299.1 3 1136 GCTCTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC

GAM7776 246 ARHGAP1 1 17742 NP_055598.1 3 294 CTCTGTCGTCCA A 3 C b b

1A GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCTG
C

GAM7776 246 ARK5 1 17859 NP_055655.1 3 2999 GAGTTTTGCCCA TT CTC - 3 C c
c

GGCCTGCTGTCT CA GCA CAG CCTGGGCAA
TGAGTACA GT TGT GTC GGACCCGTT
TC C-- C

GAM7776 246 ARPP-19 1 944 NP_006619.1 3 3491 CACTCTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 ASB16 1 14722 NP_543139.4 3 143 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCT GTGACGTGAGGTCGGACCCGTT

GAM7776 246 ASB6 2 2196 NP_060343.1 3 1136 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
AC

GAM7776 246 ASB6 2 2196 NP_821066.1 3 1699 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
AC

GAM7776 246 ASB6 2 10305 NP_060343.1 3 1442 CTCTGTCACCTA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 ASB6 2 10305 NP_821066.1 3 2005 CTCTGTCACCTA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 ASE-1 2 1741 NP_036231.1 3 451 CTCTGTCGCCCA A 3 C b b

GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTTGGACCCG
C

GAM7776 246 ASE-1 2 3101 NP_036231.1 3 743 TGGTGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 ATF7IP2 1 9602 NP_079273.1 3 541 CTCTGTTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGTCAC GTGAC TGAGGTCGGACCCGTT
A

GAM7776 246 ATM 1 1837 NP_612150.1 3 123 TCTGTCCGCCCA C------ T A 3 C c c
GGCTGGGTGCAG ATTGCAC CCAGCCTGGGC
TCACGGCT TGACGTG GGTCGGACCCG
TCGGCAC - C

GAM7776 246 ATP1B2 1 16916 NP_001669.1 3 823 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 ATP1B4 1 13042 NP_036201.1 3 1878 TGTTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 ATP6V0D 1 15039 NP_689778.1 3 853 CTCTGTCGCCCA C A 3 C b b

2 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
ATGGCGTG GTAACGTGAG TCGGACCCG
A C

GAM7776 246 ATP6V1A 1 18868 NP_001681.2 3 676 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 ATP7A 1 4112 NP_000043.1 3 1061 TTTTGCAGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
A

GAM7776 246 ATP8B2 1 8634 XP_290875.1 3 1016 TCTTGTCACCTA CA CA 3 C c c

GGCAAGAGTGCA CATTGCACTC GCCTGGG
ATGGCACA GTAACGTGAG CGGATCC
AA AC

GAM7776 246 AXL 1 11802 NP_001690.2 3 471 CTGTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 AXL 1 11802 NP_068713.2 3 471 CTGTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 B4GALT4 1 11028 NP_003769.1 3 654 AGGACCTGCCCA CACTC - 3 C c
c

GGTATGCCTTCC CATTG CA GCCTGGGCA
AGTGATGC GTGAC GT TGGACCCGT
CTTCC A

GAM7776 246 B4GALT7 1 18475 NP_009186.1 3 311 TTCACGTGCCCA A TC - 3 C c c

GGCCTGTGGGTA CATTGC C CAG CCTGGGCA
GTGGGGAG GTGATG G GTC GGACCCGT
- GT C

GAM7776 246 BA108L7 1 10888 NP_112233.2 3 1055 CTATTTTGCCCA 3 C b b .2

GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAGCGTGAGGTCGGACCCGTT

GAM7776 246 BACE2 1 11052 NP_036237.2 3 781 AGACTTTGCCCA --- TCCAG 3 C c c

GGGTCCTGTGCC CATT GCAC CCTGGGCAA
TGGATGGG GTAG CGTG GGACCCGTT
GTC TCCTG

GAM7776 246 BACE2 1 11052 NP_620476.1 3 781 AGACTTTGCCCA --- TCCAG 3 C c c

GGGTCCTGTGCC CATT GCAC CCTGGGCAA
TGGATGGG GTAG CGTG GGACCCGTT
GTC TCCTG

GAM7776 246 BACE2 1 11052 NP_620477.1 3 978 AGACTTTGCCCA --- TCCAG 3 C c c

GGGTCCTGTGCC CATT GCAC CCTGGGCAA
TGGATGGG GTAG CGTG GGACCCGTT
GTC TCCTG

GAM7776 246 BAG5 1 5695 NP_004864.1 3 1870 CTCTGTTGCCCA C 3 C b b

GGCTGCAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGCC GTGACGTGA GTCGGACCCGTT
C

GAM7776 246 BART1 1 16830 NP_036238.1 3 1112 GTTTGTATGCTT CC TG 3 C c c

TGGTTTAGTGCA CATTGCACT AGCC GGCA
ATGTGTGG GTAACGTGA TTGG TCGT
T- TT

GAM7776 246 BAZ2A 1 8852 NP_038477.1 5 23 TCTTATTGCCCA C 3 C b b

GGCTTGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGACCTG GTAACGTGAG TCGGACCCGTT
T

GAM7776 246 BCAP31 1 4861 NP_005736.2 3 467 TGTTTTGTATTT CCTGG- 3 C c c

CTCTGGAGTGCA CATTGCACTCCAG GCAA
ATGGTGCA GTAACGTGAGGTC TGTT
TCTTTA

GAM7776 246 BCL10 1 19576 NP_003912.1 3 783 CTCTATCGCCCA A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM7776 246 BDP1 1 19556 NP_060899.1 3 153 TTCTGTTGCCCA CA 3 C b b

GGCAAGAGTGCA CATTGCACTC GCCTGGGCAA
GTGGTATG GTGACGTGAG CGGACCCGTT
AA

GAM7776 246 BENE 1 6009 NP_005425.1 3 474 CTCTTCCTCCAA - CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGG
GTGACGCG GTGACGTGAGGTCGGA CCT
A CC

GAM7776 246 BHD 1 9036 NP_659434.2 3 912 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 BMF 1 759 NP_277038.1 3 2226 TTGCCAGGCCCA T-- T A 3 C c c
GGCTGGGTGCCC CAT GCAC CCAGCCTGGGC
TGTGGCCT GTG CGTG GGTCGGACCCG
TCC - G

GAM7776 246 BNIP-S 1 5845 NP_612122.1 3 333 GCTCTGTCGCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 BRIP1 1 13904 NP_114432.1 3 208 GTCTGTTGCCCA C 3 C b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGTGTG GTGACGT AGGTCGGACCCGTT
A

GAM7776 246 BTN3A1 1 2067 NP_008979.2 3 1056 ACTCTGTTGCTA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGTGCG GTGACGTGAGGTCGGATC GTT
-

GAM7776 246 BXDC1 2 4549 XP_166303.1 3 1357 CTCTGTCGCTCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACTCG
C

GAM7776 246 BXDC1 2 12129 XP_166303.1 3 686 TTCTGTCACCTA G CA 3 C c b
GGGTGGAGTGCA CATTGCACTCCA CCTGGG
GTGGCACA GTGACGTGAGGT GGATCC
G AC

GAM7776 246 C11orf1 1 11525 NP_065693.2 3 217 CTCTGTTGCCCA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 C13orf1 1 5746 NP_065189.1 3 1686 CCTTGTCACCCA C CA 3 C c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCACG GTGACGTGAG TCGGACCC
A AC

GAM7776 246 C14orf1 1 12744 NP_009107.1 3 1453 CTCTGTCACCCA C-- CA 3 C c c
GGCTGGGAATTG CATTGCA TCCAGCCTGGG
CAGTGGCA GTGACGT GGGTCGGACCC
TAA AC

GAM7776 246 C14orf1 2 5052 NP_060100.1 3 797 CTTCTGTGGTCA CAC G 3 C c b
13 GGCTGGGACAGT CATTG TCCAGCCTGG CA
GAAAGGCA GTGAC GGGTCGGACT GT

A-- G

GAM7776 246 C14orf1 2 18863 NP_060100.1 3 360 TCTTGTTGCCCA C 3 C b b
13 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCATG GTAAC TGAGGTCGGACCCGTT
A

GAM7776 246 C14orf1 1 17955 NP_660274.1 3 1620 CTTTGTCACCTA C CA 3 C c c
43 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGCGCGA GTGACGTGAGGTCG ATCC
A AC

GAM7776 246 C14orf9 1 14861 NP_055643.1 3 968 CTCTGTCACCCA CA 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 C1orf24 1 19538 NP_443198.1 3 1462 CTCTGTCGCCAA G A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGTGTG GTGACGTGAGGTCGGA CCG
A C

GAM7776 246 C1QTNF6 1 14882 NP_114116.2 3 543 CTCTGTTGCCCA C 3 C b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGTGCA GTGACGTGAG TCGGACCCGTT
A

GAM7776 246 C20orf1 1 16257 NP_689880.1 3 981 CTCTGTCGCCCA T A 3 C c c
47 GGTTGGAGTGCC CAT GCACTCCAGCCTGGGC
ATGGCACC GTA CGTGAGGTTGGACCCG
C C

GAM7776 246 C21orf6 1 6569 NP_478068.1 5 158 CGCTGTCGCCCA A A 3 C b b
7 GGCTGGAGCGCA CATTGC CTCCAGCCTGGGC
ATGGCGCG GTAACG GAGGTCGGACCCG
C C

GAM7776 246 C22orf1 1 18897 NP_003669.2 3 1825 CTCTGTTGTCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCTGTT

GAM7776 246 C4orf9 1 15574 XP_035572.1 3 370 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 C6orf33 1 6896 NP_588608.1 3 2345 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGATGCA GTGACGTGAGGTCGGACCCG
C

GAM7776 246 C6orf5 2 10099 NP_056339.2 3 1428 CTCTGTCGTCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGCTGCA GTGACGTGAGGTCGGACCTG
C

GAM7776 246 C6orf5 2 12805 NP_056339.2 3 2320 CACTCTTTCCCA C C CA 3 C c b
GGCTGCAGTACA CATTG ACT CAGCCTGGG
GTGACACA GTGAC TGA GTCGGACCC
A C TT

GAM7776 246 C6orf57 1 2114 NP_660310.1 3 501 CTCTCTCACCCA G CA 3 C c c

GGCTGGAGTGGA CATT CACTCCAGCCTGGG
GTGGCGCT GTGA GTGAGGTCGGACCC
G AC
GAM7776 246 C7 1 17778 NP_000578.1 3 631 CTTTGTTGCCCA A 3 C b b
GGCTGGAGCGCA CATTGC CTCCAGCCTGGGCAA
GTGGGGTG GTGACG GAGGTCGGACCCGTT
C
GAM7776 246 C9orf5 1 14258 NP_114401.1 3 1340 GGTTCTTGGCCA TG A C G 3 C c
c
GGCTGTAGGTGG CAT C CT CAGCCTGG CAA
TGGCTCAC GTG G GA GTCGGACC GTT
GT - T G
GAM7776 246 C9orf9 2 5477 NP_061829.2 3 856 CTCTGTCTCCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
TC
GAM7776 246 C9orf9 2 11520 NP_061829.2 3 217 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGGCGTGAGGTCGGACCCG
C
GAM7776 246 CAB2 1 9181 NP_219487.2 3 709 GAGTGTGGGCCA --- C --- 3 C c c
GGCTGAGTGCAT CAT TGCACTC AGCCTGG GCA
AGGTGACA GTG ACGTGAG TCGGACC TGT
GAT - GGG
GAM7776 246 CABP4 1 7624 NP_660201.1 5 32 CAAGGGTGCCCA TG CCAG 3 C c
c
GGGGTGTGGTGT CAT CACT CCTGGGCA
CTCTGAGC GTG GTGG GGACCCGT
GT ----
GAM7776 246 CALN1 1 17850 NP_113656.1 3 159 GTAAAGAACCCA - C - CA 3 C c c
AGGTTGAGTGCA CA TTGCACTC AGCCT GGG
ACTGGGGT GT AACGTGAG TTGGA CCC
C - A AA
GAM7776 246 CAMLG 1 18944 NP_001736.1 3 791 TCTTGTTGCCCA C 3 C b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCGCC GTAACGTGAG TCGGACCCGTT
A
GAM7776 246 CAPN6 1 2208 NP_055104.2 3 671 TGCTTAATCAAG C - ----- 3 C c c
AGCTGGAGTTCA CATTG ACTCCAGC CT GGGCA
ATGAGTCC GTAAC TGAGGTCG GA TTCGT
T A ACTAA
GAM7776 246 CAPRI 1 4271 NP_008920.3 3 1974 CTGTGTTGCCCA - 3 C b b
GGCTGGAGTGCA CATT GCACTCCAGCCTGGGCAA
AATGGCTT GTAA CGTGAGGTCGGACCCGTT
A
GAM7776 246 CARD6 1 9036 NP_115976.2 3 205 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 CASP2 1 16398 NP_001215.1 3 1634 CTCTGTCGCCCA A A 3 C c c

GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM7776 246 CASP2 1 16398 NP_116764.1 3 1245 CTCTGTCGCCCA A A 3 C c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM7776 246 CASP2 1 16398 NP_116765.1 3 2059 CTCTGTCGCCCA A A 3 C c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM7776 246 CASP2 1 16398 NP_116766.1 3 2059 CTCTGTCGCCCA A A 3 C c c
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCACG GTGACG GAGGTCGGACCCG
G C

GAM7776 246 CASP8 1 15049 NP_001219.2 3 82 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 CASP8 1 15049 NP_203519.1 3 82 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 CASP8 1 15049 NP_203520.1 3 82 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 CASP8 1 15049 NP_203521.1 3 827 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 CASPR4 1 13634 NP_620481.1 3 103 CCAGATACTGAA CC C GG 3 C c
c

CAAGTTAGTGCA CATTGCACT AGC TG CA
ATGAAGTA GTAACGTGA TTG AC GT
-- A AA

GAM7776 246 CBFA2T2 2 8242 NP_787060.1 5 594 CCCTGTCACTCA CA CA 3 C c
c

GGCTGGAGCACA CATTG CTCCAGCCTGGG
GTGGTGTG GTGAC GAGGTCGGACTC
AC AC

GAM7776 246 CBFA2T2 2 8572 NP_005084.1 3 1896 TCTTGTCTCCCA C----- CA 3 C c
c

GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATCGCGCA TAACGTGAGGTCGGACCC
ACGCGC TC

GAM7776 246 CBFA2T2 2 8572 NP_787060.1 3 1896 TCTTGTCTCCCA C----- CA 3 C c
c

GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATCGCGCA TAACGTGAGGTCGGACCC

ACGCGC TC

GAM7776 246 CCL16 1 9543 NP_004581.1 3 276 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 CCL22 2 1679 NP_002981.2 3 951 TCTTGTCACCCA C CA 3 C c b
CGCTGGAGTGCA CATTGCACTCCAGC TGGG
ATGGTGTG GTAACGTGAGGTCG ACCC
C AC

GAM7776 246 CCL22 2 15049 NP_002981.2 3 1275 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 CCNF 1 17624 NP_001752.1 3 1293 TCTTGTCTCCCC T CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCC GGG
GTGGCATG GTGACGTGAGGTCGG CCC
C TC

GAM7776 246 CCRN4L 1 4698 NP_036250.2 3 103 CTCTGTTGCCTA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCCTG GTGAC TGAGGTCGGATCCGTT
A

GAM7776 246 CD209 2 4298 NP_066978.1 3 1590 GCTCTGTCGCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 CD209 2 17051 NP_066978.1 3 625 TCTTGTCGCTCA T A 3 C c b
GGCTGGAGTGCC CAT GCACTCCAGCCTGGGC
ATGGCGCG GTA CGTGAGGTCGGACTCG
C C

GAM7776 246 CD24 1 19572 NP_037362.1 3 890 CTTTGTCGCCCA A A 3 C c c
GGCCGGAGTGCA CATTGCACTCC GCCTGGGC
GTGGTGCG GTGACGTGAGG CGGACCCG
C C

GAM7776 246 CD5 1 1049 NP_055022.1 5 31 CCCAGCTGCCCA CA------- A C 3 C c c
GGCTGAGGCAAG TTGC CTC AGCCTGGGCA
AGAAGGCC AACG GAG TCGGACCCGT
CCGGAAGAG - -

GAM7776 246 CD84 1 514 NP_003865.1 3 1303 TGAATAGTCCTA AC - A 3 C c c
GGCTGGACAGCA CATTGC TCCAGCCTGGG C
ATGGGCTG GTAACG AGGTCGGATCC G
AC T A

GAM7776 246 CDC14B 1 17127 NP_201589.1 3 632 TCTTGTTGTCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCTGTT

GAM7776 246 CDC2L2 1 15084 NP_296370.1 5 18 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGAG GTAACGTGAGGTCGGACCC
AC

GAM7776 246 CDC6 1 9211 NP_001245.1 3 414 CCCTGTTGCCCA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 CDCP1 1 12091 NP_073753.3 3 1772 TTCTGTTGCCTA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGATCCGTT

GAM7776 246 CDH1 2 5514 NP_004351.1 3 519 TTCTATCGGCCA GCA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGACC
GGC
GAM7776 246 CDH1 2 12580 NP_004351.1 3 825 CTCCATCGCCCA CT - A 3 C c c
GGCCTGGGATGC CATTGCA CCAG CCTGGGC
AGTGATGT GTGACGT GGTC GGACCCG
AG C C
GAM7776 246 CDH17 1 13851 NP_004054.2 3 190 CTCTGTCGCCCA C A 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGTGTG GTGAC TGAGGTCGGACCCG
A C
GAM7776 246 CDK11 1 8162 XP_166324.1 3 3222 CTCTGTCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACG GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 CDKAL1 1 1255 NP_060244.1 3 444 TCTTGTCCCCCA --- CA 3 C c c
GGCTGGAGTGGT CATTGCAC TCCAGCCTGGG
GCAGTGGC GTGACGTG AGGTCGGACCC
GTG CC
GAM7776 246 CEACAM8 1 17969 NP_001807.2 3 353 CTCTGTCGCCCA A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 CECR1 2 4574 NP_059120.2 3 388 TCTTGTTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 CECR1 2 4574 NP_803124.1 3 388 TCTTGTTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 CECR1 2 9037 NP_059120.2 3 1395 CTCTGTTGCCCA CA----- G 3 C c
b

GGGTGGAGTGCA TTGCACTCCA CCTGGGCAA
GCGGTGCG GACGTGAGGT GGACCCGTT
GCGTGGC G
GAM7776 246 CECR1 2 9037 NP_803124.1 3 1395 CTCTGTTGCCCA CA----- G 3 C c
b

GGGTGGAGTGCA TTGCACTCCA CCTGGGCAA
GCGGTGCG GACGTGAGGT GGACCCGTT
GCGTGGC G

GAM7776 246 CENPH 1 19549 NP_075060.1 3 263 CTTTGTTGCCCA A C 3 C b b
GACTGGAGGGCA CATTGC CTCCAG CTGGGCAA
GTGGCGCG GTGACG GAGGTC GACCCGTT
G A
GAM7776 246 CENPJ 1 13565 NP_060921.2 5 123 CTGAGCTGCCCA AC ---- 3 C c c
GGCTTCACGGAG CATTGC TCC AGCCTGGGCA
CGGTGTTG GTGGCG AGG TCGGACCCGT
-- CACT
GAM7776 246 CGI-150 1 2191 NP_057164.1 5 49 GCTCTGTCATCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCTCA GTGACGTGAGGTCGGAC CTGT
TA
GAM7776 246 CGI-18 1 18313 NP_057031.1 5 19 TCTTGTTGCCCA C- A ---- 3 C c c
GGCTGGAAATGG ATTGC C TCCAGCCTGGGCAA
CGCGATCT TAGCG G AGGTCGGACCCGTT
TC C GTAA
GAM7776 246 CGI-43 1 14860 NP_056437.1 3 376 CTCCGTGACCCA C - 3 C b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG CA
ATGGCTCA GTAACGT AGGTCGGACCC GT
A A
GAM7776 246 CHC1L 1 15582 NP_001259.1 5 208 AGGGACTGCCCA - C C - 3 C c c
GGACTGAGTCCA CAT TG ACTC AG CCTGGGCA
TATGGAAG GTA AC TGAG TC GGACCCGT
T C - A
GAM7776 246 CHRAC1 1 9475 NP_059140.1 3 960 CTCAGTTGCCCA C 3 C b b
GGCTGGATTGCG CATTGCA TCCAGCCTGGGCAA
GTGGCGCT GTGGCGT AGGTCGGACCCGTT
T
GAM7776 246 CHSY1 1 11924 NP_055733.2 3 639 CTCTGTTACCCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCA GTGACGT AGGTCGGACCC
A AT
GAM7776 246 CIAS1 1 13461 NP_004886.2 5 289 CTGTGTCGCCTA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGATCCG
C
GAM7776 246 CIP29 2 3509 NP_115740.3 3 164 CTCTGTTGCCCA C 3 C b b
GCTGGAGTGCAG CATTGCACTCCAGC TGGGCAA
TGGTGTGA GTGACGTGAGGTCG ACCCGTT
-
GAM7776 246 CIP29 2 20120 NP_115740.3 3 164 GCTCTGTTGCCC C 3 C b b
AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGTGTG GTGACGTGAGGTCG ACCCGTT
-
GAM7776 246 CLDN19 1 5914 NP_683763.1 3 1484 CTGGGTGCCTGA CC CT- 3 C c
c
AGCTATAGTGCA CATTGCACT AGC GGGCA
ATGGTTCC GTAACGTGA TCG TCCGT
TA AAG
GAM7776 246 CLECSF1 2 15296 NP_072092.2 3 320 CTTTGTTACCCA CA 3 C c c

2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 CLECSF1 2 16192 NP_072092.2 3 970 TCTTGTTGCCCA CA----- 3 C c c

2 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGCACG AACGTGAGGTCGGACCCGTT
GCACGGC
GAM7776 246 CLIC5 1 19116 NP_058625.1 5 142 CCCCGCTGCTCG GCA- 3 C c c
GGCTGGAGAATA CATT CTCCAGCCTGGGCA
GATGGTTT GTAG GAGGTCGGGCTCGT
ATAA
GAM7776 246 CLN8 1 515 NP_061764.2 3 1639 CTTTGGCTCCCA C CA 3 C c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGTGTG GTGAC TGAGGTCGGACCC
C TC
GAM7776 246 CLNS1A 1 18823 NP_001284.1 3 80 GTGCCTCTTCCA ---- CC ----- 3 C c c
CTCTGGAGTGAA CATTG CACTCCAG TGG GCA
GTTAATGA GTAAT GTGAGGTC ACC CGT
TGAA TC TTCTC
GAM7776 246 CMAR 2 5053 NP_005191.2 5 232 CGCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCTGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 CMAR 2 18767 NP_005191.2 5 364 CTGTGTTGCCAA CA----- G 3 C c c

GGCTGGAGTGCA TTGCACTCCAGCCT GGCAA
GGCCGCGA GACGTGAGGTCGGA CCGTT
AGCGCCG A
GAM7776 246 CNN2 1 9959 NP_004359.1 3 736 GGTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 CNP 1 606 NP_149124.1 3 561 TGCTATTTCCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCG GTGACGTGAGGTCG ACCC
A TT
GAM7776 246 COLEC12 1 11525 NP_110408.2 3 104 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 CORO1C 1 13595 NP_055140.1 3 1013 GCAGCTTGCCCA C C C- 3 C c
c
GCTCTTGAGTAC CATTG ACTC AG CTGGGCAA
AGTGGTGG GTGAC TGAG TC GACCCGTT
A T TC
GAM7776 246 COX15 1 7552 NP_510870.1 3 659 TCTTGTTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCGTG GTAAC TGAGGTCGGACCCGTT
A

GAM7776 246 CPA4 1 8942 NP_057436.1 3 604 TCTTGTTGCCCA TG 3 C b b
GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
ATGGGCTC GTA GTGAGGTCGGACCCGTT
GT
GAM7776 246 CPR8 1 13999 NP_065790.1 3 1691 CTTTGTCAGCCA --- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
GTGACACG GTGACGTGAGGTCGGACC TGTT
GAC
GAM7776 246 CPS1 1 14493 NP_001866.2 3 668 TCACACTCTCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCT
CT
GAM7776 246 CPSF2 2 591 XP_029311.2 3 2045 TCTTGTTGCCCA C 3 C b b
GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCACA GTAACGTGAGGTC GACCCGTT
A
GAM7776 246 CPSF2 2 1877 XP_029311.2 3 1220 CAGAGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGAG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 CR1 1 17292 NP_000564.1 3 771 CTCTGTCTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 CR1 1 17292 NP_000642.2 3 770 CTCTGTCTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 CRLF3 1 7105 NP_057070.2 3 613 TCTTGTCACTCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACTC
AC
GAM7776 246 CRSP6 1 7661 NP_004259.3 3 435 CTCTGTAGCCCA C A 3 C c c
GTCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTGTG GTGACGTGAGGTC GACCCG
T A
GAM7776 246 CRTAP 1 7107 NP_006362.1 3 267 CTCTCTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 CSE-C 1 2336 NP_061851.1 5 2 GGAGTGCCCAGG G 3 C b b
ATGGAGTGCAGT CATTGCACTCCA CCTGGGCA
GGCTATTC GTGACGTGAGGT GGACCCGT
A
GAM7776 246 CSE1L 1 6312 NP_803185.1 3 493 TCTCATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGAGCTA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 CSNK2A2 1 15382 NP_001887.1 5 1 TGTCACCCAGGC CA 3 C c c
TGGAGTGCAGTG CATTGCACTCCAGCCTGGG

GCGCAATC GTGACGTGAGGTCGGACCC
AC
GAM7776 246 CTEN 1 14746 NP_116254.3 3 767 CACTGTCACCCA CTC CA 3 C c c
GGCTGAACTGCA CATTGCA CAGCCTGGG
GTGGTGTG GTGACGT GTCGGACCC
CAA AC
GAM7776 246 CTF1 1 13287 NP_001321.1 3 196 CTCTGTCGCCCA A 3 C b b
GGCTGGGGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGGGGTCGGACCCG
C
GAM7776 246 CTSS 1 4517 NP_004070.3 3 1701 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 CXCL16 1 17688 NP_071342.1 3 340 CTCTGTCATCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCT
AC
GAM7776 246 CYCS 3 9339 NP_061820.1 3 2207 CCTTTTCGCCCA C C A 3 C c b
GGCTGAGTACAG CATTG ACTC AGCCTGGGC
TGGTGCAA GTGAC TGAG TCGGACCCG
A - C
GAM7776 246 CYCS 3 18868 NP_061820.1 3 2620 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 CYCS 3 18991 NP_061820.1 3 1817 CTGTGTCGCCAA G A 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGTGCG GTGACGTGAGGTCGGA CCG
A C
GAM7776 246 CYLC2 1 15540 NP_001331.1 3 731 CTCTGTTGCCCT C T 3 C b b
GGCTGGAGTTCA CATTG ACTCCAGCC GGGCAA
GTGACATG GTGAC TGAGGTCGG CCCGTT
T T
GAM7776 246 CYP1A2 3 6637 NP_000752.1 3 788 ACTCTGTTGCCA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCG GTGACGTGAGGTCGGACC GTT
-
GAM7776 246 CYP1A2 3 13576 NP_000752.1 3 418 GTCTGTCACCCA CA 3 C c b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTTGGACCC
AC
GAM7776 246 CYP1A2 3 18279 NP_000752.1 3 1085 CTCTGTCTCCTA C CA 3 C c b
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCATC GTGACGTGAGGTCG ATCC
A TC
GAM7776 246 CYP2B6 2 2194 NP_000758.1 3 1087 CTCTGTCTCCCA T CA 3 C c b

GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
ATGGTGCA GTA CGTGAGGTCGGACCC
T TC

GAM7776 246 CYP2B6 2 10618 NP_000758.1 3 276 CACTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 CYP4F3 1 9158 NP_000887.1 3 1396 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 CYP51A1 1 2152 NP_000777.1 3 884 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 CYP8B1 1 5978 NP_004382.1 3 1006 CTCTGTTGCCCA C 3 C b b
GGCTGCAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGTG GTGACGTGA GTCGGACCCGTT
C

GAM7776 246 DBR1 1 7961 NP_057300.1 3 86 TCTTGTCACCTA C CA 3 C c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
ATGGCGTG GTAACGTGAGGTC GATCC
A AC

GAM7776 246 DCX 1 16590 NP_000546.2 3 4962 CTCTGTCACCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 DCX 1 16590 NP_835364.1 3 4962 CTCTGTCACCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 DCX 1 16590 NP_835365.1 3 4962 CTCTGTCACCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 DCX 1 16590 NP_835366.1 3 4962 CTCTGTCACCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 DES 1 14498 NP_001918.2 3 295 GGATGGAGCCCA AC A A 3 C c c
GGCGGGAGCGGT CATTGC TCC GCCTGGGC
GGCCCTGT GTGGCG AGG CGGACCCG
-- G A

GAM7776 246 DFFB 2 2019 NP_004393.1 3 246 TTTTGTTGCCCA 3 C b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGATGTGAGGTCGGACCCGTT

GAM7776 246 DFFB 2 9091 NP_004393.1 3 889 CTCTGTCGCTCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGATGCA GTGACGTGAGGTCGGACTCG

C
GAM7776 246 DHFR 1 8052 NP_000782.1 3 920 TCTTGTTGCCCA CTCC 3 C b b
GGCTAGCATGCA CATTGCA AGCCTGGGCAA
ATGGTGTG GTAACGT TCGGACCCGTT
ACGA
GAM7776 246 DIAPH2 1 14492 NP_006720.1 3 4013 CTCTGTCACCCA C CA 3 C c c
GGCTGCAGTGTA CATTGCACT CAGCCTGGG
GTGGTGCA GTGATGTGA GTCGGACCC
C AC
GAM7776 246 DISC1 1 1298 NP_061132.1 3 3218 CTCTGTCACCCA C CA 3 C c c
AGTTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCCCC GTGACGTGAGGTTG ACCC
A AC
GAM7776 246 DKFZP43 1 4014 NP_115519.1 3 480 CTTTGTTACCCA C CA 3 C c c
4B1727 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGTGTC GTGAC TGAGGTCGGACCC
A AT
GAM7776 246 DKFZp43 1 8235 NP_060068.1 3 861 CTCTGTCACCCA C CA 3 C c c
4C0923 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 DKFZP43 1 8661 XP_044196.3 3 1560 CCCTGTTGCCCA 3 C b b
4C212 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 DKFZP43 1 2209 NP_056410.2 3 810 CTCTGTCGCCCA C C A 3 C c c
4D146 GGCTAGAGTATA CATTG ACTC AGCCTGGGC
GTGGTGTG GTGAT TGAG TCGGACCCG
A A C
GAM7776 246 DKFZp43 1 11326 NP_060082.1 5 772 GTCTGTTGCCCA 3 C b b
4E2220 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 DKFZP43 1 16771 NP_110444.1 3 2412 CTCTGTCACCTA - CA 3 C c c
4F0318 GGCTGGAGTTGC CATTGCA CTCCAGCCTGGG
AGTGGTTT GTGACGT GAGGTCGGATCC
T AC
GAM7776 246 DKFZp43 1 3951 NP_115624.1 3 1205 TCTTGTTTCCCA CA 3 C b b
4F1719 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGGTGA GTAACGTGAGGTCGGACCC
TT
GAM7776 246 DKFZp43 1 4195 NP_060076.1 3 1080 ATTTAGTGCCCA - --- AGC 3 C c
c
4K1210 GGGAGTCCAGCG CATT GC ACTCC CTGGGCA
AATGACGT GTAA CG TGAGG GACCCGT
G ACC ---

GAM7776 246 DKFZp54 1 14246 NP_064546.1 3 257 CTCCATTGCCCA CA----- C 3 C c c

7H025 GGCTGGACTGCA TTGCA TCCAGCCTGGGCAA
GCAGCGTG GACGT AGGTCGGACCCGTT
GTGCGAC C

GAM7776 246 DKFZp54 1 11057 NP_694590.1 3 1544 CACTGTCACCCA CA 3 C c c

7P234 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 DKFZP56 1 2662 NP_056416.1 5 1111 TCTTGTCGCCCA C A 3 C c c

4G092 GGCTGTAGTGCA CATTGCACT CAGCCTGGGC
GTGGTACA GTGACGTGA GTCGGACCCG
T C

GAM7776 246 DKFZP56 1 16590 XP_032397.1 3 259 CTCTGTCACCTA CA 3 C c c

4I122 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 DKFZP56 1 17964 NP_114429.1 3 215 CTCTGTTGCCCA 3 C b b

4K0322 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 DKFZp56 1 2663 NP_115497.2 3 696 CTGTGTCACACA --- 3 C b b

4K142 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCGTG GTGACGTGAGGTCGGAC CTGT
ACA

GAM7776 246 DKFZP56 1 3686 NP_115496.1 3 226 CTCTGTTGCCCA C 3 C b b

4O0523 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
A

GAM7776 246 DKFZP56 1 10539 NP_110443.1 5 181 GCGTTTGTCCCA CA- - - 3 C c c

6D1346 GGCTCGGGGGCT CATTG CTCC AGCCTGGG CAA
CAGTGGGA GTGAC GGGG TCGGACCC GTT
TCG C T

GAM7776 246 DKFZP56 1 12353 NP_056226.1 3 714 CTCTGTTGCCCA T C 3 C b b

6I1024 GGCTAGAGTGCA CA TGCACTC AGCCTGGGCAA
CTGGTGGT GT ACGTGAG TCGGACCCGTT
C A

GAM7776 246 DKFZp58 1 12173 XP_098416.1 3 3009 CTCTGTCACCCA CA 3 C b b

6C0721 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCAAG GTAACGTGAGGTCGGACCC
AC

GAM7776 246 DKFZP58 1 11134 NP_056248.1 3 473 CTCTGTCATCCA CA 3 C c c

6D0919 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCT
AC

GAM7776 246 DKFZp66 1 15574 NP_808881.1 3 966 TCTTGTTGCCCA 3 C b b

7B1218 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 DKFZp66 1 8492 XP_117353.1 3 296 CTCTGTCAGCCA TG --- 3 C c c
7E0512 GGCTGGAGTGTG CAT CACTCCAGCCTGG GCA
GTGGCACA GTG GTGAGGTCGGACC TGT
GT GAC
GAM7776 246 DKFZp76 1 13571 NP_775734.1 3 2765 CTATGTCTCCCA CA 3 C c c

1B107 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 DKFZp76 1 17969 NP_689650.1 5 1005 CTCTGTCGCCCA A 3 C b b
1B128 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 DKFZp76 1 7769 XP_046017.3 3 1995 GCCCCCTGCCCA GC-- T 3 C c
c
1G2113 GGCTGGGTAAGA CATT AC CCAGCCTGGGCA
GATGGGCT GTAG TG GGTCGGACCCGT
AGAA -
GAM7776 246 DKFZp76 1 15190 NP_061181.1 3 887 ATCTGTCGCCCA C----- A 3 C c c

1H039 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCGTG TGACGTGAGGTCGGACCCG
GTGCGA C
GAM7776 246 DKFZp76 1 5768 NP_115656.1 5 1462 TCTTGTCACCCA CA 3 C c c
1J139 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 DKFZp76 1 1317 NP_060892.1 5 136 ACTTCAGCTCCA ACTC - A 3 C c
c
1K1423 GGCTGCAGTAAT CATTGC CAGCCTGG GC
GTGTTGGT GTAATG GTCGGACC CG
AC-- T A
GAM7776 246 DKFZp76 1 13529 XP_086327.6 3 1184 ACTCTGTTGCCA C G 3 C b b

1N1114 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTC GTGACGT AGGTCGGACC GTT
A -
GAM7776 246 DKFZp76 1 7699 NP_060879.1 5 1531 TCTTGTTGCCCA C 3 C b b
1O0113 GGCTTGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGATGCA GTGACGTGAG TCGGACCCGTT
T
GAM7776 246 DKFZp76 1 9147 NP_690870.1 3 740 CTCTGTCACCCA CA 3 C c c
1P1121 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 DKFZp76 1 4056 NP_848637.1 3 168 CTCTGTGGCCCA C A 3 C c c
2C2414 GGCTGAAGTGCA CATTGCACT CAGCCTGGGC

GTGGTGTG GTGACGTGA GTCGGACCCG
A G
GAM7776 246 DKFZp76 1 1744 NP_689624.1 3 255 CTCTGTCACCCA CA 3 C c c
2I137 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 DKFZp76 1 6884 NP_689597.1 3 705 CAATGGTGCCCA 3 C b b
2I194 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCGTG GTGACGTGAGGTCGGACCCGT

GAM7776 246 DKFZp76 1 9194 NP_061189.2 3 781 TTCTGTTGCCCA AG 3 C b b
2L0311 GGAGGGAGTGCA CATTGCACTCC CCTGGGCAA
GTGGTGCA GTGACGTGAGG GGACCCGTT
GA
GAM7776 246 DKK3 1 20069 NP_037385.1 3 27 TAATCTGGACCA GC - G- 3 C c c
GGCTGTGGGTAG CATT ACTC CAGCCTGG CA
ATGTGCAA GTAG TGGG GTCGGACC GT
A- T AG
GAM7776 246 DKK3 1 20069 NP_056965.2 3 27 TAATCTGGACCA GC - G- 3 C c c
GGCTGTGGGTAG CATT ACTC CAGCCTGG CA
ATGTGCAA GTAG TGGG GTCGGACC GT
A- T AG
GAM7776 246 DNAH11 1 1214 NP_003768.1 3 43 TCCTCTAGCCTC CT A 3 C c c
TGCTGGAGTGCA CATTGCACTCCAGC GGGC
GTGAGGAT GTGACGTGAGGTCG TCCG
TC A
GAM7776 246 DNAJB5 1 5815 NP_036398.2 3 231 AGAGCTAGCCCA C A- A 3 C c c

GGCCAGGGGTCA CATTG ACTCC GCCTGGGC
ATGTTCAT GTAAC TGGGG CGGACCCG
- AC A
GAM7776 246 DRIM 1 6633 NP_055318.1 3 141 CTCTGTCACCCA A - CA 3 C c c
AGGCGGAGTGCA CATTGCACTCC GCCT GGG
GTGACGAC GTGACGTGAGG CGGA CCC
- A AC
GAM7776 246 DRPLA 1 9796 NP_001931.1 5 185 TTCAGCTGCCCA GCA A-- 3 C c c

GGCAGAGGAGAA CATT CTCC GCCTGGGCA
TGGGGTCT GTAA GAGG CGGACCCGT
--- AGA
GAM7776 246 DSC3 1 7559 NP_001932.1 3 2049 CTCTGACGCACA G A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTG GC
GTGGCTCC GTGACGTGAGGTCGGAC CG
A C
GAM7776 246 DSC3 1 7559 NP_077741.1 3 2263 CTCTGACGCACA G A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTG GC
GTGGCTCC GTGACGTGAGGTCGGAC CG
A C
GAM7776 246 DSCR6 1 14954 NP_061835.1 3 546 TCTTGTCTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGACACA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 DUSP19 2 5768 NP_543152.1 3 638 TCTTGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 DUSP19 2 15367 NP_543152.1 3 2293 TCTTATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 EBAF 1 18275 NP_003231.2 3 510 TGAAGGGCTTCA A - A 3 C c c
GGCTGGGGGCAG CATTGC CTCCAGCCTGG GC
TGGACAGG GTGACG GGGGTCGGACT CG
- T G
GAM7776 246 EDG8 1 12263 NP_110387.1 3 952 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGGCAC GTAACGTGAGGTCGGACCC
AC
GAM7776 246 EEF2K 1 2595 NP_037434.1 3 345 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACATG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 EHD1 1 7065 NP_006786.2 3 329 GGCCTTTGCTGT -- - TG 3 C c c
GGCTGGAGCTGG CATTG CA CTCCAGCC GGCAA
ACAGTGCA GTGAC GT GAGGTCGG TCGTT
AG C TG
GAM7776 246 EHD2 1 4837 NP_055416.2 3 906 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGAG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 EIF2S3 1 1744 NP_001406.1 3 347 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 EIF5A2 1 8340 NP_065123.1 3 975 CTCCATCAGCCA GCA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGACC
GAC
GAM7776 246 ELP3 1 14236 NP_060561.3 3 906 CTGTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 EMR2 2 13462 NP_038475.2 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 EMR2 2 13462 NP_690880.1 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC

GAM7776 246 EMR2 2 13462 NP_690881.1 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 EMR2 2 13462 NP_690882.1 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 EMR2 2 13462 NP_690883.1 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 EMR2 2 13462 NP_690884.1 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 EMR2 2 13462 NP_690885.1 5 151 CTCTATCACCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCACC GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 EMR2 2 17743 NP_038475.2 3 1758 CTTTGTCACCCA C C CA 3 C c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC
GAM7776 246 EMR2 2 17743 NP_690880.1 3 1758 CTTTGTCACCCA C C CA 3 C c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC
GAM7776 246 EMR2 2 17743 NP_690881.1 3 1758 CTTTGTCACCCA C C CA 3 C c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC
GAM7776 246 EMR2 2 17743 NP_690882.1 3 1758 CTTTGTCACCCA C C CA 3 C c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC
GAM7776 246 EMR2 2 17743 NP_690883.1 3 1758 CTTTGTCACCCA C C CA 3 C c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC
GAM7776 246 EMR2 2 17743 NP_690884.1 3 1758 CTTTGTCACCCA C C CA 3 C c c
TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM7776 246 EMR2 2 17743 NP_690885.1 3 1758 CTTTGTCACCCA C C CA 3 C c c

TGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGGCACA GTAAC TGAGGTCG ACCC
A T AC

GAM7776 246 ENDOGL1 1 5031 NP_005098.1 3 154 CCGTGTCATCCA CA 3 C c c

GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTGGA GTGGCGTGAGGTCGGACCT
AC

GAM7776 246 EPHA8 1 1229 NP_065387.1 3 461 CTTATCCGTTAA - A GG A 3 C c c
GGCTGGAGGCAC CAT TGC CTCCAGCCT GC
ATGTGGGT GTA ACG GAGGTCGGA TG
C - AT C

GAM7776 246 EREG 1 17956 NP_001423.1 3 2043 CTCTGTTGCCCA 3 C b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTTGGACCCGTT

GAM7776 246 EVC 1 18115 NP_055371.1 3 2225 CACTTTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 EVC 1 18115 NP_714928.1 3 2225 CACTTTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 EVI5 2 7219 NP_005656.2 3 516 GTTTGTCACCCA T CA 3 C c b
GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGTGTG GTG CGTGAGGTCGGACCC
T AC

GAM7776 246 EVI5 2 11607 NP_005656.2 3 2217 TCACTGCACTCA - - 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG G GCA
GTGGTACG GTGACGTGAGGTCGGAC C CGT
T A

GAM7776 246 EZH1 1 14083 NP_001982.2 3 288 GAAGCGAGCACA G G A 3 C c c
GGCTGGGGTGGA CATT CACTCCAGCCTG GC
TGACTTAT GTAG GTGGGGTCGGAC CG
- A A

GAM7776 246 F11R 1 2664 NP_058642.1 3 2148 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 F11R 1 2664 NP_653085.1 3 2148 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 F11R 1 2664 NP_653086.1 3 2150 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 F11R 1 2664 NP_653087.1 3 2150 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 F2RL3 1 4234 NP_003941.1 3 3005 CGCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 F3 1 18492 NP_001984.1 3 424 CTCTGTTGCCCA C----- 3 C c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCACG TGACGTGAGGTCGGACCCGTT
GCACGA
GAM7776 246 F5 1 7269 NP_000121.1 5 47 AAGCGCTGCCCA TG -- 3 C c c
GGTCCTGGGGTG CAT CACTCCAG CCTGGGCA
GTGGCAGC GTG GTGGGGTC GGACCCGT
-- CT
GAM7776 246 FABP2 1 2195 NP_000125.1 3 371 CTCTTTCACTCA C CA 3 C c c
GGCTGGAATGTA CATTGCA TCCAGCCTGGG
GTGGAGAG GTGATGT AGGTCGGACTC
A AC
GAM7776 246 FANCE 1 5597 NP_068741.1 3 280 CTCTGTCATCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGATGCG GTGACGTGAGGTCGGACCT
AC
GAM7776 246 FANCF 1 5816 NP_073562.1 3 738 CTCTGTCACCCA C CA 3 C c c
GTCTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGTG GTGACGTGAGGTC GACCC
T AC
GAM7776 246 FAT3 1 8236 XP_061871.5 3 1359 CTCTGTCACCCA C CA 3 C c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCATG GTAACGTGAG TCGGACCC
A AC
GAM7776 246 FBXW8 1 11845 NP_036306.1 3 1498 TCACCTAGACTA C GCA 3 C c
c
GACTGGAGTGCA CATTGCACTCCAG CTGG
ATGGCCTG GTAACGTGAGGTC GATC
A AGA
GAM7776 246 FBXW8 1 11845 NP_699179.2 3 1498 TCACCTAGACTA C GCA 3 C c
c
GACTGGAGTGCA CATTGCACTCCAG CTGG
ATGGCCTG GTAACGTGAGGTC GATC
A AGA
GAM7776 246 FCAR 3 3819 NP_001991.1 3 158 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGAGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FCAR 3 10448 NP_579803.1 3 158 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC

GAM7776 246 FCAR 3 10448 NP_579805.1 3 158 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM7776 246 FCAR 3 10448 NP_579806.1 3 158 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM7776 246 FCAR 3 10448 NP_579807.1 3 158 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM7776 246 FCAR 3 10448 NP_579808.1 3 282 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM7776 246 FCAR 3 10448 NP_579811.1 3 158 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM7776 246 FCAR 3 10448 NP_579812.1 3 158 CTCTGTCACCCA C CA 3 C c c
GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGAGCA GTGACGTGA GTCGGACCC
A AC
GAM7776 246 FCAR 3 17643 NP_579813.1 3 243 CTCTTTCGCCAA G A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGCACG GTGACGTGAGGTCGGA CCG
A C
GAM7776 246 FCAR 3 17643 NP_579814.1 3 243 CTCTTTCGCCAA G A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
GTGGCACG GTGACGTGAGGTCGGA CCG
A C
GAM7776 246 FCGR2A 1 497 NP_067674.1 3 523 ATCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCT GTGACGTGAGGTCGGACCC
AT
GAM7776 246 FER1L4 1 11291 XP_300246.1 3 222 CTCTGTCTCCCA CA 3 C c c
GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTTGGACCC
TC
GAM7776 246 FER1L4 1 11291 XP_300246.1 3 371 CTCTGTCTCCCA CA 3 C c c
GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTTGGACCC
TC
GAM7776 246 FEZ1 1 5204 NP_072043.1 3 826 TTCTATCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCACA GTAACGTGAGGTCGGACCCG
C
GAM7776 246 FGF5 1 14382 NP_004455.1 3 2381 GCTCTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA

GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 FGF5 1 14382 NP_149134.1 3 2712 GCTCTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 FHL2 1 16589 NP_001441.2 5 449 CTTTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FISH 1 13261 NP_055446.1 5 209 CTCTGTTGCTCA C 3 C b b
GGCTGGATTGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACTCGTT
T
GAM7776 246 FKBP9 1 7851 NP_009201.1 3 805 CGTTTGTCGCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
GTGGTGCC GTGACGTGAGGTCGGACC TGTT
GC
GAM7776 246 FLJ0000 1 14844 XP_088525.2 3 1654 AGGGGGCTGCCA - CT G 3 C c
c
1 GGCTGGCTGCCG CATTG CA CCAGCCTGG CA
ATGCTCCG GTAGC GT GGTCGGACC GT
C C- -
GAM7776 246 FLJ0006 1 11528 XP_028154.1 5 30 CTCTGTCACCCA CA 3 C c c
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ1010 1 9189 NP_078994.1 3 253 CTGTGTGGCCCA A 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
G
GAM7776 246 FLJ1023 1 19236 NP_060503.1 3 795 CTCTGTCACCCA CA 3 C c c
2 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
ATGGCGCG GTAGCGTGAGGTCGGACCC
AC
GAM7776 246 FLJ1029 1 2615 NP_060520.2 3 183 CTTTGTTGCCCA C----- 3 C c c
8 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCACG TGACGTGAGGTCGGACCCGTT
GCACGA
GAM7776 246 FLJ1034 1 19219 NP_060535.1 5 100 CTCTGTCTCCCA C CA 3 C c c
6 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGCACG GTGACGTGA GTCGGACCC
A TC
GAM7776 246 FLJ1052 1 4272 NP_060594.2 3 1711 AGTGGTTGCCCA C- CCA 3 C c
c
0 GGCCTAGTTTCA CATTG ACT GCCTGGGCAA
GTGGCAGA GTGAC TGA CGGACCCGTT
TT TC-
GAM7776 246 FLJ1053 1 9543 NP_060599.1 3 806 CTCTGTCACCCA CA 3 C c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ1056 1 15591 NP_060608.1 3 190 TTCTGTCGCCCA T A 3 C c c
0 GGCTGGCGTGCA CATTGCAC CCAGCCTGGGC
GTGGCGCG GTGACGTG GGTCGGACCCG
C C
GAM7776 246 FLJ1071 1 7909 NP_060659.1 3 360 CACTGTTGCCCA 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ1084 1 11528 NP_060711.1 3 352 CTCTGTCACCCA CA 3 C c c
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ1084 1 19357 NP_060712.2 3 490 CTCTGTCATGCA --- 3 C b b
7 GGCTGGAGTGCG CATTGCACTCCAGCCTG GGCA
GTGGTGCG GTGGCGTGAGGTCGGAC CTGT
GTA
GAM7776 246 FLJ1092 1 18818 NP_060743.1 3 2051 GCTTGTTGCCCA C 3 C b b
2 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
ATGGCGTG GTAACGT AGGTCGGACCCGTT
A
GAM7776 246 FLJ1132 1 2044 NP_060860.1 3 97 TCTCGTTGCCGA C----- G 3 C c c
3 GGCTGGAGTGTA ATTGCACTCCAGCCT GGCAA
GTAGTGTG TGATGTGAGGTCGGA CCGTT
GTGTGA G
GAM7776 246 FLJ1146 1 834 NP_079239.2 3 145 TCCTGTCACCCA C CA 3 C c c
7 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 FLJ1171 1 9688 NP_079122.1 3 1011 CTCTGTCTCCCA CA 3 C c c
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 FLJ1171 1 3305 NP_078840.1 3 898 CACCGTTGCCCA A 3 C b b
5 GGCTGGAGGGCA CATTGC CTCCAGCCTGGGCAA
GTGACGTG GTGACG GAGGTCGGACCCGTT
G
GAM7776 246 FLJ1180 1 10847 NP_079250.1 3 1242 CACTGTCACCCA A CA 3 C c c

0 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
C AC
GAM7776 246 FLJ1207 1 8886 NP_079463.2 3 158 AGGTTGGGCTCA TT T A 3 C c c
6 GGCTGGGTGCTC CA GCAC CCAGCCTGGGC
TGCCATGG GT CGTG GGTCGGACTCG
CT - G
GAM7776 246 FLJ1236 1 17722 NP_115543.1 3 51 CACCGTCCCCCA T CA 3 C c c
3 GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
GTGGCGTG GTG CGTGAGGTCGGACCC

C CC
GAM7776 246 FLJ1257 1 17515 NP_075056.2 5 117 CTCTGTCACCCA C CA 3 C c c
2 GGCTGGAGTATA CATTG ACTCCAGCCTGGG
GTGGTGTG GTGAT TGAGGTCGGACCC
A AC
GAM7776 246 FLJ1258 1 10410 NP_078896.2 5 38 CTGTCTCACCCA CA 3 C c c
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ1264 1 3686 XP_291344.1 3 951 CTCTGTTGCCCA C 3 C b b
9 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
A
GAM7776 246 FLJ1268 1 3324 NP_079193.2 3 212 CACTCTTGCCCA T 3 C b b
7 GGCTGGGGTGTC CAT GCACTCCAGCCTGGGCAA
GTGGCGTG GTG TGTGGGGTCGGACCCGTT
C
GAM7776 246 FLJ1274 1 10683 XP_290972.1 3 2540 TCTTGTCACCCA CA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ1278 1 14839 NP_115551.1 3 1020 CTTTATCGCCCA C A 3 C c c
7 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGATGCA GTGAC TGAGGTCGGACCCG
A C
GAM7776 246 FLJ1280 1 4261 NP_075054.1 3 1087 ACTGGCTGCCCA ACTC 3 C c
c
0 GGCTGAATGGCA CATTGC CAGCCTGGGCA
GTGCCTGG GTGACG GTCGGACCCGT
GTAA
GAM7776 246 FLJ1288 1 17723 NP_079221.1 3 241 CTCTGTTGCCCA C 3 C b b
8 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCATG GTGACGTGAG TCGGACCCGTT
A
GAM7776 246 FLJ1290 1 10224 NP_073590.1 3 1559 TGTTGTTGCCCA 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ1296 1 11523 NP_078914.1 3 1535 CTCTGTCGCCCA A 3 C b b
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ1297 1 5230 NP_079184.1 3 294 TCTTGTTGCCCA C----- 3 C b b
3 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCG TAACGTGAGGTCGGACCCGTT
GCGCGA
GAM7776 246 FLJ1297 1 2409 NP_079085.2 3 355 CTCTGTCACCCA CA 3 C c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCACAA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 FLJ1298 1 6037 XP_290685.1 3 1798 AAACCAAGCCCA A A A 3 C c c
6 GGCCGGGGGCGG CATTGC CTCC GCCTGGGC
TGGCTCAC GTGGCG GGGG CGGACCCG
- C A
GAM7776 246 FLJ1307 2 2223 XP_117117.2 3 698 CTCTGTCGGCCA --- 3 C b b
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
GGC
GAM7776 246 FLJ1307 2 13729 XP_117117.2 3 2202 GGAGTGTGCCCA T CTCCA 3 C c
b
2 GGTCACTGCTAT CAT GCA GCCTGGGCA
GGCCTTCG GTA CGT TGGACCCGT
T CAC--
GAM7776 246 FLJ1311 1 11919 NP_078817.1 3 610 CTCTGTCGCCCA C A 3 C c c
4 GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGTG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 FLJ1319 1 8231 NP_078890.1 3 403 CTCTGTTGCCCA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ1335 2 10493 NP_078868.1 3 519 CAAAATAATAAC T GGCA 3 C c
c
2 AGGCTGGGTGCA CATTGCAC CCAGCCTG
ATGGCTCA GTAACGTG GGTCGGAC
- AATA
GAM7776 246 FLJ1335 2 13318 NP_078868.1 3 519 AAAATAATAACA T GGCA 3 C c
c
2 GGCTGGGTGCAA CATTGCAC CCAGCCTG
TGGCTCAC GTAACGTG GGTCGGAC
- AATA
GAM7776 246 FLJ1345 1 8163 XP_038291.5 3 2588 CTCTGTCGCCCA C A 3 C c c
6 AGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCACA GTGACGTGAGGTCG ACCCG
A C
GAM7776 246 FLJ1391 1 7691 NP_073617.1 3 1668 GGGATTGGCCCA T- C A 3 C c c

0 GCTTGGAGTGCT CAT GCACTCCAG CTGGGC
TGTGTGGT GTG CGTGAGGTT GACCCG
TT C G
GAM7776 246 FLJ1398 2 4819 NP_079046.1 3 897 ATACAAGTTGTT CCA G 3 C c c
4 AGGCCAGGTGCA CATTGCACT GCCTGG CAA
ATGGCTCG GTAACGTGG CGGATT GTT
AC- -
GAM7776 246 FLJ1398 2 10809 NP_079046.1 5 245 CTCTGTCACCTA CA 3 C c c
4 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGATCC
AC
GAM7776 246 FLJ1410 1 12143 NP_079301.1 3 386 TCCTGCCGCCCA T A -- A 3 C c c

0 GGCCTTGGAGGT CA TGC CTCCA GCCTGGGC
ACTGCTGC GT ATG GAGGT CGGACCCG
C - TC C
GAM7776 246 FLJ1426 1 921 NP_079303.2 3 414 TGTTTTGCATCA GC-- C - 3 C c c
0 AGCTGGAGTACT CATT ACTCCAGC TGG GCAA
GGATGGAA GTAG TGAGGTCG ACT CGTT
GTCA A A
GAM7776 246 FLJ1435 1 8586 NP_079008.1 3 317 CTTTGTCGCCCA A 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCAGT GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ1444 1 16259 NP_116174.1 3 2236 CTCTGTTACCCA C CA 3 C c c
2 GGCTAGAGTGTA CATTGCACTC AGCCTGGG
GTGGCATG GTGATGTGAG TCGGACCC
A AT
GAM7776 246 FLJ1480 1 939 NP_116231.1 3 437 TCTGTCAACGCA C ---- 3 C c c
3 GACTGGAGTGCA CATTGCACTCCAG CTG GGCA
GTGGCACG GTGACGTGAGGTC GAC CTGT
A GCAA
GAM7776 246 FLJ1495 1 13527 NP_116255.1 3 572 TCTTGTTGCCGA G 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
ATGGCGCA GTAACGTGAGGTCGGA CCGTT
G
GAM7776 246 FLJ2004 1 12557 NP_060108.1 3 132 CTTTGTTTCCCA CA 3 C c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
TT
GAM7776 246 FLJ2007 1 7530 NP_060122.1 3 626 CTGAAGAAGTGC CAGCCT 3 C c
c
0 CTTTTGAGTGCA CATTGCACTC GGGCA
ATGAATGT GTAACGTGAG TCCGT
TTT---
GAM7776 246 FLJ2007 1 14265 NP_060126.1 3 2037 TCTTGTTGCCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTATG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 FLJ2009 1 7385 NP_060136.1 3 1358 CTCTGTCACCCA CA 3 C c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ2013 1 4536 NP_060154.1 3 461 CTCTGTCGCCCA C A 3 C c c
6 GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 FLJ2014 1 2624 NP_060157.1 3 399 CTGTGTTGCCCA CA----- C 3 C c c
7 GGCTAGAGTGCA TTGCACTC AGCCTGGGCAA
GCAGTGAC GACGTGAG TCGGACCCGTT
CAGTGAC A
GAM7776 246 FLJ2024 2 5275 NP_060193.1 3 2299 TCTTGTTGCCCA 3 C b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGACACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ2024 2 8581 NP_060193.1 3 542 TCAGGAGCTCAA TT - A 3 C c b
5 GGCTGGAGTGTC CA GCACTCCAGCCT GGGC
TTGACAGT GT TGTGAGGTCGGA CTCG
TC A A
GAM7776 246 FLJ2025 1 7206 NP_062552.1 3 257 CCCAGCCTCCCA T AC CA 3 C c
c
7 GGCTGGATGGCA CAT GC TCCAGCCTGGG
TGGACTGT GTA CG AGGTCGGACCC
- GT TC
GAM7776 246 FLJ2034 1 4079 NP_060246.1 3 705 CTCTGTCATCCA CC CA 3 C c c
4 AACTGGAGTGCA CATTGCACTCCAG TGGG
GTGGCACA GTGACGTGAGGTC ACCT
AA AC
GAM7776 246 FLJ2035 1 11024 NP_060251.1 3 284 GCCGAGGGCCCA TCCA- A 3 C c
c
9 GGCCCTGTGTGC CATTGCAC GCCTGGGC
GGTGCCCA GTGGCGTG CGGACCCG
TGTCC G
GAM7776 246 FLJ2037 1 9357 NP_060264.2 3 181 CATGCCTCCTAA T AGC ---- 3 C c c

5 GAGAGGAGTGCA CA TGCACTCC CT GGGCA
TTGCTTTA GT ACGTGAGG GA TCCGT
T AGA ATCC
GAM7776 246 FLJ2051 1 17759 NP_060323.1 3 676 TCTTGTCACCCA CA 3 C c c
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ2052 1 17075 NP_060333.1 5 132 AAGCGGTGCCCA - - - A 3 C c c
7 GGCCGGTGGTGA CA TTG CACT CC GCCTGGGCA
CAACTGGG GT AAC GTGG GG CGGACCCGT
C A T C
GAM7776 246 FLJ2067 2 13041 NP_060394.1 3 632 GTTGTCACTTAA C G---- 3 C c b
1 GTTTGGAGTGCA CATTGCACTCCAG CT GGCAA
GTGGCATG GTGACGTGAGGTT GA CTGTT
T ATTCA
GAM7776 246 FLJ2067 2 16491 NP_060394.1 3 1539 GTCTGTTGCCCA 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ2070 1 18943 NP_060402.1 3 424 CTCTCTCGCCCA A 3 C b b
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ2081 1 10574 NP_060431.1 3 96 CTCTTTCACCCA CA 3 C c c
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 FLJ2112 1 17516 NP_079359.2 3 1349 TGTGTCTGCCCA - ACT- 3 C c c
8 GGCTGGCTGAGC CATT GC CCAGCCTGGGCA
GGGTGGAT GTGG CG GGTCGGACCCGT
G AGTC
GAM7776 246 FLJ2160 1 15047 NP_079038.1 3 482 CTCTGTCACCCA C CA 3 C c c
3 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATA GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 FLJ2167 1 1435 NP_112160.1 5 802 TTCTGTCACCTA CA 3 C c c
3 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGACATG GTGATGTGAGGTCGGATCC
AC
GAM7776 246 FLJ2177 1 4203 NP_115585.1 3 785 TTGTGTCACCCA CA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCA GTAACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ2232 1 9543 NP_078932.2 3 528 CTCTGTCACCCA CA 3 C c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ2253 1 5636 NP_078926.2 5 342 CTCTGTTACCCA A CA 3 C c c
1 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCGCA GTGACGTGAGG CGGACCC
C AT
GAM7776 246 FLJ2279 1 5559 NP_071357.1 3 256 CTCTGTCGCCTG C TG A 3 C c c
4 GGCTGGAGTACA CATTG ACTCCAGCC GGC
GTGGTGCG GTGAC TGAGGTCGG CCG
A GT C
GAM7776 246 FLJ2296 1 2808 NP_071384.1 3 232 CTCTTTCGCCCA G A 3 C c c
5 GGATGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGTGCG GTGACGTGAGGT GGACCCG
A C
GAM7776 246 FLJ2302 1 9682 NP_079212.1 3 330 CTCTGTCTCCCA C CA 3 C c c
4 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACA GTAACGTGAG TCGGACCC
A TC
GAM7776 246 FLJ2305 1 8693 NP_075058.1 3 212 CTCTATTGCCCA 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCTCA GTGACGTGAGGTCGGACCCGTT
GAM7776 246 FLJ2318 1 1340 NP_078892.1 3 368 GTTCTGTCGCTT C A 3 C c c
6 AGCTGGAGTGCG CATTGCACTCCAGC TGGGC
GTGGCGTG GTGGCGTGAGGTCG ATTCG
- C
GAM7776 246 FLJ2326 1 11523 NP_079391.1 5 182 CTCTGTCGCCCA A 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 FLJ2335 1 12273 NP_115613.1 3 241 CTCTGTTGCTGA G 3 C b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
GTGATGTG GTGACGTGAGGTCGGA TCGTT
G
GAM7776 246 FLJ2339 3 5554 NP_079060.1 3 607 CTCTGTCCCCCA CA 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
CC
GAM7776 246 FLJ2339 3 9148 NP_079060.1 3 197 CTCTGTCACCCA C CA 3 C c c
2 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCGCG GTGACGTGAGGTC GACCC
A AC
GAM7776 246 FLJ2339 3 20052 NP_079060.1 3 497 CTCTGTCACTGA G CA 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCT GG
GTGGCGCA GTGACGTGAGGTCGGA TC
G AC
GAM7776 246 FLJ2341 1 2152 NP_115614.1 3 1323 CTCTGTTGCCCA 3 C b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ2355 1 17969 NP_079156.1 3 425 CTCTGTCGCCCA A 3 C b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ2356 1 15048 XP_041701.4 3 1724 TCTTGTTGCCCA C 3 C b b
3 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCACA GTAACGTGAG TCGGACCCGTT
A
GAM7776 246 FLJ2386 1 1374 NP_689875.1 3 1366 GGTGGGGGTCCA -- A- A 3 C c c

7 GGCTGGAGGGGC CATT GC CTCCAGCCTGGGC
CCAATGTA GTAA CG GAGGTCGGACCTG
CC GG G
GAM7776 246 FLJ2541 1 16915 NP_659455.2 5 107 CTCTGTCACCCA T CA 3 C c c
6 GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
ATGGCATC GTA CGTGAGGTCGGACCC
C AC
GAM7776 246 FLJ2579 1 934 NP_689633.1 3 563 CTCTGTCTCCCA A CA 3 C c c
5 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACG GTGACGTGAGG CGGACCC
C TC
GAM7776 246 FLJ3050 1 17957 NP_694555.1 5 68 CCCTGTTGCCCA CAC 3 C c c
7 GGCTGGAATACA CATTG TCCAGCCTGGGCAA
GTGGCACG GTGAC AGGTCGGACCCGTT
ATA
GAM7776 246 FLJ3053 1 19834 NP_653325.1 3 191 TCTTGTTGCCCA C 3 C b b
2 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGTATG GTGAC TGAGGTCGGACCCGTT
A
GAM7776 246 FLJ3113 3 3952 NP_775928.1 3 691 TCTTGTCACCCA A CA 3 C c b

9 GGCAGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCGTT GTGACGTGAGG CGGACCC
A AC
GAM7776 246 FLJ3113 3 15200 NP_775928.1 5 145 CTCTCTGGCCCA C A 3 C c b
9 AGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCACG GTGACGTGAGGTCG ACCCG
A G
GAM7776 246 FLJ3113 3 18868 NP_775928.1 3 397 TCTTGTTGCCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3115 1 7373 NP_653201.1 3 275 CTCTGTCACCCA C CA 3 C c c
3 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCACG GTGACGTGAGGTC GACCC
A AC
GAM7776 246 FLJ3116 1 19301 NP_694567.1 3 1140 TCTTGTAGCCCA CT A 3 C c c

6 GGCTGGGATGCA CATTGCA CCAGCCTGGGC
ATGGCATG GTAACGT GGTCGGACCCG
AG A
GAM7776 246 FLJ3133 1 1672 NP_689682.1 3 268 TCTTGTTGCCCA C 3 C b b
8 CGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGTGCA GTAACGTGAGGTCG ACCCGTT
C
GAM7776 246 FLJ3138 1 14326 NP_689685.1 3 927 TCTTGCTGCCCA C 3 C b b
4 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCA
ATGGTGCG GTAACGTGAG TCGGACCCGT
A
GAM7776 246 FLJ3139 1 9670 NP_694569.1 5 140 CTTTGTTGCCCA TT 3 C b b
3 GGCTGGAGTGCC CA GCACTCCAGCCTGGGCAA
TTGGCGCG GT CGTGAGGTCGGACCCGTT
TC
GAM7776 246 FLJ3140 1 16543 NP_689877.1 3 351 CTCTGTTGGCCA G 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGTTCGA GTGACGTGAGGTCGGACC GTT
G
GAM7776 246 FLJ3209 2 1025 NP_776156.1 3 1416 CTTTGTTGCCCA 3 C b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3209 2 16043 NP_776156.1 3 1113 CTCTGTTGCCCA 3 C b b
6 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAATGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3213 3 2061 NP_689671.2 3 1143 CTCTGTTGCCTG TG 3 C b b
0 GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGGCCCA GTGACGTGAGGTCGG CCGTT
GT
GAM7776 246 FLJ3213 3 4630 NP_689671.2 3 1440 TCTTGTTGCCCA C 3 C b b
0 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA

ATGGCATG GTAACGTGAG TCGGACCCGTT
A

GAM7776 246 FLJ3213 3 15049 NP_689671.2 3 519 CTCTGTCGCCCA A 3 C b b
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 FLJ3220 1 3860 NP_689710.1 3 41 CTCTGTCGCCCA A A 3 C c c
6 GGCTGGAGGGCA CATTGC CTCCAGCCTGGGC
GTGGCGTG GTGACG GAGGTCGGACCCG
G C

GAM7776 246 FLJ3233 1 8493 NP_653166.1 3 1145 TCTCCTGGCCCA T A - - A 3 C c c
4 GGCCTGGCGGGC CA TGC CT CCAG CCTGGGC
ACTGCTTC GT ACG GG GGTC GGACCCG
C - C C G

GAM7776 246 FLJ3249 1 4681 NP_653208.1 3 744 CTCTGTCACCCA C CA 3 C c c
9 GTCTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCAAA GTGACGTGAGGTC GACCC
T AC

GAM7776 246 FLJ3273 1 16099 NP_689632.1 3 733 AGCCGCTGCCCA T - AG 3 C c c
1 GGGGAGTGGCTG CAT GC ACTCC CCTGGGCA
TGGGGAGG GTG CG TGAGG GGACCCGT
T G --

GAM7776 246 FLJ3280 1 1856 NP_694584.1 3 643 CTCTGTCACCCA CA 3 C c c
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGAA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 FLJ3286 1 2146 NP_653214.1 3 1248 TCTTGTCACCCA C CA 3 C c c
5 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
ATGATGCG GTAAC TGAGGTCGGACCC
A AC

GAM7776 246 FLJ3289 1 7467 NP_653268.1 3 705 CTCTGTTGTCCA CA----- 3 C c c
4 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGATATG GACGTGAGGTCGGACCTGTT
GTATAGC

GAM7776 246 FLJ3293 1 9555 NP_690873.1 3 604 CTCTGTCACCCA CA 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCTGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 FLJ3350 1 13693 NP_689530.1 3 741 CACTGTTGCCCA 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3365 1 16113 NP_775912.1 3 326 CTCTGTTGCCCA T 3 C b b
5 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCTTG GT ACGTGAGGTCGGACCCGTT
C

GAM7776 246 FLJ3481 2 4004 NP_689516.1 5 271 CCGCTGGTCCCA T C - A 3 C c c
7 GGCTGGATTGCC CAT GCA TCCAGCCTGGG C
GTGGCACA GTG CGT AGGTCGGACCC G

C T T G

GAM7776 246 FLJ3481 2 7075 NP_689516.1 3 208 GTCTGCCACCCA C CA 3 C c c
7 GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGCGTG GTGAC TGAGGTCGGACCC
C AC

GAM7776 246 FLJ3492 1 18132 NP_689483.1 5 153 CTTTGACCCCCA CA 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
CC

GAM7776 246 FLJ3496 1 581 XP_114353.1 3 1548 TCTTGTTGCCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3510 1 18938 NP_689890.1 5 161 CTCTGTCGTCCA T A 3 C c c
5 GGCTGGAGTGCC CAT GCACTCCAGCCTGGGC
GTGGCGTA GTG CGTGAGGTCGGACCTG
C C

GAM7776 246 FLJ3568 2 1653 NP_787096.1 3 1370 CTCTGTTGCCCA CAC 3 C c c
1 GGCTGGACTACA CATTG TCCAGCCTGGGCAA
GTGGCACA GTGAC AGGTCGGACCCGTT
ATC

GAM7776 246 FLJ3568 2 11521 NP_787096.1 3 1071 CTCTGTCACCCA C CA 3 C c c
1 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGCACA GTGACGTGAGGTC GACCC
A AC

GAM7776 246 FLJ3584 1 14986 XP_290755.1 3 1062 CTTTGTCACCCA C CA 3 C c c
8 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCATG GTGACGTGAG TCGGACCC
A AC

GAM7776 246 FLJ3644 1 2147 NP_694965.1 3 231 CTCTGTCACCCA CA 3 C c c
5 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGATGTGAGGTCGGACCC
AC

GAM7776 246 FLJ3704 1 9497 NP_787085.1 3 765 CTCTGTCGCCCA C A 3 C c c
5 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGTGCG GTGAC TGAGGTCGGACCCG
A C

GAM7776 246 FLJ3707 1 11528 NP_694588.1 5 43 CTCTGTCACCCA CA 3 C c c
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 FLJ3743 1 8582 NP_848612.1 3 198 CTCTGTTACCCA CA 3 C c c
3 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCC GTGATGTGAGGTCGGACCC
AT

GAM7776 246 FLJ3754 1 5495 NP_775938.1 3 744 CTCTGTTGCCCA 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATT GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3810 1 5589 NP_694993.2 3 742 GCTCTGTTGCCA A G 3 C b b
1 GGCTGGAGGGCA CATTGC CTCCAGCCTGG CAA
GTGGCACG GTGACG GAGGTCGGACC GTT
G -
GAM7776 246 FLJ3814 3 9373 XP_091919.5 3 259 CTCTGTCTCCCA CA 3 C c b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGAGTG GTGACGTGAGGTCGGACCC
TC
GAM7776 246 FLJ3814 3 15044 XP_091919.5 3 1432 CTCTGTTGCCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3814 3 18971 XP_091919.5 5 26 CTCTATTGCCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FLJ3828 2 6885 NP_689814.1 3 109 CTCTGTTGCCCT C----- T 3 C c b
1 GGCTGGAGTGCA ATTGCACTCCAGCC GGGCAA
GTAGAGTG TGACGTGAGGTCGG CCCGTT
GTGAGA T
GAM7776 246 FLJ3828 2 9492 NP_689814.1 3 1966 CTCTGTCGCCCA A 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ3860 2 7382 NP_689867.1 3 288 CTCTGTCGCCCA A 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ3860 2 16688 NP_689867.1 3 544 CTCTGTCACCCA CA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ3879 1 14861 NP_848615.1 3 1162 CTCTGTCACCCA CA 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ3881 2 9791 NP_665872.1 3 1041 CTCTGTCACTCA C CA 3 C c c
9 TGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCGTG GTGACGTGAGGTCG ACTC
T AC
GAM7776 246 FLJ3881 2 18642 NP_665872.1 3 214 GTCTCTTACCCA C CA 3 C c c
9 GGCTAGGGTGCA CATTGCACTC AGCCTGGG
GTGGTGTG GTGACGTGGG TCGGACCC
A AT
GAM7776 246 FLJ3899 2 10356 NP_776188.1 3 1037 CTCTGTCACCTA CA 3 C c c
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGATCC
AC
GAM7776 246 FLJ3899 2 14236 NP_776188.1 3 731 CTGTGTCACCCA CA 3 C c c

1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ3941 1 11673 NP_775952.1 3 342 GTCTTTCACCCA CA 3 C c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGCTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ3959 2 8232 NP_776164.1 3 1104 CTCTGTCACCCA CA 3 C c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FLJ3959 2 16001 NP_776164.1 3 627 TGCTGTCTCCCC A T CA 3 C c c

9 GGCTGGAGCGCA CATTGC CTCCAGCC GGG
GTGGCACG GTGACG GAGGTCGG CCC
C C TC
GAM7776 246 FLJ3963 1 9190 XP_290687.1 3 682 CTCTGTCGTCCA A 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGAGGTCGGACCTG
C
GAM7776 246 FLJ9023 1 10357 NP_775852.1 3 74 CTTTGTCGCCCA A 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FLJ9072 1 19889 NP_787115.1 3 525 CTCTGTCGCCCA A 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGCCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 FNBP1 1 16354 XP_052666.3 3 1012 CTCTATTGTTCA C 3 C b b
GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATG GTGACGTGAGGTC GACTTGTT
A
GAM7776 246 FOXE2 1 15626 NP_036317.1 5 631 AAGCTGCGTCCG T AC A 3 C c
c
GGCTGGAGCACT CA TGC TCCAGCCTGGGC
GGAACCCG GT ACG AGGTCGGGCCTG
C -- C
GAM7776 246 FOXO1A 1 736 NP_002006.2 3 13 AGCTGGGTGTCA C G 3 C c c
GGCTGGGGTTAG CATTG ACTCCAGCCTGG CA
TGAGCAGG GTGAT TGGGGTCGGACT GT
- -
GAM7776 246 FSHPRH1 1 11528 NP_006724.1 5 15 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 FUT1 2 11525 NP_000139.1 3 613 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 FUT1 2 16365 NP_000139.1 3 935 CTCTGTAGCCCA CA A 3 C c b

GGCCAGAGTGCA CATTGCACTC GCCTGGGC
GTGGCGCG GTGACGTGAG CGGACCCG
AC A

GAM7776 246 FZD4 1 4487 NP_036325.2 3 3982 CTCTGTCACCCA A CA 3 C c c
GGCTGGGGCGCA CATTGC CTCCAGCCTGGG
ATGGCACG GTAACG GGGGTCGGACCC
C AC

GAM7776 246 G2A 1 8714 NP_037477.1 3 1257 CTCTGTTGCCTG CA TG 3 C c c
GGCTGGAGAACA CATTG CTCCAGCC GGCAA
GTGGCACC GTGAC GAGGTCGG CCGTT
AA GT

GAM7776 246 G6PC 1 4204 NP_000142.1 3 1429 ACCTATCACCCA G CA 3 C c c
GGCTGGAGTGGA CATT CACTCCAGCCTGGG
GTGGCACG GTGA GTGAGGTCGGACCC
G AC

GAM7776 246 GAL3ST-4 1 4518 NP_078913.3 3 252 CTCTGTCCCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC

GAM7776 246 GATA2 1 16014 NP_116027.2 3 225 GACTGCTGCCCA T ----- G 3 C c c
GGTGGGGTTTCC CAT GC ACTCCA CCTGGGCA
TGCATGGA GTA CG TGGGGT GGACCCGT
- TCCTT -

GAM7776 246 GGA2 2 5631 NP_055859.1 3 1712 CTCTGTCACTCA CA 3 C c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTATA GTGGCGTGAGGTCGGACTC
AC

GAM7776 246 GGA2 2 5631 NP_619581.1 3 2800 CTCTGTCACTCA CA 3 C c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTATA GTGGCGTGAGGTCGGACTC
AC

GAM7776 246 GGA2 2 6391 NP_055859.1 5 66 CCGCAGCGTCGG AC G A 3 C c c
GGCTGGAGCGAT CATTGC TCCAGCCT GGC
GGCGGCGA GTAGCG AGGTCGGG CTG
-- G C

GAM7776 246 GGA2 2 6391 NP_619581.1 5 66 CCGCAGCGTCGG AC G A 3 C c c
GGCTGGAGCGAT CATTGC TCCAGCCT GGC
GGCGGCGA GTAGCG AGGTCGGG CTG
-- G C

GAM7776 246 GM2A 1 11286 NP_000396.1 3 761 GCTTTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
GTGGTGCA GTGACGTGAGGTCGGACC TGTT
AC

GAM7776 246 GNE 1 8367 NP_005467.1 3 618 GCATGAACCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTCA GTGACGTGAGGTCGGACCC
CA

GAM7776 246 GNG4 1 559 NP_004476.1 3 608 CTCTGTCACCCA CA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 GNPNAT1 1 8464 XP_085119.1 3 2471 CTCCATCACCCA C CA 3 C c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGTGTG GTGAC TGAGGTCGGACCC
C AC
GAM7776 246 GNRPX 1 12243 NP_060519.1 3 147 CTGTGTTGCCCA C 3 C b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGTGCC GTGACGTGAG TCGGACCCGTT
A
GAM7776 246 GOLGA3 1 15049 NP_005886.2 3 601 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 GP5 1 5681 NP_004479.1 3 596 CTCTGTGGCCCA T A 3 C c c
GGCTGGCGTGCA CATTGCAC CCAGCCTGGGC
GTGGGCCG GTGACGTG GGTCGGACCCG
C G
GAM7776 246 GPP34R 1 14203 NP_060648.2 3 870 TGCTCTTGCCCA --- A 3 C c c
GGCAGGAGTACA CATTGC ACTCC GCCTGGGCAA
GTAGTGCA GTGATG TGAGG CGGACCCGTT
ACA A
GAM7776 246 GPR26 1 3010 NP_703143.1 3 1152 TCTTATTGCCCA C 3 C b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGTGCG GTAACGTGAG TCGGACCCGTT
A
GAM7776 246 GPR4 1 4965 NP_005273.1 3 280 CTGTGTTGCCCA C----- 3 C c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGTGCA TGACGTGAGGTCGGACCCGTT
ACGTGA
GAM7776 246 GPR56 1 8622 NP_005673.2 5 25 CTCTGTCACACA --- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGTGTG GTGACGTGAGGTCGGAC CTGT
ACA
GAM7776 246 GPR66 1 19237 NP_006047.2 3 530 CTCTGTCGCCCA C A 3 C c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCGCG GTGACGTGAG TCGGACCCG
A C
GAM7776 246 GPR81 1 13260 NP_115943.1 3 375 CTCTGTGTCCCA - 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG CA
GTGGCACA GTGACGTGAGGTCGGACCC GT
T
GAM7776 246 GR6 1 2604 NP_031380.1 5 287 CTCTGTCACCCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCATG GTGACGT AGGTCGGACCC
A AC
GAM7776 246 GRAF 1 4362 NP_055886.1 3 2801 CTCTGTGGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

GTGGCGCG GTGACGTGAGGTCGGACCCG
G
GAM7776 246 GREB1 3 9792 NP_055483.2 3 1722 TCTTGCTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
ATGGTGCA GTAACGTGAGGTCGGACCCGT

GAM7776 246 GREB1 3 11815 NP_055483.2 3 1726 CCCAGGCTGGAG CA 3 C b b

TGCAATGGTGCA CATTGCACTCCAGCCTGGG
ATGATCTC GTAACGTGAGGTCGGACCC
--
GAM7776 246 GREB1 3 14861 NP_055483.2 3 1092 CTCTGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 GRID1 1 17390 XP_043613.8 3 2299 GGGAGGTGCCCA C---- --- T G 3 C c c

GGTGGGTGGACC ATTG CAC CCA CCTGGGCA
AGTACTCC TGAC GTG GGT GGACCCGT
CCTCA CAG - -
GAM7776 246 GRINL1A 1 5433 NP_056347.1 3 713 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCAGG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 GRM6 1 10398 NP_000834.1 3 2444 CTCAATTTCTTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGATTC
TT
GAM7776 246 GRWD 1 7996 NP_113673.2 3 372 GTCTGTCGCCCA C----- A 3 C c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCACG TGACGTGAGGTCGGACCCG
GCACGA C
GAM7776 246 GSDM 1 3199 NP_835465.1 3 296 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 GSDM 1 3199 XP_209009.1 3 294 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 GSTM1 1 12752 NP_000552.2 3 71 GCCTGCTGCCCA - A C-- 3 C c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM7776 246 GSTM1 1 12752 NP_666533.1 3 71 GCCTGCTGCCCA - A C-- 3 C c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM7776 246 GSTM2 1 12752 NP_000839.1 3 71 GCCTGCTGCCCA - A C-- 3 C c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA

CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM7776 246 GSTM4 1 12752 NP_000841.1 3 71 GCCTGCTGCCCA - A C-- 3 C c c
GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM7776 246 GSTM4 1 12752 NP_671490.1 3 358 GCCTGCTGCCCA - A C-- 3 C c c

GGCTGTGCAGCG CA TTGC CT CAGCCTGGGCA
CAGCTGGA GT GACG GA GTCGGACCCGT
C C CGT
GAM7776 246 GTF2E1 1 15661 NP_005504.1 3 306 TCTTGTACCCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
CA
GAM7776 246 GTF2IRD 1 11522 NP_115579.3 3 143 CTCTGTCGCCCA A 3 C b b
2 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTTGGACCCG
C
GAM7776 246 GTF2IRD 1 11522 NP_775808.1 3 143 CTCTGTCGCCCA A 3 C b b
2 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTTGGACCCG
C
GAM7776 246 GTPBG3 2 7812 NP_116009.1 3 467 GTCTATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 GTPBG3 2 10292 NP_116009.1 3 631 CTCTGTCACCCA C CA 3 C c
b
GGCTGGAGTTCA CATTG ACTCCAGCCTGGG
GTGGTGCG GTGAC TGAGGTCGGACCC
T AC
GAM7776 246 GYG 1 4258 NP_004121.2 3 443 TAGAATTGCCCA G --- - 3 C b b
GTGCTGCCAGAG CATT CACTC CAGC CTGGGCAA
TGAGTGAG GTGA GTGAG GTCG GACCCGTT
- ACC T
GAM7776 246 H-plk 1 12753 NP_056936.1 5 982 GCTGTGTCACCA G -- 3 C b b
GGATGGAGTGCA CATTGCACTCCA CCTGG GCA
GTGGCATG GTGACGTGAGGT GGACC TGT
A AC
GAM7776 246 H2AV 1 18864 NP_619541.1 3 585 TCTTGTCACCCA C CA 3 C c c
GACTGGAGTGCG CATTGCACTCCAG CTGGG
ATGGCACG GTAGCGTGAGGTC GACCC
A AC
GAM7776 246 H63 1 4554 NP_612432.2 3 465 TCTTGTTTCCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACA GTAACGTGAGGTCGGACCC
TT
GAM7776 246 H63 1 4554 NP_816929.1 3 465 TCTTGTTTCCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

ATGGCACA GTAACGTGAGGTCGGACCC
TT
GAM7776 246 HAVCR2 1 16260 NP_116171.2 3 497 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 HE9 1 7942 NP_741997.1 3 210 CTCTGTTGCCCA C 3 C b b
GCCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCACA GTAACGTGAGGTC GACCCGTT
C
GAM7776 246 HEPH 1 15338 NP_055614.1 5 130 CTGGCGGACTCA -- CA 3 C c c
GGCTGGGGTCTG CATTGC ACTCCAGCCTGGG
CAGTGCAG GTGACG TGGGGTCGGACTC
TC AG
GAM7776 246 HEXA 1 14035 NP_000511.1 3 270 AGGGCACAGCCA C GCA 3 C c
c
GGCTGGAGTCAG CATTG ACTCCAGCCTGG
TGTCTGCC GTGAC TGAGGTCGGACC
- GAC
GAM7776 246 HLCS 1 2142 NP_000402.2 5 180 TTCTGTCGTCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCTG
C
GAM7776 246 HMG20A 1 5040 NP_060670.1 3 1222 CTGTGTTGCCCA 3 C b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCTAT GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 HPRN 1 12916 NP_071938.1 3 220 TGGCTCTGCCCA G G 3 C c c
GGTGGGGGTGGGG CATT CACTCCA CCTGGGCA
TGGCCCAG GTGG GTGGGGT GGACCCGT
G -
GAM7776 246 HRH4 2 3116 NP_067637.2 3 1950 CTCTGTTGCCCA A C 3 C b b
CGCAGGAGTGCA CATTGCACTCC GC TGGGCAA
GTGGCATG GTGACGTGAGG CG ACCCGTT
A C
GAM7776 246 HRH4 2 18211 NP_067637.2 3 1339 CTGTGTTGCCCA C----- - T C 3 C c b

GCCTGGGTGTCA ATTG CAC CCAG CTGGGCAA
ATAATTAT TAAC GTG GGTC GACCCGTT
TATTAA T - C
GAM7776 246 HRMT1L3 1 18437 NP_062828.2 5 195 CCCAGCTGCCCA GCA AG 3 C
c c
GGACGGGGCAAG CATT CTCC CCTGGGCA
ATGTCCAA GTAG GGGG GGACCCGT
AAC CA
GAM7776 246 HSD3B7 1 2674 NP_079469.2 3 210 CTCTGTCACCCA C CA 3 C c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGTG GTGACGTGAGGTC GACCC
A AC
GAM7776 246 HSMPP8 1 7797 XP_167894.1 3 330 TCTTGTTGCCCA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 HSPA4 1 15189 XP_114482.1 3 1414 GAGTGTTACAGG CC-- - 3 C c c

CTCTAAAGTGCA CATTGCACT AGCCTG GGCA
ATGGAGAA GTAACGTGA TCGGAC TTGT
AATC A
GAM7776 246 HSPC065 2 713 NP_054876.2 3 2293 CTCTGTCCCCCA C CA 3 C c
b

TGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGCATG GTGACGTGAGGTCG ACCC
T CC
GAM7776 246 HSPC065 2 4676 NP_054876.2 3 2126 CTCTGTCCCCAA --- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGGCA
GTGGTGCA GTGACGTGAGGTCGGA CCTGT
ACC
GAM7776 246 HTR1D 1 2563 NP_000855.1 3 290 GCCCTCTCGCCA GCA 3 C c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGG
GTGGCACA GTGATGTGAGGTCGGACC
GCT
GAM7776 246 HUNK 1 17952 NP_055401.1 3 2963 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 HUS1 1 14238 NP_004498.1 3 1024 TTCTGTCACCCA C CA 3 C c c
GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGCCACA GTGACGTGAGGTC GACCC
A AC
GAM7776 246 HYAL4 1 2143 NP_036401.1 5 83 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM7776 246 HYPB 1 14422 NP_036403.1 3 1551 AGAATCCTGAGG -- G CA 3 C c c

ACCTGGAGTGCA CATTGCACTCCAG CCT GG
ATGAGAAT GTAACGTGAGGTC GGA TC
CA G CT
GAM7776 246 ICAM1 1 12075 NP_000192.1 3 1135 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 ICK 1 7385 NP_055735.1 3 1470 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 ICK 1 7385 NP_057597.2 3 1470 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 IGF1 1 6279 NP_000609.1 3 5348 CACTGTCCCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC
GAM7776 246 IGHMBP2 1 17385 NP_002171.1 5 29 TCTAGGGGCCCA A- - A A 3 C c
c
GGCCGGCGGCGG CATTGC CT CC GCCTGGGC
CGATGGCC GTAGCG GG GG CGGACCCG
GC C C G
GAM7776 246 IGLL1 1 4573 NP_064455.1 5 2 GGCCACATGGAC - - - A 3 C c c
TGGGGTGCAATG CATTGCACTCCAG CC TG GGC
GGACAGCT GTAACGTGGGGTC GG AC CCG
A T A G
GAM7776 246 IGLL1 1 4573 NP_690594.1 5 2 GGCCACATGGAC - - - A 3 C c c
TGGGGTGCAATG CATTGCACTCCAG CC TG GGC
GGACAGCT GTAACGTGGGGTC GG AC CCG
A T A G
GAM7776 246 IL11 1 11544 NP_000632.1 3 700 CTCTGTTGCCTA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGAGGCA GTGACGTGAGGTCGGATCCGTT

GAM7776 246 IL12RB1 1 10756 NP_714912.1 3 315 AGTCTGTTGGCA C----- C -- 3 C c c
GACTGGAGTGCA ATTGCACTCCAG CTG GGCA
ATCATGGC TAACGTGAGGTC GAC TTGT
CGGTAC A GG
GAM7776 246 IL16 1 19554 NP_757366.1 5 100 CTCTGTTGCCCA --- 3 C b b
GGCTGGAGTTCA CATTGC ACTCCAGCCTGGGCAA
GCGGTGCA GTGGCG TGAGGTCGGACCCGTT
ACT
GAM7776 246 IL21R 1 498 NP_068570.1 3 1362 TCTCGTCGCCCA C A 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 IL21R 1 498 NP_851564.1 3 1362 TCTCGTCGCCCA C A 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 IL21R 1 498 NP_851565.1 3 1362 TCTCGTCGCCCA C A 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 IL28RA 1 7046 NP_734464.1 3 2268 TCTTTTTGCCTA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM7776 246 IL28RA 1 7046 NP_775087.1 3 2268 TCTTTTTGCCTA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM7776 246 IL28RA 1 7046 NP_775088.1 3 2965 TCTTTTTGCCTA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGATCCGTT

GAM7776 246 IL5RA 1 8557 NP_000555.2 3 453 CATTTTGCATCA TG-- C - 3 C c c
GCCTGGAGTGAA CAT CACTCCAG CTGG GCAA
CCATGAAC GTA GTGAGGTC GACT CGTT
CCAA C A
GAM7776 246 IL5RA 1 8557 NP_783853.1 3 453 CATTTTGCATCA TG-- C - 3 C c c
GCCTGGAGTGAA CAT CACTCCAG CTGG GCAA
CCATGAAC GTA GTGAGGTC GACT CGTT
CCAA C A
GAM7776 246 ILF3 1 17287 NP_036350.2 3 581 GGTGTCTGACCC CCA C-- - 3 C c c
ACCAGCAGTGCA CATTGCACT GC TGGG CA
ATGGGCAG GTAACGTGA CG ACCC GT
--- ACC A
GAM7776 246 IMPACT 1 8975 NP_060909.1 3 2007 CTCTGTCACCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGATCC
AC
GAM7776 246 INHBE 1 16283 NP_113667.1 3 663 GCTCTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGACACG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 INMT 2 9149 NP_006765.3 3 445 CTCTGTCACCCA C CA 3 C c b
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACG GTAACGTGAG TCGGACCC
A AC
GAM7776 246 INMT 2 11523 NP_006765.3 3 622 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 IRF4 2 1517 NP_002451.1 3 1184 CGGGGACTCCCA T A CA 3 C c c
GGCTGGAGAGCA CA TGC CTCCAGCCTGGG
CTGCCAGG GT ACG GAGGTCGGACCC
C A TC
GAM7776 246 IRF4 2 2698 NP_002451.1 3 102 CTCTGTCTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 ITGAX 1 559 NP_000878.1 3 396 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 JAK3 1 18060 NP_000206.1 3 401 GCTCGTTACCCA G CA 3 C c c
GGGTGGAGTGCA CATTGCACTCCA CCTGGG
GTGGTAGC GTGACGTGAGGT GGACCC
G AT
GAM7776 246 JM11 1 10197 NP_296375.1 3 1440 GCTCTGTCACCA CA----- -- 3 C c c
GGCTGGAGTGCA TTGCACTCCAGCCTGG GCA
GCGGCGCA GACGTGAGGTCGGACC TGT

```
                                        ACGCGGC          AC
GAM7776  246  JRK   1  3927  NP_003715.1  3  1242  CTCTGTTGACCA   G       G       3  C  b  b
                                GGCTGGAGTGAA CATT CACTCCAGCCTGG CAA
                                GTGGTGTG    GTGA GTGAGGTCGGACC GTT
                                        A         A
GAM7776  246  KCNJ11  1  15049 NP_000516.2  5  53   CTCTGTCGCCCA          A       3  C  b  b
                                GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                GTGGCGTG    GTGACGTGAGGTCGGACCCG
                                                C
GAM7776  246  KCNJ16  1  2456  NP_061128.1  3  625   GCTACTTGCCCA   --  CCA         3  C  c  c
                                GGTAGTGATCAG CATTG  CACT   GCCTGGGCAA
                                TGAGAGTT    GTGAC  GTGA   TGGACCCGTT
                                        TA   ---
GAM7776  246  KCNJ16  1  2456  NP_733937.1  3  625   GCTACTTGCCCA   --  CCA         3  C  c  c
                                GGTAGTGATCAG CATTG  CACT   GCCTGGGCAA
                                TGAGAGTT    GTGAC  GTGA   TGGACCCGTT
                                        TA   ---
GAM7776  246  KCNJ16  1  2456  NP_733938.1  3  625   GCTACTTGCCCA   --  CCA         3  C  c  c
                                GGTAGTGATCAG CATTG  CACT   GCCTGGGCAA
                                TGAGAGTT    GTGAC  GTGA   TGGACCCGTT
                                        TA   ---
GAM7776  246  KENAE   1  14862 NP_789786.1  3  211   CTCTGTCACCCA          CA      3  C  c  c
                                GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
                                GTGGTGTG    GTGACGTGAGGTTGGACCC
                                                AC
GAM7776  246  KIAA006 1  5884  NP_055691.1  3  627   TCTTGTTGCCCA                3  C  b  b
          3                     GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                ATGGCACC    GTAACGTGAGGTCGGACCCGTT

GAM7776  246  KIAA008 1  18751 NP_055865.1  3  1279  TCCCCACCCCCA  T  -  -      CA      3  C  c
c
          2                     GGCTGGCAGTAG CA TGC ACT CCAGCCTGGG
                                CACTGCTG    GT ACG TGA GGTCGGACCC
                                        C  A  C       CC
GAM7776  246  KIAA008 2  7956  NP_055584.1  3  1558  GCCCATTTTATG   GC      -------  A  3  C  c  c

          7                     GGCTGGAGTTAA CATT  ACTCCAGCCT     GGGC
                                ATGGAAGT    GTAA  TGAGGTCGGG     CCCG
                                        AT        TATTTTA   -
GAM7776  246  KIAA008 2  10179 NP_055584.1  3  2190  TTCTGTCACCCA          CA      3  C  c  c
          7                     GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                GTGGCGTG    GTGACGTGAGGTCGGACCC
                                                AC
GAM7776  246  KIAA011 1  9255  XP_290939.1  3  248   TGTTGTCTCCCA          CA      3  C  c  c
          7                     GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                GTGGCGTG    GTGACGTGAGGTCGGACCC
                                                TC
GAM7776  246  KIAA018 1  2218  XP_050495.4  3  2250  GAGGTCTGCCCA    A T  G          3  C  c  c

          2                     GGGTGGGAGCAG CATTGC C CCA CCTGGGCA
```

TGTCACTG GTGACG G GGT GGACCCGT
A - G

GAM7776 246 KIAA018 1 2625 NP_066545.1 3 1108 TTCTGTCACCCA CA 3 C c c
6 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGGGGTCGGACCC
AC

GAM7776 246 KIAA020 1 3429 NP_055688.1 3 1258 CTCTGTCACCCA C CA 3 C c c
5 GGCTGTAGTGCA CATTGCACT CAGCCTGGG
GTGGCATA GTGACGTGA GTCGGACCC
T AC

GAM7776 246 KIAA023 1 17386 NP_055562.1 3 5053 CCCTGATGCCCA CA------ T 3 C c
c
7 GGCTGGGTGCAG TTGCAC CCAGCCTGGGCA
GCTCTCAT GACGTG GGTCGGACCCGT
TACTCTCG -

GAM7776 246 KIAA029 1 10742 XP_042833.2 3 3373 GCTGGAGGCCCG A- A 3 C c
c
5 GGCTGGAGGGGC CATTGC CTCCAGCCTGGGC
AGTGTTGC GTGACG GAGGTCGGGCCCG
GG G

GAM7776 246 KIAA043 1 5041 NP_055616.1 5 677 CTCTGTCACCCA C CA 3 C c c
5 GTTTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGCA GTGACGTGAGGTT GACCC
T AC

GAM7776 246 KIAA044 1 1475 XP_044155.1 5 2280 CACTGTCTCCTA CA 3 C c c
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGATCC
TC

GAM7776 246 KIAA045 1 4531 XP_027862.1 3 3704 CTTTGTTGCCCA TG 3 C b b
9 GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
GTGGGGCA GTG GTGAGGTCGGACCCGTT
GT

GAM7776 246 KIAA046 2 9147 NP_055666.1 3 702 CTCTGTCACCCA CA 3 C c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 KIAA046 2 9493 NP_055666.1 3 350 CTCTGTCACCCA CA 3 C c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 KIAA047 1 16940 NP_055679.1 3 1231 CTCTGTTGCCCA 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA049 1 17206 XP_034717.1 5 926 CTCTCTTACCCA C CA 3 C c c
3 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGACATG GTGACGTGAGGTCG ACCC
A AT

GAM7776 246 KIAA049 2 5442 XP_031397.1 3 1639 AGATGCCTTCCA C C --- 3 C c b
5 GGCTGCAGTCAG CATTG ACT CAGCCTGG GCA

TGCAGATG GTGAC TGA GTCGGACC CGT
- C TTC

GAM7776 246 KIAA049 2 14759 XP_031397.1 3 2802 CCCTGTCACCCA CA 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCG GTAACGTGAGGTCGGACCC
AC

GAM7776 246 KIAA051 1 3931 NP_055547.1 3 3674 TCTTGTTGCCCA 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA052 1 19745 XP_171054.1 3 365 TGCTGTTGCCCA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGTCCCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA053 1 12455 XP_047659.6 3 1245 TTCTGTCACCCA C C CA 3 C c
c
2 GGCTAGAGTACA CATTG ACTC AGCCTGGG
GTGGGAAC GTGAC TGAG TCGGACCC
A A AC

GAM7776 246 KIAA055 1 5555 NP_055605.1 3 2301 CTCTGTTGCCCA T C 3 C b b
5 TGCTGGAGTGCA CA TGCACTCCAGC TGGGCAA
TTGGCACA GT ACGTGAGGTCG ACCCGTT
T T

GAM7776 246 KIAA056 1 9629 XP_038150.2 3 321 CTCTGTTGCCCG CA----- 3 C c c
1 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGGCGTG GACGTGAGGTCGGGCCCGTT
GTGCGGC

GAM7776 246 KIAA056 1 16544 NP_055519.1 3 2049 CTCTGTTGCCTA 3 C b b
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGATCCGTT

GAM7776 246 KIAA056 1 16377 NP_055649.1 5 604 TCTTGTTGCCCA C 3 C b b
3 GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGTTGTG GTGACGTGA GTCGGACCCGTT
A

GAM7776 246 KIAA068 1 6522 NP_055667.1 3 32 TGGCACCGAGAG ---- - A 3 C c c
2 GGCTGGAGTGCA CATTGCACTCCAGCCT GG GC
GTGGCGTG GTGACGTGAGGTCGGG CC CG
AGAG A G

GAM7776 246 KIAA080 1 14656 XP_291080.1 3 453 AGTGGTTGGCCA - C C G 3 C c
c
4 GGCTGCAGTATA CA TTG ACT CAGCCTGG CAA
ACTGAAGC GT AAT TGA GTCGGACC GTT
C A C G

GAM7776 246 KIAA083 1 3260 NP_055739.1 3 1918 CTCAGCTGCCCA TG 3 C b b
1 GGCTGGAGTGTG CAT CACTCCAGCCTGGGCA
GTGGCGCC GTG GTGAGGTCGGACCCGT
GT

GAM7776 246 KIAA084 2 5490 XP_049237.1 3 1172 TTCTGTTGCCCA C 3 C b b
1 AGTTGGAGTGCA CATTGCACTCCAGC TGGGCAA

GTGGCATG GTGACGTGAGGTTG ACCCGTT
A
GAM7776 246 KIAA084 2 8185 XP_049237.1 3 1521 GGCTGTTTCCCA C CA 3 C c b
1 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGCATG GTGACGTGA GTCGGACCC
A TT
GAM7776 246 KIAA086 1 2153 NP_055893.2 3 955 CTCTGTCGCCCA A 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 KIAA088 1 13271 NP_056192.1 3 736 TCTTGTCCCCCA C CA 3 C c c
9 GGCTTGAGTGCA CATTGCACTC AGCCTGGG
ATGACTCA GTAACGTGAG TCGGACCC
T CC
GAM7776 246 KIAA092 2 7655 NP_055712.1 3 2517 TTCTGTTGCCTG TG 3 C b b
4 GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGGCGTG GTGACGTGAGGTCGG CCGTT
GT
GAM7776 246 KIAA092 2 13297 NP_055712.1 3 1717 CTATGTTGCCCA C 3 C b b
4 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCTAT GTGACGTGAG TCGGACCCGTT
A
GAM7776 246 KIAA093 1 14272 XP_041191.2 3 162 CTCAGTCGCTCA A 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGTGGG GTAACGTGAGGTCGGACTCG
C
GAM7776 246 KIAA093 1 11958 XP_052620.6 3 1214 CTCTGTCGCCCA A 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGTCAAG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 KIAA096 1 8976 XP_290942.1 3 1524 TCTTGTTGCCCA G 3 C b b
2 GGCTGGAGTGAA CATT CACTCCAGCCTGGGCAA
ATGGTGCG GTAA GTGAGGTCGGACCCGTT
A
GAM7776 246 KIAA100 1 12518 XP_290584.1 5 0 CGCCTAGGCTGG T A A 3 C c c
2 AGCGCCGTGGTA CAT GC CTCCAGCCTGGGC
CAGTCTTG GTG CG GAGGTCGGATCCG
C C C
GAM7776 246 KIAA104 1 11846 XP_051091.3 3 2456 CTCTGTCACCCA C CA 3 C c c
0 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACG GTGACGT AGGTCGGACCC
A AC
GAM7776 246 KIAA104 1 3653 NP_055762.1 3 968 CCCTGTTGCCCA 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 KIAA105 1 14832 XP_043493.5 3 3278 CTCTGTTGCCCA 3 C b b
4 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGTGGG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA111 1 9842 NP_055746.1 3 688 TCCCTCCTCCCA G T CA 3 C c c
5 GGCTGGTGTGAG CATT CAC CCAGCCTGGG
TGTGCGTG GTGA GTG GGTCGGACCC
- T TC

GAM7776 246 KIAA112 1 5783 NP_061872.1 3 1959 CTCCATTGCCCA CAC 3 C c c
8 GGCTGGATTACA CATTG TCCAGCCTGGGCAA
GTGGCGCA GTGAC AGGTCGGACCCGTT
ATT

GAM7776 246 KIAA114 1 7385 XP_044014.1 3 3995 CTCTGTCACCCA CA 3 C c c
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 KIAA114 1 17532 NP_065749.1 3 887 AAATATTGCTCA CA------ CT 3 C c
c
5 GGCTGGTTGCAA TTGCA CCAGCCTGGGCAA
ACTCCTTG AACGT GGTCGGACTCGTT
GTTCCTCA T-

GAM7776 246 KIAA115 1 2664 XP_030864.2 3 2954 CTCTGTCACCCA CA 3 C c c
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 KIAA117 1 10162 XP_045907.2 3 1245 TCTTGTTGCCCA C 3 C b b
0 AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCACG GTAACGTGAGGTCG ACCCGTT
A

GAM7776 246 KIAA118 1 5755 NP_065761.1 3 154 GCTCTGTCGCCA -- 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 KIAA119 1 17517 XP_041843.1 3 1645 ACACTGTCGCCA -- 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 KIAA119 5 12389 NP_065765.1 3 421 TCTTGTTGCCCA 3 C b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA119 5 12478 NP_065765.1 3 993 CTCTGTTGCCTA G- 3 C b b
8 GGCTGGAGTGAA CATT CACTCCAGCCTGGGCAA
AGTGGCGC GTGA GTGAGGTCGGATCCGTT
AA

GAM7776 246 KIAA119 5 13749 NP_065765.1 3 1272 AGTCCTTGCCCA 3 C b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA119 5 16088 NP_065765.1 3 3710 TCACTGTTGCCA G 3 C b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA

GTGGCACA GTGACGTGAGGTCGGACC GTT
-
GAM7776 246 KIAA119 5 16471 NP_065765.1 3 724 TCTGTTGCCCCA - 3 C b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG CAA
GTGGTGTG GTGACGTGAGGTCGGACCC GTT
C
GAM7776 246 KIAA120 1 8271 XP_027307.2 3 1885 CCCTGTTGCCCA C----- C 3 C c c
9 AGTTGGAGTGCA ATTGCACTCCAGC TGGGCAA
ATCTTGGC TAACGTGAGGTTG ACCCGTT
CGGTTC A
GAM7776 246 KIAA121 1 9144 XP_172801.1 3 105 CTCTGTTACCCA GC CA 3 C c c
0 GATTGGAGTGCA CATTGCACTCCA CTGGG
GTGGCGCG GTGACGTGAGGT GACCC
TA AT
GAM7776 246 KIAA125 2 9032 XP_031577.2 3 3566 TCTTGTTGCCCA C 3 C b b
7 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCGCG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 KIAA125 2 11523 XP_031577.2 3 1695 CTCTGTCGCCCA A 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 KIAA126 1 3236 XP_291055.1 3 898 TCTTGTTGCCCA 3 C b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 KIAA127 2 4555 XP_300760.1 5 675 CTCTGTCCCCCA T C CA 3 C c c
3 GTCTGGCGTGCA CATTGCAC CCAG CTGGG
ATGGTTTG GTAACGTG GGTC GACCC
C T CC
GAM7776 246 KIAA127 2 7374 XP_300760.1 5 380 GTCCAAGCTCAA C- A 3 C c c
3 AGCTGGAGTGCA CATTGCACTCCAGC TGGGC
ATGGCGCA GTAACGTGAGGTCG ACTCG
AA A
GAM7776 246 KIAA127 1 1905 XP_039169.1 5 90 GACGGTGGCGCC GCA T - A 3 C c
c
6 GGCTGGAGAATG CATT CTCCAGCC GG GC
GACTGTGA GTAA GAGGTCGG CC CG
--- - G G
GAM7776 246 KIAA128 1 9573 NP_065799.1 3 1243 CCCTGTTGCCCA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGGATG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 KIAA139 1 10123 XP_050793.2 3 1500 CTCTGTTGCCCA CA----- 3 C c c
3 GGCTGGAGTGTA TTGCACTCCAGCCTGGGCAA
GAGACACA GATGTGAGGTCGGACCCGTT
ACACAGA

GAM7776 246 KIAA144 1 15171 NP_065885.1 3 712 CTCTGTCGCCCA C A 3 C b b
3 GGCTGTAGTGCA CATTGCACT CAGCCTGGGC
ATGGCGCA GTAACGTGA GTCGGACCCG
T C
GAM7776 246 KIAA145 1 5529 XP_040100.3 3 2060 CTCTGTCGCCCA T A 3 C b b
6 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
CTGGCGCG GT ACGTGAGGTCGGACCCG
C C
GAM7776 246 KIAA146 1 1667 XP_051160.2 3 1298 CTTTGGTGCCCA GC CCA 3 C c
c
3 GGCCAAGTAGAA CATT ACT GCCTGGGCA
TGAGATGA GTAA TGA CGGACCCGT
GA AC-
GAM7776 246 KIAA146 2 18838 XP_027396.4 3 449 GCCAGCCAAGGC T --- G A 3 C c
b
5 CAGTGGAGTGCT CAT GCACTCCA GCCT GGC
GTGGGGTC GTG CGTGAGGT CGGA CCG
T GAC A A
GAM7776 246 KIAA146 2 18992 XP_027396.4 3 570 GGTCTGTCGCCA -- 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC
GAM7776 246 KIAA149 1 15045 XP_034415.1 3 2966 CTCTGTTGCCCA C C 3 C b b
3 GTCTGGAGTTCA CATTG ACTCCAG CTGGGCAA
GTGGCGCG GTGAC TGAGGTC GACCCGTT
T T
GAM7776 246 KIAA150 1 8820 XP_290952.1 3 78 GCTCGTCACCCA C----- CA 3 C c c
8 GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATTGTGCA TAACGTGAGGTCGGACCC
ACGTGT AC
GAM7776 246 KIAA151 1 13383 XP_170889.1 3 95 CTCTGTCGCCCA G A 3 C c c
8 GGGTGGAGTGCG CATTGCACTCCA CCTGGGC
GTGGCACG GTGGCGTGAGGT GGACCCG
G C
GAM7776 246 KIAA153 2 4028 XP_042661.5 3 1177 GCTCTGTCGCCA -- 3 C b b
0 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
ATGGCGTG GTAACGTGAGGTCGGACC TGT
GC
GAM7776 246 KIAA153 2 15284 XP_042661.5 3 818 TGCTCTTACCCA C CA 3 C c b
0 GGCTGAGTGCAG CATTGCACTC AGCCTGGG
TGGCAGAA GTGACGTGAG TCGGACCC
- AT
GAM7776 246 KIAA155 1 3790 XP_039393.3 3 663 GCAAGCAGCCCA A TC --- A 3 C c
c
0 GGCAGCTGTGGG CATTGC C CA GCCTGGGC
CAGTGCTG GTGACG G GT CGGACCCG
- GT CGA A
GAM7776 246 KIAA155 1 4029 XP_054472.2 3 1629 CTTTGTCCCCCA CA 3 C c c
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC

CC

GAM7776 246 KIAA157 1 14154 XP_027744.1 3 882 CTGTCTTGCCCA 3 C b b
1 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCCTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KIAA161 2 8549 NP_066002.1 3 1381 TCTTGTTGCCTA 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGATCCGTT

GAM7776 246 KIAA161 2 10111 NP_066002.1 3 1687 GCTCTGTCACCA A -- 3 C b b
5 GGCCGGAGTGCA CATTGCACTCC GCCTGG GCA
GTGGTGTC GTGACGTGAGG CGGACC TGT
C AC

GAM7776 246 KIAA167 2 7194 XP_037809.1 3 1742 CTCTGTTGCTCA G C 3 C c b
1 AGCTGGAGTGGA CATT CACTCCAGC TGGGCAA
GTGGCACG GTGA GTGAGGTCG ACTCGTT
G A

GAM7776 246 KIAA167 2 17191 XP_037809.1 3 4094 CTCTGTTGGCCA C G 3 C b b

1 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCACA GTGACGT AGGTCGGACC GTT
A G

GAM7776 246 KIAA171 2 1142 NP_085136.1 3 1318 CTCTATTGCCCA T 3 C b b
2 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCGTG GT ACGTGAGGTCGGACCCGTT
C

GAM7776 246 KIAA171 2 1142 XP_041497.2 3 1487 CTCTATTGCCCA T 3 C b b
2 GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
CTGGCGTG GT ACGTGAGGTCGGACCCGTT
C

GAM7776 246 KIAA171 2 14165 NP_085136.1 3 740 TGTTGTTGCCCA C----- 3 C b b
2 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCACG TAACGTGAGGTCGGACCCGTT
GCACGA

GAM7776 246 KIAA171 2 14165 XP_041497.2 3 740 TGTTGTTGCCCA C----- 3 C b b
2 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCACG TAACGTGAGGTCGGACCCGTT
GCACGA

GAM7776 246 KIAA172 1 14630 XP_040280.2 5 25 CATCCTTGCCCA T- --- A C 3 C c c
4 GCCGGTGTGGTG CAT GCACT CC GC TGGGCAA
CTTGTGTG GTG CGTGG GG CG ACCCGTT
TT TGT C -

GAM7776 246 KIAA173 1 10602 NP_219494.1 3 1428 TCTTGTTGCCCA C A 3 C b b
7 GGCGGAGTACAA CATTG ACTCC GCCTGGGCAA
TGGTGGGA GTAAC TGAGG CGGACCCGTT
A -

GAM7776 246 KIAA177 1 1618 NP_149091.1 3 2168 AGGACAAGCCCA T CT A A 3 C c
c
5 GGCAGGGCTGCA CAT GCA CC GCCTGGGC
TGGAGAGG GTA CGT GG CGGACCCG

```
                                        -  CG  A       A
GAM7776  246    KIAA178 1  11058  NP_115820.1  3  342   CTGTGTCACCTA              CA        3  C  c  c
          4                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     GTGGCACA    GTGACGTGAGGTCGGATCC
                                                   AC
GAM7776  246    KIAA182 1  10095  XP_041566.2  3  992   CGGGGCTGACCA    CA-       G        3  C  c
c
          2                          GGCTGGGGGTCC CATTG   CTCCAGCCTGG CA
                                     AGTGAAAC    GTGAC   GGGGTCGGACC GT
                                                 CTG         A
GAM7776  246    KIAA182 2  2143   XP_290834.1  3  938   CTCTGTTGCCCA                    3  C  b  b
          7                          GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
                                     GTGGTGTG    GTGATGTGAGGTCGGACCCGTT

GAM7776  246    KIAA182 2  12636  XP_290834.1  3  1306  CCTTGTCACCCA       C       CA        3  C  c  b

          7                          GGCTGTAGTGCG CATTGCACT CAGCCTGGG
                                     GTGGCGCG    GTGGCGTGA GTCGGACCC
                                                   T        AC
GAM7776  246    KIAA182 1  14863  XP_030378.2  3  210   CTCTGTTGCCCA                    3  C  b  b
          9                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                     GTGGTGTA    GTGACGTGAGGTCGGACCCGTT

GAM7776  246    KIAA183 1  12627  XP_114087.2  3  1679  CTCTGCCAGCCA            ---       3  C  b  b
          6                          GGCTGGAGTGCA CATTGCACTCCAGCCTGG   GCA
                                     GTGGCATG    GTGACGTGAGGTCGGACC   CGT
                                                   GAC
GAM7776  246    KIAA185 1  19095  XP_045184.1  3  1021  CCCCTCTGCCCA  TT  ACTC             3  C  c
 c
          3                          GGCTGCCACGCC CA  GC    CAGCCTGGGCA
                                     CTGGATGC    GT  CG    GTCGGACCCGT
                                               CC  CACC
GAM7776  246    KIAA190 1  16492  XP_056282.1  3  3672  AGCCTGTGTCCA   T-  A              3  C  c  c
          4                          GGCTGGGGAGCC CAT  GC CTCCAGCCTGGGCA
                                     CGTGTCTG    GTG  CG GGGGTCGGACCTGT
                                               CC  A
GAM7776  246    KIAA192 1  7553   XP_057040.1  5  322   TCTTGTTGCCCA                    3  C  b  b
          2                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                     ATGGCATG    GTAACGTGAGGTCGGACCCGTT

GAM7776  246    KIAA192 2  1857   NP_694971.2  3  597   CTCTGTCGCCCA        G     A        3  C  c  c
          4                          GGATGGAGTGCA CATTGCACTCCA CCTGGGC
                                     GTGGCGCG    GTGACGTGAGGT GGACCCG
                                                   A      C
GAM7776  246    KIAA192 2  8341   NP_694971.2  3  407   TTCTGTCACCTA       C       CA        3  C  c  c
          4                          GGCTGGAATGCA CATTGCA TCCAGCCTGGG
                                     GTGGTGCA    GTGACGT AGGTCGGATCC
                                                   A          AC
GAM7776  246    KIAA193 1  2983   XP_057107.3  5  301   ACGCGCTGTCCT    GCA      T         3  C  c  c
```

7 GGCTGGAGGAGG CATT CTCCAGCC GGGCA
TGGAGCAG GTGG GAGGTCGG CCTGT
AG- T

GAM7776 246 KIAA197 2 6902 XP_058720.4 3 214 CTCTGTCGCCCA A 3 C b b
1 GGCTGGGGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCC GTGACGTGGGGTCGGACCCG
C

GAM7776 246 KIAA197 2 11506 XP_058720.4 3 264 CTCCGCTTCCCA CA 3 C c b
1 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGGGGTCGGACCC
TT

GAM7776 246 KIAA198 1 7554 XP_113870.1 5 202 TCTTGTTGCCCA C 3 C b b
7 GGTTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCACG GTGACGTGAG TTGGACCCGTT
A

GAM7776 246 KIAA202 1 12100 XP_059415.2 3 1063 TCTGGTTGCCCA 3 C b b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 KLF12 1 1127 NP_009180.3 3 950 TGGGGCTGCCCA C CCA 3 C c c

GGCAAAGTCAGT CATTG ACT GCCTGGGCA
GAACATGA GTGAC TGA CGGACCCGT
- AA-

GAM7776 246 KLRD1 1 2353 NP_002253.1 3 396 TCACACTGCCCA CA 3 C c c
GGCTGGAGCATA CATTG CTCCAGCCTGGGCA
GTGGCAAG GTGAT GAGGTCGGACCCGT
AC

GAM7776 246 KLRD1 1 2353 NP_031360.1 3 396 TCACACTGCCCA CA 3 C c c
GGCTGGAGCATA CATTG CTCCAGCCTGGGCA
GTGGCAAG GTGAT GAGGTCGGACCCGT
AC

GAM7776 246 KMO 1 6338 NP_003670.1 3 716 CTCTGTTGACCA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGTGAG GTGACGTGAGGTCGGACC GTT
A

GAM7776 246 LAMP3 1 17760 NP_055213.1 3 565 TCTTGTCACCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC

GAM7776 246 LARS 1 2620 NP_064502.8 5 54 TTGCACAGTCGG -- --- G 3 C c c
CTGGGCGGTGCA CATTGCACT CCAGCC TG GCAA
ATGGCGGA GTAACGTGG GGTCGG AC CGTT
CG CTG A

GAM7776 246 LASP1 1 17709 NP_006139.1 3 840 GCCTGCCTCCTA T AC --- 3 C c c
GGCTGGAAGCCA CAT GC TCCAGCCT GGGCA
TGGTCCCG GTA CG AGGTCGGA TCCGT
C A- TCC

GAM7776 246 LCN7 1 15937 NP_071447.1 3 400 CTCCGTTGCCCA 3 C b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGCCCA GTGACGTGAGGTTGGACCCGTT

GAM7776 246 LETM1 1 18695 NP_036450.1 3 1029 GCAGCATGGCCA T A -- G 3 C c c

GGCTGGCCAGGG CAT GC CT CCAGCCTGG CA
CGTGGGCA GTG CG GA GGTCGGACC GT
- G CC G

GAM7776 246 LGP2 1 8032 NP_077024.1 5 165 AGAGTGGCACCA GC C - A 3 C c c

GGCTGAGTTAAG CATT ACTC AGCCTGG GC
TGGGACTG GTGA TGAG TCGGACC CG
AT - A G

GAM7776 246 LHX2 1 4178 NP_004780.3 5 506 CGCCGTCGCCCA ACTCCA A 3 C c c

GGCGCCCCGCAA CATTGC GCCTGGGC
TGTAGCTG GTAACG CGGACCCG
CCCCG- C

GAM7776 246 LIN-28 1 4726 NP_078950.1 3 2144 CTGTGTCGCCCA A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGAGCTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 Link-GE 1 19936 NP_057423.1 3 677 CCTGCATGCCCA GCA- - - 3 C c c

FII GGCTTGTGAGCC CATT CTC CA GCCTGGGCA
AAGGTGCT GTGG GAG GT CGGACCCGT
AACC T T

GAM7776 246 LIPH 1 10379 NP_640341.1 3 3 TTCTTTGCCCAG T - C - 3 C c c

AGTTGCAGTTGT CA TGCA CT CAGC CTGGGCAA
ACTGTTGC GT ATGT GA GTTG GACCCGTT
C T C A

GAM7776 246 LLGL2 1 15172 NP_004515.1 3 6 GCTGAGCGTCCA ACTC A 3 C c c

GGCTGCGCGATG CATTGC CAGCCTGGGC
GCACACAC GTAGCG GTCGGACCTG
C--- C

GAM7776 246 LNK 2 1866 NP_005466.1 3 1845 CCATGTTGGCCA GCACT G 3 C c c

GGCTGGTCTCGA CATT CCAGCCTGG CAA
ATGTCTGA GTAA GGTCGGACC GTT
GCTCT G

GAM7776 246 LNK 2 13992 NP_005466.1 3 1683 TCTTGTCAACCG GCA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCA GTGACGTGAGGTCGGGCC
AAC

GAM7776 246 LOC1126 3 793 XP_053145.1 3 1145 AAAACTGGTAAC T GGCA 3 C c c

87 AGGCTGGGTGCA CATTGCAC CCAGCCTG
ATGGCTCA GTAACGTG GGTCGGAC
- AATG

GAM7776 246 LOC1126 3 7988 XP_053145.1 3 1145 AAACTGGTAACA T GGCA 3 C c c

87 GGCTGGGTGCAA CATTGCAC CCAGCCTG
TGGCTCAC GTAACGTG GGTCGGAC
- AATG
GAM7776 246 LOC1126 3 16673 XP_053145.1 3 169 CCCTGTCACCCA CA 3 C c c
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1128 1 16256 NP_612422.2 3 419 CTCTGTCACCCA CA 3 C b b
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1134 3 5336 NP_612437.2 3 852 TTCTGTCACCCG CA 3 C c b
44 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGGCCC
AC
GAM7776 246 LOC1134 3 15899 NP_612437.2 3 590 CTCTGTCACACA C----- --- 3 C c b
44 GGCTGGAGTGCA ATTGCACTCCAGCCTG GGCA
GTACAATT TGACGTGAGGTCGGAC CTGT
TTAACA ACA
GAM7776 246 LOC1134 3 18294 NP_612437.2 3 1177 CTGTATTGCCCA 3 C b b
44 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1138 1 5632 NP_612444.1 5 268 TCCTGCCGCCCA -- C A A 3 C c
c
28 GGCAGGATGTCA CATT GCA TCC GCCTGGGC
GATGAGGA GTAG TGT AGG CGGACCCG
AC - A C
GAM7776 246 LOC1151 1 15271 XP_055276.1 5 257 CTCTATGGCCCA C A 3 C c c
23 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGACACG GTGAC TGAGGTCGGACCCG
A G
GAM7776 246 LOC1152 1 12422 XP_055499.2 5 1755 CTTTGTCCCCCA CA 3 C c c

19 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
ATGGCAGG GTAGCGTGAGGTCGGACCC
CC
GAM7776 246 LOC1156 1 7429 NP_663299.1 3 657 GCTCTGTCGCCT T A 3 C c c
48 GGCTGGAGTGCA CATTGCACTCCAGCC GGGC
GTGGTGTG GTGACGTGAGGTCGG TCCG
- C
GAM7776 246 LOC1164 1 14720 XP_058095.1 5 1241 CAATGGTGTCCA 3 C b b
11 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCGTG GTGACGTGAGGTCGGACCTGT

GAM7776 246 LOC1184 1 456 XP_060981.3 3 219 CTCTGTTGCCCA CA----- 3 C c c
90 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGGCATG GACGTGAGGTCGGACCCGTT
GTACGGC
GAM7776 246 LOC1188 1 2649 NP_849154.1 3 581 TACTCTCGCCCA C A 3 C c c

12 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCATG GTGACGTGAG TCGGACCCG
A C
GAM7776 246 LOC1188 1 2649 XP_058346.2 3 581 TACTCTCGCCCA C A 3 C c c
12 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCATG GTGACGTGAG TCGGACCCG
A C
GAM7776 246 LOC1193 1 745 XP_061446.3 5 191 CCCACCCACCCA T AC CA 3 C c
c
95 GGCTGGAGCCAT CAT GC TCCAGCCTGGG
GGATAAAT GTA CG AGGTCGGACCC
C -- AC
GAM7776 246 LOC1205 1 17112 XP_058475.1 3 679 CTCTGTCGCGCC C - A 3 C c c
26 AGCTGGAGTGCA CATTGCACTCCAGC TGG GC
GTGCCATG GTGACGTGAGGTCG ACC CG
- G C
GAM7776 246 LOC1219 1 9891 XP_062872.2 5 585 CTCTGTCACCCG T CA 3 C c c
52 GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGCTTG GTG CGTGAGGTCGGGCCC
T AC
GAM7776 246 LOC1242 1 14576 XP_058785.3 5 257 AACTTCAGTCCG T A A 3 C c c
21 GGCTGGAGGCCG CAT GC CTCCAGCCTGGGC
TGCACAAC GTG CG GAGGTCGGGCCTG
C - A
GAM7776 246 LOC1250 1 1744 XP_058889.3 3 407 CTCTGTCACCCA CA 3 C c c
61 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1266 1 3477 XP_060121.4 3 194 CTGTGTTGCCCA 3 C b b
69 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC1272 1 18918 XP_059122.1 3 141 CTTTGTTGCCCA C------ - AGC 3 C c
c
53 GAGGATGTGCAG ATTGCAC TCC CTGGGCAA
TTGTCATC TGACGTG AGG GACCCGTT
CTACTGT T A--
GAM7776 246 LOC1278 1 18516 XP_059184.1 5 112 TGGTGTTGCCCA A CA- 3 C c
c
41 GGCAGAGAGGGC CATTGC CTC GCCTGGGCAA
AGTGTGGA GTGACG GAG CGGACCCGTT
G AGA
GAM7776 246 LOC1283 1 15173 XP_059243.2 3 561 TGTTGTTGCCCA 3 C b b
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC1322 1 509 XP_059583.1 5 83 CTTTGCTTCCCA CA 3 C c c
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGTGCG GTGACGTGAGGTCGGACCC
TT
GAM7776 246 LOC1352 2 3512 XP_072402.4 3 1277 CTTGCTCTCCCA CA 3 C c b
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 LOC1352 2 10443 XP_072402.4 3 564 CTCTGTTGCCCA C 3 C b b
93 GGCTGAAGTGTA CATTGCACT CAGCCTGGGCAA
GTGGCACA GTGATGTGA GTCGGACCCGTT
A
GAM7776 246 LOC1357 1 17207 NP_612639.1 3 39 CTCCGTCACCCA CA 3 C c c
63 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCAAG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1358 1 19136 XP_059804.4 3 736 TCTTGTTGCCCA C----- C 3 C c c
18 GCCTGGAGTGCA ATTGCACTCCAG CTGGGCAA
ATAGCGTG TAACGTGAGGTC GACCCGTT
GTGCGA C
GAM7776 246 LOC1378 1 19990 XP_059929.3 3 683 TCTTGTTGCCCA 3 C b b
86 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATA GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC1394 1 9489 XP_066687.2 5 64 CTCTGTTGCCCA C 3 C b b
22 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGTGTG GTGACGTGAGGTC GACCCGTT
A
GAM7776 246 LOC1432 1 15574 NP_620167.1 5 54 TCTTGTTGCCCA 3 C b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC1442 1 3159 XP_084786.1 5 399 CTCTTTCGCCCA A 3 C b b
48 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGTGTG GTAACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1442 1 17498 XP_084795.1 5 1526 ATGCTCAGCCCA TG CA- A 3 C c
c
66 GGCATTGAGTGT CAT CACTC GCCTGGGC
GATGCTGA GTA GTGAG CGGACCCG
GT TTA A
GAM7776 246 LOC1444 3 1633 XP_084852.6 3 1294 ATCTGTTACCCA CA 3 C c b
04 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACACA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 LOC1444 3 5897 XP_084852.6 3 1129 GTCTGTTGCCTA A 3 C b b
04 GGCGGGAGTGCA CATTGCACTCC GCCTGGGCAA
GTGGCATC GTGACGTGAGG CGGATCCGTT
G
GAM7776 246 LOC1444 3 15352 XP_084852.6 3 421 TTACCAGGCCCA TG A 3 C c
b

```
          04                          GGCTGGGGTGGT CAT  CACTCCAGCCTGGGC
                                     GTGAACCC    GTG  GTGGGGTCGGACCCG
                                              TG           G
GAM7776  246   LOC1444 1  5733  NP_612482.1  5  153   CCTTGAAGCCCA  TT  CTC       A        3  C  c
c
          67                          GGCTGATGCTTG CA  GCA   CAGCCTGGGC
                                     AAGTAACT    GT  CGT   GTCGGACCCG
                                              T-  A--         A
GAM7776  246   LOC1444 1  19220 XP_096611.2  3  209   CTCTGTCACTCA            CA        3  C  c  c
          81                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     GTGGTATA    GTGACGTGAGGTCGGACTC
                                                    AC
GAM7776  246   LOC1446 1  12712 XP_096648.1  3  520   CTCTGTCATCCA     A        CA        3  C  c  c

          67                          GGCTGGAGGGTA CATTGC CTCCAGCCTGGG
                                     GTGGCGTG    GTGATG GAGGTCGGACCT
                                              G          AC
GAM7776  246   LOC1447 1  17736 XP_084949.1  5  57    CTCTGTTGCCTA     C                3  C  b  b
          42                          GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
                                     GTGGCAAG    GTGAC TGAGGTCGGATCCGTT
                                              A
GAM7776  246   LOC1447 1  8972  XP_084963.2  5  181   CTTTGTCACCCA     C        CA        3  C  c  c
          66                          GGCTGGAGTACA CATTG ACTCCAGCCTGGG
                                     GTGGCGTG    GTGAC TGAGGTCGGACCC
                                              A          AC
GAM7776  246   LOC1447 2  444   XP_084964.1  5  134   CTCCATCACTCA     C        CA        3  C  c  b
          76                          GGCTGGAGTACA CATTG ACTCCAGCCTGGG
                                     GTGCTGAG    GTGAC TGAGGTCGGACTC
                                              A          AC
GAM7776  246   LOC1447 2  16275 XP_084964.1  5  252   TTCTGTTGCCCA                     3  C  b  b
          76                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                     ATGGCATG    GTAACGTGAGGTCGGACCCGTT

GAM7776  246   LOC1448 1  12065 XP_084972.1  5  233   CTCTGTCGCCCA             A        3  C  b  b
          17                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                     GTGGTGCG    GTGACGTGAGGTCGGACCCG
                                                    C
GAM7776  246   LOC1449 1  12130 XP_084990.1  5  26    CTTCGTGTTTGC   TG-      CTG         3  C  c
c
          62                          TGCTGGAGTGAC CAT   CACTCCAGC   GGCAA
                                     TGTGTGTT    GTG   GTGAGGTCG   TCGTT
                                              TCA        ---
GAM7776  246   LOC1450 1  675   XP_085022.1  5  469   TTATAGAGCCTA   -  A--        A      3  C  c  c
          98                          GGCTGGAGGAGG CAT TGC   CTCCAGCCTGGGC
                                     TACATGGG    GTA ATG   GAGGTCGGATCCG
                                              C   GAG           A
GAM7776  246   LOC1452 1  6417  XP_096740.1  3  2362  TTACGAAATGCT        CA  CTG         3  C  c
c
          31                          AGCCAGGGTGCA CATTGCACTC  GC   GGCA
                                     ATGGCTCA    GTAACGTGGG  CG   TCGT
```

```
                                                AC  A--
GAM7776  246    LOC1452 1   18805  XP_085072.1  5  637   CTCTTTTGCCCA    GCA                3  C  c  c
          68                          GGCTGGAGCGAA CATT   CTCCAGCCTGGGCAA
                                     GTGACGAG    GTGA   GAGGTCGGACCCGTT
                                               AGC
GAM7776  246    LOC1457 1   4773   XP_085211.1  3  988   GCTCTGTCACCA    C        --        3  C  c  c
          25                          GGCTGGAGTACA CATTG ACTCCAGCCTGG  GCA
                                     GTGATGAC    GTGAC TGAGGTCGGACC  TGT
                                               A         AC
GAM7776  246    LOC1457 2   7370   XP_085227.1  5  95    CTCTGTCGCCCA             A        3  C  b  b
          57                          GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
                                     GTGGCGCG    GTGGCGTGAGGTCGGACCCG
                                                  C
GAM7776  246    LOC1457 2   11523  XP_085227.1  5  213   CTCTGTCGCCCA             A        3  C  b  b
          57                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                     GTGGCGCG    GTGACGTGAGGTCGGACCCG
                                                  C
GAM7776  246    LOC1457 1   2196   XP_085231.2  5  1119  CTCTGTCACCCA             CA       3  C  b  b
          83                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     ATGGTGCA    GTAACGTGAGGTCGGACCC
                                                  AC
GAM7776  246    LOC1458 1   16256  XP_096873.1  5  60    CTCTGTCACCCA             CA       3  C  b  b
          13                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     ATGGCATG    GTAACGTGAGGTCGGACCC
                                                  AC
GAM7776  246    LOC1459 1   11009  XP_085290.3  5  555   CTCTGTCACCCA        GCC   CA       3  C  c
c
          88                          AGATGGAGTGCA CATTGCACTCCA   TGGG
                                     ATGGCACG    GTAACGTGAGGT   ACCC
                                                  AGA   AC
GAM7776  246    LOC1461 1   16175  NP_778229.1  5  198   TCTTGTTGCCCA C-----               3  C  c  c
          77                          GGCTGGAGTGCA      ATTGCACTCCAGCCTGGGCAA
                                     GTAGCACT         TGACGTGAGGTCGGACCCGTT
                                            TCACGA
GAM7776  246    LOC1462 4   1644   XP_085387.1  3  3210  CTCTGTCGCCCA        C      A        3  C  c  b
          29                          GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
                                     GTGGCACA    GTGACGTGAG TCGGACCCG
                                                  A       C
GAM7776  246    LOC1462 4   5551   XP_085387.1  3  1707  CTCTGTCGCCCA             A        3  C  b  b
          29                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
                                     GTGGCGCC    GTGACGTGAGGTCGGACCCG
                                                  C
GAM7776  246    LOC1462 4   5672   XP_085387.1  3  4034  CTCTGTTGCCTA    C                3  C  b  b
          29                          GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
                                     GTGGTGCA    GTGAC TGAGGTCGGATCCGTT
                                                  A
GAM7776  246    LOC1462 4   8706   XP_085387.1  3  2310  TCTTGTTGCCTA                    3  C  b  b
          29                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                     ATGGCGAG    GTAACGTGAGGTCGGATCCGTT
```

GAM7776 246 LOC1463 2 5798 XP_085430.1 5 736 ACTCGTTGCCCA 3 C b b
46 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1463 2 17670 XP_085430.1 5 388 ACTCCGTTGCCA T G 3 C b b
46 GGCTGGAGTGCT CAT GCACTCCAGCCTGG CAA
GTGGCGCT GTG CGTGAGGTCGGACC GTT
T -
GAM7776 246 LOC1464 1 2457 XP_096998.2 5 536 GCTCTGTCACCA -- 3 C b b
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGTG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC1464 1 813 XP_085461.6 5 101 ACTTGTCACCCA CA 3 C b b
43 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGTG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1464 1 9246 XP_097006.1 5 119 AAGCCCACGTGA TG ----- A 3 C c
c
75 GGCTGGAGTGAT CAT CACTCCAGCCT GGGC
GTGGCCAC GTG GTGAGGTCGGA CCCG
TA GTGCA A
GAM7776 246 LOC1465 1 3374 XP_097013.1 3 40 TGGGAGGTCCCA -- TC - A 3 C c c

13 GGCTGTGTGCAC CAT TGCAC CAGCCTGGG C
AGTGACAG GTG ACGTG GTCGGACCC G
AC T- T G
GAM7776 246 LOC1466 1 7382 XP_085514.2 5 1114 CTCTGTCGCCCA A 3 C b b
03 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1467 1 13448 XP_085588.1 5 890 TCTTGTTGCCCA 3 C b b
84 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC1468 1 1745 XP_097107.1 3 677 CTCTGTTGCCCA 3 C b b
39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1468 1 8315 NP_660316.1 3 1177 TGCTGCTGCCCA 3 C b b
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACG GTGACGTGAGGTCGGACCCGT

GAM7776 246 LOC1468 1 8232 XP_097120.1 5 550 CTCTGTCACCCA CA 3 C c c
95 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1469 1 6392 XP_097121.1 3 1204 TGTCAAAAATCA GCA 3 C c c

01 GGCTGGAGTGCA CATTGCACTCCAGCCTGG

GTGGCATG GTGACGTGAGGTCGGACT
AAA
GAM7776 246 LOC1469 2 9492 XP_085634.2 3 662 CTCTGTCGCCCA A 3 C b b
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1469 2 19550 XP_085634.2 3 995 CTCTGTCGCCCA A 3 C b b
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGGC GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1470 1 16699 XP_054031.5 5 604 TCTTGTTGCCCA C 3 C b b
71 GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
ATGTTGTG GTAACGTGA GTCGGACCCGTT
A
GAM7776 246 LOC1470 1 12558 XP_097182.1 5 18 CTCTGTCCGCCA --- 3 C b b
80 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GCC
GAM7776 246 LOC1471 1 10618 XP_085722.2 3 252 CACTGTTGCCCA 3 C b b
66 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1473 1 19915 XP_097230.2 3 1189 TTGATCTGCCCA T CT AG- 3 C c
c
81 GGAAAGGGATGC CA TGCA CC CCTGGGCA
ATTGACAC GT ACGT GG GGACCCGT
T AG AAA
GAM7776 246 LOC1474 1 12065 XP_084000.1 3 143 CTCTGTCGCCCA A 3 C b b
07 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1478 2 1634 XP_085903.1 3 281 CTCTGTCACCCA G C CA 3 C c
b
17 GGCTGTAGTGGA CATT CACT CAGCCTGGG
GTGGTGTG GTGA GTGA GTCGGACCC
G T AC
GAM7776 246 LOC1478 2 19233 XP_085903.1 3 445 CTCTGTCGCCCA A 3 C b b
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCG GTAACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1478 2 8642 XP_085924.2 3 146 TCTTGTTGTCCA C 3 C b b
41 GTCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCACA GTAACGTGAGGTC GACCTGTT
T
GAM7776 246 LOC1478 2 12065 XP_085924.2 3 458 CTCTGTCGCCCA A 3 C b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1479 1 17952 XP_085974.1 3 579 CTCTGTCACCCA CA 3 C c c
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1481 2 5784 NP_653293.1 3 2524 CCTTGTTGCCCA C C 3 C b b

37 GGCTGTAGTACA CATTG ACT CAGCCTGGGCAA
ATGGCATG GTAAC TGA GTCGGACCCGTT
A T
GAM7776 246 LOC1481 2 17935 NP_653293.1 3 2097 CTCTGTCACCCA --- CA 3 C c
b

37 GGCTGGAGTGCC CATT GCACTCCAGCCTGGG
ATAGTGTG GTGA CGTGAGGTCGGACCC
TAC AC
GAM7776 246 LOC1481 1 11563 XP_047554.4 3 983 GTCGCCCACCCA C CA 3 C c
c

98 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 LOC1487 1 15671 XP_086286.4 3 1372 CTCTGTCGCCCA A 3 C b b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1487 2 6922 XP_086281.1 3 397 TCTAGTTGCCCA C CC 3 C b b

09 CACTAGAGTGCA CATTGCACTC AG TGGGCAA
ATGGCGCA GTAACGTGAG TC ACCCGTT
A AC
GAM7776 246 LOC1487 2 9201 XP_086281.1 5 143 CTCTGGTACTCA CA 3 C c b
09 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTGTG GTGGCGTGAGGTCGGACTC
AT
GAM7776 246 LOC1491 1 2184 XP_097598.1 5 3317 TCTTGTTGCCCA C 3 C b b
49 AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCGCG GTGACGTGAGGTCG ACCCGTT
A
GAM7776 246 LOC1491 1 12637 XP_086458.1 3 41 TTTTGTTGCCCA C----- CACT 3 C c
c

94 GGCTGGTCTCCA ATTG CCAGCCTGGGCAA
ATTTCTGG TAAC GGTCGGACCCGTT
GGTCTT CTCT
GAM7776 246 LOC1493 1 13354 NP_787072.1 3 371 CCCCGTCGCACA G A 3 C c c

71 GGCTGGAGTGCA CATTGCACTCCAGCCTG GC
GTGGCAAA GTGACGTGAGGTCGGAC CG
A C
GAM7776 246 LOC1494 1 16260 XP_086546.1 3 564 CTCTGTTGCCCA 3 C b b
66 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1494 1 5016 XP_086536.1 3 76 CTCTGTCGTCGA G A 3 C c c
78 GGCTGGAGTGTA CATTGCACTCCAGCCT GGC

GTGGTGCG GTGATGTGAGGTCGGA CTG
G C
GAM7776 246 LOC1495 1 2139 XP_097661.1 3 1639 CGCTGTTGCCCA C 3 C b b
06 GGCTGTAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGCG GTGACGTGA GTCGGACCCGTT
T
GAM7776 246 LOC1496 1 8887 XP_086600.1 3 1141 AGATTTTGCCCA GC AGC 3 C c
c
06 GAGGAGTAAATG CATT ACTCC CTGGGCAA
GAGGTGGG GTAA TGAGG GACCCGTT
A- A--
GAM7776 246 LOC1496 1 11025 XP_097706.1 3 613 CTCTGTCACCCA CA 3 C c c
92 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1497 1 10508 XP_097719.1 5 453 TTCTGCTGCCCA - C 3 C b b
03 AGCTGGAGTGGC CATTGC ACTCCAGC TGGGCA
AGTGGCAT GTGACG TGAGGTCG ACCCGT
G A
GAM7776 246 LOC1498 1 17917 XP_097733.1 5 13 GGTAGTTTGACC CT CT - 3 C c
c
32 TCCGTTGGTGCA CATTGCA CCAGC GGG CAA
ATGCCAGA GTAACGT GGTTG TCC GTT
-- CC A
GAM7776 246 LOC1500 1 5157 XP_097797.1 5 593 CTCTGTCGCCCA A 3 C b b
54 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCC GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1502 1 7207 XP_097870.1 3 1704 CTCTGTCGCTCA A 3 C b b
25 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACTCG
C
GAM7776 246 LOC1503 1 7485 XP_097894.1 5 386 ATGGAGCCTGCC - AG T 3 C c c

84 TTGGGGAGTGCA CAT TGCACTCC CC GGGCA
TGTGTTGG GTG ACGTGAGG GG TCCGT
T -- T
GAM7776 246 LOC1503 1 19467 XP_086907.1 3 479 CTCTGTCGTCCA C A 3 C c c
97 GGTTAGAGTGCA CATTGCACTC AGCCTGGGC
ATGGCTTG GTAACGTGAG TTGGACCTG
A C
GAM7776 246 LOC1505 1 16940 XP_097917.1 5 1616 CTCTGTTGCCCA 3 C b b
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1510 1 12075 XP_097998.1 3 1067 CTCTGTCACCCA CA 3 C c c

57 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC1511 1 19774 XP_098019.1 3 458 AAATGTACACCA T --- 3 C c c
96 GGCTGGGTGCGG CATTGCAC CCAGCCTGG GCA
TGGCTCAC GTGGCGTG GGTCGGACC TGT
- ACA
GAM7776 246 LOC1512 2 2572 XP_098021.1 3 1785 TTCTGTCACCCA C CA 3 C c b
01 GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
ATGGGGCG GTAAC TGAGGTCGGACCC
C AC
GAM7776 246 LOC1512 2 12725 XP_098021.1 3 367 ACGCTGTCACCA -- 3 C b b
01 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC1514 2 4174 XP_098063.1 5 739 CTCTGTCATCCA CA 3 C c b
75 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCT
AC
GAM7776 246 LOC1514 2 4371 XP_098063.1 5 100 CTCTGTGGCCCA A 3 C b b
75 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGATGTGAGGTCGGACCCG
G
GAM7776 246 LOC1516 1 2599 XP_087245.1 5 765 TGAGCCTGCACA CCA - G 3 C c
c
10 GAGCCAGGTGCA CATTGCACT GC CTG GCA
ATGGGCAG GTAACGTGG CG GAC CGT
AC- A A
GAM7776 246 LOC1516 3 2693 NP_612144.1 3 222 CTCTGTCGCTCG C A 3 C c c
36 CGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCATG GTGACGTGAGGTCG GCTCG
C C
GAM7776 246 LOC1516 3 4151 NP_612144.1 3 2151 CTGTGTCCCCCA CA 3 C c c
36 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
CC
GAM7776 246 LOC1516 3 14731 NP_612144.1 3 891 CTCTGTCACCCA C CA 3 C c
c
36 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGTGTG GTGACGT AGGTCGGACCC
A AC
GAM7776 246 LOC1516 1 4248 XP_098100.2 5 2082 CTGTGTCACCAA C----- A - -- 3 C c c
57 GGCTGGAGGGCA ATTGC CTCCAGCCT GG GCA
ATAGCATG TAACG GAGGTCGGA CC TGT
GTACGA G A AC
GAM7776 246 LOC1518 1 4677 XP_098132.1 3 897 CTGTGTTGCCCA TT C C----- 3 C c
c
77 GGCTAATATCGA CA GCA TC AGCCTGGGCAA
ATGCTTGG GT CGT AG TCGGACCCGTT
T- A CTATAA
GAM7776 246 LOC1522 1 9470 XP_098182.1 3 1274 CTCTGTCGCCCA ---- A 3 C c c

45 GGCTGGAGTGAG CATTGCAC TCCAGCCTGGGC
TGCAGTGG GTGACGTG AGGTCGGACCCG
AGTG C

GAM7776 246 LOC1524 1 2922 XP_098231.1 3 524 ATCTGTTGCCCA 3 C b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGAGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1526 1 1745 XP_011108.2 3 709 CTCTGTTGCCCA 3 C b b
20 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1527 2 11919 XP_098257.1 5 116 CTCTGTCGCCCA C A 3 C c c
19 GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGTG GTGACGT AGGTCGGACCCG
A C

GAM7776 246 LOC1527 2 17637 XP_098257.1 5 423 CTCTGTCGCCCA C A 3 C c c
19 GCCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGCACC GTGACGTGAGGTC GACCCG
C C

GAM7776 246 LOC1527 1 2010 XP_087525.1 5 422 GTCTGTTACCCA CA 3 C c c
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AT

GAM7776 246 LOC1528 1 9568 XP_098266.2 3 1700 TTTCTCGCACAG - G A 3 C c c
04 GCTTGGAGTGCA CATTGCACTCCA GCCTG GC
GTGGTGCG GTGACGTGAGGT CGGAC CG
T A C

GAM7776 246 LOC1530 1 5304 XP_098307.1 3 805 TGATATCACCCA CA 3 C c c
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC1538 3 9683 XP_087779.2 3 42 CTCTGTCACCCA A CA 3 C c b
11 GGCAGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
A AC

GAM7776 246 LOC1538 3 17512 XP_087779.2 3 1384 CTCTGTTGCCCA C 3 C b b
11 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGTGTA GTGACGTGAGGTC GACCCGTT
A

GAM7776 246 LOC1538 3 19665 XP_087779.2 3 962 ACCTGGTGCCCA - G 3 C b b
11 GGTGGAGGTGCA CATTGCAC TCCA CCTGGGCA
GTGGGGGT GTGACGTG AGGT GGACCCGT
G -

GAM7776 246 LOC1538 1 15929 XP_087798.1 5 128 TTCTTTTGCCCA 3 C b b
83 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1539 1 2882 XP_087801.1 5 188 CTCTGTAGCCCA C A 3 C c c
10 GTCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTACA GTGACGTGAGGTC GACCCG

T A

GAM7776 246 LOC1542 1 4307 XP_098505.1 5 117 GCTCTGTCGCCA -- 3 C b b
82 GGTTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTTGGACC TGT
GC

GAM7776 246 LOC1548 1 19205 XP_098618.3 5 2827 CTTTGTCAGCCA --- 3 C b b
22 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCAA
ATGTGCAA GTAACGTGAGGTCGGACC TGTT
GAC

GAM7776 246 LOC1548 3 3200 XP_098626.1 5 110 CTCTGTTGCCCA C 3 C b b
77 GTCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCGCA GTGACGTGAGGTC GACCCGTT
T

GAM7776 246 LOC1548 3 16089 XP_098626.1 3 1270 CTCTGTCGCCCA G A 3 C c
b
77 GGGTGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGCGTG GTGACGTGAGGT GGACCCG
G C

GAM7776 246 LOC1548 3 17731 XP_098626.1 3 3542 CCTCTGTTGCCA T C G 3 C c
b
77 GGCTGGAATGCC CAT GCA TCCAGCCTGG CAA
GTGGCGCA GTG CGT AGGTCGGACC GTT
C A -

GAM7776 246 LOC1550 1 17980 XP_088142.4 3 57 TGCTCCGGCCCA C A-- A 3 C c
c
66 GGCGGGGGAGTC CATTG ACTCC GCCTGGGC
AGTGCCCA GTGAC TGAGG CGGACCCG
- GGG G

GAM7776 246 LOC1580 1 2542 XP_088442.1 5 3580 TCTTGTCACCCA CA 3 C c c
14 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGATGTGAGGTCGGACCC
AC

GAM7776 246 LOC1582 1 5779 XP_098903.4 3 1267 CTCTTTCGCCCA C A A 3 C c c
28 GGCCGGACTGCA CATTGCA TCC GCCTGGGC
GTGGCAGG GTGACGT AGG CGGACCCG
C C C

GAM7776 246 LOC1583 1 14859 XP_098919.1 5 371 CTCTGTCGCCCA A 3 C b b
10 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C

GAM7776 246 LOC1583 1 6212 XP_048461.1 5 2535 TTGTGGAGGTTT T ----- GG 3 C c
c
81 TGTTGGTGTGCA CATTGCAC CCA GCCT GCAA
ATGGAGGA GTAACGTG GGT TGGA TGTT
T TGTTT GG

GAM7776 246 LOC1584 1 17964 XP_098936.1 5 140 CTCTGTTGCCCA 3 C b b
02 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1584 1 1263 XP_098942.1 3 643 CTCTGTCACTCA CA 3 C c c
36 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACTC
AC
GAM7776 246 LOC1584 1 935 XP_098955.1 3 893 CTCTGTCGCCCA A 3 C b b
76 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC1585 1 12003 XP_088608.1 3 908 GGACTCTGCCCA TT TCCA 3 C c
c
72 GGCCAGCGTGTT CA GCAC GCCTGGGCA
CTGAAAAT GT TGTG CGGACCCGT
CT CGAC
GAM7776 246 LOC1586 1 16260 XP_045161.1 3 426 CTCTGTTGCCCA 3 C b b
68 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1608 1 17208 XP_090573.3 5 537 CTCCGTAGCCCA A 3 C b b
97 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
A
GAM7776 246 LOC1624 2 8231 NP_835227.1 3 823 CTCTGTTGCCCA 3 C b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1624 2 8231 XP_091549.3 3 817 CTCTGTTGCCCA 3 C b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1624 2 12068 NP_835227.1 3 488 CTCTGTTGCCCA 3 C b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1624 2 12068 XP_091549.3 3 488 CTCTGTTGCCCA 3 C b b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC1629 1 3249 XP_091886.7 3 255 TCTCTGTCGCCA C -- 3 C b b
62 GGCTGGAATGCA CATTGCA TCCAGCCTGG GCA
GTGCAGTG GTGACGT AGGTCGGACC TGT
A GC
GAM7776 246 LOC1629 1 13831 XP_091890.6 3 380 CTCTGTCGCCCA C A 3 C c c
67 CGTTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGATGTG GTGACGTGAGGTTG ACCCG
C C
GAM7776 246 LOC1632 2 9147 NP_775802.1 3 1668 CTCTGTCACCCA CA 3 C c b
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC1632 2 11854 NP_775802.1 3 3358 TCTTGTTGCCCA C 3 C b b

27 AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGTGCA GTGACGTGAGGTCG ACCCGTT
A

GAM7776 246 LOC1640 1 7989 XP_089356.1 3 827 TCTTGTTGGCTA GC G 3 C c c
91 GGCTGGAGTAAA CATT ACTCCAGCCTGG CAA
ATGGTGCG GTAA TGAGGTCGGATC GTT
AA G

GAM7776 246 LOC1684 1 19786 XP_095114.2 3 696 CTCTGTAACCCA CA 3 C c c
51 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCCTG GTGACGTGAGGTCGGACCC
AA

GAM7776 246 LOC1704 1 15561 XP_096330.1 5 66 CAGCCTCATAAG T ----- A 3 C c c
09 GGCTGGAGTGCT CAT GCACTCCAGCCT GGGC
GTGGTGCC GTG CGTGAGGTCGGG TCCG
T AATAC A

GAM7776 246 LOC1962 1 2452 XP_113683.1 3 810 ACTCTGTCGCCA -- 3 C b b
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGTG GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 LOC1973 1 2432 XP_113869.1 3 2117 AAGAGAGGCCCA TT A- A 3 C c
c
42 GGCTGGGGCAGC CA GC CTCCAGCCTGGGC
CCTGAGAG GT CG GGGGTCGGACCCG
CC AC G

GAM7776 246 LOC1973 2 4625 XP_113872.2 3 1712 TCTTGTCGCCCA A 3 C b b
58 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 LOC1973 2 6387 XP_113872.2 3 2114 ATCTGTCACCCA CA 3 C c b
58 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC1997 1 10884 XP_117119.1 5 143 CTCTGTCACCTA C CA 3 C c c

25 GGCTGGATTGCA CATTGCA TCCAGCCTGGG
ATGGTGCA GTAACGT AGGTCGGATCC
T AC

GAM7776 246 LOC1998 2 5253 XP_117153.1 5 184 CTCTGTGTCTCA C - 3 C b b
99 GGCTGGAGTACA CATTG ACTCCAGCCTG GGCA
GTGGTGCA GTGAC TGAGGTCGGAC CTGT
A T

GAM7776 246 LOC1998 2 8292 XP_117153.1 3 67 CTTTGTCGCCCA C A 3 C c b
99 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGTGCG GTGAC TGAGGTCGGACCCG
A C

GAM7776 246 LOC1999 1 19756 XP_114052.1 3 1225 CTGTGTTGTCCA 3 C b b
06 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCTGTT

GAM7776 246 LOC2001 2 5066 XP_211599.1 3 1 CTGTCGTCCAGG C------- A 3 C c c

69 CTGGAGTGCAGT ATTGCACTCCAGCCTGGGC
ACGCAATC TGACGTGAGGTCGGACCTG
CTAACGCA C

GAM7776 246 LOC2001 2 6122 XP_117200.1 5 523 TTCTGTCGTCCA C----- A 3 C c c
69 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCGCA TGACGTGAGGTCGGACCTG
ACGCGA C

GAM7776 246 LOC2008 1 16540 XP_114306.1 5 176 GGGCACCGCGGA A- GG A 3 C c
c

44 GGCTGGAGCCGC CATTGC CTCCAGCCT GC
AATGGTGC GTAACG GAGGTCGGA CG
CC GG C

GAM7776 246 LOC2008 2 4175 XP_117289.1 3 649 TCTTGTTGTCCA 3 C b b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCA GTAACGTGAGGTCGGACCTGTT

GAM7776 246 LOC2008 2 12075 XP_117289.1 3 1713 CTCTGTCACCCA CA 3 C c b

60 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC2008 2 11863 NP_789785.1 3 935 TCTTGTTGCCCA A 3 C b b
95 GGCGGAGTGCAG CATTGCACTCC GCCTGGGCAA
TGGAACAA GTGACGTGAGG CGGACCCGTT
-

GAM7776 246 LOC2008 2 17681 NP_789785.1 3 935 CTCTTGTTGCCC A 3 C b b
95 AGGCGGAGTGCA CATTGCACTCC GCCTGGGCAA
GTGGAACA GTGACGTGAGG CGGACCCGTT
-

GAM7776 246 LOC2009 1 3465 XP_114317.3 3 322 TTCTGTCACCCA CA 3 C c c
16 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGACTCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC2011 2 13384 XP_290750.1 3 824 CTCTGTGGCCCA A 3 C b b
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
G

GAM7776 246 LOC2011 2 16993 NP_849158.1 3 824 CTCTGTGGCCCA A 3 C b b
64 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
G

GAM7776 246 LOC2012 1 4556 NP_775818.1 3 677 CTCTGTCACTCA C CA 3 C c c
92 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACA GTGAC TGAGGTCGGACTC
A AC

GAM7776 246 LOC2015 1 15044 XP_114343.2 3 1575 CTCTGTTGCCCA 3 C b b
62 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2017 1 5492 XP_114370.1 3 1955 CTCTATTGCTCA TG 3 C b b

25 GGCTGGAGTGTG CAT CACTCCAGCCTGGGCAA
GTGGCAGG GTG GTGAGGTCGGACTCGTT
GT
GAM7776 246 LOC2024 1 9145 XP_117397.1 5 32 CTCTGTCGCCCA A 3 C b b
00 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2024 1 18628 XP_114481.4 3 52 CTCTGTTGCCCA 3 C b b
04 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2024 1 16450 XP_114493.1 5 2041 GCTCTGTCACCA -- 3 C b b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGAGGC GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC2029 2 1729 XP_117486.2 3 1523 CTCTGTCACCCA C CA 3 C c
b
34 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 LOC2029 2 4820 XP_117486.2 3 2743 GCTCTGTCACCA -- 3 C b b
34 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC2035 2 2351 XP_114719.1 3 2894 CCTTCTTGCCCA CA----- 3 C c b

47 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
AGGGCGCA AACGTGAGGTCGGACCCGTT
ACGCGGG
GAM7776 246 LOC2035 2 9545 XP_114719.1 3 1379 CTCTGTTGCCCA 3 C b b
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2042 1 10724 XP_115295.1 3 931 CTCTGTCTCCCA TG CA 3 C c
c
88 GGCTGGAGTGTG CAT CACTCCAGCCTGGG
ATGGCGTG GTA GTGAGGTCGGACCC
GT TC
GAM7776 246 LOC2192 1 19361 XP_166599.2 3 1203 CTTGCTCGCCCA G A 3 C c c

93 GGGTGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGTGTG GTGACGTGAGGT GGACCCG
G C
GAM7776 246 LOC2197 1 2410 XP_167570.1 5 94 AGGAGTGCTGAG G G- 3 C c c
00 GGCTGGAGTGGG CATT CACTCCAGCCT GGCA
TGGGCCCT GTGG GTGAGGTCGGG TCGT
- AG
GAM7776 246 LOC2197 1 4678 XP_167596.1 5 1058 CTCTGTCATCCA CA 3 C c c
31 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCAAA GTGACGTGAGGTCGGACCT

AC
GAM7776 246 LOC2197 1 18913 XP_167601.1 3 868 CTCTGTTGCCCA C----- 3 C c c
35 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTCGCACA TGACGTGAGGTCGGACCCGTT
ACACGC
GAM7776 246 LOC2198 1 14588 XP_167782.1 3 1073 TCTGTTGCCCCA - 3 C b b
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG CAA
GTGGCGTG GTGACGTGAGGTCGGACCC GTT
C
GAM7776 246 LOC2200 3 6497 NP_660352.1 3 213 CTCTGTCACACA --- 3 C b b
74 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCACG GTGACGTGAGGTCGGAC CTGT
ACA
GAM7776 246 LOC2200 3 9147 NP_660352.1 3 543 CTCTGTCACCCA CA 3 C c b
74 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2200 3 16838 NP_660352.1 3 383 ACTCGTCACCCC C CA 3 C c
b
74 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCG GTGACGTGAGGTCG ACCC
- CA
GAM7776 246 LOC2211 1 17256 XP_167915.1 5 38 AGAAGCTGAAAA CTG--- A 3 C c
c
74 AGCTGGAGTGCA CATTGCACTCCAGC GGC
ATGGCACC GTAACGTGAGGTCG TCG
AAAAAG A
GAM7776 246 LOC2216 1 1939 XP_168131.1 5 811 CTCTGTTGCCAA G 3 C b b
63 GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
GTGGAACG GTGACGTGAGGTCGGA CCGTT
A
GAM7776 246 LOC2219 1 15948 XP_168340.1 3 921 GAGAATCGCTTG CT A 3 C c c

46 AGCTGGAGTGCA CATTGCACTCCAGC GGGC
GTGGTGCA GTGACGTGAGGTCG TTCG
AG C
GAM7776 246 LOC2219 1 14860 XP_165859.1 3 376 CTCCGTGACCCA C - 3 C b b
60 GGCTGGAATGCA CATTGCA TCCAGCCTGGG CA
ATGGCTCA GTAACGT AGGTCGGACCC GT
A A
GAM7776 246 LOC2219 1 17029 XP_168342.1 3 57 CTCTGTCTCCCA C CA 3 C c c
64 GGCTGGACTGCA CATTGCA TCCAGCCTGGG
GTGGTGCG GTGACGT AGGTCGGACCC
C TC
GAM7776 246 LOC2220 1 12803 XP_166594.2 5 744 TCTGTTGTCCAA C----- - 3 C c c
57 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM7776 246 LOC2220 1 3232 XP_166556.1 3 655 TCTTGTCGCCCA A 3 C b b
68 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

ATGGCGTG GTAACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2221 1 16228 XP_212100.1 5 76 CGCAGGCTGCCA C T G 3 C c c
59 GGCTGGCGTACA CATTG AC CCAGCCTGG CA
GTGGCGCA GTGAC TG GGTCGGACC GT
A C -
GAM7776 246 LOC2529 1 2959 XP_170858.2 3 279 CTCTGTCGCCCA C----- A 3 C c c
83 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
ATACTGCA TAACGTGAGGTCGGACCCG
ACGTCA C
GAM7776 246 LOC2536 1 5487 XP_172985.2 5 301 CTCTGTCTCCCA CA 3 C c c
12 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGCACA GTGGCGTGAGGTCGGACCC
TC
GAM7776 246 LOC2538 1 4532 XP_172854.1 3 1254 CTCTGTTGCCCA 3 C b b
05 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGATGTG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2548 1 6188 XP_171170.1 3 281 TGGAGAAATTCA T CA 3 C c c
75 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA
GAM7776 246 LOC2550 1 3261 XP_173187.1 3 221 GCACGGGGCCCA C A 3 C c c
31 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCGTG GTGACGTGAG TCGGACCCG
A G
GAM7776 246 LOC2551 1 6294 XP_172941.1 3 613 TCTCGTTGCCCA 3 C b b
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2554 1 6365 XP_173150.1 5 386 CAAAGCCCTTCA C --- A 3 C c c
58 GGCTGGAGTATA CATTG ACTCCAGCCT GGGC
GTGGCATG GTGAT TGAGGTCGGA CCCG
A CTT A
GAM7776 246 LOC2554 1 3150 XP_172581.2 3 2634 CTTTGTCACCCA A CA 3 C c c
88 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCATG GTGACGTGAGG CGGACCC
C AC
GAM7776 246 LOC2559 1 12803 XP_171083.2 5 864 TCTGTTGTCCAA C----- - 3 C c c
75 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM7776 246 LOC2566 1 7385 XP_172864.1 3 861 CTCTGTCACCCA CA 3 C c c
14 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2829 1 986 XP_212606.1 5 165 CTCTGTCGCCAA CTG A 3 C c c

```
          05                        AGTTGGAGTGCA CATTGCACTCCAGC  GGC
                                   GTGGCGCG   GTGACGTGAGGTTG  CCG
                                              AAA  C
GAM7776  246   LOC2829 1  986   XP_212647.1  5  165   CTCTGTCGCCAA          CTG  A       3  C  c  c

          43                        AGTTGGAGTGCA CATTGCACTCCAGC  GGC
                                   GTGGCGCG   GTGACGTGAGGTTG  CCG
                                              AAA  C
GAM7776  246   LOC2829 1  814   XP_210834.1  3  1912  ATGGCCATGCTG  T -     TG G       3  C  c
c
          63                        GGCTGGAGTGGC CAT GC ACTCCAGCC  G CA
                                   TGTGGGGT   GTG CG TGAGGTCGG  C GT
                                              T  G       GT -
GAM7776  246   LOC2829 1  18172  XP_210837.1  3  862   CTCTGTCTCCTA     A       CA       3  C  c  c

          72                        GGCTGGAGCGCA CATTGC CTCCAGCCTGGG
                                   GTGGTGCA   GTGACG GAGGTCGGATCC
                                              C          TC
GAM7776  246   LOC2829 2  12068  XP_210845.1  3  528   CTCTGTTGCCCA                    3  C  b  b
          87                        GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                   GTGGTGTG   GTGACGTGAGGTCGGACCCGTT

GAM7776  246   LOC2829 2  16541  XP_210845.1  5  34    CTTTGTCACCCA    C        CA       3  C  c  b
          87                        GGCTGGAGTATA CATTG ACTCCAGCCTGGG
                                   GTGGCACA   GTGAT TGAGGTCGGACCC
                                              A          AC
GAM7776  246   LOC2829 1  11798  XP_208473.1  3  987   CCCTGTTGCCCA    A               3  C  b  b
          97                        GGCTGGAGAGCA CATTGC CTCCAGCCTGGGCAA
                                   GTGGTGCA   GTGACG GAGGTCGGACCCGTT
                                              A
GAM7776  246   LOC2830 1  17587  XP_210870.1  3  415   CAGAGTAGTTCA    A --       A       3  C  c  c
          47                        GGCTGGGTGGAG CATTGC CT  CCAGCCTGGGC
                                   CAGTGGGA   GTGACG GG  GGTCGGACTTG
                                              A  TG         A
GAM7776  246   LOC2830 1  7252   XP_210875.1  3  1388  GTTTGTCACCCA           CA       3  C  c  c
          61                        GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                   GTGGCATG   GTGACGTGAGGTCGGACCC
                                              AC
GAM7776  246   LOC2830 1  4176   XP_208509.1  3  178   TTGTGTTCCCCA      C      CA       3  C  c  c
          87                        GGCTGAAGTGCA CATTGCACT CAGCCTGGG
                                   GTGGCATG   GTGACGTGA GTCGGACCC
                                              A        CT
GAM7776  246   LOC2830 1  2219   XP_210885.1  5  1721  CTCTGTCGCCCA       C      A       3  C  c  c
          89                        GGCTCGAGTGCA CATTGCACTC AGCCTGGGC
                                   GTGGCATG   GTGACGTGAG TCGGACCCG
                                              C        C
GAM7776  246   LOC2831 1  16397  XP_210895.1  3  712   CTCTCTTGCCCA                    3  C  b  b
          19                        GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                   GTGGTATG   GTGACGTGAGGTCGGACCCGTT
```

GAM7776 246 LOC2831 1 5323 XP_208525.3 3 380 CTCTGTCACCCA C CA 3 C c c
30 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGTG GTGACGT AGGTCGGACCC
A AC
GAM7776 246 LOC2831 1 12544 XP_210911.1 3 454 ACCCTGTTGCCA C G 3 C b b
40 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGCG GTGACGT AGGTCGGACC GTT
A -
GAM7776 246 LOC2831 1 19977 XP_210925.1 3 177 ATCTTCTCAGGC C--- CA 3 C c
c
42 TCACTGAGTGCA CATTGCACTC AGCCTGGG
ATGTCTGC GTAACGTGAG TCGGACTC
TCAC TT
GAM7776 246 LOC2831 1 2650 XP_210920.1 3 2296 ACTCTGTCACCA -- 3 C b b
43 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC2831 1 19812 XP_210917.2 5 317 CTCTGTCATCCA CA 3 C c c
52 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCT
AC
GAM7776 246 LOC2831 1 4979 XP_208535.1 3 649 CTCTGTTGCCCA 3 C b b
70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGAG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2831 1 15574 XP_210903.1 3 985 TCTTGTTGCCCA 3 C b b
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACA GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2832 1 10112 XP_208555.2 3 1675 TACTGTTGTCCA C----- A 3 C c c
15 GGCTGGAGCGCA ATTGC CTCCAGCCTGGGCAA
GTTGATTG TGACG GAGGTCGGACCTGTT
GTTAGT C
GAM7776 246 LOC2832 1 9525 NP_787089.1 5 63 CTCTGTCGCCCA A 3 C b b
41 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTTGGACCCG
C
GAM7776 246 LOC2832 1 4496 XP_208583.2 3 1432 ACAGCAGCCCTG T G -- A 3 C c
c
44 GGGGTGGGTGCA CATTGCAC CCA CCT GGGC
ATGAGGAT GTAACGTG GGT GGG CCCG
- G GT A
GAM7776 246 LOC2832 1 8223 XP_210952.1 5 554 CCTTGTTGCCCA TTG CT- 3 C c
c
62 GGCTGGTCTTGA CA CA CCAGCCTGGGCAA
ACTGGGCT GT GT GGTCGGACCCGTT
CAA TCT
GAM7776 246 LOC2832 1 9036 XP_210961.1 3 2048 TCTTGTTGCCCA 3 C b b

78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2832 1 17952 XP_210962.1 3 346 CTCTGTCACCCA CA 3 C c c
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2832 1 9585 XP_210965.1 5 438 CTCTGTCTCCGA --- 3 C b b
99 GGCTGGAGTGCA CATTGCACTCCAGCCT GGGCA
ATGTTGCA GTAACGTGAGGTCGGA TCTGT
GCC
GAM7776 246 LOC2833 1 2201 XP_210978.1 5 938 CTCTGTCGCCCA C A 3 C b b
29 GACTGGAGTGCA CATTGCACTCCAG CTGGGC
ATGGTGCG GTAACGTGAGGTC GACCCG
A C
GAM7776 246 LOC2833 2 2143 XP_210981.1 3 1369 CTCTGTTGCCCA 3 C b b
35 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGATGTGAGGTCGGACCCGTT

GAM7776 246 LOC2833 2 16144 XP_210981.1 3 1637 CTCTGTCACCCA A CA 3 C c
b
35 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGTGCG GTGACGTGAGG CGGACCC
C AC
GAM7776 246 LOC2833 1 8232 XP_208647.1 3 808 CTCTGTCACCCA CA 3 C c c
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2833 1 7265 XP_211007.1 3 1634 CTCTTACGCCCA G C A 3 C c
c
87 GGCTGGAATGAA CATT CA TCCAGCCTGGGC
GTGGCATG GTGA GT AGGTCGGACCCG
A A C
GAM7776 246 LOC2833 1 1730 XP_211021.1 5 134 CTCTGTTGCCCA C 3 C b b
94 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCACA GTGAC TGAGGTCGGACCCGTT
A
GAM7776 246 LOC2833 1 9003 XP_211020.1 3 528 ACTCTGTTGCTA G 3 C b b
95 GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCACA GTGACGTGAGGTCGGATC GTT
-
GAM7776 246 LOC2834 1 19206 XP_211024.1 5 444 CTCTGTCGCCAA A G A 3 C c
c
00 GGCTGGAGGGCA CATTGC CTCCAGCCT GGC
ATGGCATG GTAACG GAGGTCGGA CCG
G A C
GAM7776 246 LOC2834 1 16658 XP_211032.1 5 1943 GCTGTATTGCCA C G 3 C b
b
32 GACTGGAGTGCA CATTGCACTCCAG CTGG CAA
GTGGCGTG GTGACGTGAGGTC GACC GTT

A -
GAM7776 246 LOC2834 1 2220 XP_211043.1 3 165 CTCTGTCGCCCA C A 3 C c c
41 GGCTGCAGTGCG CATTGCACT CAGCCTGGGC
GTGGTGCG GTGGCGTGA GTCGGACCCG
C C
GAM7776 246 LOC2834 1 10032 XP_211037.1 5 974 CACCTCTTGCCA C --- -- G 3 C c c
42 GGCTGCAGAGCT ATTGCA CTC CAGCCTGG CAA
ATGCAGTC TGACGT GAG GTCGGACC GTT
C ATC AC -
GAM7776 246 LOC2834 1 5683 XP_211044.1 5 306 CTGTGTCATGCA --- 3 C b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCATG GTGACGTGAGGTCGGAC CTGT
GTA
GAM7776 246 LOC2834 1 7397 XP_208679.1 5 490 GTCTGACACCTG TG CA 3 C c
c
52 GGCTGGAGTGCA CATTGCACTCCAGCC GG
GTGGTGCA GTGACGTGAGGTCGG CC
GT AC
GAM7776 246 LOC2834 1 14861 XP_211049.1 5 128 CTCTGTCACCCA CA 3 C c c
54 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2834 1 13967 XP_211050.1 3 1034 AAACCTTTGTCA A T G 3 C c c
67 GGCTGGGCGCGG CATTGC C CCAGCCTGG CAA
TGGCTCAC GTGGCG G GGTCGGACT GTT
C - -
GAM7776 246 LOC2834 1 9892 XP_211056.1 3 1714 TTCTCTTGCCCA 3 C b b
75 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2834 1 17710 XP_211053.1 5 1048 CTCTGTCCCCTG --- 3 C b b
84 GGCTGGAGTGCA CATTGCACTCCAGCCT GGGCA
ATGGTGCG GTAACGTGAGGTCGGG CCTGT
TCC
GAM7776 246 LOC2834 1 7371 XP_211062.1 3 676 CTCTGTTACCCA C CA 3 C c c
87 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCGTG GTAACGTGAG TCGGACCC
A AT
GAM7776 246 LOC2835 1 12075 XP_211075.1 3 1820 CTCTGTCACCCA CA 3 C c c
07 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2835 1 3199 XP_211083.1 3 3279 CTCTGTCACCCA CA 3 C c c
34 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2835 1 13652 XP_211118.1 3 37 CTCTGCTCCCCA G C CA 3 C c
c

70 GGCTTGAGTGAG CATT CACTC AGCCTGGG
TGTGTGCC GTGA GTGAG TCGGACCC
- T CT
GAM7776 246 LOC2835 2 6183 XP_211095.1 5 421 CTCTGTTGCCCA CAT----- C 3 C c
c
75 GGCTAGAGTGCA TGCACTC AGCCTGGGCAA
CTAATACA ACGTGAG TCGGACCCGTT
ACATAATC A
GAM7776 246 LOC2835 2 10067 XP_211095.1 5 885 CTCTGTTGCCCA C TC 3 C c c

75 GGCTGAGGTACA CATTG AC CAGCCTGGGCAA
GTGGCGTG GTGAC TG GTCGGACCCGTT
A GA
GAM7776 246 LOC2835 1 10466 XP_294741.1 5 480 CTCTGTCACCCA T C CA 3 C c
c
85 AGCTGGAGTGCA CA TGCACTCCAGC TGGG
CTGGCATG GT ACGTGAGGTCG ACCC
C A AC
GAM7776 246 LOC2835 1 10638 NP_787093.1 3 911 CTCTGTTGCCCA 3 C b b
88 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGACTC GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC2836 1 4420 XP_211126.1 5 3889 CTCTGTTGCCCA C 3 C b b
24 GGCTGGAGTCCA CATTG ACTCCAGCCTGGGCAA
GTGGCATG GTGAC TGAGGTCGGACCCGTT
C
GAM7776 246 LOC2836 2 3581 XP_211134.1 5 1238 CTCTGTCGCCCA C A 3 C c b
37 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGTATG GTGACGTGAG TCGGACCCG
A C
GAM7776 246 LOC2836 2 14859 XP_211134.1 5 361 CTCTGTCGCCCA A 3 C b b
37 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2836 1 17964 XP_208764.1 3 227 CTCTGTTGCCCA 3 C b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2836 1 16674 XP_211147.1 5 893 CTCTGTCGCCCA CAC A 3 C c
c
63 GGCTGGACTACA CATTG TCCAGCCTGGGC
ATGGCACG GTAAC AGGTCGGACCCG
ATC C
GAM7776 246 LOC2836 1 8450 XP_208773.1 5 12 TTTTGTCACCCA T CA 3 C c c
64 GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
ATGGCACG GTA CGTGAGGTCGGACCC
C AC
GAM7776 246 LOC2836 1 1730 XP_211152.1 5 19 CTCTGTTGCCCA C 3 C b b
72 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCACA GTGAC TGAGGTCGGACCCGTT

A

GAM7776 246 LOC2836 1 11904 NP_787094.1 3 1229 TTTTGTCACCGA G CA 3 C c c

87 GGCTGGAGTGCA CATTGCACTCCAGCCT GG
ATGGCCCG GTAACGTGAGGTCGGA CC
G AC

GAM7776 246 LOC2836 1 5305 XP_208788.1 3 334 AGAAATTTGTCA T G 3 C b b

93 GGCTGGGTGCAG CATTGCAC CCAGCCTGG CAA
TGGCTCAT GTGACGTG GGTCGGACT GTT
- -

GAM7776 246 LOC2837 2 13716 XP_211170.3 3 1559 CCTTCTTCCCCA G - CA 3 C c b

01 GGCTGGGAGTGG CATT CACTCC AGCCTGGG
GTGAGACG GTGG GTGAGG TCGGACCC
- G CT

GAM7776 246 LOC2837 2 14381 XP_211170.3 3 3386 GCTCTGTCACCA -- 3 C b b

01 GGCTGGAGTGCG CATTGCACTCCAGCCTGG GCA
GTGGCATA GTGGCGTGAGGTCGGACC TGT
AC

GAM7776 246 LOC2837 1 9256 XP_211176.1 5 751 AAAAATTTGAAC CC - GG 3 C c c

23 GAGGCTAGTGCA CATTGCACT AGCCT G CAA
ATGTTTTG GTAACGTGA TCGGA C GTT
-- G AA

GAM7776 246 LOC2837 1 11523 XP_208115.1 3 290 CTCTGTCGCCCA A 3 C b b

41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 LOC2837 1 12479 XP_208835.1 3 299 CGCTGTTGCCCA CC 3 C b b

67 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC

GAM7776 246 LOC2837 1 4370 XP_211199.1 5 1257 CTCTGTCGCCCA A 3 C b b

78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGGG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 LOC2837 1 17644 XP_211198.1 3 2590 ACGACAGACCCA T ---- CA 3 C c c

79 GGCTGGAGTCTT CAT GC ACTCCAGCCTGGG
GGCTGTGC GTG CG TGAGGTCGGACCC
T GTTC AG

GAM7776 246 LOC2838 1 6265 XP_208122.1 3 1461 TAGTGTTGCCCA 3 C b b

01 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2838 1 16700 XP_208850.1 3 949 CTCTGTCATCCA CA 3 C c c

02 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCT
AC

GAM7776 246 LOC2838 1 9546 XP_211218.1 3 256 CTCTGTCACCCC T CA 3 C c c
18 GGCTGGAGTGCA CATTGCACTCCAGCC GGG
GTGGTGTG GTGACGTGAGGTCGG CCC
C AC
GAM7776 246 LOC2838 1 4308 NP_848611.1 5 92 TGGAGTTGCCCA GCA - -- 3 C c c
49 GGCCCTGTGAGC CATT CTC CA GCCTGGGCAA
AAGTGGCA GTGA GAG GT CGGACCCGTT
AC- T CC
GAM7776 246 LOC2838 1 4308 XP_208870.1 5 92 TGGAGTTGCCCA GCA - -- 3 C c c
49 GGCCCTGTGAGC CATT CTC CA GCCTGGGCAA
AAGTGGCA GTGA GAG GT CGGACCCGTT
AC- T CC
GAM7776 246 LOC2838 1 4974 XP_211229.1 3 679 CTCTGTCACCGA G CA 3 C c c
51 GGTTGGAGTGCA CATTGCACTCCAGCCT GG
GTGGTATG GTGACGTGAGGTTGGA CC
G AC
GAM7776 246 LOC2838 1 6184 XP_211233.1 3 694 AAAGACTGAAGA GGG 3 C c c
56 GGCTGGAGTGCA CATTGCACTCCAGCCT CA
GTGGCGCA GTGACGTGAGGTCGGA GT
GAA
GAM7776 246 LOC2838 2 1401 NP_787095.1 3 713 CTCTGTCGTCCA A 3 C b b
61 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCTG
C
GAM7776 246 LOC2838 2 1635 NP_787095.1 3 1035 CTCTGTCGACCA CA----- --- 3 C c
b
61 GGCTGGAGTGCA TTGCACTCCAGCCTGG GCA
GGGGCACA GACGTGAGGTCGGACC TGT
ACACGGG AGC
GAM7776 246 LOC2838 1 13285 XP_208875.1 3 1506 GCTTGTTGCCCA 3 C b b
63 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2838 1 18993 XP_211248.2 5 724 CTCTGTCTCCCG CA 3 C c c
87 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGGCCC
TC
GAM7776 246 LOC2838 2 11072 XP_211249.1 3 1413 GTCCCAGCTCCA CA - A 3 C c
b
88 GGCTGGAGCCAG CATTG CTCCAGCCTGG GC
TGAAGGGT GTGAC GAGGTCGGACC CG
C- T A
GAM7776 246 LOC2838 2 14104 XP_211249.1 3 1551 CTCTGCTGCCCA C 3 C b b
88 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCA
GTGGTGCC GTGACGT AGGTCGGACCCGT
A

GAM7776 246 LOC2838 2 3899 XP_208899.1 3 784 TTCTGTCACCCA A CA 3 C c c
89 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGTGTA GTGACGTGAGG CGGACCC
C AC
GAM7776 246 LOC2838 2 10739 XP_208899.1 5 290 ATTCTAGGCAGA C GG A 3 C c
c
89 GGCTGGAATGCA CATTGCA TCCAGCCT GC
ATGATGCG GTAACGT AGGTCGGA CG
A GA G
GAM7776 246 LOC2839 2 4703 XP_208909.1 5 2420 TTCTGCTGCCCA 3 C b b
28 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACG GTGACGTGAGGTTGGACCCGT

GAM7776 246 LOC2839 2 20101 XP_208909.1 5 2716 CTCTGTTGCCCA 3 C b b
28 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGTCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2839 1 15775 XP_208905.2 5 920 CTCCGTCACCCA CA 3 C c c
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2839 1 19569 XP_208145.2 3 1458 TAGTGTCACCCA CA 3 C c c

64 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGATCCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2840 2 11764 XP_208958.2 3 2380 ATCATGGGTCCA ACTC A 3 C c
c
01 GGCTGATAGCAA CATTGC CAGCCTGGGC
TGGACAGA GTAACG GTCGGACCTG
ATA- G
GAM7776 246 LOC2840 2 18161 XP_208958.2 3 1485 CACTGTCGCCCA T CC A 3 C c
c
01 ATCTGGAGTGCA CA TGCACTCCAG TGGGC
CTGGCGCT GT ACGTGAGGTC ACCCG
C TA C
GAM7776 246 LOC2840 1 3244 XP_211298.1 3 17 CTCTTGTTGCCT C 3 C b b
16 AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCGCA GTAACGTGAGGTCG ATCCGTT
-
GAM7776 246 LOC2840 1 18610 XP_208961.1 3 354 CTCTGTAACTCA CA 3 C c c
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACTC
AA
GAM7776 246 LOC2840 1 10124 XP_211302.1 3 2841 CTCTGTTGCCCT C T 3 C b b

19 GGCTGGAGTACA CATTG ACTCCAGCC GGGCAA
GTGGCATG GTGAC TGAGGTCGG CCCGTT
A T
GAM7776 246 LOC2840 2 14597 XP_208983.3 3 1018 CTGTGTCGCCCA A 3 C b b

23 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2840 2 17953 XP_208983.3 3 1473 CTCTGTTGCCCA C 3 C b b
23 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCGTG GTGACGTGAGGTC GACCCGTT
A
GAM7776 246 LOC2840 1 10847 XP_208152.1 3 1242 CACTGTCACCCA A CA 3 C c
c
48 GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCACA GTGACGTGAGG CGGACCC
C AC
GAM7776 246 LOC2840 2 1596 XP_211321.1 3 58 CCCTGTTGCCCA C 3 C b b
74 GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGCG GTGACGTGA GTCGGACCCGTT
A
GAM7776 246 LOC2840 2 15531 XP_211321.1 3 983 CTCAGTCGCCCA A 3 C b b
74 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2840 1 18527 XP_211323.1 3 2 CTGTCACCCAGG C CA 3 C c c
82 CTGAAGTGCAGT CATTGCACT CAGCCTGGG
GCAGGACC GTGACGTGA GTCGGACCC
A AC
GAM7776 246 LOC2840 3 7333 XP_211324.1 3 845 CTCTGTCACCCT T CA 3 C c b
95 GGCTGGAGTGCG CATTGCACTCCAGCC GGG
GTGGCGAT GTGGCGTGAGGTCGG CCC
T AC
GAM7776 246 LOC2840 3 11799 XP_211324.1 3 1043 CTCTTTCGCCCA C A A 3 C c
b
95 GGCCGGACTGCA CATTGCA TCC GCCTGGGC
GTGGCGCA GTGACGT AGG CGGACCCG
C C C
GAM7776 246 LOC2840 3 15513 XP_211324.1 3 143 CTCTGTCATTCA --- 3 C b b
95 GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGTGCA GTGACGTGAGGTCGGAC CTGT
TTA
GAM7776 246 LOC2840 1 8582 XP_209008.3 3 198 CTCTGTTACCCA CA 3 C c c
98 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCC GTGATGTGAGGTCGGACCC
AT
GAM7776 246 LOC2841 1 1777 XP_209015.1 3 1541 TCCAGTGCTCCA T A - 3 C c c
00 GGCTGGGGGCCG CAT GC CTCCAGCCTGG GCA
TGGATCCT GTG CG GGGGTCGGACC CGT
C - T
GAM7776 246 LOC2841 1 19537 XP_209019.1 5 411 CTCTGTTGCCCA --- 3 C b b
01 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA
GAM7776 246 LOC2841 3 3233 XP_211327.3 3 608 TTTTGTTGCCCA CA----- 3 C c b

02 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGCGCG AACGTGAGGTCGGACCCGTT
GCGCGGC
GAM7776 246 LOC2841 3 7745 XP_211327.3 5 862 CTTTGTCACCCA CA 3 C c b
02 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2841 3 18149 XP_211327.3 5 46 TCTTGCCGTCCA A 3 C b b
02 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGTG GTAACGTGAGGTCGGACCTG
C
GAM7776 246 LOC2841 2 1966 XP_211342.1 3 461 CCCTGTCGCCCA T A 3 C b b
28 GGCTGGAGTGCC CAT GCACTCCAGCCTGGGC
ATGGCGCG GTA CGTGAGGTCGGACCCG
C C
GAM7776 246 LOC2841 2 17271 XP_211342.1 3 0 TCGCCCAGGCTG A 3 C b b
28 GAGTGCAGTGGT CATTGCACTCCAGCCTGGGC
AGATCAGG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2841 1 12779 XP_209032.1 3 540 GACTGTTGCCCA 3 C b b
35 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
ATGGCGCC GTAATGTGAGGTCGGACCCGTT

GAM7776 246 LOC2841 1 4102 XP_211353.1 5 368 GCTCTGTCGCCA -- 3 C b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
ATGGCGCG GTAACGTGAGGTCGGACC TGT
GC
GAM7776 246 LOC2841 1 11530 XP_209051.1 3 1095 TGTTGTCGCCTA A 3 C b b
71 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGATGCG GTAACGTGAGGTCGGATCCG
C
GAM7776 246 LOC2841 2 1111 XP_209059.1 5 422 TCTCGTTGCCAA G 3 C b b
83 GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
ATGGCACG GTAACGTGAGGTCGGA CCGTT
A
GAM7776 246 LOC2841 2 9456 XP_209059.1 5 922 ATCGATAGCCCA C A A 3 C c b

83 GGCAGGAGTACA CATTG ACTCC GCCTGGGC
GTGGCACA GTGAC TGAGG CGGACCCG
A A A
GAM7776 246 LOC2841 1 14861 XP_209060.2 3 1162 CTCTGTCACCCA CA 3 C c c

86 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2841 1 4421 XP_211377.1 5 64 TCTTGTCGCCCA CA----- A 3 C c c
91 GGCTGGAGTGCA TTGCACTCCAGCCTGGGC
ACGGTATG AACGTGAGGTCGGACCCG
GTATGGC C
GAM7776 246 LOC2842 1 3800 XP_208174.2 3 2063 TCAGTGCTCTCA - CT- 3 C c c

02 GCTGGCAGTGCA CATTGCACT CCAGC GGGCA
ATGCTTGT GTAACGTGA GGTCG CTCGT
C ACT
GAM7776 246 LOC2842 1 8494 XP_211411.1 5 1562 ATCTGTCACCCA CA 3 C b b
67 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCATG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2842 1 1026 XP_211412.1 5 1027 CTTTGTCACCCA CA 3 C b b
76 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2842 1 19875 XP_211419.1 3 1829 CTCTGTCTCCCA CA 3 C c c
86 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 LOC2842 2 1885 XP_209105.1 3 146 TCTTGTTACCCA A CA 3 C c c
89 GGCAGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCGTG GTGACGTGAGG CGGACCC
A AT
GAM7776 246 LOC2842 2 16648 XP_209105.1 3 311 CCACATTGGCCA GCACT G 3 C
c c
89 GGCTGGTCTCAA CATT CCAGCCTGG CAA
ATGACCCT GTAA GGTCGGACC GTT
ACTCT G
GAM7776 246 LOC2842 1 1751 XP_209112.1 3 1370 GGTGCCTGCCCA GCA - AG- 3 C
c c
97 GGATGGGTAGGA CATT CT CC CCTGGGCA
AATGCTGA GTAA GA GG GGACCCGT
AG- T GTA
GAM7776 246 LOC2843 1 4849 XP_211426.1 3 315 TCTTATTGCCCA 3 C b b
04 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACGAG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2843 2 3386 XP_209162.1 3 1766 CTCTCTCGCCCA A 3 C b b
17 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2843 2 7077 XP_209162.1 3 813 TTCTGTCACACA T C --- 3 C c b
17 GTCTGGAGTGCT CAT GCACTCCAG CTG GGCA
GTGGTGCA GTG CGTGAGGTC GAC CTGT
T T ACA
GAM7776 246 LOC2843 1 1731 XP_209143.1 3 1033 TTCTGTCGTCCA A 3 C c c
25 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGGCGTGAGGTCGGACCTG
C
GAM7776 246 LOC2843 1 11986 XP_211437.1 3 437 CTTTGTGCCCTA C - 3 C b b
56 GACTGGAGTGCA CATTGCACTCCAG CT GGGCA
ATGGCGCC GTAACGTGAGGTC GA CCCGT
A T

GAM7776 246 LOC2843 1 18898 XP_211435.1 3 530 ACTTGTCACCCA CA 3 C c c
62 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2843 1 16701 XP_209154.1 3 931 CTCTGTCATCCA CA 3 C c c
75 GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTTGGACCT
AC
GAM7776 246 LOC2843 1 19718 XP_209157.1 3 664 TCTTATTGCCCA 3 C b b
76 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2843 1 9312 XP_209163.1 3 384 CTCTATTGCCCA C 3 C b b
79 GTCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATG GTGACGTGAGGTC GACCCGTT
T
GAM7776 246 LOC2843 1 16459 XP_211454.1 5 125 CTGTTTGGCCCA T ACT - A 3 C c
c
95 GGCCTGGGCCAT CAT GC CCAG CCTGGGC
GACGGATG GTA CG GGTC GGACCCG
C --- C G
GAM7776 246 LOC2843 1 10399 XP_211452.1 3 1675 CTGTGTTGTCCA 3 C b b
96 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGTG GTAACGTGAGGTCGGACCTGTT

GAM7776 246 LOC2844 2 2645 XP_209183.2 3 1651 TTCTGTCCCCGA A --- 3 C b b
05 GGCCGGAGTGCA CATTGCACTCC GCCT GGGCA
ATGGCGTG GTAACGTGAGG CGGA CCTGT
C GCC
GAM7776 246 LOC2844 2 19462 XP_209183.2 3 908 CTCTGTCACCCA C C CA 3 C c
b
05 GGCTGTAGTACA CATTG ACT CAGCCTGGG
GTGGTGCC GTGAC TGA GTCGGACCC
A T AC
GAM7776 246 LOC2844 1 14364 XP_211443.1 5 367 CTCTGTTGCCCA T 3 C b b
08 GGCTGGTGTGTA CATTGCAC CCAGCCTGGGCAA
GTGATCTC GTGATGTG GGTCGGACCCGTT
T
GAM7776 246 LOC2844 1 17304 XP_211449.1 3 638 GTGGTTGCTGAA TG- G- 3 C c
c
10 GGCTGGAGTGGG CAT CACTCCAGCCT GGCAA
TGTGGCAA GTG GTGAGGTCGGA TCGTT
TGG AG
GAM7776 246 LOC2844 2 4533 XP_209200.1 5 1199 CTCTGTTGCCCG 3 C b b
21 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGGCCCGTT

GAM7776 246 LOC2844 2 15844 XP_209200.1 5 1328 CTATGTTGCCCA CA------ CT 3 C c
b
21 GGCTGGTTGCAA TTGCA CCAGCCTGGGCAA

ACTTCTGG AACGT GGTCGGACCCGTT
GGTCTTCA T-
GAM7776 246 LOC2844 2 15844 XP_209200.1 5 1372 CTATGTTGCCCA CA------ CT 3 C c b
21 GGCTGGTTGCAA TTGCA CCAGCCTGGGCAA
ACTTCTGG AACGT GGTCGGACCCGTT
GGTCTTCA T-
GAM7776 246 LOC2844 3 4975 XP_209198.1 3 476 TGCTGCTGCCCA 3 C b b
26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGTGCA GTGACGTGAGGTCGGACCCGT

GAM7776 246 LOC2844 3 5357 XP_209198.1 3 311 CTCTGTCGCCCA A 3 C b b
26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGACATG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2844 3 13177 XP_209198.1 3 877 CTCTGTCGCCCA C A 3 C c b
26 GGTTTGAGTGCA CATTGCACTC AGCCTGGGC
ATGGCACA GTAACGTGAG TTGGACCCG
T C
GAM7776 246 LOC2844 1 8752 XP_209210.1 3 761 CCTCTGTCACCA -- 3 C b b
40 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC2844 3 3999 XP_209216.1 5 680 CACTGTCACCCG CA 3 C c b
54 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCTCG GTAACGTGAGGTCGGGCCC
AC
GAM7776 246 LOC2844 3 16031 XP_209216.1 5 1116 CTCTGTTGCCCA C 3 C b b
54 GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGTGTG GTGACGTGA GTCGGACCCGTT
A
GAM7776 246 LOC2844 3 19117 XP_209216.1 5 1282 CCATCTTGGCCA TG- T G 3 C c b
54 GGCTGGTGTGAT CAT CAC CCAGCCTGG CAA
CATGGCTC GTA GTG GGTCGGACC GTT
CTA T G
GAM7776 246 LOC2844 1 18777 XP_211470.1 3 256 CTCTGTTATCCA T CA 3 C c c
56 GGCTGGTGTGCA CATTGCAC CCAGCCTGGG
GTGATACA GTGACGTG GGTCGGACCT
T AT
GAM7776 246 LOC2844 1 19286 XP_209225.1 3 1168 CTCTGTCACCCA CT CA 3 C c c
71 GGCTGGGATGCA CATTGCA CCAGCCTGGG
GTGGCTTC GTGACGT GGTCGGACCC
AG AC
GAM7776 246 LOC2845 1 14119 XP_211500.1 3 1747 CTCTGTCGCCCA CA A 3 C c c
12 GGCTGGAGCCCA CATTG CTCCAGCCTGGGC
GTGGCGAG GTGAC GAGGTCGGACCCG
CC C

GAM7776 246 LOC2845 1 18865 XP_211502.1 5 908 CCCAATAGCCCA A 3 C b b
13 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCAGA GTGACGTGAGGTCGGACCCG
A
GAM7776 246 LOC2845 1 19112 XP_211514.1 5 89 CCTTGCCCTTTG TT - --- 3 C c c
49 GGCTGGAGATGC CA GCA CTCCAGCCT GGGCAA
TTTGCCAG GT CGT GAGGTCGGG CCCGTT
TT A TTT
GAM7776 246 LOC2845 1 9493 XP_211515.1 3 1303 CTCTGTCACCCA CA 3 C c c
51 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2845 1 19533 XP_211522.1 3 7 CTCTGTCTCCCA G C CA 3 C c c
77 GACTGGAGTGAG CATT CACTCCAG CTGGG
TGGTGTGA GTGA GTGAGGTC GACCC
- A TC
GAM7776 246 LOC2845 1 12803 XP_209278.3 5 73 TCTGTTGTCCAA C----- - 3 C c c
87 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM7776 246 LOC2846 1 12497 XP_211552.1 3 977 CTCGGTCACCTA CA 3 C c c
11 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGATGTGAGGTCGGATCC
AC
GAM7776 246 LOC2846 1 18882 XP_211561.1 5 505 CTCTGTTGCCTA C 3 C b b
28 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
ATGGCGTG GTAACGTGAGGTC GATCCGTT
A
GAM7776 246 LOC2846 2 501 XP_209319.1 5 101 TCTTATTGCCCA C C 3 C b b
75 GACTAGAGTGCG CATTGCACTC AG CTGGGCAA
ATGGTGCG GTAGCGTGAG TC GACCCGTT
A A
GAM7776 246 LOC2846 2 2389 XP_209319.1 5 558 CTCTGTCACCCA -- CA 3 C c b
75 GGCTGGAGTGTG CATTGCAC TCCAGCCTGGG
CAGTGGCG GTGACGTG AGGTCGGACCC
TG AC
GAM7776 246 LOC2846 1 5926 XP_208236.1 3 488 AGAGACTGTAGC T AGC A 3 C c
c
83 TCAGGGCGTGCA CATTGCAC CC CTGGGC
ATGTGAGG GTAACGTG GG GACTCG
C --- A
GAM7776 246 LOC2847 1 12803 XP_294994.1 5 866 TCTGTTGTCCAA C----- - 3 C c c
01 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM7776 246 LOC2847 1 5153 XP_209332.1 3 524 CTCTGTTGCCCA CA------ T 3 C c c
08 GGCTGGGTGCAG TTGCAC CCAGCCTGGGCAA
CGGTGCGA GACGTG GGTCGGACCCGTT

AGCGTGGC -

GAM7776 246 LOC2847 3 2215 XP_211602.1 3 637 CTGTGTTGGCCA G CT- G 3 C c b

23 GGCTGGTCTTGA CATT CA CCAGCCTGG CAA

ATGCCTGA GTAA GT GGTCGGACC GTT

- TCT G

GAM7776 246 LOC2847 3 3182 XP_211602.1 3 472 CTTTGTTGCCCA 3 C b b

23 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA

GTGGTGCA GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC2847 3 6498 XP_211602.1 3 61 CTCTGCCACCCA C CA 3 C c b

23 AGCTGGAGTGCA CATTGCACTCCAGC TGGG

GTGGCACG GTGACGTGAGGTCG ACCC

A AC

GAM7776 246 LOC2848 3 853 XP_209371.1 3 1213 TTTGCCCAGGCT ---- 3 C b b

05 GGATGGAGTGCA CATTGCACTCCA GCCTGGGCAA

GTGGCGTG GTGACGTGAGGT CGGACCCGTT

AGGT

GAM7776 246 LOC2848 3 1544 XP_209371.1 3 1111 CTCTGCTGCTCA 3 C b b

05 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA

GTGGTGCA GTGACGTGAGGTCGGACTCGT

GAM7776 246 LOC2848 3 8046 XP_209371.1 3 1213 CTCTTTTGCCCA ---- 3 C b b

05 GGCTGGATGGAG CATTGCACTCCA GCCTGGGCAA

TGCAGTGG GTGACGTGAGGT CGGACCCGTT

AGGT

GAM7776 246 LOC2848 1 19401 XP_211661.1 5 446 TCTTGTTGCCCG 3 C b b

39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

ATGGCGCG GTAACGTGAGGTCGGGCCCGTT

GAM7776 246 LOC2848 1 3582 XP_209383.1 3 138 CTCTGTCACCCA A CA 3 C c c

53 GGCTGGAGCGTA CATTGC CTCCAGCCTGGG

ATGGCACA GTAATG GAGGTCGGACCC

C AC

GAM7776 246 LOC2848 1 12736 XP_211668.2 3 619 TCTTGTCCCCCA C CA 3 C c c

56 GACTGGAGTGCA CATTGCACTCCAG CTGGG

ATGGCACG GTAACGTGAGGTC GACCC

A CC

GAM7776 246 LOC2848 1 12736 XP_302835.1 3 108 TCTTGTCCCCCA C CA 3 C c c

56 GACTGGAGTGCA CATTGCACTCCAG CTGGG

ATGGCACG GTAACGTGAGGTC GACCC

A CC

GAM7776 246 LOC2848 1 16785 XP_209384.2 3 315 GATGGAGGCAGT G TGG A 3 C c c

59 GGCTGGAGTGAA CATT CACTCCAGCC GC

TGAACGGC GTAA GTGAGGTCGG CG

- TGA G

GAM7776 246 LOC2848 1 16785 XP_211670.2 5 289 GATGGAGGCAGT G TGG A 3 C c c

61 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM7776 246 LOC2848 1 1645 XP_211672.1 3 70 CTCTGTTGCCCA 3 C b b
65 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC2848 1 16785 XP_209412.1 3 1421 GATGGAGGCAGT G TGG A 3 C
c c
73 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM7776 246 LOC2848 2 3846 XP_209394.1 3 1070 GCTCTGTCGCCA C -- 3 C c c
74 GGCTGGAGTACA CATTG ACTCCAGCCTGG GCA
GTGGTGTG GTGAC TGAGGTCGGACC TGT
A GC
GAM7776 246 LOC2848 2 16244 XP_209394.1 3 616 GCTCTGCGCCCA G A 3 C c c

74 GGATGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGCATG GTGACGTGAGGT GGACCCG
A C
GAM7776 246 LOC2849 1 14894 XP_211696.1 5 657 TTTTGTCGCCCA A 3 C b b
34 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2849 1 5465 XP_211705.1 3 1141 TCTTGTCTCTCA CT CA 3 C c
c
47 GGCTGGGTTGCA CATTGCA CCAGCCTGGG
ATGGCACA GTAACGT GGTCGGACTC
TG TC
GAM7776 246 LOC2849 1 4025 XP_211703.1 3 163 ACTCTGTCGCCA -- 3 C b b
50 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTG GTGACGTGAGGTCGGACC TGT
GC
GAM7776 246 LOC2850 1 3500 XP_211731.2 3 639 TGTGTGACCTTA - - 3 C b b
02 GGCTGGAGTGCA CATTGCACTCCAGCCTG GG CA
ATGGCATG GTAACGTGAGGTCGGAT CC GT
T A
GAM7776 246 LOC2850 1 17523 XP_209440.1 3 2382 CTCTGTCACCCA C CA 3 C c
c
26 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGGTGCG GTGACGTGAGGTC GACCC
A AC
GAM7776 246 LOC2850 1 2174 XP_211751.1 3 866 TTCTGTCACCCA A C CA 3 C c c

52 GGCTAGAGCGCA CATTGC CTC AGCCTGGG
GTGGCAAG GTGACG GAG TCGGACCC
C A AC
GAM7776 246 LOC2850 1 20023 XP_211753.1 5 236 TGTCACCCAGGT C --- CA 3 C c
c

58 GGCTGGAGTACA CATTG ACTCCAGCC TGGG
GTGGCCTG GTGAC TGAGGTCGG ACCC
A TGG AC
GAM7776 246 LOC2850 1 5667 XP_209464.1 3 987 CTCTATCACCCA C CA 3 C c c
83 GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGGTACG GTGACGTGA GTCGGACCC
A AC
GAM7776 246 LOC2850 1 6092 XP_209465.1 3 42 TCTTGTTGCCCA CA 3 C b b
88 GGCCAGAGTGCA CATTGCACTC GCCTGGGCAA
ATGGCGTG GTAACGTGAG CGGACCCGTT
AC
GAM7776 246 LOC2851 1 17113 XP_211773.1 3 843 GGGGATGAGCCA CA G- 3 C c
c
23 GGCTGGGGACAG CATTG CTCCAGCCTGG CA
TGGGGCTG GTGAC GGGGTCGGACC GT
A- GA
GAM7776 246 LOC2851 2 5921 XP_211771.1 3 578 CTCTGTCACCCA CA 3 C c c
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCCCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2851 2 11528 XP_211771.1 3 145 CTCTGTCACCCA CA 3 C c c
27 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2851 1 4283 XP_211791.1 3 1871 TGCAGATTCCCA T CA 3 C c c

66 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACCC
- TT
GAM7776 246 LOC2851 1 7860 XP_209500.1 3 170 CTCTTTTGCCCA C----- G C 3 C c c

76 GACTGGAGTGAA ATT CACTCCAG CTGGGCAA
GTAGCATG TGA GTGAGGTC GACCCGTT
GTACGA A A
GAM7776 246 LOC2851 1 1745 XP_209509.1 3 678 CTCTGTTGCCCA 3 C b b
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2852 1 13597 XP_209521.1 5 78 ATCTGTCACCCA A CA 3 C c c
21 GGCTGGAGCGCA CATTGC CTCCAGCCTGGG
GTGGTGTG GTGACG GAGGTCGGACCC
C AC
GAM7776 246 LOC2852 3 8001 XP_211813.1 3 723 CTCTGTCACCCA C CA 3 C c c
31 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCC
A AC
GAM7776 246 LOC2852 3 8001 XP_211813.1 3 889 CTCTGTCACCCA C CA 3 C c c
31 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCC
A AC

GAM7776 246 LOC2852 3 9352 XP_211813.1 3 1425 CTATCTTGCCCA C--------- CTCC 3 C c c
31 GGCTTGCAATTT ATTGCA AGCCTGGGCAA
ATAGAGCT TAACGT TCGGACCCGTT
TCGAGATATT ----
GAM7776 246 LOC2852 3 15366 XP_211813.1 3 1260 CACTGTCACCCA G C CA 3 C c c
31 GTCTGGAGTGGA CATT CACTCCAG CTGGG
GTGGCATA GTGA GTGAGGTC GACCC
G T AC
GAM7776 246 LOC2852 1 15575 XP_211829.1 5 565 TCTTGTTACCCA CA 3 C b b
81 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACG GTAACGTGAGGTCGGACCC
AT
GAM7776 246 LOC2852 1 9374 XP_209554.1 3 399 CTATGTCACTCA CA 3 C c c
99 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACTC
AC
GAM7776 246 LOC2853 1 1027 XP_211844.1 3 477 CTCTGTCTCCCA - CA 3 C c c
34 GGCTGGAGTTGC CATTGCA CTCCAGCCTGGG
AGTGGTGC GTGACGT GAGGTCGGACCC
T TC
GAM7776 246 LOC2853 2 556 XP_211854.1 3 1258 CTCTGTTACCCA C CA 3 C c b
45 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCGCG GTGACGTGAG TCGGACCC
A AT
GAM7776 246 LOC2853 2 18883 XP_211854.1 3 869 CAGGGTTGCCCA G 3 C b b
45 GGGTGGAGTGCA CATTGCACTCCA CCTGGGCAA
GTGGCAGG GTGACGTGAGGT GGACCCGTT
G
GAM7776 246 LOC2853 1 6117 XP_209581.1 3 515 CTCTGTCACCCA CA 3 C c c
66 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGGGGTCGGACCC
AC
GAM7776 246 LOC2853 1 10352 XP_211861.3 3 251 CTTTGTCACCCA CA 3 C c c
69 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2853 1 19692 XP_211873.1 3 1012 CTCTCTCGCCAT TG A 3 C c c
89 GGTTGGAGTGCA CATTGCACTCCAGCC GGC
GTGGTGCG GTGACGTGAGGTTGG CCG
TA C
GAM7776 246 LOC2853 2 9688 XP_211879.1 3 41 CTCTGTCTCCCA CA 3 C c b
92 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC
GAM7776 246 LOC2853 2 17969 XP_211879.1 3 344 CTCTGTCGCCCA A 3 C b b
92 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG

C
GAM7776 246 LOC2853 2 4655 XP_209593.1 3 1208 TCCTCTCGCCCA A 3 C b b
98 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTC GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2853 2 13286 XP_209593.1 3 906 CTCTGTCGCCCA C----- A 3 C c b
98 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTAGCGCG TGACGTGAGGTCGGACCCG
GCGCGA C
GAM7776 246 LOC2854 1 4171 XP_209607.3 3 1518 TTCTGTCGCCCA A 3 C b b
29 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2854 1 13804 XP_211914.1 5 572 CACTGTCGCCCA A 3 C b b
88 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGGCGTGAGGTCGGACCCG
C
GAM7776 246 LOC2854 1 11239 XP_211917.1 3 164 CTCTGTCCCTCA C----- --- 3 C c c
91 GGCTGGAGTGCA ATTGCACTCCAGCCT GGGCA
GTAGCGTG TGACGTGAGGTCGGA CCTGT
GTGCGA CTC
GAM7776 246 LOC2855 1 3519 XP_211923.1 5 176 TACTTTCATTCA CA 3 C c c
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACTT
AC
GAM7776 246 LOC2855 1 14552 XP_209643.1 3 12 CTCTTTTTGCAC C G 3 C b b
10 AGGCTGAGTGCA CATTGCACTC AGCCTG GCAA
ATGCCGTG GTAACGTGAG TCGGAC CGTT
- A
GAM7776 246 LOC2855 2 6961 XP_209654.1 5 8 CTGTGTCGCCCA - A 3 C b b
40 GGCTGGAGTGCA CATT GCACTCCAGCCTGGGC
AGTGGCAT GTGA CGTGAGGTCGGACCCG
A C
GAM7776 246 LOC2855 2 9543 XP_209654.1 5 1535 CTCTGTCACCCA CA 3 C c b
40 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2855 1 8718 XP_209660.1 3 436 CACTCTTGCCCA T C 3 C b b
60 GGCTGTAGTGCT CAT GCACT CAGCCTGGGCAA
GTGGCACG GTG CGTGA GTCGGACCCGTT
T T
GAM7776 246 LOC2855 2 12804 XP_209671.1 3 721 CTCTGTCGCCAG - -- 3 C b b
89 GACTGGAGTGCA CATTGCACTCCAG CCTGG GCA
GTGACACG GTGACGTGAGGTC GGACC TGT
A GC
GAM7776 246 LOC2855 2 17087 XP_209671.1 3 267 CTTGATCACCCA C CA 3 C c b
89 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCGTG GTGACGTGAG TCGGACCC

A AC
GAM7776 246 LOC2856 1 13843 XP_211959.1 5 850 CTCTGTTGCCCA C 3 C b b
26 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGATACG GTGACGT AGGTCGGACCCGTT
A
GAM7776 246 LOC2856 1 4949 XP_209693.1 5 3929 TTCTGTCACCCA CA 3 C c c
38 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2856 1 19299 XP_209719.2 3 204 CTCTGTTGCTCA 3 C b b
79 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACTCGTT

GAM7776 246 LOC2856 1 17726 XP_209724.1 3 1089 CTCTGTTGCCCA 3 C b b
89 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2856 1 16940 XP_211981.1 5 24 CTCTGTTGCCCA 3 C b b
93 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2857 1 18012 XP_211997.1 5 350 CTCTGTCAACCA --- 3 C b b
22 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGACTCT GTGACGTGAGGTCGGACC TGT
AAC
GAM7776 246 LOC2857 1 11141 XP_209743.1 3 1367 TTCTGTCACCCA CA 3 C c c
44 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2857 1 11528 XP_209742.1 3 2434 CTCTGTCACCCA CA 3 C c c

47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2857 1 13412 XP_209750.1 3 371 CACTCTTGCCCA - A 3 C b b
60 GGCTGGAGCGCA CATT GC CTCCAGCCTGGGCAA
AGTGGCGC GTGA CG GAGGTCGGACCCGTT
A C
GAM7776 246 LOC2857 1 16810 XP_212013.1 5 230 CTATGGTCCACA T -- - - A 3 C c c
77 GGCTGGAGGGTG CAT GCAC TCCAGCCTG GG C
CATGGAAC GTA CGTG AGGTCGGAC CC G
- GG A T G
GAM7776 246 LOC2858 1 559 XP_212055.1 3 719 CTCTGTCACCCA CA 3 C b b
12 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGTG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2858 1 12389 XP_212036.1 5 78 TCTTGTTGCCCA 3 C b b
13 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2858 2 1847 XP_209777.1 3 237 CTCTGTTGCCCA C G 3 C b b
22 GGATGGAATGCA CATTGCA TCCA CCTGGGCAA
GTGGCACA GTGACGT AGGT GGACCCGTT
A A
GAM7776 246 LOC2858 2 9753 XP_209777.1 5 1360 CTGTGTCACCCA CA 3 C c b
22 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2858 1 986 XP_212043.1 5 165 CTCTGTCGCCAA CTG A 3 C c c
30 AGTTGGAGTGCA CATTGCACTCCAGC GGC
GTGGCGCG GTGACGTGAGGTTG CCG
AAA C
GAM7776 246 LOC2858 1 17964 XP_212034.1 3 188 CTCTGTTGCCCA 3 C b b
43 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2858 1 18945 XP_212045.1 5 732 CTCTGTCACCCG CA 3 C c c
47 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGGCCC
AC
GAM7776 246 LOC2858 1 10885 XP_212061.1 3 687 TTCTGTAACCCA CA 3 C c c
72 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCCTG GTGACGTGAGGTCGGACCC
AA
GAM7776 246 LOC2859 1 6188 XP_209810.1 3 304 TGGAGAAATTCA T CA 3 C c c
14 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG
TGGCTCAC GTGACGTG GGTCGGACTT
- AA
GAM7776 246 LOC2859 1 19536 XP_212104.1 3 41 CTATGTTGCCCA 3 C b b
23 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2859 1 17126 XP_209816.1 3 595 TCTTGTTGCCCA GCAC --- 3 C c
c
24 GGCTATGGGAAG CATT TCC AGCCTGGGCAA
AAATGAAA GTAA AGG TCGGACCCGTT
AGA- GTA
GAM7776 246 LOC2859 1 12075 XP_212092.1 5 845 CTCTGTCACCCA CA 3 C c c
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2859 1 15323 XP_209821.1 3 680 TGCTGTTGCCCA 3 C b b
52 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2859 1 2604 XP_209833.1 5 934 CTCTGTCACCCA C CA 3 C c c
61 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCATG GTGACGT AGGTCGGACCC
A AC

GAM7776 246 LOC2859 1 5318 XP_212105.1 3 866 TCGTGTTGCCCC T 3 C b b
72 GGCTGGAGTGCA CATTGCACTCCAGCC GGGCAA
GTGGCGCT GTGACGTGAGGTCGG CCCGTT
C
GAM7776 246 LOC2859 2 1397 XP_212117.1 5 4 TACTGTCATACA C----- T --- 3 C c b
79 GGCTGGCGTGCA ATTGCAC CCAGCCTG GGCA
GTAGTGGG TGACGTG GGTCGGAC CTGT
GGGTGA C ATA
GAM7776 246 LOC2859 2 6388 XP_212117.1 5 548 CTCTGTCAGCCA --- 3 C b b
79 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
ATGGCATG GTAACGTGAGGTCGGACC TGT
GAC
GAM7776 246 LOC2859 1 11742 XP_212111.1 3 936 TCTTGTTGCCCA C A 3 C b b
89 GGCAGGAGTACA CATTG ACTCC GCCTGGGCAA
ATGGCAGG GTAAC TGAGG CGGACCCGTT
A A
GAM7776 246 LOC2859 1 3647 XP_212120.1 3 774 CTATGTTGCCCA C-- ACT--- 3 C c
c
99 GGCTGGCCTCAA ATTGC CCAGCCTGGGCAA
GCAATCCT TAACG GGTCGGACCCGTT
TCC AACTCC
GAM7776 246 LOC2860 1 15231 XP_209866.1 3 1642 AATCGTCACCCA CC CA 3 C c
c
29 CATTGGAGTGCA CATTGCACTCCAG TGGG
GTGGTACG GTGACGTGAGGTT ACCC
AC AC
GAM7776 246 LOC2860 1 2244 XP_209868.1 5 640 TTTTGTTGCGCA G 3 C b b
30 GGCTGGAGTGCA CATTGCACTCCAGCCTG GCAA
ATGGTGCA GTAACGTGAGGTCGGAC CGTT
G
GAM7776 246 LOC2860 1 11035 XP_209873.1 5 648 TTTTGTTGCCCA 3 C b b
39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2860 1 9367 XP_212152.1 3 1054 CTCTGTTGTCCA 3 C b b
52 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACC GTGACGTGAGGTCGGACCTGTT

GAM7776 246 LOC2860 1 17965 NP_776192.1 5 66 CTCTGTTGCCCA C 3 C b b
75 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCGTG GTGAC TGAGGTCGGACCCGTT
A
GAM7776 246 LOC2860 5 3810 XP_212163.1 3 451 CTCTGTCGCCCA A 3 C b b
78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGAGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2860 5 13100 XP_212163.1 5 790 CTGTCTTGCCCA CA----- C 3 C c
b
78 GGCTGGAGTTCA TTG ACTCCAGCCTGGGCAA
GGGGCTAT GAC TGAGGTCGGACCCGTT

TATCGGG T
GAM7776 246 LOC2860 5 15083 XP_212163.1 3 760 CTCTGTCACCCA G CA 3 C c b
78 GGATGGAGTGCA CATTGCACTCCA CCTGGG
GTGTTGTG GTGACGTGAGGT GGACCC
A AC
GAM7776 246 LOC2860 5 15589 XP_212163.1 5 1402 GCTCTGTTGCCA T G 3 C b b
78 GGCTGGAGTGCA CA TGCACTCCAGCCTGG CAA
CTGGGGCT GT ACGTGAGGTCGGACC GTT
C -
GAM7776 246 LOC2860 5 16716 XP_212163.1 5 84 CTGGGCTGCCCA TG CCAG 3 C c b
78 GGGGTGTGATGT CAT CACT CCTGGGCA
GGAGCTGG GTA GTGG GGACCCGT
GT ----
GAM7776 246 LOC2860 1 16409 XP_212166.3 5 142 GCCATGTGGAAC ----- TG-- A 3 C c c
90 TGCTGGAGTGCA CATTGCACTCCAGC C GGC
GTGGCATG GTGACGTGAGGTCG G CCG
TCAAG TGTA -
GAM7776 246 LOC2861 1 7847 XP_212185.1 3 991 CTCTGCCACCCA CA 3 C c c
26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2861 1 7113 XP_212194.1 5 446 TTTTGTCACCCA CA 3 C c c
32 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2861 1 9746 XP_212196.1 3 1354 CCATATTGCCCA GCACT 3 C c c
35 GGCTGGTCTCGA CATT CCAGCCTGGGCAA
ATGCCTGG GTAA GGTCGGACCCGTT
GCTCT
GAM7776 246 LOC2861 1 3927 XP_209925.1 5 1001 CTCTGTTGACCA G G 3 C b b
66 GGCTGGAGTGAA CATT CACTCCAGCCTGG CAA
GTGGTGTG GTGA GTGAGGTCGGACC GTT
A A
GAM7776 246 LOC2861 1 8426 XP_212211.1 5 1936 GCTGTGTCACCA AC -- 3 C b b
70 GGCTGGAGCAGT CATTGC TCCAGCCTGG GCA
GGCACGAT GTGACG AGGTCGGACC TGT
-- AC
GAM7776 246 LOC2861 2 3430 XP_212219.1 5 148 CTTTGTCACCCA C CA 3 C c c
86 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC
GAM7776 246 LOC2861 2 18020 XP_212219.1 3 390 CTCTATCACCCA CA 3 C c c
86 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGTGGCT GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2862 1 2600 XP_209953.1 3 1535 CTCTGTTGCCCA C 3 C b b
06 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCACA GTGACGT AGGTCGGACCCGTT
A
GAM7776 246 LOC2862 1 19893 XP_209941.1 3 913 CTCTGTCACCCA C CA 3 C c c
07 GACTGGAGTGCA CATTGCACTCCAG CTGGG
GTGCCACA GTGACGTGAGGTC GACCC
A AC
GAM7776 246 LOC2862 3 2849 XP_212230.1 3 1658 CTCTGTCACCCA CA 3 C c b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTCACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2862 3 4372 XP_212230.1 3 1457 CTCTGTCGCCCA C A 3 C c b
08 GGCTGGAGTTCA CATTG ACTCCAGCCTGGGC
GTGGCGCG GTGAC TGAGGTCGGACCCG
T C
GAM7776 246 LOC2862 3 9724 XP_212230.1 3 2282 CTCTGTAGCCCA A 3 C b b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGTGGCA GTGACGTGAGGTCGGACCCG
A
GAM7776 246 LOC2862 1 19240 XP_212228.1 5 554 CTCTGTCAACCA T --- 3 C b b
15 GGCTGGAGTGCA CA TGCACTCCAGCCTGG GCA
CTGGCGCA GT ACGTGAGGTCGGACC TGT
C AAC
GAM7776 246 LOC2862 1 7774 XP_212233.1 5 65 TGCCCCCTGCCA CA TC G 3 C c
c
21 GGCTGAGGGACA CATTG C CAGCCTGG CA
GTGACACA GTGAC G GTCGGACC GT
AG GA -
GAM7776 246 LOC2862 1 6118 XP_209956.1 3 768 TGGCCATGCCCA TTGC T - 3 C c
c
23 GGGCTGGTGTTG CA AC CCAGCC TGGGCA
GTTGAGGA GT TG GGTCGG ACCCGT
TGGT T G
GAM7776 246 LOC2862 1 6868 XP_212244.1 5 238 CTCTGTCGCTCA A A 3 C c c
45 GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGTGCA GTGGCG GAGGTCGGACTCG
A C
GAM7776 246 LOC2863 1 15975 XP_212278.1 3 413 TGTTGTTGCCCA 3 C b b
41 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT
GAM7776 246 LOC2863 1 522 XP_208408.1 5 131 TCCCCACTGGCC GC C G 3 C c
c
47 AGCTGGAGTAGA CATT ACTCCAGC TGG CA
TGAAGTTC GTAG TGAGGTCG ACC GT
A- - G

GAM7776 246 LOC2863 1 15730 XP_212286.1 5 688 GCTCTGTCACCA A -- 3 C c c
54 GGCTGGAGGGCA CATTGC CTCCAGCCTGG GCA
GTGGCGCC GTGACG GAGGTCGGACC TGT
G AC
GAM7776 246 LOC2863 1 7385 XP_212290.1 5 1101 CTCTGTCACCCA CA 3 C c c
56 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC2863 1 14974 XP_212285.1 5 14 CAATGTTGCCCA 3 C b b
57 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2863 1 3785 XP_212291.1 3 157 TTCTGGTGTCCA TGC- C 3 C c
c
71 GGCTGAAGTCCT CAT ACT CAGCCTGGGCA
CGTGTGAC GTG TGA GTCGGACCTGT
CTCC A
GAM7776 246 LOC2863 1 2722 XP_212308.1 5 5808 CCCTGTTGCCCA CC 3 C b b

95 GGCTACAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCATG GTAACGTGA TCGGACCCGTT
CA
GAM7776 246 LOC2864 1 1038 XP_212310.1 5 501 TCTTGTTGCCCA A C 3 C b b
01 GGCTAGAGGGCA CATTGC CTC AGCCTGGGCAA
ATGGTGCA GTAACG GAG TCGGACCCGTT
G A
GAM7776 246 LOC2864 1 2754 XP_212319.1 3 55 GTGCTGTTTCCT T -- 3 C c c
41 GGCTGGAGTGCA CATTGCACTCCAGCC GG GCA
GTGGCATG GTGACGTGAGGTCGG CC TGT
T TT
GAM7776 246 LOC2864 1 9580 XP_210063.1 3 986 TGTTGTTGCCCA 3 C b b
67 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC2865 1 3183 XP_212340.1 3 892 CTTTGTCGCCCA A 3 C b b
53 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC2865 1 9264 XP_210106.1 3 99 CTCTGTAGACCA A --- 3 C c c
58 GGCTGGAGCGCA CATTGC CTCCAGCCTGG GCA
GTGGCAGG GTGACG GAGGTCGGACC TGT
C AGA
GAM7776 246 LOC2865 1 9264 XP_210108.1 3 99 CTCTGTAGACCA A --- 3 C c c
64 GGCTGGAGCGCA CATTGC CTCCAGCCTGG GCA
GTGGCAGG GTGACG GAGGTCGGACC TGT
C AGA
GAM7776 246 LOC3385 1 13760 XP_294654.1 3 1173 GCTCCATCACCA GCA 3 C c
c
62 GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGCG GTGACGTGAGGTCGGACC

ACT

GAM7776 246 LOC3385 1 12867 XP_294653.1 3 1934 TTTTGTTGCCCA C 3 C b b
65 GGCTGGAGTTCA CATTG ACTCCAGCCTGGGCAA
GTGGCGTG GTGAC TGAGGTCGGACCCGTT
T

GAM7776 246 LOC3385 1 14074 XP_290473.1 3 981 CTATATTGCCCA CC C 3 C b b
75 AGCTACAGTGCA CATTGCACT AGC TGGGCAA
ATGATTAA GTAACGTGA TCG ACCCGTT
CA A

GAM7776 246 LOC3385 1 4528 XP_290472.1 3 1085 CCCTGTCACCCA C CA 3 C c
c
79 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
ATGGCACG GTAACGT AGGTCGGACCC
A AC

GAM7776 246 LOC3385 1 7523 XP_294658.1 5 203 CACTTTGTTTCA T-- T-- - 3 C c c
85 GGCTGGTCTGTG CAT GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T

GAM7776 246 LOC3386 1 6626 XP_290494.1 3 2436 TCTTGTTGCCCA 3 C b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGAGCG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3387 1 12803 XP_211595.2 5 683 TCTGTTGTCCAA C----- - 3 C c c
09 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM7776 246 LOC3387 1 6518 XP_294688.1 3 517 ACTCCAGGCTCA TG A- A 3 C c
c
31 GGCTGGAGCCGT CAT C CTCCAGCCTGGGC
GATGGCAC GTA G GAGGTCGGACTCG
GT CC G

GAM7776 246 LOC3387 2 14732 XP_294690.1 3 117 TTCTGATGCCCA 3 C b b
39 GGTTGGGGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACA GTGACGTGGGGTTGGACCCGT

GAM7776 246 LOC3387 2 15044 XP_294690.1 3 528 CTCTGTTGCCCA 3 C b b
39 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3387 1 16493 XP_290570.1 3 878 GTCTGTCACCCA CA 3 C c c
73 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC3388 1 11507 XP_290216.1 3 337 TTTTATTGCCCA TT CCA 3 C c
c
19 GGCAGTGCTCTG CA GCACT GCCTGGGCAA
GGCAGGAA GT CGTGA CGGACCCGTT
CT ---

GAM7776 246 LOC3388 1 12341 XP_294740.1 5 562 CTCTGTCACCAA T - -- 3 C c c

99 GGCTGGAGTGCA CA TGCACTCCAGCCT GG GCA
TTGGTGCA GT ACGTGAGGTCGGA CC TGT
T A AC
GAM7776 246 LOC3389 2 4298 XP_294742.1 3 438 GCTCTGTCGCCA -- 3 C b b
23 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
GC
GAM7776 246 LOC3389 2 8559 XP_294742.1 3 2044 TTCTGTCACTCA CA 3 C c b
23 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACTC
AC
GAM7776 246 LOC3389 1 3348 XP_294757.1 3 1068 ACTGAAGTCCCA - - - A 3 C c c
63 GGCTGGGGGTGT CATTG CACTCC AGCCTGGG C
CAATGGAC GTAAC GTGGGG TCGGACCC G
T G T A
GAM7776 246 LOC3389 1 12479 XP_290663.1 3 299 CGCTGTTGCCCA CC 3 C b b

91 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC
GAM7776 246 LOC3389 1 12479 XP_290659.1 3 299 CGCTGTTGCCCA CC 3 C b b

99 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC
GAM7776 246 LOC3390 1 17484 XP_294802.2 3 894 TCTTATCGCCCA A 3 C b b
77 GGCTGGGGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCA GTAACGTGGGGTCGGACCCG
C
GAM7776 246 LOC3390 1 9543 XP_290692.1 3 851 CTCTGTCACCCA CA 3 C c c
78 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3390 1 1843 XP_290697.2 5 868 AAAAGAATATTG T G CA 3 C c c

83 AGGCTGGGTGCA CATTGCAC CCAGCCT GG
ATGCATCA GTAACGTG GGTCGGA TT
- G AT
GAM7776 246 LOC3391 1 14266 XP_290711.1 5 144 TTTGGCTGCCCA TT ACTCC 3 C
c c
08 GGCTCGCCTTGA CA GC AGCCTGGGCA
CTCCAAAT GT CG TCGGACCCGT
TC C----
GAM7776 246 LOC3391 1 15614 XP_294825.1 5 449 GCTCTGTTGCCA G 3 C b b
46 GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGTGCG GTGACGTGAGGTCGGACC GTT
-
GAM7776 246 LOC3391 1 16261 XP_290742.1 3 674 CTCTGTCACCCA C CA 3 C c c

78 GGCTGGAGTACA CATTG ACTCCAGCCTGGG

ATGGCGTG GTAAC TGAGGTCGGACCC
A AC
GAM7776 246 LOC3392 1 4056 XP_290756.1 3 357 CTCTGTGGCCCA C A 3 C c c
01 GGCTGAAGTGCA CATTGCACT CAGCCTGGGC
GTGGTGTG GTGACGTGA GTCGGACCCG
A G
GAM7776 246 LOC3392 1 19537 XP_290762.2 5 411 CTCTGTTGCCCA --- 3 C b b
16 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA
GAM7776 246 LOC3392 1 19597 XP_294879.1 3 545 TGGAAGCCTTCA TC -- A 3 C c
c
48 GGTTGCTGTGCA CATTGCAC CAGCCTG GGC
ATGGAATA GTAACGTG GTTGGAC CCG
TC TT A
GAM7776 246 LOC3392 1 19597 XP_294883.1 3 545 TGGAAGCCTTCA TC -- A 3 C c
c
50 GGTTGCTGTGCA CATTGCAC CAGCCTG GGC
ATGGAATA GTAACGTG GTTGGAC CCG
TC TT A
GAM7776 246 LOC3392 1 19537 XP_294900.2 5 411 CTCTGTTGCCCA --- 3 C b b
82 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAGTGCC GTGACG TGAGGTTGGACCCGTT
ACA
GAM7776 246 LOC3392 1 11314 XP_294899.2 5 1180 CTCTGTTGCCCA --- 3 C b b
83 GGTTGGAGTACA CATTGC ACTCCAGCCTGGGCAA
GCAATGCC GTAACG TGAGGTTGGACCCGTT
ACA
GAM7776 246 LOC3393 1 9544 XP_290838.1 3 2392 TCTTGTTGCCCA C 3 C b b
24 GGCTGCAGTGCA CATTGCACT CAGCCTGGGCAA
ATGGCACA GTAACGTGA GTCGGACCCGTT
C
GAM7776 246 LOC3393 2 16940 XP_290830.1 3 372 CTCTGTTGCCCA 3 C b b
25 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3393 2 17114 XP_290830.1 3 143 AGCCTTTCTCCA A CA 3 C c b

25 GGTGGGAGTGCA CATTGCACTCC GCCTGGG
GTGGCATG GTGACGTGAGG TGGACCT
G CT
GAM7776 246 LOC3394 1 2027 XP_294944.1 5 627 CTCTGTTGCCCA CA----- 3 C c c
17 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GGGGCGTA GACGTGAGGTCGGACCCGTT
ATGCGGG
GAM7776 246 LOC3394 1 10679 XP_290902.1 3 308 TCTTGTCGCCCA A 3 C b b
48 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCA GTAACGTGAGGTCGGACCCG
C
GAM7776 246 LOC3394 1 5488 XP_290911.1 3 1340 CTCTGTCGCCCA A 3 C b b

58 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACT GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC3394 1 13513 XP_290907.2 3 838 CTCTGTCGCCTA A 3 C b b
59 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGATCCG
C
GAM7776 246 LOC3394 3 695 XP_290919.1 3 1557 CCATGTTGGCCA GCACT G 3 C c
b
92 GGCTGGTCTCGA CATT CCAGCCTGG CAA
ATGCCTGG GTAA GGTCGGACC GTT
GCTCT G
GAM7776 246 LOC3394 3 7386 XP_290919.1 3 1081 CTCTGTCGCGCA G G A 3 C c
b
92 GGGTGGAGTGCG CATTGCACTCCA CCTG GC
GTGGCACG GTGGCGTGAGGT GGAC CG
G G C
GAM7776 246 LOC3394 3 8590 XP_290919.1 3 1387 TCTTGTTGCCCA T 3 C b b
92 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
TTGGCGTG GT GCGTGAGGTCGGACCCGTT
T
GAM7776 246 LOC3395 2 12075 XP_295005.1 3 1040 CTCTGTCACCCA CA 3 C c c
77 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3395 2 14733 XP_295005.1 3 1187 CTACGTGACCCA C----- - 3 C c c
77 GGCTGGAGTGTA ATTGCACTCCAGCCTGGG CA
GTAGCTAT TGATGTGAGGTCGGACCC GT
TATCGA A
GAM7776 246 LOC3396 1 15295 XP_295014.1 3 1461 CTCTGTCACTTA CA 3 C c c
00 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGATTC
AC
GAM7776 246 LOC3396 1 17076 XP_290981.1 3 1596 GCCCTGTTGCCA C G 3 C b
b
59 GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM7776 246 LOC3396 1 1982 XP_295032.1 5 166 CTCTACCACCCA CA 3 C c c
85 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3396 1 15954 XP_295035.1 5 835 AGACAGGGTCTT CCT A 3 C c
c
94 GACTGGAGTGCA CATTGCACTCCAG GGGC
GTGGTGCG GTGACGTGAGGTC TCTG
AGT G
GAM7776 246 LOC3397 1 11528 XP_295038.1 3 1272 CTCTGTCACCCA CA 3 C c c

11 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3397 1 16942 XP_295041.1 5 880 CTCTGTCGCCCA A 3 C b b
20 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC3398 1 13337 XP_295072.1 3 1492 GTCTGTCACCCA CA 3 C c c
03 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3398 1 6146 XP_295071.1 3 813 CTTACCATTTTG TCCA G 3 C c
c
08 CTAGGGTGTGCA CATTGCAC GCCT GGCAA
ATGCCCAC GTAACGTG TGGG TCGTT
---- A
GAM7776 246 LOC3398 2 1744 XP_291020.1 5 1637 CTCTGTCACCCA CA 3 C c c
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3398 2 17750 XP_291020.1 5 1174 CACTGTCACCTA CA 3 C c c
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTAAA GTGACGTGAGGTCGGATCC
AC
GAM7776 246 LOC3398 2 7633 XP_291031.1 5 575 CTCTGTTGCCCA C 3 C b b
33 GCCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATT GTGACGTGAGGTC GACCCGTT
C
GAM7776 246 LOC3398 2 10421 XP_291031.1 3 561 CTGTGATGCCGA G G 3 C b b
33 GGGTGGAGTGCA CATTGCACTCCA CCT GGCA
GTGGCACA GTGACGTGAGGT GGA CCGT
G G
GAM7776 246 LOC3398 1 14645 NP_835467.1 5 48 TTCTGTCGCCCA A 3 C b b
34 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGACGCG GTGATGTGAGGTCGGACCCG
C
GAM7776 246 LOC3398 1 14645 XP_291033.1 5 48 TTCTGTCGCCCA A 3 C b b
34 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGACGCG GTGATGTGAGGTCGGACCCG
C
GAM7776 246 LOC3398 3 4026 XP_291050.1 3 183 CTGTGTTGCCCA C----- 3 C c b
72 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
GTAGCTAT TGACGTGAGGTCGGACCCGTT
TATCGA
GAM7776 246 LOC3398 3 5858 XP_291050.1 5 768 CTCAGTCGCTCA A 3 C b b
72 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACTCG

C

GAM7776 246 LOC3398 3 9299 XP_291050.1 5 471 GTCTGTTGCCCA 3 C b b
72 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGGG GTGACGTGAGGTTGGACCCGTT

GAM7776 246 LOC3398 1 1081 XP_295095.1 5 133 CTCTGTTGCCCA C 3 C b b
94 GGTTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCTTG GTGACGTGAG TTGGACCCGTT
A

GAM7776 246 LOC3399 1 3425 XP_291065.1 3 1461 CTCTGTTGCCCA CA----- 3 C c c
07 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GGGGCACG GACGTGAGGTCGGACCCGTT
GCACGGG

GAM7776 246 LOC3399 1 10709 XP_291069.1 5 122 CTCTGTTGCCCA 3 C b b
09 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3399 1 714 XP_295099.1 5 595 CAGAATCGCCCA - - T- A- A 3 C c c
14 GGCCAGGCTGTG CAT TGC AC CC GCCTGGGC
GCAGATGA GTA ACG TG GG CGGACCCG
G G TC AC C

GAM7776 246 LOC3399 1 16942 XP_291095.1 3 714 CTCTGTCGCCCA A 3 C b b
70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 LOC3400 1 12244 XP_295137.1 3 37 TCTTGTTGCCCA 3 C b b
37 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGCGCGA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3401 1 12803 XP_291150.1 5 683 TCTGTTGTCCAA C----- - 3 C c c
25 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM7776 246 LOC3401 1 11753 XP_291153.1 3 2141 CTCTGTCACTCA CA 3 C c c
38 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGACGTG GTAACGTGAGGTCGGACTC
AC

GAM7776 246 LOC3401 1 10096 XP_291158.1 3 1441 GCTCTGTCACGA - - 3 C b b
56 GGCTGGAGTGCA CATTGCACTCCAGCCT G GGCA
GTGGCCCC GTGACGTGAGGTCGGA C CTGT
G A

GAM7776 246 LOC3402 1 12803 XP_291203.1 5 683 TCTGTTGTCCAA C----- - 3 C c c
27 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM7776 246 LOC3402 1 2179 XP_295188.1 5 340 TCCAGCGGCCCA CA A A 3 C c
c
38 GGCGGGGGACAG CATTG CTCC GCCTGGGC
TGCCGTTC GTGAC GGGG CGGACCCG

AG - G

GAM7776 246 LOC3402 1 18147 XP_295190.1 5 998 CTGTGTGGCCTA A 3 C b b
59 GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGCA GTAACGTGAGGTTGGATCCG
G

GAM7776 246 LOC3402 1 15740 XP_291214.1 5 1350 TCTCTTGTCCAA C----- - 3 C c c
90 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A

GAM7776 246 LOC3403 1 18868 XP_291269.1 3 1383 TCTTGTTGCCCA 3 C b b
90 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3404 1 1309 XP_291274.1 5 647 TTTTGTTGCCCA 3 C b b
08 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGATGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3404 1 1744 XP_295240.1 3 174 CTCTGTCACCCA CA 3 C c c
14 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC3404 1 1744 XP_295252.1 5 244 CTCTGTCACCCA CA 3 C c c
50 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC3405 1 13053 XP_295268.1 5 225 TCTCTGTAGCCA C----- A -- 3 C c c
28 GGCTGGAGGGCA ATTGC CTCCAGCCTGG GCA
ATTGTACA TAACG GAGGTCGGACC TGT
ACATGT G GA

GAM7776 246 LOC3429 1 13464 XP_292790.2 3 811 CTCTGTCACCCA CA 3 C c c
26 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC

GAM7776 246 LOC3434 1 439 XP_295563.1 5 222 TGTTCATGCCCA --- CTC -- 3 C c c
35 GGATCTGCTGCG CAT TGCA CAG CCTGGGCA
CTCATGGA GTA GCGT GTC GGACCCGT
CTC C-- TA

GAM7776 246 LOC3452 1 523 NP_835236.1 3 952 CTCTTTCGCCCA A 3 C b b
75 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTATG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 LOC3458 1 12611 XP_293993.2 5 33 AGGAGATGTCCA TG A C 3 C c
c
78 GGCTGAAGGTGG CAT C CT CAGCCTGGGCA
TGATTTGA GTG G GA GTCGGACCTGT
GT - A

GAM7776 246 LOC3466 1 17927 XP_294357.2 3 372 GCTCTGTCTCCA C -- 3 C c c
53 GGCTGGAGTACA CATTG ACTCCAGCCTGG GCA
GTGGTGCG GTGAC TGAGGTCGGACC TGT

A TC
GAM7776 246 LOC3476 1 9837 XP_300226.1 3 110 CATTGCCCTTCG TT - --- 3 C c c
48 GGCTGGAGATGC CA GCA CTCCAGCCT GGGCAA
TTTGCCGG GT CGT GAGGTCGGG CCCGTT
TT A CTT
GAM7776 246 LOC3477 1 11420 XP_300530.1 5 15 AACTATCACCTG TG CA 3 C c c
64 GGCTGGAGTGCG CATTGCACTCCAGCC GG
ATGGCATG GTAGCGTGAGGTCGG CC
GT AC
GAM7776 246 LOC3479 1 9505 XP_302624.1 5 368 TCTTGTTGTCCA C 3 C b b
05 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCATG GTAACGTGAG TCGGACCTGTT
A
GAM7776 246 LOC3479 1 17689 XP_300565.1 5 189 TTTTATTGCCCA 3 C b b
18 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGATGTGAGGTCGGACCCGTT
GAM7776 246 LOC3480 2 13716 XP_302653.1 3 1556 CCTTCTTCCCCA G - CA 3 C c
b
75 GGCTGGGAGTGG CATT CACTCC AGCCTGGG
GTGAGACG GTGG GTGAGG TCGGACCC
- G CT
GAM7776 246 LOC3480 2 14381 XP_302653.1 3 3385 GCTCTGTCACCA -- 3 C b b
75 GGCTGGAGTGCG CATTGCACTCCAGCCTGG GCA
GTGGCATA GTGGCGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC3480 2 13332 XP_300615.1 3 234 TCCCGTCCAACA C --- A 3 C c c
94 GGCTGGAGTACA CATTG ACTCCAGCCT GGGC
ATGGCGAG GTAAC TGAGGTCGGA CCTG
A CAA C
GAM7776 246 LOC3480 2 16473 XP_300615.1 5 57 GAGACCGACGGC T CTG A 3 C c
c
94 CGCTGGAGTGCA CA TGCACTCCAGC GGC
CTGGCATG GT ACGTGAGGTCG CCG
C --- G
GAM7776 246 LOC3481 1 12479 XP_300623.1 3 299 CGCTGTTGCCCA CC 3 C b b
13 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC
GAM7776 246 LOC3481 1 13705 XP_300626.1 5 554 TCTTGTTGCCCA CA 3 C b b
15 GGCCCGAGTGCA CATTGCACTC GCCTGGGCAA
GTGGTGCG GTGACGTGAG CGGACCCGTT
CC
GAM7776 246 LOC3481 1 12479 XP_300635.1 3 299 CGCTGTTGCCCA CC 3 C b b
37 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT

TC
GAM7776 246 LOC3481 1 12479 XP_300636.1 3 299 CGCTGTTGCCCA CC 3 C b b

42 GGCTCTAGTGCA CATTGCACT AGCCTGGGCAA
ATGGCACG GTAACGTGA TCGGACCCGTT
TC
GAM7776 246 LOC3482 1 15852 XP_300670.1 3 1531 CTCTGTTGCCCA C 3 C b b
35 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGTACG GTGACGT AGGTCGGACCCGTT
A
GAM7776 246 LOC3482 1 7306 XP_300683.1 5 58 CTCTGTTGCCTG TG 3 C b b
62 GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGCCACG GTGACGTGAGGTCGG CCGTT
GT
GAM7776 246 LOC3483 1 16669 XP_302716.1 5 317 CTTTGTTGCCCA 3 C b b
14 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC3483 1 19778 XP_300696.1 3 1763 AGTCTGTCACCA -- 3 C b b
26 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC3483 1 8820 XP_030209.2 3 79 GCTCGTCACCCA C----- CA 3 C c c

27 GGCTGGAGTGCA ATTGCACTCCAGCCTGGG
ATTGTGCA TAACGTGAGGTCGGACCC
ACGTGT AC
GAM7776 246 LOC3483 2 872 XP_302741.1 3 1206 CGCCGTTGCCCA 3 C b b
93 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC3483 2 11192 XP_302741.1 3 744 CTAGGAGGCCCA TG A 3 C c
b
93 GGCTGGAGTGAG CAT CACTCCAGCCTGGGC
GTGGCACG GTG GTGAGGTCGGACCCG
GA G
GAM7776 246 LOC3483 3 1569 XP_300729.1 5 150 CTCTGTCACCCA C CA 3 C c b

96 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGCAGTG GTGACGT AGGTCGGACCC
A AC
GAM7776 246 LOC3483 3 9545 XP_300729.1 3 184 CTCTGTTGCCCA 3 C b b
96 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3483 3 10270 XP_300729.1 3 1031 TCTTGTTATCCA CA 3 C c b
96 GGCTGGGGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCG GTAACGTGGGGTCGGACCT
AT
GAM7776 246 LOC3484 3 695 XP_300730.1 3 798 CCATGTTGGCCA GCACT G 3 C c
b

02 GGCTGGTCTCGA CATT CCAGCCTGG CAA
ATGCCTGG GTAA GGTCGGACC GTT
GCTCT G
GAM7776 246 LOC3484 3 7386 XP_300730.1 3 322 CTCTGTCGCGCA G G A 3 C c
b
02 GGGTGGAGTGCG CATTGCACTCCA CCTG GC
GTGGCACG GTGGCGTGAGGT GGAC CG
G G C
GAM7776 246 LOC3484 3 8590 XP_300730.1 3 628 TCTTGTTGCCCA T 3 C b b
02 GGCTGGAGTGCG CA TGCACTCCAGCCTGGGCAA
TTGGCGTG GT GCGTGAGGTCGGACCCGTT
T
GAM7776 246 LOC3484 1 19778 XP_300738.1 3 1763 AGTCTGTCACCA -- 3 C b b
45 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC3484 1 15049 XP_302760.1 3 2633 CTCTGTCGCCCA A 3 C b b
55 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC3484 2 4143 XP_300743.1 3 130 ACTCTGTCACCA -- 3 C b b
60 GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGCCGCA GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 LOC3484 2 13465 XP_300743.1 5 247 CTCTGTCACCCA C CA 3 C c
b
60 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
ATGGCACC GTAACGTGAG TCGGACCC
A AC
GAM7776 246 LOC3484 1 17206 XP_209299.2 3 230 CTCTCTTACCCA C CA 3 C c c

74 AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGACATG GTGACGTGAGGTCG ACCC
A AT
GAM7776 246 LOC3484 1 6119 XP_302789.1 5 27 CTCTGTCACCCA CA 3 C b b
94 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCC GTAACGTGAGGTCGGACCC
AC
GAM7776 246 LOC3485 1 19361 XP_300762.1 3 1203 CTTGCTCGCCCA G A 3 C c c

03 GGGTGGAGTGCA CATTGCACTCCA CCTGGGC
GTGGTGTG GTGACGTGAGGT GGACCCG
G C
GAM7776 246 LOC3485 1 12803 XP_302806.1 5 745 TCTGTTGTCCAA C----- - 3 C c c
08 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA
GTAGTGCT TGATGTGAGGTCGGA CCTGTT
TCGTGA A
GAM7776 246 LOC3485 1 5488 XP_300778.1 3 1340 CTCTGTCGCCCA A 3 C b b
25 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACT GTGACGTGAGGTCGGACCCG

C

GAM7776 246 LOC3485 2 872 XP_302818.1 3 1206 CGCCGTTGCCCA 3 C b b
32 GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGCATG GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 LOC3485 2 11192 XP_302818.1 3 744 CTAGGAGGCCCA TG A 3 C c
b
32 GGCTGGAGTGAG CAT CACTCCAGCCTGGGC
GTGGCACG GTG GTGAGGTCGGACCCG
GA G
GAM7776 246 LOC3485 1 8544 XP_302833.1 3 313 TGGAGTCTCGCT CCT A 3 C c
c
83 CTCTGGAGTGCA CATTGCACTCCAG GGGC
ATGGCGCA GTAACGTGAGGTC CTCG
T-- C
GAM7776 246 LOC3485 1 16785 XP_302834.1 5 1212 GATGGAGGCAGT G TGG A 3 C
c c
94 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM7776 246 LOC3485 1 16785 XP_302837.1 3 1593 GATGGAGGCAGT G TGG A 3 C
c c
95 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM7776 246 LOC3486 1 16785 XP_302844.1 5 289 GATGGAGGCAGT G TGG A 3 C c
c
03 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM7776 246 LOC3486 1 16785 XP_300793.1 3 1421 GATGGAGGCAGT G TGG A 3 C
c c
05 GGCTGGAGTGAA CATT CACTCCAGCC GC
TGAACGGC GTAA GTGAGGTCGG CG
- TGA G
GAM7776 246 LOC3487 1 7387 XP_300808.1 5 298 CTCTGTCACCCA C CA 3 C c c
02 GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCACG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 LOC3487 1 810 XP_300843.1 3 447 GCTTGTTGCCCA 3 C b b
90 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3487 1 7741 XP_302888.1 3 342 TGCTCTCGCCCA A 3 C b b
97 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGGTGG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LOC3487 1 19402 XP_300845.1 5 24 TCTTGTTGCCCA C 3 C b b
98 GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
ATGGCGCG GTAACGT AGGTCGGACCCGTT

A

GAM7776 246 LOC3488 1 15126 XP_300853.1 5 279 CCCTGTTGCCCA --- 3 C b b

25 GGCTGGAGTATA CATTGC ACTCCAGCCTGGGCAA

GTAGTGCA GTGATG TGAGGTCGGACCCGTT

ATA

GAM7776 246 LOC3488 1 12803 XP_300861.1 5 475 TCTGTTGTCCAA C----- - 3 C c c

42 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA

GTAGTGCT TGATGTGAGGTCGGA CCTGTT

TCGTGA A

GAM7776 246 LOC3489 1 8605 XP_302929.1 3 301 TTCTGTCGCCCT G T A 3 C c c

47 GGCTGGAGTGGA CATT CACTCCAGCC GGGC

ATGCCGTG GTAA GTGAGGTCGG CCCG

G T C

GAM7776 246 LOC3489 1 1900 XP_300434.1 3 607 AGAGTCTTGCTC CT 3 C c c

95 TGCTGGAGTGCG CATTGCACTCCAGC GGGCAA

GTGGTGCA GTGGCGTGAGGTCG CTCGTT

T-

GAM7776 246 LOC3490 2 1746 XP_300250.1 5 533 CTCTGTCACCCA C CA 3 C c c

24 GACTGGAGTGCA CATTGCACTCCAG CTGGG

GTGGCATG GTGACGTGAGGTC GACCC

A AC

GAM7776 246 LOC3490 2 4617 XP_300250.1 3 144 TCTTGTCACCCA CA 3 C c c

24 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCACA GTGACGTGAGGTCGGACCC

AC

GAM7776 246 LOC3490 1 16022 XP_300932.1 3 177 CTCTGTCACCCA C CA 3 C c c

75 GGCTGAAGTGCA CATTGCACT CAGCCTGGG

GTGGTACA GTGACGTGA GTCGGACCC

A AC

GAM7776 246 LOC3490 1 6188 XP_300937.1 3 287 TGGAGAAATTCA T CA 3 C c c

96 GGCTGGGTGCAG CATTGCAC CCAGCCTGGG

TGGCTCAC GTGACGTG GGTCGGACTT

- AA

GAM7776 246 LOC3491 1 12803 XP_302960.1 5 184 TCTGTTGTCCAA C----- - 3 C c c

14 GGCTGGAGTGTA ATTGCACTCCAGCCT GGGCAA

GTAGTGCT TGATGTGAGGTCGGA CCTGTT

TCGTGA A

GAM7776 246 LOC3491 5 958 XP_300969.1 3 1370 CTCTATTACTCA GC CA 3 C c b

70 GGCTGGAGTAAA CATT ACTCCAGCCTGGG

ATGGTGCC GTAA TGAGGTCGGACTC

AA AT

GAM7776 246 LOC3491 5 3349 XP_300969.1 3 832 CCCTATTGCCCA 3 C b b

70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

ATGGCGTG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3491 5 9545 XP_300969.1 3 469 CTCTGTTGCCCA 3 C b b

70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 LOC3491 5 11508 XP_300969.1 5 1053 CTCTGCCAGCCA T C --- 3 C c b
70 GACTGGAGTGCA CA TGCACTCCAG CTGG GCA
TTGGCGAG GT ACGTGAGGTC GACC CGT
T A GAC
GAM7776 246 LOC3491 5 18074 XP_300969.1 5 147 TTCTGTGGCCCA A 3 C b b
70 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCTGT GTGACGTGAGGTCGGACCCG
G
GAM7776 246 LOC3492 2 2323 XP_300251.1 5 413 GGGGCATGCCCA CA--- - CA 3 C c c
51 GGCAGAGTGACA TTG CACTC GCCTGGGCA
GGAGAG GAC GTGAG CGGACCCGT
GAGAG A A-
GAM7776 246 LOC3492 2 4454 XP_300251.1 3 444 CACTATCACCCA A C CA 3 C c c
51 GGCTAGAGGGCA CATTGC CTC AGCCTGGG
GTGGCACA GTGACG GAG TCGGACCC
G A AC
GAM7776 246 LOC3493 1 10639 XP_088528.1 5 447 TCTGGTTGCCCA C 3 C b b
60 GGCTGGGGTACA CATTG ACTCCAGCCTGGGCAA
GTGGTGGA GTGAC TGGGGTCGGACCCGTT
A
GAM7776 246 LOC3494 1 13466 XP_303044.1 5 14 CTCCGTTGCCCA C 3 C b b
08 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 LOC3494 1 4112 XP_300513.1 3 1060 TTTTGCAGCCCA A 3 C b b
40 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
A
GAM7776 246 LOC3501 1 18715 XP_303810.1 5 16 TCCCTCTGCCCA T A G 3 C c c
06 GGTGGGGGCCGT CAT GC CTCCA CCTGGGCA
GGCTGGAA GTG CG GGGGT GGACCCGT
C - -
GAM7776 246 LOC3509 1 19860 XP_304556.1 5 119 AAGGAATGCCCA - A CAG 3 C c c
14 GGAGAGAGCACA CAT TGC CTC CCTGGGCA
TGGTTG GTA ACG GAG GGACCCGT
C A A--
GAM7776 246 LOC5105 1 5678 NP_056995.1 3 405 GTGAACTGCTTA T A 3 C c c
8 GGTAGGAGTGCA CA TGCACTCC GCCTGGGCA
CTGCAGTT GT ACGTGAGG TGGATTCGT
C A
GAM7776 246 LOC5119 2 3111 NP_057415.1 5 98 TCCTGTTACCCA CA CA 3 C c b
3 GGCTGGAGGACA CATTG CTCCAGCCTGGG
GTGATGTG GTGAC GAGGTCGGACCC
AG AT

GAM7776 246 LOC5119 2 14721 NP_057415.1 3 733 TTCTGTTGTCCA G 3 C b b
3 GGATGGAGTGCA CATTGCACTCCA CCTGGGCAA
GTGGTTGA GTGACGTGAGGT GGACCTGTT
A
GAM7776 246 LOC5125 1 14855 NP_057580.2 5 156 CTCTGTTACCCA CA 3 C c c
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AT
GAM7776 246 LOC5133 1 8243 NP_057728.1 5 337 CTCTGTTGCCCA C 3 C b b
4 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
ATGGCACA GTAACGTGAG TCGGACCCGTT
A
GAM7776 246 LOC5133 1 18703 NP_057730.1 3 665 CTCTGTTACCCA CA 3 C b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGAGTG GTAACGTGAGGTCGGACCC
AT
GAM7776 246 LOC5595 1 17853 NP_061976.1 5 0 GTCACCCAGGCT CA 3 C c c
4 GGAGTGTAGTGG CATTGCACTCCAGCCTGGG
CGCAATCT GTGATGTGAGGTCGGACCC
AC
GAM7776 246 LOC5690 1 5945 NP_064528.1 3 518 CTTTGTCACCCA C CA 3 C c c
2 GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGTGCA GTGACGTGAG TCGGACCC
A AC
GAM7776 246 LOC5692 1 8643 NP_064555.1 3 1847 GTCTGGGGCTCA G T A 3 C c
c
6 GGCTGGTGTGGG CATT CAC CCAGCCTGGGC
ATGCAGCC GTAG GTG GGTCGGACTCG
G T G
GAM7776 246 LOC5710 1 16916 NP_065114.2 3 587 TCTTGTTGCCCA 3 C b b
7 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC5714 1 11036 NP_065155.2 3 736 TCTTGTTGCCCA CA----- 3 C c c

6 GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGTGCA AACGTGAGGTCGGACCCGTT
ACGTGGC
GAM7776 246 LOC8989 1 14184 NP_612350.1 5 445 CCATGTTTGCCA G CT- G 3 C c
c
4 GGCTGGTCCTGA CATT CA CCAGCCTGG CAA
ATGCCTGA GTAA GT GGTCGGACC GTT
- CCT -
GAM7776 246 LOC9040 1 7704 XP_031517.1 5 1646 TCTTGTTACCCA CA 3 C c c
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCG GTGACGTGAGGTCGGACCC
AT
GAM7776 246 LOC9048 2 6896 XP_032059.1 3 1341 CTCTGTCGCCCA A 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGATGCA GTGACGTGAGGTCGGACCCG

C

GAM7776 246 LOC9048 2 18698 XP_032059.1 3 1183 CTCTGTCACCCA C CA 3 C c b

5 GGCTAGAGTGCA CATTGCACTC AGCCTGGG

GTGGAGCG GTGACGTGAG TCGGACCC

A AC

GAM7776 246 LOC9071 1 13994 XP_033704.1 3 121 AGTCACATCCCA G - CA 3 C c c

9 GGCTGGGGATGG CATT CA CTCCAGCCTGGG

ATGCTCTG GTAG GT GGGGTCGGACCC

- A TA

GAM7776 246 LOC9099 1 15038 XP_035410.1 3 115 CTCTGTTGCCCA C 3 C b b

9 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA

GTGGCACG GTGAC TGAGGTCGGACCCGTT

A

GAM7776 246 LOC9111 3 12591 XP_036218.1 3 758 GTCTTTCACCCA T CA 3 C c b

5 GGCTGGAGTGCT CAT GCACTCCAGCCTGGG

GTGGCACG GTG CGTGAGGTCGGACCC

T AC

GAM7776 246 LOC9111 3 17831 XP_036218.1 3 2144 ACTTGTTGCCCA 3 C b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA

ATGGTACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 LOC9111 3 19989 XP_036218.1 3 285 TCTTGTCACCCA CA 3 C b b

5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

ATGGCACG GTAACGTGAGGTCGGACCC

AC

GAM7776 246 LOC9117 1 16178 XP_036612.1 5 209 CTTTGTCGCCCG A A 3 C c c

0 GGCAGGAGTGCA CATTGCACTCC GCCTGGGC

GTGGCTCA GTGACGTGAGG CGGGCCCG

A C

GAM7776 246 LOC9125 1 8577 XP_037135.1 5 2207 CTCTGTCACCCA C- CA 3 C c c

0 GGCTGGAGTTAT CATTG ACTCCAGCCTGGG

AGTGACGT GTGAT TGAGGTCGGACCC

AT AC

GAM7776 246 LOC9126 1 18355 XP_037268.1 5 267 GCAGGATGCCCA C---- AC - - 3 C c c

6 GGGCTCGGAAGC ATTGC TCC AGCC TGGGCA

AGTAAGGA TGACG AGG TCGG ACCCGT

AGGAA A- C G

GAM7776 246 LOC9137 1 9077 XP_038063.5 3 1526 TCTTGTTGCCCA G 3 C b b

3 GGCTGGAGTGAA CATT CACTCCAGCCTGGGCAA

GTGGCGTG GTGA GTGAGGTCGGACCCGTT

A

GAM7776 246 LOC9154 1 17238 XP_039115.1 5 1290 GCCCTGTGGCTG TG G 3 C c c

9 GGCTGGAGTGCA CATTGCACTCCAGCC G CA

ATGGCGCG GTAACGTGAGGTCGG C GT

GT G
GAM7776 246 LOC9166 1 8303 NP_612381.1 3 517 CTCTGTCGGCCA C --- 3 C b b
1 GGCTGGAATGCA CATTGCA TCCAGCCTGG GCA
ATGGTGCC GTAACGT AGGTCGGACC TGT
A GGC
GAM7776 246 LOC9166 1 8075 NP_612382.1 3 339 CTCTGTGGCCCA A 3 C b b
3 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCG GTGACGTGAGGTCGGACCCG
G
GAM7776 246 LOC9189 1 14589 XP_041340.1 3 205 CTCTGCCGCCCA A A 3 C c c
3 GGCGGGAGTGCA CATTGCACTCC GCCTGGGC
GTGGCAGT GTGACGTGAGG CGGACCCG
G C
GAM7776 246 LOC9214 1 4097 XP_043160.1 5 761 CCCTGCCGCCCA C A 3 C c c
8 GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGCACG GTGACGTGAG TCGGACCCG
A C
GAM7776 246 LOC9259 1 19339 NP_775739.1 3 3527 CTCTGTTGCCCG C 3 C b b
7 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCATG GTAAC TGAGGTCGGGCCCGTT
A
GAM7776 246 LOC9313 1 9953 XP_049396.1 5 1234 GCTCTGTCACCA A -- 3 C c c
2 GGCTGGAGGGCA CATTGC CTCCAGCCTGG GCA
GTGGTGCG GTGACG GAGGTCGGACC TGT
G AC
GAM7776 246 LSS 1 6091 NP_002331.2 3 1071 GTCTCATGCCCA TT T G 3 C c c
GGTGGGTGCTCT CA GCAC CCA CCTGGGCA
GGGCTGGA GT CGTG GGT GGACCCGT
CT - -
GAM7776 246 LTB4R 1 1022 NP_000743.1 5 303 CTCTGTCATTCA --- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGTGCG GTGACGTGAGGTCGGAC CTGT
TTA
GAM7776 246 LTB4R2 1 15504 NP_062813.1 5 1345 CAGTTTTGCCCA --- TCCAGC 3 C
c c
GATGTGCTAGAA CATT GCAC CTGGGCAA
TGGGGCTG GTAA CGTG GACCCGTT
GAT TA----
GAM7776 246 LY75 1 17724 NP_002340.1 3 573 CTCTGTTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGCGTG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 LYZ 1 7382 NP_000230.1 3 331 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 LZTS1 1 4518 NP_066300.1 3 1445 CTCTGTCCCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
CC

GAM7776 246 MAC30 1 5069 XP_031536.2 3 228 CTCTGTTGCCCA ----- 3 C b b
GGCTGGAGTAAA CATTGC ACTCCAGCCTGGGCAA
GGGCAGTG GTGACG TGAGGTCGGACCCGTT
GGAAA
GAM7776 246 MAIL 1 2338 NP_113607.1 3 872 CTCTGGCGCCCA C A 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
GTGGCATG GTGAC TGAGGTCGGACCCG
A C
GAM7776 246 MAK 1 1989 NP_005897.1 3 644 CTCTTGTGTCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCACT GTGACGTGAGGTCGGACCTGT

GAM7776 246 MAPA 1 5231 NP_660299.1 3 806 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGCTGCG GTAACGTGAGGTCGGACCC
AC
GAM7776 246 MAPK8IP 1 14298 NP_203750.1 3 1043 CCCTGTGCTCAG GCA- - 3 C c
c
3 GGCTGGAGAGAG CATT CTCCAGCC TGGGCA
GGTGGCGG GTGG GAGGTCGG ACTCGT
GAGA G
GAM7776 246 MCLC 1 7270 NP_055942.1 3 316 CTCTGTCACCCA TG CA 3 C c c
GGCTGGAGTGAG CAT CACTCCAGCCTGGG
GTGGTACA GTG GTGAGGTCGGACCC
GA AC
GAM7776 246 MDM2 1 6671 NP_002383.1 3 355 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 MDM2 1 6671 NP_006869.1 3 355 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 MDM2 1 6671 NP_006870.1 3 355 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 MDM2 1 6671 NP_006871.1 3 355 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 MDM2 1 6671 NP_006872.1 3 355 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 MDM2 1 6671 NP_006873.1 3 299 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGTGA GTGACGTGAGGTCGGACCC
AT
GAM7776 246 MDM4 1 7078 NP_002384.1 3 548 TTCTGTCTCCCA C CA 3 C c c

GGCTGAAGTGCA CATTGCACT CAGCCTGGG
GTGAGTCA GTGACGTGA GTCGGACCC
A TC
GAM7776 246 MEFV 2 5443 NP_000234.1 3 511 CTCTGTGGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
G
GAM7776 246 MEFV 2 19829 NP_000234.1 3 823 TCTTGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 MESDC2 1 6523 XP_051854.1 3 74 GCTCTTTGCCCA - G C-- 3 C c c
GCTCCTGGGGTG CA TT CACTCCAG CTGGGCAA
GGAGTGGT GT AG GTGGGGTC GACCCGTT
G G CTC
GAM7776 246 MFTC 1 16545 NP_110407.2 3 548 CTTTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 MGAT2 1 9699 NP_079374.1 3 986 TCTTGTCGCTCA C A 3 C c c
GCCTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGAGCTG GTGACGTGAGGTC GACTCG
C C
GAM7776 246 MGC1077 1 5386 NP_085044.2 5 225 CTAGAGATGCCC G CC 3 C c
c
2 ATCTGGAGTGAG CATT CACTCCAG TGGGCA
TGCAGGAC GTGA GTGAGGTC ACCCGT
- T-
GAM7776 246 MGC1081 1 2199 NP_085045.2 3 89 CTCTGTCGCCCA C A 3 C b b
8 GGCTGGAGTACA CATTG ACTCCAGCCTGGGC
ATGGTGCG GTAAC TGAGGTCGGACCCG
A C
GAM7776 246 MGC1110 1 17609 NP_115701.2 3 1315 CTGTGTTGCTCA 3 C b b
2 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACTCGTT

GAM7776 246 MGC1226 1 12220 NP_116085.1 5 203 TGATGTTGCCCA C 3 C b b
2 GGCTAGAGTGCA CATTGCACTC AGCCTGGGCAA
GTGGCACA GTGACGTGAG TCGGACCCGTT
A
GAM7776 246 MGC1251 1 18251 NP_291026.1 3 0 CCCCAGGTTGGA CA 3 C c c
8 GTGCAGTGGCGT CATTGCACTCCAGCCTGGG
GTCTTGGG GTGACGTGAGGTTGGACCC
C-
GAM7776 246 MGC1301 1 11562 NP_542387.1 3 458 CTCTGTTGCCCA CCA 3 C b
b
7 GGCAGTAGTGCA CATTGCACT GCCTGGGCAA
GTGGCGCG GTGACGTGA CGGACCCGTT
TGA
GAM7776 246 MGC1302 1 13564 NP_689501.1 3 433 GTCTGTTTCCCA CA 3 C c c

4 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGATACA GTGATGTGAGGTCGGACCC
TT

GAM7776 246 MGC1313 2 6646 NP_219363.1 3 766 TCTTGTTGCCCA C----- 3 C b b
8 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCA TAACGTGAGGTCGGACCCGTT
ACGCGA

GAM7776 246 MGC1313 2 9543 NP_219363.1 3 456 CTCTGTCACCCA CA 3 C c b
8 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 MGC1317 1 20116 NP_116101.1 3 289 CACTTCTGCCCA G CA-- 3 C c
c
0 GGCAGCAGGGTG CATT CACTC GCCTGGGCA
GGTGGGTA GTGG GTGGG CGGACCCGT
- ACGA

GAM7776 246 MGC1320 1 9494 NP_113653.1 3 129 CTCTGTTGCCCA 3 C b b
4 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTATG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 MGC1428 1 3677 NP_542391.1 3 452 CTCTGTTGCCCA 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGACGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 MGC1443 1 17347 NP_116286.1 5 825 CCCTGTCACCCA C CA 3 C c
c
6 GGCTGGGGTACG CATTG ACTCCAGCCTGGG
GTGGCATG GTGGC TGGGGTCGGACCC
A AC

GAM7776 246 MGC1483 1 15044 NP_219480.1 3 381 CTCTGTTGCCCA 3 C b b
6 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 MGC1541 1 15115 NP_079011.2 3 1453 TCCCATTGCCCA T- CC C 3 C c
c
9 GCCTCAGTGCAT CA TGCACT AG CTGGGCAA
TTGGCAAA GT ACGTGA TC GACCCGTT
TT C- C

GAM7776 246 MGC1560 1 10968 NP_659474.1 5 287 CTCTGTTGCCCA T C 3 C b b

6 GGCTGGAGTACA CA TG ACTCCAGCCTGGGCAA
TTGGTGTG GT AC TGAGGTCGGACCCGTT
T A

GAM7776 246 MGC1566 1 3620 NP_116145.1 3 25 CTAGGATGCCCA CA----- T - 3 C c
c
8 GGGCTGGGTGCA TTGCAC CCAGCC TGGGCA
GCCAGCTG GACGTG GGTCGG ACCCGT
GTCGACC - G

GAM7776 246 MGC1587 1 2894 NP_116309.1 5 81 CTCTGTCGCCCA G T A 3 C c c

3 GGCTGGCGTGAA CATT CAC CCAGCCTGGGC
GTGGCGCA GTGA GTG GGTCGGACCCG
A C C
GAM7776 246 MGC1842 1 15046 XP_037797.2 3 1420 CTCTGTTGCCCA C 3 C b b

GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCACG GTGACGTGAGGTC GACCCGTT
A
GAM7776 246 MGC2167 1 16916 NP_443093.1 3 500 TCTTGTTGCCCA 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 MGC2173 1 8134 NP_659481.1 3 997 GGGATGCTGATG -- -- 3 C c c
8 GGTTGGAGTGCC CATT GCACTCCAGCCTG GGCA
TAATGGCT GTAA CGTGAGGTTGGGT TCGT
TC AG
GAM7776 246 MGC2306 1 7160 NP_002041.2 3 225 GACCGCTGCCCA T ----- G 3 C c
c
GGTGGGGTTTCC CAT GC ACTCCA CCTGGGCA
TGCATGGA GTA CG TGGGGT GGACCCGT
- TCCTT -
GAM7776 246 MGC2474 2 7797 NP_076420.1 3 954 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 MGC2474 2 18665 NP_076420.1 3 1312 GCTCCTCACCCA C CA 3 C c
b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGTGTG GTGACGT AGGTCGGACCC
A AC
GAM7776 246 MGC2477 3 5609 NP_077004.1 5 1480 CTCTGTTGCCCA C 3 C b b
GCTGGAGTGCAG CATTGCACTCCAGC TGGGCAA
TGGCGTGA GTGACGTGAGGTCG ACCCGTT
-
GAM7776 246 MGC2477 3 8610 NP_077004.1 5 1291 TCTGTCGCCCAG - A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCC TGGGC
GTGGCGCG GTGACGTGAGGTCGG ACCCG
G C
GAM7776 246 MGC2477 3 19729 NP_077004.1 5 1480 ACTCTGTTGCCC C 3 C b b

AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCGTG GTGACGTGAGGTCG ACCCGTT
-
GAM7776 246 MGC2603 1 5845 NP_076942.1 3 419 GCTCTGTCGCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCG GTGACGTGAGGTCGGACC TGT
GC
GAM7776 246 MGC2718 1 3976 NP_076972.2 3 437 GAGCTGAGCCCA ACTC A 3 C c
c

GGCTGCGTAGTG CATTGC CAGCCTGGGC
ACCACAAG GTGATG GTCGGACCCG
C--- A

GAM7776 246 MGC2734 2 18352 XP_300964.1 5 1668 TCTTGTTGCCCA - 3 C b b
5 GGGCTGGAGTGC CATTGCACTCCAGCC TGGGCAA
AGTGGCAT GTGACGTGAGGTCGG ACCCGTT
G

GAM7776 246 MGC2734 2 19385 XP_300964.1 5 1668 CTTGTTGCCCAG - 3 C b b
5 GGCTGGAGTGCA CATTGCACTCCAGCC TGGGCAA
GTGGCATG GTGACGTGAGGTCGG ACCCGTT
G

GAM7776 246 MGC2989 1 14858 NP_653219.1 3 606 CTCTGTCACCCA CA 3 C c c
1 GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGTGCA GTGGCGTGAGGTCGGACCC
AC

GAM7776 246 MGC2989 1 16672 NP_659485.1 3 503 CTTTGTTGCCCA C 3 C b b
8 GACTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGGCATA GTGACGTGAGGTC GACCCGTT
A

GAM7776 246 MGC3113 1 10136 NP_076940.1 3 713 CTCTGTTCCCCA A CA 3 C c
c
GGCCGGAGTGCA CATTGCACTCC GCCTGGG
GTGGTACG GTGACGTGAGG CGGACCC
C CT

GAM7776 246 MGC3207 2 5157 NP_115661.1 3 1437 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCC GTGACGTGAGGTCGGACCCG
C

GAM7776 246 MGC3207 2 13812 NP_115661.1 3 788 ACTCGTTGCCCA CA----- 3 C c
b
GGCTGGAGTGTA TTGCACTCCAGCCTGGGCAA
GAGGCGAG GATGTGAGGTCGGACCCGTT
GAGCGGA

GAM7776 246 MGC3329 1 4477 NP_076991.2 3 1597 TCTTGTTGTCTA T 3 C b b
GGCTGGAGTGCC CAT GCACTCCAGCCTGGGCAA
GTGGTGCG GTG CGTGAGGTCGGATCTGTT
C

GAM7776 246 MGC3363 1 12069 NP_689809.1 3 684 CTCTGTCACCCA CA 3 C c c
7 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGTA GTGATGTGAGGTCGGACCC
AC

GAM7776 246 MGC3388 1 8724 NP_659473.1 3 49 ATGCAATTTCCA T TCC ----- 3 C c
c
7 GGCTGTGCTGTG CAT GCAC AGCCTGG GCA
GACTTCTT GTG CGTG TCGGACC CGT
T --- TTTAA

GAM7776 246 MGC3403 1 9529 NP_694956.1 5 278 TTCAGCAGTCCA CTC A 3 C c
c

```
          4                          GGCTGATGCAGT CATTGCA   CAGCCTGGGC
                                     GGCTTCAA    GTGACGT   GTCGGACCTG
                                               A--         A
GAM7776  246   MGC3407 1  19817  NP_689688.1  3  189   TTCTGTCACCCA            CA        3  C  c  c

          9                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     GTGGTGCA    GTGACGTGAGGTCGGACCC
                                                 AC
GAM7776  246   MGC3413 2  8232   XP_291029.1  3  501   CTCTGTCACCCA            CA        3  C  c  c
          2                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     GTGGCATG    GTGACGTGAGGTCGGACCC
                                                 AC
GAM7776  246   MGC3413 2  9087   XP_291029.1  3  335   CACTGTCACCCA            CA        3  C  c  c
          2                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
                                     GTGGCATG    GTGACGTGAGGTCGGACCC
                                                 AC
GAM7776  246   MGC3513 1  8535   NP_689640.1  5  174   CTCTCTCACCCA    GC      CA        3  C  c
c
          6                          GGCTGGAGTAGA CATT  ACTCCAGCCTGGG
                                     GTGACAAT    GTGA  TGAGGTCGGACCC
                                               GA          AC
GAM7776  246   MGC3544 2  6886   NP_694952.1  3  493   CTCTGTCGCCCA      C       A        3  C  c  c
          0                          GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
                                     GTGGTGCA    GTGACGT AGGTCGGACCCG
                                               A         C
GAM7776  246   MGC3544 2  7378   NP_694952.1  3  184   CTCTGTCACCCA            CA        3  C  c  c
          0                          GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
                                     GTGGCGCA    GTGGCGTGAGGTCGGACCC
                                                 AC
GAM7776  246   MGC3546 1  7484   NP_694976.1  3  87    CCTTGTTGCCCA                    3  C  b  b
          8                          GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                     ATGGCGCG    GTAACGTGAGGTCGGACCCGTT

GAM7776  246   MGC3552 1  18741  NP_659502.1  3  487   TCCCACATGCCC      TC - CT         3  C  c
c
          1                          CGCATGCGTGCA CATTGCAC  CA GC  GGGCA
                                     ATGCCTCC    GTAACGTG  GT CG  CCCGT
                                               C-  A  C-
GAM7776  246   MGC3771 1  3231   NP_112232.1  5  748   CTCTTCTTCCCA        C   CA        3  C  c  c

                                     TGCTGGAGTGCA CATTGCACTCCAGC TGGG
                                     ATGGCGCA    GTAACGTGAGGTCG ACCC
                                                 T    TT
GAM7776  246   MGC3932 1  13428  NP_689642.2  3  697   CTGGCTTGCCCA                    3  C  b  b
          0                          GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
                                     GTGGCTAG    GTGGCGTGAGGTCGGACCCGTT

GAM7776  246   MGC4015 1  10743  NP_689563.1  3  318   CTGTATTGCCCA   TG               3  C  b  b

          7                          GGCTGGAGTGTG CAT  CACTCCAGCCTGGGCAA
```

GTGGCACA GTG GTGAGGTCGGACCCGTT
GT
GAM7776 246 MGC4016 1 7220 NP_714920.1 5 285 CTCTGTTGCCAA C G 3 C b b

8 GGCTGGAATGCA CATTGCA TCCAGCCT GGCAA
GTGGCGAG GTGACGT AGGTCGGA CCGTT
A A
GAM7776 246 MGC4057 2 16218 NP_689989.1 3 904 TCTTGTCTCCCA C CA 3 C c
c

9 GACTGGAGTGCA CATTGCACTCCAG CTGGG
ATGGCATG GTAACGTGAGGTC GACCC
A TC
GAM7776 246 MGC4057 2 19220 NP_689989.1 3 333 CTCTGTCACTCA CA 3 C c c

9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTATA GTGACGTGAGGTCGGACTC
AC
GAM7776 246 MGC4248 1 3338 NP_115709.2 3 277 AATTGACTGCCA T G 3 C b b
GGCTGGGTGCAG CATTGCAC CCAGCCTGG CA
TGGCTCAC GTGACGTG GGTCGGACC GT
- -
GAM7776 246 MGC4312 1 12783 NP_775784.1 3 200 CTCTGTCACCCA T CA 3 C c
c

2 GGTTGGAGTGCA CA TGCACTCCAGCCTGGG
TTGGTGTG GT ACGTGAGGTTGGACCC
T AC
GAM7776 246 MGC5033 1 2959 NP_848604.1 3 279 CTCTGTCGCCCA C----- A 3 C c c

7 GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
ATACTGCA TAACGTGAGGTCGGACCCG
ACGTCA C
GAM7776 246 MGC5045 1 16867 NP_775733.1 3 89 ACTTCTTGCCCA C 3 C b b
2 GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 MGC5055 2 11296 NP_776163.1 3 459 ACTTTGCTCCCA C CA 3 C c
b

9 GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCTAT GTGACGT AGGTCGGACCC
A TC
GAM7776 246 MGC5055 2 15151 NP_776163.1 3 561 CTCTGTCGTCCA A 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGACTCA GTGACGTGAGGTCGGACCTG
C
GAM7776 246 MGC9912 1 12221 NP_542395.1 3 351 GCTCTGTCGCCA C -- 3 C b b

GACTGGAGTGCA CATTGCACTCCAG CTGG GCA
GTGGCGCA GTGACGTGAGGTC GACC TGT
A GC
GAM7776 246 MGRN1 1 16616 XP_048119.4 3 1594 TCTTGCTGCCCA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCA
GTGGCTCA GTGACGTGAGGTCGGACCCGT

GAM7776 246 MHC2TA 3 783 NP_000237.1 3 439 CACTGTTGCCCA T 3 C b b
GGCTGGCGTGCA CATTGCAC CCAGCCTGGGCAA
GTGGTGCG GTGACGTG GGTCGGACCCGTT
C
GAM7776 246 MHC2TA 3 922 NP_000237.1 3 809 CAGATTGCAACA CAC G- 3 C c b
GGCTGGGCTTCA CATTG TCCAGCCTG GCAA
GTGGCAGC GTGAC GGGTCGGAC CGTT
TTC AA
GAM7776 246 MHC2TA 3 2053 NP_000237.1 3 2660 CTCTTATGCCCA C 3 C b b
CGCTGGAGTGCA CATTGCACTCCAGC TGGGCA
GTGAGCCG GTGACGTGAGGTCG ACCCGT
C
GAM7776 246 MIRAB13 1 11523 NP_203744.1 3 1732 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 MIRAB13 1 11523 XP_039236.6 3 2297 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 MKRN4 1 12075 NP_110384.1 3 373 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 MLANA 1 13029 NP_005502.1 3 611 TTTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGCG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 MLC1 2 14833 NP_055981.1 3 825 CTGTCATGCCCA T-- C 3 C c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACATGGCC GTA CGTGAGGTT GACCCGT
CAC C
GAM7776 246 MLC1 2 14833 NP_631941.1 3 825 CTGTCATGCCCA T-- C 3 C c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACATGGCC GTA CGTGAGGTT GACCCGT
CAC C
GAM7776 246 MLC1 2 19859 NP_055981.1 3 775 CTGTCATGCCCA T-- C 3 C c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM7776 246 MLC1 2 19859 NP_055981.1 3 877 CTGTCATGCCCA T-- C 3 C c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM7776 246 MLC1 2 19859 NP_631941.1 3 775 CTGTCATGCCCA T-- C 3 C c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA

ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM7776 246 MLC1 2 19859 NP_631941.1 3 877 CTGTCATGCCCA T-- C 3 C c c
GCTTGGAGTGCC CAT GCACTCCAG CTGGGCA
ACGTGGCC GTG CGTGAGGTT GACCCGT
CAC C
GAM7776 246 MLZE 1 9728 NP_113603.1 5 585 CGGAGTTGCCCA CA----- 3 C c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGCATGG GACGTGAGGTCGGACCCGTT
GGTACGC
GAM7776 246 MMPL1 1 4374 NP_004133.1 3 511 TTCTGTCCTCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGACATG GTAACGTGAGGTCGGACCT
CC
GAM7776 246 MOAP1 1 1744 NP_071434.2 3 300 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 moblak 1 19657 NP_570719.1 3 1259 CCGGCCTAACCA GCA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGG
GTGGTGGG GTGACGTGAGGTCGGACC
AAT
GAM7776 246 MOCS3 1 12064 NP_055299.1 3 579 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGATGTGAGGTCGGACCCGTT
GAM7776 246 MPL 2 11185 NP_005364.1 3 569 CTCTGTCACCCA C CA 3 C c b
GGCTGCAGTGCA CATTGCACT CAGCCTGGG
ATGGCGCG GTAACGTGA GTCGGACCC
C AC
GAM7776 246 MPL 2 16608 NP_005364.1 3 750 TGCCTGTTGCCA C G 3 C b b
GACTGGAGTGCA CATTGCACTCCAG CTGG CAA
GTGGCACG GTGACGTGAGGTC GACC GTT
A -
GAM7776 246 MRPL35 1 9545 NP_057706.2 3 1060 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT
GAM7776 246 MRPL44 1 14596 NP_075066.1 3 259 CTCTGTCGCCCA C A 3 C c c
GGCTGGACTGCA CATTGCA TCCAGCCTGGGC
GTGGTGCG GTGACGT AGGTCGGACCCG
C C
GAM7776 246 MRPL49 1 5438 NP_004918.1 3 324 CTCTGTTGCCCA G 3 C b b
GGGTGGAGTGCA CATTGCACTCCA CCTGGGCAA
GTGGCATG GTGACGTGAGGT GGACCCGTT
G
GAM7776 246 MRPS27 1 4179 NP_055899.1 3 430 TTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCA GTGACGTGAGGTCGGACCC

AC
GAM7776 246 MSTP028 1 12951 NP_114160.1 3 1907 CTCTATTGGCCA G 3 C b b

GGCTGGAGTGTA CATTGCACTCCAGCCTGG CAA
GTGGCACC GTGATGTGAGGTCGGACC GTT
G
GAM7776 246 MTH2 1 15874 NP_060753.1 3 851 CTCTGTTGCCCA CC 3 C b b
CATTGGAGTGCA CATTGCACTCCAG TGGGCAA
GTGGCACG GTGACGTGAGGTT ACCCGTT
AC
GAM7776 246 MYCL2 1 16868 NP_005368.1 3 1431 TCTTGTCGCCCA CA A 3 C c c

GGCTGGAGGTTA CATTG CTCCAGCCTGGGC
ATGGCATG GTAAT GAGGTCGGACCCG
TG C
GAM7776 246 MYLC2PL 1 3580 NP_612412.1 5 369 CTCTGTCGCCCA A A 3 C b b

GGCTGGAGCGCA CATTGC CTCCAGCCTGGGC
ATGGCATG GTAACG GAGGTCGGACCCG
C C
GAM7776 246 MYO5C 1 4306 NP_061198.1 3 628 GCTCTATCGCCA GCA 3 C c c
GGCTGGAGTGTA CATTGCACTCCAGCCTGG
GTGGCATG GTGATGTGAGGTCGGACC
GCT
GAM7776 246 NACT 1 19968 NP_808218.1 3 552 GCAACCTCCCAC - C- CA 3 C c c
TGCTGGAGTGCG CATT GCACTCCAGC TGGG
AGTGGGAA GTGA CGTGAGGTCG ACCC
G TC TC
GAM7776 246 Nanog 1 11523 NP_079141.1 3 282 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 NCAG1 1 3766 NP_115536.1 3 3665 CTTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTCTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 NCOA6 2 12826 NP_054790.1 5 1279 CTCTGTCACCGA G CA 3 C c
c
GGCTGGAGTGCA CATTGCACTCCAGCCT GG
GTGGCGCG GTGACGTGAGGTCGGA CC
G AC
GAM7776 246 NCOA6 2 19446 NP_054790.1 5 884 CTCTGTCGCCCA C----- A 3 C c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGC
GTCGTGCC TGACGTGAGGTCGGACCCG
CCGTGC C
GAM7776 246 NCOA6IP 2 8841 NP_079107.5 3 280 TTTTACCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGCCATG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 NCOA6IP 2 10534 NP_079107.5 3 444 CCATGTTGCCCA CA------ C T 3 C c
b

GGCTGGTGTCAA TTG AC CCAGCCTGGGCAA
ACTCCTGG AAC TG GGTCGGACCCGTT
GGTCCTCA - T

GAM7776 246 NDP52 1 15337 NP_005822.1 3 1122 CTCTGTCACCCA T CA 3 C c c
GGCTGGCGTGCA CATTGCAC CCAGCCTGGG
ATGGCGCA GTAACGTG GGTCGGACCC
C AC

GAM7776 246 NDRG3 1 15102 NP_114402.1 3 1152 CGCTGTTACCCA CA 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCGCA GTAACGTGAGGTCGGACCC
AT

GAM7776 246 NDUFC2 1 10192 NP_004540.1 3 1240 GCTCTGTCATCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGCA
GTGGCGCA GTGACGTGAGGTCGGAC CTGT
TA

GAM7776 246 NEU3 1 12075 NP_006647.2 5 71 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 NF2 1 9169 NP_057502.1 5 480 CTTTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCGTG GTAACGTGAGGTCGGACCCG
C

GAM7776 246 NONO 1 17960 NP_031389.2 3 447 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGATGTGAGGTCGGACCCG
C

GAM7776 246 NOSIP 1 7311 NP_057037.1 5 53 TCTTGTTGCCTA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGCG GTAACGTGAGGTCGGATCCGTT

GAM7776 246 NPTXR 1 5189 NP_055108.2 3 3926 CACATGGGCCCA - C A 3 C c c
GGCTGAGTGTGA CATT GCACTC AGCCTGGGC
GTGAGCAT GTGA TGTGAG TCGGACCCG
G - G

GAM7776 246 NPTXR 1 5189 NP_478058.1 3 3926 CACATGGGCCCA - C A 3 C c c
GGCTGAGTGTGA CATT GCACTC AGCCTGGGC
GTGAGCAT GTGA TGTGAG TCGGACCCG
G - G

GAM7776 246 NQO1 1 14855 NP_000894.1 3 685 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGACCC
AT

GAM7776 246 NR2E1 1 13178 NP_003260.1 5 598 AGGAGCCTTGCA - A --- A 3 C c c
GGCTGGAGGGCG CA TTGC CTCCAGCCTG GGC
GCTGGAGA GT GGCG GAGGTCGGAC CCG
C G GTT A

GAM7776 246 NRLN1 1 15825 NP_660277.1 5 22 GGCCAGTGCCCA -- CC 3 C b b
GGTTAGTGAGCA CATTGC ACT AGCCTGGGCA

GTGCCCGG GTGACG TGA TTGGACCCGT
AG --
GAM7776 246 NT5C2 1 4030 NP_036361.1 5 35 CTCTGCTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCA
GTGATGTG GTGAC TGAGGTCGGACCCGT
A
GAM7776 246 NUDT4 1 18879 NP_061967.2 3 1290 CTTTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACA GTAACGTGAGGTCGGACCC
AC
GAM7776 246 NUMA1 1 14343 NP_006176.1 5 119 CTTCCACCAGGA --- GCA 3 C c
c
GTCTGGAGTGCA CATTGCACTCCAG CCTGG
ATGGCACG GTAACGTGAGGTC GGACC
TGA ACC
GAM7776 246 NUP43 1 1900 NP_078923.2 3 606 AGAGTCTTGCTC CT 3 C c c
TGCTGGAGTGCG CATTGCACTCCAGC GGGCAA
GTGGTGCA GTGGCGTGAGGTCG CTCGTT
T-
GAM7776 246 NXN 1 935 NP_071908.1 3 876 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACC GTGACGTGAGGTCGGACCCG
C
GAM7776 246 OR51E2 1 4096 NP_110401.1 3 439 GCTCTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCG GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 ORC1L 1 17969 NP_004144.1 3 92 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 OSBPL2 1 7553 NP_055650.1 3 1126 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 OSBPL2 1 7553 NP_653081.1 3 1126 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 P2RXL1 1 4425 NP_005437.1 3 954 GCTCTGATCCCA G C CA 3 C c
c
GGCTGGATGGAG CATT CA TCCAGCCTGGG
TGGCTGGA GTGA GT AGGTCGGACCC
G - TA
GAM7776 246 P2RY1 1 8453 NP_002554.1 3 822 ATTTACTTGCCC TC CCT 3 C c c
CACTGCTGTGCA CATTGCAC CAG GGGCAA
ATGCCTTA GTAACGTG GTC CCCGTT
TC AC-
GAM7776 246 P450RAI 1 18160 NP_063938.1 3 48 CAGCCCAGCCCA TG A-- A 3 C c
c

-2 GGCAGCGGGGTG CAT CACTCC GCCTGGGC
GTGGTTGT GTG GTGGGG CGGACCCG
-- CGA A
GAM7776 246 PAICS 1 16852 NP_006443.1 3 413 CACTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 PASK 1 2769 NP_055963.1 5 805 TCTTGTTGCTGA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCT GGCAA
GTGGCACC GTGACGTGAGGTCGGA TCGTT
G
GAM7776 246 PCDHA9 2 10427 NP_054724.1 3 1915 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PCDHA9 2 16048 NP_054724.1 3 1315 TTCTGCCACCCA C CA 3 C c
b
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 PCDHB11 1 10723 NP_061754.1 3 192 TTCTGTCGCCCT T A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCC GGGC
ATGGTGTG GTAACGTGAGGTCGG CCCG
T C
GAM7776 246 PCDHB16 1 4617 NP_066008.1 3 581 TCTTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 PCDHB9 1 11523 NP_061992.2 3 527 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 PDE6B 1 936 NP_000274.1 3 197 CTCTGTCACCCA T CA 3 C c c
GGCTGGAGTGCC CAT GCACTCCAGCCTGGG
GTGGCACG GTG CGTGAGGTCGGACCC
C AC
GAM7776 246 PDGFC 1 905 NP_057289.1 3 45 AGCTCTTGCCCA C-- - 3 C b b
GAGCTGTGCAGT CATTGCACT CAGC CTGGGCAA
GCAGTGGC GTGACGTGA GTCG GACCCGTT
CGT A
GAM7776 246 PDLIM2 1 14973 NP_789847.1 3 1201 CTCTATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PDZK1 1 4194 NP_002605.2 5 44 TTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PDZRN1 1 5270 NP_699202.1 3 522 CACTCTCACCCA CA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 PELI1 3 5491 NP_065702.2 5 2686 CTCTGTTGCCCA 3 C b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACT GTGACGTGAGGTTGGACCCGTT

GAM7776 246 PELI1 3 7382 NP_065702.2 5 2122 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM7776 246 PELI1 3 14861 NP_065702.2 5 1442 CTCTGTCACCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AC

GAM7776 246 PER2 1 19703 NP_073728.1 3 1370 TCTTTTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCC GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PFAS 1 16261 NP_036525.1 3 674 CTCTGTCACCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
ATGGCGTG GTAAC TGAGGTCGGACCC
A AC

GAM7776 246 PHAX 1 12159 NP_115553.1 3 698 CCTGAACCCCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCAGG GTGAC TGAGGTCGGACCC
A CC

GAM7776 246 PIGR 1 11059 NP_002635.2 3 814 CACTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM7776 246 PIK3C2B 1 10488 NP_002637.2 3 1447 GCCCTGTCGCCA -- 3 C b b
GGCTGGAGTGTA CATTGCACTCCAGCCTGG GCA
GTGGCATG GTGATGTGAGGTCGGACC TGT
GC

GAM7776 246 PIK3C3 1 8874 NP_002638.1 3 2 AGTTTGCCCAGT GCA C- 3 C c c
ACTGGAGAAAAT CATT CTCCAG CTGGGCAA
GAACTGGG GTAA GAGGTC GACCCGTT
AA- AT

GAM7776 246 PIK3CD 1 9545 NP_005017.2 3 822 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PKNOX1 1 8826 NP_004562.2 3 1821 TCTTGTTGCCCA A 3 C b b
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGCAA
ATGGTGCA GTAACG GAGGTCGGACCCGTT
G

GAM7776 246 PLA2G6 1 16143 NP_003551.1 3 514 TGGGAAAGCCCA G A--- A 3 C c
c
GGCCGCAGGAGT CATT CACTCC GCCTGGGC

GGGATGCC GTAG GTGAGG CGGACCCG
G ACGC A

GAM7776 246 PMCHL1 1 16917 NP_114093.1 3 526 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 PMCHL2 1 16917 NP_114094.1 3 524 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 PMPCA 1 7640 NP_055975.1 3 246 TGAAGTGCCCAG CA----- - 3 C c c
CGCTGGAGTGCA TTGCACTCCAGC CTGGGCA
GCGTGCCA GACGTGAGGTCG GACCCGT
ACCGTGC C
GAM7776 246 PNMA2 2 8006 NP_009188.1 3 1714 CTCTATCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGACGTGAGGTCGGACCC
AC
GAM7776 246 PNMA2 2 17067 NP_009188.1 3 265 TCTCATCACCCA C CA 3 C c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGCACA GTGACGTGAG TCGGACCC
A AC
GAM7776 246 POFUT1 1 11287 NP_056167.1 3 1737 CTCTGTCTCCCA CA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
TC
GAM7776 246 POLE3 1 6151 NP_059139.2 3 1144 CTCTGTGGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCATG GTGACGTGAGGTCGGACCCG
G
GAM7776 246 POLR2D 2 2798 NP_004796.1 3 520 AACTCTTGTCCA C-- --- 3 C c c
GGCTGGAGGAGT ATTGCACTCC AGCCTGGGCAA
GCAGTCGT TGACGTGAGG TCGGACCTGTT
TGC AGG
GAM7776 246 POLR2D 2 5412 NP_004796.1 3 520 TCTTGTCCAGGC C----- --- 3 C c c
TGGAGGAGTGCA ATTGCACTCC AGCCTGGGCAA
GTCGTACA TGACGTGAGG TCGGACCTGTT
ACATGC AGG
GAM7776 246 PON1 1 2152 NP_000437.3 3 1197 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 POU2AF1 1 20135 NP_006226.1 3 1375 CTCCATTGCCCA C 3 C b b

GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAC TGAGGTCGGACCCGTT
A
GAM7776 246 POU2F3 1 16114 NP_055167.1 3 1109 TGCTCCAGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

```
                                GTGGCATG    GTGACGTGAGGTCGGACCCG
                                                  A
GAM7776  246   PP1628  1  10180 NP_079477.1  5  1279  ATTGCTCAGCCA  -   A TC      ----       3  C  c
c
                                GGCTGTGGAGCA CA TTGC C  CAGCCTGG   GCAA
                                GCTGAGGC    GT GACG G  GTCGGACC   CGTT
                                      C    A GT       GACT
GAM7776  246   PP3111  1  10883 NP_071439.2  3  190   GAGCAGGCCCCA  TT  C-       - A       3  C  c
c
                                GGCTGGACCTGC CA  GCA  TCCAGCCTGGG C
                                CCTGTCCT    GT  CGT  AGGTCGGACCC G
                                      CC   CC         C G
GAM7776  246   PP3856  1  10744 NP_660202.1  5  509   TCCAGGTGCCCT C------  C       T       3  C  c
c
                                GGCTGGAGTCAG       ATTG ACTCCAGCC GGGCA
                                TCCTCATC           TGAC TGAGGTCGG CCCGT
                                      CTACTCC   -        T
GAM7776  246   PPAP2C  1  7299  NP_003703.1  3  35    GGACCCCGCCCA  T  -  A-      A       3  C  c  c

                                GGCAGGGAGCTG CAT GCA CTCC  GCCTGGGC
                                CTGTGAGT    GTG CGT GAGG  CGGACCCG
                                      T  C    GA       C
GAM7776  246   PPAP2C  1  7299  NP_803545.1  3  35    GGACCCCGCCCA  T  -  A-      A       3  C  c  c

                                GGCAGGGAGCTG CAT GCA CTCC  GCCTGGGC
                                CTGTGAGT    GTG CGT GAGG  CGGACCCG
                                      T  C    GA       C
GAM7776  246   PPAP2C  1  7299  NP_808211.1  3  35    GGACCCCGCCCA  T  -  A-      A       3  C  c  c

                                GGCAGGGAGCTG CAT GCA CTCC  GCCTGGGC
                                CTGTGAGT    GTG CGT GAGG  CGGACCCG
                                      T  C    GA       C
GAM7776  246   PPEF2   1  2954  NP_006230.2  3  368   TCTTGTTGCCCA  T                  3  C  b  b
                                GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
                                TTGGCGCG    GT ACGTGAGGTCGGACCCGTT
                                      T
GAM7776  246   PPEF2   1  2954  NP_690910.1  3  1000  TCTTGTTGCCCA  T                  3  C  b  b
                                GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
                                TTGGCGCG    GT ACGTGAGGTCGGACCCGTT
                                      T
GAM7776  246   PPEF2   1  2954  NP_690911.1  3  2213  TCTTGTTGCCCA  T                  3  C  b  b
                                GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
                                TTGGCGCG    GT ACGTGAGGTCGGACCCGTT
                                      T
GAM7776  246   PPFIA4  1  16851 XP_046751.3  5  91    CAGTGCTGCCCA   GCAC   --          3  C  c  c

                                GGACCTGGACCG CATT   TCCAG  CCTGGGCA
                                AATGGGGG    GTAA   AGGTC  GGACCCGT
                                      GCC-    CA
GAM7776  246   PPFIBP1 3  8231  NP_003613.2  3  2295  CTCTGTTGCCCA                       3  C  b  b
```

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PPFIBP1 3 10708 NP_003613.2 3 1168 TTCTGTTGCCCA C 3 C b b
TGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
GTGGCGTG GTGACGTGAGGTCG ACCCGTT
T
GAM7776 246 PPFIBP1 3 12217 NP_003613.2 3 861 CTCTGTCACCCA T CA 3 C c b

GGTTGGAGTGCC CAT GCACTCCAGCCTGGG
ATGGCATG GTA CGTGAGGTTGGACCC
C AC
GAM7776 246 PPID 1 7378 NP_005029.1 3 247 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCG CATTGCACTCCAGCCTGGG
GTGGCGCA GTGGCGTGAGGTCGGACCC
AC
GAM7776 246 PPIL2 1 13122 NP_055152.1 3 392 CTCTGTTGCCCA CC 3 C b b
GGCTCCAGTGCA CATTGCACT AGCCTGGGCAA
GTGGTGTG GTGACGTGA TCGGACCCGTT
CC
GAM7776 246 PPP1R12 1 3861 NP_002472.1 3 4497 CTCTCTCGCCCA A 3 C b b
B GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 PPP1R12 1 3861 NP_115288.1 3 4630 CTCTCTCGCCCA A 3 C b b
B GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 PRKR 1 4790 NP_002750.1 3 275 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGACACA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 PRKWNK3 1 14862 NP_065973.1 3 639 CTCTGTCACCCA CA 3 C c
c

GGTTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTTGGACCC
AC
GAM7776 246 PRND 2 1539 NP_036541.1 3 839 TCTTGTTGCCCA CA----- 3 C c b
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
ACGGCATG AACGTGAGGTCGGACCCGTT
GTACGGC
GAM7776 246 PRND 2 4170 NP_036541.1 3 2764 TTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PRO0297 1 10574 NP_054800.1 5 53 CTCTTTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 PRO0365 1 18148 NP_054845.1 5 883 GCTCTGTCGCCA C -- 3 C b b

GGCTGAAGTGCA CATTGCACT CAGCCTGG GCA
GTGGCGCA GTGACGTGA GTCGGACC TGT
A GC
GAM7776 246 PRO1048 1 12596 NP_060967.1 3 319 CTCTGCTGCCCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCA
GTGGCACA GTGAC TGAGGTCGGACCCGT
A
GAM7776 246 PRO2730 1 2048 NP_079498.1 3 320 TGGTCAGGCCCA TG C A 3 C c
c
GGCTGAGTGAGA CAT CACTC AGCCTGGGC
TGAGCTGC GTA GTGAG TCGGACCCG
GA - G
GAM7776 246 PROM2 2 2147 NP_653308.1 3 786 CTCTGTCACCCA CA 3 C c b
GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGTGCA GTGATGTGAGGTCGGACCC
AC
GAM7776 246 PROM2 2 13176 NP_653308.1 3 951 CCATGTTGCCCA T- - 3 C b b
GGCTGGAAGTGT CAT GCACT CCAGCCTGGGCAA
CTATGTTT GTA TGTGA GGTCGGACCCGTT
TC A
GAM7776 246 PRPF31 1 11313 NP_056444.1 3 145 TGGGACTGCCCA TT A AG 3 C c
c
GGGAGGAGGCCT CA GC CTCC CCTGGGCA
TGGAAGAG GT CG GAGG GGACCCGT
TC - AG
GAM7776 246 PSMD9 1 17758 NP_002804.2 3 752 CTTTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGTCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 PSPH 1 15044 NP_004568.1 3 276 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 PTGES 1 16070 NP_004869.1 3 528 CTCTGTTGCCCA G C 3 C b b
AGCTGGAGTGAA CATT CACTCCAGC TGGGCAA
GTGGTACA GTGA GTGAGGTCG ACCCGTT
A A
GAM7776 246 PTGIS 2 10783 NP_000952.1 3 3269 GCTTATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 PTGIS 2 17361 NP_000952.1 3 2840 CTCTGCTGCCCA C 3 C b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCA
GTGGCGTG GTGACGTGAG TCGGACCCGT
A
GAM7776 246 PTK2 1 10355 NP_005598.3 5 129 CCCAGGCTGCCA G G 3 C b b
GGCTGGAGTGGA CATT CACTCCAGCCTGG CA
GTGGCATG GTGA GTGAGGTCGGACC GT
G -
GAM7776 246 PYGM 1 15938 NP_005600.1 5 741 GCTCCACTCCTT A ------ - A 3 C c c

GGCTGGAGGCAG CATTGC CTCCAGCC TGG GC
TGCTGAGG GTGACG GAGGTCGG ACC CG
- TTCCTC T -

GAM7776 246 RAB11-F 1 13848 NP_116321.2 3 2596 CTCTGTTGCCCA 3 C b b
IP4 GGCTGGAGTGTA CATTGCACTCCAGCCTGGGCAA
GTGGTATG GTGATGTGAGGTCGGACCCGTT

GAM7776 246 RAB21 1 7076 NP_055814.1 3 289 CTCTGTCACCCA T CA 3 C c c
GGCTGGAGTGCA CA TGCACTCCAGCCTGGG
CTGGCTTG GT ACGTGAGGTCGGACCC
C AC

GAM7776 246 RAB33B 1 7910 NP_112586.1 3 839 GCTCTGTCTCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGTC GTGACGTGAGGTCGGACC TGT
TC

GAM7776 246 RAB36 2 808 NP_004905.1 3 1408 CCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTA GTAACGTGAGGTCGGACCCGTT

GAM7776 246 RAB36 2 1652 NP_004905.1 3 1726 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACG GTAACGTGAGGTCGGACCC
AC

GAM7776 246 RAB39 1 3754 XP_084662.1 3 753 TTTTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGGCA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 RAB4A 1 16568 NP_004569.2 5 27 GCGCCTGCGCGG - C - G 3 C c c
AGCTGGAGTCCG CA TTG ACTCCAGC CTG GCA
GCTGGGCC GT GGC TGAGGTCG GGC CGT
C C A G

GAM7776 246 RABL2A 1 2648 NP_038198.1 3 578 GCTCTGTCGCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 RABL2B 1 2648 NP_009012.1 3 585 GCTCTGTCGCCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGCGCA GTGACGTGAGGTCGGACC TGT
GC

GAM7776 246 RAI 1 8937 NP_006654.1 5 22 CAAGTGAGTCTC T A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCC GGGC
GTGGTGCA GTGACGTGAGGTCGG TCTG
C A

GAM7776 246 RAI16 1 4335 NP_073586.3 3 417 GTCAGGAGCCCA TG CCA A 3 C c
c
GGCCAGTGAGAT CAT CACT GCCTGGGC
GGGGCCTG GTA GTGA CGGACCCG
GA C-- A

GAM7776 246 RAI17 1 7523 NP_065071.1 3 1485 CACTTTGTTTCA T-- T-- - 3 C c c
GGCTGGTCTGTG CAT GCAC CCAGCCTGGG CAA

CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM7776 246 RAI17 1 7523 XP_166091.2 3 1485 CACTTTGTTTCA T-- T-- - 3 C c c
GGCTGGTCTGTG CAT GCAC CCAGCCTGGG CAA
CCCCGTGA GTG CGTG GGTCGGACTT GTT
CCC TCT T
GAM7776 246 RAI3 1 12784 NP_003970.1 3 343 CTCTGTCACCCA C CA 3 C c c
GGCTTGAGTGCA CATTGCACTC AGCCTGGG
GTGGTGCG GTGACGTGAG TCGGACCC
T AC
GAM7776 246 RAP140 1 16472 NP_056039.1 3 1919 CTCTGTCGCCCA C C A 3 C c
c
AGCTGGAGTACA CATTG ACTCCAGC TGGGC
GTGGTGCA GTGAC TGAGGTCG ACCCG
A A C
GAM7776 246 RARG 1 11090 NP_000957.1 5 41 CGGAGCCTCCCA A T CA 3 C c c

GGCTGGGGCAGT CATTGC C CCAGCCTGGG
GGGCATGG GTGACG G GGTCGGACCC
- - TC
GAM7776 246 RASSF2 1 19336 NP_055552.1 3 3347 TTCTGTTTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGGG GTGACGTGAGGTCGGACCC
TT
GAM7776 246 RASSF2 1 19336 NP_739579.1 3 3573 TTCTGTTTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGGG GTGACGTGAGGTCGGACCC
TT
GAM7776 246 RASSF2 1 19336 NP_739580.1 3 3347 TTCTGTTTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGGG GTGACGTGAGGTCGGACCC
TT
GAM7776 246 RBBP1 1 11014 NP_002883.2 3 542 GCAGTGTGCCCA - C- - 3 C c c
GGATTGAAGGTG CATT GCACT CAG CCTGGGCA
TAAATGGG GTAA TGTGG GTT GGACCCGT
A AA A
GAM7776 246 RBBP1 1 11014 NP_075376.1 3 542 GCAGTGTGCCCA - C- - 3 C c c
GGATTGAAGGTG CATT GCACT CAG CCTGGGCA
TAAATGGG GTAA TGTGG GTT GGACCCGT
A AA A
GAM7776 246 RBBP1 1 11014 NP_075377.1 3 542 GCAGTGTGCCCA - C- - 3 C c c
GGATTGAAGGTG CATT GCACT CAG CCTGGGCA
TAAATGGG GTAA TGTGG GTT GGACCCGT
A AA A
GAM7776 246 RBBP9 1 16100 NP_006597.2 3 1856 CTCTGTCTCCCA CA CA 3 C c
c
GGCTGGAGGTCA CATTG CTCCAGCCTGGG
GTGGCACA GTGAC GAGGTCGGACCC
TG TC
GAM7776 246 RBL2 1 6615 NP_005602.2 3 607 AGTCCTTGATTG TCCA 3 C c c

```
                                TTCGGGTGTGCA CATTGCAC   GCCTGGGCAA
                                ATGTCTGA    GTAACGTG    TGGGCTTGTT
                                      ----
GAM7776  246   RCBTB1  1  13829 NP_060661.2  5  129   CTCTCTTGCCCA     CAC    C          3  C  c
c
                                GACTGGAATACA CATTG   TCCAG CTGGGCAA
                                GTGGTGTG    GTGAC   AGGTC GACCCGTT
                                      ATA     A
GAM7776  246   RCD-8   1  13335 NP_055144.2  3  595   CTGCCTTGCCCA  T  AC-   G -        3  C  c  c

                                GGGGTGGGATGG CA TGC   TCCA CC TGGGCAA
                                CACTGAAG    GT ACG   GGGT GG ACCCGTT
                                      C   GTA   G  G
GAM7776  246   RDH13   1  9713  NP_612421.1  5  227   ACTCTGTCGCCA C-----     C       --     3  C  c  c
                                GGCTGGAATGCA      ATTGCA TCCAGCCTGG  GCA
                                GTAGGGCA          TGACGT AGGTCGGACC  TGT
                                      ACGGGA      A         GC
GAM7776  246   RGS3    1  3344  NP_570613.1  5  61    GTGCTCATGCCA     C  --      G       3  C  c  c
                                GGCTGACGGGTC CATTG ACTC  CAGCCTGG CA
                                CAGTGCGG    GTGAC TGGG  GTCGGACC GT
                                      C   CA      -
GAM7776  246   RHD     2  4143  NP_057208.2  3  690   ACTCTGTCACCA             --        3  C  b  b
                                GGCTGGAGTGCA CATTGCACTCCAGCCTGG  GCA
                                GTGCCGCA    GTGACGTGAGGTCGGACC  TGT
                                      AC
GAM7776  246   RHD     2  4143  NP_057309.2  3  779   ACTCTGTCACCA             --        3  C  b  b
                                GGCTGGAGTGCA CATTGCACTCCAGCCTGG  GCA
                                GTGCCGCA    GTGACGTGAGGTCGGACC  TGT
                                      AC
GAM7776  246   RHD     2  13465 NP_057208.2  3  281   CTCTGTCACCCA        C      CA       3  C  c  b
                                GGCTAGAGTGCA CATTGCACTC AGCCTGGG
                                ATGGCACC    GTAACGTGAG TCGGACCC
                                      A       AC
GAM7776  246   RHD     2  13465 NP_057309.2  3  370   CTCTGTCACCCA        C      CA       3  C  c  b
                                GGCTAGAGTGCA CATTGCACTC AGCCTGGG
                                ATGGCACC    GTAACGTGAG TCGGACCC
                                      A       AC
GAM7776  246   RHPN2   1  11803 NP_149094.2  3  890   CTGTGTTGCCCA                          3  C  b  b
                                GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
                                GTGGTGTG    GTGACGTGAGGTCGGACCCGTT

GAM7776  246   RIP60   1  5556  NP_037532.1  3  100   GTGCCTGCCTAG     C-----      -        3  C  c  c
                                TGCTGGAGTAGG CATTG     ACTCCAGC CTGGGCA
                                GGACAATG    GTAAC      TGAGGTCG GATCCGT
                                      AGGGGA       T
GAM7776  246   RIP60   1  5556  NP_055189.1  3  100   GTGCCTGCCTAG     C-----      -        3  C  c  c
                                TGCTGGAGTAGG CATTG     ACTCCAGC CTGGGCA
                                GGACAATG    GTAAC      TGAGGTCG GATCCGT
                                      AGGGGA       T
GAM7776  246   RNF137  2  7446  NP_060543.4  3  163   TCTTTGCTACCA   T  --  C      --       3  C  c  b
```

GGCTGAAGTCTG CAT GC ACT CAGCCTGG GCAA
TCATGAAA GTA TG TGA GTCGGACC CGTT
C TC A AT

GAM7776 246 RNF137 2 16940 NP_060543.4 3 829 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 RNF144 1 4727 NP_055561.1 3 3167 TTTTGTCCCCCA C C CA 3 C c c

AGCTGGAGTACA CATTG ACTCCAGC TGGG
ATGACAGG GTAAC TGAGGTCG ACCC
A A CC

GAM7776 246 RNF8 2 9745 NP_003949.1 3 959 CCCAAGCTGGAG --- C CA 3 C c c
TACAGTAGTGCA CATTGC ACTCCAGC TGGG
ATCTCAGC GTGATG TGAGGTCG ACCC
ACA A --

GAM7776 246 RNF8 2 13778 NP_003949.1 3 954 CTCTGTTGCCCA --- C 3 C c c
AGCTGGAGTACA CATTGC ACTCCAGC TGGGCAA
GTAGTGCA GTGATG TGAGGTCG ACCCGTT
ACA A

GAM7776 246 RP2 1 6582 NP_008846.1 3 1766 TCTTGTTGCCCA C 3 C b b
AGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCGCG GTAACGTGAGGTCG ACCCGTT
A

GAM7776 246 RPH3AL 1 2614 NP_008918.1 3 641 CTTTGTTGCCCA 3 C b b
GGCTGGGGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGGGGTCGGACCCGTT

GAM7776 246 RPP30 2 445 NP_006404.1 3 358 CTTTGTTGCTCA C 3 C b b
GGCTGGAGTACA CATTG ACTCCAGCCTGGGCAA
GTGGCATA GTGAC TGAGGTCGGACTCGTT
A

GAM7776 246 RPP30 2 19325 NP_006404.1 3 1203 CTCTGTCCCCCA CA 3 C c b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCTCG GTGACGTGAGGTCGGACCC
CC

GAM7776 246 S100A15 1 19723 NP_789793.1 3 3404 CTCTGTCGCCCG T A 3 C c c

GGCTGGAGTGCT CAT GCACTCCAGCCTGGGC
GTGAGCTG GTG CGTGAGGTCGGGCCCG
T C

GAM7776 246 SARM1 2 4282 NP_055892.1 3 3667 CTCTGTTGTCCA A 3 C b b
GGCTGGAGGGCA CATTGC CTCCAGCCTGGGCAA
GTGACATA GTGACG GAGGTCGGACCTGTT
G

GAM7776 246 SARM1 2 7147 NP_055892.1 3 416 AGGCAATGCCCA T A --- A 3 C c b

GGCGGGCCTGGG CA TGC CT CC GCCTGGGCA
CACTGTAT GT ACG GG GG CGGACCCGT
C - TCC G

GAM7776 246 SAS 1 17726 NP_005972.1 3 511 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCATG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 SBLF 1 14551 NP_006864.2 3 1609 CTCTGTTGCCCA C 3 C b b
GCCTGGAGTGCA CATTGCACTCCAG CTGGGCAA
GTGTGTCA GTGACGTGAGGTC GACCCGTT
C

GAM7776 246 SCAMP-4 1 2153 NP_524558.1 3 873 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 SCAND2 1 7179 NP_071333.2 3 1783 TTCTATCACCCA G CA 3 C c c

GGCTGGAGTGGA CATT CACTCCAGCCTGGG
GTGGTATG GTGA GTGAGGTCGGACCC
G AC

GAM7776 246 SCARF1 1 5158 NP_003684.1 3 410 CTCTGTCCCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
CC

GAM7776 246 SCD 1 3800 NP_005054.2 3 2066 TCAGTGCTCTCA - CT- 3 C c c
GCTGGCAGTGCA CATTGCACT CCAGC GGGCA
ATGCTTGT GTAACGTGA GGTCG CTCGT
C ACT

GAM7776 246 SCML2 1 3898 NP_006080.1 3 1313 CTCTTGTGCCCA C----- 3 C b b
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCA
ATAGCTCG TAACGTGAGGTCGGACCCGT
GCTCGA

GAM7776 246 SCN2B 1 13704 NP_004579.1 3 496 GAGCAGCCATCA - - -- A 3 C c c
GGCTGGAGGTGA CATTG CAC TCCAGCCTG GGC
CGATGAGT GTAGC GTG AGGTCGGAC CCG
A G TA A

GAM7776 246 SCN3B 1 4399 NP_060870.1 3 2013 CTCTGTCTCCCA C CA 3 C c c
GGCTAGAGTGCA CATTGCACTC AGCCTGGG
GTGGTGCA GTGACGTGAG TCGGACCC
A TC

GAM7776 246 SDS-RS1 1 14127 NP_612441.1 5 91 ATCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
AC

GAM7776 246 SEDL 3 926 NP_055378.1 3 1000 TCCTGTTGTGCA G 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTG GCAA
GTGGCACA GTGACGTGAGGTCGGAC TGTT
G

GAM7776 246 SEDL 3 11591 NP_055378.1 3 1346 CTCTGTTGTCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCAGT GTAACGTGAGGTCGGACCTGTT

GAM7776 246 SEDL 3 15576 NP_055378.1 3 308 ACTCTGTTGCCA G 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGG CAA
GTGGCGCA GTGACGTGAGGTCGGACC GTT
-

GAM7776 246 SEMA3E 1 13353 NP_036563.1 3 5 TGCCCAGGCACA G ----- ------ 3 C c c
CGCTGGACTCCT CATT CAC TCCA GCCTGGGC
GTGGGGTG GTGG GTG AGGT CGGACCCG
G TCCTC CGCACA

A
T

GAM7776 246 SEPN1 1 18255 NP_065184.1 3 1557 CTCTGTCACCCA T CA 3 C c c

GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
ATGGCTCG GTA CGTGAGGTCGGACCC
T AC
GAM7776 246 SERF1A 2 9219 NP_068802.1 3 243 ACTCTGTCACCA C -- 3 C b b
GACTGGAGTGCA CATTGCACTCCAG CTGG GCA
GTGGCGCC GTGACGTGAGGTC GACC TGT
A AC
GAM7776 246 SERF1A 2 15849 NP_068802.1 3 410 CACTGTTGCCCA C 3 C b b
GGCTGGACTGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
C
GAM7776 246 SERF1B 2 9219 NP_075267.1 3 243 ACTCTGTCACCA C -- 3 C b b
GACTGGAGTGCA CATTGCACTCCAG CTGG GCA
GTGGCGCC GTGACGTGAGGTC GACC TGT
A AC
GAM7776 246 SERF1B 2 15849 NP_075267.1 3 410 CACTGTTGCCCA C 3 C b b
GGCTGGACTGCA CATTGCA TCCAGCCTGGGCAA
GTGGCGTG GTGACGT AGGTCGGACCCGTT
C
GAM7776 246 SERPINB 2 4363 NP_004146.1 3 511 CTCTGTCGCCCA A 3 C b b
9 GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCTCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 SERPINB 2 9152 NP_004146.1 3 2359 CTCTGTCACCCA CA 3 C c b

9 GGCTGGAGTGTA CATTGCACTCCAGCCTGGG
GTGGCATG GTGATGTGAGGTCGGACCC
AC
GAM7776 246 SFXN2 1 3678 NP_849189.1 3 594 CTCTGTCGCCCA C A 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGCG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 SFXN2 1 3678 XP_058359.2 3 595 CTCTGTCGCCCA C A 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCGCG GTGACGT AGGTCGGACCCG
A C
GAM7776 246 SH3BGRL 1 2741 NP_113657.1 3 3337 ACTGAAGCCACA T ACT - A 3 C c
c

2 GGCTGGTGGCCA CAT GC CCAGCCTG GGC
TGTTCTCT GTA CG GGTCGGAC CCG
C GT- A A

GAM7776 246 SH3BP2 3 1122 NP_003014.2 3 3271 CTCTGTCGCCCA TTG C A 3 C c b
GGCTAGAGTGGA CA CACTC AGCCTGGGC
TTGGCGTG GT GTGAG TCGGACCCG
TAG A C

GAM7776 246 SH3BP2 3 3836 NP_003014.2 3 1850 CCCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGCCGTG GTAACGTGAGGTCGGACCCG
C

GAM7776 246 SH3BP2 3 9440 NP_003014.2 5 157 CTCAGTTGCCCA A C 3 C b b
GACTGGAGAGCA CATTGC CTCCAG CTGGGCAA
GTGGCCAA GTGACG GAGGTC GACCCGTT
A A

GAM7776 246 SHOX 1 4375 NP_006874.1 3 0 GCCCAGGCTGGA C A 3 C b b
GTATAATGGCAT CATTG ACTCCAGCCTGGGC
GTCTCGAC GTAAT TGAGGTCGGACCCG
A -

GAM7776 246 SIGLEC8 1 4513 NP_055257.1 3 516 CTCTGTCACCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGGGCA GTGACGTGAGGTCGGATCC
AC

GAM7776 246 SIL 1 12411 NP_003026.1 3 361 TCTTGTAGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCAGG GTAACGTGAGGTCGGACCCG
A

GAM7776 246 SIRPB1 1 14771 NP_006056.1 3 2041 ACCTTATTCCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGTCGTG GTAACGTGAGGTCGGACCC
TT

GAM7776 246 SLA2 1 19573 NP_115590.1 3 689 CCCTGTTGCCCA C 3 C b b
TGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCACG GTAACGTGAGGTCG ACCCGTT
T

GAM7776 246 SLA2 1 19573 NP_778252.1 3 792 CCCTGTTGCCCA C 3 C b b
TGCTGGAGTGCA CATTGCACTCCAGC TGGGCAA
ATGGCACG GTAACGTGAGGTCG ACCCGTT
T

GAM7776 246 SLC12A8 1 5190 NP_078904.1 3 209 CCTTGTCACCCA C CA 3 C c c
GGCTGGAGTCCA CATTG ACTCCAGCCTGGG
GTGGCACA GTGAC TGAGGTCGGACCC
C AC

GAM7776 246 SLC13A1 1 4370 NP_071889.2 3 1480 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGGG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 SLC14A2 1 4514 NP_009094.2 5 33 CTCTGTCACCCA T C CA 3 C c c

GGCTGGAGTACA CA TG ACTCCAGCCTGGG
CTGGCACT GT AC TGAGGTCGGACCC
C A AC

GAM7776 246 SLC15A1 1 18930 NP_005064.1 3 219 TCTTGTTGTCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCTGTT

GAM7776 246 SLC16A4 1 611 NP_004687.1 3 183 CTCTTTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCA GTGACGTGAGGTCGGACCCG
C

GAM7776 246 SLC19A3 1 6713 NP_079519.1 3 1013 ACAGGAGTCAGA G- A 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCT GGC
ATGGCGTG GTAACGTGAGGTCGGA CTG
GA A

GAM7776 246 SLC1A5 1 1277 NP_005619.1 3 177 GGGATGCCTGGC - C -- TG 3 C c
c

TGCTGGAGTACA CAT TG ACTCCAGC C GGCA
TGTGTTCA GTG AC TGAGGTCG G CCGT
T A TC GT

GAM7776 246 SLC24A1 1 10966 NP_004718.1 3 687 TCTTGTTGCCCA T 3 C b b
GGCTGGTGTGCA CATTGCAC CCAGCCTGGGCAA
ATGGCGTG GTAACGTG GGTCGGACCCGTT
T

GAM7776 246 SLC30A5 1 3692 NP_076960.1 3 153 CTCCATCGCCCA C A 3 C c c
GGCTGCAGTGCA CATTGCACT CAGCCTGGGC
GTGACACG GTGACGTGA GTCGGACCCG
C C

GAM7776 246 SLC30A6 1 5362 NP_060434.2 3 507 CTCTGTCGCCCA C A 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGGC
GTGGCATG GTGACGT AGGTCGGACCCG
A C

GAM7776 246 SLC35E2 1 13336 XP_049733.6 3 1607 GTCTGTCACCCA C CA 3 C c
c

GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC

GAM7776 246 SLC39A1 1 9528 NP_055252.2 5 88 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCG CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGGCGTGAGGTCGGACCCGTT

GAM7776 246 SLC4A11 1 806 NP_114423.1 3 251 AGCTTCTGCCCA - G T G 3 C c c
GGGTGGGTGGGA CA TT CAC CCA CCTGGGCA
CTGAGCAG GT AG GTG GGT GGACCCGT
C G - G

GAM7776 246 SLC5A1 1 2571 NP_000334.1 3 123 AAATTTTGCCCA - ----- G 3 C c c
GGTGGATAAATG CAT TGCAC TCCA CCTGGGCAA
TGTACATG GTA ATGTG AGGT GGACCCGTT
C TAAAT -

GAM7776 246 SLC6A14 1 13830 NP_009162.1 3 1676 TTCTGTTGCCTG TG 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCC GGCAA
GTGGCATG GTGACGTGAGGTCGG CCGTT
GT

GAM7776 246 SLC6A3 1 12941 NP_001035.1 3 1594 GTGGGCTCCAGG -- - A 3 C c c

GACTGGAGTGTA CATTGCACTCCAG CCTGG GC
ATGCTCGG GTAATGTGAGGTC GGACC CG
AG T G

GAM7776 246 SMAC 2 1861 NP_620308.1 5 482 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGAG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 SMAC 2 18165 NP_620308.1 5 656 CTCTGTTGCCCA C 3 C b b
GGCTGAAGTGCA CATTGCACT CAGCCTGGGCAA
GTGGGGCG GTGACGTGA GTCGGACCCGTT
A

GAM7776 246 SNAP23 1 19007 NP_003816.2 3 673 CTCTCTTGTCCA C----- 3 C c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCG TAACGTGAGGTCGGACCTGTT
GCGCGA

GAM7776 246 SNAP23 1 19007 NP_570710.1 3 673 CTCTCTTGTCCA C----- 3 C c c
GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA
ATAGCGCG TAACGTGAGGTCGGACCTGTT
GCGCGA

GAM7776 246 SNARK 1 18622 NP_112214.1 3 602 TCTTGGTGCCCA C 3 C b b
GGCTAGAGTGCA CATTGCACTC AGCCTGGGCA
ATGGCGCG GTAACGTGAG TCGGACCCGT
A

GAM7776 246 SNPH 1 15041 NP_055538.1 3 2430 GCCCTGGCCCAG - C- A 3 C c c

CTCTGGAGTGCA CAT TGCACTCCAG CTGGGC
TGTGTGTG GTG ACGTGAGGTC GACCCG
T TC G

GAM7776 246 SNX15 1 7625 NP_037438.2 3 270 CTGTGTCGCCCA C A 3 C c c
GACTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTGGG GTGACGTGAGGTC GACCCG
A C

GAM7776 246 SNX15 1 7625 NP_680086.1 3 270 CTGTGTCGCCCA C A 3 C c c
GACTGGAGTGCA CATTGCACTCCAG CTGGGC
GTGGTGGG GTGACGTGAGGTC GACCCG
A C

GAM7776 246 SNX22 1 13596 NP_079074.1 3 519 TCTTGTTGCCCA C 3 C b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGCACG GTGACGT AGGTCGGACCCGTT
A

GAM7776 246 SNX27 1 16941 NP_112180.4 3 3109 CTCTGTCGCCCA A 3 C b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCACG GTGACGTGAGGTTGGACCCG

C

GAM7776 246 SPN 1 16209 NP_003114.1 3 185 CTTTGTCGCCCA A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

ATGCACGA GTAACGTGAGGTCGGACCCG

C

GAM7776 246 SPOP 1 5610 NP_003554.1 5 130 CTCTGTCACCCG CA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCGCG GTGACGTGAGGTCGGGCCC

AC

GAM7776 246 SQV7L 1 7375 XP_047287.1 5 1345 CTCTGTTGCCCA C A 3 C b b

GGCAGGAGTACA CATTG ACTCC GCCTGGGCAA

GTGGCATT GTGAC TGAGG CGGACCCGTT

A A

GAM7776 246 SRL 1 6681 XP_064152.3 3 585 CTCTGTCGGCCA --- 3 C b b

GGTTGGAGTGCA CATTGCACTCCAGCCTGG GCA

GTGGTGCA GTGACGTGAGGTTGGACC TGT

GGC

GAM7776 246 SRRM2 1 18975 NP_057417.2 5 1 GCGGCCCAGGCG - A A 3 C c c

GGGTGCGAGTGG CATT GCACTCC GCCTGGGC

CGCAGTCG GTGA CGTGGGG CGGACCCG

G - G

GAM7776 246 SS18 1 17762 NP_005628.1 3 1674 TCTTGTCGCCCA A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

GTGGCGCA GTGACGTGAGGTCGGACCCG

C

GAM7776 246 STAF65(1 2196 NP_055675.1 3 1380 CTCTGTCACCCA CA 3 C b b

gamma) GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

ATGGTGCA GTAACGTGAGGTCGGACCC

AC

GAM7776 246 STAU 1 3950 NP_004593.1 5 275 TCTTGTCGCCCA A 3 C b b

GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC

GTGGCGTG GTGACGTGAGGTCGGACCCG

C

GAM7776 246 STE 1 3303 NP_005411.1 3 196 CTCTGTTGCCTA CA 3 C b b

GGCTGGAGGACA CATTG CTCCAGCCTGGGCAA

GTGGCACA GTGAC GAGGTCGGATCCGTT

AG

GAM7776 246 STEAP2 1 9147 NP_694544.1 3 1987 CTCTGTCACCCA CA 3 C c c

GGCTGGAGTGCA CATTGCACTCCAGCCTGGG

GTGGCACG GTGACGTGAGGTCGGACCC

AC

GAM7776 246 STOM 1 2907 NP_004090.3 3 495 TCTTGTTGCCCA C----- 3 C b b

GGCTGGAGTGCA ATTGCACTCCAGCCTGGGCAA

ATAGCATG TAACGTGAGGTCGGACCCGTT

GTACGA

GAM7776 246 STX12 1 12575 NP_803173.1 3 1621 AGTGTGTAGAGA C TGG--- 3 C c c

TGGCTGAGTGCA CATTGCACTC AGCC GCA

ATGGCTCA GTAACGTGAG TCGG TGT

- TAGAGA

GAM7776 246 SYT11 1 9033 NP_689493.2 3 281 TCTTGTTGCCCG 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGTGAG GTAACGTGAGGTCGGGCCCGTT

GAM7776 246 SYT13 1 15294 NP_065877.1 3 1526 CTTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TADA3L 1 9087 NP_597814.1 3 289 CACTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCATG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 TAL1 1 18260 NP_003180.1 3 2375 TTCTGTCACTCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGTGCC GTGAC TGAGGTCGGACTC
A AC
GAM7776 246 TAPBP 3 11523 NP_003181.3 3 837 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 TAPBP 3 12247 NP_003181.3 3 230 CTCTTCCGCCCA C A 3 C c b
GGCTGCAGTGCA CATTGCACT CAGCCTGGGC
GTGGCATG GTGACGTGA GTCGGACCCG
C C
GAM7776 246 TAPBP 3 16940 NP_003181.3 3 1142 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TAT 1 18942 NP_000344.1 3 779 CTCTGTCGCCCA C A 3 C c c
TGCTGGAGTGCA CATTGCACTCCAGC TGGGC
GTGGCGCG GTGACGTGAGGTCG ACCCG
T C
GAM7776 246 TBC1D5 2 14859 NP_055559.1 5 590 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGTGCA GTGACGTGAGGTCGGACCCG
C
GAM7776 246 TBC1D5 2 16449 NP_055559.1 5 920 CGCTCTTGTCCA C 3 C b b
GGCTGGAGTATA CATTG ACTCCAGCCTGGGCAA
ATGGTGCG GTAAT TGAGGTCGGACCTGTT
A
GAM7776 246 TBX3 1 19690 NP_005987.2 5 243 GCCCAGCGCCCC G ------ - A 3 C c c
GCCTGGAGTGGA CATT CACTCCA GC CTGGGC
TGAGCCTC GTAG GTGAGGT CG GACCCG
- CCGCCC C -
GAM7776 246 TBX3 1 19690 NP_057653.2 5 243 GCCCAGCGCCCC G ------ - A 3 C c c
GCCTGGAGTGGA CATT CACTCCA GC CTGGGC
TGAGCCTC GTAG GTGAGGT CG GACCCG
- CCGCCC C -
GAM7776 246 TCF2 1 625 NP_006472.1 3 2022 CTCTGTCACCCG C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG

GTGGTGCA GTGACGTGAGGTCG GCCC
A AC
GAM7776 246 TCL6 1 17450 NP_036600.2 5 645 CTCTGTCACTCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM7776 246 TCL6 1 17450 NP_055233.1 5 645 CTCTGTCACTCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM7776 246 TCL6 1 17450 NP_065575.1 5 645 CTCTGTCACTCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM7776 246 TCL6 1 17450 NP_065577.2 5 645 CTCTGTCACTCA C CA 3 C c c
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCGCG GTGACGT AGGTCGGACTC
A AC
GAM7776 246 TDGF1 1 8563 NP_003203.1 3 321 CTCTGTCACCCA C CA 3 C c c
GGCTGGACTGCA CATTGCA TCCAGCCTGGG
ATGACGCG GTAACGT AGGTCGGACCC
C AC
GAM7776 246 TERA 2 14491 NP_067061.1 3 305 CCACGTTGGCCA GCACT G 3 C c
c
GGCTGGTCTTAA CATT CCAGCCTGG CAA
ATGACCCT GTAA GGTCGGACC GTT
ATTCT G
GAM7776 246 TERA 2 17755 NP_067061.1 3 140 TCTTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AT
GAM7776 246 TERF1 1 1745 NP_003209.1 3 419 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TERF1 1 1745 NP_059523.1 3 419 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGCA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TERF2 1 1744 NP_005643.1 3 141 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 TGIF2 1 6881 NP_068581.1 3 1452 CTCTGTCACCCG CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGGCCC
AC
GAM7776 246 TIGD6 1 4933 NP_112215.1 3 909 TTATATTGCCTA C 3 C b b
GGCTGGAATGCA CATTGCA TCCAGCCTGGGCAA
GTGGTTAT GTGACGT AGGTCGGATCCGTT

A

GAM7776 246 TIM50L 2 5989 XP_053074.2 3 614 CACTGTTGCCCA T 3 C b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGCAA
TTGATGTG GT ACGTGAGGTCGGACCCGTT

T

GAM7776 246 TIM50L 2 10157 XP_053074.2 3 1407 TCTTATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCACG GTAACGTGAGGTCGGACCCGTT

GAM7776 246 TLK1 1 6551 NP_036422.2 5 279 TCCGGGAGGCCC CCAG A 3 C c c

AGGGAAGGTGCA CATTGCACT CCTGGGC
ATGGATGA GTAACGTGG GGACCCG

AAG- G

GAM7776 246 TLR5 1 16229 NP_003259.2 5 97 CTCTGCCGCCCA C A 3 C c c
GGCTGGACTGCA CATTGCA TCCAGCCTGGGC
GTGACACA GTGACGT AGGTCGGACCCG

C C

GAM7776 246 TMC1 1 2152 NP_619636.2 5 128 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TMEM14A 1 5271 NP_054770.1 5 75 CTCGGGGCTGCA - A 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTG GGC
GTGGGACA GTGACGTGAGGTCGGAC TCG

G G

GAM7776 246 TMPRSS3 1 6625 NP_076927.1 3 245 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TMPRSS3 1 6625 NP_115777.1 3 245 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TMPRSS3 1 6625 NP_115780.1 3 245 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCGAA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TNFAIP2 2 13948 NP_006282.2 3 637 ACGGCCCCTACA CT- ---- A 3 C c b

GGCTGGCCCTGC CATTGCA CCAGCCT GGGC
AATGGGGC GTAACGT GGTCGGA CCCG

CCC CATC G

GAM7776 246 TNFAIP2 2 17621 NP_006282.2 3 1221 CTGTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCCTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TNFRSF1 2 4398 NP_003833.3 3 454 CTCTGTCTCCCA CA 3 C b b
0B GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC

TC
GAM7776 246 TNFRSF1 2 4398 NP_671716.1 3 454 CTCTGTCTCCCA CA 3 C b b
0B GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGTGCA GTAACGTGAGGTCGGACCC
TC
GAM7776 246 TNFRSF1 2 15107 NP_003833.3 3 2022 CTCTCTCGCCCA CA----- A 3 C c
b
0B GGCTGGAGTGCA TTGCACTCCAGCCTGGGC
ACGGTACG AACGTGAGGTCGGACCCG
GCATGGC C
GAM7776 246 TNFRSF1 2 15107 NP_671716.1 3 2022 CTCTCTCGCCCA CA----- A 3 C c
b
0B GGCTGGAGTGCA TTGCACTCCAGCCTGGGC
ACGGTACG AACGTGAGGTCGGACCCG
GCATGGC C
GAM7776 246 TNFRSF1 1 2200 NP_003830.1 3 503 GGCTCTGGCCCA C A 3 C c c
1A GGCTAGAGTGCA CATTGCACTC AGCCTGGGC
GTGGTGCG GTGACGTGAG TCGGACCCG
A G
GAM7776 246 TNFRSF2 1 16759 NP_055267.1 3 747 TAATATGCTCTG GCA TG - 3 C c
c
1 GGCTGGAGAAAT CATT CTCCAGCC G GCA
GAAATCCT GTAA GAGGTCGG C CGT
A-- GT T
GAM7776 246 TNFRSF9 1 13464 NP_001552.2 3 227 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACC GTGACGTGAGGTCGGACCC
AC
GAM7776 246 TNS 1 8787 NP_072174.2 3 34 GCCCCTTGCCCA T CCAG 3 C c c
GGGCCAGTGCCA CAT GCACT CCTGGGCAA
TGGGGAAG GTA CGTGA GGACCCGTT
C CCG-
GAM7776 246 TOLLIP 2 3306 NP_061882.2 3 933 CTGCTGTGCCCA T --- CAG- 3 C c c
GGACGTGGGTTC CAT GC ACTC CCTGGGCA
AGCGTGGG GTG CG TGGG GGACCCGT
- ACT TGCA
GAM7776 246 TOLLIP 2 13694 NP_061882.2 3 526 GGCCCCTGCCCA C C - 3 C c c
GGGCTTGGGTCT CATTG ACTC AGCC TGGGCA
GGTGAGCT GTGGT TGGG TCGG ACCCGT
C T G
GAM7776 246 TOP3B 1 4495 NP_003926.1 3 39 CTCCCTCACCCA T C CA 3 C c c
GGCTGCAGTGCC CAT GCACT CAGCCTGGG
ATGCAGAC GTA CGTGA GTCGGACCC
C C AC
GAM7776 246 TOR1B 1 14221 NP_055321.1 3 180 CTCCGTCATCCA C CA 3 C c c
AGCTGGAGTGCA CATTGCACTCCAGC TGGG
GTGGTGCA GTGACGTGAGGTCG ACCT

A AC
GAM7776 246 TOSO 1 5682 NP_005440.1 3 356 TGTTGCTGCCCA - CA CC 3 C c c
GGCTCTAGATCA CAT TG CT AGCCTGGGCA
CATGGCAT GTA AC GA TCGGACCCGT
C TA TC
GAM7776 246 TP53 1 4654 NP_000537.2 3 833 CTTTGTTGCCCA G 3 C b b
GGCTGGAGTGGA CATT CACTCCAGCCTGGGCAA
GTGGCGTG GTGA GTGAGGTCGGACCCGTT
G
GAM7776 246 TP53I11 1 14987 XP_029347.6 5 217 CTGCAGAGGCCG GCA-- ----- 3 C c
c
GGCTGGAGGAGA CATT CTCCAGCCTGG GCA
AGATGGCG GTAG GAGGTCGGGCC CGT
AAGAG GGAGA
GAM7776 246 TPMT 1 19670 NP_000358.1 3 426 TCTTGTTGCCCA CC 3 C b b
ACCTGGAGTGCA CATTGCACTCCAG TGGGCAA
GTGGTGCG GTGACGTGAGGTC ACCCGTT
CA
GAM7776 246 TRAF5 1 7045 NP_004610.1 3 1091 CATTGTCACCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 TRAF5 1 7045 NP_665702.1 3 1091 CATTGTCACCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 TRIM16 1 4601 NP_006461.2 3 249 CACTGTTGCCCA A 3 C b b
GGCTGGAGAGCA CATTGC CTCCAGCCTGGGCAA
GTGGCGCG GTGACG GAGGTCGGACCCGTT
A
GAM7776 246 TRIM5 1 5879 NP_149023.1 3 651 TCTTGTTCCCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGGCACG GTAACGTGAGGTCGGACCC
CT
GAM7776 246 TRIM6 1 13572 NP_477514.1 3 172 CTCTGTCGCCCA T A 3 C b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
CTGGCGCA GT ACGTGAGGTCGGACCCG
C C
GAM7776 246 TRIP-Br 1 19574 NP_055570.1 3 2988 GACAGTTATTGA TC CC GG 3 C c
c
2 CACTGATGTGCA CATTGCAC CAG TG CAA
ATGAAGTG GTAACGTG GTC AC GTT
TA -- A-
GAM7776 246 TRPM6 1 18177 NP_060132.3 3 857 TCTTTTTACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGATGCG GTAACGTGAGGTCGGACCC
AT
GAM7776 246 TRPV1 2 16980 NP_061197.3 3 364 TCTTCTCACCCA C CA 3 C c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC

A AC
GAM7776 246 TRPV1 2 16980 NP_542435.1 3 364 TCTTCTCACCCA C CA 3 C c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC
GAM7776 246 TRPV1 2 16980 NP_542436.1 3 364 TCTTCTCACCCA C CA 3 C c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC
GAM7776 246 TRPV1 2 16980 NP_542437.1 3 364 TCTTCTCACCCA C CA 3 C c b
GGCTGGAATGCA CATTGCA TCCAGCCTGGG
GTGGCACA GTGACGT AGGTCGGACCC
A AC
GAM7776 246 TRPV1 2 19833 NP_061197.3 3 685 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TRPV1 2 19833 NP_542435.1 3 686 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TRPV1 2 19833 NP_542436.1 3 686 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TRPV1 2 19833 NP_542437.1 3 685 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGTG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TSC1 1 15082 NP_000359.1 3 786 ATTGTGACCACA - T - - 3 C c c
GGCTGGTGTGTA CAT TGCAC CCAGCCTG GG CA
GGTGGTAA GTG ATGTG GGTCGGAC CC GT
G T A A
GAM7776 246 TSPYL 1 15042 XP_166325.1 3 658 CTCTGTCGCCCA A 3 C b b
GGTTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTTGGACCCG
C
GAM7776 246 TTY7 1 1016 NP_114132.1 5 521 CCCCCATGCCCA G TC G 3 C c c
GGTGTGGTGAAG CATT CAC CA CCTGGGCA
TGAATCCC GTGA GTG GT GGACCCGT
A GT -
GAM7776 246 TU12B1-TY 3 4256 NP_057659.1 3 3182 TCTTTTTGCCCA A 3 C b b
GGCCGGAGTGCA CATTGCACTCC GCCTGGGCAA
ATGGCACG GTAACGTGAGG CGGACCCGTT
C
GAM7776 246 TU12B1-TY 3 15780 NP_057659.1 3 1305 TCTTATTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGCACA GTGACGTGAGGTCGGACCCGTT

GAM7776 246 TU12B1- 3 16036 NP_057659.1 3 2855 CTCTGTTGCCCA CC 3 C b b

TY TTCTGGAGTGCA CATTGCACTCCAG TGGGCAA
GTGGTGTG GTGACGTGAGGTC ACCCGTT
TT
GAM7776 246 TUCAN 2 7106 NP_055774.1 3 2766 CTCTGTCATCTA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGTG GTGACGTGAGGTCGGATCT
AC
GAM7776 246 TUCAN 2 9530 NP_055774.1 3 2457 CTCTGTTACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGTGCG GTGACGTGAGGTCGGACCC
AT
GAM7776 246 TXL-2 1 15381 NP_835231.1 5 95 AATTGCCCTGCA CA----- --- 3 C c c
GGCTGGAGTGCA TTGCACTCCAGCCT GGGCAA
GCGGCATG GACGTGAGGTCGGA CCCGTT
GTACGGC CGT
GAM7776 246 TXNL2 2 9147 NP_006532.1 3 68 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 TXNL2 2 19232 NP_006532.1 3 766 AATTAAGTGCCA CA T G 3 C c c
GGCTGGGCACAA CATTG C CCAGCCTGG CA
TGGCTCGT GTAAC G GGTCGGACC GT
AC - -
GAM7776 246 U1SNRNP 1 9590 NP_008951.1 5 122 GGGAGTCGCCCA A A 3 C c
c
BP GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C
GAM7776 246 U1SNRNP 1 9590 NP_851030.1 5 122 GGGAGTCGCCCA A A 3 C c
c
BP GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C
GAM7776 246 U1SNRNP 1 9590 NP_851034.1 5 122 GGGAGTCGCCCA A A 3 C c
c
BP GGCTGGAGAGCG CATTGC CTCCAGCCTGGGC
GTGGCGCG GTGGCG GAGGTCGGACCCG
A C
GAM7776 246 UCK1 1 11791 NP_113620.1 3 710 TGTGCGGGGCCA C ---- - ---- 3 C c c
GGCTGGGAGCCC ATTGCA CTCC AGCCTGG GCA
ATGCAGTA TGACGT GAGG TCGGACC CGT
A ACCC G GGGG
GAM7776 246 UGDH 1 7909 NP_003350.1 3 153 CACTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCA GTGACGTGAGGTCGGACCCGTT
GAM7776 246 UGT1A1 1 10967 NP_000454.1 3 534 AATGAATGAATG T - TGGG 3 C c
c
GCTTGGAGTGCA CA TGCACTCCA GCC CA
CTGAGAAC GT ACGTGAGGT CGG GT

```
                                        C       T  TAA-
GAM7776  246   UGT1A10 1  10967 NP_061948.1  3 535   AATGAATGAATG  T      -  TGGG        3  C  c
c
                                GCTTGGAGTGCA CA TGCACTCCA GCC   CA
                                CTGAGAAC    GT ACGTGAGGT CGG   GT
                                        C       T  TAA-
GAM7776  246   UGT1A4  1  10967 NP_009051.1  3 534   AATGAATGAATG  T      -  TGGG        3  C  c
c
                                GCTTGGAGTGCA CA TGCACTCCA GCC   CA
                                CTGAGAAC    GT ACGTGAGGT CGG   GT
                                        C       T  TAA-
GAM7776  246   UGT1A6  1  10967 NP_001063.1  3 533   AATGAATGAATG  T      -  TGGG        3  C  c
c
                                GCTTGGAGTGCA CA TGCACTCCA GCC   CA
                                CTGAGAAC    GT ACGTGAGGT CGG   GT
                                        C       T  TAA-
GAM7776  246   UGT1A8  1  10967 NP_061949.3  3 535   AATGAATGAATG  T      -  TGGG        3  C  c
c
                                GCTTGGAGTGCA CA TGCACTCCA GCC   CA
                                CTGAGAAC    GT ACGTGAGGT CGG   GT
                                        C       T  TAA-
GAM7776  246   UGT1A9  1  10967 NP_066307.1  3 534   AATGAATGAATG  T      -  TGGG        3  C  c
c
                                GCTTGGAGTGCA CA TGCACTCCA GCC   CA
                                CTGAGAAC    GT ACGTGAGGT CGG   GT
                                        C       T  TAA-
GAM7776  246   UMPS    1  2144  NP_000364.1  3 391   CTCTGTTGCCCA          G             3  C  b  b
                                GGATGGAGTGCA CATTGCACTCCA CCTGGGCAA
                                GTGGTGAG    GTGACGTGAGGT GGACCCGTT
                                            A
GAM7776  246   UNC84B  1  13541 NP_056189.1  3 1393  TCTGGAGCATGA      C      GG- A       3  C  c
c
                                GGCTGGATGCAG CATTGCA TCCAGCCT   GC
                                TGGTGGTG    GTGACGT AGGTCGGA   CG
                                        -       GTA  A
GAM7776  246   UNC84B  1  13541 XP_039332.1  3 1393  TCTGGAGCATGA      C      GG- A       3  C  c
c
                                GGCTGGATGCAG CATTGCA TCCAGCCT   GC
                                TGGTGGTG    GTGACGT AGGTCGGA   CG
                                        -       GTA  A
GAM7776  246   URG4    1  6788  NP_060390.2  3 565   GACCCCTGCCCA  T  C   CAG           3  C  c
c
                                GGAAGAGTTCAC CA TG ACTC   CCTGGGCA
                                TGGTCGCT    GT AC TGAG   GGACCCGT
                                        C  T   AA-
GAM7776  246   USP22   1  11288 XP_042698.2  3 2025  GTTTGTTGCCCA   G               3  C  b  b
                                GGCTGGAGTGAG CATT CACTCCAGCCTGGGCAA
                                TGGCACAG    GTGA GTGAGGTCGGACCCGTT
                                        -
GAM7776  246   VDU1    1  3187  NP_055832.2  3 278   CTTTGTCACCCA  T          CA        3  C  c  c
```

GGCTGGAGTGCT CAT GCACTCCAGCCTGGG
GTGGTGTT GTG CGTGAGGTCGGACCC
T AC

GAM7776 246 VENTX2 1 19331 NP_055283.1 3 305 CTCTGTCACCCA CA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
ATGACGCA GTAACGTGAGGTCGGACCC
AC

GAM7776 246 VHL 2 3873 NP_000542.1 3 2569 CTCTGTTGCCCA CA----- 3 C c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GAGGTGCG GACGTGAGGTCGGACCCGTT
GCGTGGA

GAM7776 246 VHL 2 8786 NP_000542.1 3 989 TCTTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCC GTGACGTGAGGTCGGACCC
AC

GAM7776 246 VIPR2 1 7754 NP_003373.2 3 314 CTCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCCTG GTGACGTGAGGTCGGACCCG
C

GAM7776 246 VPS39 1 18246 XP_031720.2 3 1284 CAGAGGTGCACA T ----- G 3 C c c

GGCTGGAGTTTC CA TGC ACTCCAGCCTG GCA
AGGCACTG GT ACG TGAGGTCGGAC CGT
C GACTT A

GAM7776 246 VTI1A 1 2313 NP_660207.1 3 358 GCCCTGTCGCCT G T A 3 C c c
GGCTGGAGTGGA CATT CACTCCAGCC GGGC
GTGGCACA GTGA GTGAGGTCGG TCCG
G - C

GAM7776 246 WBSCR18 1 2152 NP_115693.2 3 832 CTCTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
GTGGTGCG GTGACGTGAGGTCGGACCCGTT

GAM7776 246 WDR6 1 12628 NP_439891.1 5 93 TCCCAGTGACGG T - GG 3 C c c
GTCTGGAGTGCG CAT GCACTCCAG CCTG CA
TGGGGGAC GTG CGTGAGGTC GGGC GT
- T A-

GAM7776 246 WHSC1 1 9245 NP_579889.1 3 3922 CCCTGTTGGCCA C----- G 3 C c
c
GGCTGGAGTGCA ATTGCACTCCAGCCTGG CAA
GTAAGTGG TGACGTGAGGTCGGACC GTT
GGTGAA G

GAM7776 246 WNT5A 1 10269 NP_003383.1 5 751 GCTTTGGGGATG - T------ A 3 C c c

GCTGGAAGTGCA CATTGCACT CCAGCC GGGC
ATGTCTTC GTAACGTGA GGTCGG TTCG
A TAGGGGT -

GAM7776 246 XRCC2 3 9688 NP_005422.1 3 99 CTCTGTCTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACA GTGACGTGAGGTCGGACCC
TC

GAM7776 246 XRCC2 3 10148 NP_005422.1 3 278 TGTCTCCCAGGC --- CA 3 C c c
TGCTGGAGTGCA CATTGCACTCCA GCCTGGG
GTGGCACA GTGACGTGAGGT CGGACCC
CGT TC
GAM7776 246 XRCC2 3 12605 NP_005422.1 3 278 CTCTGTCTCCCA --- CA 3 C c c
GGCTGCTGGAGT CATTGCACTCCA GCCTGGG
GCAGTGGC GTGACGTGAGGT CGGACCC
CGT TC
GAM7776 246 YES1 1 16112 NP_005424.1 3 1378 CTCTGCCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCCG
C
GAM7776 246 ZAP 2 508 NP_064504.2 3 204 TTCTGATGCCCA - CTC---- 3 C c b
GGTTGCACCCCA CATTG CA CAGCCTGGGCA
TGCCAATG GTAAC GT GTTGGACCCGT
C ACCCCAC
GAM7776 246 ZAP 2 3071 NP_064504.2 3 308 CTCCATCGTCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
GTGGCGCG GTGACGTGAGGTCGGACCTG
C
GAM7776 246 ZFP30 1 9331 NP_055713.1 3 1854 CTCTTTCGCCCA T A 3 C c c
GGCTGGCGTGCA CATTGCAC CCAGCCTGGGC
GTGGCACA GTGACGTG GGTCGGACCCG
C C
GAM7776 246 ZFP42 1 10587 NP_777560.1 3 643 CTCTGTCACCCA C CA 3 C c c
GGCTGGAGTCTA CATTG ACTCCAGCCTGGG
GTGTCGTG GTGAT TGAGGTCGGACCC
C AC
GAM7776 246 ZFP64 1 15043 NP_060667.1 3 151 CTCTGTTTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCT GTGACGTGAGGTCGGACCC
TT
GAM7776 246 ZFP64 1 15043 NP_071371.2 3 151 CTCTGTTTCCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGCT GTGACGTGAGGTCGGACCC
TT
GAM7776 246 ZFYVE26 1 12160 XP_031077.1 3 3 CCCATGGCCCAG TT - --- A 3 C c c
GCTCCAGGAAGT CA GCACT CC AGCCTGGGC
GCCTTGGG GT CGTGA GG TCGGACCCG
TC A ACC G
GAM7776 246 ZMYND17 1 456 NP_848546.1 3 219 CTCTGTTGCCCA CA----- 3 C c c
GGCTGGAGTGCA TTGCACTCCAGCCTGGGCAA
GCGGCATG GACGTGAGGTCGGACCCGTT
GTACGGC
GAM7776 246 ZNF18 1 19151 XP_085596.2 5 97 AAGGACTTGCCA CAC G 3 C b b
GGCTGGACAATG CATTG TCCAGCCTGG CAA
CCCGTTGA GTAAC AGGTCGGACC GTT
--- -

GAM7776 246 ZNF253 1 19746 NP_066385.1 3 292 TCTTGTCACCGA G CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCT GG
ATGACATG GTAACGTGAGGTCGGA CC
G AC
GAM7776 246 ZNF264 2 3319 NP_003408.1 3 2604 CTCTGTCACCCA T C CA 3 C c c
CGCTGGAGTGCT CAT GCACTCCAGC TGGG
GTGATGCG GTG CGTGAGGTCG ACCC
T C AC
GAM7776 246 ZNF264 2 9147 NP_003408.1 3 2978 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCACG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 ZNF273 1 18868 XP_088082.1 3 843 TCTTGTTGCCCA 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGCAA
ATGGCGTG GTAACGTGAGGTCGGACCCGTT
GAM7776 246 ZNF281 1 16434 NP_036614.1 3 34 CAAAAGTGGCCA CA---- G 3 C c c
GGCTGGAGGTCT CATTG CTCCAGCCTGG CA
TCTAATGT GTAAT GAGGTCGGACC GT
CTTCTG G
GAM7776 246 ZNF289 1 13159 NP_115765.2 3 77 CCACAGTTCCCA TT - CA 3 C c c
GGCTGGGGATGC CA GCA CTCCAGCCTGGG
TTTGCCTT GT CGT GGGGTCGGACCC
TT A TT
GAM7776 246 ZNF305 1 18505 NP_055539.1 3 2909 TCCTGTCGCCCA A 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGGGC
ATGGCACG GTAACGTGAGGTCGGACCCG
C
GAM7776 246 ZNF334 2 5064 NP_060572.2 5 42 TGTCACCCAGGC C --- CA 3 C c c
TGCTGGAGTACA CATTG ACTCCA GCCTGGG
GTGGCACA GTGAC TGAGGT CGGACCC
A CGT AC
GAM7776 246 ZNF334 2 9628 NP_060572.2 5 42 CACTGTCACCCA C --- CA 3 C c c
GGCTGCTGGAGT CATTG ACTCCA GCCTGGG
ACAGTGGC GTGAC TGAGGT CGGACCC
A CGT AC
GAM7776 246 ZNF339 1 1729 NP_067043.1 3 655 CTCTGTCACCCA C CA 3 C c c
GGCTGGAGTACA CATTG ACTCCAGCCTGGG
GTGGCATG GTGAC TGAGGTCGGACCC
A AC
GAM7776 246 ZNF345 1 1011 NP_003410.1 3 601 TCACTGTCACCA -- 3 C b b
GGCTGGAGTGCA CATTGCACTCCAGCCTGG GCA
GTGGTGCA GTGACGTGAGGTCGGACC TGT
AC
GAM7776 246 ZNF398 1 8530 NP_065832.1 5 255 CTCTGTCGCCCA C A A 3 C c c
GGCGGGAATGCA CATTGCA TCC GCCTGGGC
GTGGCGCA GTGACGT AGG CGGACCCG
A G C

GAM7776 246 ZNF409 1 2388 NP_055709.1 5 10 AGCGAGTGCCCA CACTC G 3 C c c
GGGTGAATCAAT CATTG CA CCTGGGCA
GGAAACCC GTAAC GT GGACCCGT
TAA-- G
GAM7776 246 ZNF431 1 8477 XP_086098.2 3 1487 CTCTTTCGCCCA T A 3 C b b
GGCTGGAGTGCA CA TGCACTCCAGCCTGGGC
TTGGCATG GT ACGTGAGGTCGGACCCG
T C
GAM7776 246 ZNF432 1 5065 NP_055465.1 3 1769 TCTTGTTGCCCA C----- 3 C c c
GGTTGGAGTGTA ATTGCACTCCAGCCTGGGCAA
ATAGCACG TAATGTGAGGTTGGACCCGTT
GCACGA
GAM7776 246 ZNF440 1 1744 NP_689570.1 3 1224 CTCTGTCACCCA CA 3 C c c
GGCTGGAGTGCA CATTGCACTCCAGCCTGGG
GTGGCGTG GTGACGTGAGGTCGGACCC
AC
GAM7776 246 ZNF70 1 17076 NP_068735.1 3 1596 GCCCTGTTGCCA C G 3 C b b
GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM7776 246 ZNF70 1 17076 NP_852101.1 3 1596 GCCCTGTTGCCA C G 3 C b b
GGCTGGAATGCA CATTGCA TCCAGCCTGG CAA
GTGGCGTG GTGACGT AGGTCGGACC GTT
A -
GAM7776 246 ZNF74 1 12340 NP_003417.1 5 610 TGTCACCCAGGC --- A CA 3 C c c
GGGAGTGGTGCA CATTGCAC TCC GCCTGGG
ATGGCTTG GTAACGTG AGG CGGACCC
GTG G AC
GAM7809 398 APAF1 1 11564 NP_001151.1 3 2048 TCACTCAGATGT - ------ T T 3 A c c
ATTTTAGATAAG TAGCTTATC AGA CTGA GT GA
CTATTTAG ATCGAATAG TTT GACT CA CT
A TATGTA - -
GAM7809 398 APAF1 1 11564 NP_037361.1 3 2048 TCACTCAGATGT - ------ T T 3 A c c
ATTTTAGATAAG TAGCTTATC AGA CTGA GT GA
CTATTTAG ATCGAATAG TTT GACT CA CT
A TATGTA - -
GAM7809 398 C10orf5 1 3002 NP_848931.1 3 1137 TTAAATCCAACT C AC T 3 A c c
CAACTTTATAAG TAGCTTAT AG TGA GTTG
CTAAGGAA ATCGAATA TT ACT CAAC
T CA -
GAM7809 398 C20orf1 1 8641 NP_543018.1 3 278 AAATTGTAAGAT CT G 3 A c c
73 CAGTCTGGTACT TAG TATCAGACTGAT TTG
GAATAAAA GTC ATGGTCTGACTA AAT
-- G
GAM7809 398 C8orf7 1 2030 XP_088376.1 3 365 TGTCTTCAACAT CT C 3 A c c
CATTTGATACTA TAG TATCAGA TGATGTTGA
TAGACTTA ATC ATAGTTT ACTACAACT
-- -
GAM7809 398 CCL1 1 10810 NP_002972.1 3 133 GAGGATCTGCTT - TG T T 3 A c c

GGTCTTGATAAG TAGCTTATCA GAC A GT GA
CTATGTTG ATCGAATAGT CTG T CG CT
T GT - T

GAM7809 398 COX7A2L 1 3657 NP_004709.2 3 302 GCTTGTTAATGT TTAT 3 A c c

CAGTCTGTGCTG TAGC CAGACTGATGTTGA
AGGACCTC GTCG GTCTGACTGTAATT
T---

GAM7809 398 CTNND1 1 15144 NP_001322.1 3 421 TGCAATGTCCAG C ---- 3 A c c
CAGTCTGATAAA TAG TTATCAGACT GATGTTG
CTGACGAT GTC AATAGTCTGA CTGTAAC
A CGAC

GAM7809 398 DDX11 1 7637 NP_085913.1 3 1770 CTTCCCCAACAT AT - 3 A c c
CAGGTCTGCAGA TAGCTT CAGAC TGATGTTG
GCTGCAGG GTCGAG GTCTG ACTACAAC
AC G

GAM7809 398 DDX39 1 8028 NP_620551.1 3 566 GCGAGTCAACAT C TC T 3 A c c
CGTCTTTAACTA TAG TTA AGAC GATGTTGA
CGACATGC ATC AAT TCTG CTACAACT
- T- -

GAM7809 398 DGAT1 1 9487 NP_036211.1 3 207 GCAGGCCAGACA -- A G 3 A c c
CAGTCTGATGCC TAGCT TATCAGACTG TGTT
AGCTGGGA GTCGA GTAGTCTGAC ACAG
CC - A

GAM7809 398 DIO2 1 17701 NP_000784.2 3 1968 TCATGGCAACAT CT C --- 3 A c c
CAGCTTTCTAAT TAG TAT AGA CTGATGTTG
GTTCTAAA ATC GTA TCT GACTACAAC
TT A TTC

GAM7809 398 DIO2 1 17701 NP_054644.1 3 1968 TCATGGCAACAT CT C --- 3 A c c
CAGCTTTCTAAT TAG TAT AGA CTGATGTTG
GTTCTAAA ATC GTA TCT GACTACAAC
TT A TTC

GAM7809 398 DKFZp43 1 11265 NP_060047.1 5 768 TGAAACATTATT A ---- G 3 A c c
4C0328 CAGGCTGATAAG TAGCTTATCAG CTGA TGTT
CTAAGTGC ATCGAATAGTC GACT ACAA
G TATT A

GAM7809 398 DKFZP43 1 9242 NP_115512.2 3 303 CCTAATACAAAT - CT G 3 A c c
4L1717 ATTTCTGATAAG TAG CTTATCAGA GATGTT
ACTACAAA ATC GAATAGTCT TTATAA
A -- A

GAM7809 398 DKFZP56 1 4432 NP_056448.1 3 1167 GTGCTTTAACAT C A A 3 A c c

4O1863 CAGTTGAAACCT TAG TT TCAG CTGATGTTGA
AAATTTTC ATC AA AGTT GACTACAATT
C - -

GAM7809 398 DKFZp76 1 7056 NP_115673.1 3 749 GCAGATTTATGA CAGACT 3 A c
c

1D112 CATCCATATAAG TAGCTTAT GATGTTG
CTATCTGG ATCGAATA CTACAGT
TAC---

GAM7809 398 DKFZp76 1 15876 NP_690870.1 3 224 TGAGGAGCAGCA - --- GA 3 A c c
1P1121 GAGTCTGATACT TAG CT TATCAGACT TGTTG
AGGTCTAG ATC GG ATAGTCTGA ACGAC
T ATC G-
GAM7809 398 DUSP16 1 12004 XP_039106.1 3 842 ACCTGGCAACAT TCAGAC 3 A c c
CACGATTTAAGC TAGCTTA TGATGTTG
TAAGGTTG ATCGAAT ACTACAAC
TTAGC-
GAM7809 398 EDG3 1 16612 NP_005217.1 5 2684 CGTCATCAACAT A AGAC 3 A c c
CACAGAAGGCTG TAGCTT TC TGATGTTGA
ATCGATAT GTCGGA AG ACTACAACT
- AC--
GAM7809 398 FLJ1236 1 766 NP_115543.1 3 604 CACAGGGTTTCA - ---- G 3 A c c 3
CAGTCTGATGAG TAG CTTATCAGACTG AT TTG
ACTGTGCC GTC GAGTAGTCTGAC TG GAC
A ACTT G
GAM7809 398 FLJ2283 1 4756 NP_073748.1 3 1191 TATAGTAACATG TA---- - 3 A c c 3
CAGTCTGAAGTC TAGCT TCAGACTG ATGTTG
CTAGTTAC ATTGA AGTCTGAC TACAAT
TCCTGA G
GAM7809 398 FOXP1 1 4211 NP_116071.2 3 296 AACCGTCAACAT TTAT--- - 3 A c c
CAGTGTTGTAAA TAGC CAG ACTGATGTTGA
TTTGCTAA ATCG GTT TGACTACAACT
TTTAAAT G
GAM7809 398 HGNT-IV 1 8444 NP_037376.1 3 218 GAAGTTGAATAT TATC G 3 A c c
-H CAGTCTATAGCT TAGCT AGACTGATGTT
AATGCTAC ATCGA TCTGACTATAA
TA-- G
GAM7809 398 HNMT 1 558 NP_008826.1 3 247 CATGCAGGCTCA CAGACTG 3 A c c
ACATAACATAAG TAGCTTAT ATGTTGA
CTAGAAAA ATCGAATA TACAACT
CAA----
GAM7809 398 HSMPP8 1 14992 XP_167894.1 3 1399 ATAAATCAAGCT TAT TG 3 A c c
CAGTCTGGGTTA TAGCT CAGACTGA TTGA
TGGAGAAG ATTGG GTCTGACT AACT
--- CG
GAM7809 398 ITGB2 1 2700 NP_000202.1 3 293 AAGTCAGGACAT G -- G 3 A c c
CAGTCTGATTAA TA CTT ATCAGACTGATGTT
AGGTGGTG GT GAA TAGTCTGACTACAG
G AT G
GAM7809 398 KIAA047 1 9743 NP_055672.1 3 1775 TCTCTACATGGT - -- T 3 A c c 1
GGTCTAGATAAG TAGCTTATC AGACTG ATGT GA
CTAATTTT ATCGAATAG TCTGGT TACA CT
A GG T

GAM7809 398 KIAA074 1 6982 XP_045277.3 5 93 CCCTGACGACAT ----- AG 3 A c c
6 CAGTGATACCCA TAGCT TATC ACTGATGTTG
AAGCTGAG GTCGA ATAG TGACTACAGC
AACCC --
GAM7809 398 KIAA101 1 12780 NP_055782.1 3 1322 GTGAGCCAACAT T C - 3 A c c
8 CACGTTTTGTTA TAGCT AT AGAC TGATGTTG
GCTGTGAT GTCGA TG TTTG ACTACAAC
T T C
GAM7809 398 KIAA167 1 7267 XP_037809.1 3 360 CTCCAAGAACAT TA G G 3 A c c
1 CAGTGTGAGGCT TAGCT TCA ACTGATGTT
GGAATTGT GTCGG AGT TGACTACAA
-- G G
GAM7809 398 KIAA172 1 9351 XP_040860.3 3 5737 TGTGTAGTGCAA C C AT 3 A c c
6 CCATCTGATAAA TAG TTATCAGA TG GTTG
CTAGTGTG ATC AATAGTCT AC CAAC
A - --
GAM7809 398 LOC1218 1 17414 XP_071772.1 5 1280 TTAAGTCAACAT ATC ACT 3 A c
c
38 CCTTTAAAGCTA TAGCTT AG GATGTTGA
AGAGTATG ATCGAA TC CTACAACT
ATT ---
GAM7809 398 LOC1305 1 15342 XP_065771.1 5 33 GGACTGCAACAT C GAC- 3 A c
c
36 CACGGATGGTGA TAG TTATCA TGATGTTG
CTACTACG ATC AGTGGT ACTACAAC
- AGGC
GAM7809 398 LOC1487 1 19661 XP_086281.1 5 979 CTTGTGCAACAT A AGAC 3 A c
c
09 CAAGGAGAAGCT TAGCTT TC TGATGTTG
GCGGAAAT GTCGAA AG ACTACAAC
G GA--
GAM7809 398 LOC1496 1 15051 XP_097686.1 3 23 TGCGTATAACAT - A AG 3 A c c
00 CAGTGAGGAAGA TAG CTT TC ACTGATGTTG
CTGCA GTC GAA GG TGACTACAAT
A - AG
GAM7809 398 LOC1510 1 6610 XP_097998.1 3 1723 GTCTAAAACGTA TA - G 3 A c c
57 CAGTCTGAGGCT TAGCT TCAGACTG ATGTT
GGGGCGGG GTCGG AGTCTGAC TGCAA
-- A A
GAM7809 398 LOC1522 1 19176 XP_098174.1 3 678 CTTTCTCAACAT AT- GACT 3 A c
c
00 CTTCATGTTGAA TAGCTT CA GATGTTGA
GCTAAAAC ATCGAA GT CTACAACT
GTT ACTT
GAM7809 398 LOC1575 2 10657 XP_098767.1 3 891 TCCACTCAACAT AGAC 3 A c
c
03 CAAGATAAGCTG TAGCTTATC TGATGTTGA
CTCTATAT GTCGAATAG ACTACAACT

```
                                                A---
GAM7809  398    LOC1575 2  20114  XP_098767.1  3  891    ATTTCCACTCAA        AGAC            3  A  c
c
         03                          CATCAAGATAAG TAGCTTATC    TGATGTTGA
                                    CTGCTCTA    GTCGAATAG    ACTACAACT
                                                A---
GAM7809  398    LOC1575 1  1783   XP_088328.1  3  876    TAGTGAAAAACT       CA     T  G        3  A  c  c

         67                          CAGTTCTATAAG TAGCTTAT  GACTGA GTT
                                    CTAGCTGT    ATCGAATA  TTGACT CAA
                                                TC     -  A
GAM7809  398    LOC2830 1  14565  XP_210849.1  5  376    ACCCTTAAACAT      A   ---       G      3  A  c  c
         07                          CAGTAGACTGGG TAGCTT TCAG   ACTGATGTT
                                    AGCTGTAC    GTCGAG GGTC   TGACTACAA
                                                -   AGA       A
GAM7809  398    LOC2836 1  9650   XP_208764.1  3  1129   GCTCAGCCCCAT      ATC      ---        3  A  c
c
         41                          CAGTCTCAAAGG TAGCTT   AGACTGAT   GTTGA
                                    TTAAGCCA    ATTGGA   TCTGACTA   CGACT
                                                AAC       CCC
GAM7809  398    LOC2840 1  16558  XP_211302.1  3  2587   CTGCCTGGACAT      A        G        3  A  c  c

         19                          CAGTCTGGAAGC TAGCTT TCAGACTGATGTT
                                    TGTGCATT    GTCGAA GGTCTGACTACAG
                                                -          G
GAM7809  398    LOC2843 1  9920   XP_210786.1  5  441    TGCAATGTCCAG   C        ----          3  A  c  c
         94                          CAGTCTGATAAA TAG TTATCAGACT    GATGTTG
                                    CTGATGAT    GTC AATAGTCTGA    CTGTAAC
                                                A         CGAC
GAM7809  398    LOC2852 1  5963   XP_209518.1  5  1222   AAAATTCAACAT      ATC  AC            3  A  c
c
         19                          CACTTCAAGTTA TAGCTT   AG  TGATGTTGA
                                    AAGACACT    ATTGAA   TC  ACTACAACT
                                                CT-  --
GAM7809  398    LOC2854 1  6690   XP_209631.1  3  281    GAAGTTCAACAT      T    AC            3  A  c  c
         83                          CACTGATAGTTA TAGCT ATCAG  TGATGTTGA
                                    GAGAACTG    ATTGA TAGTC  ACTACAACT
                                                -    --
GAM7809  398    LOC2860 1  2701   XP_209873.1  5  2556   TCAGCTCAACAT      TAT   CT            3  A  c
c
         39                          CTTCTGTTAGTT TAGCT   CAGA  GATGTTGA
                                    ATAGCTGC    ATTGA   GTCT  CTACAACT
                                                TT-    T-
GAM7809  398    LOC2861 1  16153  XP_209922.1  3  2557   GCTTTTTCAGAT      TATC      G         3  A  c
c
         63                          CAGTCTCCACAG TAGCT    AGACTGAT TTGA
                                    CTACCATC    ATCGA    TCTGACTA GACT
                                                CACC       -
GAM7809  398    LOC2864 1  13979  XP_208420.1  5  833    TGGCTGGCTAAC        AGAC  T         3  A  c
 c
```

```
          25                          TTCATGGATAAG TAGCTTATC    TGA GTTG
                                     CTACAAAT    ATCGAATAG    ACT CAAT
                                                   GT--   T
GAM7809  398   LOC3385 1  15746  XP_290465.1  5  3976  CAGGCTCAACAT     A   GAC          3  A  c
c
          58                          CACATGGAAGCT TAGCTT TCA   TGATGTTGA
                                     GCCAATGC    GTCGAA GGT   ACTACAACT
                                                   -  AC-
GAM7809  398   LOC3401 1  8010   XP_295183.1  3  2814  GATGTTCAACAT   C   C  AC          3  A  c
c
          84                          CACTAATAACTA TAG TTAT AG  TGATGTTGA
                                     GAAGAAAT    ATC AATA TC  ACTACAACT
                                                   -   A  --
GAM7809  398   LOC3404 1  2701   XP_291274.1  5  2561  TCAGCTCAACAT    TAT   CT          3  A  c
c
          08                          CTTCTGTTAGTT TAGCT   CAGA  GATGTTGA
                                     ATAGCTGC    ATTGA   GTCT  CTACAACT
                                                   TT-    T-
GAM7809  398   LOC3408 1  19394  XP_291740.1  5  473   CTCCGTCAACAT     AT--  ACT          3  A  c
c
          52                          CTGCTGCTCCAA TAGCTT    CAG   GATGTTGA
                                     GCTGGTGA    GTCGAA    GTC   CTACAACT
                                                   CCTC   GT-
GAM7809  398   LOC3451 1  5096   XP_298539.1  5  205   GAAGCTCGGACT    T-       T  G       3  A  c  c

          19                          CAGTCTGATCTA TAGCT  ATCAGACTGA GTT
                                     GCTGAGCT    GTCGA  TAGTCTGACT CAG
                                                   TC        -  G
GAM7809  398   LOC3466 1  18192  XP_294357.2  3  964   CAAATCATATAT     TAT        -        3  A  c  c
          53                          CAGTCTGCTCAG TAGCT   CAGACTGATGT TGA
                                     TTGAAACC    GTTGA   GTCTGACTATA ACT
                                                   CTC         T
GAM7809  398   LOC3492 1  9015   XP_300477.1  3  1594  GGAGGTCAACAT     ----  C   CT          3  A  c
c
          89                          CTATCTAATTTA TAGCTT    AT AGA  GATGTTGA
                                     AAAGCTAT    ATCGAA    TA TCT  CTACAACT
                                                   AATT  A   AT
GAM7809  398   LOC5690 1  16105  NP_064532.1  3  28    AAAACTCAACAT    T     C----          3  A  c  c
          6                           CAAATGCTCTGA TAGC TATCAGA    TGATGTTGA
                                     TGTGCTAT    ATCG GTAGTCT    ACTACAACT
                                                   T      CGTAA
GAM7809  398   LOC9291 1  11212  NP_775740.1  3  319   CCAAGTCAACAT     ATC-  A          3  A  c
c
          2                           CAGGCTACTGAA TAGCTT    AG CTGATGTTGA
                                     GTTGAGGC    GTTGAA    TC GACTACAACT
                                                   GTCA  G
GAM7809  398   MEGF11  1  9381   NP_115821.1  3  289   ACTCATCAACAT     TATC--  A          3  A  c
c
                                     CAGCTAAATATA TAGCT     AG CTGATGTTGA
                                     GCTGATAT    GTCGA     TC GACTACAACT
```

TATAAA -

GAM7809 398 MGC1440 1 10181 NP_116297.1 3 259 ACTGAGTGACAT A A 3 A c c

7 CAGTTAGAGAGG TAGCTT TC GACTGATGTTG
TTACCTCA ATTGGA AG TTGACTACAGT
G A

GAM7809 398 MGC1955 1 4710 NP_291029.1 5 1419 TCATCTCAACAT T A 3 A c c

6 CGGCTGGTGGTT TAGCT ATCAG CTGATGTTGA
GGTAGGGG GTTGG TGGTC GGCTACAACT
- -

GAM7809 398 MGC2664 1 11055 NP_689919.1 5 128 TGGCAGCATAAA GACTG--- 3 A c c

7 TATTATGATAAG TAGCTTATCA ATGTTG
CTAAAAGC ATCGAATAGT TACGAC
ATTATAAA

GAM7809 398 MGC3961 1 4954 NP_775847.1 3 1489 GATGGACAGTAT CTT - 3 A c c

6 CAGTCTTGATCT TAG ATCA GACTGATGTTG
AAATTGTA ATC TAGT CTGACTATGAC
--- T

GAM7809 398 MGC4737 1 13111 NP_113654.1 5 1906 CACAATCAACAT TA GAC 3 A c c

CAAAGTGAAGCT TAGCT TCA TGATGTTGA
GGATTTCT GTCGA AGT ACTACAACT
-- GAA

GAM7809 398 MHC2TA 1 16477 NP_000237.1 3 2219 TGCCCACAGGAT T- ---- G 3 A c c

CAGTCTGATTCC AGCTT ATCAGACTGAT TTG
CAAGCTCT TCGAA TAGTCTGACTA GAC
TC CCCT G

GAM7809 398 MKI67IP 1 14713 NP_115766.2 3 447 AGATTTCAACAT -- GA 3 A c c

CAGATGGTTGAA TAGCTT ATCA CTGATGTTGA
GCTGGAAG GTCGAA TGGT GACTACAACT
GT A-

GAM7809 398 MS4A6A 1 9874 NP_071744.2 3 161 GATGGCAATTGA A AT-- 3 A c c

GTAGCTGATAAG TAGCTTATCAG CTG GTTG
CTGAAAAT GTCGAATAGTC GAT TAAC
- GAGT

GAM7809 398 NET-2 1 14668 NP_036470.1 3 649 TCAGTCGATTTC - - T 3 A c c

AGTTCTGATAAT TAGC TTATCAGA CTGA GTTGA
GTTAAGAA ATTG AATAGTCT GACT TAGCT
T T T

GAM7809 398 NFIB 1 1182 NP_005587.1 3 449 ATGCCTTAATAT GACT 3 A c c

TTGCATGATAAG TAGCTTATCA GATGTTGA
CTAGTTTT ATCGAATAGT TTATAATT
ACGT

GAM7809 398 NTRK2 1 9600 NP_006171.2 5 325 CGGACCAGCTCA -- T 3 A c c

GCCTCTGATAAG TAGCTTATCAGA CTGA GTTG
CTGGACTC GTCGAATAGTCT GACT CGAC
CC -

GAM7809 398 NY-REN-1 14494 XP_027116.6 3 1087 TCAAATCAACAT C- - CT 3 A c c

25 CTTTCTGGATAA TAG TTATC AGA GATGTTGA
ATCTATTT ATC AATAG TCT CTACAACT
TA G TT

GAM7809 398 NYD-SP1 1 19585 NP_114157.2 5 612 CCGCTTCAACAT TTAT- A 3 A c c

1 CAGCTGCCTCTG TAGC CAG CTGATGTTGA
CTATGACC ATCG GTC GACTACAACT
TCTCC -

GAM7809 398 OTOP3 1 17220 XP_292588.2 5 525 CTGCCTCAACAT - A CT 3 A c c
CTTCCGAGTGGG TAGCTTA TC GA GATGTTGA
CTACGATG ATCGGGT AG CT CTACAACT
G C T-

GAM7809 398 PCLO 1 17329 XP_168530.1 3 1285 ATTCAAAGAACT C T G 3 A c c
CAGTCTGATAAT TAG TTATCAGACTGA GTT
CTGCCTCC GTC AATAGTCTGACT CAA
T - G

GAM7809 398 PDGFRB 1 8445 NP_002600.1 5 241 GGGACCAGCAGT C CT - 3 A c c

CTTTCTGATAAC TAG TTATCAGA GA TGTTG
TGGGAGAG GTC AATAGTCT CT ACGAC
- TT G

GAM7809 398 PDZK3 1 13968 NP_055837.2 3 764 TTACAGAATAGC CTGA 3 A c c

ACTTCTGATAAG TAGCTTATCAGA TGTTG
CTGTATTA GTCGAATAGTCT ACGAT
TC--

GAM7809 398 PDZK3 1 13968 NP_835260.1 3 764 TTACAGAATAGC CTGA 3 A c c

ACTTCTGATAAG TAGCTTATCAGA TGTTG
CTGTATTA GTCGAATAGTCT ACGAT
TC--

GAM7809 398 PHYHIP 1 4208 NP_055574.1 3 2 CCTGCAACATCA TTA GA 3 A c c
GCGTGGGCCGCT TAGC TCA CTGATGTTG
AGGACTCC ATCG GGT GACTACAAC
CCG GC

GAM7809 398 PRO0365 1 15355 NP_054845.1 3 569 ATCCTCCAAGAA GAC G- 3 A c c

TTAAATGATAAG TAGCTTATCA TGAT TTG
CTAGGATT ATCGAATAGT ATTA AAC
AA- AG

GAM7809 398 PRPF4B 1 11905 NP_003904.2 3 568 AACCATCAACAT CT CT 3 A c c

CTCTGGTGTTTT TAG TATCAGA GATGTTGA
AAGATGTT ATT GTGGTCT CTACAACT
TT --

GAM7809 398 PTPRH 1 14651 NP_002833.1 3 402 CAGAAACCAAAT C C-- G 3 A c c

CAGTCTTCTATA TAG TTAT AGACTGAT TTG

ATCTGGGG GTC AATA TCTGACTA AAC
T TCT -
GAM7809 398 RANBP17 1 18307 NP_075048.1 3 569 CCTGCCTCAGCT - C AT 3 A c c
GCATCTGATAAA TAGCTT ATCAGA TG GTTGA
GTTGAGAG GTTGAA TAGTCT AC CGACT
A - GT
GAM7809 398 RECK 1 6244 NP_066934.1 3 1147 ATGTGTCTCACA -- A TT 3 A c c
GTTTGAAATAAG TAGCTTA TCAGACTG TG GA
CTATTTGA ATCGAAT AGTTTGAC AC CT
AA - T-
GAM7809 398 SDCCAG3 1 6557 NP_005777.2 3 303 TATTCTCAACAT T ----- T 3 A c c
3 CTGTTTTTGGTG TAGCTTA CA GAC GATGTTGA
TTAAGCTA ATCGAAT GT TTG CTACAACT
T GGTTT T
GAM7809 398 SFRS11 1 14777 NP_004759.1 3 782 CCACATCTACAT A AG T 3 A c c
CAGTGAAAGCTA TAGCTT TC ACTGATGT GA
TCTACCTA ATCGAA AG TGACTACA CT
- -- T
GAM7809 398 SOX5 1 9808 NP_008871.3 3 234 TCAACAACAAGA -- A GA 3 A c c
GATTGAAATAAG TAGCTTA TCAG CT TGTTG
CTATGGGT ATCGAAT AGTT GA ACAAC
AA A GA
GAM7809 398 SOX5 1 9808 NP_694534.1 3 234 TCAACAACAAGA -- A GA 3 A c c
GATTGAAATAAG TAGCTTA TCAG CT TGTTG
CTATGGGT ATCGAAT AGTT GA ACAAC
AA A GA
GAM7809 398 SOX5 1 9808 NP_821078.1 3 234 TCAACAACAAGA -- A GA 3 A c c
GATTGAAATAAG TAGCTTA TCAG CT TGTTG
CTATGGGT ATCGAAT AGTT GA ACAAC
AA A GA
GAM7809 398 SPOCK 1 10241 NP_004589.1 3 1534 TTTCCTTCAGTA C A 3 A c c
CCAGTCTATAAG TAGCTTAT AGACTG TGTTGA
CTACTGTC ATCGAATA TCTGAC ATGACT
- C
GAM7809 398 SRGAP2 1 14316 NP_055665.1 3 1780 AAGGTCAAACAT A- AG G 3 A c c
CAGTGAGCAAGC TAGCTT TC ACTGATGTT
TGTGTACA GTCGAA AG TGACTACAA
CG -- A
GAM7809 398 STAF65(1 1623 NP_055675.1 3 943 CCTGAACAACAT TAT AC 3 A c c
gamma) CACTGTGGTTAC TAGCT CAG TGATGTTG
TCATCCAT ATTGG GTC ACTACAAC
T-- --
GAM7809 398 STARD4 1 7431 NP_631903.1 3 565 TCTTAAAAGCAT C T G 3 A c c
CAGTCTGTAACT TAG TTA CAGACTGATGTT
AGAACAAA ATC AAT GTCTGACTACGA
- - A

GAM7809 398 TAF1L 1 10086 NP_722516.1 3 83 GGATAGCAACAT ATCA 3 A c c
CAGTTATGGGAG TAGCTT GACTGATGTTG
CTGTGAGG GTCGAG TTGACTACAAC
GGTA
GAM7809 398 TGFBI 1 14063 NP_000349.1 3 437 CTGGAGAAATGG CAGAC 3 A c
c
CATCATTATAAG TAGCTTAT TGATGTTG
CTATGAGT ATCGAATA ACTACGGT
TT---
GAM7809 398 TTK 1 10374 NP_003309.2 3 112 TGAAGACAACAT TTA C 3 A c c
CACTCTGAAGTG TAGC TCAGA TGATGTTG
TTATCAGC ATTG AGTCT ACTACAAC
TGA C
GAM7809 398 UAP1 1 14376 NP_003106.2 3 317 GATGTTCAACAT - TC- 3 A c c
CAGTTTACTTGC TAGCT TA AGACTGATGTTGA
AGCTGGAA GTCGA GT TTTGACTACAACT
C TCA
GAM7809 398 WBSCR21 1 9104 NP_112585.2 3 442 GGCCATCAACAT AGAC 3 A c
c
CGCAGATGAGCT TAGCTTATC TGATGTTGA
GCCCCGCT GTCGAGTAG GCTACAACT
AC--
GAM7809 398 WBSCR21 1 9104 NP_683713.1 3 272 GGCCATCAACAT AGAC 3 A c
c
CGCAGATGAGCT TAGCTTATC TGATGTTGA
GCCCCGCT GTCGAGTAG GCTACAACT
AC--
GAM7809 398 WFDC13 1 17697 NP_742002.1 3 670 TGACAGTGTGGC AC 3 A c c
ATTACTGATAAG TAGCTTATCAG TGATGTTG
TTATGGAA ATTGAATAGTC ATTACGGT
--
GAM7809 398 ZBTB1 1 19264 NP_055765.1 3 289 TTCATACAACAT TATCAG 3 A c
c
CAGTGGTTACAG TAGCT ACTGATGTTG
CTATACTA ATCGA TGACTACAAC
CATTGG
GAM7809 398 ZNF228 1 14011 NP_037512.1 3 198 GAACTTTAACAT AT--- -- 3 A c c
CAGTCATTGCAC TAGCTT CA GACTGATGTTGA
AGGAGCTA ATCGAG GT CTGACTACAATT
GACAC TA
GAM7933 203 ADAM10 1 17173 NP_001101.1 5 405 TTCTCCCTCCGG AA A 7 A c c
ATCGATGTGCTG TAGCAGCACAT TGGTTTG
CTGTTAAC GTCGTCGTGTA GCTAGGC
-- C
GAM7933 203 ADAMTS1 1 11726 NP_620597.1 3 706 CCTCCTTCTACC A- A TT 7 A c
c
3 ACTGGGGTGCTG TAGCAGCAC TA TGGT GAA
CTGTACCA GTCGTCGTG GT ACCA CTT

GG C T-
GAM7933 203 ARHGEF1 1 19923 NP_056128.1 3 1959 AAACCAAATGGT --- G A 7 A c c
2 TACATTGTGCTG TAGCAGCACA TAAT GTTTG
CTAGAAAT ATCGTCGTGT ATTG TAAAC
TAC G C
GAM7933 203 BRD2 1 14556 NP_005095.1 5 188 CCCGGTCAGCCA ATAA-- T 7 A c c
ATCTGGGTGCTG TAGCAGCAC TGGTT GA
CTGACGTG GTCGTCGTG ACCGA CT
GGTCTA -
GAM7933 203 C1orf21 1 12125 NP_110433.1 3 227 GTTATCGAACTT - TAAT- 7 A c c
TCTTTGTTGCTG TAGCAGCA CA GGTTTGA
CTAGTTAA ATCGTCGT GT TCAAGCT
T TTCTT
GAM7933 203 CCL28 1 10807 NP_062820.1 3 568 CTATTGCTTCAG ---- GG 7 A c c
AATTATGTGGAG TAGCAG CACATAAT TTTGAA
TCTGTTAC ATTGTC GTGTATTA AGACTT
TGAG --
GAM7933 203 CENTD1 1 9614 NP_631921.1 5 230 TTAATGACCAGG AT A 7 A c c
CTCTATGTGCTG TAGCAGCACATA GGTTTG
CTGTAGTG GTCGTCGTGTAT TCGGAC
C- C
GAM7933 203 CRI1 1 16632 NP_055150.1 3 789 AAGAAAACAAAC CA-- A 7 A c c
CATTGCTTATGC TAGCAGCA TAATGGTTTG
TGTTATAT ATTGTCGT GTTACCAAAC
ATTC A
GAM7933 203 DKFZp54 1 4932 XP_091486.2 3 1675 CTCCGATCAAAG ATAA - 7 A c c
7J144 CCGGCCGTGCTG TAGCAGCAC TGGTTT GA
CTGGCCGG GTCGTCGTG GCCGAA CT
CCG- A
GAM7933 203 DKFZP76 1 16574 XP_295135.1 3 1386 TGGGATTCAAAC - ATAAT 7 A c c
1M1511 CCGGGAGTGTCT TAGCAG CAC GGTTTGAA
GCTGCCAC GTCGTC GTG CCAAACTT
T AGGGC
GAM7933 203 DKFZp76 1 17576 XP_048721.1 3 134 TTTGTGTTTACT TAATG 7 A c c
2K222 TAAACTGTGCTG TAGCAGCACA GTTTGA
CTAAGTAG ATCGTCGTGT CAAATT

GAM7933 203 DMTF1 1 15923 NP_066968.1 3 149 CTTAAGCCACAC - TAA---- 7 A c c
ACATTGTTGCTG TAGCAGCA CA TGGTTTGA
CTATGACT ATCGTCGT GT ACCGAATT
T TACACAC
GAM7933 203 EGFL5 1 10302 XP_098838.1 5 1334 GTCATCATCATT - TG T- 7 A c c
GTTGTGGTGCTG TAGCAGCAC ATAA GT TGA
CTAATGGG ATCGTCGTG TGTT TA ACT
G GT CT

GAM7933 203 ENAM 1 16108 NP_114095.1 3 1262 AAGGGATTCTAC C A TT 7 A c c

CAGTATGTGCTA TAG AGCACATA TGGT GAA
CTACTAAC ATC TCGTGTAT ACCA CTT
A G T-

GAM7933 203 B EPB41L4 1 4101 NP_060894.1 3 815 TTAATGTCTTAA A G T- 7 A c c
TGATTGGTGCTG TAGCAGCAC TAAT GTT GA
CTAACTTG ATCGTCGTG GTTA TAA CT
- G TT

GAM7933 203 EZH1 1 4202 NP_001982.2 3 845 CAGCTGCAGGCA CA --- A 7 A c c
AGCATTATGCTG TAGCAGCA TAATG GTTTG
CTATTGAA ATCGTCGT ATTAC CGGAC
-- GAA G

GAM7933 203 FACL4 1 7615 NP_004449.1 3 1986 ATTAACACTTAA A GG 7 A c c
GGTTGGGTGCTG TAGCAGCAC TAAT TTTGA
CTAATTCT ATCGTCGTG GTTG GAATT
G --

GAM7933 203 FACL4 1 7615 NP_075266.1 3 1986 ATTAACACTTAA A GG 7 A c c
GGTTGGGTGCTG TAGCAGCAC TAAT TTTGA
CTAATTCT ATCGTCGTG GTTG GAATT
G --

GAM7933 203 FGF2 1 1793 NP_001997.3 3 5608 TCTGTAATTTAA CAT G 7 A c c
AATATTTTGCTG TAGCAGCA AATG TTTGAA
CTAGTTAA ATCGTCGT TTAT AAATTT
T-- A

GAM7933 203 0 FLJ1052 1 17571 NP_060594.2 3 270 GCCTTCATTAAC - C -- 7 A c c
CATTATTGTATG TAGCA GCA ATAATGGTT TGAA
TTGGAAAT GTTGT TGT TATTACCAA ACTT
A - TT

GAM7933 203 2 FLJ1070 1 17057 NP_060654.1 3 934 TCTCCAGTCATT ATAA 7 A c c
AAATCAGTGCTG TAGCAGCAC TGGTTTGA
CTGCATGA GTCGTCGTG ACTAAATT

GAM7933 203 4 FLJ1087 1 5958 NP_060722.1 3 1139 GAGTTTTAAATT - - 7 A c c
ATTTATGTGCCT TAGCAG CACATAA TGGTTTGAA
GTTGCTTC GTTGTC GTGTATT ATTAAATTT
C T

GAM7933 203 1 FLJ1089 1 8768 NP_060730.1 3 1306 AAATTCAATTAA AT-- GGT 7 A c c
TTTTTGGTGCTG TAGCAGCAC AAT TTGAA
CTATTGCA ATCGTCGTG TTA AACTT
GTTT ATT

GAM7933 203 7 FLJ1274 1 13605 XP_290972.1 3 3278 CACTGCTCACAT TG T 7 A c c
ACTTATGTGCTG TAGCAGCACATAA GT TGA
CTAGTCTC ATCGTCGTGTATT TA ACT
CA C

GAM7933 203 8 FLJ1288 1 3021 NP_079221.1 5 267 ATTCTGTCATCA TAAT 7 A c c
AATCCTGTGCTG TAGCAGCACA GGTTTGA
CTGTTCCT GTCGTCGTGT CTAAACT
C---

GAM7933 203 FLJ1305 1 18278 NP_848526.1 3 260 TATCTGTCAAAC CACAT 7 A c c
7 CATTTCTGTTAG TAGCAG AATGGTTTGA
AACGATGT ATTGTC TTACCAAACT
T----
GAM7933 203 FLJ1320 1 2848 NP_079037.2 3 190 GTGCTCTTAACC A AT- T- 7 A c c
4 TTCTGAGTGCTG TAGCAGCAC TA GGTT GA
CTAGCCCA ATCGTCGTG GT CCAA CT
A CTT TT
GAM7933 203 FLJ1467 1 14019 NP_116212.3 3 106 CATCAAAGGAGG - GG---- 7 A c c
5 GATTATGTGGCT TAGCAGC ACATAAT TTTGA
GCTAAAGC ATCGTCG TGTATTA AAACT
G GGGAGG
GAM7933 203 FLJ2027 1 19345 NP_060206.1 3 223 ACGTAGAGGCAG AAT A 7 A c c
4 ACCCATGTGCTG TAGCAGCACAT GGTTTG
CTGTTGCA GTCGTCGTGTA CCAGAC
C-- G
GAM7933 203 FLJ2305 1 17879 NP_078858.1 3 350 TAATACTCAAAC AC- 7 A c c
6 CATTGTAAAGTT TAGCAGC ATAATGGTTTGA
GCTGACTA GTCGTTG TGTTACCAAACT
AAA
GAM7933 203 FLJ3197 1 1522 NP_653270.1 3 1689 GTTGTCTTAGAT - AAT 7 A c c
8 CTGATGATGCTG TAGCAGCA CAT GGTTTGA
CTATTTAC ATCGTCGT GTA CTAGATT
A GT-
GAM7933 203 FLJ3253 1 8740 NP_689760.1 5 168 TCTGCCATTTCA CATAAT 7 A c c
5 GACCTTTTGCTG TAGCAGCA GGTTTGAA
CTACCTGC ATCGTCGT CCAGACTT
TTT---
GAM7933 203 FLJ3268 1 14845 NP_689747.1 3 246 GATGTCAGAGCT AA ---- 7 A c c
5 ACCAGTGTGCTG TAGCAGCACAT TGGT TTGA
CTGGGAGA GTCGTCGTGTG ACCA GACT
-- TCGA
GAM7933 203 FLJ3937 1 8161 NP_689613.1 3 122 TGCCTTGTTTCA - TAA 7 A c c
0 AATCATGTGCTG TAGC AGCACA TGGTTTGAA
GCTGTTTT GTCG TCGTGT ACTAAACTT
G ---
GAM7933 203 GABRP 1 9698 NP_055026.1 3 974 GTCGCTGTCATT C A TT 7 A c c
CTGTCATTGCTG TAGCAGCA AT ATGG TGA
CTACTCTA ATCGTCGT TA TGTC ACT
- C TT
GAM7933 203 GDI2 1 3115 NP_001485.2 3 330 TTTAATCAGTGT A- GT 7 A c c
AGCTATGTGCTG TAGCAGCACATA TG TTGA
CTGCTGCT GTCGTCGTGTAT AT GACT
CG GT
GAM7933 203 GPIG4 1 1050 NP_689758.1 3 374 TTTAATTTGGTT CAT G TG 7 A c c

GAACATTTGCTG TAGCAGCA AATG TT A
CTAATGGG ATCGTCGT TTAC AA T
--- - GT

GAM7933 203 KCNMB4 1 7510 NP_055320.4 3 334 TAGTATACAAAC GCA-- A 7 A c c

CATTATGATTTA TAGCA CATAATGGTTTG
TGCTACTT ATCGT GTATTACCAAAC
ATTTA A

GAM7933 203 KIAA017 1 4948 XP_035973.4 3 340 TGAACTTTAAAT ATAA 7 A c c
9 CAATCAGTGCTG TAGCAGCAC TGGTTTGAA
CTGGCACA GTCGTCGTG ACTAAATTT
ACTA

GAM7933 203 KIAA021 1 8133 NP_055575.1 3 1840 ATTTAGATTATC ---- 7 A c c
8 ATTTATGTGCTG TAGCAGCACATA ATGGTTTGAA
TTGCACAG GTTGTCGTGTAT TATTAGATTT
TTAC

GAM7933 203 KIAA024 1 13278 NP_055549.1 3 2566 TTCTTAACCATC A---- T- 7 A c c
7 AGCCATGTGCTG TAGCAGCACAT ATGGTT GAA
CTATTTCT ATCGTCGTGTA TACCAA CTT
CCGAC TT

GAM7933 203 KIAA064 1 3596 NP_055477.1 3 108 TAGGAGTCAGGT CAT --- 7 A c c
5 GTCCGTTTGCTG TAGCAGCA AATGG TTTGA
CTATCAGT ATCGTCGT TTGCC GGACT
--- TGT

GAM7933 203 KIAA116 1 1382 XP_045358.2 3 2400 ACTCACTCAAAA ATAA - 7 A c c
4 CCAGCAGTGCTG TAGCAGCAC TGGTTT GA
CTATCAGA ATCGTCGTG ACCAAA CT
ACG- A

GAM7933 203 KIAA130 1 19660 NP_079357.1 3 696 TTGCCCTTAAAC ACAT 7 A c c

5 CATTTCTAGCTG TAGCAGC AATGGTTTGA
TTAACCCT ATTGTCG TTACCAAATT
ATCT

GAM7933 203 KIAA172 1 13195 XP_040860.3 3 5651 CTCCCAAACCAG C AA--- A 7 A c c

6 AGTCATATGCTG TAGCAGCA AT TGGTTTG
CTAGTAGA ATCGTCGT TA ACCAAAC
A CTGAG C

GAM7933 203 KIFAP3 1 5824 NP_055785.2 3 224 CACTCATCAAAC G CATAA 7 A c c

CACATCTTGATG TAGCA CA TGGTTTGA
CTAAGTAA ATCGT GT ACCAAACT
A TCTAC

GAM7933 203 LOC1136 1 6871 XP_054492.1 3 197 GACAGCTCAAAC C A TA- 7 A c c

12 CATCTTTGGCTA TAG AGC CA ATGGTTTGA
CTGTGCCC GTC TCG GT TACCAAACT
A - TTC

GAM7933 203 LOC1456 1 12056 XP_096827.1 5 24 AGAATTCAGAGC T---- - A - 7 A c c
52 CAATATGTGCTT AGCA GCACATA TGG TTTGAA

GCTTATTA TCGT CGTGTAT ACC AGACTT
ATTAT T A G
GAM7933 203 LOC1532 1 7489 NP_705835.1 3 2707 TTATATGATTCC CAT TT 7 A c
c
22 TGCCATTTGCTG TAGCAGCA AATGGT GAA
CTAAATCT ATCGTCGT TTACCG CTT
--- TC
GAM7933 203 LOC1538 1 18705 XP_087798.1 5 989 CCACATTCAAAC ACA- - 7 A c c

83 CTGTTAATTCGC TAGCAGC TAAT GGTTTGAA
TGTTATCA ATTGTCG ATTG CCAAACTT
CTTA T
GAM7933 203 LOC2209 1 11165 XP_166128.1 5 211 CTCTTTTCAAAC TAAT 7 A c c

26 CCAACTGTGCTG TAGCAGCACA GGTTTGAA
CTAACCCA ATCGTCGTGT CCAAACTT
CAAC
GAM7933 203 LOC2210 1 17864 XP_167640.1 3 1018 CAAGCTTGGCAT --- ---- A 7 A c c

35 TGACATGTGCTG TAGCAGCACAT AATG GTTTG
CTAGTTTA ATCGTCGTGTA TTAC CGAAC
CAG GGTT -
GAM7933 203 LOC2226 1 4311 XP_167095.3 3 275 TCTCTGTTCATG C AT - 7 A c c
74 GCCTGTTTGCTG TAGCAGCA ATA GGTT TGAA
CTATGAGG ATCGTCGT TGT CCGG ACTT
T -- T
GAM7933 203 LOC2553 1 10238 XP_172920.1 3 1389 TATTTTCAGAGA AT- GG 7 A c
c
28 ATTCAGGTGCTG TAGCAGCAC AAT TTTGAA
CTGGTTTT GTCGTCGTG TTA AGACTT
GAC AG
GAM7933 203 LOC2565 1 8974 XP_172816.1 5 448 ATGAAGGTTAAG ATAA 7 A c c

98 CTGGCGGTGCTG TAGCAGCAC TGGTTTGA
CTGGTGAC GTCGTCGTG GTCGAATT
GCG-
GAM7933 203 LOC2571 1 12899 XP_171239.1 5 197 TCACTGCCATTT AT----- T- 7 A c c

22 TGTGAGGTGCTG TAGCAGCAC AATGGT TGA
CTGTCTCT GTCGTCGTG TTACCG ACT
GAGTGTT TC
GAM7933 203 LOC2574 1 12573 XP_171176.1 3 203 ATGCCTGCTTCA - TAA T 7 A c
c
08 TGCCATGTGCTG TAG CAGCACA TGGT TGAA
ACTGAGCC GTC GTCGTGT ACCG ACTT
A --- T
GAM7933 203 LOC2829 1 4311 XP_212622.1 3 274 TCTCTGTTCATG C AT - 7 A c c
59 GCCTGTTTGCTG TAGCAGCA ATA GGTT TGAA
CTATGAGG ATCGTCGT TGT CCGG ACTT
T -- T

GAM7933 203 LOC2832 1 13264 XP_208566.1 3 1150 TAGAATTAACAC C-- - 7 A c c
13 CATTATGTATTT TAGCAG ACATAATGGT TTGA
TGTTATTT ATTGTT TGTATTACCA AATT
TTA C
GAM7933 203 LOC2834 1 492 XP_211031.1 3 919 ACCTTAAATTGA ATAA GA 7 A c
c
23 AAGCCAGTGCTG TAGCAGCAC TGGTTT
CTACTTTC ATCGTCGTG ACCGAA
---- AG
GAM7933 203 LOC2837 1 4062 XP_208800.1 5 256 GCTCAAAGCCAA - A--- - 7 A c c
15 CTGTATGTGCTG TAG CAGCACATA TGGTTT GA
ACTGGGTG GTC GTCGTGTAT ACCGAA CT
A GTCA A
GAM7933 203 LOC2837 1 16313 XP_211184.1 3 133 AGCGTCAGACTC - C -- 7 A c c
31 CATTATGTACTG TAG CAG ACATAATGG TTTGA
ACTGTGTG GTC GTC TGTATTACC AGACT
A A TC
GAM7933 203 LOC2838 1 6496 NP_775885.1 3 121 GTCAGCTAACTT TAAT T 7 A c
c
20 CAGCCTGTGCTG TAGCAGCACA GGTT GAA
CTGGGCCC GTCGTCGTGT CCGA CTT
---- -
GAM7933 203 LOC2846 1 15385 XP_211569.1 3 1735 GCATCATTTCAT ATAA T 7 A c
c
47 GCCAAAGTGCTG TAGCAGCAC TGGT TGAA
CTATGGGC ATCGTCGTG ACCG ACTT
AA-- T
GAM7933 203 LOC2852 1 8711 XP_208017.1 3 141 GCAACTTCAGAC T - A---- 7 A c c
83 CATTATGATAGA AGCAG C CATAATGGTTTGAA
GCCTGCTC TCGTC G GTATTACCAGACTT
C C AGATA
GAM7933 203 LOC2853 1 19928 XP_211844.1 3 1006 AGATTCTCAAAC -- ATAA 7 A c
c
34 CACACGTGCTTT TAGCA GCAC TGGTTTGA
GTTAAAGC ATTGT CGTG ACCAAACT
TT CAC-
GAM7933 203 LOC2857 2 4221 XP_209755.1 5 122 TAAGCTTCAAAC T--- TAA-- 7 A c c
69 CAGACTCTGTGC AGCAGCACA TGGTTTGAA
TGCTTCTG TCGTCGTGT ACCAAACTT
GTCT CTCAG
GAM7933 203 LOC2857 2 8378 XP_209755.1 5 122 AGCTTCAAACCA T----- TAA-- 7 A c
c
69 GACTCTGTGCTG AGCAGCACA TGGTTTGAA
CTTCTGCT TCGTCGTGT ACCAAACTT
TCGTCT CTCAG
GAM7933 203 LOC2857 1 4100 XP_212026.1 3 453 TGACCTCCCCAT TAAT T 7 A c
c
97 CAGCCTGTGCTG TAGCAGCACA GGTT GA
CTAGGTCT ATCGTCGTGT CCGA CT

```
                                                  ----   -
GAM7933  203   LOC2857 1  2760  XP_212024.1  3  3612  CTTCTTCAGGCT      CA  T-          7  A  c  c

         98                          TCTTAGCTGCTG TAGCAGCA  TAA  GGTTTGAA
                                    CTATCCAT    ATCGTCGT  ATT  TCGGACTT
                                                CG   CT
GAM7933  203   LOC3389 1  610   XP_294767.2  5  554   TGTGCTATTCAG       A A   T        7  A  c  c
         81                          CCAATAGTGCTG TAGCAGCAC TA TGGTT GAA
                                    CTGGCCCA    GTCGTCGTG AT ACCGA CTT
                                                - A   -
GAM7933  203   LOC3402 1  17638 XP_295200.1  3  593   AGCATTTTAAAC   C   CAT            7  A  c  c

         86                          CATTTGTTTTTA TAG AGCA   AATGGTTTGAA
                                    AAATTAAT    ATT TTGT   TTACCAAATTT
                                                T   ---
GAM7933  203   LOC3481 1  610   XP_302662.1  5  553   TGTGCTATTCAG       A A   T        7  A  c  c
         27                          CCAATAGTGCTG TAGCAGCAC TA TGGTT GAA
                                    CTGGCCCA    GTCGTCGTG AT ACCGA CTT
                                                - A   -
GAM7933  203   LOC3481 1  610   XP_302666.1  5  554   TGTGCTATTCAG       A A   T        7  A  c  c
         30                          CCAATAGTGCTG TAGCAGCAC TA TGGTT GAA
                                    CTGGCCCA    GTCGTCGTG AT ACCGA CTT
                                                - A   -
GAM7933  203   LOC3488 1  7451  XP_302901.1  3  709   GGGCTCCACCAG      - TAAT    A      7  A  c
c
         17                          ACCCTGATGCTG TAGCAGCA CA   GGTTTG
                                    CTACGTAT    ATCGTCGT GT   CCAGAC
                                                A  C---     C
GAM7933  203   LOC3490 1  4500  XP_300935.1  3  1506  TTGTATCTATTA       --     TT       7  A  c  c
         81                          TTACATGTGCTG TAGCAGCACA  TAATGGT  GA
                                    CTGAAGGG    GTCGTCGTGT  ATTATTA  CT
                                                AC      T-
GAM7933  203   LOC3491 1  13194 XP_302970.1  5  633   GGGGCTTCAAAC     CACA---  -         7  A  c
c
         61                          CACTTAGGACCG TAGCAG      TAA TGGTTTGAA
                                    ACTGCTGA    GTCGTC      ATT ACCAAACTT
                                                AGCCAGG   C
GAM7933  203   LRRN3   1  11739 NP_060804.2  5  375   AACTGCTTTTCA      CATAATG          7  A  c
c
                                    AGCATCATGCTG TAGCAGCA      GTTTGAA
                                    CTATTCCT    ATCGTCGT      CGAACTT
                                                ACTA---
GAM7933  203   LZTS1   1  5068  NP_066300.1  3  2137  GGAATTTCAAAC   C   CATA           7  A  c  c

                                    CATTGCTCTTAG TAG AGCA   ATGGTTTGAA
                                    TCCCAAGC    ATT TCGT   TACCAAACTT
                                                C   ----
GAM7933  203   MADH7   1  2946  NP_005895.1  3  66    GCCACACTTCAA      CATAA          7  A  c  c

                                    ACTACTTTGCTG TAGCAGCA    TGGTTTGAA
```

CTAATATT ATCGTCGT ATCAAACTT
TTC--
GAM7933 203 MAGEG1 1 10063 NP_619649.1 3 562 ATTCATAATTAT CAT--- - 7 A c c

TCAGCTCTGCTG TAGCAGCA AATGGTT TGAA
CTAAACAC ATCGTCGT TTATTAA ACTT
CTCGAC T
GAM7933 203 MGC1673 1 13414 NP_291025.1 3 237 CCACCTAGCAAA - G A 7 A c c

3 TATTATGTGCCT TAGCAG CACATAATG TTTG
GCTGTGTG GTCGTC GTGTATTAT AAAC
C - G
GAM7933 203 MGC2989 1 9508 NP_653219.1 3 744 CAGATACTTATC CA TT 7 A c c

1 CATTATGTGTCT TAG GCACATAATGG TGA
ATAGTTCA ATC TGTGTATTACC ATT
-- T-
GAM7933 203 MGC5576 1 7009 NP_076961.1 3 345 AGGTTATCAAAC AG A----- 7 A c
c

CATGGAGTGATG TAGC CACAT ATGGTTTGA
TGGAGCTA ATCG GTGTA TACCAAACT
AG GTGAGG
GAM7933 203 MMP16 1 5291 NP_005932.2 3 149 GACCTTTCAAAC ACATAA 7 A c
c

CAGAGGGTTGCT TAGCAGC TGGTTTGAA
GGTCCTGC GTCGTTG ACCAAACTT
GGAG--
GAM7933 203 NKX3-1 1 15691 NP_006158.2 3 1979 TGCAATGTTCAA ATAA - 7 A c c

TGCCACGTGCTG TAGCAGCAC TGGT TTGAA
CTGACACC GTCGTCGTG ACCG AACTT
C--- T
GAM7933 203 NUP153 1 18750 NP_005115.2 3 348 CTTTGTCTACAC A TT- 7 A c c
CATTATGTGCGC TAGC GCACATAATGGT GA
TGATAAGC GTCG CGTGTATTACCA CT
- CAT
GAM7933 203 PLAG1 1 8200 NP_002646.1 3 5229 CAGATTTAAAAT CA- G 7 A c c
ATTAATTTGCTG TAGCAGCA TAATG TTTGAA
CTAATTAA ATCGTCGT ATTAT AAATTT
TTA A
GAM7933 203 PLS1 1 14544 NP_002661.1 3 1217 TTTAGCATTAGT CAT T 7 A c c
CCATTTCTGCTG TAGCAGCA AATGG TTGA
CTAACAAT ATCGTCGT TTACC GATT
CT- T
GAM7933 203 PM5 1 6496 NP_055102.2 3 121 GTCAGCTAACTT TAAT T 7 A c c
CAGCCTGTGCTG TAGCAGCACA GGTT GAA
CTGGGCCC GTCGTCGTGT CCGA CTT
---- -
GAM7933 203 PP35 1 15536 NP_008947.1 3 3 ACCTTACAGACC --- A A 7 A c c
ATTATGGCATTT TAGCA GC CATAATGGTTTG

GCTAGACT ATCGT CG GTATTACCAGAC
TTA - A
GAM7933 203 PP35 1 15536 NP_853559.1 3 3 ACCTTACAGACC --- A A 7 A c c
ATTATGGCATTT TAGCA GC CATAATGGTTTG
GCTAGACT ATCGT CG GTATTACCAGAC
TTA - A
GAM7933 203 PPM1D 1 10407 NP_003611.1 3 834 CTATTTCAATAA ATAA GT- 7 A c
c
CAGATGGTGCTG TAGCAGCAC TG TTGAA
CTAATTCC ATCGTCGTG AC AACTT
GTAG AAT
GAM7933 203 PPP1R3A 1 500 NP_002702.1 3 2795 GTTATCTCAAAC C ATAA 7 A c
c
CAGTCTGCTGGT TAGCAG AC TGGTTTGA
TAAATGGA GTCGTC TG ACCAAACT
- ----
GAM7933 203 PPT2 1 7654 NP_620312.1 3 1012 GAATCTCTCAGC - AA -- 7 A c c
GACCAGGTGCTG TAGCAGCA CAT TGGTT TGA
CTGCTGGA GTCGTCGT GTG ACCAG ACT
C G- CG
GAM7933 203 PRO0327 1 8711 NP_054844.1 3 141 GCAACTTCAGAC T - A---- 7 A c c
CATTATGATAGA AGCAG C CATAATGGTTTGAA
GCCTGCTC TCGTC G GTATTACCAGACTT
C C AGATA
GAM7933 203 PSMD7 1 11380 NP_002802.2 3 72 CTTACAAACTAA AA--- A 7 A c c
ATCAGTGTGCTG TAGCAGCACAT TGGTTTG
CTAGAGGG ATCGTCGTGTG ATCAAAC
ACTAA A
GAM7933 203 RAB3B 1 17468 NP_002858.2 3 135 CACTCAGAGCAA --- AA G 7 A c c
GATGAGTTGCTG TAGCAGCA CAT TG TTTGA
CTATTCTT ATCGTCGT GTA AC AGACT
TGA GA G
GAM7933 203 RECK 1 11196 NP_066934.1 3 823 CATCAATCTTTA CATAA 7 A c c
AACCAATTGCTG TAGCAGCA TGGTTTGAA
CTACTTAT ATCGTCGT ACCAAATTT
TA---
GAM7933 203 RFX3 1 19639 NP_002910.1 3 531 TGATTTTCAAAC C C AAT 7 A c c
CCATATGCTTCT TAG AGCA AT GGTTTGAA
AACCACTA ATC TCGT TA CCAAACTT
T A C--
GAM7933 203 RNAC 1 12142 NP_005763.2 3 284 TGCCTTCAGGCC - AA 7 A c c
ACAGTCGTGCTG TAGCAGCAC AT TGGTTTGAA
CTAGAACA ATCGTCGTG TG ACCGGACTT
C AC
GAM7933 203 SCA1 1 8968 NP_000323.1 5 356 TTTGAAGCTTCA ATAAT 7 A c c
AACTTAGTGCTG TAGCAGCAC GGTTTGAA
CTGCAGAC GTCGTCGTG TCAAACTT
AT---
GAM7933 203 SE20-4 1 3595 NP_071400.1 3 244 GCCCCCGCAGGC AT A 7 A c c

TTCTGTGTGCTG TAGCAGCACATA GGTTTG
CTAACTGT ATCGTCGTGTGT TCGGAC
CT G

GAM7933 203 SH3BP2 1 13854 NP_003014.2 3 719 TCAGGTCAGGCC ATAA- 7 A c c

AGGGCAGTGCTG TAGCAGCAC TGGTTTGA
CTGCAGAG GTCGTCGTG ACCGGACT
ACGGG

GAM7933 203 SIAH1 1 11362 NP_003022.1 3 453 TTTGTGAGTCAA ATA GT 7 A c c

TACATAGTGCTG TAGCAGCAC ATG TTGA
CTGTGTGC GTCGTCGTG TAC AACT
A-- AT

GAM7933 203 SIGLEC8 1 18948 NP_055257.1 5 46 GCGCCTTCAAAC - AAT-- 7 A c c

CCAGACATGCTG TAGCAGCA CAT GGTTTGAA
CTGCTGCT GTCGTCGT GTA CCAAACTT
C CAGAC

GAM7933 203 SKIP 1 13806 XP_051221.2 3 982 GCCTGTTTCATC A GTT 7 A c c

ACGTATGTGCTG TAGCAGCACATA TG TGAA
CTACCTGT ATCGTCGTGTAT GC ACTT
- ACT

GAM7933 203 SON 1 7402 NP_115571.1 3 412 GCCGCCTGATTA AATG 7 A c c

AATAATGTGCTG TAGCAGCACAT GTTTGA
CTAAATAT ATCGTCGTGTA TAAATT
A---

GAM7933 203 SPG7 1 5110 NP_003110.1 5 0 TTTCAGGCCAAC ATAA---- 7 A c c

ATGGCCGTGCTG TAGCAGCAC TGGTTTGAA
CTGCTGCT GTCGTCGTG ACCGGACTT
CCGGTACA

GAM7933 203 STXBP1 1 11449 NP_003156.1 3 1336 GTGGTGAGCACA T T A 7 A c c

CCATTTGTGCTG TAGCAGCACA AATGGT TG
CTGCTGTT GTCGTCGTGT TTACCA AC
- C G

GAM7933 203 TFAP2A 1 8195 NP_003211.1 3 106 GATCAGCAACCC - TAAT- -- 7 A c c

TTCCTGCTGCTG TAGCAGCA CA GGTT TGA
CTACTGCT ATCGTCGT GT CCAA ACT
C CCTTC CG

GAM7933 203 UNC5H2 1 13226 NP_734465.1 3 545 AAAGCTTCAAAC AGC T 7 A c c

CGTTTGTAAGGT TAGC ACA AATGGTTTGAA
TAAAGAAA ATTG TGT TTGCCAAACTT
GAA -

GAM7933 203 WDR5B 1 20162 NP_061942.2 5 314 AAACTTGAAGTC ATAAT A 7 A c c

CAAGCCGTGCTG TAGCAGCAC GGTTTG
CTGATTCC GTCGTCGTG CCGAAC
----- C

GAM7933 203 WHSC1 1 12260 NP_579889.1 3 1957 AGAGTACAGAAA CA --- A 7 A c c

TTCATTATGCTG TAGCAGCA TAATGG TTTG
CTAATTTA ATCGTCGT ATTACT AGAC
-- TAA A

GAM7933 203 ZFYVE1 1 16631 NP_067083.1 5 414 CATCAAACCAAA CATAA---- 7 A c c

TCAACGTTGCTG TAGCAGCA TGGTTTGA
CTAATACA ATCGTCGT ACCAAACT
TGCAACTAA

GAM7933 203 ZFYVE1 1 16631 XP_027302.5 5 389 CATCAAACCAAA CATAA---- 7 A c c

TCAACGTTGCTG TAGCAGCA TGGTTTGA
CTAATACA ATCGTCGT ACCAAACT
TGCAACTAA

GAM7957 297 15E1.2 1 13155 XP_290596.1 3 959 CTACTCGGGAGG A AAC T 3 C c c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 3PAP 1 868 NP_061934.2 3 1629 GAGCCTGGGAGG C TG 3 C c c

TGGAGTTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCTAA AGTGACGTT GAG GGAGGGT
T GT

GAM7957 297 ABCC13 1 2331 NP_742021.1 3 1651 GAACCTGTAAGG CCC 3 C c c

CGGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCCGA AGTGACGTTGGAGGCGGA
ATG

GAM7957 297 ABCF2 2 3809 NP_009120.1 3 1185 GAGCCCAGGAGG TG C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 ABCF2 2 7251 NP_009120.1 3 1487 GAGCCCAGGAGG A T C 3 C c c

TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCAGA AGTGACGT GGAG TGGAGG
C T A

GAM7957 297 ABL1 1 4947 NP_005148.1 3 884 GGACAAGGGAGG G A--- T 3 C c c

CAGTGGCTAGTG TCACT CA CC CTGCCTCCC
GGGTGAAC AGTGG GT GG GACGGAGGG
G GATC T

GAM7957 297 ABL1 1 4947 NP_009297.1 3 884 GGACAAGGGAGG G A--- T 3 C c c

CAGTGGCTAGTG TCACT CA CC CTGCCTCCC
GGGTGAAC AGTGG GT GG GACGGAGGG
G GATC T

GAM7957 297 ABLIM1 1 16503 NP_002304.2 3 4184 TTATTTGGGACT C- TGCC 3 C c c

TGAGATTTGCAG TCACTGCAA CTC TCCCG
TGATACCA AGTGACGTT GAG AGGGT
TA TTC-

GAM7957 297 ABLIM1 1 16503 NP_006710.2 3 4184 TTATTTGGGACT C- TGCC 3 C c c

TGAGATTTGCAG TCACTGCAA CTC TCCCG
TGATACCA AGTGACGTT GAG AGGGT
TA TTC-

GAM7957 297 ABLIM1 1 16503 NP_006711.2 3 4184 TTATTTGGGACT C- TGCC 3 C c c

TGAGATTTGCAG TCACTGCAA CTC TCCCG
TGATACCA AGTGACGTT GAG AGGGT
TA TTC-

GAM7957 297 ACATE2 1 10237 NP_036464.1 3 544 GAGTCCGGGAGT AC TGC 3 C c c

TTGAGTCTGCAG TCACTGCA CTC CTCCCG
TGAGCTAT AGTGACGT GAG GAGGGC
CT TTT

GAM7957 297 ACE 1 3398 NP_690044.1 3 891 GAACCTGGGAGC A C 3 C c c

CGGAGGCTGCAG TCACTGCA CCTCTG CTCCCG
TGAGCCAA AGTGACGT GGAGGC GAGGGT
C C

GAM7957 297 ADAMTS1 1 7897 NP_112217.1 5 39 GCATGCGGGAGG A TG AA 3 C c c

2 CGGAGGGGTGGG TC C C CCTCTGCCTCCCG
ACCGGGTG AG G G GGAGGCGGAGGGC
- GT G-

GAM7957 297 ADAMTS4 1 15594 NP_005090.1 3 200 TGCCCTGGGAGG CA ---- 3 C c c

CAGTGATGGGTT TCACTG ACCT CTGCCTCCCG
AGTGGATG GGTGAT TGGG GACGGAGGGT
-- TAGT

GAM7957 297 ADAR3 1 6712 NP_061172.1 5 25 CAGAGCAGGAGG A AAC C 3 C c c

CAGAGCCCGCGG TC CTGC CTCTGCCTCC
GAAGCTCG AG GGCG GAGACGGAGG
- CCC A

GAM7957 297 ADAT1 1 15089 NP_036223.1 3 1030 CTACTCGGGAGG A AAC T 3 C c c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 ADCY1 2 17764 NP_066939.1 3 1740 GGCTTTGCAGGG ACCTCT T 3 C c b

CGGCCAGTGCAG TCACTGCA GCC CCC
TGATGCCT AGTGACGT CGG GGG
GAC--- C

GAM7957 297 ADCY1 2 18690 NP_066939.1 3 6468 GAACCCGGGAGG 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 ADCYAP1 1 13163 NP_001108.1 3 916 TATTGGAAGAGG G AC -- 3 C c c

CAGAGCCTGAGG TCACT CA CTCTGCCTC CCG
TGGTAGGA GGTGG GT GAGACGGAG GGT
A CC AA

GAM7957 297 ADH4 1 8767 NP_000661.1 5 246 TCACTGGGAGCA - -- C 3 C c c
ATGGGGTTGCAG TCA CTGCAACCTC TGC TCCCG
CTGAAGTC AGT GACGTTGGGG ACG AGGGT
C TA -

GAM7957 297 AF02059 2 5252 NP_055295.1 3 651 GGACTTGGGAGG CT 3 C b b
1 CGGTTGTTGCAG TCACTGCAAC CTGCCTCCCG
TGAGCTGT AGTGACGTTG GGCGGAGGGT
TT

GAM7957 297 AF02059 2 10612 NP_055295.1 3 1285 GAACATGGGAGG C C 3 C c
b
1 CGTAGCTTGCAG TCACTGCAA CT TGCCTCCCG
TGAGCTGA AGTGACGTT GA GCGGAGGGT
C T

GAM7957 297 AGMAT 1 17097 NP_079034.2 3 704 GGGCCCGGGAGG TG 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 AGRP 1 6741 NP_001129.1 5 284 GAATCCCGGAGG CT A-- C 3 C c c

CAGAGGCCATGC TCA GCA CCTCTGCCTCC
TGACCGCA AGT CGT GGAGACGGAGG
-- ACC C

GAM7957 297 AHR 1 4150 NP_001612.1 3 1770 CTACTCGGGAGG A AAC T 3 C c c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATAGCCT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 AIPL1 1 14786 NP_055151.2 3 828 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 AIRE 1 18688 NP_000374.1 3 352 GAACTCGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 AKAP11 1 3323 NP_652761.1 3 1312 GAACCTGGGAGG C 3 C b b
CAGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGACGGAGGGT
A

GAM7957 297 AKR1B10 2 10437 NP_064695.2 5 122 GAACCCAGGAGA C C 3 C c
c
CAGAGGTTGTAG TCACTGCAACCTCTG CTCC
TGAGCTGA AGTGATGTTGGAGAC GAGG
A A

GAM7957 297 AKR1B10 2 15089 NP_064695.2 5 88 CTACTCGGGAGG A AAC T 3 C c
c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 AKR1D1 1 19497 NP_005980.1 3 1304 GAACCCGGGAGG C G 3 C b b
AGGAGCTTGCAG TCACTGCAA CTCT CCTCCCG
TGAGCCGA AGTGACGTT GAGG GGAGGGC
C A
GAM7957 297 ALDH3B1 3 10057 NP_000685.1 3 685 GAACCCGGGAGG T TG 3 C c c
TGGAGGTTGCCG TCAC GCAACCTC CCTCCCG
TGAGCTGA AGTG CGTTGGAG GGAGGGC
C GT
GAM7957 297 ALDH3B1 3 14700 NP_000685.1 3 235 TGGGAGGCATGG A----- C 3 C c c
GAAACAGTGCAG TCACTGCA CCT TGCCTCCCG
TGACTCAC AGTGACGT GGG ACGGAGGGT
GACAAA T
GAM7957 297 ALDH3B1 3 15516 NP_000685.1 3 234 CGAGGTGGGAGG A----- C 3 C c c
CATGGGAAACAG TCACTGCA CCT TGCCTCCCG
TGCAGTGA AGTGACGT GGG ACGGAGGGT
GACAAA T
GAM7957 297 ALDH5A1 1 6817 NP_001071.1 3 2050 GAACCCAGGAGG C C 3 C c c
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCAGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 ALDH5A1 1 6817 NP_733936.1 3 2050 GAACCCAGGAGG C C 3 C c c
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCAGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 ALDH8A1 1 15129 NP_072090.1 3 582 GAGCCCAGGCGG A T T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCC CC
TGAGCCAT AGTGACGT GGAG TGG GG
C T C A
GAM7957 297 ALDH8A1 1 15129 NP_739577.1 3 582 GAGCCCAGGCGG A T T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCC CC
TGAGCCAT AGTGACGT GGAG TGG GG
C T C A
GAM7957 297 ALPP 1 15341 NP_001623.2 3 979 GAACCCGGGCGG C T 3 C b b
CGGAGATTGCAG TCACTGCAA CTCTGCC CCCG
TGAGCCGA AGTGACGTT GAGGCGG GGGC
A C
GAM7957 297 ALS2CR9 1 16955 NP_079528.1 5 138 AGGAGGCGGAGG - AA C 3 C c c
CAGCGGCTGGAG TCA CTGC CCTCTGCCTCC

GAGCGCGA GGT GGCG GGAGGCGGAGG
C AC A
GAM7957 297 ALTE 1 6238 NP_004720.1 3 1200 GAGCCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 ANAPC7 1 17768 NP_057322.1 5 198 GAACCCAGGAGA C C C 3 C c
c
CATGGGTTGCAG TCACTGCAACCT TG CTCC
TGAGCCGA AGTGACGTTGGG AC GAGG
T A A
GAM7957 297 ANKFY1 1 17805 NP_057460.2 3 3338 CCAGCCTGGTGG - AA T C 3 C c
c
CAGAGGAAGCAG TCAC TGC CCTCTGCC CC
GTGGCACC GGTG ACG GGAGACGG GG
G AA T T
GAM7957 297 ANKH 1 6937 NP_473368.1 3 2235 GATCCTGGGAGG 3 C b b
CAGAGGTTGTAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGATGTTGGAGACGGAGGGT
GAM7957 297 AOAH 1 3636 NP_001628.1 3 56 AGCACAGGGAGG TC----- G - 3 C c c
CAGAGGCTTGGG ACT CAA CCTCTGCCTCCC
TAAACTCA TGG GTT GGAGACGGAGGG
ACTCAAA - C
GAM7957 297 AP1GBP1 1 9627 NP_542118.1 3 2261 GAACCCAGGAGG C C 3 C c
c
CGGAGGTTGCAC TCA TGCAACCTCTGCCTCC
TGAGCCGA AGT ACGTTGGAGGCGGAGG
C A
GAM7957 297 AP1S3 2 10435 NP_848929.1 3 1844 GAACCCAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 AP1S3 2 14818 NP_848929.1 3 1680 GAACCTGGGAGG C 3 C b b
CAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCTGA AGTGACGTTG AGACGGAGGGT
A
GAM7957 297 AP4S1 1 17888 NP_009008.2 3 838 GAGCCTGGGGGA A TG- C 3 C c
c
CTGAGGCTGCAG TCACTGCA CCTC CCTCC
TGAGCCAT AGTGACGT GGAG GGGGG
C TCA T
GAM7957 297 APBB3 1 479 NP_006042.2 5 323 AGTGCGGGCCGG A AA- T- 3 C c c
CAGAGGCTGGCG TC CTGC CCTCTGCC CCCG
GGGAGCAG AG GGCG GGAGACGG GGGC
G GTC CC
GAM7957 297 APBB3 1 479 NP_573418.1 5 323 AGTGCGGGCCGG A AA- T- 3 C c c
CAGAGGCTGGCG TC CTGC CCTCTGCC CCCG

GGGAGCAG AG GGCG GGAGACGG GGGC
G GTC CC
GAM7957 297 APBB3 1 479 NP_573419.1 5 323 AGTGCGGGCCGG A AA- T- 3 C c c

CAGAGGCTGGCG TC CTGC CCTCTGCC CCCG
GGGAGCAG AG GGCG GGAGACGG GGGC
G GTC CC
GAM7957 297 APBB3 1 479 NP_573420.1 5 323 AGTGCGGGCCGG A AA- T- 3 C c c

CAGAGGCTGGCG TC CTGC CCTCTGCC CCCG
GGGAGCAG AG GGCG GGAGACGG GGGC
G GTC CC
GAM7957 297 APBB3 1 479 NP_573421.1 5 323 AGTGCGGGCCGG A AA- T- 3 C c c

CAGAGGCTGGCG TC CTGC CCTCTGCC CCCG
GGGAGCAG AG GGCG GGAGACGG GGGC
G GTC CC
GAM7957 297 APBB3 1 479 NP_573422.1 5 323 AGTGCGGGCCGG A AA- T- 3 C c c

CAGAGGCTGGCG TC CTGC CCTCTGCC CCCG
GGGAGCAG AG GGCG GGAGACGG GGGC
G GTC CC
GAM7957 297 APG10L 1 10656 NP_113670.1 3 443 TAACCCAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 APOBEC3 1 7049 NP_663745.1 3 396 GAACCCGGGAGG C 3 C b
b
A CAGAGCTTGCGG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGGCGTT GAGACGGAGGGC
C
GAM7957 297 APOBEC3 1 10042 NP_660341.2 3 867 GAGCCGGGGAGG A TG 3 C b
b
F TGGAGGCTGCAG TCACTGCA CCTC CCTCCC
TGAACTGA AGTGACGT GGAG GGAGGG
C GT
GAM7957 297 APOL1 1 4061 NP_003652.2 3 819 GAACCTGGGAGG C TG 3 C c c
TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCGA AGTGACGTT GAG GGAGGGT
C GT
GAM7957 297 APOL1 1 4061 NP_663318.1 3 819 GAACCTGGGAGG C TG 3 C c c
TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCGA AGTGACGTT GAG GGAGGGT
C GT
GAM7957 297 APXL2 1 14254 NP_597713.1 3 362 GAACCTGGGAGG C TG 3 C c c

TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCGGA AGTGACGTT GAG GGAGGGT
C GT
GAM7957 297 ARHGEF6 1 14790 NP_004831.1 3 1603 GAGCCCAGGAGG A CT C 3 C
c c

TCAAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCTGT AGTGACGT GGA TGGAGG
C AC A

GAM7957 297 ARLTS1 2 1904 NP_612459.1 3 746 GAACCCAGGAAG TG C C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC C TCC
TGAGCCGA AGTGACGTTGGAG G AGG
GT A A

GAM7957 297 ARLTS1 2 11695 NP_612459.1 3 314 GAGCCCAAGAGG CC 3 C c c

TAGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCAA AGTGACGTTGGAGATGGAG
AA

GAM7957 297 ARNT2 1 13998 NP_055677.1 3 2505 CCTCAACAGGGG A T CC 3 C c c

TCCAGGGTGCAG TCACTGCA CC CTG TCCC
TGAACTCA AGTGACGT GG GAC GGGG
- - CT

GAM7957 297 ASB8 1 4423 NP_077000.1 3 632 GAACCTGTGAGG CC 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCAA AGTGACGTTGGAGACGGAG
TG

GAM7957 297 ASK 1 838 NP_006707.1 3 860 GAACCTGGGAAG C C 3 C c c

TGCAGGTTGCAG TCACTGCAACCT TGC TCCCG
TGAGCCAA AGTGACGTTGGA GTG AGGGT
C A

GAM7957 297 ASTN2 1 14819 NP_054729.1 3 484 AGGAAGCTCTGA TCTG CC 3 C c c

GGATGGTTGCAG TCACTGCAACC CCTC
TGAGGAAG AGTGACGTTGG GGAG
TA-- TC

GAM7957 297 ATP1A2 1 15326 NP_000693.1 3 1430 GAACCTGTGAGG G CC 3 C c c

AAGAGGTTGCAG TCACTGCAACCTCT CCTC
TGAGCTGA AGTGACGTTGGAGA GGAG
A TG

GAM7957 297 ATP1B4 1 13338 NP_036201.1 3 543 GAGCCCAGGAGG A CT C 3 C c c

TCAAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCTGC AGTGACGT GGA TGGAGG
C AC A

GAM7957 297 AXL 1 1792 NP_001690.2 5 271 GAGGGAAGGAGG CT A C 3 C c c

CAGGGGTGCTGA TCA GCA CCTCTGCCTCC
GAAGGCGG AGT CGT GGGGACGGAGG
-- - A

GAM7957 297 AXL 1 1792 NP_068713.2 5 271 GAGGGAAGGAGG CT A C 3 C c c

CAGGGGTGCTGA TCA GCA CCTCTGCCTCC
GAAGGCGG AGT CGT GGGGACGGAGG
-- - A

GAM7957 297 B4GALT2 1 2774 NP_003771.1 3 603 TTGCATGGGAGG ACT AA - 3 C c c

CAGGTGGGGCTT TC GC CC TCTGCCTCCCG
GGATCAGT AG CG GG GGACGGAGGGT
GTT G- T
GAM7957 297 B4GALT2 1 2774 NP_085076.1 3 1267 TTGCATGGGAGG ACT AA - 3 C c c
CAGGTGGGGCTT TC GC CC TCTGCCTCCCG
GGATCAGT AG CG GG GGACGGAGGGT
GTT G- T
GAM7957 297 BANP 1 13451 NP_060339.2 3 256 CACGAGGGGAGG A A TC 3 C c c
CACGGTGCGGAG TC CTGCA CC TGCCTCCC
AGCGTCGC AG GGCGT GG ACGGAGGG
A - C-
GAM7957 297 BANP 1 13451 NP_524576.1 3 256 CACGAGGGGAGG A A TC 3 C c c
CACGGTGCGGAG TC CTGCA CC TGCCTCCC
AGCGTCGC AG GGCGT GG ACGGAGGG
A - C-
GAM7957 297 BCAR1 1 16661 NP_055382.1 3 40 CCAGGAGGGAGG A A---- 3 C c c
CAGGGGAGGGGT TC CTGCA CCTCTGCCTCCC
GCGGCGGT GG GGCGT GGGGACGGAGGG
C GGGGA
GAM7957 297 BCAS1 1 13893 NP_003648.1 3 543 GTACCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 BFAR 1 15922 NP_057645.1 3 957 GAACCCAGGAGG A C 3 C c c
CGGAGGTTGCAG TC CTGCAACCTCTGCCTCC
GGAGGGAG AG GACGTTGGAGGCGGAGG
G A
GAM7957 297 BHMT2 2 5830 NP_060084.2 3 790 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 BHMT2 2 10571 NP_060084.2 3 824 GAACCCAGGAGG C C 3 C c c
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 BIRC1 1 12796 NP_004527.1 3 1209 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGC
GAM7957 297 BIRC5 1 1829 NP_001159.1 5 22 GGGACCCGTTGG A A ------ 3 C c c
CAGAGGTGGCGG TC CTGC ACCTCTGCC TCCC
CGGCGGCA GG GGCG TGGAGACGG AGGG
C G TTGCCC
GAM7957 297 BIVM 1 14233 NP_060163.2 3 766 GAACCCGGGAGG C TG 3 C b b

TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCGGA AGTGACGTT GAG GGAGGGC
C GT

GAM7957 297 BMF 1 1509 NP_277038.1 3 942 GGGACATCGGGG C C T 3 C c c
GCAAGTTTGCAG TCACTGCAA CT TGCC CCCG
TGGGGCCG GGTGACGTT GA ACGG GGGC
T - -

GAM7957 297 BMP8 1 11740 NP_001711.2 3 2118 GAACCTGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCAGA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 BPNT1 2 3605 NP_006076.2 3 242 GAGCCCGGAAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCTGA AGTGACGTTGGAGGCGGA GGC
A

GAM7957 297 BPNT1 2 3936 XP_035738.1 3 242 GAGCCCGGAAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCTGA AGTGACGTTGGAGACGGA GGC
A

GAM7957 297 BRCA1 2 9421 NP_009226.1 5 263 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 BRCA1 2 19976 NP_009225.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009226.1 3 804 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009227.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009228.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009229.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009230.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009231.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009232.1 3 1315 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009233.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009234.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009235.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009236.1 3 803 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BRCA1 2 19976 NP_009237.1 3 6331 CAGCCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 BTBD5 1 1201 NP_060128.1 3 1240 GGGCCCGGGAGT C TGC 3 C c c

TTGAAGTTGCAG TCACTGCAAC TC CTCCCG
TGAGCTAT AGTGACGTTG AG GAGGGC
A TTT

GAM7957 297 BTN3A2 2 14305 NP_008978.1 3 442 GAACCCGGAAGG C C 3 C b b

CAGAGCTTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCCGA AGTGACGTT GAGACGGA GGC
C A

GAM7957 297 BTN3A2 2 15108 NP_008978.1 3 408 CTACTCGGGAGG A AAC T 3 C c b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 C12orf2 1 9765 NP_009142.2 3 465 GAACCCGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 C13orf1 1 13358 NP_065189.1 3 1469 GAACCCGGGAGA CCT C 3 C c c
CGGCGCTTGCAG TCACTGCAA CTG CTCCCG
TGAGCCGA AGTGACGTT GGC GAGGGC
CGC A

GAM7957 297 C14orf1 1 11463 NP_060440.1 3 2047 GAACCTGGGAGG C 3 C b b
02 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGACGTT GAGACGGAGGGT
C

GAM7957 297 C14orf1 1 13632 NP_060638.1 3 950 GAACCCAGGAGA C C C 3 C c c
05 TAGAGGTTGCAA TCA TGCAACCTCTG CTCC
TGAGCCAA AGT ACGTTGGAGAT GAGG
A A A

GAM7957 297 C14orf1 1 4003 NP_061148.1 3 371 TAACCCAAAAGG CCC 3 C c c
17 CGGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCCAA AGTGACGTTGGAGGCGGA
AAA

GAM7957 297 C14orf1 1 19330 NP_078909.1 3 949 CCATCCTGGAGG -- A-- - C 3 C c c
39 CAGCAGGTCGGG TCACT GC ACCT CTGCCTCC
TAGAGTGA AGTGA TG TGGA GACGGAGG
GA GGC C T

GAM7957 297 C14orf1 2 2780 NP_660274.1 3 1849 GGACCTGGGAGG C 3 C b b
43 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGT
C

GAM7957 297 C14orf1 2 4559 NP_660274.1 3 1815 CTGCTCGGGAGG A AAC T 3 C c b
43 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATAGCAT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 C14orf2 2 8019 XP_096757.2 3 258 GAACCCGGGAAG C C 3 C b b
3 CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A

GAM7957 297 C14orf2 2 13155 XP_096757.2 3 224 CTACTCGGGAGG A AAC T 3 C c b
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 C14orf2 2 7122 NP_775878.1 3 1227 GAACCAGGGAGG TG 3 C b b
4 TGGAGGTTGCAG TCACTGCAACCTC CCTCCC
TGAGCCAA AGTGACGTTGGAG GGAGGG
GT

GAM7957 297 C14orf2 2 16828 NP_775878.1 3 1193 CTGCTCGGGAGG A AAC T 3 C c b
4 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 C14orf4 1 10582 XP_041104.1 5 1780 CTTCGTCGGTGG T A- T C 3 C c c
CAGAGGTGGGCG TCAC GC ACCTCTGCC CC
TGGGTGCT GGTG CG TGGAGACGG GG
- GG T C
GAM7957 297 C14orf4 1 14786 XP_040343.3 3 2027 GAACCTGGGAGG 3 C b b
3 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT
GAM7957 297 C14orf4 1 4702 XP_040376.1 3 1383 GAATTCGGGAGG TG 3 C b b
6 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 C14orf7 1 14106 XP_211096.1 5 595 GGCAGTGGGAGG A- AAC- - 3 C c c
0 CAAGAGTGAAGC TC CTGC CTCT GCCTCCCG
AGAGGAGA AG GACG GAGA CGGAGGGT
GA AAGT A
GAM7957 297 C1orf24 1 10419 NP_443198.1 3 2947 GAGCGAGGGAAG A T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GC TCCC
TGAACTAT AGTGACGT GGAG TG AGGG
C T A
GAM7957 297 C1orf33 1 15057 NP_057267.2 3 382 GAACCCGGGAGG T TG 3 C c c
TGGAGGTTGCCG TCAC GCAACCTC CCTCCCG
TGAGTTGA AGTG CGTTGGAG GGAGGGC
C GT
GAM7957 297 C1orf34 2 18691 XP_027172.1 3 4794 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT
GAM7957 297 C1orf34 2 18827 XP_027172.1 3 3326 GACTTAGGGAGG GCAAC-- 3 C c b
CAGAGTGGAGGA TCACT CTCTGCCTCCC
AGTGAGAG AGTGA GAGACGGAGGG
AGGAGGT
GAM7957 297 C20orf1 1 9763 NP_543011.1 3 1296 GAACCCAGGAGG TG C 3 C c c
08 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 C20orf1 1 4680 NP_060622.2 3 269 GAACCCGGGAGG C 3 C b b
2 CAGAGGTTACAG TCACTG AACCTCTGCCTCCCG
TGAGCCAA AGTGAC TTGGAGACGGAGGGC

A

GAM7957 297 C20orf1 1 12434 XP_300782.1 3 663 GGACCTAGGAGG TG C 3 C c c
42 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 C20orf1 1 5441 NP_079194.2 3 663 GAGCCCAGGAGG A T C 3 C c c
72 TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGTTCT AGTGACGT GGAG TGGAGG
C T A

GAM7957 297 C20orf1 1 2547 NP_543019.1 3 540 GGACCCGGGAGG 3 C b b
75 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 C20orf1 1 18683 XP_290955.1 3 2356 GAACCCGGGAGG TG 3 C b b

77 CGGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCCAA AGTG GTTGGAGGCGGAGGGC
GT

GAM7957 297 C20orf2 2 17737 NP_060817.1 3 162 AAGGGGGCTGGG A G A -- 3 C c
b
9 CAGAGGGTGGAG TC CT CA CCTCTGCCT CCC
GAGGTCCT AG GA GT GGAGACGGG GGG
- G G TC

GAM7957 297 C20orf2 2 19584 NP_060817.1 3 582 GAACCTGGGAGG C 3 C b b
9 CAGAGTTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGT
T

GAM7957 297 C21orf1 1 5823 XP_114191.2 3 631 CTACTCGGGAGG A- AAC CT 3 C c
c
08 CTAAGGCAGGGG TC CTGC CT GCCTCCCG
AATCGCTT AG GACG GA CGGAGGGC
GG --- AT

GAM7957 297 C21orf6 1 8800 NP_062542.1 5 0 TGGCCAGGCAGA G --- C- 3 C c c
2 GGTCTGTGGAGT TCACT CA ACCTCTGCCT CCG
GGAGAGGC GGTGA GT TGGAGACGGA GGT
G GTC CC

GAM7957 297 C21orf9 1 14711 NP_068760.1 3 24 TGGTGTGGGAGG CT A 3 C b b
7 CAGAGGTGCTGA TCA GCA CCTCTGCCTCCCG
CGTTCTGG AGT CGT GGAGACGGAGGGT
-- -

GAM7957 297 C22orf1 3 4658 NP_003669.2 3 1025 GAACCCATGAGG CC 3 C c c
9 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGACGTTGGAGGCGGAG
TA

GAM7957 297 C22orf1 3 9519 NP_003669.2 3 2527 GAATCCCCGAGG C CC 3 C c c
9 CGGAGGTTGCAC TCA TGCAACCTCTGCCTC
TGAGCCGA AGT ACGTTGGAGGCGGAG
C CC

GAM7957 297 C22orf1 3 15217 NP_003669.2 3 2493 CCGCTCGGGAGG A AAC T 3 C c
c

9 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 C22orf2 1 18684 NP_079501.2 3 924 GAACCCAGGAGG C 3 C b b
0 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGGCGTTGGAGGCGGAGG
A

GAM7957 297 C6orf14 1 1454 NP_065141.2 3 109 TGAAGCCAGAGG C CC 3 C c c
9 CAGAGGTTGCAA TCA TGCAACCTCTGCCTC
TGAGCCGG AGT ACGTTGGAGACGGAG
A AC

GAM7957 297 C6orf15 1 14568 NP_612450.1 3 169 GGGCCCGGGAGG TG 3 C b b

0 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGTCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 C6orf16 1 10236 NP_060534.1 5 352 CTGCCGCGGAGG A AA T - 3 C c
c
6 CAGCGGCGGCAG TC CTGC CC CTGCCTCC CG
CGGCTCTC GG GACG GG GACGGAGG GC
C GC C C

GAM7957 297 C6orf29 2 5830 NP_116183.1 3 297 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 C6orf29 2 10438 NP_116183.1 3 331 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 C6orf5 3 1492 NP_056339.2 3 869 CTACTCGGGAGG A AAC T 3 C c b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 C6orf5 3 2576 NP_056339.2 3 1905 CAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 C6orf5 3 10438 NP_056339.2 3 903 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 C6orf57 1 17417 NP_660310.1 3 323 GAACCCAGGAGG TG C 3 C c c

TGGAGGTTGCGG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGGCGTTGGAG GGAGG
GT A

GAM7957 297 C6orf96 1 15978 NP_060379.1 3 296 GAACTTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG

TGAGCTAA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 C7orf3 1 11428 XP_049384.6 3 524 GGACCCTGGAGG A C 3 C c c
TAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCCAA AGTGACGT GGAGATGGAGG
C T
GAM7957 297 C8orf17 1 19452 NP_064622.1 3 126 GAACCCCAGAGG TG CC 3 C c
c
TGGAGGTTGCAG TCACTGCAACCTC CCTC
TGAGCCGA AGTGACGTTGGAG GGAG
GT AC
GAM7957 297 C9orf5 1 2784 NP_114401.1 3 1562 GAGTCCAGGAGG A T C 3 C c c
TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCCAA AGTGACGT GGAG TGGAGG
C C A
GAM7957 297 CAB5618 1 18474 NP_115909.1 3 32 GTGGTGGGAGAG A- A--- - 3 C c
c
4 CAGAGGTGGACG TC CTGC ACCTCTGC CTCCCG
CGGCCGAG AG GGCG TGGAGACG GAGGGT
CC CAGG A
GAM7957 297 CACNG1 1 7002 NP_000718.1 3 245 AGTTGGGGGAGG - AAC 3 C c
c
CAGAGCCAGCAG TCAC TGC CTCTGCCTCCC
GTGGACAG GGTG ACG GAGACGGAGGG
G ACC
GAM7957 297 CAM-KII 1 10376 NP_150284.1 5 4 CGGCCCGGGAGG A- AA 3 C c c
N CGGAGGCGCGGG TC CTGC CCTCTGCCTCCCG
GGAGGAGG AG GGCG GGAGGCGGAGGGC
GG C-
GAM7957 297 CAMKK1 1 8891 NP_115670.1 3 345 TGGGGCAGGAGG A AAC C 3 C c
c
CAGAGGCAGGAG TC CTGC CTCTGCCTCC
ACCAAGAT AG GACG GAGACGGAGG
- --- A
GAM7957 297 CAMKK1 1 8891 NP_757343.1 3 345 TGGGGCAGGAGG A AAC C 3 C c
c
CAGAGGCAGGAG TC CTGC CTCTGCCTCC
ACCAAGAT AG GACG GAGACGGAGG
- --- A
GAM7957 297 CAMKK2 2 6443 NP_006540.3 5 347 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 CAMKK2 2 6443 NP_705719.2 5 347 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 CAMKK2 2 6443 NP_705720.1 5 347 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 CAMKK2 2 6443 NP_757363.1 5 347 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 CAMKK2 2 6443 NP_757364.1 5 347 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 CAMKK2 2 6443 NP_757365.1 5 347 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 CAMKK2 2 9311 NP_757380.1 5 36 GAGCGCGGGAGG AC AA T 3 C c
b
CGGCGGCGGCGC TC TGC CC CTGCCTCCCG
GGAGCCCA AG GCG GG GGCGGAGGGC
GC GC C
GAM7957 297 CAP2 1 16561 NP_006357.1 5 7 TCTTTGGGGAGG TG A C-- 3 C c c
CAACTAGGATGG TCAC CA CCT TGCCTCCC
TGTGGCCG GGTG GT GGA ACGGAGGG
TG A TCA
GAM7957 297 CAPNS1 1 16623 NP_001740.1 5 85 CGCTCCGGGAGG AAC --- 3 C c
c
CCCGGGAGCGGC TCACTGC CTCT GCCTCCCG
AGTGGAAC GGTGACG GAGG CGGAGGGC
GC- GCC
GAM7957 297 CARKL 1 13435 NP_037408.1 3 1598 GAACTCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 CASP10 2 1694 NP_001221.1 3 1086 GAATCCAGGAGG TG A C 3 C c
c
CAGAGGCTGTGG TCAC CA CCTCTGCCTCC
TGAGCCAA AGTG GT GGAGACGGAGG
GT C A
GAM7957 297 CASP10 2 1694 NP_116758.1 3 1741 GAATCCAGGAGG TG A C 3 C c
c
CAGAGGCTGTGG TCAC CA CCTCTGCCTCC
TGAGCCAA AGTG GT GGAGACGGAGG
GT C A
GAM7957 297 CASP10 2 1694 NP_116759.1 3 1086 GAATCCAGGAGG TG A C 3 C c
c
CAGAGGCTGTGG TCAC CA CCTCTGCCTCC
TGAGCCAA AGTG GT GGAGACGGAGG
GT C A
GAM7957 297 CASP10 2 17083 NP_001221.1 3 1052 CTACTCGGGAGG A CAAC T 3 C
c c
CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCTCTT AG GAC GAG CGGAGGGC

```
                                        -  A---  T
GAM7957  297   CASP10  2  17083  NP_116758.1  3  1707  CTACTCGGGAGG  A  CAAC  T          3  C
c  c
                                CTGAGACAGGAG TC CTG   CTC GCCTCCCG
                                AATCTCTT    AG GAC   GAG CGGAGGGC
                                        -  A---  T
GAM7957  297   CASP10  2  17083  NP_116759.1  3  1052  CTACTCGGGAGG  A  CAAC  T          3  C
c  c
                                CTGAGACAGGAG TC CTG   CTC GCCTCCCG
                                AATCTCTT    AG GAC   GAG CGGAGGGC
                                        -  A---  T
GAM7957  297   CASP8   1  7316   NP_203519.1  5  117   CATGGAGGGAGG    ---  AACC          3  C  c
c
                                CAGAAGAGCCAG TCACT  GC   TCTGCCTCCC
                                GGTGGTTA   GGTGG  CG   AGACGGAGGG
                                           GAC  AGA-
GAM7957  297   CASP8   1  7316   NP_203521.1  5  117   CATGGAGGGAGG    ---  AACC          3  C  c
c
                                CAGAAGAGCCAG TCACT  GC   TCTGCCTCCC
                                GGTGGTTA   GGTGG  CG   AGACGGAGGG
                                           GAC  AGA-
GAM7957  297   CBCIP2  1  614   NP_116220.1  3  1611  GAACCCGGGAGG       C          3  C  b  b
                                CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                TGAGCTGA    AGTGACGTT GAGACGGAGGGC
                                        C
GAM7957  297   CCL5    3  3753   NP_002976.2  3  565   GAACCCAGGAGG     A  TG   C      3  C  c  b

                                TGGAGGCTGCAG TCACTGCA CCTC  CCTCC
                                TGAGCTGA    AGTGACGT GGAG  GGAGG
                                        C   GT   A
GAM7957  297   CCL5    3  13155  NP_002976.2  3  351   CTACTCGGGAGG  A  AAC  T          3  C  c
b
                                CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                AATGGCGT    AG GACG  GAG CGGAGGGC
                                        -   ---  T
GAM7957  297   CCL5    3  15343  NP_002976.2  3  385   GAACCCGGGAGG       C          3  C  b  b
                                CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                        C
GAM7957  297   CCNL2   1  2911   NP_112199.1  3  19    CATCGGAGGTGG       T  TC         3  C  c  c
                                GCGGGGTTGCAG TCACTGCAACC CTGCC  CC
                                TGACTGGT    AGTGACGTTGG GGCGG  GG
                                        -   GT
GAM7957  297   CCR6    1  12792  NP_004358.1  3  1519  GAACCCAGGAGG          C       3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGAGCCGA    AGTGACGTTGGAGACGGAGG
                                            A
GAM7957  297   CCR6    1  12792  NP_113597.1  3  1519  GAACCCAGGAGG          C       3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGAGCCGA    AGTGACGTTGGAGACGGAGG
```

A

GAM7957 297 CD19 1 8851 NP_001761.2 3 329 TAAGGAAGGAAG A --- G C 3 C c c
TCAAGGCTGCAG TCACTGCA CCT CT CCT CC
TGAGCTAT AGTGACGT GGA GA GGA GG
C ACT A A

GAM7957 297 CD28 1 13593 NP_006130.1 3 1043 GAACCTGGCAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCGA AGTGACGTTGGAGGCGGA GGT
C

GAM7957 297 CD59 1 6036 NP_000602.1 3 289 CTCTTGGGAAGA CCT CC-- 3 C c c

CCAGCTTTGCAG TCACTGCAA CTG TCCCG
TGACAGCT AGTGACGTT GAC AGGGT
TC- CAGA

GAM7957 297 CD68 1 17185 NP_001242.1 3 365 GAACCCTGGAAG TG C C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC C TCC
TGAGCCTG AGTGACGTTGGAG G AGG
GT A T

GAM7957 297 CD84 1 3814 NP_003865.1 3 2197 GAACCCAGGAAG TG C C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC C TCC
TGAGCTGA AGTGACGTTGGAG G AGG
GT A A

GAM7957 297 CDAN1 1 6264 XP_085300.3 3 714 TGAACCTGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT T

GAM7957 297 CDC42EP 1 8291 NP_006440.2 5 715 GCCCGCGGGAGG - AA T- 3 C c
c

3 CCCGGGGCAGCG TCA CTGC CCTC GCCTCCCG
GCTGGGAT GGT GGCG GGGG CGGAGGGC
C AC CC

GAM7957 297 CDCA4 1 6066 NP_060425.2 3 215 TGGAGGGCCAGG CT A -- 3 C c c

CAGAGGCTGTTC TCA GCA CCTCTGCCT CCC
TGGAAGGC GGT TGT GGAGACGGA GGG
CT C CC

GAM7957 297 CDH6 1 19638 NP_004923.1 5 246 GGAATGAGGCTG A --- - --- 3 C c c
GATACGGTGCAG TCACTGCA CC TCT GCCTC CC
TGAAAAAG AGTGACGT GG AGG CGGAG GG
- CAT T TAA

GAM7957 297 CDT1 1 5446 NP_112190.1 3 665 GAACCCAGGAGG C C C 3 C c c
CACAGCTTGCAG TCACTGCAA CT TGCCTCC
TGAGCGAA AGTGACGTT GA ACGGAGG
C C A

GAM7957 297 CEACAM5 2 3562 NP_004354.1 3 251 TTACTCGGGAGG A AAC T 3 C c
b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC

```
                                        -   ---  T
GAM7957  297   CEACAM5 2   14555  NP_004354.1  3  285   GAACCCGGGAGG       C  TG          3  C  b
 b
                                TGGAGATTGCAG TCACTGCAA CTC  CCTCCCG
                                TGAGCCCA    AGTGACGTT GAG  GGAGGGC
                                          A  GT
GAM7957  297   CENTG1  1   15422  NP_055585.1  3  1320  TCTCCTTGGAGG    TGCA  T     C       3  C
c  c
                                CAGTGGTGTGAA TCAC    ACC CTGCCTCC
                                TCTTCTTC    AGTG    TGG GACGGAGG
                                          ----  T      T
GAM7957  297   CERK   1   1617   NP_073603.2  3  1993   GAACCCAAGAGG         TG   CC       3  C  c
c
                                TGGAGGTTGCGG TCACTGCAACCTC  CCTC
                                TGAGCCAA    AGTGGCGTTGGAG  GGAG
                                          GT   AA
GAM7957  297   CG012  4   5067   XP_096710.1  3  649   CAACCCAGGAGG     CAA       C       3  C  c  b

                                CAGAGGCTACAG TCACTG   CCTCTGCCTCC
                                TGAGCTGA    AGTGAC   GGAGACGGAGG
                                          ATC         A
GAM7957  297   CG012  4   10655  XP_096710.1  5  51    GAACCCAGGACA       C   CC  C       3  C  c  b

                                CGGAGATTGCAG TCACTGCAA CTCTG  TCC
                                TGAGCCAA    AGTGACGTT GAGGC  AGG
                                          A    AC  A
GAM7957  297   CG012  4   11098  XP_096710.1  3  1289   GAATCCGGGAGG       CC            3  C  b  b

                                CGGGTCTTGCAG TCACTGCAA  TCTGCCTCCCG
                                TGAGCAGA    AGTGACGTT  GGGCGGAGGGC
                                          CT
GAM7957  297   CG012  4   15105  XP_096710.1  3  1257   CTACTCGGGAGG  A-   AAC  T          3  C  c
b
                                CTGAGGCAGGGG TC  CTGC   CTC GCCTCCCG
                                AATGGCGT    AG  GACG   GAG CGGAGGGC
                                          GG   ---  T
GAM7957  297   CGI-119 1   7927   NP_057140.1  3  494   GAACCTGGGAGG   C      TG          3  C  c  c
                                TGGAGGTTGCAT TCA TGCAACCTC  CCTCCCG
                                TGAGCCAA    AGT ACGTTGGAG  GGAGGGT
                                          T       GT
GAM7957  297   CGI-57  1   4207   NP_056495.2  5  40    GCCCCGGGGAGG   -  AACC           3  C  c  c

                                CAGGCTGGCAGG TCAC TGC    TCTGCCTCCC
                                TGGACAGG    GGTG ACG    GGACGGAGGG
                                          G  GTC-
GAM7957  297   CHRFAM7 1   19583  NP_683709.1  5  775   AGATGCAGGAGG     CAACC      C       3  C
c  c
          A                      CAGATATCAGTG TCACTG     TCTGCCTCC
                                GCT         GGTGAC     AGACGGAGG
                                          TAT--        A
```

GAM7957 297 CKLiK 2 1797 NP_705718.1 3 793 GAACCCGGGAGA C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTG CTCCCG
TGAGCTGA AGTGACGTTGGAGGC GAGGGC
A
GAM7957 297 CKLiK 2 15089 NP_705718.1 3 759 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 CLCN7 1 11937 NP_001278.1 3 1109 CTCACGGGGCGG T-- CAA--- - 3 C c
c
CAGAGGCAACTT CACTG CCTCTGCC TCCCG
CAGTGTCC GTGAC GGAGACGG GGGGC
CCT TTCAAC C
GAM7957 297 CLDN15 1 4226 NP_055158.1 5 116 GGAAGAGGCAGG - G A C 3 C c
c
CAGAGGCTGAGG TCA CT CA CCTCTGCCT CC
CTGATTCC AGT GG GT GGAGACGGA GG
C A C C
GAM7957 297 CLDN15 1 4226 NP_612438.1 5 31 GGAAGAGGCAGG - G A C 3 C c c
CAGAGGCTGAGG TCA CT CA CCTCTGCCT CC
CTGATTCC AGT GG GT GGAGACGGA GG
C A C C
GAM7957 297 CLDN19 2 5830 NP_683763.1 3 1907 CTACTCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 CLDN19 2 10568 NP_683763.1 3 1941 GAACTCGGGAGG TC----- TG 3 C c
c
TGGAGGTTGCAG ACTGCAACCTC CCTCCCG
TCAGCCAA TGACGTTGGAG GGAGGGC
AACCGAC GT
GAM7957 297 CLN8 2 8497 NP_061764.2 3 3665 GAACCTGGGAGG C 3 C b b
CAGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGT
A
GAM7957 297 CLN8 2 18690 NP_061764.2 3 738 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 CLSPN 1 15905 NP_071394.2 5 64 GCGCAGGGGAGG A- - -- C 3 C c c
CAGAAGTCATGA TC CTG CA AC TCTGCCTCCC
CAGGCGAG AG GAC GT TG AGACGGAGGG
CG A AC A
GAM7957 297 CNNM1 2 5830 NP_065081.1 3 1356 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG

AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 CNNM1 2 10439 NP_065081.1 3 1390 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 COE2 1 13624 XP_034639.1 3 1575 GAACCCAGGAGG C C C 3 C c
c
CACAGATTGCAG TCACTGCAA CT TGCCTCC
TGAGCCAA AGTGACGTT GA ACGGAGG
A C A
GAM7957 297 COPS7B 1 5797 NP_073567.1 5 38 GGCGCCGGGAGG A CAAC T 3 C
c c
CCGAGCCAGCGA TC CTG CTC GCCTCCCG
CTAAGAGG AG GAC GAG CGGAGGGC
C C--- C
GAM7957 297 CPM 2 5015 NP_001865.1 3 626 GAACCCTAGAGG C CC 3 C c c
CGGAGTTTGCAG TCACTGCAA CTCTGCCTC
TGAGCCGA AGTGACGTT GAGGCGGAG
T AT
GAM7957 297 CPM 2 14439 NP_001865.1 3 592 CCTTTCGGGAGG A CAAC T 3 C c
c
CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCGCTT AG GAC GAG CGGAGGGC
- A--- T
GAM7957 297 CPR2 1 3265 NP_112162.1 3 1377 GAACCCGGGAGG A TG 3 C b b

TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAGTTAA AGTGACGT GGAG GGAGGGC
C GT
GAM7957 297 CPT2 1 15223 NP_000089.1 3 276 GAACCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 CRACC 1 9770 NP_067004.3 3 1222 GAACCTGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 CRAMP1L 1 7133 XP_034570.4 3 3345 GAACCTCAGCGG TCCC 3 C c
c
CGGAGGTTGCAG TCACTGCAACCTCTGCC
TGAGTCGA AGTGACGTTGGAGGCGG
CGAC
GAM7957 297 CREB1 2 5925 NP_004370.1 3 1735 GAACCCAGGAGG - C 3 C b b
CAGAGGGTTGCA TCACTGCAACC TCTGCCTCC
GTGAGCCG AGTGACGTTGG AGACGGAGG
G A
GAM7957 297 CREB1 2 5925 NP_604391.1 3 1735 GAACCCAGGAGG - C 3 C b b
CAGAGGGTTGCA TCACTGCAACC TCTGCCTCC

GTGAGCCG AGTGACGTTGG AGACGGAGG
G A
GAM7957 297 CREB1 2 14278 NP_004370.1 3 1735 AACCCAGGAGGC - C 3 C b b
AGAGGGTTGCAG TCACTGCAACC TCTGCCTCC
TGAGCCGA AGTGACGTTGG AGACGGAGG
G A
GAM7957 297 CREB1 2 14278 NP_604391.1 3 1735 AACCCAGGAGGC - C 3 C b b
AGAGGGTTGCAG TCACTGCAACC TCTGCCTCC
TGAGCCGA AGTGACGTTGG AGACGGAGG
G A
GAM7957 297 CROT 1 13250 NP_066974.2 3 779 GAGCCCAGGAGG A TCT C 3 C c
c
TTGTGGCTGCAG TCACTGCA CC GCCTCC
TGAGCTGT AGTGACGT GG TGGAGG
C TGT A
GAM7957 297 CRTAM 1 2833 NP_062550.1 3 683 GAACCTGGGAGG C TG 3 C c
c
TGGAGATTGCAG TCACTGCAA CTC CCTCCCG
TGAGTCAA AGTGACGTT GAG GGAGGGT
A GT
GAM7957 297 CRY2 1 17056 NP_066940.1 3 900 TACCAGGAGGAG --- G C 3 C c c
ACCAGGTTGCAG TCACTGCAACC TCT CCTCC
TGGCGTAA GGTGACGTTGG AGA GGAGG
ACC - A
GAM7957 297 CRYZL1 1 5251 NP_660354.1 3 1246 GAACCTGGGAGG C 3 C b b
CAGAGGTTTCAG TCACTG AACCTCTGCCTCCCG
TGAGCCAA AGTGAC TTGGAGACGGAGGGT
T
GAM7957 297 CSAD 1 6679 NP_057073.2 3 302 GAACCCAGGGGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGGGG
A
GAM7957 297 CTMP 1 16622 NP_444283.1 3 443 GAACCCAGGAGG G C 3 C b b
AAGAGGTTGCAG TCACTGCAACCTCT CCTCC
TGAGCCAA AGTGACGTTGGAGA GGAGG
A A
GAM7957 297 CTMP 1 16622 NP_789823.1 3 1074 GAACCCAGGAGG G C 3 C b b
AAGAGGTTGCAG TCACTGCAACCTCT CCTCC
TGAGCCAA AGTGACGTTGGAGA GGAGG
A A
GAM7957 297 CTSS 1 1951 NP_004070.3 3 1068 GAGCCCAGGAGG AC T C 3 C c
c
TTGAGAATGCAG TCACTGCA CTC GCCTCC
TGAGCTTG AGTGACGT GAG TGGAGG
AA T A
GAM7957 297 CUBN 1 13063 NP_001072.1 3 384 GAACCCAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 CX40.1 1 4730 NP_699199.1 3 259 GAGCCTGGGAGA A TGC 3 C c c

TCGAGGCTGCAG TCACTGCA CCTC CTCCCG
TGAGCCAA AGTGACGT GGAG GAGGGT
C CTA

GAM7957 297 CXorf12 1 9618 NP_003483.1 5 196 TCAGCCGGGAGG TCA -- - -- 3 C c c

CCCAGAGTGTTC CTGCA AC CTCT GCCTCCCG
TGCAGAGG GACGT TG GAGA CGGAGGGC
GGA CT T CC

GAM7957 297 CXYorf1 1 8398 XP_088704.2 3 177 GGACAGAGGTGG AC--- TG --- 3 C c c

AGACAGGTGCAG TCACTGCA CTC CCTC CC
TGACCCAG AGTGACGT GAG GGAG GG
GGACA GT ACA

GAM7957 297 CYB561 1 7117 NP_001906.2 3 1299 GAACCCGGGAGA CCT GC 3 C c c

TGGCGCTTGCAG TCACTGCAA CT CTCCCG
TGAGCTGA AGTGACGTT GG GAGGGC
CGC TA

GAM7957 297 CYCS 1 18947 NP_061820.1 3 3545 GAACTTGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAG AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 CYorf14 1 14752 NP_061012.1 3 297 AGCCCAGGAGAT C T -- C 3 C c c

GCAGGCTTGCAG TCACTGCAA C CTGC CTCC
TGAGCCAT AGTGACGTT G GACG GAGG
C - TA A

GAM7957 297 CYP4F3 2 16247 NP_000887.1 3 1829 GAAACCCACAGG CCC 3 C c c

CGGAGGTTGCGG TCACTGCAACCTCTGCCT
TGGGCTGG GGTGGCGTTGGAGGCGGA
CAC

GAM7957 297 CYP4F3 2 18962 NP_000887.1 3 2832 GAACCCAGGAGT C C C 3 C c c

CAGAGGTTTCAG TCACTG AACCTCTG CTCC
TGAGCCGA AGTGAC TTGGAGAC GAGG
T T A

GAM7957 297 D21S205 2 13060 NP_003674.1 3 1448 GAACCTGGGAGG TG 3 C b b

6E CAGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCTAA AGTG GTTGGAGACGGAGGGT
GT

GAM7957 297 D21S205 2 15089 NP_003674.1 3 1414 CTACTCGGGAGG A AAC T 3 C c b

6E CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 DAPP1 1 2773 NP_055210.1 3 1750 GAACCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAACCAA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 DBCCR1 1 2272 NP_055433.1 5 124 AGAGCCGGGAGG AA 3 C b b
CAGAGGGAGTAG TCACTGC CCTCTGCCTCCCG
TGACCGCC AGTGATG GGAGACGGAGGGC
AG
GAM7957 297 DBT 1 9770 NP_001909.1 3 510 GAACCTGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 DCLRE1C 2 9270 NP_071932.1 3 475 GAACCTGGGAGG T TG 3 C c c
TGGTGGTTGCAG TCACTGCAACC C CCTCCCG
TGAGCTGA AGTGACGTTGG G GGAGGGT
T GT
GAM7957 297 DCLRE1C 2 9533 NP_071932.1 3 316 GAGCCCAGGAGA A TGC C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCCAT AGTGACGT GGAG GAGG
C TTA A
GAM7957 297 DDOST 2 15593 NP_005207.2 3 483 GAATCCAGGAGG C C 3 C b b
CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 DDOST 2 17654 NP_005207.2 3 451 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AAAGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DDX34 2 2125 NP_055496.1 3 2235 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGAGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DDX34 2 7047 NP_055496.1 3 2269 GAACCCGGGAGG C 3 C b b
CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGACGTT GAGACGGAGGGC
C
GAM7957 297 DDX51 1 17424 NP_778236.1 3 582 GAACCCGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 DEGS 1 2834 NP_003667.1 3 530 AGGAGGCGGAGG A C 3 C b b
CAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGACCCAA AGTGACGT GGAGACGGAGG
C C

GAM7957 297 DEGS 1 2834 NP_659004.1 3 153 AGGAGGCGGAGG A C 3 C b b
CAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGACCCAA AGTGACGT GGAGACGGAGG
C C
GAM7957 297 DF 1 8534 NP_001919.1 3 310 GAACGCAGGAGG A T C 3 C c c
CTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGTTGT AGTGACGT GGAG CGGAGG
C T A
GAM7957 297 DFFA 1 19036 NP_004392.1 3 511 GAACCTGGGAGG C 3 C b b
CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGACGGAGGGT
C
GAM7957 297 DGKI 1 13155 NP_004708.1 5 95 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DIS3 2 15204 NP_055768.2 3 2299 GAACCTGGGAGG C 3 C b b
CGGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCGA AGTGACGTTG AGGCGGAGGGT
A
GAM7957 297 DIS3 2 17399 NP_055768.2 3 2476 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 DJ122O8 1 3814 NP_065199.1 3 523 GAACCCAGGAAG TG C C 3 C c
c
.2 TGGAGGTTGCAG TCACTGCAACCTC C TCC
TGAGCTGA AGTGACGTTGGAG G AGG
GT A A
GAM7957 297 DKFZp31 1 9281 XP_087728.2 3 328 GAACCCGGGAGG CT 3 C b b
3G1735 CAGCAGTTGCAG TCACTGCAAC CTGCCTCCCG
TGAGCTGA AGTGACGTTG GACGGAGGGC
AC
GAM7957 297 DKFZp31 1 7349 NP_776187.1 3 267 GAGCCCAGGAGG CT C 3 C c
c
3N0621 CCAAGGTTGCAG TCACTGCAACCT GCCTCC
TGGGCCCA GGTGACGTTGGA CGGAGG
AC A
GAM7957 297 DKFZP43 1 8751 NP_061864.1 3 1472 GAGCCCAGGAAG A TG C C 3 C
c c
4A0131 TGGAGGCTGCAG TCACTGCA CCTC C TCC
TGACCTAT AGTGACGT GGAG G AGG
C GT A A
GAM7957 297 DKFZP43 2 4428 XP_166485.3 3 729 CTACTCGGGAGG A AAC T 3 C c
b
4B0335 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGTTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 DKFZP43 2 7885 XP_166485.3 3 763 GAACCCGGGAGG A 3 C b b
4B0335 CGGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAGCCGA AGTGACGT GGAGGCGGAGGGC
C
GAM7957 297 DKFZP43 1 11706 NP_056459.1 5 593 CAAGGGCAAGTG C - - -- 3 C b b
4B103 CTAGAGTTGCAG TCACTGCAAC TCT GC CT CCC
TGAATTTA AGTGACGTTG AGA CG GA GGG
- T T AC
GAM7957 297 DKFZP43 1 2483 NP_056249.1 3 396 GAACCTGGGAGG C 3 C b b
4B168 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT
C
GAM7957 297 DKFZP43 1 17129 NP_056436.1 3 1764 GAACCCAGGAGG C C 3 C c
c
4C171 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCAT AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 DKFZp43 1 6416 NP_115623.1 3 2337 GAACCTGGGAGG C 3 C b b
4E0519 CGGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCAA AGTGACGTTG AGGCGGAGGGT
A
GAM7957 297 DKFZp43 1 14786 NP_060082.1 5 1232 GAACCTGGGAGG 3 C b b
4E2220 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT
GAM7957 297 DKFZP43 1 744 NP_056268.1 3 399 GAACCCAGCAGG CCC 3 C c
c
4F091 CGGAGGTTGCGG TCACTGCAACCTCTGCCT
TGAGTCGA AGTGGCGTTGGAGGCGGA
CGA
GAM7957 297 DKFZp43 2 4428 XP_290829.1 3 1748 CTACTCGGGAGG A AAC T 3 C c
b
4H247 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGTTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DKFZp43 2 17399 XP_290829.1 3 1782 GAACCTGGGAGG 3 C b b
4H247 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 DKFZP43 1 3132 XP_113763.3 3 652 GAACCTGGCAGG C 3 C b b
4I1735 CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCAA AGTGACGTTGGAGACGGA GGT
C
GAM7957 297 DKFZP43 1 17403 XP_044070.6 3 852 GAACCCAGGAGG C 3 C b b
4L187 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 DKFZP43 1 7178 XP_041116.1 3 82 GGCAAGGGGAGG ACT AA- - 3 C c c

4P0111 CAGGAGGGTGGC TC GC CCTC TGCCTCCC

CTGGACCT AG CG GGAG ACGGAGGG

GTC GTG G

GAM7957 297 DKFZP43 1 6448 NP_055364.1 3 3070 AAAGTATTGGGG TG CC 3 C c c

4P211 TGGAGGTTGCAG TCACTGCAACCTC CCTC

TGAGCAGA AGTGACGTTGGAG GGGG

GT TT

GAM7957 297 DKFZp54 1 5830 XP_040799.2 3 678 CTACTCGGGAGG A AAC T 3 C c c

7C176 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG

AATCGCTT AG GACG GAG CGGAGGGC

- --- T

GAM7957 297 DKFZp54 2 9762 NP_061175.1 3 1412 GAACCTGGGAGG 3 C b b

7G183 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG

TGAGTTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 DKFZp54 2 18018 NP_061175.1 3 1378 CTGTTCGGGAGG A AAC T 3 C c b

7G183 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG

AATCACTT AG GACG GAG CGGAGGGC

- --- T

GAM7957 297 DKFZp54 1 11012 NP_115531.1 3 1428 GAGCCCTGGAGT A C C- C 3 C c c

7I094 TCAAGGCTGCAG TCACTGCA CCT TG CTCC

TGAGCTGT AGTGACGT GGA AC GAGG

C - TT T

GAM7957 297 DKFZP56 1 8377 XP_032397.1 3 327 GAACCAGGGAGG C 3 C b b

4I122 CAGAGATTGCAG TCACTGCAA CTCTGCCTCCC

TGAGCCGA AGTGACGTT GAGACGGAGGG

A

GAM7957 297 DKFZP56 1 14509 NP_056274.1 3 743 GAACCTGCGAGG C CC 3 C c c

4J0863 CAGAGATTGCAG TCACTGCAA CTCTGCCTC

TGAGCCAA AGTGACGTT GAGACGGAG

A CG

GAM7957 297 DKFZp56 1 1903 NP_115497.2 3 1171 ATACCTGGGAGG C 3 C b b

4K142 CGGAGATTGCAG TCACTGCAA CTCTGCCTCCCG

TGAGCCGA AGTGACGTT GAGGCGGAGGGT

A

GAM7957 297 DKFZP56 2 7401 XP_085525.3 3 366 GAACCTGGGAGG 3 C b b

4M182 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG

TGAGCCAC AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 DKFZP56 2 16630 XP_085525.3 3 2535 TAACCCGGGAGG TG 3 C b b

4M182 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG

TGAGCTGA AGTGACGTTGGAG GGAGGGC

GT
GAM7957 297 DKFZP56 1 2876 XP_166254.2 3 2171 TGCTGTGGGAGG - G AC - 3 C c c
4O0423 CATGAGCTGGAG TCA CT CA CTC TGCCTCCCG
ATGGGGGC GGT GA GT GAG ACGGAGGGT
A G C- T
GAM7957 297 DKFZp56 2 7863 NP_060005.1 3 304 AAACCCAGGAGG TG C 3 C c b
6H0824 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 DKFZp56 2 8019 NP_060005.1 5 39 GAACCCGGGAAG C C 3 C b b
6H0824 CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A
GAM7957 297 DKFZP56 1 1200 NP_112485.1 3 324 GAACCCGGGAGG C C 3 C b b
6J2046 CGGAGCTTACAG TCACTG AA CTCTGCCTCCCG
TGAGCTGA AGTGAC TT GAGGCGGAGGGC
A C
GAM7957 297 DKFZP56 1 12521 NP_056420.1 5 17 CTGGCGAGGCTG A T--- - 3 C c c
6K0524 CTGGGGTTGCAG TC CTGCAACCTC GCCTC CCG
CGGGACAG GG GACGTTGGGG CGGAG GGT
C TCGT C
GAM7957 297 DKFZp58 1 19501 XP_098416.1 3 4289 TAACCCGGAAGG C TG C 3 C c c
6C0721 TGGAGTTTGCAG TCACTGCAA CTC CCT CCG
TGAGCCGA AGTGACGTT GAG GGA GGC
T GT A
GAM7957 297 DKFZP58 1 6014 XP_045876.1 3 738 GAACCTGGAAGG C 3 C b b
6C1324 CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCAGA AGTGACGTTGGAGGCGGA GGT
A
GAM7957 297 DKFZP58 1 5614 NP_112584.1 3 435 GAGACTAGGAGT A TGC C 3 C c c
6M1120 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAACTAA AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 DKFZp72 1 9974 NP_689481.1 5 38 TCTTGCGGGAGG T ------ C 3 C c c
7A071 CGTGGGCTGGGA CACTGCAA CCT TGCCTCCCG
TTGCGGTG GTGGCGTT GGG GCGGAGGGC
- AGGGTC T
GAM7957 297 DKFZP72 1 7653 XP_038689.1 5 681 TCTCTGGGGAGG T AA -- 3 C c c
7C091 CAGTAAGGGGCC TCAC GC CCT CTGCCTCCC
GTGGAGCT GGTG CG GGA GACGGAGGG
C G- AT
GAM7957 297 DKFZp72 1 1693 NP_659802.1 3 247 AAACCAGGAAGG C C 3 C b b

7G131 CAGAGATTGCAG TCACTGCAA CTCTGCCT CC
TGAGCTGA AGTGACGTT GAGACGGA GG
A A
GAM7957 297 DKFZp76 1 5957 XP_054098.4 3 491 CGGGCCTCTGGG C A ----- 3 C c c
1A052 CAGAGGATGCAA TCA TGCA CCTCTGCCT CCCG
TGGCACGG GGT ACGT GGAGACGGG GGGC
A A TCTCC
GAM7957 297 DKFZp76 1 920 NP_689874.1 3 1521 TGTGCAGGGTGG A ----- T 3 C c c
1G0122 CAGAGGTGCCTC TC CTGCA ACCTCTGCC CCC
TGCAGAGA AG GACGT TGGAGACGG GGG
A CTCCG T
GAM7957 297 DKFZp76 1 10014 XP_046017.3 3 407 CGACCCGGGAGG - G- CT- 3 C c c
1G2113 CTGTGGGTTGGA TCA CT CAACCT GCCTCCCG
AGCTGAGC AGT GA GTTGGG CGGAGGGC
C AG TGT
GAM7957 297 DKFZp76 2 13155 NP_775102.1 3 412 CTACTCGGGAGG A AAC T 3 C c c
1H0421 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DKFZp76 2 15340 NP_775102.1 3 446 GAACCCAGGAGG C C 3 C c c
1H0421 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCAA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 DKFZp76 1 17403 XP_166582.2 3 856 GAACCCAGGAGG C 3 C b b
1I2123 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 DKFZp76 1 9330 NP_115656.1 5 792 GAGCCCTGGCGG T C 3 C b b
1J139 CAGAGGTTGCAG TCACTGCAACCTCTGCC CC
TGAGCCAA AGTGACGTTGGAGACGG GG
C T
GAM7957 297 DKFZp76 2 6861 NP_690877.1 3 1120 GAACCCGGGAGG C 3 C b b
1L1417 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCCA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 DKFZp76 2 11920 NP_690877.1 3 1086 CTACTCGGGAGG A AAC T 3 C c b
1L1417 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGC AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DKFZp76 1 19710 XP_294685.2 5 53 GAACCCGGGAGG C 3 C b b
1L1518 CGGATGTTGCGG TCACTGCAAC TCTGCCTCCCG
TGAGCCGA AGTGGCGTTG AGGCGGAGGGC

T
GAM7957 297 DKFZp76 1 2921 NP_689624.1 3 730 AGCCCAGGGAGG A CT 3 C c
c
2I137 TCAAGGCTGCAG TCACTGCA CCT GCCTCCC
TGAGCAAT AGTGACGT GGA TGGAGGG
C AC
GAM7957 297 DKFZp76 1 8890 XP_290525.1 5 288 GGCGGCGGGAGG A AA 3 C c
c
2N1910 CGGAGGAGGCGG TC CTGC CCTCTGCCTCCCG
CGGCGGCG GG GGCG GGAGGCGGAGGGC
C GA
GAM7957 297 DMC1 1 6684 NP_008999.2 3 888 GAACCCAGGAGG C C 3 C c c
CAGAGATTGCGG TCACTGCAA CTCTGCCTCC
TGAGCCAA AGTGGCGTT GAGACGGAGG
A A
GAM7957 297 DNAM-1 1 14329 NP_006557.1 5 49 GAGGGAGCAGCG C-- -- 3 C c c
GGGAGCTTGCAG TCACTGCAA CTCTGC CTCCC
TGACCAAG AGTGACGTT GGGGCG GAGGG
CGA AC
GAM7957 297 DNASE2 2 12684 NP_001366.1 3 494 CTCCTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DNASE2 2 17444 NP_001366.1 3 528 GAACTCGGGAGG CT 3 C b
b
CAGAGGTTGTCA TCA GCAACCTCTGCCTCCCG
TGAGCTGA AGT TGTTGGAGACGGAGGGC
AC
GAM7957 297 DNCL2A 1 9496 NP_054902.1 5 54 GGTCGGAAATGG A G A TC-- 3 C c
c
CAGAGGTGGAGG TC CT CA CCTCTGCC CCG
AGACACTG AG GA GT GGAGACGG GGC
- G - TAAA
GAM7957 297 DNCL2A 1 9496 NP_808853.1 5 54 GGTCGGAAATGG A G A TC-- 3 C c
c
CAGAGGTGGAGG TC CT CA CCTCTGCC CCG
AGACACTG AG GA GT GGAGACGG GGC
- G - TAAA
GAM7957 297 DNCL2B 1 908 NP_570967.1 5 114 CCTCCGCGATGG A G A - C 3 C c
c
CAGAGGTGGAGG TC CT CA CCTCTGCC TC CG
AAACCTTA AG GA GT GGAGACGG AG GC
- G - T C
GAM7957 297 DPP9 2 5830 NP_631898.1 3 688 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 DPP9 2 9761 NP_631898.1 3 722 GAACCCGGGAGG TG 3 C b b

TGGAGGTTGCGG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGGCGTTGGAG GGAGGGC
GT

GAM7957 297 DRF1 2 11050 NP_079380.1 3 490 GAACCTGAGAGG TG CC 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTC
TGAGCCGA AGTGACGTTGGAG GGAG
GT AG

GAM7957 297 DRF1 2 19029 NP_079380.1 3 1753 GAACCCAGGAGG TC----- C 3 C c c

CAGAGGTTGCAG ACTGCAACCTCTGCCTCC
TCAGCCAA TGACGTTGGAGACGGAGG
AACCGAC A

GAM7957 297 DRIM 1 18872 NP_055318.1 3 144 TCTGTCACCCAA AC CCC 3 C c c

GGCGGAGTGCAG TCACTGCA CTCTGCCT
TGACGACA AGTGACGT GAGGCGGA
-- ACC

GAM7957 297 DSC1 1 1568 NP_004939.1 3 1418 GAATCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 DSC1 1 1568 NP_077739.1 3 1210 GAATCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 DSC2 1 19615 NP_004940.1 3 125 GGCTGGGTCTGT C- CT- 3 C c c
AGGTTGTTGCAG TCACTGCAAC TCTGC CCCG
TGAACGAC AGTGACGTTG GGATG GGGT
TT TCT

GAM7957 297 DSCR6 1 13664 NP_061835.1 3 1004 GAACCCGGGAGG T 3 C b b
CGGAGGTTGCCG TCAC GCAACCTCTGCCTCCCG
TGAGTCGA AGTG CGTTGGAGGCGGAGGGC
C

GAM7957 297 DTNB 1 2938 NP_068707.1 3 8 GAATGGGAAAGA A- C C -- 3 C c c
CAGAGGTTACAG TC CTG AACCTCTG C TCCCG
AGGAGCCG AG GAC TTGGAGAC G AGGGT
GA A A AA

GAM7957 297 DTNB 1 2938 NP_149160.1 3 8 GAATGGGAAAGA A- C C -- 3 C c c
CAGAGGTTACAG TC CTG AACCTCTG C TCCCG
AGGAGCCG AG GAC TTGGAGAC G AGGGT
GA A A AA

GAM7957 297 DVL3 1 7466 NP_004414.2 3 1929 CCAGGAAGCAAG --- C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGC CT CC
TGAGTTGA AGTGACGTTGGAGGCG GA GG
AAC A

GAM7957 297 EDG3 2 6041 NP_005217.1 5 2512 GAACCCAGGAGG C T C 3 C c b

CAGTGGTTGCAA TCA TGCAACC CTGCCTCC
TGAGCCGA AGT ACGTTGG GACGGAGG

A T A
GAM7957 297 EDG3 2 19288 NP_005217.1 3 2009 AAACCCGGGAGG C 3 C b b
CGGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGACGTT GAGGCGGAGGGC
A
GAM7957 297 EGFL4 1 15055 XP_290821.1 3 2106 GAACCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTCA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 EGFL5 1 4534 XP_098838.1 3 1486 GAACCTGGGAGG C 3 C b b
CAGAGGTTACAG TCACTG AACCTCTGCCTCCCG
TGAGCCGA AGTGAC TTGGAGACGGAGGGT
A
GAM7957 297 EHD1 1 15638 NP_006786.2 3 192 TGGCGGGGGAGG - GCA- 3 C c
c
CAGGGGTGAGAG TCA CT ACCTCTGCCTCCC
GATGGAAT GGT GG TGGGGACGGAGGG
A AGAG
GAM7957 297 EIF1A 1 13049 NP_001403.1 3 454 ATTTGAGGGAGG - - C 3 C b b
CAGAAGTCTGCA TCA CTGCA AC TCTGCCTCCC
GTTGAAGA AGT GACGT TG AGACGGAGGG
T C A
GAM7957 297 EIF2AK4 1 11505 XP_031612.6 3 330 AGCCTCAGGAGG A T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCTGT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 EIF3S2 1 17403 NP_003748.1 3 243 GAACCCAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 ELAVL2 1 6187 NP_004423.1 5 72 AGTTGAAGGAGG TG ----- C 3 C c c
CAGAGAAGGGGT TCAC CAACC TCTGCCTCC
TGGTGATA AGTG GTTGG AGACGGAGG
-- GGAAG A
GAM7957 297 EP300 1 14306 NP_001420.1 5 808 GCGCCGAGGAGG A ---- G - 3 C c c
AAGAGGTTGATG TC CTGC AACCTCT CCTCC CG
GCGGCGGC GG GGCG TTGGAGA GGAGG GC
C GTAG A A
GAM7957 297 EPHB1 1 3606 NP_004432.1 3 74 GTCAAGGGGGAC TG---- C- 3 C c c
CAGAGGTTGACC TCAC CAACCTCTG CTCCC
ACTGTGGA GGTG GTTGGAGAC GGGGG
TCACCA CA
GAM7957 297 ERAP140 2 12831 XP_059748.2 3 1533 GAATCCGGGAAG C 3 C b b
CAGAGGTTGTAG TCACTGCAACCTCTGC TCCCG
TGAGCCAA AGTGATGTTGGAGACG AGGGC
A

GAM7957 297 ERAP140 2 15089 XP_059748.2 3 1499 CTACTCGGGAGG A AAC T 3 C c b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 ET 1 11097 NP_077287.1 3 849 GAGCCTGGGAGG 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 EXO70 1 6447 NP_056034.1 3 1793 AACTGGGGGAGG A CAAC 3 C c c

CAGGGCACAGGG TC CTG CTCTGCCTCCC
AGATGCTC AG GAC GGGACGGAGGG
G AC--

GAM7957 297 F2RL3 4 4424 NP_003941.1 3 1217 TGGCGGCAGAGG GCAAC -- 3 C c b

CAGAGATGGGAG TCACT CTCTGCCTC CCG
TGATGCGG AGTGA GAGACGGAG GGC
GGGTA AC

GAM7957 297 F2RL3 4 10569 NP_003941.1 3 1084 GAACCTGGGAGG TC----- 3 C c b

CGGAGGTTGCGG ACTGCAACCTCTGCCTCCCG
TCAGCTGA TGGCGTTGGAGGCGGAGGGT
AGTCGAC

GAM7957 297 F2RL3 4 13066 NP_003941.1 3 415 GAACCTGGGAGG 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 F2RL3 4 18740 NP_003941.1 3 749 GAGCCTGGGAGG TCT 3 C c b

TTGTGGTTGCAG TCACTGCAACC GCCTCCCG
TGAGCTAT AGTGACGTTGG TGGAGGGT
TGT

GAM7957 297 FADS1 1 10611 NP_037534.2 3 460 GAACCGGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCC
TGAGCTGA AGTGACGTTGGAG GGAGGG
GT

GAM7957 297 FADS2 1 7605 NP_004256.1 5 71 CCGGCTGGGAGG A --- CT 3 C c c

CAGCCGTCTGTG TC CTGCA AC CTGCCTCCCG
CAGCGAGC AG GACGT TG GACGGAGGGT
C GTC CC

GAM7957 297 FANCC 1 16815 NP_000127.1 3 2339 GCCGCAGGGAGG ---- AAC 3 C c c

CAGGGATGGCAA TCAC TGC CTCTGCCTCCC
GGCGTGAA AGTG ACG GGGACGGAGGG
CGGA GTA

GAM7957 297 FBLP-1 2 13065 XP_290943.1 3 921 GAACCCGGGAGG 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 FBLP-1 2 15697 NP_060026.1 3 621 CAATCTGGAAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGATTG AGTGACGTTGGAGACGGA GGT
A
GAM7957 297 FBLP-1 2 15697 XP_290943.1 3 621 CAATCTGGAAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGATTG AGTGACGTTGGAGACGGA GGT
A
GAM7957 297 FBXO13 1 5802 XP_098421.2 3 725 GAGCTCAAGAGG T CC 3 C c c
CCGAGGTTGCAG TCACTGCAACCTC GCCTC
TGAGCCGT AGTGACGTTGGAG CGGAG
C AA
GAM7957 297 FBXO26 1 6268 NP_079183.4 3 276 GAGACCAGGAGG A T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCCGT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 FBXO26 1 6268 NP_680474.1 3 276 GAGACCAGGAGG A T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCCGT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 FBXO27 2 15089 NP_849142.1 3 784 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FBXO27 2 15089 XP_059045.1 3 784 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FBXO27 2 19101 NP_849142.1 3 818 GAGCCCGGGAGG A 3 C b b
CAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAACCAA AGTGACGT GGAGACGGAGGGC
C
GAM7957 297 FBXO27 2 19101 XP_059045.1 3 818 GAGCCCGGGAGG A 3 C b b
CAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAACCAA AGTGACGT GGAGACGGAGGGC
C
GAM7957 297 FBXO6 1 14305 NP_060908.1 3 400 GAACCCGGAAGG C C 3 C b b
CAGAGCTTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCCGA AGTGACGTT GAGACGGA GGC
C A
GAM7957 297 FBXO9 1 7864 NP_258441.1 3 1510 GAGCCTGGGAAG C TG C 3 C c
c

TGGAAGTTGCAG TCACTGCAAC TC C TCCCG
TGAGCCAA AGTGACGTTG AG G AGGGT
A GT A

GAM7957 297 FCAR 1 9833 NP_579813.1 3 650 GAACCCAGGAGG CT C 3 C c c
CAGCTGTTGCAG TCACTGCAAC CTGCCTCC
TGAGCCAA AGTGACGTTG GACGGAGG
TC A

GAM7957 297 FCAR 1 9833 NP_579814.1 3 317 GAACCCAGGAGG CT C 3 C c c
CAGCTGTTGCAG TCACTGCAAC CTGCCTCC
TGAGCCAA AGTGACGTTG GACGGAGG
TC A

GAM7957 297 FCMD 1 1356 NP_006722.1 3 5236 GAACCCGGGAAG AC C 3 C b
b
CAGAGTCTGCAG TCACTGCA CTCTGC TCCCG
TGAGCCAA AGTGACGT GAGACG AGGGC
CT A

GAM7957 297 FCN2 1 12186 NP_056653.1 3 63 GGGGGAGGCTGG T------ G ---- 3 C c c
GAGAGGTTGGGT CACT CAACCTCT GCCTCCC
GCTCTCCT GTGG GTTGGAGA CGGAGGG
TCCTCTC - GGGT

GAM7957 297 FCN2 1 12186 NP_056654.1 3 769 GGGGGAGGCTGG T------ G ---- 3 C c
c
GAGAGGTTGGGT CACT CAACCTCT GCCTCCC
GCTCTCCT GTGG GTTGGAGA CGGAGGG
TCCTCTC - GGGT

GAM7957 297 FGF2 1 15312 NP_001997.3 3 2138 GAGGCTGAGAGG CT ---- 3 C c c
TCAAGGTTGCAG TCACTGCAACCT GCCTC CC
TGAGCCAT AGTGACGTTGGA TGGAG GG
AC AGTC

GAM7957 297 FGFR1 1 16118 NP_075595.1 3 876 GAACCCAGAAGG CCC 3 C c c
CAGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGACGTTGGAGACGGA
AGA

GAM7957 297 FGFR1 1 16118 NP_075596.1 3 876 GAACCCAGAAGG CCC 3 C c c
CAGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGACGTTGGAGACGGA
AGA

GAM7957 297 FGFR2 1 5528 NP_075262.1 3 232 TACTCCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AGTCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 FGFR2 1 5528 NP_075263.1 3 232 TACTCCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AGTCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 FGFRL1 1 19614 NP_068742.1 3 1353 GATGGAAGGAAG A --- G C 3 C c c

ACTGGGTTGCAG TC CTGCAACC TCT CCT CCG
GGACTGTG AG GACGTTGG AGA GGA GGT
G GTC A A

GAM7957 297 FKBP14 2 6269 NP_060416.1 3 1381 CTACTCGGGAGG A CAAC T 3 C c b

CTGAGACAGGAG TC CTG CTC GCCTCCCG
ATTTGCTT AG GAC GAG CGGAGGGC
- A--- T

GAM7957 297 FKBP14 2 19054 NP_060416.1 3 1415 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 FKSG17 1 9322 NP_114420.1 3 459 GAATCCAGAAGG CCC 3 C c c

CGGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGACGTTGGAGGCGGA
AGA

GAM7957 297 FLJ0006 1 11462 XP_028154.1 3 1963 GAACCCAGGAGG C C 3 C b b
0 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
C A

GAM7957 297 FLJ0022 1 8941 XP_084552.3 3 1029 TTGGAGAGGAGG AACCT C 3 C c c
5 CAGCCAGCAGTG TCACTGC CTGCCTCC
GCAGTCCA GGTGACG GACGGAGG
ACC-- A

GAM7957 297 FLJ1005 1 6015 NP_060455.1 3 1734 GAACCCAGGAGG - TG C 3 C c c
8 TGGAGGTTGCAA TCACT GCAACCTC CCTCC
GTGAGCTG AGTGA CGTTGGAG GGAGG
A GT A

GAM7957 297 FLJ1012 1 5141 NP_060471.1 3 919 GAGGTGGGAAGG A CAAC - 3 C c c
0 CAGAGCATCAGG TC CTG CTCTGCCT CCCG
AGGGAACA AG GAC GAGACGGA GGGT
- TAC- A

GAM7957 297 FLJ1013 1 17277 NP_060475.1 3 1294 GAACCTGGGTGG A T T 3 C c c
9 TCGAGGCTGCAG TCACTGCA CCTC GCC CCCG
TGAGCCGA AGTGACGT GGAG TGG GGGT
C C T

GAM7957 297 FLJ1024 1 11741 NP_060507.1 3 740 GAACACAGGAGG C 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 FLJ1030 1 2126 NP_060521.2 5 1196 GAGGCCGGGAGG TGCAA T 3 C c c

0 CGAGGAAACCGT TCAC CCTC GCCTCCCG
GGAAATTG GGTG GGAG CGGAGGGC
CCAAA -
GAM7957 297 FLJ1035 1 5754 NP_060541.2 5 246 CGGGTCGGGAGG C A TCT--- 3 C c
c
7 CTGTGCTGGCTG TCA TGCA CC GCCTCCCG
CACTGGCC GGT ACGT GG CGGAGGGC
C C TCGTGT
GAM7957 297 FLJ1046 1 3325 NP_060567.1 3 975 GAACCCAGGAGG TC----- C 3 C c
c
0 CAGAGGTTGCAG ACTGCAACCTCTGCCTCC
TAAGCCAA TGACGTTGGAGACGGAGG
AACCGAA A
GAM7957 297 FLJ1052 1 2838 NP_060594.2 3 2164 AACCCTGGGAGG 3 C b b
0 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGTCGA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 FLJ1053 1 6240 NP_060598.2 3 1361 GAACTTGGGAGG - G 3 C b b
4 GGTAGGTTGCAG TCACTGCAACCT CT CCTCCCG
TGAGCTGA AGTGACGTTGGA GG GGAGGGT
T -
GAM7957 297 FLJ1054 1 18846 NP_060604.1 3 435 TTACTCGGGAGG A CAAC T 3 C c
c
7 CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCGCTT AG GAC GAG CGGAGGGC
- A--- T
GAM7957 297 FLJ1078 1 909 NP_060685.1 3 1077 GAATCCAGGAGG C C 3 C b b
1 CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCAA AGT ACGTTGGAGACGGAGG
A A
GAM7957 297 FLJ1080 1 15983 NP_060694.1 3 2247 GAACCCGGGAGG TG 3 C b
b
3 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 FLJ1082 1 19057 NP_060703.1 3 875 GAACCCAGGAGG C 3 C b b
6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 FLJ1093 1 15224 NP_060747.1 3 1272 GAACCTGGGAGG TG 3 C b
b
2 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 FLJ1093 2 1291 NP_060749.2 5 19 GGCGCCGGGAGG CT- -- C 3 C c c
6 CGCGGGCTTTGC TCA GCAA CCT TGCCTCCCG
TCCTGGGG GGT CGTT GGG GCGGAGGGC
CCT TC C
GAM7957 297 FLJ1093 2 16966 NP_060749.2 3 1651 GAACCTGGGATG TG C 3 C c
c

6 TGGAGGTTGCAG TCACTGCAACCTC C TCCCG
TGAGCCAA AGTGACGTTGGAG G AGGGT
GT T
GAM7957 297 FLJ1102 3 8904 NP_060774.1 3 1134 GCATCCTGGAGG CT C 3 C c b

9 TGAAGGTTGCAG TCACTGCAACCT GCCTCC
TGAGCCAA AGTGACGTTGGA TGGAGG
AG T
GAM7957 297 FLJ1102 3 17631 NP_060774.1 3 825 GGGCCCCGGAGG C 3 C b b
9 TAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGATGGAGG
C
GAM7957 297 FLJ1102 3 18691 NP_060774.1 3 260 GAACCTGGGAGG 3 C b b
9 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 FLJ1103 1 7218 NP_060776.2 3 799 GAGCCCAGGAGT A T C- C 3 C c
c
6 TCAGGGCTGCAG TCACTGCA CC CTG CTCC
TGAGGTAC AGTGACGT GG GAC GAGG
C - TT A
GAM7957 297 FLJ1104 1 19379 NP_060778.1 3 313 GAGCCCTGGAGT GC C 3 C c
c
2 TGGAGGTTGCAG TCACTGCAACCTCT CTCC
TGAGCAGA AGTGACGTTGGAGG GAGG
TT T
GAM7957 297 FLJ1110 2 4880 NP_060794.1 3 344 CTACTCGGGAGG A AAC T 3 C c
c
6 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1110 2 10375 NP_060794.1 3 378 GAACCTGGGAGG C TG 3 C c
c
6 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAACCGA AGTGACGTT GAG GGAGGGT
C GT
GAM7957 297 FLJ1112 1 11721 NP_060802.1 3 1165 CTACTCGGGAGG A GCA T 3 C c
c
6 CTGAGGTAGGAG TC CT ACCTC GCCTCCCG
GATCGCTT AG GA TGGAG CGGAGGGC
- GGA T
GAM7957 297 FLJ1115 2 3794 NP_060810.1 3 1721 CTACTCGGGAGG A AAC T 3 C c
b
1 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
ATCGCTGG AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1115 2 12335 NP_060810.1 3 1754 GAACTCAGGAGG C 3 C b b
1 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 FLJ1125 1 18025 NP_060840.1 3 1783 GAGCCCAGGAGG A TG C 3 C c c
9 TGGAGGCTGCAG TCACTGCA CCTC CCTCC
TGAGCCAT AGTGACGT GGAG GGAGG
C GT A
GAM7957 297 FLJ1130 2 1492 NP_060855.1 3 350 CTACTCGGGAGG A AAC T 3 C c b
1 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1130 2 5229 NP_060855.1 3 384 GAACCAGGGAGG C 3 C b b
1 CAGAGTTTGCAG TCACTGCAA CTCTGCCTCCC
TGAATGGA AGTGACGTT GAGACGGAGGG
T
GAM7957 297 FLJ1137 1 1492 NP_079237.1 3 1404 CTACTCGGGAGG A AAC T 3 C c c
0 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1157 1 4977 NP_079435.1 3 572 GAACCTGAGAGG CC 3 C b b
7 CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGACGTTGGAGACGGAG
AG
GAM7957 297 FLJ1170 1 8533 NP_079168.1 3 995 AAACCCGGGAAG TG C 3 C c c
0 TGGAGGTTGCAG TCACTGCAACCTC C TCCCG
TGAGCCAA AGTGACGTTGGAG G AGGGC
GT A
GAM7957 297 FLJ1171 1 12055 NP_079122.1 5 201 GGGCCAGGGAGG A T 3 C b b
0 TTGAGGCTGCAG TCACTGCA CCTC GCCTCCC
TGAGCTAT AGTGACGT GGAG TGGAGGG
C T
GAM7957 297 FLJ1171 1 16495 NP_078840.1 3 1555 TTAGCCTGGAGG A CT C 3 C c c
5 TCAAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCCAT AGTGACGT GGA TGGAGG
C AC T
GAM7957 297 FLJ1172 1 8840 NP_079246.1 3 1701 AGGCAGGAGAAT C-- C 3 C c c
2 CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAACCGA AGTGACGTTGGAGAC GAGG
TAA A
GAM7957 297 FLJ1180 1 10310 NP_079250.1 3 1674 GGGCCTGGGAGG A T 3 C c c
0 TCGAGGCTGCAG TCACTGCA CCTC GCCTCCCG
TGAGCTGT AGTGACGT GGAG TGGAGGGT
C C
GAM7957 297 FLJ1199 2 3322 NP_079252.1 3 2323 GGACCCGGGAGG 3 C b b
6 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 FLJ1199 2 12331 NP_079252.1 3 1270 CGGAGGCGGAGG C 3 C b b

6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
C

GAM7957 297 FLJ1205 2 5828 NP_079209.1 3 919 CTATTCGGGAGG A AAC T 3 C c
c

6 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 FLJ1205 2 12398 NP_079209.1 3 953 GAACCCAGGAGA GC C 3 C c
c

6 TGGAGGTTGCGG TCACTGCAACCTCT CTCC
TGAGCTGA AGTGGCGTTGGAGG GAGG
TA A

GAM7957 297 FLJ1207 2 8723 NP_079253.1 5 443 CTACTCGGGAGG - GCA- T 3 C c
b

8 CTGAGGTGGAAA TCA CT ACCTC GCCTCCCG
GATGGCCC GGT GA TGGAG CGGAGGGC
A AAGG T

GAM7957 297 FLJ1207 2 13066 NP_079253.1 3 2222 GAACCTGGGAGG 3 C b b

8 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 FLJ1219 1 10438 NP_079347.1 3 1591 GAACCCGGGAGG 3 C b b

0 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 FLJ1229 1 6415 NP_115540.1 3 202 GAACCCAGGAGG C C 3 C c c

8 CGGAAGTTGCAG TCACTGCAAC TCTGCCTCC
TGAGCTGA AGTGACGTTG AGGCGGAGG
A A

GAM7957 297 FLJ1230 2 16879 NP_115541.1 3 985 GAACCCGGGAGG CC 3 C b b

3 CAGACCTTGCAG TCACTGCAA TCTGCCTCCCG
TGAGCCAA AGTGACGTT AGACGGAGGGC
CC

GAM7957 297 FLJ1230 2 16943 NP_115541.1 3 951 CTACCCGGGAGG A AAC T 3 C c
b

3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 FLJ1233 1 10982 NP_079262.1 3 1402 GAACCCGGGAGG TC----- C 3 C c
c

1 CAAAGGTTGCGG ACTGCAACCT TGCCTCCCG
TAAGCTGC TGGCGTTGGA ACGGAGGGC
CGTCGAA A

GAM7957 297 FLJ1244 1 13668 NP_075046.1 3 1056 GAACCCAGGAGG C C 3 C c c

8 TGCAGGTTGCAG TCACTGCAACCT TGCCTCC

TGAGCCGA AGTGACGTTGGA GTGGAGG
C A
GAM7957 297 FLJ1248 1 2963 NP_073604.2 3 110 TGGGCAGGGTGG ACC - 3 C c c
4 GGCAGGATGCAG TCACTGCA TCTGCCTC CC
TGAGCCAG AGTGACGT GGACGGGG GG
A-- T
GAM7957 297 FLJ1258 1 1908 NP_078896.2 3 1155 GAGCCTGGGAGG TG 3 C b b
6 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 FLJ1260 1 5039 NP_079080.1 3 319 GAACCCGGGAGG CC 3 C b b
6 CGGAACTTGCGG TCACTGCAA TCTGCCTCCCG
TGAGCCGA AGTGGCGTT AGGCGGAGGGC
CA
GAM7957 297 FLJ1261 1 17753 NP_079160.1 3 540 GAGCCCAGGAGG A CT C 3 C c
c
8 TCTAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCTTA AGTGACGT GGA TGGAGG
C TC A
GAM7957 297 FLJ1266 2 7966 NP_079428.1 3 1037 CTACTCGGGAGG A AAC T 3 C c
b
0 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCATTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1266 2 8107 NP_079428.1 3 1071 CAACCCGGGAGG T 3 C b b
0 CTGAGGTTGCAG TCACTGCAACCTC GCCTCCCG
TGAGTGGA AGTGACGTTGGAG CGGAGGGC
T
GAM7957 297 FLJ1266 1 19695 NP_078871.1 3 1201 GAACCCTGGAGG T TG C 3 C c
c
6 TGGCGGTTGCAG TCACTGCAACC C CCTCC
TGAGCACA AGTGACGTTGG G GGAGG
C GT T
GAM7957 297 FLJ1267 1 14567 NP_112242.1 3 674 GAGCCCAGGAGG C C 3 C c c
1 CGGAGATTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
A A
GAM7957 297 FLJ1268 2 6150 NP_079193.2 3 970 GGACCTGGGAGG TG 3 C b b
7 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 FLJ1268 2 13584 NP_079193.2 3 938 CTACTCGGGAGG A AAC T 3 C c
b
7 CTGAGGCAGGAT TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1280 1 1400 NP_075054.1 3 1662 GAACCTGGGAAG C C 3 C b b

0 CAGAGTTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCAA AGTGACGTT GAGACG AGGGT
T A
GAM7957 297 FLJ1292 2 15108 NP_079151.1 3 791 CTACTCGGGAGG A AAC T 3 C c c
1 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1292 2 15316 NP_079151.1 3 825 GAACCTGGAAGG C C 3 C c c
1 CGGAGCTTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCTGA AGTGACGTT GAGGCGGA GGT
C A
GAM7957 297 FLJ1298 1 6600 XP_290685.1 3 767 GAAGATGGGAAG C C C 3 C c c
6 CACAGATTGCAG TCACTGCAA CT TGC TCCCG
TGAACCGA AGTGACGTT GA ACG AGGGT
A C A
GAM7957 297 FLJ1315 1 13134 NP_078874.1 5 30 TCCGGGTGCCGG - T T--- 3 C c c
4 TTGAGGTTGCTG TCACT GCAACCTC GCC CCCG
GTGGGCCT GGTGG CGTTGGAG TGG GGGC
T T CCGT
GAM7957 297 FLJ1316 1 19052 NP_079278.1 3 1490 GAACCCAGGAGG C 3 C b b
2 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGGCGTTGGAGGCGGAGG
A
GAM7957 297 FLJ1317 1 9763 NP_076412.1 3 927 GAACCCAGGAGG TG C 3 C c c
1 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 FLJ1323 1 6757 NP_079178.2 3 345 GAACCTGAGAGG CC 3 C c c
6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGACGTTGGAGGCGGAG
AG
GAM7957 297 FLJ1324 1 9173 NP_079364.1 3 1866 GAGTCTGGGAGG A TG 3 C c
c
1 TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAGCCGT AGTGACGT GGAG GGAGGGT
C GT
GAM7957 297 FLJ1330 2 7048 XP_291019.1 3 747 GAACCCAGGAGG C C 3 C b b
5 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 FLJ1330 2 8647 XP_291019.1 3 713 CTACTTGGGAGG A AAC 3 C b b
5 CAGAGGCAGGAG TC CTGC CTCTGCCTCCCG
AATGGCAT AG GACG GAGACGGAGGGT
- ---
GAM7957 297 FLJ1344 1 17453 NP_079423.1 3 709 GAACCCGGGAGG TC----- 3 C c c
8 CGGAGGTTGCAG ACTGCAACCTCTGCCTCCCG

TTAGCCAA TGACGTTGGAGGCGGAGGGC
AACCGAT
GAM7957 297 FLJ1345 1 8296 XP_038291.5 3 2455 GAACCCAGGAAG TG C C 3 C c
c
6 TGGAGGTTGCAG TCACTGCAACCTC C TCC
TGAGCTAA AGTGACGTTGGAG G AGG
GT A A
GAM7957 297 FLJ1354 1 16514 NP_079284.1 3 388 AAAGCCGGGAGG A CAA - - 3 C c
c
4 CAAGTAGGACAG TC CTG CCT CT GCCTCCCG
AGAGATGA AG GAC GGA GA CGGAGGGC
A A-- T A
GAM7957 297 FLJ1361 1 12723 NP_079217.1 3 527 GAACCGGGGAGG TC----- 3 C c
c
1 CAGAGGTTGCAG ACTGCAACCTCTGCCTCCC
TTAAGCCG TGACGTTGGAGACGGAGGG
GCCGAAT
GAM7957 297 FLJ1362 1 15343 NP_079285.1 3 1056 GAACCCGGGAGG C 3 C b b
1 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 FLJ1376 2 15089 NP_079288.1 3 4482 CTACTCGGGAGG A AAC T 3 C c
b
9 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ1376 2 19422 NP_079288.1 3 4516 GAGCCTGGGAGG - TG 3 C b
b
9 TGGAGGTTGCCA TCACTG CAACCTC CCTCCCG
GTGAGTCG AGTGAC GTTGGAG GGAGGGT
C GT
GAM7957 297 FLJ1398 1 7450 NP_079046.1 3 1109 GAGCCTCGGAGG C 3 C b b
4 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
C
GAM7957 297 FLJ1406 1 19033 NP_079299.1 3 733 GAACCCAGGAGG C C 3 C b b
9 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCAA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 FLJ1410 2 4061 NP_079301.1 3 955 GAACCTGGGAGG C TG 3 C c c
0 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCGA AGTGACGTT GAG GGAGGGT
C GT
GAM7957 297 FLJ1410 2 4880 NP_079301.1 3 921 CTACTCGGGAGG A AAC T 3 C c
c
0 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGT AG GACG GAG CGGAGGGC

```
                                        -   ---  T
GAM7957  297    FLJ1411 3  4313  NP_073614.1  3  907   GAGCCTGGGAGG                  3  C  b  b
         7                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCCAA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297    FLJ1411 3  7796  NP_073614.1  3  1723  GAACCCGCGAGG      AC      C       3  C  c
b
         7                          CGGAGACTGCAG TCACTGCA  CTCTGCCTC CG
                                    TGAGCCGA    AGTGACGT  GAGGCGGAG GC
                                              CA       C
GAM7957  297    FLJ1411 3  10125 NP_073614.1  3  1207  GAGCCTGGGAGG   C   C           3  C  b
b
         7                          CAGAGATTGCAC TCA TGCAA CTCTGCCTCCCG
                                    TGAGCCGA    AGT ACGTT GAGACGGAGGGT
                                         C    A
GAM7957  297    FLJ1412 1  10918 NP_112157.1  3  797   GAACCTGGGAGG                  3  C  b  b
         9                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCGGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297    FLJ1432 2  13517 NP_079188.1  3  4825  CACTTCGGGAGG    GCAA   T         3  C  c
 b
         7                          CCGAGGCAGGTG TCACT   CCTC GCCTCCCG
                                    GAACACTT    GGTGG   GGAG CGGAGGGC
                                         AC--   C
GAM7957  297    FLJ1432 2  17423 NP_079188.1  3  4992  GAACCTGGGAGG         TG         3  C  b
b
         7                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                    TGAGCCGA    AGTGACGTTGGAG  GGAGGGT
                                                GT
GAM7957  297    FLJ1434 2  1492  NP_079009.1  3  211   CTACTCGGGAGG  A   AAC  T         3  C  c
b
         5                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATCACTT    AG GACG   GAG CGGAGGGC
                                        -   ---  T
GAM7957  297    FLJ1434 2  14502 NP_079009.1  3  245   GAACCTGGGAGG                  3  C  b  b
         5                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCGAG    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297    FLJ1439 2  4880  NP_116168.2  3  358   CTACTCGGGAGG  A   AAC  T         3  C  c
b
         7                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATGGTGT    AG GACG   GAG CGGAGGGC
                                        -   ---  T
GAM7957  297    FLJ1439 2  15345 NP_116168.2  3  392   GAACCTGGGAGG       C          3  C  b  b
         7                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                    TGAGCTGA    AGTGACGTT GAGGCGGAGGGT
                                              C
GAM7957  297    FLJ1445 1  18269 NP_116177.1  3  1573  GAATCGGGGAGG TC-----     C         3  C  c
c
         7                          CAGAGCTTGCAG       ACTGCAA CTCTGCCTCCC
```

TCAGCCGA TGACGTT GAGACGGAGGG
AGCCGAC C

GAM7957 297 FLJ1446 3 5830 NP_116179.1 3 947 CTACTCGGGAGG A AAC T 3 C c b
6 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 FLJ1446 3 14789 NP_116179.1 3 981 GAACCCAGGAGG C 3 C b b
6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 FLJ1446 3 16279 NP_116179.1 3 682 AAGCCCAGGAGG AC CT C 3 C c b
6 CCAAGTCTGCAG TCACTGCA CT GCCTCC
TGAGCTAT AGTGACGT GA CGGAGG
CT AC A

GAM7957 297 FLJ1449 1 10571 NP_116182.1 3 1055 GAACCCAGGAGG C C 3 C c c
0 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A

GAM7957 297 FLJ1464 1 16502 NP_116207.1 3 324 CACTTTGGGAAG A A C 3 C c c
2 CAGAGGTGGCAG TC CTGC ACCTCTGC TCCCG
GATCATTC AG GACG TGGAGACG AGGGT
- G A

GAM7957 297 FLJ2000 2 6217 NP_060088.1 3 439 TGAACCTGGAGG C C 3 C b b
6 CAGAGATTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGACGGAGG
A T

GAM7957 297 FLJ2000 2 14201 NP_060088.1 3 761 GAGTCTGGGAGG 3 C b b
6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 FLJ2001 1 14786 NP_060091.1 3 495 GAACCTGGGAGG 3 C b b
3 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 FLJ2001 1 10518 NP_060094.1 3 414 GAGCCTGGGAGT A TGC 3 C c c
9 TCGAGGCTGCAG TCACTGCA CCTC CTCCCG
TGAGCAAT AGTGACGT GGAG GAGGGT
C CTT

GAM7957 297 FLJ2004 1 13209 NP_060108.1 3 796 GAACCCAGGAGG CT C 3 C c c
5 TGAAGGTTGCAG TCACTGCAACCT GCCTCC
TGACCGGA AGTGACGTTGGA TGGAGG
AG A

GAM7957 297 FLJ2006 1 17194 NP_060121.3 3 696 TGACCCAGGAGG C 3 C b b
9 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG

```
                                                                A
GAM7957  297   FLJ2013 1  12593 NP_060155.1  3  914   GAGCCCGGGAGG                    3  C  b  b
         9                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAT    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   FLJ2015 1  17280 NP_060159.1  3  1449  TGATCAGGGAGG      AACCTC          3  C
c  c
         1                      CATAGCAGTGAG TCACTGC     TGCCTCCC
                                AGCCATAG    AGTGACG     ACGGAGGG
                                          AT----
GAM7957  297   FLJ2015 1  17311 NP_061873.2  5  4    ATTCAAGGGAGG   CT  AACC           3  C  c
c
         2                      CAGGCGCTTTGG TCA  GC    TCTGCCTCCC
                                AAGTTTGT    GGT  CG    GGACGGAGGG
                                          TT  C---
GAM7957  297   FLJ2020 2  3492  NP_115668.2  3  339   CTGCTTGGGAGG   A   AAC            3  C  b
b
         3                      CAGAGGCAGGAG TC CTGC   CTCTGCCTCCCG
                                AATTGCTT    AG GACG   GAGACGGAGGGT
                                          -   ---
GAM7957  297   FLJ2020 2  15426 NP_115668.2  3  373   GAGCCCGAGAGA          C  C       3  C  b  b

         3                      CAGAGGTTGCAG TCACTGCAACCTCTG CTC CG
                                TGAGCCGA    AGTGACGTTGGAGAC GAG GC
                                          A  A
GAM7957  297   FLJ2021 1  13691 NP_060183.1  3  1086  GAACCTGGGAGG TC-----            3  C  c
c
         1                      CAGAGGTTGCAG      ACTGCAACCTCTGCCTCCCG
                                TAAGCCAA         TGACGTTGGAGACGGAGGGT
                                       AACCGAA
GAM7957  297   FLJ2025 1  17007 NP_062552.1  3  486   CTGGCAGGGAGG   TGCA  C--          3  C  c
 c
         7                      CACGCAGGTACT TCAC   ACCT   TGCCTCCC
                                GTGAAAAT    AGTG   TGGA   ACGGAGGG
                                          TCA-   CGC
GAM7957  297   FLJ2028 1  12403 NP_060211.1  3  396   GAACCCAGGAGA          C  C       3  C  c  c
         0                      CGGAGGTTGCGG TCACTGCAACCTCTG CTCC
                                TGAGTTGA    AGTGGCGTTGGAGGC GAGG
                                          A  A
GAM7957  297   FLJ2030 2  3975  NP_060226.1  3  762   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         6                      CTGAGGCAGGGA TC CTGC   CTC GCCTCCCG
                                GAATCGCT    AG GACG   GAG CGGAGGGC
                                          G   ---  T
GAM7957  297   FLJ2030 2  15330 NP_060226.1  3  795   GAACCTGGGAGG        - G         3  C  b  b
         6                      AGAAGGTTGCAG TCACTGCAACCT CT CCTCCCG
                                TGAGCTGA    AGTGACGTTGGA GA GGAGGGT
                                          A  -
GAM7957  297   FLJ2033 1  4177  NP_060242.1  3  1032  TAGAACGGGAGG   -   A-  C  T---       3  C  c
c
```

7 CTGCTGAAGTGA TCA CTGC AC TC GCCTCCCG
GTAGCTGA AGT GATG TG AG CGGAGGGC
C AG A TCGT
GAM7957 297 FLJ2041 2 10318 NP_060278.1 3 1680 GAACCAGGGAGG C G 3 C b
b
3 AGGAGCTTGCAG TCACTGCAA CTCT CCTCCC
TGAGCCGA AGTGACGTT GAGG GGAGGG
C A
GAM7957 297 FLJ2041 2 13155 NP_060278.1 3 1646 CTACTCGGGAGG A AAC T 3 C c
b
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ2045 1 11133 NP_060298.2 3 94 CTCTTCGGGAGG A C T--- 3 C c c
2 CAGCCCTGGTTC TC CTG AACC CTGCCTCCCG
TAGGATGC AG GAT TTGG GACGGAGGGC
- C TCCC
GAM7957 297 FLJ2046 2 15056 NP_060304.1 3 726 GAACCTGGGAGG T 3 C b b
4 CGGAGGTTGCCG TCAC GCAACCTCTGCCTCCCG
TGAGCCGA AGTG CGTTGGAGGCGGAGGGT
C
GAM7957 297 FLJ2046 2 16904 NP_060304.1 3 897 GAACCCGGGAGG C 3 C b b
4 CGGAGTTGCGGT TCACTGCAAC TCTGCCTCCCG
GAGCCGAG AGTGGCGTTG AGGCGGAGGGC
-
GAM7957 297 FLJ2053 1 7783 NP_060335.2 5 101 AGGCCCGGGAGG AA----- C 3 C c
c
1 CGCAGGCGCAGG TCACTGC CCT TGCCTCCCG
CGCAGTGG GGTGACG GGA GCGGAGGGC
CGGACGC C
GAM7957 297 FLJ2067 1 19100 NP_060394.1 3 1956 CACTTTGGGAGG CAA 3 C c
c
1 CAGAGGCCGGTG TCACTG CCTCTGCCTCCCG
GGTTGCTT GGTGGC GGAGACGGAGGGT
C--
GAM7957 297 FLJ2068 1 2852 NP_060395.2 3 763 CTTGAACTGAGG CAA CC 3 C c
c
6 CAGAGGCTACAG TCACTG CCTCTGCCTC
TGAGTGGA AGTGAC GGAGACGGAG
ATC TC
GAM7957 297 FLJ2069 1 17403 NP_060398.1 3 2086 GAACCCAGGAGG C 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 FLJ2070 1 16856 NP_060402.1 3 1211 GAACCCGGGTGG CCT T 3 C c
c
0 CGGCGCTTGCAG TCACTGCAA CTGCC CCCG
TGAGCTGA AGTGACGTT GGCGG GGGC
CGC T
GAM7957 297 FLJ2080 1 4334 NP_060429.1 3 653 GAACCTGGTAGG C 3 C b b

2 CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCGA AGTGACGTTGGAGACGGA GGT
T

GAM7957 297 FLJ2082 5 805 NP_060432.1 5 46 GGGTACAGGTGG A C TC 3 C c b
5 GCATAGGTGCAG TCACTGCA CCT TGCC CC
TGAGTGCA AGTGACGT GGA ACGG GG
- T GT

GAM7957 297 FLJ2082 5 6040 NP_060432.1 3 654 GAACCCAGGAGG C C 3 C c b
5 CAGAGGTTGCGT TCA TGCAACCTCTGCCTCC
TGAGCCAA AGT GCGTTGGAGACGGAGG
T A

GAM7957 297 FLJ2082 5 6889 NP_060432.1 5 207 GGGTACAGATGG A C ------- 3 C c b
5 GCATAGGTGCAG TCACTGCA CCT TGCCT CCC
TGAGTGCA AGTGACGT GGA ACGGG GGG
- T TAGACAT

GAM7957 297 FLJ2082 5 8889 NP_060432.1 5 71 GAGTGCAGGTGG A C TC 3 C c b

5 GCATAGGTGCAG TCACTGCA CCT TGCC CC
TGAGTGCA AGTGACGT GGA ACGG GG
- T GT

GAM7957 297 FLJ2082 5 19263 NP_060432.1 3 803 CTCTTGGGGAGG A AAC 3 C b
b
5 CAGAGGCAGGAG TC CTGC CTCTGCCTCCC
GATCGCTT AG GACG GAGACGGAGGG
- ---

GAM7957 297 FLJ2090 1 18412 NP_078969.2 3 25 GTGTGGTGGAGG GCAA C 3 C c
c
9 CAGAGGAGTGAG TCACT CCTCTGCCTCC
GCCCACGG AGTGA GGAGACGGAGG
---- T

GAM7957 297 FLJ2097 1 13690 NP_079306.1 3 1500 GAACCCAGGAGG C C 3 C b
b
2 CAGAGATTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
A A

GAM7957 297 FLJ2113 1 14182 NP_079142.1 3 390 CAGGTGCGGGGG TGCAA T 3 C
c c
5 CAGAGGGTGACT TCAC CCTCTGCC CCCG
TACCAAGA AGTG GGAGACGG GGGC
----- -

GAM7957 297 FLJ2114 1 3619 NP_073611.1 3 822 GAACCTGAGAGG C CC 3 C c c

4 CAGAGGTTACAG TCACTG AACCTCTGCCTC
TGAGCTGA AGTGAC TTGGAGACGGAG
A AG

GAM7957 297 FLJ2124 1 16290 NP_079123.1 3 730 GAACCCAGGAGG C TG C 3 C c
c
0 TGGAGTTTGCAG TCACTGCAA CTC CCTCC
TGAGCTGA AGTGACGTT GAG GGAGG
T GT A

GAM7957 297 FLJ2160 1 13858 NP_079038.1 3 304 GAGCCTGGGAGG 3 C b b
3 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 FLJ2165 1 13061 NP_071928.2 3 1878 GAACCTGGGAGG 3 C b b
7 CAGAGGTTGTAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGATGTTGGAGACGGAGGGT

GAM7957 297 FLJ2167 2 16286 NP_112160.1 3 542 GAACCCGGGAGG A 3 C b b
3 CAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAGCTGA AGTGACGT GGAGACGGAGGGC
C

GAM7957 297 FLJ2167 2 19796 NP_112160.1 3 225 GAACCCCAGAGG CC 3 C c b
3 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGACGTTGGAGGCGGAG
AC

GAM7957 297 FLJ2168 2 17803 NP_079135.1 3 1985 CTACTCGGGAGG A AAC T 3 C c
c
7 CTGAGGCAGAGA TC CTGC CTC GCCTCCCG
ATTGCTTG AG GACG GAG CGGAGGGC
A --- T

GAM7957 297 FLJ2168 2 19018 NP_079135.1 3 2016 GAATCCAGGAGG A TG C 3 C c
c
7 TGGAGGTTGCAG TC CTGCAACCTC CCTCC
CGAGCCAA AG GACGTTGGAG GGAGG
C GT A

GAM7957 297 FLJ2177 2 627 NP_115585.1 5 45 GAACCCGGGAGG C 3 C b b
7 CGGAGGTTTCAG TCACTG AACCTCTGCCTCCCG
TGAGCCGA AGTGAC TTGGAGGCGGAGGGC
T

GAM7957 297 FLJ2177 2 11407 NP_115585.1 3 330 GAACCCTGGAGG C 3 C b b
7 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTGGA AGTGACGTTGGAGGCGGAGG
T

GAM7957 297 FLJ2187 1 6605 NP_075392.1 3 2513 AAACCTGAGAGG - TG CC 3 C c
c
0 TGGAGGTTGCAG TCA CTGCAACCTC CCTC
TTGAGCCA AGT GACGTTGGAG GGAG
T GT AG

GAM7957 297 FLJ2205 1 17423 NP_078837.2 3 634 GAACCTGGGAGG TG 3 C b b
4 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 FLJ2217 1 17804 NP_079317.1 5 249 GCTCAGAGGAGG G AC C 3 C c
c
3 CAGAGATGGGGT TCACT CA CTCTGCCTCC
GGTGGCTG GGTGG GT GAGACGGAGG
G A- A

GAM7957 297 FLJ2231 1 14789 NP_071768.2 3 553 GAACCCAGGAGG C 3 C b b

```
          3                    CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                               TGAGCTGA    AGTGACGTTGGAGGCGGAGG
                                           A
GAM7957  297   FLJ2241 1  4373  NP_079045.1  3  1095  AAATCCAGCAGG         TG  CCC       3  C  c
c
          5                    TGGAGGTTGCAG TCACTGCAACCTC  CCT
                               TGAGCCAA    AGTGACGTTGGAG  GGA
                                           GT  CGA
GAM7957  297   FLJ2269 1  7048  NP_079325.1  3  558   GAACCCAGGAGG       C       C       3  C  b  b
          2                    CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
                               TGAGCCGA    AGTGACGTT GAGACGGAGG
                                           C       A
GAM7957  297   FLJ2281 3  2026  NP_079192.1  3  331   CTACTCGGGAGG  A   AAC  T          3  C  c
c
          4                    CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                               GATCACTT    AG GACG  GAG CGGAGGGC
                                           -   ---  T
GAM7957  297   FLJ2281 3  8877  NP_079192.1  3  1747  GAACCCAGGAGG       C       C       3  C  c  c
          4                    CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
                               TGAGCTGA    AGTGACGTT GAGGCGGAGG
                                           C       A
GAM7957  297   FLJ2281 3  15203 NP_079192.1  3  1331  CCCCACGCGGAG       ACCT  C   -       3  C  c
 c
          4                    CCAGCGCTGCAG TCACTGCA   CTG CTCC CG
                               TGAAAGAG    AGTGACGT   GAC GAGG GC
                                           CGC-  C   C
GAM7957  297   FLJ2296 2  17741 NP_071384.1  3  439   CTACTTGGGAGG  A   AAC            3  C  b
b
          5                    CAGAGGCAGGAG TC CTGC  CTCTGCCTCCCG
                               AATTGCTT    AG GACG  GAGACGGAGGGT
                                           -   ---
GAM7957  297   FLJ2296 2  18688 NP_071384.1  3  473   GAACTCGGGAGG         TG          3  C  b  b

          5                    TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                               TGAGCTGA    AGTGACGTTGGAG  GGAGGGC
                                           GT
GAM7957  297   FLJ2302 2  5830  NP_079327.1  3  812   CTACTCGGGAGG  A   AAC  T          3  C  c
b
          2                    CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                               AATCGCTT    AG GACG  GAG CGGAGGGC
                                           -   ---  T
GAM7957  297   FLJ2302 2  9765  NP_079327.1  3  846   GAACCCGGGAGG         TG          3  C  b  b
          2                    TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                               TGAGCCGA    AGTGACGTTGGAG  GGAGGGC
                                           GT
GAM7957  297   FLJ2304 1  5732  NP_079450.1  3  713   GAACCTGGGAGG TC-----              3  C  c  c
          0                    CGGAGGTTGCAG       ACTGCAACCTCTGCCTCCCG
                               TAAGCCCA          TGACGTTGGAGGCGGAGGGT
                                           ACCCGAA
GAM7957  297   FLJ2304 1  9948  NP_079433.1  3  890   GAACCCAGGACG          C  C       3  C  c  c
```

```
          2                          CAGAGGTTGCGG TCACTGCAACCTCTGC TCC
                                     TGAGCCAA    AGTGGCGTTGGAGACG AGG
                                                   C   A
GAM7957  297   FLJ2318 2  10998  NP_079332.1  3  268   GAGCCCTAGAGG      A   T   CC       3  C  c
c
          5                          TTGAGGCTGCAG TCACTGCA CCTC GCCTC
                                     TGAGCTAT    AGTGACGT GGAG TGGAG
                                               C   T    AT
GAM7957  297   FLJ2318 2  11247  NP_079332.1  3  897   GAGCCCTAGAGG      A   T   CC       3  C  c
c
          5                          TCGAGGCTGCAG TCACTGCA CCTC GCCTC
                                     TGAGCTAT    AGTGACGT GGAG TGGAG
                                               C   C    AT
GAM7957  297   FLJ2323 1  17838  NP_079219.1  3  808   GAACCTGGCAGG      C     C        3  C  b  b

          5                          CAGAGTTTGCAG TCACTGCAA CTCTGCCT CCG
                                     TGAACCAA    AGTGACGTT GAGACGGA GGT
                                                  T      C
GAM7957  297   FLJ2332 2  8548   NP_079231.3  3  1356  AGACCCGGGAGG                    3  C  b  b
          2                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   FLJ2332 2  11740  NP_079231.3  3  1679  GAACCTGGGAGG         TG          3  C  b
b
          2                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCAGA    AGTGACGTTGGAG  GGAGGGT
                                                   GT
GAM7957  297   FLJ2335 1  2436   NP_115613.1  3  244   TCTGTTGCTGAG      AC  -   CC       3  C  c  c

          6                          GCTGGAGTGCAG TCACTGCA  CTCT GCCTC
                                     TGATGTGA    AGTGACGT  GAGG CGGAG
                                               --   T    TC
GAM7957  297   FLJ2336 2  5830   NP_075564.1  3  1139  CTACTCGGGAGG  A   AAC  T          3  C  c
b
          0                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATCGCTT    AG GACG   GAG CGGAGGGC
                                               -   ---  T
GAM7957  297   FLJ2336 2  13066  NP_075564.1  3  1173  GAACCTGGGAGG                    3  C  b  b
          0                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   FLJ2343 1  8839   NP_078947.2  5  177   TGGAGCGGGAGG   T   CTCT          3  C  c
c
          6                          CGTTGCCGTGGG TCAC GCAAC   GCCTCCCG
                                     GCCTCGAG    GGTG CGTTG   CGGAGGGC
                                               C    ----
GAM7957  297   FLJ2349 1  4310   NP_073598.1  3  1217  GAACCCAGGAAG          C  C       3  C  b  b
          9                          CAGAGGTTGCAG TCACTGCAACCTCTGC TCC
                                     TGAGCTGA    AGTGACGTTGGAGACG AGG
                                                  A  A
```

GAM7957 297 FLJ2353 1 10013 NP_079165.1 3 2079 AGAACCGGGAGG C 3 C b b
7 CGGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCAA AGTGACGTTG AGGCGGAGGGC
A
GAM7957 297 FLJ2375 1 13853 NP_689888.1 3 1300 GAACCTGGGAAG C 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCCGA AGTGACGTTGGAGACG AGGGT
A
GAM7957 297 FLJ2386 1 7778 NP_689882.1 3 1351 GGACTCAGGAGG C C 3 C c c
5 CGGAGTTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGGCGGAGG
T A
GAM7957 297 FLJ2387 2 15315 NP_659427.1 3 968 GAACCCGGAAGG C C 3 C b b
8 CGGAGCTTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCCGA AGTGACGTT GAGGCGGA GGC
C A
GAM7957 297 FLJ2387 2 19119 NP_659427.1 3 934 CTACTCGGGAGG A AAC T 3 C c
b
8 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ2500 1 19211 NP_653211.1 3 115 GGGCCCAGGAGA GC C 3 C c
c
6 TGGAGGTTGCGG TCACTGCAACCTCT CTCC
TGAGTGGG AGTGGCGTTGGAGG GAGG
TA A
GAM7957 297 FLJ2561 1 8469 NP_775865.1 3 1339 GAGCCTGGGAGG A CT 3 C c
c
3 TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAGCTGT AGTGACGT GGA TGGAGGGT
C AC
GAM7957 297 FLJ3009 1 6927 NP_659420.1 3 594 CAGCCTGGGAGG A CT 3 C c c
2 TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAGCTGT AGTGACGT GGA TGGAGGGT
C AC
GAM7957 297 FLJ3031 2 6683 NP_742148.1 3 203 GAACCTGGGAGG TC----- 3 C c c
7 CAGAGGTTGCAG ACTGCAACCTCTGCCTCCCG
TAAGCTAA TGACGTTGGAGACGGAGGGT
AATCGAA
GAM7957 297 FLJ3031 2 7121 NP_742148.1 3 1412 GAACCTGGGAGG TG C 3 C c
c
7 CAGATGTTGTGG TCAC CAAC TCTGCCTCCCG
TGAGCCGA AGTG GTTG AGACGGAGGGT
GT T
GAM7957 297 FLJ3050 1 5647 NP_694555.1 5 305 TTTTAGGGCAAG C C CT- 3 C c c
7 TATAGGTTGCAC TCA TGCAACCT TGC CCC
TGATCCTG AGT ACGTTGGA ATG GGG

C T AAC
GAM7957 297 FLJ3059 1 9422 NP_694556.1 3 1157 GAACCCAGGAGG C 3 C b b
4 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 FLJ3067 1 8173 NP_694562.1 3 1256 GAGCCCAGGAGT A TGC C 3 C c
c
9 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAACTAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 FLJ3079 1 7170 NP_653295.1 5 254 CGGGGGCGGAGG - AAC T 3 C c
c
1 CAGCTGAGGCGC TCA CTGC CTCTGCC CCCG
TTCTTTCC AGT GACG GAGGCGG GGGC
C --- -
GAM7957 297 FLJ3089 1 19054 NP_689943.1 3 483 GAACCCGGGAGG 3 C b b
9 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 FLJ3103 1 9589 NP_689937.1 3 876 GAACCCGGGAGG C 3 C b b
4 CAGAGGTTGCAC TCA TGCAACCTCTGCCTCCCG
TGAGCTGA AGT ACGTTGGAGACGGAGGGC
C
GAM7957 297 FLJ3105 1 15521 NP_689591.1 5 210 CCGGGAGGGAGG C AACCTC 3 C
c c
2 CAAATGAGCATT TCA TGC TGCCTCCC
GAGAAATT AGT ACG ACGGAGGG
T AGTAA-
GAM7957 297 FLJ3115 1 2160 NP_689782.1 3 708 GAACCCGGGAGG C 3 C b b
8 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAACCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 FLJ3120 1 14200 NP_694568.1 3 1080 GAATCTGGGAAG C 3 C b b
8 CGGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCTGA AGTGACGTTGGAGGCG AGGGT
A
GAM7957 297 FLJ3132 2 6650 NP_689600.1 3 1720 GAACCCAGGAGG C C 3 C b b
2 CAGAAGTTGCAG TCACTGCAAC TCTGCCTCC
TGAGCCGA AGTGACGTTG AGACGGAGG
A A
GAM7957 297 FLJ3132 2 13125 NP_689600.1 3 1143 GAACCCGGGAGG TC----- T 3 C c
b
2 CAGAGGTTGCTG AC GCAACCTCTGCCTCCCG
TAAGCTGA TG CGTTGGAGACGGAGGGC
AGTCGAA T
GAM7957 297 FLJ3133 1 9421 NP_689743.1 3 822 GAACCCGGGAGG 3 C b b
1 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 FLJ3143 2 1420 NP_689709.1 3 229 TGATGGGAACGG - AA- -- 3 C c b
4 CAGAGGCTGGCA TCAC TGC CCTCTGCC TCCCG
GGTGACTG AGTG ACG GGAGACGG AGGGT
G GTC CA
GAM7957 297 FLJ3143 2 15343 NP_689709.1 3 1293 GAACCCGGGAGG C 3 C b b
4 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 FLJ3145 1 15977 NP_659401.1 3 236 GAACTCGGGAGG C 3 C b b
5 CGAAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCCGA AGTGACGTTGGA GCGGAGGGC
A
GAM7957 297 FLJ3156 2 18229 NP_689722.1 3 1081 GAACCCGGGTGG T 3 C b b
8 CAGAGGTTGCAG TCACTGCAACCTCTGCC CCCG
TGAGCCGA AGTGACGTTGGAGACGG GGGC
T
GAM7957 297 FLJ3156 2 20105 NP_689722.1 3 336 GTATCTGGGAGG T C 3 C b b
8 CAGAGTTTGCCG TCAC GCAA CTCTGCCTCCCG
TGAGCTGA AGTG CGTT GAGACGGAGGGT
C T
GAM7957 297 FLJ3173 1 6645 NP_659421.1 3 1534 AAACCCAGGAGG A C C 3 C c c
7 CAAAGGCTGCAG TCACTGCA CCT TGCCTCC
TGAGCCAA AGTGACGT GGA ACGGAGG
C A A
GAM7957 297 FLJ3181 1 12402 NP_689742.2 3 574 GAATCTGGGAGG T 3 C b b
9 CAGAGGTTGCTG TCAC GCAACCTCTGCCTCCCG
TGAGCCGA AGTG CGTTGGAGACGGAGGGT
T
GAM7957 297 FLJ3184 2 5671 NP_689700.1 3 378 GAACCCGAGAGA C C 3 C b b
2 CGGAGGTTGCAG TCACTGCAACCTCTG CTC CG
TGAGCTGA AGTGACGTTGGAGGC GAG GC
A A
GAM7957 297 FLJ3184 2 5830 NP_689700.1 3 344 CTACTCGGGAGG A AAC T 3 C c
b
2 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ3184 1 17941 NP_659411.1 5 43 GCTGCCGGGAGG CT A-- - 3 C c
c
6 CGGGAGGGAGTG TCA GCA CCTCT GCCTCCCG
CCCTGAAA AGT CGT GGAGG CGGAGGGC
CC GAG G
GAM7957 297 FLJ3188 1 11921 NP_689673.1 3 969 GAACCTGGGAGG C TG 3 C c
c
2 TGGAGATTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCCA AGTGACGTT GAG GGAGGGT
A GT
GAM7957 297 FLJ3195 1 8772 NP_653283.1 3 1046 GAATCCTGGAGG C 3 C b b

2 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
T
GAM7957 297 FLJ3195 1 694 NP_694575.1 3 591 GTTGTGGATGAG ACC -- -- 3 C c c
8 CTGCAGGTGCAG TCACTGCA TCTGC CTC CCG
TGACTCCA AGTGACGT GGACG GAG GGT
--- TC TA
GAM7957 297 FLJ3202 3 1492 NP_775853.2 3 5283 CTACTCGGGAGG A AAC T 3 C c
c
9 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ3202 3 15089 NP_775853.2 3 1425 CTACTCGGGAGG A AAC T 3 C c
c
9 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ3202 3 19975 NP_775853.2 3 1459 GAACCTAGGAGG C T C 3 C c
c
9 CTGAGATTGCAG TCACTGCAA CTC GCCTCC
TGAGCCGA AGTGACGTT GAG CGGAGG
A T A
GAM7957 297 FLJ3221 1 3464 NP_689686.1 3 1002 GAACCCGGGAGG CT 3 C b b
4 CAGAGGTTGTGT TCA GCAACCTCTGCCTCCCG
TGAGCCAA AGT TGTTGGAGACGGAGGGC
TG
GAM7957 297 FLJ3238 1 12664 NP_653209.1 3 95 GTCTCAAGGAGG - A CT C 3 C c
c
4 CAGGTGGCAGAT TCA CTGC ACCT GCCTCC
GAAAACCA AGT GACG TGGA CGGAGG
A G -- A
GAM7957 297 FLJ3253 1 8019 NP_689760.1 3 980 GAACCCGGGAAG C C 3 C b b
5 CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A
GAM7957 297 FLJ3291 1 8190 NP_659451.1 5 183 GAACCCGGGAGG A 3 C b b
5 CGGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAGTCGA AGTGACGT GGAGGCGGAGGGC
C
GAM7957 297 FLJ3320 1 5805 NP_848649.1 3 222 TGACTGAGGGGG AAC C 3 C c
c
7 CAGAGGCAGTGG TCACTGC CTCTGCCTCC
CTCTTTAG GGTGACG GAGACGGGGG
--- A
GAM7957 297 FLJ3329 1 4903 NP_775907.1 3 585 GAGCCTGGGATG A CT C 3 C c
c
8 TCAAGGCTGCAG TCACTGCA CCT GC TCCCG
TGAGCTGT AGTGACGT GGA TG AGGGT
C AC T

GAM7957 297 FLJ3350 1 7314 NP_689530.1 3 1397 GAGCCCGGGAGG C 3 C b b
5 CGGAGCTTGCGG TCACTGCAA CTCTGCCTCCCG
TGGGCCGG GGTGGCGTT GAGGCGGAGGGC
C
GAM7957 297 FLJ3361 1 11488 NP_775968.1 3 1183 TGACCATAGAGG G C CC 3 C c
c
0 CAGAGATTGGAG TCACT CAA CTCTGCCTC
TGAAGTGG AGTGA GTT GAGACGGAG
G A AT
GAM7957 297 FLJ3367 2 1928 XP_291074.1 3 289 CTACTCGGGAGG A AAC T 3 C c
b
4 CTGAGGCGGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GGCG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ3367 2 11561 XP_291074.1 3 322 TGAACAGGGAGG 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCCGA AGTGACGTTGGAGACGGAGGG

GAM7957 297 FLJ3379 1 12060 NP_775854.1 3 419 GAACCTGGGAGG C 3 C b b
0 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCCA AGTGACGTT GAGGCGGAGGGT
C
GAM7957 297 FLJ3397 1 592 NP_689849.1 3 2656 TGAAGCTGGAGG G C C 3 C c c

9 CAGAGATTGGAG TCACT CAA CTCTGCCTCC
TGATACAT AGTGA GTT GAGACGGAGG
G A T
GAM7957 297 FLJ3404 1 15371 NP_775940.1 3 2246 GAGCCCAGGAGC A GC C 3 C c
c
7 TGGAGGCTGCAG TCACTGCA CCTCT CTCC
TGAACTAT AGTGACGT GGAGG GAGG
C TC A
GAM7957 297 FLJ3427 1 12930 NP_775873.1 3 1296 CAGGGAGACAGA C---- 3 C b b

8 CAGAGGTTGCAG TCACTGCAACCTCTG CTCCC
TGAGCCGA AGTGACGTTGGAGAC GAGGG
AGACA
GAM7957 297 FLJ3481 1 9991 NP_689516.1 3 567 GAACCCGGGAGG C TG 3 C b
b
7 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCAA AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 FLJ3496 1 9420 XP_114353.1 3 1000 GAACCTGGGAGG 3 C b b
9 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 FLJ3511 2 4404 NP_787067.1 3 434 GAACCCAGGAAG C C 3 C c b
9 CGGAGGTTGCAG TCACTGCAACCTCTGC TCC
TGAGCCGA AGTGACGTTGGAGGCG AGG
A A

GAM7957 297 FLJ3511 2 13065 NP_787067.1 3 881 GAACCCGGGAGG 3 C b b
9 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 FLJ3568 1 13398 NP_787096.1 3 951 CTTTAGGGGAGG G A -- 3 C b b
1 CAGGCAGGTGGG TCACT CA CCT CTGCCTCCC
TGAGCAGC AGTGG GT GGA GACGGAGGG
- - CG
GAM7957 297 FLJ3574 1 7183 NP_671728.1 3 234 CCAAGGCAGAGT A C-- C -- 3 C c c
0 CAGAGGTTCCAC TC CTG AACCTCTG CTC CC
AGGAGGAG AG GAC TTGGAGAC GAG GG
- ACC T AC
GAM7957 297 FLJ3584 1 9398 XP_290755.1 3 269 AAACCCAGGAGG C 3 C b b
8 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTGAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 FLJ3593 1 13467 NP_775735.1 3 67 GAACCTGGGAGG C C C 3 C c c
6 CAGAGATTACAC TCA TG AA CTCTGCCTCCCG
TGACCTGA AGT AC TT GAGACGGAGGGT
C A A
GAM7957 297 FLJ3681 2 12792 NP_694992.1 3 1142 GAACCCAGGAGG C 3 C b b
2 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 FLJ3681 2 15984 NP_694992.1 3 813 GAACCCAGGAGG TG C 3 C c
b
2 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 FLJ3713 1 19393 NP_775958.1 3 1072 GAACCTAGGAGG C C 3 C b b
1 CAGAGTTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
T A
GAM7957 297 FLJ3722 1 12334 NP_787113.1 3 578 GAACCCGGGAGG 3 C b b
8 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGTCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 FLJ3731 1 10438 NP_689799.1 3 283 GAACCCGGGAGG 3 C b b
8 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 FLJ3756 1 11700 NP_689622.1 3 1121 AAATCCAGGAGG C 3 C b b
2 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 FLJ3835 1 10720 NP_689731.1 3 1036 AGTTGAAGGAGG GCAA - C 3 C c
c

9 CAGAAGGGAGAG TCACT CCT CTGCCTCC
TGATGCAC AGTGA GGA GACGGAGG
GAG- A A
GAM7957 297 FLJ3842 1 11462 NP_775882.1 3 2058 GAACCCAGGAGG C C 3 C b b
6 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 FLJ3848 1 3131 NP_689894.1 3 798 GGACCCAGGAGG C C 3 C b b
2 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 FLJ3866 2 9420 NP_689482.1 3 432 GAACCTGGGAGG 3 C b b
3 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 FLJ3866 2 19910 NP_689482.1 3 398 CTACTCGGGAGG A AAC T 3 C c b
3 CCGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCGT AG GACG GAG CGGAGGGC
- --- C
GAM7957 297 FLJ3869 3 1620 NP_848608.1 3 1625 GAACCCAGGAGG C 3 C b b
0 CGGGGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTCGA AGTGACGTTGGGGGCGGAGG
A
GAM7957 297 FLJ3869 3 3523 NP_848608.1 3 1591 CTACTCGGGAGG A A CTCT 3 C c b
0 CTGTGGCAGGAG TC CTGC AC GCCTCCCG
AATTGCTT AG GACG TG CGGAGGGC
- G T---
GAM7957 297 FLJ3869 3 15308 NP_848608.1 3 635 GAACCCAGGAGA C C 3 C b b
0 CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCAA AGTGACGTTGGAGAC GAGG
A A
GAM7957 297 FLJ3877 3 7759 NP_848623.1 3 1293 GAACCCAGGAGG T C 3 C c c
3 CGGCGGTTGCAG TCACTGCAACC CTGCCTCC
TGAGCCAA AGTGACGTTGG GGCGGAGG
C A
GAM7957 297 FLJ3877 3 18950 NP_848623.1 5 278 CTGACCAGGAGT A TGC C 3 C c c
3 TCGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCCGA AGTGACGT GGAG GAGG
C CTT A
GAM7957 297 FLJ3877 3 19941 NP_848623.1 3 1259 CTATTCGGGAGG A AAC T 3 C c c
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ3894 2 948 NP_689574.1 3 1073 GAACCCGGGAGG TC----- 3 C c c
4 CGGAGGTTGCAG ACTGCAACCTCTGCCTCCCG

TAAGCCGA TGACGTTGGAGGCGGAGGGC
AGCCGAA
GAM7957 297 FLJ3894 2 1492 NP_689574.1 3 1039 CTACTCGGGAGG A AAC T 3 C c c
4 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ3899 1 13139 NP_776188.1 3 374 GAACCTGGAATA C CC- C 3 C c c
1 CAGAGGTTTCAG TCACTG AACCTCTG TCC
TGAGCTGA AGTGAC TTGGAGAC AGG
T ATA T
GAM7957 297 FLJ3900 1 12307 NP_848616.1 3 1415 GAACCTAGGAGG C 3 C b b
5 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAACCGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 FLJ3936 1 15223 NP_689576.1 3 822 GAACCCAGGAGG TG C 3 C c c
9 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 FLJ3941 1 14355 NP_775952.1 3 497 GAACTTGTGGGG TG CC 3 C c c
5 TGGAGGTTGCAG TCACTGCAACCTC CCTC
TGAGCTGA AGTGACGTTGGAG GGGG
GT TG
GAM7957 297 FLJ3944 1 8873 XP_084736.6 3 2930 GAACCTGGGAGG TC----- 3 C c c
1 CGGAGGTTGCAG ACTGCAACCTCTGCCTCCCG
TCAGCCAA TGACGTTGGAGGCGGAGGGT
AACCGAC
GAM7957 297 FLJ3965 2 13908 NP_689897.1 3 1049 GAATCCGGGAGG 3 C b b
3 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAACCGA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 FLJ3965 2 19119 NP_689897.1 3 1015 CTACTCGGGAGG A AAC T 3 C c b
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ4016 1 15055 NP_775755.2 3 1237 GAACCCAGGAGG C 3 C b b
0 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTCA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 FLJ4018 1 9550 NP_775967.1 3 657 GAACCCGGGAGT GC 3 C b b
2 TGGAGGTTGCAG TCACTGCAACCTCT CTCCCG
TGAGCCAA AGTGACGTTGGAGG GAGGGC
TT
GAM7957 297 FLJ4028 1 17816 NP_775953.1 3 655 GGGAGGTGGAGG C AA- TG 3 C c c

8 CAGGCACTGAAT TCA TGC CCTC CCTCCC
AAGGTCCC AGT ACG GGAG GGAGGG
C GAC GT
GAM7957 297 FLJ4041 2 631 NP_775921.1 5 177 CTACTCGGGAGG A AAC T 3 C c
c
7 CTGAGGCAGGAA TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 FLJ4041 2 4629 NP_775921.1 5 209 GCACCCAGGAGG TG C 3 C c c

7 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 FLJ4054 1 14572 NP_848598.1 3 1345 GACCCCGGGAGG A TG 3 C b
b
2 TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAGTTGT AGTGACGT GGAG GGAGGGC
C GT
GAM7957 297 FLJ9016 1 12468 NP_699169.1 3 631 GAACCCGAGAGG TG C 3 C c
c
5 TGGAGGTTGCAG TCACTGCAACCTC CCTC CG
TGAACCAA AGTGACGTTGGAG GGAG GC
GT A
GAM7957 297 FLJ9065 1 7434 NP_775889.1 3 274 CTGCTGGGGAGG C AC-- 3 C c c

2 CAGAGACCCTGC TCA TGCA CTCTGCCTCCC
AATGGCCA GGT ACGT GAGACGGAGGG
A CCCA
GAM7957 297 FLJ9073 1 17403 NP_699206.1 3 1517 GAACCCAGGAGG C 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 FLJ9079 1 19895 NP_699198.1 3 673 GCATGGGGGAGG ACT AC C 3 C
c c
8 CACAGAATGCTG TC GCA CT TGCCTCCC
GAGAGATG AG CGT GA ACGGAGGG
GT- AA C
GAM7957 297 FRSB 1 9067 NP_005678.2 3 1277 TGAACCAGGAGG C TG C 3 C c
c
TGGACGTTGCAG TCACTGCAAC TC CCTCC
TGATCCCA AGTGACGTTG AG GGAGG
C GT A
GAM7957 297 FUSIP1 1 14886 NP_473357.1 3 711 GAACCTGGGAGG C 3 C b b
TAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCAA AGTGACGTTG AGATGGAGGGT
A
GAM7957 297 FUT6 1 3076 NP_000141.1 3 809 GAACCTGTGAGG C TG CC 3 C c c

TGGAGCTTGCAG TCACTGCAA CTC CCTC
TGAGCCAA AGTGACGTT GAG GGAG

```
                                                C  GT   TG
GAM7957  297   FZD2   1  19131 NP_001457.1  5 22    AGGCGCGGGAGG  A   AAC -          3  C  c  c

                                                CGGCAGCCGCAG TC CTGC  CT CTGCCTCCCG
                                                CGAGGAGG    AG GACG  GA GGCGGAGGGC
                                                        C   CC- C
GAM7957  297   GALNT6 1  10435 NP_009141.1  3 939   GAACCCAGGAGG             C       3  C  b  b
                                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                                TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                                                  A
GAM7957  297   GALNT7 1  17403 NP_473451.2  3 1088  GAACCCAGGAGG             C       3  C  b  b

                                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                                TGAGCTGA    AGTGACGTTGGAGACGGAGG
                                                                  A
GAM7957  297   GALT   1  14368 NP_667342.1  3 2100  GGGCCCAGGAGT      A   TG---  ---      3  C  c
c
                                                TTGAGGCTGCAG TCACTGCA CCTC    CCT  CCC
                                                TGAGCCAT    AGTGACGT GGAG    GGA  GGG
                                                        C   TTTGA  CCC
GAM7957  297   GALT   1  14368 NP_667343.1  3 1611  GGGCCCAGGAGT      A   TG---  ---      3  C  c
c
                                                TTGAGGCTGCAG TCACTGCA CCTC    CCT  CCC
                                                TGAGCCAT    AGTGACGT GGAG    GGA  GGG
                                                        C   TTTGA  CCC
GAM7957  297   GAS7   1  19102 NP_005881.1  3 2931  GAACCTGGGAGG      C            3  C  b  b
                                                CGGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
                                                TGAACCAA    AGTGACGTT GAGGCGGAGGGT
                                                          A
GAM7957  297   GATS   1  19105 NP_849153.1  5 839   GAGCCCAGGAGG TC-----          C    3  C  c
c
                                                CAGAGGTTGCAG      ACTGCAACCTCTGCCTCC
                                                TAAGCCGA          TGACGTTGGAGACGGAGG
                                                        AGCCGAA           A
GAM7957  297   GBP4   2  4182  NP_443173.2  3 2670  CTACACGGGAGG  A   AAC  T          3  C  c
c
                                                CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                                AATGGCGT    AG GACG  GAG CGGAGGGC
                                                        -   ---  T
GAM7957  297   GBP4   2  14599 NP_443173.2  3 2704  GAGCCCAGGAGG      C      C       3  C  c  c
                                                CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
                                                TGAGTCGA    AGTGACGTT GAGGCGGAGG
                                                          C       A
GAM7957  297   GCNT2  1  9733  NP_001482.1  5 428   CAAACGGGGAGG  A GCAA-           3  C  c
c
                                                CAGAGGGAGGAG TC CT    CCTCTGCCTCCC
                                                GGAAGGCT    AG GG    GGAGACGGAGGG
                                                        - AGGAG
GAM7957  297   GDF11  1  5161  NP_005802.1  3 167   AACAGAGGGAGG    G-  --- -          3  C  c  c
                                                CAGGTGGGAATT TCACT  CAA  CC TCTGCCTCCC
```

GAGGGTGA AGTGG GTT GG GGACGGAGGG
GA AAG T
GAM7957 297 GGCX 1 17049 NP_000812.2 3 502 GGGCCCAGGAGG TG C 3 C c
c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 GL012 1 1572 NP_110441.1 3 415 GGGTGGGGGAGG CT AA - 3 C c
c
CAGGAGGAGGCT TCA GC CCTC TGCCTCCC
GAGCGTAG AGT CG GGAG ACGGAGGG
-- GA G
GAM7957 297 GLTP 1 17424 NP_057517.1 3 637 GAACCCGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 GNB4 2 10438 NP_067642.1 3 1940 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 GNB4 2 16402 NP_067642.1 3 1906 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
ATTCGCCT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 GNE 1 15108 NP_005467.1 3 587 CTACTCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 GNG11 1 2988 NP_004117.1 5 95 CCGGGCAGGCCT A CT--- - 3 C c c

CCTGGGTTGCAG TC CTGCAACCT GCCT CCCG
GGACTTGA AG GACGTTGGG CGGA GGGC
G TCCTC C
GAM7957 297 GNPNAT1 1 17400 XP_085119.1 3 1685 GAACCCGGGAGG C 3 C b
b
CAAAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCTGA AGTGACGTTGGA ACGGAGGGC
A
GAM7957 297 GOLGA2 2 5830 NP_004477.2 3 452 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 GOLGA2 2 6239 NP_004477.2 3 486 GAACCTGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGGGCTGA GGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 GOLGIN- 1 9854 NP_851421.1 5 608 AGGAGGCTCTGG A C--- 3 C c c

67 GCGGAGGTGCAG TCACTGCA CCTCTGCCT CC
TGACCCCG AGTGACGT GGAGGCGGG GG
- TCTC

GAM7957 297 GP2 1 3379 NP_001493.1 3 396 GAACTCAGGGGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGTTGA AGTGACGTTGGAG GGGGG
GT A

GAM7957 297 GP5 1 9421 NP_004479.1 3 2264 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 GPA33 1 16908 NP_005805.1 5 193 GCTGAGGCTGGG G A C- 3 C c c

CAGAGGTGGGTG TCACT CA CCTCTGCCT CC
AGAAGAGG AGTGG GT GGAGACGGG GG
- - TC

GAM7957 297 GPR1 2 2031 NP_005270.1 3 578 CTACTCGGGAGG A AACC T 3 C c b

CTGAAGCAGGAG TC CTGC TC GCCTCCCG
AATCACTT AG GACG AG CGGAGGGC
- A--- T

GAM7957 297 GPR1 2 10434 NP_005270.1 3 612 GAACCTGGGAGG TG 3 C b b
CAGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCCAA AGTG GTTGGAGACGGAGGGT
GT

GAM7957 297 GRAF 1 14162 NP_055886.1 3 3981 GAGCCCGGGAGG C 3 C b b
CGGAGATTGCGG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGGCGTT GAGGCGGAGGGC
A

GAM7957 297 GREB1 1 13343 NP_683701.1 3 724 GAACTTGGGAGG TG 3 C b b
CAGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCCGA AGTG GTTGGAGACGGAGGGT
GT

GAM7957 297 GRM6 1 9275 NP_000834.1 3 953 GAACCTGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTGT AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 GRTP1 1 18691 NP_078995.1 3 650 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 GSG2 1 19193 NP_114171.1 3 276 CTACTCGGGAGG A AAC T 3 C c c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
GATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 GTF2F1 1 13402 NP_002087.1 3 633 GAACCTGGGAGG T TG 3 C c c

TGGAGGTTGCTG TCAC GCAACCTC CCTCCCG
TGAGCTGA AGTG CGTTGGAG GGAGGGT
T GT
GAM7957 297 GTPBP5 3 2483 NP_056481.1 3 1623 GAACCTGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT
C
GAM7957 297 GTPBP5 3 12059 NP_056481.1 3 1306 GAGCCTGGGAGG A CT 3 C c b
TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAGCCGT AGTGACGT GGA TGGAGGGT
C AC
GAM7957 297 GTPBP5 3 15564 NP_056481.1 3 1589 CTACTCGGGAGG A AACC T 3 C c b
CTGAAGCAGGAG TC CTGC TC GCCTCCCG
AATGGCGT AG GACG AG CGGAGGGC
- A--- T
GAM7957 297 GZMH 1 6446 NP_219491.1 3 91 AGGGGTGGGCAG A --- - 3 C c c
TCAGGGTTGCAG TC CTGCAACCT CTGCCT CCC
GACTGTAA AG GACGTTGGG GACGGG GGG
- ACT T
GAM7957 297 H2-ALPH 1 15749 XP_054284.3 5 13 GCGCGCACAGGC - - CCC 3 C c c
A AGGAGGTTGCAG TCA CTGCAACCTC TGCCT
TTGGGCGC GGT GACGTTGGAG ACGGA
T G CAC
GAM7957 297 H2AFX 1 2926 NP_002096.1 3 802 TTTAGGGGAGGG TC---- A- - 3 C c c
CAGAGGCCTGCA ACTGCA CCTCTGCC TCCC
GTTTGGCT TGACGT GGAGACGG AGGG
TCGGTT CC G
GAM7957 297 HBS1L 1 12190 NP_006611.1 3 1795 GAGCCCAGGAGG A T C 3 C c c
TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCCAT AGTGACGT GGAG TGGAGG
C C A
GAM7957 297 HCGIX 1 641 NP_005835.2 3 298 GAGCCCAGGAGT A TGC C 3 C c c
TCGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C CTT A
GAM7957 297 HCNGP 2 15274 NP_037392.1 3 1349 TTTTGTGGGAGG -- AACCT 3 C c c
CAGCATGGCACC TCAC TGC CTGCCTCCCG
GTGGAAAG GGTG ACG GACGGAGGGT
CC GTAC-
GAM7957 297 HCNGP 2 20026 NP_037392.1 3 1054 TCAGTGGGTGGG GC---- - 3 C c c
CAGAGGTTTAGA TCACT AACCTCTGCCT CCCG
AAGGTGGT GGTGG TTGGAGACGGG GGGT

```
                                        AAAGAT         T
GAM7957  297   HEMK   1  9386  NP_057257.1  3  4119  CTGTAAAGGAGG    ---  A CT      C       3  C  c
c
                                CAGGAGTGTCAG TCACT   GCA C  CTGCCTCC
                                AGTGACGG    AGTGA   TGT G  GACGGAGG
                                          GAC   - AG       A
GAM7957  297   HES2   3  5827  XP_290879.1  3  1178  CTACTCGGGAGG  A  GCAA   T           3  C  c
c
                                CTGAGGCAAGAG TC CT    CCTC GCCTCCCG
                                AATCACTT    AG GA    GGAG CGGAGGGC
                                          A  AC--    T
GAM7957  297   HES2   3  15984 XP_290879.1  3  3024  GAACCCAGGAGG          TG    C       3  C  c  c

                                TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                          GT     A
GAM7957  297   HES2   3  19032 XP_290879.1  3  1210  GAACCTCGGAGG        C  T    C       3  C  c  c

                                CTGAAGTTGCAG TCACTGCAAC TC GCCTCC
                                TGAGCCAA    AGTGACGTTG AG CGGAGG
                                          A  T     C
GAM7957  297   HES6   1  2945  NP_061115.2  3  343   GGGCTCTGGGGG  A   A        C       3  C  c  c
                                CAGAGGTGGCAG TC CTGC ACCTCTGCCTCC
                                GAATGGTG    AG GACG TGGAGACGGGGG
                                          -   G          T
GAM7957  297   HHLA2  1  5686  NP_009003.1  5  207   GAACCCGGGAGG     C                3  C  b  b
                                CGGAGGTTACAG TCACTG AACCTCTGCCTCCCG
                                TGAGCCTT    AGTGAC TTGGAGGCGGAGGGC
                                          A
GAM7957  297   HIC    1  19869 XP_041273.1  3  645   GAACCCGAGAGG        C      C        3  C  b  b
                                CGGAAGTTGCAG TCACTGCAAC TCTGCCTC CG
                                TGAGCCGA    AGTGACGTTG AGGCGGAG GC
                                          A       A
GAM7957  297   HIG2   1  2455  NP_037464.1  3  398   TGAACCCGGGGA          C T         3  C  b  b
                                CGGAGGTTGCAG TCACTGCAACCTCTG C CCCG
                                TGAACCGA    AGTGACGTTGGAGGC G GGGC
                                          A -
GAM7957  297   HIP1   1  19132 NP_005329.2  3  2391  GAACCCCAGAGG             CC       3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
                                TGAGCTGA    AGTGACGTTGGAGACGGAG
                                            AC
GAM7957  297   HM13   1  18691 NP_848697.1  3  1414  GAACCTGGGAGG                    3  C  b  b
                                CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   HMGA2  1  3859  NP_003474.1  3  71    TTTTGAAGGGAG       ACC  GC          3  C  c
c
                                AAGACACTGCAG TCACTGCA   TCT  CTCCC
                                TGACCACT    AGTGACGT   AGA  GAGGG
                                          CAC   A-
```

GAM7957 297 HRH1 1 15027 NP_000852.1 3 1283 GAACCCGGGAGG T TG 3 C c c

TGGAGGTTGCCG TCAC GCAACCTC CCTCCCG
TGAGCCAA AGTG CGTTGGAG GGAGGGC
C GT

GAM7957 297 HRH4 1 16196 NP_067637.2 3 1048 CTACTCGGGAGG A- AAC T 3 C c c

CTGAGGCAGGGG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
GG --- T

GAM7957 297 HSD17B7 1 16464 NP_057455.1 3 205 GAGGCTGGGAGG 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 HSH2 1 10438 NP_116244.1 3 687 GAACCCGGGAGG 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 HSMPP8 1 4558 XP_167894.1 3 1128 GAGCCAGGGAGG A CT 3 C c c

TCAAGGCTGCAG TCACTGCA CCT GCCTCCC
TGAGCCGT AGTGACGT GGA TGGAGGG
C AC

GAM7957 297 HSPA5 1 10438 NP_005338.1 3 1303 GAACCCGGGAGG 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 HSPC043 1 12141 NP_067041.1 3 971 GAACCTGGGAGG 3 C b b

CAGGGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGGGACGGAGGGT

GAM7957 297 HUNK 1 2603 NP_055401.1 3 2039 GAACCTAGGAGG A T C 3 C c c

TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCCAA AGTGACGT GGAG TGGAGG
C C A

GAM7957 297 HYPK 1 9495 NP_057484.3 3 703 GAAATTGGAAAG C- C 3 C c c

CAGAGGTTGCAG TCACTGCAACCTCTGC TCC
TGAGCTGA AGTGACGTTGGAGACG AGG
AA T

GAM7957 297 IAPP 1 19057 NP_000406.1 3 596 GAACCCAGGAGG C 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 IFIT4 1 3297 NP_001540.2 3 377 GAACCTGGAAGG G C 3 C b b

AAGAGGTTGCAG TCACTGCAACCTCT CCT CCG
TGAGCCAA AGTGACGTTGGAGA GGA GGT
A A

GAM7957 297 IFNAR1 1 7044 NP_000620.1 3 416 GAAAACAGGAGG TG C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG

```
                                                GT    A
GAM7957  297   IFNGR2  1  17119 NP_005525.1  5  4    GTTGACTGGAGG            C       3  C  b  b
                                  CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                  TGAGCCGA    AGTGACGTTGGAGGCGGAGG
                                                  T
GAM7957  297   IHPK3   1  18598 NP_473452.1  5  460  GTCTCCCGGGAG  C C     C         3  C  c  c
                                  CAGAGGTTCTAT TCA TG AACCTCTGC TCCCG
                                  GAATCCCT    AGT AT TTGGAGACG AGGGC
                                            - C       -
GAM7957  297   IL10    1  8482  NP_000563.1  3  836  GAACCCAGGAGA       C  GC   C       3  C  c  c
                                  TGGAAGTTGCAG TCACTGCAAC TCT  CTCC
                                  TGAGCTGA    AGTGACGTTG AGG  GAGG
                                              A  TA   A
GAM7957  297   IL10RB  1  18976 NP_000619.3  3  545  GGGAGGAGGAGG         G   C       3  C  c  c

                                  AGGAGGTTGCAG TCACTGCAACCTCT CCTCC
                                  TGAGCCGA    AGTGACGTTGGAGG GGAGG
                                               A    A
GAM7957  297   IL13RA1 1  11740 NP_001551.1  3  739  GAACCTGGGAGG         TG          3  C  b  b

                                  TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                  TGAGCAGA    AGTGACGTTGGAG  GGAGGGT
                                              GT
GAM7957  297   IL17R   1  11720 NP_055154.3  3  625  GAATCTGGGAGG                    3  C  b  b
                                  CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   IL18    1  9399  NP_001553.1  3  245  GCACTCCGGAGG    TG        C       3  C  c  c
                                  TAGAGGTTGTGG TCAC  CAACCTCTGCCTCC
                                  TGAGCCGA    AGTG  GTTGGAGATGGAGG
                                            GT          C
GAM7957  297   IL1R1   1  10406 NP_000868.1  3  454  GAACCGGGGAGA          C         3  C  b  b
                                  CGGAGGTTGCAG TCACTGCAACCTCTG CTCCC
                                  TGAGCCGA    AGTGACGTTGGAGGC GAGGG
                                               A
GAM7957  297   IL23R   1  9056  NP_653302.2  3  783  GAACCAGGAAGG   C        C       3  C  b  b
                                  CAGAGGTTGCAC TCA TGCAACCTCTGCCT CC
                                  TGAGCTGA    AGT ACGTTGGAGACGGA GG
                                            C          A
GAM7957  297   IL28RA  1  15436 NP_734464.1  3  258  GTGGGCTGAGGT    TG     -  --      3  C  c  c
                                  CAGAGGTTGGTG TCAC  CAACCTCTG CCTC  CC
                                  GGGTGTCA    GGTG  GTTGGAGAC GGAG  GG
                                            --       T   TC
GAM7957  297   IL28RA  1  15436 NP_775087.1  3  258  GTGGGCTGAGGT    TG     -  --      3  C  c  c
                                  CAGAGGTTGGTG TCAC  CAACCTCTG CCTC  CC
                                  GGGTGTCA    GGTG  GTTGGAGAC GGAG  GG
                                            --       T   TC
GAM7957  297   IL28RA  1  15436 NP_775088.1  3  955  GTGGGCTGAGGT    TG     -  --      3  C  c  c
                                  CAGAGGTTGGTG TCAC  CAACCTCTG CCTC  CC
                                  GGGTGTCA    GGTG  GTTGGAGAC GGAG  GG
```

```
                                        --       T   TC
GAM7957  297   IL6R   1  17754 NP_000556.1  3 1415  GAGCCTGGGAGG       A  CT          3  C  c  c
                                  TCAAGGCTGCAG TCACTGCA CCT  GCCTCCCG
                                  TGAGCCGA    AGTGACGT GGA  TGGAGGGT
                                        C   AC
GAM7957  297   IL6R   1  17754 NP_852004.1  3 1630  GAGCCTGGGAGG       A  CT          3  C  c  c
                                  TCAAGGCTGCAG TCACTGCA CCT  GCCTCCCG
                                  TGAGCCGA    AGTGACGT GGA  TGGAGGGT
                                        C   AC
GAM7957  297   IL8RB  1  10438 NP_001548.1  3 497   GAACCCGGGAGG                    3  C  b  b
                                  CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   INE1   2  13712 NP_003660.1  3 415   CTACTCGGGAGG  A GCA    T          3  C  c  c

                                  CTGAGGTGGGAG TC CT   ACCTC GCCTCCCG
                                  GATCGCTG    AG GA   TGGAG CGGAGGGC
                                        - GGG    T
GAM7957  297   INE1   2  18648 NP_003660.1  3 447   GAGCCTGGGAAG       A   T C         3  C  c  c
                                  TTGAGGCTGCAG TCACTGCA CCTC GC TCCCG
                                  TGAGCCGT    AGTGACGT GGAG TG AGGGT
                                        C   T A
GAM7957  297   ING2   1  13415 NP_477519.1  3 353   CTATTCGGGAGG  A   AAC  T          3  C  c  c

                                  CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                  AATGGCNT    AG GACG   GAG CGGAGGGC
                                        -   ---  T
GAM7957  297   INHBC  1  16412 NP_005529.1  3 38    GGTATGGGCAGC   C      ----     C--     3  C  c  c
                                  CCAAGGTTGCAT TCA TGCAACCT    CTGCCT   CC
                                  GGGAAAAC    GGT ACGTTGGA    GACGGG   GG
                                        -       ACCC      TAT
GAM7957  297   INPP5B 2  12792 XP_300739.1  3 1656  GAACCCAGGAGG             C       3  C  b  b
                                  CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                  TGAGCCGA    AGTGACGTTGGAGACGGAGG
                                              A
GAM7957  297   INPP5B 2  16413 XP_300739.1  3 2269  GAACCCAGGAGG T-----            C     3  C  c
b
                                  CAGAGGTTGCAG      CACTGCAACCTCTGCCTCC
                                  TGCGCTGA          GTGACGTTGGAGACGGAGG
                                        AGTCGC              A
GAM7957  297   INPP5D 1  9965  NP_005532.1  5 42    GAGGCAACGGGC          CT  T         3  C  b  b
                                  GGCAGGTTGCAG TCACTGCAACCT  GCC CCCG
                                  TGGAGGGG    GGTGACGTTGGA  CGG GGGC
                                        --  C
GAM7957  297   IPP    2  7118  NP_005888.1  3 1145  CTGCTTGGGAGG  A       T          3  C  b  b
                                  CTGAGGTTGCAG TC CTGCAACCTC GCCTCCCG
                                  GATCGCTT    AG GACGTTGGAG CGGAGGGT
                                        -        T
GAM7957  297   IPP    2  11184 NP_005888.1  3 1177  GAGCCCAGGAGG      A T  -   C       3  C  c  b
                                  TCAGGGCTGCAG TCACTGCA CC CTG CCTCC
```

TGAGCCGA AGTGACGT GG GAC GGAGG
C - T A
GAM7957 297 IRAK1 1 12737 NP_001560.1 3 704 ATGCTTGGGAGG A T 3 C c c
TCGAGGCTGCAG TCACTGCA CCTC GCCTCCCG
TGAGTCAT AGTGACGT GGAG TGGAGGGT
C C
GAM7957 297 IRAK4 1 10607 NP_057207.1 3 1291 GAACCAGGGAGG 3 C b b
TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCTGA AGTGACGTTGGAGATGGAGGG

GAM7957 297 ITGAD 1 5341 XP_113880.1 3 316 TTGCCTAGGGGG A C 3 C c c
CAGAGGGTGCAG TCACTGCA CCTCTGCCTCC
TGGCAGTG GGTGACGT GGAGACGGGGG
G A
GAM7957 297 ITGAL 1 15224 NP_002200.1 3 1231 GAACCTGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 JPH2 1 7268 NP_065166.2 3 761 GTGGGAAGAGGG A CT ----- 3 C c c
GTTAAGGTGCAG TCACTGCA CCT GCC TCCCG
TGATGATG AGTGACGT GGA TGG AGGGT
- AT GGAGA
GAM7957 297 KAI1 1 4535 NP_002222.1 3 585 TGAACCCGGGAG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCTGA AGTGACGTTGGAGGCG AGGGC
-
GAM7957 297 KBRAS2 1 3310 NP_060065.2 3 828 GAACTCAGAAGG A CCC 3 C c
c
CGGAGGCTGCAG TCACTGCA CCTCTGCCT
TGAGCCGA AGTGACGT GGAGGCGGA
C AGA
GAM7957 297 KCNA7 2 2483 NP_114092.2 3 2093 GAACCTGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT
C
GAM7957 297 KCNA7 2 15108 NP_114092.2 3 2059 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KCNH6 2 18166 NP_775115.1 3 150 GAACCCTAAAGG CCC 3 C c c

CAGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCCGA AGTGACGTTGGAGACGGA
AAT
GAM7957 297 KCNH6 2 19242 NP_110406.1 3 285 GAACCCGGGAGG A TG 3 C c
c
TGGAGGTTGCAG TC CTGCAACCTC CCTCCCG
GGAGCCGA AG GACGTTGGAG GGAGGGC
G GT

```
GAM7957  297   KCNIP2  1  14673  NP_055406.2  3  999   GAAGGAGGGAGG   C-  AACC          3  C  c
c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNIP2  1  14673  NP_775283.1  3  999   GAAGGAGGGAGG   C-  AACC          3  C  c
c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNIP2  1  14673  NP_775284.1  3  999   GAAGGAGGGAGG   C-  AACC          3  C  c
c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNIP2  1  14673  NP_775285.1  3  999   GAAGGAGGGAGG   C-  AACC          3  C  c
c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNIP2  1  14673  NP_775286.1  3  999   GAAGGAGGGAGG   C-  AACC          3  C  c
c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNIP2  1  14673  NP_775287.1  3  999   GAAGGAGGGAGG   C-  AACC          3  C  c
c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNIP2  1  14673  NP_775464.1  3  1438  GAAGGAGGGAGG   C-  AACC          3  C
c  c
                                 CAGGCATAGCAT TCA  TGC   TCTGCCTCCC
                                 CTGAACCC    AGT  ACG   GGACGGAGGG
                                         CT   ATAC
GAM7957  297   KCNJ14  1  18135  NP_733838.1  5  10    GGTTGCAGTGAG        T  C  CC       3  C  c
c
                                 CTGAGGTTGCGG TCACTGCAACCTC GC TC
                                 TGAGCTGA    AGTGGCGTTGGAG CG AG
                                           T  -  TG
GAM7957  297   KCNJ5   1  15224  NP_000881.3  3  1271  GAACCTGGGAGG        TG          3  C  b  b

                                 TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                 TGAGCCAA    AGTGACGTTGGAG  GGAGGGT
                                           GT
GAM7957  297   KCNK6   1  2853   NP_004814.1  3  1391  GAGGCCAGGAGT      A   TGC   C       3  C  c
c
                                 TTGAGGCTGCAG TCACTGCA CCTC   CTCC
                                 TGAGTTAT    AGTGACGT GGAG   GAGG
                                           C   TTT   A
```

GAM7957 297 KCNMB3 1 7035 NP_741981.1 5 45 CCTGGGAGGCGG --- 3 C b b
AGGAGGTTGCAG TCACTGCAACCTCT GCCTCCCG
TGAACTGA AGTGACGTTGGAGG CGGAGGGT
AGG
GAM7957 297 KIAA012 1 4129 NP_055607.1 3 2650 CTCGGGAAAGGG - G --- --- 3 C c c
5 CAGAGGTCACTG TCAC T CA ACCTCTGCC TCCCG
GGGGTGGG GGTG G GT TGGAGACGG AGGGC
G G CAC GAA
GAM7957 297 KIAA014 1 1809 NP_055476.1 3 2099 TCCTGTGGAAGG AAC C 3 C c
c
0 CAGAGGCAGTGA TCACTGC CTCTGCCT CCG
GGGAGGTG AGTGACG GAGACGGA GGT
--- A
GAM7957 297 KIAA021 1 12651 NP_055445.1 5 24 TCGGGCGGGAGG A AACC 3 C c
c
1 CGGGAGGCGGGA TC CTGC TCTGCCTCCCG
GGCCGGGC AG GGCG GGGCGGAGGGC
- GA--
GAM7957 297 KIAA023 1 8698 NP_055562.1 3 1502 AGGGTGAAAGGC AC- - ---- 3 C c c
7 GAGAGGTTGCAC TC TGCAACCTCT GCCT CCC
AGGACATG AG ACGTTGGAGA CGGA GGG
GAC G AAGT
GAM7957 297 KIAA026 1 15976 NP_067677.1 3 1155 GAAACTGGAAGG C 3 C b b
6 CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCAA AGTGACGTTGGAGACGGA GGT
A
GAM7957 297 KIAA027 1 17630 XP_048199.1 5 19 CCTCAGCTTCGA A T C CC 3 C c
c
6 GCCGAGGTGCAG TCACTGCA CCTC GC TC
TGAGCTGG AGTGACGT GGAG CG AG
- C - CT
GAM7957 297 KIAA035 1 6039 NP_055501.1 3 1663 GAACCCGGGAGG C 3 C b b
5 CGGAGGTTACAG TCACTG AACCTCTGCCTCCCG
TGAGCTGA AGTGAC TTGGAGGCGGAGGGC
A
GAM7957 297 KIAA039 1 9795 XP_029438.2 3 967 GACTGCGGGAGG T-- --- A 3 C c c
7 CAGGGGATGCAT CACT GCA CCTCTGCCTCCCG
GGGTGTCC GTGG CGT GGGGACGGAGGGC
CCT GTA A
GAM7957 297 KIAA040 1 11277 NP_055517.1 3 3715 GAACCCGGGAGG C 3 C b b
8 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCAGA AGTGACGTT GAGACGGAGGGC
C
GAM7957 297 KIAA041 1 10439 NP_055526.2 3 1203 GAACCTGGGAGG 3 C b b
9 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 KIAA042 1 5274 NP_055587.1 3 137 GAGGAGGGCAGG CAAC - 3 C c c
7 CAGAGTCGGTGG TCACTG CTCTGCCT CCC
CCAGTCTG GGTGGC GAGACGGA GGG
T--- C
GAM7957 297 KIAA044 1 19849 XP_044155.1 5 1475 GAACCCGGGAGG C TG 3 C c c
6 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGGGTGGA GGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 KIAA044 1 19104 NP_060066.1 3 1314 GGAGACACCAGC A - ------ C 3 C c c
9 AGGTGGCTGCAG TCACTGCA CC TCTGC CTCC
TGACGTTA AGTGACGT GG GGACG GAGG
C T ACCACA -
GAM7957 297 KIAA046 1 7582 NP_055666.1 3 2730 CTTCCCGGGAGG C CA- ---- 3 C c c
9 CCCTGGGAGGTG TCA TG ACCTCT GCCTCCCG
ATCATTGA AGT AC TGGAGG CGGAGGGC
T TAG GTCC
GAM7957 297 KIAA047 1 2975 NP_055672.1 3 2389 GAACCCAGGAGG C 3 C b b
1 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGGGCCAA GGTGACGTTGGAGACGGAGG
A
GAM7957 297 KIAA047 1 18691 XP_290898.1 3 916 GAACCTGGGAGG 3 C b b
2 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 KIAA047 2 1492 NP_055679.1 3 2960 CTACTCGGGAGG A AAC T 3 C c c
5 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA047 2 11624 NP_055679.1 3 2994 GAATCCAGGAGG C C 3 C c c

5 CGAAGGTTGCAG TCACTGCAACCT TGCCTCC
TGAGCTGA AGTGACGTTGGA GCGGAGG
A A
GAM7957 297 KIAA047 1 10354 NP_055671.1 5 387 GAAGCGCGGGAC ACC -- 3 C b b
6 AGGCAGATGCAG TCACTGCA TCTGCC TCCCG
TGAGTGAG AGTGACGT AGACGG AGGGC
--- AC
GAM7957 297 KIAA047 1 18191 NP_055685.1 3 1964 TGGGATGGGGCT - T- --- 3 C c c
8 TGGGAGTTGCAG TCACTGCAAC CTC GCC TCCCG
TGAATGTC AGTGACGTTG GGG CGG AGGGT
A TT GGT
GAM7957 297 KIAA051 1 1907 NP_055511.1 3 4967 GAGCCCAGGAGG TG C 3 C c c
4 TGGAGGTTGCAG TCACTGCAACCTC CCTCC

TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 KIAA052 1 4002 NP_055617.1 5 40 AAGCAGGGGCGG A CAA-- T 3 C c c
8 CAGAGGCTCAAC TC CTG CCTCTGCC CCC
GGGATGCT AG GGC GGAGACGG GGG
- AACTC C
GAM7957 297 KIAA055 2 2342 XP_085507.1 3 1978 GAGCCCAGGAAG A T C C 3 C c b
7 TTGAGGCTGCAG TCACTGCA CCTC GC TCC
TGAGCTGT AGTGACGT GGAG TG AGG
C T A A
GAM7957 297 KIAA055 2 2789 XP_085507.1 3 1817 GAACCAGGGAGG 3 C b b
7 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCCGA AGTGACGTTGGAGGCGGAGGG

GAM7957 297 KIAA056 2 609 NP_055649.1 3 925 GAACCTGGGAGG C 3 C b b
3 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGT
C
GAM7957 297 KIAA056 2 15108 NP_055649.1 3 891 CTACTCGGGAGG A AAC T 3 C c b
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA056 1 12789 XP_039912.1 3 2443 GAACCTGGGAGG C 3 C b b
5 CAAAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCTGA AGTGACGTTGGA ACGGAGGGT
A
GAM7957 297 KIAA059 1 9935 NP_055529.1 5 14 TCAGCGGCCTGG C --- TC- 3 C c c
0 CAGAGGTTTCAG TCA TGC AACCTCTGCC CCG
CGCTGAGG AGT GCG TTGGAGACGG GGC
C ACT TCC
GAM7957 297 KIAA062 1 16922 NP_055604.1 3 3558 CTGCTCGGGAGG A AAC T 3 C c c
8 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA064 1 17488 NP_055477.1 3 279 GCAGGTGGGAGG T- C C 3 C c c
5 CACAGATTGTCC TCAC GCAA CT TGCCTCCCG
GTGGGAGG GGTG TGTT GA ACGGAGGGT
CC A C
GAM7957 297 KIAA071 1 6186 NP_055682.1 3 2487 CTGCAGGGAGGG CT -- - 3 C b b
1 CAGAGGCATTGC TCA GCAA CCTCTGCC TCCC
TGAGACTG AGT CGTT GGAGACGG AGGG
-- AC G
GAM7957 297 KIAA075 1 16933 NP_056120.1 5 14 TGAGGGAGGACC A TCTG--- 3 C c c

9 TGCTGGCTGCAG TCACTGCA CC CCTCCC
TGAGGAGC AGTGACGT GG GGAGGG
C TCGTCCA
GAM7957 297 KIAA077 1 11119 NP_055505.1 3 1090 TCCCTCAGCCAG - T CCC 3 C c
c
3 GCAGGGTTGCAG TCA CTGCAACC CTGCCT
CTGAGGGC AGT GACGTTGG GACGGA
C - CCG
GAM7957 297 KIAA082 1 15983 XP_027906.5 3 4039 GAACCCGGGAGG TG 3 C b
b
5 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 KIAA083 1 3413 NP_055739.1 3 1328 TGAACCGGGAGG 3 C b b
1 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 KIAA087 2 4557 NP_055755.1 3 2397 GAACCCGGGAGG TGC 3 C b
b
2 CAGAGGTTATCG TCAC AACCTCTGCCTCCCG
TGAGCTGA AGTG TTGGAGACGGAGGGC
CTA
GAM7957 297 KIAA087 2 19196 NP_055755.1 3 2093 GAACCCGAGAGG C 3 C b b
2 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC CG
TGAGCCGA AGTGACGTTGGAGGCGGAG GC
A
GAM7957 297 KIAA088 2 3610 XP_046660.4 3 1600 AAACCTGGGATG TG C 3 C c c
4 TGGAGGTTGCAG TCACTGCAACCTC C TCCCG
TGAACTGA AGTGACGTTGGAG G AGGGT
GT T
GAM7957 297 KIAA088 2 5856 XP_046660.4 3 1433 CACTTTGGGAGG GCAA C 3 C c
c
4 CAAAGGCAGGTG TCACT CCT TGCCTCCCG
GATCACCT GGTGG GGA ACGGAGGGT
AC-- A
GAM7957 297 KIAA088 3 3264 NP_056192.1 3 2093 GAACCCAGGAGG A C 3 C c c
9 CGGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCTGA AGTGACGT GGAGGCGGAGG
C A
GAM7957 297 KIAA088 3 7577 NP_056192.1 3 223 GAACCCAGTAGG C CCC 3 C c
c
9 CGGAAGTTGCAG TCACTGCAAC TCTGCCT
TGAGCTGA AGTGACGTTG AGGCGGA
A TGA
GAM7957 297 KIAA088 3 13091 NP_056192.1 5 12 GAGCCCAGGAGT A TGC C 3 C c
c
9 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C TTT A

GAM7957 297 KIAA088 3 13091 NP_689470.1 5 203 GAGCCCAGGAGT A TGC C 3 C c c
9 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 KIAA089 1 12683 XP_048457.1 3 2248 GAGCCCAGGAGA A TGC C 3 C c c
2 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCATG AGTGACGT GGAG GAGG
C TTA A
GAM7957 297 KIAA090 2 3136 NP_055764.1 3 245 CAACCTGGGAGG 3 C b b
7 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 KIAA090 2 11102 NP_055764.1 3 633 GAACTTGGGAGG TG 3 C b b
7 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGGGCCGA GGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 KIAA091 1 13066 XP_044347.3 3 259 GAACCTGGGAGG 3 C b b
3 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 KIAA092 1 10571 NP_055712.1 3 3236 GAACCCAGGAGG C C 3 C c c
4 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 KIAA093 1 2363 XP_052620.6 3 1982 CTACTCGGGAGG A AAC T 3 C c c
5 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCAATC AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA098 1 2679 XP_028867.2 3 1296 GAACCTGGGAGG A 3 C b b
1 CGGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAGCTGG AGTGACGT GGAGGCGGAGGGT
C
GAM7957 297 KIAA100 3 1269 NP_055775.1 3 2213 GAGCCTGGGAGG TG 3 C b b

1 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGTGGA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 KIAA100 3 15875 NP_055775.1 3 1879 CTACTCGGGAGG A AAC T 3 C c b
1 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AGAATCGC AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA100 3 19927 NP_055775.1 3 1913 GAACCGGGGAGG A TG 3 C b b
1 TGGAGGCTGCAG TCACTGCA CCTC CCTCCC
TGAGCCGA AGTGACGT GGAG GGAGGG

C GT
GAM7957 297 KIAA103 1 5109 XP_038604.4 3 2172 GAACCCTGGAGG C 3 C b b
2 CAGAGGTTGTAG TCACTGCAACCTCTGCCTCC
TGAGTCGT AGTGATGTTGGAGACGGAGG
T
GAM7957 297 KIAA103 1 9356 NP_055724.1 3 2855 TTTCTGGGGAGG A AAC 3 C c
c
6 CAGAGAGGCAGG TC CTGC CTCTGCCTCCC
GACTTTGG AG GACG GAGACGGAGGG
G GA-
GAM7957 297 KIAA108 2 1442 XP_047610.1 3 967 CTACTCGGGAGG A AA T 3 C c c
6 CTGAGGCCGTAG TC CTGC CCTC GCCTCCCG
GATCCCTT AG GATG GGAG CGGAGGGC
- CC T
GAM7957 297 KIAA108 2 6649 XP_047610.1 3 1915 GAAATTGGGAGG A GCAA-- 3 C c
c
6 CAGGGGGAATAA TC CT CCTCTGCCTCCCG
AGGAAATC AG GA GGGGACGGAGGGT
- AATAAG
GAM7957 297 KIAA111 1 6299 NP_055746.1 5 219 GGAGGAGGGAGG - GCA - 3 C c
c
5 CAGGAGGTGAGG TCA CT ACCTC TGCCTCCC
TTGGAAGT GGT GG TGGAG ACGGAGGG
T AG- G
GAM7957 297 KIAA112 2 2893 XP_050325.1 3 2728 CTTCCTGGGAGG G ACC 3 C c
c
6 CAGGTGTGGGTG TCACT CA TCTGCCTCCCG
ACCGGGGC AGTGG GT GGACGGAGGGT
- GT-
GAM7957 297 KIAA112 2 18121 XP_050325.1 3 3429 GGCGGGAAGGGG T AAC --- 3 C c
c
6 CAGAGGCCGTGA TCAC GC CTCTGCC TCCCG
GCTCTCAG AGTG CG GAGACGG AGGGC
C --- GGA
GAM7957 297 KIAA113 1 6682 XP_166110.3 5 348 CTCTCTGGGAGG CT AA - 3 C c c
6 CAGATGGGAGCC TCA GC CC TCTGCCTCCCG
ATGGCTTA GGT CG GG AGACGGAGGGT
AC AG T
GAM7957 297 KIAA115 1 3204 XP_030864.2 3 1519 GTGGCTGTGGGA A G- CC 3 C c
c
5 CAGAGGTTGGAA TC CT CAACCTCTG TCCCG
GGAAAGGA AG GA GTTGGAGAC AGGGT
- AG --
GAM7957 297 KIAA116 2 6420 XP_045358.2 3 2871 GAACCCAGGAGG CCT C 3 C c
b
4 CAGTGATTGCAG TCACTGCAA CTGCCTCC
TGAGCTGA AGTGACGTT GACGGAGG
AGT A

GAM7957 297 KIAA116 2 6526 XP_045358.2 3 1257 GAACCCGGCAGG C 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCGA AGTGACGTTGGAGACGGA GGC
C
GAM7957 297 KIAA118 2 9991 NP_065195.1 3 1854 GAACCCGGGAGG C TG 3 C b
b
1 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCAA AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 KIAA118 2 16802 NP_065195.1 3 346 AAGCATCAGGGA AC CT C 3 C c
b
1 TGCTAAGTGCAG TCACTGCA CT GC TCCC
TGATGAGG AGTGACGT GA CG AGGG
-- AT T
GAM7957 297 KIAA119 2 8382 XP_041843.1 3 1510 GGGCACAGAGGG G---- ------ 3 C c
c
3 CAGAGGTTGGGC TCACT CAACCTCTGCCT CCC
GGGGTGGG GGTGG GTTGGAGACGGG GGG
GGCGG AGACAC
GAM7957 297 KIAA119 2 8722 XP_041843.1 5 13 TCGCTGGGGAGG T AAC-- 3 C c c
3 CAGAGTCCTCGC TCAC GC CTCTGCCTCCC
GTGGTCTC GGTG CG GAGACGGAGGG
- CTCCT
GAM7957 297 KIAA120 2 8547 XP_050478.1 3 1354 GAACCTGGAAGG C C 3 C b b
2 CAGAGATTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCTGA AGTGACGTT GAGACGGA GGT
A A
GAM7957 297 KIAA120 2 15089 XP_050478.1 3 1320 CTACTCGGGAGG A AAC T 3 C c
b
2 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA122 2 9422 XP_036408.3 3 2835 GAACCCAGGAGG C 3 C b b
8 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 KIAA122 2 15089 XP_036408.3 3 2801 CTACTCGGGAGG A AAC T 3 C c
b
8 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA124 1 15329 XP_039676.1 3 1335 GTTGCAATGAGG A C CC 3 C c
c
0 CAAAGGATGCAG TCACTGCA CCT TGCCTC
TGACTTTT AGTGACGT GGA ACGGAG
A A TA
GAM7957 297 KIAA127 1 3813 XP_291190.1 3 497 GAACCTGGGAGG TG 3 C b b
0 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGGGCCAA GGTGACGTTGGAG GGAGGGT

GT
GAM7957 297 KIAA127 1 18088 XP_045472.1 3 2434 GAACCCAGGATG C C 3 C c c

1 CGGAGGTTGCAG TCACTGCAACCTCTGC TCC
TGAGCCGA AGTGACGTTGGAGGCG AGG
T A
GAM7957 297 KIAA127 1 13059 XP_039169.1 3 387 GAACCTAGGAGG C 3 C b b

6 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 KIAA127 1 3417 XP_035114.3 3 1766 GAACTGGGGAGG - G 3 C b b

7 AGAAGGTTGCAG TCACTGCAACCT CT CCTCCC
TGAGCCGA AGTGACGTTGGA GA GGAGGG
A -
GAM7957 297 KIAA134 1 3882 XP_044836.2 3 2489 TCTCCCTTCAGG CCC 3 C c c

0 CGGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCCGA AGTGACGTTGGAGGCGGA
CTT
GAM7957 297 KIAA134 2 9419 XP_043826.2 3 2025 GAACCCGGGAGG 3 C b b

8 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGGCGTTGGAGGCGGAGGGC

GAM7957 297 KIAA134 2 12559 XP_043826.2 3 1993 CTACTCGGGAGG A AAC T 3 C c
b

8 CTGAGGCAGGAA TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA137 1 20104 XP_040708.2 3 898 CAACCTGGGAGG A T 3 C c c

7 TTGAGGCTGCAG TCACTGCA CCTC GCCTCCCG
TGAGCTGT AGTGACGT GGAG TGGAGGGT
C T
GAM7957 297 KIAA139 1 10279 XP_046685.4 3 115 AGAGGGAGCAGG A G A --- 3 C c
c

9 CAGAGGGTGGGG TC CT CA CCTCTGCC TCCC
GACCTGGC AG GG GT GGAGACGG AGGG
- G G ACG
GAM7957 297 KIAA140 1 6419 NP_066363.1 3 328 AAACCCAGGAGG C 3 C b b

4 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 KIAA142 1 12788 XP_029703.1 3 1128 GAGCCCTGGAGG A CT C 3 C c
c

3 TCAAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCCAT AGTGACGT GGA TGGAGG
C AC T
GAM7957 297 KIAA144 1 10517 XP_290770.2 5 2710 CGTCCCAGGAGG AACCT C 3 C
c c

7 CAGGCAGTGGCT TCACTGC CTGCCTCC
ATGACAGT GGTGACG GACGGAGG
----- A

GAM7957 297 KIAA145 2 3412 XP_040100.3 5 234 GAACCCGTGAGG C 3 C b b
6 CAGAGGTTGCAG TCACTGCAACCTCTGCCTC CG
TGAACCGA AGTGACGTTGGAGACGGAG GC
T
GAM7957 297 KIAA145 2 18691 XP_040100.3 3 3420 GAACCTGGGAGG 3 C b b
6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 KIAA147 2 1492 XP_047550.1 3 1876 CTACTCGGGAGG A AAC T 3 C c
b
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA147 2 5557 XP_047550.1 3 1910 GAACCCGGGAAG C 3 C b b
3 CAGAGGTTGCGG TCACTGCAACCTCTGC TCCCG
TGAGCCGA AGTGGCGTTGGAGACG AGGGC
A
GAM7957 297 KIAA148 1 15677 XP_041126.4 3 2401 GAACCTGGGAGG C TG 3 C c
c
6 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCTGA AGTGACGTT GAG GGAGGGT
C GT
GAM7957 297 KIAA151 4 10439 XP_170889.1 3 741 GAACCTGGGAGG 3 C b b
8 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 KIAA151 4 14466 NP_056308.2 5 124 GAACCTGGGAGG T 3 C b b
8 CAGAGGTTGCCG TCAC GCAACCTCTGCCTCCCG
TGAGCTGA AGTG CGTTGGAGACGGAGGGT
C
GAM7957 297 KIAA151 4 17403 XP_170889.1 3 1203 GAACCCAGGAGG C 3 C b b
8 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 KIAA151 4 18859 XP_170889.1 3 266 GAACCCAGGAGG TG C 3 C c
b
8 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAG AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 KIAA153 2 5273 XP_049474.4 3 2000 AAGGCCTGGAGG GCAA C 3 C c
c
8 CAGGGGCAGAGG TCACT CCTCTGCCTCC
TGACGACA AGTGG GGGGACGGAGG
AGAC T
GAM7957 297 KIAA153 2 17039 XP_049474.4 3 2002 TGGAGGCAGGGG GCAA C 3 C
c c
8 CAGAGGTGACGA TCACT CCTCTGCCTCC
CAGTGCCC AGTGG GGGGACGGAGG
AGAC T
GAM7957 297 KIAA154 1 9321 XP_290536.2 5 9 GCACGGCGGCGG A AA - - 3 C c c

2 CAGAGGCGGCGG TC CTGC CCTCTGCC TC CCG
CGGCCGGG GG GGCG GGAGACGG GG GGC
C GC C C
GAM7957 297 KIAA155 1 16064 XP_290768.1 3 2711 GAGCCTGGGAGT A TGC 3 C c
c
4 TTGAGGCTGCAG TCACTGCA CCTC CTCCCG
TGAGCTAT AGTGACGT GGAG GAGGGT
C TTT
GAM7957 297 KIAA155 1 15359 XP_054472.2 3 2152 GAACCCAAGAGG C CC 3 C c
c
9 CAGAGTTTGCAG TCACTGCAA CTCTGCCTC
TGAGCTGA AGTGACGTT GAGACGGAG
T AA
GAM7957 297 KIAA159 1 17403 XP_050754.5 3 1597 GAACCCAGGAGG C 3 C b b
4 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 KIAA161 1 12333 XP_046531.1 3 462 GAACCCGGGAGG 3 C b b
4 TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGATGGAGGGC

GAM7957 297 KIAA161 1 17901 XP_290769.2 3 344 GAACCCGGGAGG AAC 3 C b
b
8 CAGAGATAGCAG TCACTGC CTCTGCCTCCCG
TGAACTGA AGTGACG GAGACGGAGGGC
ATA
GAM7957 297 KIAA163 1 15143 NP_061176.2 3 279 GAATCTGGGAGG 3 C b b
0 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAG AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 KIAA165 1 7120 XP_038022.1 5 730 GAACCCAGGAGG TG C 3 C c c

6 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCAGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 KIAA167 1 17218 XP_047672.4 5 30 GGCACCGGGAGG A AA T 3 C c
c
3 CGGTGGCGGCGG TC CTGC CC CTGCCTCCCG
CGGCGGCG GG GGCG GG GGCGGAGGGC
C GC T
GAM7957 297 KIAA167 1 10619 XP_290462.1 3 2880 GAACCCAGGAGA C C C 3 C c
c
4 CGGAGCTTGCAG TCACTGCAA CTCTG CTCC
TGAGCCGA AGTGACGTT GAGGC GAGG
C A A
GAM7957 297 KIAA171 1 1763 NP_085136.1 5 132 GGTTGCGGGAGG GCAACC - 3 C
c c
2 CTGGACTCTGGT TCACT TCT GCCTCCCG
GACTGTAA AGTGG AGG CGGAGGGC
TCTC-- T

GAM7957 297 KIAA171 1 2721 XP_042834.1 3 4232 GAACACGGGAGG 3 C b b
5 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCAGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 KIAA172 1 7563 XP_040280.2 3 5270 GAACCTGGGAGA C GC 3 C c
c
4 TGGAGATTGCAG TCACTGCAA CTCT CTCCCG
TGAGCAGA AGTGACGTT GAGG GAGGGT
A TA
GAM7957 297 KIAA173 1 10758 XP_290496.1 3 2892 GAGCCCAGGAGT TGC C 3 C c
c
5 TTGAGGTTGCAG TCACTGCAACCTC CTCC
TGAGCTGA AGTGACGTTGGAG GAGG
TTT A
GAM7957 297 KIAA177 1 3051 XP_086404.1 3 327 GAGCCCAAGAGG A T CC 3 C c
c
1 TTGAGGCTGCAG TCACTGCA CCTC GCCTC
TGAGCCAT AGTGACGT GGAG TGGAG
C T AA
GAM7957 297 KIAA182 1 13774 XP_290834.1 5 212 ATGGGAACGAGG A CAA --- 3 C c
c
7 CAGAGGAAATAG TC CTG CCTCTGCCTC CC
AGAAATTT AG GAT GGAGACGGAG GG
A AAA CAA
GAM7957 297 KIAA183 1 9403 XP_114087.2 3 2703 GAGCCCAGGAAG C C 3 C b b
6 CAGAGGTTGCAG TCACTGCAACCTCTGC TCC
TGAGCCTC AGTGACGTTGGAGACG AGG
A A
GAM7957 297 KIAA184 1 1419 XP_087056.4 3 1879 GAACCCGGGTGG T 3 C b b
1 CAGAGGTTGCAG TCACTGCAACCTCTGCC CCCG
TGAGCTGA AGTGACGTTGGAGACGG GGGC
T
GAM7957 297 KIAA185 1 17219 XP_166549.1 5 105 GGGAGGTGAAGG A G A ------ 3 C c
c
6 CAGAGGTGGAGG TC CT CA CCTCTGCC TCCC
ACATGGAC AG GA GT GGAGACGG AGGG
- G - AAGTGG
GAM7957 297 KIAA187 1 9531 NP_116277.1 3 195 ATCACTAGGAGG C 3 C b b
0 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCAGT AGTGACGTTGGAGACGGAGG
A
GAM7957 297 KIAA187 1 17416 XP_290737.1 3 1702 GAACCTGGGAGG TG 3 C b
b
1 TGGAGGTTGCGG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGGCGTTGGAG GGAGGGT
GT
GAM7957 297 KIAA187 1 16024 NP_149053.1 3 1362 AAACCTGAGAGG C CC 3 C c
c
2 CAGAGGTTACAG TCACTG AACCTCTGCCTC

TGAGCCAA AGTGAC TTGGAGACGGAG
A AG
GAM7957 297 KIAA187 1 5944 XP_056635.1 3 821 AAGCCCGGGAGG ACC 3 C b b
9 CAGAACCTGCAG TCACTGCA TCTGCCTCCCG
TGAGCCAA AGTGACGT AGACGGAGGGC
CCA
GAM7957 297 KIAA190 2 2653 XP_056282.1 3 4228 AGACTAGAGGGA TGC 3 C c c
4 GTGGGGTTGCAG TCACTGCAACCTC CTCCC
TGGCTGCC GGTGACGTTGGGG GAGGG
T--
GAM7957 297 KIAA190 2 19541 XP_056282.1 3 3784 GTCCCCGGGAGG T AA---- -- 3 C c c
4 CAGCTGGGGCAG CACTGC CCT CTGCCTCCCG
CAGCAGTG GTGACG GGG GACGGAGGGC
- ACGACG TC
GAM7957 297 KIAA191 3 5830 XP_290732.1 3 1360 CTACTCGGGAGG A AAC T 3 C c b
7 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 KIAA191 3 15343 XP_290732.1 3 857 GAACCCGGGAGG C 3 C b b
7 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 KIAA191 3 19051 XP_290732.1 3 1394 GAACTCAGGAGG TG C 3 C c b
7 TGGAGGTTGCGG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGGCGTTGGAG GGAGG
GT A
GAM7957 297 KIAA192 1 10532 XP_085210.1 5 3099 GAAGCAGGGATA A CT -- 3 C c c
0 GGTGGGCTGCAG TCACTGCA CCT GCC TCCC
TGACATCA AGTGACGT GGG TGG AGGG
C -- AT
GAM7957 297 KIAA193 3 9047 XP_056082.5 3 998 GAGCCTGGTAGG A T C 3 C c b
6 CTGAGGCTGCAG TCACTGCA CCTC GCCT CCG
TGAGCCAA AGTGACGT GGAG CGGA GGT
C T T
GAM7957 297 KIAA193 3 14501 XP_056082.5 3 594 GAACCCGGGAGG C G 3 C b b
6 AAGAGCTTGCAG TCACTGCAA CTCT CCTCCCG
TGAGCCGA AGTGACGTT GAGA GGAGGGC
C A
GAM7957 297 KIAA193 3 19057 XP_056082.5 3 296 GAACCCAGGAGG C 3 C b b
6 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 KIAA194 1 10268 XP_086981.2 3 2320 CTGCACTAGAGG GCAA CC 3 C c c

```
          0                        CAGAGGGGTGAA TCACT    CCTCTGCCTC
                                   CAAGATAC    AGTGG    GGAGACGGAG
                                               ----         AT
GAM7957  297   KIAA194 1  9414   XP_059318.2  3  2379   GAACCTGGGAGG          TG          3  C  b  b

          1                        TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                   TGAGTTGA     AGTGACGTTGGAG  GGAGGGT
                                                GT
GAM7957  297   KIAA194 1  17575  XP_166376.1  5  455    CGGTGGGGGAGG    TG AACC            3  C
c  c
          9                        CAGGCGGTGGTG TCAC  C    TCTGCCTCCC
                                   ACAGGACA     AGTG  G    GGACGGAGGG
                                                GT GC--
GAM7957  297   KIAA194 1  17575  XP_300167.1  5  455    CGGTGGGGGAGG    TG AACC            3  C
c  c
          9                        CAGGCGGTGGTG TCAC  C    TCTGCCTCCC
                                   ACAGGACA     AGTG  G    GGACGGAGGG
                                                GT GC--
GAM7957  297   KIAA194 1  17575  XP_300202.1  5  455    CGGTGGGGGAGG    TG AACC            3  C
c  c
          9                        CAGGCGGTGGTG TCAC  C    TCTGCCTCCC
                                   ACAGGACA     AGTG  G    GGACGGAGGG
                                                GT GC--
GAM7957  297   KIAA195 2  13263  XP_057401.1  3  1731   ATATGAGGGAGA       A    TGC          3  C  c
b
          1                        TTGAGGCTGCAG TCACTGCA CCTC   CTCCC
                                   TGAGCTGT     AGTGACGT GGAG   GAGGG
                                                C    TTA
GAM7957  297   KIAA195 2  15343  XP_057401.1  3  1290   GAACCCGGGAGG        C             3  C  b  b

          1                        CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                   TGAGCCGA     AGTGACGTT GAGGCGGAGGGC
                                                C
GAM7957  297   KIAA195 1  11132  XP_085375.4  3  1383   GGAACCCGGGAG       AC     C          3  C  b
b
          4                        CAGAGACTGCAG TCACTGCA  CTCTGC TCCCG
                                   TGAGCTGA     AGTGACGT  GAGACG AGGGC
                                                CA     -
GAM7957  297   KIAA195 1  4403   XP_085836.1  5  4      TCGGTGGGGAGG  A    AA    -          3  C  c  c
          6                        CAAGAGGGCGGC TC CTGC  CCTCT GCCTCCC
                                   GAGGAGGT     AG GGCG  GGAGA CGGAGGG
                                                C   --    A
GAM7957  297   KIAA195 1  18691  XP_088566.2  3  2670   GAACCTGGGAGG                        3  C  b  b
          8                        CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                   TGAGCCGA     AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   KIAA197 2  10065  XP_113984.2  3  3110   GAACCTGGGAGG        C  CT          3  C  c
c
          9                        TCAAGATTGCAG TCACTGCAA CT  GCCTCCCG
                                   TGAGCTAT     AGTGACGTT GA  TGGAGGGT
```

```
                                                A  AC
GAM7957  297   KIAA197 2  10353  XP_113984.2  3  3579   GAACCCAGGAGG      A   TG    C       3  C  c
c
          9                          TGGAGGATGCAG TCACTGCA CCTC  CCTCC
                                     TGAACTGA    AGTGACGT GGAG  GGAGG
                                                   A   GT    A
GAM7957  297   KIAA198 1  7592   XP_114000.1  3  1079   CCTGTGGGGAGA  ACT     T -         3  C  c
c
          1                          GTGAGGTTGCTG TC  GCAACCTC GC CTCCC
                                     GAGCCACG    AG   CGTTGGAG TG GAGGG
                                               GT-       -  A
GAM7957  297   KIAA199 2  10265  XP_068710.3  3  6530   GAACCTGGGAGC         TGC          3  C  c
c
          8                          CTGAGGTTGCAG TCACTGCAACCTC  CTCCCG
                                     TGAGCCAA    AGTGACGTTGGAG  GAGGGT
                                                   TCC
GAM7957  297   KIAA199 2  10487  XP_068710.3  3  5630   GAACCTGGAACG   C       C-  C       3  C  c
c
          8                          CGGAGGTTGCAA TCA TGCAACCTCTGC  TCC
                                     TGAGCCGA    AGT ACGTTGGAGGCG  AGG
                                                   A         CA  T
GAM7957  297   KIF11  1  5160   NP_004514.2  3  327    TGAACCCAGGAA        T  C  C       3  C  c  c
                                     GCGGGGTTGCAG TCACTGCAACC CTGC TCC
                                     TGAGCCAA    AGTGACGTTGG GGCG AGG
                                                  -  A  A
GAM7957  297   KIF13B 1  19613  NP_056069.1  3  2123   TGGCTGGGAAAG      A---   GCC       3  C  c
c
                                     AGGGATGTGCAG TCACTGCA   CCTCT  TCCCG
                                     TGACGTGG    AGTGACGT   GGAGA  AGGGT
                                                   GTAG    A--
GAM7957  297   KIF14  1  2937   NP_055690.1  3  374    GAACCTGAGAGG            CC       3  C  b  b
                                     CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
                                     TGAGCCAA    AGTGACGTTGGAGACGGAG
                                                   AG
GAM7957  297   KIF1B  1  10435  NP_055889.1  3  1296   GAACCCAGGAGG            C       3  C  b  b
                                     CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                                   A
GAM7957  297   KIF3B  1  17418  NP_004789.1  3  2261   GAACCTGGGAGG                  3  C  b  b
                                     CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGTCGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   KIF5C  1  2807   NP_004513.1  3  3117   TACTGGGAAAGG  A  G  A     --        3  C  c  c
                                     CAGAGGGTGGAG TC CT CA CCTCTGCC  TCCCG
                                     GGAAGATT    AG GA GT GGAGACGG  AGGGT
                                               G  G  G       AA
GAM7957  297   KLC2L  1  13397  NP_660318.1  3  413    GAACCCAGGAGG   T     TG    C       3  C  c
c
                                     TGGAGGTTGCTG TCAC GCAACCTC  CCTCC
                                     TGAGCCAA    AGTG CGTTGGAG  GGAGG
```

T GT A

GAM7957 297 KLRG1 1 13091 NP_005801.2 3 105 GAGCCCAGGAGT A TGC C 3 C c c

TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG

C TTT A

GAM7957 297 KREMEN1 2 9420 NP_114434.3 3 1175 GAACCTGGGAGG 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 KREMEN1 2 14776 NP_114434.3 3 200 GAGCCCAGGAGG A T C 3 C c b

TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCTAT AGTGACGT GGAG TGGAGG

C C A

GAM7957 297 KSR 1 3327 XP_290793.1 5 740 ACCCCAGGGAGG C AA -- 3 C c c

CACAGGGGGAGC TCA TGC CCTCT GCCTCCC
ATGAAGAG AGT ACG GGGGA CGGAGGG

- AG CA

GAM7957 297 LAMP2 2 2602 NP_054701.1 3 1187 TTACTCGGGAGG A AAC T 3 C c b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC

- --- T

GAM7957 297 LAMP2 2 10440 NP_054701.1 3 1221 GAACCCGGGAGG 3 C b b

CAGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGGCGTTGGAGACGGAGGGC

GAM7957 297 LANO 1 4084 NP_079444.1 3 1211 GAACCCGGGAGG CT 3 C b b

CTAAGGTTGCAG TCACTGCAACCT GCCTCCCG
TGAGCCGA AGTGACGTTGGA CGGAGGGC

AT

GAM7957 297 LAP1B 1 948 NP_056417.1 3 972 GAACCCGGGAGG TC----- 3 C c c

CGGAGGTTGCAG ACTGCAACCTCTGCCTCCCG
TAAGCCGA TGACGTTGGAGGCGGAGGGC

AGCCGAA

GAM7957 297 LASP1 1 9055 NP_006139.1 3 1363 AGGGTGGAAGGT TG - ---- 3 C c c

AAGAGGTTGGTG TCAC CAACCTCT GCCT CCC
TGGAGTTG GGTG GTTGGAGA TGGA GGG

TG A AGGT

GAM7957 297 LDB3 1 14268 XP_084376.6 3 1948 TATGCAGGGACA CT GCC 3 C c c

AGGAGGTTGCTG TCA GCAACCTCT TCCC
ACTGTACT AGT CGTTGGAGG AGGG

-- AAC

GAM7957 297 LDLR 3 4260 NP_000518.1 3 1830 GAGCCCAGGAGG TG C 3 C c b

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAT AGTGACGTTGGAG GGAGG

GT A
GAM7957 297 LDLR 3 4880 NP_000518.1 3 1314 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LDLR 3 8019 NP_000518.1 3 1348 GAACCCGGGAAG C C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A
GAM7957 297 LEP 1 5562 NP_000221.1 3 2719 CCACTCGGGAGG A CAAC T 3 C c c
CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCGCTT AG GAC GAG CGGAGGGC
- A--- T
GAM7957 297 LILRB1 1 7591 NP_006660.1 3 594 GAACCAGGGAGT C C 3 C b b
CAGAGGTTTCAG TCACTG AACCTCTG CTCCC
TGAGCCAA AGTGAC TTGGAGAC GAGGG
T T
GAM7957 297 LIM 2 1052 NP_006448.1 3 750 GAACCCGGGAGG G 3 C b b
GAGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCCAA AGTGACGTTGGAGA GGAGGGC
G
GAM7957 297 LIM 2 15993 NP_006448.1 3 1360 GAACCCAGGAGA C C C 3 C c b
CGGAAGTTGCAG TCACTGCAAC TCTG CTCC
TGAGCTGA AGTGACGTTG AGGC GAGG
A A A
GAM7957 297 LMNB2 1 5883 NP_116126.2 3 819 TTGCCTTGGAGG T AACC C 3 C c c
CAGAAGCTGTGA TCAC GC TCTGCCTCC
GTTTCAGA AGTG CG AGACGGAGG
T A--- T
GAM7957 297 LMOD1 1 6842 NP_036266.1 3 1169 GAAGGCGGCAGG G AC- C 3 C c c
CAGAGAAGTGGA TCACT CA CTCTGCCT CCG
GTGACTAT AGTGA GT GAGACGGA GGC
G GAA C
GAM7957 297 LMOD3 2 14217 XP_067529.3 3 1548 GAACTGGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGACAA AGTGACGTTGGAGACGGAGGG

GAM7957 297 LMOD3 2 15089 XP_067529.3 3 1514 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1126 1 7318 XP_053145.1 3 1364 GAACCCAGGAGA GC C 3 C c c
87 TGGAGGTTGCAG TCACTGCAACCTCT CTCC
TGAGCTGA AGTGACGTTGGAGG GAGG

```
                                                TA   A
GAM7957  297   LOC1128 1  12290  NP_612424.1  3  684   CATCTGGGCGCC      ACCTCT  C          3  C
c  c
          85                      GGGACGCTGCAG TCACTGCA     GC TCCCG
                                 TGATCCCC    AGTGACGT     CG AGGGC
                                             ------  C
GAM7957  297   LOC1149 1  9417   NP_660284.1  3  902   GAACCCAGGAGG             C        3  C  b  b
          87                      CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
                                 TGAGCCGA    AGTGGCGTTGGAGGCGGAGG
                                                A
GAM7957  297   LOC1150 1  9418   XP_291162.1  3  303   GAACCCAGGAGG         TG    C        3  C  c
c
          04                      TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                 TGAGTCAA    AGTGACGTTGGAG  GGAGG
                                               GT    A
GAM7957  297   LOC1151 3  1147   XP_055292.1  5  516   GAACCTGGGAGG  A       TG          3  C  c
c
          29                      TGGAGGTTGCAG TC CTGCAACCTC  CCTCCCG
                                 CGAGCCAA    AG GACGTTGGAG  GGAGGGT
                                          C        GT
GAM7957  297   LOC1151 3  1418   XP_055292.1  3  811   GAACCCAGGAGG        T TG    C        3  C  c
c
          29                      TGGTGGTTGCAG TCACTGCAACC C  CCTCC
                                 TGAGCCTA    AGTGACGTTGG G  GGAGG
                                              T GT    A
GAM7957  297   LOC1151 3  9914   XP_055292.1  5  155   CTGAACCCAGGA        CT C   C        3  C  c
c
          29                      GACAGGTTGCAG TCACTGCAACCT  G CTCC
                                 TGAGCCGA    AGTGACGTTGGA  C GAGG
                                             -- A   A
GAM7957  297   LOC1157 1  13386  NP_660288.1  3  314   TTAACAGGAGGG  A-   AA      TC         3  C  c
c
          04                      CAGAGGGCAGGG TC  CTGC  CCTCTGCC  CC
                                 GACAGACG    AG  GACG  GGAGACGG  GG
                                          GG   --       GA
GAM7957  297   LOC1161 2  3378   NP_612467.1  3  1040  GAACCCAGGAGG       C  TG    C        3  C  c
b
          43                      TGGAGATTGCAG TCACTGCAA CTC  CCTCC
                                 TGAGCTGA    AGTGACGTT GAG  GGAGG
                                             A  GT    A
GAM7957  297   LOC1161 2  9421   NP_612467.1  3  252   GAACCCGGGAGG                    3  C  b  b
          43                      CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                 TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC1162 2  1671   XP_300752.1  3  1511  AGGTGGGGCAGG TC-----          -      3  C  c
c
          28                      CGGAGGTTGCAG       ACTGCAACCTCTGCCT CCC
                                 TAAGCCAA          TGACGTTGGAGGCGGA GGG
                                        AACCGAA            C
GAM7957  297   LOC1162 2  12210  XP_300752.1  5  225   CAGGGCGGGAGG    T  AA  T           3  C  c
c
```

```
          28                          CGGCGGCGCGTG TCAC GC  CC CTGCCTCCCG
                                     GGGGCGGG    GGTG CG  GG GGCGGAGGGC
                                               - C- C
GAM7957  297   LOC1162 2  2487  XP_057674.5  3  1836  GAACCCGGGAGG       C            3  C  b  b

          36                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCTGA    AGTGACGTT GAGGCGGAGGGC
                                                 C
GAM7957  297   LOC1162 2  18886 XP_057674.5  3  558   TGAGAAGGGCGG      AAC    T        3  C  c
b
          36                          CAGAGGCAGTGG TCACTGC  CTCTGCC CCC
                                     GGCTGGCT    GGTGACG  GAGACGG GGG
                                                 ---     C
GAM7957  297   LOC1163 2  10572 XP_057993.1  3  881   GAACCCGGGAGG       C            3  C  b  b

          49                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTT GAGGCGGAGGGC
                                                 C
GAM7957  297   LOC1163 2  13155 XP_057993.1  3  847   CTACTCGGGAGG  A   AAC  T          3  C  c
 b
          49                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATGGCGT    AG GACG  GAG CGGAGGGC
                                               -   ---  T
GAM7957  297   LOC1187 1  11340 XP_058338.2  5  1272  GCCTCGGACAGG   TGCAA     C-       3  C
c  c
          09                          CAGAGGCTGTGA TCAC    CCTCTGCCT  CCG
                                     AATACGTG    AGTG    GGAGACGGA  GGC
                                                 TC---       CA
GAM7957  297   LOC1202 2  10567 NP_620143.1  3  1082  TGAACCCGGTAG      C   G  C       3  C  c
c
          24                          GGGAGCTTGCAG TCACTGCAA CTCT CCT CCG
                                     TGAGCCCA    AGTGACGTT GAGG GGA GGC
                                                 C   -  T
GAM7957  297   LOC1202 2  20099 NP_620143.1  3  1050  CTACTCGGGAGG  A GCAA  T          3  C
c  c
          24                          CTGAGGCAAGAG TC CT   CCTC GCCTCCCG
                                     AATGGCAT    AG GA   GGAG CGGAGGGC
                                               A  AC--   T
GAM7957  297   LOC1204 1  10342 XP_061976.2  3  1014  GTCGTCAGGAGG        TG   C       3  C  c
c
          06                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                     TGAGCCAA    AGTGACGTTGGAG  GGAGG
                                                 GT    A
GAM7957  297   LOC1214 2  957   XP_062645.2  3  1272  CTACTTGGGAGG  A   AAC           3  C  b
b
          56                          CAGAGGCAGGAG TC CTGC  CTCTGCCTCCCG
                                     AATCGTTT    AG GACG  GAGACGGAGGGT
                                               -   ---
GAM7957  297   LOC1214 2  3524  XP_062645.2  3  1306  GAACCCAGGAGG        T    C       3  C  b
b
```

56 CTGAGGTTGCAG TCACTGCAACCTC GCCTCC
TGAGCCCA AGTGACGTTGGAG CGGAGG
T A
GAM7957 297 LOC1227 1 6651 XP_058647.1 3 474 AAACTCGGGAGG 3 C b b
04 TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGATGGAGGGC

GAM7957 297 LOC1237 3 5759 XP_058721.2 3 1367 TGAACCCGGGGG A T 3 C b
b
22 CAGAGGCTGCAG TCACTGCA CCTCTGCC CCCG
TGAGCCGA AGTGACGT GGAGACGG GGGC
C -
GAM7957 297 LOC1237 3 13155 XP_058721.2 3 1912 CTACTCGGGAGG A AAC T 3 C c
b
22 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1237 3 15675 XP_058721.2 3 1946 GAACCCGGGAGG C TG 3 C b
b
22 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCGA AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 LOC1244 1 12083 XP_058804.4 3 1528 CATTTCGGGAGG A AAC T 3 C c
c
11 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
GATCATTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1247 1 12792 XP_064298.4 3 427 GAACCCAGGAGG C 3 C b b
51 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC1261 2 5860 XP_058997.2 3 1040 AAGCCCAGGAGA C C 3 C b
b
67 CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCAA AGTGACGTTGGAGAC GAGG
A A
GAM7957 297 LOC1261 2 12793 XP_058997.2 3 707 GAACCTGGGAGG 3 C b b
67 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC1266 2 6238 XP_060121.4 3 2065 GAGCCCAGGAGG TG C 3 C c
c
69 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC1266 2 14979 XP_060121.4 3 3858 CCTTCCAGGGTT AC CCT 3 C c
c
69 TAGGGAGTGCAG TCACTGCA CTCTG CCC
TGATGTCG AGTGACGT GGGAT GGG
GA TT-

GAM7957 297 LOC1272 1 5861 XP_072073.5 3 1067 GAGCCCAGGAGG C 3 C b b

62 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 LOC1300 2 2487 NP_612477.3 3 1582 GAACCCGGGAGG C 3 C b b

26 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 LOC1300 2 3640 NP_612477.3 3 2412 GAACCCAGGCGG T C 3 C b
b

26 CAGAGGTTGCAG TCACTGCAACCTCTGCC CC
TGAGTCGA AGTGACGTTGGAGACGG GG
C A

GAM7957 297 LOC1305 1 17423 NP_620156.1 3 773 GAACCTGGGAGG TG 3 C b
b

89 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 LOC1339 2 12792 XP_059674.1 3 713 GAACCCAGGAGG C 3 C b b

26 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 LOC1339 2 13155 XP_059674.1 3 679 CTACTCGGGAGG A AAC T 3 C c
b

26 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC1341 1 8199 XP_059692.1 3 848 TCATGCGGGAGG ACT AC -- 3 C c
c

21 CAATGAGCTGCT TC GCA CTC TGCCTCCCG
GGAGCACA AG CGT GAG ACGGAGGGC
GT- C- TA

GAM7957 297 LOC1341 2 1453 NP_620164.1 3 444 GAACCCAGGAGG AC TG C 3 C c
b

47 TGGAGACTGCAG TCACTGCA CTC CCTCC
TGAGCCAA AGTGACGT GAG GGAGG
CA GT A

GAM7957 297 LOC1341 2 9760 NP_620164.1 3 841 TGAACCTGGAGG C 3 C b b

47 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTCGA AGTGACGTTGGAGACGGAGG
T

GAM7957 297 LOC1362 1 15223 NP_660311.1 3 1134 GAACCCAGGAGG TG C 3 C c
c

63 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 LOC1384 1 10454 XP_059972.1 3 523 GAACCTGGGAGG T 3 C b b

28 CGGAGGTTGCTG TCAC GCAACCTCTGCCTCCCG

TGAGCTGA AGTG CGTTGGAGGCGGAGGGT
T
GAM7957 297 LOC1394 1 5043 XP_066687.2 3 612 AAACCCGGGAGG C 3 C b b
22 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC1395 3 7063 XP_066765.1 3 737 GAACCCGGGAGG A 3 C b b
62 CGGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGGGCCGG GGTGACGT GGAGGCGGAGGGC
C
GAM7957 297 LOC1395 3 7286 XP_066765.1 3 545 ATACTCGGGAGG A AAC CT 3 C c
b
62 CTAAGGCAGGAG TC CTGC CT GCCTCCCG
AATCGCTT AG GACG GA CGGAGGGC
- --- AT
GAM7957 297 LOC1395 3 7773 XP_066765.1 3 576 CTTGACGGGAAG C 3 C b b
62 CGGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCCGA AGTGACGTTGGAGGCG AGGGC
A
GAM7957 297 LOC1427 1 5071 XP_084337.1 3 1678 GAACCAGGGAGT C C 3 C b
b
79 CGGAGATTGCAG TCACTGCAA CTCTG CTCCC
TGAGCTGA AGTGACGTT GAGGC GAGGG
A T
GAM7957 297 LOC1428 1 15983 XP_084355.1 3 1431 GAACCCGGGAGG TG 3 C b
b
26 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 LOC1429 1 8865 XP_096364.1 3 1064 GAACCCGGGAGG C TG 3 C b
b
48 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCTGG AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 LOC1444 2 1996 XP_096611.2 3 2224 GAGCCCAGGAGG A T C 3 C c
c
81 TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAACTAA AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 LOC1444 2 10867 XP_096611.2 3 2564 CTACTCGGGAGG A CAAC T 3 C
c c
81 CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCACTT AG GAC GAG CGGAGGGC
- A--- T
GAM7957 297 LOC1448 1 12140 XP_084972.1 3 625 GAACCCAGGAGG C C 3 C b
b
17 CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCAA AGT ACGTTGGAGACGGAGG
A A
GAM7957 297 LOC1448 2 3092 NP_612483.1 3 565 GAACCCGGGAGG 3 C b b

45 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGGTAA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC1448 2 12559 NP_612483.1 3 533 CTACTCGGGAGG A AAC T 3 C c
b
45 CTGAGGCAGGAA TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1452 1 10554 XP_096730.1 3 1560 TGAACCCGGAAG C C C 3 C c
c
16 CGAAGGTTGCAG TCACTGCAACCT TGC TCC
TGAGCCAA AGTGACGTTGGA GCG AGG
A A C
GAM7957 297 LOC1452 3 15089 XP_096740.1 3 2909 CTACTCGGGAGG A AAC T 3 C c
b
31 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1452 3 16122 XP_096740.1 3 2573 CAACCTGGGAGA GC 3 C b
b
31 TGGAGGTTGCAG TCACTGCAACCTCT CTCCCG
TGAGCCGA AGTGACGTTGGAGG GAGGGT
TA
GAM7957 297 LOC1452 3 19055 XP_096740.1 3 2943 GAACCCGGGAGG 3 C b b
31 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGGCGTTGGAGGCGGAGGGC

GAM7957 297 LOC1453 2 2001 XP_096791.1 3 494 GGGTCCAGGAGG A TG C 3 C c
b
87 TGGAGGCTGCAG TCACTGCA CCTC CCTCC
TGAGCTAT AGTGACGT GGAG GGAGG
C GT A
GAM7957 297 LOC1453 2 14786 XP_096791.1 3 1079 GAACCTGGGAGG 3 C b b
87 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC1454 1 10439 XP_085120.1 3 750 GAACCTGGGAGG 3 C b b
53 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC1456 2 5360 XP_096817.1 3 55 AATTTCGGGAGG A AAC T 3 C c
b
09 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AACGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1456 2 15343 XP_096817.1 3 89 GAACCCGGGAGG C 3 C b b
09 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC1456 1 13155 XP_096829.1 3 814 CTACTCGGGAGG A AAC T 3 C c
c

```
          63                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATGGCGT    AG GACG  GAG CGGAGGGC
                                             -   ---  T
GAM7957  297   LOC1456 1  15903 XP_085205.1  5 1281  TTCTCTGGGAGG   C  AA-  C          3  C  c
c
          93                          CAAAGGCTGGCA TCA TGC  CCT TGCCTCCCG
                                     CTGGACTG    GGT ACG  GGA ACGGAGGGT
                                               C  GTC  A
GAM7957  297   LOC1457 1  11897 XP_085227.1  3 814   GAACCCAGGAGG        C    C       3  C  b
b
          57                          CAAAGGTTGCAG TCACTGCAACCT TGCCTCC
                                     TGAGCCAC    AGTGACGTTGGA ACGGAGG
                                                A     A
GAM7957  297   LOC1457 1  6791  XP_096858.1  5 614   GATAGGAGGAGG  ACT  A-      C       3  C  c
c
          58                          CAGAGGGGTGCC TC  GCA  CCTCTGCCTCC
                                     TGGAGTTT    AG  CGT  GGAGACGGAGG
                                               GTC  GG       A
GAM7957  297   LOC1458 1  15343 XP_085246.1  3 1755  GAACCCGGGAGG       C             3  C  b
b
          20                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                                C
GAM7957  297   LOC1462 1  19900 XP_085387.1  3 1336  GAACCCGGAAGG           C        3  C  b  b

          29                          CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
                                     TGAGCCAA    AGTGACGTTGGAGGCGGA GGC
                                                   A
GAM7957  297   LOC1463 1  18065 XP_085421.2  3 1136  CAGGGCGGGAGG    ----  ACC          3  C  c
c
          36                          CAGGCTGTGTCC TCACT   GCA  TCTGCCTCCCG
                                     TCGGTGGG    GGTGG   TGT  GGACGGAGGGC
                                               CTCC  GTC
GAM7957  297   LOC1467 2  10438 XP_097071.2  3 2061  GAACCCGGGAGG                    3  C  b  b
          13                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   LOC1467 2  14497 XP_097071.2  3 936   GAACCCGGGAGG  C                 3  C  b  b

          13                          CGGAGGTTGCAT TCA TGCAACCTCTGCCTCCCG
                                     GAGCTGAG    AGT ACGTTGGAGGCGGAGGGC
                                               -
GAM7957  297   LOC1467 2  9770  XP_097074.1  5 1479  GAACCTGGGAGG         TG          3  C  b
b
          28                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCTGA    AGTGACGTTGGAG  GGAGGGT
                                                GT
GAM7957  297   LOC1467 2  17996 XP_097074.1  3 231   GAGCTTAGGAGG      A  T   C       3  C  c
b
          28                          TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
```

TGAGCTGT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 LOC1467 1 15343 XP_097085.5 3 1540 GAACCCGGGAGG C 3 C b b
56 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC1468 1 4338 XP_097120.1 3 180 GAACCTGGGAGG C 3 C b b
95 CAGATGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCGA AGTGACGTTG AGACGGAGGGT
T
GAM7957 297 LOC1469 1 1262 XP_097121.1 3 464 AATCCCAGGAGA C C 3 C b b
01 CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCGA AGTGACGTTGGAGAC GAGG
A A
GAM7957 297 LOC1469 1 12758 XP_097142.1 3 425 CCTCCAATGAGG CC 3 C b b
58 CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCTGA AGTGACGTTGGAGACGGAG
TA
GAM7957 297 LOC1470 2 609 XP_054031.5 3 925 GAACCTGGGAGG C 3 C b b
71 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGT
C
GAM7957 297 LOC1470 2 13155 XP_054031.5 3 891 CTACTCGGGAGG A AAC T 3 C c b
71 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1470 1 9281 XP_097182.1 3 263 GAACCCGGGAGG CT 3 C b b
80 CAGCAGTTGCAG TCACTGCAAC CTGCCTCCCG
TGAGCTGA AGTGACGTTG GACGGAGGGC
AC
GAM7957 297 LOC1470 1 6900 XP_097184.4 3 393 TGCAAGGAGAGG T------- CAA - 3 C c c
93 CAGAGGCCAGTG CACTG CCTCTGCCTC CC
CTTGCGCG GTGAC GGAGACGGAG GG
GCGCGTTC C-- A
GAM7957 297 LOC1476 1 10707 XP_085831.1 5 366 GGTTGGGGGAGG C A 3 C b b
45 CAGAGGTGGCAC TCA TGC ACCTCTGCCTCCC
TGGAGGCC GGT ACG TGGAGACGGAGGG
C G
GAM7957 297 LOC1476 2 2487 XP_085830.1 3 797 GAACCCGGGAGG C 3 C b b
49 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC1476 2 13155 XP_085830.1 3 763 CTACTCGGGAGG A AAC T 3 C c b

```
          49                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATGGCGT    AG GACG  GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC1476 1  472   XP_097262.1  3  569   GAGTCCAGGAAT          CC  C       3  C  c  c
          69                          TAGAGGTTGCAG TCACTGCAACCTCTG  TCC
                                     TGAGGTAT    AGTGACGTTGGAGAT  AGG
                                                  TA  A
GAM7957  297   LOC1477 3  630   XP_085862.1  5  1885  GAACCTGGGAGG   C  C             3  C  b  b

          27                          CAGAGGTTACAA TCA TG AACCTCTGCCTCCCG
                                     TGAGCCGA    AGT AC TTGGAGACGGAGGGT
                                              A  A
GAM7957  297   LOC1477 3  16906  XP_085862.1  5  1382  TGACCTGGCAGG           C       3  C  b  b

          27                          CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGA GGT
                                                    C
GAM7957  297   LOC1477 3  19057  XP_085862.1  5  1706  GAACCCAGGAGG            C       3  C  b  b

          27                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGG
                                                    A
GAM7957  297   LOC1477 1  12969  XP_097293.2  3  804   GAAGCCGGGAGG    G-  AC  CT          3  C
c  c
          91                          CTCAGCCTGAAA TCACT  CA  CT  GCCTCCCG
                                     GTGGCTCC    GGTGA  GT  GA  CGGAGGGC
                                              AA  CC  CT
GAM7957  297   LOC1478 2  4707  NP_660319.1  3  1039  GAATCCGGGAGG                  3  C  b  b
          37                          CGGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCAA    AGTGGCGTTGGAGGCGGAGGGC

GAM7957  297   LOC1478 2  18983  NP_660319.1  3  523   GAGCCGAGGGGG          TG   -       3  C  c
b
          37                          TGGGGGTTGCAG TCACTGCAACCTC  CCTCC CG
                                     TGAGCCAA    AGTGACGTTGGGG  GGGGG GC
                                                  GT    A
GAM7957  297   LOC1479 1  14271  XP_085974.1  3  1456  GAGTCCAGGAGT      A  C  C-   C       3  C  c
 c
          47                          TCAAGGCTGCAG TCACTGCA CCT TG  CTCC
                                     TGAGTTGT    AGTGACGT GGA AC  GAGG
                                                 C  -  TT   A
GAM7957  297   LOC1481 1  10028  NP_653293.1  3  2643  GAACTCAGAAGG           CCC       3  C  c
c
          37                          CAGAGGTTGCAG TCACTGCAACCTCTGCCT
                                     TGGAAAAA    GGTGACGTTGGAGACGGA
                                                    AGA
GAM7957  297   LOC1481 1  5018  XP_086077.1  3  46    GAACCTGGGAGA          C          3  C  b  b
          66                          CGGAGGTTGCAG TCACTGCAACCTCTG CTCCCG
                                     TGAGCCAT    AGTGACGTTGGAGGC GAGGGT
                                                    A
```

GAM7957 297 LOC1481 2 1492 XP_047554.4 3 1872 CTACTCGGGAGG A AAC T 3 C c b

98 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC1481 2 10436 XP_047554.4 3 1906 GAACCCAGGAGG C 3 C b b

98 CAGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGGCGTTGGAGACGGAGG
A

GAM7957 297 LOC1482 2 17263 XP_086096.2 3 33 CTACTTGGGAGG A AAC 3 C b b

06 CAGAGGCAGGAG TC CTGC CTCTGCCTCCCG
AATCATTT AG GACG GAGACGGAGGGT
- ---

GAM7957 297 LOC1482 2 17399 XP_086096.2 3 67 GAACCTGGGAGG 3 C b b

06 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC1489 1 9014 XP_086361.1 5 2093 GAACCCAGAAGG C CCC 3 C c c

18 CAGAGGTTGCAT TCA TGCAACCTCTGCCT
GATGCAAT AGT ACGTTGGAGACGGA
- AGA

GAM7957 297 LOC1491 1 13065 XP_086458.1 5 554 GAACCCGGGAGG 3 C b b

94 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC1492 1 17044 XP_086475.1 3 1648 GAACCCAGGAGG C C 3 C b b

71 CAGAGTTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCAA AGTGACGTT GAGACGGAGG
T A

GAM7957 297 LOC1494 1 13110 XP_097642.1 3 1686 GAGGCCAGGAGT A TGC C 3 C c c

48 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C TTT A

GAM7957 297 LOC1494 2 1492 XP_097645.1 3 778 CTACTCGGGAGG A AAC T 3 C c b

64 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC1494 2 17317 XP_097645.1 5 1114 TGGCCCAGGAGG C 3 C b b

64 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 LOC1495 1 6656 XP_097661.1 3 2996 CCCAGCAGGAGG GCA C 3 C c c

```
          06                          CAGGGGTAGAGT TCACT   ACCTCTGCCTCC
                                    GATGGAAG    AGTGA   TGGGGACGGAGG
                                              GA-          A
GAM7957  297   LOC1496 1   18837  XP_086669.2  5  50    GAAGTAGGGAGG           G          3  C  b  b
          72                          AGGAGGTTGCAG TCACTGCAACCTCT CCTCCC
                                    TGAGCTGA    AGTGACGTTGGAGG GGAGGG
                                                 A
GAM7957  297   LOC1497 2   5361   XP_097711.4  3  1754   GAACCTGGGAGG TC-----       T          3  C  c
c
          05                          CAGCGGTTGCAG       ACTGCAACC CTGCCTCCCG
                                    TAAGCCAA          TGACGTTGG GACGGAGGGT
                                           AACCGAA        C
GAM7957  297   LOC1497 2   6755   XP_097711.4  3  1000   AAACCCAGGTGG            T C        3  C  c  c

          05                          CGGAGGTTGCAG TCACTGCAACCTCTGCC CC
                                    TGAGCCGA    AGTGACGTTGGAGGCGG GG
                                                  T A
GAM7957  297   LOC1500 2   2125   XP_097805.1  3  160    CTACTCGGGAGG  A   AAC  T          3  C  c
b
          95                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATGGAGT    AG GACG   GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC1500 2   18254  XP_097805.1  3  194    GAACCCGGGAGG                  3  C  b  b
          95                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAACCCA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   LOC1501 2   2222   XP_097820.1  5  908    GGAACGCGGAGG    T-- AAC-       -      3  C  c
c
          50                          CAGGGAGAGGCT TCAC   GC    CTCTGCCTCC CG
                                    CCGTGACG    AGTG   CG    GGGACGGAGG GC
                                              CCT  GAGA         C
GAM7957  297   LOC1501 2   16255  XP_097820.1  5  628    AGAAACCGGGCT         CTCT  T--         3  C  c
c
          50                          TGGTTGTTGCAG TCACTGCAAC    GCC   CCCG
                                    TGGGAAGA    GGTGACGTTG    TGG   GGGC
                                                 T---   TTC
GAM7957  297   LOC1501 2   6243   XP_086802.2  3  3072   AAAGTATTGGGG           TG   CC        3  C  c
c
          74                          TGGAGGTTGCAG TCACTGCAACCTC  CCTC
                                    TGAGCGGA    AGTGACGTTGGAG  GGGG
                                                  GT    TT
GAM7957  297   LOC1501 2   14331  XP_086802.2  3  908    GGGCCCGGGAGG     ------  ACC          3  C  c
c
          74                          CAGACCTGCCCT TCACT     GCA   TCTGCCTCCCG
                                    AAGGGTGA    AGTGG     CGT   AGACGGAGGGC
                                              GAATCC   CC-
GAM7957  297   LOC1502 5   2979   XP_086827.2  3  2172   TGAGTCAGGAGG       A   T    C        3  C  c
c
          12                          TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
                                    TGAGCTAT    AGTGACGT GGAG TGGAGG
```

```
                                                C   T    A
GAM7957  297   LOC1502 5  3584   XP_086827.2  3  1212   GAACACAGAAGG          TG   CCC        3   C   c
 c
          12                          TGGAGGTTGCAG TCACTGCAACCTC  CCT
                                     TGAGCCAA    AGTGACGTTGGAG  GGA
                                                   GT   AGA
GAM7957  297   LOC1502 5  5019   XP_086827.2  3  1530   AAACCTGGGAGT       ACC  TGC          3   C
c   c
          12                          TTGAAGCTGCAG TCACTGCA   TC   CTCCCG
                                     TGAGCCAT    AGTGACGT   AG   GAGGGT
                                                   CGA  TTT
GAM7957  297   LOC1502 5  17190  XP_086827.2  3  2474   GAGCCCGAGAGG          TG   C          3   C   c
 c
          12                          TGGAGGTTGCAG TCACTGCAACCTC  CCTC CG
                                     TGAGCCGA    AGTGACGTTGGAG  GGAG GC
                                                   GT   A
GAM7957  297   LOC1502 5  19451  XP_086827.2  3  1179   CCACTCGGGAGG   A  GCAA   T           3   C
c   c
          12                          CTGAGGCAAGAG TC CT    CCTC GCCTCCCG
                                     AGTTACTT    AG GA    GGAG CGGAGGGC
                                              A  AC--    T
GAM7957  297   LOC1502 2  6243   XP_059324.1  3  3071   AAAGTATTGGGG          TG   CC         3   C   c
c
          13                          TGGAGGTTGCAG TCACTGCAACCTC  CCTC
                                     TGAGCGGA    AGTGACGTTGGAG  GGGG
                                                   GT   TT
GAM7957  297   LOC1502 2  14331  XP_059324.1  3  909    GGGCCCGGGAGG     ------  ACC          3   C   c
 c
          13                          CAGACCTGCCCT TCACT     GCA   TCTGCCTCCCG
                                     AAGGGTGA    AGTGG     CGT   AGACGGAGGGC
                                              GAATCC   CC-
GAM7957  297   LOC1502 1  9421   XP_097870.1  3  4158   GAACCCGGGAGG                    3   C   b   b
          25                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC1502 1  13945  XP_097859.2  3  9      ATGCTGGGGACG   A   CA--      C          3   C   c
c
          71                          CAGAGGTGACCC TC CTG    ACCTCTGC TCCC
                                     AGAGACAT    AG GAC    TGGAGACG AGGG
                                              A   CCAG       C
GAM7957  297   LOC1502 1  6687   XP_086820.1  3  320    AAGATGCTGGTG       ACC    C -        3   C   c
c
          79                          AAGCAGGTGCAG TCACTGCA   TCTGC TC CCG
                                     TGAGGATC    AGTGACGT   GGACG AG GGT
                                              ---    A  T
GAM7957  297   LOC1502 1  6090   XP_097869.2  3  606    GAACCCAGGAGG      A         C          3   C   b   b

          99                          CAGAGGTCGCAG TCACTGC ACCTCTGCCTCC
                                     TGAGTCGA    AGTGACG TGGAGACGGAGG
                                                   C          A
```

GAM7957 297 LOC1506 2 4127 XP_097931.1 3 810 CTACTCGGGAGG A AAC CT 3 C c c

30 CTAAGGCAGGAG TC CTGC CT GCCTCCCG
AATCGCTT AG GACG GA CGGAGGGC
- --- AT

GAM7957 297 LOC1506 2 7317 XP_097931.1 3 844 GAACCCCAGAGG CC 3 C c c

30 CAGAGGTTGCGG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGGCGTTGGAGACGGAG
AC

GAM7957 297 LOC1509 1 17018 XP_097971.1 5 413 GAGGAGGGGTGG CT - T 3 C c c

33 CAGAGGATTGTT TCA GCAA CCTCTGCC CCC
TGGCCAGG GGT TGTT GGAGACGG GGG
T- A T

GAM7957 297 LOC1511 1 20012 XP_087106.2 5 256 GGAACTGGGAGG T A ------ 3 C c c

46 CAGGTTTGGAGG CACTGCA CCTCT GCCTCCCG
CTGCAGTG GTGACGT GGAGG CGGAGGGT
- C TTTGGA

GAM7957 297 LOC1511 2 9002 NP_660323.2 3 842 CTGCTCGGGAGG A- AAC T 3 C c b

94 CTGAGGCAGGGG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
GG --- T

GAM7957 297 LOC1511 2 9420 NP_660323.2 3 874 GAACCTGGGAGG 3 C b b

94 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC1516 1 5532 XP_098096.5 3 792 GAACCCAGGAGG ACC C 3 C c c

23 TAGAAGCTGCAG TCACTGCA TCTGCCTCC
TGAGCAGG AGTGACGT AGATGGAGG
CGA A

GAM7957 297 LOC1517 1 16954 XP_087279.6 3 182 GAACCCAGGAGG C C 3 C c c

20 CAGAGCTTGTAG TCACTGCAA CTCTGCCTCC
TGAGCCTA AGTGATGTT GAGACGGAGG
C A

GAM7957 297 LOC1520 1 10971 XP_087365.1 3 632 GACCCAGGGAGG ACC T 3 C c c

24 TCGATGCTGCAG TCACTGCA TC GCCTCCC
TGAGCTAT AGTGACGT AG TGGAGGG
CGT C

GAM7957 297 LOC1524 1 10654 XP_098231.1 3 2012 GAACCTGGGAGT GC 3 C b b

45 TGGAGGTTGCAG TCACTGCAACCTCT CTCCCG
TGAAACGA AGTGACGTTGGAGG GAGGGT
TT

GAM7957 297 LOC1526 2 7628 XP_087495.1 3 203 GAACCTGGGAGG TC----- A 3 C c b

27 CAGAGGGTGCAG ACTGCA CCTCTGCCTCCCG
TAAGCTGA TGACGT GGAGACGGAGGGT
AGTCGAA G
GAM7957 297 LOC1526 2 19899 XP_087495.1 5 1819 GGAACGTGGAGG - 3 C b b
27 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC CG
TGAGCCGA AGTGACGTTGGAGACGGAGG GC
T
GAM7957 297 LOC1528 2 13066 XP_098266.2 3 2438 GAACCTGGGAGG 3 C b b
04 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC1528 2 14782 XP_098266.2 3 805 GAACTCAGGAGG TG C 3 C c
b
04 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC1528 1 11843 XP_087532.1 5 8 GAATCCAGGAAG C C 3 C c c
29 CAGAGGTTGCGG TCACTGCAACCTCTGC TCC
TGAGCCGA AGTGGCGTTGGAGACG AGG
A A
GAM7957 297 LOC1530 2 15345 XP_098307.1 3 2344 GAACCTGGGAGG C 3 C b b

77 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGT
C
GAM7957 297 LOC1530 2 16654 XP_098307.1 3 744 CTACTCGGGAGG A GCA T 3 C c
b
77 CTGAGGTGAAAG TC CT ACCTC GCCTCCCG
GATCACTT AG GA TGGAG CGGAGGGC
- AAG T
GAM7957 297 LOC1531 1 13434 XP_098319.1 3 605 GAACCTGGGAGG C 3 C b b
46 TACAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCCCA AGTGACGTTGGA ATGGAGGGT
C
GAM7957 297 LOC1533 1 14393 XP_098361.1 3 1073 AAACCCAGGAGG TG C 3 C c
c
38 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC1535 2 8369 XP_087708.6 3 896 CTGCTCGGGAGG A AAC T 3 C c
c
61 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC1535 2 8646 XP_087708.6 3 930 GAACCCAGGAGT C GC C 3 C c
c
61 TGGAGCTTGCAG TCACTGCAA CTCT CTCC
TGAGCCGA AGTGACGTT GAGG GAGG
C TT A
GAM7957 297 LOC1536 1 609 XP_098414.1 3 493 GAACCTGGGAGG C 3 C b b

```
          82                          CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTT GAGACGGAGGGT
                                                 C
GAM7957  297   LOC1537 1  14924 XP_098419.1  3 219   TAGGTCGGGAGG   C  AACCTC          3  C
c  c
          11                          CACCTCTAGCAT TCA TGC    TGCCTCCCG
                                     GAGACAGT    AGT ACG     ACGGAGGGC
                                               -  ATCTCC
GAM7957  297   LOC1537 1  20181 XP_098422.1  3 707   AACCTAGGGAGG                  3  C  b  b
          27                          CAGAGGTTGTAG TCACTGCAACCTCTGCCTCCC
                                     TGAGCCAA    AGTGATGTTGGAGACGGAGGG

GAM7957  297   LOC1547 1  7965  XP_098602.1  3 659   AGCCTGGAGATG      A    --  C      3  C  c  c
          39                          TAGAGGCTGCAG TCACTGCA CCTCTGC  CTCC
                                     TGAGCTGT    AGTGACGT GGAGATG  GAGG
                                                 C     TA   T
GAM7957  297   LOC1547 1  2550  XP_088045.1  3 480   GAACCCGGGAGG   C      TG          3  C  c
c
          91                          TGGAGGTTGCGA TCA TGCAACCTC  CCTCCCG
                                     TGAGCTGA    AGT GCGTTGGAG  GGAGGGC
                                               A       GT
GAM7957  297   LOC1548 1  9421  XP_098626.1  3 3104  GAACCCGGGAGG                  3  C  b  b
          77                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC1550 1  15060 XP_088117.1  3 656   GAACCTCGGAGG            C      3  C  b  b
          06                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGGCGGAGG
                                                 C
GAM7957  297   LOC1550 1  1423  XP_088140.1  3 325   GAGCCCAGGAGG      A       C      3  C  b  b

          54                          CAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
                                     TGAGCCAT    AGTGACGT GGAGACGGAGG
                                                 C         A
GAM7957  297   LOC1550 3  614   XP_098661.1  3 1229  GAACCCGGGAGG       C           3  C  b  b
          72                          CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCTGA    AGTGACGTT GAGACGGAGGGC
                                                 C
GAM7957  297   LOC1550 3  13155 XP_098661.1  3 1195  CTACTCGGGAGG  A   AAC  T          3  C  c
 b
          72                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATGGCGT    AG GACG   GAG CGGAGGGC
                                               -   ---  T
GAM7957  297   LOC1550 3  19036 XP_098661.1  3 900   GAACCTGGGAGG       C           3  C  b  b
          72                          CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCTGA    AGTGACGTT GAGACGGAGGGT
                                                 C
GAM7957  297   LOC1554 1  1716  XP_088257.3  5 297   GCACGGACGAGG    GCAA       --       3  C  c
c
          35                          CAGAGGAGTGGC TCACT    CCTCTGCCTC  CCG
```

```
                                  CGGTCCCA    GGTGA   GGAGACGGAG  GGC
                                              ----        CA
GAM7957  297   LOC1572 2  10646  XP_098741.2  3  1587  CTACTCGGGAGG  A  GCA   T          3  C
c  c
         78                        CTGAGGTGGGAG TC CT   ACCTC GCCTCCCG
                                  GATCACTT    AG GA   TGGAG CGGAGGGC
                                          - GGG    T
GAM7957  297   LOC1572 2  15781  XP_098741.2  3  1619  GAACCCAGGAGG      A       C       3  C  c
c
         78                        TAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
                                  TGAGCCGG    AGTGACGT GGAGATGGAGG
                                              C         A
GAM7957  297   LOC1575 3  3765   XP_088331.2  3  1791  TGAACCCGGGAG      C  T          3  C  b  b

         70                        GCGAGCTTGCAG TCACTGCAA CTC GCCTCCCG
                                  TGAGCCGA    AGTGACGTT GAG CGGAGGGC
                                              C   -
GAM7957  297   LOC1575 3  13155  XP_088331.2  3  1757  CTACTCGGGAGG  A   AAC  T          3  C  c
 b
         70                        CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                  AATGGCGT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   LOC1575 3  14946  XP_088331.2  3  1791  GAACCCGGGAGG      C  T          3  C  b
b
         70                        CGAGCTTGCAGT TCACTGCAA CTC GCCTCCCG
                                  GAGCCGAG    AGTGACGTT GAG CGGAGGGC
                                              C   -
GAM7957  297   LOC1576 1  3676   NP_808880.1  3  1526  CTACTCGGGAGG  A   AAC  T          3  C  c
 c
         57                        CCGAGGCAGGAA TC CTGC   CTC GCCTCCCG
                                  AATTTATT    AG GACG   GAG CGGAGGGC
                                          -   ---  C
GAM7957  297   LOC1577 1  14124  XP_098819.1  3  286   GAACCCAGGAGA        C   C       3  C  c  c

         37                        CGGAGGTTGCAG TCACTGCAACCTCTG CTCC
                                  TGAGCCGA    AGTGACGTTGGAGGC GAGG
                                                A   A
GAM7957  297   LOC1578 1  13066  XP_098828.1  3  401   GAACCTGGGAGG                  3  C  b  b
         13                        CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   LOC1579 1  4539   XP_098842.1  3  1098  GGGCCCAGGAGG  C     --     C       3  C  c
c
         18                        CAGCTGGGTTGC TCA TGCAACCT  CTGCCTCC
                                  ATGGAGAG    GGT ACGTTGGG  GACGGAGG
                                          -       TC       A
GAM7957  297   LOC1579 1  4539   XP_088420.1  5  236   GGGCCCAGGAGG  C     --     C       3  C  c
c
         19                        CAGCTGGGTTGC TCA TGCAACCT  CTGCCTCC
                                  ATGGAGAG    GGT ACGTTGGG  GACGGAGG
```

```
                                        -      TC       A
GAM7957  297    LOC1580 1   10572  XP_098872.1  3  787    GAACCCGGGAGG        C              3  C  b  b

         88                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                    TGAGCCAA    AGTGACGTT GAGGCGGAGGGC
                                             C
GAM7957  297    LOC1581 1   15220  XP_054490.2  3  443    GAGGCTGGGAGG                    3  C  b  b
         60                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297    LOC1581 1   13065  XP_098892.1  3  1151   GAACCCGGGAGG                    3  C  b  b
         87                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297    LOC1588 1   9422   XP_098995.1  3  539    GAACCCAGGAGG              C       3  C  b  b
         19                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                    TGAGCCAA    AGTGACGTTGGAGGCGGAGG
                                                A
GAM7957  297    LOC1590 2   13155  XP_099021.1  3  1832   CTACTCGGGAGG  A   AAC  T          3  C  c
 b
         53                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATGGCGT    AG GACG   GAG CGGAGGGC
                                          -    ---   T
GAM7957  297    LOC1590 2   17424  XP_099021.1  3  1210   GAACCCGGGAGG         TG         3  C  b
b
         53                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAG  GGAGGGC
                                                GT
GAM7957  297    LOC1591 1   18709  XP_088753.1  3  1255   GAACCCAGGAGG       C       C       3  C  b
b
         10                          CAGAGTTTGCAG TCACTGCAA CTCTGCCTCC
                                    TGAGCTGA    AGTGACGTT GAGACGGAGG
                                             T        A
GAM7957  297    LOC1591 1   17699  XP_088768.3  3  376    GAACCCTGGAGG         TG    C       3  C  c
c
         76                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                    TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                                GT    T
GAM7957  297    LOC1612 1   5801   XP_090783.3  5  72     TGTGTAGGGTTG       AC   G  --       3  C  c  c
         47                          GGGAGAGTGCAG TCACTGCA  CTCT CCT  CCC
                                    TGATGGGA    AGTGACGT  GAGA GGG  GGG
                                             --   G   TT
GAM7957  297    LOC1629 1   3275   XP_091892.3  3  562    TTCCGAGGGAGG  A  -  AA-             3  C  c
c
         68                          CAGGGGACGGCC TC CT GC   CCTCTGCCTCCC
                                    AGCGGCAG    GG GA CG   GGGGACGGAGGG
                                             C  C  GCA
GAM7957  297    LOC1632 1   17144  XP_088769.6  3  387    GAACCTGGGAGG       C  T          3  C  b
b
         59                          CTGAGCTTGCAG TCACTGCAA CTC GCCTCCCG
```

```
                                    TGAGCTGA    AGTGACGTT GAG CGGAGGGT
                                                C   T
GAM7957  297   LOC1635 2  11882  XP_088979.6  3  563   TTCACACGGAGG   - G A       C       3  C  c
c
         56                          CAGAGGTGGGGA TCA CT CA CCTCTGCCTCC
                                    TGAGGTAT    AGT GG GT GGAGACGGAGG
                                              A G -       C
GAM7957  297   LOC1635 2  14783  XP_088979.6  3  1034  GAGCCCAGGAGG      A   T   C       3  C  c
c
         56                          TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
                                    TGAGCCAT    AGTGACGT GGAG TGGAGG
                                                C   T    A
GAM7957  297   LOC1645 2  12796  XP_104562.1  3  693   GAACCCGGGAGG                    3  C  b  b
         80                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCCAA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   LOC1645 2  15089  XP_104562.1  3  659   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         80                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATTGCTT    AG GACG   GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC1653 1  7877   XP_092518.1  3  588   CTACTCGGGAGG  A   AAC  T          3  C  c
c
         24                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATCTCTT    AG GACG   GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC1664 1  14199  XP_093876.5  3  421   GAACCCAGGAGG      C       C       3  C  b
b
         49                          CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
                                    TGAGCCTA    AGTGACGTT GAGACGGAGG
                                                C       A
GAM7957  297   LOC1665 2  4880   XP_093920.5  3  696   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         22                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATGGTGT    AG GACG   GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC1665 2  15343  XP_093920.5  3  730   GAACCCGGGAGG      C             3  C  b  b

         22                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                    TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                                C
GAM7957  297   LOC1703 1  17945  NP_775812.1  3  185   TCCGGGAGAAGG  A   AA----     ---     3  C  c
c
         93                          CAGAGGGCAGAG TC CTGC    CCTCTGCC  TCCCG
                                    GCAGGAAA    AG GACG    GGAGACGG  AGGGC
                                              -  GAGACG      AAG
GAM7957  297   LOC1703 1  4679   XP_096329.1  5  115   AGGAGGGGGATG  -   --     C       3  C  c  c
         94                          CAGAGGTGATGC TCA CTGCA  ACCTCTGC TCCC
                                    AGCTGGGG    GGT GACGT  TGGAGACG AGGG
                                              C    AG      T
```

GAM7957 297 LOC1962 1 16370 XP_116897.1 5 1398 CAATGTGGGAGG A ACC 3 C c c

14 CAGGATGCAGGG TC CTGCA TCTGCCTCCCG
ATGGGCTC AG GACGT GGACGGAGGGT
G A--

GAM7957 297 LOC1965 1 18391 XP_116933.1 3 894 GAGCCCCGGGGG T T T 3 C c c

40 CTGAGGTTGCTG TCAC GCAACCTC GCC CCCG
TGAGCCGA AGTG CGTTGGAG CGG GGGC
T T -

GAM7957 297 LOC1972 1 4083 XP_113839.2 3 2651 GAACCAGGGAGG TG 3 C b b

01 CAGAGGTTGTGG TCAC CAACCTCTGCCTCCC
TGAGCCGA AGTG GTTGGAGACGGAGGG
GT

GAM7957 297 LOC1973 1 18190 XP_113869.1 3 162 CAGGGGAAGGGT A- - TG -- 3 C c c

42 GGGTGGTTGCAG TC CTGCAACC TC CC TCCC
GGGAAGTT AG GACGTTGG GG GG AGGG
GG T GT GA

GAM7957 297 LOC1996 1 12792 XP_117107.2 5 1009 GAACCCAGGAGG C 3 C b b

76 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 LOC1998 1 15343 XP_114040.1 3 368 GAACCCGGGAGG C 3 C b b

58 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 LOC2002 1 14572 XP_117217.2 3 1346 GACCCCGGGAGG A TG 3 C b b

98 TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAGTTGT AGTGACGT GGAG GGAGGGC
C GT

GAM7957 297 LOC2007 1 3813 XP_117268.1 3 247 GAACCTGGGAGG TG 3 C b b

31 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGGGCCAA GGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 LOC2017 1 9125 XP_117329.2 3 214 GAGCCTAGGAAG A T C C 3 C c c

05 TCGAGGCTGCAG TCACTGCA CCTC GC TCC
TGAGCTGA AGTGACGT GGAG TG AGG
C C A A

GAM7957 297 LOC2018 2 17081 XP_114393.1 5 253 CTACTCGGGAGG A AAC T 3 C c c

68 CCGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- C

GAM7957 297 LOC2018 2 19499 XP_114393.1 3 927 GAACCCAAAAGG CC CCC 3 C c c

68 CAGACATTGCAG TCACTGCAA TCTGCCT
TGAGCCAA AGTGACGTT AGACGGA
AC AAA

GAM7957 297 LOC2018 1 2773 NP_777581.1 3 1146 GAACCCGGGAGG TG 3 C b b

95 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAACCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 LOC2019 1 2545 XP_117339.1 3 1512 GAACCCGGGAGG C 3 C b b

11 CGGAGATTGCGG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGGCGTT GAGGCGGAGGGC
A

GAM7957 297 LOC2021 1 15085 XP_117365.1 5 734 GACCTCAGGAGG C 3 C b b

34 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 LOC2024 1 5365 XP_114493.1 3 346 GATTCTGGGAGG GCAA TC 3 C c c

60 CAATGGGGAGTG TCACT CC TGCCTCCCG
ACTGCTAA AGTGA GG ACGGAGGGT
GG-- TA

GAM7957 297 LOC2027 1 17055 XP_117455.1 3 298 GAACTCGGGTGG C G T 3 C c c

81 GGGAGGTTGCAA TCA TGCAACCTCT CC CCCG
TGAGCCGA AGT ACGTTGGAGG GG GGGC
A G T

GAM7957 297 LOC2028 3 614 XP_117477.1 3 1229 GAACCCGGGAGG C 3 C b b

68 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGACGGAGGGC
C

GAM7957 297 LOC2028 3 2487 XP_117477.1 3 900 GAACCCGGGAGG C 3 C b b

68 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 LOC2028 3 15108 XP_117477.1 3 1195 CTACTCGGGAGG A AAC T 3 C c b

68 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2029 2 2071 XP_117486.2 5 1569 GTGGGAGGGAGG - AA - 3 C c c

34 CAGTGGGAAGTA TCA CTGC CCT CTGCCTCCC
GTTGAATC AGT GATG GGG GACGGAGGG
T AA T

GAM7957 297 LOC2029 2 13454 XP_117486.2 5 1930 CTGGGAAACAGG TC-- --- ---- 3 C c c

34 CAGAGGTTGGAA ACTG CAACCTCTGCC TCCCG

```
                                  CAGTTTGG      TGAC  GTTGGAGACGG   AGGGT
                                        GGTT   AAG        ACAA
GAM7957  297   LOC2032 2  2549  XP_114657.1  3  1366  GAACCCAGGAGG      C      C       3  C  c
c
         45                     CGGAGATTGCAG TCACTGCAA CTCTGCCTCC
                                TGAGCCGA    AGTGACGTT GAGGCGGAGG
                                          A       A
GAM7957  297   LOC2032 2  3440  XP_114657.1  3  1332  CTACCCGGGAGG  A   AAC  T          3  C  c
 c
         45                     CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                AATCGCTT    AG GACG  GAG CGGAGGGC
                                      -   ---  T
GAM7957  297   LOC2042 1  11765 XP_115295.1  3  669   GAACCAGAGAGG        TG   CC       3  C  c
c
         88                     TGGAGGTTGCAG TCACTGCAACCTC  CCTC
                                TGAACCGA    AGTGACGTTGGAG  GGAG
                                          GT   AG
GAM7957  297   LOC2052 1  12156 XP_115760.2  5  262   CCCAGAAGGAGG  -  AAC-      C      3  C  c
c
         72                     CAGAGCTCCGCA TCA CTGC   CTCTGCCTCC
                                GCTGGATC    GGT GACG   GAGACGGAGG
                                      C   CCTC       A
GAM7957  297   LOC2064 2  1492  XP_116497.2  5  543   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         12                     CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATCACTT    AG GACG   GAG CGGAGGGC
                                      -   ---  T
GAM7957  297   LOC2064 2  4032  XP_116497.2  5  576   TGAAACGGGAGG                  3  C  b  b
         12                     CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC2192 4  3056  XP_166599.2  5  856   AGGATGGGGAGG   CT  AA  ---          3  C  c
b
         93                     CAGGGCTGGGGG TCA  GC  CC   TCTGCCTCCC
                                CTTTGAGG    AGT  CG  GG   GGACGGAGGG
                                      TT  GG  TCG
GAM7957  297   LOC2192 4  9335  XP_166599.2  3  869   GAGCATGGGAGG                  3  C  b  b
         93                     CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   LOC2192 4  13988 XP_166599.2  3  703   GAGCCCGGGAAG   C      TG C         3  C  c
b
         93                     TGGAGGTTGCAC TCA TGCAACCTC  C TCCCG
                                TGAGCTGA    AGT ACGTTGGAG  G AGGGC
                                      C       GT A
GAM7957  297   LOC2192 4  17505 XP_166599.2  5  526   CTACTCGGGAGG    GCAA--   T          3  C  c
b
         93                     CTGAGGCAGGAG TCACT     CCTC GCCTCCCG
                                AGTGACGT    AGTGA     GGAG CGGAGGGC
                                      GAGGAC   T
```

GAM7957 297 LOC2193 1 614 XP_167564.2 3 1573 GAACCCGGGAGG C 3 C b b
47 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGACGGAGGGC
C
GAM7957 297 LOC2196 3 4880 XP_167562.1 3 1259 CTACTCGGGAGG A AAC T 3 C c
b
49 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2196 3 6149 XP_167562.1 3 1293 GAACCCGGGCGG C TG T 3 C c
b
49 TGGAGCTTGCAG TCACTGCAA CTC CC CCCG
TGAGCCGA AGTGACGTT GAG GG GGGC
C GT C
GAM7957 297 LOC2196 3 19057 XP_167562.1 3 686 GAACCCAGGAGG C 3 C b b
49 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2196 1 5800 XP_167572.1 3 431 GCTCAGGGGAGG A G ACC- 3 C c
c
90 CAGGAAGATGAA TC CT CA TCTGCCTCCC
GGACTGTT AG GA GT GGACGGAGGG
- A AGAA
GAM7957 297 LOC2197 1 4908 XP_167593.1 5 797 GAACCTGGGAGG 3 C b b
22 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGGTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC2199 1 15762 XP_169057.2 3 822 CTACTCGGGAGG A AAC T 3 C c
c
08 CTGAGGCGGGAG TC CTGC CTC GCCTCCCG
GATCAGTT AG GGCG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2199 2 1492 XP_167785.1 3 315 CTACTCGGGAGG A AAC T 3 C c
c
19 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2199 2 19952 XP_167785.1 3 349 GAGCCCAGGAGG TG C 3 C c
c
19 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCAGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC2200 1 645 NP_660351.1 3 1064 GAGCCCAGGAGT A TGC C 3 C c
c
70 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCCAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 LOC2209 2 5882 XP_166133.1 3 221 GAACCCAGGAGG C C 3 C c b

06 CAGAGATTGCGG TCACTGCAA CTCTGCCTCC

TGAGCCGG AGTGGCGTT GAGACGGAGG
A A
GAM7957 297 LOC2209 2 12432 XP_166133.1 3 822 GGACCTGGGAGG TG 3 C b
b
06 TGGAGGTTGCGG TCACTGCAACCTC CCTCCCG
TGAGCTGA AGTGGCGTTGGAG GGAGGGT
GT
GAM7957 297 LOC2210 2 5830 XP_167669.2 3 2170 CTACTCGGGAGG A AAC T 3 C c
b
42 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2210 2 10438 XP_167669.2 3 2204 GAACCCGGGAGG 3 C b b
42 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC2210 1 11627 XP_169026.1 3 1051 GAACCCGGGAGG CC 3 C b
b
91 CGGATCTTGCAG TCACTGCAA TCTGCCTCCCG
TGAGCGGA AGTGACGTT AGGCGGAGGGC
CT
GAM7957 297 LOC2212 2 11276 XP_168058.1 3 2699 GAACCCGGGAGG C 3 C b
b
88 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCGGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC2212 2 17328 XP_168058.1 3 2665 CTACTCGGGAGG A AAC T 3 C c
b
88 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCCT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2215 2 5859 XP_168091.1 3 2026 GAATCTGGGAGG 3 C b b
43 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC2215 2 17535 XP_168091.1 5 1043 GAACCGGGGAGG C 3 C b
b
43 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCC
TGAGCCAA AGTGACGTT GAGGCGGAGGG
C
GAM7957 297 LOC2215 1 16121 XP_166388.1 3 181 GAACCTGGGAGG G 3 C b b

50 AGGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCTGA AGTGACGTTGGAGG GGAGGGT
A
GAM7957 297 LOC2218 1 8562 XP_166513.1 3 740 AGGGAGTCCACG AC-- C--- 3 C c
c
89 GAGAAGATGCAG TCACTGCA CTCTG CTCCC
TGAATGCT AGTGACGT GAGGC GAGGG
AGAA ACCT

GAM7957 297 LOC2219 2 3974 XP_168343.1 5 539 GAACCCAGGAGG C 3 C b b
43 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGACCCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2219 2 4428 XP_168343.1 5 505 CTACTCGGGAGG A AAC T 3 C c
b
43 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGTTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2219 2 5782 XP_168349.1 5 749 GAGCCCAGGAGG A C 3 C b b
54 CAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCCGA AGTGACGT GGAGACGGAGG
C A
GAM7957 297 LOC2219 2 19058 XP_168349.1 5 571 GAACCTGGGAGG 3 C b b
54 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGGCGTTGGAGGCGGAGGGT
GAM7957 297 LOC2219 2 14360 XP_166554.1 3 1802 CTACTCGGGAGG A GCA T 3 C
c c
62 CTGAGGTGGGAG TC CT ACCTC GCCTCCCG
GATCGCTT AG GA TGGAG CGGAGGGC
- GGG T
GAM7957 297 LOC2219 2 15781 XP_166554.1 3 1834 GAACCCAGGAGG A C 3 C c
c
62 TAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCCGG AGTGACGT GGAGATGGAGG
C A
GAM7957 297 LOC2220 1 10696 XP_168371.1 3 2476 GGGCGTGGGAGG C CAACC 3 C
c c
31 CAGAAGACACTG TCA TG TCTGCCTCCCG
AAGAATTT AGT AC AGACGGAGGGT
C AGA--
GAM7957 297 LOC2220 1 18690 XP_168427.1 5 227 GAACCCGGGAGG 3 C b b
60 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 LOC2221 4 2116 XP_168431.1 3 843 GAACCCAGGAGG A T C 3 C c
b
60 TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGTCAT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 LOC2221 4 9832 XP_168431.1 3 1276 GAACCTGGGAGG C 3 C b b
60 CAGAGTTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCGGA AGTGACGTT GAGACGGAGGGT
T
GAM7957 297 LOC2221 4 10916 XP_168431.1 5 883 CTACTTGGGAGG A AAC 3 C b
b
60 CAGAGGCAGGAG TC CTGC CTCTGCCTCCCG
AATCGCTT AG GACG GAGACGGAGGGT

```
                                        -   ---
GAM7957  297    LOC2221 4  15984  XP_168431.1  5  917   GAACCCAGGAGG          TG    C        3  C  c
b
          60                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                     TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                                   GT    A
GAM7957  297    LOC2222 1  18049  XP_168633.1  3  675   GAGCCCAGGAGT       A   TGC   C        3  C  c
 c
          25                          TTGAGGCTGCAG TCACTGCA CCTC   CTCC
                                     TGAGCTGT    AGTGACGT GGAG   GAGG
                                               C   TTT   A
GAM7957  297    LOC2226 1  10395  XP_167086.2  3  214   CTTTCTGGGGAA       ACC    C         3  C  c
c
          62                          GCAGAACTGCAG TCACTGCA   TCTGC TCCC
                                     TGACCCAC    AGTGACGT   AGACG AGGG
                                               CA-    A
GAM7957  297    LOC2226 1  10435  XP_167095.3  3  144   GAACCCAGGAGG             C        3  C  b  b
          74                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                                   A
GAM7957  297    LOC2532 1  6471   XP_170765.2  5  55    TCCACAGGGAGG  A  CAA -            3  C  c
c
          16                          CAGGTGGCCACG TC CTG   CC TCTGCCTCCC
                                     GCGAGGTC    AG GGC   GG GGACGGAGGG
                                               C   ACC  T
GAM7957  297    LOC2536 2  5924   XP_172985.2  5  607   GAACCCGGAAGG          TG  C        3  C  c
b
          12                          TGGAGGTTGCAG TCACTGCAACCTC  CCT CCG
                                     TGAGCCGA    AGTGACGTTGGAG  GGA GGC
                                                   GT   A
GAM7957  297    LOC2536 2  10438  XP_172985.2  3  1326  GAACCCGGGAGG                    3  C  b  b
          12                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297    LOC2541 1  14304  XP_172851.1  3  748   TGAACCGGGAGG        C             3  C  b  b
          00                          CAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTG AGACGGAGGGC
                                                   A
GAM7957  297    LOC2542 1  9572   XP_173221.1  3  615   GAACCCAGGAGG       C   G    C        3  C  c
c
          66                          AGGAGCTTGCAG TCACTGCAA CTCT CCTCC
                                     TGAGCCGA    AGTGACGTT GAGG GGAGG
                                               C   A    A
GAM7957  297    LOC2548 1  15343  XP_173100.1  3  1192  GAACCCGGGAGG       C             3  C  b
b
          08                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                               C
GAM7957  297    LOC2548 2  2306   XP_171170.1  3  101   GAGCCTGGGAGG          G          3  C  b  b
          75                          AAGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
```

TGAGCCGA AGTGACGTTGGAGA GGAGGGT
A
GAM7957 297 LOC2548 2 7908 XP_171170.1 3 493 GAATCCGGGAGA CTC -- 3 C b b
75 TGCATGTTGCAG TCACTGCAAC TGC CTCCCG
TGAGCTGA AGTGACGTTG ACG GAGGGC
T-- TA
GAM7957 297 LOC2549 1 9560 XP_171161.2 3 519 GAACCTGGGAGG TC----- C 3 C c c
46 CAGAGCTTGCAG ACTGCAA CTCTGCCTCCCG
TAAGCCGA TGACGTT GAGACGGAGGGT
AGCCGAA C
GAM7957 297 LOC2550 1 8789 XP_173187.1 3 440 GAACTTGGGAGG C 3 C b b
31 CAGAGGTTTCAG TCACTG AACCTCTGCCTCCCG
TGAGCCGA AGTGAC TTGGAGACGGAGGGT
T
GAM7957 297 LOC2551 2 1492 XP_172941.1 3 1387 CTACTCGGGAGG A AAC T 3 C c b
77 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2551 2 6524 XP_172941.1 3 1421 AAACATGGGAGG 3 C b b
77 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC2553 2 1492 XP_172920.1 3 2944 CTACTCGGGAGG A AAC T 3 C c b
28 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2553 2 11775 XP_172920.1 3 2978 GAACGTGGGAGG C 3 C b b
28 CAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCAA AGTGACGTTG AGACGGAGGGT
A
GAM7957 297 LOC2553 1 6760 XP_171171.1 5 35 GAGCCCAGGAGG A T C 3 C c c

74 TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGGTAT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 LOC2559 1 5830 XP_172907.1 3 690 CTACTCGGGAGG A AAC T 3 C c c
71 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2560 1 12654 XP_171084.1 3 1091 GAACCCGGCGGG G C 3 C b b
19 AAGAGGTTGCAG TCACTGCAACCTCT CCT CCG
TGAGCCAA AGTGACGTTGGAGA GGG GGC
A C

GAM7957 297 LOC2561 1 18825 XP_172187.1 3 1863 GAGCCCAGGAGT A TGC C 3 C c c

06 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGTTAT AGTGACGT GGAG GAGG
C TTT A

GAM7957 297 LOC2564 1 10018 XP_171439.1 5 526 CTATCCCAGAGG A T CC 3 C c c

70 TCGAGGCTGCAG TCACTGCA CCTC GCCTC
TGAGCTGT AGTGACGT GGAG TGGAG
C C AC

GAM7957 297 LOC2565 2 1492 XP_172866.1 3 315 CTACTCGGGAGG A AAC T 3 C c c

15 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2565 2 7125 XP_172866.1 3 349 GAGCCCAGGAAG TG C C 3 C c c

15 TGGAGGTTGCAG TCACTGCAACCTC C TCC
TGAGCAGA AGTGACGTTGGAG G AGG
GT A A

GAM7957 297 LOC2565 2 1492 XP_173127.1 3 315 CTACTCGGGAGG A AAC T 3 C c c

94 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2565 2 2732 XP_173127.1 3 349 CAGCCCAGGAGG TG C 3 C c c

94 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCGGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 LOC2829 1 16121 XP_212580.1 3 181 GAACCTGGGAGG G 3 C b b

10 AGGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCTGA AGTGACGTTGGAGG GGAGGGT
A

GAM7957 297 LOC2829 1 5928 XP_212579.1 3 1286 GAACCCAGGAGA C C 3 C c c

15 CAGGGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCAA AGTGACGTTGGGGAC GAGG
A A

GAM7957 297 LOC2829 1 16121 XP_212628.1 3 181 GAACCTGGGAGG G 3 C b b

47 AGGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCTGA AGTGACGTTGGAGG GGAGGGT
A

GAM7957 297 LOC2829 1 5928 XP_212627.1 3 1286 GAACCCAGGAGA C C 3 C c c

51 CAGGGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCAA AGTGACGTTGGGGAC GAGG
A A

GAM7957 297 LOC2829 1 10435 XP_212622.1 3 144 GAACCCAGGAGG C 3 C b b
59 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2829 2 15108 XP_210834.1 3 2201 CTACTCGGGAGG A AAC T 3 C c
b
63 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2829 2 15343 XP_210834.1 3 2235 GAACCCGGGAGG C 3 C b
b
63 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC2829 1 18905 XP_210845.1 3 288 TTACCTGGGAGG CT A 3 C c
c
87 CAGAGGGTGTTA TCA GCA CCTCTGCCTCCCG
TGGGAGGA GGT TGT GGAGACGGAGGGT
AT G
GAM7957 297 LOC2830 1 9858 XP_208481.1 3 1299 GAACAGGGGAGA GC 3 C b
b
05 TGGAGGTTGCAG TCACTGCAACCTCT CTCCC
TGAGCTGA AGTGACGTTGGAGG GAGGG
TA
GAM7957 297 LOC2830 2 1557 XP_210872.1 3 1333 ATAAGAGGGAGG GC -- 3 C c
c
50 CAGGAGGGTTAG TCACT AACCT CTGCCTCCC
AGTGAGTA AGTGA TTGGG GACGGAGGG
GA AG
GAM7957 297 LOC2830 2 4180 XP_210872.1 3 1375 AACAGTGGAAGC G - C C 3 C c
c
50 AAGAGGTTGGGG TCACT CAACCTCT GC TCC
TGATGTGG AGTGG GTTGGAGA CG AGG
G A A T
GAM7957 297 LOC2830 2 18041 XP_210875.1 3 484 CTACTCGGGAGG A CAAC T 3 C
c c
61 CTGAGTCAGGAG TC CTG CTC GCCTCCCG
AATCACTT AG GAC GAG CGGAGGGC
- T--- T
GAM7957 297 LOC2830 2 19246 XP_210875.1 3 517 GAACCTGGGAGG C TG 3 C c
c
61 TGGATGTTGCAG TCACTGCAAC TC CCTCCCG
TGAGCTGA AGTGACGTTG AG GGAGGGT
T GT
GAM7957 297 LOC2830 1 8877 XP_210883.1 3 1115 GAACCCAGGAGG C C 3 C c
c
83 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 LOC2831 1 16476 XP_210889.1 3 1485 GAACTCAGGTGG T C 3 C b
b

```
          07                          CAGAGGTTGCAG TCACTGCAACCTCTGCC CC
                                     TGAGCCGA    AGTGACGTTGGAGACGG GG
                                                   T  A
GAM7957  297   LOC2831 1  13229 XP_210897.1  3 1396  TGGGAGGTGGAG      A-----   TG        3  C  c
 c
          25                          GGGAGGCTGCAG TCACTGCA    CCTC  CCTCCCG
                                     TGAGCTGA    AGTGACGT    GGAG  GGAGGGT
                                                   CGGAGG   GT
GAM7957  297   LOC2831 1  16945 XP_210920.1  3 1045  CATTTTGGGAGG  A   AAC            3  C  b
b
          43                          CAGAGGCAGGAG TC CTGC  CTCTGCCTCCCG
                                     GATTGCTT    AG GACG  GAGACGGAGGGT
                                              -   ---
GAM7957  297   LOC2831 1  19057 XP_210910.1  3 1027  GAACCCAGGAGG            C        3  C  b  b

          68                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGG
                                                   A
GAM7957  297   LOC2831 1  12613 XP_210903.1  3 1158  TGTGACAGGAGG  A    -- -     C       3  C  c
c
          77                          CAGCAGAAGTTG TC CTGCAAC  CT CTGCCTCC
                                     CAGAGAAG    AG GACGTTG  GA GACGGAGG
                                              A      AA  C       A
GAM7957  297   LOC2832 1  9151  XP_208559.2  3 724   CAACCTGGGAGG                  3  C  b  b
          08                          TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGATGGAGGGT

GAM7957  297   LOC2832 2  8878  XP_208555.2  3 2913  GAACCTGGGAGG       C             3  C  b  b
          15                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTT GAGGCGGAGGGT
                                                   C
GAM7957  297   LOC2832 2  9770  XP_208555.2  3 3482  GAACCTGGGAGG          TG          3  C  b
b
          15                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCTGA    AGTGACGTTGGAG  GGAGGGT
                                                   GT
GAM7957  297   LOC2832 1  18691 XP_208578.1  3 840   GAACCTGGGAGG                  3  C  b  b
          35                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC2832 2  11352 XP_210947.2  3 792   GAACCCAGGAGG       A       C       3  C  c  c

          43                          TAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
                                     TGAGCAGG    AGTGACGT GGAGATGGAGG
                                                   C         A
GAM7957  297   LOC2832 2  14360 XP_210947.2  3 760   CTACTCGGGAGG  A GCA    T          3  C  c
 c
          43                          CTGAGGTGGGAG TC CT   ACCTC GCCTCCCG
                                     GATCGCTT    AG GA   TGGAG CGGAGGGC
                                              -  GGG    T
```

```
GAM7957  297   LOC2832 1  18377 XP_208583.2  3  1056  AGGCCAGGGAGG  A   AA  T          3  C  c
 c
          44                      CAGTGGAGGCAG TC CTGC  CC CTGCCTCCC
                                 GAGAGGCT    AG GACG  GG GACGGAGGG
                                         -   GA  T
GAM7957  297   LOC2832 1  1906  XP_210953.1  3  946   GAACCCAGGAGG        TG   C       3  C  c
c
          69                      TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                 TGGGCCGA    GGTGACGTTGGAG  GGAGG
                                             GT    A
GAM7957  297   LOC2832 1  19053 XP_208601.1  3  968   GAACCCAGAAGG       C     CCC       3  C  c
 c
          83                      CGGAAGTTGCAG TCACTGCAAC TCTGCCT
                                 TGAGCCGA    AGTGACGTTG AGGCGGA
                                           A     AGA
GAM7957  297   LOC2832 1  12929 XP_210964.1  3  2033  GACCCCAGGAGG       CC  TG   C       3  C
c  c
          95                      TGGACATTGCAG TCACTGCAA  TC  CCTCC
                                 TGAGCCGA    AGTGACGTT  AG  GGAGG
                                           AC  GT    A
GAM7957  297   LOC2832 1  12796 XP_210965.1  3  632   GAACCCGGGAGG                  3  C  b  b
          99                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                 TGAGCCAA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   LOC2833 2  14571 XP_210969.1  3  582   GAGCTCGGAAGA       A   GC  C       3  C  c
 b
          14                      TGGAGGCTGCAG TCACTGCA CCTCT  CT CCG
                                 TGAGCCAT    AGTGACGT GGAGG  GA GGC
                                           C    TA  A
GAM7957  297   LOC2833 2  18826 XP_210969.1  3  1487  GAACCTGGGAGG       A             3  C  b  b

          14                      CGGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
                                 TGAGCCGA    AGTGACGT GGAGGCGGAGGGT
                                           C
GAM7957  297   LOC2833 1  15781 XP_208618.1  3  1773  GAACCCAGGAGG       A       C       3  C  c
c
          25                      TAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
                                 TGAGCCGG    AGTGACGT GGAGATGGAGG
                                           C        A
GAM7957  297   LOC2833 2  12188 XP_210978.1  5  215   GAGCCCAGGAGG       A  T    C       3  C  c
b
          29                      TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
                                 TGAGCTAT    AGTGACGT GGAG TGGAGG
                                           C   T    A
GAM7957  297   LOC2833 2  18024 XP_210978.1  3  622   GAACCCGAGAGG       C      C       3  C  b
b
          29                      CGGAGCTTGCAG TCACTGCAA CTCTGCCTC CG
                                 TGAGCTGA    AGTGACGTT GAGGCGGAG GC
                                           C       A
GAM7957  297   LOC2833 1  15018 XP_210991.1  3  649   ACCCGGTAGAGG           --       3  C  b  b
```

```
          57                        CGGAGGTTGCAG TCACTGCAACCTCTGCCTC  CCG
                                    TGAGCCGA    AGTGACGTTGGAGGCGGAG  GGC
                                                  AT
GAM7957  297   LOC2833 1  9260  XP_211005.1  3  779   GAACCCAGGAGG        C       C        3  C  c  c

          82                        TAGAAGTTGCAG TCACTGCAAC TCTGCCTCC
                                    TGAGCCGA    AGTGACGTTG AGATGGAGG
                                              A       A
GAM7957  297   LOC2833 1  17398 XP_211021.1  3  666   GAACCTGGGAGG    TG                3  C  b
b
          94                        CAGAGGTTGTGG TCAC  CAACCTCTGCCTCCCG
                                    TGAGCTGA    AGTG  GTTGGAGACGGAGGGT
                                              GT
GAM7957  297   LOC2834 1  19054 XP_208084.1  3  443   GAACCCGGGAGG                    3  C  b  b
          15                        CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCCAA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC2834 1  13667 XP_211038.1  3  962   GAACCCGGGAGG         C           3  C  b  b

          37                        TGCAGGTTGCAG TCACTGCAACCT TGCCTCCCG
                                    TGAGCCAA    AGTGACGTTGGA GTGGAGGGC
                                                C
GAM7957  297   LOC2834 1  15747 XP_211042.1  5  594   GAACCCAGGAGG       C       C        3  C  c
c
          38                        CGGAGTTTGCAG TCACTGCAA CTCTGCCTCC
                                    TGAGCTGA    AGTGACGTT GAGGCGGAGG
                                              T       A
GAM7957  297   LOC2834 1  15984 XP_211037.1  3  869   GAACCCAGGAGG         TG    C        3  C  c
c
          42                        TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                    TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                                GT    A
GAM7957  297   LOC2834 1  19898 XP_211047.1  5  562   GAACTCGGGAGG        CTC            3  C  c
c
          53                        TGAAAGTTGCAG TCACTGCAAC   TGCCTCCCG
                                    TGAGCCGA    AGTGACGTTG   GTGGAGGGC
                                              AAA
GAM7957  297   LOC2834 3  1620  XP_208682.1  3  1625  GAACCCAGGAGG             C       3  C  b  b
          60                        CGGGGGTTGCAG TCACTGCAACCTCTGCCTCC
                                    TGAGTCGA    AGTGACGTTGGGGGCGGAGG
                                                  A
GAM7957  297   LOC2834 3  3523  XP_208682.1  3  1591  CTACTCGGGAGG  A   A  CTCT           3  C
c  b
          60                        CTGTGGCAGGAG TC CTGC AC    GCCTCCCG
                                    AATTGCTT    AG GACG TG    CGGAGGGC
                                              -   G  T---
GAM7957  297   LOC2834 3  15308 XP_208682.1  3  635   GAACCCAGGAGA          C   C        3  C  b
b
          60                        CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
                                    TGAGCCAA    AGTGACGTTGGAGAC GAGG
```

A A
GAM7957 297 LOC2834 1 16897 XP_211050.1 3 1245 CAACCAGGGAGG 3 C b b
67 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCCGA AGTGACGTTGGAGACGGAGGG

GAM7957 297 LOC2835 1 15343 XP_211073.1 3 401 GAACCCGGGAGG C 3 C b b

06 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC2835 2 14789 XP_211070.1 3 1417 GAACCCAGGAGG C 3 C b b

08 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2835 2 15089 XP_211070.1 3 1383 CTACTCGGGAGG A AAC T 3 C c
b
08 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2835 2 5830 XP_211078.1 3 747 CTACTCGGGAGG A AAC T 3 C c
b
31 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2835 2 14787 XP_211078.1 3 781 GAACCAGGGAAG C 3 C b b
31 CGGAGGTTGCAG TCACTGCAACCTCTGC TCCC
TGAGCCGA AGTGACGTTGGAGGCG AGGG
A
GAM7957 297 LOC2835 1 9763 XP_211114.1 3 709 GAACCCAGGAGG TG C 3 C c
c
66 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC2835 2 3025 XP_211118.1 5 870 CTACTTGAGAGG A AAC CC 3 C c
b
70 CAGAGGCAGGAG TC CTGC CTCTGCCTC
AATCGCTT AG GACG GAGACGGAG
- --- AG
GAM7957 297 LOC2835 2 18691 XP_211118.1 5 904 GAACCTGGGAGG 3 C b b
70 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC2836 1 1548 XP_208762.1 5 3898 GGGCCCAGGAGT A ---- G --- 3 C c
c
33 TCAAGGCTGCAG TCACTGCA CCT CT CCT CCC
TGAGCTAT AGTGACGT GGA GA GGA GGG
C ACTT - CCC
GAM7957 297 LOC2836 4 9536 XP_211144.1 3 1764 GAATCCGGGAGG TG 3 C b
b

```
          55                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCCAA    AGTGACGTTGGAG  GGAGGGC
                                                 GT
GAM7957  297   LOC2836 4  13166  XP_211144.1  3  563   GAACCCAGGGGG   C      TG   C       3  C  c
b
          55                          TGGAGGTTGCAC TCA TGCAACCTC  CCTCC
                                     TGAGCCGA    AGT ACGTTGGAG  GGGGG
                                           C       GT    A
GAM7957  297   LOC2836 4  14905  XP_211144.1  3  860   GAACCCGGGAGG   - -              3  C  b  b
          55                          CAGAGGTTGTGA TCA CT GCAACCTCTGCCTCCCG
                                     GCTGAGAT    AGT GA TGTTGGAGACGGAGGGC
                                           C G
GAM7957  297   LOC2836 4  17452  XP_211144.1  5  542   GAACCCGGGAGG       C            3  C  b  b

          55                          CGGAGTTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTT GAGGCGGAGGGC
                                              T
GAM7957  297   LOC2836 1  4155   XP_211164.1  3  1926  CTGCTTGGGAGG  A  CA   C           3  C  c
c
          86                          CACAGGTCCTGG TC CTG  ACCT TGCCTCCCG
                                     GACATGAA    AG GGT  TGGA ACGGAGGGT
                                           -  CC   C
GAM7957  297   LOC2836 1  9781   XP_211167.1  3  5834  CTTCTCGGGAGG  A  AAC  T           3  C  c
c
          90                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATCACTT    AG GACG   GAG CGGAGGGC
                                           -   ---  T
GAM7957  297   LOC2836 2  2070   XP_208788.1  3  546   AAACCTGGGAGG   CT  A-              3  C  c  c

          93                          CAGAGGTGAGCT TCA  GC  ACCTCTGCCTCCCG
                                     GAGATCGC    AGT  CG  TGGAGACGGAGGGT
                                           --  AG
GAM7957  297   LOC2836 2  5830   XP_208788.1  3  512   CTACTCGGGAGG  A  AAC  T           3  C  c
c
          93                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATCGCTT    AG GACG   GAG CGGAGGGC
                                           -   ---  T
GAM7957  297   LOC2836 1  18836  XP_211173.1  5  1225  CTGGTGGGGAGG    TG AACC            3  C
c  c
          97                          CAGGCTGGTGGT TCAC  C   TCTGCCTCCC
                                     GGAGTCAT    GGTG  G   GGACGGAGGG
                                           GT GTC-
GAM7957  297   LOC2837 2  2678   XP_208804.3  5  1965  AAGGGCAGGAGG  AC--  A  -     C      3  C  c
b
          06                          CAGCAGGTGCAC TC   TGCA CCT CTGCCTCC
                                     CAGGAGCA    AG   ACGT GGA GACGGAGG
                                           GACC   -  C      A
GAM7957  297   LOC2837 2  15592  XP_208804.3  3  1744  GAACCCAGGAGG    C        C       3  C  b
b
          06                          CAGAGGTTACAG TCACTG AACCTCTGCCTCC
```

```
                                    TGAGCAGA    AGTGAC TTGGAGACGGAGG
                                              A          A
GAM7957  297   LOC2837 1  8067  XP_211184.1  3  423   AATCTCGGGAGG                    3  C  b  b
          31                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   LOC2837 1  13155 XP_208819.1  3  545   CTACTCGGGAGG  A   AAC  T          3  C  c
 c
          40                      CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                    AATGGCGT    AG GACG  GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   LOC2837 1  14124 XP_208826.2  3  3085  GAACCCAGGAGA          C  C       3  C  c
c
          60                      CGGAGGTTGCAG TCACTGCAACCTCTG CTCC
                                    TGAGCCGA    AGTGACGTTGGAGGC GAGG
                                                A   A
GAM7957  297   LOC2837 1  10439 XP_208835.1  5  584   GAACCTGGGAGG                    3  C  b  b
          67                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   LOC2837 2  14438 XP_211199.1  5  4201  GAACCCGGCAGG  C      G  C        3  C  c
 c
          78                      AAGAGGTTGCAT TCA TGCAACCTCT CCT CCG
                                    TGAGCTGA    AGT ACGTTGGAGA GGA GGC
                                          T       A  C
GAM7957  297   LOC2837 2  15089 XP_211199.1  5  4167  CTACTCGGGAGG  A   AAC  T          3  C  c
 c
          78                      CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                    AATTGCTT    AG GACG  GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   LOC2838 1  16120 XP_211229.1  3  2839  GAACCCAGGAGG       C      C       3  C  b
b
          51                      CAGAAGTTGCAG TCACTGCAAC TCTGCCTCC
                                    TGAGCTGA    AGTGACGTTG AGACGGAGG
                                              A       A
GAM7957  297   LOC2838 1  20057 XP_208875.1  3  2825  CTACCCGGGAGG      A  T          3  C  b
b
          63                      CAGTGGCTGCAG TCACTGCA CC CTGCCTCCCG
                                    TGAGCTGA    AGTGACGT GG GACGGAGGGC
                                            C  T
GAM7957  297   LOC2838 1  8987  XP_211241.1  3  585   CAGTTCGGGAGG    GC  C          3  C  c
c
          75                      CAGAGTTAGGTG TCACT  AAC TCTGCCTCCCG
                                    GATCAATT    GGTGG  TTG AGACGGAGGGC
                                            A-  -
GAM7957  297   LOC2838 1  2881  XP_208899.1  3  1279  GGGCCCACAAAG      A  C  C -------     3  C  c
c
          89                      TCAAGGCTGCAG TCACTGCA CCT TG CT      CCC
                                    TGAGCTGT    AGTGACGT GGA AC GA      GGG
                                            C   -  T  AACACCC
```

GAM7957 297 LOC2838 1 9765 XP_211250.1 3 390 GAACCCGGGAGG TG 3 C b b

94 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 LOC2839 1 9765 XP_211256.1 3 390 GAACCCGGGAGG TG 3 C b b

09 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 LOC2839 2 4977 XP_208906.1 3 971 GAACCTGAGAGG CC 3 C b b

24 CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGACGTTGGAGACGGAG
AG

GAM7957 297 LOC2839 2 18690 XP_208906.1 3 554 GAACCCGGGAGG 3 C b b

24 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC2839 1 962 XP_208909.1 3 162 GAACCCAGGAGG A C 3 C c c

28 CGGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCCCA AGTGACGT GGAGGCGGAGG
C A

GAM7957 297 LOC2839 3 1734 XP_208905.2 3 162 GACCCCAGGAGG G C 3 C b b

29 CAGAGGTTGAAG TCACT CAACCTCTGCCTCC
TGAGCCAG AGTGA GTTGGAGACGGAGG
A A

GAM7957 297 LOC2839 3 7877 XP_208905.2 5 1947 CTACTCGGGAGG A AAC T 3 C c b

29 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCTCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2839 3 9417 XP_208905.2 5 1981 GAACCCAGGAGG C 3 C b b

29 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGGCGTTGGAGGCGGAGG
A

GAM7957 297 LOC2839 2 6418 NP_787097.1 3 2637 GAACCTGGAAGG C 3 C b b

32 CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCAA AGTGACGTTGGAGGCGGA GGT
A

GAM7957 297 LOC2839 2 8956 NP_787097.1 3 2143 CACTTCGGGAGG A GCA CT 3 C c b

32 CCAAGGTGAGAG TC CT ACCT GCCTCCCG
GATAACTT AG GA TGGA CGGAGGGC
- GAG AC

GAM7957 297 LOC2839 1 12303 XP_208928.1 3 494 GAACCTGGGAGA C 3 C b b

49 CAGAGGTTGCAG TCACTGCAACCTCTG CTCCCG
TGAGCCAA AGTGACGTTGGAGAC GAGGGT
A

GAM7957 297 LOC2839 1 18689 XP_208931.1 3 1537 GAACCTGGGAGG C 3 C b b

54 CGAAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCCAA AGTGACGTTGGA GCGGAGGGT
A

GAM7957 297 LOC2839 1 471 XP_211282.1 3 1004 GAACCGAGGAGG C - 3 C b b
72 CGAAGGTTGCAG TCACTGCAACCT TGCCTCC CG
TGAGCCGA AGTGACGTTGGA GCGGAGG GC
A A

GAM7957 297 LOC2839 1 9983 XP_208941.1 3 809 CATGTCGGGAGG A GCA T 3 C c
c

81 CTGAGGTGGGAG TC CT ACCTC GCCTCCCG
GATCGCTT AG GA TGGAG CGGAGGGC
- GGG T

GAM7957 297 LOC2839 1 15983 NP_835229.1 3 927 GAACCCGGGAGG TG 3 C b
b

85 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 LOC2839 1 15983 XP_208951.2 3 927 GAACCCGGGAGG TG 3 C b
b

85 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 LOC2839 1 11864 XP_208945.1 3 1333 CTTCCCGGGAGG CT A ---- 3 C c
c

95 CAGCCCCGGGAT TCA GCA CCT CTGCCTCCCG
GCTGAGAG AGT CGT GGG GACGGAGGGC
-- A CCCC

GAM7957 297 LOC2840 1 17795 XP_208958.2 3 115 GCTCAGGTGGGA A- TG TC 3 C c
c

01 CGAGGGCTGCAG TCACTGCA CCTC CC CC
TGAAGGCC AGTGACGT GGAG GG GG
CG CA GT

GAM7957 297 LOC2840 1 12796 XP_211299.1 5 507 GAACCCGGGAGG 3 C b b
09 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC2840 1 5830 XP_211300.2 3 1718 CTACTCGGGAGG A AAC T 3 C c
c

14 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2840 1 9417 XP_208970.1 3 375 GAACCCAGGAGG C 3 C b b
24 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGGCGTTGGAGGCGGAGG
A

GAM7957 297 LOC2840 1 9422 XP_208982.1 3 1028 GAACCCAGGAGG C 3 C b b
31 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG

A

GAM7957 297 LOC2840 1 723 XP_211310.1 3 438 GAACCTGGGAGG C 3 C b b
44 CGGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCTGA AGTGACGTTG AGGCGGAGGGT

A

GAM7957 297 LOC2840 1 12193 XP_208152.1 3 1675 GAGCCTGGGAGG A T 3 C c
c
48 TCGAGGCTGCAG TCACTGCA CCTC GCCTCCCG
TGAGCTGT AGTGACGT GGAG TGGAGGGT

C C

GAM7957 297 LOC2840 3 2483 XP_211316.1 5 570 GAACCTGGGAGG C 3 C b b
62 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT

C

GAM7957 297 LOC2840 3 6320 XP_211316.1 5 526 CTGCTCGGGAGG A AAC T 3 C c
b
62 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGT AG GACG GAG CGGAGGGC

- --- T

GAM7957 297 LOC2840 3 8856 XP_211316.1 3 689 GAGGCCAGGAGT AC C C 3 C c
b
62 TAGAGACTGCAG TCACTGCA CTCTG CTCC
TGAGCTAT AGTGACGT GAGAT GAGG

CA T A

GAM7957 297 LOC2840 1 947 XP_211319.1 3 880 GGACCCGGGAGG 3 C b b
72 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC2840 3 1199 XP_211321.1 3 818 GCAGAGGCTGGG A- G TC 3 C c
c
74 GGAGGGATGCAG TCACTGCA CCTCT CC CC
TGACTTTT AGTGACGT GGAGG GG GG

AG G TC

GAM7957 297 LOC2840 3 3337 XP_211321.1 3 2161 GAGCCCTGGAGG A T C 3 C c
c
74 TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCTGG AGTGACGT GGAG TGGAGG

C T T

GAM7957 297 LOC2840 3 11071 XP_211321.1 3 1798 GAGCCCAGGAGT A TGC C 3 C
c c
74 TTGAGGATGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG

A TTT A

GAM7957 297 LOC2841 2 8019 XP_209019.1 5 784 GAACCCGGGAAG C C 3 C b b

01 CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC

C A

GAM7957 297 LOC2841 2 13155 XP_209019.1 5 750 CTACTCGGGAGG A AAC T 3 C c
b

```
          01                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATGGCGT    AG GACG  GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC2841 1  10901  XP_211327.3  5  591   GAACCGGGGAGG                    3  C  b  b
          02                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
                                     TGAGCTGA    AGTGACGTTGGAGACGGAGGG

GAM7957  297   LOC2841 1  4377   XP_209026.1  3  300   GAACCCGGGAAG    T      TG C         3  C  c
c
          21                          TGGAGGTTGCCG TCAC GCAACCTC  C TCCCG
                                     TGAGTCGA    AGTG CGTTGGAG  G AGGGC
                                               C      GT A
GAM7957  297   LOC2841 1  5042   XP_211353.1  3  871   GAACTGGGGAAG           C         3  C  b  b
          45                          CAGAGGTTGTAG TCACTGCAACCTCTGC TCCC
                                     TGAGCCGA    AGTGATGTTGGAGACG AGGG
                                                 A
GAM7957  297   LOC2841 1  12886  XP_211354.1  5  511   GAATGTGGGAGG                    3  C  b  b
          55                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGTCAG    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC2841 2  1163   XP_209041.1  5  485   GTGTGTCGGGGG  A  GCAA     T        3  C
c  b
          58                          CAGAGGGAAGGA TC CT   CCTCTGCC CCCG
                                     GGGAAGGA    AG GA   GGAGACGG GGGC
                                              -  AG--       -
GAM7957  297   LOC2841 2  3397   XP_209041.1  3  3     AGCCCGGGAGGC       A            3  C  b  b
          58                          AGAGGCTGCAGT TCACTGCA CCTCTGCCTCCCG
                                     GGCTGAGA    GGTGACGT GGAGACGGAGGGC
                                                   C
GAM7957  297   LOC2841 1  19278  XP_209047.2  3  687   GAACCCGGGAGG       A            3  C  b  b

          61                          CAGAGGCTGTAG TCACTGCA CCTCTGCCTCCCG
                                     TGAGCCAA    AGTGATGT GGAGACGGAGGGC
                                                   C
GAM7957  297   LOC2841 1  18300  XP_211357.1  5  39    CACTTTGGGAGG     GCAAC            3  C  c
c
          70                          CAGAGACAGGTG TCACT    CTCTGCCTCCCG
                                     GATCACGA    GGTGG    GAGACGGAGGGT
                                                ACA--
GAM7957  297   LOC2841 1  6740   XP_211363.1  5  533   GTACATGGGAGG    T  ACCTC          3  C  c
 c
          74                          CATGTGTGTGAT TCAC GCA    TGCCTCCCG
                                     GTGTACAC    AGTG TGT    ACGGAGGGT
                                              -  GT---
GAM7957  297   LOC2841 1  11754  XP_211369.1  3  1118  TGGCTCGGGGGA   -      CTGC         3  C  c
 c
          79                          TCCAGGTTGCAG TCA CTGCAACCT    CTCCCG
                                     ATGAAATA    AGT GACGTTGGA    GGGGGC
                                                A       CCTA
GAM7957  297   LOC2841 2  7321   XP_209061.1  3  620   GAACCCAGGAAG          C  C       3  C  c  c
```

```
          81                          TAGAGGTTGCAG TCACTGCAACCTCTGC TCC
                                     TGAGCCGA    AGTGACGTTGGAGATG AGG
                                                   A   A
GAM7957  297   LOC2841 2  14790  XP_209061.1  3  1163   GAGCCCAGGAGG       A  CT    C        3  C  c
 c
          81                          TCAAGGCTGCAG TCACTGCA CCT  GCCTCC
                                     TGAGCTGT    AGTGACGT GGA  TGGAGG
                                                  C  AC     A
GAM7957  297   LOC2841 1  19195  XP_209059.1  3  602    GGCCACGGGAGG   C   A  T            3  C  c
c
          83                          CGGGGCTGCATG TCA TGCA CC CTGCCTCCCG
                                     GCTGGGGG    GGT ACGT GG GGCGGAGGGC
                                              -   C  -
GAM7957  297   LOC2841 3  5070   XP_211366.2  3  1265   GAACCTGGGAAG       A   TG C          3  C  c
b
          87                          TGGAGGCTGCAG TCACTGCA CCTC  C TCCCG
                                     TGAGCCGA    AGTGACGT GGAG  G AGGGT
                                                  C   GT A
GAM7957  297   LOC2841 3  12259  XP_211366.2  3  1571   GAACCAGGGAGG       A             3  C  b  b

          87                          CAGAGGCTGCGG TCACTGCA CCTCTGCCTCCC
                                     TGAGCCGA    AGTGGCGT GGAGACGGAGGG
                                                  C
GAM7957  297   LOC2841 3  19057  XP_211366.2  3  2403   GAACCCAGGAGG             C        3  C  b  b

          87                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGG
                                                    A
GAM7957  297   LOC2841 1  4105   XP_211380.1  5  2271   GCATCCAGGAGA       C   C   C        3  C  c
c
          98                          TAGAAGTTGCAG TCACTGCAAC TCTG CTCC
                                     TGAGCTGA    AGTGACGTTG AGAT GAGG
                                                  A   A   A
GAM7957  297   LOC2842 1  16896  XP_211386.1  3  716    GAACCCGGCAGG             C         3  C  b  b

          11                          CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
                                     TGAGCGGA    AGTGACGTTGGAGGCGGA GGC
                                                    C
GAM7957  297   LOC2842 1  11749  XP_211410.1  3  1284   GAAGCTGGGAGG     C  C             3  C  b
b
          59                          CAGAGTTTTCAG TCACTG AA CTCTGCCTCCCG
                                     TGAGCCAA    AGTGAC TT GAGACGGAGGGT
                                                  T  T
GAM7957  297   LOC2842 2  1030   XP_211403.1  3  735    GGGAGGCTGAGG    CT   --------   T        3  C  c
b
          66                          CAGAAGTATTGC TCA  GCAA       CCTC GCCTCCC
                                     TTGAACCC    AGT  CGTT       GGAG CGGAGGG
                                              T-    ATGAAGAC    T
GAM7957  297   LOC2842 2  17403  XP_211403.1  3  765    GAACCCAGGAGG             C        3  C  b  b
          66                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
```

TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2842 1 19637 XP_211411.1 3 10 CCCCATGGGAGG - AACCTC 3 C c c
67 CACATTAGCTAG TCACT GC TGCCTCCCG
TGGCAAGT GGTGA CG ACGGAGGGT
T ATTAC-
GAM7957 297 LOC2842 1 7322 XP_211416.1 5 1226 GAACCCGAGAGG C C 3 C b b
80 CGGAGCTTGCAG TCACTGCAA CTCTGCCTC CG
TGAGCCAA AGTGACGTT GAGGCGGAG GC
C A
GAM7957 297 LOC2843 1 13066 XP_211426.1 3 1132 GAACCTGGGAGG 3 C b b
04 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC2843 1 14092 XP_302720.1 3 651 GAGCCCAGGAGG AC CT C 3 C c c
11 TCAAGACTGCAG TCACTGCA CT GCCTCC
TGAGCTAT AGTGACGT GA TGGAGG
CA AC A
GAM7957 297 LOC2843 1 12307 XP_209116.1 3 1415 GAACCTAGGAGG C 3 C b b

13 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAACCGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2843 1 13433 XP_209149.1 3 3 AACCTGGGAGGC 3 C b b
18 GGAGGTTGCAGT TCACTGCAACCTCTGCCTCCCG
GGCCGAGA GGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC2843 1 698 XP_209120.1 5 25 CTACTCGGGAGG TG 3 C b b
47 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 LOC2843 1 15609 XP_209155.1 3 403 GAACCCTGGAGG C 3 C b b
71 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
T
GAM7957 297 LOC2843 1 7223 XP_209157.1 3 1716 GATCCGGGGAGG C TG 3 C c c
76 TGGAAGTTGCAG TCACTGCAAC TC CCTCCC
TGGGCCAA GGTGACGTTG AG GGAGGG
A GT
GAM7957 297 LOC2844 4 5830 XP_209185.1 3 435 CTACTCGGGAGG A AAC T 3 C c b
07 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2844 4 5831 XP_209185.1 3 469 GAATCCAGGAGG G C 3 C c b

```
          07                      AGGAGGTTGCAG TCACTGCAACCTCT CCTCC
                                  TGAGCCGA    AGTGACGTTGGAGG GGAGG
                                              A    A
GAM7957  297   LOC2844 4  9066  XP_209185.1  3  1334  AGCTAAAGGAGG        T    C       3  C  b  b

          07                      CTGAGGTTGCAG TCACTGCAACCTC GCCTCC
                                  TGAGCTGA    AGTGACGTTGGAG CGGAGG
                                              T    A
GAM7957  297   LOC2844 4  9857  XP_209185.1  3  165   GAACCCAGGAGG           C       3  C  b  b
          07                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                  TGAGCTGT    AGTGACGTTGGAGACGGAGG
                                              A
GAM7957  297   LOC2844 1  9500  XP_211449.1  3  353   GAACCCCGGAGG    C       C       3  C  b  b

          10                      CAGAGGTTTCAG TCACTG AACCTCTGCCTCC
                                  TGAGCCGA    AGTGAC TTGGAGACGGAGG
                                              T         C
GAM7957  297   LOC2844 1  9777  XP_209184.1  5  772   GAACCCGTGTGG          TCC       3  C  c  c

          12                      CAGAGGTTGCGG TCACTGCAACCTCTGCC  CG
                                  TGAGTGTA    AGTGGCGTTGGAGACGG  GC
                                              TGT
GAM7957  297   LOC2844 2  3681  XP_209187.1  3  411   CTACGTGGGAGG  A   AAC           3  C  b
b
          17                      CAGAGGCAGGAG TC CTGC  CTCTGCCTCCCG
                                  AATCATTT    AG GACG  GAGACGGAGGGT
                                              -   ---
GAM7957  297   LOC2844 2  17423 XP_209187.1  3  445   GAACCTGGGAGG         TG          3  C  b
b
          17                      TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                  TGAGCCGA    AGTGACGTTGGAG  GGAGGGT
                                              GT
GAM7957  297   LOC2844 1  15017 XP_209193.1  3  339   GAAACTGGAAGG          C       3  C  b  b
          19                      CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
                                  TGAGCCGA    AGTGACGTTGGAGACGGA GGT
                                              A
GAM7957  297   LOC2844 2  9421  XP_211460.1  3  2220  GAACCCGGGAGG                  3  C  b  b
          34                      CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC2844 2  18690 XP_211460.1  3  1918  GAACCCGGGAGG                  3  C  b  b
          34                      CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCTGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC2844 1  11942 XP_209209.1  3  270   AACACCAGGGGG  A  CA       C       3  C  c
c
          44                      CAGAGGTCAGGA TC CTG  ACCTCTGCCTCC
                                  GAATCATC    AG GAC  TGGAGACGGGGG
                                              -   --         A
GAM7957  297   LOC2844 1  19196 XP_209231.1  3  1529  GAACCCGAGAGG          C       3  C  b  b
```

```
          86                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTC CG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAG GC
                                                    A
GAM7957  297   LOC2845 1  15933  XP_209244.1  3  539   GGGCCCTGGAGG      A  CT    C       3  C  c
c
          14                          TCAAGGCTGCAG TCACTGCA CCT  GCCTCC
                                     TGAGTCAA    AGTGACGT GGA  TGGAGG
                                                   C  AC     T
GAM7957  297   LOC2845 1  19461  XP_209254.1  5  502   CAAGTGGGGAGG  A  CA   CT          3  C  c
c
          42                          CAGGTGACAGGG TC CTG  ACCT  GCCTCCC
                                     ACTCCGAG    AG GAC  TGGA  CGGAGGG
                                              G  AG   --
GAM7957  297   LOC2845 1  7964   XP_209256.1  5  68    GGATGGGAACCG T       --   CC         3  C  c  c

          57                          GATTGGTTGCAG  CACTGCAACC  TCTG  TCCCG
                                     TGT        GTGACGTTGG  AGGC  AGGGT
                                           T        TT   CA
GAM7957  297   LOC2845 1  8381   XP_211527.1  3  1106  GAACCCGGGAGG TC-----              3  C  c
c
          74                          CAGAGGTTGCAG       ACTGCAACCTCTGCCTCCCG
                                     TAAGCAGA          TGACGTTGGAGACGGAGGGC
                                           AGACGAA
GAM7957  297   LOC2845 1  15308  XP_211522.1  3  1234  GAACCCAGGAGA          C   C       3  C  b
b
          77                          CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
                                     TGAGCCAA    AGTGACGTTGGAGAC GAGG
                                                    A   A
GAM7957  297   LOC2846 2  1244   XP_211548.1  3  1393  CTATTCGGGAGG  A  CAAC  T          3  C  c
c
          00                          CTGAGACAGGAG TC CTG    CTC GCCTCCCG
                                     AATCACTT    AG GAC    GAG CGGAGGGC
                                              -  A---   T
GAM7957  297   LOC2846 2  16341  XP_211548.1  3  1427  GAACCCGGGAGG  A  GC              3  C  c
c
          00                          CGGAGGTTATGG TC CT  AACCTCTGCCTCCCG
                                     AGAGCCAA    AG GG  TTGGAGGCGGAGGGC
                                              A  TA
GAM7957  297   LOC2846 2  9474   XP_211561.1  5  1176  CTACTCGGGAGG  A   AAC  T          3  C  c
b
          28                          CTGAGGCGGGAG TC CTGC   CTC GCCTCCCG
                                     AATCACTT    AG GGCG   GAG CGGAGGGC
                                              -   ---   T
GAM7957  297   LOC2846 2  14786  XP_211561.1  5  901   GAACCTGGGAGG                  3  C  b  b
          28                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC2846 1  9946   XP_211562.1  5  194   TCGGCACTGAGG  AC  AA       ----      3  C  c
c
          30                          CAGAGGAGGCAA TC  TGC  CCTCTGCCTC   CCG
```

GGGCTGGT GG ACG GGAGACGGAG GGC
GA GA TCAC
GAM7957 297 LOC2846 1 17403 XP_211567.1 3 734 GAACCCAGGAGG C 3 C b b
39 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2846 1 9422 XP_211571.1 5 740 GAACCCAGGAGG C 3 C b b
50 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2846 1 2812 XP_211581.1 5 1344 GAGCTCAGGAGG C 3 C b b
65 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2846 1 9421 XP_211591.1 3 977 GAACCCGGGAGG 3 C b b
73 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC2847 3 8917 XP_211598.1 3 1039 CTGCTCGGGAGG A AAC T 3 C c
b
07 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGTTG AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2847 3 15308 XP_211598.1 3 178 GAACCCAGGAGA C C 3 C b
b
07 CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCAA AGTGACGTTGGAGAC GAGG
A A
GAM7957 297 LOC2847 3 18690 XP_211598.1 3 1072 GAACCCGGGAGG 3 C b b
07 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC2847 2 12933 XP_209343.1 3 896 GAACCCTGGGAG C C 3 C b
b
36 CGGAGATTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCTGA AGTGACGTT GAGGCG AGGGT
A -
GAM7957 297 LOC2847 2 19053 XP_209343.1 3 561 GAACCCAGAAGG C CCC 3 C c
b
36 CGGAAGTTGCAG TCACTGCAAC TCTGCCT
TGAGCCGA AGTGACGTTG AGGCGGA
A AGA
GAM7957 297 LOC2847 1 17060 XP_211616.1 3 1003 GAATCTAGGAGG C 3 C b b

57 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAACTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2848 3 9535 XP_211642.1 3 457 GAACCCGGGAGG TC----- C 3 C c
c
03 CAGAGCTTGCAG ACTGCAA CTCTGCCTCCCG

TAAGCCGA TGACGTT GAGACGGAGGGC
AGCCGAA C
GAM7957 297 LOC2848 3 13751 XP_211642.1 5 149 ACCAGCCCCCGG T A T -- 3 C c c
03 CAGAGGCTGAGG CACTGC ACCTC GCCTC CCG
TGGCAGTG GTGACG TGGAG CGGAG GGC
- G T AC
GAM7957 297 LOC2848 3 17328 XP_211642.1 3 423 CTACTCGGGAGG A AAC T 3 C c c
03 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCCT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2848 3 7759 XP_209372.1 3 1293 GAACCCAGGAGG T C 3 C c c
08 CGGCGGTTGCAG TCACTGCAACC CTGCCTCC
TGAGCCAA AGTGACGTTGG GGCGGAGG
C A
GAM7957 297 LOC2848 3 18950 XP_209372.1 5 278 CTGACCAGGAGT A TGC C 3 C c c
08 TCGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCCGA AGTGACGT GGAG GAGG
C CTT A
GAM7957 297 LOC2848 3 19941 XP_209372.1 3 1259 CTATTCGGGAGG A AAC T 3 C c c
08 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2848 2 3325 XP_211662.1 3 1302 GAACCCAGGAGG TC----- C 3 C c c
44 CAGAGGTTGCAG ACTGCAACCTCTGCCTCC
TAAGCCAA TGACGTTGGAGACGGAGG
AACCGAA A
GAM7957 297 LOC2848 2 9844 XP_211662.1 3 646 ATCTCCGGGAGG A GC TCT 3 C c c
44 CCCTGGTTAAAG TC CT AACC GCCTCCCG
GAGGCTAA AG GA TTGG CGGAGGGC
- AA TCC
GAM7957 297 LOC2848 1 9422 XP_211663.1 3 1340 GAACCCAGGAGG C 3 C b b
45 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2848 1 15742 XP_209383.1 3 260 GTACCCAGGAGG C C 3 C b b
53 CAGAGATTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
A A
GAM7957 297 LOC2848 1 19058 XP_211671.1 3 464 GAACCTGGGAGG 3 C b b
57 CGGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGGCGTTGGAGGCGGAGGGT

GAM7957 297 LOC2848 4 2488 XP_209386.1 3 1518 GAACCCGGGAGG C 3 C b b

58 CGGAGCTTGTAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGATGTT GAGGCGGAGGGC
C

GAM7957 297 LOC2848 4 5830 XP_209386.1 3 1185 CTACTCGGGAGG A AAC T 3 C c b

58 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2848 4 13155 XP_209386.1 3 1484 CTACTCGGGAGG A AAC T 3 C c b

58 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2848 4 19500 XP_209386.1 3 1219 GAACCTGTGGGT - CCC 3 C c b

58 CAGAGGTTGCAG TCACTGCAACCTCTG CCT
TGAACCAA AGTGACGTTGGAGAC GGG
T TGT

GAM7957 297 LOC2848 1 16401 XP_209384.2 3 311 TGCAGATGGAGG G A T C 3 C c c

59 CAGTGGCTGGAG TCACT CA CC CTGCCTCC
TGAATGAA AGTGA GT GG GACGGAGG
G C T T

GAM7957 297 LOC2848 1 16401 XP_211670.2 5 285 TGCAGATGGAGG G A T C 3 C c c

61 CAGTGGCTGGAG TCACT CA CC CTGCCTCC
TGAATGAA AGTGA GT GG GACGGAGG
G C T T

GAM7957 297 LOC2848 1 9439 XP_211666.1 3 699 CTCCTGCTGAGG C TG CC 3 C c c

62 TGGAGATTGCAG TCACTGCAA CTC CCTC
TGAACTAA AGTGACGTT GAG GGAG
A GT TC

GAM7957 297 LOC2848 1 16401 XP_209412.1 3 1417 TGCAGATGGAGG G A T C 3 C c c

73 CAGTGGCTGGAG TCACT CA CC CTGCCTCC
TGAATGAA AGTGA GT GG GACGGAGG
G C T T

GAM7957 297 LOC2848 4 2520 XP_211680.1 3 1503 ATGAGGGAGGCA ACC-- 3 C c b

99 GGCAATATGCAG TCACTGCA TCTGCCTCCC
TGAAAACC AGTGACGT GGACGGAGGG
ATAAC

GAM7957 297 LOC2848 4 12699 XP_211680.1 3 1503 CAATGAGGGAGG ACC-- 3 C c b

99 CAGGCAATATGC TCACTGCA TCTGCCTCCC
AGTGAAAA AGTGACGT GGACGGAGGG
ATAAC

GAM7957 297 LOC2848 4 15979 XP_211680.1 5 886 GAACCCGGGAGG 3 C b b
99 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGTCAA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC2848 4 17082 XP_211680.1 5 852 CTACTCGGGAGG A AAC T 3 C c
b
99 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGTTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2849 2 4952 XP_211684.1 3 1772 CTACTCGGGAGG A CAAC T 3 C
c b
11 CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATTGCTT AG GAC GAG CGGAGGGC
- A--- T
GAM7957 297 LOC2849 2 13631 XP_211684.1 3 1806 GAACCTGGAAGG C 3 C b b

11 CAGGGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGACCTGA AGTGACGTTGGGGACGGA GGT
A
GAM7957 297 LOC2849 2 15344 XP_209410.1 3 1515 GAACCCGGGAGG TC----- 3 C c
c
15 CGGAGGTTGCAG ACTGCAACCTCTGCCTCCCG
TCAGCCGA TGACGTTGGAGGCGGAGGGC
AGCCGAC
GAM7957 297 LOC2849 2 16573 XP_209410.1 3 1188 TGCTGAAGGGAA - GCC 3 C c
c
15 GAGAGGTTGCAG TCA CTGCAACCTCT TCCC
CTGAGCAA AGT GACGTTGGAGA AGGG
C GA-
GAM7957 297 LOC2849 3 5093 XP_211699.1 3 474 AAGCCCGGGAGG TG 3 C b b

36 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCCA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 LOC2849 3 9420 XP_211699.1 3 296 GAACCTGGGAGG 3 C b b
36 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC2849 3 17279 XP_211699.1 3 440 CTACTCGGGAGG A AAC T 3 C c
b
36 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGTCT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2849 1 14786 XP_211700.1 5 533 GAACCTGGGAGG 3 C b b
39 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC2849 1 10463 XP_211708.1 5 214 AGAAGGGACAGA C- C -- 3 C c
c
59 CAGAGGTTCTCA TCACTG AACCTCTG C TCCC

```
                                    GTGATGAG    AGTGAC  TTGGAGAC G  AGGG
                                                TC      A AC
GAM7957  297   LOC2849 1  6191  XP_211712.1  5  1029  GAGCCAGGAAGG        T   C       3  C  b
b
         72                          TTGAGGTTGCAG TCACTGCAACCTC GCCT CC
                                    TGAGCTAT    AGTGACGTTGGAG TGGA GG
                                                T   A
GAM7957  297   LOC2849 2  9420  XP_211711.1  3  2388  GAACCTGGGAGG                  3  C  b  b
         75                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC2849 2  12954 XP_211711.1  3  2354  CTACTCGGGAGG  A   AACC  T         3  C
c  b
         75                          CTGACGCAGGAG TC CTGC   TC GCCTCCCG
                                    AATCACTT    AG GACG   AG CGGAGGGC
                                            -   C---  T
GAM7957  297   LOC2849 1  10672 XP_211714.1  3  1821  GAACCAAGGAGG        TG   C       3  C  c
c
         76                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                    TGAGCCGG    AGTGACGTTGGAG  GGAGG
                                                GT    A
GAM7957  297   LOC2849 1  2521  XP_211721.1  3  109   ACACAGGGGAGG  A   AA---           3  C  c
c
         82                          CAGGGGAAGAGG TC CTGC    CCTCTGCCTCCC
                                    CAGGAGGG    AG GACG    GGGGACGGAGGG
                                            -   GAGAA
GAM7957  297   LOC2849 1  13912 XP_211722.1  5  55    GAATCCAGGAGG            C       3  C  b  b
         93                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                    TGAACCAA    AGTGACGTTGGAGGCGGAGG
                                                A
GAM7957  297   LOC2849 2  1706  XP_211729.1  3  514   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         95                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                    AATGTCGT    AG GACG   GAG CGGAGGGC
                                            -   ---  T
GAM7957  297   LOC2849 2  15343 XP_211729.1  3  548   GAACCCGGGAGG       C             3  C  b  b

         95                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                    TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                                C
GAM7957  297   LOC2850 1  9938  XP_211742.1  5  370   TGACCACGTGGG       ACCT  CC         3  C  c
 c
         43                          AACAGCCTGCAG TCACTGCA   CTG  TCCCG
                                    TGAGCGGT    AGTGACGT   GAC  AGGGT
                                            CC--   A-
GAM7957  297   LOC2850 1  10474 XP_211753.1  3  1527  GAGCCCAGGAGG  C      TG   C       3  C  c
 c
         58                          TGGAGGTTGCAA TCA TGCAACCTC  CCTCC
                                    TGAGCCGA    AGT ACGTTGGAG  GGAGG
                                            A       GT    A
```

GAM7957 297 LOC2850 1 470 XP_211759.1 3 1668 GAACCTGGGAGG C C 3 C b b

82 CAGAGTTTACAG TCACTG AA CTCTGCCTCCCG
TGAGCCGA AGTGAC TT GAGACGGAGGGT
A T

GAM7957 297 LOC2850 1 19057 XP_209464.1 3 2100 GAACCCAGGAGG C 3 C b b

83 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 LOC2850 1 8468 XP_209471.1 5 802 GAGCCTGGGAGG A T 3 C c c

94 TTGAGGCTGCAG TCACTGCA CCTC GCCTCCCG
TGAGCCAT AGTGACGT GGAG TGGAGGGT
C T

GAM7957 297 LOC2851 1 4060 XP_211766.1 5 464 GAACCCGGGAGG C TG 3 C b b

03 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCTGA AGTGACGTT GAG GGAGGGC
C GT

GAM7957 297 LOC2851 1 12145 XP_209478.1 3 1065 AAACCCAGAAGG CCC 3 C c c

08 CAGGGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCCAA AGTGACGTTGGGGACGGA
AGA

GAM7957 297 LOC2851 1 629 XP_211769.1 3 743 GAACCCAGGAGG TG C 3 C c c

25 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGGCAA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 LOC2851 1 2936 XP_211771.1 3 697 GAACCTGGGAGG C 3 C b b

27 CAGAGGTTGCAA TCA TGCAACCTCTGCCTCCCG
TGAGCCAA AGT ACGTTGGAGACGGAGGGT
A

GAM7957 297 LOC2851 1 9735 XP_211782.1 5 13 GAACCTGGGAGG ACC TG 3 C c c

51 TGGAAGCTGCAG TCACTGCA TC CCTCCCG
TGAGCCAA AGTGACGT AG GGAGGGT
CGA GT

GAM7957 297 LOC2851 1 12791 XP_211791.1 3 2081 GAACCCGGGAGG 3 C b b

66 CAGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGGCGTTGGAGACGGAGGGC

GAM7957 297 LOC2851 4 7413 XP_211790.1 3 2623 AAATCCAGGAGG C C 3 C b b

67 CAAAGGTTGCAG TCACTGCAACCT TGCCTCC
TGAGCCAA AGTGACGTTGGA ACGGAGG
A A

GAM7957 297 LOC2851 4 7557 XP_211790.1 3 2211 CTACTTGGGAGG - GCA- 3 C c b

67 CAGAGGTGGGAA TCA CT ACCTCTGCCTCCCG

GATGGTTT GGT GA TGGAGACGGAGGGT
A AGGG
GAM7957 297 LOC2851 4 15370 XP_211790.1 3 2243 GAGCCCAGGAGG CC C 3 C c b
67 CAGAATTTGCAG TCACTGCAA TCTGCCTCC
TGAGCTGA AGTGACGTT AGACGGAGG
TA A
GAM7957 297 LOC2851 4 18453 XP_211790.1 3 1437 GAACCCGGGAAG C 3 C b b
67 CAGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGACAGAG AGTGACGTTGGAGACG AGGGC
A
GAM7957 297 LOC2851 4 5046 XP_211799.1 3 698 GAACCCGGGAGG CC 3 C b b
71 CGGAACTTGCAG TCACTGCAA TCTGCCTCCCG
TGAGCCAA AGTGACGTT AGGCGGAGGGC
CA
GAM7957 297 LOC2851 4 13155 XP_211799.1 3 664 CTACTCGGGAGG A AAC T 3 C c b
71 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2851 4 13690 XP_211799.1 3 305 GAACCCAGGAGG C C 3 C b b
71 CAGAGATTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
A A
GAM7957 297 LOC2851 4 19794 XP_211799.1 5 811 GAACCCCCAAGG C CCC 3 C c b
71 CGGAGCTTGCAG TCACTGCAA CTCTGCCT
TGAGCCGA AGTGACGTT GAGGCGGA
C ACC
GAM7957 297 LOC2852 1 13065 XP_209520.1 5 933 GAACCCGGGAGG 3 C b b
16 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC
GAM7957 297 LOC2852 1 12792 XP_209518.1 3 939 GAACCCAGGAGG C 3 C b b
19 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2852 1 9913 XP_211809.1 5 607 AGAGTGGTGGGA ACCT C- 3 C c c
22 GAACAGCTGCAG TCACTGCA CTG CTCCCG
TGAAGCAC AGTGACGT GAC GAGGGT
C--- AA
GAM7957 297 LOC2852 2 2944 XP_211814.1 3 939 GAGCCCGGGAGG 3 C b b
30 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGT AGTGACGTTGGAGACGGAGGGC
GAM7957 297 LOC2852 2 6423 XP_211814.1 5 467 CCAGCGGCCTGC - T CTC 3 C c b

30 CGGGAGTTGCAG TCACTGCAAC CTC GC CCG
TGAACCCA AGTGACGTTG GGG CG GGC
A C TCC
GAM7957 297 LOC2852 1 7927 XP_209537.1 3 438 GAACCTGGGAGG C TG 3 C c
c
63 TGGAGGTTGCAT TCA TGCAACCTC CCTCCCG
TGAGCCAA AGT ACGTTGGAG GGAGGGT
T GT
GAM7957 297 LOC2852 1 5047 XP_211833.1 3 349 GAGCCCAGGAGG C TG C 3 C c
c
95 TGGAGGTTGCAC TCA TGCAACCTC CCTCC
TGAGCGGA AGT ACGTTGGAG GGAGG
C GT A
GAM7957 297 LOC2853 2 1492 XP_211839.1 3 315 CTACTCGGGAGG A AAC T 3 C c
c
09 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2853 2 9203 XP_211839.1 3 349 GAGCCCAGGAGG TG C 3 C c
c
09 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCGGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC2853 3 10559 XP_211845.1 3 2416 AAACCCGGGAGG A CT 3 C c
b
32 TGAAGGATGCAG TCACTGCA CCT GCCTCCCG
TGAGCCAA AGTGACGT GGA TGGAGGGC
A AG
GAM7957 297 LOC2853 3 10634 XP_211845.1 3 2114 GATCTGGGGAGG CA 3 C b
b
32 CAGAGGTGACAG TCACTG ACCTCTGCCTCCC
TGAGCTGA AGTGAC TGGAGACGGAGGG
AG
GAM7957 297 LOC2853 3 15405 XP_211845.1 3 1295 TTAAGGAGAAGG A CT - - 3 C c
b
32 TCAAGGCTGCAG TCACTGCA CCT GCCT C CC
TGAGCCAT AGTGACGT GGA TGGA G GG
C AC A A
GAM7957 297 LOC2853 1 15984 XP_211858.1 3 659 GAACCCAGGAGG TG C 3 C c
c
59 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC2853 1 18691 XP_211864.1 3 1311 GAACCTGGGAGG 3 C b b
76 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 LOC2853 1 10435 XP_211859.1 5 394 GAACCCAGGAGG C 3 C b b
78 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG

```
                                                                A
GAM7957  297   LOC2853 2  1492   XP_211868.1  3  1104  CTACTCGGGAGG  A   AAC  T          3  C  c
c
         79                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                    AATCACTT    AG GACG  GAG CGGAGGGC
                                             -   ---  T
GAM7957  297   LOC2853 2  9203   XP_211868.1  3  1138  GAGCCCAGGAGG        TG   C       3  C  c
c
         79                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                    TGAGCGGA    AGTGACGTTGGAG  GGAGG
                                                GT    A
GAM7957  297   LOC2853 1  15219  XP_209588.1  3  1395  GAACCTAGGAGG        TG   C       3  C  c
c
         87                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                    TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                                GT    A
GAM7957  297   LOC2853 1  14204  XP_211875.1  3  258   GAGCCGGGGAGG         G          3  C  b
b
         95                          AGGGGGTTGCAG TCACTGCAACCTCT CCTCCC
                                    TGAGCCGA    AGTGACGTTGGGGG GGAGGG
                                                A
GAM7957  297   LOC2854 1  15520  XP_211885.1  3  1324  GAACCCAGGAGA       T  C   C       3  C  c
c
         04                          CGGTGGTTGCAG TCACTGCAACC CTG CTCC
                                    TGAGCCAA    AGTGACGTTGG GGC GAGG
                                                T  A   A
GAM7957  297   LOC2854 2  14360  XP_211886.3  3  759   CTACTCGGGAGG  A  GCA   T          3  C  c
c
         08                          CTGAGGTGGGAG TC CT   ACCTC GCCTCCCG
                                    GATCGCTT    AG GA   TGGAG CGGAGGGC
                                             -  GGG    T
GAM7957  297   LOC2854 2  14913  XP_211886.3  3  791   GAACCCAGGAGG       A       C       3  C  c  c

         08                          TAGAGGCTGCAG TCACTGCA CCTCTGCCTCC
                                    TGAGCTGG    AGTGACGT GGAGATGGAGG
                                                C         A
GAM7957  297   LOC2854 4  1571   XP_211900.1  3  614   GAACCCCGGAGG            C       3  C  b  b
         47                          TAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                    TGAGCCGA    AGTGACGTTGGAGATGGAGG
                                                C
GAM7957  297   LOC2854 4  5830   XP_211900.1  3  888   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         47                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                    AATCGCTT    AG GACG  GAG CGGAGGGC
                                             -   ---  T
GAM7957  297   LOC2854 4  8585   XP_211900.1  3  588   CTCCTCGGGAGG  CT  AAC-  -          3  C  c
b
         47                          CAGGAGAATCGC TCA  GC   CTC TGCCTCCCG
                                    TTGAACCC    AGT  CG   GAG ACGGAGGGC
                                             T-  CTAA  G
```

GAM7957 297 LOC2854 4 19799 XP_211900.1 3 922 GAACCCGAGAGG C 3 C b b
47 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC CG
TGAGCCCA AGTGACGTTGGAGGCGGAG GC
A
GAM7957 297 LOC2854 1 13061 XP_209622.1 3 1664 GAACCTGGGAGG 3 C b b
65 CAGAGGTTGTAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGATGTTGGAGACGGAGGGT

GAM7957 297 LOC2854 1 8189 XP_211912.1 5 821 GAACCCGGGAGG A TG 3 C b
b
81 TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAGCCGA AGTGACGT GGAG GGAGGGC
C GT
GAM7957 297 LOC2854 2 6846 XP_209630.1 3 1864 GAATCTGGGAGG TG 3 C b b

84 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 LOC2854 2 10306 XP_209630.1 3 702 GGAAGGACGAGG C AAC- -- 3 C c
b
84 CAGAGCTCCGCG TCA TGC CTCTGCCTC CC
CTGACGAA AGT GCG GAGACGGAG GG
C CCTC CA
GAM7957 297 LOC2854 1 961 XP_211913.1 5 729 TGGGAGCCCAGG AC AA ----- 3 C c
c
85 CAGAGGAGGCAC TC TGC CCTCTGCC TCCCG
CGAGAGTG AG ACG GGAGACGG AGGGT
CC GA ACCCG
GAM7957 297 LOC2854 2 8855 XP_211918.1 5 873 GAACCGAGGAGG C - 3 C b b
95 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC CG
TGAGCCAA AGTGACGTT GAGACGGAGG GC
C A
GAM7957 297 LOC2854 2 18458 XP_211918.1 5 838 CTACTCGGGAGG A AAC T 3 C c
b
95 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGAAGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2855 1 837 XP_211929.1 5 1469 GAACCTGGGAGG A TG 3 C c
c
31 TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAACCGA AGTGACGT GGAG GGAGGGT
C GT
GAM7957 297 LOC2855 1 13066 XP_209669.1 5 504 GAACCTGGGAGG 3 C b b
92 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC2855 1 13062 XP_211946.2 3 955 GAACCCAGGAGG C 3 C b b
94 CAGAGGTTGTAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGATGTTGGAGACGGAGG
A

GAM7957 297 LOC2856 4 1965 XP_211952.1 3 1606 AACCTGGGAGAC - C C 3 C c c

08 AGAAGTTTGCAG TCACTGCAA C TCTG CTCCCG
TGATCCGA AGTGACGTT G AGAC GAGGGT
T A A

GAM7957 297 LOC2856 4 2726 XP_211952.1 3 774 GAACCTGGCAGG TG C 3 C c
c

08 TGGAGGTTGCAG TCACTGCAACCTC CCT CCG
TGAGTGGA AGTGACGTTGGAG GGA GGT
GT C

GAM7957 297 LOC2856 4 4337 XP_211952.1 3 1783 CAGCCTAGGACG A T C C 3 C c
c

08 TTGAGGCTGCAG TCACTGCA CCTC GC TCC
TGAGCTGT AGTGACGT GGAG TG AGG
C T C A

GAM7957 297 LOC2856 4 17557 XP_211952.1 3 1299 CTCTTTGGAAGG A AAC C 3 C c
c

08 CAGAGGCAGGAG TC CTGC CTCTGCCT CCG
GATCACTT AG GACG GAGACGGA GGT
- --- A

GAM7957 297 LOC2856 1 10438 XP_211953.1 3 433 GAACCCGGGAGG 3 C b b
14 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC2856 2 11452 XP_211950.1 5 248 GAACCCGGCAGG C C 3 C b
b

17 CAGAGCTTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCCGA AGTGACGTT GAGACGGA GGC
C C

GAM7957 297 LOC2856 2 15207 XP_211950.1 3 804 GAACCTGGAAGG C 3 C b b
17 CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCGA AGTGACGTTGGAGGCGGA GGT
A

GAM7957 297 LOC2856 1 10435 XP_211978.1 3 601 GAACCCAGGAGG C 3 C b b
65 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 LOC2856 1 13322 XP_211977.1 3 199 TGAACCCGGAGG C 3 C b b
66 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
C

GAM7957 297 LOC2856 2 10438 XP_209718.1 3 408 GAACCCGGGAGG 3 C b b
76 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC2856 2 15108 XP_209718.1 3 374 CTACTCGGGAGG A AAC T 3 C c
b

76 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2857 1 2856 XP_211987.1 5 1051 CTCCTGCTGAGG AC CC 3 C c c
07 CGGAGACTGCAG TCACTGCA CTCTGCCTC
TGAGCTGA AGTGACGT GAGGCGGAG
CA TC
GAM7957 297 LOC2857 1 12495 XP_211992.1 3 1460 TGAACCCAGGAG T C C 3 C c c
13 ACGAGGTTGCAG TCACTGCAACCTC G CTCC
TGAGCCGA AGTGACGTTGGAG C GAGG
- A A
GAM7957 297 LOC2857 1 1146 XP_212000.1 3 2029 GAATTCGCGAGG A C 3 C b b
27 CAGAGGTTGCAG TC CTGCAACCTCTGCCTC CG
CGAACCCA AG GACGTTGGAGACGGAG GC
C C
GAM7957 297 LOC2857 2 4824 XP_212007.1 3 1758 ATACTCGGGAGG A AAC T 3 C c b
45 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2857 2 19057 XP_212007.1 3 1792 GAACCCAGGAGG C 3 C b b
45 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2857 1 9762 XP_209742.1 3 1175 GAACCTGGGAGG 3 C b b
47 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGTTGA AGTGACGTTGGAGGCGGAGGGT
GAM7957 297 LOC2857 1 10490 XP_212015.1 5 633 GAACCCGGGAGG TG 3 C b b
71 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGGTGA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 LOC2858 1 2460 XP_212028.1 3 3799 GAATCCAGGAGG AC TG C 3 C c c
06 TGGAGCCTGCAG TCACTGCA CTC CCTCC
TGAGCCAA AGTGACGT GAG GGAGG
CC GT A
GAM7957 297 LOC2858 1 5928 XP_209790.1 3 1282 GAACCCAGGAGA C C 3 C c c
33 CAGGGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCCAA AGTGACGTTGGGGAC GAGG
A A
GAM7957 297 LOC2858 1 13726 XP_212041.1 3 806 CAGTGGGGAAGG --- AA - 3 C c c
42 CAGAGGAGTAAC TCAC TGC CCTCTGCCT CCC
TGTGGGGA GGTG ATG GGAGACGGA GGG
TCA A- A
GAM7957 297 LOC2858 1 8380 XP_209770.1 3 1949 GAACTGGGGAGG 3 C b b

54 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGGCCCGA GGTGACGTTGGAGACGGAGGG

GAM7957 297 LOC2858 2 3330 XP_209769.1 3 477 GAACCCAGGAGG C C 3 C b b

55 CAGAGATTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCAA AGTGACGTT GAGACGGAGG
A A
GAM7957 297 LOC2858 2 5929 XP_209769.1 3 1066 GAACCTGGGAGG C TG 3 C c
b
55 TGGAAGTTGCAG TCACTGCAAC TC CCTCCCG
TGAGCTGA AGTGACGTTG AG GGAGGGT
A GT
GAM7957 297 LOC2858 2 4206 XP_209775.1 3 1399 CTACTCGGGAGG C AA--- T 3 C c
b
59 CTGAGGCGGGAG TCA TGC CCTC GCCTCCCG
CATGGCAT GGT ACG GGAG CGGAGGGC
- AGGGC T
GAM7957 297 LOC2858 2 15343 XP_209775.1 3 1433 GAACCCGGGAGG C 3 C b
b
59 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC2858 1 14367 XP_212058.1 3 201 GAGCCCGGGAGG C 3 C b b

69 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC2858 2 1492 XP_212065.1 3 1335 CTACTCGGGAGG A AAC T 3 C c
b
87 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC2858 2 13063 XP_212065.1 3 1369 GAACCCAGGAGG C 3 C b b

87 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC2859 1 11641 XP_209811.1 3 1130 GAACCTAGGAGG C C 3 C b
b
09 CAGAAGTTGCAG TCACTGCAAC TCTGCCTCC
TGAGCAGA AGTGACGTTG AGACGGAGG
A A
GAM7957 297 LOC2859 3 2159 XP_212078.1 3 1325 GAACCTGGGAGA C C 3 C c b

12 CGGAGCTTGCAG TCACTGCAA CTCTG CTCCCG
TGAGCTGA AGTGACGTT GAGGC GAGGGT
C A
GAM7957 297 LOC2859 3 16368 XP_212078.1 3 289 GAACCTGGTAGG C 3 C b b
12 CAGAGGTTGTAG TCACTGCAACCTCTGCCT CCG

TGAGCCGA AGTGATGTTGGAGACGGA GGT
T
GAM7957 297 LOC2859 3 16843 XP_212078.1 3 1726 GAACCCGGGATG C 3 C b b

12 CAGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCTGA AGTGACGTTGGAGACG AGGGC
T
GAM7957 297 LOC2859 3 16369 XP_212074.1 3 289 GAACCCGGTAGG C 3 C b b
13 CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCGA AGTGACGTTGGAGACGGA GGC
T
GAM7957 297 LOC2859 3 16843 XP_212074.1 3 1722 GAACCCGGGATG C 3 C b b

13 CAGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCTGA AGTGACGTTGGAGACG AGGGC
T
GAM7957 297 LOC2859 3 19036 XP_212074.1 3 1327 GAACCTGGGAGG C 3 C b b

13 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGACGGAGGGT
C
GAM7957 297 LOC2859 2 2306 XP_209810.1 3 126 GAGCCTGGGAGG G 3 C b b
14 AAGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCCGA AGTGACGTTGGAGA GGAGGGT
A
GAM7957 297 LOC2859 2 7908 XP_209810.1 3 516 GAATCCGGGAGA CTC -- 3 C b
b
14 TGCATGTTGCAG TCACTGCAAC TGC CTCCCG
TGAGCTGA AGTGACGTTG ACG GAGGGC
T-- TA
GAM7957 297 LOC2859 1 475 XP_212082.1 3 668 GAACCCAGGAGG T C 3 C b b
16 CCGAGGTTGCAG TCACTGCAACCTC GCCTCC
TGAGCCAA AGTGACGTTGGAG CGGAGG
C A
GAM7957 297 LOC2859 1 15752 XP_212091.1 5 298 GAACCCAGGAGG TC----- C 3 C c
c
20 CAGAGGTTGCAG ACTGCAACCTCTGCCTCC
TAAGCCTA TGACGTTGGAGACGGAGG
ATCCGAA A
GAM7957 297 LOC2859 1 9763 XP_212104.1 3 832 GAACCCAGGAGG TG C 3 C c
c
23 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC2859 1 18617 XP_209816.1 3 1212 GAGCCCAGCAGG CCC 3 C c
c
24 CAGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGACGTTGGAGACGGA
CGA
GAM7957 297 LOC2859 1 15676 NP_777609.1 3 237 CTGCAGGAAGGC C - C 3 C c
c

```
          31                        CAGAGGTTCTGG TCACTG AACCTCTG CCT CC
                                   TGGAGTTG    GGTGGT TTGGAGAC GGA GG
                                              C      C  A
GAM7957  297   LOC2859 2  7352  XP_209820.1  3  1140  GAACCAGGGAGG                    3  C  b  b
          53                        CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
                                   TGAGCCCA    AGTGACGTTGGAGACGGAGGG

GAM7957  297   LOC2859 2  9781  XP_209820.1  3  1106  CTTCTCGGGAGG  A   AAC  T          3  C  c
b
          53                        CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                   AATCACTT    AG GACG  GAG CGGAGGGC
                                             -   ---  T
GAM7957  297   LOC2859 1  18690 XP_212088.1  3  1067  GAACCCGGGAGG                    3  C  b  b
          60                        CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                   TGAGCTGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   LOC2859 1  3055  XP_212127.1  3  2700  GAGCCTGTGAGG      A   T   CC       3  C  c
c
          87                        TCGAGGCTGCAG TCACTGCA CCTC GCCTC
                                   TGAGCCGA    AGTGACGT GGAG TGGAG
                                              C   C    TG
GAM7957  297   LOC2859 1  11322 XP_212111.1  5  881   GAACCCGGGAGG  C                 3  C  b  b

          89                        CAGAGGTTGCAT TCA TGCAACCTCTGCCTCCCG
                                   TGAGCCGA    AGT ACGTTGGAGACGGAGGGC
                                               T
GAM7957  297   LOC2859 3  13066 XP_212128.1  3  1004  GAACCTGGGAGG                    3  C  b  b
          96                        CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                   TGAGCCGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   LOC2859 3  15893 XP_212128.1  3  517   GAGCCCAGGAGT      A T  C-   C      3  C  c
b
          96                        TCAGGGCTGCAG TCACTGCA CC CTG  CTCC
                                   TGAGCCTT    AGTGACGT GG GAC  GAGG
                                              C  -  TT   A
GAM7957  297   LOC2859 3  15983 XP_212128.1  3  1680  GAACCCGGGAGG          TG          3  C  b
b
          96                        TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                   TGAGCCAA    AGTGACGTTGGAG  GGAGGGC
                                                GT
GAM7957  297   LOC2860 1  4082  XP_212133.1  3  809   GAGCCCAGGAGG      A   T    C       3  C  c
c
          07                        TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
                                   TGAGCCCT    AGTGACGT GGAG TGGAGG
                                              C   C     A
GAM7957  297   LOC2860 2  11466 XP_209866.1  3  856   CTACTCGGGAGG  A GCAA   T          3  C
c  b
          29                        CTGAGGAAGGAG TC CT    CCTC GCCTCCCG
                                   AATGGTGT    AG GG    GGAG CGGAGGGC
                                             A  AA--   T
```

GAM7957 297 LOC2860 2 19031 XP_209866.1 3 890 GAACCCGGGAGG C 3 C b b

29 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGC
C

GAM7957 297 LOC2860 1 925 XP_209868.1 3 1098 GAGCTCAGGAGG C 3 C b b
30 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 LOC2860 1 925 XP_209873.1 3 1098 GAGCTCAGGAGG C 3 C b b
39 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 LOC2860 1 4734 XP_209872.1 3 804 AGGCCAGGGAGG A AA 3 C b b
47 CAGGGGAGGCAG TC CTGC CCTCTGCCTCCC
GAGAGGCT AG GACG GGGGACGGAGGG
- GA

GAM7957 297 LOC2860 1 13065 XP_212141.3 3 1171 GAACCCGGGAGG 3 C b b
48 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC2860 1 9871 NP_776192.1 3 70 CTGGGTCCTGAG AC G ---- 3 C c c
75 GGAGAGCTGCAG TCACTGCA CTCT CCTC CC
TGAGAAGT AGTGACGT GAGA GGAG GG
C- G TCCT

GAM7957 297 LOC2861 1 4600 XP_212176.1 3 469 GCTGCAAGGAGG A AA- C 3 C c c
12 CAGGGGCCAGCG TC CTGC CCTCTGCCTCC
GGAAGGAG AG GGCG GGGGACGGAGG
- ACC A

GAM7957 297 LOC2861 1 8922 XP_212185.1 3 1857 GAACCCGGTAGG C C 3 C b b
26 CGGAGCTTGCAG TCACTGCAA CTCTGCCT CCG
TGAGCTGA AGTGACGTT GAGGCGGA GGC
C T

GAM7957 297 LOC2861 1 10132 XP_212199.2 3 592 CTGCTCGGGAGG A AAC T 3 C c c
47 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC2861 1 2949 XP_212204.1 5 753 TGAACAGGGAAG C 3 C b b
54 CAGAGGTTGCGG TCACTGCAACCTCTGC TCCC
TGAACCGG AGTGGCGTTGGAGACG AGGG
A

GAM7957 297 LOC2861 1 9764 XP_209925.1 5 3640 AAGCCCAGGAGT A TGC C 3 C c c
66 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGTTAT AGTGACGT GGAG GAGG

C TTT A
GAM7957 297 LOC2861 1 6044 XP_212216.1 5 782 GAATCTAAGAAG C CC 3 C c c

84 CAGAGGTTGCAG TCACTGCAACCTCTGC TC
TGAGCTGA AGTGACGTTGGAGACG AG
A AA
GAM7957 297 LOC2861 1 3979 XP_212219.1 3 878 GAAGCCAGGAGG C 3 C b b
86 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC2861 1 17423 XP_209933.1 3 2388 GAACCTGGGAGG TG 3 C b
b
88 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 LOC2861 1 12144 XP_209940.1 3 324 GAACCTGGGAGG C 3 C b b
97 CAGAGGTTGCAA TCA TGCAACCTCTGCCTCCCG
TGAGCTGA AGT ACGTTGGAGACGGAGGGT
A
GAM7957 297 LOC2862 1 11327 XP_209953.1 3 648 GAACCCGTGAGG C 3 C b b
06 CAGAGGTTGCAG TCACTGCAACCTCTGCCTC CG
TGAGCCGA AGTGACGTTGGAGACGGAG GC
T
GAM7957 297 LOC2862 1 13066 XP_212230.1 3 1260 GAACCTGGGAGG 3 C b b
08 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC2862 1 5322 XP_212235.1 3 2233 GAGGCCAGGAGG C C 3 C c
c
18 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 LOC2862 1 19821 XP_212236.1 3 929 CACTTTGAGAGG A AAC CC 3 C c
c
19 CAGAGGCAGGAG TC CTGC CTCTGCCTC
GATCAGGA AG GACG GAGACGGAG
- --- AG
GAM7957 297 LOC2862 1 8306 XP_212238.1 3 148 AGGCAGGGCAGC A C - 3 C c c

35 CAGGGGCTGCAG TCACTGCA CCTCTG CT CCC
TGAAATGA AGTGACGT GGGGAC GA GGG
C C C
GAM7957 297 LOC2862 1 12289 XP_212241.1 3 153 AGGCAGGGCAGC A C - 3 C c
c
37 CAGGGGCTGCAG TCACTGCA CCTCTG CT CCC
TGAAATGG AGTGACGT GGGGAC GA GGG
C C C
GAM7957 297 LOC2862 1 13199 XP_209977.1 5 596 AAACCCGGGAGG A A 3 C b
b
55 CAGAGGCTGCAG TC CTGCA CCTCTGCCTCCCG

```
                                  AGAGCCAA    AG GACGT GGAGACGGAGGGC
                                         A    C
GAM7957  297   LOC2862 2  10659  XP_209972.1  3  1642  ATACTCGGGAGG  A   AAC  T          3  C  c
c
         58                       CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                  AATCACTT    AG GACG   GAG CGGAGGGC
                                         -   ---  T
GAM7957  297   LOC2862 2  17108  XP_209972.1  3  1676  GAACCTGGGAGA  A       GC         3  C  c
c
         58                       TGGAGGTTGCAG TC CTGCAACCTCT  CTCCCG
                                  AGAGCCAA    AG GACGTTGGAGG  GAGGGT
                                         A         TA
GAM7957  297   LOC2862 2  2924   XP_209976.1  3  1229  AGCCCCAGGAGG      A  T    C       3  C  c
c
         60                       TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
                                  TGAGCCAT    AGTGACGT GGAG TGGAGG
                                           C   C     A
GAM7957  297   LOC2862 2  15984  XP_209976.1  3  911   GAACCCAGGAGG        TG   C       3  C  c
c
         60                       TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                  TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                           GT    A
GAM7957  297   LOC2863 1  15675  XP_212274.3  3  1696  GAACCCGGGAGG      C  TG         3  C  b
b
         37                       TGGAGCTTGCAG TCACTGCAA CTC  CCTCCCG
                                  TGAGCCGA    AGTGACGTT GAG  GGAGGGC
                                           C   GT
GAM7957  297   LOC2863 1  7590   XP_212278.1  3  2502  TGAGCCTGGGAG       TC  C         3  C  b
b
         41                       CAAGGGTTGCAG TCACTGCAACC  TGC TCCCG
                                  TGAGCTGA    AGTGACGTTGG  ACG AGGGT
                                           GA   -
GAM7957  297   LOC2863 2  3561   XP_212290.1  3  155   GTACTCGGGAGG  A   AAC  T          3  C  c
b
         56                       CTGAGGCAGAGA TC CTGC   CTC GCCTCCCG
                                  ATTGCTTG    AG GACG   GAG CGGAGGGC
                                         A   ---  T
GAM7957  297   LOC2863 2  16262  XP_212290.1  3  186   GAACGCGGGAGG      AC           3  C  b
b
         56                       CAGAGACTGCAG TCACTGCA  CTCTGCCTCCCG
                                  TGAGCCGA    AGTGACGT  GAGACGGAGGGC
                                           CA
GAM7957  297   LOC2863 2  9990   XP_212294.1  5  448   GAACCCAGGAGG      C  TG   C       3  C  c
c
         72                       TGGAGCTTGCAG TCACTGCAA CTC  CCTCC
                                  TGAGCCGA    AGTGACGTT GAG  GGAGG
                                           C   GT    A
GAM7957  297   LOC2863 2  13155  XP_212294.1  5  414   CTACTCGGGAGG  A   AAC  T          3  C  c
c
         72                       CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
```

```
                                AATGGCGT    AG GACG   GAG CGGAGGGC
                                        -   ---  T
GAM7957  297   LOC2863 2  14789  XP_212293.1  5  1432  GAACCCAGGAGG            C       3  C  b  b

         74                      CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGAGCTGA    AGTGACGTTGGAGGCGGAGG
                                              A
GAM7957  297   LOC2863 2  15343  XP_212293.1  5  747   GAACCCGGGAGG       C            3  C  b  b

         74                      CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                           C
GAM7957  297   LOC2863 1  18691  XP_210027.1  3  105   GAACCTGGGAGG                  3  C  b  b
         76                      CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC2863 3  3091   XP_212308.1  5  4008  AATAACCGGAGG       A --      C       3  C  c  b

         95                      CAGGCTGGGTGC TCACTGCA CC  TCTGCCTCC
                                AGTGGCTC    GGTGACGT GG  GGACGGAGG
                                          G  TC       C
GAM7957  297   LOC2863 3  13180  XP_212308.1  5  4055  CTCTTAGGGAGG  A   AAC             3  C  b
b
         95                      CAGAGGCAGGAG TC CTGC   CTCTGCCTCCC
                                GATAGCTT    AG GACG   GAGACGGAGGG
                                        -   ---
GAM7957  297   LOC2863 3  14790  XP_212308.1  5  2364  GAGCCCAGGAGG      A  CT    C       3  C  c
 b
         95                      TCAAGGCTGCAG TCACTGCA CCT  GCCTCC
                                TGAGCTGT    AGTGACGT GGA  TGGAGG
                                          C  AC     A
GAM7957  297   LOC2864 1  7351   XP_210036.1  3  2064  TGGAGAGGCAGG      AA      C       3  C  b
b
         04                      CAGAGGGCAGTG TCACTGC  CCTCTGCCT CC
                                GTTCTCCC    GGTGACG  GGAGACGGA GG
                                         --       C
GAM7957  297   LOC2864 1  19200  XP_212312.1  3  986   GAACCCAAGAGG            CC       3  C  c  c

         11                      CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
                                TGAGCCAA    AGTGACGTTGGAGGCGGAG
                                              AA
GAM7957  297   LOC2864 1  3830   XP_210041.1  3  873   GAACCCAGGAGG       CC  TG    C       3  C  c
c
         16                      TGGGCATTGCAG TCACTGCAA  TC  CCTCC
                                TGAGCCGA    AGTGACGTT  GG  GGAGG
                                          AC  GT    A
GAM7957  297   LOC2864 2  6817   XP_212316.1  5  591   GAACCCAGGAGG       C       C       3  C  c  c

         31                      CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
                                TGAGCAGA    AGTGACGTT GAGGCGGAGG
```

```
                                                C        A
GAM7957  297    LOC2864 2  8014   XP_212316.1  5  557   CTAGTCGGGAGG  A   AAC  T          3  C  c
c
          31                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATGGCGT    AG GACG  GAG CGGAGGGC
                                              -   ---  T
GAM7957  297    LOC2864 3  5210   XP_210047.1  3  1989  CTACCCGGGAGG  A   AAC  T          3  C  c
 b
          35                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATCACTT    AG GACG  GAG CGGAGGGC
                                              -   ---  T
GAM7957  297    LOC2864 3  9769   XP_210047.1  3  2023  GTACCTGGGAAG        C  C         3  C  c  b

          35                          CGCAGGTTGCAG TCACTGCAACCT TGC TCCCG
                                     TGAGCTGA    AGTGACGTTGGA GCG AGGGT
                                                 C  A
GAM7957  297    LOC2864 3  13491  XP_210047.1  3  713   GAACTCGGGAGG  A  C              3  C  b
b
          35                          CAGAGGTTTCAG TC CTG AACCTCTGCCTCCCG
                                     GGAGCCAA    AG GAC TTGGAGACGGAGGGC
                                              G  T
GAM7957  297    LOC2864 2  6500   XP_212325.1  3  1484  GAACCCGGGAGG    C              3  C  b  b

          70                          CGGAGGTTACAG TCACTG AACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGAC TTGGAGGCGGAGGGC
                                              A
GAM7957  297    LOC2864 2  17423  XP_212325.1  3  1178  GAACCTGGGAGG         TG         3  C  b
b
          70                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAG  GGAGGGT
                                                 GT
GAM7957  297    LOC2864 1  2822   XP_210077.1  3  514   GAACCCAAGAGG           CC       3  C  b  b

          86                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
                                     TGAACTGA    AGTGACGTTGGAGACGGAG
                                                    AA
GAM7957  297    LOC2865 1  8258   NP_835230.1  3  875   GACCACGGGAGG  A   A  CT          3  C  c
c
          30                          CCCAGGTGCGGA TC CTGCA CCT  GCCTCCCG
                                     GAGGAGGC    AG GGCGT GGA  CGGAGGGC
                                              A   -  CC
GAM7957  297    LOC3385 1  11411  XP_294650.1  3  330   CAACCTCGGAGG           C        3  C  b  b
          45                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGGCGGAGG
                                                    C
GAM7957  297    LOC3385 3  3956   XP_294651.1  3  166   CTGCTCGGGAGG  A   AAC CT          3  C  c
 b
          49                          CTAAGGCAGGAG TC CTGC  CT  GCCTCCCG
                                     AATTGCTT    AG GACG  GA  CGGAGGGC
                                              -   ---  AT
```

GAM7957 297 LOC3385 3 5588 XP_294651.1 3 199 TGAGCCCAGAGG CC 3 C c b

49 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCGA AGTGACGTTGGAGGCGGAG
AC

GAM7957 297 LOC3385 3 10572 XP_294651.1 3 583 GAACCCGGGAGG C 3 C b b

49 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 LOC3385 1 7048 XP_290481.1 3 1898 GAACCCAGGAGG C C 3 C b
b

93 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGACGGAGG
C A

GAM7957 297 LOC3385 2 15837 XP_294660.1 5 78 GAGCCCGGGAGG CT 3 C b b

94 TCAAGGTTGCAG TCACTGCAACCT GCCTCCCG
TGAGTCAT AGTGACGTTGGA TGGAGGGC
AC

GAM7957 297 LOC3385 2 17423 XP_294660.1 3 439 GAACCTGGGAGG TG 3 C b
b

94 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 LOC3386 1 4376 XP_294665.1 5 650 GAGCCTTGGAGG C 3 C b b
04 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
T

GAM7957 297 LOC3386 2 5830 XP_290518.1 5 94 CTACTCGGGAGG A AAC T 3 C c
b

90 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC3386 2 14785 XP_290518.1 5 128 GAACCCGGGAGG TG 3 C b
b

90 CGGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCCGA AGTG GTTGGAGGCGGAGGGC
GT

GAM7957 297 LOC3388 2 12726 XP_294725.1 3 396 AATGCCGGGAGG A AAC T 3 C c
b

37 CTGAGGCGGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GGCG GAG CGGAGGGC
- --- T

GAM7957 297 LOC3388 2 18690 XP_294725.1 3 430 GAACCCGGGAGG 3 C b b
37 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 LOC3388 2 9815 XP_294736.1 5 1000 GAGCCCAGGAGG ACC T C 3 C c
c

66 TCGAAGCTGCAG TCACTGCA TC GCCTCC
TGAGGTAT AGTGACGT AG TGGAGG
CGA C A
GAM7957 297 LOC3388 2 11040 XP_294736.1 5 271 AGCTCCGGGAGG - AA T --- 3 C c
c
66 CTGCAGTGGCGG TCA CTGC CC CT GCCTCCCG
CAGCTGAG AGT GACG GG GA CGGAGGGC
C GC T CGT
GAM7957 297 LOC3389 1 6154 XP_290630.1 3 1194 GAACCCGGGAGG TC----- TG 3 C c
c
10 TGGAGGTTGCAG ACTGCAACCTC CCTCCCG
TAAGCCGA TGACGTTGGAG GGAGGGC
AGCCGAA GT
GAM7957 297 LOC3389 1 15384 XP_294742.1 3 1431 AAGGCCAGGAGT A TGC C 3 C
c c
23 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 LOC3389 2 6095 XP_294757.1 5 936 GAACCCGGGAAG C 3 C b b
63 CGGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCCGA AGTGACGTTGGAGGCG AGGGC
A
GAM7957 297 LOC3389 2 12559 XP_294757.1 5 904 CTACTCGGGAGG A AAC T 3 C c
b
63 CTGAGGCAGGAA TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3389 1 17403 XP_294762.1 5 1217 GAACCCAGGAGG C 3 C b b
76 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC3389 1 10439 XP_290663.1 5 584 GAACCTGGGAGG 3 C b b
91 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC3389 1 10439 XP_290659.1 5 584 GAACCTGGGAGG 3 C b b
99 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC3390 1 7867 XP_290682.1 3 1333 AAACCCAGGAGG C 3 C b b
59 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTTGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC3390 1 14359 XP_294800.1 3 503 GAACCTGGGAGG A 3 C b b
71 CAGAGGTTGCAG TC CTGCAACCTCTGCCTCCCG
GGAACCTA AG GACGTTGGAGACGGAGGGT
G
GAM7957 297 LOC3390 2 6790 XP_290692.1 3 2423 CTACTCGGGAGG A AAC T 3 C c
c

```
          78                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATCGCCT    AG GACG  GAG CGGAGGGC
                                             -   ---  T
GAM7957  297   LOC3390 2  12011  XP_290692.1  3  2456  TGAACCCAGAAG          C  CC       3  C  c
c
          78                          CGGAGGTTGCAG TCACTGCAACCTCTGC TC
                                     TGAGCTGA    AGTGACGTTGGAGGCG AG
                                               A  AC
GAM7957  297   LOC3390 4  2987   XP_290697.2  5  1081  GAACCTTGGAGG            C       3  C  b  b
          83                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCTGA    AGTGACGTTGGAGACGGAGG
                                                 T
GAM7957  297   LOC3390 4  9420   XP_290697.2  3  190   GAACCTGGGAGG                  3  C  b  b
          83                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCTGA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC3390 4  12337  XP_290697.2  5  1974  GAACCCAGGAGG            C       3  C  b  b

          83                          TAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGATGGAGG
                                                 A
GAM7957  297   LOC3390 4  13093  XP_290697.2  5  2290  GAACCCAGGAGG        C    C       3  C  b
b
          83                          CACAGGTTGCAG TCACTGCAACCT TGCCTCC
                                     TGAGCCAG    AGTGACGTTGGA ACGGAGG
                                               C     A
GAM7957  297   LOC3391 1  10720  XP_294813.2  3  755   AGTTGAAGGAGG    GCAA  -     C       3  C  c
 c
          11                          CAGAAGGGAGAG TCACT   CCT CTGCCTCC
                                     TGATGCAC    AGTGA   GGA GACGGAGG
                                             GAG-  A      A
GAM7957  297   LOC3391 1  10489  XP_290723.2  5  1616  CATCTTGGAAAG  A   -----     C-  C    3  C  c
c
          30                          CAGAGGTGTCCC TC CTGCA    ACCTCTGC  TCC
                                     TGCAGGAT    AG GACGT    TGGAGACG  AGG
                                             -   CCCTG      AA  T
GAM7957  297   LOC3391 1  19056  XP_294825.1  3  256   GAACCTGGGAGG        C           3  C  b  b
          46                          CGAAGGTTGCAG TCACTGCAACCT TGCCTCCCG
                                     TGAGCTGA    AGTGACGTTGGA GCGGAGGGT
                                               A
GAM7957  297   LOC3391 1  4314   XP_294829.1  3  784   GAACCCGGGAAG          C          3  C  b  b
          52                          CAGAGGTTGCGG TCACTGCAACCTCTGC TCCCG
                                     TGAGCTGA    AGTGGCGTTGGAGACG AGGGC
                                               A
GAM7957  297   LOC3391 1  14392  XP_290743.1  3  614   GAACCCAGAAGG        TG  CCC       3  C  c
 c
          84                          TGGAGGTTGCAG TCACTGCAACCTC  CCT
                                     TGAGCCGA    AGTGACGTTGGAG  GGA
                                               GT   AGA
GAM7957  297   LOC3391 1  15984  XP_290759.1  3  1816  GAACCCAGGAGG        TG   C       3  C  c
c
```

99 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 LOC3392 2 8019 XP_290762.2 5 784 GAACCCGGGAAG C C 3 C b b

16 CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A
GAM7957 297 LOC3392 2 13155 XP_290762.2 5 750 CTACTCGGGAGG A AAC T 3 C c
b

16 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3392 1 13438 XP_290774.1 3 560 GAATCCGGGAGG C 3 C b b

23 CAGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
TGGGCCTA GGTGACGTT GAGACGGAGGGC
A
GAM7957 297 LOC3392 1 18686 XP_290777.1 3 436 GAACCTGGGAGG TG 3 C b
b

31 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGTCGA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 LOC3392 1 18140 XP_290783.1 3 629 GAACCCCGGAGG C 3 C b b

38 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
C
GAM7957 297 LOC3392 1 18140 XP_290784.1 3 559 GAACCCCGGAGG C 3 C b b

38 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
C
GAM7957 297 LOC3392 2 8019 XP_294900.2 5 784 GAACCCGGGAAG C C 3 C b b

82 CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A
GAM7957 297 LOC3392 2 13155 XP_294900.2 5 750 CTACTCGGGAGG A AAC T 3 C c
b

82 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3392 2 1493 XP_294901.1 5 2823 CTACTCGGGAGG A GCAA T 3 C
c b

90 CTGAGGCAAGAG TC CT CCTC GCCTCCCG
AATCGCTT AG GA GGAG CGGAGGGC
A AC-- T
GAM7957 297 LOC3392 2 16582 XP_294901.1 5 2855 GAACCTGGGAGG C 3 C b b

90 CAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG

TGAAACAA AGTGACGTTG AGACGGAGGGT
A
GAM7957 297 LOC3393 1 1686 XP_290819.1 3 686 GAACCTAAGTGG TCCC 3 C c c
27 CAGAGGTTGCAG TCACTGCAACCTCTGCC
TGAGCTGA AGTGACGTTGGAGACGG
TGAA
GAM7957 297 LOC3393 2 5830 XP_290846.1 3 91 CTACTCGGGAGG A AAC T 3 C c c
43 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3393 2 19994 XP_290846.1 3 609 GAGCCCAGGAGG T C 3 C c c
43 TCGAGGTTGCAG TCACTGCAACCTC GCCTCC
TGAGCAGT AGTGACGTTGGAG TGGAGG
C A
GAM7957 297 LOC3393 1 4402 XP_294921.1 3 1339 GAACCCGGGAAG C 3 C b b
73 CGGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCCAA AGTGACGTTGGAGGCG AGGGC
A
GAM7957 297 LOC3394 1 14129 XP_294932.1 5 1047 GAACCCAGGAGG C 3 C b b
01 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAACCGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 LOC3394 1 14425 XP_294944.1 5 1256 GAATTGGGGAGG 3 C b b
17 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCTGA AGTGACGTTGGAGGCGGAGGG
GAM7957 297 LOC3394 1 12654 XP_294952.2 3 3005 GAACCCGGCGGG G C 3 C b b
39 AAGAGGTTGCAG TCACTGCAACCTCT CCT CCG
TGAGCCAA AGTGACGTTGGAGA GGG GGC
A C
GAM7957 297 LOC3394 1 15409 XP_290903.1 3 937 AAGGGGCAGGTG A A - -- 3 C c c
52 CAGAGGTGGCAG TC CTGC ACCTCTGC CT CCC
GGATGGCT AG GACG TGGAGACG GG GGG
G G T AC
GAM7957 297 LOC3394 1 18690 XP_290907.2 3 2212 GAACCCGGGAGG 3 C b b
59 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 LOC3394 1 6550 XP_294966.1 5 630 TCCCTGGCGAGG - ACC - 3 C c c
62 CAGACGCTGCGG TCACT GCA TCTGCCTC CCG
GTGGAGAC GGTGG CGT AGACGGAG GGT
G CGC C
GAM7957 297 LOC3394 1 6390 XP_290919.1 3 2179 GAGCACAGGAGT A TGC C 3 C c c

92 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGACCTAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 LOC3394 1 17699 XP_290927.1 3 218 GAACCCTGGAGG TG C 3 C c
c
93 TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT T
GAM7957 297 LOC3394 1 13092 XP_290925.1 3 899 GAACCCAGCGGG GCC 3 C b
b
94 AAGAGGTTGCAG TCACTGCAACCTCT TCCCG
TGAGCCAA AGTGACGTTGGAGA AGGGC

GAM7957 297 LOC3395 1 4458 XP_290953.1 5 193 CGCGGCCGGAGG A- CAA C 3 C c
c
59 CAGAGGCCAGGC TC CTG CCTCTGCCTCC
GAGACACC AG GAC GGAGACGGAGG
CG C-- C
GAM7957 297 LOC3395 1 15343 XP_290957.1 3 127 GAACCCGGGAGG C 3 C b b
87 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC3397 1 10720 XP_290339.1 3 1036 AGTTGAAGGAGG GCAA - C 3 C
c c
40 CAGAAGGGAGAG TCACT CCT CTGCCTCC
TGATGCAC AGTGA GGA GACGGAGG
GAG- A A
GAM7957 297 LOC3397 4 4154 XP_291005.1 3 2381 AAGTCTGGGAGG A T 3 C c b
61 TTGAGGCTGCAG TCACTGCA CCTC GCCTCCCG
TGAGCTGT AGTGACGT GGAG TGGAGGGT
C T
GAM7957 297 LOC3397 4 12437 XP_291005.1 3 799 GAGCTCAGGAGG - CT C 3 C c
b
61 TTGGGTCTGCAG TCACTGCA ACCT GCCTCC
TGAGCTAT AGTGACGT TGGG TGGAGG
C T- A
GAM7957 297 LOC3397 4 17629 XP_291005.1 3 2789 GAACCTGGGAGG CCT 3 C b
b
61 CAGTTTGCAGTG TCACTGCAA CTGCCTCCCG
AGCTGAGA AGTGACGTT GACGGAGGGT
T--
GAM7957 297 LOC3397 4 18770 XP_291005.1 3 2789 TTGAACCTGGGA CCT 3 C b
b
61 GGCAGTTTGCAG TCACTGCAA CTGCCTCCCG
TGAGCTGA AGTGACGTT GACGGAGGGT
T--
GAM7957 297 LOC3398 1 16895 XP_295072.1 3 928 GAACCCGGCGGG TC----- C 3 C c
c

03 CAGAGGTTGCAG ACTGCAACCTCTGCCT CCG
TAAGCAGA TGACGTTGGAGACGGG GGC
AGACGAA C
GAM7957 297 LOC3398 1 15343 XP_295071.1 3 2016 GAACCCGGGAGG C 3 C b b
08 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC3398 1 13277 XP_291020.1 5 121 GCTAACGGGAGG TGCA CT 3 C c c
09 CAGTGTGATGTG TCAC AC CTGCCTCCCG
GAGGGGAA GGTG TG GACGGAGGGC
TAG- T-
GAM7957 297 LOC3398 2 11987 XP_295080.1 5 865 GAGCCTGGGAGG A 3 C b b
31 CAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAGCCGA AGTGACGT GGAGACGGAGGGT
C
GAM7957 297 LOC3398 2 13584 XP_295080.1 5 833 CTACTCGGGAGG A AAC T 3 C c b
31 CTGAGGCAGGAT TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3398 1 1325 XP_295079.1 5 246 GTCTTCGGGAGG G CC 3 C b b
32 CAGAATTGAAGT TCACT CAA TCTGCCTCCCG
GAACATGA AGTGA GTT AGACGGAGGGC
A A-
GAM7957 297 LOC3398 1 17278 XP_291032.1 5 216 GAACCCGGGAGT C C 3 C b b
35 TAAAGGTTGCAG TCACTGCAACCT TG CTCCCG
TGAGCCGA AGTGACGTTGGA AT GAGGGC
A T
GAM7957 297 LOC3398 1 13065 XP_291038.1 3 865 GAACCCGGGAGG 3 C b b
41 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC
GAM7957 297 LOC3398 2 1816 XP_295086.1 3 366 GAGCTGGGGAGA A GC 3 C c c
52 TGGAGGCTGCAG TCACTGCA CCTCT CTCCC
TGAGCTAT AGTGACGT GGAGG GAGGG
C TA
GAM7957 297 LOC3398 2 15089 XP_295086.1 3 841 CTACTCGGGAGG A AAC T 3 C c c
52 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3398 1 5805 XP_291041.1 3 222 TGACTGAGGGGG AAC C 3 C c c
55 CAGAGGCAGTGG TCACTGC CTCTGCCTCC

```
                                  CTCTTTAG    GGTGACG   GAGACGGGGG
                                              ---         A
GAM7957  297    LOC3398 1   9765  XP_295089.1  3  820   GAACCCGGGAGG          TG           3  C  b  b

          65                       TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                  TGAGCCGA    AGTGACGTTGGAG  GGAGGGC
                                                GT
GAM7957  297    LOC3398 1   13689 XP_295094.1  3  1155  GAACCTGGGAGG TC-----                 3  C  c
c
          87                       CAGAGGTTGCGG       ACTGCAACCTCTGCCTCCCG
                                  TAAGCCGA          TGGCGTTGGAGACGGAGGGT
                                        AGCCGAA
GAM7957  297    LOC3399 1   5256  XP_295105.1  3  1299  GAACCCGGGAGG     C    C            3  C  b
b
          29                       CAAAGGTTTTAG TCACTG AACCT TGCCTCCCG
                                  TGAGCCGA    AGTGAT TTGGA ACGGAGGGC
                                              T    A
GAM7957  297    LOC3400 1   9766  XP_291125.2  3  370   GAACTCAGGAGG              C        3  C  b  b
          38                       CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
                                  TGAGCCGA    AGTGGCGTTGGAGGCGGAGG
                                                A
GAM7957  297    LOC3400 1   11266 XP_295152.1  3  1573  GAACCCAGGAGT           C    C        3  C  c
c
          85                       CGGAGGTTGCAG TCACTGCAACCTCTG CTCC
                                  TGAGTTGA    AGTGACGTTGGAGGC GAGG
                                                T    A
GAM7957  297    LOC3400 1   3445  XP_295153.1  3  873   GGGAGGTGGAGG          TG    C        3  C  c
c
          87                       TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                  TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                                GT    T
GAM7957  297    LOC3401 1   12654 XP_295164.2  3  336   GAACCCGGCGGG          G  C         3  C  b
b
          28                       AAGAGGTTGCAG TCACTGCAACCTCT CCT CCG
                                  TGAGCCAA    AGTGACGTTGGAGA GGG GGC
                                                A  C
GAM7957  297    LOC3401 1   12306 XP_291151.1  3  1515  GAACCTGGGAGG                        3  C  b  b
          33                       CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAACCAA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297    LOC3401 3   10571 XP_291153.1  3  3673  GAACCCAGGAGG        C        C        3  C  c
b
          38                       CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
                                  TGAGCCGA    AGTGACGTT GAGGCGGAGG
                                              C         A
GAM7957  297    LOC3401 3   13155 XP_291153.1  3  3639  CTACTCGGGAGG  A   AAC  T           3  C  c
 b
          38                       CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                  AATGGCGT    AG GACG   GAG CGGAGGGC
                                              -   ---  T
```

GAM7957 297 LOC3401 3 15675 XP_291153.1 3 649 GAACCCGGGAGG C TG 3 C b
b
38 TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCGA AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 LOC3401 1 12654 XP_295176.1 3 336 GAACCCGGCGGG G C 3 C b
b
53 AAGAGGTTGCAG TCACTGCAACCTCT CCT CCG
TGAGCCAA AGTGACGTTGGAGA GGG GGC
A C
GAM7957 297 LOC3401 2 8198 XP_295183.1 3 1371 GAACCTGGGAGG 3 C b b
84 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGATCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC3401 2 19035 XP_295183.1 3 3211 GAACCTGGGAGG C 3 C b b

84 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGATTGGA AGTGACGTT GAGACGGAGGGT
C
GAM7957 297 LOC3402 3 9994 XP_295187.1 5 336 GAACTCAGGAGG C C 3 C c b
08 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 LOC3402 3 14091 XP_295187.1 3 638 AACCCGGGAAGG C - 3 C b b

08 CGGAAGTTGCAG TCACTGCAAC TCTGCCT CCCG
TGAGCCGA AGTGACGTTG AGGCGGA GGGC
A A
GAM7957 297 LOC3402 3 15108 XP_295187.1 5 302 CTACTCGGGAGG A AAC T 3 C c
b
08 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3403 1 3560 XP_295216.1 3 190 GTTGAGGGCAGG CT A - 3 C b
b
19 CAGAGGTAGCTG TCA GC ACCTCTGCCT CCC
AGGGTAGC AGT CG TGGAGACGGA GGG
-- A C
GAM7957 297 LOC3403 2 8552 XP_295212.1 3 297 GAACTTGGGAGG G 3 C b b
21 GAGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCCCA AGTGACGTTGGAGA GGAGGGT
G
GAM7957 297 LOC3403 2 13857 XP_295212.1 5 663 GAACCCGGGAAG C 3 C b b
21 CAGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCTGA AGTGACGTTGGAGACG AGGGC
A
GAM7957 297 LOC3403 1 9208 XP_290402.1 3 549 AGTTATCAGGGA TG GCC 3 C c
c
24 AAGAGGTTGATG TCAC CAACCTCT TCCC
TGAACTCA AGTG GTTGGAGA AGGG

```
                                          TA       A--
GAM7957  297    LOC3403 2  9767   XP_295218.1  5  80    GAACTCGGGAGG                    3  C  b  b
          35                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297    LOC3403 2  12218  XP_295218.1  3  898   GAACCCCAGAGG     G A       CC        3  C  c
 b
          35                          CAGAGGCTGAAG TCACT CA CCTCTGCCTC
                                     TGAGCCAA    AGTGA GT GGAGACGGAG
                                               A  C        AC
GAM7957  297    LOC3403 1  3934   XP_295221.1  5  1285  GAGCCAGAGAGG       A       CC        3  C  c
c
          53                          TAGAGGCTGCAG TCACTGCA CCTCTGCCTC
                                     TGAGCTAT    AGTGACGT GGAGATGGAG
                                                  C        AG
GAM7957  297    LOC3403 1  15223  XP_295225.1  3  457   GAACCCAGGAGG          TG    C        3  C  c
c
          62                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                     TGAGCTGA    AGTGACGTTGGAG  GGAGG
                                                  GT    A
GAM7957  297    LOC3403 1  15468  XP_291269.1  5  25    CTGAAATGGAGG  A TG  A       C        3  C  c
c
          90                          CAGAGGTGTGGG TC C  CA CCTCTGCCTCC
                                     AGGCAGAA    AG G  GT GGAGACGGAGG
                                              - GT  -         T
GAM7957  297    LOC3403 1  12796  XP_295235.1  3  221   GAACCCGGGAGG                    3  C  b  b
          94                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297    LOC3404 1  925    XP_291274.1  3  1098  GAGCTCAGGAGG             C        3  C  b  b
          08                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                                  A
GAM7957  297    LOC3404 1  4087   XP_295240.1  3  1327  GAACCTGGGAGG          CT           3  C  b
b
          14                          CCAAGGTTGCAG TCACTGCAACCT  GCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGA  CGGAGGGT
                                                  AC
GAM7957  297    LOC3404 1  19885  XP_291298.1  3  87    GAAGTCCCTTGG  A      TCTGC          3  C  c
 c
          56                          GGAGGGTTGCAG TC CTGCAACC    CTCCC
                                     AGAGAGTG    AG GACGTTGG    GAGGG
                                              A       -----
GAM7957  297    LOC3404 2  7183   XP_290428.1  3  284   CCAAGGCAGAGT  A  C--      C  --       3  C  c
c
          94                          CAGAGGTTCCAC TC CTG   AACCTCTG CTC  CC
                                     AGGAGGAG    AG GAC   TTGGAGAC GAG  GG
                                              -  ACC       T  AC
GAM7957  297    LOC3404 2  10536  XP_290428.1  3  429   CAGAGTGGGAGG  ACT  AC---           3  C
c  c
```

```
          94                          CAGAGAAGTGTG TC   GCA    CTCTGCCTCCCG
                                     CTCAGAGG    AG  CGT    GAGACGGAGGGT
                                            ACT  GTGAA
GAM7957  297   LOC3405 1  15984  XP_291331.1  3  1156  GAACCCAGGAGG         TG    C       3  C  c
c
          47                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                     TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                            GT    A
GAM7957  297   LOC3406 1  1950   XP_294645.1  5  532   GCAGTAGGGAGG    GCAAC-            3  C  c
 c
          15                          CAGAGTATCTTG TCACT     CTCTGCCTCCC
                                     GTGGGGAG    GGTGG     GAGACGGAGGG
                                            TTCTAT
GAM7957  297   LOC3437 1  3216   XP_297855.1  5  311   CAGTACTAGGAG        TC  C  C       3  C  c
c
          88                          CATTGGTTGCAG TCACTGCAACC  TGC TCC
                                     TGGAGGAG    GGTGACGTTGG  ACG AGG
                                            TT  -  A
GAM7957  297   LOC3461 1  5901   XP_299316.1  5  302   AGTGGTGGGAGG  A    A  T---          3  C  c
c
          10                          CAGCTGTGGTGC TC CTGCA CC    CTGCCTCCCG
                                     AGGAGCTG    AG GACGT GG    GACGGAGGGT
                                            -   - TGTC
GAM7957  297   LOC3477 2  8739   XP_300253.1  5  1     GGAGGGAGGCAG  A   AA  T           3  C  c
c
          58                          GGAGGCAGGGAG TC CTGC  CC CTGCCTCCC
                                     GCAGGGAG    AG GACG  GG GACGGAGGG
                                            G   GA  -
GAM7957  297   LOC3477 2  12606  XP_300253.1  5  9     GAGGCAGGGAGG  A   AA  T           3  C  c
c
          58                          CAGGGAGGCAGG TC CTGC  CC CTGCCTCCC
                                     GAGGAACG    AG GACG  GG GACGGAGGG
                                            G   GA  -
GAM7957  297   LOC3477 2  12061  XP_084325.1  3  1023  GAGCCCAGGAGG      A   T    C       3  C  c
b
          59                          TCGAGGCTGCAG TCACTGCA CCTC GCCTCC
                                     TGAGCTGT    AGTGACGT GGAG TGGAGG
                                            C   C    A
GAM7957  297   LOC3477 2  14817  XP_084325.1  3  660   GAACCCGGAAGG           C        3  C  b  b
          59                          CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
                                     TGAGCCGA    AGTGACGTTGGAGACGGA GGC
                                            A
GAM7957  297   LOC3479 1  1911   XP_302639.1  3  907   GAACCTGGGAGG         TG          3  C  b  b

          71                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGGGCTAA    GGTGACGTTGGAG  GGAGGGT
                                            GT
GAM7957  297   LOC3480 2  2678   XP_300620.1  5  1966  AAGGGCAGGAGG  AC--  A  -     C      3  C  c
 b
          71                          CAGCAGGTGCAC TC    TGCA CCT CTGCCTCC
```

CAGGAGCA AG ACGT GGA GACGGAGG
GACC - C A
GAM7957 297 LOC3480 2 15592 XP_300620.1 3 1744 GAACCCAGGAGG C C 3 C b
b
71 CAGAGGTTACAG TCACTG AACCTCTGCCTCC
TGAGCAGA AGTGAC TTGGAGACGGAGG
A A
GAM7957 297 LOC3480 1 17403 XP_302652.1 5 1693 GAACCCAGGAGG C 3 C b b
72 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC3481 1 13342 XP_302651.1 5 1542 GAACCCAGGAGG C 3 C b b
02 TAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGATGGAGG
A
GAM7957 297 LOC3481 1 10439 XP_300623.1 5 584 GAACCTGGGAGG 3 C b b
13 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 LOC3481 1 6043 XP_302665.1 5 477 AAGAGGCCCTGG A T C--- 3 C c
c
25 GCCGAGGTGCAG TCACTGCA CCTC GCCT CC
TGACCCTG AGTGACGT GGAG CGGG GG
- C TCCC
GAM7957 297 LOC3481 1 10439 XP_300635.1 5 356 GAACCTGGGAGG 3 C b b
37 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 LOC3481 1 10439 XP_300636.1 5 584 GAACCTGGGAGG 3 C b b
42 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 LOC3481 1 3778 XP_208864.1 3 2175 GAACCCGGGAGG C CC 3 C c
c
61 CGGATCTTGCAT TCA TGCAA TCTGCCTCCCG
TGAGCCAA AGT ACGTT AGGCGGAGGGC
T CT
GAM7957 297 LOC3481 1 16944 XP_300643.1 5 936 GATTGTTGGCAG AC CT C 3 C c
c
62 GCCAGCCTGCAG TCACTGCA CT GCCT CCG
TGACAGTG AGTGACGT GA CGGA GGT
CC C- C
GAM7957 297 LOC3482 1 7332 XP_302697.1 3 347 GAAACTGGGAGG TG 3 C b b
33 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 LOC3482 1 10439 XP_209014.1 3 407 GAACCTGGGAGG 3 C b b

```
          45                        CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   LOC3482 1  11153  XP_302704.1  3  553   GTGCCCAGGGGT      ACC   CT        3  C  c
 c
          61                        TGCAGGCTGCAG TCACTGCA  TCTGC  CCC
                                    TGAGCTGT    AGTGACGT  GGACG  GGG
                                              C--    TT
GAM7957  297   LOC3482 4  825    XP_302706.1  3  1722  GAACCCGGGAGG  A  C  C           3  C  c
b
          64                        CGGAAGTTTCAG TC CTG AAC TCTGCCTCCCG
                                    CGAGCCGA    AG GAC TTG AGGCGGAGGGC
                                           C  T  A
GAM7957  297   LOC3482 4  1479   XP_302706.1  3  1024  GACGCTGGGAGG      ACC  TG         3  C
c  b
          64                        TGGATGCTGCAG TCACTGCA  TC  CCTCCCG
                                    TGAGCAGT    AGTGACGT  AG  GGAGGGT
                                              CGT  GT
GAM7957  297   LOC3482 4  6470   XP_302706.1  3  2020  GAACCCGGGAGG      A             3  C  b  b

          64                        TAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
                                    TGAGCCGA    AGTGACGT GGAGATGGAGGGC
                                              C
GAM7957  297   LOC3482 4  9499   XP_302706.1  3  1688  CTACTCGGGAGG  A  CAAC  T          3  C
c  b
          64                        CTGAGACAGGAG TC CTG   CTC GCCTCCCG
                                    AATCGCTT    AG GAC   GAG CGGAGGGC
                                           -  A---  T
GAM7957  297   LOC3482 4  825    XP_302705.1  3  1722  GAACCCGGGAGG  A  C  C           3  C  c
b
          65                        CGGAAGTTTCAG TC CTG AAC TCTGCCTCCCG
                                    CGAGCCGA    AG GAC TTG AGGCGGAGGGC
                                           C  T  A
GAM7957  297   LOC3482 4  1479   XP_302705.1  3  1024  GACGCTGGGAGG      ACC  TG         3  C
c  b
          65                        TGGATGCTGCAG TCACTGCA  TC  CCTCCCG
                                    TGAGCAGT    AGTGACGT  AG  GGAGGGT
                                              CGT  GT
GAM7957  297   LOC3482 4  6470   XP_302705.1  3  2020  GAACCCGGGAGG      A             3  C  b  b

          65                        TAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
                                    TGAGCCGA    AGTGACGT GGAGATGGAGGGC
                                              C
GAM7957  297   LOC3482 4  9499   XP_302705.1  3  1688  CTACTCGGGAGG  A  CAAC  T          3  C
c  b
          65                        CTGAGACAGGAG TC CTG   CTC GCCTCCCG
                                    AATCGCTT    AG GAC   GAG CGGAGGGC
                                           -  A---  T
GAM7957  297   LOC3483 1  19588  XP_302732.1  5  712   GGCTGCGGGAGG T-----  TG           3  C  c
 c
```

```
          69                          CGGGGGTTGGCG      CAC  CAACCTCTGCCTCCCG
                                     TGCCTGAG         GTG  GTTGGGGGCGGAGGGC
                                           GAGTCC   CG
GAM7957  297   LOC3483 1  9275  XP_300723.1  3  1601  GAACCTGGGAGG          TG          3  C  b
b
          78                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCTGT    AGTGACGTTGGAG  GGAGGGT
                                                 GT
GAM7957  297   LOC3483 2  15224 XP_302741.1  3  422   GAACCTGGGAGG          TG          3  C  b
b
          93                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCCAA    AGTGACGTTGGAG  GGAGGGT
                                                 GT
GAM7957  297   LOC3483 2  15307 XP_302741.1  3  1325  GAACCTGGGAGG                    3  C  b  b
          93                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAACTGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   LOC3484 1  6390  XP_300730.1  3  1420  GAGCACAGGAGT      A   TGC   C       3  C  c
 c
          02                          TTGAGGCTGCAG TCACTGCA CCTC   CTCC
                                     TGACCTAT    AGTGACGT GGAG   GAGG
                                                 C   TTT   A
GAM7957  297   LOC3484 2  1671  XP_057659.1  3  1536  AGGTGGGGCAGG TC-----          -      3  C  c
c
          42                          CGGAGGTTGCAG       ACTGCAACCTCTGCCT CCC
                                     TAAGCCAA          TGACGTTGGAGGCGGA GGG
                                           AACCGAA            C
GAM7957  297   LOC3484 2  12210 XP_057659.1  5  227   CAGGGCGGGAGG    T  AA  T           3  C  c
 c
          42                          CGGCGGCGCGTG TCAC GC  CC CTGCCTCCCG
                                     GGGGCGGG    GGTG CG  GG GGCGGAGGGC
                                           - C-  C
GAM7957  297   LOC3484 1  18285 XP_302760.1  3  4581  ACAGGCACGGCT      -  T  -  TC-       3  C  c
c
          55                          GGTGGTGTGCAG TCACTGCA ACC CT GCC   CC
                                     TGAACAGC    AGTGACGT TGG GG CGG   GG
                                                 G   T  T   CAC
GAM7957  297   LOC3484 2  2031  XP_302761.1  3  337   CTACTCGGGAGG   A   AACC  T          3  C  c
 b
          56                          CTGAAGCAGGAG TC CTGC    TC GCCTCCCG
                                     AATCACTT    AG GACG    AG CGGAGGGC
                                           -   A---  T
GAM7957  297   LOC3484 2  12336 XP_302761.1  3  371   GAACCCAGGAGG              C       3  C  b  b
          56                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGTCAA    AGTGACGTTGGAGACGGAGG
                                                 A
GAM7957  297   LOC3484 1  7449  XP_302764.1  3  1213  GAACATGGTAGA          C  C        3  C  b  b

          61                          CAGAGGTTGCAG TCACTGCAACCTCTG CT CCG
                                     TGAGCCAA    AGTGACGTTGGAGAC GA GGT
```

```
                                                A  T
GAM7957  297    LOC3484 1   4185   XP_209299.2  3  1055   CAACCCAGGAGG  A     C       C        3  C  c
c
          74                          CAGACGTTGCAG TC CTGCAAC TCTGCCTCC
                                     CGAGCCAA    AG GACGTTG AGACGGAGG
                                              C      C        A
GAM7957  297    LOC3484 1   5613   XP_300748.1  5  9      GAACCTGGGAGG        C              3  C  b  b
          75                          CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCTA    AGTGACGTT GAGACGGAGGGT
                                                 C
GAM7957  297    LOC3484 1   5321   XP_302773.1  3  2272   GAACCCGGGAGG        C              3  C  b  b

          80                          TAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAAACCGA    AGTGACGTT GAGATGGAGGGC
                                                 C
GAM7957  297    LOC3484 1   5613   XP_300753.1  5  9      GAACCTGGGAGG        C              3  C  b  b
          82                          CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCTA    AGTGACGTT GAGACGGAGGGT
                                                 C
GAM7957  297    LOC3484 2   3203   XP_300352.1  5  832    CCCTCTCAGGCA     --       --   CCC      3  C  c
c
          88                          GAGAGGTTGCCG TCACT  GCAACCTCT  GCCT
                                     AGTGATTC    AGTGA  CGTTGGAGA  CGGA
                                               GC       GA   CTC
GAM7957  297    LOC3484 2   19709  XP_300352.1  5  831    CTCCCTCTCAGG     --       --   CCC      3  C  c
c
          88                          CAGAGAGGTTGC TCACT  GCAACCTCT  GCCT
                                     CGAGTGAT    AGTGA  CGTTGGAGA  CGGA
                                               GC       GA   CTC
GAM7957  297    LOC3484 2   5830   XP_302795.1  3  1133   CTACTCGGGAGG  A   AAC  T           3  C  c
 c
          96                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATCGCTT    AG GACG   GAG CGGAGGGC
                                               -   ---  T
GAM7957  297    LOC3484 2   7670   XP_302795.1  3  872    GAGTCCAGGAGG        A        C        3  C  c  c
          96                          CGGAGGCTGCAG TCACTGCA CCTCTGCCTCC
                                     TGAGCTGT    AGTGACGT GGAGGCGGAGG
                                                 C         A
GAM7957  297    LOC3485 2   9335   XP_300762.1  3  869    GAGCATGGGAGG                        3  C  b  b
          03                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297    LOC3485 2   13988  XP_300762.1  3  703    GAGCCCGGGAAG  C       TG C           3  C  c
 b
          03                          TGGAGGTTGCAC TCA TGCAACCTC  C TCCCG
                                     TGAGCTGA    AGT ACGTTGGAG  G AGGGC
                                               C        GT A
GAM7957  297    LOC3485 1   17081  XP_300769.1  5  251    CTACTCGGGAGG  A   AAC  T           3  C  c
c
          04                          CCGAGGCAGGAG TC CTGC   CTC GCCTCCCG
```

AATTGCTT AG GACG GAG CGGAGGGC
- --- C
GAM7957 297 LOC3485 1 6989 XP_300772.1 3 44 TGAACCAGGATG G - C 3 C c c
20 GGGAGGTTGCAG TCACTGCAACCTCT CC TCC
TGAGCCGA AGTGACGTTGGAGG GG AGG
- T A
GAM7957 297 LOC3485 1 15409 XP_300774.1 3 937 AAGGGGCAGGTG A A - -- 3 C c
c
22 CAGAGGTGGCAG TC CTGC ACCTCTGC CT CCC
GGATGGCT AG GACG TGGAGACG GG GGG
G G T AC
GAM7957 297 LOC3485 4 2031 XP_300779.1 3 290 CTACTCGGGAGG A AACC T 3 C c
b
27 CTGAAGCAGGAG TC CTGC TC GCCTCCCG
AATCACTT AG GACG AG CGGAGGGC
- A--- T
GAM7957 297 LOC3485 4 3911 XP_300779.1 5 2153 GAACCCCGGAGG C C 3 C c
b
27 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C C
GAM7957 297 LOC3485 4 12336 XP_300779.1 3 324 GAACCCAGGAGG C 3 C b b
27 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTCAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC3485 4 18885 XP_300779.1 5 2119 GTACTCGGGAGG A AAC T 3 C c
b
27 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC3485 2 15224 XP_302818.1 3 422 GAACCTGGGAGG TG 3 C b
b
32 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 LOC3485 2 15307 XP_302818.1 3 1325 GAACCTGGGAGG 3 C b b
32 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAACTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC3485 1 12654 XP_302819.1 3 336 GAACCCGGCGGG G C 3 C b
b
33 AAGAGGTTGCAG TCACTGCAACCTCT CCT CCG
TGAGCCAA AGTGACGTTGGAGA GGG GGC
A C
GAM7957 297 LOC3485 1 13091 XP_302820.1 3 1296 GAGCCCAGGAGT A TGC C 3 C
c c
41 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 LOC3485 3 1492 XP_300243.1 3 999 CTACTCGGGAGG A AAC T 3 C c
c

```
          44                          CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATCACTT    AG GACG   GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LOC3485 3  5164  XP_300243.1  3  441   GAACCCTGGAGG    TG         C       3  C  c
c
          44                          CAGAGGTTGTGG TCAC  CAACCTCTGCCTCC
                                     TGAGCTGA    AGTG  GTTGGAGACGGAGG
                                               GT          T
GAM7957  297   LOC3485 3  16953 XP_300243.1  3  1033  GAACCCTGGAGG      A       C       3  C  c
c
          44                          CAGAGGTGGTAG TCACTGC ACCTCTGCCTCC
                                     TGAGCCGA    AGTGATG TGGAGACGGAGG
                                               G          T
GAM7957  297   LOC3485 1  16401 XP_302834.1  5  1208  TGCAGATGGAGG    G  A  T     C       3  C  c
c
          94                          CAGTGGCTGGAG TCACT CA CC CTGCCTCC
                                     TGAATGAA    AGTGA GT GG GACGGAGG
                                               G  C  T      T
GAM7957  297   LOC3485 1  16401 XP_302837.1  3  1589  TGCAGATGGAGG    G  A  T     C       3  C  c
c
          95                          CAGTGGCTGGAG TCACT CA CC CTGCCTCC
                                     TGAATGAA    AGTGA GT GG GACGGAGG
                                               G  C  T      T
GAM7957  297   LOC3486 1  16401 XP_302844.1  5  285   TGCAGATGGAGG    G  A  T     C       3  C  c
c
          03                          CAGTGGCTGGAG TCACT CA CC CTGCCTCC
                                     TGAATGAA    AGTGA GT GG GACGGAGG
                                               G  C  T      T
GAM7957  297   LOC3486 1  16401 XP_300793.1  3  1417  TGCAGATGGAGG    G  A  T     C       3  C  c
c
          05                          CAGTGGCTGGAG TCACT CA CC CTGCCTCC
                                     TGAATGAA    AGTGA GT GG GACGGAGG
                                               G  C  T      T
GAM7957  297   LOC3486 1  14111 XP_209400.1  3  1401  GAACCTGGGAAG      A   TG C        3  C  c
c
          29                          TGGAGGCTGCAG TCACTGCA CCTC  C TCCCG
                                     TGAGCCCA    AGTGACGT GGAG  G AGGGT
                                               C   GT A
GAM7957  297   LOC3486 1  15983 XP_300816.1  5  548   GAACCCGGGAGG         TG          3  C  b
b
          99                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                     TGAGCCAA    AGTGACGTTGGAG  GGAGGGC
                                                GT
GAM7957  297   LOC3487 1  7320  XP_300826.1  3  1081  GAACCCGGGAGG       CC          3  C  b
b
          38                          CAGACTTTGCAG TCACTGCAA  TCTGCCTCCCG
                                     TGAGCTGA    AGTGACGTT  AGACGGAGGGC
                                               TC
GAM7957  297   LOC3487 2  10423 XP_300843.1  5  41    GAGCCTGGGAGG   C      TG          3  C  c
b
```

```
          90                          TGGAGGTTGCAC TCA TGCAACCTC  CCTCCCG
                                     TGAGTAGA    AGT ACGTTGGAG  GGAGGGT
                                              C       GT
GAM7957  297   LOC3487 2  16164  XP_300843.1  3  1055  GAACCTGGGAGG  A                3  C  b  b

          90                          CGGAGGTTGCAG TC CTGCAACCTCTGCCTCCCG
                                     GGAGCTGA    AG GACGTTGGAGGCGGAGGGT
                                              G
GAM7957  297   LOC3488 1  18336  XP_302902.1  3  508   AAACCCTGGAGG            C       3  C  b  b
          35                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                                       T
GAM7957  297   LOC3488 2  17081  XP_302903.1  5  253   CTACTCGGGAGG  A   AAC  T          3  C  c
c
          43                          CCGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATTGCTT    AG GACG  GAG CGGAGGGC
                                              -   ---  C
GAM7957  297   LOC3488 2  19499  XP_302903.1  3  922   GAACCCAAAAGG       CC     CCC       3  C  c
 c
          43                          CAGACATTGCAG TCACTGCAA  TCTGCCT
                                     TGAGCCAA    AGTGACGTT  AGACGGA
                                                    AC      AAA
GAM7957  297   LOC3488 1  8189   XP_302914.1  5  817   GAACCCGGGAGG       A   TG          3  C  b
b
          99                          TGGAGGCTGCAG TCACTGCA CCTC  CCTCCCG
                                     TGAGCCGA    AGTGACGT GGAG  GGAGGGC
                                              C   GT
GAM7957  297   LOC3490 1  15984  XP_300917.1  3  1464  GAACCCAGGAGG         TG   C       3  C  c
c
          50                          TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                     TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                                 GT    A
GAM7957  297   LOC3490 1  14367  XP_302949.1  3  201   GAGCCCGGGAGG       C             3  C  b  b

          63                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCTGA    AGTGACGTT GAGGCGGAGGGC
                                              C
GAM7957  297   LOC3490 2  2306   XP_300937.1  3  126   GAGCCTGGGAGG          G          3  C  b  b
          96                          AAGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGA GGAGGGT
                                                 A
GAM7957  297   LOC3490 2  7908   XP_300937.1  3  499   GAATCCGGGAGA       CTC  --         3  C  b
b
          96                          TGCATGTTGCAG TCACTGCAAC  TGC  CTCCCG
                                     TGAGCTGA    AGTGACGTTG  ACG  GAGGGC
                                              T--  TA
GAM7957  297   LOC3491 2  9421   XP_302967.1  3  614   GAACCCGGGAGG                  3  C  b  b
          51                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTTGGAGGCGGAGGGC
```

GAM7957 297 LOC3491 2 12920 XP_302967.1 3 580 CTGCTCGGGAGG A AAC 3 C b b

51 CAGAGGCAGGAG TC CTGC CTCTGCCTCCCG
AATGGCGT AG GACG GAGACGGAGGGC
- ---

GAM7957 297 LOC3491 1 10438 XP_302978.1 3 1775 GAACCCGGGAGG 3 C b b

69 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC3491 1 4313 XP_300969.1 3 2449 GAGCCTGGGAGG 3 C b b

70 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 LOC3491 1 10440 XP_302985.1 3 1664 GAACCCGGGAGG 3 C b b

86 CAGAGGTTGCGG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGGCGTTGGAGACGGAGGGC

GAM7957 297 LOC3491 1 18689 XP_300974.1 3 336 GAACCTGGGAGG C 3 C b b

97 CGAAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCCAA AGTGACGTTGGA GCGGAGGGT
A

GAM7957 297 LOC3492 1 3491 XP_301005.1 3 236 GTGCGGCGGTGC A - - C 3 C c c

76 TGGAGGTTGCGG TC CTGCAACCTCT GC CT CCG
CGGCGGCT GG GGCGTTGGAGG CG GG GGC
C T T C

GAM7957 297 LOC3492 1 17262 XP_301008.1 3 934 GAACCCGGGAGG CC TG 3 C c c

82 TGGAACTTGCAG TCACTGCAA TC CCTCCCG
TGAGCCGA AGTGACGTT AG GGAGGGC
CA GT

GAM7957 297 LOC3492 1 1755 XP_301016.1 3 664 GGGCGGCGGTGC A ------ T 3 C c c

98 TGGAGGTTGCGG TC CTGCAACCTCT GCC CCC
CGGCGGCT GG GGCGTTGGAGG CGG GGG
C TCGTGG C

GAM7957 297 LOC3493 1 17262 XP_301024.1 3 909 GAACCCGGGAGG CC TG 3 C c c

13 TGGAACTTGCAG TCACTGCAA TC CCTCCCG
TGAGCCGA AGTGACGTT AG GGAGGGC
CA GT

GAM7957 297 LOC3493 1 10438 XP_301033.1 5 7 GAACCCGGGAGG 3 C b b

32 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 LOC3493 1 11100 XP_303039.1 5 18 TTCAGCGGGAGG GCAA --- 3 C c c

81 CAGCAGAGGGGA TCACT CCTCT GCCTCCCG
AGTGGTCA GGTGA GGAGA CGGAGGGC
AGG- CGA

GAM7957 297 LOC3494 1 18825 XP_301075.1 3 1863 GAGCCCAGGAGT A TGC C 3 C c c

20 TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGTTAT AGTGACGT GGAG GAGG
C TTT A

GAM7957 297 LOC3494 3 5210 XP_301084.1 3 1989 CTACCCGGGAGG A AAC T 3 C c b

30 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC3494 3 9769 XP_301084.1 3 2023 GTACCTGGGAAG C C 3 C c b

30 CGCAGGTTGCAG TCACTGCAACCT TGC TCCCG
TGAGCTGA AGTGACGTTGGA GCG AGGGT
C A

GAM7957 297 LOC3494 3 13491 XP_301084.1 3 713 GAACTCGGGAGG A C 3 C b b

30 CAGAGGTTTCAG TC CTG AACCTCTGCCTCCCG
GGAGCCAA AG GAC TTGGAGACGGAGGGC
G T

GAM7957 297 LOC3494 1 13491 XP_301086.1 3 713 GAACTCGGGAGG A C 3 C b b

32 CAGAGGTTTCAG TC CTG AACCTCTGCCTCCCG
GGAGCCAA AG GAC TTGGAGACGGAGGGC
G T

GAM7957 297 LOC3494 1 18709 XP_088752.1 3 1255 GAACCCAGGAGG C C 3 C b b

47 CAGAGTTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGACGGAGG
T A

GAM7957 297 LOC3510 1 10900 XP_304617.1 5 1177 GAGTCTGGGAGG A ------- CT 3 C c c

12 CAGGTTTCCAAG TC CTGC AACCT GCCTCCCG
AGCAGGGA AG GACG TTGGA CGGAGGGT
G AGAACCT --

GAM7957 297 LOC5114 1 12025 NP_057242.1 3 1550 GTACCCAGGAGG TG C 3 C c c

5 TGGAGGTTGCGG TCACTGCAACCTC CCTCC
TGAACTGA AGTGGCGTTGGAG GGAGG
GT A

GAM7957 297 LOC5121 1 7047 NP_057464.1 3 297 GAACCCGGGAGG C 3 C b b

2 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCAA AGTGACGTT GAGACGGAGGGC
C

GAM7957 297 LOC5127 2 1492 NP_057630.1 3 1171 CTACTCGGGAGG A AAC T 3 C c b

9 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 LOC5127 2 19061 NP_057630.1 3 1205 GAACCTGGGAGG 3 C b b

```
          9                         CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCTAA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC5133 1  4982  NP_057727.1  3  816   GAACCTGGGAGA   C       C          3  C  b  b

          3                         CAGAGGTTGCAA TCA TGCAACCTCTG CTCCCG
                                    TGAACCGA    AGT ACGTTGGAGAC GAGGGT
                                          A         A
GAM7957  297   LOC5597 1  15223 NP_061333.1  3  490   GAACCCAGGAGG         TG    C       3  C  c
c
          4                         TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                    TGAGCTGA    AGTGACGTTGGAG  GGAGG
                                          GT    A
GAM7957  297   LOC5709 1  18987 NP_065088.1  3  1214  GATGGAGGGAGG  A  CAAC             3  C
c  c
          0                         CAGAGTAACAGC TC CTG    CTCTGCCTCCC
                                    GAAGAGGG    AG GAC    GAGACGGAGGG
                                          C   AAT-
GAM7957  297   LOC6392 1  9770  NP_071381.1  3  986   GAACCTGGGAGG         TG          3  C  b  b

          9                         TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                    TGAGCTGA    AGTGACGTTGGAG  GGAGGGT
                                          GT
GAM7957  297   LOC6416 1  17267 NP_071745.1  3  248   AAACCCGGGAGG       C  TG          3  C  b
b
          7                         TGGAGCTTGCAG TCACTGCAA CTC  CCTCCCG
                                    TGAGCCGA    AGTGACGTT GAG  GGAGGGC
                                          C   GT
GAM7957  297   LOC8156 1  15437 XP_030465.1  3  473   TGGCCAGGGAGG   -  ACCTC           3  C
c  c
          9                         CATTGCTGCAGG TCAC TGCA    TGCCTCCC
                                    TGAGCCTG    AGTG ACGT    ACGGAGGG
                                          G   CGTT-
GAM7957  297   LOC8369 1  17437 NP_113651.3  3  2202  GAGCCCAGGATG    G       C  C       3  C  c
c
          3                         CAGAGGTTGAAG TCACT CAACCTCTGC TCC
                                    TGAGCCAA    AGTGA GTTGGAGACG AGG
                                          A       T  A
GAM7957  297   LOC9012 1  19914 XP_291299.1  3  521   TGGGACGGGAGG   - AA   -          3  C  c
c
          0                         CGGGAGGGGGCT TCACT GC  CCTCT GCCTCCCG
                                    GGTGGTGC    GGTGG CG  GGAGG CGGAGGGC
                                          T GG    G
GAM7957  297   LOC9023 1  14788 NP_612356.1  3  1458  GAACCCAGAAGG       C     CCC       3  C  c
c
          3                         CGGAAGTTGCAG TCACTGCAAC TCTGCCT
                                    TGAGCTGA    AGTGACGTTG AGGCGGA
                                          A      AGA
GAM7957  297   LOC9032 1  2487  XP_030896.3  5  280   GAACCCGGGAGG       C             3  C  b  b
          1                         CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
```

TGAGCTGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 LOC9057 1 17837 XP_032669.1 3 657 GAACCCATAAGG CCC 3 C c c
3 CAGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGACGTTGGAGACGGA
ATA
GAM7957 297 LOC9078 1 11847 XP_034109.1 5 856 GAACCGGGGAGT GC 3 C b b
4 TGGAGGTTGCAG TCACTGCAACCTCT CTCCC
TGAGCCGA AGTGACGTTGGAGG GAGGG
TT
GAM7957 297 LOC9078 2 12572 XP_034110.1 3 1975 CTACTCGGGAGG A AAC CT 3 C c b
5 CTCAGGCAGGAG TC CTGC CT GCCTCCCG
AATCACTT AG GACG GA CGGAGGGC
- --- CT
GAM7957 297 LOC9078 2 13437 XP_034110.1 3 2009 GAACCTGGGAGG 3 C b b
5 TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGATGGAGGGT

GAM7957 297 LOC9091 1 7710 XP_034863.1 5 976 GAAGCCAGGAGG TC----- C 3 C c c
8 CAGAGGTTGCAG ACTGCAACCTCTGCCTCC
TTAGCCCA TGACGTTGGAGACGGAGG
ACCCGAT A
GAM7957 297 LOC9103 2 10462 XP_035622.1 3 411 GAAGCCAGGAGG C 3 C b b

5 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A
GAM7957 297 LOC9103 2 16454 XP_035622.1 3 377 CTACTCGGGAGG A AAC T 3 C c b
5 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTA AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC9105 1 15158 NP_612377.1 3 1895 GAACCTGGGAGG C 3 C b b
6 CAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCGA AGTGACGTTG AGACGGAGGGT
A
GAM7957 297 LOC9125 1 5988 XP_037135.1 5 779 GAACCTGGGAGG A 3 C b b
0 CAGAGGTTGTAG TC CTGCAACCTCTGCCTCCCG
CGAGCCAA AG GATGTTGGAGACGGAGGGT
C
GAM7957 297 LOC9131 1 7955 XP_037686.2 3 202 GGGAATCTGAGG GCAA ------ 3 C c c
9 CAGAGGAGGGTG TCACT CCTCTGCC TCCC
AGGCCTGT AGTGG GGAGACGG AGGG
GA-- AGTCTA

GAM7957 297 LOC9152 1 13402 NP_710181.1 3 790 GAACCTGGGAGG T TG 3 C c c
6 TGGAGGTTGCTG TCAC GCAACCTC CCTCCCG
TGAGCTGA AGTG CGTTGGAG GGAGGGT
T GT
GAM7957 297 LOC9186 1 6686 NP_443090.1 3 473 GAATCTGGGAGG C 3 C b b
2 CGGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT
A
GAM7957 297 LOC9207 1 15724 XP_042684.1 3 521 GTGGGAGGTAGG A AA-- ---- 3 C c c
8 CAGAGGGCAGGC TC CTGC CCTCTGCC TCCCG
AGGAGAAA AG GACG GGAGACGG AGGGT
- GACG ATGG
GAM7957 297 LOC9222 1 9420 XP_043731.1 3 1117 GAACCTGGGAGG 3 C b b
8 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT
GAM7957 297 LOC9223 1 15751 XP_043733.1 5 649 GCACCTGGGAGG - A- -- 3 C c c
0 CAGGCAGGCATG TCAC TGCA CCT CTGCCTCCCG
CATGTGGG GGTG ACGT GGA GACGGAGGGT
T AC CG
GAM7957 297 LOC9223 1 1042 XP_043739.2 3 168 GCATAAGGGCAG A A-- CT 3 C c c
5 CAGAGGTGGAGT TC CTGC ACCTCTGC CCC
AGGGAGGA AG GATG TGGAGACG GGG
G AGG AC
GAM7957 297 LOC9229 2 8662 XP_044075.1 3 451 GAACCCGGGCGG C T 3 C b b
9 CGGAAGTTGCAG TCACTGCAAC TCTGCC CCCG
TGAGCCGA AGTGACGTTG AGGCGG GGGC
A C
GAM7957 297 LOC9229 2 15089 XP_044075.1 3 417 CTACTCGGGAGG A AAC T 3 C c b
9 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 LOC9231 1 15597 XP_044166.4 3 156 GGGGGAGGGAGG T ----- A T 3 C c c
2 CAGTGGTGGCTG CACT GC ACC CTGCCTCCC
GAGGGTGC GTGG CG TGG GACGGAGGG
C GAGGT G T
GAM7957 297 LOC9236 2 722 XP_044589.1 5 20 AAACCCGGGAGG 3 C b b
0 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC
GAM7957 297 LOC9236 2 11410 XP_044589.1 3 157 GAACCCTGGAGG T C 3 C c b
0 TTGAGGTTGCAG TCACTGCAACCTC GCCTCC

```
                                    TGAGCTGA    AGTGACGTTGGAG TGGAGG
                                                T     T
GAM7957  297   LOC9240 1  12688 XP_044914.1  3 971   CTACTCGGGAGG  A GCAA   T          3  C
c  c
         5                          CTGAGGAAGGAG TC CT   CCTC GCCTCCCG
                                    AATCGCTT    AG GG   GGAG CGGAGGGC
                                           A  AA--   T
GAM7957  297   LOC9248 1  15548 XP_045310.1  3 768   GAATCCAGGTGG           T C       3  C  c  c

         2                          CGGAGGTTGCAG TCACTGCAACCTCTGCC CC
                                    TGAGCCGA    AGTGACGTTGGAGGCGG GG
                                                T A
GAM7957  297   LOC9249 2  4848  XP_045450.1  5 350   GAACCTGGGCGG           T         3  C  b  b
         9                          CAGAGGTTGCAG TCACTGCAACCTCTGCC CCCG
                                    TGAGTCAA    AGTGACGTTGGAGACGG GGGT
                                                C
GAM7957  297   LOC9249 2  5830  XP_045450.1  5 316   CTACTCGGGAGG  A   AAC  T          3  C  c
b
         9                          CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                    AATCGCTT    AG GACG  GAG CGGAGGGC
                                           -   ---  T
GAM7957  297   LOC9265 1  11153 XP_046434.3  3 553   GTGCCCAGGGGT      ACC   CT         3  C  c
 c
         9                          TGCAGGCTGCAG TCACTGCA  TCTGC  CCC
                                    TGAGCTGT    AGTGACGT  GGACG  GGG
                                              C--    TT
GAM7957  297   LOC9297 1  12985 XP_048529.2  5 1039  ATGTCCATGAGG   CT     G   CC        3  C  c
 c
         3                          GAGAGGTTGCTG TCA  GCAACCTCT CCTC
                                    AGAAGTAC    AGT  CGTTGGAGA GGAG
                                           --       G   TA
GAM7957  297   LOC9313 2  10438 XP_049396.1  5 622   GAACCCGGGAGG                  3  C  b  b
         2                          CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   LOC9313 2  14699 XP_049396.1  5 1552  GAAGCTGGGAGG                  3  C  b  b
         2                          CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                    TGAGCCAA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297   LOC9361 1  19262 XP_052568.1  3 792   GAGCCCAGGAGG      A  C    C        3  C  c
c
         3                          CACAGGCTGCAG TCACTGCA CCT TGCCTCC
                                    TGAGCAGA    AGTGACGT GGA ACGGAGG
                                              C  C     A
GAM7957  297   LOC9443 1  9856  NP_660280.1  5 1074  TATCCCGGGAAT        C  CC-         3  C  b
b
         1                          TCAAGGTTGCAG TCACTGCAACCT TG  TCCCG
                                    TGAGCTAT    AGTGACGTTGGA AC  AGGGC
                                              -  TTA
GAM7957  297   LOC9659 1  17714 XP_039922.1  5 2463  GAACCCAGGCAG          ---   CCC      3  C  c
 c
```

```
          7                          TGGAGGTTGCAG TCACTGCAACCTCT  GCCT
                                     TGAGCCAA    AGTGACGTTGGAGG  CGGA
                                                   TGA   CCC
GAM7957  297   LOST1  1  1927  NP_758955.1  3  92   CACCGCGGGAGG   CT  A  CT          3  C  c
c
                                     CCAGGGTGCTGA TCA  GCA CCT  GCCTCCCG
                                     CTGTCAAG    AGT  CGT GGG  CGGAGGGC
                                              --  -  AC
GAM7957  297   LRG    1  16201 NP_443204.1  3  268  CAACTCGGGAGG  A   AAC  T          3  C  c  c

                                     CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                     AATGGCGT    AG GACG  GAG CGGAGGGC
                                              -   ---  T
GAM7957  297   LRRC2  1  10418 NP_078788.1  3  583  TGAACCTGGGAG       C  TG          3  C  b  b

                                     GTGGAGTTGCAG TCACTGCAAC TC  CCTCCCG
                                     TGAGCCGA    AGTGACGTTG AG  GGAGGGT
                                                 -  GT
GAM7957  297   LRRC2  1  10418 NP_079026.2  3  583  TGAACCTGGGAG       C  TG          3  C  b  b

                                     GTGGAGTTGCAG TCACTGCAAC TC  CCTCCCG
                                     TGAGCCGA    AGTGACGTTG AG  GGAGGGT
                                                 -  GT
GAM7957  297   LRRFIP1 1  14509 NP_004726.1  3  1070  GAACCTGCGAGG       C      CC       3  C  c
c
                                     CAGAGATTGCAG TCACTGCAA CTCTGCCTC
                                     TGAGCCAA    AGTGACGTT GAGACGGAG
                                                 A       CG
GAM7957  297   LUZP1  1  9422  NP_361013.1  3  1272  GAACCCAGGAGG            C       3  C  b  b
                                     CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                     TGAGCCAA    AGTGACGTTGGAGGCGGAGG
                                                    A
GAM7957  297   LYNX1  1  2417  NP_076435.1  5  243  GCGCAGGGGAGG   CT  AA  -           3  C  c
c
                                     CAGGCGGAGGCC TCA  GC  CC TCTGCCTCCC
                                     ATGGGCAG    GGT  CG  GG GGACGGAGGG
                                              AC  GA  C
GAM7957  297   LYNX1  1  2417  NP_803252.1  5  243  GCGCAGGGGAGG   CT  AA  -           3  C  c
c
                                     CAGGCGGAGGCC TCA  GC  CC TCTGCCTCCC
                                     ATGGGCAG    GGT  CG  GG GGACGGAGGG
                                              AC  GA  C
GAM7957  297   LZLP   1  16039 NP_037476.1  3  126  GAGCCTGGGAAG      A   TG C         3  C  c  c

                                     TGGAGGCTGCAG TCACTGCA CCTC  C TCCCG
                                     TGAGCCTA    AGTGACGT GGAG  G AGGGT
                                                 C   GT A
GAM7957  297   LZTS1  1  8918  NP_066300.1  3  1349  CGGAGCGGGAGG  A  GCA  T          3  C  c
c
                                     CGGTGGTAGAGA TC CT   ACC CTGCCTCCCG
```

GAGATAAA AG GA TGG GGCGGAGGGC
A GA- T
GAM7957 297 MACF1 2 1172 NP_149033.1 3 619 AGGAGAATGGTG C ------ C 3 C c c
CGGAGCTTGCAG TCACTGCAA CTCTGC CTCC
TGAGCCGA AGTGACGTT GAGGCG GAGG
C TGGTAA A
GAM7957 297 MACF1 2 11920 NP_149033.1 3 597 CTACTCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGTGC AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 MAFF 1 5558 NP_036455.1 3 1444 AAGCCCAGAAGG CCC 3 C c c
CAGAGGTTGTAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGATGTTGGAGACGGA
AGA
GAM7957 297 MAFF 1 5558 NP_690617.1 3 1444 AAGCCCAGAAGG CCC 3 C c c
CAGAGGTTGTAG TCACTGCAACCTCTGCCT
TGAGCTGA AGTGATGTTGGAGACGGA
AGA
GAM7957 297 MAL2 1 6717 NP_443118.1 5 18 GAGCCCGGGAGG A AA---- 3 C c c
CGGAGGCGGGAG TC CTGC CCTCTGCCTCCCG
GCGGCGGC GG GGCG GGAGGCGGAGGGC
C GAGGGC
GAM7957 297 MAP2K7 2 8514 NP_663302.1 3 1176 GAACCCGGGAGG C 3 C b b
CGGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCTGA AGTGACGTT GAGGCGGAGGGC
A
GAM7957 297 MAP2K7 2 19795 NP_663302.1 3 1142 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AACCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 MAP3K9 3 9732 XP_027237.1 5 407 TCTGGATAGGGG T TG --- 3 C c
b
ATGAGGTTGCTG TCAC GCAACCTC CCTC CCG
TGAAAGCA AGTG CGTTGGAG GGGG GGT
T TA ATA
GAM7957 297 MAP3K9 3 14786 XP_027237.1 3 2188 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGT
GAM7957 297 MAP3K9 3 17642 XP_027237.1 3 2019 CGCTTTGGGAGG GCAA 3 C c
b
CAGAGGCAGGTG TCACT CCTCTGCCTCCCG
GATCACCT GGTGG GGAGACGGAGGGT
AC--
GAM7957 297 MAP4 1 16329 NP_002366.1 5 131 CTCGGCGGCGGC C- - - 3 C c c
GGGCAGTTGCAG TCACTGCAAC TCTGCC TC CCG
TGGTGCAG GGTGACGTTG GGGCGG GG GGC

```
                                                AC     C  C
GAM7957  297   MAP4   1  16329 NP_112146.1  5  131   CTCGGCGGCGGC        C-     - -       3  C  c  c
                                GGGCAGTTGCAG TCACTGCAAC  TCTGCC TC CCG
                                TGGTGCAG    GGTGACGTTG  GGGCGG GG GGC
                                                AC     C  C
GAM7957  297   MAP4   1  16329 NP_112147.1  5  131   CTCGGCGGCGGC        C-     - -       3  C  c  c
                                GGGCAGTTGCAG TCACTGCAAC  TCTGCC TC CCG
                                TGGTGCAG    GGTGACGTTG  GGGCGG GG GGC
                                                AC     C  C
GAM7957  297   MAP4   1  16329 NP_112245.1  5  131   CTCGGCGGCGGC        C-     - -       3  C  c  c
                                GGGCAGTTGCAG TCACTGCAAC  TCTGCC TC CCG
                                TGGTGCAG    GGTGACGTTG  GGGCGG GG GGC
                                                AC     C  C
GAM7957  297   MAPK8IP 1  6843  NP_203750.1  3  2443  GCTGGGCAGAGG   C  A-       --        3  C  c
c
          3                      CAGAGGTCAGCA TCA TGC  ACCTCTGCCTC  CC
                                CTGGCCAT    GGT ACG  TGGAGACGGAG  GG
                                          C  AC         AC
GAM7957  297   MAPKBP1 1  8123  XP_031706.7  3  1812  TGGAGGTGGAGG          TG    C        3  C  c
 c
                                TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                             GT     T
GAM7957  297   MAWBP  1  14181 NP_071412.1  3  361   GAACCCAGGAGG        C       C        3  C  b
b
                                CAGAAGTTGCAG TCACTGCAAC TCTGCCTCC
                                TGAGCAGA    AGTGACGTTG AGACGGAGG
                                             A        A
GAM7957  297   MBTD1  1  2975  NP_060113.1  3  1095  GAACCCAGGAGG             C        3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGGGCCAA    GGTGACGTTGGAGACGGAGG
                                                A
GAM7957  297   MCAM   1  3363  NP_006491.1  3  842   GAATCCAGGAGG        C  TG    C        3  C  c
c
                                TGGAGCTTGCAG TCACTGCAA CTC  CCTCC
                                TGAGCCGA    AGTGACGTT GAG  GGAGG
                                             C  GT     A
GAM7957  297   MCM4   1  8108  XP_030274.1  3  435   AAACCCAGGCGG           T  C        3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCC CC
                                TGAGCCAA    AGTGACGTTGGAGACGG GG
                                                C  A
GAM7957  297   MECP2  1  3575  NP_004983.1  3  6573  CTGGGATAGGGG   AC   AA      ----        3  C  c
c
                                CAGAGGAGGCGA TC  TGC  CCTCTGCC    TCCCG
                                GGAGGCCG    AG  GCG  GGAGACGG    AGGGT
                                          GA   GA       GGAT
GAM7957  297   MEGF10 1  11788 NP_115822.1  3  318   CTCCCTCGGAGA         C  C    C        3  C  c
c
                                CGCAGGTTGCAG TCACTGCAACCT TG CTCC
                                TGGACATT    GGTGACGTTGGA GC GAGG
```

```
                                                C A   C
GAM7957  297   MEGF11  1   5685  NP_115821.1  3  2273  AGAAGGGAAAGG   TGCAA     --        3  C  c
 c
                                CAGAGGGTGTGA TCAC    CCTCTGCC  TCCC
                                TTATGGTG    AGTG    GGAGACGG  AGGG
                                          TG---       AA
GAM7957  297   MEN1    1   7241  NP_570715.1  5  103   GAGCCCGTGAAG      A   T  C  C       3  C  c  c

                                TCGAGGCTGCAG TCACTGCA CCTC GC TC CG
                                TGAGCCCA    AGTGACGT GGAG TG AG GC
                                          C   C  A  T
GAM7957  297   MEN1    1   7241  NP_570716.1  5  103   GAGCCCGTGAAG      A   T  C  C       3  C  c  c

                                TCGAGGCTGCAG TCACTGCA CCTC GC TC CG
                                TGAGCCCA    AGTGACGT GGAG TG AG GC
                                          C   C  A  T
GAM7957  297   MGC1020 1   17423 NP_659497.1  3  646   GAACCTGGGAGG         TG          3  C  b
b
          0                     TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                TGAGCCGA    AGTGACGTTGGAG  GGAGGGT
                                            GT
GAM7957  297   MGC1076 1   7629   NP_077321.1  3  1765  GAACCCGGGAGG TC-----    A          3  C  c
 c
          5                     CAGAGGGTGCAG       ACTGCA CCTCTGCCTCCCG
                                TAAGCCGA          TGACGT GGAGACGGAGGGC
                                        AGCCGAA     G
GAM7957  297   MGC1077 1   19103 NP_078782.2  3  237   GAATCCAGGAGG            C       3  C  b  b

          1                     CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGAGTGGA    AGTGACGTTGGAGACGGAGG
                                              A
GAM7957  297   MGC1081 2   14900 NP_116060.1  5  222   GAACCCGGGAGG    T  A             3  C  b
b
          4                     CAGAGGTGGCTG TCAC GC ACCTCTGCCTCCCG
                                TGAGCCGA    AGTG CG TGGAGACGGAGGGC
                                          T  G
GAM7957  297   MGC1081 2   15216 NP_116060.1  3  318   GAACCCGGGAGG         TG          3  C  b
b
          4                     TGGAGGTTGCGG TCACTGCAACCTC  CCTCCCG
                                TGAGCTGA    AGTGGCGTTGGAG  GGAGGGC
                                            GT
GAM7957  297   MGC1099 1   10844 NP_116044.1  5  213   CTGGGTAACAGG TC--   ---        ----    3  C  c
c
          7                     CAGAGGTTGGAA    ACTG   CAACCTCTGCCT   CCCG
                                CAGTTTGG       TGAC   GTTGGAGACGGA   GGGT
                                        GGTT    AAG         CAAT
GAM7957  297   MGC1099 1   11306 NP_115683.2  3  367   GAACTCAGAAGG         TG   CCC        3  C
c  c
          9                     TGGAGGTTGCAG TCACTGCAACCTC  CCT
                                TGAGGCGA    AGTGACGTTGGAG  GGA
```

```
                                                GT   AGA
GAM7957  297    MGC1136 1  15748  NP_076930.1  3  244    CAGGGAAGGAGG   -    A  --      C       3  C  c
c
                                  CAGCTAGGCTGT TCA CTGCA CCT  CTGCCTCC
                                  AGATGGAA    GGT GATGT GGA  GACGGAGG
                                            A    C  TC       A
GAM7957  297    MGC1138 1  14786  NP_116322.1  3  1473   GAACCTGGGAGG                    3  C  b  b

         6                        CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCAA    AGTGACGTTGGAGGCGGAGGGT

GAM7957  297    MGC1294 1  11532  NP_115694.1  3  27    TGACCCAGGAAG           C  C       3  C  c  c

         5                        CGGAGGTTGCAG TCACTGCAACCTCTGC TCC
                                  TGAGCCAA    AGTGACGTTGGAGGCG AGG
                                              A  A
GAM7957  297    MGC1302 1  804    NP_689501.1  3  307    ATAGAGGGGAGG    T-  AAC             3  C  c
c
         4                        CAGGGAGAGCTT TCAC  GC   CTCTGCCTCCC
                                  GTGGGACC    GGTG  CG   GGGACGGAGGG
                                              TT  AGA
GAM7957  297    MGC1305 2  8676   NP_116099.1  3  1459   CTACTCGGGAGG   A-   AAC   T          3  C
c  c
         3                        CTGAGGCAGGGG TC  CTGC   CTC GCCTCCCG
                                  AATCACTT    AG  GACG   GAG CGGAGGGC
                                              GG   ---   T
GAM7957  297    MGC1305 2  10475  NP_116099.1  3  1031   CTTCTCGGGAGG   A   AAC   T          3  C
c  c
         3                        CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                  AATGGCGT    AG GACG   GAG CGGAGGGC
                                              -    ---   T
GAM7957  297    MGC1327 1  2998   NP_115731.1  5  162    CCATGGGTCCGG      AA      T--        3  C  c
c
         2                        CAGAGGGCAGTG TCACTGC  CCTCTGCC   CCCG
                                  ACCGGCAC    AGTGACG  GGAGACGG   GGGT
                                              --       CCT
GAM7957  297    MGC1412 1  12370  NP_116287.1  3  450    GAACCTGGGAGG        C  T           3  C  b
b
         6                        CTGAAGTTGCAG TCACTGCAAC TC GCCTCCCG
                                  TGAGCCGA    AGTGACGTTG AG CGGAGGGT
                                              A  T
GAM7957  297    MGC1427 1  12189  NP_694980.1  3  2043   GAGCCCAGGAGG       A  CT    C        3  C
c  c
         6                        TCAAGGCTGCAG TCACTGCA CCT  GCCTCC
                                  TGAGCCGT    AGTGACGT GGA  TGGAGG
                                              C  AC     A
GAM7957  297    MGC1440 2  4378   NP_116297.1  3  1052   CTACTCGGGAGG   A   CAAC             3  C
c  b
         7                        CGGAGTCAGGAG TC CTG    CTCTGCCTCCCG
                                  ACTCTCTT    AG GAC    GAGGCGGAGGGC
```

```
                                        -  T---
GAM7957  297   MGC1440 2  10435  NP_116297.1  3  1085  GAACCCAGGAGG            C       3  C  b
b
         7                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                              A
GAM7957  297   MGC1443 1  18050  NP_116286.1  3  45    GAGCCCGGGAGG     C  C            3  C  b
b
         6                      CGGAGCTTACAG TCACTG AA CTCTGCCTCCCG
                                TGAGCTGA    AGTGAC TT GAGGCGGAGGGC
                                          A  C
GAM7957  297   MGC1479 1  6876   NP_115712.1  3  244   GAACCTGGGAGC          GC         3  C  b
b
         9                      AGGAGGTTGCAG TCACTGCAACCTCT  CTCCCG
                                TGAGCCGA    AGTGACGTTGGAGG  GAGGGT
                                              AC
GAM7957  297   MGC1481 2  6787   NP_115714.1  3  639   GAACCCAGGAGA          GC   C       3  C  c
c
         7                      TGGAGGTTGCAG TCACTGCAACCTCT  CTCC
                                TGAGCCAA    AGTGACGTTGGAGG  GAGG
                                              TA   A
GAM7957  297   MGC1481 2  13584  NP_115714.1  3  607   CTACTCGGGAGG  A   AAC  T          3  C  c
 c
         7                      CTGAGGCAGGAT TC CTGC   CTC GCCTCCCG
                                AATTGCTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   MGC1483 1  17854  NP_219480.1  3  482   CTGCTCGGGAGG  A   AAC  T          3  C
c  c
         6                      CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATCTCTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   MGC1539 1  15089  NP_542383.1  3  436   CTACTCGGGAGG  A   AAC  T          3  C  c
 c
         7                      CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATTGCTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   MGC1603 1  10438  NP_116276.1  3  273   GAACCCGGGAGG                3  C  b  b
         7                      CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   MGC1614 1  14332  NP_116152.1  3  621   GAACCCAGGAGG     AAC      C       3  C  c
 c
         2                      CAGAGATCGCAG TCACTGC   CTCTGCCTCC
                                TGAGTTGA    AGTGACG   GAGACGGAGG
                                          CTA        A
GAM7957  297   MGC1633 1  17692  NP_612635.2  3  396   GATCACTGGAGT     A   TGC  C       3  C  c
 c
         2                      TCGAGGCTGCAG TCACTGCA CCTC   CTCC
                                TGAGCTAT    AGTGACGT GGAG   GAGG
                                          C   CTT   T
```

GAM7957 297 MGC1638 1 11946 NP_444276.1 3 922 CAGGAGGTCAGG A ---- - C 3 C c c
4 TCAAGGCTGCAG TCACTGCA CCT CTG CCTCC
TGAGCCAT AGTGACGT GGA GAC GGAGG
C ACTG T A
GAM7957 297 MGC1670 2 4657 NP_659479.1 3 788 CTATTCGGGAGG A AAC T 3 C c b
3 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
GATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 MGC1670 2 18312 NP_659479.1 3 820 GAACCCGGGAGG C 3 C b b
3 CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGTCGA AGTGACGTT GAGACGGAGGGC
C
GAM7957 297 MGC1779 5 646 NP_689575.1 3 1289 GTTGCAGGGAGG 3 C b b
1 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCCGA AGTGACGTTGGAGGCGGAGGG
GAM7957 297 MGC1779 5 6756 NP_689575.1 3 1272 GAACCTGGGAGG A C 3 C c b
1 CGCAGGTTGCAG TC CTGCAACCT TGCCTCCCG
GGAGGCGG AG GACGTTGGA GCGGAGGGT
G C
GAM7957 297 MGC1779 5 10818 NP_689575.1 3 821 TGAGCCAGGAGG G C 3 C c b
1 AGGAGGTTGCAG TCACTGCAACCTCT CCTCC
TGAGCCGA AGTGACGTTGGAGG GGAGG
A A
GAM7957 297 MGC1779 5 11137 NP_689575.1 3 1460 AGCCCAGGAGTT A GC- C 3 C c b
1 AAGAGGCTGCAG TCACTGCA CCTCT CTCC
TGACCGAT AGTGACGT GGAGA GAGG
C ATT A
GAM7957 297 MGC1779 5 16675 NP_689575.1 3 790 CTACTCGGGAGG A AAC T 3 C c b
1 CTGAGGCAGGAT TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 MGC1798 1 9086 NP_705836.1 3 566 AAACCTGGGAGG C 3 C b b
6 CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT
C
GAM7957 297 MGC2023 1 6648 NP_659478.1 3 807 GAAACCGGAAGG C 3 C b b
5 CAGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCAA AGTGACGTTGGAGACGGA GGC
A
GAM7957 297 MGC2048 2 973 NP_443081.1 3 1272 GGGCCTGGGAGG 3 C b b
1 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 MGC2048 2 19193 NP_443081.1 3 1240 CTACTCGGGAGG A AAC T 3 C c b

1 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
GATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 MGC2074 2 11529 NP_061031.2 3 572 CACTTTGGGAGG A AAC 3 C b b

1 CAGAGGCGGGAG TC CTGC CTCTGCCTCCCG
GATTGCTT AG GGCG GAGACGGAGGGT
- ---

GAM7957 297 MGC2074 2 17399 NP_061031.2 3 333 GAACCTGGGAGG 3 C b b

1 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 MGC2078 1 19781 NP_443167.1 5 7 ACGAGGGGATGG GCAA - 3 C c c

1 CAGAGGAGGTGA TCACT CCTCTGCC TCCC
GGAGGGAG AGTGG GGAGACGG AGGG
A--- T

GAM7957 297 MGC2324 1 18691 NP_653216.1 3 187 GAACCTGGGAGG 3 C b b

4 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 MGC2388 1 11744 NP_689714.1 3 612 GAACCAGGGAGG TG 3 C b b

5 TGGAGGTTGCAG TCACTGCAACCTC CCTCCC
TGAGCTGA AGTGACGTTGGAG GGAGGG
GT

GAM7957 297 MGC2396 1 8496 NP_443084.1 3 184 GAACCCTGGAGG TG C 3 C c c

CAGAGGTTGTGG TCAC CAACCTCTGCCTCC
TGAGTCGA AGTG GTTGGAGACGGAGG
GT T

GAM7957 297 MGC2562 3 6525 NP_115750.1 3 1836 GAACCCAGCAGG CCC 3 C c b

CAGAGGTTGCAG TCACTGCAACCTCTGCCT
TGAGCCAA AGTGACGTTGGAGACGGA
CGA

GAM7957 297 MGC2562 3 15818 NP_115750.1 3 519 GAACCCAGGAGG C 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGATCCAA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 MGC2562 3 19241 NP_115750.1 3 1480 GAACCCGGTAGG TG C 3 C c b

TGGAGGTTGCAG TCACTGCAACCTC CCT CCG
TGAGCCGA AGTGACGTTGGAG GGA GGC
GT T

GAM7957 297 MGC2687 1 16438 NP_653228.1 5 22 GAACCTGGGAGG 3 C b b

7 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAACAGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 MGC2731 1 6364 NP_076973.1 3 468 GAAACCGGGAGG G 3 C b b

CGGAGGTTGAGG TCACT CAACCTCTGCCTCCCG
TGAGCCGA AGTGG GTTGGAGGCGGAGGGC
A

GAM7957 297 MGC2989 2 15224 NP_653219.1 3 1428 GAACCTGGGAGG TG 3 C b
b

1 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 MGC2989 2 18690 NP_653219.1 3 1611 GAACCCGGGAGG 3 C b b

1 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 MGC3169 2 6847 NP_076979.1 3 569 GAATCCAGGAGG TG C 3 C c
c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 MGC3169 2 11898 NP_076979.1 3 535 CTACTCGGGAGG A AAC T 3 C c
c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACAT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 MGC3195 1 8791 NP_114111.2 3 865 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGGTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 MGC3202 1 18690 NP_689479.1 3 306 GAACCCGGGAGG 3 C b b
0 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 MGC3207 1 2485 NP_115661.1 3 494 GAAACTGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGT
C

GAM7957 297 MGC3329 1 17423 NP_076991.2 3 1677 GAACCTGGGAGG TG 3 C b
b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 MGC3348 1 16907 NP_612359.1 3 36 AGGCTCCGGACG A C C 3 C c
c

8 CAGAGGTGGCAG TCACTGC ACCTCTGC TCC
TGGCACCA GGTGACG TGGAGACG AGG
G C C

GAM7957 297 MGC3354 1 20039 NP_653262.1 5 1 AGCGGGGGCAGA GCAA T 3 C c c

7 GGCCAAGTGGGC TCACT CCTCTGCC CCCG
ACCGGATA GGTGA GGAGACGG GGGC
ACC- -

GAM7957 297 MGC3365 1 4802 NP_699177.1 3 915 GAACCTGGGAGG AC TG 3 C c c

3 TGGAGACTGCAG TCACTGCA CTC CCTCCCG
TGAGCCGA AGTGACGT GAG GGAGGGT
CA GT

GAM7957 297 MGC3397 1 14635 NP_699174.1 3 1631 GAGCCCAGGAGG A CT C 3 C c c

1 TCAAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCTTT AGTGACGT GGA TGGAGG
C AC A

GAM7957 297 MGC3403 1 3186 NP_694956.1 3 1394 GAGGCCAGGAGG A T C 3 C c c

4 TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCTGT AGTGACGT GGAG TGGAGG
C T A

GAM7957 297 MGC3407 1 743 NP_689688.1 3 1626 GGGCCTGGGAGG C 3 C b b

9 CATAGGTTGCAG TCACTGCAACCT TGCCTCCCG
TGAGCCGA AGTGACGTTGGA ACGGAGGGT
T

GAM7957 297 MGC3472 2 6790 NP_775908.1 5 435 CTACTCGGGAGG A AAC T 3 C c b

5 CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCCT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 MGC3472 2 18691 NP_775908.1 5 469 GAACCTGGGAGG 3 C b b

5 CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 MGC3529 1 15007 NP_689930.1 3 745 CTCCCAATGGAG A- G C 3 C c c

5 GGGAGGTTGCAG TC CTGCAACCTCT CCTCC
GGGAGAGC AG GACGTTGGAGG GGAGG
GG - T

GAM7957 297 MGC3535 1 6472 NP_689773.1 3 35 CGGAGCAGGAGG - AA C 3 C c c

2 CAGAGGAGCAGA TCA CTGC CCTCTGCCTCC
TGGAGCAG GGT GACG GGAGACGGAGG
A A- A

GAM7957 297 MGC3536 1 9208 NP_671727.1 3 549 AGTTATCAGGGA TG GCC 3 C c c

1 AAGAGGTTGATG TCAC CAACCTCT TCCC
TGAACTCA AGTG GTTGGAGA AGGG
TA A--

GAM7957 297 MGC3544 1 12759 NP_694952.1 3 1434 GAACTCGGGAGG G 3 C b b

```
          0                          AAGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
                                     TGAGCTGA    AGTGACGTTGGAGA GGAGGGC
                                                 A
GAM7957  297   MGC3951 1  8988  NP_776183.1  5  15    TGCTGCGGGAGG  A   AA  T           3  C  c
c
          8                          CGGCGGCGGTAG TC CTGC  CC CTGCCTCCCG
                                     GAAGCCGG    AG GATG  GG GGCGGAGGGC
                                             -   GC  C
GAM7957  297   MGC3963 1  5211  NP_689762.1  5  299   GATGGTCGGAGG     CA---        C      3  C  c
c
          3                          CAGAGGTGTTTC TCACTG    ACCTCTGCCTCC
                                     CAGTGATC    AGTGAC    TGGAGACGGAGG
                                                 CTTTG          C
GAM7957  297   MGC4248 2  5210  NP_115709.2  3  455   CTACCCGGGAGG  A   AAC  T           3  C  c
 b
                                     CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                     AATCACTT    AG GACG   GAG CGGAGGGC
                                             -   ---  T
GAM7957  297   MGC4248 2  15981 NP_115709.2  3  489   GAACCTGGGAGG         TG          3  C  b
b
                                     TGGAGGTTGCGG TCACTGCAACCTC  CCTCCCG
                                     TGAGCTGA    AGTGGCGTTGGAG  GGAGGGT
                                                 GT
GAM7957  297   MGC4303 1  11412 NP_689924.1  3  634   GAACCTAGGAGG        - G   C       3  C  c
c
          3                          GGAAGGTTGCAG TCACTGCAACCT CT CCTCC
                                     TGAGCCGA    AGTGACGTTGGA GG GGAGG
                                                 A -    A
GAM7957  297   MGC4353 1  1686  NP_848639.1  3  685   GAACCTAAGTGG           TCCC        3  C  c
c
          7                          CAGAGGTTGCAG TCACTGCAACCTCTGCC
                                     TGAGCTGA    AGTGACGTTGGAGACGG
                                                   TGAA
GAM7957  297   MGC4562 1  972   NP_588616.1  3  364   GAACCCAGGAAG          GCC  C       3  C  c
c
                                     AGGAGGTTGCAG TCACTGCAACCTCT   TCC
                                     TGAGCCGA    AGTGACGTTGGAGG   AGG
                                                 AGA  A
GAM7957  297   MGC4580 1  13687 NP_689517.1  3  405   GAACCTGGGAGG       C             3  C  b
b
          6                          CAGAGATTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCAA    AGTGACGTT GAGACGGAGGGT
                                                 A
GAM7957  297   MGC4633 1  15343 XP_290712.1  3  458   GAACCCGGGAGG       C             3  C  b
b
          6                          CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                     TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                                 C
GAM7957  297   MGC4771 2  9499  NP_116057.1  3  1031  CTACTCGGGAGG  A  CAAC  T           3  C
c  b
```

CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCGCTT AG GAC GAG CGGAGGGC
- A--- T

GAM7957 297 MGC4771 2 13162 NP_116057.1 3 1065 GAATCCGGGAGG A 3 C b b

CAGAGGTTGCAG TC CTGCAACCTCTGCCTCCCG
GAGCTGAG AG GACGTTGGAGACGGAGGGC
-

GAM7957 297 MGC4840 2 2546 NP_113678.2 3 779 GAACCCAGGAGG TG C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGG AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 MGC4840 2 9736 NP_113678.2 3 1639 GGATGAGGGAGG A T 3 C c c

TCGGGGCTGCAG TCACTGCA CCTC GCCTCCC
TGAGCCAA AGTGACGT GGGG TGGAGGG
C C

GAM7957 297 MGC5083 1 5072 XP_171060.1 3 632 GAATCCCTGAGG CC 3 C b b

6 CAGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCTGA AGTGACGTTGGAGACGGAG
TC

GAM7957 297 MMP8 1 6716 NP_002415.1 3 735 TGAAGACAGAGG G C CC 3 C c c

CAGAGATTGGAG TCACT CAA CTCTGCCTC
TGACGCAT AGTGA GTT GAGACGGAG
G A AC

GAM7957 297 MOG 1 17403 NP_002424.1 3 1050 GAACCCAGGAGG C 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 MOST2 1 18624 NP_064635.1 5 2121 GTACCTGGGAGG G 3 C b b

AGGAGGTTGCAG TCACTGCAACCTCT CCTCCCG
TGAGCTGA AGTGACGTTGGAGG GGAGGGT
A

GAM7957 297 MRE11A 1 5020 NP_005581.2 3 1554 TACCAGGGGAGG - GCA CT 3 C c c

CAGTGTCTGGAT TCA CT AC CTGCCTCCC
GATGCTGT AGT GG TG GACGGAGGG
A TC- T-

GAM7957 297 MRE11A 1 5020 NP_005582.1 3 1554 TACCAGGGGAGG - GCA CT 3 C c c

CAGTGTCTGGAT TCA CT AC CTGCCTCCC
GATGCTGT AGT GG TG GACGGAGGG
A TC- T-

GAM7957 297 MRP63 2 4128 NP_076931.1 3 692 GAACCTCAGAGG C CC 3 C c c

CAGAGGTTGCAA TCA TGCAACCTCTGCCTC
TGAAGCGG AGT ACGTTGGAGACGGAG

```
                                        A           AC
GAM7957  297   MRP63  2  4181  NP_076931.1  3  710   GTTGCAATGAAG          C  CC       3  C  c  c
                                CGGAGGTTGCAG TCACTGCAACCTCTGC TC
                                TGAGCCGA    AGTGACGTTGGAGGCG AG
                                          A  TA
GAM7957  297   MRPL24 1  16165 NP_663781.1  5  109   CCGTCCGAGAGG  AC  -  AC      C       3  C  c
 c
                                CAGAGCTGACAA TC  TG CA  CTCTGCCTC CG
                                GGAAGGTT    AG  AC GT  GAGACGGAG GC
                                         GA  A  C-       A
GAM7957  297   MRPL30 2  2031  NP_660213.1  3  289   CTACTCGGGAGG  A   AACC  T          3  C  c
 b
                                CTGAAGCAGGAG TC CTGC    TC GCCTCCCG
                                AATCACTT    AG GACG    AG CGGAGGGC
                                         -   A---  T
GAM7957  297   MRPL30 2  13065 NP_660213.1  3  323   GAACCCGGGAGG                  3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCTGA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   MRPL4  1  1750  NP_666500.1  3  308   GAGCTCAGGGGG      A  CT    C       3  C  c
c
                                CCAAGGCTGCAG TCACTGCA CCT  GCCTCC
                                TGAGTCAT    AGTGACGT GGA  CGGGGG
                                          C  AC     A
GAM7957  297   MRPL52 1  6651  NP_848026.1  3  474   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGATGGAGGGC

GAM7957  297   MRPL52 1  6651  NP_851312.1  3  755   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGATGGAGGGC

GAM7957  297   MRPL52 1  6651  NP_851313.1  3  474   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGATGGAGGGC

GAM7957  297   MRPL52 1  6651  NP_851821.1  3  474   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGATGGAGGGC

GAM7957  297   MRPL52 1  6651  NP_851822.1  3  474   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGATGGAGGGC

GAM7957  297   MRPL52 1  6651  NP_851823.1  3  474   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA    AGTGACGTTGGAGATGGAGGGC

GAM7957  297   MRPL52 1  6651  NP_851824.1  3  517   AAACTCGGGAGG                  3  C  b  b
                                TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
```

TGAGCCAA AGTGACGTTGGAGATGGAGGGC

GAM7957 297 MRPS10 1 3585 NP_060611.2 3 999 ACCCGGGCCCGG A TG T-- 3 C c c

TGGAGGCTGCAG TCACTGCA CCTC CC CCCG
TGAGACGA AGTGACGT GGAG GG GGGC
C GT CCC

GAM7957 297 MRPS18B 2 12993 NP_054765.1 3 255 GGCGGAGGTTGC TCCC 3 C c b

AGTGAGTTGCAG TCACTGCAACCTCTGCC
TCACACCC AGTGACGTTGGAGGCGG

GAM7957 297 MRPS18B 2 13965 NP_054765.1 3 249 GATCCCAGGAGG C 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTTGC AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 MS4A2 1 18691 NP_000130.1 3 1177 GAACCTGGGAGG 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 MSCP 1 5159 NP_057696.1 3 313 CAGAGGAGGGAA CC-- G- C 3 C c c

GAAAATTTGCAG TCACTGCAA TCT CCTCC
TGACTGAA AGTGACGTT AGA GGAGG
TAAA AG A

GAM7957 297 MSCP 1 5159 NP_061049.2 3 2877 CAGAGGAGGGAA CC-- G- C 3 C c c

GAAAATTTGCAG TCACTGCAA TCT CCTCC
TGACTGAA AGTGACGTT AGA GGAGG
TAAA AG A

GAM7957 297 MSH3 1 6752 NP_002430.1 3 714 GAACCTGGGAGG C 3 C b b

CGGAGGTTGCAA TCA TGCAACCTCTGCCTCCCG
TGAGCCGA AGT ACGTTGGAGGCGGAGGGT
A

GAM7957 297 MSH5 1 12084 NP_002432.1 5 146 GCGCGTGGTTGG A AAC TC 3 C c c

CAGAGGCAGAGA TC CTGC CTCTGCC CCG
CATAAGAC AG GACG GAGACGG GGT
A --- TT

GAM7957 297 MTMR9 2 14781 NP_056273.2 3 2016 GAGCCTAGGAGG A T C 3 C c b

TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCTAT AGTGACGT GGAG TGGAGG
C T A

GAM7957 297 MTMR9 2 19031 NP_056273.2 3 4129 GAACCCGGGAGG C 3 C b b

CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGC
C

GAM7957 297 MTNR1A 1 4731 NP_005949.1 3 850 GAGCCCCAGAGG TG CC 3 C c c

CAGAGGTTGTGG TCAC CAACCTCTGCCTC
TGAGCCGA AGTG GTTGGAGACGGAG
GT AC

GAM7957 297 MU 1 17421 NP_071368.1 3 1305 GAACTCAGGAGG C 3 C b b

CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGGCGTTGGAGGCGGAGG
A

GAM7957 297 MUC13 1 13548 NP_149038.1 3 750 AATGCTAGGAGG A AA - C 3 C c c

CAGAAGGGGCAG TC CTGC CCT CTGCCTCC
AGAGTAAA AG GACG GGA GACGGAGG
A G- A A

GAM7957 297 MUC6 1 2101 XP_290540.1 3 501 AGTCAGGGAGGG A AA- - 3 C c c

CAGAGGGTGGCA TC CTGC CCTCTGCC TCCC
GCGAGGGC AG GACG GGAGACGG AGGG
C GTG G

GAM7957 297 MUCDHL 1 3704 NP_112555.1 3 1087 TCCGGATGGAGG CT G C 3 C c c

GAGAGGTTGTGC TCA GCAACCTCT CCTCC
TGACCACC AGT TGTTGGAGA GGAGG
CG G T

GAM7957 297 MXI1 1 17318 NP_005953.2 5 13 TTTCCCAGGGGG A AA--- C 3 C c c

CAGAGGCAGGGG TC CTGC CCTCTGCCTCC
CGGGAGGG AG GGCG GGAGACGGGGG
- GGGAC A

GAM7957 297 MYBL2 1 14569 NP_002457.1 3 69 GGGTTGTGGGGG T- AA C 3 C c c

CAGAGGGGGTCT TCAC GC CCTCTGCCTCC
GTGAATCT AGTG TG GGAGACGGGGG
TC GG T

GAM7957 297 MYH7B 1 8697 NP_219492.1 3 735 GAACCCAGGAGG T C 3 C c c

CGGAGGTTGCCG TCAC GCAACCTCTGCCTCC
TGAGCCAA AGTG CGTTGGAGGCGGAGG
C A

GAM7957 297 MYO1D 1 1521 XP_050041.4 3 1308 AGGTGGAGTGGG A - A C-- 3 C c c

CAGAGGTGCAAG TC CT GCA CCTCTGCCT CCG
AGAGGGAT AG GA CGT GGAGACGGG GGT
A A - TGA

GAM7957 297 MYOZ3 1 8407 NP_588612.1 3 503 TGAACTAGGAGG C 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 N4BP2 1 4033 NP_060647.2 3 1102 AAACCTGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGACCCGA AGTGACGTTGGAG GGAGGGT
GT

GAM7957 297 N4BP3 1 10245 XP_038920.2 3 3521 GCAAAGAGGGCG ACC CT 3 C c c

CAGGCCCTGCAG TCACTGCA TCTGC CCC
TGACGGTT AGTGACGT GGACG GGG
CCC C-
GAM7957 297 NALP12 2 9765 NP_653288.1 3 394 GAACCCGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 NALP12 2 19050 NP_150639.1 5 859 GAACCCGGGAGG TG 3 C b b

CGGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCTGA AGTG GTTGGAGGCGGAGGGC
GT
GAM7957 297 NAP4 1 9627 XP_294897.2 3 3195 GAACCCAGGAGG C C 3 C c c
CGGAGGTTGCAC TCA TGCAACCTCTGCCTCC
TGAGCCGA AGT ACGTTGGAGGCGGAGG
C A
GAM7957 297 NAT5 1 19510 NP_057184.1 3 662 GAACCCTGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT T
GAM7957 297 NAT5 1 19510 NP_852668.1 3 662 GAACCCTGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT T
GAM7957 297 NAT5 1 19510 NP_852669.1 3 717 GAACCCTGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT T
GAM7957 297 NCAG1 2 12727 NP_115536.1 3 2136 CTACACGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCAT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 NCAG1 2 20079 NP_115536.1 3 2170 GAACCTGGGAGG C 3 C b b

CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGTGGA AGTGACGTT GAGACGGAGGGT
C
GAM7957 297 NDUFS2 1 4978 NP_004541.1 5 14 CCCCAGGAGAGG A G AC - 3 C c
c
CAGAGAGTGAGG TC CT CA CTCTGCCTC CC
GAAAGGGC AG GG GT GAGACGGAG GG
- A GA A
GAM7957 297 NFATC3 1 10867 NP_775187.1 3 314 CTACTCGGGAGG A CAAC T 3 C
c c
CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCACTT AG GAC GAG CGGAGGGC
- A--- T
GAM7957 297 NFKBIL2 1 15343 NP_038460.2 3 283 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG

TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 NFX1 1 12058 NP_667345.1 3 559 GAACTCGGGAGG C 3 C b b
CGGATGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAGCCAA AGTGACGTTG AGGCGGAGGGC
T
GAM7957 297 NHLH1 1 5156 NP_005589.1 3 553 GCCCTGGGGAGG T------- TG 3 C c
c
CAGGGGTTGGTG CAC CAACCTCTGCCTCCC
CCCTGACT GTG GTTGGGGACGGAGGG
TCAGTCCC --
GAM7957 297 NMNAT1 3 13691 NP_073624.2 3 770 GAACCTGGGAGG TC----- 3 C c
b
CAGAGGTTGCAG ACTGCAACCTCTGCCTCCCG
TAAGCCAA TGACGTTGGAGACGGAGGGT
AACCGAA
GAM7957 297 NMNAT1 3 15904 NP_073624.2 3 219 GACCCCAGGTGG TG T C 3 C c
b
TGGAGGTTGCAG TCACTGCAACCTC CC CC
TGAGCCAA AGTGACGTTGGAG GG GG
GT T A
GAM7957 297 NMNAT1 3 16965 NP_073624.2 3 469 GAACCCGGGAGG C C 3 C b
b
CACAGGTTCCAG TCACTG AACCT TGCCTCCCG
TGGGCCAA GGTGAC TTGGA ACGGAGGGC
C C
GAM7957 297 NMT2 1 8031 NP_004799.1 3 937 TGAACCTGAGAG T CC 3 C c c
GTGAGGTTGCAG TCACTGCAACCTC GCCTC
TGAGCCGA AGTGACGTTGGAG TGGAG
- AG
GAM7957 297 NODAL 1 12796 NP_060525.2 3 411 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 NONO 1 5857 NP_031389.2 3 208 GTATGCTGGAGG AC AA C 3 C c
c
CAGAGGGCAAGG TC TGC CCTCTGCCTCC
GAGGGGTG GG ACG GGAGACGGAGG
GA -- T
GAM7957 297 NPHP1 1 15224 NP_000263.1 3 1410 GAACCTGGGAGG TG 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 NPHS1 1 14789 NP_004637.1 3 498 GAACCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 NPTXR 1 5234 NP_055108.2 3 1645 GAACTGAGGAGG TG C 3 C c
c

```
                                TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                            GT    A
GAM7957  297   NPTXR  1  5234  NP_478058.1  3  1645  GAACTGAGGAGG         TG    C       3  C  c
c
                                TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                TGAGCCGA    AGTGACGTTGGAG  GGAGG
                                            GT    A
GAM7957  297   NPY2R  1  11027 NP_000901.1  3  240   AGTTGGTTGGGT  C--     -    C-      3  C  c  c
                                AGTAGGTTGCAT TCA   TGCAACCT CTGCCT  CCG
                                TATGAGTA    AGT   ACGTTGGA GATGGG  GGT
                                          ATT      T     TT
GAM7957  297   NT5C2  1  19192 NP_036361.1  3  1217  GAACCCAGGAGG            C       3  C  b  b
                                CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                TGAGCCAG    AGTGACGTTGGAGGCGGAGG
                                              A
GAM7957  297   NUP43  1  2851  NP_078923.2  3  1582  AAACCCGGGAGG                  3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGACCCAA    AGTGACGTTGGAGACGGAGGGC

GAM7957  297   NUP62  2  1492  NP_036478.2  3  602   CTACTCGGGAGG  A   AAC  T          3  C  c
c
                                CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATCACTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   NUP62  2  1492  NP_057637.2  3  602   CTACTCGGGAGG  A   AAC  T          3  C  c
c
                                CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATCACTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   NUP62  2  1492  NP_714940.1  3  602   CTACTCGGGAGG  A   AAC  T          3  C  c
c
                                CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATCACTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   NUP62  2  1492  NP_714941.1  3  602   CTACTCGGGAGG  A   AAC  T          3  C  c
c
                                CTGAGGCAGGAG TC CTGC   CTC GCCTCCCG
                                AATCACTT    AG GACG   GAG CGGAGGGC
                                          -   ---  T
GAM7957  297   NUP62  2  12360 NP_036478.2  3  635   ACTTGAACCCAG        CTCT    C       3  C  c
c
                                GAGGTGTTGCAG TCACTGCAAC   GCCTCC
                                TGAACCAA    AGTGACGTTG   TGGAGG
                                            ----     A
GAM7957  297   NUP62  2  12360 NP_057637.2  3  635   ACTTGAACCCAG        CTCT    C       3  C  c
c
                                GAGGTGTTGCAG TCACTGCAAC   GCCTCC
                                TGAACCAA    AGTGACGTTG   TGGAGG
                                            ----     A
```

GAM7957 297 NUP62 2 12360 NP_714940.1 3 635 ACTTGAACCCAG CTCT C 3 C c c
GAGGTGTTGCAG TCACTGCAAC GCCTCC
TGAACCAA AGTGACGTTG TGGAGG
---- A
GAM7957 297 NUP62 2 12360 NP_714941.1 3 635 ACTTGAACCCAG CTCT C 3 C c c
GAGGTGTTGCAG TCACTGCAAC GCCTCC
TGAACCAA AGTGACGTTG TGGAGG
---- A
GAM7957 297 NUPL1 1 4937 NP_054808.1 3 731 GAAGCCGGGAGG TG 3 C b b
TGGGGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGGG GGAGGGC
GT
GAM7957 297 ODAG 2 6298 NP_066990.2 3 387 GAACCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCAGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 ODAG 2 15089 NP_066990.2 3 1026 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 OGG1 1 15343 NP_002533.1 5 11 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 OGG1 1 15343 NP_058212.1 5 11 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 OGG1 1 15343 NP_058213.1 5 11 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 OPA3 2 1507 NP_079412.1 3 768 GAACCCATGAGG TG CC 3 C c c
TGGAGGTTGCGG TCACTGCAACCTC CCTC
TGAGCCAA AGTGGCGTTGGAG GGAG
GT TA
GAM7957 297 OPA3 2 15089 NP_079412.1 3 734 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 ORC6L 1 8790 NP_055136.1 3 477 GAACGTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 OS4 1 18554 NP_005721.2 3 850 ATGTCGGCGGCG A T - C 3 C c c
CTGGGGTTGCAG TC CTGCAACCTC GC CT CCG

```
                                  GGAAAAGA    AG GACGTTGGGG CG GG GGC
                                         G       T C  C
GAM7957  297   OTX3   1  12921 NP_671725.1  3  1666  CAATCTGGGAGG       C TG          3  C  c  c

                                  TGGAAGTTGCAG TCACTGCAAC TC  CCTCCCG
                                  TGAGCCGA    AGTGACGTTG AG  GGAGGGT
                                           A  GT
GAM7957  297   OTX3   1  12921 NP_757379.1  3  1666  CAATCTGGGAGG       C TG          3  C  c  c

                                  TGGAAGTTGCAG TCACTGCAAC TC  CCTCCCG
                                  TGAGCCGA    AGTGACGTTG AG  GGAGGGT
                                           A  GT
GAM7957  297   P2RX7  2  11148 NP_002553.2  3  1199  GAACCTGGGAGG   C      TG          3  C  c
b
                                  TGGAGGTTGCAT TCA TGCAACCTC  CCTCCCG
                                  TGAGCTGA    AGT ACGTTGGAG  GGAGGGT
                                         T       GT
GAM7957  297   P2RX7  2  11148 NP_803176.1  3  2440  GAACCTGGGAGG   C      TG          3  C  c
b
                                  TGGAGGTTGCAT TCA TGCAACCTC  CCTCCCG
                                  TGAGCTGA    AGT ACGTTGGAG  GGAGGGT
                                         T       GT
GAM7957  297   P2RX7  2  15480 NP_002553.2  3  230   GAACCCGGGAGG                  3  C  b  b
                                  CAGAGGTTGTAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCCA    AGTGATGTTGGAGACGGAGGGC

GAM7957  297   P2RX7  2  15480 NP_803176.1  3  1471  GAACCCGGGAGG                  3  C  b  b
                                  CAGAGGTTGTAG TCACTGCAACCTCTGCCTCCCG
                                  TGAGCCCA    AGTGATGTTGGAGACGGAGGGC

GAM7957  297   P2RY11 1  11772 NP_002557.2  3  495   GGGGTGGGTGGG   --  AA---      -     3  C  c
c
                                  CAGAGGACGGGG TCAC  TGC    CCTCTGCCT CCCG
                                  TAATGTGA    AGTG  ATG    GGAGACGGG GGGT
                                           TA  GGGCA       T
GAM7957  297   PABPN1 1  18682 NP_004634.1  5  215   ATGAGGGGAAGC       -  T C         3  C  c  c

                                  TGGGGTTTGCAG TCACTGCAA CCTC GC TCCC
                                  TGGTTTGA    GGTGACGTT GGGG CG AGGG
                                           T   T  A
GAM7957  297   PAF53  2  1595  NP_071935.1  3  291   CTACTCGGGAGG  A   AAC  T          3  C  c
c
                                  CTGAGGCAGGAC TC CTGC   CTC GCCTCCCG
                                  GATTACTT    AG GACG   GAG CGGAGGGC
                                           -   ---  T
GAM7957  297   PAF53  2  9204  NP_071935.1  3  323   GAGCTTGGGAAA         C CC-         3  C  c  c
                                  TCAAGGTTGCAG TCACTGCAACCT TG   TCCCG
                                  TGAGCTAT    AGTGACGTTGGA AC   AGGGT
                                           - TAA
GAM7957  297   PAFAH2 1  17420 NP_000428.2  3  1113  GAACCTAGGAGG            C      3  C  b  b
```

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGTCAA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 PAICS 1 16560 NP_006443.1 3 1380 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCTG AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 PCDH11X 2 4124 NP_116749.1 3 767 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATAGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PCDH11X 2 15343 NP_116749.1 3 801 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 PCDH11Y 2 13155 NP_116753.1 3 794 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PCDH11Y 2 13155 NP_116754.1 3 794 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PCDH11Y 2 15343 NP_116753.1 3 828 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 PCDH11Y 2 15343 NP_116754.1 3 828 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C

GAM7957 297 PCDHA9 1 3570 NP_054724.1 3 3085 GAGCCTGGGACA A TGCC 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC TCCCG
TGAACTGT AGTGACGT GGAG AGGGT
C TTAC

GAM7957 297 PCDHB9 1 5830 NP_061992.2 3 1455 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PDCD7 1 18337 NP_005698.1 3 1116 AAACCCAGGAGG C C 3 C b b
CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC

TGAGCCGA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 PDCL 1 9532 NP_005379.2 3 2022 GAGCCTGGGAGG A CT 3 C c c
TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAACCAT AGTGACGT GGA TGGAGGGT
C AC
GAM7957 297 PDE4A 1 8124 NP_006193.1 3 952 CGGCCACAGGCA -- C--- 3 C c c
AGGGGGTTGCAG TCACTGCAACCTCT GCCT CCG
TGGCCGCC GGTGACGTTGGGGG CGGA GGC
AA CACC
GAM7957 297 PDE4C 1 1567 NP_000914.1 3 1165 GAATTCAGGAGG TG C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 PDE7A 1 17399 NP_002595.1 3 1629 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 PECR 1 4310 NP_060911.2 3 594 GAACCCAGGAAG C C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGC TCC
TGAGCTGA AGTGACGTTGGAGACG AGG
A A
GAM7957 297 PHAX 2 4459 NP_115553.1 3 666 CTACTCGGGAGG A AAC T 3 C c
c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACCT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 PHAX 2 15984 NP_115553.1 3 1620 GAACCCAGGAGG TG C 3 C c
c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 PHKB 2 12490 NP_000284.1 3 763 CACTTCGGGAGG GCAA T 3 C c
c

CTGAGGCAGGTG TCACT CCTC GCCTCCCG
GATCACTT GGTGG GGAG CGGAGGGC
AC-- T
GAM7957 297 PHKB 2 14137 NP_000284.1 3 931 TGAACCAGGAGA C C 3 C c c
CGGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCTGA AGTGACGTTGGAGGC GAGG
A A
GAM7957 297 PIGO 1 5114 NP_116023.2 3 310 CACTTTGGGAGG A GCA 3 C c c
CAGAGGTGGGAG TC CT ACCTCTGCCTCCCG
GATTGCTT AG GA TGGAGACGGAGGGT
- GGG
GAM7957 297 PIGO 1 5114 NP_690577.1 3 310 CACTTTGGGAGG A GCA 3 C c c
CAGAGGTGGGAG TC CT ACCTCTGCCTCCCG
GATTGCTT AG GA TGGAGACGGAGGGT
- GGG

GAM7957 297 PIP5K2B 1 3903 NP_619632.1 3 27 TGACCCAGGAGG C 3 C b b
CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGACCCTC AGTGGCGTTGGAGGCGGAGG
A
GAM7957 297 PIWIL2 1 9765 NP_060538.2 3 514 GAACCCGGGAGG TG 3 C b b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 PLA2G2D 1 15631 NP_036532.1 3 2077 GGACCTGGGAGG C 3 C b
b
CAGAGGTTTCAG TCACTG AACCTCTGCCTCCCG
TGAGCCCA AGTGAC TTGGAGACGGAGGGT
T
GAM7957 297 PLEKHB2 2 8068 NP_060428.1 3 938 CTACTCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATAGTGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 PLEKHB2 2 15340 NP_060428.1 3 972 GAACCCAGGAGG C C 3 C c
c
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCAA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 PLK 1 1508 NP_005021.2 5 54 GCTTCGGGAGCA AC- - C 3 C c c
TGAGTGCTGCAG TCACTGCA CTC TGC TCCCG
TGACTGCA AGTGACGT GAG ACG AGGGC
CGT T -
GAM7957 297 PLPL 1 699 NP_064566.1 3 602 TGGAGGGGGAGG TC--- T - - 3 C c c
CAGGAGGATTGC AC GCAA CCTC TGCCTCCC
TGTCAGCC TG CGTT GGAG ACGGAGGG
CCGAC T A G
GAM7957 297 PNPLA1 2 1493 NP_775947.1 3 576 CTACTCGGGAGG A GCAA T 3 C c
c
CTGAGGCAAGAG TC CT CCTC GCCTCCCG
AATCGCTT AG GA GGAG CGGAGGGC
A AC-- T
GAM7957 297 PNPLA1 2 18749 NP_775947.1 3 607 GAACCCAGGAGG T----- C 3 C c
c
CAGAGGTTGCAG CACTGCAACCTCTGCCTCC
TGCACCAA GTGACGTTGGAGACGGAGG
AACCAC A
GAM7957 297 PODXL 1 19168 NP_005388.1 3 3750 TGATGGGGGAGG AC AAC - 3 C c
c
CAAGAGAGGGCA TC TGC CTCT GCCTCCC
AAGAGTAA AG ACG GAGA CGGAGGG
AA GGA A
GAM7957 297 POFUT1 1 17423 NP_056167.1 3 3686 GAACCTGGGAGG TG 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGT

```
                                                GT
GAM7957  297   POLA2  1  3957  NP_002680.2  3  140   CCAGCCAGGGAG      ACCT    -       3  C  c
c
                                GGGCAGCTGCAG TCACTGCA   CTGCCTC CC
                                TGACCAGG    AGTGACGT   GACGGGG GG
                                          C---      A
GAM7957  297   POLH   3  6653  NP_006493.1  3  654   TAACCTTGGAGG   C          C       3  C  c  c
                                CGGAGGTTGCAT TCA TGCAACCTCTGCCTCC
                                TGAGCTGA    AGT ACGTTGGAGGCGGAGG
                                          T           T
GAM7957  297   POLH   3  8681  NP_006493.1  3  911   CTACTCGGGAGG  A   AAC  CT          3  C  c
c
                                CTAAGGCAGGAG TC CTGC   CT  GCCTCCCG
                                AATCACTT    AG GACG   GA  CGGAGGGC
                                          -   ---  AT
GAM7957  297   POLH   3  10896 NP_006493.1  3  945   GAACCCAGGAGG    G         C       3  C  c  c
                                CAGAGGTTGGGG TCACT CAACCTCTGCCTCC
                                TGAGCTGA    AGTGG GTTGGAGACGGAGG
                                          G          A
GAM7957  297   POLR1B 1   732   NP_061887.1  3  3286  GAACCCAAGAGG      A   T   CC       3  C  c
c
                                TCGAGGCTGCAG TCACTGCA CCTC GCCTC
                                TGAGCCAA    AGTGACGT GGAG TGGAG
                                          C   C    AA
GAM7957  297   PPARD  2   1622  NP_803184.1  3  434   GAACCCGAGAGG        TG   C       3  C  c  c

                                TGGAGGTTGCAG TCACTGCAACCTC  CCTC CG
                                TGAGCCAA    AGTGACGTTGGAG  GGAG GC
                                          GT   A
GAM7957  297   PPARD  2   8364  NP_006229.1  3  852   TCTCCGGGGAGG TCA---   --          3  C  c
c
                                CAGGGGTCCTGC     CTGCA  ACCTCTGCCTCCC
                                AGGTCCTG         GACGT  TGGGGACGGAGGG
                                        GTCCTG    CC
GAM7957  297   PPM1F  1   2607  NP_055449.1  3  1052  TTGTTAGGGAGG   TG  CC -         3  C  c
c
                                CATGATTTTGGT TCAC  CAA  TC TGCCTCCC
                                GAGATCTT    AGTG  GTT  AG ACGGAGGG
                                          --  TT  T
GAM7957  297   PPP1R12 1   8779  NP_002472.1  3  2272  GAACCCGGGAGG      C           3  C  b  b

          B                      CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                TGAGCCTT    AGTGACGTT GAGGCGGAGGGC
                                          C
GAM7957  297   PPP1R12 1   8779  NP_115288.1  3  2405  GAACCCGGGAGG      C           3  C  b  b

          B                      CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                TGAGCCTT    AGTGACGTT GAGGCGGAGGGC
                                          C
GAM7957  297   PPP1R3B 2   1492  NP_078883.1  3  1771  CTACTCGGGAGG  A   AAC  T          3  C  c
 c
```

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PPP1R3B 2 15984 NP_078883.1 3 1805 GAACCCAGGAGG TG C 3 C c
c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 PPP2R1B 1 9028 NP_002707.2 3 1308 GAACCTGGGAGG C 3 C b b

TAGAGGTTGCAC TCA TGCAACCTCTGCCTCCCG
TGAGCCGA AGT ACGTTGGAGATGGAGGGT
C

GAM7957 297 PQBP1 1 15439 NP_005701.1 5 161 GTTTACGGGAGG A C TC- 3 C c
c

CGCTTGGTTACG TC CTG AACC TGCCTCCCG
GGATCCAG AG GGC TTGG GCGGAGGGC
- A TTC

GAM7957 297 PRDM14 1 13304 NP_078780.1 3 235 GAGCACAGGAGA T C C 3 C c
c

CGGAGGTTGCTG TCAC GCAACCTCTG CTCC
TGAGCTGA AGTG CGTTGGAGGC GAGG
T A A

GAM7957 297 PRIC285 1 13230 NP_208384.1 3 637 GACTCCAGGAGG A C C 3 C c
c

CGCAGGCTGCAG TCACTGCA CCT TGCCTCC
TGAGCTCT AGTGACGT GGA GCGGAGG
C C A

GAM7957 297 PRKX 2 5830 NP_005035.1 3 2475 CTACTCGGGAGG A AAC T 3 C c
b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PRKX 2 13758 NP_005035.1 3 2509 GAACCCGGGAGG A 3 C b b

CAGAGGCTGCAG TCACTGCA CCTCTGCCTCCCG
TGAGCCGA AGTGACGT GGAGACGGAGGGC
C

GAM7957 297 PRKY 2 1053 NP_002751.1 3 4050 TTAGTCGGGAGG A AAC T 3 C c
c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATATGGA AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 PRKY 2 5494 NP_002751.1 3 1156 GAGCTCAAGAGG A T CC 3 C c c

TTGAGGCTGCAG TCACTGCA CCTC GCCTC
TGAGCCCT AGTGACGT GGAG TGGAG
C T AA

GAM7957 297 PRO0255 2 5830 NP_054843.1 3 613 CTACTCGGGAGG A AAC T 3 C c
b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG

AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 PRO0255 2 18286 NP_054843.1 3 647 GAGCCTGGGAGA GC 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTCT CTCCCG
TGAGCTGA AGTGACGTTGGAGG GAGGGT
TA
GAM7957 297 PRO0478 5 1171 NP_054848.1 5 413 GAGCCCAGGAAG C C C 3 C c
b
CGGAGGTTGCAA TCA TGCAACCTCTGC TCC
TGAGCCGA AGT ACGTTGGAGGCG AGG
A A A
GAM7957 297 PRO0478 5 3871 NP_054848.1 5 379 GTACTCGGGAGG A AACC T 3 C
c b
CTGAAGCAGGAG TC CTGC TC GCCTCCCG
AATCGCTT AG GACG AG CGGAGGGC
- A--- T
GAM7957 297 PRO0478 5 5635 NP_054848.1 3 108 GAACCAGGGAGG TCA----- 3 C c
b
CGGAGGTTGCAG CTGCAACCTCTGCCTCCC
CAAGCCAA GACGTTGGAGGCGGAGGG
AACCGAAC
GAM7957 297 PRO0478 5 12098 NP_054848.1 3 500 CCACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGATGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 PRO0478 5 12922 NP_054848.1 3 534 GAACCCGGGAGG C C 3 C b
b
CATAGCTTGCAG TCACTGCAA CT TGCCTCCCG
TGAGCCGA AGTGACGTT GA ACGGAGGGC
C T
GAM7957 297 PRO0483 2 4309 NP_054849.1 5 261 GAACCCGGGAGG C TG 3 C b
b
TGGAGATTGCAG TCACTGCAA CTC CCTCCCG
TGAGCTGA AGTGACGTT GAG GGAGGGC
A GT
GAM7957 297 PRO0483 2 8189 NP_054849.1 5 815 GAACCCGGGAGG A TG 3 C b
b
TGGAGGCTGCAG TCACTGCA CCTC CCTCCCG
TGAGCCGA AGTGACGT GGAG GGAGGGC
C GT
GAM7957 297 PRO0618 2 5830 NP_054852.1 3 1243 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 PRO0618 2 12796 NP_054852.1 3 1277 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG

TGAGCCAA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 PRO1048 3 7048 NP_060967.1 5 4 GAACCCAGGAGG C C 3 C b b
CAGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGACGGAGG
C A
GAM7957 297 PRO1048 3 11467 NP_060967.1 3 1438 GAACCCGGGAGG TG C 3 C c
b
CAGAGCTTGTGG TCAC CAA CTCTGCCTCCCG
TGAGCCGA AGTG GTT GAGACGGAGGGC
GT C
GAM7957 297 PRO1048 3 12433 NP_060967.1 5 300 GGGCCCGGGAGG CT 3 C b
b
TCAAGGTTGCAG TCACTGCAACCT GCCTCCCG
TGAGCTGT AGTGACGTTGGA TGGAGGGC
AC
GAM7957 297 PRO1496 1 4729 NP_061073.1 3 990 AGCCCTGGGAGG A CT 3 C c
c
TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAGCTGC AGTGACGT GGA TGGAGGGT
C AC
GAM7957 297 PRO2015 1 18687 NP_060982.1 3 750 GAACCCGGGAGG 3 C b b
CGGAGGTTGTAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGATGTTGGAGGCGGAGGGC

GAM7957 297 PRO2198 1 8909 NP_061091.1 5 240 CAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTTA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 PRO2730 1 17419 NP_079498.1 3 1146 GAACCCAGGAGG C 3 C b
b
CGGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGTTGA AGTGGCGTTGGAGGCGGAGG
A
GAM7957 297 PRO2964 2 13155 NP_061017.1 3 490 CTACTCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 PRO2964 2 15343 NP_061017.1 3 524 GAACCCGGGAGG C 3 C b b

CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 PRPF4 1 3935 NP_004688.2 3 501 AAGCCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 PRX 2 6121 NP_066007.1 3 3556 AGGAAGGGAGGG T AA - 3 C c c
CAGAGGGGGCTG TCAC GC CCTCTGCC TCCC

TGGCCGTC GGTG CG GGAGACGG AGGG
T GG G
GAM7957 297 PRX 2 14564 NP_066007.1 3 3812 CTCTGCCTGGAG - CT C C 3 C c c

CCCAGGTTGCAG TCAC TGCAACCT GC TCC
GTGGTGAG GGTG ACGTTGGA CG AGG
G CC - T
GAM7957 297 PSCD3 1 1543 NP_004218.1 3 107 GTGGCAGGGAGG T--- ACCT-- 3 C c
c

CAGTCGCCCTGC CACTGCA CTGCCTCCC
GGTGCAAG GTGGCGT GACGGAGGG
GAAC CCCGCT
GAM7957 297 PSK 1 2797 NP_057235.1 5 27 GAAGAGGAGAGG A AA -- - 3 C c c
CAGAGAGGGCGC TC CTGC CCTCT GCCTC CC
GGGGACCG AG GGCG GGAGA CGGAG GG
G CG GA A
GAM7957 297 PSMD5 1 2976 NP_005038.1 3 565 GAGCCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 PTAFR 1 18066 NP_000943.1 3 589 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAACCTA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 PTGIS 1 7315 NP_000952.1 3 1472 GAACCCAGGAGG TG C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAACTGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 PTGS1 1 12185 NP_000953.2 3 863 GGCTGGGCGTGC -- - CT- 3 C c c

TAGAGGTTGCAG TCA CTGCAACCTCT GC CCCG
CATGAGAC AGT GACGTTGGAGA CG GGGT
AC T TGC
GAM7957 297 PTGS1 1 12185 NP_542158.1 3 863 GGCTGGGCGTGC -- - CT- 3 C c c

TAGAGGTTGCAG TCA CTGCAACCTCT GC CCCG
CATGAGAC AGT GACGTTGGAGA CG GGGT
AC T TGC
GAM7957 297 PTK6 1 15675 NP_005966.1 3 1059 GAACCCGGGAGG C TG 3 C b
b

TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCGA AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 PTRF 1 11379 NP_036364.1 3 188 CCGATGGGGAGG AACCT 3 C c
c

CAGCCCCCGCAG TCACTGC CTGCCTCCC
TGGACAGC GGTGACG GACGGAGGG
CCCCC
GAM7957 297 QRSL1 1 17699 NP_060762.2 3 257 GAACCCTGGAGG TG C 3 C c c

TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCGA AGTGACGTTGGAG GGAGG
GT T

GAM7957 297 RAB3D 1 19319 NP_004274.1 3 246 CTGCATGGCAGG A CAA C 3 C c c

CAGAGGCCCAGG TC CTG CCTCTGCCT CCG
GACACTGA AG GAC GGAGACGGA GGT
G CC- C

GAM7957 297 RAB4B 2 15089 NP_057238.2 5 590 CTACTCGGGAGG A AAC T 3 C c b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 RAB4B 2 15221 NP_057238.2 5 624 GAACCTGGGAGG TG 3 C b b
TGGAGGTTGCGG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGGCGTTGGAG GGAGGGT
GT

GAM7957 297 RAB5B 1 14174 NP_002859.1 3 648 AGAATGGGGAGG A CAAC C 3 C c c

CAAGATCTCAGG TC CTG CT TGCCTCCC
GACACCAA AG GAC GA ACGGAGGG
G TCTA -

GAM7957 297 RAB7L1 2 2925 NP_003920.1 3 842 GAGACTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAACCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 RAB7L1 2 16970 NP_003920.1 3 1737 GAACCTGGGAGT C 3 C b b
TAGAGGTTGCAG TCACTGCAACCTCTG CTCCCG
TGAGCTGA AGTGACGTTGGAGAT GAGGGT
T

GAM7957 297 RAB9B 1 20013 NP_057454.1 5 58 AGGACGAGGAGG AA - - 3 C b b
CAGCAGGAGCAG TCACTGC CCT CTGCCTCC CG
TGACGGTG AGTGACG GGA GACGGAGG GC
A- C A

GAM7957 297 RAD1 2 19050 NP_002844.1 3 521 GAACCCGGGAGG TG 3 C b b
CGGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCTGA AGTG GTTGGAGGCGGAGGGC
GT

GAM7957 297 RAD1 2 19050 NP_579816.1 3 521 GAACCCGGGAGG TG 3 C b b
CGGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCTGA AGTG GTTGGAGGCGGAGGGC
GT

GAM7957 297 RAD1 2 19050 NP_596868.1 3 521 GAACCCGGGAGG TG 3 C b b
CGGAGGTTGTGG TCAC CAACCTCTGCCTCCCG
TGAGCTGA AGTG GTTGGAGGCGGAGGGC
GT

GAM7957 297 RAD1 2 20138 NP_002844.1 3 489 CTACTCGGGAGG A AAC T 3 C c b

CTGAGGCAGGAA TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC

```
                                        -   ---   T
GAM7957  297   RAD1   2   20138 NP_579816.1  3  489   CTACTCGGGAGG  A   AAC  T          3  C  c
b
                                CTGAGGCAGGAA TC CTGC   CTC GCCTCCCG
                                AATTGCTT    AG GACG   GAG CGGAGGGC
                                        -   ---   T
GAM7957  297   RAD1   2   20138 NP_596868.1  3  489   CTACTCGGGAGG  A   AAC  T          3  C  c
b
                                CTGAGGCAGGAA TC CTGC   CTC GCCTCCCG
                                AATTGCTT    AG GACG   GAG CGGAGGGC
                                        -   ---   T
GAM7957  297   RAD51  1   3609  NP_002866.2  3  851   AAGCCTGGAAGG       C  TG  C       3  C  c
c
                                TGGAAGTTGCAG TCACTGCAAC TC  CCT CCG
                                TGAGTCGA    AGTGACGTTG AG  GGA GGT
                                          A  GT   A
GAM7957  297   RAD51  1   3609  NP_597994.1  3  851   AAGCCTGGAAGG       C  TG  C       3  C  c
c
                                TGGAAGTTGCAG TCACTGCAAC TC  CCT CCG
                                TGAGTCGA    AGTGACGTTG AG  GGA GGT
                                          A  GT   A
GAM7957  297   RBBP5  1   6786  NP_005048.1  3  1517  GAACGTGGGAGG                  3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGTGGA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   RBL1   1   19648 NP_002886.1  3  433   GGGAGGCTGAGG   CT   -----   T       3  C  c  c

                                CAGAATTGCTTG TCA  GCAA    CCTC GCCTCCC
                                AACCCAGG    AGT  CGTT    GGAG CGGAGGG
                                  T-   AAGAC   T
GAM7957  297   RBM10  1   14218 NP_005667.2  5  199   GGTGGCGGCGGG  A --  --      C       3  C  c
c
                                CAGAGGTGATGT TC CT  GCA  ACCTCTGCCT CCG
                                CTGGGAGC    AG GG  TGT  TGGAGACGGG GGC
                                        - TC   AG        C
GAM7957  297   RBM10  1   14218 NP_690595.1  5  199   GGTGGCGGCGGG  A --  --      C       3  C  c
c
                                CAGAGGTGATGT TC CT  GCA  ACCTCTGCCT CCG
                                CTGGGAGC    AG GG  TGT  TGGAGACGGG GGC
                                        - TC   AG        C
GAM7957  297   RBM3   1   14780 NP_006734.1  3  587   GAACCCGGGAGG                  3  C  b  b
                                CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCTAA    AGTGACGTTGGAGGCGGAGGGC

GAM7957  297   RCN1   1   904   NP_002892.1  3  364   GGTTGAGGGAGG    G  ACCT-          3  C  c
c
                                CAGTAATATGAA TCACT CA    CTGCCTCCC
                                GTGACTGC    AGTGA GT    GACGGAGGG
                                  A  ATAAT
GAM7957  297   RDC1   1   15888 NP_064707.1  3  429   TTGTTTGGGAGG   CT   AC  C          3  C  c
c
```

```
                                CATAGTGCTGAC TCA  GCA  CT TGCCTCCCG
                                ATATATTC    AGT  CGT  GA ACGGAGGGT
                                         --  -- T
GAM7957  297   RDC1   1  15888 XP_051522.2  3  429   TTGTTTGGGAGG   CT  AC  C          3  C  c
c
                                CATAGTGCTGAC TCA  GCA  CT TGCCTCCCG
                                ATATATTC    AGT  CGT  GA ACGGAGGGT
                                         --  -- T
GAM7957  297   RERE   1  9174  NP_036234.2  3  1929  TTCACAGGGAGG   C - AC  C          3  C  c
c
                                CAAAGCTGACAT TCA TG CA  CT TGCCTCCC
                                GAACCTTT    AGT AC GT  GA ACGGAGGG
                                         - A  C-  A
GAM7957  297   RET    1  17434 NP_065681.1  3  535   CCATCAGGGGTA  A       T  CT        3  C  c  c
                                GCGAGGTTGCAG TC CTGCAACCTC GC  CCC
                                GAGCTGGC    AG GACGTTGGAG CG  GGG
                                         -       - AT
GAM7957  297   REV3L  1  6680  NP_002903.1  5  432   AGTGAAGGGAGG  A   AA  T          3  C  c  c

                                CAGTGGCGGCGG TC CTGC  CC CTGCCTCCC
                                CGGCGAAC    GG GGCG  GG GACGGAGGG
                                         C   GC  T
GAM7957  297   RFC2   2  9763  NP_002905.2  3  356   GAACCCAGGAGG        TG   C       3  C  c  c
                                TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                TGAGCCAA    AGTGACGTTGGAG  GGAGG
                                            GT    A
GAM7957  297   RFC2   2  9763  NP_852136.1  3  356   GAACCCAGGAGG        TG   C       3  C  c  c
                                TGGAGGTTGCAG TCACTGCAACCTC  CCTCC
                                TGAGCCAA    AGTGACGTTGGAG  GGAGG
                                            GT    A
GAM7957  297   RFC2   2  9778  NP_002905.2  3  322   CTACTCGGGAGG  A   A  CTCT         3  C  c
c
                                CTGTGGCAGGAG TC CTGC AC   GCCTCCCG
                                AATCGCTT    AG GACG TG   CGGAGGGC
                                         -   G  T---
GAM7957  297   RFC2   2  9778  NP_852136.1  3  322   CTACTCGGGAGG  A   A  CTCT         3  C  c
c
                                CTGTGGCAGGAG TC CTGC AC   GCCTCCCG
                                AATCGCTT    AG GACG TG   CGGAGGGC
                                         -   G  T---
GAM7957  297   RGSL2  1  15343 NP_115643.1  3  305   GAACCCGGGAGG       C           3  C  b  b
                                CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
                                TGAGCCGA    AGTGACGTT GAGGCGGAGGGC
                                            C
GAM7957  297   RHO6   1  1080  NP_055285.1  5  6     GTTGGAGGGAGG   CT  AAC---        3  C  c  c

                                CAGGGAATCTGG TCA  GC     CTCTGCCTCCC
                                CTTGATTG    AGT  CG     GGGACGGAGGG
                                         T-  GTCTAA
GAM7957  297   RHOBTB3 1  18151 NP_055714.1  3  1875  GAACCTGGGAGG       C  TG         3  C  c
 c
```

TGGAAGTTGCAG TCACTGCAAC TC CCTCCCG
TGAGCCGA AGTGACGTTG AG GGAGGGT
A GT

GAM7957 297 RIMS1 1 10435 NP_055804.1 3 3171 GAACCCAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 RNF125 1 11101 NP_060301.1 3 764 GAGCCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 ROCK2 1 9205 NP_004841.1 3 1735 GAACCCAGGAGA T C C 3 C c
c
CGGTGGTTGCAG TCACTGCAACC CTG CTCC
TGAGCGAA AGTGACGTTGG GGC GAGG
T A A

GAM7957 297 RoXaN 1 9947 NP_060060.3 3 2328 GAGAGTGGGAGG A- G -- - 3 C c c
CAGAGTGTGATG TC CT CA AC CTCTGCCTCCCG
GGGAGGAG AG GG GT TG GAGACGGAGGGT
GA G AG T

GAM7957 297 RPN1 2 9619 NP_002941.1 5 72 GAACCCGGGAGG TCA----- 3 C c c
CAGAGGTTGCAG CTGCAACCTCTGCCTCCCG
CCGGCTGA GACGTTGGAGACGGAGGGC
AGTCGGCC

GAM7957 297 RPN1 2 15089 NP_002941.1 5 38 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 RPS6KC1 1 2652 NP_036556.2 5 126 TGGCGGCGGCGG A AA - - 3 C c
c
CAGAGGCGGCGG TC CTGC CCTCTGCC TC CCG
GAGGATGA AG GGCG GGAGACGG GG GGC
- GC C C

GAM7957 297 RRP4 1 9420 NP_055100.2 3 704 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 SBP1 1 15055 NP_835222.1 5 223 GAACCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCTCA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 SC65 2 10571 NP_006446.1 3 610 GAACCCAGGAGG C C 3 C c b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A

GAM7957 297 SC65 2 15304 NP_006446.1 3 335 GAACCTGGGAGG C 3 C b b
CAAAGGTTGCGG TCACTGCAACCT TGCCTCCCG
TGAACTGA AGTGGCGTTGGA ACGGAGGGT

A

GAM7957 297 SCAND2 1 12555 NP_378666.1 3 1198 CTACTCGGGAGG A AA CT 3 C c c

CTGGGGCAGGAG TC CTGC CCT GCCTCCCG
AATCACTT AG GACG GGG CGGAGGGC
- -- T-

GAM7957 297 SCAP2 1 16383 NP_003921.2 3 930 GAACAAGGTAGG C 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCT CC
TGAGCCAA AGTGACGTTGGAGACGGA GG
T

GAM7957 297 SCIN 1 17536 NP_149119.1 3 337 GAACCCAGGAGG T C 3 C b b

CTGAGGTTGCAG TCACTGCAACCTC GCCTCC
TGAGCCAG AGTGACGTTGGAG CGGAGG
T A

GAM7957 297 SCN11A 1 15992 NP_054858.1 3 509 AAACCTGGGAGA C 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTG CTCCCG
TGAGCCAA AGTGACGTTGGAGGC GAGGGT
A

GAM7957 297 SCN2B 2 1782 NP_004579.1 3 1329 GAGCCCGGGAAG C 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAACTGA AGTGACGTTGGAGACG AGGGC
A

GAM7957 297 SCN2B 2 3358 NP_004579.1 3 278 GTCCTGGGGAGG TGCAA - 3 C c b

CAGGAGGCACAT TCAC CCTC TGCCTCCC
GTGAGGGT AGTG GGAG ACGGAGGG
TACAC G

GAM7957 297 SCR59 1 3264 NP_075559.1 3 918 GAACCCAGGAGG A C 3 C c c

CGGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCTGA AGTGACGT GGAGGCGGAGG
C A

GAM7957 297 SEC24C 1 7132 NP_004913.1 3 743 TGGGGAGAGAGG ACT AA ---- 3 C c c

CAGAGGCAGCTG TC GC CCTCTGCC TCCC
GAGCGCCG AG CG GGAGACGG AGGG
GT- AC AGAG

GAM7957 297 SEC61A1 1 7817 NP_037468.1 3 779 AGCTAGGTGGAC CC- - T C 3 C c c

AGACCCTTGCAG TCACTGCAA TCTG CC CC
TGATGTCC AGTGACGTT AGAC GG GG
CCC A T A

GAM7957 297 SEMA3E 1 8019 NP_036563.1 3 3621 GAACCCGGGAAG C C 3 C b b

CGGAGCTTGCAG TCACTGCAA CTCTGC TCCCG
TGAGCCGA AGTGACGTT GAGGCG AGGGC
C A

GAM7957 297 SEMA5A 1 5826 NP_003957.1 3 4133 TGAGCCAGGAGG T C 3 C c c

TTGAGGTTGCAG TCACTGCAACCTC GCCTCC
TGAGCTGA AGTGACGTTGGAG TGGAGG

T A

GAM7957 297 SEPT1 1 19489 NP_443070.1 5 150 AGTGGGGAGAGA A - C-- 3 C c c
CGGCAGGTGCAG TCACTGCA CCT CTG CTCCC
TGATGGCT AGTGACGT GGA GGC GAGGG
- C AGA

GAM7957 297 SGKL 2 9421 NP_037389.4 3 820 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 SGKL 2 9421 NP_733827.2 3 820 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 SGKL 2 15249 NP_037389.4 5 79 GGGGTGGGTGCC C - --- - 3 C c b
CGAAGGTTGCAT TCA TGCAACCT C TGCCT CCC
GATGGAAT AGT ACGTTGGA G GTGGG GGG
- A CCC T

GAM7957 297 SGKL 2 15249 NP_733827.2 5 79 GGGGTGGGTGCC C - --- - 3 C c b
CGAAGGTTGCAT TCA TGCAACCT C TGCCT CCC
GATGGAAT AGT ACGTTGGA G GTGGG GGG
- A CCC T

GAM7957 297 SH3YL1 1 1043 NP_056492.1 5 330 TGCCAGAGGAGG - - C 3 C c c
CAGCGGGATTGT TCACTGCAA CCT CTGCCTCC
AGTGGCGC GGTGATGTT GGG GACGGAGG
A C A

GAM7957 297 SHCBP1 1 4225 NP_079021.2 3 916 GAGCCCAGGAGG A T C 3 C c
c
TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGGTGT AGTGACGT GGAG TGGAGG
C T A

GAM7957 297 SHFM3 1 15889 NP_071322.1 5 409 AGCAGAGGGAGG A G ACC- 3 C c
c
CAGAAGCGTGGA TC CT CA TCTGCCTCCC
GGAAGGGG AG GA GT AGACGGAGGG
- G GCGA

GAM7957 297 SHOC2 1 10301 NP_031399.1 3 796 GTTTGGGGGAAG C--- G C 3 C c
c
AGAAACTTGCAG TCACTGCAA CTCT CCTCC
TGAAAAGG AGTGACGTT GAGA GGGGG
CAAA A T

GAM7957 297 SIAT8A 1 4881 NP_003025.1 5 28 CAGCGCGGGAGG A AA --- 3 C c c
CGGCGAAGGGCG TC CTGC CCT CTGCCTCCCG
CAGGAGCA AG GACG GGA GGCGGAGGGC
- CG AGC

GAM7957 297 SIGLEC1 1 9765 NP_443116.1 3 909 GAACCCGGGAGG TG 3 C b b
1 TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCGA AGTGACGTTGGAG GGAGGGC
GT

GAM7957 297 SIM2 1 15218 NP_033664.1 3 989 GAACCCGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCTAA AGTGACGTTGGAG GGAGGGC
GT
GAM7957 297 SLC14A1 1 4653 NP_056949.1 3 1337 GAGCCCAGGAGG A G C 3 C c c

AGGAGGCTGCAG TCACTGCA CCTCT CCTCC
TGAGCTAA AGTGACGT GGAGG GGAGG
C A A
GAM7957 297 SLC14A2 1 9991 NP_009094.2 3 521 GAACCCGGGAGG C TG 3 C b b

TGGAGCTTGCAG TCACTGCAA CTC CCTCCCG
TGAGCCAA AGTGACGTT GAG GGAGGGC
C GT
GAM7957 297 SLC16A2 1 8449 NP_006508.1 5 26 AGCTGGGGGAGG ACT AA T 3 C c c

CAGTGGCGGCTG TC GC CC CTGCCTCCC
GAGTAGGT AG CG GG GACGGAGGG
GT- GC T
GAM7957 297 SLC17A5 1 7865 NP_036566.1 3 988 GAACCTGGGAGA C GC 3 C c c

TGGAAGTTGCAG TCACTGCAAC TCT CTCCCG
TGAACCAA AGTGACGTTG AGG GAGGGT
A TA
GAM7957 297 SLC21A9 1 19542 NP_009187.1 3 567 GCCCCCTGGAGG C AACC C 3 C c c

CAGAGCACTGAG TCA TGC TCTGCCTCC
CTGGACCC AGT ACG AGACGGAGG
C ---- T
GAM7957 297 SLC22A2 1 2052 NP_694861.1 3 690 CATGTGTGGGGG A TG -- C 3 C c c

CAGAGGTTATGT TC C CA ACCTCTGCCTCC
GGGAAATC AG G GT TGGAGACGGGGG
- GT AT T
GAM7957 297 SLC23A3 1 7727 NP_653313.1 3 1457 GAGCCTGGGAGG T 3 C b b

CAGAGGTTGCTG TCAC GCAACCTCTGCCTCCCG
TGAGCCGA AGTG CGTTGGAGACGGAGGGT
T
GAM7957 297 SLC25A1 1 12480 NP_055067.1 3 570 GAACCCGGGAGG C 3 C b b

5 CAGAAGTTGCAG TCACTGCAAC TCTGCCTCCCG
TGAACTGA AGTGACGTTG AGACGGAGGGC
A
GAM7957 297 SLC26A4 1 15343 NP_000432.1 3 1867 GAACCCGGGAGG C 3 C b b

CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 SLC28A2 1 16463 NP_004203.1 3 369 GAATCCGGGAGG A C 3 C b b

CGGAGCTTGCAG TC CTGCAA CTCTGCCTCCCG
CGAGCCGG AG GACGTT GAGGCGGAGGGC
C C
GAM7957 297 SLC2A3 1 15860 NP_008862.1 3 1920 GAACCCGGGACG C 3 C b b

CAGGGGTTGCAG TCACTGCAACCTCTGC TCCCG
TGAGCGGA AGTGACGTTGGGGACG AGGGC
C
GAM7957 297 SLC31A1 1 18685 NP_001850.1 3 740 GAACCTAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 SLC35E1 1 6652 NP_079157.2 3 1274 GAACCTGGGAGG TG C 3 C c
c
CAGAAGTTGTGG TCAC CAAC TCTGCCTCCCG
TGAGCCGA AGTG GTTG AGACGGAGGGT
GT A
GAM7957 297 SLC35E2 1 6363 XP_049733.6 3 2206 GAACCCCGGAGA GC C 3 C c
c
TGGAGGTTGCAG TCACTGCAACCTCT CTCC
TGAGCCAA AGTGACGTTGGAGG GAGG
TA C
GAM7957 297 SLC35E3 2 4801 NP_061126.1 3 316 GAACCCGGGAGG C G 3 C b
b
AGGAGGTTGCAC TCA TGCAACCTCT CCTCCCG
TGAGCCGA AGT ACGTTGGAGG GGAGGGC
C A
GAM7957 297 SLC35E3 2 16325 NP_061126.1 3 642 TGAGCCTGGGAG C CT - 3 C c
b
CGCAGGTTGCAA TCA TGCAACCT GC CTCCCG
TGAGCCAA AGT ACGTTGGA CG GAGGGT
A -- C
GAM7957 297 SLC6A6 2 10881 NP_003034.1 3 268 TCCGTGGAGAGG C-- C C - 3 C c
c
CAGAGCTTTCAT TCA TG AA CTCTGCCTC CCG
ACTGAATT AGT AC TT GAGACGGAG GGT
CAT T C A
GAM7957 297 SLC6A6 2 11013 NP_003034.1 3 1541 CCTTATGTGGAG CT- C C 3 C c
c
CAGAGGTTGTCT TCA GCAACCTCTGC TCC
CTGAACCA AGT TGTTGGAGACG AGG
CTC - T
GAM7957 297 SLC7A11 1 19054 NP_055146.1 3 1569 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 SMA3 1 18653 NP_006771.1 3 546 GAACCTGGGAGG AC 3 C b b
CAGAGTCTGCAG TCACTGCA CTCTGCCTCCCG
TGAGCCGA AGTGACGT GAGACGGAGGGT
CT

GAM7957 297 SMAP-5 1 10571 NP_110426.3 3 692 GAACCCAGGAGG C C 3 C c c

CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A

GAM7957 297 SMC1L1 1 938 NP_006297.2 3 4854 GATCAGGACAGG A - A C- 3 C c c

CAGAGGTGGTCA TC CTG C ACCTCTGCCT CC
GGGAGAAG AG GAC G TGGAGACGGA GG
G T G CA

GAM7957 297 SMG1 2 10571 NP_054725.1 3 1738 GAACCCAGGAGG C C 3 C c c

CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A

GAM7957 297 SMG1 2 10571 NP_055907.2 3 1738 GAACCCAGGAGG C C 3 C c c

CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCCGA AGTGACGTT GAGGCGGAGG
C A

GAM7957 297 SMG1 2 13155 NP_054725.1 3 1704 CTACTCGGGAGG A AAC T 3 C c c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 SMG1 2 13155 NP_055907.2 3 1704 CTACTCGGGAGG A AAC T 3 C c c

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATGGCGT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 SNAPC2 1 5533 NP_003074.1 3 210 ACAGGGGTTGGG A TG -- 3 C c c

TGGGGGTTGCAG TC CTGCAACCTC CCT CCC
GACTCCAC AG GACGTTGGGG GGG GGG
- GT TT

GAM7957 297 SNX22 1 876 NP_079074.1 3 805 GAAGCCGGGAGG TG C 3 C c c
CGGAAGTTGTGG TCAC CAAC TCTGCCTCCCG
TGAGCCGA AGTG GTTG AGGCGGAGGGC
GT A

GAM7957 297 SOX7 1 15980 NP_113627.1 3 945 GAACCTAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 SPG4 1 12724 NP_055761.2 5 83 GTCTGCGGGAGG A AA ---- 3 C c c
CGGGTTATGGCG TC CTGC CC TCTGCCTCCCG
GCGGCGGC GG GGCG GG GGGCGGAGGGC
C GC TATT

GAM7957 297 SPIB 1 7007 NP_003112.1 3 558 TACTCGGGGAGG T------ A T 3 C c c
CAGGGTAGCAGT CACTGC ACC CTGCCTCCC
GCTTCCAG GTGACG TGG GACGGAGGG

GACCTTC A -
GAM7957 297 Spir-2 1 17700 XP_047462.4 3 761 GAACCCGGGAGG CT 3 C b b
TGTAGGTTGCAG TCACTGCAACCT GCCTCCCG
TGAGCCGA AGTGACGTTGGA TGGAGGGC
TG
GAM7957 297 SPTLC1 1 13585 NP_847894.1 3 416 CAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 SPTLC2 3 6941 NP_004854.1 3 4885 GAACCCAAGAGG C A CC 3 C c
b
CAGAGGATGCAA TCA TGCA CCTCTGCCTC
TGAGCCAA AGT ACGT GGAGACGGAG
A A AA
GAM7957 297 SPTLC2 3 14784 NP_004854.1 3 4187 GAGCCTGGGAGG A CT 3 C c
b
TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAGCCAT AGTGACGT GGA TGGAGGGT
C AC
GAM7957 297 SPTLC2 3 15328 NP_004854.1 3 1741 GAACCCAGGAGG C 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGACGA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 SRGAP1 1 10721 XP_051143.3 5 1168 GAACCCGGGACG C C 3 C b
b
CAGAGGTTACAG TCACTG AACCTCTGC TCCCG
TGAACCGA AGTGAC TTGGAGACG AGGGC
A C
GAM7957 297 SS18L1 1 7922 NP_056373.1 3 822 GAACCCAGGAGA TG C C 3 C c
c
CAGAGGTTGTGG TCAC CAACCTCTG CTCC
TGGGGCAA GGTG GTTGGAGAC GAGG
GT A A
GAM7957 297 SSH2 1 10439 NP_203747.1 3 407 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 SSR3 1 12338 NP_009038.1 3 1719 GAACCCAGGAGG C 3 C b b
CAGAGGTTGCGG TCACTGCAACCTCTGCCTCC
TGAGTCGA AGTGGCGTTGGAGACGGAGG
A
GAM7957 297 SSRP1 1 11518 NP_003137.1 3 240 TAGGGTGGGAGG A AC- 3 C c
c
CAGGGCAATGCA TC CTGCA CTCTGCCTCCCG
GGATCCAA AG GACGT GGGACGGAGGGT
- AAC
GAM7957 297 SSX2IP 1 8979 NP_054740.1 5 19 GAGGCCGGGAGG A AA ----- 3 C c c

CGGCTGCAAGGG TC CTGC CCT CTGCCTCCCG

GCGGGGAA AG GGCG GGA GGCGGAGGGC
G G- ACGTC
GAM7957 297 STAT3 2 5830 NP_003141.2 3 780 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 STAT3 2 5830 NP_644805.1 3 780 CTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 STAT3 2 18951 NP_003141.2 3 814 GAACCTGAGAGG CC 3 C c c
CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCAA AGTGACGTTGGAGGCGGAG
AG
GAM7957 297 STAT3 2 18951 NP_644805.1 3 814 GAACCTGAGAGG CC 3 C c c
CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
TGAGCCAA AGTGACGTTGGAGGCGGAG
AG
GAM7957 297 STX1A 1 5464 NP_004594.1 3 730 CAGCTAGGGAGG TC-- A - -- 3 C c c
CAAAGCAGGCTG ACTGCA CCT CT GCCTCCC
CAGTCAGT TGACGT GGA GA CGGAGGG
TGAC C C AA
GAM7957 297 SUDD 1 13065 NP_003822.2 3 1178 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC
GAM7957 297 SUDD 1 13065 NP_665913.1 3 1555 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC
GAM7957 297 SULT2A1 2 11833 NP_003158.2 3 662 AGCCCAGGGATG C C 3 C b b
CAAAGGTTGCAG TCACTGCAACCT TGC TCCC
TGAGTTGA AGTGACGTTGGA ACG AGGG
A T
GAM7957 297 SULT2A1 2 16320 NP_003158.2 3 541 GAACTCAGGAGG C C 3 C b b
CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCAA AGT ACGTTGGAGACGGAGG
A A
GAM7957 297 SUV39H2 1 2697 NP_078946.1 3 1740 GAATTCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A
GAM7957 297 SV2A 1 15941 NP_055664.1 3 3 AGACCCGGGGGC ACC T 3 C c c
AGGTGCTGCAGT TCACTGCA TCTGCC CCCG
GAGGGGTC AGTGACGT GGACGG GGGC

CGT -

GAM7957 297 SWAP70 1 18423 NP_055870.1 3 317 GAACGTGGGAGG A 3 C b b

CGGAGGTTGCAG TC CTGCAACCTCTGCCTCCCG
CGAGCTGA AG GACGTTGGAGGCGGAGGGT
C

GAM7957 297 SWAP70 1 18423 XP_049197.2 3 318 GAACGTGGGAGG A 3 C b b

CGGAGGTTGCAG TC CTGCAACCTCTGCCTCCCG
CGAGCTGA AG GACGTTGGAGGCGGAGGGT
C

GAM7957 297 SYAP1 1 4339 NP_116185.2 3 799 GAACCCAGGAGG A C 3 C b b
CAGAGGTTGCAG TC CTGCAACCTCTGCCTCC
CGAGCTGA AG GACGTTGGAGACGGAGG
C A

GAM7957 297 SYNGR1 1 18392 NP_004702.2 3 1334 CCCTATGGGAGG AC AAC 3 C c c

CAGAGCGGCAAG TC TGC CTCTGCCTCCCG
GACAGGGC AG ACG GAGACGGAGGGT
GA GC-

GAM7957 297 SYT11 1 18126 NP_689493.2 3 1973 TGAGCCCAGAGG A CC 3 C c c

TAGAGGCTGCAG TCACTGCA CCTCTGCCTC
TGAGCCAT AGTGACGT GGAGATGGAG
C AC

GAM7957 297 TA-LRRP 1 4246 NP_056165.1 3 281 GAACCAGGGAGG TG 3 C b b

TGGAGGTTGCAG TCACTGCAACCTC CCTCCC
TGAGCCGA AGTGACGTTGGAG GGAGGG
GT

GAM7957 297 TACC1 1 14784 NP_006274.1 3 2702 GAGCCTGGGAGG A CT 3 C c c

TCAAGGCTGCAG TCACTGCA CCT GCCTCCCG
TGAGCCAT AGTGACGT GGA TGGAGGGT
C AC

GAM7957 297 TACTILE 1 19031 NP_005807.1 3 2023 GAACCCGGGAGG C 3 C b b

CAGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGACGGAGGGC
C

GAM7957 297 TADA2L 1 9344 NP_001479.2 3 380 GAACACAGGAGG A C 3 C b b
CAGAGGTTGCAG TC CTGCAACCTCTGCCTCC
CGAGCTGA AG GACGTTGGAGACGGAGG
C A

GAM7957 297 TADA3L 1 9420 NP_597814.1 3 634 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 TAF1L 2 585 NP_722516.1 3 337 ATACTCGGGAGG A AACC T 3 C c b

CTGAAGCAGGAG TC CTGC TC GCCTCCCG
AATTGCTT AG GACG AG CGGAGGGC
- A--- T

GAM7957 297 TAF1L 2 4247 NP_722516.1 3 371 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGTGGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 TARSH 1 9763 NP_079077.1 3 1393 GAACCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 TBRG1 2 10438 NP_116200.1 3 2044 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 TBRG1 2 19130 NP_116200.1 3 2011 CTACTCGGGAGG A AAC T 3 C c b
CTGAGGCAGGAA TC CTGC CTC GCCTCCCG
GAATCGCT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 TBX1 1 9841 NP_005983.1 3 162 TTACTCGGGAGG A AAC T 3 C c c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
GATCACTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 TBX19 1 7816 NP_005140.1 3 856 GATCTCAGGAGG A T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAATTAT AGTGACGT GGAG TGGAGG
C T A

GAM7957 297 TBX6 1 19047 NP_542936.1 3 487 GAACCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGTCGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 TCF4 1 839 NP_003190.1 5 57 GCGGCGGGGAGG A AA - 3 C c c
CAGCAGGCGCGG TC CTGC CCT CTGCCTCCC
GAGCGGGC AG GGCG GGA GACGGAGGG
- C- C

GAM7957 297 TCF7 1 2362 NP_003193.1 3 1715 GAACCCGGGAGG C 3 C b b
CGGAGGTTCCAG TCACTG AACCTCTGCCTCCCG
TGAGCCGA AGTGAC TTGGAGGCGGAGGGC
C

GAM7957 297 TCTA 2 17399 NP_071503.1 3 601 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 TCTA 2 20025 NP_071503.1 3 567 CTACTCGGGAGG A AACC T 3 C c b
CTGAAGCAGGAG TC CTGC TC GCCTCCCG
ATTTGCTT AG GACG AG CGGAGGGC
- A--- T

```
GAM7957  297   TDE1L  1  2974  NP_065806.1  3  979   GAGCCCAGGAGG              C       3  C  b  b
                                 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
                                 TGAGCCAA    AGTGACGTTGGAGACGGAGG
                                                A
GAM7957  297   TEM6   1  19194 NP_073585.6  3  397   CAGCCCTTGAGG    --  A      CC      3  C  c  c
                                 CAGAGGTGCCGA TCACT  GCA CCTCTGCCTC
                                 GTGACTGC    AGTGA  CGT GGAGACGGAG
                                              GC  -       TT
GAM7957  297   TEM7   1  17985 NP_065138.2  3  1184  GAACCTGGGAGG                      3  C  b  b
                                 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                 TGAGCTCA    AGTGACGTTGGAGACGGAGGGT

GAM7957  297   TIP47  1  18951 NP_005808.2  3  541   GAACCTGAGAGG              CC      3  C  c  c
                                 CGGAGGTTGCAG TCACTGCAACCTCTGCCTC
                                 TGAGCCAA    AGTGACGTTGGAGGCGGAG
                                                AG
GAM7957  297   TIX1   1  17424 NP_055850.1  3  5491  GAACCCGGGAGG          TG          3  C  b  b
                                 TGGAGGTTGCAG TCACTGCAACCTC  CCTCCCG
                                 TGAGCTGA    AGTGACGTTGGAG  GGAGGGC
                                                GT
GAM7957  297   TJP1   2  7287  NP_003248.2  5  209   AGCTGCGGGAGG    G  AC   T          3  C  c  c
                                 CCGAGTGGGTGG TCACT CA  CTC GCCTCCCG
                                 CCGCGCTC    GGTGG GT  GAG CGGAGGGC
                                              - --  C
GAM7957  297   TJP1   2  7287  NP_783297.1  5  209   AGCTGCGGGAGG    G  AC   T          3  C  c  c
                                 CCGAGTGGGTGG TCACT CA  CTC GCCTCCCG
                                 CCGCGCTC    GGTGG GT  GAG CGGAGGGC
                                              - --  C
GAM7957  297   TJP1   2  18566 NP_003248.2  5  140   GACGCCGGGAGG   CT-  A  CT-         3  C  c
c
                                 CCACGGGTGCTG TCA   GCA CCT   GCCTCCCG
                                 CTGACGGG    AGT   CGT GGG   CGGAGGGC
                                              CGT   -  CAC
GAM7957  297   TJP1   2  18566 NP_783297.1  5  140   GACGCCGGGAGG   CT-  A  CT-         3  C  c
c
                                 CCACGGGTGCTG TCA   GCA CCT   GCCTCCCG
                                 CTGACGGG    AGT   CGT GGG   CGGAGGGC
                                              CGT   -  CAC
GAM7957  297   TMEM1  1  19683 NP_003265.2  3  1418  GCTTGCGGGAGG   C  AA  T          3  C  c
 c
                                 CGGTGGGGCATG TCA TGC  CC CTGCCTCCCG
                                 GGAGGAAG    GGT ACG  GG GGCGGAGGGC
                                              -  G-  T
GAM7957  297   TMEM4  1  12891 NP_055070.1  5  380   CGGCCCTGGGAG  A  G  A    C       3  C  c
c
                                 CAGAGGTGGAGC TC CT CA CCTCTGC TCCCG
                                 GACCCCAT    AG GA GT GGAGACG AGGGT
                                              C  G  -     -
GAM7957  297   TMG4   1  3326  NP_076986.1  3  248   GAACCTGGGAGG TC-----              3  C  c  c
                                 CAGAGGTTGCAG       ACTGCAACCTCTGCCTCCCG
```

TAAGCTGA TGACGTTGGAGACGGAGGGT
AGTCGAA
GAM7957 297 TNFRSF1 1 13649 NP_001057.1 3 837 GAACCCGGGAAG A C 3 C b
b
B CGGAGGTTGCAG TC CTGCAACCTCTGC TCCCG
GGAGCCGA AG GACGTTGGAGGCG AGGGC
G A
GAM7957 297 TNFSF10 1 6521 NP_003801.1 3 694 GAACCCGGGAGG T----- 3 C b b

CAGAGGTTGCAG CACTGCAACCTCTGCCTCCCG
TGTGGTGA GTGACGTTGGAGACGGAGGGC
AGTGGT
GAM7957 297 TNFSF14 1 722 NP_003798.2 3 317 AAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 TNFSF14 1 722 NP_742011.1 3 317 AAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 TNFSF15 1 1981 NP_005109.2 3 1067 GAACTGGGGAGG 3 C b b
CAGAGGTTGCGG TCACTGCAACCTCTGCCTCCC
TGAGCCCA AGTGGCGTTGGAGACGGAGGG

GAM7957 297 TNIP3 1 16969 NP_079149.2 3 920 AGCCCAGGGAGG TC----- T 3 C c c

CAGAGGTTGCTG AC GCAACCTCTGCCTCCC
TAAGTTGA TG CGTTGGAGACGGAGGG
AGTTGAA T
GAM7957 297 TNRC5 1 17344 NP_006577.1 5 253 GCGGGCGGGAGG T CT - 3 C c
c
CTAGCTGTTGTC TCAC GCAAC CT GCCTCCCG
GTGGTTGC GGTG TGTTG GA CGGAGGGC
C TC T
GAM7957 297 TP53I5 1 13608 XP_290532.2 3 1407 TGGCATGGAAGG G A C 3 C c c

CAGAGGCTGGGT TCACT CA CCTCTGCCT CCG
GGGGTGGG GGTGG GT GGAGACGGA GGT
- C A
GAM7957 297 TPM4 1 19193 NP_003281.1 3 908 CTACTCGGGAGG A AAC T 3 C c
c
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
GATCGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 TRADD 1 15543 NP_003780.1 3 361 TCCTGGGTGCTG ACC CT-- 3 C c
c
CAGATACTGCAG TCACTGCA TCTGC CCCG
TGAAGTAA AGTGACGT AGACG GGGT
CAT TCGT
GAM7957 297 TRADD 1 15543 NP_700474.1 3 361 TCCTGGGTGCTG ACC CT-- 3 C c
c

```
                                CAGATACTGCAG TCACTGCA  TCTGC  CCCG
                                TGAAGTAA   AGTGACGT  AGACG  GGGT
                                           CAT   TCGT
GAM7957  297   TRAM2  2  5830  NP_036420.1  3  1545  CTACTCGGGAGG  A  AAC  T          3  C  c
c
                                CTGAGGCAGGAG TC CTGC  CTC GCCTCCCG
                                AATCGCTT   AG GACG  GAG CGGAGGGC
                                         -  ---  T
GAM7957  297   TRAM2  2  9810  NP_036420.1  3  1579  GAACCTAGAAGG        TG  CCC       3  C  c
 c
                                TGGAGGTTGCAG TCACTGCAACCTC  CCT
                                TGAGCGGA   AGTGACGTTGGAG  GGA
                                           GT  AGA
GAM7957  297   TRB2   1  15438 NP_067675.1  3  1851  ACCTTGGAGGAG   TG     G   C       3  C  c
c
                                GAGAGGTTGGTG TCAC  CAACCTCT CCTCC
                                ACATGCAT   AGTG  GTTGGAGA GGAGG
                                         --      -   A
GAM7957  297   TRIAD3 1  17399 NP_061884.2  3  1615  GAACCTGGGAGG                  3  C  b  b
                                CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
                                TGAGCCAA   AGTGACGTTGGAGACGGAGGGT

GAM7957  297   TRIM14 2  2835  NP_055603.2  3  2730  GAACCCAGGAGG      C      C       3  C  c  b
                                CGGAGATTGCAG TCACTGCAA CTCTGCCTCC
                                TGAGCTGA   AGTGACGTT GAGGCGGAGG
                                         A       A
GAM7957  297   TRIM14 2  2835  NP_150090.1  3  2536  GAACCCAGGAGG      C      C       3  C  c  b
                                CGGAGATTGCAG TCACTGCAA CTCTGCCTCC
                                TGAGCTGA   AGTGACGTT GAGGCGGAGG
                                         A       A
GAM7957  297   TRIM14 2  17397 NP_150089.1  3  372   GAACCCGGGCAG          CT        3  C  b  b
                                CGGAGGTTGCAG TCACTGCAACCTCTGC  CCCG
                                TGAGCCGA   AGTGACGTTGGAGGCG  GGGC
                                           AC
GAM7957  297   TRIM28 1  8138  NP_005753.1  5  86    GCCTTCGGGAGG TC---   AA  - -       3  C  c
c
                                CGAGCAGGCAGC    ACTGC  CCT CT GCCTCCCG
                                AGTTGGCC       TGACG  GGA GA CGGAGGGC
                                       CCGGT   AC  C  G
GAM7957  297   TRIM35 1  16080 NP_055881.1  3  532   AAATGGGCAAGG  A-  AAC     --       3  C  c
c
                                CAGAGTAAGCAG TC  CTGC  CTCTGCCT  CCCG
                                GGGAGACA   AG  GACG  GAGACGGA  GGGT
                                         GG   AAT     AC
GAM7957  297   TRIM35 1  16080 NP_741983.1  3  1505  AAATGGGCAAGG  A-  AAC     --       3  C  c
c
                                CAGAGTAAGCAG TC  CTGC  CTCTGCCT  CCCG
                                GGGAGACA   AG  GACG  GAGACGGA  GGGT
                                         GG   AAT     AC
GAM7957  297   TRIM46 1  9420  NP_079334.1  3  40    GAACCTGGGAGG                  3  C  b  b
```

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 TRIM56 1 1762 NP_112223.1 3 992 GAGCCGAGGAGT AC TGC - 3 C c c

TTGAGTCTGCAG TCACTGCA CTC CTCC CG
TGAGCTAT AGTGACGT GAG GAGG GC
CT TTT A

GAM7957 297 TRIM56 1 1762 XP_168586.1 3 992 GAGCCGAGGAGT AC TGC - 3 C c c

TTGAGTCTGCAG TCACTGCA CTC CTCC CG
TGAGCTAT AGTGACGT GAG GAGG GC
CT TTT A

GAM7957 297 TRIM8 1 6715 NP_112174.1 3 214 ATCTCCTGGACG CA C C 3 C c c

CAGAGGTGACAG TCACTG ACCTCTGC TCC
TGGGAGCT GGTGAC TGGAGACG AGG
AG C T

GAM7957 297 TRPM2 1 782 NP_003298.1 5 403 TGAGGGCAGCAG - --- CT 3 C c c

GCCTGGTTGCAG TCA CTGCAACC TCTGC CCC
CTGGCGTG GGT GACGTTGG GGACG GGG
C TCC AC

GAM7957 297 TRPM3 1 16946 NP_079247.2 3 3341 GAACCCTGGAGG C C 3 C c c

CGGAAGTTGCAG TCACTGCAAC TCTGCCTCC
TGAGCCGA AGTGACGTTG AGGCGGAGG
A T

GAM7957 297 TRPM4 1 2740 NP_060106.2 5 38 GCCCTGGGCTGC A - CT 3 C c c

AGGAGGTTGCGG TC CTGCAACCTC TGC CCCG
CGGCCGCG GG GGCGTTGGAG ACG GGGT
C G TC

GAM7957 297 TRPM8 1 9731 NP_076985.3 3 1550 GAACCTGGGAGG 3 C b b

CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAACCAA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 TRPV1 1 14712 NP_542437.1 5 125 TGGGGAGGGAGG AACCT 3 C c c

CAGCGCGGTGGT TCACTGC CTGCCTCCC
TATCAACC GGTGGCG GACGGAGGG
C----

GAM7957 297 TSAP6 1 15578 NP_060704.1 5 45 AGCGGCGGGCCG A GC CT 3 C c c

CAGAGGTTCAAG TC CT AACCTCTGC CCCG
CGATTCTC AG GA TTGGAGACG GGGC
C AC CC

GAM7957 297 TSNAX 1 13066 NP_005990.1 3 766 GAACCTGGGAGG 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 TTF2 1 6501 NP_003585.2 3 565 GAGTCCAGGAGG A T C 3 C c c

TTGAGGCTGCAG TCACTGCA CCTC GCCTCC

TGAGCTGT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 TU12B1-1 9085 NP_057659.1 5 33 CTACCCGGGAGG AC AAC -- 3 C c c
TY CGAAGAGAAGCA TC TGC CTCT GCCTCCCG
CAGAAGAA AG ACG GAGA CGGAGGGC
AC AA- AG
GAM7957 297 U1SNRNP 2 1492 NP_851030.1 5 547 CTACTCGGGAGG A AAC T 3 C c b
BP CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATCACTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 U1SNRNP 2 13066 NP_851030.1 5 581 GAACCTGGGAGG 3 C b b
BP CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 U1SNRNP 2 13066 NP_851034.1 5 465 GAACCTGGGAGG 3 C b b
BP CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGT
GAM7957 297 U2AF65 1 12063 NP_009210.1 3 105 GAAGACGATGGG GCAA CC 3 C c c
CAGAGGAGTGAC TCACT CCTCTGCCT CG
AGCCGCAG AGTGA GGAGACGGG GC
---- TA
GAM7957 297 UBCE7IP 1 14779 NP_055763.1 3 1929 GAGCCGGGGAGG 3 C b b
5 CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCC
TGAGCCGA AGTGACGTTGGAGACGGAGGG
GAM7957 297 UBE2B 2 1890 NP_003328.1 3 1389 CACTTTGGGAGG A AAC C 3 C c c
CAAAGGCGGGAG TC CTGC CT TGCCTCCCG
GATCACTT AG GGCG GA ACGGAGGGT
- --- A
GAM7957 297 UBE2B 2 12734 NP_003328.1 3 1559 ATGCCTAGGAGG A T C 3 C c c
TTGAGGCTGCAG TCACTGCA CCTC GCCTCC
TGAGCTGT AGTGACGT GGAG TGGAGG
C T A
GAM7957 297 UBE2G2 2 8877 NP_003334.2 3 1927 GAACCCAGGAGG C C 3 C c b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCC
TGAGCTGA AGTGACGTT GAGGCGGAGG
C A
GAM7957 297 UBE2G2 2 11556 NP_003334.2 3 890 GAACCCGGGAGG A 3 C b b
CAGAGGTAGTAG TCACTGC ACCTCTGCCTCCCG

TGAGCTGA AGTGATG TGGAGACGGAGGGC
A
GAM7957 297 UNC5CL 1 8143 NP_775832.1 3 231 CCTCCTGGCCGG A AA TC 3 C c c
CAGAGGGCGCAG TC CTGC CCTCTGCC CCG
GAGCCCAG AG GACG GGAGACGG GGT
- CG CC
GAM7957 297 UNC5H2 1 14996 NP_734465.1 3 56 ACTGGCAGGAGG A ACC C 3 C c c
CAGGTGCAGGGA TC CTGCA TCTGCCTCC
GGCCTGGG AG GACGT GGACGGAGG
G --- A
GAM7957 297 UPK1B 1 19696 NP_008883.1 3 854 TTGACCGGGAGA C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTG CTCCCG
TGAGCTGA AGTGACGTTGGAGAC GAGGGC
A
GAM7957 297 USP14 1 10433 NP_005142.1 3 1267 GAACCTGGAAGG C C 3 C b b
CAGAAGTTGCAG TCACTGCAAC TCTGCCT CCG
TGAGCTGA AGTGACGTTG AGACGGA GGT
A A
GAM7957 297 UST 2 11817 NP_005706.1 5 81 GGCTGTGGGAGG A- AA T 3 C c c
CAGCGGAGCAGG TC CTGC CC CTGCCTCCCG
CGATGAAG AG GACG GG GACGGAGGGT
CG A- C
GAM7957 297 UST 2 19210 NP_005706.1 3 566 GAGCCCAGGAGT TGC C 3 C c c
TTGAGGTTGCAG TCACTGCAACCTC CTCC
TGAGCTGT AGTGACGTTGGAG GAGG
TTT A
GAM7957 297 VDR 1 15223 NP_000367.1 3 2212 GAACCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 VEGF 1 13604 NP_003367.3 5 67 TCTGTCGGGAGG GC T -- 3 C c c
CGCAGCGGTTAG TCACT AACC CT GCCTCCCG
GTGGACCG GGTGG TTGG GA CGGAGGGC
A- C CG
GAM7957 297 VHL 3 5896 NP_000542.1 3 2349 GACCCCAGGAGG C C C 3 C c b
CGAAGATTGCAG TCACTGCAA CT TGCCTCC
TGAGCTGA AGTGACGTT GA GCGGAGG
A A A
GAM7957 297 VHL 3 17264 NP_000542.1 3 3238 GAACCTGGAAGG C TG C 3 C c b
TGGAGCTTGCAG TCACTGCAA CTC CCT CCG
TGAGCTGA AGTGACGTT GAG GGA GGT
C GT A
GAM7957 297 VHL 3 19054 NP_000542.1 3 3389 GAACCCGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGGCGGAGGGC

GAM7957 297 VIK 1 18691 NP_612503.1 3 1900 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 VIPL 1 19197 NP_110432.1 3 279 TCCATGTGGGAG TGCA C 3 C c c

CAGAGGTGTGAA TCAC ACCTCTGC TCCCG
GAGAATTT AGTG TGGAGACG AGGGT
---- -
GAM7957 297 VprBP 1 5044 NP_055518.1 3 442 ATAACAGGGAGG CT - ----- 3 C c c
CAGAATTCAGGT TCA GC AACC TCTGCCTCCC
TGGCTTGA AGT CG TTGG AGACGGAGGG
T- G ACTTA
GAM7957 297 VPS4B 1 10439 NP_004860.2 3 831 GAACCTGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGT

GAM7957 297 WBSCR1 1 8562 NP_071496.1 3 740 AGGGAGTCCACG AC-- C--- 3 C c
c
GAGAAGATGCAG TCACTGCA CTCTG CTCCC
TGAATGCT AGTGACGT GAGGC GAGGG
AGAA ACCT
GAM7957 297 WBSCR1 1 8562 NP_114381.1 3 740 AGGGAGTCCACG AC-- C--- 3 C c
c
GAGAAGATGCAG TCACTGCA CTCTG CTCCC
TGAATGCT AGTGACGT GAGGC GAGGG
AGAA ACCT
GAM7957 297 WBSCR21 1 15303 NP_112585.2 3 1056 GAACCCTGGAGG C C 3 C b
b
CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCGA AGT ACGTTGGAGACGGAGG
A T
GAM7957 297 WBSCR21 1 15303 NP_683710.1 3 249 GAACCCTGGAGG C C 3 C b
b
CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCGA AGT ACGTTGGAGACGGAGG
A T
GAM7957 297 WBSCR21 1 15303 NP_683711.1 3 249 GAACCCTGGAGG C C 3 C b
b
CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCGA AGT ACGTTGGAGACGGAGG
A T
GAM7957 297 WBSCR21 1 15303 NP_683713.1 3 886 GAACCCTGGAGG C C 3 C b
b
CAGAGGTTGCAA TCA TGCAACCTCTGCCTCC
TGAGCCGA AGT ACGTTGGAGACGGAGG
A T
GAM7957 297 WBSCR23 2 14797 NP_079318.1 3 1637 GAACCCTGGAGG T C 3 C c
c
CGGAGGTTGCCG TCAC GCAACCTCTGCCTCC

TGAGCCAA AGTG CGTTGGAGGCGGAGG
C T
GAM7957 297 WBSCR23 2 19838 NP_079318.1 3 1399 AGTCATGGGAGG A G AC 3 C c c
CAGAGCTGGGGG TC CT CA CTCTGCCTCCCG
AGCGAGGC AG GG GT GAGACGGAGGGT
- G C-
GAM7957 297 WDR23 2 10486 NP_079506.3 3 1682 TGAACTTGGGAG T-- -- A- C 3 C c c
CAGAGGTGAGCT CACT GC ACCTCTGC TCCCG
GAGTGCAG GTGA CG TGGAGACG AGGGT
GAC GT AG -
GAM7957 297 WDR23 2 10486 NP_852002.1 3 1682 TGAACTTGGGAG T-- -- A- C 3 C c c
CAGAGGTGAGCT CACT GC ACCTCTGC TCCCG
GAGTGCAG GTGA CG TGGAGACG AGGGT
GAC GT AG -
GAM7957 297 WDR23 2 14277 NP_079506.3 3 1691 GGAGCAGAGGTG -------- C C 3 C c c
AGCTGAGTGCAG TCACTGCA ACCTCTGC TCC
TGAGCCAA AGTGACGT TGGAGACG AGG
GAGTCGAG - -
GAM7957 297 WDR23 2 14277 NP_852002.1 3 1691 GGAGCAGAGGTG -------- C C 3 C c c
AGCTGAGTGCAG TCACTGCA ACCTCTGC TCC
TGAGCCAA AGTGACGT TGGAGACG AGG
GAGTCGAG - -
GAM7957 297 WIG1 1 15343 NP_071915.1 3 1226 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 WIG1 1 15343 NP_689426.1 3 1226 GAACCCGGGAGG C 3 C b b
CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C
GAM7957 297 WNT7B 1 1621 NP_478679.1 3 1025 GAACCCGGGAGG C TG 3 C c c
TGGAGGTTGCAA TCA TGCAACCTC CCTCCCG
TGAGCCAA AGT ACGTTGGAG GGAGGGC
A GT
GAM7957 297 WNT8B 1 3133 NP_003384.1 3 595 GGTTCCTAGAGG - G CC 3 C c c
CAGAGGTTGAAG TCA CT CAACCTCTGCCTC
ATGGAAGA GGT GA GTTGGAGACGGAG
A A AT
GAM7957 297 XRCC2 1 15223 NP_005422.1 3 2095 GAACCCAGGAGG TG C 3 C c c
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCTGA AGTGACGTTGGAG GGAGG
GT A

GAM7957 297 YEA 1 7319 NP_116215.1 3 969 GAACCCGGGAGA CT C 3 C c c
TGAAGGTTGCAG TCACTGCAACCT G CTCCCG
TGAGCTGA AGTGACGTTGGA T GAGGGC
AG A
GAM7957 297 YME1L1 2 9763 NP_055078.1 3 1035 GAACCCAGGAGG TG C 3 C c
b
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 YME1L1 2 9763 NP_647473.1 3 1035 GAACCCAGGAGG TG C 3 C c
b
TGGAGGTTGCAG TCACTGCAACCTC CCTCC
TGAGCCAA AGTGACGTTGGAG GGAGG
GT A
GAM7957 297 YME1L1 2 18286 NP_055078.1 3 851 GAGCCTGGGAGA GC 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTCT CTCCCG
TGAGCTGA AGTGACGTTGGAGG GAGGGT
TA
GAM7957 297 YME1L1 2 18286 NP_647473.1 3 851 GAGCCTGGGAGA GC 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTCT CTCCCG
TGAGCTGA AGTGACGTTGGAGG GAGGGT
TA
GAM7957 297 ZADH1 1 9120 NP_689657.1 3 1059 GAACCTGGGAGG T G 3 C c c
GGGAGGTTGCCG TCAC GCAACCTCT CCTCCCG
TGAGCTGA AGTG CGTTGGAGG GGAGGGT
C G
GAM7957 297 ZAK 1 13065 NP_598407.1 3 4011 GAACCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 ZBTB2 1 15154 NP_065912.1 5 25 AGCAGCGAGAGG A AA C 3 C c c

CAGAGGCGGCGG TC CTGC CCTCTGCCTC CG
CGGCGGGG GG GGCG GGAGACGGAG GC
C GC A
GAM7957 297 ZFD25 1 19287 NP_057304.1 3 1419 AAACCTGGGAGG C C 3 C c c
CGAAGATTGCAG TCACTGCAA CT TGCCTCCCG
TGAGCTGA AGTGACGTT GA GCGGAGGGT
A A
GAM7957 297 ZFP106 2 13058 NP_071918.1 3 1496 GAACCCGGGAGG TC----- C 3 C c
c
CAGAGATTGCAG ACTGCAA CTCTGCCTCCCG
TAAGCTGA TGACGTT GAGACGGAGGGC
AGTCGAA A
GAM7957 297 ZFP106 2 17808 NP_071918.1 3 2112 GAACCCTGGAGG C C 3 C c c

TAGAAGTTGCAG TCACTGCAAC TCTGCCTCC
TGAGCCAA AGTGACGTTG AGATGGAGG

A T
GAM7957 297 ZFP30 1 14388 NP_055713.1 3 1557 GGGCCCGGGAGG 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGA AGTGACGTTGGAGACGGAGGGC

GAM7957 297 ZFP91 1 883 NP_444251.1 3 1563 ATTTCCTTGGGA CT CC 3 C c c
TAGAGGTTGTGT TCA GCAACCTCTG TCCCG
TGGGGAAT GGT TGTTGGAGAT AGGGT
TG --
GAM7957 297 ZIM3 2 10267 NP_443114.1 3 534 CTACCCGGGAGG A AAC T 3 C c
b
CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T
GAM7957 297 ZIM3 2 19880 NP_443114.1 3 568 GAACCTGGGAGG 3 C b b
TAGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCAA AGTGACGTTGGAGATGGAGGGT

GAM7957 297 ZNF11B 1 15224 NP_008886.1 3 2158 GAACCTGGGAGG TG 3 C b
b
TGGAGGTTGCAG TCACTGCAACCTC CCTCCCG
TGAGCCAA AGTGACGTTGGAG GGAGGGT
GT
GAM7957 297 ZNF14 1 5303 NP_066358.1 3 514 TGAACCTGGAGA C C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTG CTCC
TGAGCTGA AGTGACGTTGGAGAC GAGG
A T
GAM7957 297 ZNF197 1 2173 NP_008922.1 3 366 AACCTGGGAGGG - 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCC TCCCG
TGAGCCAG AGTGACGTTGGAGGCGG AGGGT
G
GAM7957 297 ZNF264 1 2367 NP_003408.1 3 1424 GAACGTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCTGA AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 ZNF271 1 13091 NP_006620.2 3 159 GAGCCCAGGAGT A TGC C 3 C c
c
TTGAGGCTGCAG TCACTGCA CCTC CTCC
TGAGCTAT AGTGACGT GGAG GAGG
C TTT A
GAM7957 297 ZNF297B 2 3235 NP_054726.1 3 3103 CTACTCGGGAGG A AAC 3 C b
b
CGGAGGCAGGAG TC CTGC CTCTGCCTCCCG
AATCACTT AG GACG GAGGCGGAGGGC
- ---
GAM7957 297 ZNF297B 2 15000 NP_054726.1 3 3137 GAACCTGGGAGG 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCCCG
TGAGCCGC AGTGACGTTGGAGGCGGAGGGT

GAM7957 297 ZNF333 1 12792 NP_115809.1 3 808 GAACCCAGGAGG C 3 C b b

CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 ZNF339 1 2484 NP_067043.1 3 1114 GAAACTGGGAGG G 3 C b b
CAGGGGTTGGAG TCACT CAACCTCTGCCTCCCG
TGAGCCAG AGTGA GTTGGGGACGGAGGGT
G

GAM7957 297 ZNF33A 1 19246 NP_008905.1 3 2158 GAACCTGGGAGG C TG 3 C c
c

TGGATGTTGCAG TCACTGCAAC TC CCTCCCG
TGAGCTGA AGTGACGTTG AG GGAGGGT
T GT

GAM7957 297 ZNF347 1 9422 NP_115973.1 3 337 GAACCCAGGAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGGCGGAGG
A

GAM7957 297 ZNF36 1 10435 XP_168302.1 3 2468 GAACCCAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCAA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 ZNF409 1 15207 NP_055709.1 3 2432 GAACCTGGAAGG C 3 C b b
CGGAGGTTGCAG TCACTGCAACCTCTGCCT CCG
TGAGCCGA AGTGACGTTGGAGGCGGA GGT
A

GAM7957 297 ZNF426 1 9759 NP_077011.1 3 321 GAACCCAGGAAG C C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGC TCC
TGAGCAGA AGTGACGTTGGAGACG AGG
A A

GAM7957 297 ZNF430 2 10917 NP_079465.1 3 987 GAACCCGGGAGG G 3 C b b
CAGAGGTTGAAG TCACT CAACCTCTGCCTCCCG
TGAGCTGA AGTGA GTTGGAGACGGAGGGC
A

GAM7957 297 ZNF430 2 15089 NP_079465.1 3 953 CTACTCGGGAGG A AAC T 3 C c
b

CTGAGGCAGGAG TC CTGC CTC GCCTCCCG
AATTGCTT AG GACG GAG CGGAGGGC
- --- T

GAM7957 297 ZNF431 1 7868 XP_086098.2 3 263 GAACCTGGGAGG C TG 3 C c c

TGGAAGTTGCAG TCACTGCAAC TC CCTCCCG
TGAGCCAA AGTGACGTTG AG GGAGGGT
A GT

GAM7957 297 ZNF432 1 5251 NP_055465.1 3 1213 GAACCTGGGAGG C 3 C b b
CAGAGGTTTCAG TCACTG AACCTCTGCCTCCCG
TGAGCCAA AGTGAC TTGGAGACGGAGGGT
T

GAM7957 297 ZNF440 1 14055 NP_689570.1 3 2038 GAATATAGGAGG C 3 C b b
CAGAGGTTGCAG TCACTGCAACCTCTGCCTCC
TGAGCCGA AGTGACGTTGGAGACGGAGG
A

GAM7957 297 ZNF444 1 7772 NP_060807.1 3 532 GGTTGGGGGAGG CT A--- - 3 C c c

CAGCGGGTGATG TCA GC ACCT CTGCCTCCC
GCTCTGAA AGT CG TGGG GACGGAGGG
CT GTAG C

GAM7957 297 ZNF450 2 6071 NP_055612.1 3 2794 GAGCCCAGGAGG A C 3 C c c

CGGAGGCTGCAG TCACTGCA CCTCTGCCTCC
TGAGCTGA AGTGACGT GGAGGCGGAGG
C A

GAM7957 297 ZNF450 2 10867 NP_055612.1 3 2760 CTACTCGGGAGG A CAAC T 3 C c c

CTGAGACAGGAG TC CTG CTC GCCTCCCG
AATCACTT AG GAC GAG CGGAGGGC
- A--- T

GAM7957 297 ZNF74 1 12062 NP_003417.1 3 536 GAGCCTAGGAGG A CT C 3 C c c

TCAAGGCTGCAG TCACTGCA CCT GCCTCC
TGAGCCAT AGTGACGT GGA TGGAGG
C AC A

GAM7957 297 ZNF91 1 15343 NP_003421.1 3 110 GAACCCGGGAGG C 3 C b b

CGGAGCTTGCAG TCACTGCAA CTCTGCCTCCCG
TGAGCCGA AGTGACGTT GAGGCGGAGGGC
C

GAM8145 328 1 1692 NP_061085.1 3 863 AGGAAGCTGTAG T T GG 3 C c c

GTGAGGAGATCT ACA GATCTCCTCAC CTA
GTATAATA TGT CTAGAGGAGTG GAT
- - GT

GAM8145 328 ADRA2A 1 4823 NP_000672.2 3 1210 TCCGTGCTTTTC CTCACT 3 C c c

TGGTTGAGATCA ACATGATCTC CTAGGA
TGTCATTG TGTACTAGAG GGTCTT
TT----

GAM8145 328 ADRB1 1 10737 NP_000675.1 3 57 CTTCCCAGGGGA - A-- A 3 C c c

ACGAGGAGATCT ACAT GATCTCCTC CTCT GG
GTGTTTAC TGTG CTAGAGGAG GGGG CC
T CAA A

GAM8145 328 ARSB 1 9103 NP_000037.1 3 471 CTTCTCCCTGTC CC C- 3 C c c

GGTGAAGGATCA ACATGATCT TCACT TAGG
TGTTCAGG TGTACTAGG AGTGG GTCC
A- CT

GAM8145 328 ATP6IP2 1 7285 NP_005756.2 3 176 TGTTTTTCTAGA - CTCC 3 C c c

GTGAATTATAGT AC ATGAT TCACTCTAGGA
ATTGACGT TG TATTA AGTGAGATCTT
A ----

GAM8145 328 BSPRY 1 5340 NP_060158.1 3 856 GGCCCTCAGAGG CA-- - 3 C c c

ACCAGGGGATCA ACATGATCTCCT CTCT AGG
TGTCTCCA TGTACTAGGGGA GAGA TCC
CCAG C

GAM8145 328 C1orf1 1 14716 NP_001204.1 3 935 AGAGATTCCAGT A----- -- CTA 3 C c c

GAGTTGAGATCA CATGATCTC CTCACT GGA
TGCCCCTG GTACTAGAG GAGTGA CCT
GTCCCC TT ---
GAM8145 328 C1orf22 1 10321 NP_079467.2 3 2319 CCTAGTTAAGAA G A--- --- 3 C c c
AAGAGGAGATAA ACAT ATCTCCTC CT CTAGG
TGTTCGTC TGTA TAGAGGAG GA GATCC
A AAAA ATT
GAM8145 328 C1QDC1 1 11118 NP_076414.2 5 480 GTTAGGGCTGGT T - G 3 C c c
GGTGAGGGATCA ACATGATC CCTCACT CTAG
TGTAAAGA TGTACTAG GGAGTGG GGTC
- T G
GAM8145 328 C1QDC1 1 11118 NP_115532.1 5 480 GTTAGGGCTGGT T - G 3 C c c
GGTGAGGGATCA ACATGATC CCTCACT CTAG
TGTAAAGA TGTACTAG GGAGTGG GGTC
- T G
GAM8145 328 C20orf7 1 3280 NP_443097.1 3 739 TTTCTGGCGTGA C---- T 3 C c c
2 GTCAACAGATCA ACATGATCT CTCAC CTAGGA
TGTAGATA TGTACTAGA GAGTG GGTCTT
CAACT C
GAM8145 328 C6orf5 1 4879 NP_056339.2 3 916 AGAGGTTGCAGT -- C G 3 C c c
GAGCCGAGATCA ACATGATCTC CTCACT TAG
TGTCACTG TGTACTAGAG GAGTGA GTT
CC C G
GAM8145 328 CABC1 1 14186 NP_064632.1 3 443 TGTGTTTCTAGA TG TCTC 3 C c
c
GTGAGATTTGTG ACA A CTCACTCTAGGA
TTTTCTGC TGT T GAGTGAGATCTT
GT TA--
GAM8145 328 CACNG3 1 8825 NP_006530.1 5 237 ACCCTTCCTAGA A ---- A- 3 C c c
GCGGAGGAACCG CATGATC TCCTC CTCTAGGA
GGTCGTGC GTGCTGG AGGAG GAGATCCT
C GCCA GC
GAM8145 328 CAPN1 1 3309 NP_005177.2 5 137 CCCCCAGGATGT C -- - A 3 C c c
CGGAGGAGATCA A ATGATCTCCTC AC TCT GG
TCACGCCG A TACTAGAGGAG TG AGG CC
C GC T A
GAM8145 328 CASP2 1 7205 NP_001215.1 3 853 TTTTGTCCTAGA GA C---- 3 C c c
GTGAGAGTTTGG ACAT TCT CTCACTCTAGGA
AAGGTGTC TGTG AGG GAGTGAGATCCT
GA TTTGA
GAM8145 328 CASP2 1 7205 NP_116764.1 3 464 TTTTGTCCTAGA GA C---- 3 C c c
GTGAGAGTTTGG ACAT TCT CTCACTCTAGGA
AAGGTGTC TGTG AGG GAGTGAGATCCT
GA TTTGA
GAM8145 328 CASP2 1 7205 NP_116765.1 3 1278 TTTTGTCCTAGA GA C---- 3 C c c
GTGAGAGTTTGG ACAT TCT CTCACTCTAGGA
AAGGTGTC TGTG AGG GAGTGAGATCCT
GA TTTGA

GAM8145 328 CASP2 1 7205 NP_116766.1 3 1278 TTTTGTCCTAGA GA C---- 3 C c c
GTGAGAGTTTGG ACAT TCT CTCACTCTAGGA
AAGGTGTC TGTG AGG GAGTGAGATCCT
GA TTTGA
GAM8145 328 CD151 1 12932 NP_004348.2 5 59 TGGTAGCCTAGA T T- --- 3 C c c
GTCCTGGGGAGC ACA GA CTCCTC ACTCTAGG
TTCTGTCC TGT CT GAGGGG TGAGATCC
- TC TCC
GAM8145 328 CG012 1 2753 XP_096710.1 5 1021 GTTGTTGCCTGG CCTCAC 3 C c
c
ATTTCCAGATCA ACATGATCT TCTAGG
TGTGACAG TGTACTAGA AGGTCC
CCTTT-
GAM8145 328 CHEK1 1 15806 NP_001265.1 3 84 ATTCTTCCTAGA C CCTCA 3 C c
c
GAAGATTATCCT A ATGATCT CTCTAGGA
GTCCTGCA C TATTAGA GAGATCCT
C A----
GAM8145 328 COX8 1 15358 NP_004065.1 3 13 CAGGAGGCCAGA C AT A 3 C c c
GTGAGGGGTCCG A ATG CTCCTCACTCT GG
TTCTGTCC C TGC GGGGAGTGAGA CC
T CT -
GAM8145 328 DKFZp72 1 18597 NP_689481.1 3 130 CACAGCTCATGG C A G 3 C c
c
7A071 AGGGTGAGATCA ACATGATCTC TC CTCTA GA
TGTTAGGG TGTACTAGAG GG GAGGT CT
T - A
GAM8145 328 DMWD 1 17090 XP_027569.1 3 546 GTCTGTCCCCTT G ACTCT 3 C c
c
CGGAGGAGATGA ACAT ATCTCCTC AGG
TGTAGAGG TGTA TAGAGGAG TCC
G GCT--
GAM8145 328 DPF3 1 15298 NP_036206.1 3 1420 ACATGACTCCCA A -- CTA 3 C c c
GTGAGGAGAATT AC TGA TCTCCTCACT GGA
CAGGTGAT TG ACT AGAGGAGTGA CCT
G TA C--
GAM8145 328 Ells1 2 18457 NP_690006.1 3 5167 CCTCCCCTGAGA C TC - 3 C c c
GTGAGGACCTCA A ATGA TCCTCACTCT AGG
TCCGACCA C TACT AGGAGTGAGA TCC
C CC G
GAM8145 328 Ells1 2 19837 NP_690006.1 3 2930 ACTTACCTGAGA G C - 3 C c c
GTGAGAGATGTG ACAT ATCTC TCACTCT AGG
TAGGAAGA TGTG TAGAG AGTGAGA TCC
- - G
GAM8145 328 ERAP140 1 7182 XP_059748.2 3 269 CAAATCCATACA A- C C - 3 C c c
GTGAGGAATCAG AC TGAT TCCTCACT TA GGA
AGTGTTTA TG ACTA AGGAGTGA AT CCT

```
                                        AG   -      C  A
GAM8145  328    FBXO11  1   11365  NP_061163.2  3  88    TTAGTGCCTAGA    GA-   CTC          3  C  c
c
                                GTTAAGAGACAA ACAT   TCTC   ACTCTAGG
                                ATGTTTAC    TGTA   AGAG   TGAGATCC
                                          AAC    AAT
GAM8145  328    FLJ1046 1   455    NP_060567.1  3  674   TGGGAGGCCTAG A-----      C    T       3  C  c  c
         0                      GTGGGCAGATCA      CATGATCT CTCAC CTAGG
                                TGAGGTCA         GTACTAGA GGGTG GATCC
                                       ACTGGA       C    -
GAM8145  328    FLJ1127 1   13401  NP_060845.1  3  802   CACATTCCTAGA   A  AT     AC          3  C  c
c
         4                      GAGGAGCCAAGT AC TG  CTCCTC  TCTAGGA
                                TCTAGTAG    TG AC  GAGGAG  AGATCCT
                                         A  C-      --
GAM8145  328    FLJ2067 1   11719  NP_060394.1  3  2244  CTATGTCCTAGA     A    T  -          3  C  c  c
         1                      GATGGGGGAATG ACATG TCTCC CA CTCTAGGA
                                TGTTATTG    TGTGT AGGGG GT GAGATCCT
                                          A    - A
GAM8145  328    FLJ2358 1   14763  NP_078864.1  3  241   GCTCCCAGCAGA  C   TC       A--        3  C  c
c
         4                      GTGAGGACTTCA A ATGA  TCCTCACTCT   GG
                                TTCTCTAG    C TACT  AGGAGTGAGA   CC
                                         T   TC        CGA
GAM8145  328    FLJ3188 1   3175   NP_689673.1  3  1213  CAACCTGGATGG  C       --- AC          3  C  c
c
         2                      AGTTGGAGATCA A ATGATCTCC   TC  TCTAGG
                                TTATTCTA    A TACTAGAGG   AG  AGGTCC
                                         T       TTG  GT
GAM8145  328    FLJ3195 1   15807  NP_653283.1  3  1059  AGAGGTTGCAGT        --    C  G       3  C  c  c

         2                      GAGCTGAGATCA ACATGATCTC  CTCACT TAG
                                TGTCACTG    TGTACTAGAG  GAGTGA GTT
                                          TC     C  G
GAM8145  328    FLJ3399 1   10522  NP_787090.1  3  229   TTGTTGCTTAGG   T  -      CT          3  C  c  c
         6                      ATGAGGAGACTC ACA GA TCTCCTCA  CTAGG
                                TGTAATTT    TGT CT AGAGGAGT  GATTC
                                          -  C       AG
GAM8145  328    FOXL2   1   2486   NP_075555.1  3  1074  CAAGTCCTGGAG A----  -       CA-        3  C  c  c

                                GCAGGGAGATCA     CA TGATCTCCT   CTCTAGGA
                                CTGCCTGC         GT ACTAGAGGG   GAGGTCCT
                                         CGTCC  C        ACG
GAM8145  328    FUT10   1   3533   NP_116053.2  3  309   AATTCACCTAGA   T- TCTC-           3  C  c  c
                                GTGAGTACTTTC ACA  GA    CTCACTCTAGG
                                CTTGTGCA    TGT  CT    GAGTGAGATCC
                                          TC  TTCAT
GAM8145  328    GALNT13 1   16038  XP_054951.3  3  11    CATGACCTTGGG        CTCA-  T         3  C  c
c
                                CACATGAGATCA ACATGATCTC    CTC AGG
```

TGTCCTCC TGTACTAGAG GGG TCC
TACAC T
GAM8145 328 GCNT2 1 12041 NP_001482.1 3 1227 CATGATACCAGG A CAC A 3 C c c
CCCAGGAGATCA AC TGATCTCCT TCT GG
GTAATTAC TG ACTAGAGGA GGA CC
- CCC -
GAM8145 328 GCNT2 1 12041 NP_663624.1 3 1227 CATGATACCAGG A CAC A 3 C c c
CCCAGGAGATCA AC TGATCTCCT TCT GG
GTAATTAC TG ACTAGAGGA GGA CC
- CCC -
GAM8145 328 GCNT2 1 12041 NP_663630.1 3 1227 CATGATACCAGG A CAC A 3 C c c
CCCAGGAGATCA AC TGATCTCCT TCT GG
GTAATTAC TG ACTAGAGGA GGA CC
- CCC -
GAM8145 328 GPLD1 1 1243 NP_001494.2 5 92 AGAAGCCGGTGG ---- CTA 3 C c c
GCAATGAGATCA ACATGATCTC CTCACT GG
TGTCTGCT TGTACTAGAG GGGTGG CC
TAAC ---
GAM8145 328 GPLD1 1 1243 NP_803436.1 5 41 AGAAGCCGGTGG ---- CTA 3 C c c
GCAATGAGATCA ACATGATCTC CTCACT GG
TGTCTGCT TGTACTAGAG GGGTGG CC
TAAC ---
GAM8145 328 GPR30 1 7529 NP_001496.1 5 477 CACCATGCCGGT T - T A 3 C c c
GTGAGGAGCATC ACA GAT CTCCTCAC CT GG
TGTTCTTC TGT CTA GAGGAGTG GG CC
- C T -
GAM8145 328 GPR55 1 8432 NP_005674.1 3 984 TAGACAGCTGAG TCC A A 3 C c c
AGGACCTGATCA ACATGATC TC CTCT GG
TGTAGGGA TGTACTAG AG GAGA TC
TCC - G
GAM8145 328 GTF2F1 1 8940 NP_002087.1 3 85 CGCCATCCTAGA T TCT 3 C c c
GTGAGGCTCTGT ACA GA CCTCACTCTAGGA
CCAATACA TGT CT GGAGTGAGATCCT
- C--
GAM8145 328 HIC2 1 18759 NP_055909.1 3 4457 TAATTGGAACTG T AC G 3 C c c
GAAGAGGGATCA ACATGATC CCTC TCTAG
TGTTTTGT TGTACTAG GGAG AGGTC
- A- A
GAM8145 328 HIC2 1 18759 XP_036937.2 3 4457 TAATTGGAACTG T AC G 3 C c c
GAAGAGGGATCA ACATGATC CCTC TCTAG
TGTTTTGT TGTACTAG GGAG AGGTC
- A- A
GAM8145 328 HPSE 1 454 NP_006656.1 3 685 GACAATTCAGAG T A- A 3 C c c
GCGAGGAGATTC ACA GATCTCCTC CTCT GGA
TGTAAACT TGT TTAGAGGAG GAGA CTT
C CG -

GAM8145 328 HSPC009 1 6013 NP_054738.1 3 24 TCCTATCTGGAT TC-- C 3 C c c
GGGTATTGATCA ACATGATC CTCA TCTAGG
TGTCCAAC TGTACTAG GGGT AGGTCT
TTAT -
GAM8145 328 KIAA026 1 16213 XP_045954.2 3 1828 CCTTTCTGGGGA GATC A- 3 C c
c
5 GTGAGGAATGTG ACAT TCCTCACTCT GGA
GGAGAGAG TGTA AGGAGTGAGG TCT
---- GG
GAM8145 328 KIAA035 1 18748 NP_055687.1 3 2290 CTTAATTATAGT TCTCC T 3 C c
c
4 CTGGCGTGATCA ACATGA TCAC CTAGG
TGTAGAAT TGTACT AGTG GGTCT
----- C
GAM8145 328 KIAA056 1 16594 XP_038664.6 3 712 CTTGCTGCTAGA GA- -- G 3 C c c

4 GTGGGAGGAGAA ACAT TCTCCTC ACTCTAG
AGATGTCT TGTA AGAGGAG TGAGATC
GAA GG G
GAM8145 328 KIAA057 1 16814 XP_291018.1 3 2337 AATTATCCTAGA A------ T TC 3 C c
c
0 GTGAGGACTTCT CA GA TCCTCACTCTAGGA
GCAGCTTA GT CT AGGAGTGAGATCCT
ATTCGAC - TC
GAM8145 328 KIAA079 1 8567 NP_079286.1 3 1595 CCGTATCCAGAA ---- CAC A 3 C c
c
5 GGATAGTGATCA ACATGATC TCCT TCT GGA
TGTCTAGT TGTACTAG AGGA AGA CCT
TGAT --- -
GAM8145 328 KIAA087 1 3812 NP_055755.1 3 2106 GGAGGTTGCAGT -- C G 3 C c c

2 GAGCCGAGATCA ACATGATCTC CTCACT TAG
TGTCACTG TGTACTAGAG GAGTGA GTT
CC C G
GAM8145 328 KIAA103 1 14136 XP_085748.1 5 4 CAACATTCCGGG CAC A 3 C c c
9 ACAGGGAGATCA ACATGATCTCCT TCT GGA
TGTTTCAC TGTACTAGAGGG AGG CCT
AC- G
GAM8145 328 KIAA182 1 15750 XP_041566.2 3 113 ACGTGTTCTAGA A - - 3 C c c
2 GTGAAGGGGGTG AC TG ATCTCCT CACTCTAGGA
CGGGTGTG TG GC TGGGGGA GTGAGATCTT
G G A
GAM8145 328 KIAA184 1 5943 XP_087056.4 3 1892 AGAGGTTGCAGT -- C G 3 C c c
1 GAGCTGAGATCA ACATGATCTC CTCACT TAG
TGTTTCTG TGTACTAGAG GAGTGA GTT
TC C G
GAM8145 328 KIAA189 1 4184 NP_056212.1 3 529 AAATTACCTGGA TGATC 3 C c
c
2 GTGAGGATTACT ACA TCCTCACTCTAGG
TGTAATTA TGT AGGAGTGAGGTCC

```
                                                TCATT
GAM8145  328   KIAA198 1   15733  XP_114000.1  3  464   ATCGAGATGCCT A-----          CTC        3  C  c
c
          1                          ATGAGGAGATCG      CATGATCTCCTCA  TAGG
                                     TGAGGCTG          GTGCTAGAGGAGT  ATCC
                                           GTCGGA            ---
GAM8145  328   KLHL8   1   12192  NP_065854.1  3  414   GTTTTTCCTAGA  A      C  A           3  C  c  c
                                     GGAGAGATTAGT AC TGATCTC TC CTCTAGGA
                                     ACCTATTC     TG ATTAGAG AG GAGATCCT
                                              -      - -
GAM8145  328   KNG    1   1846   NP_000884.1  5  25    TCAGCTCCTAGA A      C-----  A         3  C  c  c
                                     GGGAGATTGTTA  CATGATCT     CTC CTCTAGGA
                                     GATCATGA      GTACTAGA     GAG GAGATCCT
                                           A       TTGTTA  G
GAM8145  328   KRTHBP2 1   11295  XP_303553.1  3  488   AACTGCTGGAGG    -----          A-      3  C  c
c
                                     GTGAGGAGATCC ACAT     GATCTCCTCACTCT  GG
                                     GGCTGTGT     TGTG     CTAGAGGAGTGGGA  TC
                                              TCGGC            GG
GAM8145  328   LOC1344 1   8992   NP_660309.1  3  317   AAAAGAACATTA        CCTC      G         3  C  c
c
          92                         GAGTATAGATCA ACATGATCT    ACTCTAG
                                     TGTGAAAT     TGTACTAGA    TGAGATT
                                              TA--       A
GAM8145  328   LOC1491 1   12363  XP_097598.1  5  675   GTGACTTCTGTG   -  --        C         3  C  c  c
          49                         GTGAGGAGGCTT ACA TGA  TCTCCTCACT TAGGA
                                     CAGTGTTC     TGT ACT  GGAGGAGTGG GTCTT
                                              G  TC         T
GAM8145  328   LOC1493 1   12288  XP_086503.1  3  508   TGGAGTCCTAGA    GA  -   AC           3  C  c
c
          51                         GAGGCAGACAAT ACAT  TCT CCTC  TCTAGGA
                                     GTTGATGA     TGTA  AGA GGAG  AGATCCT
                                              AC   C    --
GAM8145  328   LOC1496 1   20142  XP_086647.4  5  666   ACGTGATTGACC         C  CTCT          3  C  c
c
          70                         TTGGCGAGATCA ACATGATCTC TCA    AGG
                                     TGTTTCTA     TGTACTAGAG GGT    TCC
                                              C   ----
GAM8145  328   LOC1509 1   11545  XP_097977.2  3  496   AGCTGCCCCAGA    G-  CT       A         3  C  c
c
          46                         GTGAGGGTGTAG ACAT  AT  CCTCACTCT GG
                                     ATGTCTGT     TGTA  TG  GGAGTGAGA CC
                                              GA  TG        C
GAM8145  328   LOC1540 1   17934  XP_087842.1  3  113   ATAAAGCCTAGA     ATCTCC             3  C  c
c
          62                         GTGATATGTTTA ACATG     TCACTCTAGG
                                     TCTATAAA     TGTAT     AGTGAGATCC
                                              ------
GAM8145  328   LOC1584 1   12592  XP_098936.1  5  1817  CATGTAGCCCTA    G       ACTC          3  C  c
c
```

02 TCGAGGAGATGA ACAT ATCTCCTC TAGG
TGTAGGGG TGTA TAGAGGAG ATCC
G CT--
GAM8145 328 LOC2214 1 5393 XP_168138.1 3 1027 ATAAATTCAGAA G AC- A 3 C c
c
05 GGGAGGAGATGT ACAT ATCTCCTC TCT GGA
GTGTACAG TGTG TAGAGGAG AGA CTT
- GGA -
GAM8145 328 LOC2217 1 17794 XP_166471.2 5 428 CACAGGATCCCA A----- TCA A 3 C c
c
10 AGAGGGAGATCA CATGATCTCC CTCT GG
TGAGCCTT GTACTAGAGG GAGA CC
TTCCGA --- A
GAM8145 328 LOC2222 1 10921 XP_168633.1 3 722 GCTCCAGCCTGG TGA T 3 C c
c
25 GTGAGGAGACCC ACA TCTCCTCAC CTAGG
TGTCCTAA TGT AGAGGAGTG GGTCC
CCC -
GAM8145 328 LOC2532 1 4153 XP_171113.3 3 280 CCAAGGACCGCA GA CTA 3 C c
c
28 GTGAGGAGGAAT ACAT TCTCCTCACT GG
GTACCACT TGTA GGAGGAGTGA CC
A- CG-
GAM8145 328 LOC2549 1 18473 XP_171161.2 5 30 GCCCCTTCTGGG A AT- 3 C c c

46 GTGAGGAGTACC AC TG CTCCTCACTCTAGGA
AAGTGCAC TG AC GAGGAGTGGGGTCTT
A CAT
GAM8145 328 LOC2831 1 9794 XP_210921.1 3 807 TGTCCTTATAAG A AC ---- 3 C c c
67 AAGAGGAGATTA AC TGATCTCCTC TCT AGGA
GGTCACAG TG ATTAGAGGAG AGA TCCT
G A- ATAT
GAM8145 328 LOC2833 1 9046 XP_210977.1 5 1457 TCTGTTCTTAAG - --- C - 3 C c c
31 ATGAGGAGAGTA ACAT GA TCTCCTCA TCT AGGA
TCTGTGTT TGTG CT AGAGGAGT AGA TTCT
T ATG - A
GAM8145 328 LOC2835 1 13165 XP_210264.2 3 571 AGCTAGCCGGGC CT A 3 C c
c
14 ATGAGGAGATCG ACATGATCTCCTCA CT GG
TGTCTCCA TGTGCTAGAGGAGT GG CC
AC G
GAM8145 328 LOC2838 1 15479 XP_211247.1 3 1118 ATGGTTCCTAGA A TCA 3 C c
c
93 GCCTGGGGGTCA AC TGATCTCC CTCTAGGA
AGTGTTCC TG ACTGGGGG GAGATCCT
A TCC
GAM8145 328 LOC2839 1 15479 XP_211252.3 3 1117 ATGGTTCCTAGA A TCA 3 C c
c
08 GCCTGGGGGTCA AC TGATCTCC CTCTAGGA
AGTGTTCC TG ACTGGGGG GAGATCCT

```
                                        A       TCC
GAM8145  328   LOC2843 1  1483  XP_209156.1  5  675   TATTGTTCAAGA   T    CTC    A        3  C  c
c
         20                          GTGAGATCTTGT ACA GATCTC   ACTCT GGA
                                    AGAGTGGC    TGT CTAGAG   TGAGA CTT
                                           T    ---    A
GAM8145  328   LOC2844 1  7639  XP_209212.1  3  1859  TCAGGGTCTAGA   A  --   CT           3  C  c
c
         45                          GTGGAGAGAAAT AC TGA  TCTC  CACTCTAGG
                                    CGGTAAGA    TG GCT  AGAG  GTGAGATCT
                                           -  AA   AG
GAM8145  328   LOC2844 1  10899 XP_211478.1  5  132   ATTGGTCCTAGA    A  CCTCA           3  C  c
 c
         75                          GAAAAGACTATG ACATG TCT    CTCTAGGA
                                    TCATTTAC    TGTAT AGA    GAGATCCT
                                           C  AAA--
GAM8145  328   LOC2846 1  13805 XP_211586.1  5  963   CTGCCACCAGAG   T T-     -  A        3  C  c
c
         82                          GTGAGGAGTCTC ACA GA  CTCCTCAC TCT GG
                                    TTGTCACT    TGT CT  GAGGAGTG AGA CC
                                           T  CT      G  -
GAM8145  328   LOC2850 1  16224 XP_209474.1  3  1488  CCAAAACCTAGA     T-  C T          3  C  c
c
         99                          GTGGTAGTTTTA ACATGA  CT C CACTCTAGG
                                    TGTAAATG    TGTATT  GA G GTGAGATCC
                                           TT  T -
GAM8145  328   LOC2851 1  8036  XP_211766.1  5  586   GGAAATCCGAGA  C  A  -     A        3  C  c  c

         03                          GTGAGAGAGACA A ATG TCTC CTCACTCT GGA
                                    TCCAGGCT    C TAC AGAG GAGTGAGA CCT
                                           C  -  A      G
GAM8145  328   LOC2854 1  19642 XP_211913.1  3  97    TTTTCACCCAGA A-----      CC     A-     3  C  c
c
         85                          GAGTGAAGATCA     CATGATCT  TCACTCT  GG
                                    TGGAGGAG         GTACTAGA  AGTGAGA  CC
                                           GAGGAG      --      GA
GAM8145  328   LOC2856 1  5278  XP_209713.1  3  49    CAGGTCCACTGG    GA       TA-        3  C  c
c
         62                          GTGAGGAGAGAT ACAT  TCTCCTCACTC   GGA
                                    GTGTGGGC    TGTA  AGAGGAGTGGG   CCT
                                           G-         TCA
GAM8145  328   LOC2856 1  12958 XP_211984.1  3  702   GGATTGTTCCTA   T   -     CT         3  C  c  c

         92                          GTGAGGAAGGTC ACA GATCT CCTCACT  AGGA
                                    TTGTCCCA    TGT CTGGA GGAGTGA  TCCT
                                           T    A     --
GAM8145  328   LOC2858 1  6980  XP_212070.1  3  139   GTGACCCTGGGT A------   A      -       3  C  c  c

         89                          GTGAGGAGACGT       CATG TCTCCTCAC TCTAGG
                                    GGTCTGTG          GTGC AGAGGAGTG GGGTCC
```

GTGTCTG - T
GAM8145 328 LOC2859 1 18029 XP_212131.1 3 19 AAACCTTATAGA CTC --- 3 C c c
78 GTGAGATTATCA ACATGAT CTCACTCT AGG
TGTACAAG TGTACTA GAGTGAGA TCC
TTA TAT
GAM8145 328 LOC2859 1 18029 XP_212114.1 3 19 AAACCTTATAGA CTC --- 3 C c c
81 GTGAGATTATCA ACATGAT CTCACTCT AGG
TGTACAAG TGTACTA GAGTGAGA TCC
TTA TAT
GAM8145 328 LOC2860 1 3075 XP_212130.1 3 272 CTCCTGGAGTGA A----- - -- - 3 C c c
22 GTGAGGATTCAA CAT GA TCTC CTCACTCTAGGA
TGAGATAT GTA CT GGAG GAGTGAGGTCCT
TATAGA A TA T
GAM8145 328 LOC2861 1 12097 XP_212176.1 5 58 CAAGGTCATAGA C T ----- G 3 C c
c
12 GTGAGTGCCTGA A ATGA CTC CTCACTCTA GA
GTCATCCA C TACT GAG GAGTGAGAT CT
C - TCCGT A
GAM8145 328 LOC2863 1 19146 NP_789789.1 3 1096 CCCGCTCCCTAG A----- T CA 3 C c
c
99 AGCAGGAGATCT CA GATCTCCT CTCTAGG
TGAGTGGG GT CTAGAGGA GAGATCC
GGGTGA T C-
GAM8145 328 LOC2864 1 19962 XP_210044.1 5 833 CGGCACCCATGG CCT T - 3 C c
c
30 TGTGCTGGATCA ACATGATCT CAC CTA GG
TGTGCATG TGTACTAGG GTG GGT CC
TC- T A
GAM8145 328 LOC3401 1 17436 XP_291151.1 3 727 CGCCAGCCTGGA A- T ----- 3 C c
c
33 GTGAGGGAGCAG CA GATCT CCTCACTCTAGG
GATCTGGG GT CTAGG GGAGTGAGGTCC
GG - ACGAG
GAM8145 328 LOC3402 1 17407 XP_295197.1 5 10 GGTGGCTGGGGT TC -- G 3 C c
c
76 GGCAGCTGATCA ACATGATC CT CACTCTAG
TGTCAGGA TGTACTAG GA GTGGGGTC
TC CG G
GAM8145 328 LOC3405 1 4381 XP_295268.1 3 1087 ACATCTCCTAGA GATC CA 3 C c
c
28 GCTGGGAATGTG ACAT TCCT CTCTAGGA
TCCCTAAC TGTA AGGG GAGATCCT
---- TC
GAM8145 328 LOC3479 1 16665 XP_301398.1 5 36 CATGGCTTCCAG AC C A A 3 C c
c
41 AGGACGAGATCA ATGATCTC TC CTCT GGA
TA TACTAGAG AG GAGA CCT
A- C - -
GAM8145 328 LOC3483 1 5706 XP_300723.1 3 1440 TGGGAGGCCGAG TC A- TA 3 C c
c

```
          78                          GCGGGTGGATCA ACATGATC  CTC  CTC  GG
                                     TGTGAGGC    TGTACTAG  GGG  GAG  CC
                                                   GT   CG   --
GAM8145  328   LOC3493 1  7639  XP_301042.1  3  1884  TCAGGGTCTAGA  A  --  CT          3  C  c
c
          39                          GTGGAGAGAAAT AC TGA  TCTC  CACTCTAGG
                                     CGGTAAGA    TG GCT  AGAG  GTGAGATCT
                                               -  AA   AG
GAM8145  328   LOC3517 1  20137 XP_305099.1  5  46   AAGGTTCCAAGA A-----  GA       A      3  C  c
c
          43                          GTGAGGAGAGAA      CAT  TCTCCTCACTCT GGA
                                     TGCATGGG         GTA  AGAGGAGTGAGA CCT
                                           GGGTAC   AG          A
GAM8145  328   LOC3522 1  1767  XP_305558.1  5  3    CTTTCTTGAAGT       --  C  C        3  C  c  c
          87                          TAGGTTAGATCA ACATGATCT  CCT ACT TAGGA
                                     TGTTCTCA    TGTACTAGA  GGA TGA GTTCT
                                                  TT   T   A
GAM8145  328   LOC5127 1  16462 NP_057630.1  3  80   AGAGGGCCTGGA A--  -  A  --          3  C  c  c

          9                           GTGAGGACTGAA    CA TG TC  TCCTCACTCTAGG
                                     CACTGGGG       GT AC AG  AGGAGTGAGGTCC
                                           GGG  C  A  TC
GAM8145  328   LOC8994 1  19307 NP_612351.2  3  691   CTCTGGTGTTCA     A       -----       3  C  c  c
          4                           GTGAGGAGGACA ACATG TCTCCTCACT     CTAGG
                                     TGTGAGTC    TGTAC GGAGGAGTGA     GGTCT
                                                  A        CTTGT
GAM8145  328   LOC9082 1  3263  NP_612373.1  5  1280  CCACAAGTCCTA     ATC      CT         3  C  c
c
          6                           GTGAGGAAACAT ACATG   TCCTCACT  AGGA
                                     GTTGGGAA    TGTAC   AGGAGTGA  TCCT
                                                  AA-       --
GAM8145  328   LOC9146 1  6655  XP_038589.1  3  660   GAGCATCTCAGA    GA-   C     AG        3  C  c
c
          4                           GTGAGAGAAAAA ACAT   TCTC TCACTCT  GA
                                     TGTAGAAA    TGTA   AGAG AGTGAGA  CT
                                                  AAA   -      CT
GAM8145  328   LOC9580 1  9601  XP_047816.5  3  206   TGCCTTCCTAGA   -  CT  C           3  C  c  c
          3                           GTTGGGTTGTCA ACA TGAT  CCT ACTCTAGGA
                                     CTGTCCTG    TGT ACTG  GGG TGAGATCCT
                                                  C   TT   T
GAM8145  328   MAN1A1  1  14751 NP_005898.2  3  372   TTTTCCTCCTCT    G      ACTCT         3  C  c
c
                                     AAGAGGAGATGA ACAT ATCTCCTC     AGGA
                                     TGTCTGCT    TGTA TAGAGGAG     TCCT
                                                  G       AATC-
GAM8145  328   MAN2A1  1  9444  NP_002363.1  5  463   TGTCTCCTTTGG    GA      - CT        3  C  c
c
                                     CTGAGGAGAGTG ACAT  TCTCCTCA CT  AGGA
                                     TCCTGGCC    TGTG  AGAGGAGT GG  TCCT
                                                  --       C  TT
```

GAM8145 328 MBNL2 1 1692 NP_659002.1 3 976 AGGAAGCTGTAG T T GG 3 C c c

GTGAGGAGATCT ACA GATCTCCTCAC CTA
GTATAATA TGT CTAGAGGAGTG GAT
- - GT

GAM8145 328 MEOX2 1 10706 NP_005915.1 3 404 GAACATTCCAGA CT - A 3 C c c

TGTGTGAGATCA ACATGATCTC CAC TCT GGA
TGTGTATT TGTACTAGAG GTG AGA CCT
T- T -

GAM8145 328 MGC1110 1 11974 NP_115701.2 3 1668 TGGCCTCCTAGA ---- CT 3 C c c

2 GTGCTGGGATTA ACAT GATCTC CACTCTAGGA
CAGGTGTG TGTG TTAGGG GTGAGATCCT
GACA TC

GAM8145 328 MGC2078 1 1066 NP_443167.1 5 288 AGCCTGGGCGGG A----- - --- 3 C c c

1 TGCAGGAGATCG CATGATCTCCT CACT CTAGG
TGGGCGCC GTGCTAGAGGA GTGG GGTCC
CCGCGG C GCG

GAM8145 328 MGC2743 1 7480 NP_659487.1 3 82 TGATGGCCAGCA - C - A 3 C c c

4 GTGAGGAATCTG ACAT GAT TCCTCACT CT GG
TGTGTTCT TGTG CTA AGGAGTGA GA CC
T - C -

GAM8145 328 NCOA6 1 11974 NP_054790.1 5 1102 TGGCCTCCTAGA ---- CT 3 C c c

GTGCTGGGATTA ACAT GATCTC CACTCTAGGA
CAGGTGTG TGTG TTAGGG GTGAGATCCT
GACA TC

GAM8145 328 OCRL 1 11613 NP_000267.2 3 766 AGTATCTGAAGA T-- C A- 3 C c c

GTGAGAGCATTC ACATGA CTC TCACTCT GGA
ATGTTTGA TGTACT GAG AGTGAGA TCT
TAC - AG

GAM8145 328 OCRL 1 11613 NP_001578.2 3 766 AGTATCTGAAGA T-- C A- 3 C c c

GTGAGAGCATTC ACATGA CTC TCACTCT GGA
ATGTTTGA TGTACT GAG AGTGAGA TCT
TAC - AG

GAM8145 328 PCDHA11 1 10904 NP_061725.1 5 170 GCCCACAGAGAT C-- - A- 3 C c c

GAGAATAGATCA ACATGATCT CTCA CTCT GG
TGTGGAAC TGTACTAGA GAGT GAGA CC
TAA A CA

GAM8145 328 PCDHA11 1 10904 NP_114067.1 5 170 GCCCACAGAGAT C-- - A- 3 C c c

GAGAATAGATCA ACATGATCT CTCA CTCT GG
TGTGGAAC TGTACTAGA GAGT GAGA CC
TAA A CA

GAM8145 328 PEF 1 5634 NP_036524.1 3 71 TGGCTTCTTAGA A- C 3 C c c

GTGAGAGAAGTA ACATG TCTC TCACTCTAGGA
TGTGGACA TGTAT AGAG AGTGAGATTCT

GA -

GAM8145 328 PKD1-li 1 2164 NP_079150.2 3 2 GGAGCCCGCGGG T A CTA 3 C c c
ke AGGAGATCCTGT ACA GATCTCCTC CT GG
ACCACCTG TGT CTAGAGGAG GG CC
C - CG-

GAM8145 328 PLSCR3 1 11017 NP_065093.2 3 29 GGCCACCATGGT C A T - 3 C c c

GTGAGGAGACCA A ATG TCTCCTCAC CTA GG
TCACCTCG A TAC AGAGGAGTG GGT CC
C C T A

GAM8145 328 PML 1 18322 NP_150241.1 3 286 GGGAGGTCCTGA A----- A - T 3 C c c
GTGAGGAAGGCA CATG TCT CCTCACTC AGGA
TGACCTCT GTAC GGA GGAGTGAG TCCT
TCTCCA - A -

GAM8145 328 PNPLA1 1 17384 NP_775947.1 5 55 AAGGCTTCTTGG C G A 3 C c c
AGGAGGAGATGA A AT ATCTCCTC CTCTAGGA
TTGAGCTG G TA TAGAGGAG GAGGTTCT
T G -

GAM8145 328 POU3F2 1 19075 NP_005595.1 3 286 CTCCTGGAGAGA GA ---- 3 C c c

GTGAGGAGAGTG ACAT TCTCCTCACTCT AGGA
TGTGATAG TGTG AGAGGAGTGAGA TCCT
TG GAGG

GAM8145 328 PPEF2 1 9035 NP_690911.1 3 109 CAACCTGTTACA --- C--- 3 C c c
GTGAGGAGATCA ACA TGATCTCCTCACT TAGG
CAGTGTGT TGT ACTAGAGGAGTGA GTCC
GAC CATT

GAM8145 328 PRKAR2B 1 6242 NP_002727.1 3 700 AACAGTGTTTTA C C C 3 C c c

GATGAGAGATCA A ATGATCTC TCA TCTAGGA
TTAATGCA A TACTAGAG AGT AGATTTT
T - -

GAM8145 328 PTPN9 1 6603 NP_002824.1 3 725 TGGACTAGCTTG T TC T 3 C c c
GGTTGGTGATCA ACATGATC CC AC CTAGG
TGTCTCCT TGTACTAG GG TG GGTTC
T T- -

GAM8145 328 PTPRT 2 6604 NP_008981.2 3 405 TCTCCTTAGGAG G - -- 3 C c c
TGGAGGAGATGT ACAT ATCTCCTC ACTCT AGGA
GTGTTCTG TGTG TAGAGGAG TGAGG TCCT
- G AT

GAM8145 328 PTPRT 2 6604 NP_573400.1 3 405 TCTCCTTAGGAG G - -- 3 C c c
TGGAGGAGATGT ACAT ATCTCCTC ACTCT AGGA
GTGTTCTG TGTG TAGAGGAG TGAGG TCCT
- G AT

GAM8145 328 PTPRT 2 19034 NP_008981.2 3 7066 TGAGATCTTGTG T TCA G 3 C c
c

GAGCTGGGATCA ACATGATC CC CTCTA GA
TGTTTGAA TGTACTAG GG GAGGT TT
- TC- G

GAM8145 328 PTPRT 2 19034 NP_573400.1 3 7066 TGAGATCTTGTG T TCA G 3 C c
c

GAGCTGGGATCA ACATGATC CC CTCTA GA
TGTTTGAA TGTACTAG GG GAGGT TT
- TC- G

GAM8145 328 RHOBTB3 1 10064 NP_055714.1 5 318 GCCCTGCCCTTG CTCAC 3 C c c

GATTTGAGATCA ACATGATCTC TCTAGG
TGTCCATC TGTACTAGAG AGGTTC
TTT--

GAM8145 328 RNF14 1 11351 NP_004281.1 3 1330 TGTGTGTCCAGA C-- A 3 C c c

GTGAGCAAGGAT ACATGATCT CTCACTCT GGA
TATGTTTT TGTATTAGG GAGTGAGA CCT
AAC -

GAM8145 328 SCNN1G 1 1599 NP_001030.1 3 599 CCCTTGGAGTGT A- T---- 3 C c c

TGGTGGAGATCA AC TGATCTCC CACTCTAGG
GAGTGCCG TG ACTAGAGG GTGAGGTTC
AG TGGTT

GAM8145 328 SH3GL2 1 10145 NP_003017.1 3 1294 TGTGCCACCTGC TC C C 3 C c c

AGTAGTGGATCA ACATGATC CT ACT TAGG
TGTGGAGT TGTACTAG GA TGA GTCC
GT - C

GAM8145 328 TACTILE 1 16831 NP_005807.1 3 207 GCTTAACCAAGA ---- TC A 3 C c c

GTGAGAGGATAT ACATGA TC CTCACTCT GG
GTCATGTT TGTACT AG GAGTGAGA CC
GTAT GA A

GAM8145 328 TAF6 1 1733 NP_005632.1 5 332 GCCTCCACTGAT T C- TA- 3 C c c

CTGAGGAGATCC ACA GATCTCCTCA TC GGA
TGTGACTG TGT CTAGAGGAGT AG CCT
C CT TCA

GAM8145 328 TAF6 1 1733 NP_620835.1 5 332 GCCTCCACTGAT T C- TA- 3 C c c

CTGAGGAGATCC ACA GATCTCCTCA TC GGA
TGTGACTG TGT CTAGAGGAGT AG CCT
C CT TCA

GAM8145 328 TBL1X 1 2978 NP_005638.1 3 2930 GACCTTCCTAGA A TCCT 3 C c c

GTGTTTGGTCGG AC TGATC CACTCTAGGA
GTTCACAG TG GCTGG GTGAGATCCT
G TTT-

GAM8145 328 TCL1B 1 4847 NP_004909.1 3 83 CATGCCCCCTCA TC- CT 3 C c c

GTGAGGATCTTC ACATGA TCCTCACT AGG
ATGTACCT TGTACT AGGAGTGA TCC
TCT C-

GAM8145 328 TKTL1 1 10570 NP_036385.1 5 1 GCTTCTATGAGG A CTC 3 C c c

AGACCATGTGCC ACATG TCTCCTCA TAGGA
GAGGTCGT TGTAC AGAGGAGT ATCTT
C ---

GAM8145 328 TTTY9 1 17970 NP_114133.1 3 985 CAGACCTCTAGA T CCT- 3 C c c

GTGTCCTAGATT ACA GATCT CACTCTAGG
TTGTGGCA TGT TTAGA GTGAGATCT
T TCCT
GAM8145 328 UXS1 1 9295 NP_079352.1 5 519 GCTCATCGTCTA A - CT 3 C c c
GTGAGGAAGGCA ACATG TCT CCTCACT AGG
TGTGTGAA TGTAC GGA GGAGTGA TCT
- A --
GAM8145 328 VPS4A 1 12450 NP_037377.1 3 594 TGTCTTCCTTGG G A 3 C c c
GGGAGGAGATGG ACAT ATCTCCTC CTCTAGG
TGTCGTTT TGTG TAGAGGAG GGGGTTC
G -
GAM8145 328 WDR17 1 15836 NP_851782.1 3 81 AATTTTTCTTAG C - T 3 C c c
GTGAGGAGGATT A ATGATC TCCTCAC CTAGGA
ATTAACTG A TATTAG AGGAGTG GATTCT
T G -
GAM8145 328 ZNF187 1 1570 NP_689949.1 3 936 AAAGTCAGCTTG A----- AC 3 C c c
GAGAGGAGATCA CATGATCTCCTC TCTAGG
TGATCTTT GTACTAGAGGAG AGGTTC
TTTCTA --
GAM8297 367 ABCF2 1 2015 NP_005683.2 5 64 CGAGGCCCAGCT A- CAC 3 B c c
CCCTGAAACAAC GCTGTTGTT AGGG TTGGG
AGTAACCT TGACAACAA TCCC GACCC
AG TC-
GAM8297 367 ABCF2 1 2015 NP_009120.1 5 64 CGAGGCCCAGCT A- CAC 3 B c c
CCCTGAAACAAC GCTGTTGTT AGGG TTGGG
AGTAACCT TGACAACAA TCCC GACCC
AG TC-
GAM8297 367 ADAM2 1 6042 NP_001455.2 5 28 TAACCACCAACT TT T C 3 B c c
GCCCTTATTCCG GCTG GT AAGGGCA TTGG
GCTGGGAC CGGC TA TTCCCGT AACC
CT - C
GAM8297 367 ADCY1 1 13856 NP_066939.1 3 5255 GCAGGGCCAAGT T AA- 3 B c
c
GCCCATGAGCAC GCTGT GTT GGGCACTTGG
AGCCCCAG CGACA CGA CCCGTGAACC
- GTA
GAM8297 367 ADORA3 1 2855 NP_000668.1 5 761 TGGGAAGGCAAG AA - G 3 B c
c
ATGCCCAACAAC GCTGTTGTT GGGCA CTTG
AGCACTGC CGACAACAA CCCGT GAAC
-- A G
GAM8297 367 ALK7 1 7726 NP_660302.1 3 140 CAGTATTTAAGT G A 3 B c c
GCCCATAAGGCA GCTGTT TTA GGGCACTTGGG
GCATGAAA CGACGG AAT CCCGTGAATTT
- A
GAM8297 367 ARHF 1 11640 NP_061907.1 3 269 GGACTCGCAAGT T TTA G 3 B c
c
GCCCTCATCACA GCTGT G AGGGCACTTG

GCCACCCC CGACA C TCCCGTGAAC
- TAC G
GAM8297 367 ARHGEF1 1 19384 NP_055444.1 5 1742 CTGGGTCCCAGG G G A 3 B c c
0 AGCCTTAACAAG GCT TTGTTAAGG C CTTGGG
GCATTGAG CGG AACAATTCC G GGACCC
- - A
GAM8297 367 ASB17 1 491 NP_543144.1 3 37 CAGTGTCCTAAG T C 3 B c c
TTCCTTAACAAT GC GTTGTTAAGGG ACTTGGG
GCTTACCA CG TAACAATTCCT TGAATCC
- -
GAM8297 367 B3GAT1 1 1556 NP_061114.1 3 1845 AGCCAGCCAAGT -- TTAAG 3 B c c
GCCAAGGTCAGC GCT GTTG GGCACTTGG
TTGGCTGG CGG CGAC CCGTGAACC
TT TGGAA
GAM8297 367 B3GAT1 1 1556 NP_473366.1 3 1827 AGCCAGCCAAGT -- TTAAG 3 B c c
GCCAAGGTCAGC GCT GTTG GGCACTTGG
TTGGCTGG CGG CGAC CCGTGAACC
TT TGGAA
GAM8297 367 BGN 1 14465 NP_001702.1 3 327 CCAAACCCAAGT TT AA 3 B c c
GTCCAAGGCTCC GCTG GTT GGGCACTTGGG
AGTCCTAG TGAC CGG CCTGTGAACCC
CT AA
GAM8297 367 BLR1 1 18216 NP_001707.1 3 723 CTGACTCTAGGT - TG 3 B c c
GCCCTTGGAGGC GCTG T TTAAGGGCACTTGGG
CAGCCAGT CGAC G GGTTCCCGTGGATCT
C GA
GAM8297 367 BLR1 1 18216 NP_116743.1 3 723 CTGACTCTAGGT - TG 3 B c c
GCCCTTGGAGGC GCTG T TTAAGGGCACTTGGG
CAGCCAGT CGAC G GGTTCCCGTGGATCT
C GA
GAM8297 367 C1orf2 1 11170 NP_006580.1 5 526 ATGCTCCCAAGT -- G AAG 3 B c c
GCCAGGGAGGGC GCT GTT TT GGCACTTGGG
CGAGCGAG CGA CGG AG CCGTGAACCC
GC G GGA
GAM8297 367 C21orf1 1 3476 XP_114191.2 3 2830 CTTGACCTAGGT - T T-- 3 B c c
08 GCCCTTTCTGCT GC TGT GT AAGGGCACTTGGG
ACATGCAA CG ACA CG TTCCCGTGGATCC
T T TCT
GAM8297 367 C6orf33 1 10725 NP_588608.1 3 1827 TGTTACCCAAGT GT TA 3 B c c
GTCTTATACAAG GCT TGT AGGGCACTTGGG
CTTCTGGT CGA ACA TTCTGTGAACCC
-- TA
GAM8297 367 C6orf50 1 16763 XP_166460.1 3 207 TACAATCCAAGT - TTAAGG 3 B c c
GCATTCAACAAG GCT GTTG GCACTTGGG
TGATATGG TGA CAAC CGTGAACCT
A TTA---

GAM8297 367 C9orf14 1 17546 XP_098859.2 5 315 CCATTTCTCTGT TT TT 3 B c c
GCCCTTTTGACA GCTGTTG AAGGGCAC GGG
GCTCCAGG CGACAGT TTCCCGTG CTC
T- T-
GAM8297 367 CACNA1D 1 7620 NP_000711.1 5 73 GCCCAGCACAGT - TA ---- 3 B c c

GCCCTGCACACA GCTGT TGT AGGGCACT TGGG
GTAGTCGC TGACA ACG TCCCGTGA ACCC
C -- CACG
GAM8297 367 CACNA1H 1 14959 NP_066921.1 3 402 TGGGGGCCCTGT T TT 3 B c
c
GCCCTTGCCGGC GCTGTTG TAAGGGCAC GGG
GGCAGGTT CGGCGGC GTTCCCGTG CCC
C T-
GAM8297 367 CACNB1 1 17887 NP_000714.2 3 184 CAGCTCCCGGGA TT - A 3 B c
c
GCCCTTAAGCCC GCTG GTT AAGGGC CTTGGG
CAGCTGTC CGAC CGA TTCCCG GGGCCC
CC A A
GAM8297 367 CCL14 1 12494 NP_004157.1 5 884 CCAGGCCAGCTC TA---- A-- 3 B c c

TCCTCCCACAAC GCTGTTGT AGGGC CTTGG
AGCTTCCC CGACAACA TCTCG GGACC
CCCTCC ACC
GAM8297 367 CCL14 1 12494 NP_116738.1 5 884 CCAGGCCAGCTC TA---- A-- 3 B c c

TCCTCCCACAAC GCTGTTGT AGGGC CTTGG
AGCTTCCC CGACAACA TCTCG GGACC
CCCTCC ACC
GAM8297 367 CCL14 1 12494 NP_116739.1 5 21 CCAGGCCAGCTC TA---- A-- 3 B c c
TCCTCCCACAAC GCTGTTGT AGGGC CTTGG
AGCTTCCC CGACAACA TCTCG GGACC
CCCTCC ACC
GAM8297 367 CCL15 1 12494 NP_004158.1 3 93 CCAGGCCAGCTC TA---- A-- 3 B c c
TCCTCCCACAAC GCTGTTGT AGGGC CTTGG
AGCTTCCC CGACAACA TCTCG GGACC
CCCTCC ACC
GAM8297 367 CCL15 1 12494 NP_116740.1 3 93 CCAGGCCAGCTC TA---- A-- 3 B c c
TCCTCCCACAAC GCTGTTGT AGGGC CTTGG
AGCTTCCC CGACAACA TCTCG GGACC
CCCTCC ACC
GAM8297 367 CDK5RAP 1 3296 NP_079473.2 3 722 AGATTGCCAAGT T AAG 3 B c
c
3 GCCAGCAGCTGC GCTGT GTT GGCACTTGG
AGCAAGAA CGACG CGA CCGTGAACC
T CGA
GAM8297 367 CDK5RAP 1 3296 NP_788275.1 3 722 AGATTGCCAAGT T AAG 3 B c
c
3 GCCAGCAGCTGC GCTGT GTT GGCACTTGG
AGCAAGAA CGACG CGA CCGTGAACC

T CGA
GAM8297 367 CGA 1 6094 NP_000726.1 3 32 GTTTTACCAAGT T TG -- 3 B c c
GCTGTCTTGATG GC GT TTAAG GGCACTTGG
ACTGCTGA CG CA AGTTC TCGTGAACC
T GT TG
GAM8297 367 CGI-69 1 15577 NP_057100.1 3 87 ACCCAGCCAAGT TTGTT 3 B c c
GCCTTTTCCTCA GCTG AAGGGCACTTGG
GCACTGAG CGAC TTTCCGTGAACC
TCCT-
GAM8297 367 CNNM2 1 9355 NP_060119.2 3 151 CAAAGACCTTGT G TT TT 3 B c
c
GCCCTTCCCAGG GCT TTG AAGGGCAC GG
AGCCGCGG CGA GAC TTCCCGTG CC
G CC TT
GAM8297 367 CNR1 1 8385 NP_057167.1 3 1013 TTCATGCCTGGG AA G TG 3 B c
c
TGGCCAAACAAC GCTGTTGTT GG CACT GG
AGTCTTCA TGACAACAA CC GTGG CC
A- G GT
GAM8297 367 COL1A1 1 10598 NP_000079.1 3 501 AAACACCCAAGT TTGTTAA - 3 B c
c
GGCCCCCACCCT GCTG GGGC ACTTGGG
CAGCCCGC CGAC CCCG TGAACCC
TCCCACC G
GAM8297 367 CPR2 1 19074 NP_112162.1 3 16 AGCTGGCCAAGT T AG 3 B c c
GCTTGTGCCAGC GCTGTTG TA GGCACTTGG
AGCATGGA CGACGAC GT TCGTGAACC
C GT
GAM8297 367 CRHR1 1 6267 NP_004373.2 3 901 CCCTGCCCAAGT - -- - 3 B c c
GGCTCTTGGGAC GC TGTTGTT AAGGGC ACTTGGG
AACGTGCT CG GCAACAG TTCTCG TGAACCC
T GG G
GAM8297 367 CRTL1 1 1537 NP_001875.1 3 20 TACAACTGATGT T G - TG 3 B c c
GCCCTTAGAGCG GC GTT TTAAGGGCAC T G
CACTAGTT CG CGA GATTCCCGTG A C
- - T GT
GAM8297 367 CSNK1G2 1 10903 NP_001310.2 3 16 AGCGACACAAGT --- TA G 3 B c
c
GCCCTGGGCGCG GCTGT TGT AGGGCACTTG
TGCAGCCC CGACG GCG TCCCGTGAAC
TGC GG A
GAM8297 367 CYC1 1 2163 NP_001907.2 3 16 GGCCGCCCAAGT TTGTTA 3 B c c
GCCCTGTCCAGT GCTG AGGGCACTTGGG
GTCTGCTT TGAC TCCCGTGAACCC
CTG---
GAM8297 367 CYFIP2 1 7131 NP_055191.1 5 132 GACTTGCTGTGT TTG T 3 B c c
GCCCTTAAACCA GCTG TTAAGGGCAC TGG
GCCACTAC CGAC AATTCCCGTG GTC
CA- T

GAM8297 367 DAAM1 1 13477 NP_055807.1 3 727 TCTCTGCCAAGT CT 3 B c c
GCTCTTGATAAT G GTTGTTAAGGGCACTTGG
TTCTTCAG C TAATAGTTCTCGTGAACC
TT
GAM8297 367 DEFB1 1 7595 NP_005209.1 3 7 GGAAGGCCAAGT - TAAG 3 B c c
GCTGCAAGTGGC GCTG TTGT GGCACTTGG
TGGGAGTG CGGT AACG TCGTGAACC
G ----
GAM8297 367 DEPC-1 1 9065 NP_631917.1 5 219 GGAAAAGGAAGT -- --- GG 3 B c c
GCCCTTATCCAC GCT GTTGT TAAGGGCACTT
GACCAAGC CGA CAGCA ATTCCCGTGAA
AC CCT GG
GAM8297 367 DIO3 1 3054 NP_001353.2 3 314 CCTCAGCCAAGT TT G 3 B c c
GCTTTGGCCCGG GCTG GTTAAGG CACTTGG
TGCTTCCC TGGC CGGTTTC GTGAACC
C- -
GAM8297 367 DKFZP43 1 2459 NP_061864.1 3 1188 AGCCACCCTCGG AA A --- 3 B c
c
4A0131 AGAGTCCACAAC GCTGTTGTT GGGC CTT GGG
AGCAGCCA CGACGACAA CCTG GAG CCC
CA A GCT
GAM8297 367 DKFZp54 1 9218 XP_091486.2 3 301 GGCACTCCAAGT G ---- -- 3 B c c
7J144 GCATCCTCCACT CTGTTGTTA AGG GCACTTGGG
GGCAACAG GACAACGGT TCC CGTGAACCT
- CACC TA
GAM8297 367 DKFZP56 1 17456 NP_054761.1 3 127 GTGCCTGAAAGT GTTGT -- 3 B c
c
4M082 GCCCTTGGGCAC GCT TAAGGGCACTT GGG
CTCCTCAG CGG GTTCCCGTGAA TCC
----- AG
GAM8297 367 DKFZp76 1 1345 XP_086327.6 3 1787 CCTGTCCCAAGT - T- AG 3 B c
c
1N1114 GCTGTGATTCAC GC TGT GTTA GGCACTTGGG
ACGCCTGA CG ACA TAGT TCGTGAACCC
C CT G-
GAM8297 367 DKFZp76 1 20098 NP_689801.1 3 1205 CTTCTGCCAAGT TTGTT 3 B c
c
2A217 GCTTTTCTCAGT GCTG AAGGGCACTTGG
TGAAAACT TGAC TTTTCGTGAACC
TC---
GAM8297 367 DOCK3 1 3680 XP_039259.5 3 2833 CATCTCCCAAGT - TAA G 3 B c c
GGCCACATACAG GCTGT TGT GG CACTTGGG
CAACCCAC CGACA ACA CC GTGAACCC
T --- G
GAM8297 367 DRIL2 1 1268 NP_006456.1 3 2061 ACCCTCACTGCC A--- CTT- 3 B c c
CTCAAGGACAAC GCTGTTGTT AGGGCA GGG
AGCAGGGT CGACAACAG TCCCGT CCC
GAAC CACT
GAM8297 367 EDG1 1 11979 NP_001391.2 3 1114 CCACCCTCTTGT GTTGT TT-- 3 B c
c

GCCCTTAAGCAT GCT TAAGGGCAC GGG
TACTTTAA CGA ATTCCCGTG CCC
----- TTCT

GAM8297 367 EDN3 1 18442 NP_000105.1 5 122 CCCGGCCCCAGT TGTT T 3 B c c

GCCCTTTCGCGG GCTGT AAGGGCACT GGG
CCACAAGC CGGCG TTCCCGTGA CCC
CT-- C

GAM8297 367 EDNRA 1 14062 NP_001948.1 3 683 CAAATACTACAG TG- A - 3 B c c

GCCCTTAAAGCA GCTGT TTAAGGGC CT TGG
CAGTCTGA TGACA AATTCCCG GA ATC
CGA - C

GAM8297 367 EGFL4 1 15348 XP_290821.1 3 495 GGAGACCCAAGT TTAA- -- 3 B c c

GGGCCCGGCGCC GCTGTTG GGGC ACTTGGG
AACGGCTC CGGCAAC CCCG TGAACCC
CGCGG GG

GAM8297 367 ERN1 1 14185 NP_001424.1 3 131 CCCAAACCAAGT T- T A 3 B c c

GCCTTGAGCTGC GC GT GTT AGGGCACTTGG
CTGCTCTG CG CG CGA TTCCGTGAACC
TC T G

GAM8297 367 FLJ1052 1 9343 NP_060595.1 3 697 CATCTGGCAGGT -- G 3 B c c
1

GCCCTTGATGCT GCTGT TGTTAAGGGCACTTG
ATAGCGCC CGATA GTAGTTCCCGTGGAC
TC G

GAM8297 367 FLJ1078 1 3362 NP_060689.1 3 60 ACCAGGCCCAGT TG TTA T 3 B c c

6

GCCCTCAAATGC GC TTG AGGGCACT GGG
CTCCCTCA CG AAC TCCCGTGA CCC
TA --- -

GAM8297 367 FLJ1080 1 13516 NP_060694.1 3 580 GAAAATCCCAGG - G A 3 B c c
3

GCCCTTAAGATA GC TGTT TTAAGGGC CTTGGG
TGCTGTAT CG ATAG AATTCCCG GGACCC
T - -

GAM8297 367 FLJ1089 1 15940 NP_061957.1 3 2036 ATAGAGATCCCA AA CAC 3 B c c

5

ACTTGAAACAAC GCTGTTGTT GGG TTGGG
AGCCAGTG CGACAACAA TTC AACCC
AG ---

GAM8297 367 FLJ1153 1 12818 NP_079024.1 3 278 CCTCAATCAAGT GTTG 3 B c c

9

GCCTTTAAATAG GCT TTAAGGGCACTTGG
AGCTGCAC CGA AATTTCCGTGAACT
GATA

GAM8297 367 FLJ1266 1 1015 NP_079428.1 3 27 TGTTCCCCAAGT T- GTTA 3 B c c
0

GTCCTGGAAATT GC GTT AGGGCACTTGGG
TGCCTGGT CG TAA TCCTGTGAACCC
TT AGG-

GAM8297 367 FLJ1278 1 16212 NP_071937.1 3 1539 TACCTCCCAAGT T TAA 3 B c c

8 GCCTGGTACATA GCTGT GT GGGCACTTGGG
GTGGGTGC TGATA CA TCCGTGAACCC
- TGG
GAM8297 367 FLJ1426 1 10780 NP_079303.2 5 435 GATCCTAAAAGT T- T -- 3 B c c
0 GCCCTTGGCTGC GC GT GTTAAGGGCACT TGGG
CTGCTGGA CG CG CGGTTCCCGTGA ATCC
TC T AA
GAM8297 367 FLJ1482 1 5731 NP_116237.1 3 331 TTGCTGCCAAGT GTTAAGG 3 B c
c
7 GCGAATAAACGG GCTGTT GCACTTGG
CGTGATTG CGGCAA CGTGAACC
ATAAG--
GAM8297 367 FLJ2007 1 2651 NP_060126.1 3 673 ATAACTGCCAGT T TT T 3 B c c
9 GCCCTTTCACAG GCTGT G AAGGGCACT GG
CTGATTAT CGACA C TTCCCGTGA CC
- T- -
GAM8297 367 FLJ2036 1 12890 NP_060255.2 3 3 CAGAGACCCAGT TTA T 3 B b b
4 GCCCTCAACAGT GCTGTTG AGGGCACT GGG
AAGACTTT TGACAAC TCCCGTGA CCC
--- -
GAM8297 367 FLJ2050 1 19215 NP_060315.1 3 840 GTAACCTCAGTT - GC- T 3 B c c
2 AACTTTAACAAC GCT GTTGTTAAGG ACT GGG
AAGCATTC CGA CAACAATTTC TGA TCC
A AAT C
GAM8297 367 FLJ2060 1 2121 NP_060368.2 3 78 GGGATTGACTGA GCA TG 3 B c
c
5 GATCTTAACAAC GCTGTTGTTAAGG CT G
AGCAGCAA CGACAACAATTCT GA C
A-- GT
GAM8297 367 FLJ2305 1 15786 NP_078858.1 5 69 GCAATCCCCCAT - G CT 3 B c c
6 GCCCTTAGGAGC GCT GTT TTAAGGGCA TGGG
AAGCAGTT CGA CGA GATTCCCGT ACCC
A G --
GAM8297 367 FLJ2332 1 18937 NP_078930.1 3 117 GCCATGAATGGT --- ----- 3 B c c
3 GCCCTTATTAAC GCTGTTGTTA AGGGCACT TGG
AACAGTGT TGACAACAAT TCCCGTGG ACC
TAT TAAGT
GAM8297 367 FLJ3093 1 18669 NP_689973.1 3 956 GTGGTCACTAGT G TT T 3 B c c

4 GCCCTTCCCAAG GCT TTG AAGGGCACT GG
GCAAGTCA CGG AAC TTCCCGTGA TC
- CC -
GAM8297 367 FLJ3134 1 10144 NP_775786.1 3 60 CCTGCCCCAAGT TGTTA- 3 B c
c
9 GCCTTGCTTTTA GCTGT AGGGCACTTGGG
CAGTGGAC TGACA TTCCGTGAACCC
TTTTCG
GAM8297 367 FLJ3202 1 15817 NP_775853.2 3 608 TCTGTTTCAGGT TGT 3 B c c
9 GCCCTTGGTGCA GCTGT TAAGGGCACTTGGG
GTATAAAT TGACG GTTCCCGTGGACTT

TG-

GAM8297 367 FLJ3329 1 10479 NP_775907.1 3 48 CACAAAATCCCT GT CTT 3 B c c

8 GCCCTTAACAAG GCT TGTTAAGGGCA GGG
CTCACATT CGA ACAATTCCCGT CCC
-- ---

GAM8297 367 FLJ3361 1 2606 NP_775968.1 3 971 AAGACCAGGGAG ---- G A-- 3 B c c

0 GCCCTTAAGAAA GCTGT T TTAAGGGC CTTGG
ATATAGCA CGATA A AATTCCCG GGACC
TAAA G GAG

GAM8297 367 FLJ3583 1 6529 NP_775803.1 3 389 TCCACTTCATGA TA G 3 B c c

8 GTGTTTTACAAC GCTGTTGT AGGGCACTTG
AGCACTTG CGACAACA TTTTGTGAGT
-- A

GAM8297 367 FLJ3657 1 8645 NP_775793.1 3 637 AAACTCACTCAG A GC T 3 B c c

6 TATCATGACAAC GCTGTTGTTA GG ACT GGG
AGCATGGG CGACAACAGT CT TGA CTC
A A- -

GAM8297 367 FLJ3731 1 5684 NP_689799.1 5 112 CTGCAAGGCTCT ----- A G 3 B c c

8 AGGTGTGACAAC GCTGTTGTTA AGGGC CTTG
AGCAGTTG CGACAACAGT TCTCG GAAC
GTGGA - G

GAM8297 367 FLJ3860 1 5277 NP_694947.1 3 850 AGGGTCCCAAGT TT- TAA 3 B c
c

8 GTCCGGGCCCCC GCTG GT GGGCACTTGGG
AGCTACCC CGAC CG CCTGTGAACCC
CCC GG-

GAM8297 367 FLJ3911 1 8551 NP_689577.1 3 124 AAAATCCCAAGT G TAA - 3 B c c

7 GACCCACAGAAG GCT TTGT GGG CACTTGGG
CTGTCCTA CGA GACA CCC GTGAACCC
A --- A

GAM8297 367 FLJ4016 1 14835 NP_775755.2 3 587 GGACATCCAGGT GTT T 3 B c
c

0 GCCCTTCATCCA GCT GT AAGGGCACTTGGG
AGCTCCTA CGA TA TTCCCGTGGACCT
ACC C

GAM8297 367 FOXD2 1 11152 NP_004465.1 5 1516 GGCGCCCGAGTG G---- T- G- 3 B c
c

AGCCTTAACATC CTG TGTTAAGG CACTTGGG
CAGGGGCT GAC ACAATTCC GTGAGCCC
TCGGG CT GA

GAM8297 367 FRABIN 1 6720 NP_640334.1 5 325 AAAGCCACAAGT G TTAA - 3 B c
c

GCCTCCAAAGCC GCT TTG GGGCACTTG GG
ATTACACC CGA AAC TCCGTGAAC CC
- C--- A

GAM8297 367 FRCP2 1 9651 NP_715637.1 3 1820 CTTTGCCCAAGT GTTAAGG 3 B c
c

GTGACAGCACTG GCTGTT GCACTTGGG
GGGAGGAG CGACAG TGTGAACCC

```
                                                -------
GAM8297  367   FSTL1   1  17836 NP_009016.1  3  1937  CCCTGTCCAAGT    T-  AA---          3  B  c  c
                                 GCCTTGGAGAAC GCTGT  GTT    GGGCACTTGGG
                                 TCACAGCA    CGACA  CAA    TCCGTGAACCT
                                                CT   GAGGT
GAM8297  367   G2A     1  18565 NP_037477.1  3  672   CCAAATGTCCAC       AA   ACT        3  B  c  c
                                 GCCCAGAACAAC GCTGTTGTT  GGGC   TGGG
                                 AGTTGGCA    TGACAACAA  CCCG   ACCT
                                                GA   C--
GAM8297  367   GAB3    1  14391 NP_542179.1  3  1944  GTAGGCCCAAGT  C   T   AAG            3  B  c
c
                                 GTCAAGAACCAC G TGT GTT   GGCACTTGGG
                                 ACCAGATT    C ACA CAA   CTGTGAACCC
                                              C   C   GAA
GAM8297  367   GFPT2   1  12066 NP_005101.1  3  169   TTCTACCCAAGT    TGT              3  B  c  c
                                 GCTTTTGCTTAC GCTGT   TAAGGGCACTTGGG
                                 AGCAGATA    CGACA   GTTTTCGTGAACCC
                                                TTC
GAM8297  367   GPR87   1  11836 NP_076404.2  5  308   TCGTCCCCAAGT  T  T   A  --          3  B  c  c
                                 GTTTCCTGACAC GC GT GTTA GG  GCACTTGGG
                                 GCATCTTT    CG CA CAGT CC  TGTGAACCC
                                              -  -   -  TT
GAM8297  367   GPRC5C  1  8211  NP_061123.2  5  22    TCCCTGAAGAGT    T TTA      ----      3  B  c  c

                                 GCCCTGGTCACA GCTGT G   AGGGCACTT    GGG
                                 GCACCCTT    CGACA C   TCCCGTGAG    CCC
                                              - TGG        AAGT
GAM8297  367   GPS2    1  13607 NP_004480.1  5  371   AATGCCACCGGC       AA--   ACT        3  B  c
c
                                 CCCATGGACAAC GCTGTTGTT    GGGC   TGG
                                 AGCCTGGC    CGACAACAG    CCCG   ACC
                                                GTAC    GCC
GAM8297  367   GUK1    1  11774 NP_000849.1  3  109   CGGCAGCTCTGT    TT       TT        3  B  c  c
                                 GCCCTTGGCCAG GCTG  GTTAAGGGCAC  GGG
                                 CATGTGGA    CGAC  CGGTTCCCGTG  CTC
                                              --         T-
GAM8297  367   HDAC1   1  4562  NP_004955.2  3  311   GAAATGCCAAGT      TTAA           3  B  c  c
                                 GCCTGCTTAGTA GCTGTTG   GGGCACTTGG
                                 GCTTTGGA    CGATGAT    TCCGTGAACC
                                                TCG-
GAM8297  367   HHIP    1  842   NP_071920.1  5  538   TGTCTCTGGAGT  T--   TA      G       3  B  c  c
                                 GCCCTACAGCCC GC   GTTGT  AGGGCACTT GG
                                 CGCAAACT    CG   CGACA  TCCCGTGAG TC
                                              CCC    --       G
GAM8297  367   HNRPH3  1  13944 NP_036339.1  3  41    CACCAACATACA         GGC    G        3  B  c
c
                                 AGTCTTGACAAC GCTGTTGTTAAG   ACTTG
                                 AGCATCTG    CGACAACAGTTC   TGAAC
                                                ---    A
GAM8297  367   HNRPH3  1  13944 NP_067676.2  3  41    CACCAACATACA         GGC    G        3  B  c
c
```

AGTCTTGACAAC GCTGTTGTTAAG ACTTG
AGCATCTG CGACAACAGTTC TGAAC
--- A

GAM8297 367 HOXA1 1 18845 NP_705873.1 3 420 GAGGCGGCTCCA AA ACT 3 B c c

GCCCCAGACAAC GCTGTTGTT GGGC TGGG
AGCCCAGG CGACAACAG CCCG ACCT
AC ---

GAM8297 367 HSD11B2 2 13964 NP_000187.2 3 446 TAAATCCCAAGT GTT - 3 B c c

GTCTCTTGACTG GCT GTTAAG GGCACTTGGG
GCTCAAGA CGG CAGTTC CTGTGAACCC
T-- T

GAM8297 367 HSD11B2 2 15068 NP_000187.2 3 112 GATCCCCCAAGT TT A 3 B c c

GTCCTGGACCCT GCTG GTT AGGGCACTTGGG
GGCCTAAA CGGT CAG TCCTGTGAACCC
CC G

GAM8297 367 HSPA5 1 12356 NP_005338.1 3 546 CTGGGCCCAAGT TT T- - 3 B c c

GATCCTTCCACC GCTG GT AAGGG CACTTGGG
TCAGTCTC TGAC CA TTCCT GTGAACCC
TC CC A

GAM8297 367 IFIT2 1 13164 NP_001538.2 3 1388 AAAAATTCTAAC - - CAC 3 B c c

CACTGTAACAAC GCTGTTGTTA AG GG TTGGG
AGTTTTTG TGACAACAAT TC CC AATCT
G A ---

GAM8297 367 IL17D 1 1766 NP_612141.1 3 131 AGCAAACCAAGT T AAG 3 B c c

GCCGGAGCACCA GCTG TGTT GGCACTTGG
GCGCCGCC CGAC ACGA CCGTGAACC
C GG-

GAM8297 367 IL8RA 1 1110 NP_000625.1 5 3 TATTCATCAAGT GTT-- - 3 B c c

GCCCTCTAGCTG GCT GTTA AGGGCACTTGG
TTAAGTCA TGA CGAT TCCCGTGAACT
ATTGT C

GAM8297 367 IRS3L 1 14904 XP_295210.1 5 139 GGTGGCCCAAGT -- TG 3 B c c

GCTCTTGGTGGC GCT GT TTAAGGGCACTTGGG
CCAGCTTG CGA CG GGTTCTCGTGAACCC
CC GT

GAM8297 367 Jade-1 1 7801 NP_079176.2 3 1161 AGGTACCCAAGT GTTA G 3 B c c

GGCCTGAAACAG GCTGTT AGG CACTTGGG
TGTAGGGA TGACAA TCC GTGAACCC
AG-- G

GAM8297 367 KCNA6 1 12111 NP_002226.1 3 508 TGTTATTCCAGT ---- - T 3 B c c

GCCCTGTAACAA GCT GTTGTTA AGGGCACT GGG
TCACTGGT TGG TAACAAT TCCCGTGA CCT
TCAC G -

GAM8297 367 KCNIP4 1 4158 NP_671711.1 5 206 TGTGTACCAAGT G- G- --- 3 B c c

GCTGTCCTTGAC CT TTGTTAAGG GCACTTGG
AAGAAGAC GA AACAGTTCC CGTGAACC

CA AG TGT

GAM8297 367 KIAA004 1 1670 NP_055471.1 3 692 GCTCAGGCAAGT - TA G 3 B c c
0 GCCTTGCACACA GCTGT TGT AGGGCACTTG
GTAGGTAC TGACA ACG TTCCGTGAAC
C -- G

GAM8297 367 KIAA012 1 5670 NP_055607.1 3 651 TAGTGACCCAGT TT TA-- T 3 B c c
5 GCCCTCACTGCC GCTG GT AGGGCACT GGG
CAGCCCCG CGAC CG TCCCGTGA CCC
C- TCAC -

GAM8297 367 KIAA026 1 7732 XP_045954.2 3 3256 TAAACCATTCAT GT CT-- 3 B c c
5 GCCCTTAAATAG GCTGTT TAAGGGCA TGG
CTAGATTT CGATAA ATTCCCGT ACC
-- ACTT

GAM8297 367 KIAA029 1 12348 XP_042833.2 3 32 ATGACACCAAGT --- AA 3 B c c
5 GCCCGGATAAAG GCTG TTGTT GGGCACTTGG
TCAGCTTC CGAC AATAG CCCGTGAACC
TGA G-

GAM8297 367 KIAA029 1 19626 NP_055514.1 3 682 TCCAGGCCCAGC AAGG C 3 B c
c
6 TGCAGCAACAAC GCTGTTGTT GCA TTGGG
AGTCATTA TGACAACAA CGT GACCC
CGA- C

GAM8297 367 KIAA037 1 4379 NP_055474.1 3 726 TCATCCCCAAGT TT TAA-- 3 B c c
7 GCCCCTTCTGCC GCTG GT GGGCACTTGGG
TCAGTCCT TGAC CG CCCGTGAACCC
TC TCTTC

GAM8297 367 KIAA065 1 15617 XP_051017.2 3 1604 GGCCAGGCGGGT GT G 3 B c
c
7 GCCCTTGGACAG GCTGTT TAAGGGCACTTG
CTTGGAAG CGACAG GTTCCCGTGGGC
-- G

GAM8297 367 KIAA079 1 18730 NP_079286.1 5 272 ATGGACCCAAGT GTTGTTA 3 B c
c
5 GCCCTGGAGGCT GCT AGGGCACTTGGG
CTGATCAA CGG TCCCGTGAACCC
AGG----

GAM8297 367 KIAA095 1 4538 XP_039733.2 3 807 TACAGTTCAACC TA- CTT 3 B c c
3 TGCCTTAACACA GCTGTTGT AGGGCA GG
ACAGTATC TGACAACA TTCCGT CC
CAA ---

GAM8297 367 KIAA101 1 19015 XP_050742.5 3 1414 GTTCCTCCAAGT T- TAAGG 3 B c
c
0 GCACATTTAGCC GCTG TGT GCACTTGGG
TTAAAATC CGAT ACA CGTGAACCT
TT -----

GAM8297 367 KIAA106 1 5233 XP_042635.3 3 1715 CAACTGCCAAGT G TTAAG 3 B c
c

```
          9                    GCTATATTCAAA GCT TTG    GGCACTTGG
                               GCAGGATG    CGA AAC    TCGTGAACC
                                        -  TTATA
GAM8297  367   KIAA112 1  18824 XP_050325.1  3  2454  AGGCCATTCAGT    T  TA     ---       3  B  c  c

          6                    GCCCTCCACATG GCTGT GT  AGGGCACT   TGG
                               GCCTTGCC    CGGTA CA  TCCCGTGA   ACC
                                        -  CC       CTT
GAM8297  367   KIAA119 1  12870 NP_065765.1  3  2688  GTCACCATCCAC       --   CACT       3  B  c
c
          8                    CCTCGTAACAAC GCTGTTGTTA  AGGG    TGG
                               AGTCTCCC    TGACAACAAT  TCCC    ACC
                                           GC    ACCT
GAM8297  367   KIAA127 1  11062 XP_045472.1  3  921   TGTTTGCCAAGT   G   TTAA           3  B  c
c
          1                    GCCTGGCCCAGA GCT TTG    GGGCACTTGG
                               GCAAGTGG    CGA GAC    TCCGTGAACC
                                        -  CCGG
GAM8297  367   KIAA132 1  6018  NP_065824.1  3  2292  CCCCGGCCAGGG    T--       CA       3  B  c
c
          2                    TCCCTTAACACC GCTG   TGTTAAGGG  CTTGG
                               TCGGCACA    CGGC   ACAATTCCC  GGACC
                                        TCC        TG
GAM8297  367   KIAA132 1  11039 XP_029429.4  3  823   ATTTACCCAAGT    TTGTTAAG          3  B  c
 c
          8                    GTTCAGCTTATT GCTG       GGCACTTGGG
                               CACCCCAC    CGAC       TTGTGAACCC
                                        --------
GAM8297  367   KIAA137 1  11705 XP_290527.1  3  232   TTACACCCAAGT   GTT-   ---         3  B  c  c
          2                    GTCCTGGTTAAC GCT   GTTA   AGGGCACTTGGG
                               TTGAAGCA    CGA    CAAT   TCCTGTGAACCC
                                        AGTT    TGG
GAM8297  367   KIAA179 1  8257  XP_027074.3  3  208   TTTAACCAGGTA       AG-  C         3  B  c  c
          8                    CTGTCTAACAAC GCTGTTGTTA   GG ACTTGG
                               AGTCATCT    TGACAACAAT   TC TGGACC
                                           CTG  A
GAM8297  367   KIAA193 1  15618 XP_057107.3  3  128   CAGGAGCCAAGT     GT              3  B  c  c
          7                    GCTTTTGGATGG GCTGTT  TAAGGGCACTTGG
                               TGAGGGTG    TGGTAG  GTTTTCGTGAACC
                                        --
GAM8297  367   KIAA199 1  7678  XP_114447.2  3  1792  CTGAACCCAAGT G    ----   --       3  B  c  c
          9                    GTTTATTTAAAT  CTGTTG   TTAAG  GGCACTTGGG
                               GTCAACAG     GACAAC    AATTT  TTGTGAACCC
                                        -    TGTA    AT
GAM8297  367   KIF2   1  4157  NP_004511.1  3  10    AAGAGACCCCGT    TT   -    TT       3  B  c  c
                               GCCCTTTAACCG GCTG  GTTAA GGGCAC  GGG
                               GCATTTGC    CGGC  CAATT CCCGTG  CCC
                                        --    T     C-
GAM8297  367   KLK10  1  17457 NP_002767.2  3  368   GGCAAGCCAAGT    TT  A----          3  B  c  c
                               GCCCTCTCTGAA GCTG  GTT    AGGGCACTTGG
```

CCTCAGTT TGAC CAA TCCCGTGAACC
TC GTCTC
GAM8297 367 KLK10 1 17457 NP_665895.1 3 368 GGCAAGCCAAGT TT A---- 3 B c c
GCCCTCTCTGAA GCTG GTT AGGGCACTTGG
CCTCAGTT TGAC CAA TCCCGTGAACC
TC GTCTC
GAM8297 367 KPNA3 1 3939 NP_002258.1 3 80 TGGCTACCAAAT AAGGG C 3 B c
c
GATAAGAACAAC GCTGTTGTT CA TTGG
AGCAACAA CGACAACAA GT AACC
GAATA A
GAM8297 367 KRT8 1 9986 NP_002264.1 3 16 TCCTGCCCAAGT TAAGGG 3 B c c

GACAGCTGCGGC GCTGTTGT CACTTGGG
AGCCCCTC CGACGGCG GTGAACCC
TCGACA
GAM8297 367 LASS1 1 8142 NP_067090.1 3 1330 ATCTCCGTGCTC ---- TT 3 B c c
TTCTTTGACAAC GCTGTTGTTA AGGGCAC GGG
AGCGACAA CGACAACAGT TCTCGTG CCT
TTCT --
GAM8297 367 LGI3 1 566 NP_644807.1 3 781 CCCTCTGCCCGA A------ CTT 3 B c c
AGCAATAACAAC GCTGTTGTTA GGGCA GGG
AGCAGCAG CGACAACAAT CCCGT CCC
AACGAAG CT-
GAM8297 367 LIMS1 1 9951 NP_004978.2 5 98 GGCCTCCCAAGC -- -- AC 3 B c c
CCTGATAACAAC GCT GTTGTTA AGGGC TTGGG
ATGGCCAA CGG CAACAAT TCCCG AACCC
TA AG --
GAM8297 367 LOC1149 1 7181 NP_660284.1 3 1532 CCCTGCCCAAGT ---- AA- 3 B c c

87 GCCTAGGGGCAG GCTGT TGTT GGGCACTTGGG
TAGACAGC CGACA ACGG TCCGTGAACCC
GATG GGA
GAM8297 367 LOC1152 1 12944 XP_055499.2 5 2305 TCAGCGGCCAAG AGGGCA 3 B
c c
19 GGGAGTGACAAC GCTGTTGTTA CTTGG
AGCCAGAC CGACAACAGT GAACC
GAGGG-
GAM8297 367 LOC1213 1 18517 XP_062574.2 5 87 AGATTGTCCATG AA- CT 3 B c c

01 TCCAGAAACAAC GCTGTTGTT GGGCA TGGG
AGTGTCTT TGACAACAA CCTGT ACCT
AGA --
GAM8297 367 LOC1226 1 10278 NP_776245.1 5 53 TCACCCCCAAGT T TAA 3 B c c

64 GTCTCCCACGAC GC GTTGT GGGCACTTGGG
TGCCCTCC CG CAGCA TCTGTGAACCC
T CCC
GAM8297 367 LOC1266 1 17931 XP_059059.1 5 14 AACACCCCAAGT G AA- 3 B c c

```
          16                        GTCCGGGAACAA GCT TTGTT  GGGCACTTGGG
                                   AGGCAAGT    CGG AACAA  CCTGTGAACCC
                                             A    GGG
GAM8297  367   LOC1275 1  8397  XP_059164.6  5  531   TGGACCCTCAGT       A     T-       3  B  c  c
          40                        GCCCTGGCAACA GCTGTTGTTA GGGCACT  GGG
                                   GCTCTGTG    CGACAACGGT CCCGTGA  CCC
                                             -     CT
GAM8297  367   LOC1363 1  12191 XP_072455.2  3  310   GATAACCCAAGT   GT  TAA           3  B  c
c
          45                        GTCCCACAGGCC GCT  TGT  GGGCACTTGGG
                                   AAGGTACA    CGG  ACA  CCTGTGAACCC
                                             --  C--
GAM8297  367   LOC1392 1  10411 XP_208439.1  3  8    ATAGACCCAAGT   GT  TAAGG          3  B  c
c
          01                        GCATCATGCAAG GCT  TGT   GCACTTGGG
                                   CATATGAT    CGA  ACG   CGTGAACCC
                                             --  TACTA
GAM8297  367   LOC1434 1  10575 NP_777562.1  3  991   GGCCTCCAAAGT  TGT      C   -       3  B  c
c
          58                        TCCCTTAACACT GC   TGTTAAGGG ACTT GGG
                                   TGCAAAGT    CG   ACAATTCCC TGAA CCT
                                             TTC       T   A
GAM8297  367   LOC1458 1  7193  XP_096879.1  5  1091  TCAGTCCCAAGT G-------   TGTT          3  B  c
c
          28                        GCCCTTTTACAG       CTGT   AAGGGCACTTGGG
                                   AGAATGCC          GACA   TTCCCGTGAACCC
                                          CCGTAAGA   TT--
GAM8297  367   LOC1479 1  9617  XP_085993.3  3  2876  AGGTAACCAAGT  - TTG  AG          3  B  c
c
          91                        GCCTCTAAGTCA GC TG   TTA  GGCACTTGG
                                   TGCTTATT    CG AC   AAT  CCGTGAACC
                                             T  TG-  CT
GAM8297  367   LOC1494 1  8650  NP_690048.1  3  741   GAACTCTCCAGT  T    TA     T       3  B  c  c

          20                        GCCCTATAGCTG GC GTTGT  AGGGCACT GGG
                                   CAAGAGTT    CG CGATA  TCCCGTGA CCT
                                             T    --       -
GAM8297  367   LOC1497 1  18798 XP_097719.1  5  240   ATCCTTCCATTT      TA   - CT       3  B  c  c

          03                        GATCCTCACAAC GCTGTTGT  AGGG CA  TGGG
                                   AGCCATGT    CGACAACA  TCCT GT  ACCT
                                             C-   A  TT
GAM8297  367   LOC1507 1  18707 XP_086996.2  5  709   AGGCTGGGCCAA   G  --     AC        3  B  c
c
          63                        GCCCTTAAGTCA GCT TTG  TTAAGGGC  TTGG
                                   GGAGCAGT    CGA GAC  AATTCCCG  AACC
                                             G  TG      --
GAM8297  367   LOC1511 1  798   XP_098008.1  5  65    GTCCGCCCAAGT G---     TTA--          3  B  c  c

          54                        GCCCTCCTCTCA    CTGTTG    AGGGCACTTGGG
```

GCAGGCGG GACGAC TCCCGTGAACCC
GGCG TCTCC
GAM8297 367 LOC1511 1 4822 XP_087117.1 5 596 AACGCGATGAGT G - G 3 B c c
78 GCCCTTACACAA GCT TTGT TAAGGGCACTTG
AAGCCTGG CGA AACA ATTCCCGTGAGT
A C A
GAM8297 367 LOC1535 2 7669 NP_612500.1 3 76 ACCAGCCCAAGT TT-- -- 3 B c c
16 GCCGTCTTAGCC GCTG GTTAAG GGCACTTGGG
ATTCAGTG TGAC CGATTC CCGTGAACCC
TTAC TG
GAM8297 367 LOC1535 2 9799 NP_612500.1 3 53 CGGATCTAAGAT TTG-- - 3 B c c
16 GCCCTTAGAAGA GCTG TTAAGGGCA CTTGGG
CCAGCCCA CGAC GATTCCCGT GAATCT
CAGAA A
GAM8297 367 LOC1550 1 7006 XP_088116.2 5 257 TGCTTTCCAAGT - - TAAGG- 3 B c
c
08 GCAAAACTACAG GC TGT TGT GCACTTGGG
ACACGCGC CG ACA ACA CGTGAACCT
C G TCAAAA
GAM8297 367 LOC1550 1 12191 XP_098647.1 5 77 GATAACCCAAGT GT TAA 3 B c
c
32 GTCCCACAGGCC GCT TGT GGGCACTTGGG
AAGGTACA CGG ACA CCTGTGAACCC
-- C--
GAM8297 367 LOC1580 1 13911 XP_088442.1 5 3123 TTTCACCCAAGT G------- TTAAG 3 B
c c
14 GCCAGTCAACAG CTGTTG GGCACTTGGG
AGTACATG GACAAC CCGTGAACCC
GTACATGA TGA--
GAM8297 367 LOC1580 1 6216 XP_098861.2 3 1235 TAGGCGCGGCCA TAA A 3 B c
c
62 GGGCCCCACAAC GCTGTTGT GGGC CTTGG
AGCAGGTC CGACAACA CCCG GGACC
C-- -
GAM8297 367 LOC1584 1 17142 XP_098942.1 5 238 CCCGCCGCGGGT - GTT- - 3 B c
c
36 GCCCTTCGGAAA GC TGTT AAGGGCACTTG GG
CGCGCTGA CG GCAA TTCCCGTGGGC CC
C AGGC G
GAM8297 367 LOC1591 1 16800 XP_099028.1 5 600 TGCAGCTCCAGT TT- A T 3 B c
c
21 GCCCTGAGCTCC GCTG GTT AGGGCACT GGG
CAGCCACA CGAC CGA TCCCGTGA CCT
CCT G -
GAM8297 367 LOC1686 1 1796 XP_166592.1 3 2505 GATTTACCAAGT G A-- 3 B c c
67 GCTTCAATGAGA GCTGTT TTA GGGCACTTGG
GCAGTCCT TGACGA AGT TTCGTGAACC
G AAC
GAM8297 367 LOC1973 1 16515 NP_777577.1 3 319 CCGCCCCACAGT TG TA - 3 B c
c

```
          22                    GCCCTGCAGTTG GC  TTGT  AGGGCACT TGGG
                               CCAGGCTC    CG  GACG  TCCCGTGA ACCC
                                        TT   --      C
GAM8297  367   LOC2001 1  9656  XP_114148.1  3  1763  CTGCATTCAAGT   ---   TA-          3  B  c  c
          97                    GCCCTGCTACAA GCT  GTTGT  AGGGCACTTGGG
                               TTCTGGCT   CGG  TAACA  TCCCGTGAACTT
                                        TCT    TCG
GAM8297  367   LOC2020 1  5326  XP_114422.3  3  198   GAACCACAAAGT  C   --  -     ---      3  B  c  c
          24                    GCCCTCTAATAA G TGTT  GTTA AGGGCACT  TGG
                               GACATCGG    C ACAG  TAAT TCCCGTGA  ACC
                                        T   AA   C      AAC
GAM8297  367   LOC2193 1  9192  XP_167564.2  3  1369  CCTCCTTAGAAG        A  GCA  ---       3  B  c
c
          47                    ATACCTAACAAC GCTGTTGTTA GG  CTT  GGG
                               AGCACTGT    CGACAACAAT CC  GAA  TCC
                                        - ATA  GAT
GAM8297  367   LOC2206 1  10547 XP_167540.4  3  186   TCTGCCCCATGT  T  G       T         3  B  c  c

          86                    GCCCTTGAAGCT GC GTT TTAAGGGCAC TGGG
                               GCCCCACA    CG CGA AGTTCCCGTG ACCC
                                        T  -       T
GAM8297  367   LOC2210 2  6759  XP_167709.1  3  898   ATGCTGCCAAGT   TTG   -          3  B  c  c
          61                    GCCATTTGGGGT GCTG  TTAAG GGCACTTGG
                               CAGCATCC    CGAC  GGTTT CCGTGAACC
                                        TGG    A
GAM8297  367   LOC2210 2  19881 XP_167709.1  3  760   TTAACTCCAAGT     TT              3  B  c  c
          61                    GCCTTTTTGACA GCTGTTG  AAGGGCACTTGGG
                               GTGACAAC    TGACAGT  TTTCCGTGAACCT
                                        T-
GAM8297  367   LOC2214 1  8039  XP_168138.1  5  217   GTATGGACCAGT   - TA     T         3  B  c  c
          05                    GCCCTCCGCAGA GCTGT TGT  AGGGCACT GG
                               CAGCTCAC    CGACA ACG  TCCCGTGA CC
                                        G  CC      -
GAM8297  367   LOC2530 1  18869 XP_171068.2  3  1073  GGAGCAACCTAG G-----     AA          3  B  c
c
          17                    GTGTCCAACAAC     CTGTTGTT  GGGCACTTGGG
                               AGATGAAT        GACAACAA  CCTGTGGATCC
                                        TAAGTA      --
GAM8297  367   LOC2533 1  8311  XP_172857.1  5  330   GAACCCAGCAGT    TGTTA     --        3  B  c
c
          92                    GCCCTGCCCTGC GCTGT    AGGGCACT  TGGG
                               AGTCTGAG    TGACG    TCCCGTGA  ACCC
                                        TCCCG      CG
GAM8297  367   LOC2541 1  5139  XP_171440.3  5  93    CTTCTCCCAAGT       AAGGG          3  B  c
c
          11                    GGGCAGCAGCAG GCTGTTGTT    CACTTGGG
                               CAGCTTCT    CGACGACGA    GTGAACCC
                                        CGG--
GAM8297  367   LOC2551 1  7969  XP_173156.1  5  42    AACCCCATGGGG      TA  GCA --       3  B  c
c
```

```
          67                        GACCTCGACAAC GCTGTTGT  AGG   CT  TGGG
                                   AGCGCCT     CGACAACA  TCC   GG  ACCC
                                               GC   AGG  GT
GAM8297  367   LOC2559 1  3149  XP_171083.2  5  1226  CAGATGAGCCTA       TAA    CT          3  B  c
c
          75                        CTGCCTCACAAC GCTGTTGT  GGGCA  TGGG
                                   AGCCTCCA    CGACAACA   TCCGT  ATCC
                                               C--    C-
GAM8297  367   LOC2569 1  18153 XP_173031.1  3  633   GTCAGTCTTCCA       AAGG   T          3  B  c
c
          05                        CGTGTAAACAAC GCTGTTGTT   GCAC TGGG
                                   AGTGTGTG    TGACAACAA    TGTG ACCT
                                               A---   C
GAM8297  367   LOC2570 1  11089 XP_173226.1  3  397   GTTGTGCCAAGT    TT  AAGG           3  B  c
 c
          85                        GCAATAAACCAG GCTG  GTT   GCACTTGG
                                   TCACAAAA    TGAC  CAA   CGTGAACC
                                               --  ATAA
GAM8297  367   LOC2830 1  7748  XP_208495.1  5  727   ACTCCGCCAAGT    TT  AA ---          3  B  c
c
          46                        GCTAACCAAAGC GCTG  GTT  GG   GCACTTGG
                                   TCAGCAAC    CGAC  CGA  CC   CGTGAACC
                                               T-   AA  AAT
GAM8297  367   LOC2830 1  6474  XP_210880.1  5  1168  TGGGTCCCCAGT    T--  A     T        3  B  c
c
          73                        GCCCTCAGCCCC GCTGT   GTT AGGGCACT GGG
                                   GCAGCGTA    CGACG   CGA TCCCGTGA CCC
                                               CCC   C       C
GAM8297  367   LOC2831 1  7758  XP_210910.1  5  2090  TTTCAGCCAAGT   G  TTAA            3  B  c
c
          68                        GCCTGCCCAGAG GCT TTG   GGGCACTTGG
                                   CTCTGCAG    CGA GAC   TCCGTGAACC
                                               -  CCG-
GAM8297  367   LOC2832 1  12493 XP_210941.1  5  282   GCCAGGAGTTTG       TAA   --------      3  B  c
c
          05                        ATTGCTTACAAC GCTGTTGT  GGGCA      CTTGG
                                   AGCTCTTT    CGACAACA  TTCGT      GGACC
                                               ---    TAGTTTGA
GAM8297  367   LOC2832 1  17415 XP_208600.1  3  1265  TGGTCAGCTAAT         G  C         3  B  c  c

          71                        TGCTTTGACAAC GCTGTTGTTAAGG CA TTGG
                                   AGCGCAGT    CGACAACAGTTTC GT AATC
                                               -  T
GAM8297  367   LOC2832 1  3938  XP_210957.1  5  1273  TGGTACCCAGGT   GTTGTT            3  B  c
 c
          74                        GCCCTTCAGGCT GCT     AAGGGCACTTGGG
                                   CTAACCAA    CGG     TTCCCGTGGACCC
                                               AC----
GAM8297  367   LOC2833 1  17261 XP_211002.1  5  70    GGGTCTGCAAGT    ---  AA-      G     3  B  c
c
```

```
          76                    GCCCCTCAGCAG GCTGT  TGTT  GGGCACTTG
                                GAACAGCT   CGACA  ACGA  CCCGTGAAC
                                      AGG  CTC      G
GAM8297  367   LOC2835 1  6241  XP_208096.1  3 65   AGGTCGTTCCTA      TA    CT        3  B  c  c
          32                    CTGTTTTACAAC GCTGTTGT  AGGGCA  TGGG
                                AGCATGTC   CGACAACA  TTTTGT  ATCC
                                     --    C-
GAM8297  367   LOC2835 1  16651 XP_211083.1  3 1449  TGTCTCCTAAGT      A-            3  B  c  c
          34                    GCCCTCAGACAG GCTGTTGTT  AGGGCACTTGGG
                                CAGTGACG   TGACGACAG  TCCCGTGAATCC
                                      AC
GAM8297  367   LOC2837 1  8051  XP_208817.1  3 198   TGAGCTCCAAGT      AAG           3  B  c  c
          44                    GCTAAATAACAG GCTGTTGTT  GGCACTTGGG
                                CATCTCAT   CGACAATAA  TCGTGAACCT
                                      A--
GAM8297  367   LOC2837 1  9843  XP_211196.1  5 439   AAGACCCCGAGC   T--      CA        3  B  c  c

          76                    ATCCTTAACATC GCTG  TGTTAAGGG  CTTGGG
                                CCAGCACC   CGAC  ACAATTCCT  GAGCCC
                                     CCT       AC
GAM8297  367   LOC2837 1  13762 XP_211199.1  5 2574  ATGAACTACGGT      A G   -       3  B  c  c

          78                    GTGTTAAACAAC GCTGTTGTT AG GCACT TGG
                                AGCAGTGG   CGACAACAA TT TGTGG ATC
                                     A G   C
GAM8297  367   LOC2838 1  10880 XP_211227.1  3 407   GAGAGCTGAAGT      TTAA     G        3  B  c
c
          41                    GCCCCAGCCAGC GCTGTTG   GGGCACTT GG
                                AGCTAGCC   CGACGAC   CCCGTGAA TC
                                     CGAC      G
GAM8297  367   LOC2839 1  10210 NP_787097.1  3 634   TGTCACCAAAGT   TT  AA     -       3  B  c
c
          32                    GCCCAACTCTGG GCTG  GTT  GGGCACTT GG
                                CACGGGGC   CGGT  CAA  CCCGTGAA CC
                                     CT  --      A
GAM8297  367   LOC2840 1  14152 XP_210324.1  5 186   ACAGCTCCAGAC      AA   C--       3  B  c
c
          15                    ATGTCCAACAAC GCTGTTGTT  GGGCA  TTGGG
                                AGCCCCGA   CGACAACAA  CCTGT  GACCT
                                     --    ACA
GAM8297  367   LOC2840 1  6093  XP_211318.1  5 1210  CCCAGCCCAAGT   -  AA           3  B  b  b

          61                    GCCTGGCACACA GCTGT TGTT  GGGCACTTGGG
                                GCTAATGT   CGACA ACGG  TCCGTGAACCC
                                     C  --
GAM8297  367   LOC2840 1  875   XP_211322.1  5 285   GCCTCTGCAGGT  -     A G   G       3  B  c  c

          80                    GACCGTAACAAC GC TGTTGTTA GG CACTTG
                                ATGCAAAT   CG ACAACAAT CC GTGGAC
                                     T      G A    G
```

GAM8297 367 LOC2840 2 812 XP_211324.1 3 230 AGCCTCCCAAGT G - ----- G 3 B c c
95 GGCTAAGACTTA CTGTT GTTAAG G CACTTGGG
ACAAACAG GACAA CAATTC C GTGAACCC
- A AGAAT G
GAM8297 367 LOC2840 2 3574 XP_211324.1 3 231 CCCAAGTGGCTA G---- - ----- G 3 B c
c
95 AGACTTAACAAA CTGTT GTTAAG G CACTTGG
CAGGCACA GACAA CAATTC C GTGAACC
ACACG A AGAAT G

G
C

GAM8297 367 LOC2841 1 8034 XP_209021.1 5 401 CAGAAACCAAGT TT A 3 B c c
13 GCTCTAGCCTCA GCTG GTTA GGGCACTTGG
GCCCTAAA CGAC CGAT CTCGTGAACC
TC -
GAM8297 367 LOC2841 1 7562 XP_211346.1 3 688 AATATCCCAAGT TTAA- 3 B c c
33 GCCTGGCTTTGA GCTGTTG GGGCACTTGGG
TAGTTAAA TGATAGT TCCGTGAACCC
TTCGG
GAM8297 367 LOC2842 1 17032 XP_209091.1 3 390 CTTACAGTTTCC AAG CT 3 B c
c
52 ATTGCCAACAAC GCTGTTGTT GGCA TGGG
AGCCATCC CGACAACAA CCGT ACCT
--- T-
GAM8297 367 LOC2846 1 6319 XP_209289.1 3 1369 TAGATCATGGCA AA A G 3 B c
c
13 AGGCCTGACAAC GCTGTTGTT GGGC CTTG
AGCTGAGC CGACAACAG TCCG GAAC
-- - G
GAM8297 367 LOC2846 1 1268 XP_208231.1 3 2831 ACCCTCACTGCC A--- CTT- 3 B c
c
42 CTCAAGGACAAC GCTGTTGTT AGGGCA GGG
AGCAGGGT CGACAACAG TCCCGT CCC
GAAC CACT
GAM8297 367 LOC2846 1 16211 XP_010647.5 3 2248 CAGCCCCCAAGT GTT AA 3 B c
c
67 GTCCAGCCTGGC GCT GTT GGGCACTTGGG
ACTTCCCA CGG CGA CCTGTGAACCC
TC- --
GAM8297 367 LOC2847 1 9135 XP_211608.1 3 412 TCCCATCTCAAG - A 3 B c c
32 GTCCTTAACAGC GC TGTTGTTAAGGGC CTTGGG
ATGTGGAA TG ACGACAATTCCTG GAACTC
T -
GAM8297 367 LOC2849 1 11674 XP_211692.1 5 847 TGCTACCCATCG - ACT 3 B c c

30 GCCCTTAATAAA GCTGTT GTTAAGGGC TGGG
TGGCCTCA CGGTAA TAATTCCCG ACCC
A GCT

GAM8297 367 LOC2850 1 13545 XP_211739.1 5 689 ATGATACCAAGT G A ---- 3 B c c
33 GCTGAACCTGAG GCTGTT TTA GG GCACTTGG
AGCAGCCC CGACGA AGT CC CGTGAACC
G - AAGT
GAM8297 367 LOC2850 1 20075 XP_211751.1 3 964 GAAAGGGCCAGT G----- G - T 3 B c
c
52 GCCCTTATACAA CT TTGT TAAGGGCACT GG
AGACTGGA GA AACA ATTCCCGTGA CC
AGGTCA - T -
GAM8297 367 LOC2851 1 20164 XP_211783.1 5 266 GTTGTCCCAAGT ---- AGGG 3 B c
c
52 GGACATAATTAT GCTGTT GTTA CACTTGGG
AAATAGCT CGATAA TAAT GTGAACCC
ATAT ACAG
GAM8297 367 LOC2853 1 5993 XP_211876.1 5 524 GGGCACCCAAGT G TAA---- 3 B c
c
97 GCCCCCTGTCTG GCT TTGT GGGCACTTGGG
CGAAGTCC TGA AGCG CCCGTGAACCC
- TCTGTCC
GAM8297 367 LOC2854 1 19782 XP_211907.1 3 202 TCAGGGAGCCGT G TT 3 B c
c
67 GCCCTTGAAAGC GCTGTT TTAAGGGCAC GG
GGTGTATT TGGCGA AGTTCCCGTG CC
A --
GAM8297 367 LOC2854 1 15176 XP_211914.1 3 451 CAGGGTCCCAGT - T A-- T 3 B c
c
88 GCCCTCTGGACA GC TG TGTT AGGGCACT GGG
CTATGCCA CG AT ACAG TCCCGTGA CCC
T C GTC -
GAM8297 367 LOC2856 1 12828 XP_209693.1 5 1405 TGTGTTTTAAGT T AA-- 3 B c c
38 GCCCAGTGAACA GCTGT GTT GGGCACTTGGG
CAGTTCCA TGACA CAA CCCGTGAATTT
- GTGA
GAM8297 367 LOC2857 1 1780 XP_209729.1 5 540 AATTCCCTGTCT TT C-- TT 3 B c
c
08 CCCCTTAACCAG GCTG GTTAAGGG AC GGG
CACTGGAA CGAC CAATTCCC TG CCC
-- CTC T-
GAM8297 367 LOC2858 1 679 XP_212034.1 5 1235 GATATCCCAAGT T AAGGG-- 3 B c
c
43 GACACAGAAACA GCTGT GTT CACTTGGG
CAGCTCCT CGACA CAA GTGAACCC
- AGACACA
GAM8297 367 LOC2860 1 5140 XP_212150.1 3 280 ATTCCCTCAAGT --- G A 3 B c c
44 GCCCTGAGGAGC GC TGTT TT AGGGCACTTGGG
ATTTGCAA CG ACGA GA TCCCGTGAACTC
TTT G G
GAM8297 367 LOC2860 1 4656 XP_210815.1 5 18 GAAGGCCCAAGT T TTAA 3 B c
c

```
          55                          GTCCCCACAGTC GCTGT G   GGGCACTTGGG
                                     TTAGGGGG    TGACA C   CCTGTGAACCC
                                               - C---
GAM8297  367   LOC2860 1  8210  XP_212156.1  3  1015  TCTCTTTCAAGT    TGTTAAG          3  B  c
 c
          59                          GCCATTACAGCT GCTGT     GGCACTTGGG
                                     GAACATTA    CGACA     CCGTGAACTT
                                               TTA----
GAM8297  367   LOC2864 1  10137 XP_208415.1  3  70   AAGGACCCAAGT   G   TA-----  -      3  B  c
c
          02                          GACTCTGATGTT GCT TTGT      AGGG CACTTGGG
                                     TACAAAGC    CGA AACA      TCTC GTGAACCC
                                               -  TTTGTAG   A
GAM8297  367   LOC2865 1  4342  XP_210093.1  3  255   CCCCTCCCAAGG  T-   --    A       3  B  c  c
          32                          GCCCTTAAAGCG GC  GTTGT  TAAGGGC CTTGGG
                                     ACCTGTCA    TG  CAGCG  ATTCCCG GAACCC
                                               TC    AA     G
GAM8297  367   LOC3388 1  17184 XP_290588.1  3  1503  CGTCTACCTTTT     T-     CTT       3  B  c
c
          17                          GCCCTTATTCAA GCTGTTG  TAAGGGCA   GGG
                                     TAGTGGGA    TGATAAC  ATTCCCGT   TCC
                                               TT      TT-
GAM8297  367   LOC3389 1  4981  XP_292272.2  5  316   TTTTCTCAACCC       AAGGGC          3  B  c
 c
          13                          AAGTCAAACAAC GCTGTTGTT     ACTTGGG
                                     AGTTTGTG    TGACAACAA     TGAACCC
                                               AC----
GAM8297  367   LOC3391 1  11902 XP_294832.1  3  2116  TCCTACCCAAGT  T   TTA  G          3  B  c
c
          54                          GGCCTCCAGCTG GC GTTG   AGG CACTTGGG
                                     TCCGTTAG    TG CGAC   TCC GTGAACCC
                                               T   C--  G
GAM8297  367   LOC3392 1  19822 XP_290800.1  3  2107  AAAGTTCCAAGT    T  AAGG          3  B  c
 c
          87                          GCAAAATTACAG GCTGT GTT    GCACTTGGG
                                     TGTGTTAG    TGACA TAA    CGTGAACCT
                                               T  AA--
GAM8297  367   LOC3394 1  2239  XP_294926.1  3  3408  GTTAAGTCAAGT    --   AA          3  B  c  c
          00                          GCCTGGAACAGA GCTGT  TGTT  GGGCACTTGG
                                     ACAGCCAT    CGACA  ACAA  TCCGTGAACT
                                               AG   GG
GAM8297  367   LOC3394 1  14065 XP_291487.1  5  26    CGGTCTCCAAGT    TG  A           3  B  c  c
          45                          GCCCCTGGTTAC GCTGT  TTA GGGCACTTGGG
                                     AGCTCCTG    CGACA  GGT CCCGTGAACCT
                                               TT  C
GAM8297  367   LOC3394 1  11960 XP_290911.1  3  250   ACCTGACCCAGT  -    TA     T       3  B  c  c

          58                          GCCCTGCGACAC GC TGTTGT  AGGGCACT GGG
                                     GCCCACAG    CG ACAGCG  TCCCGTGA CCC
                                               C    --      -
```

GAM8297 367 LOC3398 1 11787 XP_295094.1 3 1197 TTGCACTCCAGC AA-- ACT 3 B c c

87 CCGGGCAACAAC GCTGTTGTT GGGC TGGG
AGCGAAAC CGACAACAA CCCG ACCT
CGGG ---

GAM8297 367 LOC3399 1 1575 XP_295107.1 3 84 CCTAGCAGCTCT - --- -- 3 B c c

42 GTCCTTAACACA GCTGT TGTTAAGGGCA CT TGGG
CAGCAGGT CGACA ACAATTCCTGT GA ATCC
C CTC CG

GAM8297 367 LOC3399 1 9814 XP_295116.1 5 120 TTTGATCCAAGT TGTTAA 3 B c c

78 GCCCACAGTTCT GCTGT GGGCACTTGGG
GATGAATG TGACA CCCGTGAACCT

GAM8297 367 LOC3413 1 18471 XP_296117.1 5 49 CAGAGACCAAGT TT TAA 3 B c c

33 GCCCACTTAGCC GCTG GT GGGCACTTGG
GTGAAAAA CGAT CA CCCGTGAACC
T- ---

GAM8297 367 LOC3418 1 17370 XP_292256.1 5 103 AGCGGTTCCAGT G TTA T 3 B c c

67 GCCCTCAAAGCA GCT TTG AGGGCACT GGG
ATCTGTCT CGA AAC TCCCGTGA CCT
- --- -

GAM8297 367 LOC3424 1 5255 XP_296905.2 3 191 TTTAGGACCAAG --- CA 3 B c c

90 CCCCTTAACAAC GCT GTTGTTAAGGG CTTGG
TCAGGCCT CGG CAACAATTCCC GAACC
ACT C-

GAM8297 367 LOC3426 1 7400 XP_297028.1 5 1390 GCCCAGCGGAGT G-- --- ---- 3 B c c

63 GCCCTTCTGAGC CTGTTGTT AAGGGCACT TGGG
AGCGGGCG GGCGACGA TTCCCGTGA ACCC
GCG GTC GGCG

GAM8297 367 LOC3431 1 3845 XP_291421.1 5 47 ACACCCGCGAGT T- GTT - 3 B c c

41 GCCCTTTCAAGC GC GTT AAGGGCACTTG GG
CTGCTGGG CG CGA TTCCCGTGAGC CC
TC ACT G

GAM8297 367 LOC3435 1 7356 XP_291629.1 5 112 ACCAGTCCCGGC TAA G -- 3 B c c

32 AGTGGCCACAAC GCTGTTGT GG CACT TGGG
AGCACATC CGACAACA CC GTGA GCCC
--- G CG

GAM8297 367 LOC3454 1 19581 XP_298768.2 5 327 TATTTTCCAAGT G- TTA 3 B c c

22 GCCTTCACCAAA GCT TTG AGGGCACTTGGG
AGGCCAAG CGG AAC TTCCGTGAACCT
AA CAC

GAM8297 367 LOC3463 1 13991 XP_299473.1 3 28 TGCTCCTTCAAG ---- G A 3 B c c

51 GCCCTTAAAACT GCT GTT TTAAGGGC CTTGGG

GTGGGCTC CGG CAA AATTCCCG GAACTT
GTGT - -
GAM8297 367 LOC3464 1 2854 XP_299501.1 5 84 TCCTGCCCAAGT TTAA G- 3 B c
c
30 GGACCCAGCGGC GCTGTTG GG CACTTGGG
AAAGGTGA CGGCGAC CC GTGAACCC
---- AG
GAM8297 367 LOC3481 1 2548 XP_211219.1 5 2048 CAAATCCCAAGT T AGG 3 B c
c
55 GTTGACACAGCC GCTGT GTTA GCACTTGGG
ATCTTGTC CGACA CAGT TGTGAACCC
- ---
GAM8297 367 LOC3485 1 11960 XP_300778.1 3 250 ACCTGACCCAGT - TA T 3 B c c

25 GCCCTGCGACAC GC TGTTGT AGGGCACT GGG
GCCCACAG CG ACAGCG TCCCGTGA CCC
C -- -
GAM8297 367 LOC3486 1 10547 XP_300790.1 3 186 TCTGCCCCATGT T G T 3 B c c

00 GCCCTTGAAGCT GC GTT TTAAGGGCAC TGGG
GCCCCACA CG CGA AGTTCCCGTG ACCC
T - T
GAM8297 367 LOC3490 1 17698 XP_302954.1 5 890 CAGTATTCAAGT GTTA 3 B c
c
79 GCCTTGAACAGT GCTGTT AGGGCACTTGGG
GTCCCCTC TGACAA TTCCGTGAACTT
G---
GAM8297 367 LOC3492 1 9993 XP_303002.1 5 294 CATCTACTGCGT GT- T 3 B c c
13 GCCCTTGCCAAA GCTGTT TAAGGGCAC TGG
CAGCTGTG CGACAA GTTCCCGTG GTC
ACC C
GAM8297 367 LOC3492 1 14405 XP_303011.1 5 861 GCCCTCCCAAGT T AAGG 3 B c
c
62 GCAGCTGCAGCC GCTGT GTT GCACTTGGG
ACCCAAGC CGACG CGA CGTGAACCC
T ----
GAM8297 367 LOC3492 1 14405 XP_303012.1 5 861 GCCCTCCCAAGT T AAGG 3 B c
c
69 GCAGCTGCAGCC GCTGT GTT GCACTTGGG
ACCCAAGC CGACG CGA CGTGAACCC
T ----
GAM8297 367 LOC3492 1 14140 XP_300476.1 5 434 ATTTCAATGACT --- - C 3 B c c
88 TTTAAGAACAAC GCTGTTGT TAAGGG CA TTGGG
AGCCCTTC CGACAACA ATTTTC GT AACTT
AGA A -
GAM8297 367 LOC3492 1 14405 XP_303017.1 5 861 GCCCTCCCAAGT T AAGG 3 B c
c
91 GCAGCTGCAGCC GCTGT GTT GCACTTGGG
ACCCAAGC CGACG CGA CGTGAACCC
T ----

GAM8297 367 LOC3494 1 2271 XP_303044.1 5 391 AAAACACCAAGT TT AA 3 B c c

08 GCCTGGAATCAG GCTG GTT GGGCACTTGG
TTGTTTGT TGAC TAA TCCGTGAACC
-- GG

GAM8297 367 LOC3505 1 3074 XP_304238.1 5 112 AAAACCCCAAGT GTT AA- 3 B c
c

98 GCCTGGAGACCC GCT GTT GGGCACTTGGG
GAGCCCCA CGA CAG TCCGTGAACCC
GCC AGG

GAM8297 367 LOC5106 1 17350 NP_057000.2 5 146 ATGGCCACAAGT - TAA - 3 B c
c

3 GCCCACAGCTGG GCT GTTGT GGGCACTTG GG
CCCCAGGT CGG CGACA CCCGTGAAC CC
T --- A

GAM8297 367 LOC9076 1 4499 NP_849160.1 3 132 AAGTTGCTAAGT T AA 3 B c c

8 GCCCGAGCGCAG GCTGT GTT GGGCACTTGG
CGCGTTAA CGACG CGA CCCGTGAATC
- G-

GAM8297 367 LOC9260 1 1231 XP_046097.1 3 219 ATTACCAATTTG AA A TG 3 B c
c

6 AGGCCCAACAAC GCTGTTGTT GGGC CT GG
AGTGTATT TGACAACAA CCCG GA TT
-- - GT

GAM8297 367 LOC9308 1 16872 NP_612406.1 3 251 ATACGGCCAAGT - T TA-- 3 B c
c

2 GCCCTGTGTGCC GCT GT GT AGGGCACTTGG
GCTGGCAG CGG CG CG TCCCGTGAACC
T C TGTG

GAM8297 367 LYRIC 1 7749 NP_848927.1 3 287 AGAATATTATCC GGGC T 3 B c c
TGGTTTAACAAC GCTGTTGTTAA ACT GGG
AGTGCCCT TGACAACAATT TGG CCT
---- T

GAM8297 367 LYRIC 1 7749 XP_043070.5 3 287 AGAATATTATCC GGGC T 3 B c c
TGGTTTAACAAC GCTGTTGTTAA ACT GGG
AGTGCCCT TGACAACAATT TGG CCT
---- T

GAM8297 367 MADH7 1 7744 NP_005895.1 3 829 TGCTCACCCAGT TTGTTA- T 3 B c
c

GCCCTCTCCCCT GCTG AGGGCACT GGG
CAGCCTCT CGAC TCCCGTGA CCC
TCCCCTC -

GAM8297 367 MAP2K3 1 7679 NP_002747.2 5 155 ATATGTGCAAGT GT-- G 3 B c c
GCCCTTGACAGA GCT TGTTAAGGGCACTTG
GAGGCTGG CGG ACAGTTCCCGTGAAC
AGAG G

GAM8297 367 MAPKAPK 1 1041 NP_004626.1 3 1135 TGCCTGACAAGT - AA G 3 B c
c

3 GCCTGACACGCA GCTGT TGTT GGGCACTTG
GCCTAGTT CGACG ACAG TCCGTGAAC

```
                                        C  --      A
GAM8297  367   MCC   1  5308  NP_002378.1  3 233   GCTCTTCCCTCC      TAA   ACTT--       3  B  c
c
                                TGGGCCCACAAC GCTGTTGT  GGGC    GGG
                                AGCGTGTA   CGACAACA  CCCG    CCC
                                       ---   GGTCCT
GAM8297  367   MDA5  1  15518 NP_071451.2  5 155   CATTTCACCTGT      AA-  C  TT       3  B  c  c

                                CCCGCAGACAAC GCTGTTGTT  GGG AC  GG
                                AGCACCAT   CGACAACAG  CCC TG  CC
                                       ACG  -  T-
GAM8297  367   MESDC1  1  17738 NP_072088.1  5 477   CCGCAGCCCAGT    T-  TA     T        3  B  c
c
                                GCCCTCTGCCCG GCTGT  GT  AGGGCACT GGG
                                CGGCGGTG   CGGCG  CG  TCCCGTGA CCC
                                       CC  TC      -
GAM8297  367   MGC1064 1  8894  NP_116082.1  3 213   TGGACACAAGAG      TA  -  A   G       3  B  c
c
         6                      CCACTGCACAAC GCTGTTGT  AG GGC CTTG
                                AGCCAAGG   CGACAACA  TC CCG GAAC
                                       CG  A   A   A
GAM8297  367   MGC1081 1  2986  NP_085045.2  3 219   ATGGGAACAAGT   G-   A       G       3  B  c
c
         8                      GCCCTCAGCAAG GCT  TTGTT AGGGCACTTG
                                AAGCCGTG   CGA  AACGA TCCCGTGAAC
                                       AG   C       A
GAM8297  367   MGC1098 2  1625  NP_116043.1  3 81    CAAATCCCAAGT      TAAGGG           3  B  c
c
         1                      GGCGATGGCATG GCTGTTGT    CACTTGGG
                                TAACCACA   CGGTAGCG    GTGAACCC
                                       ------
GAM8297  367   MGC1098 2  5612  NP_116043.1  3 1171  ACTCGAACCCGT      T--    ACTT       3  B  c
c
         1                      CCTTTTCACAAC GCTGTTGT  AAGGGC   GGG
                                AGCCGCGG   CGACAACA  TTCCTG   CCC
                                       CTT    ----
GAM8297  367   MGC1290 1  6475  NP_112496.1  5 631   CATTTCCCAAGT   TT   ----          3  B  c  c
         4                      GCTTCATGTTAG GCTG  GTTAA   GGGCACTTGGG
                                CCAGCAAA   CGAC  CGATT   TTCGTGAACCC
                                       --   GTAC
GAM8297  367   MGC1296 1  4628  NP_116095.1  3 596   GACCCACCAAGT   G  TT             3  B  c
c
         6                      GCTTTTCCCAAG GCT TTG  AAGGGCACTTGG
                                GGTCTGGG   TGG AAC  TTTTCGTGAACC
                                       G  CC
GAM8297  367   MGC1304 1  13016 NP_116098.1  3 68    TGAATTCCAAGT   TTG  - -          3  B  c  c

         7                      GCTCCATTGGAT GCTG  TTAA GG GCACTTGGG
                                CAGCTTCC   CGAC  GGTT CC CGTGAACCT
                                       TA-   A  T
```

GAM8297 367 MGC1483 1 11725 NP_115715.1 3 259 CCCAGGGTAAGT G TAA ----- 3 B c c

2 GCCCACGAAAGC GCT TTGT GGGCACT TGGG
CCAGTCCA CGA AGCA CCCGTGA ACCC
A --- ATGGG

GAM8297 367 MGC1629 1 1591 NP_116159.2 3 648 ATGAGTGGCCTG - GCA TG 3 B c c

1 AGCCTTAACAAC GC TGTTGTTAAGG CT GG
ATGTTTTT TG ACAACAATTCC GA CC
T --- GT

GAM8297 367 MGC1663 1 13782 NP_777593.1 5 406 AAGCCGCCCAGT ----- A T 3 B c c

8 GCCCTGAGCGTC GCTGT TGTT AGGGCACT GGG
TCCATGGC CGGTA GCGA TCCCGTGA CCC
CCTCT G -

GAM8297 367 MGC2046 1 14116 NP_444271.1 5 1146 GCCTGTTCAAGT T T 3 B c c

0 GCCCTTGCTACC GCTG TG TAAGGGCACTTGGG
AGTTCCGA TGAC AT GTTCCCGTGAACTT
C C

GAM8297 367 MGC2452 1 10266 NP_116033.1 5 41 GTCTGCCCAAGT ---- G G 3 B c c

GTCTTAGGAACC GCT GTT TTAAGG CACTTGGG
AAAAGCAA CGA CAA GATTCT GTGAACCC
AAAC G -

GAM8297 367 MGC2670 1 5445 NP_689794.1 3 619 TGTTTCTCAGTG T- - T 3 B c c

6 TTCCTTAACAGC GC GTTGTTAAGGG CACT GGG
CTGCCTTT CG CGACAATTCCT GTGA CTC
TC T -

GAM8297 367 MGC3067 1 13227 NP_077271.1 3 73 CCAGTGCTGGGT T G TG 3 B c c

GCGCTTAACAAC GC GTTGTTAAG GCACT G
TGCGTTCT CG CAACAATTC CGTGG C
T G GT

GAM8297 367 MGC3318 1 17019 NP_660204.1 5 408 TTGCCTCTCAGG AAGGG - 3 B c c

2 ATGACAAACAAC GCTGTTGTT CA CTTGGG
AGCGGCTC CGACAACAA GT GGACTC
ACA-- A

GAM8297 367 MGC3320 1 17059 NP_775811.1 3 19 AACATCTCTAGT G T T 3 B c c

2 GCCCTTGCAAGA GCT TTGT AAGGGCACT GGG
GCCTTTAA CGA AACG TTCCCGTGA CTC
G - T

GAM8297 367 MGC3969 1 13115 NP_689984.1 5 46 CGCCGTCCCAGT G TTA T 3 B c c

6 GCCCTCAGAGGC GCT TTG AGGGCACT GGG
ACCTAGAC CGG GAC TCCCGTGA CCC
A --- -

GAM8297 367 MGC4005 1 16179 NP_689796.1 3 1886 CTAATACTAAGT G-- A--- 3 B c c

3 GCCCAACCTGAC CTGTTGTTA GGGCACTTGG
AACAGAGA GACAACAGT CCCGTGAATC
AGA CCAA
GAM8297 367 MGC4540 1 2651 NP_689502.1 3 488 ATAACTGCCAGT T TT T 3 B c c

8 GCCCTTTCACAG GCTGT G AAGGGCACT GG
CTGATTAT CGACA C TTCCCGTGA CC
- T- -
GAM8297 367 MGC4584 1 19671 NP_775855.1 3 515 CAGCTGCAGGAA A A GG 3 B c
c

0 GGCTCTGACAAC GCTGTTGTTA GGGC CTT
AGCCCGCC CGACAACAGT CTCG GAA
- - GG
GAM8297 367 MGC4737 1 4951 NP_113654.1 5 1126 CCTGCCACCGGT GTT T -- 3 B c
c

GCCCTTCACCAA GCT GT AAGGGCACT TGG
GCTTCCCA CGA CA TTCCCGTGG ACC
AC- C CC
GAM8297 367 MGC4796 1 4380 NP_114406.1 3 1002 ACATATCCCAGT G- ---- T 3 B c c

GCCCTTGCCTCA CTGTTGT TAAGGGCACT GGG
TAATAGAT GATAATA GTTCCCGTGA CCC
TA CTCC -
GAM8297 367 MGC5391 1 13373 NP_116129.2 3 1251 GGATCCCAGTGT G -- T 3 B c
c

TGCCTTAACAGG GCT TTGTTAAGG GCACT GGG
GTGTCTGT TGG GACAATTCC TGTGA CCC
- GT -
GAM8297 367 MGC5508 1 4031 NP_076997.1 3 645 TCTCTTTCAAGT -- TTA- 3 B c c
GCCTTAATCCGA GCTG TTG AGGGCACTTGGG
GCCAGCAG CGAC AGC TTCCGTGAACTT
CG CTAA
GAM8297 367 MIRO-2 1 10083 NP_620124.1 3 257 GAGCTCCCAAGT T T AAG 3 B c
c

GCCGGCCACCGC GC GT GTT GGCACTTGGG
TGTCAGGG CG CA CGG CCGTGAACCC
C C ---
GAM8297 367 MLC1 1 1467 NP_055981.1 5 179 GTGTCCCCAAGT G TTAAG- 3 B c
c

GCCATGACCCAG GCT TTG GGCACTTGGG
GAGCCATT CGA GAC CCGTGAACCC
G CCAGTA
GAM8297 367 MLC1 1 1467 NP_631941.1 5 219 GTGTCCCCAAGT G TTAAG- 3 B c
c

GCCATGACCCAG GCT TTG GGCACTTGGG
GAGCCATT CGA GAC CCGTGAACCC
G CCAGTA
GAM8297 367 MRPS27 1 15026 NP_055899.1 3 84 GGACTCAGCAGT A G -- 3 B c c
GGCCTGGACAAC GCTGTTGTT AGG CACT TGGG
AGCCTCAG CGACAACAG TCC GTGA ACTC

```
                                                G  G  CG
GAM8297  367  MSTP028 1  2725  NP_114160.1  3  2760  CAGGACCCAAGT  T-  AAGG          3  B  c
 c
                                GTGAACAACACT GCTG  TGTT  GCACTTGGG
                                CAGCCCGC  CGAC  ACAA  TGTGAACCC
                                          TC  CAAG
GAM8297  367  MTHFD2  1  11949  NP_006627.1  3  354  CATTTCCCAAGT      AAG--          3  B  c  c

                                GCTATTGCAATA GCTGTTGTT  GGCACTTGGG
                                ACAGTTGA  TGACAATAA  TCGTGAACCC
                                          CGTTA
GAM8297  367  MUC6  1  5705  XP_290540.1  3  141  TGGCCCCCAAGT  TG T  TA            3  B  c  c

                                GCCCTGGGCCGT GC  T GT  AGGGCACTTGGG
                                GGCTCCCT  CG  G CG  TCCCGTGAACCC
                                          GT C  GG
GAM8297  367  MYO1D  1  12931  XP_050041.4  3  1403  AACCCACCAAGT  TGTTAA          3  B  c
 c
                                GCCTGTGTGCAG GCTGT  GGGCACTTGG
                                CCTCCTGT  CGACG  TCCGTGAACC
                                          TGTG--
GAM8297  367  MYO3A  1  9274  NP_059129.2  3  167  CGGCCCTCAAGT  TT  TAA          3  B  c
c
                                GCCCGGGCCGGC GCTG  GT  GGGCACTTGGG
                                CTTCGTGC  CGGC  CG  CCCGTGAACTC
                                          -- GG-
GAM8297  367  MYOZ2  1  7556  NP_057683.1  5  28  TCAGGCCCAAGT  TGTTAAG          3  B  c
 c
                                GCCATCCATAGT GCTGT  GGCACTTGGG
                                CCATCTCC  TGATA  CCGTGAACCC
                                          CCTA---
GAM8297  367  NAV3  1  5758  NP_055718.2  3  719  CCACCTGCCCAC  G      CACT       3  B  c  c

                                TCCCTTAACAAG GCT TTGTTAAGGG  TGGG
                                AGTTTTAT  TGA AACAATTCCC  ACCC
                                          G      TC--
GAM8297  367  NDP  1  17354  NP_000257.1  5  39  CTCTCCCTGTGT      - -  TT      3  B  c  c
                                CGCTTAAACAAC GCTGTTGTT AAG GGCAC  GGG
                                AGTCCTAA  TGACAACAA TTC CTGTG  CCC
                                          A  G  T-
GAM8297  367  NETO1  1  3758  NP_620552.1  3  160  ACCACGATTTGT  T  G      --- -    3  B  c  c
                                GCCCTTGAAAAT GC GTT TTAAGGGCAC  TTG GG
                                GCTGTTTG  CG TAA AGTTCCCGTG  AGC CC
                                          - A      TTT  A
GAM8297  367  NFKBIL1 1  7331  NP_004998.2  3  15  AGGCCCTCAAGT  G- G TA          3  B  c  c

                                GCCCTAGGGAAG GCT  TT T  AGGGCACTTGGG
                                AAGCAAGA  CGA  AA G  TCCCGTGAACTC
                                          AG  G GA
GAM8297  367  NKTR  1  4907  NP_005376.2  3  1385  TGTTCCCCAAGT  --- T  GG        3  B  c  c
```

GTACTTAATCAC GCT GT GTTAAG CACTTGGG
CTTAGTGC TGA CA TAATTC GTGAACCC
TTC C AT
GAM8297 367 NLI-IF 1 15666 NP_067021.1 3 414 TGGACATCAAGT G TA 3 B c c
GCCTTGCATAGA GCT TTGT AGGGCACTTGG
GCCCCCTC CGA GATA TTCCGTGAACT
- CG
GAM8297 367 NPC2 1 14591 NP_006423.1 3 88 CTCCAGCTCTGC - - C-- 3 B c c
TGCTTCAACAAC GCTGTTGTT AAG GGCA TTGGG
AGTGACTT TGACAACAA TTC TCGT GACCT
C G CTC
GAM8297 367 NSG-X 1 2106 NP_055226.1 3 855 CCTTCCCCAAGT TTA GG 3 B c c

GAGCTCAGCAGC GCTGTTG AG CACTTGGG
ATGTGCTA CGACGAC TC GTGAACCC
--- GA
GAM8297 367 NXPH3 1 12898 NP_009156.1 3 193 AGGGTCCCAAGT ---- TTAAG 3 B c
c
GCTGGTCCCAAC GCT GTTG GGCACTTGGG
CTGAAGCT CGA CAAC TCGTGAACCC
AGTC CCTGG
GAM8297 367 NYD-SP1 1 9259 NP_114157.2 3 947 CTATTCCCAAGT T -- G 3 B c c
1 GGTCTTCAAGCA GCTG TGTT AAGG CACTTGGG
CCAGTGTA TGAC ACGA TTCT GTGAACCC
C AC G
GAM8297 367 OAS3 1 3720 NP_006178.1 3 1096 TCTCCTGACCTC AAG C 3 B c c
AAGTCCAACAAC GCTGTTGTT GG ACTTGGG
AGTGTCCA TGACAACAA CC TGAACTC
--- -
GAM8297 367 P2RX1 1 2491 NP_002549.1 5 258 TCCAACCCAAGT ---- - AA 3 B c c
GCCTCCAGCTGA GCT GTT GTT GGGCACTTGGG
CCTCTGGC CGG CAG CGA TCCGTGAACCC
TCTC T CC
GAM8297 367 PCDH11X 1 11504 NP_116750.1 3 3898 TTAAAAGCAGTT AGGGC 3 B
c c
CAAGTTGACAAC GCTGTTGTTA ACTTGGG
AGCAGAAA CGACAACAGT TGAACTT

GAM8297 367 PCDH11X 1 11504 NP_116751.1 3 3898 TTAAAAGCAGTT AGGGC 3 B
c c
CAAGTTGACAAC GCTGTTGTTA ACTTGGG
AGCAGAAA CGACAACAGT TGAACTT

GAM8297 367 PCDH11Y 1 11504 NP_116755.1 3 3890 TTAAAAGCAGTT AGGGC 3 B
c c
CAAGTTGACAAC GCTGTTGTTA ACTTGGG
AGCAGAAA CGACAACAGT TGAACTT

GAM8297 367 PCDHGA1 1 3215 NP_061735.1 3 1471 AACCCCAGACCT T C-- 3 B c
c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA1 1 3215 NP_061736.1 3 1471 AACCCCAGACCT T C-- 3 B c c

0 GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA1 1 3215 NP_061737.1 3 1471 AACCCCAGACCT T C-- 3 B c c

1 GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA1 1 3215 NP_114481.1 3 1471 AACCCCAGACCT T C-- 3 B c c

1 GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA1 1 3215 NP_003726.1 3 1471 AACCCCAGACCT T C-- 3 B c c

2 GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA2 1 3215 NP_061738.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA3 1 3215 NP_061739.2 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA4 1 3215 NP_061740.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA5 1 3215 NP_061741.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA6 1 3215 NP_061742.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA7 1 3215 NP_061743.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA8 1 3215 NP_114477.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGA9 1 3215 NP_061744.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB1 1 3215 NP_061745.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB2 1 3215 NP_061746.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB3 1 3215 NP_061747.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB4 1 3215 NP_003727.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB5 1 3215 NP_061748.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB6 1 3215 NP_061749.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGB7 1 3215 NP_061750.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGC3 1 3215 NP_002579.2 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGC3 1 3215 NP_115779.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGC4 1 3215 NP_061751.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PCDHGC5 1 3215 NP_061752.1 3 1471 AACCCCAGACCT T C-- 3 B c c

GCCCTTACAGTA GCTGTTGT AAGGGCA TTGGG
GTGTAGCG TGATGACA TTCCCGT GACCC
- CCA

GAM8297 367 PDGFRB 1 10084 NP_002600.1 3 113 GTCAGCCAGGCT T T - 3 B c c

GCCCTTATCAGC GC GTTG TAAGGGCA CTTGG
TGTCCCCT TG CGAC ATTCCCGT GGACC
T T C

GAM8297 367 PELO 1 2948 NP_057030.2 5 860 CGCCAGGCAAGT -- G G 3 B c c

GCCCTTAGAAAC GCT GTT TTAAGGGCACTTG
CGGGCCCC CGG CAA GATTCCCGTGAAC
GC A G

GAM8297 367 PHB 1 9136 NP_002625.1 3 256 AAATTGCCAAGT -- TAA 3 B c c

GCCTATGCAAAC GCTG TTGT GGGCACTTGG
CAGCTTTA CGAC AACG TCCGTGAACC
CA TA-

GAM8297 367 PIGR 1 15327 NP_002635.2 5 22 GCAGCGTCCAGT TTA T 3 B c c

GCCCTGCCAGTA GCTGTTG AGGGCACT GGG
GCTCCTAG CGATGAC TCCCGTGA CCT
CG- -

GAM8297 367 PIM2 1 12815 NP_006866.1 3 558 GTTATCCCAAGT GTTGT 3 B c c

GCTCTTATTCTG GCT TAAGGGCACTTGGG
GTGAGAAG TGG ATTCTCGTGAACCC
TCTT-

GAM8297 367 PLAG1 1 12375 NP_002646.1 5 442 CAGTTCCCAAGT G-- AA 3 B c c

GTCCAACAAGAA GCT TTGTT GGGCACTTGGG
GGCCTGGT CGG AACAA CCTGTGAACCC
AAG --

GAM8297 367 PP2CE 1 6865 NP_640338.1 5 208 CGACTCCCAGAG GT AC 3 B c c

GCCCTTAAACAG GCTGTT TAAGGGC TTGGG
CATCTTCA CGACAA ATTCCCG GACCC
-- GA

GAM8297 367 PPAP2B 1 4950 NP_003704.3 3 196 AGTGTTTGCCTA AAGGG T 3 B c c

TGTGGAAACAAC GCTGTTGTT CAC TGGG
AGCAAACT CGACAACAA GTG ATCC
AG--- T

GAM8297 367 PPAP2B 1 4950 NP_803133.1 3 196 AGTGTTTGCCTA AAGGG T 3 B c c

TGTGGAAACAAC GCTGTTGTT CAC TGGG
AGCAAACT CGACAACAA GTG ATCC
AG--- T

GAM8297 367 PPIL3 1 2401 NP_115861.1 5 122 TTGCATTTTTCC G CTT 3 B c c

TGTTTTAACAAC GCTGTTGTTAAGG CA GGG
GGCTGTGC CGGCAACAATTTT GT CCT
- ---

GAM8297 367 PPIL3 1 2401 NP_570981.1 5 57 TTGCATTTTTCC G CTT 3 B c c

TGTTTTAACAAC GCTGTTGTTAAGG CA GGG
GGCTGTGC CGGCAACAATTTT GT CCT
- ---

GAM8297 367 PPIL3 1 2401 NP_572028.1 5 272 TTGCATTTTTCC G CTT 3 B c c

TGTTTTAACAAC GCTGTTGTTAAGG CA GGG
GGCTGTGC CGGCAACAATTTT GT CCT
- ---

GAM8297 367 PPM1F 1 13090 NP_055449.1 3 959 AGCCATTCAAGT T TA 3 B c c

GCCTTACACAGC GCTGT GT AGGGCACTTGGG
TTTGAAGA CGACA CA TTCCGTGAACTT
- --

GAM8297 367 PRDM1 1 6451 NP_001189.1 5 163 CTGCCCCCAAGT TT AAGG 3 B c c

GTAACTCCAGCA GCTG GTT GCACTTGGG
CTGTGAGG CGAC CAA TGTGAACCC
CT ----

GAM8297 367 PRND 1 937 NP_036541.1 3 2072 CGCTCTCCTAAG TAAG C 3 B c c

TTTAATTACAAC GCTGTTGT GG ACTTGGG
AGCACGTG CGACAACA TT TGAATCC
TTAA -

GAM8297 367 PRO0149 1 7715 NP_054836.1 3 117 TCTATACACTGG AA TG 3 B c c

GTGCCCAACAAC GCTGTTGTT GGGCACT G
AGCCCCTT CGACAACAA CCCGTGG C
-- GT

GAM8297 367 Prostei 1 10314 NP_149093.1 3 429 CCCATCTCTAAG T- CA 3 B c c
n CCCCTTAACCTG GCTGT GTTAAGGG CTTGGG
CAGCTTCG CGACG CAATTCCC GAATCT
TC C-

GAM8297 367 PRX 1 13569 NP_066007.1 3 1584 GCTTCCAAAAGT GTTAA -- 3 B c c

GCCCGAGGCAGC GCTGTT GGGCACT TGGG
CCTTCCAG CGACGG CCCGTGA ACCT
AG--- AA

GAM8297 367 PSCD1 1 20040 NP_004753.1 3 797 TCCATCCCAAGT G TAA 3 B c c

GCCTGCGGAGCC GCT TTGT GGGCACTTGGG
CGAGGAGA CGA GGCG TCCGTGAACCC
- ---
GAM8297 367 PSCD1 1 20040 NP_059430.1 3 797 TCCATCCCAAGT G TAA 3 B c c

GCCTGCGGAGCC GCT TTGT GGGCACTTGGG
CGAGGAGA CGA GGCG TCCGTGAACCC
- ---
GAM8297 367 PTP4A1 1 7509 NP_003454.1 3 2695 CTCCTATTCCCA T G ACT 3 B c c

CGCCTTAACACA GCTGT GTTAAGG C TGGG
GCTCTATA CGACA CAATTCC G ACCC
- - C--
GAM8297 367 PTPRU 1 3003 NP_005695.2 3 825 TGACAATCTGCA AAG A G 3 B c c

AGGCTGAACAAC GCTGTTGTT GGC CTTG
AGCCCCTG CGACAACAA TCG GAAC
G-- - G
GAM8297 367 PTPRU 1 3003 NP_573438.1 3 825 TGACAATCTGCA AAG A G 3 B c c

AGGCTGAACAAC GCTGTTGTT GGC CTTG
AGCCCCTG CGACAACAA TCG GAAC
G-- - G
GAM8297 367 PTPRU 1 3003 NP_573439.1 3 825 TGACAATCTGCA AAG A G 3 B c c

AGGCTGAACAAC GCTGTTGTT GGC CTTG
AGCCCCTG CGACAACAA TCG GAAC
G-- - G
GAM8297 367 PYC1 1 15258 NP_690865.1 3 98 CGCGCACCAGTC AAGG - T 3 B c c

GCGTAAGACAAC GCTGTTGTT GC ACT GG
AGCAGTGT CGACAACAG CG TGA CC
AATG C -
GAM8297 367 RAB-R 1 14904 NP_006067.2 3 459 GGTGGCCCAAGT -- TG 3 B c c
GCTCTTGGTGGC GCT GT TTAAGGGCACTTGGG
CCAGCTTG CGA CG GGTTCTCGTGAACCC
CC GT
GAM8297 367 RAI1 1 5307 NP_109590.2 3 2760 GCCACCAAGAAG TA - A- 3 B c c
CTCCTCGACAAC GCTGTTGT AGG GC CTTGG
AGCCACTT CGACAACA TCC CG GAACC
GC T AA
GAM8297 367 RASSF2 1 8667 NP_055552.1 3 456 CTCCTCTCAAGT G TAAG 3 B c c

GCCAGGGAGCAG GCTGTT T GGCACTTGGG
CCACACGT CGACGA G CCGTGAACTC
G GA--
GAM8297 367 RASSF2 1 8667 NP_739579.1 3 682 CTCCTCTCAAGT G TAAG 3 B c c

GCCAGGGAGCAG GCTGTT T GGCACTTGGG
CCACACGT CGACGA G CCGTGAACTC

G GA--
GAM8297 367 RASSF2 1 8667 NP_739580.1 3 456 CTCCTCTCAAGT G TAAG 3 B c c
GCCAGGGAGCAG GCTGTT T GGCACTTGGG
CCACACGT CGACGA G CCGTGAACTC
G GA--
GAM8297 367 RBM3 1 9588 NP_006734.1 3 629 CCACTGTACTCC AA ACT 3 B c c
AGCCTGGACAAC GCTGTTGTT GGGC TGGG
AGCGAGAG CGACAACAG TCCG ACCT
G- ---
GAM8297 367 RDH-E2 1 6845 NP_620419.1 3 766 CCCGCCTCCAGT GTT----- ----- 3 B c c
GCCCTTCTTTCC GCTGTT AAGGGCACT TGG
AAAACAGC CGACAA TTCCCGTGA GCC
AACCTTTC CCTCC

G
C

GAM8297 367 RERG 1 16494 NP_116307.1 5 248 ACTCAGTGCTTT ----- T 3 B c c
AGTTTTAACAAC GCTGTTGTTAAG GGCACT GGG
AGTAAATT TGACAACAATTT TCGTGA CTC
TGATT -
GAM8297 367 RGL 1 5364 NP_055964.2 5 156 GCCGGACCGAGT TGTTA 3 B c c
GCCCTGCAGTTG GCTGT AGGGCACTTGG
GTAGGAGT TGACG TCCCGTGAGCC

GAM8297 367 RGS11 1 2788 NP_003825.1 3 801 CATCCCCCAAGT T TTAA 3 B c c

GCCTCACCAGTC GCTG TG GGGCACTTGGG
CCCCAGAC TGAC AC TCCGTGAACCC
C ----
GAM8297 367 RNF7 1 1071 NP_055060.1 3 78 TTGTAATCCAGT G TA T 3 B c c
GCCCTACAAAGG GCT TTGT AGGGCACT GGG
CTAGAACA CGG AACA TCCCGTGA CCT
A -- -
GAM8297 367 ROBO1 1 17266 NP_598334.1 5 315 CATCCCCCAAGT G AAGGG 3 B c c
GATGGGAACAAG GCT TTGTT CACTTGGG
GGCCCGCC CGG AACAA GTGAACCC
G GGGTA
GAM8297 367 RYR1 1 5163 NP_000531.1 3 53 CCCACCTCAAGT TGTTA- 3 B c c
GCCTTATTCTCA GCTGT AGGGCACTTGGG
CAGCAAGC CGACA TTCCGTGAACTC
CTCTTA
GAM8297 367 SARM1 1 3114 NP_055892.1 3 565 TAATCACTCAGT TT T 3 B c c
GCCCTTAGCTAG GCTG GTTAAGGGCACT GGG
CCTGACTA CGAT CGATTCCCGTGA CTC
-- -
GAM8297 367 SDC3 1 2696 NP_055469.1 3 216 GCCCCAGACTGT GT T --- 3 B c c

GCCCTTACGAGC GCT TGT AAGGGCAC TTGGG
TCATCTCT CGA GCA TTCCCGTG GACCC
-- - TCA

GAM8297 367 SEF 1 2366 NP_060033.1 3 245 GGCATGTCCATA AA A - 3 B c c
AGGTCTGACAAC GCTGTTGTT GGGC CTTG GG
AGCTTGCC CGACAACAG TCTG GAAT CC
-- - A

GAM8297 367 SEMA4F 1 17986 NP_004254.2 3 1177 TCAGATTTTCAA G G A 3 B c c
GGCCTTAACAAA GCT TTGTTAAGG C CTTGGG
GTTAAAGG TGA AACAATTCC G GAACTT
- - -

GAM8297 367 SERPINB 1 16752 NP_004559.3 3 91 TGCAACCCAAGT TGT-- G 3 B c c
6 GGCCTTATCCGT GCTGT TAAGG CACTTGGG
GCAGTGGT TGACG ATTCC GTGAACCC
TGCCT G

GAM8297 367 SH2B 1 4036 NP_056318.1 3 342 GGCCACCCCAGG - G A 3 B c c
GCCATTAACAAC GCTG TTGTTAA GGC CTTGGG
CAGTACTC TGAC AACAATT CCG GGACCC
C A -

GAM8297 367 SH3BP2 1 14484 NP_003014.2 3 4424 CAGCACCCAAGT TGTTA- 3 B c c
GCCCTCCCCTCA GCTGT AGGGCACTTGGG
CAGTGTCA TGACA TCCCGTGAACCC
CTCCCC

GAM8297 367 SHAPY 1 18309 NP_620148.1 3 1204 ATCATTCACAGT TGTTA - 3 B c c
GCCCTCCCCACA GCTGT AGGGCACT TGGG
GCACTACC CGACA TCCCGTGA ACTT
CCCC- C

GAM8297 367 SLC17A2 1 2863 NP_005826.1 3 247 TAGCATGCGCCC AGG A 3 B c c
GGGGTTGACAAC GCTGTTGTTA GC CTTGGG
AGCTGGAC CGACAACAGT TG GGGCCC
--- -

GAM8297 367 SLC26A1 1 8035 NP_071325.2 3 486 ACACACCCAAGT - T-- TAA 3 B c c
GCCCCTCACACC GC TG TGT GGGCACTTGGG
TCGTGCCT CG GC ACA CCCGTGAACCC
T TCC CTC

GAM8297 367 SLC6A1 1 2172 NP_003033.1 5 136 TCCTCCTAGGGT T TG - 3 B c c
GCCCTTGAGCCG GC GT TTAAGGGCACT TGGG
CAAAACTG CG CG AGTTCCCGTGG ATCC
C -- G

GAM8297 367 SLC9A8 1 1781 XP_030524.2 3 4089 TCTCCCCCAAGT G- TA GG 3 B c c
GAGCTGCAAGAG GCT TTGT AG CACTTGGG
GCCCCTGT CGG AACG TC GTGAACCC
AG -- GA

GAM8297 367 SON 1 2947 NP_115571.1 3 134 ACATAGCCCATT TG CT 3 B c c
GCCCTTAATGAT GCTGT TTAAGGGCA TGGG
GGTTTCTT TGGTA AATTCCCGT ACCC
GT T-
GAM8297 367 Spir-1 1 18344 XP_290818.1 3 672 TGTTGTCCCAGT TTGTTA T 3 B c c
GCCCTGGTTCAG GCTG AGGGCACT GGG
TGTCTCCT TGAC TCCCGTGA CCC
TTGG-- -
GAM8297 367 SPRY3 1 16967 NP_005831.1 3 1031 TCTGACCCAAGT - - AAG 3 B c c
GCCAAAGGCAGA GC TGT TGTT GGCACTTGGG
CGTGCTTT CG GCA ACGG CCGTGAACCC
T G AAA
GAM8297 367 SRRM1 1 4656 NP_005830.1 3 248 GAAGGCCCAAGT T TTAA 3 B c
c
GTCCCCACAGTC GCTGT G GGGCACTTGGG
TTAGGGGG TGACA C CCTGTGAACCC
- C---
GAM8297 367 SSB1 1 8921 NP_079382.2 3 1067 GATTTCCCAAGT G TTA -- 3 B c c
GCATCCTCAGAA GCT TTG AGG GCACTTGGG
GCTCTGGG CGA GAC TCC CGTGAACCC
A --- TA
GAM8297 367 SYT8 1 6528 NP_612634.1 3 1411 CACCTTCCTGGT TTGTT T 3 B c c
GCCCTTCAGCCA GCTG AAGGGCACT GGG
GGTCCAGA CGAC TTCCCGTGG CCT
----- T
GAM8297 367 TAZ 1 490 NP_000107.1 3 134 ACCCTCTCAAGT GT TTA 3 B c c
GCCCTCTCCGAG GCT TG AGGGCACTTGGG
CTGGTAGG CGA GC TCCCGTGAACTC
-- CTC
GAM8297 367 TAZ 1 490 NP_851828.1 3 134 ACCCTCTCAAGT GT TTA 3 B c c
GCCCTCTCCGAG GCT TG AGGGCACTTGGG
CTGGTAGG CGA GC TCCCGTGAACTC
-- CTC
GAM8297 367 TAZ 1 490 NP_851829.1 3 134 ACCCTCTCAAGT GT TTA 3 B c c
GCCCTCTCCGAG GCT TG AGGGCACTTGGG
CTGGTAGG CGA GC TCCCGTGAACTC
-- CTC
GAM8297 367 TAZ 1 490 NP_851830.1 3 134 ACCCTCTCAAGT GT TTA 3 B c c
GCCCTCTCCGAG GCT TG AGGGCACTTGGG
CTGGTAGG CGA GC TCCCGTGAACTC
-- CTC
GAM8297 367 TAZ 1 490 NP_851831.1 3 741 ACCCTCTCAAGT GT TTA 3 B c c
GCCCTCTCCGAG GCT TG AGGGCACTTGGG
CTGGTAGG CGA GC TCCCGTGAACTC
-- CTC
GAM8297 367 TBC1D4 1 748 NP_055647.1 3 1625 ATAGCTCAGTGT TG---- - 3 B c c
GCCCTTGAATCC GCTGT TTAAGGGCAC TTGGG

ATACAGTT TGACA AGTTCCCGTG GACTC
TACCTA T
GAM8297 367 TBX6 1 6888 NP_004599.2 5 121 GCGGCCCCGAGT TTG - 3 B c c
GCCCTGTGAAAT GCTG TTA AGGGCACTTGGG
CAGCTCAG CGAC AGT TCCCGTGAGCCC
TAA G
GAM8297 367 TBX6 1 6888 NP_542936.1 5 121 GCGGCCCCGAGT TTG - 3 B c c
GCCCTGTGAAAT GCTG TTA AGGGCACTTGGG
CAGCTCAG CGAC AGT TCCCGTGAGCCC
TAA G
GAM8297 367 TCL6 1 18755 NP_036600.2 5 211 ACACAGCCAAGT T AA - 3 B c c
GCATCCGAGCAG GC GTTGTT GG GCACTTGG
CGCAGGAT CG CGACGA CT CGTGAACC
- GC A
GAM8297 367 TCL6 1 18755 NP_055233.1 5 211 ACACAGCCAAGT T AA - 3 B c c
GCATCCGAGCAG GC GTTGTT GG GCACTTGG
CGCAGGAT CG CGACGA CT CGTGAACC
- GC A
GAM8297 367 TCL6 1 18755 NP_065575.1 5 211 ACACAGCCAAGT T AA - 3 B c c
GCATCCGAGCAG GC GTTGTT GG GCACTTGG
CGCAGGAT CG CGACGA CT CGTGAACC
- GC A
GAM8297 367 TCL6 1 18755 NP_065577.2 5 211 ACACAGCCAAGT T AA - 3 B c c
GCATCCGAGCAG GC GTTGTT GG GCACTTGG
CGCAGGAT CG CGACGA CT CGTGAACC
- GC A
GAM8297 367 TJP2 1 15651 NP_004808.1 3 971 TTAAACCCAAGT G TAAG 3 B c c
GCTGCACAAAAG GCT TTGT GGCACTTGGG
CAGATACT CGA AACA TCGTGAACCC
A CG--
GAM8297 367 TMEM2 1 1387 NP_037522.1 3 1528 CTAATTGTAAGT G T G 3 B c c
GCCCTTACTAAG GCT TTG TAAGGGCACTTG
GGCACATG CGG AAT ATTCCCGTGAAT
G C G
GAM8297 367 TMPRSS2 1 5188 NP_005647.2 3 1220 GCATTGCCAAGT - T AG 3 B c
c
GCCATAACCATG GCT GT GTTA GGCACTTGG
AGCACTAC CGA TA CAAT CCGTGAACC
G C A-
GAM8297 367 TNFRSF1 1 11026 NP_001057.1 3 150 AGTTCCTCTAGT T TA T 3 B c
c
B GCCCTCCACAGC GC GTTGT AGGGCACT GGG
CGCAGCCT CG CGACA TCCCGTGA CTC
C CC T
GAM8297 367 TOMM70A 1 18168 NP_055635.1 3 647 TACATTCTTCTT TAA AC 3 B c
c
AAAGTCCACAAC GCTGTTGT GGGC TTGGG
AGCAGATT CGACAACA CCTG AATTC
--- A-
GAM8297 367 TOP2A 1 15250 NP_001058.2 3 163 TAAAGCCCAAGT TTGTT 3 B c
c

GTTCTTTAGCTT GCTG AAGGGCACTTGGG
TTTATAAT CGAT TTCTTGTGAACCC

GAM8297 367 TRIM26 1 6153 NP_003440.1 3 1155 CCCATTCCAAGT TTGTTA 3 B c c

GCTCTGCCAGCC GCTG AGGGCACTTGGG
CCTGTTCA CGAC TCTCGTGAACCT
CG----
GAM8297 367 TRIPIN 1 13987 NP_689737.1 3 342 GAAGACCCAAGT --- G GG 3 B c c

GAGTTTGAAACA GC TGTT TTAAG CACTTGGG
CCTGCTCT CG ACAA AGTTT GTGAACCC
TCC - GA
GAM8297 367 TUB 1 4633 NP_003311.2 3 522 TGGCCAAGCCTG T - A--- 3 B c c
GCCCTTAAACAA GC GTTGTT AAGGGC CTTGG
CTGCAGAA CG CAACAA TTCCCG GAACC
T A GTCC
GAM8297 367 TUB 1 4633 NP_813977.1 3 522 TGGCCAAGCCTG T - A--- 3 B c c
GCCCTTAAACAA GC GTTGTT AAGGGC CTTGG
CTGCAGAA CG CAACAA TTCCCG GAACC
T A GTCC
GAM8297 367 UBE2V1 1 8584 NP_003340.1 3 420 GCCTCCCACCCT A- CACT 3 B c c

CCCTGCAACAAC GCTGTTGTT AGGG TGGG
AGCCCTCT CGACAACAA TCCC ACCC
CG TCCC
GAM8297 367 UBE2V1 1 8584 NP_068823.1 3 420 GCCTCCCACCCT A- CACT 3 B c c

CCCTGCAACAAC GCTGTTGTT AGGG TGGG
AGCCCTCT CGACAACAA TCCC ACCC
CG TCCC
GAM8297 367 UBE2V1 1 8584 NP_071887.1 3 420 GCCTCCCACCCT A- CACT 3 B c c

CCCTGCAACAAC GCTGTTGTT AGGG TGGG
AGCCCTCT CGACAACAA TCCC ACCC
CG TCCC
GAM8297 367 UEV3 1 10736 NP_060784.2 3 144 CCTCAATCCACA AA C - 3 B c c
GTCTCCAACAAC GCTGTTGTT GGG ACT TGGG
AGTTAAAA TGACAACAA CCT TGA ACCT
-- C C
GAM8297 367 UNC5C 1 8079 NP_003719.2 3 683 GACCCTTCTGGT G ---- T--- 3 B c c
GCCCTTTGGGAA GCT TTGTT AAGGGCACT GGG
TAAAGCTG CGA AATAA TTCCCGTGG CCC
- GGGT TCTT
GAM8297 367 UROS 1 1029 NP_000366.1 5 164 GGTCCCGCGAGT T G - - 3 B c c
GCCCTATAAGGA GC GTT TTA AGGGCACTTG GG
CTGCCAGG CG CAG AAT TCCCGTGAGC CC
T G A G
GAM8297 367 VIM 1 14629 NP_003371.1 3 104 CAGCTTTCAAGT TGTT 3 B c c
GCCTTTCTGCAG GCTGT AAGGGCACTTGGG

TTTTTCAG TGACG TTTCCGTGAACTT
TC--
GAM8297 367 VIP32 1 14426 NP_068378.1 5 43 TGTGACCCAAGT TT AA G 3 B c c
GGCCCGGACCAG GCTG GTT GG CACTTGGG
TTTGGGGC TGAC CAG CC GTGAACCC
-- GC G
GAM8297 367 WISP1 1 2051 NP_003873.1 3 1044 CAAGAAGTGGGT TT G 3 B c c
GCCCTTGGTAGC GCTGTTG AAGGGCACTTG
AGCCTGGG CGACGAT TTCCCGTGGGT
GG G
GAM8297 367 ZNF282 1 11281 NP_003566.1 3 290 ACCTCCTCGAGT -- T A- 3 B c c
GCCCTGGGACCA GCT GT GTT AGGGCACTTGGG
CTGGGCCA CGG CA CAG TCCCGTGAGCTC
GT C GG
GAM8297 367 ZNF282 1 11281 XP_114578.1 3 290 ACCTCCTCGAGT -- T A- 3 B c c
GCCCTGGGACCA GCT GT GTT AGGGCACTTGGG
CTGGGCCA CGG CA CAG TCCCGTGAGCTC
GT C GG
GAM8297 367 ZNF337 1 5587 NP_056470.1 3 617 ATGGGATCAGGT G GT- 3 B c c
GCCCTTATGAAA GCT TT TAAGGGCACTTGG
AGGCTTGA CGG AA ATTCCCGTGGACT
A AGT
GAM8297 367 ZNF76 1 14384 NP_003418.2 3 236 GCATCATCCTCG AAG A 3 B c c
GGAGCTGACAAC GCTGTTGTT GGC CTTGGG
AGCCAGGC CGACAACAG TCG GGGCTC
--- A
GAM8297 367 ZNFN1A1 1 1221 NP_006051.1 3 514 CGCCACCCAAGT T AAG 3 B c c
GCCAAGACACAG GCTGT GTT GGCACTTGGG
CAGGGCCA CGACA CAG CCGTGAACCC
- AA-
GAM8358 255 1 11587 NP_061052.1 5 525 GCAGGCACCCCA AG T 3 C c c
GTGGCCTCATCC GATGAGGC CACT GGG
TAGT CTACTCCG GTGA CCC
-- C
GAM8358 255 A1BG 1 18906 NP_570602.2 3 1777 TTTTCCCCAAGT A- -- 3 C c c
GCTTAGTTGCCA GATG GGC AGCACTTGGG
TCTA CTAC TTG TCGTGAACCC
CG AT
GAM8358 255 ABCC3 1 12771 NP_003777.2 3 461 GTACTCTGGGGT G- G 3 C c c
GCTGCCTGAATC GAT AGGCAGCACTT GG
CATT CTA TCCGTCGTGGG TC
AG G
GAM8358 255 ABCC3 1 12771 NP_064421.1 3 1477 GTACTCTGGGGT G- G 3 C c c
GCTGCCTGAATC GAT AGGCAGCACTT GG
CATT CTA TCCGTCGTGGG TC
AG G
GAM8358 255 ABCC3 1 12771 NP_064422.1 3 3716 GTACTCTGGGGT G- G 3 C c c

GCTGCCTGAATC GAT AGGCAGCACTT GG
CATT CTA TCCGTCGTGGG TC
AG G

GAM8358 255 ACATE2 1 11855 NP_036464.1 5 15 CGACTCCAAGAC T A- 3 C c c
GCTGCCTCTTCC GA GAGGCAGC CTTGGG
TGCG CT CTCCGTCG GAACCT
T CA

GAM8358 255 ACTR1A 1 19684 NP_005727.1 3 442 CCCCAGGCAGCT ---- ---- 3 C c c
GCTGCCTCCACT GAT GAGGCAGCA CTTGGG
ATCG CTA CTCCGTCGT GGACCC
TCAC CGAC

GAM8358 255 ADAR 1 12787 NP_001102.1 3 1197 ATTTATCCAAGT GC 3 C c c
GCTTTCATTTTT GATGAG AGCACTTGGG
CCAG TTACTT TCGTGAACCT
--

GAM8358 255 ADAR 1 12787 NP_056655.1 3 1197 ATTTATCCAAGT GC 3 C c c
GCTTTCATTTTT GATGAG AGCACTTGGG
CCAG TTACTT TCGTGAACCT
--

GAM8358 255 ADAR 1 12787 NP_056656.1 3 1197 ATTTATCCAAGT GC 3 C c c
GCTTTCATTTTT GATGAG AGCACTTGGG
CCAG TTACTT TCGTGAACCT
--

GAM8358 255 AK2 1 1267 NP_037543.1 3 879 AACTGACCAAAT TG C 3 C c c
GCTGCCTTGTTT GA AGGCAGCA TTGG
GGCC TT TCCGTCGT AACC
GT A

GAM8358 255 AKAP6 1 19508 NP_004265.3 3 82 TGCAACTCAGGG A A 3 C c c
GTGGCCTCATCC GATGAGGC GC CTTGGG
TCCC CTACTCCG TG GGACTC
G G

GAM8358 255 ALEX1 1 14775 NP_057692.1 5 244 GAACCAAGTCGA GA----- --- 3 C c c
GCTGCCTCAGAG TGAGGCAGC ACTTGG
CCGG ACTCCGTCG TGAACC
GGCCGAG AGC

GAM8358 255 AMOT 1 13810 NP_573572.1 3 3395 TGTCTTCCAAGT - CA- 3 C c c
GCCATCCATCAT GATGA GG GCACTTGGG
CAGT CTACT CC CGTGAACCT
A TAC

GAM8358 255 ANXA13 1 17250 NP_004297.1 3 241 GCAAGCATCTAG T A T 3 C c c

GCTGCCTCTTCA GA GAGGCAGC CT GG
CTTT CT CTCCGTCG GA CT
T - T

GAM8358 255 AP3S2 1 3119 NP_005820.1 3 1376 ACTAGGAGCAGG T A G 3 C c c
GCTGCCTCTTCT GA GAGGCAGC CTTG
CCCT CT CTCCGTCG GGAC
T - G

GAM8358 255 APM1 1 12520 NP_004788.1 3 710 CCATCTCTAAGT G- 3 C c c
GCTGAACTCATC GATGAG CAGCACTTGGG

CCTG CTACTC GTCGTGAATCT
AA
GAM8358 255 APPL 1 1547 NP_036228.1 3 2003 ATGGTAGCAAGT -- G 3 C c c
GCTGCCCTTTAT GATGA GGCAGCACTTG
CAGC CTATT CCGTCGTGAAC
TC G
GAM8358 255 AR 1 6654 NP_000035.2 5 357 TTCTCTCCCGCA - ACT 3 C c c
GCTGCCTCAGTC GA TGAGGCAGC TGGG
GGCT CT ACTCCGTCG GCCC
G AC-
GAM8358 255 BHD 1 13544 NP_653207.1 3 173 TGATAGCCAAGT G -- 3 C c c
GCTTGGCCTGGT GAT AGGC AGCACTTGG
CGAC CTG TCCG TCGTGAACC
G GT
GAM8358 255 BMI1 1 19346 NP_005171.4 3 430 TAGAAAACAAGT C G 3 C c c
GCTTTTTATCTT GATGAGG AGCACTTG
GAAA CTATTTT TCGTGAAC
- A
GAM8358 255 BRF1 2 674 NP_663718.1 3 1100 TCACTGACCCCA AGCA 3 C c c
GGGGCCTCATCC GATGAGGC CTTGGG
TCCC CTACTCCG GGACCC
G---
GAM8358 255 BRF1 2 13302 NP_001510.2 3 1101 CACTGACCCCCA AGCA 3 C c
c
GGGGCCTCATCC GATGAGGC CTTGGG
TCCC CTACTCCG GGACCC
G---
GAM8358 255 BRF1 2 13302 NP_663734.1 3 62 CACTGACCCCCA AGCA 3 C c c
GGGGCCTCATCC GATGAGGC CTTGGG
TCCC CTACTCCG GGACCC
G---
GAM8358 255 BRP17 1 3850 NP_072094.1 3 234 CCGCAGCGCGAG A G 3 C c c
GCTGCCTCATCA GATGAGGCAGC CTTG
ACGG CTACTCCGTCG GAGC
- G
GAM8358 255 BTBD5 1 9813 NP_060128.1 3 230 ATCTCCCCAAGT CA- 3 C c c
GCACACTTTATC GATGAGG GCACTTGGG
CACC CTATTTC CGTGAACCC
ACA
GAM8358 255 BTBD9 1 9655 NP_689946.1 5 90 TATTGTTCCAAG AGCA 3 C c c
GGAGCCTCATCA GATGAGGC CTTGGG
AAAC CTACTCCG GAACCT
AGG-
GAM8358 255 BTN1A1 1 19954 NP_001723.1 3 1044 GCTTTCCTACAT T CT 3 C c c
GCTGCCTCTCCT GA GAGGCAGCA TGGG
CAGG CT CTCCGTCGT ATCC
- AC
GAM8358 255 BZRAP1 1 2350 NP_004749.1 3 552 GTGTCCCACAGT G - - 3 C c c
GCTGCGCTAGTC GAT AG GCAGCACT TGGG
CCTT CTG TC CGTCGTGA ACCC

A G C

GAM8358 255 c-MIR 1 6685 NP_659458.1 3 521 CCCTCTGCCGAT T C 3 C c c
GCTGCCTCCTCC GA GAGGCAGCA TTGG
ATGC CT CTCCGTCGT AGCC
C -

GAM8358 255 C10orf6 1 14001 NP_060591.2 5 19 GGAAGCCCAAGT T - - 3 C c c
GTTGGCCATCCT GA GA GGC AGCACTTGGG
CAAC CT CT CCG TTGTGAACCC
C A G

GAM8358 255 C11orf1 1 11350 NP_006124.1 3 709 TGTGCCTCTCAT T CT 3 C c c
1 GCTGCCTCCTCT GA GAGGCAGCA TGGG
GCCC CT CTCCGTCGT ACTC
C --

GAM8358 255 C11orf1 1 19991 NP_065696.1 3 660 CAAGACTCCCAT CT 3 C b b
4 GCTGCCTCATTT GATGAGGCAGCA TGGG
GTAT TTACTCCGTCGT ACCC
--

GAM8358 255 C14orf5 1 9425 NP_060261.1 3 899 ATCAGCCCAAGT - 3 C c c
8 GCTTGTTTTATT GATGAGGCA GCACTTGGG
CCAA TTATTTTGT CGTGAACCC
T

GAM8358 255 C14orf7 1 2248 XP_040910.3 3 246 AGAGCTCTCAAT G C 3 C c c
3 GCTGCCTATCGG GAT AGGCAGCA TTGGG
GCGG CTA TCCGTCGT AACTC
- -

GAM8358 255 C14orf9 1 10799 NP_060285.1 3 54 TTCTGCATAGCT --- - - G 3 C c c
4 GCTGCCTCCTAA GAT GAGGCAGCA CT TG
TCTT CTA CTCCGTCGT GA AC
ATC C T G

GAM8358 255 C18orf1 1 18134 NP_004329.1 3 978 GTATCATGCAGT - TGG 3 C c c
GCTGCCCTCATC GATGAGG CAGCACT
CTCC CTACTCC GTCGTGA
C CGT

GAM8358 255 C18orf2 1 8513 NP_113604.1 3 460 GGTCTCTCAAGT T --- 3 C c c
GCTTATGCTTTT GA GAGGCA GCACTTGGG
CTTC CT TTTCGT CGTGAACTC
- ATT

GAM8358 255 C1orf17 1 7471 NP_055916.1 3 1812 TAGGTAGTCAAG A A 3 C c c
GCAGCCTCATCT GATGAGGC GC CTTGG
CCCC CTACTCCG CG GAACT
A -

GAM8358 255 C20orf1 1 14369 NP_036601.1 5 46 TTTCCCTCTTCC ACTT-- 3 C c c
4 GCTGCCTCATTC GATGAGGCAGC GGG
CTTT TTACTCCGTCG CCC
CCTTCT

GAM8358 255 C20orf1 1 1203 XP_037265.1 3 1236 GCGCTCCAGCTA AC- 3 C c c
50 GCTGCCTCATCA GATGAGGCAGC TTGGG
AAAA CTACTCCGTCG GACCT
ATC

GAM8358 255 C20orf1 1 15257 NP_848558.1 5 39 CCCCCACCAAGT AGGCA 3 C c
c

66 GCGGACGCATCG GATG GCACTTGG
AGCT CTAC CGTGAACC
GCAGG
GAM8358 255 C20orf1 1 15257 XP_170976.2 5 413 CCCCCACCAAGT AGGCA 3 C c
c
66 GCGGACGCATCG GATG GCACTTGG
AGCT CTAC CGTGAACC
GCAGG
GAM8358 255 C20orf1 1 14749 XP_290955.1 3 2008 TTATGCTGAGTT T - TG 3 C c c
77 GCTGCCTTTCCC GA GAGGCAGCA CT G
CGTC CT TTCCGTCGT GA C
- T GT
GAM8358 255 C20orf2 1 15423 NP_061328.1 3 36 CAGCTCCCAAGT A C 3 C c c
4 GCTCCCTATCCA GATG GG AGCACTTGGG
GTCC CTAT CC TCGTGAACCC
C -
GAM8358 255 C21orf9 1 2575 NP_694936.1 3 17 ATGATTGGAAGT - GG 3 C c c
0 GCTGCCTACGTC GATG AGGCAGCACTT
TTCT CTGC TCCGTCGTGAA
A GG
GAM8358 255 C22orf5 1 8084 NP_036396.1 3 1774 CCAGGCCAAAGT TGA - 3 C c c
GCTGCTGATTCC GA GGCAGCACTT GG
CACT CT TCGTCGTGAA CC
TAG A
GAM8358 255 C6orf55 1 6070 NP_057569.2 3 662 GATTTCCCAAGT C-- 3 C b b
GCTTTACCTTAT GATGAGG AGCACTTGGG
CTGT CTATTCC TCGTGAACCC
ATT
GAM8358 255 CAMKK1 1 8178 NP_115670.1 3 1677 TGATCCCCAAGT --- C 3 C c c
GTTTCTTGAGCA GATG AGG AGCACTTGGG
TCTG CTAC TTC TTGTGAACCC
GAG T
GAM8358 255 CAMKK1 1 8178 NP_757343.1 3 1677 TGATCCCCAAGT --- C 3 C c c
GTTTCTTGAGCA GATG AGG AGCACTTGGG
TCTG CTAC TTC TTGTGAACCC
GAG T
GAM8358 255 CCBP2 1 17116 NP_001287.2 5 82 GAATTACTCAAG T A 3 C b b
GCTGCCTCTCTG GA GAGGCAGC CTTGGG
CAAA CT CTCCGTCG GAACTC
- -
GAM8358 255 CCNE1 1 6758 NP_001229.1 3 502 TGTTTTGTAAGT A G 3 C c c
GCTGCTATATCT GATG GGCAGCACTTG
ATCC CTAT TCGTCGTGAAT
A G
GAM8358 255 CCNE1 1 6758 NP_476530.1 3 502 TGTTTTGTAAGT A G 3 C c c
GCTGCTATATCT GATG GGCAGCACTTG
ATCC CTAT TCGTCGTGAAT
A G
GAM8358 255 CCNT2 1 2221 NP_001232.1 3 241 ATATTTGTAAGT G 3 C c c
GCTGCTTTATTC GATGAGGCAGCACTTG

TTCA TTATTTCGTCGTGAAT
G
GAM8358 255 CCNT2 1 2221 NP_490595.1 3 141 ATATTTGTAAGT G 3 C c c
GCTGCTTTATTC GATGAGGCAGCACTTG
TTCA TTATTTCGTCGTGAAT
G
GAM8358 255 CCR9 1 8222 NP_006632.2 3 379 TTCAGTTCTCAT T CT 3 C c c
GCTGCCTCTTCC GA GAGGCAGCA TGGG
AAAA CT CTCCGTCGT ACTC
T --
GAM8358 255 CCR9 1 8222 NP_112477.1 3 379 TTCAGTTCTCAT T CT 3 C c c
GCTGCCTCTTCC GA GAGGCAGCA TGGG
AAAA CT CTCCGTCGT ACTC
T --
GAM8358 255 CCRK 1 14303 NP_036251.2 3 360 GCTTCCCCGAGT --- 3 C b b
GCTGCCTCCTGG GAT GAGGCAGCACTTGGG
TCAA CTG CTCCGTCGTGAGCCC
GTC
GAM8358 255 CCRK 1 14303 NP_848519.1 3 360 GCTTCCCCGAGT --- 3 C b b
GCTGCCTCCTGG GAT GAGGCAGCACTTGGG
TCAA CTG CTCCGTCGTGAGCCC
GTC
GAM8358 255 CD34 1 18960 NP_001764.1 3 1391 CCCTTATCACCA T ACT 3 C c c
GCTGCCTCTTCT GA GAGGCAGC TGG
GTGG CT CTCCGTCG ACC
T ---
GAM8358 255 CDC42EP 1 19471 NP_006770.1 3 501 GACCAGATGTGT -- -- 3 C b b
2 CCTGCCTCATCC GATGAGGCAG CAC TTGG
CTAG CTACTCCGTC GTG GACC
CT TA
GAM8358 255 CDK11 1 18586 XP_166324.1 3 4041 TTACCTATGTGT T-- 3 C c c
GCTGCCTCATTC GATGAGGCAGCAC TGGG
CTGG TTACTCCGTCGTG ATCC
TGT
GAM8358 255 CGN 1 16231 NP_065821.1 3 70 ATCCCAGCAAGT TG - --- 3 C c c
GCTGCTCTGCTC GA AG GCAGCACT TGGG
TGCC CT TC CGTCGTGA ACCC
CG T ACG
GAM8358 255 CHRD 1 18550 NP_817087.1 3 2031 CTCCCGACCAGT GA --- 3 C c c
GCTGCCCTGTTT GAT GGCAGCACT TGGG
GCCC TTG CCGTCGTGA GCCC
TC CCA
GAM8358 255 CHRD 1 18550 NP_817088.1 3 1208 CTCCCGACCAGT GA --- 3 C c c
GCTGCCCTGTTT GAT GGCAGCACT TGGG
GCCC TTG CCGTCGTGA GCCC
TC CCA
GAM8358 255 CHST7 1 12624 NP_063939.2 3 431 TAAGGGCCAAGT GA A 3 C c c

GCAGTCCTGTCT GAT GGC GCACTTGG
TGAT CTG CTG CGTGAACC

TC A
GAM8358 255 CKN1 1 10649 NP_000073.1 3 710 GTATGACCAAAT CAC 3 C c c
CCTGCCTCATTA GATGAGGCAG TTGG
ATTC TTACTCCGTC AACC
CTA
GAM8358 255 CLECSF1 1 16381 NP_569708.1 5 302 CTGCTCCCAAGT - CA 3 C c c

1 GCAACCTCTGTC GAT GAGG GCACTTGGG
TGAC CTG CTCC CGTGAACCC
T AA
GAM8358 255 CLONE25 1 3547 NP_056196.1 3 896 TCTCCCGTGACT CT-- 3 C c c
003 GCTGCCTCATCG GATGAGGCAGCA TGGG
ATAC CTACTCCGTCGT GCCC
CAGT
GAM8358 255 CNTN2 1 19963 NP_005067.1 3 939 CACCTCTCCAGT - - T 3 C c c
GCTGCCTGCAGT GA TG AGGCAGCACT GGG
CAGC CT AC TCCGTCGTGA CCT
G G -
GAM8358 255 COBRA1 1 9964 NP_056271.2 3 547 TTGCCCAGCAGT GA---- - -- 3 C c c

GCTGCCTTCAGC TGA GGCAGCACT TGGG
GGCC ACT CCGTCGTGA ACCC
CCGGCG T CG
GAM8358 255 COL5A3 1 12577 NP_056534.1 3 681 GATCCTAATGGT A -- 3 C c c
GCTGCCCTATTT GATG GGCAGCACT TGGG
ATAC TTAT CCGTCGTGG ATCC
C TA
GAM8358 255 COPS7B 1 10817 NP_073567.1 3 517 TGCTTTCCCTCT CACTT 3 C c
c
CCTGCCTCATTC GATGAGGCAG GGG
CTTG TTACTCCGTC CCC
CTCT-
GAM8358 255 CRAMP1L 1 8892 XP_034570.4 3 1346 CATCTCTCCCTT CACTT 3 C c
c
CCTGCCTCATTT GATGAGGCAG GGG
CATC TTACTCCGTC CCC
CTT--
GAM8358 255 CSNK1G1 1 2519 NP_071331.1 3 302 AGGAAGCTAAGT TGA 3 C c
c
GCTGCTGTTTCT GA GGCAGCACTTGG
TTAA CT TCGTCGTGAATC
TTG
GAM8358 255 CT120 1 4706 NP_079068.1 3 50 AGCCTCACACCA T ACT 3 C c c
GCTGCCTCCTCC GA GAGGCAGC TGG
ACTC CT CTCCGTCG ACC
C ---
GAM8358 255 CYP2B6 1 11117 NP_000758.1 3 1432 TCCTCATTCCCA T ACT 3 C c
c
GCTGCCTCTTCC GA GAGGCAGC TGGG
TACT CT CTCCGTCG ACCC

T ---
GAM8358 255 D12S248 1 712 NP_031386.1 3 247 GATATCCCCAAG T A 3 C b b
9E GCTGCCTCTCCC GA GAGGCAGC CTTGGG
ACCA CT CTCCGTCG GAACCC
- -
GAM8358 255 DDX11 1 7256 NP_085913.1 3 430 CCAGCTGGTGGT A ------ 3 C c c
GCTGCCCTATCA GATG GGCAGCACT TGG
GATG CTAT CCGTCGTGG ACC
C TGGTCG
GAM8358 255 DDX20 1 2897 NP_009135.3 5 63 AGCGACTCACCA ACT 3 C c c
GTTGCCTCATCT GATGAGGCAGC TGGG
TTCC CTACTCCGTTG ACTC
ACC
GAM8358 255 DKFZp43 1 6913 NP_115630.1 5 13 CCAGGCCCAGCA A CAC 3 C c
c
4F142 TCTGCCTCACCG G TGAGGCAG TTGGG
TGGC C ACTCCGTC GACCC
C TAC
GAM8358 255 DKFZp43 1 16331 NP_115631.1 3 52 GGGGCCTCCAGT T -- T 3 C c c
4I1930 GCTGCCCCTCCT GA GA GGCAGCACT GGG
CCCT CT CT CCGTCGTGA CTC
C CC C
GAM8358 255 DKFZp43 1 9070 XP_097012.2 5 762 TGGTGCCCAAGT A AG 3 C c c

4O0320 GAGTCACATCCA GATG GGC CACTTGGG
GGTA CTAC CTG GTGAACCC
A A-
GAM8358 255 DKFZp54 2 9992 XP_040799.2 3 1192 GGGGAACTAAGT G G 3 C c c

7C176 GCTGACTAGTTT GAT AG CAGCACTTGG
GTTT TTG TC GTCGTGAATC
A A
GAM8358 255 DKFZp54 2 13108 XP_040799.2 3 51 ATACCCTGGAAC CA-- T 3 C c c

7C176 ACTGCCTCATTG GATGAGGCAG CT GGG
TCTT TTACTCCGTC GG CCC
ACAA T
GAM8358 255 DKFZP56 1 5804 NP_114429.1 5 635 TGCCGTCCCCCG CAC 3 C c
c
4K0322 ACTGCCTCATTC GATGAGGCAG TTGGG
TTTG TTACTCCGTC AGCCC

GAM8358 255 DKFZP56 1 15465 NP_064715.1 5 99 TCTTGGTCTCAA GC 3 C b b
4O043 GTTGCCTCATTG GATGAGGCA ACTTGGG
CGGC TTACTCCGT TGAACTC
--
GAM8358 255 DKFZP56 1 8396 NP_056424.1 3 432 CCACCCCCAAGT - - 3 C b b
6C0424 GCATGTCTCCAT GATG AGGCA GCACTTGGG
CACT CTAC TCTGT CGTGAACCC
C A

GAM8358 255 DKFZP72 1 6607 XP_045308.2 3 1336 CAACATTCAAAT CAC 3 C c c

7G051 TCTGCCTCATCT GATGAGGCAG TTGGG
GGAG CTACTCCGTC AACTT
TTA

GAM8358 255 DKFZp76 1 3724 NP_115665.1 3 521 ATGCCCAGGTCT -- C-- 3 C c c
1B0514 CCTGCCTCACAT GA TGAGGCAG ACTTGGG
CACA CT ACTCCGTC TGGACCC
AC CTC

GAM8358 255 DKFZp76 1 1697 NP_848634.1 3 392 TGTATCCCAAGT -- - -- 3 C c c
1E1217 GCACTGTCCTTC GAT GAGG CA GCACTTGGG
TGTC CTG TTCC GT CGTGAACCC
TC T CA

GAM8358 255 DKFZp76 1 7508 NP_612212.1 3 235 TCCAAGGCCAAT TG ----- 3 C c c
1H2121 GCTGCCTGCTCT GA AGGCAGCA CTTGGG
GTTT CT TCCGTCGT GAACCT
CG AACCG

GAM8358 255 DKFZp76 1 1386 NP_060892.1 3 255 GAATACTCAAGT ATG - 3 C c c
1K1423 GCTAGCTTAGCA G AGGC AGCACTTGGG
GCTT C TTCG TCGTGAACTC
GA- A

GAM8358 255 DMPK 1 2249 NP_004400.3 5 754 AGGGGCCATGGT G - 3 C c c
GCTGCCTGTCCA GAT AGGCAGCACT TGG
ACAT CTG TCCGTCGTGG ACC
- T

GAM8358 255 DMRT2 1 2892 NP_006548.1 3 870 TTTGGCCCAAGT A A 3 C c c
GTGGCCCCATTA GATG GGC GCACTTGGG
GCGA TTAC CCG TGTGAACCC
C G

GAM8358 255 DNAJB2 1 960 NP_006727.2 3 2 AGGCCTCTCGCT ACTT 3 C c c
GCCTCATCCTCT GATGAGGCAGC GG
GACA CTACTCCGTCG CC
CTCT

GAM8358 255 DNAJC8 1 9424 NP_055095.1 3 268 GCCACCATTGGT T -- 3 C c c
GCTGCCTTCTCT GA GAGGCAGCACT TGG
TCCC CT TTCCGTCGTGG ACC
C TT

GAM8358 255 DNMT2 1 5113 NP_004403.1 3 1334 AGCAGCCCAAGT A CA- 3 C c c

GTCATCCCATTC GATG GG GCACTTGGG
ACCC TTAC CC TGTGAACCC
- TAC

GAM8358 255 DNMT2 1 5113 NP_788270.1 3 1334 AGCAGCCCAAGT A CA- 3 C c c

GTCATCCCATTC GATG GG GCACTTGGG
ACCC TTAC CC TGTGAACCC
- TAC

GAM8358 255 DNMT2 1 5113 NP_788271.1 3 1334 AGCAGCCCAAGT A CA- 3 C c c

GTCATCCCATTC GATG GG GCACTTGGG

ACCC TTAC CC TGTGAACCC
- TAC
GAM8358 255 DNMT2 1 5113 NP_788272.1 3 2175 AGCAGCCCAAGT A CA- 3 C c c

GTCATCCCATTC GATG GG GCACTTGGG
ACCC TTAC CC TGTGAACCC
- TAC
GAM8358 255 DNMT2 1 5113 NP_788273.1 3 2145 AGCAGCCCAAGT A CA- 3 C c c

GTCATCCCATTC GATG GG GCACTTGGG
ACCC TTAC CC TGTGAACCC
- TAC
GAM8358 255 DNMT2 1 5113 NP_788274.1 3 1941 AGCAGCCCAAGT A CA- 3 C c c

GTCATCCCATTC GATG GG GCACTTGGG
ACCC TTAC CC TGTGAACCC
- TAC
GAM8358 255 DPF3 1 15008 NP_036206.1 3 2273 AGATCTCCAATT - C 3 C c c
GCTGCCTCCATT GATG AGGCAGCA TTGGG
GATG TTAC TCCGTCGT AACCT
C T
GAM8358 255 DPH2L2 1 14115 NP_001375.2 5 155 CACCACCCAAGC G----- G - 3 C c
c

TGTGCCTCATGG ATGAGGCA CA CTTGGG
AGTC TACTCCGT GT GAACCC
CTGAGG - C
GAM8358 255 DRD5 1 14601 NP_000789.1 3 105 TGCCTTTCCAGT ---- T 3 C c c
GCTGCTCCCTTT GATGA GGCAGCACT GGG
ATCA CTATT TCGTCGTGA CCT
TCCC -
GAM8358 255 DSCR6 1 3793 NP_061835.1 3 2 GTGGCAAGTGCT C G 3 C b b
CCTCATCCAAAT GATGAGG AGCACTTG
GATC CTACTCC TCGTGAAC
- G
GAM8358 255 DT1P1A1 1 15919 NP_477511.1 3 569 CCTCCCAGGAAT T-- -- 3 C c c
0 GCTGCCTTCCTT GA GAGGCAGCA CTTGGG
CAGC CT TTCCGTCGT GGACCC
TCC AA
GAM8358 255 DVL3 1 10388 NP_004414.2 3 546 ATCCCCCTGCCT - CTT- 3 C c c
GCTGCCTCAGTC GA TGAGGCAGCA GGG
TGCA CT ACTCCGTCGT CCC
G CCGT
GAM8358 255 E2IG4 1 5803 NP_056331.1 3 306 TATCCCCCAAGT G--- CA-- 3 C c c
GCCTTCCCTCAT ATGAGG GCACTTGGG
GCCT TACTCC CGTGAACCC
TCCG CTTC
GAM8358 255 EB-1 1 571 NP_690001.1 3 881 AGGCCCGGAAGT AGG---- -- 3 C c c
GCTGACGCAGCC GATG CAGCACTT GGG
ATCA CTAC GTCGTGAA CCC
CGACGCA GG

GAM8358 255 EDEM 1 3301 NP_055489.1 3 29 TCTGCTCTCTGT AG TT- 3 C c c
GAGGCCTCATCT GATGAGGC CAC GGG
TGAA CTACTCCG GTG CTC
GA TCT
GAM8358 255 EIF2B5 1 6190 XP_291076.1 5 24 CGCATTTCAAGT T --- 3 C c c
GCTGGATCCTTT GA GAGG CAGCACTTGGG
TTGT TT TTCC GTCGTGAACTT
T TAG
GAM8358 255 ENTPD6 1 10345 NP_001238.1 3 165 AGAAGGCCTGGT A--- T 3 C c c
GCTGCCCTGGCA GATG GGCAGCACT GG
TCAG CTAC CCGTCGTGG CC
GGTC T
GAM8358 255 EPHB4 1 1248 NP_004435.2 3 512 CCTCCCCCAGCT G---- - C 3 C c c
GCTGCCTTCATA ATGA GGCAGCA TTGGG
TTGA TACT CCGTCGT GACCC
AGTTA T C
GAM8358 255 ERAP140 1 5927 XP_059748.2 3 107 GCCCCAGCCCAG CAC 3 C c
c
CCTGCCTCATCC GATGAGGCAG TTGGG
CACC CTACTCCGTC GACCC
C--
GAM8358 255 EVPL 1 6608 NP_001979.1 3 88 TCTTGCCTCAGA A A T 3 C c c
GCAGCCTCATCC GATGAGGC GC CT GGG
CAGG CTACTCCG CG GA TCC
A A C
GAM8358 255 FBXW5 1 13135 NP_839891.1 3 43 GGCTCACCGAGA AGCA 3 C c
c
CCAGCCTCATCT GATGAGGC CTTGG
CGGG CTACTCCG GAGCC
ACCA
GAM8358 255 FLJ0000 1 19793 XP_088525.2 3 1117 CTCACCCGAAGG - A - 3 C b b
1 GCTGCCTCACTC GA TGAGGCAGC CTT GGG
TGTG CT ACTCCGTCG GAA CCC
C G G
GAM8358 255 FLJ1034 1 14374 NP_060535.1 5 1 GGCACGAGGCTG - A G 3 C c c
6 CCTCAGTCTCCT GA TGAGGCAGC CTTG
GAGT CT ACTCCGTCG GAGC
G - A
GAM8358 255 FLJ1053 1 11608 NP_060600.1 3 746 TCATTCCCAAGT GA ----- 3 C c c
9 GCCCTTGTGCCC GAT GGCA GCACTTGGG
TGTT TTG CCGT CGTGAACCC
TC GTTCC
GAM8358 255 FLJ1098 1 6098 XP_035527.2 3 452 AATGTGTTAAGT G 3 C c c
0 GCTGTTCATTTA GATGAG CAGCACTTGG
AGTT TTACTT GTCGTGAATT
-
GAM8358 255 FLJ1178 1 6450 NP_079167.1 5 155 GTCTCTCGGGTG AG- 3 C c c
3 ATGGCCTCATCC GATGAGGC CACTTGGG
AGGG CTACTCCG GTGGGCTC

GTA

GAM8358 255 FLJ1207 1 1230 NP_079463.2 3 1113 ATTAACTCATGT AGC T 3 C c c
6 ACAGCCTCATCC GATGAGGC AC TGGG
TGTA CTACTCCG TG ACTC
ACA T

GAM8358 255 FLJ1254 1 19280 NP_079268.1 3 200 TTGCAGCTCGGC G C 3 C c c
7 TGTGCCTCATCT GATGAGGCA CA TTGGG
TCCC CTACTCCGT GT GGCTC
- C

GAM8358 255 FLJ1268 1 3627 NP_079193.2 5 83 GTGCCGGAGCCT A -- G 3 C c c
7 GCTGCCTCGCCG G TGAGGCAGCA CTT GG
ACGC C GCTCCGTCGT GAG CC
C CC G

GAM8358 255 FLJ1280 3 7968 NP_075054.1 3 892 AGGTTTTCCATG - CT 3 C c c
0 ACTGCCTCATCA GATGAGGCAG CA TGGG
GCAG CTACTCCGTC GT ACCT
A --

GAM8358 255 FLJ1280 3 10088 NP_075054.1 3 949 CTACTCCCAGGT AGC 3 C c c

0 CCAGCCTCATCA GATGAGGC ACTTGGG
TGCC CTACTCCG TGGACCC
ACC

GAM8358 255 FLJ1280 3 14600 NP_075054.1 5 96 AGGGCCCCAAGT A G - 3 C c c
0 GTCTGACTCGCA G TGAG CAG CACTTGGG
AAGG C GCTC GTC GTGAACCC
- A T

GAM8358 255 FLJ1287 1 12746 NP_078820.1 3 223 CCCTGTCCATGT A T 3 C c c
5 GCAGCCTCATCA GATGAGGC GCAC TGGG
GAGC CTACTCCG CGTG ACCT
A T

GAM8358 255 FLJ1298 1 4980 NP_079200.1 3 941 TTATTTCAGGTT GC- 3 C c c
5 CATGCCTCATTA GATGAGGCA ACTTGGG
CACA TTACTCCGT TGGACTT
ACT

GAM8358 255 FLJ1307 1 14989 XP_117117.2 3 2090 CGCCCGCCGAGT GA 3 C c c

2 GCTGCTGGGTTG GAT GGCAGCACTTGG
GGCA TTG TCGTCGTGAGCC
GG

GAM8358 255 FLJ1319 1 7714 NP_078890.1 3 855 GTGCCCACTCGT T T-- 3 C c c
7 GCTGCCTCTTCT GA GAGGCAGCAC TGGG
TAAC CT CTCCGTCGTG ACCC
T CTC

GAM8358 255 FLJ1363 1 9712 NP_078981.1 3 681 ATATCAATCCAT G CT 3 C c c
9 GCTGCCTGATCC GAT AGGCAGCA TGGG
CTGT CTA TCCGTCGT ACCT
G --

GAM8358 255 FLJ1384 1 8727 NP_079047.1 3 276 TCCTCCACAGTG T - - 3 C c c
8 GCTGCCTCCTCA GA GAGGCAGC ACT TGGG
TTTG CT CTCCGTCG TGA ACCT

C G C

GAM8358 2552 FLJ1385 1 1028 NP_075566.1 3 459 ACAGCCAGGCCG A-- 3 C b b
GCTGCCTCATCT GATGAGGCAGC CTTGG
CAGC CTACTCCGTCG GGACC
GCC

GAM8358 2559 FLJ1439 1 15886 NP_116169.2 3 988 GACCAACCCATG ACT 3 C c c
GTTGCCTCATCA GATGAGGCAGC TGGG
GCAG CTACTCCGTTG ACCC
GT-

GAM8358 2556 FLJ1481 1 3978 NP_116234.1 3 829 ACGGTCCTGAGA AG - TG 3 C c c
TGAGCCTCATCC GATGAGGC CA CT GG
CTGG CTACTCCG GT GA CC
A- A GT

GAM8358 2552 FLJ2023 1 17239 NP_061881.2 3 333 TGGCCCATGTTT - CT-- 3 C c c
GCTGCCTCTATC GAT GAGGCAGCA TGGG
TGGT CTA CTCCGTCGT ACCC
T TTGT

GAM8358 2550 FLJ2030 1 10271 NP_060223.1 3 387 ATTACCACAGTT T - - 3 C c c
GCTGCCTCCTCC GA GAGGCAGCA CT TGG
AGAA CT CTCCGTCGT GA ACC
C T C

GAM8358 2553 FLJ2030 1 952 NP_060225.2 5 259 GCTCCTCAACGT A - 3 C b b
GCGGCCTCATCA GATGAGGC GCAC TTGGG
TAAG CTACTCCG CGTG AACTC
G C

GAM8358 2558 FLJ2050 1 2977 NP_060320.1 3 806 TTTCCAAGGTCT - --- 3 C b b
GCTGCCTTCATC GATGA GGCAGCA CTTGGG
TATG CTACT CCGTCGT GAACCT
T CTG

GAM8358 2551 FLJ2051 1 11948 NP_060323.1 3 1056 TTCCCAGAAGCT T - -- 3 C c c
GCTGCCTCTTCC GA GAGGCAGCA CT TGGG
TGAG CT CTCCGTCGT GA ACCC
T C AG

GAM8358 2552 FLJ2080 1 19763 NP_060429.1 5 141 TTCTCAGGTCAT T --- 3 C c c
GCTGCCTCTCCC GA GAGGCAGC ACTTGGG
TATC CT CTCCGTCG TGGACTC
- TAC

GAM8358 2558 FLJ2143 1 7158 XP_029084.5 3 28 CTGGCTGCCCAT CACT 3 C c c
CCTGCCTCATCA GATGAGGCAG TGGG
CACG CTACTCCGTC ACCC
CT--

GAM8358 2551 FLJ2323 1 3342 NP_079355.1 3 484 CTCTACGCCAAT AG C 3 C c c
GAGGCCTCATCT GATGAGGC CA TTGG
GTGC CTACTCCG GT AACC
GA -

GAM8358 2552 FLJ2332 1 14095 NP_079231.3 3 332 CCCGTCTCAAGT T C 3 C c c
GCTCCTCTTCCT GA GAGG AGCACTTGGG
TCCA CT CTCC TCGTGAACTC
T -

GAM8358 255 FLJ2537 1 18933 NP_689756.1 3 99 TAATCCACAAGT G------ C - 3 C c c
1 GCTTCTCATATT ATGAGG AGCACTTG GG
GCCC TACTCT TCGTGAAC CC
CCCGTTA - A
GAM8358 255 FLJ3031 1 5561 NP_689970.1 3 369 ACCCCGGGCAGG T A--- 3 C c c
3 GCTGCCTCCTCA GA GAGGCAGC CTTGGG
CCTC CT CTCCGTCG GGGCCC
C GGAC
GAM8358 255 FLJ3063 1 3937 NP_694559.1 3 53 CTGGCCCCTGCT -- CTT 3 C c c
4 GCTGCCTCCCGT GAT GAGGCAGCA GGG
CCTC CTG CTCCGTCGT CCC
CC CGT
GAM8358 255 FLJ3171 1 15771 NP_689745.1 3 79 GACGGGGAGAGT - GG 3 C c c
5 GCTGCTTCTATC GAT GAGGCAGCACTT
GATG CTA CTTCGTCGTGAG
T AG
GAM8358 255 FLJ3195 1 17080 NP_694575.1 3 949 GGCTGCCCCAGT GA- T 3 C c c
8 GCTGCCACAGTC GAT GGCAGCACT GGG
CCAT CTG CCGTCGTGA CCC
ACA C
GAM8358 255 FLJ3233 1 18443 NP_653166.1 3 784 GGGAGTGGGTGA -- G 3 C c c
4 CCTGCCTCATCA GATGAGGCAG CACTTG
CTGC CTACTCCGTC GTGGGT
CA G
GAM8358 255 FLJ3279 1 6527 NP_705834.1 5 359 AAGACCCAGAGA A CA - 3 C c c
6 CCTGCCTCACCA G TGAGGCAG CT TGGG
GTGC C ACTCCGTC GA ACCC
C CA G
GAM8358 255 FLJ3666 1 19178 NP_689695.1 3 910 CACAGCCTGGGA A A- TG 3 C c
c
6 GGCGCCTCATCC GATGAGGC GC CT GG
AGAA CTACTCCG CG GG CC
- GA GT
GAM8358 255 FMOD 1 1281 NP_002014.1 3 483 ACCTCTTGCCCA T ACT 3 C c c
GCTGCCTCTTCT GA GAGGCAGC TGGG
GAAA CT CTCCGTCG ACCC
T ---
GAM8358 255 FOXO1A 1 4341 NP_002006.2 5 322 TCCGCCCCCAGT T G T 3 C c c
GCTGCGTTCTCC GA GA GCAGCACT GGG
CCCT CT TT CGTCGTGA CCC
C G C
GAM8358 255 FUT6 1 5232 NP_000141.1 3 76 CTCACCTGAGTG AG- TG 3 C c c
GGGGCCTCATCT GATGAGGC CACT GG
ACCT CTACTCCG GTGA CC
GGG GT
GAM8358 255 GABBR1 1 7815 NP_001461.1 3 294 CACTGCTCACAC T ACT 3 C c
c
GCTGCCTCCTCA GA GAGGCAGC TGGG

```
                                GCAG       CT CTCCGTCG   ACTC
                                        C       CAC
GAM8358  255   GABBR1  1   7815  NP_068703.1  3  294   CACTGCTCACAC  T      ACT          3  C  c
c
                                GCTGCCTCCTCA GA GAGGCAGC   TGGG
                                GCAG       CT CTCCGTCG   ACTC
                                        C       CAC
GAM8358  255   GABBR1  1   7815  NP_068704.1  3  294   CACTGCTCACAC  T      ACT          3  C  c
c
                                GCTGCCTCCTCA GA GAGGCAGC   TGGG
                                GCAG       CT CTCCGTCG   ACTC
                                        C       CAC
GAM8358  255   GABBR1  1   7815  NP_068705.1  3  1291  CACTGCTCACAC  T      ACT          3  C  c
c
                                GCTGCCTCCTCA GA GAGGCAGC   TGGG
                                GCAG       CT CTCCGTCG   ACTC
                                        C       CAC
GAM8358  255   GAC1    1   18086 NP_006329.1  3  519   GGGATGCCCAGG       AGCA         3  C  c
c
                                AACGCCTCATCT GATGAGGC    CTTGGG
                                CAGC       CTACTCCG    GGACCC
                                            CAA-
GAM8358  255   GAL3ST2 1   19391 NP_149025.1  3  76    GTCCAGCCAGGG   ---      A        3  C  c  c
                                GCTGCCTCCATG GAT   GAGGCAGC CTTGG
                                TCCT       CTG   CTCCGTCG GGACC
                                            TAC       G
GAM8358  255   GALNAC4 1   14898 NP_055678.1  3  840   GGCTCTCTCTCT  T      CTT          3  C  c
c
          S-6ST                    GCTGCCTCTTCA GA GAGGCAGCA   GGG
                                TACG       CT CTCCGTCGT   CTC
                                        T       CT-
GAM8358  255   GALNAC4 1   14898 NP_056976.1  3  1018  GGCTCTCTCTCT  T      CTT          3  C  c
 c
          S-6ST                    GCTGCCTCTTCA GA GAGGCAGCA   GGG
                                TACG       CT CTCCGTCGT   CTC
                                        T       CT-
GAM8358  255   GALNT3  1   1308  NP_004473.1  3  134   CTTATTCCAAGT       CA---          3  C  c  c
                                GCATTTTTCTTA GATGAGG    GCACTTGGG
                                TTTA       TTATTCT    CGTGAACCT
                                            TTTTA
GAM8358  255   GARP    1   18213 NP_005503.1  3  791   CCTGACCCCAGT  ATG  -      T        3  C  c  c

                                GCTGCTCTAAGC G   AG GCAGCACT GGG
                                ACCG       C   TC CGTCGTGA CCC
                                        GAA  T       C
GAM8358  255   GATA4   1   17802 NP_002043.1  3  604   ACCCACCACAGC       A  A  ----       3  C  c  c
                                GCAGCCTCATCA GATGAGGC GC CT    TGGG
                                AAAT       CTACTCCG CG GA    ACCC
                                            A  C  CACC
GAM8358  255   GCHFR   1   18283 NP_005249.1  3  85    GACCTCCAAGCT  A      CA-          3  C  c  c
```

CCTGCCTCACCG G TGAGGCAG CTTGGG
TCTG C ACTCCGTC GAACCT
C CTC

GAM8358 255 GGT1 1 5411 NP_005256.1 5 8 GGCAAGTGAGGT - GG 3 C c c
GCTGCCGTCATC GATGA GGCAGCACTT
CAGG CTACT CCGTCGTGGA
G GT

GAM8358 255 GGT1 1 5411 NP_038265.1 5 427 GGCAAGTGAGGT - GG 3 C c c
GCTGCCGTCATC GATGA GGCAGCACTT
CAGG CTACT CCGTCGTGGA
G GT

GAM8358 255 GGT1 1 5411 NP_038347.1 5 137 GGCAAGTGAGGT - GG 3 C c c
GCTGCCGTCATC GATGA GGCAGCACTT
CAGG CTACT CCGTCGTGGA
G GT

GAM8358 255 GGT2 1 5411 XP_290331.1 5 11 GGCAAGTGAGGT - GG 3 C c c
GCTGCCGTCATC GATGA GGCAGCACTT
CAGG CTACT CCGTCGTGGA
G GT

GAM8358 255 GIT1 1 599 NP_054749.1 3 130 AGTGCCCTTAGT - A T- 3 C c c
GCTGCCACACTC GA TG GGCAGCACT GGG
CCTG CT AC CCGTCGTGA CCC
C A TT

GAM8358 255 GPS2 1 16530 NP_004480.1 5 692 TGGTGGCCCAGG T- A 3 C c c
GCTGCCTCCTTC GA GAGGCAGC CTTGGG
CCTG CT CTCCGTCG GGACCC
TC -

GAM8358 255 GRM4 1 1955 NP_000832.1 3 728 GTGTTGCCAAGT T G 3 C c c
GCTGCGTCCTCC GA GA GCAGCACTTGG
TGGT CT CT CGTCGTGAACC
C G

GAM8358 255 GTF2E1 1 17008 NP_005504.1 3 525 GCCTCCCAAAGT ----- - 3 C c c
GCTGTATTTTCT GATGAG GCAGCACTT GGG
TATC CTATTC TGTCGTGAA CCC
TTTTA A

GAM8358 255 GYPB 1 731 NP_002091.1 3 52 TATTGCCTGCAT G CT 3 C c c
GCTGCCTGATCT GAT AGGCAGCA TGGG
TGCG CTA TCCGTCGT GTCC
G AC

GAM8358 255 GYPE 1 14090 NP_002093.1 3 47 TGTGGCCTGCAT G CT 3 C c c
GCTGCCTGATCT GAT AGGCAGCA TGGG
TGCC CTA TCCGTCGT GTCC
G AC

GAM8358 255 HD 1 11900 NP_002102.2 3 2889 CAGCTGCCAAGT TG C 3 C c c
GCTCTTTGTTAC GA AGG AGCACTTGG
TGTC TT TTC TCGTGAACC
GT -

GAM8358 255 HECA 1 2910 NP_057301.1 3 558 AGTGGCACAAGT - G 3 C c c
GCTGTTTCTATC GAT GAGGCAGCACTTG
ACTA CTA CTTTGTCGTGAAC

T A
GAM8358 255 HEM1 1 7159 NP_005328.1 5 712 GTGCCCAACTTC -- CAC 3 C c c
TAAGCCTCATCA GATGAGGC AG TTGGG
GCAA CTACTCCG TC AACCC
AA TTC
GAM8358 255 HEYL 1 781 NP_055386.1 3 971 CCAGACGTCTGT G ------ 3 C c c
GCTGCCTGGTTT GAT AGGCAGCAC TTGG
GCAT TTG TCCGTCGTG GACC
G TCTGCA
GAM8358 255 HHLA1 1 11901 NP_005703.1 3 91 CTTGTCCCAAGT A AG 3 C c c
GGGCTACATTTG GATG GGC CACTTGGG
AAGA TTAC TCG GTGAACCC
A G-
GAM8358 255 HLA-DRA 1 9798 NP_061984.1 3 166 GCCACCCCAAGT T ----- 3 C c c
GTGGTTATGCCT GA GAGGCA GCACTTGGG
CCTC CT CTCCGT TGTGAACCC
C ATTGG
GAM8358 255 HOXC13 1 12196 NP_059106.2 3 397 ATGGCCCCAATT CAC 3 C c
c
CTTGCCTCATCC GATGAGGCAG TTGGG
TATG CTACTCCGTT AACCC
CTT
GAM8358 255 HRC 1 7926 NP_002143.1 5 146 GCTGGAGCCAGT --- T 3 C c c
GCTGCCTGTCCG GATG AGGCAGCACT GG
TCCC CTGC TCCGTCGTGA CC
CTG -
GAM8358 255 HRH1 1 9207 NP_000852.1 3 1522 AAGGAACCAAGT CA 3 C c c
GCATTTTTATCT GATGAGG GCACTTGG
GTGA CTATTTT CGTGAACC
TA
GAM8358 255 HRI 1 17628 NP_055228.2 3 456 CATTACCTGAAG AGCA - 3 C c c
GACGCCTCATCA GATGAGGC CTT GGG
TTTC CTACTCCG GAA TCC
CAG- G
GAM8358 255 HS3ST3B 1 16195 NP_006032.1 3 355 AGTTCTCCAGTT --- C 3 C c c
1 GCTGCCTCCTTG GAT GAGGCAGCA TTGGG
TCTT CTG CTCCGTCGT GACCT
TTC T
GAM8358 255 HSD3B2 1 3135 NP_000189.1 3 119 AGCCCAGGTCCT T --- 3 C b b
GCTGCCTCTCTT GA GAGGCAGC ACTTGGG
TCAC CT CTCCGTCG TGGACCC
- TCC
GAM8358 255 ID2 1 19404 NP_002157.1 3 90 AATCTTTTAAGT G- 3 C c c
GCTGAACTTATT GATGAG CAGCACTTGGG
TTTC TTATTC GTCGTGAATTT
AA
GAM8358 255 IDH3A 1 14914 NP_005521.1 3 216 CTTTTTCCAAGT - 3 C c c
GCTTGTTTTATT GATGAGGCA GCACTTGGG
TATT TTATTTTGT CGTGAACCT
T

GAM8358 255 IFNAR2 1 11246 NP_000865.2 3 870 GCATCCTAACTT C- 3 C c c
GCTGCCTTATCG GATGAGGCAGCA TTGGG
TCTG CTATTCCGTCGT AATCC
TC
GAM8358 255 IGSF2 1 15726 NP_004249.1 3 128 ATGAACCCAAGT CAG--- 3 C c c
GAACTTTCCTCA GATGAGG CACTTGGG
TTAC TTACTCC GTGAACCC
TTTCAA
GAM8358 255 IL16 1 10757 NP_757366.1 3 288 ACCATCTTAAGA GCA 3 C c c
GATGCCTCATTT GATGAGGCA CTTGGG
TAGA TTACTCCGT GAATTC
AGA
GAM8358 255 IL17C 2 15783 NP_037410.1 3 0 CCTGCGTGCTGC A T 3 C c c
CCCGTTCAGTGT GATG GGCAGCAC TGGG
GCCG TTGC CCGTCGTG GTCC
C C
GAM8358 255 IL17C 2 17730 NP_037410.1 3 327 AGGCCCCCGCAG T A - 3 C c c
GCTGCCTCTTCC GA GAGGCAGC CT TGGG
CAAC CT CTCCGTCG GA GCCC
T - C
GAM8358 255 ITCH 1 8893 NP_113671.3 3 1774 ATGAGTGAAAGG A GG 3 C c c
GTTGCCTCATCA GATGAGGCAGC CTT
AGCA CTACTCCGTTG GAA
G AG
GAM8358 255 ITPR2 1 7682 NP_002214.1 5 172 CTGGGCGCCTGG T A T 3 C c c
GCTGCCTCTTCG GA GAGGCAGC CT GG
CGGG CT CTCCGTCG GG CC
T - T
GAM8358 255 JMJ 1 1204 NP_004964.2 3 1291 ACATTTATAAGT - G 3 C c c
GCTGCTTACATC GATG AGGCAGCACTTG
ACTG CTAC TTCGTCGTGAAT
A A
GAM8358 255 KCNE1L 1 5757 NP_036414.1 3 109 TCCCTTCCAGGG - A 3 C c c
TTCGCCTCATCT GATGAGGC AGC CTTGGG
GAGG CTACTCCG TTG GGACCT
C -
GAM8358 255 KIAA019 1 19449 NP_055581.2 3 1474 GTTGGGCCTAAT CAC 3 C c
c
3 CCTGCCTCATCA GATGAGGCAG TTGGG
TTCT CTACTCCGTC AATCC
CT-
GAM8358 255 KIAA023 1 19327 NP_055562.1 3 392 CCACTGGTCGGT G ------ 3 C c c
7 GCTGCCTGGTCC GAT AGGCAGCACT TGG
TGGC CTG TCCGTCGTGG ACC
G CTGGTC
GAM8358 255 KIAA029 1 19243 XP_084529.6 3 276 CTCAAGATCTGT T ----- 3 C c c
8 GCTGCCTCCTCA GA GAGGCAGCAC TTGGG
GGAG CT CTCCGTCGTG AACTC
C TCTAG
GAM8358 255 KIAA032 1 4476 NP_055659.1 3 289 GATTACCCACGT --- - T 3 C c c

```
          9                    GCTGCCGTCCTG GAT   GA GGCAGCAC TGGG
                               GTCT       CTG   CT CCGTCGTG ACCC
                                    GTC  G       C
GAM8358  255   KIAA037 1  1638  NP_055474.1  3  727   TCATCCCCAAGT GA     ------          3  C  c  c
          7                    GCCCCTTCTGCC  TGAGGCA     GCACTTGGG
                               TCAG         ACTCCGT     CGTGAACCC
                                  G-       CTTCCC
GAM8358  255   KIAA040 1  18934 XP_290517.1  3  265   TGGGCCCACACT  T      CT-          3  C  c  c

          4                    GCTGCCTTCTCC GA GAGGCAGCA   TGGG
                               CAGG        CT TTCCGTCGT   ACCC
                                    C        CAC
GAM8358  255   KIAA047 1  10981 XP_290898.1  5  389   CAGATCTTAAAT   G      C            3  C  c  c
          2                    GCTGCCTATCAT GAT AGGCAGCA TTGGG
                               GTTG        CTA TCCGTCGT AATTC
                                    -       A
GAM8358  255   KIAA049 1  7638  XP_031397.1  5  1051  GGCCACCTGAAT         C TG          3  C  c  c

          5                    GCTGCCTTATCA GATGAGGCAGCA T  GG
                               CAAG        CTATTCCGTCGT A  CC
                                             A GT
GAM8358  255   KIAA053 1  14353 XP_049349.8  3  3880  TTGGGTCAAAGT   --        GG         3  C  c  c

          4                    GCTGCCTTTAAT GAT  GAGGCAGCACTT
                               CGAC        CTA  TTCCGTCGTGAA
                                          AT          AC
GAM8358  255   KIAA055 1  14105 XP_039796.7  3  245   ATCCCCAAGAAT  TG      --          3  C  c  c
          1                    GCTGCCTTGTCT GA  AGGCAGCA  CTTGGG
                               GTGG        CT  TCCGTCGT  GAACCC
                                         GT       AA
GAM8358  255   KIAA055 1  10997 NP_055605.1  3  1823  ATTATTACAAGT    G       G          3  C  c  c
          5                    GCTGTATTATTT GATGA GCAGCACTTG
                               GACT        TTATT TGTCGTGAAC
                                            A         A
GAM8358  255   KIAA072 1  13136 NP_067680.2  3  805   AGGCCACCATTG        - CT          3  C  c  c
          1                    TCTGCCTCATCA GATGAGGCAG CA  TGG
                               GGAA        CTACTCCGTC GT  ACC
                                             T  T-
GAM8358  255   KIAA084 1  3729  NP_055760.1  3  204   TCTTTTCTAAGT   GAG              3  C  c  c
          3                    GCTGTGGGATCT GAT   GCAGCACTTGGG
                               GGGA        CTA   TGTCGTGAATCT
                                          GGG
GAM8358  255   KIAA096 2  9385  XP_290942.1  3  1292  AGTGGACCCCAG G-----      G A          3  C  c
c
          2                    GGTGCCTCATAC      ATGAGGCA C CTTGGG
                               CAGC             TACTCCGT G GGACCC
                                       CGACCA      - -
GAM8358  255   KIAA096 2  18634 XP_290942.1  3  1080  TACCCTAAAAGT  T        ---         3  C  c  c
          2                    GCTGTCTCTTCA GA GAGGCAGCACTT   GGG
                               AGTC        CT CTCTGTCGTGAA   CCC
```

T AAT
GAM8358 255 KIAA104 1 16854 XP_048592.1 3 3034 TAACCTTCAAGT T C 3 C c c
5 GCTCCTCTTCAT GA GAGG AGCACTTGGG
TTGA CT CTCC TCGTGAACTT
T -
GAM8358 255 KIAA119 1 18347 NP_065177.2 3 1282 TTTTCACCAAAA AGCAC 3 C c
c
1 TGAGCCTCATCC GATGAGGC TTGG
CTTT CTACTCCG AACC
AGTAA
GAM8358 255 KIAA132 1 19188 XP_029429.4 3 823 ATTTACCCAAGT TG -- 3 C c c
8 GTTCAGCTTATT GA AGGC AGCACTTGGG
CACC CT TTCG TTGTGAACCC
TA AC
GAM8358 255 KIAA139 1 17260 XP_208522.1 3 531 GGTGGCATCCAA CAC 3 C c c
4 CCTGCCTCATTC GATGAGGCAG TTGGG
GGCC TTACTCCGTC AACCT
C--
GAM8358 255 KIAA140 2 1732 NP_066363.1 3 1114 CCTATCCCAAGT CA-- 3 C c b
4 GTGATCCTTCAT GATGAGG GCACTTGGG
CCCA CTACTTC TGTGAACCC
CTAG
GAM8358 255 KIAA140 2 7163 NP_066363.1 3 1219 AGACCCAGGCCT - -- 3 C b b
4 GCTGCCTGCATC GATG AGGCAGCA CTTGGG
TGCA CTAC TCCGTCGT GGACCC
G CC
GAM8358 255 KIAA144 1 16287 NP_065883.1 3 73 GTTTTCCCTACT G CTT 3 C c c
1 GCTGCCTGATCC GAT AGGCAGCA GGG
CTCG CTA TCCGTCGT CCC
G CAT
GAM8358 255 KIAA155 1 19407 XP_290768.1 3 2449 GTTTCCGCCATG GCACT 3 C c
c
4 GATGCCTCATCA GATGAGGCA TGG
CCAA CTACTCCGT ACC
AGGT-
GAM8358 255 KIAA168 1 6606 XP_290870.2 5 60 GAAAGGCTGAAG T A G 3 C c c
3 GCTGCCTCCTCT GA GAGGCAGC CTT GG
TGCA CT CTCCGTCG GAA TC
C - G
GAM8358 255 KIAA173 1 8127 XP_290496.1 3 655 GTAAGACCTTGG T A T 3 C c c
5 GCTGCCTCTTCT GA GAGGCAGC CT GGG
GTCT CT CTCCGTCG GG TCC
T - T
GAM8358 255 KIAA175 1 2837 NP_277047.1 3 1561 TAAGACCCAAGT TGA ---- 3 C c c
0 GCCTCCTGCTGT GA GGCA GCACTTGGG
TTCC CT TCGT CGTGAACCC
TTG CCTC
GAM8358 255 KIAA187 1 2574 NP_149053.1 3 105 CCCAGATCTCAT CAC----- 3 C c c

2 CCTGCCTCATCC GATGAGGCAG TTGGG
TGAG CTACTCCGTC GACCC
CTACTCTA

GAM8358 2555 KIAA191 1 8633 XP_055481.1 3 1272 TAAGCAGTCAAT C 3 C b b
GCTGCCTCATTT GATGAGGCAGCA TTGG
ATTG TTACTCCGTCGT AACT
-

GAM8358 2550 KIAA194 1 20086 XP_086981.2 3 2018 AGAACCAGAGGT ---- -- 3 C c c
GCTGCCTTCCCT GAT GAGGCAGCACT TGG
GTCT CTG TTCCGTCGTGG ACC
TCCC AG

GAM8358 2559 KIAA194 1 18390 XP_166376.1 5 986 CATTAACCCTGT A TT 3 C c c
GCTGCCACATCT GATG GGCAGCAC GGG
GGCT CTAC CCGTCGTG CCC
A T-

GAM8358 2559 KIAA194 1 18390 XP_300167.1 5 986 CATTAACCCTGT A TT 3 C c c
GCTGCCACATCT GATG GGCAGCAC GGG
GGCT CTAC CCGTCGTG CCC
A T-

GAM8358 2559 KIAA194 1 18390 XP_300202.1 5 986 CATTAACCCTGT A TT 3 C c c
GCTGCCACATCT GATG GGCAGCAC GGG
GGCT CTAC CCGTCGTG CCC
A T-

GAM8358 2558 KIAA201 1 14076 XP_291062.1 3 441 TCATAATCAAGT -- G 3 C c c
GCTGGCTAATGT GATG AG CAGCACTTGG
CAGC CTGT TC GTCGTGAACT
AA G

GAM8358 255 KIF5B 1 13109 NP_004512.1 5 198 GCGCAGCTGACT T C TG 3 C c c
GCTGCCTCTCAC GA GAGGCAGCA T G
GGCC CT CTCCGTCGT A C
- C GT

GAM8358 255 KPNA6 1 15175 NP_036448.1 3 1574 TGATCACCCATG T ACT 3 C c c
GCTGCCTCTCCT GA GAGGCAGC TGGG
ATTA CT CTCCGTCG ACCC
- GT-

GAM8358 255 LBP-9 1 18984 NP_055368.1 3 365 GGGTATCTTGGT - T 3 C c c
GCTGCCTGTATT GATG AGGCAGCACT GGG
GGTC TTAT TCCGTCGTGG TCT
G T

GAM8358 255 LDLR 1 13935 NP_000518.1 3 405 GGACCCCCTGGC CA T 3 C c c
CCTGCCTCATCC GATGAGGCAG CT GGG
ACCA CTACTCCGTC GG CCC
CC T

GAM8358 255 LMOD1 1 15622 NP_036266.1 3 1231 CTAGGGCTCAGA ------- A 3 C c c
GGGGCCTCATCT GATGAGGC AGC CTTGG
TCCC CTACTCCG TCG GGATC
GGGAGAC -

GAM8358 255 LOC1128 1 8726 NP_612424.1 3 749 GGGGTCCTCAAG T- A 3 C c c

85 GCTGCCTCCTTC GA GAGGCAGC CTTGGG
CTTT CT CTCCGTCG GAACTC
TC -
GAM8358 255 LOC1151 1 5560 XP_049825.5 3 1643 GCCCAAGACCCG T A---- 3 C c
c
10 GCTGCCTCCTCC GA GAGGCAGC CTTGGG
TCTT CT CTCCGTCG GAACCC
C GCCCA
GAM8358 255 LOC1218 1 9861 XP_071772.1 5 2717 CTGGAACCAAGT T G- 3 C c c
38 GCTGAACTCTCA GA GAG CAGCACTTGG
CATC CT CTC GTCGTGAACC
- AA
GAM8358 255 LOC1283 1 8512 XP_059233.2 5 112 CTCGGCCTCTGT A TT 3 C c c
08 GCAGCCTCATCT GATGAGGC GCAC GGG
CCTG CTACTCCG CGTG TCC
A TC
GAM8358 255 LOC1341 1 13019 NP_620164.1 3 240 CTGACCAGGTGT G----- -- 3 C c c

47 AGTGCCTCATGC ATGAGGCA GCACTTGG
CTGT TACTCCGT TGTGGACC
TGTCCG GA
GAM8358 255 LOC1392 1 7841 XP_060020.3 3 284 TTTTTAACAAGT GG G 3 C c c
31 GCTGGGTTATTC GATGA CAGCACTTG
TGAT TTATT GTCGTGAAC
GG A
GAM8358 255 LOC1464 1 17130 XP_047748.5 3 144 CCCACCCACAGT T - - 3 C b b
88 GCTGCACTCCTC GA GAG GCAGCACT TGGG
CTGC CT CTC CGTCGTGA ACCC
C A C
GAM8358 255 LOC1468 1 19317 XP_097109.2 3 201 AGACCCAGAAGT - C -- 3 C c c
50 TCTGCCTCACTC GA TGAGGCAG ACT TGGG
CCAG CT ACTCCGTC TGA ACCC
C T AG
GAM8358 255 LOC1479 1 12919 XP_097351.2 3 119 AACATCCCAAGT T - 3 C c c
75 GTATGTCTCTTC GA GAGGCA GCACTTGGG
CCTG CT CTCTGT TGTGAACCC
T A
GAM8358 255 LOC1481 1 1685 XP_086087.1 5 826 CCTCGTTATCCG T ACT 3 C c c

89 GCTGCCTCCTCC GA GAGGCAGC TGGG
TCCC CT CTCCGTCG GCCT
C ---
GAM8358 255 LOC1489 1 8018 XP_086369.1 3 1373 CTCCACCCAGCT TG C 3 C c
c
30 GCTGCCTATTCC GA AGGCAGCA TTGGG
CTGC CT TCCGTCGT GACCC
TA C
GAM8358 255 LOC1492 1 1162 XP_086475.1 3 425 AAGTTCCCAAGT GA - 3 C c c
71 GATTGCTGGTCC GAT GGCAG CACTTGGG
AGGG CTG TCGTT GTGAACCC

```
                                        G-    A
GAM8358  255   LOC1494 1  3902  XP_097642.1  3  1411  TGCGGCCCAAGT  T  GCAG            3  C  c
 c
         48                          GATACTTTCTTT GA GAG   CACTTGGG
                                    ACCG       CT TTC   GTGAACCC
                                            -  ATA-
GAM8358  255   LOC1494 1  19340 XP_097645.1  5  1826  AAGCTCCCAAGT  GA              3  C  c  c

         64                          GTTGCTGGATCT GAT  GGCAGCACTTGGG
                                    CTGC       CTA  TCGTTGTGAACCC
                                            GG
GAM8358  255   LOC1509 1  12653 XP_097977.2  3  445   GATTTCCCAAGT  T  GCA             3  C  c
c
         46                          GCCCACTCTCCT GA GAG   GCACTTGGG
                                    TTGT       CT CTC   CGTGAACCC
                                            -  ACC
GAM8358  255   LOC1511 1  12623 XP_098008.1  5  65    GTCCGCCCAAGT  T  CA-             3  C  c  c

         54                          GCCCTCCTCTCA GA GAGG  GCACTTGGG
                                    GCAG       CT CTCC   CGTGAACCC
                                            -  TCC
GAM8358  255   LOC1521 1  9697  XP_045692.1  5  554   AAAGATCCAAGT  T  C            3  C  c  c
         90                          GCTTTCTTTTCA GA GAGG AGCACTTGGG
                                    TTTC       CT TTCT TCGTGAACCT
                                            T  T
GAM8358  255   LOC1548 1  12900 XP_098626.1  3  2469  ATGCATCTCCCA G-----     AGC          3  C  c
 c
         77                          AGTGCCTCATGC      ATGAGGC  ACTTGGG
                                    TTGC           TACTCCG  TGAACCC
                                         CGTTCG      ---
GAM8358  255   LOC1573 2  11073 XP_098754.5  3  1418  CTCTAATTAAGA       CA           3  C  c  c
         81                          ACTGCCTCATTG GATGAGGCAG  CTTGG
                                    AGCC       TTACTCCGTC  GAATT
                                               AA
GAM8358  255   LOC1573 2  13288 XP_098754.5  5  1576  CTCTGCTCTTCT      A  CTT          3  C  c
c
         81                          GCAGCCTCATCT GATGAGGC GCA   GGG
                                    CTGC       CTACTCCG CGT   CTC
                                               A  CTT
GAM8358  255   LOC1575 1  8038  XP_212210.1  5  1481  TCTGAGCCAGAT  G-     C          3  C  c  c

         31                          GCTGCCTGGGTC GAT  AGGCAGCA TTGG
                                    GGTT       CTG  TCCGTCGT GACC
                                            GG      A
GAM8358  255   LOC1583 1  10509 XP_098925.7  3  176   GAGGGATTCCAT  T      CT          3  C  c  c

         18                          GCTGCCTTCTCC GA GAGGCAGCA  TGGG
                                    GGAC       CT TTCCGTCGT  ACCT
                                            C       --
GAM8358  255   LOC1647 1  3977  XP_104657.1  5  1974  CAGGAGGCAGGT   A       G          3  C  c
c
```

14 GCTGCCCGTCTG GATG GGCAGCACTTG
CAAC CTGC CCGTCGTGGAC
- G
GAM8358 255 LOC1647 1 1980 XP_092976.1 3 713 GTGGCTGCCGGA T A T 3 C c c
29 GCTGCCTCCTCC GA GAGGCAGC CT GG
TCCT CT CTCCGTCG GG CC
C A -
GAM8358 255 LOC1703 1 3757 XP_096316.5 3 397 TTGCATCTCAGT --- T 3 C c c
71 GCTGCTTTGGGG GAT GAGGCAGCACT GGG
TCTC CTG TTTCGTCGTGA CTC
GGG -
GAM8358 255 LOC1703 1 20058 XP_096329.1 5 378 ACCGCGACCCGG A A 3 C b b
94 GGCGCCTCATCC GATGAGGC GC CTTGGG
TCAG CTACTCCG CG GGGCCC
- -
GAM8358 255 LOC1969 1 10671 XP_113796.1 3 1285 TGTCCCACAACT - CACT- 3 C c c
96 CTGGCCTCATCG GATGAGGC AG TGGG
CCCT CTACTCCG TC ACCC
G TCAAC
GAM8358 255 LOC2003 1 4936 XP_117224.3 3 691 CAGGATCAATGT G - 3 C b b
12 GGTGCCTCATCC GATGAGGCA CAC TTGG
AGGG CTACTCCGT GTG AACT
G T
GAM8358 255 LOC2211 1 14736 XP_167867.1 3 638 ACTCTCTCCAGT A- T 3 C c c
22 GCTGCCAGCGTC GATG GGCAGCACT GGG
GCAC CTGC CCGTCGTGA CCT
GA -
GAM8358 255 LOC2532 1 16497 XP_170765.2 3 1350 TCCGCACCCAGT G--- -- T 3 C c c
16 GCTGCCGCTCGT ATGA GGCAGCACT GGG
GCTC TGCT CCGTCGTGA CCC
CTCG CG -
GAM8358 255 LOC2566 1 7454 XP_172864.1 3 208 CAAACTCCAAGA -- CA 3 C c c
14 CCTGCCTCACCT GA TGAGGCAG CTTGGG
CACC CT ACTCCGTC GAACCT
CC CA
GAM8358 255 LOC2569 1 1184 XP_170882.3 3 17 CCAGGTTCAGTA ------ 3 C c c
49 GCTGCCTCGTCT GATGAGGCAGC ACTTGG
GGCT CTGCTCCGTCG TGGACC
ATGACT
GAM8358 255 LOC2829 1 8517 XP_210837.1 3 1621 ATGGCTGTAAGT - G 3 C c c
72 GCTGGCCTCATT GATGAGGC AGCACTTG
TCGC TTACTCCG TCGTGAAT
G G
GAM8358 255 LOC2829 1 17627 XP_208473.1 3 81 CTCCAGAACCCA CAC 3 C b b
97 ACTGCCTCATCC GATGAGGCAG TTGGG

```
                                  CGCA       CTACTCCGTC   AACCC
                                             ---
GAM8358  255   LOC2831 1  17655  XP_210906.1  3  33    TCTCAACGACTG      -   C   G          3  C  c  c
         66                       TTGGCCTCATCA GATGAGGC AGCA TTG
                                  AGAG       CTACTCCG TTGT AGC
                                               G   C   A
GAM8358  255   LOC2833 1  13210  XP_210991.1  3  116   ATCTATCTTCCT      A   CTT          3  C  c  c

         57                       GTAGCCTCATCA GATGAGGC GCA   GGG
                                  ATCC       CTACTCCG TGT   CCT
                                               A   ---
GAM8358  255   LOC2834 1  3817   XP_211038.1  3  285   TTTCTGCCCATG      -   CT           3  C  c  c
         37                       TTCGCCTCATCT GATGAGGC AGCA  TGGG
                                  AACC       CTACTCCG TTGT  ACCC
                                               C   --
GAM8358  255   LOC2835 1  1675   XP_211108.1  3  167   AACCTTTCAAGT    A  --            3  C  c  c
         84                       GCTACGTCCATT GATG GGC  AGCACTTGGG
                                  TGTG       TTAC CTG  TCGTGAACTT
                                             -   CA
GAM8358  255   LOC2838 1  4085   XP_208859.1  5  9     CGTCCACCGTCT    -      CT           3  C  c  c
         16                       GCTGCCTACATC GATG AGGCAGCA  TGG
                                  CGCC       CTAC TCCGTCGT  GCC
                                               A       CT
GAM8358  255   LOC2839 1  3468   XP_211252.3  3  721   ACGGGCGGCAAT   T-       C   G          3  C  c
c
         08                       GCTGCCTCCTTC GA  GAGGCAGCA TTG
                                  CCCG       CT  CTCCGTCGT AAC
                                           TC       -   G
GAM8358  255   LOC2841 1  9360   XP_209021.1  5  402   CAGAAACCAAGT GA--     ---          3  C  c  c
         13                       GCTCTAGCCTCA    TGAGGC   AGCACTTGG
                                  GCCC         ACTCCG   TCGTGAACC
                                         CCCG     ATC
GAM8358  255   LOC2841 1  15015  XP_208171.1  5  663   CCTTCTTCAAGT   TG               3  C  c  c
         67                       GCTGCCTGCTCA GA  AGGCAGCACTTGGG
                                  CTGA       CT  TCCGTCGTGAACTT
                                             CG
GAM8358  255   LOC2842 1  5281   XP_302709.1  5  894   CCCAATAGACAT         C-----       3  C  c  c
         14                       GCTGCCTCATTC GATGAGGCAGCA     TTGGG
                                  AAAA       TTACTCCGTCGT     AACCC
                                               ACAGAT
GAM8358  255   LOC2842 1  2290   XP_209112.1  5  20    CCTCTCTCCCCA  T      ACT          3  C  c  c
         97                       GCTGCCTCCTCC GA GAGGCAGC   TGGG
                                  TCTT       CT CTCCGTCG   ACCC
                                             C       ---
GAM8358  255   LOC2843 1  6189   XP_211433.1  5  119   CCCAGCGCACGG    -     A ------      3  C  c  c
         60                       GCTGCCTCCATC GATG AGGCAGC CT     TGGG
                                  AGGG       CTAC TCCGTCG GG     ACCC
                                               C      -  CACGCG
GAM8358  255   LOC2845 1  1267   XP_208210.1  3  1093  AACTGACCAAAT   TG      C          3  C  c  c
```

15 GCTGCCTTGTTT GA AGGCAGCA TTGG
GGCC TT TCCGTCGT AACC
GT A
GAM8358 255 LOC2845 1 13630 XP_208213.1 5 558 ACATTCCCAAGT - - 3 C b b
41 GCCTGTCCTTAT GATGAGG CAG CACTTGGG
TGGA TTATTCC GTC GTGAACCC
T C
GAM8358 255 LOC2846 1 7866 XP_209289.1 3 1974 CCTGCCTGAGGT T - 3 C c c
13 GCTGCCTCCTCC GA GAGGCAGCACTT GGG
CAGG CT CTCCGTCGTGGA TCC
C G
GAM8358 255 LOC2846 1 8597 XP_211569.1 3 890 GCAGGCTCCAGT AG T 3 C c c
47 GGGGCCTCATCA GATGAGGC CACT GGG
TACA CTACTCCG GTGA CCT
GG -
GAM8358 255 LOC2846 1 19474 XP_209321.1 3 1189 TGATGAGTGACT ---- G 3 C c c
91 CCTGCCTCATCC GATGAGGCAG CACTTG
ATTG CTACTCCGTC GTGAGT
CTCA A
GAM8358 255 LOC2846 1 8248 XP_209323.1 5 149 TGACAGGCCCAA G C 3 C b b
93 TGTGCCTCATTG GATGAGGCA CA TTGGG
AGAA TTACTCCGT GT AACCC
- -
GAM8358 255 LOC2847 1 10087 XP_211604.2 3 104 TTCTGTCCTAAA A AC 3 C c c
31 GTCGCCTCATCT GATGAGGC GC TTGGG
TCAC CTACTCCG TG AATCC
C A-
GAM8358 255 LOC2847 1 19911 XP_211608.1 5 352 GGGGCTCCAAGT G -- 3 C c c
32 GCCTTGTTCATC GATGAG CA GCACTTGGG
CTTT CTACTT GT CGTGAACCT
- TC
GAM8358 255 LOC2848 1 1280 XP_209371.1 5 38 AAGGGATCCAAG T A 3 C b b
05 GCTGCCTCTTCC GA GAGGCAGC CTTGGG
TCTT CT CTCCGTCG GAACCT
T -
GAM8358 255 LOC2848 1 9090 XP_211680.1 3 1357 TGTGATGGAAGA A GG 3 C c
c
99 GCTGCCTCATCA GATGAGGCAGC CTT
CGTA CTACTCCGTCG GAA
A GG
GAM8358 255 LOC2850 1 5411 XP_210798.1 3 59 GGCAAGTGAGGT - GG 3 C c c
36 GCTGCCGTCATC GATGA GGCAGCACTT
CAGG CTACT CCGTCGTGGA
G GT
GAM8358 255 LOC2853 1 19896 XP_211879.1 5 241 GCTCATCTTTGG -- CT-- 3 C c c
92 ATTGCCTCATCA GATGAGGCAG CA TGGG
TCCC CTACTCCGTT GT ACTC
AG TTCT
GAM8358 255 LOC2853 1 19532 XP_211876.1 5 525 GGGCACCCAAGT G CA 3 C c
c

97 GCCCCCTGTCTG GAT AGG GCACTTGGG
CGAA CTG TCC CGTGAACCC
- CC
GAM8358 255 LOC2854 1 11311 XP_211909.1 3 496 GTTTGCATCAAT TG C 3 C c c

78 GCTGCCTTGTTA GA AGGCAGCA TTGG
TTCT TT TCCGTCGT AACT
GT -
GAM8358 255 LOC2855 1 18189 XP_211947.1 3 623 GTCTGGGCAAGT - C G 3 C c c

87 GCTCCCTCACTC GA TGAGG AGCACTTG
CCTT CT ACTCC TCGTGAAC
C C G
GAM8358 255 LOC2856 1 4457 XP_209676.1 5 1718 ATGTACACAGGT T G 3 C c c
02 GCTGCCTCTCCC GA GAGGCAGCACTTG
TGAT CT CTCCGTCGTGGAC
- A
GAM8358 255 LOC2857 1 13089 XP_209726.1 3 480 CCTTCCGGTGGA A -- 3 C c c
05 GCTGCCTCGTTC GATGAGGCAGC CT TGGG
CTTT TTGCTCCGTCG GG GCCT
A TG
GAM8358 255 LOC2857 1 12096 XP_212011.1 3 1087 TCAGCTCCCTGT G TT 3 C c
c
62 GCTGCCTGATTT GAT AGGCAGCAC GGG
CTCA TTA TCCGTCGTG CCC
G T-
GAM8358 255 LOC2858 2 4884 XP_212037.1 5 292 TCCATCTCACGC - ACT 3 C c c
58 GCTGCCTCTGTC GAT GAGGCAGC TGGG
ATTT CTG CTCCGTCG ACTC
T CGC
GAM8358 255 LOC2858 2 6422 XP_212037.1 5 105 CTCCATCCCTTT G CTT 3 C c c

58 GATGCCTCATCC GATGAGGCA CA GGG
ATCT CTACTCCGT GT CCC
A TT-
GAM8358 255 LOC2859 1 7453 XP_209816.1 3 353 CCTCCCACAAGT A - - 3 C b b
24 CGCGCCTCATCG GATGAGGC GC ACTTG GG
AGCA CTACTCCG CG TGAAC CC
- C A
GAM8358 255 LOC2859 1 17650 NP_777609.1 3 203 GTTCGTCAGCTG AC- 3 C c c

31 GCTGCCTCATTG GATGAGGCAGC TTGG
CCAC TTACTCCGTCG GACT
GTC
GAM8358 255 LOC2859 1 13769 XP_208366.1 5 121 GGCCGCCAGAAA GCAC- 3 C c
c
40 GATGCCTCATCC GATGAGGCA TTGG
TCGA CTACTCCGT GACC
AGAAA
GAM8358 255 LOC2860 1 3955 XP_209853.1 3 557 CTGCACCCTATT A CTT 3 C c c

```
          16                      GTGGCCTCATCC GATGAGGC GCA   GGG
                                  AAAC       CTACTCCG TGT   CCC
                                               G   TAT
GAM8358   255   LOC2860 2  1344  XP_212152.1  3  220   TGGTCATCAGGA  T      A            3  C  c  c
          52                      GCTGCCTCTTCT GA GAGGCAGC CTTGG
                                  GTTA       CT CTCCGTCG GGACT
                                           T      A
GAM8358   255   LOC2860 2  4733  XP_212152.1  3  197   GGGAACTCATTT  ---      CT          3  C  c  c
          52                      GCTGCCTCTTGG GAT   GAGGCAGCA  TGGG
                                  TCAT       CTG   CTCCGTCGT  ACTC
                                           GTT       TT
GAM8358   255   LOC2860 1  10597 XP_209889.1  3  321   TCAGCTCCTGGA  T      A  T          3  C  c  c

          76                      GCTGCCTCTCTG GA GAGGCAGC CT GGG
                                  CACT       CT CTCCGTCG GG CCT
                                           -      A  T
GAM8358   255   LOC2860 1  6499  XP_212163.1  5  2065  CTCACTGGCCCT  T      CTT          3  C  c
c
          78                      GCTGCCTCTTCA GA GAGGCAGCA   GGG
                                  AGTT       CT CTCCGTCGT   CCC
                                           T       ---
GAM8358   255   LOC2861 1  9669  XP_212184.3  3  352   TCCCTTTATGGG       C   -----       3  C  c  c
          21                      TCTGCCTCATTG GATGAGGCAG ACTT    GGG
                                  GATT       TTACTCCGTC TGGG    CCC
                                             -   TATTT
GAM8358   255   LOC2862 1  4906  XP_212232.1  3  1751  CAGGCCACCAGT GA-----       T        3  C  c
c
          17                      GCTGCCTCAGGG       TGAGGCAGCACT GG
                                  TGTC             ACTCCGTCGTGA CC
                                         CTGTGGG          -
GAM8358   255   LOC2863 1  18959 XP_212293.1  5  173   GCCCCAGGTGAT  ----      ---         3  C  c  c
          74                      GCTGCCTTTGCT GAT   GAGGCAGC  ACTTGGG
                                  GTCC       CTG   TTCCGTCG  TGGACCC
                                           TCGT      TAG
GAM8358   255   LOC2864 2  3416  XP_210036.1  3  1865  CCACTCCCAAGT  T   CA           3  C  c  c

          04                      GTGCCCTCTTCC GA GAGG  GCACTTGGG
                                  CTCT       CT CTCC  TGTGAACCC
                                           T   CG
GAM8358   255   LOC2864 2  4632  XP_210036.1  3  168   CTATATCCAAGT  ---  C           3  C  c  c
          04                      GCTTCCTCCAAG GAT   GAGG AGCACTTGGG
                                  TCAC       CTG   CTCC TCGTGAACCT
                                           AAC   T
GAM8358   255   LOC2864 2  4632  XP_210826.2  3  168   CTATATCCAAGT  ---  C           3  C  c  c
          04                      GCTTCCTCCAAG GAT   GAGG AGCACTTGGG
                                  TCAC       CTG   CTCC TCGTGAACCT
                                           AAC   T
GAM8358   255   LOC2864 1  1033  XP_210047.1  5  1669  GGGCTCCCCTGT    ----      TT         3  C  c  c

          35                      GCTGCCTAGCTC GATGA   GGCAGCAC  GGG
```

```
                                  GTCT       CTGCT    CCGTCGTG  CCC
                                             CGAT       TC
GAM8358  255    LOC2864 1  3469  XP_210057.1  3  101   TTAATAACCAGT          T          3  C  b  b
         56                        GTTGCCTCATTC GATGAGGCAGCACT GG
                                  AGCT       TTACTCCGTTGTGA CC
                                             -
GAM8358  255    LOC2864 1  1737  XP_208437.1  3  764   TGACTCTTATCT        CACT          3  C  c  c
         93                        ACTGCCTCATCT GATGAGGCAG    TGGG
                                  TGAT       CTACTCCGTC    ATTC
                                               ATCT
GAM8358  255    LOC2865 1  13990 XP_210090.1  5  1268  CCCCCGGGAGGT          ---          3  C  b  b

         29                        GCTGCCTCGTCT GATGAGGCAGCACT   TGGG
                                  ACCC       CTGCTCCGTCGTGG   GCCC
                                               AGG
GAM8358  255    LOC3385 1  12673 XP_294659.1  5  78    GAGGGCCTTCTT  --       CTT          3  C  c  c

         88                        GCTGCCTCACCT GA  TGAGGCAGCA   GGG
                                  CATG       CT  ACTCCGTCGT   TCC
                                           CC        TCT
GAM8358  255    LOC3387 1  5276  XP_290570.1  3  211   ATCTTACCAAGT    GGCA             3  C  c
c
         73                        GCCATCATCCTT GATGA    GCACTTGG
                                  CACC       CTACT    CGTGAACC
                                             AC--
GAM8358  255    LOC3388 1  1697  XP_290586.1  3  392   TGTATCCCAAGT   --   - --          3  C  c  c
         11                        GCACTGTCCTTC GAT  GAGG CA  GCACTTGGG
                                  TGTC       CTG  TTCC GT  CGTGAACCC
                                           TC    T  CA
GAM8358  255    LOC3389 1  4800  XP_294754.1  3  1535  ATAGCCTCGGGT   G--              3  C  c  c
         59                        GCTGCCTGTAGT GAT   AGGCAGCACTTGGG
                                  CATG       CTG   TCCGTCGTGGGCTC
                                             ATG
GAM8358  255    LOC3390 1  20096 XP_290682.1  3  815   CAGGGACCCACT   T      CT          3  C  c
c
         59                        GCTGCCTCTTCC GA GAGGCAGCA  TGGG
                                  AGGA       CT CTCCGTCGT  ACCC
                                           T       C-
GAM8358  255    LOC3391 1  10008 XP_294830.1  5  127   TCTGGCCCCGGT G----  -       T       3  C  c
c
         49                        GCTGCCTGCATG     ATG AGGCAGCACT GGG
                                  CCAA           TAC TCCGTCGTGG CCC
                                         AACCG   G        C
GAM8358  255    LOC3391 1  13786 XP_294835.1  5  298   CTGGCGCCTCCT   T      CTT          3  C  c
c
         61                        GCTGCCTCCTCC GA GAGGCAGCA   GG
                                  ATAC       CT CTCCGTCGT   CC
                                           C        CCT
GAM8358  255    LOC3392 1  11490 XP_294901.1  5  316   CTTTCTTAATTA  A      AC-          3  C  c  c
         90                        GCTGCCTCACCG G TGAGGCAGC   TTGGG
```

GCTG C ACTCCGTCG AATTC
C ATT
GAM8358 255 LOC3393 1 11710 XP_297112.1 5 215 AGGCTCCTGTTG - CT 3 C c c
05 CCTGCCTCATCC GATGAGGCAG CA TGGG
CACA CTACTCCGTC GT GTCC
C T-
GAM8358 255 LOC3394 1 14243 XP_294957.1 3 1335 GGGCAGGGCAGG CA G 3 C c
c
42 ACTGCCTCATCC GATGAGGCAG CTTG
TCTG CTACTCCGTC GGAC
A- G
GAM8358 255 LOC3394 1 10510 XP_290907.2 3 1658 AATGTTGCAGGT --- G 3 C c c
59 GCTGCCTCCGAG GAT GAGGCAGCACTTG
TCTG CTG CTCCGTCGTGGAC
AGC G
GAM8358 255 LOC3396 1 9001 XP_290962.1 5 239 AGCCCACCAAGA G A- 3 C c c
07 GGTGCCTCATTA GATGAGGCA C CTTGG
GAAC TTACTCCGT G GAACC
- GA
GAM8358 255 LOC3396 1 18585 XP_295032.1 5 766 CTCACCTCAACT -- C 3 C c c
85 GCTGCCTTCTGT GAT GAGGCAGCA TTGGG
CCAG CTG TTCCGTCGT AACTC
TC C
GAM8358 255 LOC3399 1 7941 XP_295099.1 5 314 TTGACACCAGTG AG- T 3 C c c
14 GAAGCCTCATCC GATGAGGC CACT GG
TCAG CTACTCCG GTGA CC
AAG -
GAM8358 255 LOC3402 1 4985 XP_291169.1 3 32 TCCCTCCTTCTT T CTT 3 C c c
04 GCTGCCTCCTCC GA GAGGCAGCA GGG
TCCT CT CTCCGTCGT TCC
C TCT
GAM8358 255 LOC3402 1 6120 XP_290386.1 5 170 CTGCTTTCAAGT AGG 3 C c c
32 GCTGGAACATTA GATG CAGCACTTGGG
AGTT TTAC GTCGTGAACTT
AAG
GAM8358 255 LOC3402 1 14581 XP_291214.1 3 1424 TCTTCCCTGTCT T CT 3 C c c
90 GCTGCCTCTCCA GA GAGGCAGCA TGGG
GTCC CT CTCCGTCGT GTCC
- CT
GAM8358 255 LOC3447 1 17217 XP_298281.2 5 16 GAAGCAGCAAGT GG- G 3 C c
c
82 GCTGACATCATC GATGA CAGCACTTG
ACGG CTACT GTCGTGAAC
ACA G
GAM8358 255 LOC3457 1 9069 XP_298978.1 5 358 ACTGGTCAAGTG G----- G- 3 C c c
49 AATGCCTCATGT ATGAGGCA CACTTGG
TTCT TACTCCGT GTGAACT

TCTTTG AA
GAM8358 255 LOC3471 1 13274 XP_294530.1 5 51 GCGGCTTCCGGT - T 3 C c c
66 GCTGCCTGCGTC GATG AGGCAGCACT GGG
ATCT CTGC TCCGTCGTGG CCT
G -
GAM8358 255 LOC3477 1 6985 XP_300531.1 3 1857 CTCGGCCCAAGT G CAG 3 C c
c
67 GAGTCCTGGTCC GAT AGG CACTTGGG
AAGG CTG TCC GTGAACCC
G TGA
GAM8358 255 LOC3478 1 13761 XP_302604.1 3 360 GGCTGCCCCAGT GA- T 3 C c
c
03 GCTGCCACAGTC GAT GGCAGCACT GGG
CCAC CTG CCGTCGTGA CCC
ACA C
GAM8358 255 LOC3481 1 17997 XP_302567.1 3 795 GGGAGGCTCAGG T A 3 C c c

21 GCTGCCTCCTCG GA GAGGCAGC CTTGGG
AGTT CT CTCCGTCG GGACTC
C -
GAM8358 255 LOC3481 1 2553 XP_211219.1 5 2048 CAAATCCCAAGT AGG---- 3 C c
c
55 GTTGACACAGCC GATG CAGCACTTGGG
ATCT CTAC GTTGTGAACCC
CGACACA
GAM8358 255 LOC3482 1 17130 XP_300304.1 3 144 CCCACCCACAGT T - - 3 C b b
09 GCTGCACTCCTC GA GAG GCAGCACT TGGG
CTGC CT CTC CGTCGTGA ACCC
C A C
GAM8358 255 LOC3482 1 12407 XP_300686.1 5 157 GAGAGGCCAAGG -- A 3 C b b

58 GCTGCCTCCTAT GAT GAGGCAGC CTTGG
CAGA CTA CTCCGTCG GAACC
TC G
GAM8358 255 LOC3483 1 7856 XP_302739.1 5 4 TACTGTCTCAGT A T 3 C c c
89 GCTGCTATATTT GATG GGCAGCACT GGG
AAGA TTAT TCGTCGTGA CTC
A -
GAM8358 255 LOC3483 1 10069 XP_300729.1 3 2220 TGTGGGCCTAAA CAC 3 C c
c
96 TTTGCCTCATTC GATGAGGCAG TTGGG
AGAC TTACTCCGTT AATCC
TA-
GAM8358 255 LOC3487 1 17866 XP_302869.1 3 1548 CAAAGCTTAACC -- AC 3 C c c

61 GCTGCCTCCTGT GAT GAGGCAGC TTGGG
CCCC CTG CTCCGTCG AATTC
TC CC
GAM8358 255 LOC3487 1 6580 XP_302883.1 5 345 CTCAGGAGCAAT T ----- 3 C c c
68 GCTGCCTTCTCC GA GAGGCAGCA CTTGGG

CTGT CT TTCCGTCGT GGACTC
C AACGA
GAM8358 255 LOC3491 1 7453 XP_173186.2 3 350 CCTCCCACAAGT A - - 3 C b b
01 CGCGCCTCATCG GATGAGGC GC ACTTG GG
AGCA CTACTCCG CG TGAAC CC
- C A
GAM8358 255 LOC3492 1 10509 XP_301004.1 3 176 GAGGGATTCCAT T CT 3 C c c
78 GCTGCCTTCTCC GA GAGGCAGCA TGGG
GGAC CT TTCCGTCGT ACCT
C --
GAM8358 255 LOC3493 1 10509 XP_301017.1 3 176 GAGGGATTCCAT T CT 3 C c c
02 GCTGCCTTCTCC GA GAGGCAGCA TGGG
GGAC CT TTCCGTCGT ACCT
C --
GAM8358 255 LOC3493 1 13247 XP_301037.1 5 56 TCGGGGCTGGGC T A TG 3 C c
c
37 GCTGCCTCTCGG GA GAGGCAGC CT G
TCGA CT CTCCGTCG GG C
- C GT
GAM8358 255 LOC3494 1 1033 XP_301084.1 5 1669 GGGCTCCCCTGT ---- TT 3 C c c
30 GCTGCCTAGCTC GATGA GGCAGCAC GGG
GTCT CTGCT CCGTCGTG CCC
CGAT TC
GAM8358 255 LOC3501 1 16322 XP_303855.1 5 93 AGCAGCCCAAGT G- C 3 C c c
76 GCTCCTGAGTCC GAT AGG AGCACTTGGG
TTGC CTG TCC TCGTGAACCC
AG -
GAM8358 255 LOC3507 1 1938 XP_303117.1 5 217 AGCAGCCCCTGC ACTT 3 C c
c
17 GCTGCCTCATCT GATGAGGCAGC GGG
ACAT CTACTCCGTCG CCC
CGT-
GAM8358 255 LOC3508 1 18754 XP_303256.1 5 279 CCCGTGTTGGGT T - TG 3 C c
c
97 GCTGCCATCTCT GA GA GGCAGCACT G
ACTA CT CT CCGTCGTGG T
- A GT
GAM8358 255 LOC3509 1 17196 XP_304543.1 5 157 TTGCCAGGTGAT T --- 3 C c c
35 GCTGCCTCTCTG GA GAGGCAGC ACTTGG
TGGA CT CTCCGTCG TGGACC
- TAG
GAM8358 255 LOC5123 1 19076 NP_057542.2 3 439 ATAGGTACAAGT TG G 3 C c
c
6 GCTGCTTTGTCA GA AGGCAGCACTTG
GCCT CT TTCGTCGTGAAC
GT A
GAM8358 255 LOC5595 1 17880 NP_061976.1 3 163 GCCACACCAAGT - A 3 C b b

4 GCAGCCCTCGTC GATGAGG C GCACTTGG
CTGG CTGCTCC G CGTGAACC
C A
GAM8358 255 LOC8155 1 16662 NP_110429.1 3 566 GTTTTCCCAAGT CA - 3 C c c
8 GGCATTTTCATC GATGAGG GC ACTTGGG
TCGC CTACTTT CG TGAACCC
TA G
GAM8358 255 LOC9016 1 4312 XP_029570.1 3 170 AAAGATCCAGCT C 3 C c c
7 GTTGCCTCATTC GATGAGGCAGCA TTGGG
CTTG TTACTCCGTTGT GACCT
C
GAM8358 255 LOC9207 1 1696 XP_042684.1 5 1273 CAGAGGCCTAAG GA----- A 3 C c
c
8 GCTGCCTCAGCA TGAGGCAGC CTTGGG
CCCT ACTCCGTCG GAATCC
TCCCACG -
GAM8358 255 LOC9226 1 2289 XP_043979.3 3 218 CCAGCCCCAAGT T AG 3 C c c
7 GGCTTTTTCAAT GA GAGGC CACTTGGG
TACA CT TTTCG GTGAACCC
T --
GAM8358 255 LOC9297 1 7336 XP_048529.2 5 3336 AATTCCCCAAGT A-- 3 C c c
3 GTGAAGCCTCAT GATGAGGC GCACTTGGG
TCAT TTACTCCG TGTGAACCC
AAG
GAM8358 255 LTB4R2 1 15287 NP_062813.1 5 1155 AGAGGCCCAGGA AG - 3 C c
c
TGAGCCTCATCT GATGAGGC CA CTTGGG
TGTC CTACTCCG GT GGACCC
A- A
GAM8358 255 LY9 1 3090 NP_002339.1 3 32 GGAAAAGCAGCT T C G 3 C c c
GCTGCCTCTCTC GA GAGGCAGCA TTG
CTGG CT CTCCGTCGT GAC
- C G
GAM8358 255 LYN 1 12638 NP_002341.1 3 49 TTGGCAGGGGTG - GG 3 C c c
GCTGCCTCATTT GATGAGGCAGC ACTT
AGAG TTACTCCGTCG TGGG
G GA
GAM8358 255 MADH6 1 17896 NP_005576.2 5 48 GAGCCGCCGGGC A A 3 C c c
GCTGCCTCGCCA G TGAGGCAGC CTTGG
GACC C GCTCCGTCG GGGCC
C C
GAM8358 255 MAGEB6 1 12419 NP_775794.2 5 32 AGCCTGAAAAGT A --- 3 C c c
GCTGTCACGTCA GATG GGCAGCACTT GGG
GCGG CTGC CTGTCGTGAA TCC
A AAG
GAM8358 255 MAP2K5 1 3777 NP_002748.1 5 309 AGTCCTTGCCCT T CTT 3 C c c
GCTGCCTCCTCA GA GAGGCAGCA GGG
TACC CT CTCCGTCGT CCC

C ---
GAM8358 255 MAP2K5 1 3777 NP_660143.1 5 309 AGTCCTTGCCCT T CTT 3 C c c

GCTGCCTCCTCA GA GAGGCAGCA GGG
TACC CT CTCCGTCGT CCC
C ---
GAM8358 255 MAP2K5 1 3777 NP_660144.1 5 309 AGTCCTTGCCCT T CTT 3 C c c

GCTGCCTCCTCA GA GAGGCAGCA GGG
TACC CT CTCCGTCGT CCC
C ---
GAM8358 255 MAPBPIP 1 6096 NP_054736.1 3 5 CCTCACCCAAGT AG AG 3 C c c

GGCGGCATCTTA GATG GC CACTTGGG
CGGC CTAC CG GTGAACCC
GG --
GAM8358 255 MAPK13 1 6864 NP_002745.1 5 91 GGGTGCCCGGGA AG - 3 C c c
TGAGCCTCATCC GATGAGGC CA CTTGGG
GGAA CTACTCCG GT GGGCCC
A- A
GAM8358 255 MAST205 1 6973 NP_055927.1 3 48 CATCACCCAAGT GA- ---- 3 C c c
GCCTGATGCCTC TGAGGCA GCACTTGGG
AGGT ACTCCGT CGTGAACCC
TGG AGTC
GAM8358 255 MBIP 1 6554 NP_057670.1 3 285 TAATTTACAAGT AGG G 3 C c c
GCTGGTACATCT GATG CAGCACTTG
TTTT CTAC GTCGTGAAC
ATG A
GAM8358 255 MGAT4B 1 6555 NP_463459.1 5 142 CCCCACCTCTGT A TT 3 C c c
GCTGCCCCATCC GATG GGCAGCAC GGG
ACCT CTAC CCGTCGTG TCC
C TC
GAM8358 255 MGC1136 1 2422 NP_076930.1 3 349 TTGTGCCCAAGT T C- 3 C c c
GTTTCCCTCTCT GA GAGG AGCACTTGGG
CCCT CT CTCC TTGTGAACCC
- CT
GAM8358 255 MGC1485 1 2435 XP_030295.3 3 843 GCTGCCCTCAGC -- ACTT 3 C c
c
9 TCCGCCTCATCA GATGAGGC AGC GGG
GCTA CTACTCCG TCG CCC
CC ACT-
GAM8358 255 MGC1552 1 19724 NP_612637.1 5 144 CCGGCCTTCGAG T A 3 C c
c
3 GCTGCCTCCTCC GA GAGGCAGC CTTGGG
AGGC CT CTCCGTCG GAGCTT
C -
GAM8358 255 MGC1588 1 2341 XP_294758.1 3 252 ACTGAGCTGAGT -- TG 3 C c c

5 GCTGCCCTTTAT GATGA GGCAGCACT G
TAAA TTATT CCGTCGTGA C

```
                                                TC       GT
GAM8358  255    MGC1733 1  4035  NP_443112.1  3 935   TGCTCCCCAAGT   G   AG             3  C  c
c
          0                          GGGCCTGATTTA GAT AGGC  CACTTGGG
                                     GCAG       TTA TCCG  GTGAACCC
                                              G   G-
GAM8358  255    MGC2039 1  1889  NP_443089.1  3 68    TGTATAAAAAGT   T        GG          3  C  c  c
          8                          GCTGTCTCTCAG GA GAGGCAGCACTT
                                     TAGT       CT CTCTGTCGTGAA
                                              -         AA
GAM8358  255    MGC2388 1  11074 NP_689714.1  3 349   CCTAGTTCAGTG G-----      -   ----      3  C  c
c
          5                          TCTGCCTCATGG      ATGAGGCAG CACT   TGGG
                                     GAAG           TACTCCGTC GTGA   ATCC
                                            GAAGGG       T   CTTG
GAM8358  255    MGC3206 1  15890 NP_695003.1  3 345   CACCTGGCCACT         CT          3  C  c  c

          5                          GCTGCCTTATCC GATGAGGCAGCA  TGG
                                     ATTC       CTATTCCGTCGT  ACC
                                                C-
GAM8358  255    MGC3483 1  12612 NP_689527.1  3 907   TGCCCACAAGAT      - CA   -        3  C  c
c
          0                          CTAGCCTCATCT GATGAGGC AG  CTTG GG
                                     GGAG       CTACTCCG TC  GAAC CC
                                                A  TA   A
GAM8358  255    MGC3932 2  7913  NP_671722.1  3 1165  ATGGTCTCTAGT   G       T          3  C  c  c

          5                          GCTGCCTATCAA GAT AGGCAGCACT GGG
                                     CTTG       CTA TCCGTCGTGA CTC
                                              -         T
GAM8358  255    MGC3932 2  15215 NP_671722.1  3 1278  ACCTACAAGTGG       --    G        3  C  c
c
          5                          TTTGCCTCATTG GATGAGGCAG  CACTTG
                                     CCTT       TTACTCCGTT  GTGAAC
                                                TG     A
GAM8358  255    MGC4055 1  10027 NP_689498.1  3 24    GAGCTGCCCCGT   T       TT          3  C  c
c
          5                          GCTGCCTTCTCC GA GAGGCAGCAC  GGG
                                     AGGC       CT TTCCGTCGTG  CCC
                                              C         C-
GAM8358  255    MGC4263 1  10509 NP_787119.1  3 214   GAGGGATTCCAT   T      CT          3  C  c
c
          0                          GCTGCCTTCTCC GA GAGGCAGCA  TGGG
                                     GGAC       CT TTCCGTCGT  ACCT
                                              C         --
GAM8358  255    MGC5391 1  12983 NP_116129.2  3 1161  AGCTCCCCAAGT   - CAG            3  C  c
 c
                                     GATTCTACGTTC GATG AGG   CACTTGGG
                                     CCCA       TTGC TCT   GTGAACCC
                                              A   TA-
```

GAM8358 255 MME 1 4104 NP_000893.1 3 2905 TATGTGTCCAAT AT C 3 C c c
GCTGCCTTCCCA G GAGGCAGCA TTGGG
TGAA C TTCCGTCGT AACCT
CC -
GAM8358 255 MME 1 4104 NP_009218.1 3 2905 TATGTGTCCAAT AT C 3 C c c
GCTGCCTTCCCA G GAGGCAGCA TTGGG
TGAA C TTCCGTCGT AACCT
CC -
GAM8358 255 MME 1 4104 NP_009219.1 3 2905 TATGTGTCCAAT AT C 3 C c c
GCTGCCTTCCCA G GAGGCAGCA TTGGG
TGAA C TTCCGTCGT AACCT
CC -
GAM8358 255 MME 1 4104 NP_009220.1 3 2905 TATGTGTCCAAT AT C 3 C c c
GCTGCCTTCCCA G GAGGCAGCA TTGGG
TGAA C TTCCGTCGT AACCT
CC -
GAM8358 255 MMP2 1 17651 NP_004521.1 3 319 GGCTGCCCTGGT -- A T 3 C c c
GCTGCCACACTT GA TG GGCAGCACT GGG
CAGG CT AC CCGTCGTGG CCC
TC A T
GAM8358 255 MOST2 1 993 NP_064635.1 5 677 CCAGCTCCCAGT T - T 3 C c c
GCTGCTGTCCTC GA GA GGCAGCACT GGG
TGAT CT CT TCGTCGTGA CCC
C G -
GAM8358 255 MPP2 1 3308 NP_005365.2 3 227 TTGTGCCCAGGT - A 3 C b b
GCTGCCCACTCC GA TG GGCAGCACTTGGG
TGAT CT AC CCGTCGTGGACCC
C -
GAM8358 255 MRPL9 1 14139 NP_113608.1 3 347 TTGTCTCCAGTA CAC 3 C c c
CTTGCCTCATTC GATGAGGCAG TTGGG
TCAT TTACTCCGTT GACCT
CAT
GAM8358 255 MSI2 1 13149 NP_733839.1 3 649 AGTCATCCAGGT G----- A 3 C c c
GCTGCCACATGA ATG GGCAGCACTTGGG
CAGG TAC CCGTCGTGGACCT
GGACAG A
GAM8358 255 MTHFR 1 8401 NP_005948.1 3 75 CTCCTCCACAGT T - 3 C c c
GCTGCTTCTCTT GA GAGGCAGCACT TGGG
GGGA CT CTTCGTCGTGA ACCT
- C
GAM8358 255 MYBL2 2 6152 NP_002457.1 3 305 CCCACGTCAGGC A-- --- T 3 C c c
CTGGCCTCATCT GATGAGGC GC AC TGGG
CAGA CTACTCCG CG TG ACCC
GTC GAC C
GAM8358 255 MYBL2 2 18152 NP_002457.1 3 173 ACAGGGCCATGT GA T 3 C c c
GCTGCCCTGTTG GAT GGCAGCAC TGG
CCGA TTG CCGTCGTG ACC
TC T
GAM8358 255 MYBPC1 1 14764 NP_002456.1 3 243 AGGCCCCCAAGT T- A 3 C c c

GTGGTCTTTTTC GA GAGGC GCACTTGGG
TTTC CT TTCTG TGTGAACCC
TT G

GAM8358 255 MYO1B 1 15695 XP_290989.1 5 203 ATGGAAGCTGAG T A TG 3 C c c

GCTGCCTCTTCC GA GAGGCAGC CT G
TAGC CT CTCCGTCG GA C
T - GT

GAM8358 255 N4BP2 1 13301 NP_060647.2 3 733 CTTCCAGATGTT C--- 3 C c c
GCTGCCTTATCG GATGAGGCAGCA TTGGG
AAAT CTATTCCGTCGT GACCT
TGTA

GAM8358 255 N4BP3 1 1115 XP_038920.2 3 857 CCCTAGAAGTGC -- --- 3 C c c
TCTGCCTCATTC GATGAGGCA GCACTT GGG
CCTG TTACTCCGT CGTGAA CCC
CT GAT

GAM8358 255 NAB1 1 3469 NP_005957.2 3 102 TTAATAACCAGT T 3 C b b
GTTGCCTCATTC GATGAGGCAGCACT GG
AGCT TTACTCCGTTGTGA CC
-

GAM8358 255 NDFIP1 1 8122 NP_085048.1 3 991 TTCTGCCCAAGT GCAG 3 C c c

GGTAATTCATCT GATGAG CACTTGGG
TGGT CTACTT GTGAACCC
AATG

GAM8358 255 NEBL 1 7080 NP_006384.1 3 3526 AGCAAGCAAGTT TG - G 3 C c c
GCTGCCTATTCT GA AGGCAGCA CTTG
ATAG CT TCCGTCGT GAAC
TA T G

GAM8358 255 NETO2 1 2069 NP_060562.3 3 318 AGCCAGGCTCAG T A---- 3 C c c
GCTGCCTCTTCG GA GAGGCAGC CTTGG
TTTT CT CTCCGTCG GGACC
T GACTC

GAM8358 255 NFASC 1 521 XP_046808.8 3 1558 CAGACCGAAGGT - G- 3 C c c
GCTGCCTTCATC GATGA GGCAGCACTT GG
CTCC CTACT CCGTCGTGGA CC
T AG

GAM8358 255 NINJ1 1 16214 NP_004139.1 3 139 CCAGAGCCCAGG - A T 3 C b b
CTGGCCTCATCT GATGAGGC AGC CT GGG
GCAC CTACTCCG TCG GA CCC
G - -

GAM8358 255 NKTR 1 8666 NP_005376.2 3 1385 TGTTCCCCAAGT G CA 3 C c c
GTACTTAATCAC GAT AGG GCACTTGGG
CTTA CTA TTC TGTGAACCC
A A-

GAM8358 255 NXN 1 18637 NP_071908.1 3 126 CACCACCCAAGT T A-- 3 C c c
GTCCAGCCTCTC GA GAGGC GCACTTGGG
TGTG CT CTCCG TGTGAACCC
- ACC

GAM8358 255 OAZ3 1 7561 NP_057262.1 5 206 CCGGGAGAAGAT ------ 3 C c c

GCTGCCTCGTTG GATGAGGCAGCA CTTGG
TTAT TTGCTCCGTCGT GGGCC
AGAAGA

GAM8358 255 ODF2 1 2038 NP_002531.3 5 307 TGCCTAGCCATG C T 3 C b b
TCTGCCTCATCC GATGAGGCAG AC TGG
TCAG CTACTCCGTC TG ACC
- T

GAM8358 255 ODF2 1 2038 NP_702915.1 5 260 TGCCTAGCCATG C T 3 C b b
TCTGCCTCATCC GATGAGGCAG AC TGG
TCAG CTACTCCGTC TG ACC
- T

GAM8358 255 OIP106 1 14387 NP_055780.1 3 359 AAACTCCCAAGT CA 3 C c c
GTGTTCTTATCC GATGAGG GCACTTGGG
CATG CTATTCT TGTGAACCC
TG

GAM8358 255 OPA1 1 6097 NP_056375.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570844.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570845.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570846.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570847.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570848.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570849.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OPA1 1 6097 NP_570850.1 3 1124 TCTATCTCATTT T CT 3 C c c
GCTGCCTTTTCA GA GAGGCAGCA TGGG
CTAA CT TTCCGTCGT ACTC
T TT

GAM8358 255 OSCAR 1 18649 NP_570127.1 5 113 TGGTTTTCTGAT C TG 3 C c c
GTTGCCTCATTT GATGAGGCAGCA T GG
CCTG TTACTCCGTTGT A CT

- GT
GAM8358 255 OSCAR 1 18649 NP_573398.1 5 113 TGGTTTTCTGAT C TG 3 C c c
GTTGCCTCATTT GATGAGGCAGCA T GG
CCTG TTACTCCGTTGT A CT
- GT
GAM8358 255 OSCAR 1 18649 NP_573399.1 5 113 TGGTTTTCTGAT C TG 3 C c c
GTTGCCTCATTT GATGAGGCAGCA T GG
CCTG TTACTCCGTTGT A CT
- GT
GAM8358 255 OTOP3 1 13034 XP_292588.2 5 890 TCAGCACTGAGT C TG 3 C c c
ACTGCCTCATCT GATGAGGCAG ACT G
GCTG CTACTCCGTC TGA C
A GT
GAM8358 255 P2RX4 1 5900 NP_002551.2 5 171 CCGACCGCCCGT T- TT 3 C c c
GCTGCCTCCTTC GA GAGGCAGCAC GGG
CGGG CT CTCCGTCGTG CCC
TC --
GAM8358 255 P2RX4 1 5900 NP_780776.1 5 171 CCGACCGCCCGT T- TT 3 C c c
GCTGCCTCCTTC GA GAGGCAGCAC GGG
CGGG CT CTCCGTCGTG CCC
TC --
GAM8358 255 P2RX4 1 5900 NP_780777.1 5 171 CCGACCGCCCGT T- TT 3 C c c
GCTGCCTCCTTC GA GAGGCAGCAC GGG
CGGG CT CTCCGTCGTG CCC
TC --
GAM8358 255 P2RY6 1 985 NP_004145.1 5 117 GTTTCCTCATCT T CT 3 C c c
GCTGCCTCTCCA GA GAGGCAGCA TGGG
GACT CT CTCCGTCGT ACTC
- CT
GAM8358 255 P2RY6 1 985 NP_789766.1 5 137 GTTTCCTCATCT T CT 3 C c c
GCTGCCTCTCCA GA GAGGCAGCA TGGG
GACT CT CTCCGTCGT ACTC
- CT
GAM8358 255 P2RY6 1 985 NP_789768.1 5 274 GTTTCCTCATCT T CT 3 C c c
GCTGCCTCTCCA GA GAGGCAGCA TGGG
GACT CT CTCCGTCGT ACTC
- CT
GAM8358 255 P5-1 1 18467 NP_006665.1 3 778 TTGGACCCATAG A ACT 3 C c c
GTAGCCTCATCC GATGAGGC GC TGGG
CTGC CTACTCCG TG ACCC
A GAT
GAM8358 255 PAM 1 8824 NP_055872.1 3 652 TGCAATACTGAG G TG 3 C c c
TGTGCCTCATTA GATGAGGCA CACT G
TCTT TTACTCCGT GTGA C
- GT
GAM8358 255 PC326 1 13648 NP_060912.1 5 212 AACTGTCGACGT A - 3 C c c
GCTGCCACGTCT GATG GGCAGCAC TTGG
GTTG CTGC CCGTCGTG AGCT
A C
GAM8358 255 PCDH17 1 14897 NP_055274.2 5 381 TCCTTCTTATCG CACT 3 C c
c

CCTGCCTCATCG GATGAGGCAG TGGG
CTCA CTACTCCGTC ATTC
CGCT
GAM8358 255 PCNX 1 2623 NP_055797.1 5 261 TCCTCCTCGTTT T CT 3 C c c
GCTGCCTCCTCC GA GAGGCAGCA TGGG
TCCT CT CTCCGTCGT GCTC
C TT
GAM8358 255 PCOLCE 1 16049 NP_002584.1 5 39 CAAAATTCAGCT - C 3 C c c
GCTGCCTCTGTC GAT GAGGCAGCA TTGGG
TTGA CTG CTCCGTCGT GACTT
T C
GAM8358 255 PDE1B 1 11070 NP_000915.1 3 1090 GGGCTCAGGGCT --- -- 3 C c c
GCTGCCTTCCTG GAT GAGGCAGCA CTTGGG
TCCT CTG TTCCGTCGT GGACTC
TCC CG
GAM8358 255 PDGFRB 1 1574 NP_002600.1 3 541 GCCTTGAGCAGT TGG 3 C c
c
GTTGCCTCATCC GATGAGGCAGCACT
AGAA CTACTCCGTTGTGA
CGA
GAM8358 255 PEG10 1 15770 NP_055883.1 3 64 TCCCCACAAGAT G - - 3 C b b
GATGCCTCATCT GATGAGGCA CA CTTG GG
CCAC CTACTCCGT GT GAAC CC
A A A
GAM8358 255 PET112L 1 6659 NP_004555.1 3 113 TGTGCCCTGAGA T A TG 3 C c
c
GCTGCCTCTCAA GA GAGGCAGC CT GG
TCCC CT CTCCGTCG GA CC
- A GT
GAM8358 255 PHF1 1 13506 NP_002627.1 3 17 CCCCCACTCGAT C 3 C b b
GCTGCCTCATCT GATGAGGCAGCA TTGGG
TCCT CTACTCCGTCGT AGCTC
-
GAM8358 255 PI4KII 1 17573 NP_060895.1 3 1263 GTCTTTTCCCCT - CTT 3 C c c
GCTGCCTCACTC GA TGAGGCAGCA GGG
CCCA CT ACTCCGTCGT CCC
C C--
GAM8358 255 PILRB 2 5463 NP_038468.3 5 671 TCATCCTAAAGT T - - 3 C c c
GCTGGCCTCTCA GA GAGGC AGCACTT GGG
TTCC CT CTCCG TCGTGAA TCC
- G A
GAM8358 255 PILRB 2 5463 NP_778212.2 5 739 TCATCCTAAAGT T - - 3 C c c
GCTGGCCTCTCA GA GAGGC AGCACTT GGG
TTCC CT CTCCG TCGTGAA TCC
- G A
GAM8358 255 PILRB 2 15545 NP_038468.3 5 334 AGGGTCCCAAGT GGCAG 3 C c
c
GGTACATCGTCA GATGA CACTTGGG
TAGC CTGCT GTGAACCC
ACATG

GAM8358 255 PILRB 2 15545 NP_778212.2 5 334 AGGGTCCCAAGT GGCAG 3 C c c

GGTACATCGTCA GATGA CACTTGGG
TAGC CTGCT GTGAACCC
ACATG

GAM8358 255 PIM2 1 584 NP_006866.1 3 558 GTTATCCCAAGT GC 3 C b b

GCTCTTATTCTG GATGAG AGCACTTGGG
GTGA TTATTC TCGTGAACCC
--

GAM8358 255 PIP5K2C 1 13606 NP_079055.2 3 294 TCTCTCCCAAGT G CA 3 C c c

GCCTTGATCTTT GAT AGG GCACTTGGG
GTAA CTA TTC CGTGAACCC
G --

GAM8358 255 PLAGL1 1 2458 NP_006709.2 5 2098 CAGGCCCACGAT T CT- 3 C c c

GCTGCCTCTCCC GA GAGGCAGCA TGGG
GTGG CT CTCCGTCGT ACCC
- AGC

GAM8358 255 PML 2 1247 NP_150242.1 3 71 CCCGGCCCCTGA T ACTT 3 C c c

GCTGCCTCCTCC GA GAGGCAGC GGG
AGCC CT CTCCGTCG CCC
C AGT-

GAM8358 255 PML 2 1247 NP_150243.1 3 1366 CCCGGCCCCTGA T ACTT 3 C c c

GCTGCCTCCTCC GA GAGGCAGC GGG
AGCC CT CTCCGTCG CCC
C AGT-

GAM8358 255 PML 2 1247 NP_150245.1 3 71 CCCGGCCCCTGA T ACTT 3 C c c

GCTGCCTCCTCC GA GAGGCAGC GGG
AGCC CT CTCCGTCG CCC
C AGT-

GAM8358 255 PML 2 1247 NP_150247.1 3 961 CCCGGCCCCTGA T ACTT 3 C c c

GCTGCCTCCTCC GA GAGGCAGC GGG
AGCC CT CTCCGTCG CCC
C AGT-

GAM8358 255 PML 2 1247 NP_150248.1 3 1351 CCCGGCCCCTGA T ACTT 3 C c c

GCTGCCTCCTCC GA GAGGCAGC GGG
AGCC CT CTCCGTCG CCC
C AGT-

GAM8358 255 PML 2 1247 NP_150253.1 3 71 CCCGGCCCCTGA T ACTT 3 C c c

GCTGCCTCCTCC GA GAGGCAGC GGG
AGCC CT CTCCGTCG CCC
C AGT-

GAM8358 255 PML 2 2434 NP_150241.1 3 577 TTTCATCCCAGA AGCA - 3 C c c

GGGGCCTCATCA GATGAGGC CT TGGG
GCAA CTACTCCG GA ACCC
GG-- G

GAM8358 255 POLM 1 13657 NP_037416.1 3 224 GAGCCCTCAGTG A- T- 3 C c c

CCAGCCTCATCA GATGAGGC GCACT GGG
CTGT CTACTCCG CGTGA CCC
AC CT
GAM8358 255 POLQ 1 2177 NP_006587.2 3 379 GAAAATGAAGCT - - GG 3 C c c
GCTGCCTCAATC GAT GAGGCAGCA CTT
GACC CTA CTCCGTCGT GAA
A C GT
GAM8358 255 POLR3D 1 5565 NP_001713.1 3 55 TGTGCCCACGCT TG CT- 3 C c
c
GCTGCCTGCTCC GA AGGCAGCA TGGG
AGAC CT TCCGTCGT ACCC
CG CGC
GAM8358 255 PPIL2 1 13963 NP_680480.1 3 117 TGGATGCTGGGT AG TG 3 C c c
GGCGCCTCATCT GATGAGGC CACT G
GCAT CTACTCCG GTGG C
CG GT
GAM8358 255 PPM1E 1 5899 NP_055721.3 3 3379 TGTGGTTCAAGT ---- C 3 C c c
GCTTCCTTCCCC GATG AGG AGCACTTGGG
ATCA CTAC TCC TCGTGAACTT
CCCT T
GAM8358 255 PPP1R3D 1 5493 NP_006233.1 5 197 TCGTCTCTCATC CACT 3 C c
c
CCTGCCTCATCT GATGAGGCAG TGGG
TCCG CTACTCCGTC ACTC
CCT-
GAM8358 255 PPP3R1 1 3148 NP_000936.1 3 1522 CTTCAACTGAGT AG TG 3 C c
c
GCTGCACATCAT GATG GCAGCACT G
GGGC CTAC CGTCGTGA C
A- GT
GAM8358 255 PRCC 1 9455 NP_005964.2 5 166 CCCGGTCTCAAG AGC 3 C c c
TAGGCCTCATCT GATGAGGC ACTTGGG
GCCG CTACTCCG TGAACTC
GA-
GAM8358 255 PRDM7 1 4427 NP_443722.1 3 340 TGAACCCCAAGT CA- 3 C c c
GTGTACCTCATT GATGAGG GCACTTGGG
CTTC TTACTCC TGTGAACCC
ATG
GAM8358 255 PRDM9 1 4427 NP_064612.1 3 345 TGAACCCCAAGT CA- 3 C c c
GTGTACCTCATT GATGAGG GCACTTGGG
CTTC TTACTCC TGTGAACCC
ATG
GAM8358 255 PRKRIR 1 2605 NP_004696.2 3 765 TGACTCTTATAT CACT 3 C c c
ACTGCCTCATCT GATGAGGCAG TGGG
TGAT CTACTCCGTC ATTC
ATAT
GAM8358 255 PRO0461 1 7800 NP_112558.1 5 1601 ACCGTGTTCAGT - ----- 3 C c c
GCTGCTTCACTC GA TGAGGCAGCACT TGG
TACC CT ACTTCGTCGTGA GCC
C CTTGT

GAM8358 255 PRO0650 1 12955 NP_054856.1 5 1174 CCATGTCCAAGT - - 3 C b b
GCTGTGCTCAGT GA TGAG GCAGCACTTGGG
CTC CT ACTC TGTCGTGAACCT
G G
GAM8358 255 PSMA5 1 11290 NP_002781.2 5 55 CCCCGCGTAGCC T ---- T 3 C c c
GCTGCCTCCTCC GA GAGGCAGC AC TGGG
TACC CT CTCCGTCG TG GCCC
C CCGA C
GAM8358 255 PTDSS2 1 14935 NP_110410.1 3 182 GGAGGCCCCAGC A-- ACT 3 C c
c
ACAGCCTCATCT GATGAGGC GC TGGG
CCAT CTACTCCG CG ACCC
ACA ---
GAM8358 255 PTGIS 1 3522 NP_000952.1 3 2257 TGGCAACCCTCA ACTT 3 C c c
GCTGCCTCATCG GATGAGGCAGC GGG
TGGC CTACTCCGTCG CCC
ACT-
GAM8358 255 PYGM 1 6017 NP_005600.1 5 585 GGCGGCCCAAGT T C- --- 3 C c c
GGAGCTCACCTC GA GAGG AGC ACTTGGG
TCCC CT CTCC TCG TGAACCC
- AC AGG
GAM8358 255 RAB2B 1 19612 NP_116235.2 3 1125 ACAGTGCCTAGT G T 3 C c c
GCTGCTCATTAT GATGAG CAGCACT GG
GTGT TTACTC GTCGTGA CC
- T
GAM8358 255 RAB36 1 8203 NP_004905.1 3 887 CCTGTGCCCACT T CT 3 C c c
GCTGCCTCTCCA GA GAGGCAGCA TGGG
TCCC CT CTCCGTCGT ACCC
- C-
GAM8358 255 RAE1 1 12024 NP_003601.1 3 59 GTTTCTCTCCAC CACT 3 C c c
TCTGCCTCATCT GATGAGGCAG TGGG
CTGT CTACTCCGTC ACCT
TC--
GAM8358 255 RAG2 1 15119 NP_000527.1 5 59 TCTTCCCCAAGT GAGG 3 C c c
GCTGACAATTAA GAT CAGCACTTGGG
TACC TTA GTCGTGAACCC
ACA-
GAM8358 255 RALGPS1 2 3361 NP_055451.1 3 2414 TGGGAGTTAAGT G 3 C c c
A GCTGCTTGTCTT GAT AGGCAGCACTTGG
CCCA CTG TTCGTCGTGAATT
-
GAM8358 255 RALGPS1 2 12537 NP_055451.1 3 3367 GCACTAGCAAGT ATG G 3 C c
c
A GCTGCCTATGCT G AGGCAGCACTTG
GAGA C TCCGTCGTGAAC
GTA G
GAM8358 255 RASSF2 1 11773 NP_055552.1 3 1157 CATTCCAAGAAT AG -- 3 C c c
GAAGCCTCATCT GATGAGGC CA CTTGGG
TGCT CTACTCCG GT GAACCT

```
                                                AA  AA
GAM8358  255   RASSF2  1   11773  NP_739579.1  3  1383   CATTCCAAGAAT      AG --          3  C  c  c

                                    GAAGCCTCATCT GATGAGGC  CA  CTTGGG
                                    TGCT       CTACTCCG  GT  GAACCT
                                                AA  AA
GAM8358  255   RASSF2  1   11773  NP_739580.1  3  1157   CATTCCAAGAAT      AG --          3  C  c  c

                                    GAAGCCTCATCT GATGAGGC  CA  CTTGGG
                                    TGCT       CTACTCCG  GT  GAACCT
                                                AA  AA
GAM8358  255   RBM7    1   8778   NP_057174.1  3  818    AAGCCTTTAAGT   -       --        3  C  c  c
                                    GCTGCTTCTGTC GAT GAGGCAGCACTT  GGG
                                    AGTC       CTG CTTCGTCGTGAA  TCC
                                                T         TT
GAM8358  255   RDH5    1   5992   NP_002896.1  5  110    TCCAGCTATGTG  T     - T         3  C  c  c
                                    GCTGCCTCTTCT GA GAGGCAGC AC TGG
                                    GCTG       CT CTCCGTCG TG ATC
                                                T      G  T
GAM8358  255   RGS11   1   11687  NP_003825.1  3  801    CATCCCCCAAGT  A    AGC           3  C  c
c
                                    GCCTCACCAGTC G TGAGGC   ACTTGGG
                                    CCCC       C ACTCCG   TGAACCC
                                                C     ---
GAM8358  255   RING1   1   14960  NP_002922.1  3  218    ACGCCCCCATCT  T      CT          3  C  c  c
                                    GCTGCCTTTTCT GA GAGGCAGCA  TGGG
                                    ATTG       CT TTCCGTCGT  ACCC
                                                T       CT
GAM8358  255   RIPK1   1   13476  NP_003795.1  3  266    GCCTTCCAAAGT   AGG     -         3  C  c  c
                                    GCTGGGATATCA GATG   CAGCACTT GGG
                                    GGCA       CTAT   GTCGTGAA CCT
                                                AGG      A
GAM8358  255   RNASE1  1   1512   NP_002924.1  3  66     ATCCTCTCCACA  T     ACT           3  C  c  c
                                    GCTGCCTCTTCC GA GAGGCAGC   TGGG
                                    CTCT       CT CTCCGTCG   ACCT
                                                T      AC-
GAM8358  255   RNF38   1   2759   NP_073618.2  3  1309   GATGGATCAAGT G   -----          3  C  c  c
                                    GCTGTTACAGCT  ATGAG    GCAGCACTTGG
                                    CATG       TACTC    TGTCGTGAACT
                                                G    GACAT
GAM8358  255   RNPC4   1   18636  NP_060577.2  5  62     TGTACCTGCAGT  T       -         3  C  c  c
                                    GCTGCTTTTCTT GA GAGGCAGCACT TGGG
                                    GCCT       CT TTTCGTCGTGA GTCC
                                                -        C
GAM8358  255   RODH    1   19289  NP_003716.2  5  19     AGGAAGCCGACT   G     C           3  C  c  c
                                    GCTGCCTGGTCT GAT AGGCAGCA TTGG
                                    GCAA       CTG TCCGTCGT AGCC
                                                G       C
GAM8358  255   RP4-622 1   17249  NP_061991.2  3  1193   TCCTCCCTCCTT  T      CTT-         3  C  c
c
```

```
          L5                          GCTGCCTCTTCC GA GAGGCAGCA    GGG
                                      CACC       CT CTCCGTCGT    CCC
                                               T       TCCT
GAM8358  255   S100A15 1   13112  NP_789793.1  3  1525   TCCCAGCCCCCT  T      C----          3  C  c
c
                                      GCTGCCTTCTCT GA GAGGCAGCA    TTGGG
                                      ATGC       CT TTCCGTCGT    GACCC
                                               C       CCCCC
GAM8358  255   SARM1   1   7757   NP_055892.1  3  3035   GCCAGCCCTCGT  --       TT          3  C  c  c
                                      GCTGCCTCTGGT GAT  GAGGCAGCAC  GGG
                                      CCCT       CTG  CTCCGTCGTG  CCC
                                               GT       CT
GAM8358  255   SBZF3   1   9443   XP_300732.1  5  6    GGGTTCCCGTCT  T      CT           3  C  c  c
                                      GCTGCCTCTCGG GA GAGGCAGCA  TGGG
                                      AGAG       CT CTCCGTCGT  GCCC
                                               -       CT
GAM8358  255   SEC14L1 1   13770  NP_002994.1  3  450   CGCTTCCCCCAA G-----       AC          3  C  c
c
                                      GCTGCCTCATGG     ATGAGGCAGC  TTGGG
                                      CCCG           TACTCCGTCG  AACCC
                                               GCCCGG       --
GAM8358  255   SERPINB 1   11491  NP_004559.3  3  92    TGCAACCCAAGT      AG            3  C  b  b
          6                           GGCCTTATCCGT GATGAGGC  CACTTGGG
                                      GCAG       CTATTCCG  GTGAACCC
                                                --
GAM8358  255   SH3BGRL 1   16703  NP_003013.1  3  410   TCTCATTCCTAA       GC            3  C  b  b

                                      GTTGCCTCATTA GATGAGGCA  ACTTGGG
                                      ATTT       TTACTCCGT  TGAATCC
                                                --
GAM8358  255   SH3KBP1 1   15834  NP_114098.1  3  485   TTCAGGCTAAGA  -      A           3  C  c  c
                                      GCTGCCTCGCTC GA TGAGGCAGC CTTGG
                                      TTTG       CT GCTCCGTCG GAATC
                                               C       A
GAM8358  255   SLC25A1 1   6324   NP_036272.2  3  452   GCTCACCCAAGT GA-- - - -          3  C  c  c

          0                           GCTAGCTCTGCA    TG AG GC AGCACTTGGG
                                      CTTC         AC TC CG TCGTGAACCC
                                               CTTC  G  T  A
GAM8358  255   SLC25A1 1   14932  NP_055067.1  3  820   TCACTACTTAAG      AGC           3  C  c  c

          5                           TTAGCCTCATCA GATGAGGC   ACTTGGG
                                      TTTT       CTACTCCG   TGAATTC
                                                AT-
GAM8358  255   SLC39A3 1   11947  NP_653165.1  3  2047   AGCTCCCGTGCA       ---   TT          3  C  c
c
                                      TCTGCCTCATCT GATGAGGCA   GCAC  GGG
                                      CTCC       CTACTCCGT   CGTG  CCC
                                                CTA   --
GAM8358  255   SLC6A8  1   17130  NP_005620.1  3  294   CCCACCCACAGT  T  -     -          3  C  b  b
```

GCTGCACTCCTC GA GAG GCAGCACT TGGG
CTGC CT CTC CGTCGTGA ACCC
C A C
GAM8358 255 SMARCD2 1 7747 NP_003068.2 3 653 GGATGCCAGAGG T A - 3 C c c
GCTGCCTCTCCA GA GAGGCAGC CT TGG
GCGG CT CTCCGTCG GA ACC
- G G
GAM8358 255 SMCR7 1 6215 NP_631901.2 3 936 CCCCTCCCAAGT T CAG 3 C c c
GACCCTCCTCCT GA GAGG CACTTGGG
GCCT CT CTCC GTGAACCC
C CA-
GAM8358 255 SMCR7 1 6215 NP_683684.1 3 936 CCCCTCCCAAGT T CAG 3 C c c
GACCCTCCTCCT GA GAGG CACTTGGG
GCCT CT CTCC GTGAACCC
C CA-
GAM8358 255 SMP3 1 2105 NP_079439.2 3 137 ATGACTCCCACT T CT 3 C c c
GCTGCCTCTCCT GA GAGGCAGCA TGGG
GGGC CT CTCCGTCGT ACCC
- C-
GAM8358 255 SOX12 1 2490 NP_008874.2 3 2628 TGGCTTCGGGGT T G 3 C c c
GCTGCCTCTCCC GA GAGGCAGCACTT GG
TCCC CT CTCCGTCGTGGG CT
- G
GAM8358 255 SP3 1 18359 XP_092672.2 5 565 CAGATTCCAAGT TGA 3 C c c
GCTGCTACTTCA GA GGCAGCACTTGGG
AGTG CT TCGTCGTGAACCT
TCA
GAM8358 255 SPN 1 15664 NP_003114.1 5 26 CCTGGCCCCAGT --- T 3 C c c
GCTGCGTCCTTA GATGAG GCAGCACT GGG
TCAG CTATTC CGTCGTGA CCC
CTG C
GAM8358 255 SPTBN4 1 14455 NP_079489.1 3 500 CTCACTTCCAAT - C 3 C c c
GCTGCCTTGATC GAT GAGGCAGCA TTGGG
TCTG CTA TTCCGTCGT AACCT
G -
GAM8358 255 SULT1C2 1 17465 NP_006579.2 5 286 GGTGGATAGAGT - GG 3 C c c
GCTGCCTCTATC GAT GAGGCAGCACTT
CACA CTA CTCCGTCGTGAG
T AT
GAM8358 255 SYN3 1 2991 NP_003481.2 3 66 ACTCGTCCCCCT CACTT 3 C c c
CCTGCCTCATCT GATGAGGCAG GGG
TCCT CTACTCCGTC CCC
CT---
GAM8358 255 SYN3 1 2991 NP_598343.1 3 401 ACTCGTCCCCCT CACTT 3 C c c
CCTGCCTCATCT GATGAGGCAG GGG
TCCT CTACTCCGTC CCC

CT---

GAM8358 255 SYN3 1 2991 NP_598344.1 3 182 ACTCGTCCCCCT CACTT 3 C c c

CCTGCCTCATCT GATGAGGCAG GGG

TCCT CTACTCCGTC CCC

CT---

GAM8358 255 TARBP2 1 15955 NP_599150.1 5 75 CCGTGCCCAAGT A CAG 3 C c c

GAGTCCTTACCG G TGAGG CACTTGGG

CCTC C ATTCC GTGAACCC

C TGA

GAM8358 255 TARBP2 1 15955 NP_599151.1 5 75 CCGTGCCCAAGT A CAG 3 C c c

GAGTCCTTACCG G TGAGG CACTTGGG

CCTC C ATTCC GTGAACCC

C TGA

GAM8358 255 TBL2 1 4498 NP_116783.1 3 613 GAAGGGTCAAGT -- 3 C b b

GCTGTCTACCAT GATG AGGCAGCACTTGG

CAAC CTAC TCTGTCGTGAACT

CA

GAM8358 255 TCF6L1 1 4205 NP_003192.1 5 103 TGGGGTCGGGTC C- 3 C c c

ACTGCCTCATCC GATGAGGCAG ACTTGG

ACCG CTACTCCGTC TGGGCT

AC

GAM8358 255 TCOF1 1 12390 NP_000347.1 3 389 CTAGGCCTGACC G C- TG 3 C c c

TGTGCCTCATCC GATGAGGCA CA T GG

CGTG CTACTCCGT GT A CC

- CC GT

GAM8358 255 TIAF1 1 16620 NP_004731.2 3 227 GGGAGCCCAAGT G--- G -- 3 C c c

GCAGTGCCTGGT AT AGGCA GCACTTGGG

GCTG TG TCCGT CGTGAACCC

GTCG G GA

GAM8358 255 TIAF1 1 16620 NP_510880.2 3 1145 GGGAGCCCAAGT G--- G -- 3 C c c

GCAGTGCCTGGT AT AGGCA GCACTTGGG

GCTG TG TCCGT CGTGAACCC

GTCG G GA

GAM8358 255 TITF1 1 11075 NP_003308.1 3 46 CTAGCCCAGCGC A CAC- 3 C c c

TCTGCCTCACCG G TGAGGCAG TTGGG

CTTC C ACTCCGTC GACCC

C TCGC

GAM8358 255 TK2 1 9571 NP_004605.1 3 526 CCCTTGCCCTGG T A T 3 C c c

GCTGCCTCCTCC GA GAGGCAGC CT GGG

TGAG CT CTCCGTCG GG CCC

C - T

GAM8358 255 TLN1 1 2014 NP_006280.2 3 199 CCAACCCCAAGT G------- CA 3 C c c

GCCTTCATGCCC ATGAGG GCACTTGGG

TAGG TACTTC CGTGAACCC

GGATCCCG --

GAM8358 255 TNRC4 1 3329 NP_009116.2 3 597 GGAGCCCTGAGG T A TG 3 C c c

GCTGCCTCTCTG GA GAGGCAGC CT GG
CCAG CT CTCCGTCG GA CC
- G GT
GAM8358 255 TP53I5 1 19129 XP_290532.2 5 1436 GGAGCCCCCAGC A-- ACT 3 C c c
c
CCAGCCTCATCC GATGAGGC GC TGGG
TGGA CTACTCCG CG ACCC
ACC ---
GAM8358 255 TRAF5 1 12305 NP_004610.1 3 168 AACTTCTGAAGT T G 3 C c c
GCTGTCTTTTTA GA GAGGCAGCACTT GG
CATT TT TTCTGTCGTGAA TC
T G
GAM8358 255 TRAF5 1 12305 NP_665702.1 3 168 AACTTCTGAAGT T G 3 C c c
GCTGTCTTTTTA GA GAGGCAGCACTT GG
CATT TT TTCTGTCGTGAA TC
T G
GAM8358 255 TRAM2 1 5325 NP_036420.1 3 4177 TCCCCAGTGAAA ---- T 3 C c c
GCTGCCTCATTC GATGAGGCAGC ACT GGG
TTTT TTACTCCGTCG TGA CCC
AAAG C
GAM8358 255 TRIM29 1 673 NP_036233.2 3 932 GCCCCATCAGAG T A- -- 3 C c c
GCTGCCTCCTCC GA GAGGCAGC CT TGGG
TTCT CT CTCCGTCG GA ACCC
C GA CT
GAM8358 255 TRIM47 1 3214 XP_290731.1 3 59 CTGCTCCAGGAA T A- 3 C c c
GCTGCCTCCTCT GA GAGGCAGC CTTGGG
GGGC CT CTCCGTCG GGACCT
C AA
GAM8358 255 UBE2Q 1 13750 NP_060052.3 3 1294 CATCTAGCGGGT - G 3 C c c
GCTGCCTGCATC GATG AGGCAGCACTTG
TCTT CTAC TCCGTCGTGGGC
G G
GAM8358 255 USH1G 2 4086 NP_775748.1 3 1846 AGAGCCCCAGGT TGA 3 C c
c
GCTGCCCCTTCT GA GGCAGCACTTGGG
CTCC CT CCGTCGTGGACCC
TCC
GAM8358 255 USH1G 2 12873 NP_775748.1 3 1817 CCACCCCCAAGT T ----- 3 C c c
GCCGACTTGTTT GA GAGGCA GCACTTGGG
CTCC CT CTTTGT CGTGAACCC
- TCAGC
GAM8358 255 VANGL2 1 17930 XP_049695.4 3 1027 CTCCAGAGACCT --- G 3 C c c
GTTGCCTCATCT GATGAGGCAGCA CTT GG
CTTT CTACTCCGTTGT GAG CC
CCA A
GAM8358 255 VAT1 1 7020 NP_006364.2 3 603 TTCTTAACCAAG T A 3 C b b
GCTGCCTCTTCC GA GAGGCAGC CTTGG
AACA CT CTCCGTCG GAACC
T -
GAM8358 255 VWF 1 13033 NP_000543.1 3 79 CCAGGCCAGAGT GA - 3 C c c

GCTGCCAGTCCT GAT GGCAGCACT TGG
CTGC CTG CCGTCGTGA ACC
A- G

GAM8358 255 WDR22 1 16841 XP_031102.1 3 249 AATAACCCAAGT T C - 3 C c c
GACTCCTTTCTA GA GAGG AG CACTTGGG
GTGA CT TTCC TC GTGAACCC
- - A

GAM8358 255 WDR7 1 570 NP_056100.1 3 414 CACCTCTGAAGT G- G 3 C c c
GCTGCTTGAATC GAT AGGCAGCACTT GG
TGGC CTA TTCGTCGTGAA TC
AG G

GAM8358 255 WDR7 1 570 NP_443066.1 3 414 CACCTCTGAAGT G- G 3 C c c
GCTGCTTGAATC GAT AGGCAGCACTT GG
TGGC CTA TTCGTCGTGAA TC
AG G

GAM8358 255 WDR9 1 15650 NP_061836.2 3 825 AAATGCCAAAAA G C-- 3 C c c
TGTGCCTCATTA GATGAGGCA CA TTGG
AGAG TTACTCCGT GT AACC
- AAA

GAM8358 255 WFS1 1 6581 NP_005996.1 3 601 TGGGCACCACAG G----- A - 3 C c c
GCTGCCTCATGA ATGAGGCAGC CT TGG
CCCT TACTCCGTCG GA ACC
TCCCAG - C

GAM8358 255 WHN 1 18123 NP_003584.2 3 191 ATCACCTGGGGT T - TG 3 C c c
GCTGCCTCTCAC GA GAGGCAGCAC T GG
ACAT CT CTCCGTCGTG G CC
- G GT

GAM8358 255 WHSC1L1 1 1808 NP_060248.2 3 824 TATGTTCCAAGT - - C 3 C c c
GCTACTCTCACT GA TGAG G AGCACTTGGG
CAGC CT ACTC C TCGTGAACCT
C T A

GAM8358 255 WSB2 1 17131 NP_061109.1 3 510 TGTTGGCCAAGT T C 3 C c c
GCTTTTCTTCTT GA GAGG AGCACTTGG
GGGC CT CTTT TCGTGAACC
T -

GAM8358 255 YWHAB 1 8275 NP_003395.1 3 519 GGTCTCCCAAGT GCA 3 C b b

GCACTCATCCAG GATGAG GCACTTGGG
GTCA CTACTC CGTGAACCC
A--

GAM8358 255 YWHAB 1 8275 NP_003395.1 3 1517 GGTCTCCCAAGT GCA 3 C b
b

GCACTCATCCAG GATGAG GCACTTGGG
GTCA CTACTC CGTGAACCC
A--

GAM8358 255 YWHAB 1 8275 NP_647539.1 3 1517 GGTCTCCCAAGT GCA 3 C b
b

GCACTCATCCAG GATGAG GCACTTGGG
GTCA CTACTC CGTGAACCC
A--

GAM8358 255 ZDHHC14 1 11339 NP_078906.2 3 566 GAATTTTCAAGT TG 3 C c c
GCTGTTTTGTTG GA AGGCAGCACTTGGG
GAAG TT TTTGTCGTGAACTT
GT
GAM8358 255 ZDHHC14 1 11339 NP_714968.1 3 566 GAATTTTCAAGT TG 3 C c c
GCTGTTTTGTTG GA AGGCAGCACTTGGG
GAAG TT TTTGTCGTGAACTT
GT
GAM8358 255 ZNF302 1 15235 NP_060913.1 3 741 CCAGTTCCAAGT CA- 3 C c c
GCATCCCTTATT GATGAGG GCACTTGGG
CTAT TTATTCC CGTGAACCT
CTA
GAM8358 255 ZNF302 1 15235 NP_061145.1 3 778 CCAGTTCCAAGT CA- 3 C c c
GCATCCCTTATT GATGAGG GCACTTGGG
CTAT TTATTCC CGTGAACCT
CTA
GAM8358 255 ZNF313 1 13901 NP_061153.1 3 1343 GGGGCTGCAAGT A C G 3 C c
c
GCTACCTCGCGC G TGAGG AGCACTTG
TTGT C GCTCC TCGTGAAC
- A G
GAM8554 388 ABL1 1 4735 NP_005148.1 3 259 TATCTGTGGAGT G TGG-- 3 B c c
TCCTGCTCCGTG TTCATGG AGCAGG TACAG
GACTGCAG AGGTGCC TCGTCC GTGTC
- TTGAG
GAM8554 388 ABL1 1 4735 NP_009297.1 3 259 TATCTGTGGAGT G TGG-- 3 B c c
TCCTGCTCCGTG TTCATGG AGCAGG TACAG
GACTGCAG AGGTGCC TCGTCC GTGTC
- TTGAG
GAM8554 388 AFG3L1 1 4913 NP_001123.1 3 4 CTTTAAGGTCCA - A T A 3 B c c
CCTGCGCCCACT TTCA TGGG GCAGGTGG AC
GAGCTGGA GAGT ACCC CGTCCACC TG
C G - G
GAM8554 388 ALDH4A1 1 4955 NP_003739.2 3 1298 TCCAGGATATGT CAG GT 3 B c
c
GTCATTTCCCAT TTCATGGGAG GTG ACA
GAGGGGCC GAGTACCCTT TAC TGT
--- TG
GAM8554 388 ALDH4A1 1 4955 NP_733844.1 3 285 TCCAGGATATGT CAG GT 3 B c
c
GTCATTTCCCAT TTCATGGGAG GTG ACA
GAGGGGCC GAGTACCCTT TAC TGT
--- TG
GAM8554 388 AP1G1 1 18932 NP_001119.2 3 110 CCCAACTGTACC GGGA AG 3 B c
c
ACGGGCATGAGG TTCAT GC GTGGTACAG
AGCTGAAG GAGTA CG CACCATGTC
---- GG
GAM8554 388 AP1M1 1 7039 NP_115882.1 3 660 ACTGTAGCGTCT T TG ---- 3 B c c
GCCTGCTCCCTG TTCA GGGAGCAGG G TACAG

GACTCGCA AGGT CCCTCGTCC C ATGTC
- GT TGCG

GAM8554 388 APRG1 1 9637 NP_848028.1 5 944 CACAGCTGTACC - A AG- 3 B c c
ACATGGCCCACG TTCATG GG GC GTGGTACAG
TGAAATCT AAGTGC CC CG CACCATGTC
A - GTA

GAM8554 388 APRG1 1 9637 NP_848029.1 5 944 CACAGCTGTACC - A AG- 3 B c c
ACATGGCCCACG TTCATG GG GC GTGGTACAG
TGAAATCT AAGTGC CC CG CACCATGTC
A - GTA

GAM8554 388 APRG1 1 9637 NP_848032.1 5 535 CACAGCTGTACC - A AG- 3 B c c
ACATGGCCCACG TTCATG GG GC GTGGTACAG
TGAAATCT AAGTGC CC CG CACCATGTC
A - GTA

GAM8554 388 ARH 1 18536 NP_056442.1 3 781 TAACTGGCTGCT A TG -- 3 B c c
CCCTGCTCCCAG TTC TGGGAGCAGG GTA CAG
GGACTGAC AGG ACCCTCGTCC CGT GTC
G CT CG

GAM8554 388 ARL2 1 9268 NP_001658.1 3 169 GCTCTGTGGCCA T----- A- - 3 B c c
CCCGGCTCCCAT TCATGGGAGC GGTGGT ACAG
GGCGGGAG GGTACCCTCG CCACCG TGTC
GAGGGC GC G

GAM8554 388 ARPC3 1 10193 NP_005710.1 5 50 GCTGTACCTGGA T T---- 3 B c c
TCCTGCTCCTCT TTCA GGGAGCAGG GGTACAG
GGGTTGAA GGGT TCCTCGTCC CCATGTC
C TAGGT

GAM8554 388 ASF1B 1 4386 NP_060624.1 3 516 ATCCCATTTCTG A TGGT 3 B c c
TCCTGCTCCCAG TTC TGGGAGCAGG ACAG
GAAGATTC AAG ACCCTCGTCC TGTC
G ----

GAM8554 388 ATP10A 1 12086 NP_077816.1 3 1765 TTTGGAAGGTGA T G G A 3 B c
c
CACTGCTCCCTG TTCA GGGAGCAG TG TAC
AATTAAGG AAGT CCCTCGTC AC GTG
- - A G

GAM8554 388 ATPIF1 1 19002 NP_835498.1 3 1281 GAGGATGACCAG C-- G A 3 B c
c
CTAGACTCCCAT TTCATGGGAG AG TGGT CA
GGAATTGG AGGTACCCTC TC ACCA GT
AGA G -

GAM8554 388 BACH2 2 17751 NP_068585.1 3 1362 GTGTGCAGTAGG T GG A 3 B c
c
ACCTGCTCCCCT TTCA GGGAGCAGGT TAC
GAAGGACG AAGT CCCTCGTCCA ATG
C GG A

GAM8554 388 BACH2 2 19189 NP_068585.1 3 4975 ACATTCAGTGCC GG A 3 B c c
AAGTGCTCCCAT TTCATGGGAGCA TGGTAC
GGGAATAA GGGTACCCTCGT ACCGTG
GA A

GAM8554 388 BOP 1 3691 XP_097915.2 3 1016 TTAGACTCTATC A AG C 3 B c c
ATGGGCCCCCAT TTCATGGG GC GTGGTA AG
GAAGCTCC AAGTACCC CG TACTAT TC
C GG C
GAM8554 388 C14orf1 1 13492 NP_060100.1 3 1989 GCCTCTGTGACC ATGGG - 3 B c
c
13 ACCTGCTAGAGG TTC AGCAGGTGGT ACAG
GAGATTCT GAG TCGTCCACCA TGTC
GGAGA G
GAM8554 388 C9orf19 1 4682 NP_071738.1 3 1020 CTGCAGCTGTGC T-- T 3 B c c
TCCTGCTCCCTC TTCA GGGAGCAGG GGTACAG
CTGGAATG AGGT CCCTCGTCC TCGTGTC
CCT -
GAM8554 388 C9orf25 1 1932 NP_671735.1 3 1801 ATGTGCTGGTGG CA ----- 3 B c c
ATCCACTCCCAT TTCATGGGAG GGT GGTACA
GGATCCAC AGGTACCCTC CTA TCGTGT
AC GGTGG
GAM8554 388 CA6 1 4909 NP_001206.1 3 134 GTGTCTGGAACA T - GTA 3 B c c
CGCTGCTCCCCT TTCA GGGAGCAG GTG CAG
GGGCAGCT GGGT CCCTCGTC CAC GTC
C G AAG
GAM8554 388 CACNA2D 1 8973 NP_006021.1 3 780 CTCCTGCTCACC --- GA A-- 3 B c
c
2 ACCTGCCTCTAA TTCA TGG GCAGGTGGT CAG
TCTGAGCT GAGT ATC CGTCCACCA GTC
CTA TC CTC
GAM8554 388 CAP350 1 11531 NP_055625.2 3 799 TGAATCTCTACC A G CA 3 B c c
AGCTGCTCCCAG TTC TGGGAGCAG TGGTA
AATCACAG AAG ACCCTCGTC ACCAT
- G CT
GAM8554 388 CASP8 1 14684 NP_203521.1 3 264 TTCATCTGCTGT C TG 3 B c c
ATCCTCTCCCAT TTCATGGGAG AGG GTACAG
GGAGACAA AGGTACCCTC TCC TATGTC
- --
GAM8554 388 CCR7 1 1279 NP_001829.1 3 311 GAAACTGTTCCC GGG T- 3 B c c
ACCTGCTGGAGT TTCAT AGCAGGTGG ACAG
GAAGGGGC AAGTG TCGTCCACC TGTC
AGG CT
GAM8554 388 CHD4 1 2554 NP_001264.1 3 33 CAGACTGATACC - GAGC - 3 B c c
ACCTCCACCGCT TTCA TGG AGGTGGTA CAG
GAGCAGTG GAGT GCC TCCACCAT GTC
C ACC- A
GAM8554 388 CHST2 1 5960 NP_004258.2 3 306 ACCCTGTCCTCC --- - T-- 3 B c c
ACCTGCCTTCCA TTCA TGGGAG CAGGTGG ACAG
TTTTGAAG AAGT ACCTTC GTCCACC TGTC
TTT C TCC
GAM8554 388 CNTF 1 19190 NP_000605.1 3 151 TTTTCTCTGACC - A- A 3 B c c
ACCTGCAGCCTG TTCA TGGG GCAGGTGGT CAG
TTGAAGGA AAGT GTCC CGTCCACCA GTC

T GA -
GAM8554 388 CRAT 1 8044 NP_003994.2 5 64 ATCGCCACTGCC - - CA 3 B c c
ACCTGCCTCCCG TTCA TGGGAG CAGGTGGTA
CTGAATCT AAGT GCCCTC GTCCACCGT
C C CA
GAM8554 388 CRH 1 7497 NP_000747.1 3 89 GTATTCTGTACC TT- ---- 3 B c c
ATAGCGCTGCTC CATGGGAGCAG GTGGTACAG
TTATGCCA GTATTCTCGTC TACCATGTC
ACC GCGA
GAM8554 388 CXCL9 1 548 NP_002407.1 3 1576 ATCAATTACCAC CAG-- CA 3 B c c

ACCATCTCCCAT TTCATGGGAG GTGGTA
GAAGAAAG AAGTACCCTC CACCAT
TACCA TA
GAM8554 388 DAZAP2 1 12754 NP_055579.1 3 1208 TTTGACTGTACC G CA 3 B c
c
ATTGACTGTTAT TTCATGG AG GGTGGTACAG
GGAAGTTC AGGTATT TC TTACCATGTC
G AG
GAM8554 388 DC2 1 4382 NP_067050.1 3 85 AAAGGCTGTACC GG C -- 3 B c c
AATCCTCTAATA TTCATG AG AGG TGGTACAG
TGAAATGT AAGTAT TC TCC ACCATGTC
AA - TA
GAM8554 388 DES 1 17929 NP_001918.2 3 63 CACCCCTGTCCT T GT- T 3 B c c
CACTGCTCCCTG TTCA GGGAGCAG GG ACAG
AAGCCCAG AAGT CCCTCGTC CC TGTC
- ACT -
GAM8554 388 DGUOK 1 2183 NP_550438.1 3 19 AGAATCTGTACC GAGCAGG 3 B c
c
AATACCATGAAG TTCATGG TGGTACAG
TTCAGGCT AAGTACC ACCATGTC
ATA----
GAM8554 388 DGUOK 1 2183 NP_550440.1 3 19 AGAATCTGTACC GAGCAGG 3 B c
c
AATACCATGAAG TTCATGG TGGTACAG
TTCAGGCT AAGTACC ACCATGTC
ATA----
GAM8554 388 DHDDS 1 6851 NP_079163.1 3 1507 CTTGGCTATTGT A GG T 3 B c
c
CCATGCTCCCAG TTC TGGGAGCA TGG ACAG
AATCAAGC AAG ACCCTCGT ACC TGTT
- -- -
GAM8554 388 DHRS1 1 10467 NP_612461.1 5 263 CCTGTGAGTCAT AG-- -- 3 B c c
GGCAGCTCCCAT TTCATGGGAGC GTGG TACAG
GAATGGCC AAGTACCCTCG TACT GTGTC
ACGG GA
GAM8554 388 DKFZP43 1 10822 NP_056227.1 3 102 TCTGGAAGTACC A G -- A 3 B c
c
4F2021 ACCTGGACTCAC TTC TG GAG CAGGTGGTAC
AGAGGAGC GAG AC CTC GTCCACCATG

```
                                        - A  AG       A
GAM8554  388   DKFZP43 1  12087  NP_056307.1  3  948   CTGCTGTGAGCC      GA      --        3  B  c
c
         4H132                          ACCTGCCTGTGG TTCATGG  GCAGGTGGT  ACAG
                                      AGTGCTGA    AGGTGTC  CGTCCACCG  TGTC
                                              --       AG
GAM8554  388   DKFZP43 1  12435  NP_056486.1  5  456   CCTGGATTGCTA      AGC-      ---       3  B  c
c
         4J046                          CTTTACCCCCAT TTCATGGG   AGGTGGTA  CAG
                                      GAAGCCCG    AAGTACCC   TTCATCGT  GTC
                                              CCAT       TAG
GAM8554  388   DKFZP56 1  2580   XP_166254.2  3  4532  GGAGTCTGTACC T--   --      G-        3  B  c
c
         4O0423                          AAGCTGCTTCTG   TCAT  GGGAGCAG  TGGTACAG
                                      GATGACCA      AGTA  TCTTCGTC  ACCATGTC
                                            ACC   GG       GA
GAM8554  388   DKFZP56 1  2609   NP_056278.1  3  212   TGGTGATGTACC   A    GCAG           3  B  c
c
         6K1924                          ACTCCCGAGAAT TTC TGGGA   GTGGTACA
                                      ATTCCCAT    AAG GCCCT   CACCATGT
                                              A    ----
GAM8554  388   DKFZP58 1  8692   NP_056253.2  3  1571  CTCACGCTGTCC     GGGA      T         3  B  c
c
         6I2223                          ACCTGCCAGGTG TTCAT   GCAGGTGG ACAG
                                      GAGTGTAT    AGGTG   CGTCCACC TGTC
                                              GAC-       -
GAM8554  388   DKFZP58 1  8692   NP_542768.1  3  577   CTCACGCTGTCC     GGGA      T         3  B  c
c
         6I2223                          ACCTGCCAGGTG TTCAT   GCAGGTGG ACAG
                                      GAGTGTAT    AGGTG   CGTCCACC TGTC
                                              GAC-       -
GAM8554  388   DKFZP58 1  8692   NP_542769.1  3  577   CTCACGCTGTCC     GGGA      T         3  B  c
c
         6I2223                          ACCTGCCAGGTG TTCAT   GCAGGTGG ACAG
                                      GAGTGTAT    AGGTG   CGTCCACC TGTC
                                              GAC-       -
GAM8554  388   DKFZp76 1  11144  NP_775734.1  3  1500  CCTCTTCTGGGC    T       T  TA        3  B  c
c
         1B107                          CTCTGCTCCCCT TTCA GGGAGCAGG GG  CAG
                                      GGGACCTC    GGGT CCCTCGTCT CC  GTC
                                              C       - GG
GAM8554  388   DKFZp76 1  14901  XP_044062.3  3  966   CCCACCTGGACC   AT-  AG      A         3  B  c
c
         1O2018                          ACCTGACCCCTC TTC   GGG  CAGGTGGT CAG
                                      GGGATTCC    AGG   CCC  GTCCACCA GTC
                                              GCT   CA       G
GAM8554  388   DKFZP76 1  19658  NP_067047.2  3  105   AAGTGTACCTTC T-----  G       ---       3  B  c  c

         2N2316                          ACCTGCTCCAGT      TCAT GGAGCAGGT   GGTACA
                                      GATGAGAG         AGTG CCTCGTCCA   CCATGT
```

GAGAGT A CTT

GAM8554 388 EIF4G1 1 7541 NP_004944.1 3 405 AGCCCCTGTACC T G ----- 3 B c c
ACCCCTGCTGTT TTCA GG AGCA GGTGGTACAG
GCCTGGGC GGGT CC TTGT CCACCATGTC
- G CGTCC

GAM8554 388 ENTPD6 1 12576 NP_001238.1 5 67 AGACCGGCTGCC AT CA 3 B c c
GCCTGCTCCCCG TTC GGGAGCAGGTGGTA
GAAAAGGG AAG CCCTCGTCCGCCGT
GC CG

GAM8554 388 ERK8 1 15517 NP_620590.1 3 1146 CGGCACTGGGCC T-- A TA 3 B c c
ACCTGCCCCTGC TTCA GGG GCAGGTGG CAG
TGGAGGGG AGGT CCC CGTCCACC GTC
CGT - GG

GAM8554 388 EVI5 1 5538 NP_005656.2 3 1046 TAAATCTGTACC - GGAGC 3 B c c
ACCTAACATTGA TTCA TG AGGTGGTACAG
ACATCATT AAGT AC TCCACCATGTC
T AA---

GAM8554 388 FAM10A3 1 874 XP_015334.4 5 186 GGGTAAAGTACC A - A 3 B c c
ACCTGCTACTCA TTC TGGG AGCAGGTGGTAC
GAAAGCTA AAG ACTC TCGTCCACCATG
- A A

GAM8554 388 FBXO16 1 9967 NP_758954.1 3 243 GAGCTGAATTTA -- - TA- 3 B c c
CTTGGCTCCCAT TTC ATGGGAGC AGGTGG CAG
TAGAAACT AAG TACCCTCG TTCATT GTC
AT G TAA

GAM8554 388 FLJ0000 1 4850 NP_258260.1 3 1863 AGCACCTGCCCC A - A TA 3 B c c
7 ACCTGCCCACAG TTC TG GG GCAGGTGG CAG
AGAACACA GAG AC CC CGTCCACC GTC
- A - CC

GAM8554 388 FLJ1130 1 18187 NP_060855.1 3 1251 GCTTCCTGTACC G-- C 3 B c c
1 ATCTACTGGACC TTCATGG AG AGGTGGTACAG
GTGAGCCA GAGTGCC TC TCTACCATGTC
AGG A

GAM8554 388 FLJ1289 1 18925 NP_076415.2 5 301 GGTTCTGGCACC - AG A- 3 B c c
5 ACCTGAGCCCAC TTCA TGGG CAGGTGGT CAG
TGGGCATC GGGT ACCC GTCCACCA GTC
C GA CG

GAM8554 388 FLJ1296 1 13088 NP_078914.1 3 61 TGAGCCTGTACC GGA -- 3 B c c
0 ACTGTTGTAACA TTCATG GCA GGTGGTACAG
TGGGAAGA GGGTAC TGT TCACCATGTC
AA- TG

GAM8554 388 FLJ2070 1 16918 NP_060406.1 3 43 GGTTGCCTGGCT GG A 3 B c c
7 ACCTGCTCATGA TTCAT GAGCAGGTGGT CAG
GGGACTTG GAGTA CTCGTCCATCG GTC
-- -

GAM8554 388 FLJ2089 1 12410 NP_078876.1 5 359 CTGCTGCCCACC T --- - - 3 B c c

8 CTCTGCTCCCTG TTCA GGGAGCA GGTGG TA CAG
GGATGGGC GGGT CCCTCGT CCACC GT GTC
- CTC C C
GAM8554 388 FLJ2294 1 10158 NP_079421.2 5 22 GCTGCGTGCGCT -- TG TA 3 B c
c
4 GCCTGCTCCCGC TTCA TGGGAGCAGG G CA
CTGAGGAA GAGT GCCCTCGTCC C GT
CC GT GC
GAM8554 388 FLJ2386 1 13980 NP_689875.1 3 300 GTGCTCTGCACC T T A 3 B c c
7 CCCTGCTCCCTT TTCA GGGAGCAGG GGT CAG
GGGCTGGC GGGT CCCTCGTCC CCA GTC
T C C
GAM8554 388 FLJ2575 1 3815 NP_776175.1 5 84 CTGAACTGTACC CA 3 B c c
6 ACCATTTCTGTG TTCATGGGAG GGTGGTACAG
AGGTGGCA GAGTGTCTTT CCACCATGTC
A-
GAM8554 388 FLJ3093 1 13660 NP_689973.1 3 181 GCCTGTAATACC -- - G 3 B c c
4 ATGTCTTCCCAT TTCATGGGA GCA GGTG TACAG
GAGGGGTC GAGTACCCT TGT CCAT ATGTC
TC A A
GAM8554 388 FLJ3116 1 17040 NP_694567.1 3 1383 AGAGGCCTGACC --- T A 3 B c c

6 CCCTGCTCCTGG TTCA TGGGAGCAGG GGT CAG
CCTGAAAT AAGT GTCCTCGTCC CCA GTC
CCG C -
GAM8554 388 FLJ3131 1 10740 NP_689499.1 3 327 GCCCTGTGAACC - - -- 3 B b b
8 ACCTGCTGCCCT TTCAT GGG AGCAGGTGGT ACAG
GTGAGGCC GAGTG CCC TCGTCCACCA TGTC
T G AG
GAM8554 388 FLJ3282 1 11776 NP_689705.1 5 2 GTGATGCCACCA A -- - 3 B c c
5 CTGCTCCCAGGA TTC TGGGAGCA GGTGGTA CA
GCCCACAG GAG ACCCTCGT CCACCGT GT
G CA A
GAM8554 388 FLJ3593 1 1674 NP_775735.1 3 420 TCTTGTTCCTCT A---- T T 3 B c c
6 GCCATTCCCCAT TTCATGGG GCAGG GG ACAG
GAAGCCGT AAGTACCC CGTCT CC TGTT
CTTAC - T
GAM8554 388 FLJ3849 1 16881 NP_776158.1 3 332 ATTAATTGTACC T -- G 3 B c c
9 ACATGCTAATCC TTCA GGG AGCA GTGGTACAG
TGAAGAGA AAGT CCT TCGT CACCATGTT
- AA A
GAM8554 388 FLJ3910 1 8062 NP_775900.1 3 724 AAACACTTTACA T--- G C 3 B c c
6 ACCTGCTCTCTC TTCA GGGAGCAGGT GTA AG
TCTGAAGT AAGT CTCTCGTCCA CAT TC
CTCT A T
GAM8554 388 FLJ4085 1 1720 NP_775948.1 3 1241 CAGTGTATGTTC T T T 3 B c c
2 TCCTGCTCCCTG TTCA GGGAGCAGG GG ACA
GACAAATC AGGT CCCTCGTCC CT TGT
- T -
GAM8554 388 FOXD4 1 10798 XP_095746.6 5 1 GACTGAAGCACC -- GTA 3 B c c

TGCTCCGCCATG TTCATGG GAGCAGGTG CAG
AACTTGCC AAGTACC CTCGTCCAC GTC
GC GAA

GAM8554 388 FOXD4L1 1 14436 NP_036316.1 5 1 GACTGAAGCACC -- GTA 3 B c c

TGCTCCGCCATG TTCATGG GAGCAGGTG CAG
AACCTGCC AAGTACC CTCGTCCAC GTC
GC GAA

GAM8554 388 FUK 1 16844 NP_659496.1 3 6 CCTCAACCTGTT CA T - 3 B c c

GCCCTTTCCCAT TTCATGGGAG GG GGTA CAG
GAGCTGGC GAGTACCCTT TC CCGT GTC
-- - T

GAM8554 388 FUT3 1 2915 NP_000140.1 3 302 TTACCTGCTGGG A GG - 3 B c c

ACCTGCTCCCAG TTC TGGGAGCAGGT TA CAG
AGACCTTG GAG ACCCTCGTCCA GT GTC
- GG C

GAM8554 388 FUT5 1 2915 NP_002025.1 3 352 TTACCTGCTGGG A GG - 3 B c c

ACCTGCTCCCAG TTC TGGGAGCAGGT TA CAG
AGACCTTG GAG ACCCTCGTCCA GT GTC
- GG C

GAM8554 388 FUT6 1 7499 NP_000141.1 3 369 TTACCTGCTGGG A GG - 3 B c c

ACCTGCTCCCAG TTC TGGGAGCAGGT TA CAG
AGACCTTC GAG ACCCTCGTCCA GT GTC
- GG C

GAM8554 388 FUT9 1 16065 NP_006572.1 5 58 AACAACTGTCTA T----- - G T 3 B c c

CGTGCTTCCCAT TCATGGGA GCA GTGG ACAG
GATATGTT AGTACCCT CGT CATC TGTC
TTGTAT T G -

GAM8554 388 GAB2 1 7231 NP_036428.1 3 3384 CCTCCCTCTGGC C T A 3 B c c

CCCTTCTCCCAT TTCATGGGAG AGG GGT CAG
GGGGACAT GGGTACCCTC TCC CCG GTC
T - -

GAM8554 388 GAB2 1 7231 NP_536739.1 3 3384 CCTCCCTCTGGC C T A 3 B c c

CCCTTCTCCCAT TTCATGGGAG AGG GGT CAG
GGGGACAT GGGTACCCTC TCC CCG GTC
T - -

GAM8554 388 GAS7 1 19750 NP_003635.1 3 691 ATTGAGCGCTGA G GG A 3 B c c

ATCGTGTCCCAT TTCATGGGA CA TGGT CAG
GAGATCAG GAGTACCCT GT GCTA GTC
- -- A

GAM8554 388 GAS7 1 19750 NP_005881.1 3 691 ATTGAGCGCTGA G GG A 3 B c c

ATCGTGTCCCAT TTCATGGGA CA TGGT CAG
GAGATCAG GAGTACCCT GT GCTA GTC
- -- A

GAM8554 388 GOLGA1 1 5615 NP_002068.1 3 905 CTCGCACTCTGG T- G G C 3 B c c

CACTGCTCCCTC TTCA GGGAGCAG TG TA AG
TGAAGTGC AAGT CCCTCGTC AC GT TC

CT - G C

GAM8554 388 GRIN2B 1 10992 NP_000825.1 3 247 GCTGTCAGCCAT -- -- 3 B b b
TCCTGTTCCCAT TTCATGGGAGCAGG TGGT ACAG
GAGATGAT GAGTACCCTTGTCC ACCG TGTC
TT AC

GAM8554 388 GSPT2 1 8094 NP_060564.1 3 227 TTCCTCTGTACC T - 3 B b b
ACTCTGCTTCCT TTCA GGGAGCAG GTGGTACAG
TGGACAAT AGGT CCTTCGTC CACCATGTC
T T

GAM8554 388 HDGF 1 2702 NP_004485.1 3 19 AGAGCCTGTACC ATG -- 3 B c c
ACCAATGTTTCA TTC GGAGCA GGTGGTACAG
AGAGGAGC GAG CTTTGT CCACCATGTC
AA- AA

GAM8554 388 HELSNF1 1 18562 XP_033511.7 3 166 AAAAATGTACCT ---- GT- 3 B c c

GATTGCTCCCAA TTCA TGGGAGCAG GGTACA
TTATGAGA GAGT ACCCTCGTT CCATGT
ATTA AGT

GAM8554 388 HEMK 1 15386 NP_057257.1 3 3458 ACCTTCTGTACC A GA GG 3 B c
c

ATGCCTTCAGAA TTC TGG GCA TGGTACAG
ACCTTCTT AAG ACT CGT ACCATGTC
- TC --

GAM8554 388 HMGA1 1 13844 NP_002122.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HMGA1 1 13844 NP_665906.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HMGA1 1 13844 NP_665907.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HMGA1 1 13844 NP_665908.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HMGA1 1 13844 NP_665909.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HMGA1 1 13844 NP_665910.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HMGA1 1 13844 NP_665911.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG

C T C

GAM8554 388 HMGA1 1 13844 NP_665912.1 3 31 CCCATGCGTGCC - - A 3 B c c
GCCTGCTCCTCA TTCA TG GGAGCAGGTGGTAC
CTGGAGGA AGGT AC CCTCGTCCGCCGTG
C T C

GAM8554 388 HPS1 1 8078 NP_000186.1 5 111 AGGGATGCTGTG CA TG 3 B c c
CTGCTCTCCCAT TTCATGGGAG GG GTACAG
GAGCCAGT GAGTACCCTC TC CGTGTC
-- GT

GAM8554 388 HRIHFB2 1 3658 NP_008963.2 3 702 AAGGTGTTTCTC T T- T- 3 B c c
122 TTCTGCTCCCTG TTCA GGGAGCAGG GG ACA
AACCTCTT AAGT CCCTCGTCT TC TGT
- TC TT

GAM8554 388 HS3ST2 1 3906 NP_006034.1 3 662 CTTTGTGATTCT - TG --- 3 B c c
CCCTGCTCCCTG TTCAT GGGAGCAGG G TACAG
TGGACAAA AGGTG CCCTCGTCC C GTGTT
T CT TTA

GAM8554 388 HS6ST2 1 13150 NP_671704.2 5 7 CCAGGCTGACCT A GGT- A 3 B c
c
TTATGCTCCCAG TTC TGGGAGCA GGT CAG
AATCATCA AAG ACCCTCGT CCA GTC
- ATTT -

GAM8554 388 ICOS 1 16504 NP_036224.1 3 1229 GCCACTAGGTAT A T A 3 B c c
TCTTGCTCCCAG TTC TGGGAGCAGG GGTAC
AGGCTGAA GAG ACCCTCGTTC TTATG
- - G

GAM8554 388 IL18R1 1 950 NP_003846.1 3 203 TGGGCTGTGGTC A G - 3 B c c
ACGTGCTCCCAG TTC TGGGAGCA GTGGT ACAG
AAGACCTG AAG ACCCTCGT CACTG TGTC
- G G

GAM8554 388 ITGB3BP 1 6219 NP_055103.3 3 287 ATATTCTGTACC CAG-- 3 B c c
ACATACACTTCT TTCATGGGAG GTGGTACAG
GTGGACTT AGGTGTCTTC CACCATGTC
ACATA

GAM8554 388 JUND 1 9711 NP_005345.2 3 212 ACAAGCTGGACC A T A 3 B c c
CCCTGCTCCCGG TTC TGGGAGCAGG GGT CAG
GGGCGAGC GGG GCCCTCGTCC CCA GTC
G C G

GAM8554 388 KAB 1 6558 NP_055627.1 3 395 TCTCCTGTGCCA T G- 3 B b b
AGCTGCTCCCTG TTCA GGGAGCAG TGGTACAG
AAATGGAC AAGT CCCTCGTC ACCGTGTC
- GA

GAM8554 388 KIAA037 1 12790 XP_048462.1 3 142 CCCTGTGCTGGC TT---- - --- 3 B c c
5 ACCTGCTCCCTG CAT GGGAGCAGGTG GTACAG
TGCTCAGT GTG CCCTCGTCCAC CGTGTC
TGACTC T GGT

GAM8554 388 KIAA059 1 16996 XP_085127.6 5 837 TCCTCAAGTACC A - - A 3 B c c
9 ACCTGCTGCTCC TTC TGG G AGCAGGTGGTAC
AGGAAATT AAG ACC C TCGTCCACCATG
G T G A

GAM8554 388 KIAA095 1 2253 XP_039733.2 3 166 TGTTAGGGTCCT TG T A 3 B c c
3 CCCTGCTCCCAT TTCATGGGAGCAGG G AC
GAGGATAT GAGTACCCTCGTCC C TG
CT C G
GAM8554 388 KIAA098 1 4106 XP_037557.2 5 118 CGGCTGTGCGCT A TG-- 3 B c c
4 CCCTGCTCCCAC TTC TGGGAGCAGG GTACAG
GGGCCGGT GGG ACCCTCGTCC CGTGTC
C CTCG
GAM8554 388 KIAA104 1 5832 XP_048592.1 3 3145 CCTTTCTGGTCC - GT TA 3 B c c
5 TGCTGCTCCCTA TTCAT GGGAGCAG GG CAG
TGGGATGT GGGTA CCCTCGTC CC GTC
T GT TG
GAM8554 388 KIAA139 1 3139 XP_208522.1 3 69 CACTGTGGTGCC T T A 3 B c c
4 CTCTGCTCCCTG TTCA GGGAGCAGG GGTAC
GAGCTCTT AGGT CCCTCGTCT CCGTG
- C G
GAM8554 388 KIAA171 1 10338 XP_290811.1 5 75 GGAGCCTGTACC A - -- - 3 B c c
3 AGCCTGCCTTCT TTC TGG GA GCAGG TGGTACAG
CCAGGAGG GAG ACC CT CGTCC ACCATGTC
G T TC G
GAM8554 388 KIAA184 1 15579 XP_030838.3 3 2364 CACTTTGTGCCC - C- T 3 B c c
3 CTATCTGCCCAT TTCATGGG AG AGG GGTACAG
GAAAACAG AAGTACCC TC TCC CCGTGTT
G TA -
GAM8554 388 KIAA187 1 11147 NP_116277.1 5 152 CTGGTGCTGAGC ----- T A 3 B c c
0 CTCTGCTCCCAC TTCA TGGGAGCAGG GGT CAG
CGGGTGAA AAGT ACCCTCGTCT CCG GTC
GGGCC - A
GAM8554 388 KIAA194 1 16455 XP_086981.2 3 1987 GCACCCTGTAGC T---- - T - 3 B c c
0 TCCTGCTCCCTG TCAT GGGAGCAGG GGT ACAG
TGACCCCA AGTG CCCTCGTCC TCG TGTC
ACCCC T - A
GAM8554 388 KIF13B 1 11786 NP_056069.1 3 1280 TGGCTGGGGCAC A -- GTA 3 B c
c
TTATGCTCCCAG TTC TGGGAGCA GGTG CAG
AGCCTTTG GAG ACCCTCGT TCAC GTC
- AT GGG
GAM8554 388 KIF3C 1 16548 NP_002245.2 3 519 ACAGTGTTGGGC - GT-- 3 B c c
ATCTGCTCCCCG TTCATGGG AGCAGGTG ACA
TGGACACA AGGTGCCC TCGTCTAC TGT
C GGGT
GAM8554 388 KLK3 1 14566 NP_001639.1 5 8 CCCAAGCTTACC A A CA 3 B c c
ACCTGCACCCGG TTC TGGG GCAGGTGGTA
AGAGCTGT GAG GCCC CGTCCACCAT
- A TC
GAM8554 388 KLK3 1 14566 NP_665863.1 5 8 CCCAAGCTTACC A A CA 3 B c c
ACCTGCACCCGG TTC TGGG GCAGGTGGTA
AGAGCTGT GAG GCCC CGTCCACCAT

```
                                        -  A       TC
GAM8554  388   L3MBTL2 1  796   NP_113676.2  3  764   TTTGGCTCTGCT   TG       CA       3  B  c  c

                                ACCTGCTCCTGA TTCA  GGAGCAGGTGGTA
                                AGCCCCGC    AAGT  CCTCGTCCATCGT
                                        --          CT
GAM8554  388   LAMC2  1  13196 NP_005553.1  3  1259  ACATATGTTGCA       CA  G--  -      3  B  c  c

                                AGACCCTCCCAT TTCATGGGAG  GGT  GTA CA
                                GGGGGCAC    GGGTACCCTC  CCA  CGT GT
                                        --  GAA  T
GAM8554  388   LCP2   1  7204  NP_005556.1  3  118   GGACTGAACTGA      AGC  T  A       3  B  c  c
                                ACCCCTCCCCAT TTCATGGG  AGG GGT CAG
                                GAACACAA    AAGTACCC   TCC CCA GTC
                                        C--  -  A
GAM8554  388   LIMD1  1  8280  NP_055055.1  3  1890  AGGCTGAGCCTC      AG--  T  A       3  B  c  c

                                CTGAAAACCCAT TTCATGGG   CAGG GGT CAG
                                GAACGCTG    AAGTACCC    GTCC CCG GTC
                                        AAAA   T  A
GAM8554  388   LOC1161 1  3173  NP_620139.1  5  256   GATCTGGAGCCC   TGG      TA--      3  B  c
c
         23                      ACCTGCTTTGAA TTCA  GAGCAGGTGG   CAG
                                AGAAATGA    AAGT  TTCGTCCACC   GTC
                                        ---        CGAG
GAM8554  388   LOC1219 1  15313 XP_062872.2  5  1046  TCAATCCTTTAC      G  G   CA       3  B  c
c
         52                      CAACTGTCCCAT TTCATGGGA CAG TGGTA
                                GAAGAGTA    AAGTACCCT GTC ACCAT
                                        -  A    TT
GAM8554  388   LOC1307 1  10806 XP_059468.3  3  953   TGCCTCTGTACC   T   C           3  B  c  c
         52                      ATTTTTCCTTGA TTCA GGGAG AGGTGGTACAG
                                GTGTGCTT    GAGT TCCTT TTTACCATGTC
                                        -   -
GAM8554  388   LOC1395 1  6100  XP_066756.4  3  815   CCAAGCTCTGAG   A      GT  A       3  B  c
c
         47                      CTCTGCTCCCAG TTC TGGGAGCAG  GGT CAG
                                GGAGCACG    AGG ACCCTCGTC  TCG GTC
                                        G       --  A
GAM8554  388   LOC1469 1  14000 XP_085634.2  3  413   GGACCTGTAGCC   A  GA      -       3  B  c
c
         09                      ACCTGCACCAGG TTC TGG  GCAGGTGGT ACAG
                                AGCTGGAC    GAG ACC  CGTCCACCG TGTC
                                        G  A-       A
GAM8554  388   LOC1487 1  17195 XP_097506.1  3  272   CCTGACCTTCAC   AT      -----  A      3  B  c
c
         10                      ACCTGCTCCCCA TTC  GGGAGCAGGT    GGT CAG
                                GAGAAGCC    GAG  CCCTCGTCCA    CCA GTC
                                        AC        CACTT  -
GAM8554  388   LOC1496 1  7264  XP_047499.3  3  491   TCCCTGTGCTCC   A -  -    --       3  B  c  c
```

```
          03                          ACCTGCCTCCGC TTC TG GGAG CAGGTGG  TACAG
                                     AGAAGGAA    AAG AC CCTC GTCCACC  GTGTC
                                              - G   C      TC
GAM8554  388   LOC1508 1  9583  XP_097954.1  5 672   CTCTTTCTCTGT    -      GGT        3  B  c  c
          19                          GCCTGCTCCTTA TTCATG GGAGCAGGT   ACAG
                                     TGAGTGCA    GAGTAT CCTCGTCCG   TGTC
                                                T       ---
GAM8554  388   LOC1527 1  4063  XP_087519.1  5 700   TGCCTCTGAAGC   A G      GTA        3  B  c
c
          65                          ACCTGCTCACAG TTC TG GAGCAGGTG   CAG
                                     AAGGGTGA    AAG AC CTCGTCCAC   GTC
                                              - A       GAA
GAM8554  388   LOC1582 1  7028  XP_098916.1  5 70    TCTTCTGCAGCC   A   -      A-        3  B  c  c
          98                          ACCTGCTTTCCA TTC TGGGA GCAGGTGGT  CAG
                                     GAGAGATG    GAG ACCTT CGTCCACCG  GTC
                                              -   T       AC
GAM8554  388   LOC2030 1  4227  XP_114620.1  5 63    GAGCCTGTGACC      GA      -         3  B  c  c
          82                          ACCTGTGCTGTG TTCATGG  GCAGGTGGT ACAG
                                     GAGATGGA    AGGTGTC  TGTCCACCA TGTC
                                               G-       G
GAM8554  388   LOC2534 1  16092 XP_172902.2  3 328   GCCAATGGTACC   T    A-     A       3  B  c  c

          99                          ACCCAGTTTCCT TTCA GGGAGC  GGTGGTAC
                                     GAGCTAAG    GAGT CCTTTG  CCACCATG
                                              -    AC      G
GAM8554  388   LOC2539 1  3239  XP_172953.2  3 1088  CCCGTGTACTCC   A  A     --        3  B  c  c
          92                          ACCTGCCCCAGG TTC TGGG GCAGGTGG  TACA
                                     AGCTGGAG    GAG ACCC CGTCCACC  ATGT
                                              G   -      TC
GAM8554  388   LOC2558 1  9954  XP_172855.1  3 237   AGGCACTGTACC   -  AGCA          3  B  c
c
          49                          ACCAGCCTACTG TTCA TGGG   GGTGGTACAG
                                     AGATTGTG    GAGT ATCC   CCACCATGTC
                                               C   GA--
GAM8554  388   LOC2568 1  14030 XP_173004.1  3 1406  AAGAATTGTATA      AGCA  ----        3  B  c
c
          61                          ATATACCCCCAT TTCATGGG   GGTG   GTACAG
                                     GAACTTGT    AAGTACCC   CCAT   TATGTT
                                                ----   ATAA
GAM8554  388   LOC2829 1  8045  XP_212579.1  3 66    AATGGCTTGTGC          T          3  B  c  c
          15                          TCCTGCTCCTGT TTCATGGGAGCAGG GGTACAG
                                     GGGTATAG    GGGTGTCCTCGTCC TCGTGTT
                                                -
GAM8554  388   LOC2829 1  8045  XP_212627.1  3 66    AATGGCTTGTGC          T          3  B  c  c
          51                          TCCTGCTCCTGT TTCATGGGAGCAGG GGTACAG
                                     GGGTATAG    GGGTGTCCTCGTCC TCGTGTT
                                                -
GAM8554  388   LOC2830 1  19511 XP_210862.1  3 271   GGTACTCTGCCT   T    - T   C       3  B  c  c

          28                          CTCTGCTCCCTG TTCA GGGAGCAG G GGTA AG
```

GGGGCCAA GGGT CCCTCGTC C CCGT TC
- T T C
GAM8554 388 LOC2832 1 18729 XP_210961.1 3 1221 GTGTGCAGACGT T ----- 3 B c c

78 GCCTGCTCCCTG TTCA GGGAGCAGGTG GTACA
GATGCCAG AGGT CCCTCGTCCGT CGTGT
- GCAGA
GAM8554 388 LOC2833 1 8601 XP_210969.1 3 839 ATCTAGGTGTCC GA T 3 B c c
14 ACCTGCGTCTGT TTCATGG GCAGGTGG ACA
GGAAGAAG AGGTGTC CGTCCACC TGT
TG -
GAM8554 388 LOC2836 1 11309 XP_211167.1 3 3519 TCCTGACAGAGC --- ---- A 3 B c c

90 ACCTGCTGTTTT TTCATGGG AGCAGGTG GT CAG
TATGAAGC AAGTATTT TCGTCCAC CA GTC
TTG GAGA -
GAM8554 388 LOC2838 1 2526 NP_848611.1 3 2248 AGGATGTGGACC A-- A 3 B c c

49 ACCTGCGGCCCC TTCATGGG GCAGGTGGT CA
ATGGGGTG GGGTACCC CGTCCACCA GT
CGG G
GAM8554 388 LOC2838 1 13934 NP_787095.1 3 1499 TGCTGCACCATT -- - A 3 B c c
61 TTGTATTCCCAT TTCATGGGA GCAGG TGGT CAG
GAGCAGGT GAGTACCCT TGTTT ACCA GTC
TA T C
GAM8554 388 LOC2839 1 17942 XP_211259.2 5 1464 GGACAGTGTGCC T G 3 B c
c
11 ACCTGCTGTCTG TTCA GG AGCAGGTGGTACA
AGAGGCAG GAGT CT TCGTCCACCGTGT
- G
GAM8554 388 LOC2841 1 18036 XP_211330.2 5 540 CCTATCTGACCC A- TA 3 B c c

09 ATCTGCTCCCAC TTC TGGGAGCAGGTGG CAG
CGAAGTTA AAG ACCCTCGTCTACC GTC
CC CA
GAM8554 388 LOC2849 1 11242 XP_211728.1 5 204 CACTGTTCTTGC ---- GT--- 3 B c c

99 ACCTGCTCCTAG TTCA TGGGAGCAGGTG ACAG
CCCTGAAC AAGT ATCCTCGTCCAC TGTC
CCCG GTTCT
GAM8554 388 LOC2852 1 8759 XP_211829.1 5 1931 CAGAGTAGGCCT ---- GG A 3 B c
c
81 GCTTCTTCCCAT TTCATGGGA GCAGGT TAC
GAAAGCCA AAGTACCCT CGTCCG ATG
TCTT G- A
GAM8554 388 LOC2854 1 683 XP_209617.1 5 167 CTCTAGCCTGTG -- GG 3 B c c
56 GCCTGCTCCTGG TTCA TGGGAGCAGGT TACAG
TTGAAGAA AAGT GTCCTCGTCCG GTGTC
TG --
GAM8554 388 LOC2856 1 7057 XP_209676.1 5 1835 TGAGGAGTGGGC G T TA 3 B c
c

```
          02                          TCCTGCTCCATG TTCATGG AGCAGG GG  CA
                                    AGGGACAC    GAGTACC TCGTCC TC  GT
                                              -    - GG
GAM8554  388   LOC2857 1  16880 XP_212000.1  3 1094  CCCTCCCTTGCC          T   CA       3  B  c
c
          27                          TCCTGCTCCCAT TTCATGGGAGCAGG GGTA
                                    GGGAAACA    GGGTACCCTCGTCC CCGT
                                                 T   TC
GAM8554  388   LOC2857 1  18454 XP_212006.1  3 1766  GCAGAAACATGT        CA   T        3  B  c
c
          33                          TCATTTTCCCAT TTCATGGGAG  GGTGG ACA
                                    GAAGGAAC    AAGTACCCTT  TTACT TGT
                                              --    -
GAM8554  388   LOC2857 1  10046 XP_212016.1  5 90    TTCACAATGTGA        A T  -        3  B  c  c
          79                          CCCCGCTCCCAT TTCATGGGAGC GG GGT ACA
                                    GGGCTCCC    GGGTACCCTCG CC CCA TGT
                                              - -  G
GAM8554  388   LOC2858 1  15481 XP_212029.1  5 299   GTGACCGGCTCT        ------ G   A     3  B  c
c
          04                          GGAAGTTCCCAT TTCATGGGAGC     AG TGGT CA
                                    GAATGGAC    AAGTACCCTTG     TC GCCA GT
                                              AAGGTC  G   -
GAM8554  388   LOC2858 1  8045  XP_209790.1  3 66    AATGGCTTGTGC          T          3  B  c  c
          33                          TCCTGCTCCTGT TTCATGGGAGCAGG GGTACAG
                                    GGGTATAG    GGGTGTCCTCGTCC TCGTGTT
                                              -
GAM8554  388   LOC2858 1  2900  XP_212034.1  5 2286  GGCAGTGACCTA   AT     - -  A       3  B  c
c
          43                          CTCTGCTCCCCA TTC  GGGAGCAG GT GGT CA
                                    GAGGCTCC    GAG  CCCTCGTC CA CCA GT
                                              AC       T  T  -
GAM8554  388   LOC2859 1  1695  XP_212103.1  3 3004  GCAAGCTGTACC   AT    AGG          3  B  c
 c
          46                          AGCAGCTCCTGG TTC  GGGAGC   TGGTACAG
                                    GGACGTGC    AGG  TCCTCG   ACCATGTC
                                              GG     ACG
GAM8554  388   LOC2860 1  11421 XP_209870.2  5 106   GGCCAGAAGTAC       A  GG    A       3  B  c
c
          40                          CAGGTGCCCCAT TTCATGGG GCA  TGGTAC
                                    GAAGTGCT    AAGTACCC CGT  ACCATG
                                              -  GG     A
GAM8554  388   LOC2862 1  15299 XP_209972.1  3 316   TTCCTGAGCCCC      G       TA--       3  B  c
c
          58                          ACCTGCTTCATG TTCATGG AGCAGGTGG    CAG
                                    GGTTGGCT    GGGTACT TCGTCCACC    GTC
                                              -       CCGA
GAM8554  388   LOC2863 1  10194 XP_212293.1  5 1639  GCACCGTGCCAT    --       --    A     3  B  c  c

          74                          CCCTGCTCCCAG TTCA  TGGGAGCAGG  TGGTAC
                                    CTGAGGCT    GAGT  ACCCTCGTCC  ACCGTG
```

```
                                        CG        CT     C
GAM8554  388   LOC2863 1  867   XP_208412.1  5  1     GACTGAAGCACC      --       GTA        3  B  c  c
         80                          TGCTCCTCCATG TTCATGG  GAGCAGGTG   CAG
                                    AACCTGCC    AAGTACC  CTCGTCCAC   GTC
                                          TC        GAA
GAM8554  388   LOC3386 1  10670 XP_290521.1  3  2910  CCTTTCTTGTGA      AGC      -         3  B  c
c
         82                          CCATCTCCCCAT TTCATGGG   AGGTGGT ACAG
                                    GAAAGTGC    AAGTACCC   TCTACCA TGTT
                                          C--      G
GAM8554  388   LOC3394 1  10107 NP_848641.1  3  234   TTTCTGCGCTGG    T  -      -- TA       3  B  c  c

         83                          ACCTGCTCACCT TTCA GG GAGCAGGT  GG  CAG
                                    GAGCCTGC    GAGT CC CTCGTCCA  TC  GTC
                                          - A      GG  GC
GAM8554  388   LOC3398 1  9637  XP_291056.2  5  943   CACAGCTGTACC     - A  AG-          3  B  c  c

         83                          ACATGGCCCACG TTCATG GG GC   GTGGTACAG
                                    TGAAATCT    AAGTGC CC CG   CACCATGTC
                                          A  -  GTA
GAM8554  388   LOC3403 1  4660  XP_295216.1  5  659   CCACTGGGCACC    T  AG      A--        3  B  c
c
         19                          ACCTGGGCCCTG TTCA GGG  CAGGTGGT   CAG
                                    AGTCTCCC    GAGT CCC  GTCCACCA   GTC
                                          -  GG       CGG
GAM8554  388   LOC3403 1  2836  XP_291269.1  5  2285  CTCAAACTGTAT    TG--       G         3  B  c  c

         90                          GCCTGCTCCAGC TTCA   GGAGCAGGTG TACAG
                                    CTGGACTG    AGGT    CCTCGTCCGT ATGTC
                                          CCGA        -
GAM8554  388   LOC3484 1  2990  XP_302753.1  5  27    CAAGTGTGTACC    TG- A  -           3  B  c  c
         28                          ACCATGCCTGGC TTCA   GG GCA GGTGGTACA
                                    TGAACACT    AAGT   TC CGT CCACCATGT
                                          CGG  -  A
GAM8554  388   LOC3487 1  1312  XP_302888.1  3  22    TAGGATGTGCCC     G  A      -         3  B  c  c
         97                          ACCTGCATTGGT TTCAT GG GCAGGTGG TACA
                                    GAAGGTCA    AAGTG TT CGTCCACC GTGT
                                          G  A      C
GAM8554  388   LOC3491 1  13730 XP_300973.1  5  42    GGTCAGAAGTAC      A  GG     A         3  B  c
c
         92                          CAGGTGCCCCAT TTCATGGG GCA  TGGTAC
                                    GAAGTGCT    AAGTACCC CGT  ACCATG
                                          -  GG     A
GAM8554  388   LOC3493 1  8798  XP_302590.1  5  498   TCCAGCAGGTCC    A       T  T  A        3  B  c
c
         08                          TCCTGCTCCCAG TTC TGGGAGCAGG GG AC
                                    AGGTGACC    GAG ACCCTCGTCC CC TG
                                          -        T  -  G
GAM8554  388   LOC3493 1  867   XP_300480.1  5  1     GACTGAAGCACC      --       GTA        3  B  c  c
         18                          TGCTCCTCCATG TTCATGG  GAGCAGGTG   CAG
```

AACCTGCC AAGTACC CTCGTCCAC GTC
TC GAA
GAM8554 388 LOC3493 1 867 XP_300488.1 5 1 GACTGAAGCACC -- GTA 3 B c c
34 TGCTCCTCCATG TTCATGG GAGCAGGTG CAG
AACCTGCC AAGTACC CTCGTCCAC GTC
TC GAA
GAM8554 388 LOC3494 1 7281 XP_303269.1 5 567 GAGGCCTGGACC T --- A 3 B c c
66 ACCTGGGGCTCC TTCA GGGAGC AGGTGGT CAG
CTGAGGAT GAGT CCCTCG TCCACCA GTC
- GGG G
GAM8554 388 LOC5116 1 12236 NP_057294.1 3 971 TTCACTGGGCTC TG - TA 3 B c
c
1 ACCTGCTTCTGA TTCA GGAGCAGGTG G CAG
AAACGGCT AAGT CTTCGTCCAC C GTC
-- T GG
GAM8554 388 LOC9026 1 12418 NP_612357.1 3 947 CAGTTTGTATCC A GG - 3 B c c
8 ACCTGCTTTCAG TTC TG AGCAGGTGG TACAG
AGGAGGAA GAG AC TCGTCCACC ATGTT
- TT T
GAM8554 388 LOC9049 1 2928 XP_032170.1 3 1084 TTGAATGCTGCT --- T - 3 B c c
9 TCCTGCTCCCTC TTCAT GGGAGCAGG GGTA CA
CATGGACC AGGTA CCCTCGTCC TCGT GT
CCT T C
GAM8554 388 LOXL3 1 11442 NP_115992.1 3 755 GCATTTTGTACC T--- -- 3 B c c
ATCTGCTCCCCA TCAT GGGAGCAGGTGGTACAG
ATGGCCAA GGTA CCCTCGTCTACCATGTT
AACC AC
GAM8554 388 LPHN1 1 7496 NP_055736.1 3 533 TGCGCTGTAATT T TG - 3 B c c
CCCTGCTCCCTG TTCA GGGAGCAGG GT ACAG
GAGACTGG AGGT CCCTCGTCC TA TGTC
- CT A
GAM8554 388 LRRC8 1 14275 XP_026998.2 3 1265 AGCCCTGTCACC -- G - 3 B b b
ACCTGGTCCTTC TTCATG GGA CAGGTGGT ACAG
ATGAAGAG AAGTAC CCT GTCCACCA TGTC
TT G C
GAM8554 388 LYK5 1 15716 NP_699166.1 3 130 GGAGCTCTGGCC - G A 3 B c c
ACTGCTTCCCAT TTCATGGGA GCAG TGGT CAG
GAGCTGAG GAGTACCCT CGTC ACCG GTC
T - -
GAM8554 388 MADH9 1 15488 NP_005896.1 5 10 TGAATTGGTCCC A G T A 3 B c c
AGCTGCTCCCAG TTC TGGGAGCAG TGG AC
AAGAACGG AAG ACCCTCGTC ACC TG
- G C G
GAM8554 388 MAP2K1I 1 5192 NP_068805.1 3 259 GGTTCAGTCTAT AG CA 3 B c c
P1 CACAGCTCCCAT TTCATGGGAGC GTGGTA
GGAGTTAG AGGTACCCTCG CACTAT
A- CT

GAM8554 388 MAP3K8 1 13588 NP_005195.2 3 136 GCAGTGTGACCT A- T - 3 B c c
CCTGTGACCCAT TTCATGGG GCAGG GGT ACA
GAATGTGC AAGTACCC TGTCC CCA TGT
AG T G
GAM8554 388 MCM3APA 1 5637 NP_060588.1 3 1642 ATCCACTGAGCC CA T A 3 B c
c
S TTCATCTCCCAT TTCATGGGAG GG GGT CAG
GAACTTGA AAGTACCCTC CT CCG GTC
TA T A
GAM8554 388 MFAP3 1 18666 NP_005918.1 5 459 CAAGATTTTGTC CA T 3 B c c
CCATTTTCCCAT TTCATGGGAG GGTGG ACAG
GAAGCTAC AAGTACCCTT TTACC TGTT
-- C
GAM8554 388 MGC2989 1 817 NP_659485.1 3 752 GTGAGCCACCAT A---- - A 3 B c c
8 GCCTGGCCCCAT TTCATGGG GCA GGTGGT CA
GAATACAC AAGTACCC CGT CCACCG GT
CGGTC A A
GAM8554 388 MGC3101 1 10658 NP_076948.1 3 1220 CTCCTTCTGTGT ---- G 3 B c c
ACCTGCTCCCAC TTCA TGGGAGCAGGTG TACAG
TTCTGAGC GAGT ACCCTCGTCCAT GTGTC
CTTC -
GAM8554 388 MGC3234 1 4854 NP_076436.2 3 161 CCATGTGACTCC CA ----- 3 B c c
CCATCCTCCCAT TTCATGGGAG GGTGG TACA
GAGGGGTC GAGTACCCTC CTACC GTGT
-- CCTCA
GAM8554 388 MGC3504 1 13468 NP_694940.1 5 288 GATCCGTACCTC A-- T A 3 B c
c
8 CAAGGCTCCCAT TTCATGGGAGC GG GGTAC
GGGCCCAA GGGTACCCTCG CC CCATG
GAA T C
GAM8554 388 MGC7036 1 14389 NP_659495.1 3 340 CGTGTCCTACTC A - CA 3 B c
c
ATCTGCTCCCAC TTC TGGGAGCAGGTG GTA
GGATGACC AGG ACCCTCGTCTAC CAT
C T CC
GAM8554 388 MME 1 10848 NP_000893.1 3 2907 ATGTGTCCAATG -- G-- - 3 B c c
CTGCCTTCCCAT TTCATGGGA GCAG TGG TACA
GAATCTGT AAGTACCCT CGTC ACC GTGT
TC GTA T
GAM8554 388 MME 1 10848 NP_009218.1 3 2907 ATGTGTCCAATG -- G-- - 3 B c c
CTGCCTTCCCAT TTCATGGGA GCAG TGG TACA
GAATCTGT AAGTACCCT CGTC ACC GTGT
TC GTA T
GAM8554 388 MME 1 10848 NP_009219.1 3 2907 ATGTGTCCAATG -- G-- - 3 B c c
CTGCCTTCCCAT TTCATGGGA GCAG TGG TACA
GAATCTGT AAGTACCCT CGTC ACC GTGT
TC GTA T
GAM8554 388 MME 1 10848 NP_009220.1 3 2907 ATGTGTCCAATG -- G-- - 3 B c c

CTGCCTTCCCAT TTCATGGGA GCAG TGG TACA
GAATCTGT AAGTACCCT CGTC ACC GTGT
TC GTA T
GAM8554 388 MSX2 1 14467 NP_002440.2 3 7 ATGGCATGTACC A G 3 B b b
ACCTGTCCTAGG TTC TGGGA CAGGTGGTACA
AAGACCAG AAG ATCCT GTCCACCATGT
G -
GAM8554 388 MYCBP 1 6531 NP_036465.1 3 463 AGATGCTTTTGT AGGTG 3 B c c
ACGGGTTCCCAT TTCATGGGAGC GTACAG
GAATCTTC AAGTACCCTTG CATGTT
GG---
GAM8554 388 NLGN4 1 425 NP_065793.1 5 351 CTCTCCCAGGTC T G T A 3 B c c
TACTGCTCCCTG TTCA GGGAGCAG TGG AC
GAAAGCCC AGGT CCCTCGTC ATC TG
- - - G
GAM8554 388 NLGN4 1 425 NP_851849.1 5 317 CTCTCCCAGGTC T G T A 3 B c c
TACTGCTCCCTG TTCA GGGAGCAG TGG AC
GAAAGCCC AGGT CCCTCGTC ATC TG
- - - G
GAM8554 388 P5326 1 7667 NP_113638.1 3 82 CTCCTGTCTTCC GC T T-- 3 B c c
TCCTTGTCCCAT TTCATGGGA AGG GG ACAG
GAAGGCCA AAGTACCCT TCC CC TGTC
GT T TTC
GAM8554 388 PACAP 1 19792 NP_057543.1 5 409 GTCCTGGACCGG A G-- A 3 B c c
AGCTGCTCCCGG TTC TGGGAGCAG TGGT CAG
AACTGGCA AAG GCCCTCGTC GCCA GTC
- GAG G
GAM8554 388 PDCD2 1 11383 NP_659005.1 3 209 GGGTGGGTATCC G GG - A 3 B c c
AGATGGTCCCAT TTCATGGGA CA TGG TAC
GAGTAGGG GAGTACCCT GT ACC ATG
G AG T G
GAM8554 388 PEPP3 1 1056 NP_055750.1 3 1329 CTCTCATGATCC A A TA 3 B c c
ACCTGCCCCGGG TTC TGGG GCAGGTGG CA
AGGGCAGC GAG GCCC CGTCCACC GT
G - TA
GAM8554 388 PISD 1 1719 NP_055153.1 5 14 GAAGCTGGAGCC T A- A- 3 B c c
ACCTGCGGCTCT TTCA GGG GCAGGTGGT CAG
GAGAGGGA GAGT CTC CGTCCACCG GTC
- GG AG
GAM8554 388 PLPL 1 5391 NP_064566.1 3 384 TGTACCTTCTCC A A ------ 3 B c c
ACCTGCCCCCAG TTC TGGG GCAGGT GGTACA
GAAAAAGA AAG ACCC CGTCCA CCATGT
G C CCTCTT
GAM8554 388 PLXNB1 1 15214 NP_002664.1 3 222 GGGTAGTACCCA AT -- A 3 B c c
GCCTGCTCCCCG TTC GGGAGCAGGT GGTAC
AGTCCAGC GAG CCCTCGTCCG CCATG

```
                                        C-        AC    A
GAM8554  388   PPARD  1  5618  NP_006229.1  3  1075  GTCCCTGCCCTC    ---       T  TA--      3  B  c  c

                                CCCTGCTCCCAG TTCA   TGGGAGCAGG GG    CAG
                                GTTGAGGT    GAGT   ACCCTCGTCC CC    GTC
                                        TGG        -  TCCC
GAM8554  388   PPP1R12 1  18026 NP_002472.1  3  1027  CTTCGCCCTGAC    -       GTA        3  B  c
c
         B                       ACCTGCTTCTAA TTCAT GGGAGCAGGTG   CAG
                                TGAGAAAT    GAGTA TCTTCGTCCAC   GTC
                                        A         A--
GAM8554  388   PPP1R12 1  18026 NP_115288.1  3  1160  CTTCGCCCTGAC    -       GTA        3  B  c
c
         B                       ACCTGCTTCTAA TTCAT GGGAGCAGGTG   CAG
                                TGAGAAAT    GAGTA TCTTCGTCCAC   GTC
                                        A         A--
GAM8554  388   PRKACB  1  19320 NP_002722.1  3  1704  TTCATCTGTACC     G  AGCAG            3  B
c  c
                                ACACCCTGGTGA TTCAT GG    GTGGTACAG
                                AACCTTTG    AAGTG TC    CACCATGTC
                                        G  CCA--
GAM8554  388   ProSAPi 1  13653 NP_055546.1  3  1450  AGCCCCTGACCA T-----      C  -   A     3  B  c
c
         P1                       GCCTCCTCCCAT      TCATGGGAG AGG TGGT CAG
                                GACTGGTG         AGTACCCTC TCC ACCA GTC
                                        GTGGTC       C  G   -
GAM8554  388   PRTD-NY 1  13126 NP_112186.2  3  14    ATCACATGTACC     G     --          3  B  c  c
         3                       ACTGCTGCTTTG TTCAT GGAGCAG  GTGGTACA
                                ATGGAGCT    AGGTA TTTCGTC  CACCATGT
                                        G      GT
GAM8554  388   PTPRT  1  17911 NP_008981.2  3  6672  CCACCCTGTCCC       CA--  T  T       3  B  c
c
                                TGTATCTCCCAT TTCATGGGAG    GG GG ACAG
                                GGAAGATG    AGGTACCCTC    TC CC TGTC
                                        TATG  -  -
GAM8554  388   PTPRT  1  17911 NP_573400.1  3  6672  CCACCCTGTCCC       CA--  T  T       3  B  c
c
                                TGTATCTCCCAT TTCATGGGAG    GG GG ACAG
                                GGAAGATG    AGGTACCCTC    TC CC TGTC
                                        TATG  -  -
GAM8554  388   RAB11-F 1  5886  NP_116321.2  3  1484  CTTGGGTGTGAC    A  G-       G        3  B  c
c
         IP4                       ACCTGCTTGACA TTC TG  GAGCAGGTG TACA
                                GAGGCAGG    GAG AC  TTCGTCCAC GTGT
                                        -  AG        A
GAM8554  388   RAMP3  1  19598 NP_005847.1  3  161   CTTCCTGGGCTG    AT       -  TA       3  B  c
c
                                ACCTGCTCCCTC TTC  GGGAGCAGGT GG  CAG
                                GAGGCCAG    GAG  CCCTCGTCCA TC  GTC
                                        CT        G  GG
```

GAM8554 388 RGS16 1 14356 NP_002919.1 3 1324 TCTCTCTGTACC AT-- AG 3 B c c

ATGAGCTCCTCC TTC GGGAGC GTGGTACAG
AGGAGATT GAG TCCTCG TACCATGTC
GACC AG

GAM8554 388 RIS 1 4407 NP_057647.1 3 1496 TGTGTGTGTACC T GA G 3 B c c

ACTGCCATCTGA TTCA GG GCAG TGGTACA
ACAAACTA AAGT CT CGTC ACCATGT
- AC -

GAM8554 388 RNMT 1 12208 NP_003790.1 3 3525 AGCCCTAAAGTC T T T A 3 B c c

CCCTGCTCCCTG TTCA GGGAGCAGG GG AC
GACTTCTC AGGT CCCTCGTCC CC TG
- - - A

GAM8554 388 ROR2 1 6454 NP_004551.2 3 942 TCTCTCTGTACC GGA G 3 B c c

ACGTGCACATGA TTCATG GCA GTGGTACAG
GGTCCATT GAGTAC CGT CACCATGTC
A-- G

GAM8554 388 RP4-622 1 7263 NP_061991.2 3 812 TGTGTCTGAGCA TG A 3 B c c
L5 TTCTGCTCCCAT TTCATGGGAGCAGG GT CAG
GGACATCC AGGTACCCTCGTCT CG GTC
TA A

GAM8554 388 RS1 1 17639 NP_000321.1 3 1057 TACGCAAACTGC TG GTA 3 B c c

GCCTGCTCCTGA TTCA GGAGCAGGTG CAG
AAAGCTCT AAGT CCTCGTCCGC GTC
-- ---

GAM8554 388 S164 1 15155 XP_027330.5 5 22 ACCTCATTTGAA CA A 3 B c c

TCGCCCTCCCAT TTCATGGGAG GGTGGT CAG
GGGAATCC GGGTACCCTC CCGCTA GTT
-- A

GAM8554 388 SART3 1 16857 NP_055521.1 3 639 ATTATTTGTGCC GGG 3 B c c

ACCTGCTGTGGA TTCAT AGCAGGTGGTACAG
CTGTTTTC AGGTG TCGTCCACCGTGTT

GAM8554 388 SBZF3 1 420 NP_065127.2 3 184 AGTGCCTGGACT G TG A 3 B c c

CCCTGCTCCGTG TTCATGG AGCAGG GT CAG
AGGCGAAT GAGTGCC TCGTCC CA GTC
- CT G

GAM8554 388 SBZF3 1 420 XP_300732.1 3 63 AGTGCCTGGACT G TG A 3 B c c

CCCTGCTCCGTG TTCATGG AGCAGG GT CAG
AGGCGAAT GAGTGCC TCGTCC CA GTC
- CT G

GAM8554 388 SCN4B 1 6820 NP_777594.1 3 1430 GAGATGTCGGCC - GG -- 3 B c c

AGGTGCTCCCAT TTCA TGGGAGCA TGGT ACA
TGGGGTTT GGGT ACCCTCGT ACCG TGT
T GG GC

GAM8554 388 SDC3 1 13246 NP_055469.1 5 1159 CCTTAGTGTACC T G CA 3 B c c

ACCCCTGCCTTG TTCA GG AG GGTGGTACA
AGCTTGTG GAGT CC TC CCACCATGT
T G C-
GAM8554 388 SFMBT 1 18612 NP_057413.1 3 202 CAGAAGTGGATC GGG A 3 B c c
ACCTGCTGGTGG TTCAT AGCAGGTGGT CA
AAATGTGG AGGTG TCGTCCACTA GT
G-- G
GAM8554 388 SH3GL2 1 1385 NP_003017.1 3 1287 TTCCGATGTGCC GGGA 3 B c c
ACCTGCAGTAGT TTCAT GCAGGTGGTACA
GGATCATG AGGTG CGTCCACCGTGT
ATGA
GAM8554 388 SIPA1 1 4806 NP_006738.2 3 30 CCGTCTGGAACC T AG A- 3 B c c
ACCTGGGCCCCT TTCA GGG CAGGTGGT CAG
GAGGGCAC GAGT CCC GTCCACCA GTC
C GG AG
GAM8554 388 SIPA1 1 4806 NP_694985.28 3 30 CCGTCTGGAACC T AG A- 3 B c c
ACCTGGGCCCCT TTCA GGG CAGGTGGT CAG
GAGGGCAC GAGT CCC GTCCACCA GTC
C GG AG
GAM8554 388 SLC20A1 1 17340 NP_005406.3 3 69 CATCTTAGGTAT T T A 3 B c c
TCCTGCTCCCCT TTCA GGGAGCAGG GGTAC
GAAGAATG AAGT CCCTCGTCC TTATG
C - G
GAM8554 388 SLC25A1 1 2699 NP_006349.1 3 21 CACCAACACTGG GC GTA 3 B c c
7 ACGCCTTCCCAT TTCATGGGA AGGTG CAG
GAAAAATT AAGTACCCT TCCGC GTC
-- AG-
GAM8554 388 SMARCF1 1 11978 NP_060920.4 3 265 CAAGGTGTCTAG A -- T 3 B c c
TCCAGCTCCCAT TTCATGGGAGC GG TGG ACA
GGAGGGTG AGGTACCCTCG CC ATC TGT
A TG -
GAM8554 388 SPBPBP 1 9243 NP_006683.1 3 417 CTGCCTGGACCC A GG TA- 3 B c c
AGATGCTCCCAG TTC TGGGAGCA TGG CAG
AATCAATA AAG ACCCTCGT ACC GTC
- AG CAG
GAM8554 388 SYNJ2 1 7330 NP_003889.1 3 565 AATGACTAGACT ---- G- A 3 B c c
GTACATTCCCAT TTCATGGGA GCAG TGGT CA
GAGCCTTC GAGTACCCT TGTC ATCA GT
TACA AG -
GAM8554 388 TCOF1 1 1511 NP_000347.1 3 224 AGGAGAAAGTGG T----- AGG A 3 B c c
ACCAGCTCCCAT TCATGGGAGC TGGT CA
GACCTCAC AGTACCCTCG ACCA GT
CACTCC --- G
GAM8554 388 TGFB3 1 3958 NP_003230.1 3 439 CATTGCTGTACC ATG -- 3 B c c

ACATCTGCTCTA TTC GGAGCAG GTGGTACAG
GGGAATCT AAG TCTCGTC CACCATGTC
GGA TA
GAM8554 388 TOLLIP 1 1045 NP_061882.2 3 2334 AGCCTCTGCTGC ---- T - 3 B c c
TCCTGCTCCTGG TTCA TGGGAGCAGG GGTA CAG
GTTTGAAG AAGT GTCCTCGTCC TCGT GTC
TTGG - C
GAM8554 388 TU3A 1 17216 NP_009108.1 3 128 TGTGATGTTCCC - T- 3 B c c
ACCTGCTTCTGT TTC ATGGGAGCAGGTGG ACA
AGAAATGT AAG TGTCTTCGTCCACC TGT
A CT
GAM8554 388 UGDH 1 18136 NP_003350.1 3 402 GTGAGCCACCAC AG ----- A 3 B c
c
GCCTGGGCCCAT TTCATGGG CAGGT GGT CA
GAACCAAG AAGTACCC GTCCG CCG GT
GG CACCA A
GAM8554 388 UNC84A 1 4603 XP_291219.1 3 625 ACTCGCTGTACC AGCAGG 3 B c
c
AATATCCATGGA TTCATGGG TGGTACAG
GGAATATG AGGTACCT ACCATGTC
ATA---
GAM8554 388 URF2 1 2555 NP_689519.2 3 451 AGATGATGTTGA T GGT 3 B c c
ACCTGCTCCTTG TTCA GGGAGCAGGT ACA
GACCTCTG AGGT TCCTCGTCCA TGT
- AGT
GAM8554 388 VprBP 1 5213 NP_055518.1 3 1019 CGGGTCCTGAGC G GTA 3 B c c
ACCTGCTTCATG TTCATGG AGCAGGTG CAG
AAGGAAGA AAGTACT TCGTCCAC GTC
- GA-
GAM8554 388 WDFY1 1 18013 NP_065881.1 3 2722 GAATGTATTACT C--- 3 B c c
TTGTTCTCCCAT TTCATGGGAG AGGTGGTACA
GAAAGAAT AAGTACCCTC TTCATTATGT
TTGT
GAM8554 388 WDFY1 1 18013 NP_848127.1 3 2722 GAATGTATTACT C--- 3 B c c
TTGTTCTCCCAT TTCATGGGAG AGGTGGTACA
GAAAGAAT AAGTACCCTC TTCATTATGT
TTGT
GAM8554 388 WFDC10B 1 7903 NP_742003.1 3 42 CTGGGATGTGCA T TG 3 B c
c
TCCTGCTCCCTG TTCA GGGAGCAGG GTACA
AACCCTTC AAGT CCCTCGTCC CGTGT
- TA
GAM8554 388 WFDC10B 1 7903 NP_742143.1 3 42 CTGGGATGTGCA T TG 3 B c
c
TCCTGCTCCCTG TTCA GGGAGCAGG GTACA
AACCCTTC AAGT CCCTCGTCC CGTGT
- TA
GAM8554 388 WHSC1 1 16764 NP_579889.1 3 2383 TAAAATTGCCCC G- TA 3 B c
c

ACCTGCTCTAGA TTCAT GGAGCAGGTGG CAG
TGGATCTT AGGTA TCTCGTCCACC GTT
GA CC
GAM8554 388 ZFP91 1 19190 NP_739574.1 3 726 TTTTCTCTGACC - A- A 3 B c c
ACCTGCAGCCTG TTCA TGGG GCAGGTGGT CAG
TTGAAGGA AAGT GTCC CGTCCACCA GTC
T GA -
GAM8554 388 ZNF124 1 18483 NP_003422.1 5 79 CACTTATGTGGA T----- GG 3 B c c
ATCTGCTCCCAT TCATGGGAGCAGGT TACA
GACCCAAG AGTACCCTCGTCTA GTGT
GAACCC AG
GAM8554 388 ZNF239 1 13975 NP_005665.1 5 494 AGGTCACCTGGA A - --- - A 3 B c c
CTCTGCTCCCAG TTC TGGGAGCAG GT GGT AC
GAAGCTGT AAG ACCCTCGTC CA CCA TG
G T GGT C G
GAM8554 388 ZNF289 1 14798 NP_115765.2 3 724 TCCCTCTGTACC GGG 3 B c c

ATCTGCTGTGGA TTCAT AGCAGGTGGTACAG
ATGCAGGA AGGTG TCGTCTACCATGTC

GAM8554 388 ZNF297 1 17593 NP_005444.3 3 264 GTACACTGAAGC A - T A- 3 B c c
CCCTGCTCCACA TTC TG GGAGCAGG GGT CAG
GAGTAGAT GAG AC CCTCGTCC CCG GTC
- A - AA
GAM8678 347 ABCA4 1 14902 NP_000341.1 3 209 CGAAACTGACTT ----- - C 3 C c c
GCTCACCTGGAA GTGTTCCAGG AAGTC GT TTG
CACCTGAT CACAAGGTCC TTCAG CA AGC
ACTCG T A
GAM8678 347 ADCY1 1 11743 NP_066939.1 3 3870 TTAAAGCCACCA AGTC 3 C c
c

GGGCTTCTGGAA GTGTTCCAGGA GTCTTG
CACCTGTC CACAAGGTCTT CGGGAC

GAM8678 347 AGXT 1 15028 NP_000021.1 3 197 TCCCTCCAGTGG G A C - 3 C c c
CACCTCCTGGAA GT TTCCAGGA GT GTC TTG
ACAGTCCA CA AAGGTCCT CA CGG GAC
- C - T
GAM8678 347 AMD1 1 8863 NP_001625.1 3 1633 TGGTTTGAAATC GAAG T 3 C c
c

AAGTGGTTGGAA GTGTTCCAG TCG CTTGA
CACTGTTT CACAAGGTT GGT GAACT
---- -
GAM8678 347 ANKRD10 1 2626 NP_060134.1 3 49 GAAACGCAGGAG T - TCG 3 C c
c

TCCTTCCTGGTA G GTT CCAGGAAG TCTTG
GCCAGCTC C CGA GGTCCTTC AGGAC
- T CTG
GAM8678 347 ANKTM1 1 18718 NP_015628.1 3 480 CCTAACCTAAGC G C T 3 C c
c

TGCTTCCTGGAA GT TTCCAGGAAGT G CTTG

AGCTTCAT CG AAGGTCCTTCG C GAAT
A T -
GAM8678 347 APOB48R 1 14532 NP_061160.1 5 4 ACAGACAGGATG T- -- - 3 C c c
GACTTCCTCCGG GTGT CC AGGAAGTC GTCTTG
CTATACCT CATA GG TCCTTCAG TAGGAC
TC CC G
GAM8678 347 ATP7A 1 14456 NP_000043.1 3 3387 AAAAGAATAAAG - GTC G 3 C c
c
ACATTCCTGGAA GTG TTCCAGGAA GTCTT
TCACTCCT CAC AAGGTCCTT CAGAA
T A-- A
GAM8678 347 BMP1 1 18997 NP_006122.1 3 583 GTGTGCAAGTAC --- G - 3 C c c
GACTTCGTGGAG GTGT TCCA GAAGTCGT CTTG
GTGCGCAG CGCG AGGT CTTCAGCA GAAC
TGG G T
GAM8678 347 BMP1 1 18997 NP_006123.1 3 1311 GTGTGCAAGTAC --- G - 3 C c c
GACTTCGTGGAG GTGT TCCA GAAGTCGT CTTG
GTGCGCAG CGCG AGGT CTTCAGCA GAAC
TGG G T
GAM8678 347 BRCA1 1 16053 NP_009225.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009227.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009228.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009229.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009230.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009231.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009232.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009233.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT

CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009234.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009235.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009236.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 BRCA1 1 16053 NP_009237.1 5 24 TGAGCTCGCTGA ---- G T- 3 C c c
GACTTCCTGGAC GTGT TCCAGGAAGTC TC TGA
CCCGCACC CACG AGGTCCTTCAG AG GCT
CCCC - TC
GAM8678 347 C14orf7 1 1099 XP_040910.3 5 36 CCCGACGACGGC TC - 3 C c c
3 GACTTCCTGCGC GTGT CAGGAAGTCGTC TTG
ACGCCGCG CACG GTCCTTCAGCGG AGC
C- C
GAM8678 347 C20orf1 1 14457 XP_300782.1 3 260 GTAAGACTTGAC -- - -- 3 C c c
42 CTTTATCTGGAA GTGTTCCAG GAAG TC GTCTTG
CACTCCTT CACAAGGTC TTTC AG CAGAAT
TA C TT
GAM8678 347 C20orf1 1 13151 NP_061968.1 5 38 GACTAACAAGAC T-- AA - 3 C c c
55 GAGCGCTCTGGA GTG TCCAGG G TCGTCTTG
TCTTACTA CAT AGGTCT C AGCAGAAC
TCT CG G
GAM8678 347 C21orf8 1 14253 NP_715631.1 5 225 CCGCCTCCGAGC T A T 3 C c c
1 GACTTCCGGGAG G GTTCC GGAAGTCG CTTG
CCGGGCGG C CGAGG CCTTCAGC GAGC
- G -
GAM8678 347 C4orf6 1 2254 NP_005741.1 5 138 AAGAAAAACAAG G GT 3 C c c
GACTTCCTGGGA GT TTCCAGGAAGTC CTTG
GGCTGTGG CG AGGGTCCTTCAG GAAC
G --
GAM8678 347 C5orf5 1 19983 NP_057687.1 3 540 GAGATTTCAAGT GGA - T 3 C c c
CGTACTATGGAA GTGTTCCA AGT CG CTTGA
CACCTTTC CACAAGGT TCA GC GAACT
A-- T T
GAM8678 347 C5orf6 1 5117 NP_057689.1 3 29 AAACTGAGAGGC - C G 3 C c c
TACTTCCTGGGG GTG TTCCAGGAAGT GTCTT
CCACACAG CAC GGGGTCCTTCA CGGAG
C T A
GAM8678 347 CARD15 1 7952 NP_071445.1 3 1058 TTCAAAGCAAAT T T C 3 C c c
GTCTTCCTGGAT GTG TCCAGGAAG CGT TTG
TATTCAAA TAT AGGTCCTTC GTA AAC
T T -
GAM8678 347 CARD9 1 18998 NP_071747.2 5 100 CTGCAGTGCAGG G A T 3 C c c

TGGCTCCTGGAA GT TTCCAGGA GTCG CTTG
GACCCTCA CA AAGGTCCT CGGT GGAC
G - -
GAM8678 347 CARD9 1 18998 NP_434700.1 5 100 CTGCAGTGCAGG G A T 3 C c c

TGGCTCCTGGAA GT TTCCAGGA GTCG CTTG
GACCCTCA CA AAGGTCCT CGGT GGAC
G - -
GAM8678 347 CARD9 1 18998 NP_434701.1 5 111 CTGCAGTGCAGG G A T 3 C c c

TGGCTCCTGGAA GT TTCCAGGA GTCG CTTG
GACCCTCA CA AAGGTCCT CGGT GGAC
G - -
GAM8678 347 CBR1 1 3247 NP_001748.1 5 4 CAGACTCGAGCA - AGTC T 3 C c c
GTCTCTGGAACA GTGTTCCAG GA G CTTGA
CGCTGCGG CACAAGGTC CT C GAGCT
T GA-- -
GAM8678 347 CDCP1 1 4987 NP_073753.3 3 133 GAACAGCAGGAG T TCG 3 C c
c

GTTTTCCTGGAC GTGT CCAGGAAG TCTTG
ACCGCCAA CACA GGTCCTTT AGGAC
- TGG
GAM8678 347 CDKN2A 1 18494 NP_478104.1 3 204 GCTGCCCGGGAG T G 3 C c
c

GGCTTCCTGGAC GTGT CCAGGAAGTC TCTTG
ACGCTGGT CACA GGTCCTTCGG AGGGC
- G
GAM8678 347 CDKN2B 1 18494 NP_511042.1 3 173 GCTGCCCGGGAG T G 3 C c
c

GGCTTCCTGGAC GTGT CCAGGAAGTC TCTTG
ACGCTGGT CACA GGTCCTTCGG AGGGC
- G
GAM8678 347 CDR1 1 18037 NP_004056.1 3 259 TTGGAAGACATG G --- G 3 C c c
GATTTCCTGGAA GT TTCCAGGAAGTC GTCTT
GACGTGGA CA AAGGTCCTTTAG CAGAA
G GTA G
GAM8678 347 CEACAM1 1 13671 NP_001703.2 5 8 GCCGTGCTCGAA T GT TC 3 C c
c

GCGTTCCTGGAG G GTTCCAGGAA CG TTGA
CCCAAGCT C CGAGGTCCTT GC AGCT
C -- GA
GAM8678 347 CEACAM5 1 12584 NP_004354.1 5 50 AGCCTTGACAAA T GT C 3 C c
c

ACGTTCCTGGAA G GTTCCAGGAA CGT TTG
CTCAAGCT C CAAGGTCCTT GCA AAC
T -- A
GAM8678 347 CGGBP1 1 14778 NP_003654.2 5 126 ACGTAAAGGCAT TT- -- G 3 C c
c

GACTTCCTGGCA GTG CCAGGAAGTC GTCTT
CCACAGGG CAC GGTCCTTCAG CGGAA

CAC TA A
GAM8678 347 CHST5 1 9412 NP_036258.1 5 239 AGAAGACCTCTG - ---- G 3 C c c
GCTTTCCTGGAA GTGTTCCAGGAA GTC GTCTT
CACAGATG CACAAGGTCCTT CGG CAGAA
T TCTC G
GAM8678 347 CHST6 1 20149 NP_067628.1 3 1703 AAGTAACAAAGT AA TC 3 C c
c
GATGGCTTGGAA GTGTTCCAGG GTCG TTG
CACTGTCT CACAAGGTTC TAGT AAC
GG GA
GAM8678 347 CLDN12 1 8628 NP_036261.1 5 11 TCGCTGGGAACG - - 3 C c c
CACTTCCTGGGA GTGTTCCAGGAAGT CGT CTTG
CGCTGAGA CGCAGGGTCCTTCA GCA GGGT
C A
GAM8678 347 CNR2 1 11056 NP_001832.1 3 162 GAGTGTTGGGAC G A - TG 3 C c
c
TGACTCCTGGAA GT TTCCAGGA GTC GTCT A
GACAGCCT CA AAGGTCCT CAG CAGG T
G - T GT
GAM8678 347 COL17A1 1 6300 NP_000485.2 3 409 TGGGGGTGGGGC ---- T 3 C c c
GCCTTCCTGGAG GTGT TCCAGGAAG CGTCTTG
GTGACACT CACA AGGTCCTTC GCGGGGT
GTGG C
GAM8678 347 COLEC12 1 19564 NP_110408.2 5 98 GCCGCTCGGGAC T- - 3 C c c
GACTTCCTCGGC GTGT CC AGGAAGTCGTCTTGA
TGCGCGGC CGCG GG TCCTTCAGCAGGGCT
TC C
GAM8678 347 COLEC12 1 19564 NP_569057.1 5 98 GCCGCTCGGGAC T- - 3 C c c
GACTTCCTCGGC GTGT CC AGGAAGTCGTCTTGA
TGCGCGGC CGCG GG TCCTTCAGCAGGGCT
TC C
GAM8678 347 CREG 1 5534 NP_003842.1 5 6 CGGCCGCCGGGA - TC 3 C c c
CTCTTCCTGGAG GTGT TCCAGGAAG GTCTTG
ACACCGCC CACA AGGTCCTTC CAGGGC
G T-
GAM8678 347 CYP4B1 1 16905 NP_000770.1 3 158 ATTACCATAGAC G C A - 3 C c c
GACTCCTAGAGG GT TTC AGGA GTCGTCT TG
ACAGTGCT CA GAG TCCT CAGCAGA AC
G A - T
GAM8678 347 DCX 1 18999 NP_000546.2 3 3998 CTTGCTGCAAGG G TC 3 C c c
CTCTTCCTGGGA GT TTCCAGGAAG GTCTTG
ACTAAGGG CA AGGGTCCTTC CGGAAC
- T-
GAM8678 347 DCX 1 18999 NP_835364.1 3 3998 CTTGCTGCAAGG G TC 3 C c c
CTCTTCCTGGGA GT TTCCAGGAAG GTCTTG
ACTAAGGG CA AGGGTCCTTC CGGAAC
- T-
GAM8678 347 DCX 1 18999 NP_835365.1 3 3998 CTTGCTGCAAGG G TC 3 C c c

CTCTTCCTGGGA GT TTCCAGGAAG GTCTTG
ACTAAGGG CA AGGGTCCTTC CGGAAC
- T-

GAM8678 347 DCX 1 18999 NP_835366.1 3 3998 CTTGCTGCAAGG G TC 3 C c c
CTCTTCCTGGGA GT TTCCAGGAAG GTCTTG
ACTAAGGG CA AGGGTCCTTC CGGAAC
- T-

GAM8678 347 DGCR9 1 17341 XP_097827.1 3 523 GCTGAGCTGCAA T AGTC 3 C c
c

GACATCCTGGAA G GTTCCAGGA GTCTTG
TTGGGAGC G TAAGGTCCT CAGAAC
T A---

GAM8678 347 DKFZP43 1 9302 NP_110444.1 3 8 GCGTGCAGGGCT TC- 3 C c c
4F0318 GTTTTTCTGGAA GTGTTCCAGGAAG GTCTTG
CATCCTTT TACAAGGTCTTTT CGGGAC
TGT

GAM8678 347 DKFZP43 1 1085 XP_166383.1 3 626 ATGGCAAGATGC - A -- 3 C c c
4G1411 CATATCCTGGAA GTGTT CCAGGA GT CGTCTTG
ACATATTA TACAA GGTCCT TA GTAGAAC
A A CC

GAM8678 347 DKFZP56 1 8255 NP_056469.2 3 328 CTGGAGGTGCAG AAG G 3 C c
c

4C103 GGGGACCTGGAA GTGTTCCAGG TC TCTTG
CATGGATG TACAAGGTCC AG GGGAC
--- G

GAM8678 347 DKFZP58 1 9451 NP_112584.1 3 1440 AAGCACAAGACT G - C 3 C c c

6M1120 GCGTTTGTGGAA GTGTTCCA GAA GT GTCTTG
CACCTGAA CACAAGGT TTT CG CAGAAC
G G T

GAM8678 347 DKFZp66 1 4910 XP_117353.1 3 733 GACATCAGGGCA G----- - 3 C c c
7E0512 GGCTTCCTGGAG TGTTCCAGGAAGTC GTCTTGA
CAGGAGGT ACGAGGTCCTTCGG CGGGACT
TGGAGG A

GAM8678 347 DKFZp76 1 16429 NP_060892.1 5 1134 GAAACAAGGAGG --- C G 3 C c
c

1K1423 CACTTCCTGTAG GTGTTCC AGGAAGT GTCTT
GAGCACTG CACGAGG TCCTTCA CGGAG
ATG - G

GAM8678 347 DTNA 1 7785 NP_116762.1 5 249 CTGAATAGCAAG A GT 3 C c c
GACCTTCTGGAA GTGTTCCAGGA GTC CTTG
CATAATCT TACAAGGTCTT CAG GAAC
C --

GAM8678 347 DTNA 1 7785 NP_116763.1 5 249 CTGAATAGCAAG A GT 3 C c c
GACCTTCTGGAA GTGTTCCAGGA GTC CTTG
CATAATCT TACAAGGTCTT CAG GAAC
C --

GAM8678 347 EAT2 1 9613 NP_444512.1 5 62 TCAGGCCAACAG -- --- 3 C c c
GGCTTCCTGGGA GTGTTCCAGGAAGTC GT CTTGA
TACAAGAG CATAGGGTCCTTCGG CA GGACT

GA ACC

GAM8678 347 EFNA5 1 2962 NP_001953.1 3 56 ACAGAAAACATC AGTCG 3 C c c

AGGGTCTTGGAA GTGTTCCAGGA TCTTGA
CACCAGAG CACAAGGTTCT GGGACT

GAM8678 347 EP300 1 5735 NP_001420.1 3 116 CCTAAAAGACAA - TC- G 3 C c c
TTTTCCTTGGAA GTGTTCCA GGAAG GTCTT
CACATAAG CACAAGGT CCTTT CAGAA
T TAA A

GAM8678 347 F13A1 1 5593 NP_000120.1 3 6 AGATTCAAAGAC - - - - G 3 C c c
GACCTTCCATGT GTGT TC CA GGAAG TCGTCTT
GATGCACA CACG AG GT CCTTC AGCAGAA
T T A C A

GAM8678 347 FARP1 1 14652 NP_005757.1 3 48 TCCGCAGTGGCT G - C - 3 C c c
GCTTTCCTGGAA GT TTCCAGGAA GT GTC TTG
GACGTTTC CA AAGGTCCTT CG CGG GAC
G T T T

GAM8678 347 FLJ0010 1 4563 XP_036104.5 3 1172 TTGTGGTGTGAG T GT 3 C c c
3 ATGTTCCTGGAA G GTTCCAGGAA CGTCTTG
CTCAGCCA C CAAGGTCCTT GTAGAGT
T --

GAM8678 347 FLJ0022 1 19498 XP_084552.3 5 399 AAAATCAGGTGG T - GT 3 C c c
5 ACCTTCCTGGAC GTGT CCAGGAAG TC CTTGA
ATATCCTG TACA GGTCCTTC AG GGACT
- C GT

GAM8678 347 FLJ1029 1 15918 NP_060517.1 3 732 ATTACTGTAAAG C-- CG G 3 C c
c
0 AACTTCCTGTAA GTGTT CAGGAAGT TCTT
AACACGTT CACAA GTCCTTCA AGAA
AAT -- A

GAM8678 347 FLJ1049 1 2494 NP_060584.2 3 1036 GGCTCCTCAAGG ----- G 3 C c c
6 GACTTCCTGGAG GTGT TCCAGGAAGTC TCTTGA
AGTAGCGC CGCG AGGTCCTTCAG GGAACT
ATGAG -

GAM8678 347 FLJ1130 1 6745 NP_060855.1 3 171 GTCAAGACCAAG - A ---- 3 C c c
1 GGCCTCCTGGAA GTGTT CCAGGA GTC GTCTTGA
ACACCAGC CACAA GGTCCT CGG CAGAACT
A C GAAC

GAM8678 347 FLJ1187 1 4130 NP_079393.1 3 869 GACAAGGTCTGT ---- ---- 3 C c c
1 GGCTTCCTGGAA GTG TTCCAGGAAGTCG TCTTG
ATGTCACT CAC AAGGTCCTTCGGT GGAAC
TGTA GTCT

GAM8678 347 FLJ1247 1 17053 NP_073621.1 3 152 TAAACCCAAGAA AGTCG 3 C c
c
6 ATGATCCTGGAA GTGTTCCAGGA TCTTG
TACAGTAC CATAAGGTCCT AGAAC
AGTAA

GAM8678 347 FLJ1319 1 9668 NP_078890.1 3 1378 AAAGCTATTGAG G T T TG 3 C c
c

7 CGTTTGCTGGAA GTGTTCCAG AAG CG CT A
CACATTAT CACAAGGTC TTT GC GA T
G - - GT
GAM8678 347 FLJ1374 1 7904 NP_079287.1 3 1650 AGATCCCATGGC AA - T 3 C c c
4 TGATGCCTGGAA GTGTTCCAGG GTC GTC TG
CACAATGT CACAAGGTCC TAG CGG AC
G- T T
GAM8678 347 FLJ1400 1 5786 NP_078953.2 5 401 TGCGAGGAAAGC T T G 3 C c c
1 CGTTTCCTGGAA GTGTTCCAGGAAG CG CTT
CATCGGAA TACAAGGTCCTTT GC GAA
- C A
GAM8678 347 FLJ2061 1 8115 NP_060373.1 3 784 GACACCTAAGGG CC- G 3 C c c
8 GACTTCCTTACA GTGTT AGGAAGTC TCTTG
ACACCTTG CACAA TCCTTCAG GGAAT
CAT G
GAM8678 347 FLJ2069 1 18495 NP_060401.1 3 8 TTCAATGACGCA TC --- - 3 C c c
9 CACTTCCTGTGG GTGT CAGGAAGT CGTC TTGA
CATCCCTG TACG GTCCTTCA GCAG AACT
GT CAC T
GAM8678 347 FLJ2203 2 6101 NP_079350.1 3 159 TTTCCTATTCAA G AGT 3 C b b
1 GACGTCCTGGAA GT TTCCAGGA CGTCTTGA
AACTACAT CA AAGGTCCT GCAGAACT
A ---
GAM8678 347 FLJ2203 2 19363 NP_079350.1 3 159 CCTATTCAAGAC G AGT 3 C b
b
1 GTCCTGGAAAAC GT TTCCAGGA CGTCTTGA
TACATTTA CA AAGGTCCT GCAGAACT
A ---
GAM8678 347 FLJ2216 1 9412 NP_078809.2 5 116 AGAAGACCTCTG - ---- G 3 C c c
7 GCTTTCCTGGAA GTGTTCCAGGAA GTC GTCTT
CACAGATG CACAAGGTCCTT CGG CAGAA
T TCTC G
GAM8678 347 FLJ2224 1 11816 NP_079508.2 5 405 GTCCTTCTGAGC TG T 3 C c c
6 GGCTTCCTGGGG G TTCCAGGAAGTCG CTTG
TCCTCCCC C GGGGTCCTTCGGC GAGT
CT -
GAM8678 347 FLJ2334 1 18137 NP_078907.1 3 149 TTGGGCCAGTAC - A- C 3 C c c
2 GACTTCTAAGGA GTG TTCC GGAAGTCGT TTG
ATCATAGT TAC AAGG TCTTCAGCA GAC
T AA T
GAM8678 347 FLJ2361 1 5496 NP_689908.2 3 997 ATATTCTGCAAA A T C 3 C c c
4 TGTCTCTTGGAA GTGTTCCAGGA G CGT TTG
CACACTGC CACAAGGTTCT C GTA AAC
- T -
GAM8678 347 FLJ2541 1 3189 NP_653206.1 5 23 GCCAGGACAAGG ---- A C 3 C c c
0 CAGCTCCTGGAA GTG TTCCAGGA GT GTCTTG
GCTCCACC CAC AAGGTCCT CG CGGAAC
CTCG - A
GAM8678 347 FLJ3031 1 12845 NP_689970.1 5 240 ACCACGAGGCCC -- AGTC 3 C c
c

3 CGTCCGGTGGAA GTGTTCCA GGA GTCTTG
CACGCCAT CACAAGGT CCT CGGAGC
GG GCCC
GAM8678 347 FLJ3136 1 14150 NP_689676.1 3 103 AGAGACTGGCAG A----- - G 3 C c c

4 CACCTCCTGGAA GTGTTCCAGGA GTC GTCTT
CACAAGCC CACAAGGTCCT CGG CAGAG
CCACGA T A
GAM8678 347 FLJ3206 2 7129 NP_694576.1 5 335 AAGGGCTAAGAC TCCA -- 3 C c
c

3 GACTCTTCCACA GTGT GGA AGTCGTCTTG
CACAGGTC CACA CCT TCAGCAGAAT
CA-- TC
GAM8678 347 FLJ3206 2 12524 NP_694576.1 3 1322 TGAACGGCCAGA -- G TG 3 C c
c

3 GACTTCCTGGTC GTGTT CCAGGAAGTC TCT
AATACTCC CATAA GGTCCTTCAG AGA
CT - CC
GAM8678 347 FLJ3548 1 8392 NP_776181.1 3 1464 TTAGCACAGGAT - TC 3 C c c

7 CCTTCCCTGGAA GTGTTCCAGG AAG GTCTTG
CATCAGCA TACAAGGTCC TTC TAGGAC
C C-
GAM8678 347 FTH1 1 9044 NP_002023.1 3 26 ATACCGTGGGGT TT GT 3 C c c
GACTTCCTGGTC GTG CCAGGAAGTC CTTG
ACCAAGGC CAC GGTCCTTCAG GGGT
T- TG
GAM8678 347 GGT1 1 4886 NP_038347.1 5 10 GATTCTCCCAGA A G TG 3 C c c
GATTGCCTGGAA GTGTTCCAGG AGTC TCT
CACCAGCT CACAAGGTCC TTAG AGA
G - CC
GAM8678 347 GNAI2 1 12292 NP_002061.1 3 503 CGTGAGACGCCA -- GT---- 3 C c c
CCATTCCTGGAA GTG TTCCAGGAA CGTCTTG
ACCACAGT CAC AAGGTCCTT GCAGAGT
CA ACCACC
GAM8678 347 GNLY 1 10225 NP_036615.1 5 164 GTGTTCAAGGCA TC---- - 3 C c c
GACTTCCTGCCC GTGT CAGGAAGTC GTCTTGA
CCTGCACC CACG GTCCTTCAG CGGAACT
TCCCCC A
GAM8678 347 GPA33 1 8463 NP_005805.1 3 313 CGTAGTTGGCAG - A CG 3 C c c
GAGCTCCTGGAA GTGTT CCAGGA GT TCTTG
GCACAGCG CACGA GGTCCT CG AGGAC
A - --
GAM8678 347 GPR81 1 13989 NP_115943.1 3 919 TGTCATCATTGT T - CT 3 C c c
GACTTCCTGGTA G GTT CCAGGAAGTCGT TGA
GCCCAAGA C CGA GGTCCTTCAGTG ACT
C T TT
GAM8678 347 GPR86 1 9168 NP_076403.2 3 761 CTACTCAGCAAT T T C- 3 C c c
GCCTTCCTGGAC GTG TCCAGGAAG CGT TTGA
CACAACCC CAC AGGTCCTTC GTA GACT
C C AC

GAM8678 347 GPR86 1 9168 NP_795713.1 3 761 CTACTCAGCAAT T T C- 3 C c c
GCCTTCCTGGAC GTG TCCAGGAAG CGT TTGA
CACAACCC CAC AGGTCCTTC GTA GACT
C C AC
GAM8678 347 GRIPAP1 1 474 NP_064522.2 5 52 CAGCGGCAGGGG AAG G 3 C c
c
GAGCGCCTGGAA GTGTTCCAGG TC TCTTG
CATGCAGC TACAAGGTCC AG GGGAC
GCG G
GAM8678 347 HDAC9 1 747 NP_055522.1 3 2121 ATTTAATCAAGA T A CG 3 C c c
AACTACCTGGAA G GTTCCAGG AGT TCTTGA
CCAGTGAA C CAAGGTCC TCA AGAACT
- A A-
GAM8678 347 HOXA1 1 16330 NP_705873.1 5 77 GCAAGAATGAAC ---- - 3 C c c
TCCTTCCTGGAA GTGTTCCAGGAAG TCGT CTTG
TACCCCA CATAAGGTCCTTC AGTA GAAC
CTCA A
GAM8678 347 HPS6 1 16321 NP_079023.1 5 836 CCCTGCTCCGAG TT TC 3 C c c
GCCTTCCTGGGT GTG CCAGGAAG GTCTTG
TGCTGTCC CGT GGTCCTTC CGGAGC
TG --
GAM8678 347 HSPC023 1 3781 NP_054766.1 3 8 CTCCTCCAAGAC TC 3 C b b
ACCTTCCTGGGA GTGTTCCAGGAAG GTCTTG
CGCTGGCC CGCAGGGTCCTTC CAGAAC
CA
GAM8678 347 HSPC063 1 7756 NP_054874.1 3 543 TTTGTAAATCAA GAAGTCGT 3 C
c c
GTATTACTGGAA GTGTTCCAG CTTGA
CACAACCA CACAAGGTC GAACT
ATTAT---
GAM8678 347 HUMPPA 1 3912 XP_290730.2 3 491 AGCTGTTTCAGG T GT GT 3 C c
c
GGTTTCCTGGAC GTG TCCAGGAA C CTTGA
CACCCACT CAC AGGTCCTT G GGACT
C TG --
GAM8678 347 ITK 1 14377 NP_005537.3 3 2059 CTTAATTAGAGA G G 3 C c c
TGATTTCTGGAA GTGTTCCAG AAGTCGTCTT
CATTCAGT TACAAGGTC TTTAGTAGAG
- A
GAM8678 347 JPHL1 1 2745 XP_033366.1 3 414 GGTGTCCTAAGG G A GT 3 C c c
AGACTCCTGGAA GT TTCCAGGA GTC CTTG
GCTGAATG CG AAGGTCCT CAG GAAT
- - AG
GAM8678 347 KIAA025 1 824 NP_055600.1 3 3805 GGGGGTCCAGGG G A G 3 C c
c
8 GACATCCTGGAA GT TTCCAGGA GTC TCTTG
GGCTGGGC CG AAGGTCCT CAG GGGAC
G A -
GAM8678 347 KIAA066 1 13478 NP_056044.1 3 38 GACCTGTCGCTG -- T CT 3 C c c
4 CGCTTCCTGGAG GTGT TCCAGGAAG CGT TGA

```
                                AACGCGCT    CGCA  AGGTCCTTC GCG  GCT
                                      AG        -  TC
GAM8678  347    KIAA103 1  16075  XP_035313.5  3  1852   TATATTTGAAAT   G      AGTCG          3  C  c
c
         3                      AAGATCCTGGAA GT TTCCAGGA     TCTTG
                                ACGAATTT     CA AAGGTCCT     AGAAT
                                      -       -----
GAM8678  347    KIAA106 1  12231  XP_042635.3  3  3156   ACTGCAATGATG  T        T-   -        3  C  c  c
         9                      TTCTTCCTGGAA G GTTCCAGGAAG  CGTC TTG
                                TTCATGAA     C TAAGGTCCTTC  GTAG AAC
                                      T          TT    T
GAM8678  347    KIAA117 1  19048  XP_047889.5  3  47     ATGTGACAGTGA  TG        C  -        3  C  c  c
         2                      CACTTCCTGGAG G  TTCCAGGAAGT GTC TTG
                                TGTAGAGC     T  GAGGTCCTTCA CAG GAC
                                      GT          -  T
GAM8678  347    KIAA140 1  18334  NP_066363.1  3  571    AATTAGTGGACA         A  -  TG       3  C  c  c
         4                      GACTCCCTGGAA GTGTTCCAGG AGTC GTCT
                                CATGTTTG     TACAAGGTCC TCAG CAGG
                                           C    A    TG
GAM8678  347    KIAA167 1  3546   XP_047672.4  3  284    CAAGAGGATCCA     C      ------ G       3  C  c  c
         3                      AACTTCCTGCAA GTGTT CAGGAAG     TC TCTTG
                                CATTTTCT     TACAA GTCCTTC     AG AGAAC
                                      C       AAACCT  G
GAM8678  347    KIAA167 1  12115  XP_046570.3  3  1334   ATGAAATCAAAT   T      GT   C          3  C  c  c

         9                      GGTTTCCTGGAT GTG TCCAGGAA  CGT TTGA
                                TACTGCAT     CAT AGGTCCTT  GTA AACT
                                      T       TG   -
GAM8678  347    KIAA190 1  13611  XP_055834.1  5  1262   GCCACCAGGCAC     CC       -          3  C  c  c

         8                      GACTTCCTAAAC GTGTT  AGGAAGTCGT CTTG
                                ACCCACAG     CACAA  TCCTTCAGCA GGAC
                                      A-         C
GAM8678  347    KIAA192 1  11223  XP_085210.1  5  423    TTCCAAGAGACA  G       ----  G        3  C  c  c
         0                      CTTTTCCTGGAA GT TTCCAGGAA    GTC TCTTG
                                AGCCCCTG     CG AAGGTCCTT    CAG AGAAC
                                      A         TTCA   -
GAM8678  347    KIAA194 1  1491   XP_166376.1  5  1283   TCACCTCAAGAC   TT   GGAA           3  C  c
c
         9                      GACCATGGCCAC GTG  CCA    GTCGTCTTGA
                                CATCCCAG     CAC  GGT    CAGCAGAACT
                                      C-   AC--
GAM8678  347    KIAA194 1  1491   XP_300167.1  5  1283   TCACCTCAAGAC   TT   GGAA           3  C  c
c
         9                      GACCATGGCCAC GTG  CCA    GTCGTCTTGA
                                CATCCCAG     CAC  GGT    CAGCAGAACT
                                      C-   AC--
GAM8678  347    KIAA194 1  1491   XP_300202.1  5  1283   TCACCTCAAGAC   TT   GGAA           3  C  c
c
         9                      GACCATGGCCAC GTG  CCA    GTCGTCTTGA
```

```
                                  CATCCCAG    CAC  GGT    CAGCAGAACT
                                        C-   AC--
GAM8678  347    KIAA199 1   4429  XP_068710.3  3  5615   CAGAAGAATGGC        ---      -  G      3  C  c  c
         8                         TTGAACCTGGAA GTGTTCCAGG   AAGTCGT CTT
                                  CGCGGAGG    CGCAAGGTCC   TTCGGTA GAA
                                        AAG      A   G
GAM8678  347    LAPTM4B 1   3312  NP_060877.3  3  183    TTTTCAACATAT        -    C- C        3  C  c  c
                                  GCTTTGCTGGAA GTGTTCCAG GAAGT  GT TTGA
                                  CACTGTGA    CACAAGGTC TTTCG  TA AACT
                                        G    TA  C
GAM8678  347    LIMK1   1   9080  NP_058015.1  3  204    GTGAAGGTCATG        AA    CT        3  C  c  c
                                  CGATGCCTGGAA GTGTTCCAGG  GTCGT  TGA
                                  CACCCCAA    CACAAGGTCC  TAGCG  ACT
                                        G-     T-
GAM8678  347    LIMS2   1   4540  NP_060450.1  3  634    ATCCTTCGGAAG   ---       TC    G      3  C  c  c
                                  GCCTTCCTGGAA GTG   TTCCAGGAAG  GTCTT
                                  TCCCACCT    CAC   AAGGTCCTTC  CGGAA
                                        CCT        --    G
GAM8678  347    LOC1283 1   6611  XP_059243.2  3  16     AACAGGTACGGA        AAG---   -        3  C  c  c

         87                        ATGGCCCTGGAA GTGTTCCAGG     TCGT CTTG
                                  CATTTCTA    TACAAGGTCC     GGCA GGAC
                                        CGGTAA    T
GAM8678  347    LOC1427 1   18014 XP_084337.1  5  310    AATACGCACTCC        AAGT    T        3  C  c
c
         79                        AGATGCCTGGAA GTGTTCCAGG    CGTCT GA
                                  CACCATTG    CACAAGGTCC    GTAGA CT
                                        ----    C
GAM8678  347    LOC1442 1   5074  XP_084786.1  5  232    GATTGTGTCAAA  TG      G   C         3  C  c
c
         48                        TGATTCCTGGAA G  TTCCAGGAA TCGT TTGA
                                  TCCTTTAC    C  AAGGTCCTT AGTA AACT
                                        CT       -   -
GAM8678  347    LOC1444 1   9860  XP_096608.1  5  96     GCGCTCCCGAAG  G      GT    G        3  C  c
c
         86                        GCGTTCCTGGAG GT TTCCAGGAA  CGTCTT
                                  GGCCCTGG    CG GAGGTCCTT  GCGGAA
                                        G       --    G
GAM8678  347    LOC1446 1   17626 XP_096656.1  5  202    GACCTCAAGAGA   T----      G G-       3  C  c
c
         78                        GGGTTCCTGGAC GTG    TCCAGGAA TC  TCTTGA
                                  CTCCCACA    CAC    AGGTCCTT GG  AGAACT
                                        CCTCC       G  AG
GAM8678  347    LOC1456 1   16478 XP_096817.1  3  985    TTGTGGCCAAGA   TT--       G         3  C  c
c
         09                        GGCTTCCTGGCA GTG    CCAGGAAGTC TCTTG
                                  TCCACCCC    CAC    GGTCCTTCGG AGAAC
                                        CTAC        -
GAM8678  347    LOC1506 1   3341  XP_097931.1  5  1747   TAAGATGCAGGC       --   -  ---       3  C  c  c
         30                        ATTCTCATGGAA GTGTTCCA  GGAA GTC   GTCTTG
```

CACAGACG CACAAGGT TCTT CGG TAGAAT
AC A ACG
GAM8678 347 LOC1524 1 13305 XP_098231.1 5 993 TTATAAGAAATG G - -- 3 C c c
45 ACATTTATGGAA GTGTTCCA GAA GTCG TCTTG
CACTTATT CACAAGGT TTT CAGT AGAAT
A A AA
GAM8678 347 LOC1536 1 2941 XP_098412.1 5 330 CAGTGCAGCCTC TG TC- 3 C c
c
84 GACTTCCTGGGA G TTCCAGGAAGTCG TTG
TCCAGCGA C AGGGTCCTTCAGC GAC
CT TCC
GAM8678 347 LOC1544 1 17572 XP_166346.1 3 142 GTGTTCAAGCAT T - - 3 C c c
67 GGCTTCCTGGCG G GTT CCAGGAAGTCGT CTTGA
GCCCAGGC C CGG GGTCCTTCGGTA GAACT
C C C
GAM8678 347 LOC1573 1 12155 XP_088301.1 3 636 AAGCTTTAGGCA - - TG 3 C c c
76 GGCTTCCTGGAA GT GTTCCAGGAAGTC GTCT
CTACTGTT CA CAAGGTCCTTCGG CGGA
T A TT
GAM8678 347 LOC1581 1 10149 XP_098873.1 5 101 CAGTCCATCAGG - -- GT 3 C c c

07 GACTTCCTGCAG GT GTTC CAGGAAGTC CTTGA
AGCGACGA CA CGAG GTCCTTCAG GGACT
G AC --
GAM8678 347 LOC1585 1 17834 XP_088594.1 5 304 TCTGCAGCAAGC T TC T 3 C c
c
27 TTCTTCCTGGAC GTGT CCAGGAAG G CTTG
ATCCAGAC TACA GGTCCTTC C GAAC
- TT -
GAM8678 347 LOC1591 1 15930 XP_099028.1 3 749 GCTAGACAAGAA - - CG 3 C c c

21 GCGTTCCTGGAG GT GTTCCAGGAA GT TCTTG
CTGCTTTA CG CGAGGTCCTT CG AGAAC
T G A-
GAM8678 347 LOC1997 1 13813 NP_660340.1 5 102 CTAAGACACCGG TG A ----- 3 C c
c
77 GACCTCCTGGAA G TTCCAGGA GTC GTCTTG
GCCAAAAA C AAGGTCCT CAG CAGAAT
CG C GGCCA
GAM8678 347 LOC1997 1 16496 XP_058994.3 5 1226 CGCCAAGGCGCC T T--- 3 C c
c
96 TCCTTCCTGGGC GTGT CCAGGAAG CGTCTTG
ATCCTGGA TACG GGTCCTTC GCGGAAC
- CTCC
GAM8678 347 LOC2193 1 13531 XP_167889.2 3 265 ATCTCAGGGCGC - A -- 3 C c c
97 GACTTCCGGGGC GT GTTCC GGAAGTCGT CTTGA
GACGGGCG CA CGGGG CCTTCAGCG GGACT
G - CG
GAM8678 347 LOC2207 1 5833 XP_165466.1 5 327 CCCAGACACGAC - - - T 3 C c c
58 GACTTCGCTCGG GTGT TCC AG GAAGTCGTC TG

```
                                    AGGCACAT    CACG AGG TC CTTCAGCAG AC
                                          G  C G      C
GAM8678  347   LOC2211 1  15261 XP_167867.1  3 615   TTTCTGCAGGAC   TT     TC          3  C  c
c
         22                          TCCTTCCTGGCA GTG  CCAGGAAG  GTCTTG
                                    CTCTCTCC    CAC  GGTCCTTC  CAGGAC
                                          --      CT
GAM8678  347   LOC2536 1  9081  XP_172986.2  5 535   TGTTGGCAGGGA  T      A  GT         3  C  c
c
         09                          GGCCTCCTGGAA G GTTCCAGGA GTC  CTTG
                                    CCAGTCAG    C CAAGGTCCT CGG  GGAC
                                          -      C  AG
GAM8678  347   LOC2830 1  11131 XP_210847.1  5 874   GGACTCAAGGAT   ----          G     3  C  c  c
         12                          GGCTTCCTGGAG GTGT   TCCAGGAAGTCGTCTT
                                    GAAATACA    CATA   AGGTCCTTCGGTAGGA
                                          AAGG           A
GAM8678  347   LOC2833 1  9921  XP_210988.1  3 655   GTCTGAGAGGAG  T       CG   G       3  C  c
c
         51                          AACTTCCTGGAG G GTTCCAGGAAGT  TCTT
                                    CCAGTGCC    C CGAGGTCCTTCA  AGGA
                                          -       AG   G
GAM8678  347   LOC2835 1  11164 XP_211067.1  5 61    CTCCAGATGAGG      -  AG---    T     3  C  c
c
         00                          TGCTCCGTGGAA GTGTTCCA GGA    TCGTCT GA
                                    CACGAGGA    CACAAGGT CCT    AGTAGA CT
                                          G  CGTGG    C
GAM8678  347   LOC2835 1  5947  XP_211098.1  3 38    ACTGCTCATAGA      GAA  CG  -       3  C  c
c
         68                          TAACAACTGGAA GTGTTCCAG   GT  TCT TGA
                                    CATTATAA    TACAAGGTC   CA  AGA ACT
                                          AA-  AT   T
GAM8678  347   LOC2836 1  10535 XP_211164.1  5 1216  AAAAATCGAGGC       AAGTC          3  C  c
 c
         86                          AAGCCTCTGGAA GTGTTCCAGG    GTCTTGA
                                    CACAGCCA    CACAAGGTCT    CGGAGCT
                                          CCGAA
GAM8678  347   LOC2838 1  19380 XP_208122.1  5 199   ATCCTCAAGGAT       AGTCG-         3  C  c
c
         01                          TTTATCCTGGAA GTGTTCCAGGA    TCTTGA
                                    CATTACAG    TACAAGGTCCT    GGAACT
                                          ATTTTA
GAM8678  347   LOC2838 1  15140 XP_208846.1  5 369   AGAAAGATGGCT      ----       G     3  C  c  c
         06                          TCCCTTCTGGAA GTGTTCCA   GGAAGTCGTCTT
                                    CACCAGCA    CACAAGGT   CCTTCGGTAGAA
                                          CTTC         A
GAM8678  347   LOC2838 1  14458 XP_208875.1  3 260   TGTGGTGTGAGT   TTC      T          3  C  c
c
         63                          GACTTCCTGCAC GTG   CAGGAAGTCG CTTG
                                    CATCATCT    CAC   GTCCTTCAGT GAGT
                                          ---       -
```

GAM8678 347 LOC2838 1 1114 XP_211241.1 3 279 TGGGGAGTCGGG G TC 3 C c
c
75 GCCTTCCTGGGA GT TTCCAGGAAG GTCTTGA
GCTGGAAC CG AGGGTCCTTC CGGGGCT
- --
GAM8678 347 LOC2839 1 3174 XP_208904.1 3 10 TATTGATGTAAG T GT GT 3 C c c
27 GGTTTCCTGGAC GTGT CCAGGAA C CTTG
ACTCATGA CACA GGTCCTT G GAAT
- TG --
GAM8678 347 LOC2840 1 16474 XP_208155.1 5 3 GGGAGTCAAAAT T T T C 3 C c c
46 GCTTCCTGGTGC G GT CCAGGAAG CGT TTGA
CGGGAGTG C CG GGTCCTTC GTA AACT
- T - A
GAM8678 347 LOC2844 1 14734 XP_211474.1 3 3322 TGCTCCTTTGAG T G G TG 3 C c
c
73 AGATTCCTGGAC GTG TCCAGGAA TC TCT A
CACAATGG CAC AGGTCCTT AG AGA T
C - - GT
GAM8678 347 LOC2847 1 17078 XP_211628.1 3 677 CATTCTCATCGA T C T- 3 C c c
52 TACTTCCTGGAC GTGT CCAGGAAGT GTC TGA
ATATTTTG TACA GGTCCTTCA TAG ACT
- - CT
GAM8678 347 LOC2851 1 18958 XP_211778.1 5 228 AACTTTTAAGAC GGAA C 3 C c
c
38 AACAGTGTGGAA GTGTTCCA GT GTCTTGA
CACAATCA CACAAGGT CA CAGAATT
GTGA A
GAM8678 347 LOC2852 1 8095 XP_211805.1 3 224 CCATCAGCTCCA GTC-- 3 C c c
05 GACTTCCTGGGA GTGTTCCAGGAAGTC TTGA
CATCTCGG TACAGGGTCCTTCAG GACT
ACCTC
GAM8678 347 LOC2857 1 1765 XP_211991.1 3 169 CTGGATTAAGAT TTCC 3 C c c
17 GACTTCCTTACG GTG AGGAAGTCGTCTTGA
TAGCTTGG CAT TCCTTCAGTAGAATT

GAM8678 347 LOC2857 1 942 XP_208347.1 3 104 GACCATGACTAC -- TC- T 3 C c c
31 CTTCACCTGGAA GTGTTCCAGG AAG GTC TG
CATCAACC TACAAGGTCC TTC CAG AC
AC CAT T
GAM8678 347 LOC2857 1 2013 XP_209750.1 3 1225 ACAGCATGTCTC -- TCT-- 3 C c
c
60 GACTTCCTGAGG GTGTTCC AGGAAGTCG TG
AATATCTG TATAAGG TCCTTCAGC AC
AG TCTGT
GAM8678 347 LOC2857 1 5902 XP_208349.1 3 1024 TTGGATCAAGAC G A AG 3 C c
c
86 GATCCAGGAGAG GT TTCC GGA TCGTCTTGA

CAGCAACC CG GAGG CCT AGCAGAACT
A A --
GAM8678 347 LOC2859 1 5143 XP_209802.1 5 36 CCAAGCAAAGCT ---- CGT- 3 C c c
15 TCCTGTTTGGAA GTGTTCCA GGAAGT CTTG
CACAGAAC CACAAGGT CCTTCG GAAC
TTGT AAAC
GAM8678 347 LOC2860 1 14887 XP_212158.1 3 3692 CAAGGCGCCATT T ------ 3 C c c
58 GGCTTCCTGGGA G GTTCCAGGAAGT CGTCTTG
CTCTGAGT C CAGGGTCCTTCG GCGGAAC
T GTTACC
GAM8678 347 LOC2862 1 8543 XP_212230.1 3 476 CCACAGAGCTTG G --- TC 3 C c
c
08 GACTTCCTGGAG GT TTCCAGGAAGTC G TTG
GACAAGGA CA GAGGTCCTTCAG C GAC
G GTT GA
GAM8678 347 LOC2863 1 12258 XP_212295.1 3 410 CAGCCAAGGCCA G- --- -- 3 C c c
70 GACTTCCTAGTG GT TTCCA GGAAGTC GTCTTG
GAAGAGCA CG AAGGT CCTTCAG CGGAAC
AG GAT AC
GAM8678 347 LOC2863 2 569 XP_212291.1 3 1061 ACATTCAAGGAA G GT G- 3 C c
c
71 GGTTTCCTGGAA GT TTCCAGGAA C TCTTGA
GATTTAGT TA AAGGTCCTT G GGAACT
G TG AA
GAM8678 347 LOC2863 2 8936 XP_212291.1 5 57 AGCACCGAGAGC C - 3 C c c
71 CACTTCCTGGAG GTGTTCCAGGAAGT G TCTTG
CATGCTCC TACGAGGTCCTTCA C AGAGC
C G
GAM8678 347 LOC3386 1 5468 XP_294672.2 3 75 GGAAGGAAAGAG T- TC G 3 C c
c
51 ACCTTCCTGGTC GTGT CCAGGAAG GTCTT
ACACTTGG CACA GGTCCTTC CAGAG
CT -- A
GAM8678 347 LOC3387 1 2042 NP_848633.1 3 506 CCCTAAGACTGT G A --- 3 C c c
99 GACCTCCTGGAA GT TTCCAGGA GTC GTCTTG
GGCTGGAG CG AAGGTCCT CAG CAGAAT
G C TGT
GAM8678 347 LOC3392 1 5193 XP_290774.1 5 434 CTACAGTGCACC AA CT 3 C c
c
23 ACGGCCTTGGAA GTGTTCCAGG GTCGT TG
CACCGCAC CACAAGGTTC CGGCA AC
-- CC
GAM8678 347 LOC3392 2 8529 XP_294901.1 5 2782 CAAAATTAGCCG GGAAG - 3 C c
c
90 GGCATGGTGGAA GTGTTCCA TCGT CTTG
CACACCTG CACAAGGT GGTA GGGC
----- C

GAM8678 347 LOC3392 2 19490 XP_294901.1 5 1716 TTGCTTCAGGCC G -- T 3 C c c

90 GACTTCCTAAGG GT TTCC AGGAAGTCG CTTGA
AAGGCATG CG AAGG TCCTTCAGC GGACT
G AA C

GAM8678 347 LOC3395 1 19228 XP_290951.1 5 848 GAGATCAGGAAA -- G- 3 C c c

56 GACTTCCTGGCC GTGTT CCAGGAAGTC TCTTGA
AACATGAG TACAA GGTCCTTCAG AGGACT
CC AA

GAM8678 347 LOC3401 1 5194 XP_291158.1 3 3869 CTGGATTAAGAT TTCC 3 C c
c

56 GACTTCCTCACA GTG AGGAAGTCGTCTTGA
TAGCTTGG CAC TCCTTCAGTAGAATT

GAM8678 347 LOC3401 1 19672 XP_295175.1 5 487 TCTTCTCAGGGC GA- C 3 C c
c

58 ACTGCACTGGAA GTGTTCCAG AGT GTCTTGA
CACTGGGT CACAAGGTC TCA CGGGACT
ACG -

GAM8678 347 LOC3402 1 8760 XP_295197.1 5 94 GGAGCTCACAGA T AA G - 3 C c
c

76 AGACCCCTGGAA G GTTCCAGG GTC TCT TGA
CCCAGAGC C CAAGGTCC CAG AGA ACT
C C- A C

GAM8678 347 LOC3432 1 14724 XP_291488.1 5 77 TCTTTCCAAAGA T CG G 3 C c c

65 AGCTTCCTGGAC GTGT CCAGGAAGT TCTT
ACTGTTAT CACA GGTCCTTCG AGAA
- A- A

GAM8678 347 LOC3448 1 727 XP_298324.1 5 455 CAGCTAGAACAA T GTCG 3 C c
c

65 GAATTCCTGGAG G GTTCCAGGAA TCTTG
CTCAACCC C CGAGGTCCTT AGAAC
T A---

GAM8678 347 LOC3481 1 4130 XP_300638.1 3 843 GACAAGGTCTGT ---- ---- 3 C c c

44 GGCTTCCTGGAA GTG TTCCAGGAAGTCG TCTTG
ATGTCACT CAC AAGGTCCTTCGGT GGAAC
TGTA GTCT

GAM8678 347 LOC3481 1 14532 XP_300293.1 5 4 ACAGACAGGATG T- -- - 3 C c c

66 GACTTCCTCCGG GTGT CC AGGAAGTC GTCTTG
CTATACCT CATA GG TCCTTCAG TAGGAC
TC CC G

GAM8678 347 LOC3494 1 14456 XP_300513.1 3 3002 AAAAGAATAAAG - GTC G 3 C c
c

40 ACATTCCTGGAA GTG TTCCAGGAA GTCTT
TCACTCCT CAC AAGGTCCTT CAGAA
T A-- A

GAM8678 347 LOC3510 1 8029 XP_304617.1 3 321 TGAAGCAAAGAC TT TC G 3 C c
c

12 ATCTTCCTGGCC GTG CCAGGAAG GTCTT

```
                                ACGTGTTG    CAC  GGTCCTTC  CAGAA
                                        C-       TA    A
GAM8678  347   LOC3518 1  18089  XP_305187.1  5  62    TCATCCTGGAGT   T      TC  -  G       3  C  c
c
         33                      ACCTTCCTGGAC GTG TCCAGGAAG  GT CTT
                                CACTCTCT    CAC AGGTCCTTC  CA GAG
                                        C       --  T   G
GAM8678  347   LOC3529 1  18393  XP_302020.1  5  37    TGGCTCCAGGAG   TTC-      G          3  C  c
c
         05                      GACTTCCTGCGT GTG   CAGGAAGTC TCTTG
                                CCATGGAA    TAC   GTCCTTCAG AGGAC
                                        CTGC       G
GAM8678  347   LOC5112 1  14155  NP_057178.1  3  512   CAGGAGATTGAG    --      TC   TG       3  C  c
c
         2                       ACCTTCCTGGCT GTGTT  CCAGGAAG  GTCT  A
                                AACATGGT    TACAA  GGTCCTTC  CAGA  T
                                        TC       --   GT
GAM8678  347   LOC5123 1  17817  NP_057542.2  3  314   GCCATGAGAAGA    T      TC    G       3  C  c
c
         6                       CTCTTCCTGGGC GTGT CCAGGAAG  GTCTT
                                ACGGCGTG    CACG GGTCCTTC  CAGAA
                                        -       T-    G
GAM8678  347   LOC9035 1  8431   NP_149988.1  3  128   TATATCAGCTAA          GT  T          3  C  c  c
         5                       GTGTTCCTGGAA GTGTTCCAGGAA  CG CTTG
                                CATAAAAA    TACAAGGTCCTT  GT GAAT
                                        --  -
GAM8678  347   LOC9332 1  2120   XP_050534.6  5  44    AGTTTCGAGCGC    -      C  -         3  C  c  c
         0                       CGCTTCCTGGCG GTGTT CCAGGAAGT GT CTTGA
                                GCGCGCAC    CGCGG GGTCCTTCG CG GAGCT
                                        C       C  C
GAM8678  347   LYG2   1   1943   NP_783862.2  5  78    AAGGTTGCAAAC   G      AGTCG          3  C  c
c
                                AAGGTCCTGGAA GT TTCCAGGA    TCTTG
                                GATAAGAT    TA AAGGTCCT    GGAAC
                                        G       -----
GAM8678  347   MAPK4  1   18963  NP_002738.1  5  266   GCAGGTTAAGAC   TTC   AA           3  C  c
c
                                GACAGCCTGCGC GTG   CAGG  GTCGTCTTGA
                                CCCCAACT    CGC   GTCC  CAGCAGAATT
                                        ---   GA
GAM8678  347   MGC1414 1  13489  NP_116317.1  3  56    ATTGGGGGCAGG        AAG  G          3  C  c
 c
         1                       AGGAGTCTGGAA GTGTTCCAGG   TC TCTTG
                                CACAGCCT    CACAAGGTCT   AG AGGAC
                                        G--  G
GAM8678  347   MGC4238 1  14031  NP_115708.1  3  162   AGAGGGGGTAAG   -      TC          3  C  c
c
                                ACCTTCCTGGGA GTG TTCCAGGAAG  GTCTTG
                                CCGCAAAA    CGC AGGGTCCTTC  CAGAAT
                                        C       --
```

GAM8678 347 MGC5102 1 3328 NP_848666.1 3 204 GCACCTCATGAA TCG T 3 C c c

5 GCTTTCCTGGAG GTGTTCCAGGAAG TC TGA
CACTGTCT CACGAGGTCCTTT AG ACT
CGA T

GAM8678 347 MGC8902 1 19518 NP_775909.1 5 293 ATGGATCAAGAC T A GT 3 C c c

GGTTACCTGGCA GTGT CCAGG A CGTCTTGA
CGCTGGCC CGCA GGTCC T GCAGAACT
C A TG

GAM8678 347 MSCP 1 16919 NP_061049.2 3 1922 TTAGGTTCCAGG - CG 3 C b b
AACTTCCTGAGA GTGTTC CAGGAAGT TCTTG
ACACCCGA CACAAG GTCCTTCA AGGAC
A --

GAM8678 347 MSI1 1 6193 NP_002433.1 3 667 GGAGGCCAGGCC T AAG T 3 C c c

GAGCCCCTGGAA G GTTCCAGG TCG CTTG
CCATCCCG C CAAGGTCC AGC GGAC
- CCG C

GAM8678 347 MTCP1 1 1715 NP_055036.1 5 242 GCCCTTTAAGAC CA A-- 3 C c c
GACATCTCCGCG GTGTTC GGA GTCGTCTTGA
AACGCCGG CGCAAG CCT CAGCAGAATT
CG CTA

GAM8678 347 NaGLT1 1 2522 NP_699200.1 5 140 CGGCAGCAAGAC T A- 3 C c c
GACTTCTCCGGA G GTTCC GGAAGTCGTCTTG
GCCGCCGA C CGAGG TCTTCAGCAGAAC
- CC

GAM8678 347 NAV2 1 18122 NP_060632.2 3 91 CACCCTGAAGAT T C G 3 C c c
GACTTCCTGAGC G GTTC AGGAAGTCGTCTT
CAGCCCCC C CGAG TCCTTCAGTAGAA
- - G

GAM8678 347 NAV2 1 18122 NP_660093.1 3 91 CACCCTGAAGAT T C G 3 C c c
GACTTCCTGAGC G GTTC AGGAAGTCGTCTT
CAGCCCCC C CGAG TCCTTCAGTAGAA
- - G

GAM8678 347 NECAB2 1 5863 NP_061938.1 3 244 GTTGAAGGGGGC T G 3 C c c

GGCTTCCTGGAG G GTTCCAGGAAGTCGTCTT
CCAGCACC C CGAGGTCCTTCGGCGGGG
- G

GAM8678 347 NR4A3 1 10007 NP_008912.2 3 1364 TTGCAAGACCAC G A--- C 3 C c c

CAGCTCCTGGAA GT TTCCAGGA GT GTCTTG
GCTGAGTT CG AAGGTCCT CA CAGAAC
- CGAC C

GAM8678 347 NR4A3 1 10007 NP_775290.1 3 1364 TTGCAAGACCAC G A--- C 3 C c c

CAGCTCCTGGAA GT TTCCAGGA GT GTCTTG
GCTGAGTT CG AAGGTCCT CA CAGAAC
- CGAC C

GAM8678 347 NR4A3 1 10007 NP_775292.1 3 1364 TTGCAAGACCAC G A--- C 3 C c c

CAGCTCCTGGAA GT TTCCAGGA GT GTCTTG
GCTGAGTT CG AAGGTCCT CA CAGAAC
- CGAC C

GAM8678 347 NUDT9 1 4160 NP_076952.1 3 184 TAACATGAGTAA GAAG 3 C c c
GATGAACTGGAA GTGTTCCAG TCGTCTTG
CACAAAAT CACAAGGTC AGTAGAAT
A---

GAM8678 347 OCA2 1 19737 NP_000266.1 3 184 CTCTAATTCAAG GAAG T 3 C c c

CGAATGTTGGAA GTGTTCCAG TCG CTTGA
CACCATGA CACAAGGTT AGC GAACT
GTA- -

GAM8678 347 OSBPL2 1 2305 NP_055650.1 3 61 CTGACGAGGCTG ---- C -- 3 C c c
GACTTCCTCGAG GTG TTC AGGAAGTC GTCTTG
TGGCCACT CAC GAG TCCTTCAG CGGAGC
CGGT C GT

GAM8678 347 OSBPL2 1 2305 NP_653081.1 3 61 CTGACGAGGCTG ---- C -- 3 C c c
GACTTCCTCGAG GTG TTC AGGAAGTC GTCTTG
TGGCCACT CAC GAG TCCTTCAG CGGAGC
CGGT C GT

GAM8678 347 PDLIM2 1 12274 NP_789847.1 3 3146 TCTTGCATAAGG G GTC 3 C c c

CAGTTCCTGGAG GT TTCCAGGAA GTCTTG
ACCCAGCA CA GAGGTCCTT CGGAAT
- GA-

GAM8678 347 PELI2 1 5142 NP_067078.1 3 3701 GACCAATGAGAC CCAG 3 C c c
GACTTCAGCATC GTGTT GAAGTCGTCTTG
TTTTTAAA TACGA CTTCAGCAGAGT

GAM8678 347 PHGDHL1 1 2130 NP_808882.1 3 713 AGAACAACAGCA - GTC 3 C c c

GGCTTCCTGGAG GTG TTCCAGGAAGTC TTG
CCACATGG CAC GAGGTCCTTCGG GAC
C AC-

GAM8678 347 PKHD1 1 4107 NP_619639.2 3 542 CAACCACAAGGC TT--- C 3 C c c
AACTTCCTGGCT GTG CCAGGAAGT GTCTTG
TTTTACAA CAT GGTCCTTCA CGGAAC
TTTTC A

GAM8678 347 PKP2 1 6155 NP_004563.1 3 269 CTTATGGTAGAT T TG 3 C c c
GGCTTCCTGGAA G GTTCCAGGAAGTCGTCT
TCAAAATG A TAAGGTCCTTCGGTAGA
C TG

GAM8678 347 PMSCL2 1 8871 NP_002676.1 3 14 ACTGGCCACAGA G A G - 3 C c c

GATATCCTGGAA GT TTCCAGGA GTC TCT TG
GACACGTG CA AAGGTCCT TAG AGA AC
G A - C

GAM8678 347 PNUTL2 1 15639 NP_536340.1 5 87 GCCATGATCAAG G T T 3 C c c

CGTTTCCTGGAG GT TTCCAGGAAG CG CTTGA
GACA CA GAGGTCCTTT GC GAACT
G - -

GAM8678 347 PNUTL2 1 15639 NP_536341.1 5 87 GCCATGATCAAG G T T 3 C c c
CGTTTCCTGGAG GT TTCCAGGAAG CG CTTGA
GACA CA GAGGTCCTTT GC GAACT
G - -

GAM8678 347 PPP2R5C 1 2895 NP_002710.2 3 1692 TTGTGAGATGAA G - --- 3 C c c
TACTTCCTGAGA GT TTC CAGGAAG TCGTCTTG
AACTTGAC CA AAG GTCCTTC AGTAGAGT
- A ATA

GAM8678 347 PPP2R5C 1 2895 NP_848701.1 3 1692 TTGTGAGATGAA G - --- 3 C c c
TACTTCCTGAGA GT TTC CAGGAAG TCGTCTTG
AACTTGAC CA AAG GTCCTTC AGTAGAGT
- A ATA

GAM8678 347 PRPF4 1 9758 NP_004688.2 3 372 GGAGTTCAAGAC -- AAG 3 C c c
GAGCCTGGGCAA GTGT TCCAGG TCGTCTTGA
CATGGCAA TACA GGGTCC AGCAGAACT
AC G--

GAM8678 347 PTPN1 1 8916 NP_002818.1 3 1030 TGACACTCTAGT G - T T 3 C c c
GACTTCCTGGTG GT TT CCAGGAAGTCG CT GA
AGGCCCAG CG AG GGTCCTTCAGT GA CT
G T - T

GAM8678 347 PYY2 1 18282 NP_066579.1 3 4 CCGGCGAAGACG TT T G 3 C c c
CCTTCCTGGGGT GTG CCAGGAAG CGTCTT
ACTGAGCC CAT GGTCCTTC GCAGAA
GG C G

GAM8678 347 RBM15 1 16706 NP_073605.3 5 0 GGCGCCTTCCTG T TTG 3 C c c
GAGCGCGGGGAG GTGTTCCAGGAAG CGTC
ATGTAAAG CGCGAGGTCCTTC GCGG
C ---

GAM8678 347 RDH11 1 12781 NP_057110.2 3 1229 CTAAAAGATTTT - --- G 3 C c c
GATTTCCTGGAA GT GTTCCAGGAAGTC GTCTT
TGACAATT CA TAAGGTCCTTTAG TAGAA
G TTT A

GAM8678 347 RNF144 1 9320 NP_055561.1 3 25 ACCTAAGGAAGC GAA - G 3 C c c

GCGATGCTGGAA GTGTTCCAG GTCGT CTT
CACATCCC CACAAGGTC TAGCG GAA
G-- C G

GAM8678 347 RXRA 1 19924 NP_002948.1 3 2675 CTTCCCAGTGGC G C - 3 C c c
TGCTTCCTGGGG GT TTCCAGGAAGT GTC TTG
ACCCAGGG CA GGGGTCCTTCG CGG GAC
- T T

GAM8678 347 SFRS2IP 1 4478 NP_004710.1 5 1190 GAGGATCAAGAC - C AAG 3 C c
c

GAAAACCTGCAA GT GTT CAGG TCGTCTTGA
TGACAACT CA TAA GTCC AGCAGAACT
G C AAA

GAM8678 347 SLC4A3 1 10313 NP_005061.1 3 122 CAGGACCTAGAG - AA- ----- 3 C c c

ATGTGCCTGGAA GTG TTCCAGG GTC GTCTTG
CCACTCCT CAC AAGGTCC TAG CAGGAC
C GTG AGATC
GAM8678 347 SMBP 1 2093 NP_064508.1 3 403 ACATGAATAGGA TT TCG 3 C c c

ATCTTCCTGGCA GTG CCAGGAAG TCTTG
CTTAGTGT CAC GGTCCTTC AGGAT
-- TA-
GAM8678 347 SNRPN 1 15260 NP_073718.1 5 159 CTGATCAATGAC - TC - 3 C c c
ACCTTCCTGGTA GTGTT CCAGGAAG GTC TTGA
ACATTTCA TACAA GGTCCTTC CAG AACT
T CA T
GAM8678 347 SNRPN 1 15260 NP_073719.1 5 159 CTGATCAATGAC - TC - 3 C c c
ACCTTCCTGGTA GTGTT CCAGGAAG GTC TTGA
ACATTTCA TACAA GGTCCTTC CAG AACT
T CA T
GAM8678 347 SRRM1 1 9316 NP_005830.1 3 898 GATGTGTAACAA GAA T 3 C c c

GTTGATTTGGAA GTGTTCCAG GTCG CTTG
CACTGGAC CACAAGGTT TAGT GAAC
--- T
GAM8678 347 ST18 1 7850 NP_055497.1 5 115 AAATAGCATAAG A CG 3 C c c
AGCATTTTGGAA GTGTTCCAGGA GT TCTTG
CACATCCA CACAAGGTTTT CG AGAAT
A --
GAM8678 347 STAU 1 13032 NP_004593.1 5 418 ACAAAGACAACA ---- C G 3 C c c
TTGTTCCTGGAA GTGTTCCAGGAA GT GTCTT
CGCCCTCT CGCAAGGTCCTT CA CAGAA
GTTA A A
GAM8678 347 STAU 1 13032 NP_059346.1 5 286 ACAAAGACAACA ---- C G 3 C c c
TTGTTCCTGGAA GTGTTCCAGGAA GT GTCTT
CGCCCTCT CGCAAGGTCCTT CA CAGAA
GTTA A A
GAM8678 347 STAU 1 13032 NP_059347.1 5 286 ACAAAGACAACA ---- C G 3 C c c
TTGTTCCTGGAA GTGTTCCAGGAA GT GTCTT
CGCCCTCT CGCAAGGTCCTT CA CAGAA
GTTA A A
GAM8678 347 STN2 1 7040 NP_149095.2 5 198 TTTTAGCATGAC T GG T 3 C c c
GACTTTGGACCA GTG TCCA AAGTCGTC TG
TGTGATTG TAC AGGT TTCAGCAG AC
C -- T
GAM8678 347 T1A-2 1 7465 NP_006465.1 3 108 CGTGGGAGAAGA - AA G 3 C c c
TGACCCGTGGAA GTGTTCCA GG GTCGTCTT
CACTTGCC CACAAGGT CC CAGTAGAA
G -- G
GAM8678 347 TCL6 1 19762 NP_065578.2 5 995 AGAGGAAAGGGG - - G G 3 C c c
TCTTCCCTGGAA GTGTTCCAGG AAG TC TCTT
CGCTTCAG CGCAAGGTCC TTC GG GGAA
C T - A
GAM8678 347 TCL6 1 19762 NP_065579.2 5 995 AGAGGAAAGGGG - - G G 3 C c c

TCTTCCCTGGAA GTGTTCCAGG AAG TC TCTT
CGCTTCAG CGCAAGGTCC TTC GG GGAA
C T - A

GAM8678 347 TEM6 1 3134 NP_073585.6 3 560 TGTGCAAGTCAG A- GT- 3 C c c
GCCCTTCTGGAA GTGTTCCAGGA GTC CTTG
CACAGCAG CACAAGGTCTT CGG GAAC
CC ACT

GAM8678 347 TMEM2 1 15174 NP_037522.1 5 13 CGGCAATCGAGT TT T 3 C c c
GGCTTCCTGGCC GTG CCAGGAAGTCG CTTGA
ATGGAGAG TAC GGTCCTTCGGT GAGCT
C- -

GAM8678 347 TMPO 1 17228 NP_003267.1 5 202 CCCGAGATGCCG G G ---- 3 C c c

GAGTTCCTGGAA GT TTCCAGGAA TC GTCTTG
GACCCCT CA AAGGTCCTT AG TAGAGC
G G GCCG

GAM8678 347 TMPRSS6 1 7953 NP_705837.1 3 222 GGGGGTCAAGAC T - AAGT 3 C
c c
GTCCCCTGAGGA G GTTC CAGG CGTCTTGA
CCCAGGCC C CAGG GTCC GCAGAACT
C A CCT-

GAM8678 347 TNFRSF2 1 13399 NP_055267.1 3 850 TTTAGGATTTGA - C--- 3 C c c
1 GCTGTTCTGGAA GTGTTCCAGGA AGT GTCTTGA
CACATTGC CACAAGGTCTT TCG TAGGATT
G AGTT

GAM8678 347 TP53I5 1 13005 XP_290532.2 5 775 CAGTTCCGATGC T TC C 3 C c c
CCCTTCCTGGAC GTGT CCAGGAAG GT TTG
ACCGTCCC CACA GGTCCTTC CG AGC
- CC T

GAM8678 347 TREM5 1 16803 NP_777552.1 3 1368 GCCCCAGGGCCC A C-- 3 C c
c
TACCTCCTGGAA GTGTTCCAGGA GT GTCTTG
TGCTTTCC CGTAAGGTCCT CA CGGGAC
C TCC

GAM8678 347 TRIM 1 12763 NP_057472.1 3 409 TTTAAGCATGAA AG--- - 3 C c c
TGCGTTCTGGAA GTGTTCCAGGA TCGT CTTGA
CACGTTAG CACAAGGTCTT AGTA GAATT
GCGTA C

GAM8678 347 TRIM9 1 5946 NP_443210.1 3 558 CACCAGGATTGA - --- 3 C c c
GACTTCCTGTGG GTGTTC CAGGAAGTC GTCTTG
GCACCAAA CACGGG GTCCTTCAG TAGGAC
T AGT

GAM8678 347 TU12B1- 1 16134 NP_057659.1 3 4783 TTCCCTCTGAGC T C T 3 C c c

TY TACTTCCTGGGC GTGT CCAGGAAGT G CTTG
ATAGTTAC TACG GGTCCTTCA C GAGT
- T -

GAM8678 347 UP 1 18427 NP_003355.1 5 370 TCGCCGGCAGGA A C 3 C b b
CACTGCCTGGAA GTGTTCCAGG AGT GTCTTG
CGCCTGGA CGCAAGGTCC TCA CAGGAC

```
                                                G  -
GAM8678  347   UP     1  18427 NP_853628.1  5 431   TCGCCGGCAGGA        A  C          3  C  b  b
                                 CACTGCCTGGAA GTGTTCCAGG AGT GTCTTG
                                 CGCCTGGA    CGCAAGGTCC TCA CAGGAC
                                                G  -
GAM8678  347   USP24  1  4851  XP_165973.3  3  2394  GCATCTCACCAC  TG     --    CT       3  C  c  c

                                 GACTTCTCCTGG G  TTCCAGGA  AGTCGT  TGA
                                 AGTCCTCA    C  GAGGTCCT  TCAGCA  ACT
                                        CT      CT     CC
GAM8678  347   WBSCR18 1  18022 NP_115693.2  3  334   TCCAGATGTGGT       G   ------   T    3  C  c
c
                                 CAACTTCTGGAA GTGTTCCAG AAGT     CGTCT GA
                                 CACTCGCT    CACAAGGTC TTCA     GTAGA CT
                                           -   ACTGGT    C
GAM8678  347   WHSC1  1  2577  NP_055734.1  3  4776  TGAGGACGTGGT     C      -----    G    3  C  c
c
                                 GACTTCCTGAAC GTGTTC AGGAAGTC    GTCTT
                                 ATCAGCTT    TACAAG TCCTTCAG    CAGGA
                                           -      TGGTG    G
GAM8678  347   WHSC1  1  2577  NP_579877.1  3  2515  TGAGGACGTGGT     C      -----    G    3  C  c
c
                                 GACTTCCTGAAC GTGTTC AGGAAGTC    GTCTT
                                 ATCAGCTT    TACAAG TCCTTCAG    CAGGA
                                           -      TGGTG    G
GAM8678  347   WHSC1  1  2577  NP_579878.1  3  2515  TGAGGACGTGGT     C      -----    G    3  C  c
c
                                 GACTTCCTGAAC GTGTTC AGGAAGTC    GTCTT
                                 ATCAGCTT    TACAAG TCCTTCAG    CAGGA
                                           -      TGGTG    G
GAM8678  347   WHSC1  1  2577  NP_579879.1  3  4896  TGAGGACGTGGT     C      -----    G    3  C  c
c
                                 GACTTCCTGAAC GTGTTC AGGAAGTC    GTCTT
                                 ATCAGCTT    TACAAG TCCTTCAG    CAGGA
                                           -      TGGTG    G
GAM8678  347   WHSC1  1  2577  NP_579888.1  3  4763  TGAGGACGTGGT     C      -----    G    3  C  c
c
                                 GACTTCCTGAAC GTGTTC AGGAAGTC    GTCTT
                                 ATCAGCTT    TACAAG TCCTTCAG    CAGGA
                                           -      TGGTG    G
GAM8678  347   WHSC1  1  2577  NP_579890.1  3  2515  TGAGGACGTGGT     C      -----    G    3  C  c
c
                                 GACTTCCTGAAC GTGTTC AGGAAGTC    GTCTT
                                 ATCAGCTT    TACAAG TCCTTCAG    CAGGA
                                           -      TGGTG    G
GAM8678  347   WSB2   1  7154  NP_061109.1  3  546   ACCTGCAGGACA  T       TC-          3  C  c  c
                                 GTTTTCCTGGAG G GTTCCAGGAAG   GTCTTG
                                 CCATTTGG    C CGAGGTCCTTT   CAGGAC
                                           -       TGA
GAM8678  347   ZFP106 1  19973 NP_071918.1  3  1069  GGACCTCAAGCA  G  C     GT         3  C  c
c
```

GACTTCCTAGAG GT TTC AGGAAGTC CTTGA
ACTTGTTT CA GAG TCCTTCAG GAACT
- A AC

GAM8678 347 ZNF211 1 19228 NP_006376.1 5 90 GAGATCAGGAAA -- G- 3 C c c
GACTTCCTGGCC GTGTT CCAGGAAGTC TCTTGA
AACATGAG TACAA GGTCCTTCAG AGGACT
CC AA

GAM8678 347 ZNF211 1 19228 XP_290823.1 5 849 GAGATCAGGAAA -- G- 3 C c c
GACTTCCTGGCC GTGTT CCAGGAAGTC TCTTGA
AACATGAG TACAA GGTCCTTCAG AGGACT
CC AA

GAM8678 347 ZNF79 1 9053 NP_009066.1 5 187 TGTGACTCGGGA GGAA G 3 C c
c
GACGGAGTGGAA GTGTTCCA GTC TCTTGA
CACCCGGC CACAAGGT CAG AGGGCT
GAGG -

GAM8678 347 ZNF84 1 852 NP_003419.1 5 203 TGAGATAAGAAA T G G- 3 C c c
GAGTTCCTGGAA G GTTCCAGGAA TC TCTTG
CCAGGAAT C CAAGGTCCTT AG AGAAT
- G AA

GAM8678 347 ZW10 1 10937 NP_004715.1 3 480 AGGAATTAAGGA C GT 3 C c c
GACTTCCTGTAA GTGTT CAGGAAGTC CTTGA
TATTTCTT TATAA GTCCTTCAG GAATT
T AG

GENE NAME	GAM SEQ-ID	TARGET	REFERENCES	SRC	GAM ACC	TAR ACC
GAM25	206	A1BG	Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B-glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989.	1	C	c
GAM25	206	A1BG	Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989.	1	C	c
GAM25	206	A1BG	Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.	1	C	c
GAM25	206	A1BG	Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.	1	C	c
GAM25	206	A1BG	Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988.	1	C	c
GAM25	206	ADAMTS4	Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.	1	C	c
GAM25	206	ADAMTS4	Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.	1	C	c
GAM25	206	ADAMTS4	Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999.	1	C	c
GAM25	206	ADAMTS4	Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664- 1666, 1999.	1	C	c
GAM25	206	AHR	Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002.	1	C	c
GAM25	206	AHR	Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor: functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994.	1	C	c
GAM25	206	AHR	Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994.	1	C	c
GAM25	206	AHR	Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression	1	C	c

is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001.

GAM25 206 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95-101, 1997. 1 C c

GAM25 206 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779-782, 2000. 1 C c

GAM25 206 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 (CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998. 1 C b

GAM25 206 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999. 1 C b

GAM25 206 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248-258, 2000. 1 C b

GAM25 206 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001. 1 C b

GAM25 206 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999. 1 C b

GAM25 206 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002. 1 C b

GAM25 206 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz-Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf-1 in malignant melanoma. Nature 409: 207- 211, 2001. 1 C b

GAM25 206 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998. 1 C b

GAM25 206 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998. 1 C b

GAM25 206 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 1 C b

GAM25 206 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 1 C c

GAM25 206 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at 1 C c

chromosome locus 12q13. Genomics 43: 387- 389, 1997.

GAM25 206 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: 1 C c
an intracellular vesicle water channel protein in renalepithelia. Proc. Nat.
Acad. Sci. 96: 5808- 5813, 1999.

GAM25 206 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, 1 C c
A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and
Drosophila. Genomics 26: 101- 106, 1995.

GAM25 206 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer 1 C c
protein delta- COP, encoded by the archain gene, is conservedacross diverse
eukaryotes. Mammalian Genome 7: 784- 786, 1996.

GAM25 206 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; 1 C c
Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the
beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990.

GAM25 206 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: 1 C c
Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11
near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec.
Genet. 16: 401- 405, 1990.

GAM25 206 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K- 1 C c
ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics
6:697- 699, 1990.

GAM25 206 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: 1 C c
Identification of a putative isoform of the Na,K- ATPase beta
subunit:primary structure and tissue- specific expression. J. Biol. Chem.
164:4613- 4618, 1989.

GAM25 206 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: 1 C c
Identification of a cDNA clone specific for the neural adhesionmolecule
AMOG. J. Neurosci. Res. 22: 113- 119, 1989.

GAM25 206 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 1 C c
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM25 206 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 1 C c
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM25 206 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 1 C c
membrane- associated C- type lectin that exhibits CD4- independentbinding of
human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad.
Sci. 89: 8356- 8360, 1992.

GAM25 206 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 1 C c
for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR.
Science 294: 2163- 2166, 2001.

GAM25 206 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 1 C c
Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S.
L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-
SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-
infection of T cells. Cell 100: 587- 597,2000.

GAM25 206 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 1 C c
F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a
novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune
responses. Cell 100: 575- 585, 2000.

GAM25 206 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related 1 C c

gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000.

GAM25 206 CD34 Cheng, J.; Baumhueter, S.; Cacalano, G.; Carver- Moore, K.; Thibodeaux,H.; Thomas, R.; Broxmeyer, H. E.; Cooper, S.; Hague, N.; Moore, M.;Lasky, L. A.: Hematopoietic defects in mice lacking the sialomucinCD34. Blood 87: 479- 490, 1996. 1 C c

GAM25 206 CD34 He, X.- Y.; Antao, V. P.; Basila, D.; Marx, J. C.; Davis, B. R.: Isolation and molecular characterization of the human CD34 gene. Blood 79:2296- 2302, 1992. 1 C c

GAM25 206 CD34 Howell, S. M.; Molgaard, H. V.; Greaves, M. F.; Spurr, N. K.:Localisation of the gene coding for the haemopoietic stem cell antigenCD34 to chromosome 1q32. Hum. Genet. 87: 625- 627, 1991. 1 C c

GAM25 206 CD34 Okuno, Y.; Iwasaki, H.; Huettner, C. S.; Radomska, H. S.; Gonzalez,D. A.; Tenen, D. G.; Akashi, K.: Differential regulation of the humanand murine CD34 genes in hematopoietic stem cells. Proc. Nat. Acad.Sci. 99: 6246- 6251, 2002. 1 C c

GAM25 206 CD34 Satterthwaite, A. B.; Burn, T. C.; Le Beau, M. M.; Tenen, D. G.: Structure of the gene encoding CD34, a human hematopoietic stemcell antigen. Genomics 12: 788- 794, 1992. 1 C c

GAM25 206 CD34 Simmons, D. L.; Satterthwaite, A. B.; Tenen, D. G.; Seed, B.:Molecular cloning of a cDNA encoding CD34, a sialomucin of human hematopoieticstem cells. J. Immun. 148: 267- 271, 1992. 1 C c

GAM25 206 CD34 Sutherland, D. R.; Stewart, A. K.; Keating, A.: CD34 antigen:molecular features and potential clinical applications. Stem Cells 11(suppl. 3): 50- 57, 1993. 1 C c

GAM25 206 CD34 Sutherland, D. R.; Watt, S. M.; Dowden, G.; Karhi, K.; Baker, M.A.; Greaves, M. F.; Smart, J. E.: Structural and partial amino acidsequence analysis of the human hemopoietic progenitor cell antigenCD34. Leukemia 2: 793- 803, 1988. 1 C c

GAM25 206 CD34 Tenen, D. G.; Satterthwaite, A. B.; Borson, R.; Simmons, D.; Eddy,R. L.; Shows, T. B.: Chromosome 1 localization of the gene for CD34,a surface antigen of human stem cells. Cytogenet. Cell Genet. 53:55- 57, 1990. 1 C c

GAM25 206 CDH17 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999. 1 C c

GAM25 206 CDH17 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck, P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with a protein related to the cadherin superfamily. Science 264:430- 433, 1994. 1 C c

GAM25 206 CDH17 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, D. F.: Localization of human cadherin genes to chromosomeregions exhibiting cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998. 1 C c

GAM25 206 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.; Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.; Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for Muckle- Wells syndrome and familial cold urticaria:a novel mutation underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002. 1 C c

GAM25 206 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile 1 C c

neurological cutaneous and articular syndromeis caused by mutations in CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes. Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM25 206 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature Genet. 29: 301- 305, 2001. 1 C c

GAM25 206 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu, S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci. 95: 8175- 8180, 1998. 1 C c

GAM25 206 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.: Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000. 1 C b

GAM25 206 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 1 C b

GAM25 206 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 1 C b

GAM25 206 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 1 C b

GAM25 206 CNP Bernier, L.; Colman, D. R.; D'Eustachio, P.: Chromosomal locationsof genes encoding 2- prime,3- prime cyclic nucleotide 3- prime- phosphodiesteraseand glial fibrillary acidic protein in the mouse. J. Neurosci. Res. 20:497- 504, 1988. 1 C c

GAM25 206 CNP Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J.: 2- prime,3- prime- cyclicnucleotide 3- prime- phosphodiesterase: a membrane- bound, microtubule- associatedprotein and membrane anchor for tubulin. Proc. Nat. Acad. Sci. 99:1807- 1812, 2002. 1 C c

GAM25 206 CNP Douglas, A. J.; Fox, M. F.; Abbott, C. M.; Hinks, L. J.; Sharpe,G.; Povey, S.; Thompson, R. J.: Structure and chromosomal localizationof the human 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasegene. Ann. Hum. Genet. 56: 243- 254, 1992. 1 C c

GAM25 206 CNP Douglas, A. J.; Fox, M. F.; Hinks, L. J.; Povey, S.; Thompson,R. J.: Localization of the myelin specific enzyme 2- prime,3- prime- cyclicnucleotide- 3- prime- phosphohydrolase to 17q21. (Abstract) Cytogenet.Cell Genet. 58: 2004 only, 1991. 1 C c

GAM25 206 CNP Kurihara, T.; Monoh, K.; Sakimura, K.; Takahashi, Y.: Alternativesplicing of mouse brain 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasemRNA. Biochem. Biophys. Res. Commun. 170: 1074- 1081, 1990. 1 C c

GAM25 206 CNP Monoh, K.; Kurihara, T.; Takahashi, Y.; Ichikawa, T.; Kumanishi,T.; Hayashi, S.; Minoshima, S.; Shimizu, N.: Structure, expressionand chromosomal localization of the gene encoding human 2- prime,3- prime- cyclic- nucleotide3- prime- phosphodiesterase. Gene 129: 297- 301, 1993. 1 C c

GAM25 206 CNP Sprinkle, T. J.; Kouri, R. E.; Fain, P. D.; Stoming, T. A.; Whitney,J. B., III: Chromosomal mapping of the human CNP gene using a meioticcrossover DNA 1 C c

panel, PCR, and allele- specific probes. Genomics 16:542- 545, 1993.

GAM25 206 CNP Sprinkle, T. J.; Lanclos, K. D.; Lapp, D. F.: Assignment of thehuman 2- prime,3- prime- cyclic nucleotide 3- prime- phosphohydrolase geneto chromosome 17. Genomics 13: 877- 880, 1992. 1 C c

GAM25 206 CNP Vogel, U. S.; Thompson, R. J.: Molecular structure, localization,and possible functions of the myelin- associated enzyme 2- prime,3- prime- cyclicnucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667- 1677,1988. 1 C c

GAM25 206 COG3 Suvorova, E. S.; Kurten, R. C.; Lupashin, V. V.: Identificationof a human orthologue of Sec34p as a component of the cis- Golgi vesicletethering machinery. J. Biol. Chem. 276: 22810- 22818, 2001. 1 C c

GAM25 206 COG3 Ungar, D.; Oka, T.; Brittle, E. E.; Vasile, E.; Lupashin, V. V.;Chatterton, J. E.; Heuser, J. E.; Krieger, M.; Waters, M. G.: Characterizationof a mammalian Golgi- localized protein complex, COG, that is requiredfor normal Golgi morphology and function. J. Cell Biol. 157: 405- 415,2002. 1 C c

GAM25 206 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359, 1997. 1 C b

GAM25 206 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix Biol. 18: 319- 324, 1999. 1 C b

GAM25 206 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of the gene encoding human cartilage associatedprotein (CRTAP). Cytogenet. Cell Genet. 87: 191- 194, 1999. 1 C b

GAM25 206 CSNK2A2 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 1 C c

GAM25 206 CSNK2A2 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine 392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292, 2001. 1 C c

GAM25 206 CSNK2A2 Lozeman, F. J.; Litchfield, D. W.; Piening, C.; Takio, K.; Walsh,K. A.; Krebs, E. G.: Isolation and characterization of human cDNAclones encoding the alpha and the alpha- prime subunits of casein kinaseII. Biochemistry 29: 8436- 8447, 1990. 1 C c

GAM25 206 CSNK2A2 Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C.: Globozoospermiain mice lacking the casein kinase II alpha- prime catalytic subunit. NatureGenet. 23: 118- 121, 1999. 1 C c

GAM25 206 CSNK2A2 Yang- Feng, T. L.; Naiman, T.; Kopatz, I.; Eli, D.; Dafni, N.; Canaani,D.: Assignment of the human casein kinase II alpha- prime subunitgene (CSNK2A1) to chromosome 16p13.2- p13.3. Genomics 19: 173 only,1994. 1 C c

GAM25 206 CSNK2A2 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping of the human casein kinase II catalytic subunit genes: twoloci carrying the homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125- 7129, 1991. 1 C c

GAM25 206 CXCL16 Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G.: A transmembrane CXC chemokine is a ligand for HIV- coreceptor Bonzo. 1 C c

NatureImmun. 1: 298- 304, 2000.

GAM25 206 CXCL16 Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.;Kita, T.; Yonehara, S.: Molecular cloning of a novel scavenger receptorfor oxidized low density lipoprotein, SR- PSOX, on macrophages. J.Biol. Chem. 275: 40663- 40666, 2000. 1 C c

GAM25 206 CXCL16 Wilbanks, A.; Zondlo, S. C.; Murphy, K.; Mak, S.; Soler, D.; Langdon,P.; Andrew, D. P.; Wu, L.; Briskin, M.: Expression cloning of theSTRL33/BONZO/TYMSTR ligand reveals elements of CC, CXC, CX3C chemokines. J.Immun. 166: 5145- 5154, 2001. 1 C c

GAM25 206 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996. 1 C c

GAM25 206 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989. 1 C c

GAM25 206 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000. 1 C c

GAM25 206 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. L.: The contribution of genetically determined oxidationstatus to inter- individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983. 1 C c

GAM25 206 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986. 1 C c

GAM25 206 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. Endocr. 3: 1399- 1408, 1989. 1 C c

GAM25 206 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the 3- prime nontranslated region, and localization ofgene to chromosome 15. J. Exp. Path. 3: 1- 17, 1987. 1 C c

GAM25 206 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996. 1 C c

GAM25 206 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 1 C c

GAM25 206 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 1 C c

GAM25 206 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O- deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 1 C c

GAM25 206 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva- based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 1 C c

GAM25 206 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime 1 C c

of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002.

GAM25 206 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 1 C c

GAM25 206 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 1 C c

GAM25 206 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 1 C c

GAM25 206 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 1 C c

GAM25 206 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 1 C c

GAM25 206 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4- alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 1 C c

GAM25 206 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- elongationfactor 2 kinase (calmodulin- dependent protein kinase III) antibodiesin patients with systemic lupus erythematosus. Biochem. Biophys.Res. Commun. 293: 1073- 1076, 2002. 1 C c

GAM25 206 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C. R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat. Acad. Sci. 94: 4884- 4889, 1997. 1 C c

GAM25 206 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 1 C c

GAM25 206 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 1 C c

GAM25 206 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 1 C c

GAM25 206 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998. 1 C c

GAM25 206 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985. 1 C c

GAM25 206 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985. 1 C c

GAM25 206 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988. 1 C c

GAM25 206 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional analysis of the human tissue factor promoter and inductionby serum. Proc. Nat. Acad. Sci. 87: 2254- 2258, 1990. 1 C c

GAM25 206 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: Completesequence of the human tissue factor gene, a highly regulated cellularreceptor that initiates the coagulation protease cascade. Biochemistry 28:1755- 1762, 1989. 1 C c

GAM25 206 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand mapping of RFLPs for human tissue factor (HTF) to chromosome 1p. NucleicAcids Res. 15: 9098 only, 1987. 1 C c

GAM25 206 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA sequenceand chromosome localization of the gene. Biochemistry 26: 5234- 5238,1987. 1 C c

GAM25 206 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA clones coding for human tissue factor: primary structureof the protein and cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987. 1 C c

GAM25 206 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad. Sci. 94: 6922- 6926, 1997. 1 C c

GAM25 206 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995. 1 C c

GAM25 206 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 1 C c

GAM25 206 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665- 1672, 1990. 1 C c

GAM25 206 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681- 1685, 1993. 1 C c

GAM25 206 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 1 C c

GAM25 206 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 1 C c

GAM25 206 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 1 C c

GAM25 206 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. 1 C c

Hum. Genet. 108: 128- 133, 2001.

GAM25 206 GPR48 Hsu, S. Y.; Liang, S.- G.; Hsueh, A. J. W.: Characterization oftwo LGR genes homologous to gonadotropin and thyrotropin receptorswith extracellular leucine- rich repeats and a G protein- coupled, seven- transmembraneregion. Molec. Endocr. 12: 1830- 1845, 1998. 1 C c

GAM25 206 GPR48 Loh, E. D.; Broussard, S. R.; Kolakowski, L. F.: Molecular characterizationof a novel glycoprotein hormone G- protein- coupled receptor. Biochem.Biophys. Res. Commun. 282: 757- 764, 2001. 1 C c

GAM25 206 GPR48 Loh, E. D.; Broussard, S. R.; Liu, Q.; Copeland, N. G.; Gilbert,D. J.; Jenkins, N. A.; Kolakowski, L. F., Jr. Chromosomal localizationof GPR48, a novel glycoprotein hormone receptor like GPCR, in humanand mouse with radiation hybrid and interspecific backcross mapping. Cytogenet.Cell Genet. 89: 2- 5, 2000. 1 C c

GAM25 206 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a novel secretin- like human G- protein- coupledreceptor gene. Genomics 55: 296- 305, 1999. 1 C c

GAM25 206 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected with mRNA differential display using human melanoma celllines with different metastatic potential. FEBS Lett. 446: 292- 298,1999. 1 C c

GAM25 206 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann, S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in three cases of myelodysplastic syndrome/acutemyeloid leukemia with a deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000. 1 C c

GAM25 206 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain- containingGTPase- activating protein for Rho and Cdc42 associates with focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996. 1 C c

GAM25 206 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 1 C c

GAM25 206 HTR1D Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S. J.; Duncan,A. M. V.; Rozmahel, R.; Yang, Y.; Mengod, G.; Palacios, J. M.; O'Dowd,B. F.: Characterization of the human 5- hydroxytryptamine(1B) receptor. J.Biol. Chem. 267: 5735- 5738, 1992. 1 C c

GAM25 206 HTR1D Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. 1 C c

GAM25 206 HTR1D Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T.A.; Hartig, P. R.: Human serotonin 1D receptor is encoded by a subfamilyof two distinct genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat.Acad. Sci. 89: 3630- 3634, 1992. 1 C c

GAM25 206 HTR1D Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and genome organization of mammalian G- protein- coupled receptors. Genomics 18:175- 184, 1993. 1 C c

GAM25 206 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 1 C b

M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like growth factor- I and cognitive function inhealthy older men. J. Clin. Endocr. Metab. 84: 471- 475, 1999.

GAM25 206 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993. 1 C b

GAM25 206 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and absence of association with stature among African Pygmies. Hum.Genet. 85: 349- 354, 1990. 1 C b

GAM25 206 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for insulin- like growth factors I and II and for epidermalgrowth factor in man. (Abstract) Am. J. Hum. Genet. 36: 133S only,1984. 1 C b

GAM25 206 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of genes for insulin- like growth factors I and II and epidermalgrowth factor. Nature 310: 781- 784, 1984. 1 C b

GAM25 206 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of recombinant human insulin- like growth factor I(IGF- I) therapy on the growth hormone- IGF system of a patient witha partial IGF- I gene deletion. J. Clin. Endocr. Metab. 84: 1611- 1616,1999. 1 C b

GAM25 206 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of the growth hormone receptor in children with idiopathicshort stature. New Eng. J. Med. 333: 1093- 1098, 1995. 1 C b

GAM25 206 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; Froesch, E. R.: Small stature and insulin- like growth factors:prolonged treatment of mini- poodles with recombinant human insulin- likegrowth factor I. Acta Endocr. 121: 456- 464, 1989. 1 C b

GAM25 206 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating concentrations of insulin- like growth factor- I and riskof breast cancer. Lancet 351: 1393- 1396, 1998. 1 C b

GAM25 206 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding protein- 3, and prostate- specific antigen as predictorsof clinical prostate cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000. 1 C b

GAM25 206 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith, D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival signaling in retinal endothelial cells: direct correlationwith clinical retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001. 1 C b

GAM25 206 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer prevention. Lancet 351: 1373- 1375, 1998. 1 C b

GAM25 206 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J. S.: The human gene encoding insulin- like growthfactor I is located on chromosome 12. Hum. Genet. 69: 157- 160, 1985. 1 C b

GAM25 206 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990. 1 C b

GAM25 206 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete 1 C b characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986.

GAM25 206 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; 1 C b Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF- 1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996.

GAM25 206 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: 1 C b Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat. Acad. Sci. 80: 2216- 2220, 1983.

GAM25 206 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; 1 C b Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand implications for cell type- specific growth. Nature 364: 208- 213,1993.

GAM25 206 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: 1 C b Mice carrying null mutations of the genes encoding insulin- likegrowth factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993.

GAM25 206 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like 1 C b growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83: 9343- 9347, 1986.

GAM25 206 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human 1 C b genes for insulin- like growth factors I and II and epidermalgrowth factor are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively. Cytogenet.Cell Genet. 41: 245- 249, 1986.

GAM25 206 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 1 C b 1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2 (IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985.

GAM25 206 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. 1 C b D.: Growth characteristics and response to growth hormonetherapy in patients with hypochondroplasia: genetic linkage of theinsulin- like growth factor I gene at chromosome 12q23 to the diseasein a subgroup of these patients. Clin. Endocr. 34: 265- 274, 1991.

GAM25 206 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: 1 C b IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999.

GAM25 206 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, 1 C b M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene expression sustains hypertrophy and regeneration insenescent skeletal muscle. Nature Genet. 27: 195- 200, 2001.

GAM25 206 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like 1 C b growth factor 1 regulates the location, stability,and transcriptional activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000.

GAM25 206 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, 1 C b S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993.

GAM25 206 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the 1 C b protein which binds insulin- like growth factor in human serum. Europ.J. Biochem. 172: 421- 425, 1988.

GAM25 206 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; 1 C b Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith, R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the

insulin- like growth factor I receptor and its ligandin relation to type 2 diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000.

GAM25 206 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986. 1 C b

GAM25 206 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I) reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991. 1 C b

GAM25 206 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999. 1 C b

GAM25 206 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980. 1 C b

GAM25 206 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 1991. 1 C b

GAM25 206 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984. 1 C b

GAM25 206 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984. 1 C b

GAM25 206 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984. 1 C b

GAM25 206 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-857,1992. 1 C b

GAM25 206 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002. 1 C b

GAM25 206 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980. 1 C b

GAM25 206 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999. 1 C b

GAM25 206 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy on body composition and insulin resistance in IGF- Igene deletion. J. Clin. Endocr. Metab. 85: 1407- 1411, 2000. 1 C b

GAM25 206 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 1 C b

Intrauterine growth retardation and postnatal growth failureassociated with deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335: 1363- 1367, 1996.

GAM25 206 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 1 C b
regional localization of human genes for insulin- like growthfactors I (IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell Genet. 40: 782 only, 1985.

GAM25 206 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 1 C b
growth factors and bone mineral density in African Americanand white girls. J. Pediat. 137: 826- 832, 2000.

GAM25 206 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 1 C b
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM25 206 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 1 C b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM25 206 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 1 C b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM25 206 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 1 C b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814- 819, 1992.

GAM25 206 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 1 C b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang, Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell- derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87: 7512- 7516, 1990.

GAM25 206 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 1 C b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract) Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM25 206 IL19 Blumberg, H.; Conklin, D.; Xu, W.; Grossmann, A.; Brender, T.;Carollo, S.; 1 C c
Eagan, M.; Foster, D.; Haldeman, B. A.; Hammond, A.;Haugen, H.; Jelinek, L.; and 14 others: Interleukin 20: discovery,receptor identification, and role in epidermal function. Cell 104:9- 19, 2001.

GAM25 206 IL19 Gallagher, G.; Dickensheets, H.; Eskdale, J.; Izotova, L. S.; 1 C c
Mirochnitchenko,O. V.; Peat, J. D.; Vazquez, N.; Pestka, S.; Donnelly, R. P.; Kotenko,S. V.: Cloning, expression and initial characterisation of interleukin- 19(IL- 19), a novel homologue of human interleukin- 10 (IL- 10). GenesImmunity 1: 442- 450, 2000.

GAM25 206 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel 1 C c
genes. Trends Pharm. Sci. 14: 434, 1993.

GAM25 206 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; 1 C c
Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011- 1017, 1996.

GAM25 206 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; 1 C c
Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166- 1170, 1995.

GAM25 206 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: 1 C c
Targeted overactivity of beta cell KATP channels induces profoundneonatal diabetes. Cell 100: 645- 654, 2000.

GAM25 206 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: 1 C c
Homozygositymapping, to chromosome 11p, of the gene for familial persistent
hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421,
1995.

GAM25 206 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward 1 C c
rectifier Kir6.2 also leads to familial persistent
hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812,
1996.

GAM25 206 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, 1 C c
T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium
channels in hypoxia- induced generalized seizure. Science 292:1543- 1546,
2001.

GAM25 206 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand 1 C b
characterization of human Lnk, an adaptor protein with pleckstrinhomology
and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164:
5199- 5206, 2000.

GAM25 206 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; 1 C b
Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor
protein Lnk: definition of a conserved family of signal- modulatingproteins.
Immunity 13: 599- 609, 2000.

GAM25 206 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; 1 C c
Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.;
Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2
purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363-
18367,1996.

GAM25 206 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof 1 C c
leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature
372: 179- 182, 1994.

GAM25 206 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; 1 C c
Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol.
Nature 384: 39- 43, 1996.

GAM25 206 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 1 C c
specifictranscriptional regulation of human leukotriene B4 receptor gene.
J.Exp. Med. 192: 413- 420, 2000.

GAM25 206 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 1 C c
chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM25 206 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 1 C c
Leukotrienes and lipoxins: structures, biosynthesis,and biological effects.
Science 237: 1171- 1176, 1987.

GAM25 206 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 1 C c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene
and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-
130, 1997.

GAM25 206 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 1 C c
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature
387:620- 624, 1997.

GAM25 206 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 1 C c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM25 206 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 1 C c

GAM25 206 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990. 1 C c

GAM25 206 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994. 1 C c

GAM25 206 NUMA1 Compton, D. A.; Szilak, I.; Cleveland, D. W.: Primary structureof NuMA, an intranuclear protein that defines a novel pathway forsegregation of proteins at mitosis. J. Cell Biol. 116: 1395- 1408,1992. 1 C c

GAM25 206 NUMA1 Lydersen, B. K.; Pettijohn, D. E.: Human- specific nuclear proteinthat associates with the polar region of the mitotic apparatus: distributionin a human/hamster hybrid cell. Cell 22: 489- 499, 1980. 1 C c

GAM25 206 NUMA1 Merdes, A.; Ramyar, K.; Vechio, J. D.; Cleveland, D. W.: A complexof NuMA and cytoplasmic dynein is essential for mitotic spindle assembly. Cell 87:447- 458, 1996. 1 C c

GAM25 206 NUMA1 Sparks, C. A.; Bangs, P. L.; McNeil, G. P.; Lawrence, J. B.; Fey,E. G.: Assignment of the nuclear mitotic apparatus protein NuMA geneto human chromosome 11q13. Genomics 17: 222- 224, 1993. 1 C c

GAM25 206 NUMA1 Wells, R. A.; Catzavelos, C.; Kamel- Reid, S.: Fusion of retinoicacid receptor alpha to NuMA, the nuclear mitotic apparatus protein,by a variant translocation in acute promyelocytic leukaemia. NatureGenet. 17: 109- 113, 1997. 1 C c

GAM25 206 NUMA1 Wiese, C.; Wilde, A.; Moore, M. S.; Adam, S. A.; Merdes, A.; Zheng,Y.: Role of importin- beta in coupling Ran to downstream targets inmicrotubule assembly. Science 291: 653- 656, 2001. 1 C c

GAM25 206 NUMA1 Yang, C. H.; Lambie, E. J.; Snyder, M.: NuMA: an unusually longcoiled- coil related protein in the mammalian nucleus. J. Cell Biol. 116:1303- 1317, 1992. 1 C c

GAM25 206 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 1 C c

GAM25 206 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 1 C c

GAM25 206 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine protocadherin- beta one- exon gene families show high evolutionaryconservation, despite the difference in gene number. FEBS Lett. 495:120- 125, 2001. 1 C c

GAM25 206 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 1 C c

GAM25 206 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 1 C b

an ethanol- responsive potential modulator of guanine nucleotide-
bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM25 206 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 1 C b
Cloning and characterization of the rat and human phosducin- likeprotein
genes: structure, expression and chromosomal localization. Biochim.Biophys.
Acta 1444: 346- 354, 1999.

GAM25 206 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; 1 C c
Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx
activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C.
Genomics 47: 323- 324, 1998.

GAM25 206 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, 1 C c
S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to
human chromosome 21q22.3. Genomics 41: 193- 200,1997.

GAM25 206 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 1 C c
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component
of the steroid receptor complex: cloning of thecDNA and further
characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM25 206 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 1 C c
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem.
267: 5503- 5507, 1992.

GAM25 206 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 1 C c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151
only, 1997.

GAM25 206 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 1 C c
J.- E.: The structure and complete nucleotide sequenceof the human
cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM25 206 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 1 C c
Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly,
F.: Characterization of new mutations in the codingsequence and 5- prime-
untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum.
Genet. 108: 148- 155, 2001.

GAM25 206 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 1 C c
Molecular cloning and expression of human prostacyclin synthase.
Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM25 206 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 1 C c
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.;
Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences,
gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42,
1996.

GAM25 206 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 1 C c
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM25 206 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 1 C c
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase
(PTGIS): genomic organization, chromosomal localization,and promoter
activity. Genomics 36: 296- 304, 1996.

GAM25 206 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; 1 C c
Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in
RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993.

GAM25 206 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 1 C c
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA

amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM25 206 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. Med. 339: 1775- 1777, 1998. 1 C c

GAM25 206 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand molecular genetics. Blood Rev. 8: 199- 212, 1994. 1 C c

GAM25 206 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood group polymorphism as determined by Southern analysis. Blood 78:2747- 2752, 1991. 1 C c

GAM25 206 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and its association with universal edema of the fetus, icterusgravis neonatorum and anemia of the newborn. J. Pediat. 1: 269- 309,1932. 1 C c

GAM25 206 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989. 1 C c

GAM25 206 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with sickle cell disease. Transfusion 37: 357- 361, 1997. 1 C c

GAM25 206 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 1 C c

GAM25 206 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the human RH locus: a family study of the red- cell Evans phenotypereveals a transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59: 825- 833, 1996. 1 C c

GAM25 206 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J. Hum. Genet. 58: 133- 142, 1996. 1 C c

GAM25 206 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of Rh blood group genes: association between restrictionfragment length polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994. 1 C c

GAM25 206 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine years and some observations on the biochemistry and geneticsof the system. Transfusion Med. Rev. 3: 1- 12, 1989. 1 C c

GAM25 206 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh genes revealed by analysis of unrelated donors with therare D- - phenotype. Am. J. Hum. Genet. 59: 1066- 1073, 1996. 1 C c

GAM25 206 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by alternative splicing. Blood 80: 1074- 1078, 1992. 1 C c

GAM25 206 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929, 1992. 1 C c

GAM25 206 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE genotyping for correct blood group determination inchronically transfused patients. Transfusion 39: 852- 855, 1999. 1 C c

GAM25 206 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A. 116:825- 827, 1941. 1 C c

GAM25 206 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal 1 C c

plasma. New Eng. J. Med. 339: 1734- 1738, 1998.

GAM25 206 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; 1 C c
Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases
of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome
1. Am. J. Med. Genet. 104: 250- 256, 2001.

GAM25 206 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, 1 C c
E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J.
Clin. Invest. 100: 373- 379, 1997.

GAM25 206 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 1 C c
153:771- 772, 1944.

GAM25 206 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 1 C c
ed.): 1975.

GAM25 206 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 1 C c
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII)
category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM25 206 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 1 C c
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral
transduction of K562 cells establishes the molecular basisof Rh blood group
antigens. Blood 87: 2968- 2973, 1996.

GAM25 206 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 1 C c
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang.
58: 50- 55, 1990.

GAM25 206 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 1 C c
Blood 95: 3662- 3668, 2000.

GAM25 206 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 1 C c
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393,
1999.

GAM25 206 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 1 C c
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311,
2002.

GAM25 206 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 1 C c

GAM25 206 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, 1 C b
P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.:
Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin.
Endocr. Metab. 86: 3233- 3236, 2001.

GAM25 206 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- 1 C b
linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a
common cause of early primary osteoarthritis in men. (Letter) Clin.Genet.
62: 94- 95, 2002.

GAM25 206 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. 1 C b
C.: Gene structure and expression study of the SEDL genefor
spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000.

GAM25 206 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; 1 C b
Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the
gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda.
NatureGenet. 22: 400- 404, 1999.

GAM25 206 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; 1 C b
Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.;
Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.;
Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia

tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM25 206 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 1 C b
Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset
of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J.
Med. Genet. 38: 409- 411, 2001.

GAM25 206 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 1 C b
A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five-
base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia
tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85:
3343- 3347, 2000.

GAM25 206 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 1 C b
for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a
non- canonical splice site. Gene 273: 285- 293, 2001.

GAM25 206 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, 1 C b
H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked
spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002.

GAM25 206 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; 1 C b
Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A
recurrent RNA- splicing mutation in the SEDL gene causes X-
linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398-
1407,2001.

GAM25 206 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked 1 C b
recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic
evolution in a 6- generation kindred and review ofthe literature. Medicine
78: 9- 25, 1999.

GAM25 206 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; 1 C c
Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The
granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic
cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001.

GAM25 206 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the 1 C c
gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25
by fluorescence in situ hybridization. Genomics 37:406- 408, 1996.

GAM25 206 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen 1 C c
responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a
cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec.
Endocr. 15: 1971- 1982, 2001.

GAM25 206 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, 1 C c
S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial
characterization of two novel members of the ovalbuminfamily of serine
proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995.

GAM25 206 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. 1 C c
A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to
the viral apoptotic regulator cytokine responsemodifier A is present in
cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996.

GAM25 206 SH3BP4 Dunlevy, J. R.; Berryhill, B. L.; Vergnes, J.- P.; SundarRaj, N.;Hassell, J. 1 C c
R.: Cloning, chromosomal localization, and characterizationof cDNA from a
novel gene, SH3BP4, expressed by human corneal fibroblasts. Genomics 62:519-
524, 1999.

GAM25 206 SH3BP4 Wong, W. T.; Schumacher, C.; Salcini, A. E.; Romano, A.; Castagnino,P.; 1 C c
Pelicci, P. G.; DiFiore, P. P.: A protein- binding domain, EH,identified in

the receptor tyrosine kinase substrate Eps15 and conservedin evolution. Proc. Nat. Acad. Sci. 92: 9530- 9534, 1995.

GAM25 206 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 1 C c

GAM25 206 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J recombinase activity. Science 250: 1426- 1429, 1990. 1 C c

GAM25 206 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 1 C c

GAM25 206 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990. 1 C c

GAM25 206 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995. 1 C c

GAM25 206 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic axial development and left- right specification. Nature 399:691- 694, 1999. 1 C c

GAM25 206 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human intestine:biology and function. Gastroenterology 113: 332- 340, 1997. 1 C c

GAM25 206 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563- 566, 1994. 1 C c

GAM25 206 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 1 C c

GAM25 206 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998. 1 C c

GAM25 206 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 1 C c

GAM25 206 SLC7A6 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 1 C b

GAM25 206 SLC7A6 Torrents, D.; Estevez, R.; Pineda, M.; Fernandez, E.; Lloberas,J.; Shi, Y.- B.; Zorzano, A.; Palacin, M.: Identification and characterizationof a membrane protein (y(+)L amino acid transporter- 1) that associateswith 4F2hc to encode the amino acid transport activity y(+)L: a candidategene for lysinuric protein intolerance. J. Biol. Chem. 273: 32437- 32445,1998. 1 C b

GAM25 206 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in 1 C c

mast cells. Cell 94: 537- 548, 1998.

GAM25 206 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; 1 C c
Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic
organization,chromosomal localization, alternative splicing, and isoforms of
thehuman synaptosome- associated protein- 23 gene implicated in vesicle-
membranefusion processes. Hum. Genet. 108: 211- 215, 2001.

GAM25 206 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- 1 C c
membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells.
Biochem. Biophys. Res. Commun. 231: 808- 812, 1997.

GAM25 206 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel 1 C c
syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in
non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996.

GAM25 206 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: 1 C c
Identification of three new splice variants of the SNARE proteinSNAP- 23.
Biochem. Biophys. Res. Commun. 285: 320- 327, 2001.

GAM25 206 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 1 C c
L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and
SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human
synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM25 206 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 1 C c
J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and
SSX2, encoding proteins with homology to the Kruppel- associatedbox in human
synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM25 206 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 1 C c
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand
characterization of the mouse homolog of SYT, a gene implicatedin the
development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM25 206 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 1 C c
G.: Mapping and characterization of the mouse and humanSS18 genes, two human
SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-
319, 2001.

GAM25 206 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 1 C c
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene
family with several members transcribed in normaltestis and human cancer.
Int. J. Cancer 72: 965- 971, 1997.

GAM25 206 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 1 C c
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand
prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM25 206 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 1 C c
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J.
Nat. Cancer Inst. 91: 974- 975, 1999.

GAM25 206 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 1 C c
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX
synovial sarcoma translocation proteins and co- localizationwith the SNF
protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM25 206 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 1 C c
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in
synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM25 206 TAF11 Birck, C.; Poch, O.; Romier, C.; Ruff, M.; Mengus, G.; Lavigne,A.- C.; 1 C c
Davidson, I.; Moras, D.: Human TAFII28 and TAFII18 interactthrough a histone

fold encoded by atypical evolutionary conservedmotifs also found in the SPT3 family. Cell 94: 239- 249, 1998.

GAM25 206 TAF11 Mengus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.;Davidson, I.: Cloning and characterization of hTAFII18, hTAFII20and hTAFII28: three subunits of the human transcription factor TFIID. EMBOJ. 14: 1520- 1531, 1995. 1 C c

GAM25 206 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459- 467, 1998. 1 C b

GAM25 206 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 1 C b

GAM25 206 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 1 C b

GAM25 206 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 1 C b

GAM25 206 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 1 C b

GAM25 206 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 1 C b

GAM25 206 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496- 1498, 2002. 1 C b

GAM25 206 TAT Barton, D. E.; Yang- Feng, T. L.; Francke, U.: The human tyrosineaminotransferase gene mapped to the long arm of chromosome 16 (region16q22- q24) by somatic cell hybrid analysis and in situ hybridization. Hum.Genet. 72: 221- 224, 1986. 1 C b

GAM25 206 TAT Beinfang, D. C.; Kuwabara, T.; Pueschel, S. M.: The Richner- Hanhartsyndrome: report of a case with associated tyrosinemia. Arch. Ophthal. 94:1133- 1137, 1976. 1 C b

GAM25 206 TAT Bohnert, A.; Anton- Lamprecht, I.: Richner- Hanhart's syndrome:ultrastructural abnormalities of epidermal keratinization indicatinga causal relationship to high intracellular tyrosine levels. J. Invest.Derm. 79: 68- 74, 1982. 1 C b

GAM25 206 TAT Buist, N.: Phenylketonuria and related problems.In: Nyhan, W.L.: Amino Acid Metabolism and Genetic Variation. New York: McGraw- Hill(pub.) 1967. Pp. 117 only. 1 C b

GAM25 206 TAT Chitayat, D.; Balbul, A.; Hani, V.; Mamer, O. A.; Clow, C.; Scriver,C. R.: Hereditary tyrosinaemia type II in a consanguineous AshkenaziJewish family: intrafamilial variation in phenotype; absence of parentalphenotype effects on the fetus. J. Inherit. Metab. Dis. 15: 198- 203,1992. 1 C b

GAM25 206 TAT Crovato, F.; Desirello, G.; Gatti, R.; Babbini, N.; Rebora, A.: Richner- Hanhart syndrome spares a plantar autograft. Arch. Derm. 121:539- 540, 1985. 1 C b

GAM25 206 TAT Fellman, J. H.; Vanbellinghen, P. J.; Jones, R. T.; Koler, R. D.: Soluble and mitochondrial forms of tyrosine aminotransferase: relationshipto human tyrosinemia. Biochemistry 8: 615- 622, 1969. 1 C b

GAM25 206 TAT Garibaldi, L. R.; Siliato, F.; De Martini, I.; Scarsi, M. R.; Romano,C.: Oculocutaneous tyrosinosis: report of two cases in the same family. Helv.Paediat. Acta 32: 173- 180, 1977. 1 C b

GAM25 206 TAT Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald,P. S.; Baden, H. P.: Tyrosinemia with plantar and palmar keratosisand keratitis. J. Pediat. 83: 798- 805, 1973. 1 C b

GAM25 206 TAT Hanhart, E.: Neue Sonderformen von Keratosis palmo- plantaris,u.a. eine regelmaessig- dominante mit systematisierten Lipomen, ferner2 einfach-rezessive mit Schwachsinn und z.T. mit Hornhautveraenderungendes Auges (Ektodermatosyndrom). Dermatologica 94: 286- 308, 1947. 1 C b

GAM25 206 TAT Hunziker, N.: Richner- Hanhart syndrome and tyrosinemia type II. Dermatologica 160:180- 189, 1980. 1 C b

GAM25 206 TAT Kennaway, N. G.; Buist, N. R. M.: Metabolic studies in a patientwith hepatic cytosol tyrosine aminotransferase deficiency. Pediat.Res. 5: 287- 297, 1971. 1 C b

GAM25 206 TAT Muller, G.; Scherer, G.; Zentgraf, H.; Ruppert, S.; Herrmann,B.; Lehrach, H.; Schutz, G.: Isolation, characterization and chromosomalmapping of the mouse tyrosine aminotransferase gene. J. Molec. Biol. 184:367- 373, 1985. 1 C b

GAM25 206 TAT Natt, E.; Kao, F.- T.; Rettenmeier, R.; Scherer, G.: Assignmentof the human tyrosine aminotransferase gene to chromosome 16. Hum.Genet. 72: 225- 228, 1986. 1 C b

GAM25 206 TAT Natt, E.; Kida, K.; Odievre, M.; Di Rocco, M.; Scherer, G.: Pointmutations in the tyrosine aminotransferase gene in tyrosinemia typeII. Proc. Nat. Acad. Sci. 89: 9297- 9301, 1992. 1 C b

GAM25 206 TAT Natt, E.; Westphal, E.- M.; Toth- Fejel, S. E.; Magenis, R. E.;Buist, N. R. M.; Rettenmeier, R.; Scherer, G.: Inherited and de novodeletion of the tyrosine aminotransferase gene locus at 16q22.1- q22.3in a patient with tyrosinemia type II. Hum. Genet. 77: 352- 358,1987. 1 C b

GAM25 206 TAT Pelet, B.; Antener, I.; Faggioni, R.; Spahr, A.; Gautier, E.:Tyrosinemia without liver or renal damage with plantar and palmarkeratosis and keratitis (hypertyrosinemia type II). Helv. Paediat.Acta 34: 177- 183, 1979. 1 C b

GAM25 206 TAT Rehak, A.; Selim, M. M.; Yadav, G.: Richner- Hanhart syndrome(tyrosinaemia- II) (report of four cases without ocular involvement). Brit.J. Derm. 104: 469- 475, 1981. 1 C b

GAM25 206 TAT Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.: Isolationand characterization of the human tyrosine aminotransferase gene. NucleicAcids Res. 18: 3853- 3861, 1990. 1 C b

GAM25 206 TAT Richner, H.: Hornhautaffektion bei Keratoma palmare et plantarehereditarium. Klin. Mbl. Augenheilk. 100: 580- 588, 1938. 1 C b

GAM25 206 TAT Schmid, W.; Muller, G.; Schutz, G.; Gluecksohn- Waelsch, S.: Deletionsnear the albino locus on chromosome 7 of the mouse affect the levelof tyrosine aminotransferase mRNA. Proc. Nat. Acad. Sci. 82: 2866- 2869,1985. 1 C b

GAM25 206 TAT Tallab, T.M.: Richner- Hanhart syndrome: importance of early diagnosisand early intervention. J. Am. Acad. Dermatol. 35: 857- 859, 1996. 1 C b

GAM25 206 TAT Ventura, G.; Biasini, G.; Petrozzi, M.: Cheratomia palmoplantaredissipatum associato a lesioni corneali in due fratelli. Boll. Oculist. 44:497- 510, 1965. 1 C b

GAM25 206 TAT Waardenburg, P. J.; Franceschetti, A.; Klein, D.: Genetics andOphthalmology. 1 C b

Springfield, Ill.: Charles C Thomas (pub.) 1:1961. Pp. 515- 517.

GAM25 206 TAT Westphal, E.- M.; Natt, E.; Grimm, T.; Odievre, M.; Scherer, G.: The human 1 C b
tyrosine aminotransferase gene: characterization of restrictionfragment
length polymorphisms and haplotype analysis in a family withtyrosinemia type
II. Hum. Genet. 79: 260- 264, 1988.

GAM25 206 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, 1 C b
M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and
characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and
TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020-
4027, 1998.

GAM25 206 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. 1 C b
R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune
response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature
410: 1099- 1103, 2001.

GAM25 206 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; 1 C b
Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress
different Toll- like receptors and respond to different microbialantigens.
J. Exp. Med. 194: 863- 869, 2001.

GAM25 206 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; 1 C b
Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.;
Mantovani, A.: Differential expression and regulation of Toll- likereceptors
(TLR) in human leukocytes: selective expression of TLR3in dendritic cells.
J. Immun. 164: 5998- 6004, 2000.

GAM25 206 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A 1 C b
family of human receptors structurally related to DrosophilaToll. Proc. Nat.
Acad. Sci. 95: 588- 593, 1998.

GAM25 206 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 1 C b
B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the
crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec.
Cell 4: 563- 571, 1999.

GAM25 206 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 1 C b
B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel
receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420,
1997.

GAM25 206 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 1 C b
B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi,
A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr.
Biol. 7: 1003- 1006, 1997.

GAM25 206 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 1 C b
B W. S.: Rare loss- of- function mutation of a death receptorgene in head and
neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM25 206 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 1 C b
B decoy receptor and a death domain- containing receptorfor TRAIL. Science
277: 815- 818, 1997.

GAM25 206 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 1 C b
B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334,
1997.

GAM25 206 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 1 C b
B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces
the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM25	206 B	TNFRSF10	Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.	1	C	b
GAM25	206 B	TNFRSF10	Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.	1	C	b
GAM25	206 B	TNFRSF10	Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.	1	C	b
GAM25	206	TRPM6	Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.; Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.: Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002.	1	C	c
GAM25	206	TRPM6	Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.; Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002.	1	C	c
GAM25	206	TRPM6	Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.: Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome: genetic linkage mapping and analysis of abalanced translocation breakpoint. Hum. Molec. Genet. 6: 1491- 1497,1997.	1	C	c
GAM28	260	COG3	Suvorova, E. S.; Kurten, R. C.; Lupashin, V. V.: Identificationof a human orthologue of Sec34p as a component of the cis- Golgi vesicletethering machinery. J. Biol. Chem. 276: 22810- 22818, 2001.	3	B	c
GAM28	260	COG3	Ungar, D.; Oka, T.; Brittle, E. E.; Vasile, E.; Lupashin, V. V.;Chatterton, J. E.; Heuser, J. E.; Krieger, M.; Waters, M. G.: Characterizationof a mammalian Golgi- localized protein complex, COG, that is requiredfor normal Golgi morphology and function. J. Cell Biol. 157: 405- 415,2002.	3	B	c
GAM28	260	TBL1X	Bassi, M. T.; Ramesar, R. S.; Caciotti, B.; Winship, I. M.; DeGrandi, A.; Riboni, M.; Townes, P. L.; Beighton, P.; Ballabio, A.;Borsani, G.: X- linked late- onset sensorineural deafness caused bya deletion involving OA1 and a novel gene containing WD- 40 repeats. Am.J. Hum. Genet. 64: 1604- 1616, 1999.	3	B	c
GAM28	260	TBL1X	Converse, P. J.: Personal Communication. Baltimore, Md. 8/24/2001.	3	B	c
GAM28	260	TBL1X	Disteche, C. M.; Dinulos, M. B.; Bassi, M. T.; Elliott, R. W.;Rugarli, E. I.: Mapping of the murine Tbl1 gene reveals a new rearrangementbetween mouse and human X chromosomes. Mammalian Genome 9: 1062- 1064,1998.	3	B	c
GAM28	260	TBL1X	Dong, X.; Tsuda, L.; Zavitz, K. H.; Lin, M.; Li, S.; Carthew, R.W.; Zipursky, S. L.: ebi regulates epidermal growth factor receptorsignaling pathways in Drosophila. Genes Dev. 13: 954- 965, 1999.	3	B	c
GAM28	260	TBL1X	Emes, R. D.; Ponting, C. P.: A new sequence motif linking lissencephaly,Treacher Collins and oral- facial- digital type 1 syndromes, microtubuledynamics and cell migration. Hum. Molec. Genet. 10: 2813- 2820, 2001.	3	B	c

GAM28 260 TBL1X Matsuzawa, S.; Reed, J. C.: Siah- 1, SIP, and Ebi collaborate ina novel pathway for beta- catenin degradation linked to p53 responses. Molec.Cell 7: 915- 926, 2001. 3 B c

GAM28 260 TBL1X Zhang, J.; Kalkum, M.; Chait, B. T.; Roeder, R. G.: The N- CoR- HDAC3nuclear receptor corepressor complex inhibits the JNK pathway throughthe integral subunit GPS2. Molec. Cell 9: 611- 623, 2002. 3 B c

GAM30 346 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002. 3 C c

GAM30 346 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor: functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994. 3 C c

GAM30 346 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994. 3 C c

GAM30 346 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 3 C c

GAM30 346 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95- 101, 1997. 3 C c

GAM30 346 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779- 782, 2000. 3 C c

GAM30 346 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 (CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998. 3 C b

GAM30 346 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999. 3 C b

GAM30 346 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000. 3 C b

GAM30 346 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001. 3 C b

GAM30 346 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999. 3 C b

GAM30 346 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: 3 C b

Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002.

GAM30 346 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- 3 C b
Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.;
Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf-
1 in malignant melanoma. Nature 409: 207- 211, 2001.

GAM30 346 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: 3 C b
Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization.
Molec.Cell 1: 949- 957, 1998.

GAM30 346 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; 3 C b
Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of
apoptosis and brain development. Cell 94: 739- 750, 1998.

GAM30 346 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human 3 C b
protein homologous to C. elegans CED- 4, participates in cytochromec-
dependent activation of caspase- 3. Cell 90: 405- 413, 1997.

GAM30 346 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: 3 C c
Apolipoprotein L gene family: tissue- specific expression,splicing, promoter
regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001.

GAM30 346 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya- 3 C c
Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a
new human high density lipoprotein apolipoproteinexpressed by the pancreas:
identification, cloning, characterization,and plasma distribution of
apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997.

GAM30 346 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. 3 C c
L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.;
Bahn, S.: Gene expression analysis in schizophrenia:reproducible up-
regulation of several members of the apolipoproteinL family located in a
high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat.
Acad. Sci. 99: 4680- 4685, 2002.

GAM30 346 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The 3 C c
apolipoprotein L gene cluster has emerged recently in evolutionand is
expressed in human vascular tissue. Genomics 79: 539- 546,2002.

GAM30 346 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman 3 C c
apolipoprotein L gene cluster: identification, classification,and sites of
distribution. Genomics 74: 71- 78, 2001.

GAM30 346 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, 3 C c
A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and
Drosophila. Genomics 26: 101- 106, 1995.

GAM30 346 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer 3 C c
protein delta- COP, encoded by the archain gene, is conservedacross diverse
eukaryotes. Mammalian Genome 7: 784- 786, 1996.

GAM30 346 CORO2B Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 C b
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XIII. The completesequences of 100
new cDNA clones from brain which code for large proteinsin vitro. DNA Res.
6: 63- 70, 1999.

GAM30 346 CORO2B Nakamura, T.; Takeuchi, K.; Muraoka, S.; Takezoe, H.; Takahashi,N.; Mori, 3 C b
N.: A neurally enriched coronin- like protein, ClipnC, isa novel candidate
for an actin cytoskeleton- cortical membrane- linkingprotein. J. Biol. Chem.
274: 13322- 13327, 1999.

GAM30 346 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996. 3 C b

GAM30 346 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989. 3 C b

GAM30 346 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000. 3 C b

GAM30 346 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. L.: The contribution of genetically determined oxidationstatus to inter-individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983. 3 C b

GAM30 346 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986. 3 C b

GAM30 346 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. Endocr. 3: 1399- 1408, 1989. 3 C b

GAM30 346 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the 3- prime nontranslated region, and localization ofgene to chromosome 15. J. Exp. Path. 3: 1- 17, 1987. 3 C b

GAM30 346 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996. 3 C b

GAM30 346 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 C b

GAM30 346 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 3 C b

GAM30 346 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 3 C b

GAM30 346 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 3 C b

GAM30 346 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002. 3 C b

GAM30 346 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 3 C c

GAM30 346 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 C c

GAM30 346 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. 3 C c
Lancet 355: 979- 983, 2000.

GAM30 346 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, 3 C c
T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and
desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995.

GAM30 346 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, 3 C
c
H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin.
J. Biol. Chem. 269: 26295- 26302, 1994.

GAM30 346 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The 3 C c
desmocollins of human foreskin epidermis: identification and
chromosomalassignment of a third gene and expression patterns of the three
isoforms. J.Invest. Derm. 105: 314- 321, 1995.

GAM30 346 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 C c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM30 346 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 C c
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22
suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci.
98: 10374- 10379, 2001.

GAM30 346 IFNAR2 Croze, E.; Russell- Harde, D.; Wagner, T. C.; Pu, H.; Pfeffer, L.M.; Perez, 3 C c
H. D.: The human type I interferon receptor: identificationof the interferon
beta- specific receptor- associated phosphoprotein. J.Biol. Chem. 271:
33165- 33168, 1996.

GAM30 346 IFNAR2 Croze, E.; Usacheva, A.; Asarnow, D.; Minshall, R.D.; Perez, 3 C c
H.D.;Colamonici, O.: Receptor for activated C- kinase (RACK- 1), a WD motif-
containingprotein, specifically associates with the human type I IFN
receptor. J.Immun. 165: 5127- 5132, 2000.

GAM30 346 IFNAR2 Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.;Pitha, P.; 3 C c
Colamonici, O. R.: Cloning and expression of a long formof the beta subunit
of the interferon alpha/beta receptor that isrequired for signaling. J.
Biol. Chem. 270: 21606- 21611, 1995.

GAM30 346 IFNAR2 Lutfalla, G.; Holland, S. J.; Cinato, E.; Monneron, D.; Reboul,J.; Rogers, 3 C c
N. C.; Smith, J. M.; Stark, G. R.; Gardiner, K.; Mogensen,K. E.; Kerr, I.
M.; Uze, G.: Mutant U5A cells are complemented byan interferon- alpha/beta
receptor subunit generated by alternativeprocessing of a new member of a
cytokine receptor gene cluster. EMBOJ. 14: 5100- 5108, 1995.

GAM30 346 IFNAR2 Novick, D.; Cohen, B.; Rubinstein, M.: The human interferon 3 C c
alpha/betareceptor: characterization and molecular cloning. Cell 77: 391-
400,1994.

GAM30 346 IFNAR2 Platanias, L. C.; Uddin, S.; Domanski, P.; Colamonici, O. R.:Differences in 3 C c
interferon alpha and beta signaling: interferon betaselectively induces the
interaction of the alpha and beta(L) subunitsof the type I interferon
receptor. J. Biol. Chem. 271: 23630- 23633,1996.

GAM30 346 IFNAR2 Raz, R.; Cheung, K.; Ling, L.; Levy, D. E.: Three distinct locion human 3 C c
chromosome 21 contribute to interferon- alpha/beta responsiveness.
Somat.Cell Molec. Genet. 21: 139- 145, 1995.

GAM30 346 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; 3 C c
Malherbe, P.: Cloning and functional expression of human kynurenine3-

monooxygenase. FEBS Lett. 410: 407- 412, 1997.

GAM30 346 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001. 3 C c

GAM30 346 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363- 18367,1996. 3 C c

GAM30 346 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994. 3 C c

GAM30 346 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. Nature 384: 39- 43, 1996. 3 C c

GAM30 346 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- specifictranscriptional regulation of human leukotriene B4 receptor gene. J.Exp. Med. 192: 413- 420, 2000. 3 C c

GAM30 346 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative chemoattractant receptor. Genomics 37: 187- 194, 1996. 3 C c

GAM30 346 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: Leukotrienes and lipoxins: structures, biosynthesis,and biological effects. Science 237: 1171- 1176, 1987. 3 C c

GAM30 346 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127- 130, 1997. 3 C c

GAM30 346 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- coupled receptor for leukotriene B4 that mediates chemotaxis. Nature 387:620- 624, 1997. 3 C c

GAM30 346 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990. 3 C b

GAM30 346 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994. 3 C b

GAM30 346 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C c

GAM30 346 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM30 346 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: an ethanol- responsive potential modulator of guanine nucleotide- bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993. 3 C c

GAM30 346 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 C c
Cloning and characterization of the rat and human phosducin- likeprotein
genes: structure, expression and chromosomal localization. Biochim.Biophys.
Acta 1444: 346- 354, 1999.

GAM30 346 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 3 C c
Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J
recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585,
2002.

GAM30 346 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 3 C c
cell coactivator of octamer- binding transcription factors. Nature 373:360-
362, 1995.

GAM30 346 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 3 C c
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-
specific coactivator of octamer- binding transcription factors1 and 2, to
11q23.1 by somatic cell hybridization and in situ hybridization. Genomics
33:143- 145, 1996.

GAM30 346 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 3 C c
of action of the B- cell- specific transcriptional activatorOCA- B. Molec.
Cell. Biol. 15: 4115- 4124, 1995.

GAM30 346 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 3 C c
Matthias, P.: B cell development and immunoglobulin gene transcriptionin the
absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM30 346 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 3 C c
Immun. 9: 373- 398, 1991.

GAM30 346 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 3 C c
specificcoactivator that stimulates immunoglobulin promoter activity
throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM30 346 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 3 C c
Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B,
BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-
864, 2000.

GAM30 346 PRX Boerkoel, C. F.; Takashima, H.; Stankiewicz, P.; Garcia, C. A.;Leber, S. M.; 3 C c
Rhee- Morris, L.; Lupski, J. R.: Periaxin mutationscause recessive Dejerine-
Sottas neuropathy. Am. J. Hum. Genet. 68:325- 333, 2001. Note: Erratum: Am.
J. Hum. Genet. 68: 557 only, 2001.

GAM30 346 PRX Cohn, R. D.; Campbell, K. P.: Molecular basis of muscular dystrophies. 3 C c
MuscleNerve 23: 1456- 1471, 2000.

GAM30 346 PRX Delague, V.; Bareil, C.; Tuffery, S.; Bouvagnet, P.; Chouery, E.;Koussa, S.; 3 C c
Maisonobe, T.; Loiselet, J.; Megarbane, A.; Claustres,M.: Mapping of a new
locus for autosomal recessive demyelinatingCharcot- Marie- Tooth disease to
19q13.1- 13.3 in a large consanguineousLebanese family: exclusion of MAG as
a candidate gene. Am. J. Hum.Genet. 67: 236- 243, 2000.

GAM30 346 PRX Gillespie, C. S.; Lee, M.; Fantes, J. F.; Brophy, P. J.: The geneencoding 3 C c
the Schwann cell protein periaxin localizes on mouse chromosome7 (Prx).
Genomics 41: 297- 298, 1997.

GAM30 346 PRX Gillespie, C. S.; Sherman, D. L.; Fleetwood- Walker, S. M.; Cottrell,D. F.; 3 C c
Tait, S.; Garry, E. M.; Wallace, V. C. J.; Ure, J.; Griffiths,I. R.; Smith,
A. Brophy, P. J.: Peripheral demyelination and neuropathicpain behavior in
periaxin- deficient mice. Neuron 26: 523- 531, 2000.

GAM30 346 PRX Guilbot, A.; Williams, A.; Ravise, N.; Verny, C.; Brice, A.; Sherman,D. L.; 3 C c

Brophy, P. J.; LeGuern, E.; Delague, V.; Bareil, C.; Megarbane,A.; Claustres, M.: A mutation in periaxin is responsible for CMT4F,an autosomal recessive form of Charcot- Marie- Tooth disease. Hum.Molec. Genet. 10: 415-421, 2001.

GAM30 346 PRX Schuler, G. D.: Sequence mapping by electronic PCR. Genome Res. 7:541- 550, 1997. 3 C c

GAM30 346 PRX Takashima, H.; Boerkoel, C. F.; De Jonghe, P.; Ceuterick, C.; Martin,J.- J.; Voit, T.; Schroder, J.- M.; Williams, A.; Brophy, P. J.; Timmerman,V.; Lupski, J. R.: Periaxin mutations cause a broad spectrum of demyelinatingneuropathies. Ann. Neurol. 51: 709- 715, 2002. 3 C c

GAM30 346 PSMD9 Thomas, M. K.; Yao, K.- M.; Tenser, M. S.; Wong, G. G.; Habener,J. F.: Bridge- 1, a novel PDZ- domain coactivator of E2A- mediated regulationof insulin gene transcription. Molec. Cell. Biol. 19: 8492- 8504,1999. 3 C c

GAM30 346 PSMD9 Watanabe, T. K.; Saito, A.; Suzuki, M.; Fujiwara, T.; Takahashi,E.; Slaughter, C. A.; DeMartino, G. N.; Hendil, K. B.; Chung, C. H.;Tanahashi, N.; Tanaka, K.: cDNA cloning and characterization of ahuman proteasomal modulator subunit, p27 (PSMD9). Genomics 50: 241- 250,1998. 3 C c

GAM30 346 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime-untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001. 3 C c

GAM30 346 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994. 3 C c

GAM30 346 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996. 3 C c

GAM30 346 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996. 3 C c

GAM30 346 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996. 3 C c

GAM30 346 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 C b

GAM30 346 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X-linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 C b

GAM30 346 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 C b

GAM30 346 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. 3 C b

NatureGenet. 22: 400- 404, 1999.

GAM30 346 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; 3 C b
Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.;
Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.;
Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia
tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM30 346 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 3 C b
Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset
of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J.
Med. Genet. 38: 409- 411, 2001.

GAM30 346 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 3 C b
A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five-
base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia
tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85:
3343- 3347, 2000.

GAM30 346 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 3 C b
for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a
non- canonical splice site. Gene 273: 285- 293, 2001.

GAM30 346 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, 3 C b
H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked
spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002.

GAM30 346 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; 3 C b
Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A
recurrent RNA- splicing mutation in the SEDL gene causes X-
linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398-
1407,2001.

GAM30 346 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked 3 C b
recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic
evolution in a 6- generation kindred and review ofthe literature. Medicine
78: 9- 25, 1999.

GAM30 346 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, 3 C b
C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe
transactivation domain induces bony abnormalities and cooperateswith LMO1 to
generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419,
1997.

GAM30 346 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; 3 C b
Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J
recombinase activity. Science 250: 1426- 1429, 1990.

GAM30 346 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; 3 C b
Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor
SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992.

GAM30 346 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, 3 C b
G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common
occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990.

GAM30 346 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and 3 C b
characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995.

GAM30 346 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; 3 C b
Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic
axial development and left- right specification. Nature 399:691- 694, 1999.

GAM30 346 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human 3 C b

intestine:biology and function. Gastroenterology 113: 332- 340, 1997.

GAM30 346 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563- 566, 1994. 3 C b

GAM30 346 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 3 C b

GAM30 346 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998. 3 C c

GAM30 346 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle- membranefusion processes. Hum. Genet. 108: 211- 215, 2001. 3 C c

GAM30 346 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells. Biochem. Biophys. Res. Commun. 231: 808- 812, 1997. 3 C c

GAM30 346 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996. 3 C c

GAM30 346 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: Identification of three new splice variants of the SNARE proteinSNAP- 23. Biochem. Biophys. Res. Commun. 285: 320- 327, 2001. 3 C c

GAM30 346 TAL1 Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 3 C c

GAM30 346 TAL1 Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 C c

GAM30 346 TAL1 Begley, C. G.; Aplan, P. D.; Davey, M. P.; Nakahara, K.; Tchorz,K.; Kurtzberg, J.; Hershfield, M. S.; Haynes, B. F.; Cohen, D. I.;Waldmann, T. A.; Kirsch, I. R.: Chromosomal translocation in a humanleukemic stem- cell line disrupts the T- cell antigen receptor delta- chaindiversity region and results in a previously unreported fusion transcript. Proc.Nat. Acad. Sci. 86: 2031- 2035, 1989. 3 C c

GAM30 346 TAL1 Begley, C. G.; Visvader, J.; Green, A. R.; Aplan, P. D.; Metcalf,D.; Kirsch, I. R.; Gough, N. M.: Molecular cloning and chromosomallocalization of the murine homolog of the human helix- loop- helix geneSCL. Proc. Nat. Acad. Sci. 88: 869- 873, 1991. 3 C c

GAM30 346 TAL1 Finger, L. R.; Kagan, J.; Christopher, G.; Kurtzberg, J.; Hershfield,M. S.; Nowell, P. C.; Croce, C. M.: Involvement of the TCL5 geneon human chromosome 1 in T- cell leukemia and melanoma. Proc. Nat.Acad. Sci. 86: 5039- 5043, 1989. 3 C c

GAM30 346 TAL1 Gottgens, B.; Barton, L. M.; Chapman, M. A.; Sinclair, A. M.; Knudsen,B.; Grafham, D.; Gilbert, J. G. R.; Rogers, J.; Bentley, D. R.; Green,A. R.: 3 C c

Transcriptional regulation of the stem cell leukemia gene(SCL)- - comparative analysis of five vertebrate SCL loci. Genome Res. 12:749- 759, 2002.

GAM30 346 TAL1 Gottgens, B.; Gilbert, J. G.; Barton, L. M.; Grafham, D.; Rogers,J.; Bentley, D. R.; Green, A. R.: Long- range comparison of humanand mouse SCL loci: localized regions of sensitivity to restrictionendonucleases correspond precisely with peaks of conserved noncodingsequences. Genome Res. 11: 87- 97, 2001. 3 C c

GAM30 346 TAL1 Kocher, O.; Cheresh, P.; Lee, S. W.: Identification and partialcharacterization of a novel membrane- associated protein (MAP17) up-regulatedin human carcinomas and modulating cell replication and tumor growth. Am.J. Path. 149: 493- 500, 1996. 3 C c

GAM30 346 TAL1 Kozak, M.: An analysis of 5- prime- noncoding sequences from 699vertebrate messenger RNAs. Nucleic Acids Res. 15: 8125- 8148, 1987. 3 C c

GAM30 346 TAL1 Kurtzberg, J.; Bigner, S. H.; Hershfield, M. S.: Establishmentof the DU.528 human lymphohemopoietic stem cell line. J. Exp. Med. 162:1561- 1578, 1985. 3 C c

GAM30 346 TAL1 Robb, L.; Lyons, I.; Li, R.; Hartley, L.; Kontgen, F.; Harvey,R. P.; Metcalf, D.; Begley, C. G.: Absence of yolk sac hematopoiesisfrom mice with a targeted disruption of the scl gene. Proc. Nat.Acad. Sci. 92: 7075- 7079, 1995. 3 C c

GAM30 346 TAL1 Shivdasani, R. A.; Mayer, E. L.; Orkin, S. H.: Absence of bloodformation in mice lacking the T- cell leukaemia oncoprotein tal- 1/SCL. Nature 373:432-434, 1995. 3 C c

GAM30 346 TAL1 Sinclair, A. M.; Bench, A. J.; Bloor, A. J. C.; Li, J.; Gottgens,B.; Stanley, M. L.; Miller, J.; Piltz, S.; Hunter, S.; Nacheva, E.P.; Sanchez, M.- J.; Green, A. R.: Rescue of the lethal scl- /- phenotypeby the human SCL locus. Blood 99: 3931- 3938, 2002. 3 C c

GAM30 346 TAL1 Williams, M.; Lyu, M. S.; Yang, Y. L.; Lin, E. P.; Dunbrack, R.;Birren, B.; Cunningham, J.; Hunter, K.: Ier5, a novel member of theslow- kinetics immediate- early genes. Genomics 44: 327- 334, 1999. 3 C c

GAM30 346 TAL1 Xia, Y.; Brown, L.; Yang, C. Y.- C.; Tsou Tsan, J.; Siciliano,M. J.; Espinosa, R., III; Le Beau, M. M.; Baer, R. J.: TAL2, a helix- loop-helixgene activated by the (7;9)(q34;q32) translocation in human T-cellleukemia. Proc. Nat. Acad. Sci. 88: 11416- 11420, 1991. 3 C c

GAM30 346 TBXA2R Cheng, Y.; Austin, S. C.; Rocca, B.; Koller, B. H.; Coffman, T.M.; Grosser, T.; Lawson, J. A.; FitzGerald, G. A.: Role of prostacyclinin the cardiovascular response to thromboxane A2. Science 296: 539- 541,2002. 3 C b

GAM30 346 TBXA2R Duncan, A. M. V.; Anderson, L. L.; Funk, C. D.; Abramovitz, M.;Adam, M.: Chromosomal localization of the human prostanoid receptorgene family. Genomics 25: 740- 742, 1995. 3 C b

GAM30 346 TBXA2R Fuse, I.; Mito, M.; Hattori, A.; Higuchi, W.; Shibata, A.; Ushikubi,F.; Okuma, M.; Yahata, K.: Defective signal transduction inducedby thromboxane A2 in a patient with a mild bleeding disorder: impairedphospholipase C activation despite normal phospholipase A2 activation. Blood 81:994- 1000, 1993. 3 C b

GAM30 346 TBXA2R Hirata, M.; Hayashi, Y.; Ushikubi, F.; Yokota, Y.; Kageyama, R.;Nakanishi, S.; Narumiya, S.: Cloning and expression of cDNA for ahuman thromboxane A2 receptor. Nature 349: 617- 620, 1991. 3 C b

GAM30 346 TBXA2R Hirata, T.; Kakizuka, A.; Ushikubi, F.; Fuse, I.; Okuma, M.; Narumiya,S.: Arg60- to- leu mutation of the human thromboxane A2 receptor ina dominantly 3 C b

inherited bleeding disorder. J. Clin. Invest. 94: 1662- 1667,1994.

GAM30 346 TBXA2R Hirata, T.; Ushikubi, F.; Kakizuka, A.; Okuma, M.; Narumiya, S.: Two thromboxane A(2) receptor isoforms in human platelets: oppositecoupling to adenylyl cyclase with different sensitivity to arg60- to- leumutation. J. Clin. Invest. 97: 949- 956, 1996. 3 C b

GAM30 346 TBXA2R Nusing, R. M.; Hirata, M.; Kakizuka, A.; Eki, T.; Ozawa, K.; Narumiya,S.: Characterization and chromosomal mapping of the human thromboxaneA2 receptor gene. J. Biol. Chem. 268: 25253- 25259, 1993. 3 C b

GAM30 346 TBXA2R Robinson, P. R.; Cohen, G. B.; Zhukovsky, E. A.; Oprian, D. D.: Constitutively active mutants of rhodopsin. Neuron 9: 719- 725,1992. 3 C b

GAM30 346 TBXA2R Schwengel, D. A.; Nouri, N.; Meyers, D. A.; Levitt, R. C.: Linkagemapping of the human thromboxane A2 receptor (TBXA2R) to chromosome19p13.3 using transcribed 3- prime untranslated DNA sequence polymorphisms. Genomics 18:212- 215, 1993. 3 C b

GAM30 346 TBXA2R Taketo, M.; Rochelle, J. M.; Sugimoto, Y.; Namba, T.; Honda, A.;Negishi, M.; Ichikawa, A.; Narumiya, S.; Seldin, M. F.: Mapping ofthe genes encoding mouse thromboxane A2 receptor and prostaglandinE receptor subtypes EP2 and EP3. Genomics 19: 585- 588, 1994. 3 C b

GAM30 346 TBXA2R Thomas, D. W.; Mannon, R. B.; Mannon, P. J.; Latour, A.; Oliver,J. A.; Hoffman, M.; Smithies, O.; Koller, B. H.; Coffman, T. M.:Coagulation defects and altered hemodynamic responses in mice lackingreceptors for thromboxane A(2). J. Clin. Invest. 102: 1994- 2001,1998. 3 C b

GAM30 346 TBXA2R Unoki, M.; Furuta, S.; Onouchi, Y.; Watanabe, O.; Doi, S.; Fujiwara,H.; Miyatake, A.; Fujita, K.; Tamari, M.; Nakamura, Y.: Associationstudies of 33 single nucleotide polymorphisms (SNPs) in 29 candidategenes for bronchial asthma: positive association a T924C polymorphismin the thromboxane A2 receptor gene. Hum. Genet. 106: 440- 446, 2000. 3 C b

GAM30 346 TBXA2R Ushikubi, F.; Nakajima, M.; Hirata, M.; Okuma, M.; Fujiwara, M.;Narumiya, S.: Purification of the thromboxane A2/prostaglandin H2receptor from human blood platelets.. J. Biol. Chem. 264: 16496- 16501,1989. 3 C b

GAM30 346 TBXA2R Ushikubi, F.; Okuma, M.; Kanaji, K.; Sugiyama, T.; Ogorochi, T.;Narumiya, S.; Uchino, H.: Hemorrhagic thrombocytopathy with platelletthromboxane A2 abnormality: defective signal transduction with normalbinding activity. Thromb. Haemost. 57: 158- 164, 1987. 3 C b

GAM30 346 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.; Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1 are associated with human left- right lateralitydefects. Nature Genet. 26: 365- 369, 2000. 3 C c

GAM30 346 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989. 3 C c

GAM30 346 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002. 3 C c

GAM30 346 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991. 3 C c

GAM30 346 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997. 3 C c

GAM30 346 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996. 3 C c

GAM30 346 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995. 3 C c

GAM30 346 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in vertebratedevelopment. Trends Genet. 16: 303- 309, 2000. 3 C c

GAM30 346 B TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999. 3 C b

GAM30 346 B TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997. 3 C b

GAM30 346 B TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997. 3 C b

GAM30 346 B TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998. 3 C b

GAM30 346 B TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997. 3 C b

GAM30 346 B TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997. 3 C b

GAM30 346 B TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997. 3 C b

GAM30 346 B TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997. 3 C b

GAM30 346 B TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997. 3 C b

GAM30 346 B TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997. 3 C b

GAM30 346 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; 3 C b

Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM30 346 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 C b Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM30 346 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, 3 C b R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997.

GAM30 346 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van 3 C b Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998.

GAM30 346 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; 3 C b Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997.

GAM30 346 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: 3 C b Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma. CancerRes. 39: 3119- 3128, 1979.

GAM30 346 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; 3 C b Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a follicular lymphoma cell line carrying a t(14;18)chromosomal translocation. Int. J. Cancer 39: 785- 788, 1987.

GAM30 346 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. 3 C b A.: STS map of genes and anonymous DNA fragments on human chromosome18 using a panel of somatic cell hybrids. Genomics 15: 387- 391,1993.

GAM30 346 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, 3 C b M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710- 717, 1988.

GAM30 346 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, 3 C b M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human chromosome and its expression in various tissues. Science 227:1038- 1040, 1985.

GAM30 346 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal 3 C b reassignment: YACs containing both YES1 and thymidylatesynthase map to the short arm of chromosome 18. Genomics 15: 442- 445,1993.

GAM30 346 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; 3 C b Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c- yes gene. Molec. Cell. Biol. 7: 41- 47, 1987.

GAM30 346 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; 3 C b Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985.

GAM31 250 BCL7B Jadayel, D. M.; Osborne, L. R.; Coignet, L. J. A.; Zani, V. J.;Tsui, L.- C.; 7 A c

Scherer, S. W.; Dyer, M. J. S.: The BCL7 gene family:deletion of BCL7B in Williams syndrome. Gene 224: 35- 44, 1998.

GAM31 250 BCL7B Meng, X.; Lu, X.; Li, Z.; Green, E. D.; Massa, H.; Trask, B. J.;Morris, C. A.; Keating, M. T.: Complete physical map of the commondeletion region in Williams syndrome and identification and characterizationof three novel genes. Hum. Genet. 103: 590- 599, 1998. 7 A c

GAM31 250 FUT9 Cailleau- Thomas, A.; Coullin, P.; Candelier, J.- J.; Balanzino,L.; Mennesson, B.; Oriol, R.; Mollicone, R.: FUT4 and FUT9 genesare expressed early in human embryogenesis. Glycobiology 10: 789- 802,2000. 7 A c

GAM31 250 FUT9 Kaneko, M.; Kudo, T.; Iwasaki, H.; Ikehara, Y.; Nishihara, S.;Nakagawa, S.; Sasaki, K.; Shiina, T.; Inoko, H.; Saitou, N.; Narimatsu,H.: Alpha- 1,3- fucoslytransferase (sic) IX (Fuc- TIX) is very highlyconserved between human and mouse; molecular cloning, characterizationand tissue distribution of human Fuc- TIX. FEBS Lett. 452: 237- 242,1999. 7 A c

GAM31 250 FUT9 Kaneko, M.; Kudo, T.; Iwasaki, H.; Shiina, T.; Inoko, H.; Kozaki,T.; Saitou, N.; Narimatsu, H.: Assignment of the human alpha- 1,3- fucosyltransferaseIX gene (FUT9) to chromosome band 6q16 by in situ hybridization. Cytogenet.Cell Genet. 86: 329- 330, 1999. 7 A c

GAM31 250 KCNJ10 Doupnik, C. A.; Davidson, N.; Lester, H. A.: The inward rectifierpotassium channel family. Curr. Opin. Neurobiol. 5: 268- 277, 1995. 7 A c

GAM31 250 KCNJ10 Tada, Y.; Horio, Y.; Takumi, T.; Terayama, M.; Tsuji, L.; Copeland,N. G.; Jenkins, N. A.; Kurachi, Y.: Assignment of the glial inwardlyrectifying potassium channel K(AB)- 2/Kir4.1 (Kcnj10) gene to the distalregion of mouse chromosome 1. Genomics 45: 629- 630, 1997. 7 A c

GAM31 250 KCNJ10 Takumi, T.; Ishii, T.; Horio, Y.; Morishige, K.- I.; Takahashi,N.; Yamada, M.; Yamashita, T.; Kiyama, H.; Sohmiya, K.; Nakanishi,S.; Kurachi, Y.: A novel ATP- dependent inward rectifier potassiumchannel expressed predominantly in glial cells. J. Biol. Chem. 270:16339- 16436, 1995. 7 A c

GAM31 250 MEF2B Hobson, G. M.; Krahe, R.; Garcia, E.; Siciliano, M. J.; Funanage,V. L.: Regional chromosomal assignments for four members of the MADSdomain transcription enhancer factor 2 (MEF2) gene family to humanchromosomes 15q26, 19p12, 5q14, and 1q12- q23. Genomics 29: 704- 711,1995. 7 A c

GAM31 250 MEF2B Pollock, R.; Treisman, R.: Human SRF- related proteins: DNA- bindingproperties and potential regulatory targets. Genes Dev. 5: 2327- 2341,1991. 7 A c

GAM31 250 MEF2B Youn, H.- D.; Sun, L.; Prywes, R.; Liu, J. O.: Apoptosis of T cellsmediated by Ca(2+)- induced release of the transcription factor MEF2. Science 286:790- 793, 1999. 7 A c

GAM31 250 MEF2B Yu, Y.- T.; Breitbart, R. E.; Smoot, L. B.; Lee, Y.; Mahdavi, V.;Nadal-Ginard, B.: Human myocyte- specific enhancer factor 2 comprisesa group of tissue- restricted MADS box transcription factors. GenesDev. 6: 1783- 1798, 1992. 7 A c

GAM31 250 PACE4 Kiefer, M. C.; Tucker, J. E.; Joh, R.; Landsberg, K. E.; Saltman,D.; Barr, P. J.: Identification of a second human subtilisin- likeprotease gene in the fes/fps region of chromosome 15. DNA Cell Biol. 10:757- 769, 1991. 7 A c

GAM31 250 PACE4 Mbikay, M.; Seidah, N. G.; Chretien, M.; Simpson, E. M.: Chromosomalassignment of the genes for proprotein convertases PC4, PC5, and PACE4 in mouse and human. Genomics 26: 123- 129, 1995. 7 A c

GAM31 250 PDE4B Huston, E.; Lumb, S.; Russell, A.; Catterall, C.; Ross, A. H.;Steele, M. R.; Bolger, G. B.; Perry, M. J.; Owens, R. J.; Houslay,M. D.: Molecular cloning 7 A c

and transient expression in COS7 cells ofa novel human PDE4B cAMP- specific phosphodiesterase, HSPDE4B3. Biochem.J. 328: 549- 558, 1997.

GAM31 250 PDE4B Livi, G. P.; Kmetz, P.; McHale, M. M.; Cieslinski, L. B.; Sathe,G. M.; Taylor, D. P.; Davis, R. L.; Torphy, T. J.; Balcarek, J. M.: Cloning and expression of cDNA for a human low- K(m), rolipram- sensitivecyclic AMP phosphodiesterase. Molec. Cell. Biol. 10: 2678- 2686,1990. 7 A c

GAM31 250 PDE4B Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994. 7 A c

GAM31 250 PDE4B Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins,M.; Jarnagin, K.; Shelton, E. R.: The cDNA of a human lymphocytecyclic- AMP phosphodiesterase (PDE IV) reveals a multigene family. Gene 129:239- 247, 1993. 7 A c

GAM31 250 PDE4B Szpirer, C.; Szpirer, J.; Riviere, M.; Swinnen, J.; Vicini, E.;Conti, M.: Chromosomal localization of the human and rat genes (PDE4Dand PDE4B) encoding the cAMP- specific phosphodiesterases 3 and 4. Cytogenet.Cell Genet. 69: 11- 14, 1995. 7 A c

GAM31 250 PDE4B Xu, R. X.; Hassell, A. M.; Vanderwall, D.; Lambert, M. H.; Holmes,W. D.; Luther, M. A.; Rocque, W. J.; Milburn, M. V.; Zhao, Y.; Ke,H.; Nolte, R. T.: Atomic structure of PDE4: insights into phosphodiesterasemechanism and specificity. Science 288: 1822- 1825, 2000. 7 A c

GAM31 250 PLCG1 Bristol, A.; Hall, S. M.; Kriz, R. W.; Stahl, M. L.; Fan, Y. S.;Byers, M. G.; Eddy, R. L.; Shows, T. B.; Knopf, J. L.: PhospholipaseC- 148: chromosomal location and deletion mapping of functional domains. ColdSpring Harbor Symp. Quant. Biol. 53: 915- 920, 1988. 7 A c

GAM31 250 PLCG1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 7 A c

GAM31 250 PLCG1 Nelson, K. K.; Knopf, J. L.; Siracusa, L. D.: Localization ofphospholipase C- gamma 1 to mouse chromosome 2. Mammalian Genome 3:597- 600, 1992. 7 A c

GAM31 250 PLCG1 Rothschild, C. B.; Akots, G.; Fajans, S. S.; Bowden, D. W.: Amicrosatellite polymorphism associated with the PLC1 (phospholipaseC) locus: identification, mapping, and linkage to the MODY locus onchromosome 20. Genomics 13: 560- 564, 1992. 7 A c

GAM31 250 PLCG1 Stahl, M. L.; Ferenz, C. R.; Kelleher, K. L.; Kriz, R. W.; Knopf,J. L.: Sequence similarity of phospholipase C with the non- catalyticregion of src. Nature 332: 269- 272, 1988. 7 A c

GAM31 250 PLCG1 Ye, K.; Aghdasi, B.; Luo, H. R.; Moriarity, J. L.; Wu, F. Y.; Hong,J. J.; Hurt, K. J.; Bae, S. S.; Suh, P.- G.; Snyder, S. H.: PhospholipaseC- gamma- 1 is a physiological guanine nucleotide exchange factor forthe nuclear GTPase PIKE. Nature 415: 541- 544, 2002. 7 A c

GAM31 250 SFPQ Clark, J.; Lu, Y.- J.; Sidhar, S. K.; Parker, C.; Gill, S.; Smedley,D.; Hamoudi, R.; Linehan, W. M.; Shipley, J.; Cooper, C. S.: Fusionof splicing factor genes PSF and NonO (p54- nrb) to the TFE3 gene inpapillary renal cell carcinoma. Oncogene 15: 2233- 2239, 1997. 7 A c

GAM31 250 SFPQ Patton, J. G.; Porro, E. B.; Galceran, J.; Tempst, P.; Nadal- Ginard,B.: Cloning and characterization of PSF, a novel pre- mRNA splicingfactor. Genes Dev. 7: 393- 406, 1993. 7 A c

GAM31 250 THRA Anderson, L. A.; Friedman, L.; Osborne- Lawrence, S.; Lynch, E.;Weissenbach, 7 A c

J.; Bowcock, A.; King, M.- C.: High- density genetic mapof the BRCA1 region of chromosome 17q12- q21. Genomics 17: 618- 623,1993.

GAM31 250 THRA Benbrook, D.; Pfahl, M.: A novel thyroid hormone receptor encodedby a cDNA clone from a human testis library. Science 238: 788- 791,1987. 7 A c

GAM31 250 THRA Bernal, J.; Refetoff, S.; DeGroot, L. J.: Abnormalities of triiodothyroninebinding to lymphocyte and fibroblast nuclei from a patient with peripheraltissue resistance to thyroid hormone action. J. Clin. Endocr. Metab. 47:1266- 1272, 1978. 7 A c

GAM31 250 THRA Dayton, A. I.; Selden, J. R.; Laws, G.; Dorney, D. J.; Finan, J.;Tripputi, P.; Emanuel, B. S.; Rovera, G.; Nowell, P. C.; Croce, C.M.: A human c- erbA oncogene homologue is closely proximal to thechromosome 17 breakpoint in acute promyelocytic leukemia. Proc. Nat.Acad. Sci. 81: 4495- 4499, 1984. 7 A c

GAM31 250 THRA Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, P.; Stehelin, D.: Sequencing the erbA geneof avian erythroblastosis virus reveals a new type of oncogene. Science 224:1456- 1459, 1984. 7 A c

GAM31 250 THRA Ferro, M. T.; San Roman, C.: Constitutional t(15;17). CancerGenet. Cytogenet. 4: 89- 91, 1981. 7 A c

GAM31 250 THRA Gullberg, H.; Rudling, M.; Forrest, D.; Angelin, B.; Vennstrom,B.: Thyroid hormone receptor beta- deficient mice show complete lossof the normal cholesterol 7- alpha- hydroxylase (CYP7A) response tothyroid hormone but display enhanced resistance to dietary cholesterol. Molec.Endocr. 14: 1739- 1749, 2000. 7 A c

GAM31 250 THRA Ichikawa, K.; Hughes, I. A.; Horwitz, A. L.; DeGroot, L. J.: Characterizationof nuclear thyroid hormone receptors of cultured skin fibroblastsfrom patients with resistance to thyroid hormone. Metabolism 36:392- 399, 1987. 7 A c

GAM31 250 THRA Iskaros, J.; Pickard, M.; Evans, I.; Sinha, A.; Hardiman, P.; Ekins,R.: Thyroid hormone receptor gene expression in first trimester humanfetal brain. J. Clin. Endocr. Metab. 85: 2620- 2623, 2000. 7 A c

GAM31 250 THRA Jansson, M.; Philipson, L.; Vennstrom, B.: Isolation and characterizationof multiple human genes homologous to the oncogenes of avian erythroblastosisvirus. EMBO J. 2: 561- 565, 1983. 7 A c

GAM31 250 THRA Jhanwar, S. C.; Chaganti, R. S. K.; Croce, C. M.: Germ- line chromosomallocalization of human c- erb- A oncogene. Somat. Cell Molec. Genet. 11:99- 102, 1985. 7 A c

GAM31 250 THRA Kaneshige, M.; Suzuki, H.; Kaneshige, K.; Cheng, J.; Wimbrow,H.; Barlow, C.; Willingham, M. C.; Cheng, S.: A targeted dominantnegative mutation of the thyroid hormone alpha- 1 receptor causes increasedmortality, infertility, and dwarfism in mice. Proc. Nat. Acad. Sci. 98:15095- 15100, 2001. 7 A c

GAM31 250 THRA Laudet, V.; Begue, A.; Henry- Duthoit, C.; Joubel, A.; Martin,P.; Stehelin, D.; Saule, S.: Genomic organization of the human thyroidhormone receptor alpha (c- erbA- 1) gene. Nucleic Acids Res. 19: 1105- 1112,1991. 7 A c

GAM31 250 THRA Le Beau, M. M.; Westbrook, C. A.; Diaz, M. O.; Rowley, J. D.;Oren, M.: Translocation of the p53 gene in t(15;17) in acute promyelocyticleukaemia. Nature 316: 826- 828, 1985. 7 A c

GAM31 250 THRA Mathieu- Mahul, D.; Xu, D. Q.; Saule, S.; Lidereau, R.; Galibert,F.; Berger, R.; Mauchauffe, M.; Larsen, C. J.: An EcoRI restrictionfragment length polymorphism (RFLP) in the human c- erb A locus. Hum.Genet. 71: 41- 44, 1985. 7 A c

GAM31 250 THRA McCabe, C. J.; Gittoes, N. J.; Sheppard, M. C.; Franklyn, J. A.: Thyroid 7 A c
receptor alpha- 1 and alpha- 2 mutations in nonfunctioningpituitary tumors.
J. Clin. Endocr. Metab. 84: 649- 653, 1999.

GAM31 250 THRA Menezes- Ferreira, M. M.; Eil, C.; Wortsman, J.; Weintraub, B.D.: Decreased 7 A c
nuclear uptake of [125- I]triiodo- L- thyronine in fibroblastsfrom patients
with peripheral thyroid hormone resistance. J. Clin.Endocr. Metab. 59: 1081-
1087, 1984.

GAM31 250 THRA Mitelman, F.; Manolov, G.; Manolova, Y.; Billstrom, R.; Heim,S.; 7 A c
Kristoffersson, U.; Mandahl, N.; Ferro, M. T.; San Roman, C.:High resolution
chromosome analysis of constitutional and acquiredt(15;17) maps c- erbA to
subband 17q11.2. Cancer Genet. Cytogenet. 22:95- 98, 1986.

GAM31 250 THRA Miyajima, N.; Horiuchi, R.; Shibuya, Y.; Fukushige, S.; Matsubara,K.; 7 A c
Toyoshima, K.; Yamamoto, T.: Two erbA homologs encoding proteinswith
different T(3) binding capacities are transcribed from oppositeDNA strands
of the same genetic locus. Cell 57: 31- 39, 1989.

GAM31 250 THRA Nagaya, T.; Nomura, Y.; Fujieda, M.; Seo, H.: Heterodimerizationpreferences 7 A c
of thyroid hormone receptor alpha isoforms. Biochem.Biophys. Res. Commun.
226: 426- 430, 1996.

GAM31 250 THRA Nakai, A.; Seino, S.; Sakurai, A.; Szilak, I.; Bell, G. I.; DeGroot,L. J.: 7 A c
Characterization of a thyroid hormone receptor expressed inhuman kidney and
other tissues. Proc. Nat. Acad. Sci. 85: 2781- 2785,1988.

GAM31 250 THRA Ng, L.; Rusch, A.; Amma, L. L.; Nordstrom, K.; Erway, L. C.; Vennstrom,B.; 7 A c
Forrest, D.: Suppression of the deafness and thyroid dysfunctionin Thrb-
null mice by an independent mutation in the Thra thyroid hormonereceptor
gene. Hum. Molec. Genet. 10: 2701- 2708, 2001.

GAM31 250 THRA Puzianowska- Kuznicka, M.; Krystyniak, A.; Madej, A.; Cheng, S.- Y.;Nauman, 7 A c
J.: Functionally impaired TR mutants are present in thyroidpapillary cancer.
J. Clin. Endocr. Metab. 87: 1120- 1128, 2002.

GAM31 250 THRA Refetoff, S.; DeGroot, L. J.; Benard, B.; DeWind, L. T.: Studiesof a sibship 7 A c
with apparent hereditary resistance to the intracellularaction of thyroid
hormone. Metabolism 21: 723- 756, 1972.

GAM31 250 THRA Rider, S. H.; Bailey, C. J.; Voss, R.; Sheer, D.; Hiorns, L. R.;Solomon, E.: 7 A c
RFLP for the human erb- A1 gene. Nucleic Acids Res. 15:863 only, 1987.

GAM31 250 THRA Sakurai, A.; Nakai, A.; DeGroot, L. J.: Expression of three formsof thyroid 7 A c
hormone receptor in human tissues. Molec. Endocr. 3:392- 399, 1989.

GAM31 250 THRA Sap, J.; Munoz, A.; Damm, K.; Goldberg, Y.; Ghysdael, J.; Leutz,A.; Beug, 7 A c
H.; Vennstrom, B.: The c- erb- A protein is a high- affinityreceptor for
thyroid hormone. Nature 324: 635- 640, 1986.

GAM31 250 THRA Sheer, D.; Sheppard, D. M.; Le Beau, M.; Rowley, J. D.; San Roman,C.; 7 A c
Solomon, E.: Localization of the oncogene c- erbA1 immediatelyproximal to
the acute promyelocytic leukaemia breakpoint on chromosome17. Ann. Hum.
Genet. 49: 167- 171, 1985.

GAM31 250 THRA Spurr, N. K.; Goodfellow, P. N.; Sheer, D.; Bodmer, W. F.; Vennstrom,B.: 7 A c
Mapping of cellular oncogenes: ERBA1 is on chromosome 17. (Abstract)
Cytogenet.Cell Genet. 37: 591 only, 1984.

GAM31 250 THRA Spurr, N. K.; Solomon, E.; Jansson, M.; Sheer, D.; Goodfellow,P. N.; Bodmer, 7 A c
W. F.; Vennstrom, B.: Chromosomal localisation ofthe human homologues to the
oncogenes erbA and B. EMBO J. 3: 159- 163,1984.

GAM31 250 THRA Thompson, C. C.; Weinberger, C.; Lebo, R.; Evans, R. M.: Identificationof a 7 A c
novel thyroid hormone receptor expressed in the mammalian centralnervous

system. Science 237: 1610- 1614, 1987.

GAM31 250 THRA Weinberger, C.; Thompson, C. C.; Ong, E. S.; Lebo, R.; Gruol,D. J.; Evans, 7 A c
R. M.: The c- erb- A gene encodes a thyroid hormone receptor. Nature
324:641- 646, 1986.

GAM31 250 THRA Zabel, B. U.; Fournier, R. E. K.; Lalley, P. A.; Naylor, S. L.;Sakaguchi, A. 7 A c
Y.: Cellular homologs of the avian erythroblastosisvirus erb- A and erb- B
genes are syntenic in mouse but asyntenic inman. Proc. Nat. Acad. Sci. 81:
4874- 4878, 1984.

GAM31 250 ZNF36 Rousseau- Merck, M.- F.; Duro, D.; Berger, R.; Thiesen, H. J.: 7 A c
Chromosomallocalization of two KOX zinc finger genes on chromosome bands
7q21- q22. Ann.Genet. 38: 81- 84, 1995.

GAM31 250 ZNF36 Tommerup, N.; Aagaard, L.; Lund, C. L.; Boel, E.; Baxendale, S.;Bates, G. 7 A c
P.; Lehrach, H.; Vissing, H.: A zinc- finger gene ZNF141mapping at
4p16.3/D4S90 is a candidate gene for the Wolf- Hirschhorn(4p-) syndrome.
Hum. Molec. Genet. 2: 1571- 1575, 1993.

GAM31 250 ZNF36 Tommerup, N.; Vissing, H.: Isolation and fine mapping of 16 novelhuman zinc 7 A c
finger- encoding cDNAs identify putative candidate genesfor developmental
and malignant disorders. Genomics 27: 259- 264,1995.

GAM32 384 CUL3 Du, M.; Sansores- Garcia, L.; Zu, Z.; Wu, K. K.: Cloning and 3 C c
expressionanalysis of a novel salicylate suppressible gene, Hs- CUL- 3, a
memberof cullin/Cdc53 family. J. Biol. Chem. 273: 24289- 24292, 1998.

GAM32 384 CUL3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM32 384 CUL3 Kipreos, E. T.; Lander, L. E.; Wing, J. P.; He, W. W.; Hedgecock,E. M.: cul- 3 C c
1 is required for cell cycle exit in C. elegans and identifiesa novel gene
family. Cell 85: 829- 839, 1996.

GAM32 384 CUL3 Michel, J. J.; Xiong, Y.: Human CUL- 1, but not other cullin familymembers, 3 C c
selectively interacts with SKP1 to form a complex with SKP2and cyclin A.
Cell Growth Differ. 9: 435- 449, 1998.

GAM32 384 SPP1 Ashkar, S.; Weber, G. F.; Panoutsakopoulou, V.; Sanchirico, M.E.; Jansson, 3 C c
M.; Zawaideh, S.; Rittling, S. R.; Denhardt, D. T.; Glimchar,M. J.; Cantor,
H.: Eta- 1 (osteopontin): an early component of type- 1(cell- mediated)
immunity. Science 287: 860- 864, 2000.

GAM32 384 SPP1 Baccarini- Contri, M.; Taparelli, F.; Pasquali- Ronchetti, I.: Osteopontinis 3 C c
a constitutive component of normal elastic fibers in human skinand aorta.
Matrix Biol. 14: 553- 560, 1994.

GAM32 384 SPP1 Beck, G. R., Jr.; Zerler, B.; Moran, E.: Phosphate is a specificsignal for 3 C c
induction of osteopontin gene expression. Proc. Nat. Acad.Sci. 97: 8352-
8357, 2000.

GAM32 384 SPP1 Chabas, D.; Baranzini, S. E.; Mitchell, D.; Bernard, C. C. A.;Rittling, S. 3 C c
R.; Denhardt, D. T.; Sobel, R. A.; Lock, C.; Karpuj,M.; Pedotti, R.; Heller,
R.; Oksenberg, J. R.; Steinman, L.: Theinfluence of the proinflammatory
cytokine, osteopontin, on autoimmunedemyelinating disease. Science 294:
1731- 1735, 2001.

GAM32 384 SPP1 Crosby, A. H.; Edwards, S. J.; Murray, J. C.; Dixon, M. J.: 3 C c
Genomicorganization of the human osteopontin gene: exclusion of the
locusfrom a causative role in the pathogenesis of dentinogenesis
imperfectatype II. Genomics 27: 155- 160, 1995.

GAM32 384 SPP1 Crosby, A. H.; Lyu, M. S.; Lin, K.; McBride, O. W.; Kerr, J. M.;Aplin, H. 3 C c
M.; Fisher, L. W.; Young, M. F.; Kozak, C. A.; Dixon, M.J.: Mapping of the
human and mouse bone sialoprotein and osteopontinloci. Mammalian Genome 7:
149- 151, 1996.

GAM32 384 SPP1 Fisher, L. W.; McBride, O. W.; Termine, J. D.; Young, M. F.: Humanbone 3 C c
sialoprotein: deduced protein sequence and chromosomal localization. J.Biol.
Chem. 265: 2347- 2351, 1990.

GAM32 384 SPP1 Graf, K.; Do, Y. S.; Ashizawa, N.; Meehan, W. P.; Giachelli, C.M.; Marboe, 3 C c
C. C.; Fleck, E.; Hsueh, W. A.: Myocardial osteopontinexpression is
associated with left ventricular hypertrophy. Circulation 96:3063- 3071,
1997.

GAM32 384 SPP1 Kiefer, M. C.; Bauer, D. M.; Barr, P. J.: The cDNA and derivedamino acid 3 C c
sequence for human osteopontin. Nucleic Acids Res. 17:3306, 1989.

GAM32 384 SPP1 Kim, J.- H.; Skates, S. J.; Uede, T.; Wong, K.; Schorge, J. O.;Feltmate, C. 3 C c
M.; Berkowitz, R. S.; Cramer, D. W.; Mok, S. C.: Osteopontinas a potential
diagnostic biomarker for ovarian cancer. J.A.M.A. 287:1671- 1679, 2002.

GAM32 384 SPP1 Kohri, K.; Nomura, S.; Kitamura, Y.; Nagata, T.; Yoshioka, K.;Iguchi, M.; 3 C c
Yamate, T.; Umekawa, T.; Suzuki, Y.; Sinohara, H.; Kurita,T.: Structure and
expression of the mRNA encoding urinary stone protein(osteopontin). J. Biol.
Chem. 268: 15180- 15184, 1993.

GAM32 384 SPP1 Kohri, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Amasaki, N.;Yamate, T.; 3 C c
Umekawa, T.; Iguchi, M.; Sinohara, H.; Kurita, T.: Molecularcloning and
sequencing of cDNA encoding urinary stone protein, whichis identical to
osteopontin. Biochem. Biophys. Res. Commun. 184:859- 864, 1992.

GAM32 384 SPP1 Liaw, L.; Birk, D. E.; Ballas, C. B.; Whitsitt, J. S.; Davidson,J. M.; 3 C c
Hogan, B. L. M.: Altered wound healing in mice lacking a
functionalosteopontin gene (spp1). J. Clin. Invest. 101: 1468- 1478, 1998.

GAM32 384 SPP1 Morimoto, I.; Sasaki, Y.; Ishida, S.; Imai, K.; Tokino, T.: Identificationof 3 C c
the osteopontin gene as a direct target of TP53. Genes ChromosomesCancer 33:
270- 278, 2002.

GAM32 384 SPP1 Reinholt, F. P.; Hultenby, K.; Oldberg, A.; Heinegard, D.: Osteopontin- - 3 C c
apossible anchor of osteoclasts to bone. Proc. Nat. Acad. Sci. 87:4473-
4475, 1990.

GAM32 384 SPP1 Singh, K.; Balligand, J.- L.; Fischer, T. A.; Smith, T. W.; Kelly,R. A.: 3 C c
Glucocorticoids increase osteopontin expression in cardiacmyocytes and
microvascular endothelial cells: role in regulation ofinducible nitric oxide
synthase. J. Biol. Chem. 270: 28471- 28478,1995.

GAM32 384 SPP1 Staal, A.; van Wijnen, A. J.; Birkenhager, J. C.; Pols, H. A.P.; Prahl, J.; 3 C c
DeLuca, H.; Gaub, M.- P.; Lian, J. B.; Stein, G. S.;van Leeuwen, J. P. T.
M.; Stein, J. L.: Distinct conformations ofvitamin D receptor/retinoid X
receptor- alpha heterodimers are specifiedby dinucleotide differences in the
vitamin D- responsive elements ofthe osteocalcin and osteopontin genes.
Molec. Endocr. 10: 1444- 1456,1996.

GAM32 384 SPP1 Weber, G. F.; Ashkar, S.; Glimcher, M. J.; Cantor, H.: Receptor- 3 C c
ligandinteraction between CD44 and osteopontin (Eta- 1). Science 271: 509-
512,1996.

GAM32 384 SPP1 Yoshitake, H.; Rittling, S. R.; Denhardt, D. T.; Noda, M.: Osteopontin- 3 C c
deficientmice are resistant to ovariectomy- induced bone resorption.
Proc.Nat. Acad. Sci. 96: 8156- 8160, 1999.

GAM32 384 SPP1 Young, M. F.; Kerr, J. M.; Termine, J. D.; Wewer, U. M.; Wang,M. G.; 3 C c

McBride, O. W.; Fisher, L. W.: cDNA cloning, mRNA distributionand heterogeneity, chromosomal location and RFLP analysis of humanosteopontin. Genomics 7: 491- 502, 1990.

GAM32 384 TIMELESS Koike, N.; Hida, A.; Numano, R.; Hirose, M.; Sakaki, Y.; Tei, H.: 3 C c
Identification of the mammalian homologues of the Drosophila timelessgene, timeless1. FEBS Lett. 441: 427- 431, 1998.

GAM32 384 TIMELESS Sangoram, A. M.; Saez, L.; Antoch, M. P.; Gekakis, N.; Staknis,D.; Whiteley, 3 C c
A.; Fruechte, E. M.; Vitaterna, M. H.; Shimomura, K.;King, D. P.; Young, M. W.; Weitz, C. J.; Takahashi, J. S.: Mammaliancircadian autoregulatory loop: a timeless ortholog and mPer1 interactand negatively regulate CLOCK- BMAL1- induced transcription. Neuron 21:1101- 1113, 1998.

GAM32 384 TIMELESS Zylka, M. J.; Shearman, L. P.; Levine, J. D.; Jin, X.; Weaver,D. R.; 3 C c
Reppert, S. M.: Molecular analysis of mammalian timeless. Neuron 21:1115- 1122, 1998.

GAM34 314 NGFB Breakefield, X. O.; Orloff, G.; Castiglione, C.; Coussens, L.;Axelrod, F. 3 C c
B.; Ullrich, A.: Structural gene for beta- nerve growthfactor not defective in familial dysautonomia. Proc. Nat. Acad. Sci. 81:4213- 4216, 1984.

GAM34 314 NGFB Carrier, A.; Rosier, M.- F.; Guillemot, F.; Goguel, A.- F.; Pulcini,F.; 3 C c
Bernheim, A.; Auffray, C.; Devignes, M.- D.: Integrated physical,genetic, and genic map covering 3 Mb around the human NGF gene (NGFB)at 1p13. Genomics 31: 80- 89, 1996.

GAM34 314 NGFB Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 C c
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001.

GAM34 314 NGFB Darby, J. K.; Feder, J.; Selby, M.; Riccardi, V.; Ferrell, R.;Siao, D.; 3 C c
Goslin, K.; Rutter, W.; Shooter, E. M.; Cavalli- Sforza,L. L.: A discordant sibship analysis between beta- NGF and neurofibromatosis. Am.J. Hum. Genet. 37: 52- 59, 1985.

GAM34 314 NGFB Darby, J. K.; Kidd, J. R.; Pakstis, A. J.; Sparkes, R. S.; Cann,H. M.; 3 C c
Ferrell, R. E.; Gerhard, D. G.; Riccardi, V.; Egeland, J. A.;Shooter, E. M.; Cavalli- Sforza, L. L.; Kidd, K. K.: Linkage relationshipsof the gene for the beta subunit of nerve growth factor (NGFB) withother chromosome 1 marker loci. Cytogenet. Cell Genet. 39: 158- 160,1985.

GAM34 314 NGFB Dracopoli, N. C.: Personal Communication. Cambridge, Mass. 4/29/1988. 3 C c

GAM34 314 NGFB Dracopoli, N. C.; Meisler, M. H.: Mapping the human amylase genecluster on 3 C c
the proximal short arm of chromosome 1 using a highly informative(CA)n repeat. Genomics 7: 97- 102, 1990.

GAM34 314 NGFB Dracopoli, N. C.; Rose, E.; Whitfield, G. K.; Guidon, P. T.; Bale,S. J.; 3 C c
Chance, P. A.; Kourides, I. A.; Housman, D. E.: Two thyroidhormone regulated genes, the beta- subunits of nerve growth factor(NGFB) and thyroid stimulating hormone (TSHB), are located less than310 kb apart in both human and mouse genomes. Genomics 3: 161- 167,1988.

GAM34 314 NGFB Francke, U.; de Martinville, B.; Coussens, L.; Ullrich, A.: Thehuman gene 3 C c
for the beta subunit of nerve growth factor is locatedon the proximal short arm of chromosome 1. Science 222: 1248- 1251,1983.

GAM34 314 NGFB Garson, J. A.; van den Berghe, J. A.; Kemshead, J. T.: Novelnon- isotopic in 3 C c
situ hybridization technique detects small (1 kb)unique sequences in routinely G- banded human chromosomes: fine mappingof N- myc and beta- NGF genes. Nucleic Acids Res. 15: 4761- 4770, 1987.

GAM34 314 NGFB Lee, R.; Kermani, P.; Teng, K. K.; Hempstead, B. L.: Regulationof cell survival by secreted proneurotrophins. Science 294: 1945- 1948,2001. 3 C c

GAM34 314 NGFB Levi- Montalcini, R.: The nerve growth factor thirty- five yearslater. Science 237: 1154- 1162, 1987. 3 C c

GAM34 314 NGFB MacInnis, B. L.; Campenot, R. B.: Retrograde support of neuronalsurvival without retrograde transport of nerve growth factor. Science 295:1536- 1539, 2002. 3 C c

GAM34 314 NGFB Middleton- Price, H.; van den Berghe, J.; Harding, A.; Scott, J.;Malcolm, S.: Analysis of markers on chromosome 1. (Abstract) Cytogenet.Cell Genet. 46: 662, 1987. 3 C c

GAM34 314 NGFB Mitchell, E. L. D.; Jones, D.; White, G. R. M.; Varley, J. M.;Santibanez Koref, M. F.: Determination of the gene order of the threeloci CD2, NGFB, and NRAS at human chromosome band 1p13 and refinementof their localisation at the subband level by fluorescence in situhybridization. Cytogenet. Cell Genet. 70: 183- 185, 1995. 3 C c

GAM34 314 NGFB Munke, M.; Lindgren, V.; de Martinville, B.; Francke, U.: Comparativeanalysis of mouse- human hybrids with rearranged chromosomes 1 by insitu hybridization and Southern blotting: high- resolution mappingof NRAS, NGFB, and AMY on human chromosome 1. Somat. Cell Molec.Genet. 10: 589- 599, 1984. 3 C c

GAM34 314 NGFB Ramer, M. S.; Priestley, J. V.; McMahon, S. B.: Functional regenerationof sensory axons into the adult spinal cord. Nature 403: 312- 316,2000. 3 C c

GAM34 314 NGFB Sanico, A. M.; Stanisz, A. M.; Gleeson, T. D.; Bora, S.; Proud,D.; Bienenstock, J.; Koliatsos, V. E.; Togias, A.: Nerve growth factorexpression and release in allergic inflammatory disease of the upperairways. Am. J. Resp. Crit. Care Med. 161: 1631- 1635, 2000. 3 C c

GAM34 314 NGFB Ullrich, A.; Gray, A.; Berman, C.; Dull, T. J.: Human beta- nervegrowth factor gene sequence highly homologous to that of mouse. Nature 303:821- 825, 1983. 3 C c

GAM34 314 NGFB Zabel, B. U.; Eddy, R. L.; Lalley, P. A.; Scott, J.; Bell, G.I.; Shows, T. B.: Chromosomal locations of the human and mouse genesfor precursors of epidermal growth factor and the beta subunit ofnerve growth factor. Proc. Nat. Acad. Sci. 82: 469- 473, 1985. 3 C c

GAM34 314 NGFB Zabel, B. U.; Eddy, R. L.; Scott, J.; Shows, T. B.: The humannerve growth factor gene (NGF) is located on the short arm of chromosome1. (Abstract) Cytogenet. Cell Genet. 37: 614, 1984. 3 C c

GAM34 314 RAD50 Carney, J. P.; Maser, R. S.; Olivares, H.; Davis, E. M.; Le Beau,M.; Yates, J. R., III; Hays, L.; Morgan, W. F.; Petrini, J. H. J.: The hMre11/hRad50 protein complex and Nijmegen breakage syndrome:linkage of double- strand break repair to the cellular DNA damage response. Cell 93:477- 486, 1998. 3 C c

GAM34 314 RAD50 Dolganov, G. M.; Maser, R. S.; Novikov, A.; Tosto, L.; Chong, S.;Bressan, D. A.; Petrini, J. H. J.: Human Rad50 is physically associatedwith human Mre11: identification of a conserved multiprotein complexim plicated in recombinational DNA repair. Molec. Cell Biol. 16:4832- 4841, 1996. 3 C c

GAM34 314 RAD50 Hopfner, K.- P.; Craig, L.; Moncalian, G.; Zinkel, R. A.; Usui,T.; Owen, B. A. L.; Karcher, A.; Henderson, B.; Bodmer, J.- L.; McMurray,C. T.; Carney, J. P.; Petrini, J. H. J.; Tainer, J. A.: The Rad50zinc- hook is a structure joining Mre11 complexes in DNA recombinationand repair. Nature 418: 562- 566, 2002. 3 C c

GAM34 314 RAD50 Hopfner, K.- P.; Karcher, A.; Craig, L.; Woo, T. T.; Carney, J.P.; Tainer, 3 C c

J. A.: Structural biochemistry and interaction architectureof the DNA double- strand break repair Mre11 nuclease and Rad50- ATPase. Cell 105:473-485, 2001.

GAM34 314 RAD50 Luo, G.; Yao, M. S.; Bender, C. F.; Mills, M.; Bladl, A. R.; Bradley,A.; 3 C c
Petrini, J. H. J.: Disruption of mRad50 causes embryonic stemcell lethality, abnormal embryonic development, and sensitivity toionizing radiation. Proc. Nat. Acad. Sci. 96: 7376- 7381, 1999.

GAM34 314 RAD50 Stracker, T. H.; Carson, C. T.; Weitzman, M. D.: Adenovirus 3 C c
oncoproteinsinactivate the Mre11- Rad50- NBS1 DNA repair complex. Nature 418:348- 352, 2002.

GAM34 314 RAD50 Trujillo, K. M.; Yuan, S.- S. F.; Lee, E. Y.- H. P.; Sung, P.: 3 C c
Nucleaseactivities in a complex of human recombination and DNA repair factorsRad50, Mre11, and p95. J. Biol. Chem. 273: 21447- 21450, 1998.

GAM34 314 RAD50 Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin,J.: BASC, a 3 C c
super complex of BRCA1- associated proteins involved inthe recognition and repair of aberrant DNA structures. Genes Dev. 14:927- 939, 2000.

GAM34 314 RAD50 Zhong, Q.; Chen, C.- F.; Li, S.; Chen, Y.; Wang, C.- C.; Xiao, J.;Chen, P.- 3 C c
L.; Sharp, Z. D.; Lee, W.- H.: Association of BRCA1 withthe hRad50- hMre11-p95 complex and the DNA damage response. Science 285:747- 750, 1999.

GAM34 314 RAD50 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 C c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human telomeres. Nature Genet. 25: 347- 352, 2000.

GAM36 351 FGF2 Abraham, J. A.; Mergia, A.; Whang, J. L.; Tumolo, A.; Friedman,J.; Hjerild, 3 C c
K. A.; Gospodarowicz, D.; Fiddes, J. C.: Nucleotidesequence of a bovine clone encoding the angiogenic protein, basicfibroblast growth factor. Science 233: 545- 548, 1986.

GAM36 351 FGF2 Abraham, J. A.; Whang, J. L.; Tumolo, A.; Mergia, A.; Friedman,J.; 3 C c
Gospodarowicz, D.; Fiddes, J. C.: Human basic fibroblast growthfactor: nucleotide sequence and genomic organization. EMBO J. 5:2523- 2528, 1986.

GAM36 351 FGF2 Doniach, T.: Basic FGF as an inducer of anteroposterior neuralpattern. Cell 3 C c
83: 1067- 1070, 1995.

GAM36 351 FGF2 Dono, R.; Texido, G.; Dussel, R.; Ehmke, H.; Zeller, R.: Impairedcerebral 3 C c
cortex development and blood pressure regulation in FGF2- deficientmice. EMBO J. 17: 4213- 4225, 1998.

GAM36 351 FGF2 Eckenstein, F. P.: Fibroblast growth factors in the nervous system. 3 C c
J.Neurobiol. 25: 1467- 1480, 1994.

GAM36 351 FGF2 Fukushima, Y.; Byers, M. G.; Fiddes, J. C.; Shows, T. B.: Thehuman basic 3 C c
fibroblast growth factor gene (FGFB) is assigned to chromosome4q25. Cytogenet. Cell Genet. 54: 159- 160, 1990.

GAM36 351 FGF2 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; 3 C c
Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast growth factor homologous factor 2 (FHF2): gene structure,expression and mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63, 1999.

GAM36 351 FGF2 Gritti, A.; Parati, E. A.; Cova, L.; Frolichsthal, P.; Galli, R.;Wanke, E.; 3 C c
Faravelli, L.; Morassutti, D. J.; Roisen, F.; Nickel, D.D.; Vescovi, A. L.: Multipotential stem cells from the adult mousebrain proliferate and self-renew in response to basic fibroblast growthfactor. J. Neurosci. 16: 1091-1100, 1996.

GAM36 351 FGF2 Johnson, R. L.; Tabin, C. J.: Molecular models for vertebratelimb development. Cell 90: 979- 990, 1997. 3 C c

GAM36 351 FGF2 Jung, J.; Zheng, M.; Goldfarb, M.; Zaret, K. S.: Initiation ofmammalian liver development from endoderm by fibroblast growth factors. Science 284:1998- 2003, 1999. 3 C c

GAM36 351 FGF2 Kawaguchi, H.; Nakamura, K.; Tabata, Y.; Ikada, Y.; Aoyama, I.;Anzai, J.; Nakamura, T.; Hiyama, Y.; Tamura, M.: Acceleration offracture healing in nonhuman primates by fibroblast growth factor- 2. J.Clin. Endocr. Metab. 86: 875- 880, 2001. 3 C c

GAM36 351 FGF2 Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.: Cloning andexpression of cDNA encoding human basic fibroblast growth factor. FEBSLett. 213: 189- 194, 1987. 3 C c

GAM36 351 FGF2 Lafage- Pochitaloff, M.; Galland, F.; Simonetti, J.; Prats, H.;Mattei, M.- G.; Birnbaum, D.: The human basic fibroblast growth factorgene is located on the long arm of chromosome 4 at bands q26- q27. OncogeneRes. 5: 241- 244, 1990. 3 C c

GAM36 351 FGF2 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21 by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997. 3 C c

GAM36 351 FGF2 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992. 3 C c

GAM36 351 FGF2 Mergia, A.; Eddy, R.; Abraham, J. A.; Fiddes, J. C.; Shows, T.B.: The genes for basic and acidic fibroblast growth factors areon different human chromosomes. Biochem. Biophys. Res. Commun. 138:644- 651, 1986. 3 C c

GAM36 351 FGF2 Montero, A.; Okada, Y.; Tomita, M.; Ito, M.; Tsurukami, H.; Nakamura,T.; Doetschman, T.; Coffin, J. D.; Hurley, M. M.: Disruption of thefibroblast growth factor- 2 gene results in decreased bone mass andbone formation. J. Clin. Invest. 105: 1085- 1093, 2000. 3 C c

GAM36 351 FGF2 Ortega, S.; Ittmann, M.; Tsang, S. H.; Ehrlich, M.; Basilico,C.: Neuronal defects and delayed wound healing in mice lacking fibroblastgrowth factor 2. Proc. Nat. Acad. Sci. 95: 5672- 5677, 1998. 3 C c

GAM36 351 FGF2 Plotnikov, A. N.; Hubbard, S. R.; Schlessinger, J.; Mohammadi,M.: Crystal structures of two FGF- FGFR complexes reveal the determinantsof ligand-receptor specificity. Cell 101: 413- 424, 2000. 3 C c

GAM36 351 FGF2 Plotnikov, A. N.; Schlessinger, J.; Hubbard, S. R.; Mohammadi,M.: Structural basis for FGF receptor dimerization and activation. Cell 98:641- 650, 1999. 3 C c

GAM36 351 FGF2 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast growth factor (FGF) homologous factors: new membersof the FGF family implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850- 9857, 1996. 3 C c

GAM36 351 LPHH1 Hoggard, N.; Brintell, B.; Howell, A.; Weissenbach, J.; Varley,J.: Allelic imbalance on chromosome 1 in human breast cancer. II.Microsatellite repeat analysis. Genes Chromosomes Cancer 12: 24- 31,1995. 3 C c

GAM36 351 LPHH1 White, G. R. M.; Varley, J. M.; Heighway, J.: Isolation and characterizationof a human homologue of the latrophilin gene from a region of 1p31.1implicated in breast cancer. Oncogene 17: 3513- 3519, 1998. 3 C c

GAM37 266 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double-strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence insitu hybridization. Genomics 36: 527- 529, 1996. 3 C c

GAM37 266 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence 3 C c
homologue of staufen is an RNA- binding protein thatis associated with
polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell.
Biol. 19: 2212- 2219, 1999.

GAM37 266 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: 3 C c
Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein
which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19:
2220- 2230, 1999.

GAM38 271 CD34 Cheng, J.; Baumhueter, S.; Cacalano, G.; Carver- Moore, K.; Thibodeaux,H.; 3 C c
Thomas, R.; Broxmeyer, H. E.; Cooper, S.; Hague, N.; Moore, M.;Lasky, L. A.:
Hematopoietic defects in mice lacking the sialomucinCD34. Blood 87: 479-
490, 1996.

GAM38 271 CD34 He, X.- Y.; Antao, V. P.; Basila, D.; Marx, J. C.; Davis, B. R.: Isolation 3 C c
and molecular characterization of the human CD34 gene. Blood 79:2296- 2302,
1992.

GAM38 271 CD34 Howell, S. M.; Molgaard, H. V.; Greaves, M. F.; Spurr, N. K.:Localisation of 3 C c
the gene coding for the haemopoietic stem cell antigenCD34 to chromosome
1q32. Hum. Genet. 87: 625- 627, 1991.

GAM38 271 CD34 Okuno, Y.; Iwasaki, H.; Huettner, C. S.; Radomska, H. S.; Gonzalez,D. A.; 3 C c
Tenen, D. G.; Akashi, K.: Differential regulation of the humanand murine
CD34 genes in hematopoietic stem cells. Proc. Nat. Acad.Sci. 99: 6246- 6251,
2002.

GAM38 271 CD34 Satterthwaite, A. B.; Burn, T. C.; Le Beau, M. M.; Tenen, D. G.: Structure 3 C c
of the gene encoding CD34, a human hematopoietic stemcell antigen. Genomics
12: 788- 794, 1992.

GAM38 271 CD34 Simmons, D. L.; Satterthwaite, A. B.; Tenen, D. G.; Seed, B.:Molecular 3 C c
cloning of a cDNA encoding CD34, a sialomucin of human hematopoieticstem
cells. J. Immun. 148: 267- 271, 1992.

GAM38 271 CD34 Sutherland, D. R.; Stewart, A. K.; Keating, A.: CD34 antigen:molecular 3 C c
features and potential clinical applications. Stem Cells 11(suppl. 3): 50-
57, 1993.

GAM38 271 CD34 Sutherland, D. R.; Watt, S. M.; Dowden, G.; Karhi, K.; Baker, M.A.; Greaves, 3 C c
M. F.; Smart, J. E.: Structural and partial amino acidsequence analysis of
the human hemopoietic progenitor cell antigenCD34. Leukemia 2: 793- 803,
1988.

GAM38 271 CD34 Tenen, D. G.; Satterthwaite, A. B.; Borson, R.; Simmons, D.; Eddy,R. L.; 3 C c
Shows, T. B.: Chromosome 1 localization of the gene for CD34,a surface
antigen of human stem cells. Cytogenet. Cell Genet. 53:55- 57, 1990.

GAM38 271 MAP1B Edelmann, W.; Zervas, M.; Costello, P.; Roback. L.; Fischer, I.;Hammarback, 3 C c
J. A.; Cowan, N.; Davies, P.; Wainer, B.; Kucherlapati,R.: Neuronal
abnormalities in microtubule- associated protein 1B mutantmice. Proc. Nat.
Acad. Sci. 93: 1270- 1275, 1996.

GAM38 271 MAP1B Hammarback, J. A.; Obar, R. A.; Hughes, S. M.; Vallee, R. B.:MAP1B is 3 C c
encoded as a polyprotein that is processed to form a complexN- terminal
microtubule- binding domain. Neuron 7: 129- 139, 1991.

GAM38 271 MAP1B Lien, L. L.; Boyce, F. M.; Kleyn, P.; Brzustowicz, L. M.; Menninger,J.; 3 C c
Ward, D. C.; Gilliam, T. C.; Kunkel, L. M.: Mapping of humanmicrotubule-
associated protein 1B in proximity to the spinal muscularatrophy locus at
5q13. Proc. Nat. Acad. Sci. 88: 7873- 7876, 1991.

GAM38 271 MAP1B Lien, L. L.; Feener, C. A.; Fischbach, N.; Kunkel, L. M.: Cloningof human 3 C c

microtubule- associated protein 1B and the identificationof a related gene on chromosome 15. Genomics 22: 273- 280, 1994.

GAM38 271 MAP1B Wirth, B.; Voosen, B.; Rohrig, D.; Knapp, M.; Piechaczek, B.; Rudnik- 3 C c
Schoneborn,S.; Zerres, K.: Fine mapping and narrowing of the genetic intervalof the spinal muscular atrophy region by linkage studies. Genomics 15:113- 118, 1993.

GAM38 271 MAP1B Zhang, Y. Q.; Bailey, A. M.; Matthies, H. J. G.; Renden, R. B.;Smith, M. A.; 3 C c
Speese, S. D.; Rubin, G. M.; Broadie, K.: Drosophilafragile X- related gene regulates the MAP1B homolog Futsch to controlsynaptic structure and function. Cell 107: 591- 603, 2001.

GAM38 271 PCOLN3 Halila, R.; Apostolou, S.; Winqvist, R.; Callen, D.; Prockop, D.J.; 3 C c
Peltonen, L.: Isolation and genomic assignment of a candidatecDNA clone for type III procollagen N- proteinase. (Abstract) Am.J. Hum. Genet. 51 (suppl.): A128 only, 1992.

GAM38 271 PCOLN3 Halila, R.; Peltonen, L.; Prockop, D. J.: Isolation of a candidatecDNA clone 3 C c
for type III procollagen N- proteinase from human placentalcDNA library. (Abstract) Am. J. Hum. Genet. 45 (suppl.): A192 only,1989.

GAM38 271 PCOLN3 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 C c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM38 271 PCOLN3 Scott, I. C.; Halila, R.; Jenkins, J. M.; Mehan, S.; Apostolou,S.; Winqvist, 3 C c
R.; Callen, D. F.; Prockop, D. J.; Peltonen, L.; Kadler,K. E.: Molecular cloning, expression and chromosomal localizationof a human gene encoding a 33 kDa putative metallopeptidase (PRSM1). Gene 174:135- 143, 1996.

GAM39 386 RAD1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human 3 C c
homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998.

GAM39 386 RAD1 Parker, A. E.; Van de Weyer, I.; Laus, M. C.; Oostveen, I.; Yon,J.; 3 C c
Verhasselt, P.; Luyten, W. H. M. L.: A human homologue of Schizosaccharomycespombe rad1+ checkpoint gene encodes an exonuclease. J. Biol. Chem. 273:18332- 18339, 1998.

GAM39 386 RAD1 Udell, C. M.; Lee, S. K.; Davey, S.: HRAD1 and MRAD1 encode 3 C c
mammalianhomologues of the fission yeast rad1+ cell cycle checkpoint controlgene. Nucleic Acids Res. 26: 3971- 3976, 1998.

GAM39 386 RAD1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe 3 C c
Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999.

GAM40 396 ACTG2 Miwa, T.; Manabe, Y.; Kurokawa, K.; Kamada, S.; Kanda, N.; Bruns,G.; Ueyama, 3 B c
H.; Kakunaga, T.: Structure, chromosome location, andexpression of the human smooth muscle (enteric type) gamma- actin gene:evolution of six human actin genes. Molec. Cell. Biol. 11: 3296- 3306,1991.

GAM40 396 ACTG2 Szucsik, J. C.; Lessard, J. L.: Cloning and sequence analysisof the mouse 3 B c
smooth muscle gamma- enteric actin gene. Genomics 28:154- 162, 1995.

GAM40 396 ACTG2 Ueyama, H.; Inazawa, J.; Nishino, H.; Han- Xiang, D.; Ochiai, Y.;Ohkubo, I.: 3 B c
Chromosomal mapping of the human smooth muscle actingene (enteric type, ACTA3) to 2p13.1 and molecular nature of the HindIIIpolymorphism. Genomics 25: 720- 723, 1995.

GAM40 396 CLCN6 Brandt, S.; Jentsch, T. J.: ClC- 6 and ClC- 7 are two novel broadlyexpressed 3 B c
members of the CLC chloride channel family. FEBS Lett. 377:15- 20, 1995.
GAM40 396 CLCN6 Eggermont, J.; Buyse, G.; Voets, T.; Tytgat, J.; De Smedt, H.;Droogmans, G.: 3 B c
Alternative splicing of ClC- 6 (a member of the ClCchloride- channel family)
transcripts generates three truncated isoformsone of which, ClC- 6c, is
kidney- specific. Biochem. J. 325: 269- 276,1997.
GAM40 396 CLCN6 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 B c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. II. The codingsequences of 40 new
genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell
line KG- 1. DNA Res. 1: 223- 229, 1994.
GAM40 396 CXCR4 Bleul, C. C.; Farzan, M.; Choe, H.; Parolin, C.; Clark- Lewis, I.;Sodroski, 3 B c
J.; Springer, T. A.: The lymphocyte chemoattractant SDF- 1is a ligand for
LESTR/fusin and blocks HIV- 1 entry. Nature 382:829- 833, 1996.
GAM40 396 CXCR4 Caruz, A.; Samsom, M.; Alonso, J. M.; Alcami, J.; Baleux, F.; Virelizier,J. 3 B c
L.; Parmentier, M.; Arenzana- Seisdedos, F.: Genomic organizationand
promoter characterization of human CXCR4 gene. FEBS Lett. 426:271- 278,
1998.
GAM40 396 CXCR4 Clapham, P. R.; Blanc, D.; Weiss, R. A.: Specific cell surfacerequirements 3 B c
for the infection of CD4- positive cells by human immunodeficiencyvirus
types 1 and 2 and by Simian immunodeficiency virus. Virology 181:703- 715,
1991.
GAM40 396 CXCR4 Dragic, T.; Alizon, M.: Different requirements for membrane fusionmediated 3 B c
by the envelopes of human immunodeficiency virus types 1and 2. J. Virol. 67:
2355- 2359, 1993.
GAM40 396 CXCR4 Federsppiel, B.; Melhado, I. G.; Duncan, A. M. V.; Delaney, A.;Schappert, 3 B c
K.; Clark- Lewis, I.; Jirik, F. R.: Molecular cloning ofthe cDNA and
chromosomal localization of the gene for a putative seven-
transmembranesegment (7- TMS) receptor isolated from human spleen. Genomics
16:707- 712, 1993.
GAM40 396 CXCR4 Feng, Y.; Broder, C. C.; Kennedy, P. E.; Berger, E. A.: HIV- 1entry 3 B c
cofactor: functional cDNA cloning of a seven- transmembrane,G protein-
coupled receptor. Science 272: 872- 876, 1996.
GAM40 396 CXCR4 Hendrix, C. W.; Flexner, C.; MacFarland, R. T.; Giandomenico, C.;Fuchs, E. 3 B c
J.; Redpath, E.; Bridger, G.; Henson, G. W.: Pharmacokineticsand safety of
AMD- 3100, a novel antagonist of the CXCR- 4 chemokinereceptor, in human
volunteers. Antimicrob. Agents Chemother. 44:1667- 1673, 2000.
GAM40 396 CXCR4 Herzog, H.; Hort, Y. J.; Shine, J.; Selbie, L. A.: Molecular 3 B c
cloning,characterization, and localization of the human homolog to the
reportedbovine NPY Y3 receptor: lack of NPY binding and activation. DNA
CellBiol. 12: 465- 471, 1993.
GAM40 396 CXCR4 Jazin, E. E.; Yoo, H.; Blomqvist, A. G.; Yee, F.; Weng, G.; Walker,M. W.; 3 B c
Salon, J.; Larhammar, D.; Wahlestedt, C.: A proposed bovineneuropeptide Y
(NPY) receptor cDNA clone, or its human homologue,confers neither NPY
binding sites nor NPY responsiveness on transfectedcells. Regul. Pept. 47:
247- 258, 1993.
GAM40 396 CXCR4 Liotta, L. A.: An attractive force in metastasis. Nature 410:24- 25, 2001. 3 B c
GAM40 396 CXCR4 Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini,M.; Moser, 3 B c
B.: Cloning of a human seven- transmembrane domain receptor,LESTR, that is
highly expressed in leukocytes. J. Biol. Chem. 269:232- 237, 1994.

GAM40 396 CXCR4 Lu, M.; Grove, E. A.; Miller, R. J.: Abnormal development ofthe hippocampal 3 B c
dentate gyrus in mice lacking the CXCR4 chemokinereceptor. Proc. Nat. Acad.
Sci. 99: 7090- 7095, 2002.

GAM40 396 CXCR4 Ma, Q.; Jones, D.; Borghesani, P. R.; Segal, R. A.; Nagasawa,T.; Kishimoto, 3 B c
T.; Bronson, R. T.; Springer, T. A.: Impaired B- lymphopoiesis,myelopoiesis,
and derailed cerebellar neuron migration in CXCR4- andSDF- 1- deficient
mice. Proc. Nat. Acad. Sci. 95: 9448- 9453, 1998.

GAM40 396 CXCR4 Muller, A.; Homey, B.; Soto, H.; Ge, N.; Catron, D.; Buchanan,M. E.; 3 B c
McClanahan, T.; Murphy, E.; Yuan, W.; Wagner, S. N.; Barrera,J. L.; Mohar,
A.; Verastegui, E.; Zlotnik, A.: Involvement of chemokinereceptors in breast
cancer metastasis. Nature 410: 50- 56, 2001.

GAM40 396 CXCR4 Nagasawa, T.; Hirota, S.; Tachibana, K.; Takakura, N.; Nishikawa,S.; 3 B c
Kitamura, Y.; Yoshida, N.; Kikutani, H.; Kishimoto, T.: Defectsof B- cell
lymphopoiesis and bone- marrow myelopoiesis in mice lackingthe CXC chemokine
PBSF/SDF- 1. Nature 382: 635- 638, 1996.

GAM40 396 CXCR4 Oberlin, E.; Amara, A.; Bachelerie, F.; Bessia, C.; Virelizier,J.- L.; 3 B c
Arenzana- Seisdedos, F.; Schwartz, O.; Heard, J.- M.; Clark- Lewis,I.;
Legler, D. F.; Loetscher, M.; Baggiollini, M.; Moser, B.: TheCXC chemokine
SDF- 1 is the ligand for LESTR/fusin and prevents infectionby T- cell- line-
adapted HIV- 1. Nature 382: 833- 835, 1996.

GAM40 396 CXCR4 Peled, A.; Petit, I.; Kollet, O.; Magid, M.; Ponomaryov, T.; Byk,T.; Nagler, 3 B c
A.; Ben- Hur, H.; Many, A.; Shultz, L.; Lider, O.; Alon,R.; Zipori, D.;
Lapidot, T.: Dependence of human stem cell engraftmentand repopulation of
NOD/SCID mice on CXCR4. Science 283: 845- 848,1999.

GAM40 396 CXCR4 Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E. J.;Duman, R. S.: 3 B c
Sequence and expression of a neuropeptide Y receptorcDNA. Molec. Pharm. 40:
869- 875, 1991.

GAM40 396 CXCR4 Tachibana, K.; Hirota, S.; Iizasa, H.; Yoshida, H.; Kawabata,K.; Kataoka, 3 B c
Y.; Kitamura, Y.; Matsushima, K.; Yoshida, N.; Nishikawa,S.; Kishimoto, T.;
Nagasawa, T.: The chemokine receptor CXCR4 isessential for vascularization
of the gastrointestinal tract. Nature 393:591- 594, 1998.

GAM40 396 CXCR4 Triantafilou, K.; Triantafilou, M.; Dedrick, R. L.: A CD14- independentLPS 3 B c
receptor cluster. Nature Immun. 2: 338- 345, 2001.

GAM40 396 CXCR4 Wegner, S. A.; Ehrenberg, P. K.; Chang, G.; Dayhoff, D. E.; Sleeker,A. L.; 3 B c
Michael, N. L.: Genomic organization and functional characterizationof the
chemokine receptor CXCR4, a major entry co- receptor for
humanimmunodeficiency virus type 1. J. Biol. Chem. 273: 4754- 4760, 1998.

GAM40 396 CXCR4 Weiner, D. B.; Huebner, K.; Williams, W. V.; Greene, M. I.: Humangenes other 3 B c
than CD4 facilitate HIV- 1 infection of murine cells. Pathobiology 59:361-
371, 1991.

GAM40 396 CXCR4 Xiao, H.; Neuveut, C.; Tiffany, H. L.; Benkirane, M.; Rich, E.A.; Murphy, P. 3 B c
M.; Jeang, K.- T.: Selective CXCR4 antagonism by Tat:implications for in
vivo expansion of coreceptor use by HIV- 1. Proc.Nat. Acad. Sci. 97: 11466-
11471, 2000.

GAM40 396 CXCR4 Zou, Y.- R.; Kottmann, A. H.; Kuroda, M.; Taniuchi, I.; Littman,D. R.: 3 B c
Function of the chemokine receptor CXCR4 in haematopoiesisand in cerebellar
development. Nature 393: 595- 599, 1998.

GAM40 396 DMD Abbs, S.; Roberts, R. G.; Mathew, C. G.; Bentley, D. R.; Bobrow,M.: Accurate 3 B c
assessment of intragenic recombination frequency withinthe Duchenne muscular
dystrophy gene. Genomics 7: 602- 606, 1990.

GAM40 396 DMD Ahn, A. H.; Kunkel, L. M.: The structural and functional diversityof dystrophin. Nature Genet. 3: 283- 291, 1993. 3 B c

GAM40 396 DMD Alwine, J. C.; Kemp, D. J.; Stark, G. R.: Method for detectionof specific RNAs in agarose gels by transfer to diazobenzyloxymethyl- paperand by hybridization with DNA probes. Proc. Nat. Acad. Sci. 74:5350- 5354, 1977. 3 B c

GAM40 396 DMD Angelini, C.; Beggs, A. H.; Hoffman, E. P.; Fanin, M.; Kunkel,L. M.: Enormous dystrophin in a patient with Becker muscular dystrophy. Neurology 40:808- 812, 1990. 3 B c

GAM40 396 DMD Badorff, C.; Berkely, N.; Mehrotra, S.; Talhouk, J. W.; Rhoads,R. E.; Knowlton, K. U.: Enteroviral protease 2A directly cleavesdystrophin and is inhibited by a dystrophin- based substrate analogue. J.Biol. Chem. 275: 11191- 11197, 2000. 3 B c

GAM40 396 DMD Badorff, C.; Lee, G.- H.; Lamphear, B. J.; Martone, M. E.; Campbell,K. P.; Rhoads, R. E.; Knowlton, K. U.: Enteroviral protease 2A cleavesdystrophin: evidence of cytoskeletal disruption in an acquired cardiomyopathy. NatureMed. 5: 320- 326, 1999. 3 B c

GAM40 396 DMD Bakker, E.; Hofker, M. H.; Goor, N.; Mandel, J. L.; Wrogemann,K.; Davies, K. E.; Kunkel, L. M.; Willard, H. F.; Fenton, W. A.; Sandkuyl,L.; Majoor-Krakauer, D.; van Essen, A. J.; Jahoda, M. G. J.; Sachs,E. S.; van Ommen, G. J. B.; Pearson, P. L.: Prenatal diagnosis andcarrier detection of Duchenne muscular dystrophy with closely linkedRFLPs. Lancet I: 655- 658, 1985. 3 B c

GAM40 396 DMD Bakker, E.; Pearson, P. L.: Mutation of the Duchenne musculardystrophy gene associated with meiotic recombination. (Letter) Clin.Genet. 30: 347- 349, 1986. 3 B c

GAM40 396 DMD Bakker, E.; Van Broeckhoven, C.; Bonten, E. J.; van de Vooren,M. J.; Veenema, H.; Van Hul, W.; Van Ommen, G. J. B.; Vandenberghe,A.; Pearson, P. L.: Germline mosaicism and Duchenne muscular dystrophymutations. Nature 329: 554- 556, 1987. 3 B c

GAM40 396 DMD Bar, S.; Barnea, E.; Levy, Z.; Neuman, S.; Yaffe, D.; Nudel, U.: A novel product of the Duchenne muscular dystrophy gene which greatlydiffers from the known isoforms in its structure and tissue distribution. Biochem.J. 272: 557- 560, 1990. 3 B c

GAM40 396 DMD Barbieri, A. M.; Soriani, N.; Tubiello, G. M.; Ferrari, M.; Carrera,P.: A nonsense mutation (gln- 673- term) in exon 17 of the human dystrophingene detected by heteroduplex analysis. Hum. Genet. 96: 343- 344,1995. 3 B c

GAM40 396 DMD Bartlett, R. J.; Pericak- Vance, M. A.; Koh, J.; Yamaoka, L. H.;Chen, J. C.; Hung, W.- Y.; Speer, M. C.; Wapenaar, M. C.; Van Ommen,G. J. B.; Bakker, E.; Pearson, P. L.; Kandt, R. S.; Siddique, T.;Gilbert, J. R.; Lee, J. E.; Sirotkin- Roses, M. J.; Roses, A. D.:Duchenne muscular dystrophy: high frequency of deletions. Neurology 38:1- 4, 1988. 3 B c

GAM40 396 DMD Barton- Davis, E. R.; Cordier, L.; Shoturma, D. I.; Leland, S.E.; Sweeney, H. L.: Aminoglycoside antibiotics restore dystrophinfunction to skeletal muscles of mdx mice. J. Clin. Invest. 104:375- 381, 1999. 3 B c

GAM40 396 DMD Bastianutto, C.; Bestard, J. A.; Lahnakoski, K.; Broere, D.; DeVisser, M.; Zaccolo, M.; Pozzan, T.; Ferlini, A.; Muntoni, F.; Patarnello,T.; Klamut, H. J.: Dystrophin muscle enhancer 1 is implicated inthe activation of non-muscle isoforms in the skeletal muscle of patientswith X- linked dilated cardiomyopathy. Hum. Molec. Genet. 10: 2627- 2635,2001. 3 B c

GAM40 396 DMD Baumbach, L. L.; Chamberlain, J. S.; Ward, P. A.; Farwell, N.J.; Caskey, C. T.: Molecular and clinical correlation of deletionleading to Duchenne and 3 B c

Becker muscular dystrophies. Neurology 39:465- 474, 1989.

GAM40 396 DMD Baumbach, L. L.; Ward, P. A.; Fenwick, R.; Caskey, C. T.: Analysisof 3 B c
mutations at the Duchenne muscular dystrophy locus provides noevidence for
illegitimate recombination in deletion formation. (Abstract) Am.J. Hum.
Genet. 45 (suppl.): A173, 1989.

GAM40 396 DMD Becker, P. E.: Eine neue X- chromosomale Muskeldystrophie. ActaPsychiat. 3 B c
Neurol. Scand. 193: 427, 1955.

GAM40 396 DMD Becker, P. E.: Neue Ergebnisse der Genetik der Muskeldystrophien. ActaGenet. 3 B c
Statist. Med. 7: 303- 310, 1957.

GAM40 396 DMD Becker, P. E.: Two new families of benign sex- linked recessivemuscular 3 B c
dystrophy. Rev. Canad. Biol. 21: 551- 566, 1962.

GAM40 396 DMD Beggs, A. H.; Koenig, M.; Boyce, F. M.; Kunkel, L. M.: Detectionof 98% of 3 B c
DMD/BMD gene deletions by polymerase chain reaction. Hum.Genet. 86: 45- 48,
1990.

GAM40 396 DMD Berko, B. A.; Swift, M.: X- linked dilated cardiomyopathy. NewEng. J. Med. 3 B c
316: 1186- 1191, 1987.

GAM40 396 DMD Bettecken, T.; Muller, C. R.: Identification of a 220- kb insertioninto the 3 B c
Duchenne gene in a family with an atypical course of musculardystrophy.
Genomics 4: 592- 596, 1989.

GAM40 396 DMD Bies, R. D.: X- linked dilated cardiomyopathy. (Letter) New Eng.J. Med. 330: 3 B c
368- 369, 1994.

GAM40 396 DMD Bies, R. D.; Caskey, C. T.; Fenwick, R.: An intact cysteine- richdomain is 3 B c
required for dystrophin function. J. Clin. Invest. 90:666- 672, 1992.

GAM40 396 DMD Bittner, R. E.; Streubel, B.; Shorny, S.; Schaden, G.; Voit, T.;Hoger, H.: 3 B c
Coisogenic all- plus- one immunization: a model for identifyingmissing
proteins in null- mutant conditions. Antibodies to dystrophinin mdx mouse
after transplantation of muscle from normal coisogenicdonor. Neuropediatrics
25: 176- 182, 1994.

GAM40 396 DMD Blake, D. J.; Love, D. R.; Tinsley, J.; Morris, G. E.; Turley,H.; Gatter, 3 B c
K.; Dickson, G.; Edwards, Y. H.; Davies, K. E.: Characterizationof a 4.8kb
transcript from the Duchenne muscular dystrophy locus expressedin schwannoma
cells. Hum. Molec. Genet. 1: 103- 109, 1992.

GAM40 396 DMD Bodrug, S. E.; Ray, P. N.; Gonzalez, I. L.; Schmickel, R. D.;Sylvester, J. 3 B c
E.; Worton, R. G.: Molecular analysis of a constitutionalX- autosome
translocation in a female with muscular dystrophy. Science 237:1620- 1624,
1987.

GAM40 396 DMD Boyce, F. M.; Beggs, A. H.; Feener, C.; Kunkel, L. M.: Dystrophinis 3 B c
transcribed in brain from a distant upstream promoter. Proc. Nat.Acad. Sci.
88: 1276- 1280, 1991.

GAM40 396 DMD Boyd, Y.; Buckle, V. J.: Cytogenetic heterogeneity of 3 B c
translocationsassociated with Duchenne muscular dystrophy. Clin. Genet. 29:
108- 115,1986.

GAM40 396 DMD Bulman, D. E.; Gangopadhyay, S. B.; Bebchuck, K. G.; Worton, R.G.; Ray, P. 3 B c
N.: Point mutation in the human dystrophin gene: identificationthrough
Western blot analysis. Genomics 10: 457- 460, 1991.

GAM40 396 DMD Burke, J. F.; Mogg, A. E.: Suppression of a nonsense mutationin mammalian 3 B c
cells in vivo by the aminoglycoside antibiotics G- 418and paromomycin.
Nucleic Acids Res. 13: 6265- 6272, 1985.

GAM40 396 DMD Burnette, W. N.: 'Western blotting': electrophoretic transferof proteins 3 B c
from sodium dodecyl sulfate- polyacrylamide gels to unmodifiednitrocellulose

and radiographic detection with antibody and radioiodinatedprotein A. Anal. Biochem. 112: 195- 203, 1981.

GAM40 396 DMD Bushby, K. M. D.; Cleghorn, N. J.; Curtis, A.; Haggerty, I. D.;Nicholson, L. V. B.; Johnson, M. A.; Harris, J. B.; Bhattacharya,S. S.: Identification of a mutation in the promoter region of thedystrophin gene in a patient with atypical Becker muscular dystrophy. Hum.Genet. 88: 195- 199, 1991. 3 B c

GAM40 396 DMD Chamberlain, J. S.; Pearlman, J. A.; Muzny, D. M.; Gibbs, R. A.;Ranier, J. E.; Reeves, A. A.; Caskey, C. T.: Expression of the murineDuchenne muscular dystrophy gene in muscle and brain. Science 239:1416- 1418, 1988. 3 B c

GAM40 396 DMD Chelly, J.; Concordet, J.- P.; Kaplan, J.- C.; Kahn, A.: Illegitimatetranscription: transcription of any gene in any cell type. Proc.Nat. Acad. Sci. 86: 2617- 2621, 1989. 3 B c

GAM40 396 DMD Chelly, J.; Gilgenkrantz, H.; Hugnot, J. P.; Hamard, G.; Lambert,M.; Recan, D.; Akli, S.; Cometto, M.; Kahn, A.; Kaplan, J. C.: Illegitimatetranscription: application to the analysis of truncated transcriptsof the dystrophin gene in nonmuscle cultured cells from Duchenne andBecker patients. J. Clin. Invest. 88: 1161- 1166, 1991. 3 B c

GAM40 396 DMD Chelly, J.; Hamard, G.; Koulakoff, A.; Kaplan, J.- C.; Kahn, A.;Berwald-Netter, Y.: Dystrophin gene transcribed from different promotersin neuronal and glial cells. Nature 344: 64- 65, 1990. 3 B c

GAM40 396 DMD Chelly, J.; Kaplan, J.- C.; Maire, P.; Gautron, S.; Kahn, A.:Transcription of the dystrophin gene in human muscle and non- muscletissues. Nature 333: 858- 860, 1988. 3 B c

GAM40 396 DMD Clemens, P. R.; Ward, P. A.; Caskey, C. T.; Bulman, D. E.; Fenwick,R. G.: Premature chain termination mutation causing Duchenne musculardystrophy. Neurology 42: 1775- 1782, 1992. 3 B c

GAM40 396 DMD Comi, G. P.; Ciafaloni, E.; de Silva, H. A. R.; Prelle, A.; Bardoni,A.; Rigoletto, C.; Robotti, M.; Bresolin, N.; Moggio, M.; Fortunato,F.; Ciscato, P.; Turconi, A.; Rose, A. D.; Scarlato, G.: A G(+1)- to- Atransversion at the 5- prime splice site of intron 69 of the dystrophingene causing the absence of peripheral nerve Dp116 and severe clinicalinvolvement in a DMD patient. Hum. Molec. Genet. 4: 2171- 2174, 1995. 3 B c

GAM40 396 DMD Cooper, B. J.; Valentine, B. A.; Wilson, S.; Patterson, D. F.;Concannon, P. W.: Canine muscular dystrophy: confirmation of X- linkedinheritance. J. Hered. 79: 405- 408, 1988. 3 B c

GAM40 396 DMD Covone, A. E.; Lerone, M.; Romeo, G.: Genotype- phenotype correlationand germline mosaicism in DMD/BMD patients with deletions of the dystrophingene. Hum. Genet. 87: 353- 360, 1991. 3 B c

GAM40 396 DMD Cox, G. A.; Cole, N. M.; Matsumura, K.; Phelps, S. F.; Hauschka,S. D.; Campbell, K. P.; Faulkner, J. A.; Chamberlain, J. S.: Overexpressionof dystrophin in transgenic mdx mice eliminates dystrophic symptomswithout toxicity. Nature 364: 725- 729, 1993. 3 B c

GAM40 396 DMD Cox, G. A.; Sunada, Y.; Campbell, K. P.; Chamberlain, J. S.:Dp71 can restore the dystrophin- associated glycoprotein complex inmuscle but fails to prevent dystrophy. Nature Genet. 8: 333- 339,1994. 3 B c

GAM40 396 DMD Crawford, G. E.; Lu, Q. L.; Partridge, T. A.; Chamberlain, J.S.: Suppression of revertant fibers in mdx mice by expression ofa functional dystrophin. Hum. Molec. Genet. 10: 2745- 2750, 2001. 3 B c

GAM40 396 DMD Darras, B. T.; Blattner, P.; Harper, J. F.; Spiro, A. J.; Alter,S.; Francke, U.: Intragenic deletions in 21 Duchenne muscular dystrophy(DMD)/Becker 3 B c

muscular dystrophy (BMD) families studied with the dystrophincDNA: location of breakpoints on HindIII and BglII exon- containingfragment maps, meiotic and mitotic origin of the mutations. Am. J.Hum. Genet. 43: 620- 629, 1988.

GAM40 396 DMD Darras, B. T.; Francke, U.: A partial deletion of the musculardystrophy gene transmitted twice by an unaffected male. Nature 329:556- 558, 1987. 3 B c

GAM40 396 DMD Darras, B. T.; Francke, U.: Normal human genomic restriction- fragmentpatterns and polymorphisms revealed by hybridization with the entiredystrophin cDNA. Am. J. Hum. Genet. 43: 612- 619, 1988. 3 B c

GAM40 396 DMD Davies, K. E.; Smith, T. J.; Bundey, S.; Read, A. P.; Flint, T.;Bell, M.; Speer, A.: Mild and severe muscular dystrophy associatedwith deletions in Xp21 of the human X chromosome. J. Med. Genet. 25:9- 13, 1988. 3 B c

GAM40 396 DMD De Angelis, F. G.; Sthandier, O.; Berarducci, B.; Toso, S.; Galluzzi,G.; Ricci, E.; Cossu, G.; Bozzoni, I.: Chimeric snRNA molecules carryingantisense sequences against the splice junctions of exon 51 of thedystrophin pre- mRNA induce exon skipping and restoration of a dystrophinsynthesis in delta- 48- 50 DMD cells. Proc Nat. Acad. Sci. 99: 9456- 9461,2002. 3 B c

GAM40 396 DMD den Dunnen, J. T.; Bakker, E.; Klein Breteler, E. G.; Pearson,P. L.; van Ommen, G. J. B.: Direct mutation of more than 50% of theDuchenne muscular dystrophy mutations by field inversion gels. Nature 329:640- 642, 1987. 3 B c

GAM40 396 DMD den Dunnen, J. T.; Grootscholten, P. M.; Bakker, E.; Blonden,L. A. J.; Ginjaar, H. B.; Wapenaar, M. C.; van Paassen, H. M. B.;van Broeckhoven, C.; Pearson, P. L.; van Ommen, G. J. B.: Topographyof the Duchenne muscular dystrophy (DMD) gene: FIGE and cDNA analysisof 194 cases reveals 115 deletions and 13 duplications. Am. J. Hum.Genet. 45: 835- 847, 1989. 3 B c

GAM40 396 DMD Dickson, G.; Pizzey, J. A.; Elsom, V. E.; Love, D.; Davies, K.E.; Walsh, F. S.: Distinct dystrophin mRNA species are expressedin embryonic and adult mouse skeletal muscle. FEBS Lett. 242: 47- 52,1988. 3 B c

GAM40 396 DMD Dominguez- Steglich, M.; Meng, G.; Bettecken, T.; Muller, C. R.;Schmid, M.: The dystrophin gene is autosomally located on a microchromosomein chicken. Genomics 8: 536- 540, 1990. 3 B c

GAM40 396 DMD Doolittle, R. F.: Similar amino acid sequences: chance or commonancestry? Science 214: 149- 159, 1981. 3 B c

GAM40 396 DMD Doriguzzi, C.; Palmucci, L.; Mongini, T.; Chiado- Piat, L.; Restagno,G.; Ferrone, M.: Exercise intolerance and recurrent myoglobinuriaas the only expression of Xp21 Becker type muscular dystrophy. J.Neurol. 240: 269- 271, 1993. 3 B c

GAM40 396 DMD Dubrovsky, A. L.; Taratuto, A. L.; Sevlever, G.; Schultz, M.;Pegoraro, E.; Hoop, R. C.; Hoffman, E. P.: Duchenne muscular dystrophyand myotonic dystrophy in the same patient. Am. J. Med. Genet. 55:342- 348, 1995. 3 B c

GAM40 396 DMD Emery, A. E. H.: Duchenne Muscular Dystrophy. Oxford, UK: OxfordUniversity Press (pub.) (2nd ed.): 1993. 3 B c

GAM40 396 DMD England, S. B.; Nicholson, L. V. B.; Johnson, M. A.; Forrest,S. M.; Love, D. R.; Zubrzycka- Gaarn, E. E.; Bulman, D. E.; Harris,J. B.; Davies, K. E.: Very mild muscular dystrophy associated withthe deletion of 46% dystrophin. Nature 343: 180- 182, 1990. 3 B c

GAM40 396 DMD Fabb, S. A.; Wells, D. J.; Serpente, P.; Dickson, G.: Adeno- associatedvirus vector gene transfer and sarcolemmal expression of a 144 kDamicro- dystrophin effectively restores the dystrophin- associated proteincomplex and inhibits myofibre degeneration in nude/mdx mice. Hum.Molec. Genet. 11: 3 B c

733- 741, 2002.

GAM40 396 DMD Feener, C. A.; Boyce, F. M.; Kunkel, L. M.: Rapid detection ofCA 3 B c
polymorphisms in cloned DNA: application to the 5- prime regionof the
dystrophin gene. Am. J. Hum. Genet. 48: 621- 627, 1991.

GAM40 396 DMD Ferlini, A.; Galie, N.; Merlini, L.; Sewry, C.; Branzi, A.; Muntoni,F.: A 3 B c
novel Alu- like element rearranged in the dystrophin gene causesa splicing
mutation in a family with X- linked dilated cardiomyopathy. Am.J. Hum.
Genet. 63: 436- 446, 1998.

GAM40 396 DMD Finnegan, D. J.: Eukaryotic transposable elements and genomeevolution. 3 B c
Trends Genet. 5: 103- 107, 1989.

GAM40 396 DMD Forrest, S. M.; Cross, G. S.; Speer, A.; Gardner- Medwin, D.; Burn,J.; 3 B c
Davies, K. E.: Preferential deletion of exons in Duchenne andBecker muscular
dystrophies. Nature 329: 638- 640, 1987.

GAM40 396 DMD Francke, U.; Ochs, H. D.; de Martinville, B.; Giacalone, J.; Lindgren,V.; 3 B c
Disteche, C.; Pagon, R. A.; Hofker, M. H.; van Ommen, G.- J. B.;Pearson, P.
L.; Wedgwood, R. J.: Minor Xp21 chromosome deletion ina male associated with
expression of Duchenne muscular dystrophy,chronic granulomatous disease,
retinitis pigmentosa, and McLeod syndrome. Am.J. Hum. Genet. 37: 250- 267,
1985.

GAM40 396 DMD Furst, D.; Nave, R.; Osborn, M.; Weber, K.; Bardosi, A.; Archidiacono,N.; 3 B c
Ferro, M.; Romano, V.; Romeo, G.: Nebulin and titin expressionin Duchenne
muscular dystrophy appears normal. FEBS Lett. 224: 49- 53,1987.

GAM40 396 DMD Giacalone, J. P.; Francke, U.: Common sequence motifs at therearrangement 3 B c
sites of a constitutional X/autosome translocation andassociated deletion.
Am. J. Hum. Genet. 50: 725- 741, 1992.

GAM40 396 DMD Gillard, E. F.; Chamberlain, J. S.; Murphy, E. G.; Duff, C. L.;Smith, B.; 3 B c
Burghes, A. H. M.; Thompson, M. W.; Sutherland, J.; Oss,I.; Bodrug, S. E.;
Klamut, H. J.; Ray, P. N.; Worton, R. G.: Molecularand phenotypic analysis
of patients with deletions within the deletion- richregion of the Duchenne
muscular dystrophy (DMD) gene. Am. J. Hum.Genet. 45: 507- 520, 1989.

GAM40 396 DMD Ginjaar, I. B.; Kneppers, A. L. J.; Meulen, J.- D. M.; Anderson,L. V. B.; 3 B c
Bremmer- Bout, M.; van Deutekom, J. C. T.; Weegenaar, J.;den Dunnen, J. T.;
Bakker, E.: Dystrophin nonsense mutation inducesdifferent levels of exon 29
skipping and leads to variable phenotypeswithin one BMD family. Europ. J.
Hum. Genet. 8: 793- 796, 2000.

GAM40 396 DMD Gospe, S. M., Jr.; Lazaro, R. P.; Lava, N. S.; Grootscholten,P. M.; Scott, 3 B c
M. O.; Fischbeck, K. H.: Familial X- linked myalgiaand cramps: a
nonprogressive myopathy associated with a deletion inthe dystrophin gene.
Neurology 39: 1277- 1280, 1989.

GAM40 396 DMD Greenberg, D. S.; Sunada, Y.; Campbell, K. P.; Yaffe, D.; Nudel,U.: 3 B c
Exogenous Dp71 restores the levels of dystrophin associated proteinsbut does
not alleviate muscle damage in mdx mice. Nature Genet. 8:340- 344, 1994.

GAM40 396 DMD Gussoni, E.; Soneoka, Y.; Strickland, C. D.; Buzney, E. A.; Khan,M. K.; 3 B c
Flint, A. F.; Kunkel, L. M.; Mulligan, R. C.: Dystrophin expressionin the
mdx mouse restored by stem cell transplantation. Nature 401:390- 394, 1999.

GAM40 396 DMD Hagiwara, Y.; Mizuno, Y.; Takemitsu, M.; Matsuzaki, T.; Nonaka,I.; Ozawa, 3 B c
E.: Dystrophin- positive muscle fibers following C2 myoblasttransplantation
into mdx nude mice. Acta Neuropath. 90: 592- 600,1995.

GAM40 396 DMD Hagiwara, Y.; Nishio, H.; Kitoh, Y.; Takeshima, Y.; Narita, N.;Wada, H.; 3 B c
Yokoyama, M.; Nakamura, H.; Matsuo, M.: A novel point mutation(G(- 1) to T)

in a 5- prime splice donor site of intron 13 of the dystrophingene results in exon skipping and is responsible for Becker musculardystrophy. Am. J. Hum. Genet. 54: 53- 61, 1994.

GAM40 396 DMD Hammonds, R. G., Jr.: Protein sequence of DMD gene is relatedto actin- 3 B c
binding domain of alpha- actinin. (Letter) Cell 51: 1, 1987.

GAM40 396 DMD Harper, S. Q.; Hauser, M. A.; DelloRusso, C.; Duan, D.; Crawford,R. W.; 3 B c
Phelps, S. F.; Harper, H. A.; Robinson, A. S.; Engelhardt,J. F.; Brooks, S. V.; Chamberlain, J. S.: Modular flexibility ofdystrophin: implications for gene therapy of Duchenne muscular dystrophy. NatureMed. 8: 253- 261, 2002.

GAM40 396 DMD Hart, K. A.; Hodgson, S.; Walker, A.; Cole, C. G.; Johnson, L.;Dubowitz, V.; 3 B c
Bobrow, M.: DNA deletions in mild and severe Beckermuscular dystrophy. Hum. Genet. 75: 281- 285, 1987.

GAM40 396 DMD Hodgson, S. V.; Abbs, S.; Clark, S.; Manzur, A.; Heckmatt, J.Z. H.; 3 B c
Dubowitz, V.; Bobrow, M.: Correlation of clinical and deletiondata in Duchenne and Becker muscular dystrophy, with special referenceto mental ability. Neuromusc. Disord. 2: 269- 276, 1992.

GAM40 396 DMD Hoffman, E. P.; Brown, R. H., Jr.; Kunkel, L. M.: The proteinproduct of the 3 B c
Duchenne muscular dystrophy locus. Cell 51: 919- 928,1987.

GAM40 396 DMD Hoffman, E. P.; Fischbeck, K. H.; Brown, R. H.; Johnson, M.; Medori,R.; 3 B c
Loike, J. D.; Harris, J. B.; Waterston, R.; Brooke, M.; Specht,L.; Kupsky, W.; Chamberlain, J.; Caskey, C. T.; Shapiro, F.; Kunkel,L. M.: Characterization of dystrophin in muscle- biopsy specimensfrom patients with Duchenne's or Becker's muscular dystrophy. NewEng. J. Med. 318: 1363- 1368, 1988.

GAM40 396 DMD Hoffman, E. P.; Knudson, C. M.; Campbell, K. P.; Kunkel, L. M.: Subcellular 3 B c
fractionation of dystrophin to the triads of skeletalmuscle. Nature 330: 754- 758, 1987.

GAM40 396 DMD Hoffman, E. P.; Monaco, A. P.; Feener, C. C.; Kunkel, L. M.:Conservation of 3 B c
the Duchenne muscular dystrophy gene in mice and humans. Science 238:347- 350, 1987.

GAM40 396 DMD Hoop, R. C.; Russo, L. S.; Riconda, D. L.; Schwartz, L. S.; Hoffman,E. P.: 3 B c
Restoration of half the normal dystrophin sequence in a double- deletionDuchenne muscular dystrophy family. Am. J. Med. Genet. 49: 323- 327,1994.

GAM40 396 DMD Howard, P. L.; Dally, G. Y.; Wong, M. H.; Ho, A.; Weleber, R.G.; Pillers, 3 B c
D.- A. M.; Ray, P. N.: Localization of dystrophin isoformDp71 to the inner limiting membrane of the retina suggests a uniquefunctional contribution of Dp71 in the retina. Hum. Molec. Genet. 7:1385- 1391, 1998.

GAM40 396 DMD Hu, X.; Burghes, A. H. M.; Bulman, D. E.; Ray, P. N.; Worton,R. G.: Evidence 3 B c
for mutation by unequal sister chromatid exchangein the Duchenne muscular dystrophy gene. Am. J. Hum. Genet. 44:855- 863, 1989.

GAM40 396 DMD Hu, X.; Burghes, A. H. M.; Ray, P. N.; Thompson, M. W.; Murphy,E. G.; 3 B c
Worton, R. G.: Partial gene duplication in Duchenne and Beckermuscular dystrophies. J. Med. Genet. 25: 369- 376, 1988.

GAM40 396 DMD Hu, X.; Ray, P. N.; Murphy, E. G.; Thompson, M. W.; Worton, R.G.: 3 B c
Duplicational mutation at the Duchenne muscular dystrophy locus:its frequency, distribution, origin, and phenotype- genotype correlation. Am.J. Hum. Genet. 46: 682- 695, 1990.

GAM40 396 DMD Hu, X.; Ray, P. N.; Worton, R. G.: Mechanisms of tandem duplicationin the 3 B c
Duchenne muscular dystrophy gene include both homologous andnonhomologous

intrachromosomal recombination. EMBO J. 10: 2471- 2477,1991.

GAM40 396 DMD Hu, X.; Worton, R. G.: Partial gene duplication as a cause ofhuman disease. 3 B c
Hum. Mutat. 1: 3- 12, 1992.

GAM40 396 DMD Ingram, V. M.: Gene evolution and the haemoglobins. Nature 189:704- 708, 3 B c
1961.

GAM40 396 DMD Itagaki, Y.; Saida, K.; Iwamura, K.: Regenerative capacity ofmdx mouse 3 B c
muscles after repeated applications of myo- necrotic bupivacaine.
ActaNeuropath. 89: 380- 384, 1995.

GAM40 396 DMD Kaplan, J.- C.; Kahn, A.; Chelly, J.: Illegitimate transcription:its use in 3 B c
the study of inherited disease. Hum. Mutat. 1: 357- 360,1992.

GAM40 396 DMD Kavaslar, G. N.; Telatar, M.; Serdaroglu, P.; Deymeer, F.; Ozdemir,C.; 3 B c
Tolun, A.: Identification of a one- basepair deletion in exon6 of the
dystrophin gene. Hum. Mutat. 6: 85- 86, 1995.

GAM40 396 DMD Kilimann, M. W.; Pizzuti, A.; Grompe, M.; Caskey, C. T.: Pointmutations and 3 B c
polymorphisms in the human dystrophin gene identifiedin genomic DNA
sequences amplified by multiplex PCR. Hum. Genet. 89:253- 258, 1992.

GAM40 396 DMD Kim, T.- W.; Wu, K.; Black, I. B.: Deficiency of brain synapticdystrophin in 3 B c
human Duchenne muscular dystrophy. Ann. Neurol. 38:446- 449, 1995.

GAM40 396 DMD Kingston, H. M.; Sarfarazi, M.; Thomas, N. S. T.; Harper, P. S.: 3 B c
Localisation of the Becker muscular dystrophy gene on the shortarm of the X
chromosome by linkage to cloned DNA sequences. Hum.Genet. 67: 6- 17, 1984.

GAM40 396 DMD Kingston, H. M.; Thomas, N. S. T.; Pearson, P. L.; Sarfarazi,M.; Harper, P. 3 B c
S.: Genetic linkage between Becker muscular dystrophyand a polymorphic DNA
sequence on the short arm of the X chromosome. J.Med. Genet. 20: 255- 258,
1983.

GAM40 396 DMD Kneppers, A. L. J.; Deutz- Terlouw, P. P.; van Ommen, G. J. B.;Bakker, E.: 3 B c
Point mutation screening for Duchenne muscular dystrophy(DMD) by SSCP-
analysis of multiplex PCR products by use of the PhastSystem(TM). Am. J.
Hum. Genet. Suppl. 53: Abstract- 1493, 1993.

GAM40 396 ELF5 Oettgen, P.; Kas, K.; Dube, A.; Gu, X.; Grall, F.; Thamrongsak,U.; Akbarali, 3 B c
Y.; Finger, E.; Boltax, J.; Endress, G.; Munger, K.;Kunsch, C.; Libermann,
T. A.: Characterization of ESE- 2, a novelESE- 1- related ETS transcription
factor that is restricted to glandularepithelium and differentiated
keratinocytes. J. Biol. Chem. 274:29439- 29452, 1999.

GAM40 396 ELF5 Sharrocks, A. D.; Brown, A. L.; Ling, Y.; Yates, P. R.: The ETS- 3 B c
domaintranscription factor family. Int. J. Biochem. Cell Biol. 29: 1371-
1387,1997.

GAM40 396 ELF5 Zhou, J.; Ng, A. Y. N.; Tymms, M. J.; Jermiin, L. S.; Seth, A.K.; Thomas, R. 3 B c
S.; Kola, I.: A novel transcription factor, ELF5,belongs to the ELF
subfamily of ETS genes and maps to human chromosome11p13- 15, a region
subject to LOH and rearrangement in human carcinomacell lines. Oncogene 17:
2719- 2732, 1998.

GAM40 396 EMP1 Ben Porath, I.; Kozak, C. A.; Benvenisty, N.: Chromosomal mappingof Tmp 3 B c
(Emp1), Xmp (Emp2), and Ymp (Emp3), genes encoding membraneproteins related
to Pmp22. Genomics 49: 443- 447, 1998.

GAM40 396 EMP1 Ben- Porath, I.; Benvenisty, N.: Characterization of a tumor- 3 B c
associatedgene, a member of a novel family of genes encoding membrane
glycoproteins. Gene 183:69- 75, 1996.

GAM40 396 EMP1 Chen, Y.; Medvedev, A.; Ruzanov, P.; Marvin, K. W.; Jetten, A.M.: cDNA 3 B c
cloning, genomic structure, and chromosome mapping of thehuman epithelial

membrane protein CL- 20 gene (EMP1), a member of thePMP22 family. Genomics 41: 40- 48, 1997.

GAM40 396 EMP1 Liehr, T.; Kuhlenbaumer, G.; Wulf, P.; Taylor, V.; Suter, U.; 3 B c
VanBroeckhoven, C.; Lupski, J. R.; Claussen, U.; Rautenstrauss, B.:Regional localization of the human epithelial membrane protein genes1, 2, and 3 (EMP1, EMP2, EMP3) to 12p12.3, 16p13.2, and 19q13.3. Genomics 58:106- 108, 1999.

GAM40 396 EMP1 Marvin, K. W.; Fujimoto, W.; Jetten, A. M.: Identification 3 B c
andcharacterization of a novel squamous cell- associated gene relatedto PMP22. J. Biol. Chem. 270: 28910- 28916, 1995.

GAM40 396 EMP1 Ruegg, C. L.; Wu, H.; Fagnoni, F. F.; Engleman, E. G.; Laus, R.: B4B, a 3 B c
novel growth- arrest gene, is expressed by a subset of progenitor/pre-Blymphocytes negative for cytoplasmic mu- chain. J. Immun. 157: 72- 80,1996.

GAM40 396 FBXL7 Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; 3 B c
Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol. 9: 1177- 1179, 1999.

GAM40 396 FBXL7 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 B c
and expression analysis of new members of the mammalianF- box protein family. Genomics 67: 40- 47, 2000.

GAM40 396 FBXL7 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5: 355- 364, 1998.

GAM40 396 FBXL7 Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A 3 B c
family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999.

GAM40 396 IL1R1 Copeland, N. G.; Silan, C. M.; Kingsley, D. M.; Jenkins, N. A.;Cannizzaro, 3 B b
L. A.; Croce, C. M.; Huebner, K.; Sims, J. E.: Chromosomallocation of murine and human IL- 1 receptor genes. Genomics 9: 44- 50,1991.

GAM40 396 IL1R1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 3 B b
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp) on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM40 396 IL1R1 Dower, S. K.; Kronheim, S. R.; Hopp, T. P.; Cantrell, M.; Deeley,M.; Gillis, 3 B b
S.; Henney, C. S.; Urdal, D. L.: The cell surface receptorsfor interleukin-1(alpha) and interleukin- 1(beta) are identical. Nature 324:266- 268, 1986.

GAM40 396 IL1R1 Sims, J. E.; Acres, R. B.; Grubin, C. E.; McMahan, C. J.; Wignall,J. M.; 3 B b
March, C. J.; Dower, S. K.: Cloning the interleukin 1 receptorfrom human T cells. Proc. Nat. Acad. Sci. 86: 8946- 8950, 1989.

GAM40 396 KCNAB2 Gong, J.; Xu, J.; Bezanilla, M.; van Huizen, R.; Derin, R.; Li,M.: 3 B c
Differential stimulation of PKC phosphorylation of potassiumchannels by ZIP1 and ZIP2. Science 285: 1565- 1569, 1999.

GAM40 396 KCNAB2 Leicher, T.; Bahring, R.; Isbrandt, D.; Pongs, O.: Coexpressionof the KCNA3B 3 B c
gene product with Kv1.5 leads to a novel A- type potassiumchannel. J. Biol. Chem. 273: 35095- 35101, 1998.

GAM40 396 KCNAB2 McCormack, K.; McCormack, T.; Tanouye, M.; Rudy, B.; Stuhmer, W.: 3 B c
Alternative splicing of the human Shaker K+ channel beta- 1 geneand functional expression of the beta- 2 gene product. FEBS Lett. 370:32- 36, 1995.

GAM40 396 KCNAB2 Schultz, D.; Litt, M.; Smith, L.; Thayer, M.; McCormack, K.: Localizationof 3 B c
two potassium channel beta subunit genes, KCNA1B and KCNA2B. Genomics

31:389- 391, 1996.

GAM40 396 LDB3 Faulkner, G.; Pallavicini, A.; Formentin, E.; Comelli, A.; Ievolella,C.; 3 B c
Trevisan, S.; Bortoletto, G.; Scannapieco, P.; Salamon, M.; Mouly,V.; Valle,
G.; Lanfranchi, G.: ZASP: a new Z- band alternatively splicedPDZ- motif
protein. J. Cell Biol. 146: 465- 475, 1999.

GAM40 396 LDB3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 B c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM40 396 LDB3 Zhou, Q.; Ruiz- Lozano, P.; Martone, M. E.; Chen, J.: Cypher, astriated 3 B c
muscle- restricted PDZ and LIM domain- containing protein,binds to alpha-
actinin- 2 and protein kinase C. J. Biol. Chem. 274:19807- 19813, 1999.

GAM40 396 MASP1 Dahl, M. R.; Thiel, S.; Matsushita, M.; Fujita, T.; Willis, A.C.; 3 B c
Christensen, T.; Vorup- Jensen, T.; Jensenius, J. C.: MASP- 3 andits
association with distinct complexes of the mannan- binding lectincomplement
activation pathway. Immunity 15: 127- 135, 2001.

GAM40 396 MASP1 Endo, Y.; Sato, T.; Matsushita, M.; Fujita, T.: Exon structureof the gene 3 B c
encoding the human mannose- binding protein- associatedserine protease light
chain: comparison with complement C1r and C1sgenes. Int. Immun. 8: 1355-
1358, 1996.

GAM40 396 MASP1 Matsushita, M.; Thiel, S.; Jensenius, J. C.; Terai, I.; Fujita,T.: 3 B c
Proteolytic activities of two types of mannose- binding lectin-
associatedserine protease. J. Immun. 165: 2637- 2642, 2000.

GAM40 396 MASP1 Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.: Molecular characterizationof 3 B c
a novel serine protease involved in activation of the complementsystem by
mannose- binding protein. Int. Immun. 6: 665- 669, 1994.

GAM40 396 MASP1 Takada, F.; Seki, N.; Matsuda, Y.; Takayama, Y.; Kawakami, M.:Localization 3 B c
of the genes for the 100- kDa complement- activating componentsof Ra-
reactive factor (CRARF and Crarf) to human 3q27- q28 and mouse16B2- B3.
Genomics 25: 757- 759, 1995.

GAM40 396 MASP1 Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M.: A new memberof the C1s 3 B c
family of complement proteins found in a bactericidal factor,Ra- reactive
factor, in human serum. Biochem. Biophys. Res. Commun. 196:1003- 1009, 1993.

GAM40 396 MASP1 Takayama, Y.; Takada, F.; Nowatari, M.; Kawakami, M.; Matsu- ura,N.: Gene 3 B c
structure of the P100 serine- protease component of the humanRa- reactive
factor. Molec. Immun. 36: 505- 514, 1999.

GAM40 396 NGFB Breakefield, X. O.; Orloff, G.; Castiglione, C.; Coussens, L.;Axelrod, F. 3 B c
B.; Ullrich, A.: Structural gene for beta- nerve growthfactor not defective
in familial dysautonomia. Proc. Nat. Acad. Sci. 81:4213- 4216, 1984.

GAM40 396 NGFB Carrier, A.; Rosier, M.- F.; Guillemot, F.; Goguel, A.- F.; Pulcini,F.; 3 B c
Bernheim, A.; Auffray, C.; Devignes, M.- D.: Integrated physical,genetic,
and genic map covering 3 Mb around the human NGF gene (NGFB)at 1p13.
Genomics 31: 80- 89, 1996.

GAM40 396 NGFB Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 B c
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release
the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411:
957- 962, 2001.

GAM40 396 NGFB Darby, J. K.; Feder, J.; Selby, M.; Riccardi, V.; Ferrell, R.;Siao, D.; 3 B c
Goslin, K.; Rutter, W.; Shooter, E. M.; Cavalli- Sforza,L. L.: A discordant

sibship analysis between beta- NGF and neurofibromatosis. Am.J. Hum. Genet. 37: 52- 59, 1985.

GAM40 396 NGFB Darby, J. K.; Kidd, J. R.; Pakstis, A. J.; Sparkes, R. S.; Cann,H. M.; Ferrell, R. E.; Gerhard, D. G.; Riccardi, V.; Egeland, J. A.;Shooter, E. M.; Cavalli- Sforza, L. L.; Kidd, K. K.: Linkage relationshipsof the gene for the beta subunit of nerve growth factor (NGFB) withother chromosome 1 marker loci. Cytogenet. Cell Genet. 39: 158- 160,1985. 3 B c

GAM40 396 NGFB Dracopoli, N. C.: Personal Communication. Cambridge, Mass. 4/29/1988. 3 B c

GAM40 396 NGFB Dracopoli, N. C.; Meisler, M. H.: Mapping the human amylase genecluster on the proximal short arm of chromosome 1 using a highly informative(CA)n repeat. Genomics 7: 97- 102, 1990. 3 B c

GAM40 396 NGFB Dracopoli, N. C.; Rose, E.; Whitfield, G. K.; Guidon, P. T.; Bale,S. J.; Chance, P. A.; Kourides, I. A.; Housman, D. E.: Two thyroidhormone regulated genes, the beta- subunits of nerve growth factor(NGFB) and thyroid stimulating hormone (TSHB), are located less than310 kb apart in both human and mouse genomes. Genomics 3: 161- 167,1988. 3 B c

GAM40 396 NGFB Francke, U.; de Martinville, B.; Coussens, L.; Ullrich, A.: Thehuman gene for the beta subunit of nerve growth factor is locatedon the proximal short arm of chromosome 1. Science 222: 1248- 1251,1983. 3 B c

GAM40 396 NGFB Garson, J. A.; van den Berghe, J. A.; Kemshead, J. T.: Novelnon- isotopic in situ hybridization technique detects small (1 kb)unique sequences in routinely G- banded human chromosomes: fine mappingof N- myc and beta- NGF genes. Nucleic Acids Res. 15: 4761- 4770, 1987. 3 B c

GAM40 396 NGFB Lee, R.; Kermani, P.; Teng, K. K.; Hempstead, B. L.: Regulationof cell survival by secreted proneurotrophins. Science 294: 1945- 1948,2001. 3 B c

GAM40 396 NGFB Levi- Montalcini, R.: The nerve growth factor thirty- five yearslater. Science 237: 1154- 1162, 1987. 3 B c

GAM40 396 NGFB MacInnis, B. L.; Campenot, R. B.: Retrograde support of neuronalsurvival without retrograde transport of nerve growth factor. Science 295:1536- 1539, 2002. 3 B c

GAM40 396 NGFB Middleton- Price, H.; van den Berghe, J.; Harding, A.; Scott, J.;Malcolm, S.: Analysis of markers on chromosome 1. (Abstract) Cytogenet.Cell Genet. 46: 662, 1987. 3 B c

GAM40 396 NGFB Mitchell, E. L. D.; Jones, D.; White, G. R. M.; Varley, J. M.;Santibanez Koref, M. F.: Determination of the gene order of the threeloci CD2, NGFB, and NRAS at human chromosome band 1p13 and refinementof their localisation at the subband level by fluorescence in situhybridization. Cytogenet. Cell Genet. 70: 183- 185, 1995. 3 B c

GAM40 396 NGFB Munke, M.; Lindgren, V.; de Martinville, B.; Francke, U.: Comparativeanalysis of mouse- human hybrids with rearranged chromosomes 1 by insitu hybridization and Southern blotting: high- resolution mappingof NRAS, NGFB, and AMY on human chromosome 1. Somat. Cell Molec.Genet. 10: 589- 599, 1984. 3 B c

GAM40 396 NGFB Ramer, M. S.; Priestley, J. V.; McMahon, S. B.: Functional regenerationof sensory axons into the adult spinal cord. Nature 403: 312- 316,2000. 3 B c

GAM40 396 NGFB Sanico, A. M.; Stanisz, A. M.; Gleeson, T. D.; Bora, S.; Proud,D.; Bienenstock, J.; Koliatsos, V. E.; Togias, A.: Nerve growth factorexpression and release in allergic inflammatory disease of the upperairways. Am. J. Resp. Crit. Care Med. 161: 1631- 1635, 2000. 3 B c

GAM40 396 NGFB Ullrich, A.; Gray, A.; Berman, C.; Dull, T. J.: Human beta- nervegrowth 3 B c

factor gene sequence highly homologous to that of mouse. Nature 303:821-825, 1983.

GAM40 396 NGFB Zabel, B. U.; Eddy, R. L.; Lalley, P. A.; Scott, J.; Bell, G.I.; Shows, T. 3 B c
B.: Chromosomal locations of the human and mouse genesfor precursors of epidermal growth factor and the beta subunit ofnerve growth factor. Proc. Nat. Acad. Sci. 82: 469- 473, 1985.

GAM40 396 NGFB Zabel, B. U.; Eddy, R. L.; Scott, J.; Shows, T. B.: The humannerve growth 3 B c
factor gene (NGF) is located on the short arm of chromosome1. (Abstract) Cytogenet. Cell Genet. 37: 614, 1984.

GAM40 396 NR0B2 Goodwin, B.; Jones, S. A.; Price, R. R.; Watson, M. A.; McKee,D. D.; Moore, 3 B c
L. B.; Galardi, C.; Wilson, J. G.; Lewis, M. C.; Roth,M. E.; Maloney, P. R.; Willson, T. M.; Kliewer, S. A.: A regulatorycascade of the nuclear receptors FXR, SHP- 1, and LRH- 1 represses bileacid biosynthesis. Molec. Cell 6: 517-526, 2000.

GAM40 396 NR0B2 Lee, H.- K.; Lee, Y.- K.; Park, S.- H.; Kim, Y.- S.; Park, S. H.; Lee,J. W.; 3 B c
Kwon, H.- B.; Soh, J.; Moore, D. D.; Choi, H.- S.: Structureand expression of the orphan nuclear receptor SHP gene. J. Biol.Chem. 273: 14398- 14402, 1998.

GAM40 396 NR0B2 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, 3 B c
J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000.

GAM40 396 NR0B2 Nishigori, H.; Tomura, H.; Tonooka, N.; Kanamori, M.; Yamada, S.;Sho, K.; 3 B c
Inoue, I.; Kikuchi, N.; Onigata, K.; Kojima, I.; Kohama,T.; Yamagata, K.; and 9 others: Mutations in the small heterodimerpartner gene are associated with mild obesity in Japanese subjects. Proc.Nat. Acad. Sci. 98: 575- 580, 2001.

GAM40 396 NR0B2 Seol, W.; Choi, H.- S.; Moore, D. D.: An orphan nuclear hormonereceptor that 3 B c
lacks a DNA binding domain and heterodimerizes withother receptors. Science 272: 1336- 1339, 1996.

GAM40 396 NR3C2 Arriza, J. L.; Weinberger, C.; Cerelli, G.; Glaser, T. M.; Handelin,B. L.; 3 B c
Housman, D. E.; Evans, R. M.: Cloning of human mineralocorticoidreceptor complementary DNA: structural and functional kinship withthe glucocorticoid receptor. Science 237: 268- 275, 1987.

GAM40 396 NR3C2 Berger, S.; Bleich, M.; Schmid, W.; Cole, T. J.; Peters, J.; Watanabe,H.; 3 B c
Kriz, W.; Warth, R.; Greger, R.; Schutz, G.: Mineralocorticoidreceptor knockout mice: pathophysiology of Na+ metabolism. Proc.Nat. Acad. Sci. 95: 9424- 9429, 1998.

GAM40 396 NR3C2 Chung, E.; Hanukoglu, A.; Rees, M.; Thompson, R.; Dillon, M.; Hanukoglu,I.; 3 B c
Bistritzer, T.; Kuhnle, U.; Seckl, J.; Gardiner, R. M.: Exclusionof the locus for autosomal recessive pseudohypoaldosteronism type1 from the mineralocorticoid receptor gene region on human chromosome4q by linkage analysis. J. Clin. Endocr. Metab. 80: 3341- 3345, 1995.

GAM40 396 NR3C2 Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Nowak, N. 3 B c
J.; Shows, T. B.: The human mineralocorticoid receptorgene (MLR) is located on chromosome 4 at q31.2. Cytogenet. Cell Genet. 52:83- 84, 1989.

GAM40 396 NR3C2 Geller, D. S.; Farhi, A.; Pinkerton, N.; Fradley, M.; Moritz, M.;Spitzer, 3 B c
A.; Meinke, G.; Tsai, F. T. F.; Sigler, P. B.; Lifton, R.P.: Activating mineralocorticoid receptor mutation in hypertensionexacerbated by pregnancy. Science 289: 119- 123, 2000.

GAM40 396 NR3C2 Geller, D. S.; Rodriguez- Soriano, J.; Vallo Boado, A.; Schifter,S.; Bayer, 3 B c

M.; Chang, S. S.; Lifton, R. P.: Mutations in the mineralocorticoidreceptor gene cause autosomal dominant pseudohypoaldosteronism typeI. Nature Genet. 19: 279- 281, 1998.

GAM40 396 NR3C2 Hellal- Levy, C.; Fagart, J.; Souque, A.; Wurtz, J.- M.; Moras, D.;Rafestin- 3 B c
Oblin, M.- E.: Crucial role of the H11- H12 loop in stabilizingthe active conformation of the human mineralocorticoid receptor. Molec.Endocr. 14: 1210- 1221, 2000.

GAM40 396 NR3C2 Le Menuet, D.; Isnard, R.; Bichara, M.; Viengchareun, S.; Muffat- Joly,M.; 3 B c
Walker, F.; Zennaro, M.- C.; Lombes, M.: Alteration of cardiacand renal functions in transgenic mice overexpressing human mineralocorticoidreceptor. J. Biol. Chem. 276: 38911- 38920, 2001.

GAM40 396 NR3C2 Morrison, N.; Harrap, S. B.; Arriza, J. L.; Boyd, E.; Connor, J.M.: Regional 3 B c
chromosomal assignment of the human mineralocorticoidreceptor gene to 4q31.1. Hum. Genet. 85: 130- 132, 1990.

GAM40 396 NR3C2 Morrison, N.; Harrap, S. B.; Arriza, J. L.; Boyd, E.; Connor,J. M.: Regional 3 B c
chromosomal assignment of the human mineralocorticoidreceptor gene to 4q31.1. (Abstract) Cytogenet. Cell Genet. 51: 1048,1989.

GAM40 396 NR3C2 Tajima, T.; Kitagawa, H.; Yokoya, S.; Tachibana, K.; Adachi, M.;Nakae, J.; 3 B c
Suwa, S; Katoh, S.; Fujieda, K.: A novel missense mutationof mineralocorticoid receptor gene in one Japanese family with a renalform of pseudohypoaldosteronism type 1. J. Clin. Endocr. Metab. 85:4690- 4694, 2000.

GAM40 396 NR3C2 Viemann, M.; Peter, M.; Lopez- Siguero, J. P.; Simic- Schleicher,G.; 3 B c
Sippell, W. G.: Evidence for genetic heterogeneity of pseudohypoaldosteronismtype 1: identification of a novel mutation in the human mineralocorticoidreceptor in one sporadic case and no mutations in two autosomal dominantkindreds. J. Clin. Endocr. Metab. 86: 2056- 2059, 2001.

GAM40 396 P2RY2 Dasari, V. R.; Sandhu, A. K.; Mills, D. C. B.; Athwal, R. S.; Kunapuli,S. 3 B c
P.: Mapping of the P2U purinergic receptor gene to human chromosome11q13.5-14.1. Somat. Cell Molec. Genet. 22: 75- 79, 1996.

GAM40 396 P2RY2 Katzur, A. C.; Koshimizu, T.- A.; Tomic, M.; Schultze- Mosgau, A.;Ortmann, 3 B c
O.; Stojilkovic, S. S.: Expression and responsiveness ofP2Y2 receptors in human endometrial cancer cell lines. J. Clin. Endocr.Metab. 84: 4085- 4091, 1999.

GAM40 396 P2RY2 Parr, C. E.; Sullivan, D. M.; Paradiso, A. M.; Lazarowski, E. R.;Burch, L. 3 B c
H.; Olsen, J. C.; Erb, L.; Weisman, G. A.; Boucher, R. C.;Turner, J. T.: Cloning and expression of a human P(2U) nucleotidereceptor, a target for cystic fibrosis pharmacotherapy. Proc. Nat.Acad. Sci. 91: 3275- 3279, 1994.

GAM40 396 P2RY2 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 B c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997.

GAM40 396 P2RY2 Tai, C.- J.; Kang, S. K.; Cheng, K. W.; Choi, K.- C.; Nathwani, P.S.; Leung, 3 B c
P. C. K.: Expression and regulation of P2U- purinergicreceptor in human granulosa- luteal cells. J. Clin. Endocr. Metab. 85:1591- 1597, 2000.

GAM40 396 PAX5 Adams, B.; Dorfler, P.; Aguzzi, A.; Kozmik, Z.; Urbanek, P.; Maurer- 3 B c
Fogy,I.; Busslinger, M.: Pax- 5 encodes the transcription factor BSAP andis expressed in B lymphocytes, the developing CNS, and adult testis. GenesDev. 6: 1589- 1607, 1992.

GAM40 396 PAX5 Busslinger, M.; Klix, N.; Pfeffer, P.; Graninger, P. G.; Kozmik,Z.: 3 B c
Deregulation of PAX- 5 by translocation of the E- mu enhancer ofthe IgH

locus adjacent to two alternative PAX- 5 promoters in a diffuselarge- cell lymphoma. Proc. Nat. Acad. Sci. 93: 6129- 6134, 1996.

GAM40 396 PAX5 Mikkola, I.; Heavey, B.; Horcher, M.; Busslinger, M.: Reversionof B cell commitment upon loss of Pax5 expression. Science 297:110- 113, 2002. 3 B c

GAM40 396 PAX5 Nutt, S. L.; Heavey, B.; Rolink, A. G.; Busslinger, M.: Commitmentto the B- lymphoid lineage depends on the transcription factor Pax5. Nature 401:556- 562, 1999. 3 B c

GAM40 396 PAX5 Nutt, S. L.; Vambrie, S.; Steinlein, P.; Kozmik, Z.; Rolink, A.;Weith, A.; Busslinger, M.: Independent regulation of the two Pax5alleles during B- cell development. Nature Genet. 21: 390- 395, 1999. 3 B c

GAM40 396 PAX5 Ohno, H.; Furukawa, T.; Fukuhara, S.; Zong, S. Q.; Kamesaki, H.;Shows, T. B.; Le Beau, M. M.; McKeithan, T. W.; Kawakami, T.; Honjo,T.: Molecular analysis of a chromosomal translocation, t(9;14)(p13;q32),in a diffuse large- cell lymphoma cell line expressing the Ki- 1 antigen. Proc.Nat. Acad. Sci. 87: 628- 632, 1990. 3 B c

GAM40 396 PAX5 Pasqualucci, L.; Neumeister, P.; Goossens, T.; Nanjangud, G.; Chaganti,R. S. K.; Kuppers, R.; Dalla- Favera, R.: Hypermutation of multipleproto- oncogenes in B- cell diffuse large- cell lymphomas. Nature 412:341- 346, 2001. 3 B c

GAM40 396 PAX5 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman homologs of the murine paired- box- containing genes. MammalianGenome 4: 78- 82, 1993. 3 B c

GAM40 396 PAX5 Rolink, A. G.; Nutt, S. L.; Melchers, F.; Busslinger, M.: Long- termin vivo reconstitution of T- cell development by Pax5- deficient B- cellprogenitors. Nature 401: 603- 606, 1999. 3 B c

GAM40 396 PAX5 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: Chromosomal localization of seven PAX genes and cloning of anovel family member, PAX- 9. Nature Genet. 3: 292- 298, 1993. 3 B c

GAM40 396 PAX5 Vorechovsky, I.; Koskinen, S.; Paganelli, R.; Smith, C. I. E.;Busslinger, M.; Hammarstrom, L.: The PAX5 gene: a linkage and mutationanalysis in candidate human primary immunodeficiencies. Immunogenetics 42:149- 152, 1995. 3 B c

GAM40 396 PAX5 Walther, C.; Guenet, J.- L.; Simon, D.; Deutsch, U.; Jostes, B.;Goulding, M. D.; Plachov, D.; Balling, R.; Gruss, P.: Pax: a murinemultigene family of paired box containing genes. Genomics 11: 424- 434,1991. 3 B c

GAM40 396 PPYR1 Bard, J. A.; Walker, M. W.; Branchek, T. A.; Weinshank, R. L.:Cloning and functional expression of a human Y4 subtype receptor forpancreatic polypeptide, neuropeptide Y, and peptide YY J. Biol. Chem 270:26762- 26765, 1995. 3 B c

GAM40 396 PPYR1 Darby, K.; Eyre, H. J.; Lapsys, N.; Copeland, N. G.; Gilbert, D.J.; Couzens, M.; Antonova, O.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: Assignment of the Y- 4 receptor gene (PPYR1) to humanchromosome 10q11.2 and mouse chromosome 14. Genomics 46: 513- 515,1997. 3 B c

GAM40 396 PPYR1 Lutz, C. M.; Richards, J. E.; Scott, K. L.; Sinha, S.; Yang- Feng,T. L.; Frankel, W. N.; Thompson, D. A.: Neuropeptide Y receptor genesmapped in human and mouse: receptors with high affinity for pancreaticpolypeptide are not clustered with receptors specific for neuropeptideY and peptide YY. Genomics 46: 287- 290, 1997. 3 B c

GAM40 396 PTGS1 Catella- Lawson, F.; Reilly, M. P.; Kapoor, S. C.; Cucchiara, A.J.; DeMarco, S.; Tournier, B.; Vyas, S. N.; FitzGerald, G. A.: Cyclooxygenaseinhibitors 3 B c

and the antiplatelet effects of aspirin. New Eng. J. Med. 345:1809- 1817, 2001.

GAM40 396 PTGS1 Dube, J.- N.; Drouin, J.; Aminian, M.; Plant, M. H.; Laneuville,O.: 3 B c
Characterization of a partial prostaglandin endoperoxide H synthase-1deficiency in a patient with a bleeding disorder. Brit. J. Haemat. 113:878-885, 2001.

GAM40 396 PTGS1 Funk, C. D.; Funk, L. B.; Kennedy, M. E.; Pong, A. S.; Fitzgerald,G. A.: 3 B c
Human platelet/erythroleukemia cell prostaglandin G/H synthase:cDNA cloning, expression, and gene chromosomal assignment. FASEBJ. 5: 2304- 2312, 1991.

GAM40 396 PTGS1 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; 3 B c
Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.;
Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999.

GAM40 396 PTGS1 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; 3 B c
Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.:
Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2 in the humanfetal and adult male reproductive tracts. J. Clin. Endocr. Metab. 85:3436- 3441, 2000.

GAM40 396 PTGS1 Langenbach, R.; Morham, S. G.; Tiano, H. F.; Loftin, C. D.; Ghanayem,B. I.; 3 B c
Chulada, P. C.; Mahler, J. F.; Lee, C. A.; Goulding, E. H.;Kluckman, K. D.;
Kim, H. S.; Smithies, O.: Prostaglandin synthase1 gene disruption in mice reduces arachidonic acid- induced inflammationand indomethacin- induced gastric ulceration. Cell 83: 483- 492, 1995.

GAM40 396 PTGS1 Malkowski, M. G.; Ginell, S. L.; Smith, W. L.; Garavito, R. M.: The 3 B c
productive conformation of arachidonic acid bound to prostaglandinsynthase. Science 289: 1933- 1937, 2000.

GAM40 396 PTGS1 Pareti, F. I.; Manucci, P. M.; D'Angelo, A.; Smith, J. B.; Sautebin,L.; 3 B c
Galli, G.: Congenital deficiency of thromboxane and prostacyclin. Lancet I:898- 900, 1980.

GAM40 396 PTGS1 Picot, D.; Loll, P. J.; Garavito, R. M.: The x- ray crystal structureof the 3 B c
membrane protein prostaglandin H- 2 synthase- 1. Nature 367:243- 249, 1994.

GAM40 396 PTGS1 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: 3 B c
Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93: 705- 716, 1998.

GAM40 396 PTGS1 Vane, J. R.; Mitchell, J. A.; Appleton, I.; Tomlinson, A.; Bishop- 3 B c
Bailey,D.; Croxtall, J.; Willoughby, D. A.: Inducible isoforms of cyclooxygenaseand nitric- oxide synthase in inflammation. Proc. Nat. Acad. Sci. 91:2046- 2050, 1994.

GAM40 396 PTGS1 Yokoyama, C.; Tanabe, T.: Cloning of human gene encoding 3 B c
prostaglandinendoperoxide synthase and primary structure of the enzyme. Biochem.Biophys. Res. Commun. 165: 888- 894, 1989.

GAM40 396 SFRP1 Baylin, S. B.; Herman, J. G.: DNA hypermethylation in 3 B c
tumorigenesis:epigenetics joins genetics. Trends Genet. 16: 168- 174, 2000.

GAM40 396 SFRP1 Cameron, E. E.; Bachman, K. E.; Myohanen, S.; Herman, J. G.; Baylin,S. B.: 3 B c
Synergy of demethylation and histone deacetylase inhibitionin the re-expression of genes silenced in cancer. Nature Genet. 21:103- 107, 1999.

GAM40 396 SFRP1 Finch, P. W.; He, X.; Kelley, M. J.; Uren, A.; Schaudies, R. P.;Popescu, N. 3 B c
C.; Rudikoff, S.; Aaronson, S. A.; Varmus, H. E.; Rubin,J. S.: Purification and molecular cloning of a secreted, frizzled- relatedantagonist of Wnt action. Proc. Nat. Acad. Sci. 94: 6770- 6775, 1997.

GAM40 396 SFRP1 Fukuhara, K.; Kariya, M.; Kita, M.; Shime, H.; Kanamori, T.; Kosaka,C.; Orii, A.; Fujita, J.; Fujii, S.: Secreted frizzled related protein1 is overexpressed in uterine leiomyomas, associated with a high estrogenicenvironment and unrelated to proliferative activity. J. Clin. Endocr.Metab. 87: 1729- 1736, 2002. 3 B c

GAM40 396 SFRP1 Melkonyan, H. S.; Chang, W. C.; Shapiro, J. P.; Mahadevappa, M.;Fitzpatrick, P. A.; Kiefer, M. C.; Tomei, L. D.; Umansky, S. R.:SARPs: a family of secreted apoptosis- related proteins. Proc. Nat.Acad. Sci. 94: 13636- 13641, 1997. 3 B c

GAM40 396 SFRP1 Suzuki, H.; Gabrielson, E.; Chen, W.; Anbazhagan, R.; van Engeland,M.; Weijenberg, M. P.; Herman, J. G.; Baylin, S. B.: A genomic screenfor genes upregulated by demethylation and histone deacetylase inhibitionin human colorectal cancer. Nature Genet. 31: 141- 149, 2002. 3 B c

GAM40 396 SLC9A6 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. Note: Supplement: DNA Res. 3: 341- 354, 1996. 3 B c

GAM40 396 SLC9A6 Numata, M.; Petrecca, K.; Lake, N.; Orlowski, J.: Identificationof a mitochondrial Na+/H+ exchanger. J. Biol. Chem. 273: 6951- 6959,1998. 3 B c

GAM40 396 SPAG4 Shao, X.; Tarnasky, H. A.; Schalles, U.; Oko, R.; van der Hoorn,F. A.: Interactional cloning of the 84- kDa major outer dense fiberprotein Odf84: leucine zippers mediate associations of Odf84 and Odf27. J.Biol. Chem. 272: 6105- 6113, 1997. 3 B c

GAM40 396 SPAG4 Shao, X.; van der Hoorn, F. A.: Self- interaction of the major27- kilodalton outer dense fiber protein is in part mediated by a leucinezipper domain in the rat. Biol. Reprod. 55: 1343- 1350, 1996. 3 B c

GAM40 396 SPAG4 Tarnasky, H.; Gill, D.; Murthy, S.; Shao, X.; Demetrick, D. J.;van der Hoorn, F. A.: A novel testis- specific gene, SPAG4, whoseproduct interacts specifically with outer dense fiber protein ODF27,maps to human chromosome 20q11.2. Cytogenet. Cell Genet. 81: 65- 67,1998. 3 B c

GAM40 396 SPAG4 van der Hoorn, F. A.; Tarnasky, H. A.; Nordeen, S. K.: A new ratgene RT7 is specifically expressed during spermatogenesis. Dev. Biol. 142:147- 154, 1990. 3 B c

GAM40 396 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020- 4027, 1998. 3 B c

GAM40 396 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001. 3 B c

GAM40 396 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress different Toll- like receptors and respond to different microbialantigens. J. Exp. Med. 194: 863- 869, 2001. 3 B c

GAM40 396 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.; 3 B c

Mantovani, A.: Differential expression and regulation of Toll- likereceptors (TLR) in human leukocytes: selective expression of TLR3in dendritic cells. J. Immun. 164: 5998- 6004, 2000.

GAM40 396 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A family of human receptors structurally related to DrosophilaToll. Proc. Nat. Acad. Sci. 95: 588- 593, 1998. 3 B c

GAM40 396 TRADD Hsu, H.; Xiong, J.; Goeddel, D. V.: The TNF receptor 1- associatedprotein TRADD signals cell death and NF- kappa- B activation. Cell 81:495- 504, 1995. 3 B c

GAM40 396 TRADD Pan, M.- G.; Xiong, J.; Copeland, N. G.; Gilbert, D. J.; Jenkins,N. A.; Goeddel, D. V.: Sequence, genomic organization, and chromosomelocalization of the mouse TRADD gene. J. Inflamm. 46: 168- 175, 1996. 3 B c

GAM40 396 TRADD Park, Y. C.; Ye, H.; Hsia, C.; Segal, D.; Rich, R. L.; Liou, H.- C.;Myszka, D. G.; Wu, H.: A novel mechanism of TRAF signaling revealedby structural and functional analyses of the TRADD- TRAF2 interaction. Cell 101:777- 787, 2000. 3 B c

GAM40 396 TRADD Scheuerpflug, C. G.; Lichter, P.; Debatin, K.- M.; Mincheva, A.: Assignment of TRADD to human chromosome band 16q22 by in situ hybridization. Cytogenet.Cell Genet. 92: 347- 348, 2001. 3 B c

GAM40 396 WHN Balciunaite, G.; Keller, M. P.; Balciunaite, E.; Piali, L.; Zuklys,S.; Mathieu, Y. D.; Gill, J.; Boyd, R.; Sussman, D. J.; Hollander,G. A.: Wnt glycoproteins regulate the expression of FoxN1, the genedefective in nude mice. Nature Immun. 15Oct, 2002. Note: AdvanceElectronic Publication. 3 B c

GAM40 396 WHN Frank, J.; Pignata, C.; Panteleyev, A. A.; Prowse, D. M.; Baden,H.; Weiner, L.; Gaetaniello, L.; Ahmad, W.; Pozzi, N.; Caerhalmi- Friedman,P. B.; Aita, V. M.; Uyttendaele, H.; Gordon, D.; Ott, J.; Brissette,J. L.; Christiano, A. M.: Exposing the human nude phenotype. Nature 398:473- 474, 1999. 3 B c

GAM40 396 WHN Nehls, M.; Pfeifer, D.; Schorpp, M.; Hedrich, H.; Boehm, T.: Newmember of the winged- helix protein family disrupted in mouse and ratnude mutations. Nature 372: 103- 107, 1994. 3 B c

GAM40 396 WHN Pignata, C.; Fiore, M.; Guzzetta, V.; Castaldo, A.; Sebastio, G.;Porta, F.; Guarino, A.: Congenital alopecia and nail dystrophy associatedwith severe functional T- cell immunodeficiency in two sibs. Am. J.Med. Genet. 65: 167- 170, 1996. 3 B c

GAM40 396 WHN Schorpp, M.; Hofmann, M.; Dear, T. N.; Boehm, T.: Characterizationof mouse and human nude genes. Immunogenetics 46: 509- 515, 1997. 3 B c

GAM40 396 WHN Segre, J. A.; Nemhauser, J. L.; Taylor, B. A.; Nadeau, J. H.; Lander,E. S.: Positional cloning of the nude locus: genetic, physical, andtranscription maps of the region and mutations in the mouse and rat. Genomics 28:549- 559, 1995. 3 B c

GAM40 396 YWHAG Autieri, M. V.; Carbone, C. J.: 14- 3- 3- Gamma interacts with andis phosphorylated by multiple protein kinase C isoforms in PDGF- stimulatedhuman vascular smooth muscle cells. DNA Cell Biol. 18: 555- 564,1999. 3 B c

GAM40 396 YWHAG Autieri, M. V.; Feuerstein, G. Z.; Yue, T.- L.; Ohlstein, E. H.;Douglas, S. A.: Use of differential display to identify differentiallyexpressed mRNAs induced by rat carotid artery balloon angioplasty. Lab.Invest. 72: 656- 661, 1995. 3 B c

GAM40 396 YWHAG Autieri, M. V.; Haines, D. S.; Romanic, A. M.; Ohlstein, E. H.: Expression of 14- 3- 3- gamma in injured arteries and growth factor- and cytokine- 3 B c

stimulated human vascular smooth muscle cells. CellGrowth Diff. 7: 1453-
1460, 1996.

GAM40 396 YWHAG Horie, M.; Suzuki, M.; Takahashi, E.; Tanigami, A.: Cloning, expression,and 3 B c
chromosomal mapping of the human 14- 3- 3gamma gene (YWHAG) to 7q11.23.
Genomics 60:241- 243, 1999.

GAM40 396 YWHAG Morrison, D.: 14- 3- 3: modulators of signaling proteins? Science 266:56- 3 B c
57, 1994.

GAM41 215 AF3P21 Hayakawa, A.; Matsuda, Y.; Daibata, M.; Nakamura, H.; Sano, K.: Genomic 3 C c
organization, tissue expression, and cellular localizationof AF3p21, a
fusion partner of MLL in therapy- related leukemia. GenesChromosomes Cancer
30: 364- 374, 2001.

GAM41 215 AF3P21 Sano, K.; Hayakawa, A.; Piao, J.- H.; Kosaka, Y.; Nakamura, H.:Novel SH3 3 C c
protein encoded by the AF3p21 gene is fused to the mixedlineage leukemia
protein in a therapy- related leukemia with t(3;11)(p21;q23). Blood 95:1066-
1068, 2000.

GAM41 215 AP2A1 Robinson, M. S.: Cloning of cDNAs encoding two related 100- kDcoated vesicle 3 C c
proteins (alpha- adaptins). J. Cell Biol. 108: 833- 42,1989.

GAM41 215 AP2A1 Waelter, S.; Scherzinger, E.; Hasenbank, R.; Nordhoff, E.; Lurz,R.; Goehler, 3 C c
H.; Gauss, C.; Sathasivam, K.; Bates, G. P.; Lehrach,H.; Wanker, E. E.: The
huntingtin interacting protein HIP1 is a clathrinand alpha- adaptin- binding
protein involved in receptor- mediated endocytosis. Hum.Molec. Genet. 10:
1807- 1817, 2001.

GAM41 215 CAPN1 Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.;Forbes, S. A.; 3 C c
Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B.T.; Farnebo, F.;
Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud,S.; Zhang, C. X.; Salandre,
J.; Calender, A.: Definition of the minimalMEN1 candidate area based on a 5-
Mb integrated map of proximal 11q13. Genomics 37:354- 365, 1996.

GAM41 215 CAPN1 Ohno, S.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Ohmi- Imajoh,S.; Suzuki, 3 C c
K.; Shimizu, Y.; Shimizu, N.: Four genes for the calpainfamily locate on
four distinct human chromosomes. (Abstract) Cytogenet.Cell Genet. 51: 1054-
1055, 1989.

GAM41 215 CAPN1 Ohno, S.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Shimizu, Y.;Ohmi- Imajoh, 3 C c
S.; Shimizu, N.; Suzuki, K.: Four genes for the calpainfamily locate on four
distinct human chromosomes. Cytogenet. CellGenet. 53: 225- 229, 1990.

GAM41 215 CASQ1 Bataille, N.; Schmitt, N.; Aumercier- Maes, P.; Ollivier, B.; Lucas- 3 C c
Heron,B.; Lestienne, P.: Molecular cloning of human calmitine, a
mitochondrialcalcium binding protein, reveals identity with calsequestrine.
Biochem.Biophys. Res. Commun. 203: 1477- 1482, 1994.

GAM41 215 CASQ1 Fujii, J.; Willard, H. F.; MacLennan, D. H.: Characterizationand 3 C c
localization to human chromosome 1 of human fast- twitch skeletalmuscle
calsequestrin gene. Somat. Cell Molec. Genet. 16: 185- 189,1990.

GAM41 215 CASQ1 Otsu, K.; Fujii, J.; Periasamy, M.; Difilippantonio, M.; Uppender,M.; Ward, 3 C c
D. C.; MacLennan, D. H.: Chromosome mapping of five humancardiac and
skeletal muscle sarcoplasmic reticulum protein genes. Genomics 17:507- 509,
1993.

GAM41 215 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 C c
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM41 215 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 C c
and clinical use. Blood 89: 3897- 3908, 1997.

GAM41 215 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 C c

chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814-819, 1992.

GAM41 215 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang, Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell-derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87: 7512- 7516, 1990. 3 C c

GAM41 215 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract) Cytogenet.Cell Genet. 58: 2027 only, 1991. 3 C c

GAM41 215 PITX3 Hittner, H. M.; Kretzer, F. L.; Antoszyk, J. H.; Ferrell, R. E.;Mehta, R. S.: Variable expressivity of autosomal dominant anteriorsegment mesenchymal dysgenesis in six generations. Am. J. Ophthal. 93:57- 70, 1982. 3 C c

GAM41 215 PITX3 Pellegrini- Bouiller, I.; Manrique, C.; Gunz, G.; Grino, M.; Zamora,A. J.; Figarella- Branger, D.; Grisoli, F.; Jaquet, P.; Enjalbert,A.: Expression of the members of the Ptx family of transcriptionfactors in human pituitary adenomas. J. Clin. Endocr. Metab. 84:2212- 2220, 1999. 3 C c

GAM41 215 PITX3 Semina, E. V.; Ferrell, R. E.; Mintz- Hittner, H. A.; Bitoun, P.;Alward, W. L. M.; Reiter, R. S.; Funkhauser, C.; Daack- Hirsch, S.;Murray, J. C.: A novel homeobox gene PITX3 is mutated in familieswith autosomal- dominant cataracts and ASMD. Nature Genet. 19: 167- 170,1998. 3 C c

GAM41 215 PITX3 Semina, E. V.; Murray, J. C.; Reiter, R.; Hrstka, R. F.; Graw,J.: Deletion in the promoter region and altered expression of Pitx3homeobox gene in aphakia mice. Hum. Molec. Genet. 9: 1575- 1585,2000. 3 C c

GAM41 215 PITX3 Semina, E. V.; Reiter, R. S.; Murray, J. C.: Isolation of a newhomeobox gene belonging to the Pitx/Rieg family: expression duringlens development and mapping to the aphakia region on mouse chromosome19. Hum. Molec. Genet. 6: 2109- 2116, 1997. 3 C c

GAM42 224 CDR2 Fathallah- Shaykh, H.; Wolf, S.; Wong, E.; Posner, J. B.: Cloningof a leucine- zipper protein recognized by the sera of patients withantibody-associated paraneoplastic cerebellar degeneration. Proc.Nat. Acad. Sci. 88: 3451- 3454, 1991. 3 C b

GAM42 224 CDR2 Fletcher, C. F.; Okano, H. J.; Gilbert, D. J.; Yang, Y.; Yang,C.; Copeland, N. G.; Jenkins, N. A.; Darnell, R. B.: Mouse chromosomallocations of nine genes encoding homologs of human paraneoplasticneurologic disorder antigens. Genomics 45: 313- 319, 1997. 3 C b

GAM42 224 CDR2 Furneaux, H. M.; Rosenblum, M. K.; Dalmau, J.; Wong, E.; Woodruff,P.; Graus, F.; Posner, J. B.: Selective expression of Purkinje- cellantigens in tumor tissue from patients with paraneoplastic cerebellardegeneration. New Eng. J. Med. 322: 1844- 1851, 1990. 3 C b

GAM42 224 CDR2 Furneaux, H. M.; Wong, E.; Posner, J. B.: Isolation of cDNA clonesencoding the major Yo paraneoplastic antigen. (Abstract) Neurology 40(suppl. 1): 166 only, 1990. 3 C b

GAM42 224 CDR2 Gress, T.; Baldini, A.; Rocchi, M.; Furneaux, H.; Posner, J. B.;Siniscalco, M.: In situ mapping of the gene coding for a leucinezipper DNA binding protein (CDR 2) to the region between two rarefragile sites of autosome 16 (16p12- p13.1). (Abstract) Cytogenet.Cell Genet. 58: 1999- 2000, 1991. 3 C b

GAM42 224 CDR2 Gress, T.; Baldini, A.; Rocchi, M.; Furneaux, H.; Posner, J. B.;Siniscalco, M.: In situ mapping of the gene coding for a leucinezipper DNA binding protein (CDR62) to 16p12- 16p13.1. Genomics 13:1340- 1342, 1992. 3 C b

GAM42 224 SMARCD1 Ring, H. Z.; Vameghi- Meyers, V.; Wang, W.; Crabtree, G. R.; Francke,U.: 3 C c
Five SWI/SNF- related, matrix- associated, actin- dependent regulatorof chromatin (SMARC) genes are dispersed in the human genome. Genomics 51:140-143, 1998.

GAM42 224 SMARCD1 Wang, W.; Xue, Y.; Zhou, S.; Kuo, A.; Cairns, B. R.; Crabtree,G. R.: 3 C c
Diversity and specialization of mammalian SWI/SNF complexes. GenesDev. 10: 2117- 2130, 1996.

GAM44 287 ACE Amant, C.; Bauters, C.; Bodart, J.- C.; Lablanche, J.- M.; Grollier,G.; 1 A c
Danchin, N.; Hamon, M.; Richard, F.; Helbecque, N.; McFadden,E. P.; Amouyel, P.; Bertrand, M. E.: D allele of the angiotensinI- converting enzyme is a major risk factor for restenosis after coronarystenting. Circulation 96: 56-60, 1997.

GAM44 287 ACE Arbustini, E.; Grasso, M.; Fasani, R.; Klersy, C.; Diegoli, M.;Porcu, E.; 1 A c
Banchieri, N.; Fortina, P.; Danesino, C.; Specchia, G.: Angiotensin converting enzyme gene deletion allele is independentlyand strongly associated with coronary atherosclerosis and myocardialinfarction. Brit. Heart J. 74: 584- 591, 1995.

GAM44 287 ACE Berge, K. E.; Berg, K.: No effect of insertion/deletion polymorphismat the 1 A c
ACE locus on normal blood pressure level or variability. Clin.Genet. 45: 169- 174, 1994.

GAM44 287 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: 1 A c
Insertion/deletion(I/D) polymorphism at the locus for angiotensin I-converting enzymeand myocardial infarction. Clin. Genet. 44: 292- 297, 1993.

GAM44 287 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: 1 A c
Insertion/deletion(I/D) polymorphism at the locus for angiotensin I-converting enzymeand parental history of myocardial infarction. Clin. Genet. 44:298- 301, 1993.

GAM44 287 ACE Brown, N. J.; Ray, W. A.; Snowden, M.; Griffin, M. R.: Black Americanshave 1 A c
an increased rate of angiotensin converting enzyme inhibitor-associatedangioedema. Clin. Pharmacol. Therapeutics 60: 8- 13, 1996.

GAM44 287 ACE Cambien, F.; Alhenc- Gelas, F.; Herbeth, B.; Andre, J. L.; Rakotovao,R.; 1 A c
Gonzales, M. F.; Allegrini, J.; Bloch, C.: Familial resemblanceof plasma angiotensin- converting enzyme level: the Nancy study. Am.J. Hum. Genet. 43: 774- 780, 1988.

GAM44 287 ACE Cambien, F.; Poirier, O.; Lecerf, L.; Evans, A.; Cambou, J.- P.;Arveiler, 1 A c
D.; Luc, G.; Bard, J.- M.; Bara, L.; Ricard, S.; Tiret, L.;Amouyel, P.; Alhenc- Gelas, F.; Soubrier, F.: Deletion polymorphismin the gene for angiotensin- converting enzyme is a potent risk factorfor myocardial infarction. Nature 359: 641- 644, 1992.

GAM44 287 ACE Doria, A.; Warram, J. H.; Krolewski, A. S.: Genetic predispositionto 1 A c
diabetic nephropathy: evidence for a role of the angiotensin I-convertingenzyme gene. Diabetes 43: 690- 695, 1994.

GAM44 287 ACE Ehlers, M. R. W.; Fox, E. A.; Strydom, D. J.; Riordan, J. F.:Molecular 1 A c
cloning of human testicular angiotensin- converting enzyme:the testis isozyme is identical to the C- terminal half of endothelialangiotensin-converting enzyme. Proc. Nat. Acad. Sci. 86: 7741- 7745,1989.

GAM44 287 ACE Esther, C. R., Jr.; Marino, E. M.; Howard, T. E.; Machaud, A.;Corvol, P.; 1 A c
Capecchi, M. R.; Bernstein, K. E.: The critical roleof tissue angiotensin-converting enzyme as revealed by gene targetingin mice. J. Clin. Invest. 99: 2375- 2385, 1997.

GAM44 287 ACE Evans, A. E.; Poirier, O.; Kee, F.; Lecerf, L.; McCrum, E.; Falconer,T.; 1 A c
Crane, J.; O'Rourke, D. F.; Cambien, F.: Polymorphisms of theangiotensin-
converting- enzyme gene in subjects who die from coronaryheart disease.
Quart. J. Med. 87: 211- 214, 1994.

GAM44 287 ACE Exner, D. V.; Dries, D. L.; Domanski, M. J.; Cohn, J. N.: Lesserresponse to 1 A c
angiotensin- converting- enzyme inhibitor therapy in blackas compared with
white patients with left ventricular dysfunction. NewEng. J. Med. 344: 1351-
1357, 2001.

GAM44 287 ACE Gardemann, A.; Fink, M.; Stricker, J.; Nguyen, Q. D.; Humme, J.;Katz, N.; 1 A c
Tillmanns, H.; Hehrlein, F. W.; Rau, M.; Haberbosch, W.: ACE I/D gene
polymorphism: presence of the ACE D allele increasesthe risk of coronary
artery disease in younger individuals. Atherosclerosis 139:153- 159, 1998.

GAM44 287 ACE Gayagay, G.; Yu, B.; Hambly, B.; Boston, T.; Hahn, A.; Celermajer,D. S.; 1 A c
Trent, R. J.: Elite endurance athletes and the ACE I allele:the role of
genes in athletic performance. Hum. Genet. 103: 48- 50,1998.

GAM44 287 ACE Hagaman, J. R.; Moyer, J. S.; Bachman, E. S.; Sibony, M.; Magyar,P. L.; 1 A c
Welch, J. E.; Smithies, O.; Krege, J. H.; O'Brien, D. A.:Angiotensin-
converting enzyme and male fertility. Proc. Nat. Acad.Sci. 95: 2552- 2557,
1998.

GAM44 287 ACE Hamdi, H. K.; Reznik, J.; Castellon, R.; Atilano, S. R.; Ong,J. M.; Udar, 1 A c
N.; Tavis, J. H.; Aoki, A. M.; Nesburn, A. B.; Boyer,D. S.; Small, K. W.;
Brown, D. J.; Kenney, M. C.: Alu DNA polymorphismin ACE gene is protective
for age- related macular degeneration. Biochem.Biophys. Res. Commun. 295:
668- 672, 2002.

GAM44 287 ACE Howard, T. E.; Shai, S. Y.; Langford, K. G.; Martin, B. M.; Bernstein,K. E.: 1 A c
Transcription of testicular angiotensin- converting enzyme(ACE) is initiated
within the 12th intron of the somatic ACE gene. Molec.Cell. Biol. 10: 4294-
4302, 1990.

GAM44 287 ACE Huang, W.; Gallois, Y.; Bouby, N.; Bruneval, P.; Heudes, D.; Belair,M.- F.; 1 A c
Krege, J. H.; Menteton, P.; Marre, M.; Smithies, O.; Alhenc- Gelas,F.:
Genetically increased angiotensin I- converting enzyme level andrenal
complications in the diabetic mouse. Proc. Nat. Acad. Sci. 98:13330- 13334,
2001.

GAM44 287 ACE Jeffery, S.; Malik, A. K. S.; Crosby, A.; Bland, M.; Eastwood,J. B.; Amoah- 1 A c
Danquah, J.; Acheampong, J. W.; Plange- Rhule, J.: Adominant relationship
between the ACE D allele and serum ACE levelsin a Ghanaian population.
(Letter) J. Med. Genet. 36: 869- 870, 1999.

GAM44 287 ACE Jeunemaitre, X.; Lifton, R. P.; Hunt, S. C.; Williams, R. R.;Lalouel, J.- 1 A c
M.: Absence of linkage between the angiotensin convertingenzyme locus and
human essential hypertension. Nature Genet. 1:72- 75, 1992.

GAM44 287 ACE Julier, C.; Delepine, M.; Keavney, B.; Terwilliger, J.; Davis,S.; Weeks, D. 1 A c
E.; Bui, T.; Jeunemaitre, X.; Velho, G.; Froguel, P.;Ratcliffe, P.; Corvol,
P.; Soubrier, F.; Lathrop, G. M.: Geneticsusceptibility for human familial
essential hypertension in a regionof homology with blood pressure linkage on
rat chromosome 10. Hum.Molec. Genet. 6: 2077- 2085, 1997.

GAM44 287 ACE Keavney, B.; McKenzie, C.; Parish, S.; Palmer, A.; Clark, S.;Youngman, L.; 1 A c
Delepine, M.; Lathrop, M.; Peto, R.; Collins, R.: Large- scaletest of
hypothesized associations between the angiotensin- converting-
enzymeinsertion/deletion polymorphism and myocardial infarction in about5000
cases and 6000 controls. Lancet 355: 434- 442, 2000.

GAM44 287 ACE Kehoe, P. G.; Russ, C.; McIlroy, S.; Williams, H.; Holmans, P.;Holmes, C.; 1 A c
Liolitsa, D.; Vahidassr, D.; Powell, J.; McGleenon, B.;Liddell, M.; Plomin,
R.; and 9 others: Variation in DCP1, encodingACE, is associated with
susceptibility to Alzheimer disease. (Letter) NatureGenet. 21: 71- 72, 1999.

GAM44 287 ACE Keramatipour, M.; McConnell, R. S.; Kirkpatrick, P.; Tebbs, S.;Furlong, R. 1 A c
A.; Rubinsztein, D. C.: The ACE I allele is associatedwith increased risk
for ruptured intracranial aneurysms. J. Med.Genet. 37: 498- 500, 2000.

GAM44 287 ACE Krege, J. H.; John, S. W. M.; Langenbach, L. L.; Hodgin, J. B.;Hagaman, J. 1 A c
R.; Bachman, E. S.; Jennette, J. C.; O'Brien, D. A.; Smithies,O.: Male-
female differences in fertility and blood pressure in ACE- deficientmice.
Nature 375: 146- 148, 1995.

GAM44 287 ACE Kurtz, T. W.: The ACE of hearts. Nature 359: 588- 589, 1992. 1 A c

GAM44 287 ACE Lindpaintner, K.; Lee, M.; Larson, M. G.; Rao, V. S; Pfeffer,M. A.; Ordovas, 1 A c
J. M.; Schaefer, E. J.; Wilson, A. F.; Wilson, P.W. F.; Vasan, R. S.; Myers,
R. H.; Levy, D.: Absence of associationor genetic linkage between the
angiotensin- converting- enzyme geneand left ventricular mass. New Eng. J.
Med. 334: 1023- 1028, 1996.

GAM44 287 ACE Lindpaintner, K.; Pfeffer, M. A.; Kreutz, R.; Stampfer, M. J.;Grodstein, F.; 1 A c
LaMotte, F.; Buring, J.; Hennekens, C. H.: A prospectiveevaluation of an
angiotensin- converting- enzyme gene polymorphism andthe risk of ischemic
heart disease. New Eng. J. Med. 332: 706- 711,1995.

GAM44 287 ACE Marre, M.; Bernadet, P.; Gallois, Y.; Savagner, F.; Guyene, T.- T.;Hallab, 1 A c
M.; Cambien, F.; Passa, P.; Alhenc- Gelas, F.: Relationshipsbetween
angiotensin I converting enzyme gene polymorphism, plasmalevels, and
diabetic retinal and renal complications. Diabetes 43:384- 388, 1994.

GAM44 287 ACE Marre, M.; Jeunemaitre, X.; Gallois, Y.; Rodier, M.; Chatellier,G.; Sert, 1 A c
C.; Dusselier, L.; Kahal, Z.; Chaillous, L.; Halimi, S.;Muller, A.;
Sackmann, H.; Bauduceau, B.; Bled, F.; Passa, P.; Alhenc- Gelas,F.:
Contribution of genetic polymorphism in the renin- angiotensinsystem to the
development of renal complications in insulin- dependentdiabetes. J. Clin.
Invest. 99: 1585- 1595, 1997.

GAM44 287 ACE Mattei, M.- G.; Hubert, C.; Alhenc- Gelas, F.; Roeckel, N.; Corvol,P.; 1 A c
Soubrier, F.: Angiotensin- I converting enzyme gene is on chromosome17.
(Abstract) Cytogenet. Cell Genet. 51: 1041, 1989.

GAM44 287 ACE Montgomery, H. E.; Clarkson, P.; Dollery, C. M.; Prasad, K.; Losi,M.- A.; 1 A c
Hemingway, H.; Statters, D.; Jubb, M.; Girvain, M.; Varnava,A.; World, M.;
Deanfield, J.; Talmud, P.; McEwan, J. R.; McKenna,W. J.; Humphries, S.:
Association of angiotensin- converting enzymegene I/D polymorphism with
change in left ventricular mass in responseto physical training. Circulation
96: 741- 747, 1997.

GAM44 287 ACE Montgomery, H. E.; Marshall, R.; Hemingway, H.; Myerson, S.; Clarkson,P.; 1 A c
Dollery, C.; Hayward, M.; Holliman, D. E.; Jubb, M.; World, M.;Thomas, E.
L.; Brynes, A. E.; Saeed, N.; Barnard, M.; Bell, J. D.;Prasad, K.; Rayson,
M.; Talmud, P. J.; Humphries, S. E.: Human genefor physical performance.
(Letter) Nature 393: 221- 222, 1998.

GAM44 287 ACE Ohishi, M.; Fujii, K.; Minamino, T.; Hagaki, J.; Kamitani, A.;Rakugi, H.; 1 A c
Zhao, Y.; Mikami, H.; Miki, T.; Ogihara, T.: A potentgenetic risk factor for
restenosis. (Letter) Nature Genet. 5: 324- 325,1993.

GAM44 287 ACE Oike, Y.; Hata, A.; Ogata, Y.; Numata, Y.; Shido, K.; Kondo, K.: Angiotensin 1 A c
converting enzyme as a genetic risk factor for coronaryartery spasm:

implication in the pathogenesis of myocardial infarction. J.Clin. Invest. 96: 2975- 2979, 1995.

GAM44 287 ACE Okabe, T.; Fusisawa, M.; Yotsumoto, M.; Takaru, F.; Lanzillo,J. J.; Fanburg, B. L.: Familial elevation of serum angiotensin- convertingenzyme. Quart. J. Med. 216: 55- 61, 1985. 1 A c

GAM44 287 ACE Pfeffer, M. A.; Braunwald, E.; Moye, L. A.; Basta, L.; Brown,E. J., Jr.; Cuddy, T. E.; Davis, B. R.; Geltman, E. M.; Goldman, S.;Flaker, G. C.; Klein, M.; Lamas, G. A.; Packer, M.; Rouleau, J.; Rouleau,J. L.; Rutherford, J.; Wertheimer, J. H.; Hawkins, C. M.: Effectof captopril on mortality and morbidity in patients with left ventriculardysfunction after myocardial infarction: results of the survival andventricular enlargement trial. New Eng. J. Med. 327: 669- 677, 1992. 1 A c

GAM44 287 ACE Ramaraj, P.; Kessler, S. P.; Colmenares, C.; Sen, G. C.: Selectiverestoration of male fertility in mice lacking angiotensin-convertingenzymes by sperm- specific expression of the testicular isozyme. J.Clin. Invest. 102: 371- 378, 1998. 1 A c

GAM44 287 ACE Rigat, B.; Hubert, C.; Alhenc- Gelas, F.; Cambien, F.; Corvol,P.; Soubrier, F.: An insertion/deletion polymorphism in the angiotensinI- converting enzyme gene accounting for half the variance of serumenzyme levels. J. Clin. Invest. 86: 1343- 1346, 1990. 1 A c

GAM44 287 ACE Rigat, B.; Hubert, C.; Corvol, P.; Soubrier, F.: PCR detectionof the insertion/deletion polymorphism of the human angiotensin convertingenzyme gene (DCP1) (dipeptidylcarboxypeptidase 1). Nucleic AcidsRes. 20: 1433, 1992. 1 A c

GAM44 287 ACE Ruiz, J.; Blanche, H.; Cohen, N.; Velho, G.; Cambien, F.; Cohen,D.; Passa, P.; Froguel, P.: Insertion/deletion polymorphism of theangiotensin-converting enzyme gene is strongly associated with coronaryheart disease in non- insulin- dependent diabetes mellitus. Proc. Nat.Acad. Sci. 91: 3662-3665, 1994. 1 A c

GAM44 287 ACE Schachter, F.; Faure- Delanef, L.; Guenot, F.; Rouger, H.; Froguel,P.; Lesueur- Ginot, L.; Cohen, D.: Genetic associations with humanlongevity at the APOE and ACE loci. Nature Genet. 6: 29- 32, 1994. 1 A c

GAM44 287 ACE Schmidt, S.; Schone, N.; Ritz, E.; Giesel, R.; Bergis, K.; Strojek,K.; Greszczak, W.; Schroter, W.; Willms, B. H. L.; Petzold, R.; Henrichs,H. R.; Rambausek, M.; Schwarzbeck, A.; Kohr, B.; Schneider, P.; Bosch,A.: Association of ACE gene polymorphism and diabetic nephropathy? KidneyInt. 47: 1176- 1181, 1995. 1 A c

GAM44 287 ACE Schunkert, H.; Hense, H.- W.; Holmer, S. R.; Stender, M.; Perz,S.; Keil, U.; Lorell, B. H.; Riegger, G. A. J.: Association betweena deletion polymorphism of the angiotensin- converting- enzyme geneand left ventricular hypertrophy. New Eng. J. Med. 330: 1634- 1638,1994. 1 A c

GAM44 287 ACE Singer, D. R. J.; Missouris, C. G.; Jeffery, S.: Angiotensin-convertingenzyme gene polymorphism: what to do about all the confusion? (Editorial) Circulation 94:236- 239, 1996. 1 A c

GAM44 287 ACE Soubrier, F.; Alhenc- Gelas, F.; Hubert, C.; Allegrini, J.; John,M.; Tregear, G.; Corvol, P.: Two putative active centers in humanangiotensin I-converting enzyme revealed by molecular cloning. Proc.Nat. Acad. Sci. 85: 9386- 9390, 1988. 1 A c

GAM44 287 ACE Tarnow, L.; Cambien, F.; Rossing, P.; Nielsen, F. S.; Hansen,B. V.; Lecerf, L.; Poirier, O.; Danilov, S.; Parving, H.- H.: Lackof relationship between 1 A c

an insertion/deletion polymorphism in theangiotensin I- converting enzyme gene and diabetic nephropathy andproliferative retinopathy in IDDM patients. Diabetes 44: 489- 494,1995.

GAM44 287 ACE Tiret, L.; Rigat, B.; Visvikis, S.; Breda, C.; Corvol, P.; Cambien,F.; Soubrier, F.: Evidence, from combined segregation and linkageanalysis, that a variant of the angiotensin I- converting enzyme (ACE)gene controls plasma ACE levels. Am. J. Hum. Genet. 51: 197- 205,1992. 1 A c

GAM44 287 ACE Vleming, L. J.; van der Pijl, J. W.; Lemkes, H. H. P. J.; Westendorp,R. G. J.; Maassen, J. A.; Daha, M. R.; van Es, L. A.; van Kooten,C.: The DD genotype of the ACE gene polymorphism is associated withprogression of diabetic nephropathy to end stage renal failure inIDDM. Clin. Nephrol. 51: 133- 140, 1999. 1 A c

GAM44 287 ACE Williams, A. G.; Rayson, M. P.; Jubb, M.; World, M.; Woods, D.R.; Hayward, M.; Martin, J.; Humphries, S. E.; Montgomery, H. E.:The ACE gene and muscle performance. Nature 403: 614 only, 2000. 1 A c

GAM44 287 ACE Winkelmann, B. R.; Nauck, M.; Klein, B.; Russ, A. P.; Bohm, B.O.; Siekmeier, R.; Ihnken, K.; Verho, M.; Gross, W.; Marz, W.: Deletionpolymorphism of the angiotensin I- converting enzyme gene is associatedwith increased plasma angiotensin- converting enzyme activity but notwith increased risk for myocardial infarction and coronary arterydisease. Ann. Intern. Med. 125: 19- 25, 1996. 1 A c

GAM44 287 ACE Woods, D.; Onambele, G.; Woledge, R.; Skelton, D.; Bruce, S.;Humphries, S. E.; Montgomery, H.: Angiotensin- I converting enzymegenotype- dependent benefit from hormone replacement therapy in isometricmuscle strength and bone mineral density. J. Clin. Endocr. Metab. 86:2200- 2204, 2001. 1 A c

GAM44 287 ACE Yoshida, H.; Mitarai, T.; Kawamura, T.; Kitajima, T.; Miyazaki,Y.; Nagasawa, R.; Kawaguchi, Y.; Kubo, H.; Ichikawa, I.; Sakai, O.: Role of the deletion polymorphism of the angiotensin convertingenzyme gene in the progression and therapeutic responsiveness of IgAnephropathy. J. Clin. Invest. 96: 2162- 2169, 1995. 1 A c

GAM44 287 ACE Yoshioka, T.; Xu, Y.; Yoshida, H.; Shiraga, H.; Muraki, T.; Ito,K.: Deletion polymorphism of the angiotensin converting enzyme genepredicts persistent proteinuria in Henoch- Schonlein purpura nephritis. Arch.Dis. Child. 79: 394- 399, 1998. 1 A c

GAM44 287 ACE Zhu, X.; Bouzekri, N.; Southam, L.; Cooper, R. S.; Adeyemo, A.;McKenzie, C. A.; Luke, A.; Chen, G.; Elston, R. C.; Ward, R.: Linkageand association analysis of angiotensin I- converting enzyme (ACE)- genepolymorphisms with ACE concentration and blood pressure. Am. J. Hum.Genet. 68: 1139- 1148, 2001. 1 A c

GAM44 287 ACE Zhu, X.; McKenzie, C. A.; Forrester, T.; Nickerson, D. A.; Broeckel,U.; Schunkert, H.; Doering, A.; Jacob, H. J.; Cooper, R. S.; Rieder,M. J.: Localization of a small genomic region associated with elevatedACE. Am. J. Hum. Genet. 67: 1144- 1153, 2000. Note: Erratum: Am.J. Hum. Genet. 67: 1365 only, 2000. 1 A c

GAM44 287 ASPH Jia, S.; VanDusen, W. J.; Diehl, R. E.; Kohl, N. E.; Dixon, R.A. F.; Elliston, K. O.; Stern, A. M.; Friedman, P. A.: cDNA cloningand expression of bovine aspartyl (asparaginyl) beta- hydroxylase. J.Biol. Chem. 267: 14322- 14327, 1992. 1 A c

GAM44 287 ASPH Korioth, F.; Gieffers, C.; Frey, J.: Cloning and characterizationof the human gene encoding aspartyl beta- hydroxylase. Gene 150:395- 399, 1994. 1 A c

GAM44 287 ASPH Lavaissiere, L.; Jia, S.; Nishiyama, M.; de la Monte, S.; Stern,A. M.; 1 A c
Wands, J. R.; Friedman, P. A.: Overexpression of human
aspartyl(asparaginyl)- beta- hydroxylasein hepatocellular carcinoma and
cholangiocarcinoma. J. Clin. Invest. 98:1313- 1323, 1996.

GAM44 287 ASPH Lim, K. Y.; Hong, C.- S.; Kim, D. H.: cDNA cloning and characterizationof 1 A c
human cardiac junctin. Gene 255: 35- 42, 2000.

GAM44 287 ASPH Scott, A. F.: Personal Communication. Baltimore, Md. 2/19/2001. 1 A c

GAM44 287 ASPH Treves, S.; Feriotto, G.; Moccagatta, L.; Gambari, R.; Zorzato,F.: Molecular 1 A c
cloning, expression, functional characterization, chromosomallocalization,
and gene structure of junctate, a novel integral calciumbinding protein of
sarco(endo)plasmic reticulum membrane. J. Biol.Chem. 275: 39555- 39568,
2000.

GAM44 287 ASPH Wetzel, G. T.; Ding, S.; Chen, F.: Molecular cloning of junctinfrom human 1 A c
and developing rabbit heart. Molec. Genet. Metab. 69:252- 258, 2000.

GAM44 287 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 1 A c
Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.:
Identification of Bach2 as a B- cell- specific partner for smallMaf proteins
that negatively regulate the immunoglobulin heavy chaingene 3- prime
enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM44 287 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 1 A c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-
basic leucine zipper transcription factors that interact withMafK and
regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-
6095, 1996.

GAM44 287 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, 1 A c
A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.;
Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B
cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene
19: 3739- 3749, 2000.

GAM44 287 CASP10 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 1 A c
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM44 287 CASP10 Park, W. S.; Lee, J. H.; Shin, M. S.; Park, J. Y.; Kim, H. S.;Lee, J. H.; 1 A c
Kim, Y. S.; Lee, S. N.; Xiao, W.; Park, C. H.; Lee, S.H.; Yoo, N. J.; Lee,
J. Y.: Inactivating mutations of the caspase- 10gene in gastric cancer.
Oncogene 21: 2919- 2925, 2002.

GAM44 287 CASP10 Shin, M. S.; Kim, H. S.; Kang, C. S.; Park, W. S.; Kim, S. Y.;Lee, S. N.; 1 A c
Lee, J. H.; Park, J. Y.; Jang, J. J.; Kim, C. W.; Kim,S. H.; Lee, J. Y.;
Yoo, N. J.; Lee, S. H.: Inactivating mutationsof CASP10 gene in non- Hodgkin
lymphomas. Blood 99: 4094- 4099, 2002.

GAM44 287 CASP10 Vincenz, C.; Dixit, V. M.: Fas- associated death domain proteininterleukin- 1 A c
1- beta- converting enzyme 2 (FLICE2), an ICE/Ced- 3 homologue,is proximally
involved in CD95- and p55- mediated death signaling. J.Biol. Chem. 272:
6578- 6583, 1997.

GAM44 287 CASP10 Wang, J.; Chun, H. J.; Wong, W.; Spencer, D. M.; Lenardo, M. J.: Caspase- 10 1 A c
is an initiator caspase in death receptor signaling. Proc.Nat. Acad. Sci.
98: 13884- 13888, 2001.

GAM44 287 CASP10 Wang, J.; Zheng, L.; Lobito, A.; Chan, F. K.; Dale, J.; Sneller,M.; Yao, X.; 1 A c

Puck, J. M.; Straus, S. E.; Lenardo, M. J.: Inheritedhuman caspase 10 mutations underlie defective lymphocyte and dendriticcell apoptosis in autoimmune lymphoproliferative syndrome type II. Cell 98:47- 58, 1999.

GAM44 287 CCKBR Beinborn, M.; Lee, Y.- M.; McBride, E. W.; Quinn, S. M.; Kopin,A. S.: A single amino acid of the cholecystokinin- B/gastrin receptordetermines specificity for non- peptide antagonists. Nature 362:348- 350, 1993. 1 A b

GAM44 287 CCKBR Huppi, K.; Siwarski, D.; Pisegna, J. R.; Wank, S.: Chromosomallocalization of the gastric and brain receptors for cholecystokinin(CCKAR and CCKBR) in human and mouse. Genomics 25: 727- 729, 1995. 1 A b

GAM44 287 CCKBR Lee, Y.- M.; Beinborn, M.; McBride, E. W.; Lu, M.; Kolakowski, L.F., Jr.; Kopin, A. S.: The human brain cholecystokinin- B/gastrinreceptor: cloning and characterization. J. Biol. Chem. 268: 8164- 8169,1993. 1 A b

GAM44 287 CCKBR Pisegna, J. R.; de Weerth, A.; Huppi, K.; Wank, S. A.: Molecularcloning of the human brain and gastric cholecystokinin receptor: structure,functional expression and chromosomal localization. Biochem. Biophys.Res. Commun. 189: 296- 303, 1992. 1 A b

GAM44 287 CCKBR Samuelson, L. C.; Isakoff, M. S.; Lacourse, K. A.: Localizationof the murine cholecystokinin A and B receptor genes. MammalianGenome 6: 242- 246, 1995. 1 A b

GAM44 287 CCKBR Zimonjic, D. B.; Popescu, N. C.; Matsui, T.; Ito, M.; Chihara,K.: Localization of the human cholecystokinin- B/gastrin receptorgene (CCKBR) to chromosome 11p15.5- p15.4 by fluorescence in situ hybridization.Cytogenet. Cell Genet. 65: 184- 185, 1994. 1 A b

GAM44 287 CX3CR1 Faure, S.; Meyer, L.; Costagliola, D.; Vaneensberghe, C.; Genin,E.; Autran, B.; French ALT and IMMUNOCO Study Groups; Delfraisay,J.- F.; SEROCO Study Group; McDermott, D. H.; Murphy, P. M.; Debre,P.; Theodorou, I.; Cambadiere, C.: Rapid progression to AIDS in HIV+individuals with a structural variant of the chemokine receptor CX(3)CR1. Science 287:2274- 2277, 2000. 1 A c

GAM44 287 CX3CR1 Imai, T.; Hieshima, K.; Haskell, C.; Baba, M.; Nagira, M.; Nishimura,M.; Kakizaki, M.; Takagi, S.; Nomiyama, H.; Schall, T. J.; Yoshie,O.: Identification and molecular characterization of fractalkinereceptor CX3CR1, which mediates both leukocyte migration and adhesion. Cell 91:521- 530, 1997. 1 A c

GAM44 287 CX3CR1 Maho, A.; Bensimon, A.; Vassart, G.; Parmentier, M.: Mapping ofthe CCXCR1, CX3CR1, CCBP2 and CCR9 genes to the CCR cluster withinthe 3p21.3 region of the human genome. Cytogenet. Cell Genet. 87:265- 268, 1999. 1 A c

GAM44 287 CX3CR1 Moatti, D.; Faure, S.; Fumeron, F.; Amara, M. E. W.; Seknadji,P.; McDermott, D. H.; Debre, P.; Aumont, M. C.; Murphy, P. M.; deProst, D.; Combadiere, C.: Polymorphism in the fractalkine receptorCX3CR1 as a genetic risk factor for coronary artery disease. Blood 97:1925- 1928, 2001. 1 A c

GAM44 287 CX3CR1 Raport, C. J.; Schweickart, V. L.; Eddy, R. L., Jr.; Shows, T.B.; Gray, P. W.: The orphan G- protein- coupled receptor- encoding geneV28 is closely related to genes for chemokine receptors and is expressedin lymphoid and neural tissues. Gene 163: 295- 299, 1995. 1 A c

GAM44 287 CX3CR1 Tripp, R. A.; Jones, L. P.; Haynes, L. M.; Zheng, H.; Murphy, P.M.; Anderson, L. J.: CX3C chemokine mimicry by respiratory syncytialvirus G glycoprotein. Nature Immun. 2: 732- 738, 2001. 1 A c

GAM44 287 DHCR24 Greeve, I.; Hermans- Borgmeyer, I.; Brellinger, C.; Kasper, D.;Gomez- Isla, T.; Behl, C.; Levkau, B.; Nitsch, R. M.: The human DIMINUTO/DWARF1homolog seladin- 1 confers resistance to Alzheimer's disease- associatedneurodegeneration and oxidative stress. J. Neurosci. 20: 7345- 1 A c

7352,2000.

GAM44 287 DHCR24 Nomura, N.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Kawarabayasi,Y.; Sato, S.; 1 A c
Nagase, T.; Seki, N.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. I. The codingsequences of 40 new
genes (KIAA0001- KIAA0040) deduced by analysisof randomly sampled cDNA
clones from human immature myeloid cell lineKG- 1. DNA Res. 1: 27- 35, 1994.

GAM44 287 DHCR24 Sarkar, D.; Imai, T.; Kambe, F.; Shibata, A.; Ohmori, S.; Siddiq,A.; 1 A c
Hayasaka, S.; Funahashi, H.; Seo, H.: The human homolog of
Diminuto/Dwarf1gene (hDiminuto): a novel ACTH- responsive gene overexpressed
in benigncortisol- producing adrenocortical adenomas. J. Clin. Endocr.
Metab. 86:5130- 5137, 2001.

GAM44 287 DHCR24 Waterham, H. R.; Koster, J.; Romeijn, G. J.; Hennekam, R. C. M.;Vreken, P.; 1 A c
Andersson, H. C.; FitzPatrick, D. R.; Kelley, R. I.; Wanders,R. J. A.:
Mutations in the 3- beta- hydroxysterol delta- 24- reductasegene cause
desmosterolosis, an autosomal recessive disorder of cholesterolbiosynthesis.
Am. J. Hum. Genet. 69: 685- 694, 2001.

GAM44 287 E2F3 Cloud, J. E.; Rogers, C.; Reza, T. L.; Ziebold, U.; Stone, J. R.;Picard, M. 1 A c
H.; Caron, A. M.; Bronson, R. T.; Lees, J. A.: Mutantmouse models reveal the
relative roles of E2F1 and E2F3 in vivo. Molec.Cell. Biol. 22: 2663- 2672,
2002.

GAM44 287 E2F3 He, Y.; Armanious, M. K.; Thomas, M. J.; Cress, W. D.: Identificationof E2F- 1 A c
3B, an alternative form of E2F- 3 lacking a conserved N- terminalregion.
Oncogene 19: 3422- 3433, 2000.

GAM44 287 E2F3 Lees, J. A.; Saito, M.; Vidal, M.; Valentine, M.; Look, T.; Harlow,E.; 1 A c
Dyson, N.; Helin, K.: The retinoblastoma protein binds to a familyof E2F
transcription factors. Molec. Cell. Biol. 13: 7813- 7825,1993.

GAM44 287 E2F3 Leone, G.; Sears, R.; Huang, E.; Rempel, R.; Nuckolls, F.; Park,C.- H.; 1 A c
Giangrande, P.; Wu, L.; Saavedra, H. I.; Field, S. J.; Thompson,M. A.; Yang,
H.; Fujiwara, Y.; Greenberg, M. E.; Orkin, S.; Smith,C.; Nevins, J. R.: Myc
requires distinct E2F activities to induceS phase and apoptosis. Molec. Cell
8: 105- 113, 2001.

GAM44 287 E2F3 Wu, L.; Timmers, C.; Maiti, B.; Saavedra, H. I.; Sang, L.; Chong,G. T.; 1 A c
Nuckolls, F.; Giangrande, P.; Wright, F. A.; Field, S. J.;Greenberg, M. E.;
Orkin, S.; Nevins, J. R.; Robinson, M. L.; Leone,G.: The E2F1- 3
transcription factors are essential for cellular proliferation. Nature
414:457- 462, 2001.

GAM44 287 FKBP2 Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.;Forbes, S. A.; 1 A c
Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B.T.; Farnebo, F.;
Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud,S.; Zhang, C. X.; Salandre,
J.; Calender, A.: Definition of the minimalMEN1 candidate area based on a 5-
Mb integrated map of proximal 11q13. Genomics 37:354- 365, 1996.

GAM44 287 FKBP2 DiLella, A. G.; Hawkins, A.; Craig, R. J.; Schreiber, S. L.; Griffin,C. A.: 1 A c
Chromosomal band assignments of the genes encoding human FKBP12and FKBP13.
Biochem. Biophys. Res. Commun. 189: 819- 823, 1992.

GAM44 287 FKBP2 Jin, Y. J.; Albers, M. W.; Lane, W. S.; Bierer, B. E.; Schreiber,S. L.; 1 A c
Burakoff, S. J.: Molecular cloning of a membrane- associatedhuman FK506-
and rapamycin- binding protein, FKBP- 13. Proc. Nat. Acad.Sci. 88: 6677-
6681, 1991.

GAM44 287 GPLD1 LeBoeuf, R. C.; Caldwell, M.; Guo, Y.; Metz, C.; Davitz, M. A.;Olson, L. K.; 1 A c
Deeg, M. A.: Mouse glycosylphosphatidylinositol- specificphospholipase D

(Gpld1) characterization. Mammalian Genome 9: 710- 714,1998.

GAM44 287 GPLD1 Scallon, B. J.; Fung, W.- J. C.; Tsang, T. C.; Li, S.; Kado- Fong,H.; Huang, K.- S.; Kochan, J. P.: Primary structure and functionalactivity of a phosphatidylinositol- glycan- specific phospholipase D. Science 252:446-448, 1991. 1 A c

GAM44 287 GPLD1 Schofield, J. N.; Rademacher, T. W.: Structure and expressionof the human glycosylphosphatidylinositol phospholipase D1 (GPLD1)gene. Biochim. Biophys. Acta 1494: 189- 194, 2000. 1 A c

GAM44 287 GPLD1 Tsang, T. C.; Fung, W.- J.; Levine, J.; Metz, C. N.; Davitz, M.A.; Burns, D. K.; Huang, K.- S.; Kochan, J. P.: Isolation and expressionof two human glycosylphosphatidylinositol phospholipase D (GPI- PLD)cDNAs. (Abstract) FASEB J. (supp.) 6: A1922 only, 1992. 1 A c

GAM44 287 HOXB7 Acampora, D.; D'Esposito, M.; Faiella, A.; Pannese, M.; Migliaccio,E.; Morelli, F.; Stornaiuolo, A.; Nigro, V.; Simeone, A.; Boncinelli,E.: The human HOX gene family. Nucleic Acids Res. 17: 10385- 10402,1989. 1 A c

GAM44 287 HOXB7 Lill, M. C.; Fuller, J. F.; Herzig, R.; Crooks, G. M.; Gasson,J. C.: The role of the homeobox gene, HOX B7, in human myelomonocyticdifferentiation. Blood 85: 692- 697, 1995. 1 A c

GAM44 287 HOXB7 Simeone, A.; Mavilio, F.; Acampora, D.; Giampaolo, A.; Faiella,A.; Zappavigna, V.; D'Esposito, M.; Pannese, M.; Russo, G.; Boncinelli,E.; Peschle, C.: Two human homeobox genes, c1 and c8: structure analysisand expression in embryonic development. Proc. Nat. Acad. Sci. 84:4914- 4918, 1987. 1 A c

GAM44 287 HOXB7 Yaron, Y.; McAdara, J. K.; Lynch, M.; Hughes, E.; Gasson, J. C.: Identification of novel functional regions important for the activityof HOXB7 in mammalian cells. J. Immun. 166: 5058- 5067, 2001. 1 A c

GAM44 287 IGF2R Acquati, F.; Malgaretti, N.; Hauptschein, R.; Rao, P.; Gaidano,G.; Taramelli, R.: A 2- Mb YAC contig linking the plasminogen- apoprotein(a)gene family to the insulin- like growth factor 2 receptor (IGF2R) geneon the telomeric region of chromosome 6 (6q26- q27). Genomics 22:664- 666, 1994. 1 A c

GAM44 287 IGF2R Barlow, D. P.; Stoger, R.; Herrmann, B. G.; Saito, K.; Schweifer,N.: The mouse insulin- like growth factor type- 2 receptor is imprintedand closely linked to the Tme locus. Nature 349: 84- 87, 1991. 1 A c

GAM44 287 IGF2R De Souza, A. T.; Hankins, G. R.; Washington, M. K.; Fine, R. L.;Orton, T. C.; Jirtle, R. L.: Frequent loss of heterozygosity on 6qat the mannose 6-phosphate/insulin- like growth factor II receptorlocus in human hepatocellular tumors. Oncogene 10: 1725- 1729, 1995. 1 A c

GAM44 287 IGF2R De Souza, A. T.; Hankins, G. R.; Washington, M. K.; Orton, T. C.;Jirtle, R. L.: M6P/IGF2R gene is mutated in human hepatocellularcarcinomas with loss of heterozygosity. Nature Genet. 11: 447- 449,1995. 1 A c

GAM44 287 IGF2R DeChiara, T. M.; Robertson, E. J.; Efstratiadis, A.: Parentalimprinting of the mouse insulin- like growth factor II gene. Cell 64:849- 859, 1991. 1 A c

GAM44 287 IGF2R Feinberg, A. P.: Genomic imprinting and gene activation in cancer. NatureGenet. 4: 110- 113, 1993. 1 A c

GAM44 287 IGF2R Haig, D.; Graham, C.: Genomic imprinting and the strange caseof the insulin- like growth factor II receptor. Cell 64: 1045- 1046,1991. 1 A c

GAM44 287 IGF2R Haig, D.; Westoby, M.: Parent- specific gene expression and thetriploid endosperm. Am. Nat. 134: 147- 155, 1989. 1 A c

GAM44 287 IGF2R Kalscheuer, V. M.; Mariman, E. C.; Schepens, M. T.; Rehder, H.;Ropers, H.- H.: The insulin- like- growth factor type- 2 receptor geneis imprinted in 1 A c

the mouse but not in humans. Nature Genet. 5: 74- 78,1993.

GAM44 287 IGF2R Kiess, W.; Blickenstaff, G. D.; Sklar, M. M.; Thomas, C. L.; Nissley,S. P.; 1 A c
Sahagian, G. G.: Biochemical evidence that the type II insulin- likegrowth
factor receptor is identical to the cation- independent mannose6- phosphate
receptor. J. Biol. Chem. 263: 9339- 9344, 1988.

GAM44 287 IGF2R Killian, J. K.; Oka, Y.; Jang, H.- S.; Fu, X.; Waterland, R. A.;Sohda, T.; 1 A c
Sakaguchi, S.; Jirtle, R. L.: Mannose 6- phosphate/insulin- likegrowth
factor 2 receptor (M6P/IGF2R) variants in American and Japanesepopulations.
Hum. Mutat. 18: 25- 31, 2001.

GAM44 287 IGF2R Kornfeld, S.; Mellman, I.: The biogenesis of lysosomes. Annu.Rev. Cell Biol. 1 A c
5: 483- 525, 1989.

GAM44 287 IGF2R Lau, M. M. H.; Stewart, C. E. H.; Liu, Z.; Bhatt, H.; Rotwein,P.; Stewart, 1 A c
C. L.: Loss of the imprinted IGF2/cation- independentmannose 6- phosphate
receptor results in fetal overgrowth and perinatallethality. Genes Dev. 8:
2953- 2963, 1994.

GAM44 287 IGF2R Laureys, G.; Barton, D. E.; Ullrich, A.; Francke, U.: Chromosomalmapping of 1 A c
the gene for the type II insulin- like growth factor receptor/cation-
independentmannose 6- phosphate receptor in man and mouse. Genomics 3: 224-
229,1988.

GAM44 287 IGF2R MacDonald, R. G.; Pfeffer, S. R.; Coussens, L.; Tepper, M. A.;Brocklebank, 1 A c
C. M.; Mole, J. E.; Anderson, J. K.: A single receptorbinds both insulin-
like growth factor II and mannose- 6- phosphate. Science 239:1134- 1137,
1988.

GAM44 287 IGF2R Morgan, D. O.; Edman, J. D.; Standring, D. N.; Fried, V. A.; Smith,M. C.; 1 A c
Roth, R. A.; Rutter, W. J.: Insulin- like growth factor IIreceptor as a
multifunctional binding protein. Nature 329: 301- 307,1987.

GAM44 287 IGF2R Motyka, B.; Korbutt, G.; Pinkoski, M. J.; Heibein, J. A.; Caputo,A.; Hobman, 1 A c
M.; Barry, M.; Shostak, I.; Sawchuk, T.; Holmes, C. F.B.; Gauldie, J.;
Bleackley, R. C.: Mannose 6- phosphate/insulin- likegrowth factor II
receptor is a death receptor for granzyme B duringcytotoxic T cell- induced
apoptosis. Cell 103: 491- 500, 2000.

GAM44 287 IGF2R Ogawa, O.; McNoe, L. A.; Eccles, M. R.; Morison, I. M.; Reeve,A. E.: Human 1 A c
insulin- like growth factor type I and type II receptorsare not imprinted.
Hum. Molec. Genet. 2: 2163- 2165, 1993.

GAM44 287 IGF2R Oshima, A.; Nolan, C. M.; Kyle, J. W.; Grubb, J. H.; Sly, W. S.: The human 1 A c
cation- independent mannose 6- phosphate receptor: cloningand sequence of
the full- length cDNA and expression of functionalreceptor in COS cells. J.
Biol. Chem. 263: 2553- 2562, 1988.

GAM44 287 IGF2R Puertollano, R.; Aguilar, R. C.; Gorshkova, I.; Crouch, R. J.;Bonifacino, J. 1 A c
S.: Sorting of mannose 6- phosphate receptors mediatedby the GGAs. Science
292: 1712- 1716, 2001.

GAM44 287 IGF2R Rao, P. H.; Murty, V. V. V. S.; Gaidano, G.; Hauptschein, R.;Dalla- Favera, 1 A c
R.; Chaganti, R. S. K.: Subregional mapping of 8 singlecopy loci to
chromosome 6 by fluorescence in situ hybridization. Cytogenet.Cell Genet.
66: 272- 273, 1994.

GAM44 287 IGF2R Roth, R. A.: Structure of the receptor for insulin- like growthfactor II: 1 A c
the puzzle amplified. Science 239: 1269- 1271, 1988.

GAM44 287 IGF2R Sleutels, F.; Zwart, R.; Barlow, D. P.: The non- coding Air RNAis required 1 A c
for silencing autosomal imprinted genes. Nature 415:810- 813, 2002.

GAM44 287 IGF2R Souza, R. F.; Appel, R.; Yin, J.; Wang, S.; Smolinski, K. N.;Abraham, J. M.; 1 A c

Zou, T.- T.; Shi, Y.- Q.; Lei, J.; Cottrell, J.; Cymes,K.; Biden, K.; Simms, L.; Leggett, B.; Lynch, P. M.; Frazier, M.;Powell, S. M.; Harpaz, N.; Sugimura, H.; Young, J.; Meltzer, S. J.: Microsatellite instability in the insulin- like growth factor IIreceptor gene in gastrointestinal tumours. (Letter) Nature Genet. 14:255- 257, 1996.

GAM44 287 IGF2R Szebeny, G.; Rotwein, P.: The mouse insulin- like growth factorII/cation- 1 A c
independent mannose 6- phosphate (IGF- II/MPR) receptor gene:molecular cloning and genomic organization. Genomics 19: 120- 129,1994.

GAM44 287 IGF2R Tong, P. Y.; Tollefsen, S. E.; Kornfeld, S.: The cation- independentmannose 1 A c
6- phosphate receptor binds insulin- like growth factor II. J.Biol. Chem. 263: 2585- 2588, 1988.

GAM44 287 IGF2R Waheed, A.; Braulke, T.; Junghans, U.; von Figura, K.: Mannose6- 1 A c
phosphate/insulin like growth factor II receptor: the two typesof ligands bind simultaneously to one receptor at different sites. Biochem.Biophys. Res. Commun. 152: 1248- 1254, 1988.

GAM44 287 IGF2R Xu, Y.; Goodyer, C. G.; Deal, C.; Polychronakos, C.: Functionalpolymorphism 1 A c
in the parental imprinting of the human IGF2R gene. Biochem.Biophys. Res. Commun. 197: 747- 754, 1993.

GAM44 287 IGF2R Young, L. E.; Fernandes, K.; McEvoy, T. G.; Butterwith, S. C.;Gutierrez, C. 1 A c
G.; Carolan, C.; Broadbent, P. J.; Robinson, J. J.;Wilmut, I.; Sinclair, K. D.: Epigenetic change in IGF2R is associatedwith fetal overgrowth after sheep embryo culture. Nature Genet. 27:153- 154, 2001.

GAM44 287 IGF2R Zhu, Y.; Doray, B.; Poussu, A.; Lehto, V.- P.; Kornfeld, S.: Bindingof GGA2 1 A c
to the lysosomal enzyme sorting motif of the mannose 6- phosphatereceptor. Science 292: 1716- 1718, 2001.

GAM44 287 IMMP2L Boghosian- Sell, L.; Comings, D. E.; Overhauser, J.: Tourette syndromein a 1 A c
pedigree with a 7;18 translocation: identification of a YAC spanningthe translocation breakpoint at 18q22.3. Am. J. Hum. Genet. 59:999- 1005, 1996.

GAM44 287 IMMP2L Petek, E.; Windpassinger, C.; Vincent, J. B.; Cheung, J.; Boright,A. P.; 1 A c
Scherer, S. W.; Kroisel, P. M.; Wagner, K.: Disruption ofa novel gene (IMMP2L) by a breakpoint in 7q31 associated with Tourettesyndrome. Am. J. Hum. Genet. 848- 858, 2001.

GAM44 287 ITK Cheng, G.; Ye, Z.- S.; Baltimore, D.: Binding of Bruton's tyrosinekinase to 1 A c
Fyn, Lyn, or Hck through a Src homology 3 domain- mediatedinteraction. Proc. Nat. Acad. Sci. 91: 8152- 8155, 1994.

GAM44 287 ITK Gibson, S.; Leung, B.; Squire, J. A.; Hill, M.; Arima, N.; Goss,P.; Hogg, 1 A c
D.; Mills, G. B.: Identification, cloning, and characterizationof a novel human T- cell- specific tyrosine kinase located at the hematopoietincomplex on chromosome 5q. Blood 82: 1561- 1572, 1993.

GAM44 287 ITK Janis, E. M.; Siliciano, J. D.; Isaac, D. D.; Griffin, C. A.; Hawkins,A. L.; 1 A c
Kozak, C. A.; Desiderio, S.: Mapping of the gene for the tyrosinekinase Itk to a region of conserved synteny between mouse chromosome11 and human chromosome 5q. Genomics 23: 269- 271, 1994.

GAM44 287 ITK Schaeffer, E. M.; Debnath, J.; Yap, G.; McVicar, D.; Liao, X. C.;Littman, D. 1 A c
R.; Sher, A.; Varmus, H. E.; Lenardo, M. J.; Schwartzberg,P. L.: Requirement for Tec kinases Rlk and Itk in T cell receptorsignaling and immunity. Science 284: 638- 641, 1999.

GAM44 287 ITK Woods, M. L.; Kivens, W. J.; Adelsman, M. A.; Qiu, Y.; August,A.; Shimizu, 1 A c
Y.: A novel function for the Tec family tyrosine kinaseItk in activation of beta- 1 integrins by the T- cell receptor. EMBOJ. 20: 1232- 1244, 2001.

GAM44 287 LARGE Grewal, P. K.; Holzfeind, P. J.; Bittner, R. E.; Hewitt, J. E.: Mutant glycosyltransferase and altered glycosylation of alpha- dystroglycanin the myodystrophy mouse. Nature Genet. 28: 151- 154, 2001. 1 A c

GAM44 287 LARGE Michele, D. E.; Barresi, R.; Kanagawa, M.; Saito, F.; Cohn, R.D.; Satz, J. S.; Dollar, J.; Nishino, I.; Kelley, R. I.; Somer, H.;Straub, V.; Mathews, K. D.; Moore, S. A.; Campbell, K. P.: Post- translationaldisruption of dystroglycan- ligand interactions in congenital musculardystrophies. Nature 418: 417- 422, 2002. 1 A c

GAM44 287 LARGE Peyrard, M.; Seroussi, E.; Sandberg- Nordqvist, A.- C.; Xie, Y.- G.;Han, F.- Y.; Fransson, I.; Collins, J.; Dunham, I.; Kost- Alimova, M.;Imreh, S.; Dumanski, J. P.: The human LARGE gene from 22q12.3- q13.1is a new, distinct member of the glycosyltransferase gene family. Proc.Nat. Acad. Sci. 96: 598- 603, 1999. 1 A c

GAM44 287 LTA Aggarwal, B. B.; Eessalu, T. E.; Hass, P. E.: Characterizationof receptors for human tumour necrosis factor and their regulationby gamma- interferon. Nature 318: 665- 667, 1985. 1 A c

GAM44 287 LTA Evans, A. M.; Petersen, J. W.; Sekhon, G. S.; DeMars, R.: Mappingof prolactin and tumor necrosis factor- beta genes on human chromosome6p using lymphoblastoid cell deletion mutants. Somat. Cell Molec.Genet. 15: 203- 213, 1989. 1 A c

GAM44 287 LTA Gray, P. W.; Aggarwal, B. B.; Benton, C. V.; Bringman, T. S.; Henzel,W. J.; Jarrett, J. A.; Leung, D. W.; Moffat, B.; Ng, P.; Svedersky,L. P.; Palladino, M. A.; Nedwin, G. E.: Cloning and expression ofcDNA for human lymphotoxin, a lymphokine with tumour necrosis activity. Nature 312:721- 724, 1984. 1 A c

GAM44 287 LTA Jongeneel, C. V.; Briant, L.; Udalova, I. A.; Sevin, A.; Nedospasov,S. A.; Cambon- Thomsen, A.: Extensive genetic polymorphism in thehuman tumor necrosis factor region and relation to extended HLA haplotypes. Proc.Nat. Acad. Sci. 88: 9717- 9721, 1991. 1 A c

GAM44 287 LTA Koss, K.; Satsangi, J.; Fanning, G. C.; Welsh, K. I.; Jewell, D.P.: Cytokine (TNF- alpha, LT- alpha, and IL- 10) polymorphisms in inflammatorybowel diseases and normal controls: differential effects on productionand allele frequencies. Genes Immun. 1: 185- 190, 2000. 1 A c

GAM44 287 LTA Spies, T.; Blanck, G.; Bresnahan, M.; Sands, J.; Strominger, J.L.: A new cluster of genes within the human major histocompatibilitycomplex. Science 243: 214- 217, 1989. 1 A c

GAM44 287 MEIS1 Mercader, N.; Leonardo, E.; Azpiazu, N.; Serrano, A.; Morata, G.;Martinez- A, C.; Torres, M.: Conserved regulation of proximodistallimb axis development by Meis1/Hth. Nature 402: 425- 429, 1999. 1 A c

GAM44 287 MEIS1 Moskow, J. J.; Bullrich, F.; Huebner, K.; Daar, I. O.; Buchberg,A. M.: Meis1, a PBX1- related homeobox gene involved in myeloid leukemiain BXH- 2 mice. Molec. Cell. Biol. 15: 5434- 5443, 1995. 1 A c

GAM44 287 MEIS1 Steelman, S.; Moskow, J. J.; Muzynski, K.; North, C.; Druck, T.;Montgomery, J. C.; Huebner, K.; Daar, I. O.; Buchberg, A. M.: Identificationof a conserved family of Meis1- related homeobox genes. Genome Res. 7:142- 156, 1997. 1 A c

GAM44 287 MEIS1 Thorsteinsdottir, U.; Kroon, E.; Jerome, L.; Blasi, F.; Sauvageau,G.: Defining roles for HOX and MEIS1 genes in induction of acutemyeloid leukemia. Molec. Cell. Biol. 21: 224- 234, 2001. 1 A c

GAM44 287 MFAP2 Chen, Y.; Faraco, J.; Yin, W.; Germiller, J.; Francke, U.; Bonadio,J.: 1 A c

Structure, chromosomal localization, and expression pattern ofthe murine Magp gene. J. Biol. Chem. 268: 27381- 27389, 1993.

GAM44 287 MFAP2 Faraco, J.; Bashir, M.; Rosenbloom, J.; Francke, U.: Characterizationof the human gene for microfibril- associated glycoprotein (MFAP2),assignment to chromosome 1p36.1- p35, and linkage to D1S170. Genomics 25:630- 637, 1995. 1 A c

GAM44 287 MFAP2 Gibson, M. A.; Hughes, J. L.; Fanning, J. C.; Cleary, E. G.: Themajor antigen of elastin- associated microfibrils is a 31- kDa glycoprotein.J. Biol. Chem. 261: 11429- 11436, 1986. 1 A c

GAM44 287 MFAP2 Low, F. N.: Microfibrils: fine filamentous components of the tissuespace. Anat. Rec. 142: 131- 137, 1962. 1 A c

GAM44 287 NEK6 Kimura, M.; Okano, Y.: Identification and assignment of the humanNIMA- related protein kinase 7 gene (NEK7) to human chromosome 1q31.3. Cytogenet.Cell Genet. 94: 33- 38, 2001. 1 A c

GAM44 287 NEK6 Li, M. Z.; Yu, L.; Liu, Q.; Chu, J. Y.; Zhao, S. Y.: Assignmentof NEK6, a NIMA- related gene, to human chromosome 9q33.3- q34.11 byradiation hybrid mapping. Cytogenet. Cell Genet. 87: 271- 272, 1999. 1 A c

GAM44 287 PDE5A Loughney, K.; Hill, T. R.; Florio, V. A.; Uher, L.; Rosman, G.J.; Wolda, S. L.; Jones, B. A.; Howard, M. L.; McAllister- Lucas, L.M.; Sonnenburg, W. K.; Francis, S. H.; Corbin, J. D.; Beavo, J. A.;Ferguson, K.: Isolation and characterization of cDNAs encoding PDE5A,a human cGMP- binding, cGMP- specific 3- prime,5- prime- cyclic nucleotidephosphodiesterase. Gene 216: 139- 147, 1998. 1 A c

GAM44 287 PDE5A Stacey, P.; Rulten, S.; Dapling, A.; Phillips, S. C.: Molecularcloning and expression of human cGMP- binding cGMP- specific phosphodiesterase(PDE5). Biochem. Biophys. Res. Commun. 247: 249- 254, 1998. 1 A c

GAM44 287 PDE5A Yanaka, N.; Kotera, J.; Ohtsuka, A.; Akatsuka, H.; Imai, Y.; Michibata,H.; Fujishige, K.; Kawai, E.; Takebayashi, S.- I.; Okumura, K.; Omori,K.: Expression, structure and chromosomal localization of the humancGMP- binding cGMP- specific phosphodiesterase PDE5A gene. Eur. J.Biochem. 255: 391- 399, 1998. 1 A c

GAM44 287 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 2002. 1 A c

GAM44 287 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- cell coactivator of octamer- binding transcription factors. Nature 373:360- 362, 1995. 1 A c

GAM44 287 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell- specific coactivator of octamer- binding transcription factors1 and 2, to 11q23.1 by somatic cell hybridization and in situ hybridization. Genomics 33:143- 145, 1996. 1 A c

GAM44 287 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995. 1 A c

GAM44 287 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001. 1 A c

GAM44 287 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. Immun. 9: 373- 398, 1991. 1 A c

GAM44 287 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 1 A c
specificcoactivator that stimulates immunoglobulin promoter activity
throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM44 287 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 1 A c
Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B,
BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-
864, 2000.

GAM44 287 PPP1R3A Chen, Y. H.; Hansen, L.; Chen, M. X.; Bjorbaek, C.; Vestergaard,H.; Hansen, 1 A c
T.; Cohen, P. T. W.; Pedersen, O.: Sequence of the humanglycogen- associated
regulatory subunit of type 1 protein phosphataseand analysis of its coding
region and mRNA level in muscle from patientswith NIDDM. Diabetes 43: 1234-
1241, 1994.

GAM44 287 PPP1R3A Hansen, L.; Hansen, T.; Vestergaard, H.; Bjorbaek, C.; Echwald,S. M.; 1 A c
Clausen, J. O.; Chen, Y. H.; Chen, M. X.; Cohen, P. T. W.;Pedersen, O.: A
widespread amino acid polymorphism at codon 905 ofthe glycogen- associated
regulatory subunit of protein phosphatase- 1is associated with insulin
resistance and hypersecretion of insulin. Hum.Molec. Genet. 4: 1313- 1320,
1995.

GAM44 287 PPP1R3A Hegele, R. A.; Harris, S. B.; Zinman, B.; Wang, J.; Cao, H.; Hanley,A. J. 1 A c
G.; Tsui, L.- C.; Scherer, S. W.: Variation in the AU(AT)- richelement
within the 3- prime- untranslated region of PPP1R3 is associatedwith
variation in plasma glucose in aboriginal Canadians. J. Clin.Endocr. Metab.
83: 3980- 3983, 1998.

GAM44 287 PPP1R3A Savage, D. B.; Agostini, M.; Barroso, I.; Gurnell, M.; Luan, J.;Meirhaeghe, 1 A c
A.; Harding, A.- H.; Ihrke, G.; Rajanayagam, O.; Soos,M. A.; George, S.;
Berger, D.; and 9 others: Digenic inheritanceof severe insulin resistance in
a human pedigree. Nature Genet. 31:379- 384, 2002.

GAM44 287 PPP1R3A Tang, P. M.; Bondor, J. A.; Swiderek, K. M.; DePaoli- Roach, A.A.: Molecular 1 A c
cloning and expression of the regulatory (RG1) subunitof the glycogen-
associated protein phosphatase. J. Biol. Chem. 266:15782- 15789, 1991.

GAM44 287 PRDM2 Buyse, I. M.; Shao, G.; Huang, S.: The retinoblastoma proteinbinds to RIZ, a 1 A c
zinc- finger protein that shares an epitope with theadenovirus E1A protein.
Proc. Nat. Acad. Sci. 92: 4467- 4471, 1995.

GAM44 287 PRDM2 Buyse, I. M.; Takahashi, E.; Huang, S.: Physical mapping of 1 A c
theretinoblastoma interacting zinc finger gene RIZ to D1S228 on
chromosome1p36. Genomics 34: 119- 121, 1996.

GAM44 287 PRDM2 Chadwick, R. B.; Jiang, G.- L.; Bennington, G. A.; Yuan, B.; Johnson,C. K.; 1 A c
Stevens, M. W.; Niemann, T. H.; Peltomaki, P.; Huang, S.; dela Chapelle, A.:
Candidate tumor suppressor RIZ is frequently involvedin colorectal
carcinogenesis. Proc. Nat. Acad. Sci. 97: 2662- 2667,2000.

GAM44 287 PRDM2 Mock, B. A.; Coleman, M. P.; Huang, S.: Riz maps to distal chromosome4 near 1 A c
genes involved in tumorigenesis and nerve degeneration. MammalianGenome 7:
637 only, 1996.

GAM44 287 PRDM2 Poetsch, M.; Dittberner, T.; Woenckhaus, C.: Frameshift mutationsof RIZ, but 1 A c
no point mutations in RIZ1 exons in malignant melanomaswith deletions in
1p36. Oncogene 21: 3038- 3042, 2002.

GAM44 287 PYCR1 Dougherty, K. M.; Brandriss, M. C.; Valle, D.: Cloning human pyrroline- 5- 1 A c
carboxylatereductase cDNA by complementation in Saccharomyces cerevisiae.
J.Biol. Chem. 267: 871- 875, 1992.

GAM44 287 PYCR1 Merrill, M. J.; Yeh, G. C.; Phang, J. M.: Purified human 1 A c

erythrocytepyrroline- 5- carboxylate reductase: preferential oxidation of NADPH. J.Biol. Chem. 264: 9352- 9358, 1989.

GAM44 287 RASGRP2 Kawasaki, H.; Springett, G. M.; Toki, S.; Canales, J. J.; Harlan,P.; Blumenstiel, J. P.; Chen, E. J.; Bany, I. A.; Mochizuki, N.; Ashbacher,A.; Matsuda, M.; Housman, D. E.; Graybiel, A. M.: A Rap guanine nucleotideexchange factor enriched highly in the basal ganglia. Proc. Nat.Acad. Sci. 95: 13278- 13283, 1998. 1 A c

GAM44 287 RASGRP2 Kedra, D.; Seroussi, E.; Fransson, I.; Trifunovic, J.; Clark, M.;Lagercrantz, J.; Blennow, E.; Mehlin, H.; Dumanski, J.: The germinalcenter kinase gene and a novel CDC25- like gene are located in thevicinity of the PYGM gene on 11q13. Hum. Genet. 100: 611- 619, 1997. 1 A c

GAM44 287 RING1 Kikuti, Y. Y.; Tamiya, G.; Ando, A.; Chen, L.; Kimura, M.; Ferreira,E.; Tsuji, K.; Trowsdale, J.; Inoko, H.: Physical mapping 220 kbcentromeric of the human MHC and DNA sequence analysis of the 43- kbsegment including the RING1, HKE6, and HKE4 genes. Genomics 42:422- 435, 1997. 1 A c

GAM44 287 RING1 Lovering, R.; Hanson, I. M.; Borden, K. L. B.; Martin, S.; O'Reilly,N. J.; Evan, G. I.; Rahman, D.; Pappin, D. J. C.; Trowsdale, J.; Freemont,P. S.: Identification and preliminary characterization of a proteinmotif related to the zinc finger. Proc. Nat. Acad. Sci. 90: 2112- 2116,1993. 1 A c

GAM44 287 RING1 Satijn, D. P. E.; Gunster, M. J.; van der Vlag, J.; Hamer, K. M.;Schul, W.; Alkema, M. J.; Saurin, A. J.; Freemont, P. S.; van Driel,R.; Otte, A. P.: RING1 is associated with the polycomb group proteincomplex and acts as a transcriptional repressor. Molec. Cell. Biol. 17:4105- 4113, 1997. 1 A c

GAM44 287 SFRS2IP Tanner, S.; Stagljar, I.; Georgiev, O.; Schaffner, W.; Bourquin,J.- P.: A novel SR- related protein specifically interacts with thecarboxy- terminal domain (CTD) of RNA polymerase II through a conservedinteraction domain. Biol. Chem. 378: 565- 571, 1997. 1 A c

GAM44 287 SFRS2IP Zhang, W.- J.; Wu, J. Y.: Sip1, a novel RS domain- containing proteinessential for pre- mRNA splicing. Molec. Cell. Biol. 18: 676- 684,1998. 1 A c

GAM44 287 SOX4 Critcher, R.; Stitson, R. N. M.; Wade- Martins, R.; Easty, D. J.;Farr, C. J.: Assignment of Sox4 to mouse chromosome 13 bands A3- A5by fluorescence in situ hybridization; refinement of the human SOX4location to 6p22.3 and of SOX20 to chromosome 17p12.3. Cytogenet.Cell Genet. 81: 294- 295, 1998. 1 A c

GAM44 287 SOX4 Denny, P.; Swift, S.; Connor, F.; Ashworth, A.: An SRY- relatedgene expressed during spermatogenesis in the mouse encodes a sequence- specificDNA- binding protein. EMBO J. 11: 3705- 3712, 1992. 1 A c

GAM44 287 SOX4 Farr, C. J.; Easty, D. J.; Ragoussis, J.; Collignon, J.; Lovell- Badge,R.; Goodfellow, P. N.: Characterization and mapping of the humanSOX4 gene. Mammalian Genome 4: 577- 584, 1993. 1 A c

GAM44 287 SOX4 Geijsen, N.; Uings, I. J.; Pals, C.; Armstrong, J.; McKinnon, M.;Raaijmakers, J. A. M.; Lammers, J.- W. J.; Koenderman, L.; Coffer,P. J.: Cytokine- specific transcriptional regulation through an IL- 5R- alphainteracting protein. Science 293: 1136- 1138, 2001. 1 A c

GAM44 287 SOX4 Hansen, G. M.; Skapura, D.; Justice, M. J.: Genetic profile ofinsertion mutations in mouse leukemias and lymphomas. Genome Res. 10:237- 243, 2000. 1 A c

GAM44 287 SOX4 Li, J.; et al; et al: Leukaemia disease genes: large- scale cloningand pathway predictions. Nature Genet. 23: 348- 353, 1999. 1 A c

GAM44 287 SOX4 Lund, A. H.; Turner, G.; Trubetskoy, A.; Verhoeven, E.; Wientjens,E.; Hulsman, D.; Russell, R.; DePinho, R. A.; Lenz, J.; van Lohuizen,M.: Genome- 1 A c

wide retroviral insertional tagging of genes involvedin cancer in Cdkn2a-deficient mice. Nature Genet. 32: 160- 165, 2002.

GAM44 287 SOX4 Suzuki, T.; Shen, H.; Akagi, K.; Morse, H. C., III; Malley, J.D.; Naiman, D. Q.; Jenkins, N. A.; Copeland, N. G.: New genes involvedin cancer identified by retroviral tagging. Nature Genet. 32: 166- 174,2002. Note: Erratum: Nature Genet. 32: 331 only, 2002. 1 A c

GAM44 287 SOX4 van de Wetering, M.; Oosterwegel, M.; van Norren, K.; Clevers,H.: Sox- 4, an Sry- like HMG box protein, is a transcriptional activatoris lymphocytes. EMBO J. 12: 3847- 3854, 1993. 1 A c

GAM44 287 SSA1 Frank, M. B.; Itoh, K.; Fujisaku, A.; Pontarotti, P.; Mattei, M.- G.;Neas, B. R.: The mapping of the human 52- kD Ro/SSA autoantigen geneto human chromosome 11, and its polymorphisms. Am. J. Hum. Genet. 52:183- 191, 1993. 1 A c

GAM44 287 SSA1 Frank, M. B.; Mattei, M.- G.: Mapping of the human 60000 M(r) Ro/SSAlocus: the genes for three Ro/SSA autoantigens are located on separatechromosomes. Immunogenetics 39: 428- 431, 1994. 1 A c

GAM44 287 SSA1 Itoh, K.; Itoh, Y.; Frank, M. B.: Protein heterogeneity in thehuman Ro/SSA ribonucleoproteins: the 52- and 60- kD Ro/SSA autoantigensare encoded by separate genes. J. Clin. Invest. 87: 177- 186, 1991. 1 A c

GAM44 287 SSA1 Schoenlebe, J.; Buyon, J. P.; Zitelli, B. J.; Friedman, D.; Greco,M. A.; Knisely, A. S.: Neonatal hemochromatosis associated with maternalautoantibodies against Ro/SS- A and La/SS- B ribonucleoproteins. Am.J. Dis. Child. 147: 1072- 1075, 1993. 1 A c

GAM44 287 STAT1 Chen, X.; Vinkemeier, U.; Zhao, Y.; Jeruzalmi, D.; Darnell, J.E., Jr.; Kuriyan, J.: Crystal structure of a tyrosine phosphorylatedSTAT- 1 dimer bound to DNA. Cell 93: 827- 839, 1998. 1 A c

GAM44 287 STAT1 Copeland, N. G.; Gilbert, D. J.; Schindler, C.; Zhong, Z.; Wen,Z.; Darnell, J. E., Jr.; Mui, A. L.- F.; Miyajima, A.; Quelle, F. W.;Ihle, J. N.; Jenkins, N. A.: Distribution of the mammalian Stat genefamily in mouse chromosomes. Genomics 29: 225- 228, 1995. 1 A c

GAM44 287 STAT1 Darnell, J. E., Jr.; Kerr, I. M.; Stark, G. M.: Jak- STAT pathwaysand transcriptional activation in response to IFNs and other extracellularsignaling proteins. Science 264: 1415- 1421, 1994. 1 A c

GAM44 287 STAT1 Dupuis, S.; Dargemont, C.; Fieschi, C.; Thomassin, N.; Rosenzweig,S.; Harris, J.; Holland, S. M.; Schreiber, R. D.; Casanova, J.- L.: Impairment of mycobacterial but not viral immunity by a germlinehuman STAT1 mutation. Science 293: 300- 303, 2001. 1 A c

GAM44 287 STAT1 Durbin, J. E.; Hackenmiller, R.; Simon, M. C.; Levy, D. E.: Targeteddisruption of the mouse Stat1 gene results in compromised innate immunityto viral disease. Cell 84: 443- 450, 1996. 1 A c

GAM44 287 STAT1 Haddad, B.; Pabon- Pena, C. R.; Young, H.; Sun, W. H.: Assignmentof STAT1 to human chromosome 2q32 by FISH and radiation hybrids. Cytogenet.Cell Genet. 83: 58- 59, 1998. 1 A c

GAM44 287 STAT1 Ihle, J. N.: Cytokine receptor signalling. Nature 377: 591- 594,1995. 1 A c

GAM44 287 STAT1 Ihle, J. N.: STATs: signal transducers and activators of transcription. Cell 84:331- 334, 1996. 1 A c

GAM44 287 STAT1 Ihle, J. N.; Kerr, I. M.: Jaks and Stats in signaling by the cytokinereceptor superfamily. Trends Genet. 11: 69- 74, 1995. 1 A c

GAM44 287 STAT1 Kaplan, D. H.; Shankaran, V.; Dighe, A. S.; Stockert, E.; Aguet,M.; Old, L. J.; Schreiber, R. D.: Demonstration of an interferongamma- dependent tumor surveillance system in immunocompetent mice. Proc.Nat. Acad. Sci. 95: 7556- 1 A c

7561, 1998.

GAM44 287 STAT1 Meraz, M. A.; White, J. M.; Sheehan, K. C. F.; Bach, E. A.; Rodig,S. J.; Dighe, A. S.; Kaplan, D. H.; Riley, J. K.; Greenlund, A. C.Campbell, D.; Carver- Moore, K.; DuBois, R. N.; Clark, R.; Aguet, M.;Schreiber, R. D.: Targeted disruption of the Stat1 gene in mice revealsunexpected physiologic specificity in the JAK- STAT signaling pathway. Cell 84:431- 442, 1996. 1 A c

GAM44 287 STAT1 Mowen, K. A.; Tang, J.; Zhu, W.; Schurter, B. T.; Shuai, K.; Herschman,H. R.; David, M.: Arginine methylation of STAT1 modulates IFN- alpha/beta- inducedtranscription. Cell 104: 731- 741, 2001. 1 A c

GAM44 287 STAT1 Ramana, C. V.; Chatterjee- Kishore, M.; Nguyen, H.; Stark, G. R.: Complex roles of Stat1 in regulating gene expression. Oncogene 19:2619- 2627, 2000. 1 A c

GAM44 287 STAT1 Schindler, C.; Fu, X.- Y.; Improta, T.; Aebersold, R.; Darnell,J. E., Jr.: Proteins of transcription factor ISGF- 3: one gene encodesthe 91- and 84- kDa ISGF- 3 proteins that are activated by interferonalpha. Proc. Nat. Acad. Sci. 89: 7836- 7839, 1992. 1 A c

GAM44 287 STAT1 Shankaran, V.; Ikeda, H.; Bruce, A. T.; White, J. M.; Swanson,P. E.; Old, L. J.; Schreiber, R. D.: IFN- gamma and lymphocytes preventprimary tumour development and shape tumour immunogenicity. Nature 410:1107- 1111, 2001. 1 A c

GAM44 287 STAT1 Yamamoto, K.; Kobayashi, H.; Arai, A.; Miura, O.; Hirosawa, S.;Miyasaka, N.: cDNA cloning, expression and chromosome mapping ofthe human STAT4 gene: both STAT4 and STAT1 genes are mapped to 2q32.2- q32.3. Cytogenet.Cell Genet. 77: 207- 210, 1997. 1 A c

GAM44 287 SVIL Pope, R. K.; Pestonjamasp, K. N.; Smith, K. P.; Wulfkuhle, J. D.;Strassel, C. P.; Lawrence, J. B.; Luna, E. J.: Cloning, characterization,and chromosomal localization of human supervillin (SVIL). Genomics 52:342- 351, 1998. 1 A c

GAM44 287 SVIL Ting, H.- J.; Yeh, S.; Nishimura, K.; Chang, C.: Supervillin associateswith androgen receptor and modulates its transcriptional activity. Proc.Nat. Acad. Sci. 99: 661- 666, 2002. 1 A c

GAM44 287 TUBA3 Cowan, N. J.; Dobner, P. R.; Fuchs, E. V.; Cleveland, D. W.: Expressionof human alpha- tubulin genes: interspecies conservation of 3- primeuntranslated regions. Molec. Cell. Biol. 3: 1738- 1745, 1983. 1 A c

GAM44 287 TUBA3 Gerhard, D. S.; Dobner, P. R.; Bruns, G.: Testis specific alpha- tubulinis on chromosome 2q. (Abstract) Cytogenet. Cell Genet. 40: 639- 640,1985. 1 A c

GAM44 287 TUBA3 Hall, J. L.; Cowan, N. J.: Structural features and restrictedexpression of a human alpha- tubulin gene. Nucleic Acids Res. 13:207- 223, 1985. 1 A c

GAM44 287 TUBA3 Lewis, S. A.; Cowan, N. J.: Tubulin genes: structure, expression,and regulation.In: Avila, J. (ed.): Microtubule proteins. BocaRaton: CRC Press, Inc. 1990. Pp. 37- 66. 1 A c

GAM44 287 TUBA3 Miller, F. D.; Naus, C. C. G.; Durand, M.; Bloom, F. E.; Milner,R. J.: Isotypes of alpha- tubulin are differentially regulated duringneuronal maturation. J. Cell Biol. 105: 3065- 3073, 1987. 1 A c

GAM44 287 TUBA3 Rasooly, R. S.: Personal Communication. Baltimore, Md. 2/1998. 1 A c

GAM44 287 TUBA3 Scott, A. F.: Personal Communication. Baltimore, Md. 10/3/2001. 1 A c

GAM44 287 TUBA3 Todd, S.; Naylor, S. L.: Dinucleotide repeat polymorphism in thehuman tubulin alpha 1 (testis specific) gene (TUBA1). Nucleic AcidsRes. 19: 3755 only, 1991. 1 A c

GAM44 287 UBE2V1 Deng, L.; Wang, C.; Spencer, E.; Yang, L.; Braun, A.; You, J.;Slaughter, C.; Pickart, C.; Chen, Z. J.: Activation of the I- kappa- Bcomplex by TRAF6 requires a dimeric ubiquitin- conjugating enzyme complexand a unique 1 A c

polyubiquitin chain. Cell 103: 351- 361, 2000.

GAM44 287 UBE2V1 Hofmann, R. M.; Pickart, C. M.: Noncanonical MMS2- encoded ubiquitin- 1 A c
conjugatingenzyme functions in assembly of novel polyubiquitin chains for
DNArepair. Cell 96: 645- 653, 1999.

GAM44 287 UBE2V1 Rothofsky, M. L.; Lin, S. L.: CROC- 1 encodes a protein which 1 A c
mediatestranscriptional activation of the human FOS promoter. Gene 195:141-
149, 1997.

GAM44 287 UBE2V1 Sancho, E.; Vila, M. R.; Sanchez- Pulido, L.; Lozano, J. J.; Paciucci,R.; 1 A c
Nadal, M.; Fox, M.; Harvey, C.; Bercovich, B.; Loukili, N.; Ciechanover,A.;
Lin, S. L.; Sanz, F.; Estivill, X.; Valencia, A.; Thomson, T.M.: Role of
UEV- 1, an inactive variant of the E2 ubiquitin- conjugatingenzymes, in in
vitro differentiation and cell cycle behavior of HT- 29- M6intestinal
mucosecretory cells. Molec. Cell. Biol. 18: 576- 589,1998.

GAM44 287 YWHAG Autieri, M. V.; Carbone, C. J.: 14- 3- 3- Gamma interacts with andis 1 A c
phosphorylated by multiple protein kinase C isoforms in PDGF-
stimulatedhuman vascular smooth muscle cells. DNA Cell Biol. 18: 555-
564,1999.

GAM44 287 YWHAG Autieri, M. V.; Feuerstein, G. Z.; Yue, T.- L.; Ohlstein, E. H.;Douglas, S. 1 A c
A.: Use of differential display to identify differentiallyexpressed mRNAs
induced by rat carotid artery balloon angioplasty. Lab.Invest. 72: 656- 661,
1995.

GAM44 287 YWHAG Autieri, M. V.; Haines, D. S.; Romanic, A. M.; Ohlstein, E. H.: Expression 1 A c
of 14- 3- 3- gamma in injured arteries and growth factor- and cytokine-
stimulated human vascular smooth muscle cells. CellGrowth Diff. 7: 1453-
1460, 1996.

GAM44 287 YWHAG Horie, M.; Suzuki, M.; Takahashi, E.; Tanigami, A.: Cloning, expression,and 1 A c
chromosomal mapping of the human 14- 3- 3gamma gene (YWHAG) to 7q11.23.
Genomics 60:241- 243, 1999.

GAM44 287 YWHAG Morrison, D.: 14- 3- 3: modulators of signaling proteins? Science 266:56- 1 A c
57, 1994.

GAM45 324 UNC13 Augustin, I.; Betz, A.; Herrmann, C.; Jo, T.; Brose, N.: 3 C a
Differentialexpression of two novel Munc13 proteins in rat brain. Biochem.
J. 337:363- 371, 1999.

GAM45 324 UNC13 Augustin, I.; Rosenmund, C.; Sudhof, T. C.; Brose, N.: Munc13- 1is essential 3 C a
for fusion competence of glutamatergic synaptic vesicles. Nature 400:457-
461, 1999.

GAM45 324 UNC13 Rhee, J.- S.; Betz, A.; Pyott, S.; Reim, K.; Varoqueaux, F.; Augustin,I.; 3 C a
Hesse, D.; Sudhof, T. C.; Takahashi, M.; Rosenmund, C.; Brose,N.: Beta
phorbol ester- and diacylglycerol- induced augmentation oftransmitter
release is mediated by Munc13s and not by PKCs. Cell 108:121- 133, 2002.

GAM45 324 UNC13 Richmond, J. E.; Weimer, R. M.; Jorgensen, E. M.: An open formof syntaxin 3 C a
bypasses the requirement for UNC- 13 in vesicle priming. Nature 412:338-
341, 2001.

GAM45 324 UNC13 Rosenmund, C.; Sigler, A.; Augustin, I.; Reim, K.; Brose, N.; Rhee,J.- S.: 3 C a
Differential control of vesicle priming and short- term plasticityby Munc13
isoforms. Neuron 33: 411- 424, 2002.

GAM45 324 UNC13 Song, Y.; Ailenberg, M.; Silverman, M.: Cloning of a novel genein the human 3 C a
kidney homologous to rat munc13s: its potential rolein diabetic nephropathy.
Kidney Int. 53: 1689- 1695, 1998.

GAM47 269 ABCB9 Allikmets, R.; Gerrard, B.; Hutchinson, A.; Dean, M.: Characterizationof the 3 A c

human ABC superfamily: isolation and mapping of 21 new genesusing the expressed sequence tags database. Hum. Molec. Genet. 5:1649- 1655, 1996.

GAM47 269 ABCB9 Zhang, F.; Zhang, W.; Liu, L.; Fisher, C. L.; Hui, D.; Childs,S.; Dorovini- 3 A c
Zis, K.; Ling, V.: Characterization of ABCB9, an ATPbinding cassette protein associated with lysosomes. J. Biol. Chem. 275:23287- 23294, 2000.

GAM47 269 ABCD2 Broccardo, C.; Troffer- Charlier, N.; Savary, S.; Mandel, J. L.;Chimini, G.: 3 A c
Exon organisation of the mouse gene encoding the adrenoleukodystrophyrelated protein (ALDRP). Europ. J. Hum. Genet. 6: 638- 641, 1998.

GAM47 269 ABCD2 Lombard- Platet, G.; Savary, S.; Sarde, C.- O.; Mandel, J.- L.; Chimini,G.: 3 A c
A close relative of the adrenoleukodystrophy (ALD) gene codesfor a peroxisomal protein with a specific expression pattern. Proc.Nat. Acad. Sci. 93: 1265- 1269, 1996.

GAM47 269 ABCD2 Netik, A.; Forss- Petter, S.; Holzinger, A.; Molzer, B.; Unterrainer,G.; 3 A c
Berger, J.: Adrenoleukodystrophy- related protein can compensatefunctionally for adrenoleukodystrophy protein deficiency (X- ALD):implications for therapy. Hum. Molec. Genet. 8: 907- 913, 1999.

GAM47 269 ABCD2 Savary, S.; Troffer- Charlier, N.; Gyapay, G.; Mattei, M.- G.; Chimini,G.: 3 A c
Chromosomal localization of the adrenoleukodystrophy- relatedgene in man and mice. Europ. J. Hum. Genet. 5: 99- 101, 1997.

GAM47 269 ADAM10 Hattori, M.; Osterfield, M.; Flanagan, J. G.: Regulated cleavageof a 3 A c
contact- mediated axon repellent. Science 289: 1360- 1365, 2000.

GAM47 269 ADAM10 Lunn, C. A.; Fan, X.; Dalie, B.; Miller, K.; Zavodny, P. J.; Narula,S. K.; 3 A c
Lundell, D.: Purification of ADAM 10 from bovine spleen asa TNFalpha convertase. FEBS Lett. 400: 333- 335, 1997.

GAM47 269 ADAM10 Wolfsberg, T. G.; Primakoff, P.; Myles, D. G.; White, J. M.: ADAM,a novel 3 A c
family of membrane proteins containing a disintegrin and metalloproteasedomain: multipotential functions in cell- cell and cell-matrix interactions. J.Cell Biol. 131: 275- 278, 1995.

GAM47 269 ADAM10 Yamazaki, K.; Mizui, Y.; Tanaka, I.: Radiation hybrid mappingof human ADAM10 3 A c
gene to chromosome 15. Genomics 45: 457- 459, 1997.

GAM47 269 ADAMTS5 Abbaszade, I.; Liu, R.- Q.; Yang, F.; Rosenfeld, S. A.; Ross, O.H.; Link, J. 3 A c
R.; Ellis, D. M.; Tortorella, M. D.; Pratta, M. A.; Hollis,J. M.; Wynn, R.; Duke, J. L.; and 15 others: Cloning and characterizationof ADAMTS11, an aggrecanase from the ADAMTS family. J. Biol. Chem. 274:23443- 23450, 1999.

GAM47 269 ADAMTS5 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- 3 A c
TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.

GAM47 269 AKR1B1 Bateman, J. B.; Kojis, T.; Heinzmann, C.; Klisak, I.; Diep, A.;Carper, D.; 3 A c
Nishimura, C.; Mohandas, T.; Sparkes, R. S.: Mappingof aldose reductase gene sequences to human chromosomes 1, 3, 7, 9,11, and 13. Genomics 17: 560- 565, 1993.

GAM47 269 AKR1B1 Bohren, K. M.; Bullock, B.; Wermuth, B.; Gabbay, K. H.: The aldo- 3 A c
ketoreductase superfamily: cDNAs and deduced amino acid sequences of humanaldehyde and aldose reductases. J. Biol. Chem. 264: 9547- 9551, 1989.

GAM47 269 AKR1B1 Brown, L.; Hedge, P. J.; Markham, A. F.; Graham, A.: A human 3 A c
aldehydedehydrogenase (aldose reductase) pseudogene: nucleotide sequence analysisand assignment to chromosome 3. Genomics 13: 465- 468, 1992.

GAM47 269 AKR1B1 Chung, S.; LaMendola, J.: Cloning and sequence determination ofhuman 3 A c
placental aldose reductase gene. J. Biol. Chem. 264: 14775- 14777,1989.

GAM47 269 AKR1B1 Graham, A.; Brown, L.; Hedge, P. J.; Gammack, A. J.; Markham, A.F.: Structure of the human aldose reductase gene. J. Biol. Chem. 266:6872- 6877, 1991. 3 A c

GAM47 269 AKR1B1 Graham, A.; Heath, P.; Morten, J. E. N.; Markham, A. F.: The humanaldose reductase gene maps to chromosome region 7q35. Hum. Genet. 86:509- 514, 1991. 3 A c

GAM47 269 AKR1B1 Nishimura, C.; Matsuura, Y.; Kokai, Y.; Akera, T.; Carper, D.;Morjana, N.; Lyons, C.; Flynn, T. G.: Cloning and expression of humanaldose reductase. J. Biol. Chem. 265: 9788- 9792, 1990. 3 A c

GAM47 269 AKR1B1 Shah, V. O.; Dorin, R. I.; Sun, Y.; Braun, M.; Zager, P. G.: Aldosereductase gene expression is increased in diabetic nephropathy. J.Clin. Endocr. Metab. 82: 2294- 2298, 1997. 3 A c

GAM47 269 ALOX12B Boeglin, W. E.; Kim, R. B.; Brash, A. R.: A 12R- lipoxygenase inhuman skin: mechanistic evidence, molecular cloning, and expression. Proc.Nat. Acad. Sci. 95: 6744- 6749, 1998. 3 A b

GAM47 269 ALOX12B Jobard, F.; Lefevre, C.; Karaduman, A.; Blanchet- Bardon, C.; Emre,S.; Weissenbach, J.; Ozguc, M.; Lathrop, M.; Prud'homme, J.- F.; Fischer,J.: Lipoxygenase- 3 (ALOXE3) and 12(R)- lipoxygenase (ALOX12B) aremutated in non- bullous congenital ichthyosiform erythroderma (NCIE)linked to chromosome 17p13.1. Hum. Molec. Genet. 11: 107- 113, 2002. 3 A b

GAM47 269 ALOX12B Sun, D.; McDonnell, M.; Chen, X.- S.; Lakkis, M. M.; Li, H.; Isaacs,S. N.; Elsea, S. H.; Patel, P. I.; Funk, C. D.: Human 12(R)- lipoxygenaseand the mouse ortholog: molecular cloning, expression, and gene chromosomalassignment. J. Biol. Chem. 273: 33540- 33547, 1998. 3 A b

GAM47 269 AMPH David, C.; Solimena, M.; De Camilli, P.: Autoimmunity in stiff- mansyndrome with breast cancer is targeted to the C- terminal region ofhuman amphiphysin, a protein similar to the yeast proteins, Rvs167and Rvs161. FEBS Lett. 351: 73- 79, 1994. 3 A c

GAM47 269 AMPH De Camilli, P.; Thomas, A.; Cofiell, R.; Folli, F.; Lichte, B.;Piccolo, G.; Meinck, H.- M.; Austoni, M.; Fassetta, G.; Bottazzo, G.;Bates, D.; Cartlidge, N.; Solimena, M.; Kilimann, M. W.: The synapticvesicle- associated protein amphiphysin is the 128- kD autoantigen ofstiff- man syndrome with breast cancer. J. Exp. Med. 178: 2219- 2223,1993. 3 A c

GAM47 269 AMPH Jenkins, N. A.; Gilbert, D. J.; Yamamoto, R.; Kilimann, M. W.;Copeland, N. G.: Amphiphysin (Amph) maps to the proximal region ofmouse chromosome 13. Genomics 28: 363- 365, 1995. 3 A c

GAM47 269 AMPH Lichte, B.; Veh, R. W.; Meyer, H. E.; Kilimann, M. W.: Amphiphysin,a novel protein associated with synaptic vesicles. EMBO J. 11: 2521- 2530,1992. 3 A c

GAM47 269 AMPH Yamamoto, R.; Li, X.; Francke, U.; Kilimann, M. W.: Genetic mappingof the human amphiphysin gene (AMPH) at 7p14- p13 excludes its involvementin retinitis pigmentosa 9 or dominant cystoid macular dystrophy. (Letter) Am.J. Hum. Genet. 57: 970- 972, 1995. 3 A c

GAM47 269 AMPH Yamamoto, R.; Li, X.; Winter, S.; Francke, U.; Kilimann, M. W.: Primary structure of human amphiphysin, the dominant autoantigenof paraneoplastic Stiff- Man syndrome, and mapping of its gene (AMPH)to chromosome 7p13- p14. Hum. Molec. Genet. 4: 265- 268, 1995. 3 A c

GAM47 269 ANK2 Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.: Isolationand characterization of cDNAs encoding human brain ankyrins reveala family of alternatively spliced genes. J. Cell Biol. 114: 241- 253,1991. 3 A c

GAM47 269 ANK2 Tse, W. T.; Menninger, J. C.; Yang- Feng, T. L.; Francke, U.; Sahr,K. E.; 3 A c

Lux, S. E.; Ward, D. C.; Forget, B. G.: Isolation and chromosomallocalization of a novel non- erythroid ankyrin gene. Genomics 10:858- 866, 1991.

GAM47 269 AOC3 Bono, P.; Salmi, M.; Smith, D. J.; Leppanen, I.; Horelli- Kuitunen,N.; Palotie, A.; Jalkanen, S.: Isolation, structural characterization,and chromosomal mapping of the mouse vascular adhesion protein- 1 geneand promoter. J. Immun. 161: 2953- 2960, 1998. 3 A c

GAM47 269 AOC3 Morris, N. J.; Ducret, A.; Aebersold, R.; Ross, S. A.; Keller,S. R.; Lienhard, G. E.: Membrane amine oxidase cloning and identificationas a major protein in the adipocyte plasma membrane. J. Biol. Chem. 272:9388- 9392, 1997. 3 A c

GAM47 269 AOC3 Smith, D. J.; Salmi, M.; Bono, P.; Hellman, J.; Leu, T.; Jalkanen,S.: Cloning of vascular adhesion protein 1 reveals a novel multifunctionaladhesion molecule. J. Exp. Med. 188: 17- 27, 1998. 3 A c

GAM47 269 AOC3 Zhang, X.; McIntire, W. S.: Cloning and sequencing of a copper- containing,topa quinone- containing monoamine oxidase from human placenta. Gene 179:279- 286, 1996. 3 A c

GAM47 269 AP1S1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 3 A c

GAM47 269 AP1S1 Kirchhausen, T.; Davis, A. C.; Frucht, S.; O'Brine Greco, B.; Payne,G. S.; Tubb, B.: AP17 and AP19, the mammalian small chains of theclathrin-associated protein complexes show homology to Yap17p, theirputative homolog in yeast. J. Biol. Chem. 266: 11153- 11157, 1991. 3 A c

GAM47 269 AP1S1 Peyrard, M.; Parveneh, S.; Lagercrantz, S.; Ekman, M.; Fransson,I.; Sahlen, S.; Dumanski, J. P.: Cloning, expression pattern, andchromosomal assignment to 16q23 of the human gamma- adaptin gene (ADTG). Genomics 50:275- 280, 1998. 3 A c

GAM47 269 AP1S1 Takatsu, H.; Sakurai, M.; Shin, H.- W.; Murakami, K.; Nakayama,K.: Identification and characterization of novel clathrin adaptor-relatedproteins. J. Biol. Chem. 273: 24693- 24700, 1998. 3 A c

GAM47 269 AR Abel, A.; Walcott, J.; Woods, J.; Duda, J.; Merry, D. E.: Expressionof expanded repeat androgen receptor produces neurologic disease intransgenic mice. Hum. Molec. Genet. 10: 107- 116, 2001. 3 A c

GAM47 269 AR Bailey, C. K.; Andriola, I. F. M.; Kampinga, H. H.; Merry, D. E.: Molecular chaperones enhance the degradation of expanded polyglutaminerepeat androgen receptor in a cellular model of spinal and bulbarmuscular atrophy. Hum. Molec. Genet. 11: 515- 523, 2002. 3 A c

GAM47 269 AR Batch, J. A.; Evans, B. A. J.; Hughes, I. A.; Patterson, M. N.: Mutations of the androgen receptor gene identified in perineal hypospadias. J.Med. Genet. 30: 198- 201, 1993. 3 A c

GAM47 269 AR Batch, J. A.; Williams, D. M.; Davies, H. R.; Brown, B. D.; Evans,B. A. J.; Hughes, I. A.; Patterson, M. N.: Androgen receptor genemutations identified by SSCP in fourteen subjects with androgen insensitivitysyndrome. Hum. Molec. Genet. 1: 497- 503, 1992. 3 A c

GAM47 269 AR Beitel, L. K.; Kazemi- Esfarjani, P.; Kaufman, M.; Lumbroso, R.;DiGeorge, A. M.; Killinger, D. W.; Trifiro, M. A.; Pinsky, L.: Substitutionof arginine-839 by cysteine or histidine in the androgen receptorcauses different receptor phenotypes in cultured cells and coordinatedegrees of clinical androgen resistance. J. Clin. Invest. 94: 546- 554,1994. 3 A c

GAM47 269 AR Belsham, D. D.; Pereira, F.; Greenberg, C. R.; Liao, S.; Wrogemann,K.: Leu676- to- pro mutation of the androgen receptor causes completeandrogen insensitivity syndrome in a large Hutterite kindred. Hum.Mutat. 5: 28- 33, 1995. 3 A c

GAM47 269 AR Bevan, C. L.; Brown, B. B.; Davies, H. R.; Evans, B. A. J.; Hughes,I. A.; Patterson, M. N.: Functional analysis of six androgen receptormutations identified in patients with partial androgen insensitivitysyndrome. Hum. Molec. Genet. 5: 265- 273, 1996. 3 A c

GAM47 269 AR Biancalana, V.; Serville, F.; Pommier, J.; Julien, J.; Hanauer,A.; Mandel, J. L.: Moderate instability of the trinucleotide repeatin spinobulbar muscular atrophy. Hum. Molec. Genet. 1: 255- 258,1992. 3 A c

GAM47 269 AR Boehmer, A. L. M.; Brinkmann, A. O.; Niermeijer, M. F.; Bakker,L.; Halley, D. J. J.; Drop, S. L. S.: Germ- line and somatic mosaicismin the androgen insensitivity syndrome: implications for genetic counseling.(Letter) Am. J. Hum. Genet. 60: 1003- 1006, 1997. 3 A c

GAM47 269 AR Boehmer, A. L. M.; Brinkmann, A. O.; Nijman, R. M.; Verleun- Mooijman,M. C. T.; de Ruiter, P.; Niermeijer, M. F.; Drop, S. L. S.: Phenotypicvariation in a family with partial androgen insensitivity syndromeexplained by differences in 5- alpha dihydrotestosterone availability. J.Clin. Endocr. Metab. 86: 1240- 1246, 2001. 3 A c

GAM47 269 AR Bouvattier, C.; Carel, J.- C.; Lecointre, C.; David, A.; Sultan,C.; Bertrand, A.- M., Morel, Y.; Chaussain, J.- L.: Postnatal changesof T, LH, and FSH in 46,XY infants with mutations in the AR gene. J.Clin. Endocr. Metab. 87: 29- 32, 2002. 3 A c

GAM47 269 AR Brown, C. J.; Goss, S. J.; Lubahn, D. B.; Joseph, D. R.; Wilson,E. M.; French, F. S.; Willard, H. F.: Androgen receptor locus onthe human X chromosome: regional localization to Xq11- 12 and descriptionof a DNA polymorphism. Am. J. Hum. Genet. 44: 264- 269, 1989. 3 A c

GAM47 269 AR Brown, T. R.; Lubahn, D. B.; Wilson, E. M.; Joseph, D. R.; French,F. S.; Migeon, C. J.: Deletion of the steroid- binding domain of thehuman androgen receptor gene in one family with complete androgeninsensitivity syndrome: evidence for further genetic heterogeneityin this syndrome. Proc. Nat. Acad. Sci. 85: 8151- 8155, 1988. 3 A c

GAM47 269 AR Bruggenwirth, H. T.; Boehmer, A. L. M.; Ramnarain, S.; Verleun- Mooijman,M. C. T.; Satijn, D. P. E.; Trapman, J.; Grootegoed, J. A.; Brinkmann,A. O.: Molecular analysis of the androgen- receptor gene in a familywith receptor-positive partial androgen insensitivity: an unusualtype of intronic mutation. Am. J. Hum. Genet. 61: 1067- 1077, 1997. 3 A c

GAM47 269 AR Buchanan, G.; Yang, M.; Harris, J. M.; Nahm, H. S.; Han, G.; Moore,N.; Bentel, J. M.; Matusik, R. J.; Horsfall, D. J.; Marshall, V. R.;Greenberg, N. M.; Tilley, W. D.: Mutations at the boundary of thehinge and ligand binding domain of the androgen receptor confer increasedtransactivation function. Molec. Endocr. 15: 46- 56, 2001. 3 A c

GAM47 269 AR Butler, R.; Leigh, P. N.; McPhaul, M. J.; Gallo, J.- M.: Truncatedforms of the androgen receptor are associated with polyglutamine expansionin X-linked spinal and bulbar muscular atrophy. Hum. Molec. Genet. 7:121- 127, 1998. 3 A c

GAM47 269 AR Calvo, R. M.; Asuncion, M.; Sancho, J.; San Millan, J. L.; Escobar-Morreale,H. F.: The role of the CAG repeat polymorphism in the androgen receptorgene and of skewed X- chromosome inactivation, in the pathogenesisof 3 A c

hirsutism. J. Clin. Endocr. Metab. 85: 1735- 1740, 2000.

GAM47 269 AR Caplen, N. J.; Taylor, J. P.; Statham, V. S.; Tanaka, F.; Fire,A.; Morgan, 3 A c
R. A.: Rescue of polyglutamine- mediated cytotoxicityby double- stranded
RNA- mediated RNA interference. Hum. Molec. Genet. 11:175- 184, 2002.

GAM47 269 AR Caskey, C. T.; Pizzuti, A.; Fu, Y.- H.; Fenwick, R. G., Jr.; Nelson,D. L.: 3 A c
Triplet repeat mutations in human disease. Science 256:784- 789, 1992.

GAM47 269 AR Chang, B.; Zheng, S. L.; Hawkins, G. A.; Isaacs, S. D.; Wiley,K. E.; Turner, 3 A c
A.; Carpten, J. D.; Bleecker, E. R.; Walsh, P. C.;Trent, J. M.; Meyers, D.
A.; Isaacs, W. B.; Xu, J.: Polymorphic GGCrepeats in the androgen receptor
gene are associated with hereditaryand sporadic prostate cancer risk. Hum.
Genet. 110: 122- 129, 2002.

GAM47 269 AR Chang, C.; Kokontis, J.; Liao, S.: Molecular cloning of humanand rat 3 A c
complementary DNA encoding androgen receptors. Science 240:324- 326, 1988.

GAM47 269 AR Choong, C. S.; Kemppainen, J. A.; Zhou, Z.- X.; Wilson, E. M.:Reduced 3 A c
androgen receptor gene expression with first exon CAG repeatexpansion.
Molec. Endocr. 10: 1527- 1535, 1996.

GAM47 269 AR Choong, C. S.; Quigley, C. A.; French, F. S.; Wilson, E. M.:A novel missense 3 A c
mutation in the amino- terminal domain of the humanandrogen receptor gene in
a family with partial androgen insensitivitysyndrome causes reduced
efficiency of protein translation. J. Clin.Invest. 98: 1423- 1431, 1996.

GAM47 269 AR Chu, J.; Zhang, R.; Zhao, Z.; Zou, W.; Han, Y.; Qi, Q.; Zhang,H.; Wang, J.- 3 A c
C.; Tao, S.; Liu, X.; Luo, Z.: Male fertility is compatiblewith an Arg840Cys
substitution in the AR in a large Chinese familywith divergent phenotypes of
AR insensitivity syndrome. J. Clin.Endocr. Metab. 87: 347- 351, 2002.

GAM47 269 AR Coetzee, G. A.; Ross, R. K.: Re: Prostate cancer and the androgenreceptor. 3 A c
(Letter) J. Nat. Cancer Inst. 86: 872- 873, 1994.

GAM47 269 AR Correa- Cerro, L.; Wohr, G.; Haussler, J.; Berthon, P.; Drelon,E.; Mangin, 3 A c
P.; Fournier, G.; Cussenot, O.; Kraus, P.; Just, W.; Paiss,T.; Cantu, J. M.;
Vogel, W.: (CAG)nCAA and GGN repeats in the humanandrogen receptor gene are
not associated with prostate cancer ina French- German population. Europ. J.
Hum. Genet. 7: 347- 362, 1999.

GAM47 269 AR Dowsing, A. T.; Yong, E. L.; Clark, M.; McLachlan, R. I.; de Kretser,D. M.; 3 A c
Trounson, A. O.: Linkage between male infertility and trinucleotiderepeat
expansion in the androgen- receptor gene. Lancet 354: 640- 643,1999.

GAM47 269 AR Edwards, A.; Hammond, H. A.; Jin, L.; Caskey, C. T.; Chakraborty,R.: Genetic 3 A c
variation at five trimeric and tetrameric tandem repeatloci in four human
population groups. Genomics 12: 241- 253, 1992.

GAM47 269 AR Elo, J. P.; Kvist, L.; Leinonen, K.; Isomaa, V.; Hentuu, P.; Lukkarinen,O.; 3 A c
Vihko, P.: Mutated human androgen receptor gene detected in aprostatic
cancer patient is also activated by estradiol. J. Clin.Endocr. Metab. 80:
3494- 3500, 1995.

GAM47 269 AR Gaddipati, J. P.; McLeod, D. G.; Heidenberg, H. B.; Sesterhenn,I. A.; 3 A c
Finger, M. J.; Moul, J. W.; Srivastava, S.: Frequent detectionof codon 877
mutation in the androgen receptor gene in advanced prostatecancers. Cancer
Res. 54: 2861- 2864, 1994.

GAM47 269 AR Gehring, U.; Tomkins, G. M.: Characterization of a hormone receptordefect in 3 A c
the androgen- insensitivity mutant. Cell 3: 59- 64, 1974.

GAM47 269 AR Gingrich, J. R.; Barrios, R. J.; Kattan, M. W.; Nahm, H. S.; Finegold,M. J.; 3 A c
Greenberg, N. M.: Androgen- independent prostate cancer progressionin the
TRAMP model. Cancer Res. 57: 4687- 4691, 1997.

GAM47 269 AR Gingrich, J. R.; Greenberg, N. M.: A transgenic mouse prostatecancer model. 3 A c
Toxicol. Path. 24: 502- 504, 1996.

GAM47 269 AR Giovannucci, E.; Stampfer, M. J.; Krithivas, K.; Brown, M.; Brufsky,A.; 3 A c
Talcott, J.; Hennekens, C. H.; Kantoff, P. W.: The CAG repeatwithin the
androgen receptor gene and its relationship to prostatecancer. Proc. Nat.
Acad. Sci. 94: 3320- 3323, 1997.

GAM47 269 AR Gottlieb, B.; Beitel, L. K.; Trifiro, M. A.: Variable expressivityand 3 A c
mutation databases: the androgen receptor gene mutations database.
Hum.Mutat. 17: 382- 388, 2001.

GAM47 269 AR Gottlieb, B.; Trifiro, M.; Lumbroso, R.; Pinsky, L.: The androgenreceptor 3 A c
gene mutations database. Nucleic Acids Res. 25: 158- 162,1997.

GAM47 269 AR Gottlieb, B.; Trifiro, M.; Lumbroso, R.; Vasiliou, D. M.; Pinsky,L.: The 3 A c
androgen receptor gene mutations database. Nucleic AcidsRes. 24: 151- 154,
1996.

GAM47 269 AR Griffin, J. E.: Androgen resistance- - the clinical and molecularspectrum. 3 A c
New Eng. J. Med. 326: 611- 618, 1992.

GAM47 269 AR Grino, P. B.; Griffin, J. E.; Cushard, W. G., Jr.; Wilson, J.D.: A mutation 3 A c
of the androgen receptor associated with partial androgenresistance,
familial gynecomastia, and fertility. J. Clin. Endocr.Metab. 66: 754- 761,
1988.

GAM47 269 AR Grino, P. B.; Isidro- Gutierrez, R. F.; Griffin, J. E.; Wilson,J. D.: 3 A c
Androgen resistance associated with a qualitative abnormalityof the androgen
receptor and responsive to high dose androgen therapy. J.Clin. Endocr.
Metab. 68: 578- 584, 1989.

GAM47 269 AR Hardy, D. O.; Scher, H. I.; Bogenreider, T.; Sabbatini, P.; Zhang,Z.- F.; 3 A c
Nanus, D. M.; Catterall, J. F.: Androgen receptor CAG repeatlengths in
prostate cancer: correlation with age of onset. J. Clin.Endocr. Metab. 81:
4400- 4405, 1996.

GAM47 269 AR Hellwinkel, O. J.- C.; Holterhus, P.- M.; Struve, D.; Marschke,C.; Homburg, 3 A c
N.; Hiort, O.: A unique exonic splicing mutation inthe human androgen
receptor gene indicates a physiologic relevanceof regular androgen receptor
transcript variants. J. Clin. Endocr.Metab. 86: 2569- 2575, 2001.

GAM47 269 AR Hickey, T.; Chandy, A.; Norman, R. J.: The androgen receptorCAG repeat 3 A c
polymorphism and X- chromosome inactivation in AustralianCaucasian women
with infertility related to polycystic ovary syndrome. J.Clin. Endocr.
Metab. 87: 161- 165, 2002.

GAM47 269 AR Hiort, O.; Sinnecker, G. H. G.; Holterhus, P.- M.; Nitsche, E.M.; Kruse, K.: 3 A c
Inherited and de novo androgen receptor gene mutations:investigation of
single- case families. J. Pediat. 132: 939- 943,1998.

GAM47 269 AR Holterhus, P. M.; Sinnecker, G. H. G.; Wollmann, H. A.; Struve,D.; Homburg, 3 A c
N.; Kruse, K.; Hiort, O.: Expression of two functionallydifferent androgen
receptors in a patient with androgen insensitivity. Europ.J. Pediat. 158:
702- 706, 1999.

GAM47 269 AR Holterhus, P.- M.; Bruggenwirth, H. T.; Hiort, O.; Kleinkauf- Houcken,A.; 3 A c
Kruse, K.; Sinnecker, G. H. G.; Brinkmann, A. O.: Mosaicism dueto a somatic
mutation of the androgen receptor gene determines phenotypein androgen
insensitivity syndrome. J. Clin. Endocr. Metab. 82:3584- 3589, 1997.

GAM47 269 AR Holterhus, P.- M.; Sinnecker, G. H. G.; Hiort, O.: Phenotypicdiversity and 3 A c
testosterone- induced normalization of mutant L712F androgenreceptor
function in a kindred with androgen insensitivity. J. Clin.Endocr. Metab.

85: 3245- 3250, 2000.

GAM47 269 AR Holterhus, P.- M.; Wiebel, J.; Sinnecker, G. H. G.; Bruggenwirth,H. T.; 3 A c
Sippell, W. G.; Brinkmann, A. O.; Kruse, K.; Hiort, O.: Clinicaland
molecular spectrum of somatic mosaicism in androgen insensitivitysyndrome.
Pediat. Res. 46: 684- 690, 1999.

GAM47 269 AR Hughes, I. A.; Evans, B. A. J.: Complete androgen insensitivitysyndrome 3 A c
characterized by increased concentration of a normal androgenreceptor in
genital skin fibroblasts. J. Clin. Endocr. Metab. 63:309- 315, 1986.

GAM47 269 AR Imasaki, K.; Okabe, T.; Murakami, H.; Tanaka, Y.; Haji, M.; Takayanagi,R.; 3 A c
Nawata, H.: Androgen insensitivity syndrome due to new mutationsin the DNA-
binding domain of the androgen receptor. Molec. Cell.Endocr. 120: 15- 24,
1996.

GAM47 269 AR Imperato- McGinley, J.; Ip, N. Y.; Gautier, T.; Neuweiler, J.;Gruenspan, H.; 3 A c
Liao, S.; Chang, C.; Balazs, I.: DNA linkage analysisand studies of the
androgen receptor gene in a large kindred withcomplete androgen
insensitivity. Am. J. Med. Genet. 36: 104- 108,1990.

GAM47 269 AR Irvine, R. A.; Yu, M. C.; Ross, R. K.; Coetzee, G. A.: The CAGand GGC 3 A c
microsatellites of the androgen receptor gene are in linkagedisequilibrium
in men with prostate cancer. Cancer. Res. 55: 1937- 1940,1995.

GAM47 269 AR Jakubiczka, S.; Nedel, S.; Werder, E. A.; Schleiermacher, E.;Theile, U.; 3 A c
Wolff, G.; Wieacker, P.: Mutations of the androgen receptorgene in patients
with complete androgen insensitivity. Hum. Mutat. 9:57- 61, 1997.

GAM47 269 AR Jukier, L.; Kaufman, M.; Pinsky, L.; Peterson, R. E.: Partialandrogen 3 A c
resistance associated with secondary 5- alpha- reductase
deficiency:identification of a novel qualitative androgen receptor defect
andclinical implications. J. Clin. Endocr. Metab. 59: 679- 688, 1984.

GAM47 269 AR Kang, H.- Y.; Yeh, S.; Fujimoto, N.; Chang, C.: Cloning and 3 A c
characterizationof human prostate coactivator ARA54, a novel protein that
associateswith the androgen receptor. J. Biol. Chem. 274: 8570- 8576, 1999.

GAM47 269 AR Kaufman, M.; Pinsky, L.; Bowin, A.; Au, M. W. S.: Familial externalgenital 3 A c
ambiguity due to a transformation defect of androgen- receptorcomplexes that
is expressed with 5- alpha- dihydrotestosterone and thesynthetic androgen
methyltrienolone. Am. J. Med. Genet. 18: 493- 507,1984.

GAM47 269 AR Kaufman, M.; Straisfeld, C.; Pinsky, L.: Male 3 A c
pseudohermaphroditismpresumably due to target organ unresponsiveness to
androgens: deficient5- alpha- dihydrotestosterone binding in cultured skin
fibroblasts. J.Clin. Invest. 58: 345- 350, 1976.

GAM47 269 AR Kazemi- Esfarjani, P.; Beitel, L. K.; Trifiro, M.; Kaufman, M.;Rennie, P.; 3 A c
Sheppard, P.; Matusik, R.; Pinsky, L.: Substitution ofvaline- 865 by
methionine or leucine in the human androgen receptorcauses complete or
partial androgen insensitivity, respectively withdistinct androgen receptor
phenotypes. Molec. Endocr. 7: 37- 46,1993.

GAM47 269 AR Keenan, B. S.; Meyer, W. J., III; Hadjian, A. J.; Jones, H. W.;Migeon, C. 3 A c
J.: Syndrome of androgen insensitivity in man: absenceof 5- alpha-
dihydrotestosterone binding protein in skin fibroblasts. J.Clin. Endocr. 38:
1143- 1146, 1974.

GAM47 269 AR Kittles, R. A.; Young, D.; Weinrich, S.; Hudson, J.; Argyropoulos,G.; Ukoli, 3 A c
F.; Adams- Campbell, L.; Dunston, G. M.: Extent of linkagedisequilibrium
between the androgen receptor gene CAG and GGC repeatsin human populations:
implications for prostate cancer risk. Hum.Genet. 109: 253- 261, 2001.

GAM47 269 AR Klocker, H.; Kaspar, F.; Eberle, J.; Uberreiter, S.; Radmayr,C.; Bartsch, G.: Point mutation in the DNA binding domain of theandrogen receptor in two families with Reifenstein syndrome. Am.J. Med. Genet. 50: 1318- 1327, 1992. 3 A c

GAM47 269 AR Knoke, I.; Allera, A.; Wieacker, P.: Significance of the CAGrepeat length in the androgen receptor gene (AR) for the transactivationfunction of an M780I mutant AR. Hum. Genet. 104: 257- 261, 1999. 3 A c

GAM47 269 AR Kobayashi, Y.; Miwa, S.; Merry, D. E.; Kume, A.; Mei, L.; Doyu,M.; Sobue, G.: Caspase- 3 cleaves the expanded androgen receptor proteinof spinal and bulbar muscular atrophy in a polyglutamine repeat length- dependentmanner. Biochem. Biophys. Res. Commun. 252: 145- 150, 1998. 3 A c

GAM47 269 AR Koivisto, P. A.; Schleutker, J.; Helin, H.; Ehren- van Eekelen,C.; Kallioniemi, O.- P.; Trapman, J.: Androgen receptor gene alterationsand chromosomal gains and losses in prostate carcinomas appearingduring finasteride treatment for benign prostatic hyperplasia. Clin.Cancer Res. 5: 3578- 3582, 1999. 3 A c

GAM47 269 AR Kooy, R. F.; Reyniers, E.; Storm, K.; Vits, L.; van Velzen, D.;de Ruiter, P. E.; Brinkmann, A. O.; de Paepe, A.; Willems, P. J.:CAG repeat contraction in the androgen receptor gene in three brotherswith mental retardation. Am. J. Med. Genet. 85: 209- 213, 1999. 3 A c

GAM47 269 AR La Spada, A. R.; Wilson, E. M.; Lubahn, D. B.; Harding, A. E.;Fischbeck, K. H.: Androgen receptor gene mutations in X- linked spinaland bulbar muscular atrophy. Nature 352: 77- 79, 1991. 3 A c

GAM47 269 AR La Spada, A.; Fischbeck, K. H.: Androgen receptor gene defectin X- linked spinal and bulbar muscular atrophy. (Abstract) Am. J.Hum. Genet. 49 (suppl.): 20, 1991. 3 A c

GAM47 269 AR Lewis, M.; Kaita, H.; Giblett, E. R.; Anderson, J.; Philipps,S.; Steinberg, A. G.; McAlpine, P. J.: Multiplicity of genetic polymorphismsof blood in the Schmiedeleut Hutterites. Am. J. Med. Genet. 22:477- 485, 1985. 3 A c

GAM47 269 AR Liao, S.; Witte, D.: Autoimmune anti- androgen- receptor antibodiesin human serum. Proc. Nat. Acad. Sci. 82: 8345- 8348, 1985. 3 A c

GAM47 269 AR Lim, H. N.; Chen, H.; McBride, S.; Dunning, A. M.; Nixon, R. M.;Hughes, I. A.; Hawkins, J. R.: Longer polyglutamine tracts in theandrogen receptor are associated with moderate to severe undermasculinizedgenitalia in XY males. Hum. Molec. Genet. 9: 829- 834, 2000. 3 A c

GAM47 269 AR Lin, S.- Y.; Ohno, S.: The binding of androgen receptor to DNAand RNA. Biochim. Biophys. Acta 654: 181- 186, 1981. 3 A c

GAM47 269 AR Lobaccaro, J.- M.; Lumbroso, S.; Belon, C.; Galtier- Dereure, F.;Bringer, J.; Lesimple, T.; Namer, M.; Cutuli, B. F.; Pujol, H.; Sultan,C.: Androgen receptor gene mutation in male breast cancer. Hum.Molec. Genet. 2: 1799- 1802, 1993. 3 A c

GAM47 269 AR Lubahn, D. B.; Brown, T. R.; Simental, J. A.; Higgs, H. N.; Migeon,C. J.; Wilson, E. M.; French, F. S.: Sequence of the intron/exonjunctions of the coding region of the human androgen receptor geneand identification of a point mutation in a family with complete androgeninsensitivity. Proc. Nat. Acad. Sci. 86: 9534- 9538, 1989. 3 A c

GAM47 269 AR Lubahn, D. B.; Joseph, D. R.; Sar, M.; Tan, J.; Higgs, H. N.;Larson, R. E.; French, F. S.; Wilson, E. M.: The human androgen receptor:complementary deoxyribonucleic acid cloning, sequence analysis andgene expression in prostate. Molec. Endocr. 2: 1265- 1275, 1988. 3 A c

GAM47 269 AR Lubahn, D. B.; Joseph, D. R.; Sullivan, P. M.; Willard, H. F.;French, F. S.; 3 A c

Wilson, E. M.: Cloning of human androgen receptorcomplementary DNA and localization to the X chromosome. Science 240:327- 330, 1988.

GAM47 269 AR Lumbroso, S.; Lobaccaro, J. M.; Georget, V.; Leger, J.; Poujol,N.; Terouanne, B.; Evain- Brion, D.; Czernichow, P.; Sultan, C.: Anovel substitution (leu707- to- arg) in exon 4 of the androgen receptorgene causes complete androgen resistance. J. Clin. Endocr. Metab. 81:1984- 1988, 1996. 3 A c

GAM47 269 AR Lund, A.; Udd, B.; Juvonen, V.; Andersen, P. M.; Cederquist, K.;Davis, M.; Gellera, C.; Kolmel, C.; Ronnevi, L.- O.; Sperfeld, A.- D.;Sorensen, S.- A.; Tranebjaerg, L.; Van Maldergem, L.; Watanabe, M.;Weber, M.; Yeung, L.; Savontaus, M.- L.: Multiple founder effectsin spinal and bulbar muscular atrophy (SBMA, Kennedy disease) aroundthe world. Europ. J. Hum. Genet. 9: 431- 436, 2001. 3 A c

GAM47 269 AR Macke, J. P.; Hu, N.; Hu, S.; Bailey, M.; King, V. L.; Brown,T.; Hamer, D.; Nathans, J.: Sequence variation in the androgen receptorgene is not a common determinant of male sexual orientation. Am.J. Hum. Genet. 53: 844- 852, 1993. 3 A c

GAM47 269 AR MacLean, H. E.; Chu, S.; Warne, G. L.; Zajac, J. D.: Relatedindividuals with different androgen receptor gene deletions. J. Clin.Invest. 91: 1123- 1128, 1993. 3 A c

GAM47 269 AR Madgar, I.; Green, L.; Kent- First, M.; Weissenberg, R.; Gershoni-Baruch,R.; Goldman, B.; Friedman, E.: Genotyping of Israeli infertile menwith idiopathic oligozoospermia. Clin. Genet. 62: 203- 207, 2002. 3 A c

GAM47 269 AR Marcelli, M.; Tilley, W. D.; Wilson, C. M.; Griffin, J. E.; Wilson,J. D.; McPhaul, M. J.: Definition of the human androgen receptorgene structure permits the identification of mutations that causeandrogen resistance: premature termination of the receptor proteinat amino acid residue 588 causes complete androgen resistance. Molec.Endocr. 4: 1105- 1116, 1990. 3 A c

GAM47 269 AR Marcelli, M.; Tilley, W. D.; Wilson, C. M.; Wilson, J. D.; Griffin,J. E.; McPhaul, M. J.: A single nucleotide substitution introducesa premature termination codon into the androgen receptor gene of apatient with receptor-negative androgen resistance. J. Clin. Invest. 85:1522- 1528, 1990. 3 A c

GAM47 269 AR Marcelli, M.; Tilley, W. D.; Zoppi, S.; Griffin, J. E.; Wilson,J. D.; McPhaul, M. J.: Androgen resistance associated with a mutationof the androgen receptor at amino acid 772 (arg- to- cys) results froma combination of decreased messenger ribonucleic acid levels and impairmentof receptor function. J. Clin. Endocr. 73: 318- 325, 1991. 3 A c

GAM47 269 AR McCampbell, A.; Taylor, J. P.; Taye, A. A.; Robitschek, J.; Li,M.; Walcott, J.; Merry, D.; Chai, Y.; Paulson, H.; Sobue, G.; Fischbeck,K. H.: CREB-binding protein sequestration by expanded polyglutamine. Hum.Molec. Genet. 9: 2197- 2202, 2000. 3 A c

GAM47 269 AR McGuire, W. L.; Chamness, G. C.; Fuqua, S. A. W.: Estrogen receptorvariants in clinical breast cancer. Molec. Endocr. 5: 1571- 1577,1991. 3 A c

GAM47 269 AR McPhaul, M. J.; Griffin, J. E.: Male pseudohermaphroditism causedby mutations of the human androgen receptor. J. Clin. Endocr. Metab. 84:3435-3441, 1999. 3 A c

GAM47 269 AR McPhaul, M. J.; Marcelli, M.; Tilley, W. D.; Griffin, J. E.; Isidro-Gutierrez,R. F.; Wilson, J. D.: Molecular basis of androgen resistance in afamily with a qualitative abnormality of the androgen receptor andresponsive to high- dose androgen therapy. J. Clin. Invest. 87: 1413-1421,1991. 3 A c

GAM47 269 AR McPhaul, M. J.; Marcelli, M.; Zoppi, S.; Griffin, J. E.; Wilson,J. D.: 3 A c
Genetic basis of endocrine disease 4: the spectrum of mutationsin the androgen receptor gene that causes androgen resistance. J.Clin. Endocr. Metab. 76: 17- 23, 1993.

GAM47 269 AR McPhaul, M. J.; Marcelli, M.; Zoppi, S.; Wilson, C. M.; Griffin,J. E.; 3 A c
Wilson, J. D.: Mutations in the ligand- binding domain of theandrogen receptor gene cluster in two regions of the gene. J. Clin.Invest. 90: 2097- 2101, 1992.

GAM47 269 AR McPhaul, M. J.; Schweikert, H.- U.; Allman, D. R.: Assessmentof androgen 3 A c
receptor function in genital skin fibroblasts using arecombinant adenovirus to deliver an androgen- responsive reportergene. J. Clin. Endocr. Metab. 82: 1944- 1948, 1997.

GAM47 269 AR Mifsud, A.; Ramirez, S.; Yong, E. L.: Androgen receptor geneCAG 3 A c
trinucleotide repeats in anovulatory infertility and polycysticovaries. J. Clin. Endocr. Metab. 85: 3484- 3488, 2000.

GAM47 269 AR Migeon, B. R.; Brown, T. R.; Axelman, J.; Migeon, C. J.: Studiesof the locus 3 A c
for androgen receptor: localization on the human X andevidence for homology with the Tfm locus in the mouse. Proc. Nat.Acad. Sci. 78: 6339- 6343, 1981.

GAM47 269 AR Mongan, N. P.; Jaaskelainen, J.; Green, K.; Schwabe, J. W.; Shimura,N.; 3 A c
Dattani, M.; Hughes, I. A.: Two de novo mutations in the AR genecause the complete androgen insensitivity syndrome in a pair of monozygotictwins. J. Clin. Endocr. Metab. 87: 1057- 1061, 2002.

GAM47 269 AR Mononen, N.; Syrjakoski, K.; Matikainen, M.; Tammela, T. L. J.;Schleutker, 3 A c
J.; Kallioniemi, O.- P.; Trapman, J.; Koivisto, P. A.:Two percent of Finnish prostate cancer patients have a germ- line mutationin the hormone- binding domain of the androgen receptor gene. CancerRes. 60: 6479- 6481, 2000.

GAM47 269 AR Murono, K.; Mendonca, B. B.; Arnhold, I. J. P.; Rigon, A. C. M.M.; Migeon, 3 A c
C. J.; Brown, T. R.: Human androgen insensitivity dueto point mutations encoding amino acid substitutions in the androgenreceptor steroid- binding domain. Hum. Mutat. 6: 152- 162, 1995.

GAM47 269 AR Nakao, R.; Haji, M.; Yanase, T.; Ogo, A.; Takayanagi, R.; Katsube,T.; 3 A c
Fukumaki, Y.; Nawata, H.: A single amino acid substitution (met786- to-val)in the steroid- binding domain of human androgen receptor leads tocomplete androgen insensitivity syndrome. J. Clin. Endocr. Metab. 74:1152- 1157, 1992.

GAM47 269 AR Newmark, J. R.; Hardy, D. O.; Tonb, D. C.; Carter, B. S.; Epstein,J. I.; 3 A c
Isaacs, W. B.; Brown, T. R.; Barrack, E. R.: Androgen receptorgene mutations in human prostate cancer. Proc. Nat. Acad. Sci. 89:6319- 6323, 1992.

GAM47 269 AR Nguyen, D.; Steinberg, S. V.; Rouault, E.; Chagnon, S.; Gottlieb,B.; Pinsky, 3 A c
L.; Trifiro, M.; Mader, S.: A G577R mutation in the humanAR P box results in selective decreases in DNA binding and in partialandrogen insensitivity syndrome. Molec. Endocr. 15: 1790- 1802, 2001.

GAM47 269 ASB1 Hirosawa, M.; Nagase, T.; Ishikawa, K.; Kikuno, R.; Nomura, N.;Ohara, O.: 3 A c
Characterization of cDNA clones selected by the GeneMarkanalysis from size-fractionated cDNA libraries from human brain. DNARes. 6: 329- 336, 1999.

GAM47 269 ASB1 Kile, B. T.; Viney, E. M.; Willson, T. A.; Brodnicki, T. C.; Cancilla,M. R.; 3 A c
Herlihy, A. S.; Croker, B. A.; Baca, M.; Nicola, N. A.; Hilton,D. J.; Alexander, W. S.: Cloning and characterization of the genesencoding the ankyrin repeat and SOCS box- containing proteins Asb- 1,Asb- 2, Asb- 3, and Asb- 4. Gene 258: 31- 41, 2000.

GAM47 269 ATRN Duke- Cohan, J. S.; Gu, J.; McLaughlin, D. F.; Xu, Y.; Freeman,G. J.; 3 A c
Schlossman, S. F.: Attractin (DPPT- L), a member of the CUBfamily of cell
adhesion and guidance proteins, is secreted by activatedhuman T lymphocytes
and modulates immune cell interactions. Proc.Nat. Acad. Sci. 95: 11336-
11341, 1998.

GAM47 269 ATRN Gunn, T. M.; Miller, K. A.; He, L.; Hyman, R. W.; Davis, R. W.;Azarani, A.; 3 A c
Schlessman, S. F.; Duke- Cohan, J. S.; Barsh, G. S.:The mouse mahogany locus
encodes a transmembrane form of human attractin. Nature 398:152- 156, 1999.

GAM47 269 ATRN He, L.; Gunn, T. M.; Bouley, D. M.; Lu, X.- Y.; Watson, S. J.; Schlossman,S. 3 A c
F.; Duke- Cohan, J. S.; Barsh, G. S.: A biochemical function forattractin in
agouti- induced pigmentation and obesity. Nature Genet. 27:40- 47, 2001.

GAM47 269 ATRN Nagle, D. L.; McGrail, S. H.; Vitale, J.; Woolf, E. A.; Dussault,B. J., Jr.; 3 A c
DiRocco, L.; Holmgren, L.; Montagno, J.; Bork, P.; Huszar,D.; Fairchild-
Huntress, V.; Ge, P.; Keilty, J.; Ebelling, C.; Baldini,L.; Gilchrist, J.;
Burr, P.; Carlson, G. A.; Moore, K. J.: The mahoganyprotein is a receptor
involved in suppression of obesity. Nature 398:148- 151, 1999.

GAM47 269 ATRN Tang, W.; Gunn, T. M.; McLaughlin, D. F.; Barsh, G. S.; Schlossman,S. F.; 3 A c
Duke- Cohan, J. S.: Secreted and membrane attractin resultfrom alternative
splicing of the human ATRN gene. Proc. Nat. Acad.Sci. 97: 6025- 6030, 2000.

GAM47 269 BIG1 Mansour, S. J.; Skaug, J.; Zhao, X.- H.; Giordano, J.; Scherer,S. W.; 3 A c
Melancon, P.: p200 ARF- GEP1: a Golgi- localized guanine nucleotideexchange
protein whose Sec7 domain is targeted by the drug brefeldinA. Proc. Nat.
Acad. Sci. 96: 7968- 7973, 1999.

GAM47 269 BIG1 Morinaga, N.; Moss, J.; Vaughan, M.: Cloning and expression ofa cDNA 3 A c
encoding a bovine brain brefeldin A- sensitive guanine nucleotide-
exchangeprotein for ADP- ribosylation factor. Proc. Nat. Acad. Sci. 94:
12926- 12931,1997.

GAM47 269 BIG1 Morinaga, N.; Tsai, S.- C.; Moss, J.; Vaughan, M.: Isolation ofa brefeldin 3 A c
A- inhibited guanine nucleotide- exchange protein for ADPribosylation factor
(ARF) 1 and ARF3 that contains a Sec7- like domain. Proc.Nat. Acad. Sci. 93:
12856- 12860, 1996.

GAM47 269 BIG1 Togawa, A.; Morinaga, N.; Ogasawara, M.; Moss, J.; Vaughan, M.: Purification 3 A c
and cloning of a brefeldin A- inhibited guanine nucleotide- exchangeprotein
for ADP- ribosylation factors. J. Biol. Chem. 274: 12308- 12315,1999.

GAM47 269 BMP4 Connor, J. M.: Fibrodysplasia ossificans progressiva: lessonsfrom rare 3 A c
maladies. (Editorial) New Eng. J. Med. 335: 591- 593, 1996.

GAM47 269 BMP4 Dickinson, M. E.; Kobrin, M. S.; Silan, C. M.; Kingsley, D. M.;Justice, M. 3 A c
J.; Miller, D. A.; Ceci, J. D.; Lock, L. F.; Lee, A.;Buchberg, A. M.;
Siracusa, L. D.; Lyons, K. M.; Derynck, R.; Hogan,B. L. M.; Copeland, N. G.;
Jenkins, N. A.: Chromosomal localizationof seven members of the murine TGF-
beta superfamily suggests closelinkage to several morphogenetic mutant loci.
Genomics 6: 505- 520,1990.

GAM47 269 BMP4 Dooley, C. A.; Attia, G. R.; Rainey, W. E.; Moore, D. R.; Carr,B. R.: Bone 3 A c
morphogenetic protein inhibits ovarian androgen production. J.Clin. Endocr.
Metab. 85: 3331- 3337, 2000.

GAM47 269 BMP4 McAlpine, P. J.: Personal Communication. Winnipeg, Manitoba,Canada 3 A c
7/15/1992.

GAM47 269 BMP4 Monsoro- Burq, A.- H.; le Douarin, N. M.: BMP4 plays a key rolein left- 3 A c
right patterning in chick embryos by maintaining Sonic Hedgehogasymmetry.
Molec. Cell 7: 789- 799, 2001.

GAM47 269 BMP4 Shafritz, A. B.; Shore, E. M.; Gannon, F. H.; Zasloff, M. A.; Taub,R.; Muenke, M.; Kaplan, F. S.: Overexpression of an osteogenic morphogenin fibrodysplasia ossificans progressiva. New Eng. J. Med. 335:555- 561, 1996. 3 A c

GAM47 269 BMP4 Tabas, J. A.; Hahn, G. V.; Cohen, R. B.; Seaunez, H. N.; Modi,W. S.; Wozney, J. M.; Zasloff, M.; Kaplan, F. S.: Chromosomal assignmentof the human gene for bone morphogenetic protein 4. Clin. Orthop.Rel. Res. 293: 310- 316, 1993. 3 A c

GAM47 269 BMP4 Tucker, A. S.; Matthews, K. L.; Sharpe, P. T.: Transformationof tooth type induced by inhibition of BMP signaling. Science 282:1136- 1138, 1998. 3 A c

GAM47 269 BMP4 van den Wijngaard, A.; Olde Weghuis, D.; Boersma, C. J. C.; vanZoelen, E. J. J.; Geurts van Kessel, A.; Olijve, W.: Fine mappingof the human bone morphogenetic protein- 4 gene (BMP4) to chromosome14q22- q23 by in situ hybridization. Genomics 27: 559- 560, 1995. 3 A c

GAM47 269 BMP4 van den Wijngaard, A.; van Kraay, M.; van Zoelen, E. J. J.; Olijve,W.; Boersma, C. J. C.: Genomic organization of the human bone morphogeneticprotein- 4 gene: molecular basis for multiple transcripts. Biochem.Biophys. Res. Commun. 219: 789- 794, 1996. 3 A c

GAM47 269 C1orf6 Davidson, J. D.; Riley, B.; Burright, E.N.; Duvick, L.A.; Zoghbi,H.Y.; Orr, H. T.: Identification and characterization of an ataxin- 1- interactingprotein: A1Up, a ubiquitin- like nuclear protein. Hum. Molec. Genet. 9:2305- 2312, 2000. 3 A c

GAM47 269 C1orf6 Fogli, A.; Giglio, S.; Arrigo, G.; Lo Nigro, C.; Zollo, M.; Viggiano,L.; Rocchi, M.; Archidiacono, N.; Zuffardi, O.; Carrozzo, R.: Identificationof two paralogous regions mapping to the short and long arms of humanchromosome 2 comprising LIS1 pseudogenes. Cytogenet. Cell Genet. 86:225- 232, 1999. 3 A c

GAM47 269 CAPG Dabiri, G. A.; Young, C. L.; Rosenbloom, J.; Southwick, F. S.:Molecular cloning of human macrophage capping protein cDNA: a uniquemember of the gelsolin/villin family expressed primarily in macrophages. J.Biol. Chem. 267: 16545- 16552, 1992. 3 A c

GAM47 269 CAPG Mishra, V. S.; Henske, E. P.; Kwiatkowski, D. J.; Southwick, F.S.: The human actin- regulatory protein cap G: gene structure andchromosome location. Genomics 23: 560- 565, 1994. 3 A c

GAM47 269 CAPG Southwick, F. S.; DiNubile, M. J.: Rabbit alveolar macrophagescontain a Ca(2+)- sensitive, 41,000- Dalton protein which reversiblyblocks the 'barbed' ends of actin filaments but does not sever them. J.Biol. Chem. 261: 14191- 14195, 1986. 3 A c

GAM47 269 CCND2 Inaba, T.; Matsushime, H.; Valentine, M.; Roussel, M. F.; Sherr,C. J.; Look, A. T.: Genomic organization, chromosomal localization,and independent expression of human cyclin D genes. Genomics 13:565- 574, 1992. 3 A c

GAM47 269 CCND2 Kim, H. A.; Pomeroy, S. L.; Whoriskey, W.; Pawlitzky, I.; Benowitz,L. I.; Sicinski, P.; Stiles, C. D.; Roberts, T. M.: A developmentallyregulated switch directs regenerative growth of Schwann cells throughcyclin D1. Neuron 26: 405- 416, 2000. 3 A c

GAM47 269 CCND2 Xiong, Y.; Menninger, J.; Beach, D.; Ward, D. C.: Molecular cloningand chromosomal mapping of CCND genes encoding human D- type cyclins. Genomics 13:575- 584, 1992. 3 A c

GAM47 269 CGA Amato, F.; Warnes, G. M.; Kirby, C. A.; Norman, R. J.: Infertilitycaused by hCG autoantibody. J. Clin. Endocr. Metab. 87: 993- 997,2002. 3 A c

GAM47 269 CGA Boothby, M.; Ruddon, R. W.; Anderson, C.; McWilliams, D.; Boime,I.: A single gonadotropin alpha- subunit gene in normal tissue andtumor- derived cell 3 A c

lines. J. Biol. Chem. 256: 5121- 5127, 1981.

GAM47 269 CGA Bordelon, M.; Kohler, P. O.: Synthesis of human glycoprotein hormonein somatic cell hybrids. (Abstract) J. Cell Biol. 67: 37A only,1975. 3 A c

GAM47 269 CGA Bordelon- Riser, M. E.; Siciliano, M. J.; Kohler, P. O.: Necessityfor two human chromosomes for human chorionic gonadotropin productionin human- mouse hybrids. Somat. Cell Genet. 5: 597- 613, 1979. 3 A c

GAM47 269 CGA Chin, W. W.: Personal Communication. Boston, Mass. 2/15/1982. 3 A c

GAM47 269 CGA Fiddes, J. C.; Goodman, H. M.: Isolation, cloning and sequenceanalysis of the cDNA for the alpha- subunit of human chorionic gonadotropin. Nature 281:351- 356, 1979. 3 A c

GAM47 269 CGA Fiddes, J. C.; Goodman, H. M.: The gene encoding the common alphasubunit of the four human glycoprotein hormones. J. Molec. Appl.Genet. 1: 3- 18, 1981. 3 A c

GAM47 269 CGA Hardin, J. W.; Riser, M. E.; Trent, J. M.; Kohler, P. O.: Thechorionic gonadotropin alpha- subunit gene is on human chromosome 18in JEG cells. Proc. Nat. Acad. Sci. 80: 6282- 6285, 1983. 3 A c

GAM47 269 CGA Heitz, P. U.; Kasper, M.; Kloppel, G.; Polak, J. M.; Vaitukaitis,J. L.: Glycoprotein- hormone alpha- chain production by pancreaticendocrine tumors: a specific marker for malignancy- - immunocytochemicalanalysis of tumors of 155 patients. Cancer 51: 277- 282, 1983. 3 A c

GAM47 269 CGA Hoshina, M.; Boothby, M. R.; Hussa, R. D.; Pattillo, R. A.; Camel,H. M.; Boime, I.: Segregation patterns of polymorphic restrictionsites of the gene encoding the alpha subunit of human chorionic gonadotropinin trophoblastic disease. Proc. Nat. Acad. Sci. 81: 2504- 2507, 1984. 3 A c

GAM47 269 CGA Lebo, R. V.: Personal Communication. San Francisco, Calif. 1/14/1980. 3 A c

GAM47 269 CGA Morgan, F. J.; Birken, S.; Canfield, R. E.: The amino acid sequenceof human chorionic gonadotropin: the alpha subunit and beta subunit. J.Biol. Chem. 250: 5247- 5258, 1975. 3 A c

GAM47 269 CGA Naylor, S. L.; Chin, W. W.; Goodman, H. M.; Lalley, P. A.; Grzeschik,K.- H.; Sakaguchi, A. Y.: Chromosome assignment of the genes encodingthe alpha and beta subunits of the glycoprotein hormones in man andmouse. Somat. Cell Genet. 9: 757- 770, 1983. 3 A c

GAM47 269 CGA Ruddon, R. W.; Hanson, C. A.; Addison, N. J.: Synthesis and processingof human chorionic gonadotropin subunits in cultured choriocarcinomacells. Proc. Nat. Acad. Sci. 76: 5143- 5147, 1979. 3 A c

GAM47 269 CGA Trent, J.: Personal Communication. Tucson, Ariz. 11/23/1982. 3 A c

GAM47 269 CISH Uchida, K.; Yoshimura, A.; Inazawa, J.; Yanagisawa, K.; Osada,H.; Masuda, A.; Saito, T.; Takahashi, T.; Miyajima, A.; Takahashi,T.: Molecular cloning of CISH, chromosome assignment to 3p21.3, andanalysis of expression in fetal and adult tissues. Cytogenet. CellGenet. 78: 209- 212, 1997. 3 A c

GAM47 269 CISH Yoshimura, A.; Ohkubo, T.; Kiguchi, T.; Jenkins, N. A.; Gilbert,D. J.; Copeland, N. G.; Hara, T.; Miyajima, A.: A novel cytokine- inducible gene CIS, encodes an SH2- containing protein that binds to tyrosine- phosphorylatedinterleukin 3 and erythropoietin receptors. EMBO J. 14: 2816- 2826,1995. 3 A c

GAM47 269 CIT Di Cunto, F.; Calautti, E.; Hsiao, J.; Ong, L.; Topley, G.; Turco,E.; Dotto, G. P.: Citron Rho- interacting kinase, a novel tissue- specificser/thr kinase encompassing the Rho- Rac- binding protein citron. J.Biol. Chem. 273: 29706- 29711, 1998. 3 A c

GAM47 269 CIT Di Cunto, F.; Imarisio, S.; Hirsch, E.; Broccoli, V.; Bulfone,A.; Migheli, A.; Atzori, C.; Turco, E.; Triolo, R.; Dotto, G. P.;Silengo, L.; Altruda, 3 A c

F.: Defective neurogenesis in citron kinaseknockout mice by altered cytokinesis and massive apoptosis. Neuron 28:115- 127, 2000.

GAM47 269 CIT Madaule, P.; Furuyashiki, T.; Reid, T.; Ishizaki, T.; Watanabe,G.; Morii, 3 A c
N.; Narumiya, S.: A novel partner for the GTP- bound formsof rho and rac. FEBS Lett. 377: 243- 248, 1995.

GAM47 269 CIT Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999.

GAM47 269 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 A c
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.: Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM47 269 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 3 A c
37, 2001.

GAM47 269 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: 3 A c
Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001.

GAM47 269 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification 3 A c
of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001.

GAM47 269 COPA Chow, V. T. K.; Quek, H. H.: HEP- COP, a novel human gene whoseproduct is 3 A c
highly homologous to the alpha- subunit of the yeast coatomerprotein complex. Gene 169: 223- 227, 1996.

GAM47 269 COPA Presley, J. F.; Ward, T. H.; Pfeifer, A. C.; Siggia, E. D.; Phair,R. D.; 3 A c
Lippincott- Schwartz, J.: Dissection of COPI and Arf1 dynamicsin vivo and role in Golgi membrane transport. Nature 417: 187- 193,2002.

GAM47 269 COPA Quek, H. H.; Chow, V. T. K.: Genomic organization and mappingof the human 3 A c
HEP- COP gene (COPA) to 1q. Cytogenet. Cell Genet. 76:139- 143, 1997.

GAM47 269 COPA Quek, H. H.; Chow, V. T. K.: Molecular and cellular studies ofthe human 3 A c
homolog of the 160- kD alpha- subunit of the coatomer proteincomplex. DNA Cell Biol. 16: 275- 280, 1997.

GAM47 269 CPT1B Britton, C. H.; Mackey, D. W.; Esser, V.; Foster, D. W.; Burns,D. K.; 3 A c
Yarnall, D. P.; Froguel, P.; McGarry, J. D.: Fine chromosomemapping of the genes for human liver and muscle carnitine palmitoyltransferasel (CPT1A and CPT1B). Genomics 40: 209- 211, 1997.

GAM47 269 CPT1B van der Leij, F. R.; Takens, J.; van der Veen, A. Y.; Terpstra,P.; Kuipers, 3 A c
J. R. G.: Localization and intron usage analysis ofthe human CPT1B gene for muscle type carnitine palmitoyltransferasel. Biochim. Biophys. Acta 1352: 123- 128, 1997.

GAM47 269 CPT1B Yamazaki, N.; Shinohara, Y.; Shima, A.; Yamanaka, Y.; Terada, H.: Isolation 3 A c
and characterization of cDNA and genomic clones encodinghuman muscle type carnitine palmitoyltransferase I. Biochim. Biophys.Acta 1307: 157- 161, 1996.

GAM47 269 CPT1B Yamazaki, N.; Yamanaka, Y.; Hashimoto, Y.; Shinohara, Y.; Shima,A.; Terada, 3 A c
H.: Structural features of the gene encoding human muscletype carnitine palmitoyltransferase I. FEBS Lett. 409: 401- 406,1997.

GAM47 269 CUGBP1 Good, P. J.; Chen, Q.; Warner, S. J.; Herring, D. C.: A familyof human RNA- 3 A c
binding proteins related to the Drosophila Bruno transcriptionalregulator.

J. Biol. Chem. 275: 28583- 28592, 2000.

GAM47 269 CUGBP1 Roberts, R.; Timchenko, N. A.; Miller, J. W.; Reddy, S.; Caskey,C. T.; Swanson, M. S.; Timchenko, L. T.: Altered phosphorylationand intracellular distribution of a (CUG)n triplet repeat RNA- bindingprotein in patients with myotonic dystrophy and in myotonin proteinkinase knockout mice. Proc. Nat. Acad. Sci. 94: 13221- 13226, 1997. 3 A c

GAM47 269 CUGBP1 Timchenko, L. T.; Miller, J. W.; Timchenko, N. A.; DeVore, D. R.;Datar, K. V.; Lin, L.; Roberts, R.; Caskey, C. T.; Swanson, M. S.: Identification of a (CUG)n triplet repeat RNA- binding protein andits expression in myotonic dystrophy. Nucleic Acids Res. 24: 4407- 4414,1996. 3 A c

GAM47 269 CUGBP1 Timchenko, L. T.; Timchenko, N. A.; Caskey, C. T.; Roberts, R.: Novel proteins with binding specificity for DNA CTG repeats andRNA CUG repeats: implications for myotonic dystrophy. Hum. Molec.Genet. 5: 115- 121, 1996. 3 A c

GAM47 269 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 A c

GAM47 269 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 A c

GAM47 269 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4- alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 A c

GAM47 269 DAAM2 Habas, R.; Kato, Y.; He, X.: Wnt/Frizzled activation of Rho regulatesvertebrate gastrulation and requires a novel Formin homology proteinDaam1. Cell 107: 843- 854, 2001. 3 A c

GAM47 269 DAAM2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 A c

GAM47 269 DCTN1 Collin, G. B.; Nishina, P. M.; Marshall, J. D.; Naggert, J. K.: Human DCTN1: genomic structure and evaluation as a candidate forAlstrom syndrome. Genomics 53: 359- 364, 1998. 3 A c

GAM47 269 DCTN1 Holzbaur, E. L. F.; Tokito, M. K.: Localization of the DCTN1 geneencoding p150(Glued) to human chromosome 2p13 by fluorescence in situhybridization. Genomics 31: 398- 399, 1996. 3 A c

GAM47 269 DCTN1 Holzbaur, E. L. F.; Vallee, R. B.: Dyneins: molecular structureand cellular function. Ann. Rev. Cell Biol. 10: 339- 372, 1994. 3 A c

GAM47 269 DCTN1 Jang, W.; Weber, J. S.; Tokito, M. K.; Holzbaur, E. L. F.; Meisler,M. H.: Mouse p150(Glued) (dynactin 1) cDNA sequence and evaluationas a candidate for the neuromuscular disease mutation mnd2. Biochem.Biophys. Res. Commun. 231: 344- 347, 1997. 3 A c

GAM47 269 DCTN1 Korthaus, D.; Wedemeyer, N.; Lengeling, A.; Ronsiek, M.; Jockusch,H.; Schmitt- John, T.: Integrated radiation hybrid map of human chromosome2p13: possible involvement of dynactin in neuromuscular diseases. Genomics 43:242- 244, 1997. 3 A c

GAM47 269 DCTN1 Pushkin, A.; Abuladze, N.; Newman, D.; Tatishchev, S.; Kurtz, I.: Genomic 3 A c

organization of the DCTN1- SLC4A5 locus encoding both NBC4and p150(Glued). Cytogenet. Cell Genet. 95: 163- 168, 2001.

GAM47 269 DEC1 Miura, K.; Suzuki, K.; Tokino, T.; Isomura, M.; Inazawa, J.; Matsuno,S.; Nakamura, Y.: Detailed deletion mapping in squamous cell carcinomasof the esophagus narrows a region containing a putative tumor suppressorgene to about 200 kilobases on distal chromosome 9q. Cancer Res. 56:1629- 1634, 1996. 3 A c

GAM47 269 DEC1 Nishiwaki, T.; Daigo, Y.; Kawasoe, T.; Nakamura, Y.: Isolationand mutational analysis of a novel human cDNA, DEC1 (deleted in esophagealcancer 1), derived from the tumor suppressor locus in 9q32. GenesChromosomes Cancer 27: 169- 176, 2000. 3 A c

GAM47 269 DNMT3A Baylin, S. B.; Herman, J. G.; Graff, J. R.; Vertino, P. M.; Issa,J. P.: Alterations in DNA methylation: a fundamental aspect of neoplasia. Adv.Cancer Res. 72: 141- 196, 1998. 3 A c

GAM47 269 DNMT3A Lei, H.; Oh, S. P.; Okano, M.; Juttermann, R.; Goss, K. A.; Jaenisch,R.; Li, E.: De novo DNA cytosine methyltransferase activities inmouse embryonic stem cells. Development 122: 3195- 3205, 1996. 3 A c

GAM47 269 DNMT3A Lyko, F.; Ramsahoye, B. H.; Kashevsky, H.; Tudor, M.; Mastrangelo,M.- A.; Orr- Weaver, T. L.; Jaenisch, R.: Mammalian (cytosine- 5) methyltransferasescause genomic DNA methylation and lethality in Drosophila. NatureGenet. 23: 363- 366, 1999. 3 A c

GAM47 269 DNMT3A Okano, M.; Bell, D. W.; Haber, D. A.; Li, E.: DNA methyltransferasesDnmt3a and Dnmt3b are essential for de novo methylation and mammaliandevelopment. Cell 99: 247- 257, 1999. 3 A c

GAM47 269 DNMT3A Okano, M.; Xie, S.; Li, E.: Cloning and characterization of afamily of novel mammalian DNA (cytosine- 5) methyltransferases. (Letter) NatureGenet. 19: 219- 220, 1998. 3 A c

GAM47 269 DNMT3A Robertson, K. D.; Uzvolgyi, E.; Liang, G.; Talmadge, C.; Sumegi,J.; Gonzales, F. A.; Jones, P. A.: The human DNA methyltransferases(DNMTs) 1, 3a and 3b: coordinate mRNA expression in normal tissuesand overexpression in tumors. Nucleic Acids Res. 27: 2291- 2298,1999. 3 A c

GAM47 269 DNMT3A Xie, S.; Wang, Z.; Okano, M.; Nogami, M.; Li, Y.; He, W.- W.; Okumura,K.; Li, E.: Cloning, expression and chromosome locations of the humanDNMT3 gene family. Gene 236: 87- 95, 1999. 3 A c

GAM47 269 DPYSL2 Hamajima, N.; Matsuda, K.; Sakata, S.; Tamaki, N.; Sasaki, M.;Nonaka, M.: A novel gene family defined by human dihydropyrimidinaseand three related proteins with differential tissue distribution. Gene 180:157- 163, 1996. 3 A c

GAM47 269 DPYSL2 Koyama, K.; Sudo, K.; Nakamura, Y.: Isolation of 115 human chromosome8- specific expressed- sequence tags by exon amplification. Genomics 26:245- 253, 1995. 3 A c

GAM47 269 DRG2 Schenker, T.; Lach, C.; Kessler, B.; Calderara, S.; Trueb, B.:A novel GTP- binding protein which is selectively repressed in SV40transformed fibroblasts. J. Biol. Chem. 269: 25447- 25453, 1994. 3 A c

GAM47 269 DRG2 Schenker, T.; Trueb, B.: Assignment of the gene for a developmentallyregulated GTP- binding protein (DRG2) to human chromosome bands 17p13- p12by in situ hybridization. Cytogenet. Cell Genet. 79: 274- 275, 1997. 3 A c

GAM47 269 DRG2 Vlangos, C. N.; Das, P.; Patel, P. I.; Elsea, S. H.: Assignmentof developmentally regulated GTP- binding protein (DRG2) to human chromosomeband 17p11.2 with somatic cell hybrids and localization to the 3 A c

Smith- Magenissyndrome critical interval. Cytogenet. Cell Genet. 88: 283-285,2000.

GAM47 269 DVL3 Bui, T. D.; Beier, D. R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; Kaklamanis, L.; Kearney, L.; Regan, R.; Sussman, D. J.; Harris,A. L.: cDNA cloning of a human dishevelled DVL- 3 gene, mapping to3q27, and expression in human breast and colon carcinomas. Biochem.Biophys. Res. Commun. 239: 510- 516, 1997. 3 A c

GAM47 269 DVL3 Klingensmith, J.; Nusse, R.; Perrimon, N.: The Drosophila segmentpolarity gene dishevelled encodes a novel protein required for responseto wingless signal. Genes Dev. 8: 118- 130, 1994. 3 A c

GAM47 269 DVL3 Pizzuti, A.; Amati, F.; Calabrese, G.; Mari, A.; Colosimo, A; Silani,V.; Giardino, L.; Ratti, A.; Penso, D.; Calza, L.; Palka, G.; Scarlato,G.; Novelli, G.; Dallapicolla, B.: cDNA characterization and chromosomalmapping of two human homologs of the Drosophila dishevelled polaritygene. Hum. Molec. Genet. 5: 953- 958, 1996. 3 A c

GAM47 269 DVL3 Semenov, M. V.; Snyder, M.: Human dishevelled genes constitutea DHR-containing multigene family. Genomics 42: 302- 310, 1997. 3 A c

GAM47 269 EHF Kas, K.; Finger, E.; Grall, F.; Gu, X.; Akbarali, Y.; Boltax, J.;Weiss, A.; Oettgen, P.; Kapeller, R.; Libermann, T. A.: ESE- 3, anovel member of an epithelium- specific Ets transcription factor subfamily,demonstrates different target gene specificity from ESE- 1. J. Biol.Chem. 275: 2986-2998, 2000. 3 A c

GAM47 269 EHF Kleinbaum, L. A.; Duggan, C.; Ferreira, E.; Coffey, G. P.; Buttice,G.; Burton, F. H.: Human chromosomal localization, tissue/tumor expression,and regulatory function of the ets family gene EHF. Biochem. Biophys.Res. Commun. 264: 119- 126, 1999. 3 A c

GAM47 269 EHHADH Hoefler, G.; Forstner, M.; McGuinness, M. C.; Hulla, W.; Hiden,M.; Krisper, P.; Kenner, L.; Ried, T.; Lengauer, C.; Zechner, R.;mOser, H. W.; Chen, G. L.: cDNA cloning of the human peroxisomalenoyl- CoA hydratase:3-hydroxyacyl- CoA dehydrogenase bifunctional enzymeand localization to chromosome 3q26.3- 3q28: a free left Alu arm isinserted in the 3- prime noncoding region. Genomics 19: 60- 67, 1994. 3 A c

GAM47 269 ENO1 Comings, D. E.: Evidence for ancient tetraploidy and conservationof linkage groups in mammalian chromosomes. Nature 238: 455- 457,1972. 3 A c

GAM47 269 ENO1 D'Ancona, G. G.; Chern, C. J.; Benn, P.; Croce, C. M.: Assignmentof the human gene for enolase 1 to region pter- p36 of chromosome 1. Cytogenet.Cell Genet. 18: 327- 332, 1977. 3 A c

GAM47 269 ENO1 D'Ancona, G. G.; Croce, C. M.: Assignment of the gene for enolaseto mouse chromosome 4 using somatic cell hybrids. Cytogenet. CellGenet. 19: 1- 6, 1977. 3 A c

GAM47 269 ENO1 Feo, S.; Oliva, D.; Arico, B.; Barba, G.; Cali, L.; Giallongo,A.: The human genome contains a single processed pseudogene for alphaenolase located on chromosome 1. DNA Sequence 1: 79- 83, 1990. 3 A c

GAM47 269 ENO1 Feo, S.; Oliva, D.; Barbieri, G.; Xu, W.; Fried, M.; Giallongo,A.: The gene for the muscle- specific enolase is on the short armof human chromosome 17. Genomics 6: 192- 194, 1990. 3 A c

GAM47 269 ENO1 Giallongo, A.; Feo, S.; Moore, R.; Croce, C. M.; Showe, L. C.:Molecular cloning and nucleotide sequence of a full- length cDNA forhuman alpha enolase. Proc. Nat. Acad. Sci. 83: 6741- 6745, 1986. 3 A c

GAM47 269 ENO1 Giblett, E. R.; Chen, S.- H.; Anderson, J. E.; Lewis, M.: A familystudy 3 A c

suggesting genetic linkage of phosphopyruvate hydratase (enolase)to the Rh blood group system. Cytogenet. Cell Genet. 13: 91- 92,1974.

GAM47 269 ENO1 Goss, S. J.; Harris, H.: Gene transfer by means of cell fusion.II. The mapping of 8 loci on human chromosome 1 by statistical analysisof gene assortment in somatic cell hybrids. J. Cell Sci. 25: 39- 57,1977. 3 A c

GAM47 269 ENO1 Lachant, N. A.; Jennings, M. A.; Tanaka, K. R.: Partial erythrocyteenolase deficiency: a hereditary disorder with variable clinical expression.(Abstract) Blood 68: 55a only, 1986. 3 A c

GAM47 269 ENO1 Lachant, N. A.; Tanaka, K. R.: Enolase kinetic properties inpartial erythrocyte enolase deficiency. (Abstract) Clin. Res. 35:426A only, 1987. 3 A c

GAM47 269 ENO1 Lalley, P. A.; Francke, U.; Minna, J. D.: Homologous genes forenolase, phosphogluconate dehydrogenase, phosphoglucomutase, and adenylatekinase are syntenic on mouse chromosome 4 and human chromosome 1p. Proc.Nat. Acad. Sci. 75: 2382- 2386, 1978. 3 A c

GAM47 269 ENO1 Ohno, S.: Ancient linkage groups and frozen accidents. Nature 244:259- 262, 1973. 3 A c

GAM47 269 ENO1 Ribaudo, M. R.; Di Leonardo, A.; Rubino, P.; Giallongo, A.; Feo,S.: Assignment of enolase processed pseudogene (ENO1P) to human chromosome1 bands 1q41- q42. Cytogenet. Cell Genet. 74: 201- 202, 1996. 3 A c

GAM47 269 ENO1 Van Cong, N.; Weil, D.; Rebourcet, R.; Frezal, J.: Localisationdes enolases 1 et 2 respectivement sur les chromosomes 1 et 12 parl'analyse des hybrids homme- souris. Ann. Genet. 20: 153- 157, 1977. 3 A c

GAM47 269 ENO1 Wistow, G. J.; Lietman, T.; Williams, L. A.; Stapel, S. O.; deJong, W. W.; Horwitz, J.; Piatigorsky, J.: Tau- crystallin/alpha- enolase:one gene encodes both an enzyme and a lens structural protein. J.Cell Biol. 107: 2729- 2736, 1988. 3 A c

GAM47 269 EPB49 Azim, A. C.; Knoll, J. H. M.; Beggs, A. H.; Chisti, A. H.: Isoformcloning, actin binding, and chromosomal localization of human erythroiddematin, a member of the villin superfamily. J. Biol. Chem. 270:17407- 17413, 1995. 3 A c

GAM47 269 EPB49 Azim, A. C.; Marfatia, S. M.; Korsgren, C.; Dotimas, E.; Cohen,C. M.; Chishti, A. H.: Human erythrocyte dematin and protein 4.2(pallidin) are ATP binding proteins. Biochemistry 35: 3001- 3006,1996. 3 A c

GAM47 269 EPB49 Chishti, A. H.; Faquin, W.; Wu, C.- C.; Branton, D.: Purificationof erythrocyte dematin (protein 4.9) reveals an endogenous proteinkinase that modulates actin- bundling activity. J. Biol. Chem. 264:8985- 8991, 1989. 3 A c

GAM47 269 EPB49 Gilligan, D. M.; Bennett, V.: The junctional complex of the membraneskeleton. Seminars Hemat. 30: 74- 83, 1993. 3 A c

GAM47 269 EPB49 Khanna, R.; Chang, S. H.; Andrabi, S.; Azam, M.; Kim, A.; Rivera,A.; Brugnara, C.; Low, P. S.; Liu, S.- C.; Chishti, A. H.: Headpiecedomain of dematin is required for the stability of the erythrocytemembrane. Proc. Nat. Acad. Sci. 99: 6637- 6642, 2002. 3 A c

GAM47 269 EPB49 Peters, L. L.; Eicher, E. M.; Azim, A. C.; Chishti, A. H.: Thegene encoding the erythrocyte membrane skeleton protein dematin (Epb4.9)maps to mouse chromosome 14. Genomics 26: 634- 635, 1995. 3 A c

GAM47 269 EPB49 Rana, A. P.; Ruff, P.; Maalouf, G. J.; Speicher, D. W.; Chishti,A. H.: Cloning of human erythroid dematin reveals another memberof the villin family. Proc. Nat. Acad. Sci. 90: 6651- 6655, 1993. 3 A c

GAM47 269 FACL5 Oikawa, E.; Iijima, H.; Suzuki, T.; Sasano, H.; Sato, H.; Kamataki,A.; Nagura, H.; Kang, M. J.; Fujino, T.; Suzuki, H.; Yamamoto, T.T.: A novel acyl- CoA synthetase, ACS5, expressed in intestinal epithelialcells and 3 A c

proliferating preadipocytes. J. Biochem. 124: 679- 685,1998.

GAM47 269 FACL5 Yamashita, Y.; Kumabe, T.; Cho, Y.- Y.; Watanabe, M.; Kawagishi,J.; 3 A c
Yoshimoto, T.; Fujino, T.; Kang, M.- J.; Yamamoto, T. T. Fattyacid induced
glioma cell growth is mediated by the acyl- CoA synthetase5 gene located on
chromosome 10q25.1- q25.2, a region frequently deletedin malignant gliomas.
Oncogene 19: 5919- 5925, 2000.

GAM47 269 FGF23 ADHR Consortium: Autosomal dominant hypophosphataemic ricketsis associated 3 A
c
with mutations in FGF23. Nature Genet. 26: 345- 348,2000.

GAM47 269 FGF23 Bowe, A. E.; Finnegan, R.; Jan de Beur, S. M.; Cho, J.; Levine,M. A.; Kumar, 3 A c
R.; Schiavi, S. C.: FGF- 23 inhibits renal tubular phosphatetransport and is
a PHEX substrate. Biochem. Biophys. Res. Commun. 284:977- 981, 2001.

GAM47 269 FGF23 Shimada, T.; Mizutani, S.; Muto, T.; Yoneya, T.; Hino, R.; Takeda,S.; 3 A c
Takeuchi, Y.; Fujita, T.; Fukumoto, S.; Yamashita, T.: Cloningand
characterization of FGF23 as a causative factor of tumor-
inducedosteomalacia. Proc. Nat. Acad. Sci. 98: 6500- 6505, 2001.

GAM47 269 FGF23 Strewler, G. J.: FGF23, hypophosphatemia, and rickets: has 3 A c
phosphorylationbeen found? (Commentary) Proc. Nat. Acad. Sci. 98: 5945-
5946, 2001.

GAM47 269 FGF23 White, K. E.; Jonsson, K. B.; Carn, G.; Hampson, G.; Spector, T.D.; 3 A c
Mannstadt, M.; Lorenz- Depiereux, B.; Miyauchi, A.; Yang, I. M.;Ljunggren,
O.; Meitinger, T.; Strom, T. M.; Juppner, H.; Econs, M.J.: The autosomal
dominant hypophosphatemic rickets (ADHR) gene isa secreted polypeptide
overexpressed by tumors that cause phosphatewasting. J. Clin. Endocr. Metab.
86: 497- 500, 2001.

GAM47 269 FGF23 Yamashita, T.; Yoshioka, M.; Itoh, N.: Identification of a novelfibroblast 3 A c
growth factor, FGF- 23, preferentially expressed in theventrolateral
thalamic nucleus of the brain. Biochem. Biophys. Res.Commun. 277: 494- 498,
2000.

GAM47 269 FUT6 Brinkman- Van der Linden, E. C. M.; Mollicone, R.; Oriol, R.; Larson,G.; Van 3 A c
den Eijnden, D. H.; Van Dijk, W.: A missense mutation inthe FUT6 gene
results in total absence of alpha- 3- fucosylation ofhuman alpha- 1- acid
glycoprotein. J. Biol. Chem. 271: 14492- 14495,1996.

GAM47 269 FUT6 Cameron, H. S.; Szczepaniak, D.; Weston, B. W.: Expression ofhuman 3 A c
chromosome 19p alpha- (1,3)- fucosyltransferase genes in normaltissues:
alternative splicing, polyadenylation, and isoforms. J.Biol. Chem. 270:
20112- 20122, 1995.

GAM47 269 FUT6 Koszdin, K. L.; Bowen, B. R.: The cloning and expression of ahuman alpha- 3 A c
1,3 fucosyltransferase capable of forming the E- selectinligand. Biochem.
Biophys. Res. Commun. 187: 152- 157, 1992.

GAM47 269 FUT6 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. 3 A c
C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps
of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3
and 11q21. Genomics 26: 142- 146, 1995.

GAM47 269 FUT6 Mollicone, R.; Reguigne, I.; Fletcher, A.; Aziz, A.; Rustam, M.;Weston, B. 3 A c
W.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Molecular basisfor plasma
alpha(1,3)- fucosyltransferase gene deficiency (FUT6). J.Biol. Chem. 269:
12662- 12671, 1994.

GAM47 269 FUT6 Pang, H.; Koda, Y.; Soejima, M.; Schlaphoff, T.; Du Toit, E. D.;Kimura, H.: 3 A c
Allelic diversity of the human plasma alpha(1,3)fucosyltransferasegene

(FUT6). Ann. Hum. Genet. 63: 277- 284, 1999.

GAM47 269 FUT6 Schnyder- Candrian, S.; Borsig, L.; Moser, R.; Berger, E. G.: Localizationof 3 A c
alpha- 1,3- fucosyltransferase VI in Weibel- Palade bodies of
humanendothelial cells. Proc. Nat. Acad. Sci. 97: 8369- 8374, 2000.

GAM47 269 FUT6 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of 3 A c
a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple
homologous sequences that determine expressionof the Lewis x, sialyl Lewis
x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584,
1992.

GAM47 269 GAD1 Asada, H.; Kawamura, Y.; Maruyama, K.; Kume, H.; Ding, R.- G.; Ji,F. Y.; 3 A c
Kanbara, N.; Kuzume, H.; Sanbo, M.; Yagi, T.; Obata, K.: Micelacking the 65
kDa isoform of glutamic acid decarboxylase (GAD65)maintain normal levels of
GAD67 and GABA in their brains but are susceptibleto seizures. Biochem.
Biophys. Res. Commun. 229: 891- 895, 1996.

GAM47 269 GAD1 Asada, H.; Kawamura, Y.; Maruyama, K.; Kume, H.; Ding, R.- G.; Kanbara,N.; 3 A c
Kuzume, H.; Sanbo, M.; Yagi, T.; Obata, K.: Cleft palate anddecreased brain
gamma- aminobutyric acid in mice lacking the 67- kDaisoform of glutamic acid
decarboxylase. Proc. Nat. Acad. Sci. 94:6496- 6499, 1997.

GAM47 269 GAD1 Brilliant, M. H.; Szabo, G.; Katarova, Z.; Kozak, C. A.; Glaser,T. M.; 3 A c
Greenspan, R. J.; Housman, D. E.: Sequences homologous toglutamic acid
decarboxylase cDNA are present on mouse chromosomes2 and 10. Genomics 6:
115- 122, 1990.

GAM47 269 GAD1 Bu, D.- F.; Erlander, M. G.; Hitz, B. C.; Tillakaratne, N. J. K.;Kaufman, D. 3 A c
L.; Wagner- McPherson, C. B.; Evans, G. A.; Tobin, A. J.: Two human
glutamate decarboxylases, 65- kDa GAD and 67- kDa GAD, areeach encoded by a
single gene. Proc. Nat. Acad. Sci. 89: 2115- 2119,1992.

GAM47 269 GAD1 Bu, D.- F.; Tobin, A. J.: The exon- intron organization of the genes(GAD1 3 A c
and GAD2) encoding two human glutamate decarboxylases (GAD- 67and GAD- 65)
suggests that they derive from a common ancestral GAD. Genomics 21:222- 228,
1994.

GAM47 269 GAD1 Condie, B. G.; Bain, G.; Gottlieb, D. I.; Capecchi, M. R.: Cleftpalate in 3 A c
mice with a targeted mutation in the gamma- aminobutyricacid- producing
enzyme glutamic acid decarboxylase 67. Proc. Nat.Acad. Sci. 94: 11451-
11455, 1997.

GAM47 269 GAD1 Edelhoff, S.; Grubin, C. E.; Karlsen, A. E.; Adler, D. A.; Foster,D.; 3 A c
Disteche, C. M.; Lernmark, A.: Mapping of glutamic acid decarboxylase(GAD)
genes. Genomics 17: 93- 97, 1993.

GAM47 269 GAD1 Erlander, M. G.; Tillakaratne, N. J. K.; Feldblum, S.; Patel, N.;Tobin, A. 3 A c
J.: Two genes encode distinct glutamate decarboxylases. Neuron 7:91- 100,
1991.

GAM47 269 GAD1 Kelly, C. D.; Edwards, Y.; Johnstone, A. P.; Harfst, E.; Nogradi,A.; Nussey, 3 A c
S. S.; Povey, S.; Carter, N. D.: Nucleotide sequenceand chromosomal
assignment of a cDNA encoding the large isoform ofhuman glutamate
decarboxylase. Ann. Hum. Genet. 56: 255- 265, 1992.

GAM47 269 GAD1 Krishnamoorthy, K. S.: Pyridoxine- dependency seizure: reportof a rare 3 A c
presentation. Ann. Neurol. 13: 103- 104, 1983.

GAM47 269 GAD1 Scriver, C. R.: Vitamin B6 deficiency and dependency in man. Am.J. Dis. 3 A c
Child. 113: 109- 114, 1967.

GAM47 269 GAD1 Scriver, C. R.; Hutchison, J. H.: The vitamin B6 deficiency syndromein human 3 A c
infancy: biochemical and clinical observations. Pediatrics 31:240- 250,

1963.

GAM47 269 GAD1 Sparkes, R. S.; Kaufman, D. L.; Heinzmann, C.; Tobin, A. J.; Mohandas,T.: 3 A c
Brain glutamate decarboxylase (GAD) gene assigned to human chromosome2 by somatic cell hybrid analysis. (Abstract) Cytogenet. Cell Genet. 46:696 only, 1987.

GAM47 269 GAD1 von Boehmer, H.; Sarukhan, A.: GAD, a single autoantigen fordiabetes. 3 A c
Science 284: 1135- 1136, 1999.

GAM47 269 GAD1 Yoon, J.- W.; Yoon, C.- S.; Lim, H.- W.; Huang, Q. Q.; Kang, Y.;Pyun, K. H.; 3 A c
Hirasawa, K.; Sherwin, R. S.; Jun, H.- S.: Control ofautoimmune diabetes in NOD mice by GAD expression or suppression inbeta cells. Science 284: 1183- 1187, 1999.

GAM47 269 GAN Bomont, P.; Cavalier, L.; Blondeau, F.; Ben Hamida, C.; Belal,S.; Tazir, M.; 3 A c
Demir, E.; Topaloglu, H.; Korinthenberg, R.; Tuysuz,B.; Landrieu, P.; Hentati, F.; Koenig, M.: The gene encoding gigaxonin,a new member of the cytoskeletal BTB/kelch repeat family, is mutatedin giant axonal neuropathy. Nature Genet. 26: 370- 374, 2000.

GAM47 269 GAN Bousquet, O.; Basseville, M.; Vila- Porcile, E.; Billette de Villemeur,T.; 3 A c
Hauw, J.- J.; Landrieu, P.; Portier, M.- M.: Aggregation of a subpopulationof vimentin filaments in cultured human skin fibroblasts derived frompatients with giant axonal neuropathy. Cell. Motil. Cytoskeleton 33:115- 129, 1996.

GAM47 269 GAN Kuhlenbaumer, G.; Young, P.; Oberwittler, C.; Hunermund, G.; Schirmacher,A.; 3 A c
Domschke, K.; Ringelstein, B.; Stogbauer, F.: Giant axonal neuropathy(GAN): case report and two novel mutations in the gigaxonin gene. Neurology 58:1273- 1276, 2002. Note: Erratum: Neurology 58: 1444, 2002.

GAM47 269 GAN Pena, S. D.: Giant axonal neuropathy: an inborn error of organizationof 3 A c
intermediate filaments. Muscle Nerve 5: 166- 172, 1982.

GAM47 269 GAN Prineas, J. W.; Ouvrier, R. A.; Wright, R. G.; Walsh, J. C.; McLeod,J. G.: 3 A c
Giant axonal neuropathy: a generalized disorder of cytoplasmicmicrofilament formation. J. Neuropath. Exp. Neurol. 35: 458- 470,1976.

GAM47 269 GAN Treiber- Held, S.; Budjarjo- Welim, H.; Riemann, D.; Richter, 3 A c
J.;Kretzschmar, H. A.; Hanefeld, F.: Giant axonal neuropathy: a generalizeddisorder of intermediate filaments with longitudinal grooves in thehair. Neuropediatrics 25: 89- 93, 1994.

GAM47 269 GCN5L2 Candau, R.; Moore, P. A.; Wang, L.; Barlev, N.; Ying, C. Y.; Rosen,C. A.; 3 A c
Berger, S. L.: Identification of human proteins functionallyconserved with the yeast putative adaptors ADA2 and GCN5. Molec.Cell. Biol. 16: 593- 602, 1996.

GAM47 269 GCN5L2 Carter, K. C.; Wang, L.; Shell, B. K.; Zamir, I.; Berger, S. L.;Moore, P. 3 A c
A.: The human transcriptional adaptor genes TADA2L andGCN5L2 colocalize to chromosome 17q12- q21 and display a similar tissueexpression pattern. Genomics 40: 497- 500, 1997.

GAM47 269 GCN5L2 Wang, L.; Mizzen, C.; Ying, C.; Candau, R.; Barlev, N.; Brownell,J.; Allis, 3 A c
C. D.; Berger, S. L.: Histone acetyltransferase activityis conserved between yeast and human GCN5 and is required for complementationof growth and transcriptional activation. Molec. Cell. Biol. 17:519- 527, 1997.

GAM47 269 GCN5L2 Xu, W.; Edmondson, D. G.; Evrard, Y. A.; Wakamiya, M.; Behringer,R. R.; 3 A c
Roth, S. Y.: Loss of Gcn5l2 leads to increased apoptosis andmesodermal defects during mouse development. Nature Genet. 26: 229- 232,2000.

GAM47 269 GCN5L2 Xu, W.; Edmondson, D. G.; Roth, S. Y.: Mammalian GCN5 and 3 A c

P/CAFacetyltransferases have homologous amino- terminal domains importantfor recognition of nucleosomal substrates. Molec. Cell. Biol. 18:5659- 5669, 1998.

GAM47 269 GCN5L2 Yang, X.- J.; Ogryzko, V. V.; Nishikawa, J.; Howard, B. H.; Nakatani,Y.: A 3 A c p300/CBP- associated factor that competes with the adenoviraloncoprotein E1A. Nature 382: 319- 324, 1996.

GAM47 269 GMPR Beutler, E.; Gelbart, T.; Kuhl, W.: Human red cell glucose- 6- 3 A c phosphatedehydrogenase: all active enzyme has sequence predicted by the X chromosome- encodedcDNA. Cell 62: 7- 9, 1990.

GAM47 269 GMPR Henikoff, S.; Smith, J. M.: The human mRNA that provides the N- terminusof 3 A c chimeric G6PD encodes GMP reductase. Cell 58: 1021- 1022, 1989.

GAM47 269 GMPR Kanno, H.; Huang, I.- Y.; Kan, Y. W.; Yoshida, A.: Two structuralgenes on 3 A c different chromosomes are required for encoding the majorsubunit of human red cell glucose- 6- phosphate dehydrogenase. Cell 58:595- 606, 1989.

GAM47 269 GMPR Kondoh, T.; Kanno, H.; Chang, L.; Yoshida, A.: Genomic structureand 3 A c expression of human guanosine monophosphate reductase. Hum.Genet. 88: 219- 224, 1991.

GAM47 269 GMPR Kondoh, T.; Kanno, H.; Chang, L.; Yoshida, A.: Identificationof common 3 A c variant alleles of the human guanosine monophosphate reductasegene. Hum. Genet. 88: 225- 227, 1991.

GAM47 269 GMPR Mason, P. J.; Bautista, J. M.; Vulliamy, T. J.; Turner, N.; Luzzatto,L.: 3 A c Human red cell glucose- 6- phosphate dehydrogenase is encoded onlyon the X chromosome. Cell 62: 9- 10, 1990.

GAM47 269 GMPR Murano, I.; Tsukahara, M.; Kajii, T.; Yoshida, A.: Mapping ofthe human 3 A c guanosine monophosphate reductase gene (GMPR) to chromosome6p23 by fluorescence in situ hybridization. Genomics 19: 179- 180,1994.

GAM47 269 GMPR Yoshida, A.; Kan, Y. W.: Origin of 'fused' glucose- 6- 3 A c phosphatedehydrogenase. Cell 62: 11- 12, 1990.

GAM47 269 GPR92 Lee, D. K.; Nguyen, T.; Lynch, K. R.; Cheng, R.; Vanti, W. B.;Arkhitko, O.; 3 A c Lewis, T.; Evans, J. F.; George, S. R.; O'Dowd, B. F.: Discovery and mapping of ten novel G protein- coupled receptor genes. Gene 275:83- 91, 2001.

GAM47 269 GPR92 The ADHR Consortium: Autosomal dominant hypophosphataemic ricketsis 3 A c associated with mutations in FGF23. Nature Genet. 26: 345- 348,2000.

GAM47 269 GSTM5 Pearson, W. R.; Vorachek, W. R.; Xu, S.; Berger, R.; Hart, I.;Vannais, D.; 3 A c Patterson, D.: Identification of class- mu glutathionetransferase genes GSTM1- GSTM5 on human chromosome 1p13. Am. J. Hum.Genet. 53: 220- 233, 1993.

GAM47 269 GSTM5 Takahashi, Y.; Campbell, E. A.; Hirata, Y.; Takayama, T.; Listowsky,I.: A 3 A c basis for differentiating among the multiple human mu- glutathioneS- transferases and molecular cloning of brain GSTM5. J. Biol. Chem. 268:8893- 8898, 1993.

GAM47 269 GSTM5 Xu, S.; Wang, Y.; Roe, B.; Pearson, W. R.: Characterization ofthe human 3 A c class mu glutathione S- transferase gene cluster and theGSTM1 deletion. J. Biol. Chem. 273: 3517- 3527, 1998.

GAM47 269 HDAC5 Grozinger, C. M.; Hassig, C. A.; Schreiber, S. L.: Three proteinsdefine a 3 A c class of human histone deacetylases related to yeast Hda1p. Proc.Nat. Acad. Sci. 96: 4868- 4873, 1999.

GAM47 269 HDAC5 Mahlknecht, U.; Schnittger, S.; Ottmann, O. G.; Schoch, C.; Mosebach,M.; 3 A c Hiddemann, W.; Hoelzer, D.: Chromosomal organization and localizationof the human histone deacetylase 5 gene (HDAC5). Biochim. Biophys.Acta 1493: 342- 348, 2000.

GAM47 269 HDAC5 McKinsey, T. A.; Zhang, C.- L.; Lu, J.; Olson, E. N.: Signal- 3 A c
dependentnuclear export of a histone deacetylase regulates muscle
differentiation. Nature 408:106- 111, 2000.

GAM47 269 HDAC5 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 A c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM47 269 HDAC5 Scanlan, M. J.; Chen, Y.- T.; Williamson, B.; Gure, A. O.; Stockert,E.; 3 A c
Gordan, J. D.; Tureci, O.; Sahin, U.; Pfreundschuh, M.; Old, L.J.:
Characterization of human colon cancer antigens recognized byautologous
antibodies. Int. J. Cancer 76: 652- 658, 1998.

GAM47 269 HOXB8 Greer, J. M.; Capecchi, M. R.: Hoxb8 is required for normal groomingbehavior 3 A c
in mice. Neuron 33: 23- 34, 2002.

GAM47 269 HOXB8 van den Akker, E.; Reijnen, M.; Korving, J.; Brouwer, A.; Meijlink,F.; 3 A c
Deschamps, J.: Targeted inactivation of Hoxb8 affects survivalof a spinal
ganglion and causes aberrant limb reflexes. Mech. Dev. 89:103- 114, 1999.

GAM47 269 HRH1 Inoue, I.; Taniuchi, I.; Kitamura, D.; Jenkins, N. A.; Gilbert,D. J.; 3 A c
Copeland, N. G.; Watanabe, T.: Characteristics of the mousegenomic histamine
H1 receptor gene. Genomics 36: 178- 181, 1996.

GAM47 269 HRH1 Jutel, M.; Watanabe, T.; Klunker, S.; Akdis, M.; Thomet, O. A.R.; 3 A c
Malolepszy, J.; Zak- Nejmark, T.; Koga, R.; Kobayashi, T.; Blaser,K.; Akdis,
C. A.: Histamine regulates T- cell and antibody responsesby differential
expression of H1 and H2 receptors. Nature 413: 420- 425,2001.

GAM47 269 HRH1 Le Coniat, M.; Traiffort, E.; Ruat, M.; Arrang, J.- M.; Berger,R.: 3 A c
Chromosomal localization of the human histamine H1- receptor gene.
Hum.Genet. 94: 186- 188, 1994.

GAM47 269 HRH1 Ma, R. Z.; Gao, J.; Meeker, N. D.; Fillmore, P. D.; Tung, K. S.K.; Watanabe, 3 A c
T.; Zachary, J. F.; Offner, H.; Blankenhorn, E. P.;Teuscher, C.:
Identification of Bphs, an autoimmune disease locus,as histamine receptor H-
1. Science 297: 620- 623, 2002.

GAM47 269 HRH1 Yamashita, M.; Fukui, H.; Sugama, K.; Horio, Y.; Ito, S.; Mizuguchi,H.; 3 A c
Wada, H.: Expression cloning of a cDNA encoding the bovine histamineH1
receptor. Proc. Nat. Acad. Sci. 88: 11515- 11519, 1991.

GAM47 269 IL1RL1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 3 A c
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp)
on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM47 269 IL1RL1 Kumar, S.; Tzimas, M. N.; Griswold, D. E.; Young, P. R.: Expressionof ST2, 3 A c
an interleukin- 1 receptor homologue, is induced by proinflammatorystimuli.
Biochem. Biophys. Res. Commun. 235: 474- 478, 1997.

GAM47 269 IL1RL1 Sims, J. E.; Painter, S. L.; Gow, I. R.: Genomic organizationof the type I 3 A c
and type II IL- 1 receptors. Cytokine 7: 483- 490, 1995.

GAM47 269 IL1RL1 Tago, K.; Noda, T.; Hayakawa, M.; Iwahana, H.; Yanagisawa, K.;Yashiro, T.; 3 A c
Tominaga, S.: Tissue distribution and subcellular localizationof a variant
form of the human ST2 gene product, ST2V. Biochem. Biophys.Res. Commun. 285:
1377- 1383, 2001.

GAM47 269 IL1RL1 Tominaga, S.: A putative protein of a growth specific cDNA fromBALB/c- 3T3 3 A c
cells is highly similar to the extracellular portion ofmouse interleukin 1
receptor. FEBS Lett. 258: 301- 304, 1989.

GAM47 269 IL1RL1 Tominaga, S.; Inazawa, J.; Tsuji, S.: Assignment of the humanST2 gene to 3 A c
chromosome 2 at q11.2. Hum. Genet. 97: 561- 563, 1996.

GAM47 269 IL1RL1 Tominaga, S.; Yokota, T.; Yanagisawa, K.; Tsukamoto, T.; Takagi,T.; Tetsuka, 3 A c
T.: Nucleotide sequence of a complementary DNA for humanST2. Biochim.
Biophys. Acta 1171: 215- 218, 1992.

GAM47 269 JMJ Berge- Lefranc, J.- L.; Jay, P.; Massacrier, A.; Cau, P.; Mattei,M. G.; 3 A c
Bauer, S.; Marsollier, C.; Berta, P.; Fontes, M.: Characterizationof the
human jumonji gene. Hum. Molec. Genet. 5: 1637- 1641, 1996.

GAM47 269 JMJ Toyoda, M.; Kojima, M.; Takeuchi, T.: Jumonji is a nuclear proteinthat 3 A c
participates in the negative regulation of cell growth. Biochem.Biophys.
Res. Commun. 274: 332- 336, 2000.

GAM47 269 KCNJ10 Doupnik, C. A.; Davidson, N.; Lester, H. A.: The inward rectifierpotassium 3 A c
channel family. Curr. Opin. Neurobiol. 5: 268- 277, 1995.

GAM47 269 KCNJ10 Tada, Y.; Horio, Y.; Takumi, T.; Terayama, M.; Tsuji, L.; Copeland,N. G.; 3 A c
Jenkins, N. A.; Kurachi, Y.: Assignment of the glial inwardlyrectifying
potassium channel K(AB)- 2/Kir4.1 (Kcnj10) gene to the distalregion of mouse
chromosome 1. Genomics 45: 629- 630, 1997.

GAM47 269 KCNJ10 Takumi, T.; Ishii, T.; Horio, Y.; Morishige, K.- I.; Takahashi,N.; Yamada, 3 A c
M.; Yamashita, T.; Kiyama, H.; Sohmiya, K.; Nakanishi,S.; Kurachi, Y.: A
novel ATP- dependent inward rectifier potassiumchannel expressed
predominantly in glial cells. J. Biol. Chem. 270:16339- 16436, 1995.

GAM47 269 KCNN2 Desai, R.; Peretz, A.; Idelson, H.; Lazarovici, P.; Attali, B.: Ca(2+)- 3 A c
activated K(+) channels in human leukemic Jurkat T cells:molecular cloning,
biochemical and functional characterization. J.Biol. Chem. 275: 39954-
39963, 2000.

GAM47 269 KCNN2 Schumacher, M. A.; Rivard, A. F.; Bachinger, H. P.; Adelman, J.P.: Structure 3 A c
of the gating domain of a Ca(2+)- activated K+ channelcomplexed with
Ca(2+)/calmodulin. Nature 410: 1120- 1124, 2001.

GAM47 269 KCNQ2 Berkovic, S. F.; Kennerson, M. L.; Howell, R. A.; Scheffer, I.E.; Hwang, P. 3 A c
A.; Nicholson, G. A.: Phenotypic expression of benignfamilial neonatal
convulsions linked to chromosome 20. Arch. Neurol. 51:1125- 1128, 1994.

GAM47 269 KCNQ2 Biervert, C.; Schroeder, B. C.; Kubisch, C.; Berkovic, S. F.; Propping,P.; 3 A c
Jentsch, T. J.; Steinlein, O. K.: A potassium channel mutationin neonatal
human epilepsy. Science 279: 406- 409, 1998.

GAM47 269 KCNQ2 Biervert, C.; Steinlein, O. K.: Structural and mutational analysisof KCNQ2, 3 A c
the major gene locus for benign familial neonatal convulsions. Hum.Genet.
104: 234- 240, 1999.

GAM47 269 KCNQ2 Cooper, E. C.; Aldape, K. D.; Abosch, A.; Barbaro, N. M.; Berger,M. S.; 3 A c
Peacock, W. S.; Jan, Y. N.; Jan, L. Y.: Colocalization andcoassembly of two
human brain M- type potassium channel subunits thatare mutated in epilepsy.
Proc. Nat. Acad. Sci. 97: 4914- 4919, 2000.

GAM47 269 KCNQ2 Dedek, K.; Kunath, B.; Kananura, C.; Reuner, U.; Jentsch, T. J.;Steinlein, 3 A c
O. K.: Myokymia and neonatal epilepsy caused by a mutationin the voltage
sensor of the KCNQ2 K(+) channel. Proc. Nat. Acad.Sci. 98: 12272- 12277,
2001.

GAM47 269 KCNQ2 del Giudice, E. M.; Coppola, G.; Scuccimarra, G.; Cirillo, G.;Bellini, G.; 3 A c
Pascotto, A.: Benign familial neonatal convulsions (BFNC)resulting from
mutation of the KCNQ2 voltage sensor. Europ. J. Hum.Genet. 8: 994- 997,
2000.

GAM47 269 KCNQ2 Singh, N. A.; Charlier, C.; Stauffer, D.; DuPont, B. R.; Leach,R. J.; Melis, 3 A c
R.; Ronen, G. M.; Bjerre, I.; Quattlebaum, T.; Murphy,J. V.; McHarg, M. L.;
Gagnon, D.; Rosales, T. O.; Peiffer, A.; Anderson,V. E.; Leppert, M.: A

novel potassium channel gene, KCNQ2, is mutatedin an inherited epilepsy of newborns. Nature Genet. 18: 25- 29, 1998.

GAM47 269 KCNQ2 Wang, H.- S.; Pan, Z.; Shi, W.; Brown, B. S.; Wymore, R. S.; Cohen,I. S.; 3 A c
Dixon, J. E.; McKinnon, D.: KCNQ2 and KCNQ3 potassium channelsubunits: molecular correlates of the M- channel. Science 282: 1890- 1893,1998.

GAM47 269 KCNQ2 Wang, Q.; Curren, M. E.; Splawski, I.; Burn, T. C.; Millholland,J. M.; 3 A c
VanRaay, T. J.; Shen, J.; Timothy, K. W.; Vincent, G. M.; deJager, T.; Schwartz, P. J.; Towbin, J. A.; Moss, A. J.; Atkinson,D. L.; Landes, G. M.; Connors, T. D.; Keating, M. T.: Positionalcloning of a novel potassium channel gene: KVLQT1 mutations causecardiac arrhythmias. Nature Genet. 12: 17- 23, 1996.

GAM47 269 KCNQ2 Yang, W.- P.; Levesque, P. C.; Little, W. A.; Conder, M. L.; 3 A c
Ramakrishnan,P.; Neubauer, M. G.; Blanar, M. A.: Functional expression of twoKvLQT1- related potassium channels responsible for an inherited idiopathicepilepsy. J. Biol. Chem. 273: 19419- 19423, 1998.

GAM47 269 KIF5A Hamlin, P. J.; Jones, P. F.; Leek, J. P.; Bransfield, K.; Lench,N. J.; 3 A c
Aldersley, M. A.; Howdle, P. D.; Markham, A. F.; Robinson,P. A.: Assignment of GALGT encoding beta- 1,4N- acetylgalactosaminyl- transferase(GalNAc- T) and KIF5A encoding neuronal kinesin (D12S1889) to humanchromosome band 12q13 by assignment to ICI YAC 26EG10 and in situhybridization. Cytogenet. Cell Genet. 82: 267- 268, 1998.

GAM47 269 KIF5A Niclas, J.; Navone, F.; Hom- Booher, N.; Vale, R. D.: Cloning 3 A c
andlocalization of a conventional kinesin motor expressed exclusivelyin neurons. Neuron 12: 1059- 1072, 1994.

GAM47 269 KPNA4 Ayala- Madrigal, M. L.; Doerr, S.; Ramirez- Duenas, M. L.; Hansmann,I.: 3 A c
Assignment of KPNA4 and KPNB1 encoding karyopherin alpha 4 andbeta 1 to human chromosome bands 11q22 and 17q21 respectively, byin situ hybridization. Cytogenet. Cell Genet. 89: 258- 259, 2000.

GAM47 269 KPNA4 Kohler, M.; Ansieau, S.; Prehn, S.; Leutz, A.; Haller, H.; Hartmann,E.: 3 A c
Cloning of two novel human importin- alpha subunits and analysisof the expression pattern of the importin- alpha protein family. FEBSLett. 417: 104- 108, 1997.

GAM47 269 KPNA4 Seki, T.; Tada, S.; Katada, T.; Enomoto, T.: Cloning of a cDNAencoding a 3 A c
novel importin- alpha homologue, Qip1: discrimination ofQip1 and Rch1 from hSrp1 by their ability to interact with DNA helicaseQ1/RecQL. Biochem. Biophys. Res. Commun. 234: 48- 53, 1997.

GAM47 269 MAFG Blank, V.; Kim, M. J.; Andrews, N. C.: Human MAFG is a functionalpartner for 3 A c
p45 NF- E2 in activating globin gene expression. Blood 89:3925- 3935, 1997.

GAM47 269 MAFG Blank, V.; Knoll, J. H. M.; Andrews, N. C.: Molecular characterizationand 3 A c
localization of the human MafG gene. Genomics 44: 147- 149, 1997.

GAM47 269 MAFG Iwata, T.; Kogame, K.; Toki, T.; Yokoyama, M.; Yamamoto, M.; Ito,E.: 3 A c
Structure and chromosome mapping of the human small maf genesMAFG and MAFK. Cytogenet. Cell Genet. 82: 88- 90, 1998.

GAM47 269 MAFG Motohashi, H.; Katsuoka, F.; Shavit, J. A.; Engel, J. D.; Yamamoto,M.: 3 A c
Positive or negative MARE- dependent transcriptional regulationis determined by the abundance of small Maf proteins. Cell 103:865- 875, 2000.

GAM47 269 MAFG Shavit, J. A.; Motohashi, H.; Onodera, K.; Akasaka, J.; Yamamoto,M.; Engel, 3 A c
J. D.: Impaired megakaryopoiesis and behavioral defectsin mafG- null mutant mice. Genes Dev. 12: 2164- 2174, 1998.

GAM47 269 MAFG Toki, T.; Itoh, J.; Kitazawa, J.; Arai, K.; Hatakeyama, K.; Akasaka,J.; 3 A c

Igarashi, K.; Nomura, N.; Yokoyama, M.; Yamamoto, M.; Ito, E.: Human small Maf proteins form heterodimers with CNC family transcriptionfactors and recognize the NF- E2 motif. Oncogene 14: 1901- 1910, 1997.

GAM47 269 MBD4 Bellacosa, A.; Cicchillitti, L.; Schepis, F.; Riccio, A.; Yeung,A. T.; Matsumoto, Y.; Golemis, E. A.; Genuardi, M.; Neri, G.: MED1,a novel human methyl- CpG- binding endonuclease, interacts with DNAmismatch repair protein MLH1. Proc. Nat. Acad. Sci. 96: 3969- 3974,1999. 3 A c

GAM47 269 MBD4 Boland, C. R.; Thibodeau, S. N.; Hamilton, S. R.; Sidransky, D.;Eshleman, J. R.; Burt, R. W.; Meltzer, S. J.; Rodriguez- Bigas, M.A.; Fodde, R.; Ranzani, G. N.; Srivastava, S.: A National CancerInstitute workshop on microsatellite instability for cancer detectionand familial predisposition: development of international criteriafor the determination of microsatellite instability in colorectalcancer. Cancer Res. 58: 5248- 5257, 1998. 3 A c

GAM47 269 MBD4 Hendrich, B.; Abbott, C.; McQueen, H.; Chambers, D.; Cross, S.;Bird, A.: Genomic structure and chromosomal mapping of the murineand human Mbd1, Mbd2, Mbd3, and Mbd4 genes. Mammalian Genome 10:906- 912, 1999. 3 A c

GAM47 269 MBD4 Hendrich, B.; Bird, A.: Identification and characterization ofa family of mammalian methyl- CpG binding proteins. Molec. Cell. Biol. 18:6538- 6547, 1998. 3 A c

GAM47 269 MBD4 Hendrich, B.; Hardeland, U.; Ng, H.- H.; Jiricny, J.; Bird, A.:The thymine glycosylase MBD4 can bind to the product of deaminationat methylated CpG sites. Nature 401: 301- 304, 1999. 3 A c

GAM47 269 MBD4 Millar, C. B.; Guy, J.; Sansom, O. J.; Selfridge, J.; MacDougall,E.; Hendrich, B.; Keightley, P. D.; Bishop, S. M.; Clarke, A. R.;Bird, A.: Enhanced CpG mutability and tumorigenesis in MBD4- deficientmice. Science 297: 403- 405, 2002. 3 A c

GAM47 269 MBD4 Riccio, A.; Aaltonen, L. A.; Godwin, A. K.; Loukola, A.; Percesepe,A.; Salovaara, R.; Masciullo, V.; Genuardi M.; Paravatou- Petsotas,M.; Bassi, D. E.; Ruggeri, B. A.; Klein- Szanto, A. J. P.; Testa, J.R.; Neri, G.; Bellacosa, A.: The DNA repair gene MBD4 (MED1) is mutatedin human carcinomas with microsatellite instability. (Letter) NatureGenet. 23: 266- 268, 1999. 3 A c

GAM47 269 MGA Naim, H. Y.; Sterchi, E. E.; Lentze, M. J.: Structure, biosynthesis,and glycosylation of human small intestinal maltase- glucoamylase. J.Biol. Chem. 263: 19709- 19717, 1988. 3 A c

GAM47 269 MGA Nichols, B. L.; Eldering, J.; Avery, S.; Hahn, D.; Quaroni, A.;Sterchi, E.: Human small intestinal maltase- glucoamylase cDNA cloning:homology to sucrase- isomaltase. J. Biol. Chem. 273: 3076- 3081, 1998. 3 A c

GAM47 269 MGA Schuler, G. D.; Boguski, M. S.; Stewart, E. A.; Stein, L. D.; Gyapay,G.; Rice, K.; White, R. E.; Rodriguez- Tome, P.; Aggarwal, A.; Bajorek,E.; Bentolila, S.; Birren, B. B.; Butler, A.; Castle, A. B.; Chiannilkulchai,N.; Chu, A.; Clee, C.; Cowles, S.; Day, P. J. R.; Dibling, T.; and84 others: A gene map of the human genome. Science 274: 540- 546,1996. 3 A c

GAM47 269 MINPP1 Caffrey, J. J.; Hidaka, K.; Matsuda, M.; Hirata, M.; Shears, S.B.: The human and rat forms of multiple inositol polyphosphate phosphatase:functional homology with a histidine acid phosphatase up- regulatedduring endochondral ossification. FEBS Lett. 442: 99- 104, 1999. 3 A c

GAM47 269 MINPP1 Chi, H.; Tiller, G. E.; Dasouki, M. J.; Romano, P. R.; Wang, J.;O'Keefe, R. J.; Puzas, J. E.; Rosier, R. N.; Reynolds, P. R.: Multipleinositol polyphosphate phosphatase: evolution as a distinct groupwithin the histidine phosphatase family and chromosomal localizationof the human and mouse genes 3 A c

to chromosomes 10q23 and 19. Genomics 56:324- 336, 1999.

GAM47 269 MINPP1 Chi, H.; Yang, X.; Kingsley, P. D.; O'Keefe, R. J.;Rosier, R. N.; Shears, S. B.; Reynolds, P. R.: Targeted deletionof Minpp1 provides new insight into the activity of multiple inositolpolyphosphate phosphatase in vivo. Molec. Cell. Biol. 20: 6496- 6507,2000. 3 A c

GAM47 269 MINPP1 Gimm, O.; Chi, H.; Dahia, P. L. M.; Perren, A.; Hinze, R.; Komminoth,P.; Dralle, H.; Reynolds, P. R.; Eng, C.: Somatic mutation and germlinevariants of MINPP1, a phosphatase gene located in proximity to PTENon 10q23.3, in follicular thyroid carcinomas. J. Clin. Endocr. Metab. 86:1801- 1805, 2001. 3 A c

GAM47 269 NAP1L4 Hu, R.- J.; Lee, M. P.; Johnson, L. A.; Feinberg, A. P.: A novelhuman homologue of yeast nucleosome assembly protein, 65 kb centromericto the p57(KIP2) gene, is biallelically expressed in fetal and adulttissues. Hum. Molec. Genet. 5: 1743- 1748, 1996. 3 A c

GAM47 269 NAP1L4 Rodriguez, P.; Munroe, D.; Prawitt, D.; Chu, L. L.; Bric, E.; Kim,J.; Reid, L. H.; Davies, C.; Nakagama, H.; Loebbert, R.; Winterpacht,A.; Petruzzi, M.- J.; Higgins, M. J.; Nowak, N.; Evans, G.; Shows,T.; Weissman, B. E.; Zabel, B.; Housman, D. E.; Pelletier, J.: Functionalcharacterization of human nucleosome assembly protein- 2 (NAP1L4) suggestsa role as a histone chaperone. Genomics 44: 253- 265, 1997. 3 A c

GAM47 269 NDRG1 Kalaydjieva, L.; Gresham, D.; Gooding, R.; Heather, L.; Baas, F.;de Jonge, R.; Blechschmidt, K.; Angelicheva, D.; Chandler, D.; Worsley,P.; Rosenthal, A.; King, R. H. M.; Thomas, P. K.: N- myc downstream- regulatedgene 1 is mutated in hereditary motor and sensory neuropathy- Lom. Am.J. Hum. Genet. 67: 47- 58, 2000. 3 A c

GAM47 269 NDRG1 Kalaydjieva, L.; Hallmayer, J.; Chandler, D.; Savov, A.; Nikolova,A.; Angelicheva, D.; King, R. H. H.; Ishpekova, B.; Honeyman, K.;Calafell, F.; Shmarov, A.; Petrova, J.; Turnev, I.; Hristova, A.;Moskov, M.; Stancheva, S.; Petkova, I.; Bittles, A. H.; Georgieva,V.; Middleton, L.; Thomas, P. K.: Gene mapping in Gypsies identifiesa novel demyelinating neuropathy on chromosome 8q24. Nature Genet. 14:214- 217, 1996. 3 A c

GAM47 269 NDRG1 Kokame, K.; Kato, H.; Miyata, T.: Homocysteine- respondent genesin vascular endothelial cells identified by differential display analysis:GRP78/BiP and novel genes. J. Biol. Chem. 271: 29659- 29665, 1996. 3 A c

GAM47 269 NDRG1 Park, H,; Adams, M. A.; Lachat, P.; Bosman, F.; Pang, S. C.; Graham,C. H.: Hypoxia induces the expression of a 43- kDa protein (PROXY- 1)in normal and malignant cells. Biochem. Biophys. Res. Commun. 276:321- 328, 2000. 3 A c

GAM47 269 NDRG1 Shimono, A.; Okuda, T.; Kondoh, H.: N- myc- dependent repressionof Ndr1, a gene identified by direct subtraction of whole mouse embryocDNAs between wild type and N- myc mutant. Mech. Dev. 83: 39- 52,1999. 3 A c

GAM47 269 NDRG1 van Belzen, N.; Dinjens, W. N. M.; Diesveld, M. P. G.; Groen, N.A.; van der Made, A. C. J.; Nozawa, Y.; Vliestra, R.; Trapman, J.;Bosman, F. T.: A novel gene which is up- regulated during colon epithelialcell differentiation and down- regulated in colorectal neoplasms. Lab.Invest. 77: 85- 92, 1997. 3 A c

GAM47 269 NDRG1 Zhou, D.; Salnikow, K.; Costa, M.: Cap43, a novel gene specificallyinduced by Ni2+ compounds. Cancer Res. 58: 2182- 2189, 1998. 3 A c

GAM47 269 NDUFA6 Dunbar, D. R.; Shibasaki, Y.; Dobbie, L.; Andersson, B.; Brookes,A. J.: In situ hybridisation mapping of genomic clones for five humanrespiratory chain complex I genes. Cytogenet. Cell Genet. 78: 21- 24,1997. 3 A c

GAM47 269 NDUFA6 Emahazion, T.; Brookes, A. J.: Mapping of the NDUFA2, NDUFA6,NDUFA7, NDUFB8, 3 A c

and NDUFS8 electron transport chain genes by intronbased radiation hybrid mapping. Cytogenet. Cell Genet. 82: 114 only,1998.

GAM47 269 NDUFA6 Ton, C.; Hwang, D. M.; Dempsey, A. A.; Liew, C.- C.: Identificationand primary structure of five human NADH- ubiquinone oxidoreductasesubunits. Biochem. Biophys. Res. Commun. 241: 589- 594, 1997. 3 A c

GAM47 269 NFATC4 Aramburu, J.; Garcia- Cozar, F.; Raghavan, A.; Okamura, H.; Rao,A.; Hogan, P. G.: Selective inhibition of NFAT activation by a peptidespanning the calcineurin targeting site of NFAT. Molec. Cell 1:627- 637, 1998. 3 A c

GAM47 269 NFATC4 Graef, I. A.; Chen, F.; Chen, L.; Kuo, A.; Crabtree, G. R.: Signalstransduced by Ca(2+)/calcineurin and NFATc3/c4 pattern the developingvasculature. Cell 105: 863- 875, 2001. 3 A c

GAM47 269 NFATC4 Hoey, T.; Sun, Y. L.; Williamson, K.; Xu, X.: Isolation of twonew members of the NF- AT gene family and functional characterizationof the NF- AT proteins. Immunity 2: 461- 472, 1995. 3 A c

GAM47 269 NFATC4 Horsley, V.; Pavlath, G. K.: NFAT: ubiquitous regulator of celldifferentiation and adaptation. J. Cell Biol. 156: 771- 774, 2002. 3 A c

GAM47 269 NOL3 Koseki, T.; Inohara, N.; Chen, S.; Nunez, G.: ARC, an inhibitorof apoptosis expressed in skeletal muscle and heart that interactsselectively with caspases. Proc. Nat. Acad. Sci. 95: 5156- 5160,1998. 3 A c

GAM47 269 NOL3 Li, P.- F.; Li, J.; Muller, E.- C.; Otto, A.; Dietz, R.; von Harsdorf,R.: Phosphorylation by protein kinase CK2: a signaling switch forthe caspase- inhibiting protein ARC. Molec. Cell 10: 247- 258, 2002. 3 A c

GAM47 269 NOL3 Stoss, O.; Schwaiger, F.- W.; Cooper, T. A.; Stamm, S.: Alternativesplicing determines the intracellular localization of the novel nuclearprotein Nop30 and its interaction with the splicing factor SRp30c. J.Biol. Chem. 274: 10951- 10962, 1999. 3 A c

GAM47 269 NOTCH2 Gao, X.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Gridley,T.: Assignment of the murine Notch2 and Notch3 genes to chromosomes3 and 17. Genomics 49: 160- 161, 1998. 3 A c

GAM47 269 NOTCH2 Katsanis, N.; Fitzgibbon, J.; Fisher, E. M. C.: Paralogy mapping:identification of a region in the human MHC triplicated onto humanchromosomes 1 and 9 allows the prediction and isolation of novel PBXand NOTCH loci. Genomics 35: 101- 108, 1996. 3 A c

GAM47 269 NOTCH2 Larsson, C.; Lardelli, M.; White, I.; Lendahl, U.: The human NOTCH1,2, and 3 genes are located at chromosome positions 9q34, 1p13- p11,and 19p13.2- p13.1 in regions of neoplasia- associated translocation. Genomics 24:253- 258, 1994. 3 3 A c

GAM47 269 NR2F6 Bahler, M.; Kehrer, I.; Gordon, L.; Stoffler, H.- E.; Olsen, A.S.: Physical mapping of human myosin- IXB (MYO9B), the human orthologueof the rat myosin myr 5, to chromosome 19p13.1. Genomics 43: 107- 109,1997. 3 A c

GAM47 269 NR2F6 Miyajima, N.; Kadowaki, Y.; Fukushige, S.; Shimizu, S.; Semba,K.; Yamanashi, Y.; Matsubara, K.; Toyoshima, K.; Yamamoto, T.: Identificationof two novel members of erbA superfamily by molecular cloning: thegene products of the two are highly related to each other. NucleicAcids Res. 16: 11057- 11073, 1988. 3 A c

GAM47 269 PAX2 Amiel, J.; Audollent, S.; Joly, D.; Dureau, P.; Salomon, R.; Tellier,A.- L.; Auge, J.; Bouissou, F.; Antignac, C.; Gubler, M.- C.; Eccles,M. R.; Munnich, A.; Vekemans, M.; Lyonnet, S.; Attie- Bitach, T.:PAX2 mutations in renal- coloboma syndrome: mutational hotspot andgermline mosaicism. Europ. J. Hum. Genet. 8: 820- 826, 2000. 3 A c

GAM47 269 PAX2 Dehbi, M.; Ghahremani, M.; Lechner, M.; Dressler, G.; Pelletier,J.: The paired- box transcription factor, PAX2, positively modulatesexpression of the Wilms' tumor suppressor gene. Oncogene 13: 447- 453,1996. 3 A c

GAM47 269 PAX2 Devriendt, K.; Matthijs, G.; Van Damme, B.; Van Caesbroeck, D.;Eccles, M.; Vanrenterghem, Y.; Fryns, J.- P.; Leys, A.: Missense mutationand hexanucleotide duplication in the PAX2 gene in two unrelated familieswith renal- coloboma syndrome (MIM 120330). Hum. Genet. 103: 149- 153,1998. 3 A c

GAM47 269 PAX2 Dressler, G. R.; Deutsch, U.; Chowdhury, K.; Nornes, H. O.; Gruss,P.: Pax2, a new murine paired- box- containing gene and its expressionin the developing excretory system. Development 109: 787- 795, 1990. 3 A c

GAM47 269 PAX2 Favor, J.; Sandulache, R.; Neuhauser- Klaus, A.; Pretsch, W.; Chatterjee,B.; Senft, E.; Wurst, W.; Blanquet, V.; Grimes, P.; Sporle, R.; Schughart,K.: The mouse Pax2(1Neu) mutation is identical to a human PAX2 mutationin a family with renal- coloboma syndrome and results in developmentaldefects of the brain, ear, eye, and kidney. Proc. Nat. Acad. Sci. 93:13870- 13875, 1996. 3 A c

GAM47 269 PAX2 Ford, B.; Rupps, R.; Lirenman, D.; Van Allen, M. I.; Farquharson,D.; Lyons, C.; Friedman, J. M.: Renal- coloboma syndrome: prenataldetection and clinical spectrum in a large family. Am. J. Med. Genet. 99:137- 141, 2001. 3 A c

GAM47 269 PAX2 Keller, S. A.; Jones, J. M.; Boyle, A.; Barrow, L. L.; Killen,P. D.; Green, D. G.; Kapousta, N. V.; Hitchcock, P. F.; Swank, R.T.; Meisler, M. H.: Kidney and retinal defects (Krd), a transgene- inducedmutation with a deletion of mouse chromosome 19 that includes thePax2 locus. Genomics 23: 309- 320, 1994. 3 A c

GAM47 269 PAX2 Narahara, K.; Baker, E.; Ito, S.; Yokoyama, Y.; Yu, S.; Hewitt,D.; Sutherland, G. R.; Eccles, M. R.; Richards, R. I.: Localisationof a 10q breakpoint within the PAX2 gene in a patient with a de novot(10;13) translocation and optic nerve coloboma- renal disease. J.Med. Genet. 34: 213- 216, 1997. 3 A c

GAM47 269 PAX2 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman homologs of the murine paired- box- containing genes. MammalianGenome 4: 78- 82, 1993. 3 A c

GAM47 269 PAX2 Porteous, S.; Torban, E.; Cho, N.- P.; Cunliffe, H.; Chua, L.;McNoe, L.; Ward, T.; Souza, C.; Gus, P.; Giugliani, R.; Sato, T.;Yun, K.; Favor, J.; Sicotte, M.; Goodyer, P.; Eccles, M.: Primaryrenal hypoplasia in humans and mice with PAX2 mutations: evidenceof increased apoptosis in fetal kidneys of Pax2(1Neu) +/- mutant mice. Hum.Molec. Genet. 9: 1- 11, 2000. 3 A c

GAM47 269 PAX2 Sanyanusin, P.; McNoe, L. A.; Sullivan, M. J.; Weaver, R. G.;Eccles, M. R.: Mutation of PAX2 in two siblings with renal- colobomasyndrome. Hum. Molec. Genet. 4: 2183- 2184, 1995. 3 A c

GAM47 269 PAX2 Sanyanusin, P.; Norrish, J. H.; Ward, T. A.; Nebel, A.; McNoe,L. A.; Eccles, M. R.: Genomic structure of the human PAX2 gene. Genomics 35:258- 261, 1996. 3 A c

GAM47 269 PAX2 Sanyanusin, P.; Schimmenti, L. A.; McNoe, L. A.; Ward, T. A.;Pierpont, M. E. M.; Sullivan, M. J.; Dobyns, W. B.; Eccles, M. R.: Mutation of the PAX2 gene in a family with optic nerve colobomas,renal anomalies and vesicoureteral reflux. Nature Genet. 9: 358- 364,1995. 3 A c

GAM47 269 PAX2 Schimmenti, L. A.; Cunliffe, H. E.; McNoe, L. A.; Ward, T. A.;French, M. C.; Shim, H. H.; Zhang, Y.- H.; Proesmans, W.; Leys, A.;Byerly, K. A.; Braddock, S. R.; Masuno, M.; Imaizumi, K.; Devriendt,K.; Eccles, M. R.: Further delineation of renal- coloboma syndromein patients with extreme variability 3 A c

of phenotype and identical PAX2mutations. Am. J. Hum. Genet. 60: 869- 878, 1997.

GAM47 269 PAX2 Schimmenti, L. A.; Pierpont, M. E.; Carpenter, B. L. M.; Kashtan,C. E.; Johnson, M. R.; Dobyns, W. B.: Autosomal dominant optic nervecolobomas, vesicoureteral reflux, and renal anomalies. Am. J. Med.Genet. 59: 204- 208, 1995. 3 A c

GAM47 269 PAX2 Schimmenti, L. A.; Shim, H. H.; Wirtschafter, J. D.; Panzarino,V. A.; Kashtan, C. E.; Kirkpatrick, S. J.; Wargowski, D. S.; France,T. D.; Michel, E.; Dobyns, W. B.: Homonucleotide expansion and contractionmutations of PAX2 and inclusion of Chiari 1 malformation as part ofrenal- coloboma syndrome. Hum. Mutat. 14: 369- 376, 1999. 3 A c

GAM47 269 PAX2 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: Chromosomal localization of seven PAX genes and cloning of anovel family member, PAX- 9. Nature Genet. 3: 292- 298, 1993. 3 A c

GAM47 269 PAX2 Tellier, A.- L.; Amiel, J.; Delezoide, A.- L.; Audollent, S.; Auge,J.; Esnault, D.; Encha- Razavi, F.; Munnich, A.; Lyonnet, S.; Vekemans,M.; Attie- Bitach, T.: Expression of the PAX2 gene in human embryosand exclusion in the CHARGE syndrome. Am. J. Med. Genet. 93: 85- 88,2000. 3 A c

GAM47 269 PAX2 Tellier, A.- L.; Amiel, J.; Salomon, R.; Jolly, D.; Delezoide,A.- L.; Auge, J.; Gubler, M.- C.; Munnich, A.; Lyonnet, S.; Antignac,C.; Vekemans, M.; Broyer, M.; Attie- Bitach, T.: PAX2 expression duringearly human development and its mutations in renal hypoplasia withor without coloboma. (Abstract) Am. J. Hum. Genet. 63 (suppl.):A7 only, 1998. 3 A c

GAM47 269 PAX2 Ward, T. A.; Nebel, A.; Reeve, A. E.; Eccles, M. R.: Alternativemessenger RNA forms and open reading frames within an additional conservedregion of the human PAX- 2 gene. Cell Growth Differ. 5: 1015- 1021,1994. 3 A c

GAM47 269 PAX2 Weaver, R. G.; Cashwell, L. F.; Lorentz, W.; Whiteman, D.; Geisinger,K. R.; Ball, M.: Optic nerve coloboma associated with renal disease. Am.J. Med. Genet. 29: 597- 605, 1988. 3 A c

GAM47 269 PBX1 Kamps, M. P.; Look, A. T.; Baltimore, D.: The human t(1:19) translocationin pre- B ALL produces multiple nuclear E2A- Pbx1 fusion proteins withdiffering transforming potentials. Genes Dev. 5: 358- 368, 1991. 3 A c

GAM47 269 PBX1 Kamps, M. P.; Murre, C.; Sun, X.; Baltimore, D.: A new homeoboxgene contributes the DNA binding domain of the t(1;19) translocationprotein in pre- B ALL. Cell 60: 547- 555, 1990. 3 A c

GAM47 269 PBX1 Kim, S. K.; Selleri, L.; Lee, J. S.; Zhang, A. Y.; Gu, X.; Jacobs,Y.; Cleary, M. L.: Pbx1 inactivation disrupts pancreas developmentand in Ipf1- deficient mice promotes diabetes mellitus. Nature Genet. 30:430- 435, 2002. 3 A c

GAM47 269 PBX1 Mercader, N.; Leonardo, E.; Azpiazu, N.; Serrano, A.; Morata, G.;Martinez- A, C.; Torres, M.: Conserved regulation of proximodistallimb axis development by Meis1/Hth. Nature 402: 425- 429, 1999. 3 A c

GAM47 269 PBX1 Monica, K.; Galili, N.; Nourse, J.; Saltman, D.; Cleary, M. L.: PBX2 and PBX3, new homeobox genes with extensive homology to thehuman proto- oncogene PBX1. Molec. Cell. Biol. 11: 6149- 6157, 1991. 3 A c

GAM47 269 PBX1 Nourse, J.; Mellentin, J. D.; Galili, N.; Wilkinson, J.; Stanbridge,E.; Smith, S. D.; Cleary, M. L.: Chromosomal translocation t(1;19)results in synthesis of a homeobox fusion mRNA that codes for a potentialchimeric transcription factor. Cell 60: 535- 545, 1990. 3 A c

GAM47 269 PBX1 Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.;Ando, A.; Inoko, H.; Ikemura, T.: Three genes in the human MHC classIII region near 3 A c

the junction with the class II: gene for receptorof advanced glycosylation end products, PBX2 homeobox gene and a Notchhomolog, human counterpart of mouse mammary tumor gene int- 3. Genomics 23:408- 419, 1994.

GAM47 269 PDE4B Huston, E.; Lumb, S.; Russell, A.; Catterall, C.; Ross, A. H.;Steele, M. R.; 3 A c Bolger, G. B.; Perry, M. J.; Owens, R. J.; Houslay,M. D.: Molecular cloning and transient expression in COS7 cells ofa novel human PDE4B cAMP- specific phosphodiesterase, HSPDE4B3. Biochem.J. 328: 549- 558, 1997.

GAM47 269 PDE4B Livi, G. P.; Kmetz, P.; McHale, M. M.; Cieslinski, L. B.; Sathe,G. M.; 3 A c Taylor, D. P.; Davis, R. L.; Torphy, T. J.; Balcarek, J. M.: Cloning and expression of cDNA for a human low- K(m), rolipram- sensitivecyclic AMP phosphodiesterase. Molec. Cell. Biol. 10: 2678- 2686,1990.

GAM47 269 PDE4B Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 3 A c Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM47 269 PDE4B Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins,M.; 3 A c Jarnagin, K.; Shelton, E. R.: The cDNA of a human lymphocytecyclic- AMP phosphodiesterase (PDE IV) reveals a multigene family. Gene 129:239- 247, 1993.

GAM47 269 PDE4B Szpirer, C.; Szpirer, J.; Riviere, M.; Swinnen, J.; Vicini, E.;Conti, M.: 3 A c Chromosomal localization of the human and rat genes (PDE4Dand PDE4B) encoding the cAMP- specific phosphodiesterases 3 and 4. Cytogenet.Cell Genet. 69: 11- 14, 1995.

GAM47 269 PDE4B Xu, R. X.; Hassell, A. M.; Vanderwall, D.; Lambert, M. H.; Holmes,W. D.; 3 A c Luther, M. A.; Rocque, W. J.; Milburn, M. V.; Zhao, Y.; Ke,H.; Nolte, R. T.: Atomic structure of PDE4: insights into phosphodiesterasemechanism and specificity. Science 288: 1822- 1825, 2000.

GAM47 269 PEA15 Araujo, H.; Danziger, N.; Cordier, J.; Glowinski, J.; Chneiweiss,H.: 3 A c Characterization of PEA- 15, a major substrate for protein kinaseC in astrocytes. J. Biol. Chem. 268: 5911- 5920, 1993.

GAM47 269 PEA15 Bera, T. K.; Guzman, R. C.; Miyamoto, S.; Panda, D. K.; Sasaki,M.; Hanyu, 3 A c K.; Enami, J.; Nandi, S.: Identification of a mammarytransforming gene (MAT1) associated with mouse mammary carcinogenesis. Proc.Nat. Acad. Sci. 91: 9789- 9793, 1994.

GAM47 269 PEA15 Condorelli, G.; Vigliotta, G.; Iavarone, C.; Caruso, M.; Tocchetti,C. G.; 3 A c Andreozzi, F.; Cafieri, A.; Tecce, M. F.; Formisano, P.; Beguinot,L.; Beguinot, F.: PED/PEA- 15 gene controls glucose transport andis overexpressed in type 2 diabetes mellitus. EMBO J. 17: 3858- 3866,1998.

GAM47 269 PEA15 Danziger, N.; Yokoyama, M.; Jay, T.; Cordier, J.; Glowinski, J.;Chneiweiss, 3 A c H.: Cellular expression, developmental regulation, andphylogenic conservation of PEA- 15, the astrocytic major phosphoproteinand protein kinase C substrate. J. Neurochem. 64: 1016- 1025, 1995.

GAM47 269 PEA15 Estelles, A.; Yokoyama, M.; Nothias, F.; Vincent, J.- D.; Glowinski,J.; 3 A c Vernier, P.; Chneiweiss, H.: The major astrocytic phosphoproteinPEA- 15 is encoded by two mRNAs conserved on their full length in mouseand human. J. Biol. Chem. 271: 14800- 14806, 1996.

GAM47 269 PEA15 Hwang, S.; Kuo, W.- L.; Cochran, J. F.; Guzman, R. C.; Tsukamoto,T.; 3 A c Bandyopadhyay, G.; Myambo, K.; Collins, C. C.: Assignment ofHMAT1, the human homolog of the murine mammary transforming gene (MAT1)associated with tumorigenesis, to 1q21.1, a region frequently gainedin human breast cancers. Genomics 42: 540- 542, 1997.

GAM47 269 PEA15 Wolford, J. K.; Bogardus, C.; Ossowski, V.; Prochazka, M.: 3 A c
Molecularcharacterization of the human PEA15 gene on 1q21- q22 and
associationwith type 2 diabetes mellitus in Pima Indians. Gene 241: 143-
148,2000.

GAM47 269 PFKFB3 Chesney, J.; Mitchell, R.; Benigni, F.; Bacher, M.; Spiegel, L.;Al- Abed, 3 A c
Y.; Han, J. H.; Metz, C.; Bucala, R.: An inducible geneproduct for 6-
phosphofructo- 2- kinase with an AU- rich instability element:role in tumor
cell glycolysis and the Warburg effect. Proc. Nat.Acad. Sci. 96: 3047- 3052,
1999.

GAM47 269 PFKFB3 Manzano, A.; Rosa, J. L.; Ventura, F.; Perez, J. X.; Nadal, M.;Estivill, X.; 3 A c
Ambrosio, S.; Gil, J.; Bartrons, R.: Molecular cloning,expression, and
chromosomal localization of a ubiquitously expressedhuman 6- phosphofructo-
2- kinase/fructose- 2,6- bisphosphatase gene (PFKFB3). Cytogenet.Cell Genet.
83: 214- 217, 1998.

GAM47 269 PFKFB3 Nicholl, J.; Hamilton, J. A.; Sutherland, G. R.; Sutherland, R.L.; Watts, C. 3 A c
K. W.: The third human isoform of 6- phosphofructo- 2- kinase/fructose- 2,6-
bisphosphatase(PFKFB3) map position 10p14- p15. Chromosome Res. 5: 150 only,
1997.

GAM47 269 PFKFB3 Sakai, A.; Kato, M.; Fukasawa, M.; Ishiguro, M.; Furuya, E.; Sakakibara,R.: 3 A c
Cloning of cDNA encoding for a novel isozyme of fructose 6- phosphate,2-
kinase/fructose2,6- bisphosphatase from human placenta. J. Biochem. 119:
506- 511,1996.

GAM47 269 PFKFB3 Sakakibara, R.; Kato, M.; Okamura, N.; Nakagawa, T.; Komada, Y.;Tominaga, 3 A c
N.; Shimojo, M.; Fukasawa, M.: Characterization of a humanplacental
fructose- 6- phosphate,2- kinase/fructose- 2,6- bisphosphatase. J.Biochem.
122: 122- 128, 1997.

GAM47 269 PFKFB3 Warburg, O.: On the origin of cancer cells. Science 123: 309- 314,1956. 3 A c

GAM47 269 PFKFB4 Manzano, A.; Perez, J. X.; Nadal, M.; Estivill, X.; Lange, A.;Bartrons, R.: 3 A c
Cloning, expression and chromosomal localization ofa human testis 6-
phosphofructo- 2- kinase/fructose- 2,6- bisphosphatasegene. Gene 229: 83-
89, 1999.

GAM47 269 PFKFB4 Sakai, A.; Kato, M.; Fukasawa, M.; Ishiguro, M.; Furuya, E.; Sakakibara,R.: 3 A c
Cloning of cDNA encoding for a novel isozyme of fructose 6- phosphate,2-
kinase/fructose2,6- bisphosphatase from human placenta. J. Biochem. 119:
506- 511,1996.

GAM47 269 PLAG1 Astrom, A.- K.; Voz, M. L.; Kas, K.; Roijer, E.; Wedell, B.; Mandahl,N.; Van 3 A c
de Ven, W.; Mark, J.; Stenman, G.: Conserved mechanism ofPLAG1 activation in
salivary gland tumors with and without chromosome8q12 abnormalities:
identification of SII as a new fusion partnergene. Cancer Res. 59: 918- 923,
1999.

GAM47 269 PLAG1 Kas, K.; Roijer, E.; Voz, M.; Meyen, E.; Stenman, G.; Van de Ven,W. J. M.: A 3 A c
2- Mb YAC contig and physical map covering the chromosome8q12 breakpoint
cluster region in pleomorphic adenomas of the salivaryglands. Genomics 43:
349- 358, 1997.

GAM47 269 PLAG1 Kas, K.; Voz, M. L.; Roijer, E.; Astrom, A.- K.; Meyen, E.; Stenman,G.; Van 3 A c
de Ven, W. J. M.: Promoter swapping between the genes fora novel zinc finger
protein and beta- catenin in pleiomorphic adenomaswith t(3;8)(p21;q12)
translocations. Nature Genet. 15: 170- 174,1997.

GAM47 269 PLD1 Colley, W. C.; Altshuller, Y. M.; Sue- Ling, C. K.; Copeland, N.G.; Gilbert, 3 A c
D. J.; Jenkins, N. A.; Branch, K. D.; Tsirka, S. E.;Bollag, R. J.; Bollag,

W. B.; Frohman, M. A.: Cloning and expressionanalysis of murine phospholipase D1. Biochem. J. 326: 745- 753, 1997.

GAM47 269 PLD1 Hammond, S. M.; Altshuller, Y. M.; Sung, T.- C.; Rudge, S. A.; Rose,K.; Engebrecht, J.; Morris, A. J.; Frohman, M. A.: Human ADP-ribosylationfactor- activated phosphatidylcholine- specific phospholipase D definesa new and highly conserved gene family. J. Biol. Chem. 270: 29640-29643,1995. 3 A c

GAM47 269 PLD1 Hammond, S. M.; Jenco, J. M.; Nakashima, S.; Cadwallader, K.; Gu,Q.; Cook, S.; Nozawa, Y.; Prestwich, G. D.; Frohman, M. A.; Morris,A. J.: Characterization of two alternately spliced forms of phospholipaseD1: activation of the purified enzymes by phosphatidylinositol 4,5-bisphosphate,ADP- ribosylation factor, and RHO family monomeric GTP- binding proteinsand protein kinase C- alpha. J. Biol. Chem. 272: 3860- 3868, 1997. 3 A c

GAM47 269 PLD1 Park, S. H.; Chun, Y. H.; Ryu, S. H.; Suh, P. G.; Kim, H.: Assignmentof human PLD1 to human chromosome band 3q26 by fluorescence in situhybridization. Cytogenet. Cell Genet. 82: 224 only, 1998. 3 A c

GAM47 269 PREB Fliss, M. S.; Hinkle, P. M.; Bancroft, C.: Expression cloningand characterization of PREB (prolactin regulatory element binding),a novel WD motif DNA- binding protein with a capacity to regulate prolactinpromoter activity. Molec. Endocr. 13: 644- 657, 1999. 3 A c

GAM47 269 PREB Taylor Clelland, C. L.; Levy, B.; McKie, J. M.; Duncan, A. M. V.;Hirschhorn, K.; Bancroft, C.: Cloning and characterization of humanPREB; a gene that maps to a genomic region associated with trisomy2p syndrome. Mammalian Genome 11: 675- 681, 2000. 3 A c

GAM47 269 PRKACA Skalhegg, B. S.; Huang, Y.; Su, T.; Idzerda, R. L.; McKnight, G.S.; Burton, K. A.: Mutation of the C- alpha subunit of PKA leads togrowth retardation and sperm dysfunction. Molec. Endocr. 16: 630- 639,2002. 3 A c

GAM47 269 PRKACA Tasken, K.; Solberg, R.; Zhao, Y.; Hansson, V.; Jahnsen, T.; Siciliano,M. J.: The gene encoding the catalytic subunit C- alpha of cAMP-dependentprotein kinase (locus PRKACA) localizes to human chromosome region19p13.1. Genomics 36: 535- 538, 1996. 3 A c

GAM47 269 PRKACG Beebe, S. J.; Oyen, O.; Sandberg, M.; Froysa, A.; Hansson, V.;Jahnsen, T.: Molecular cloning of a tissue- specific protein kinase(C gamma) from human testis- - representing a third isoform for thecatalytic subunit of cAMP-dependent protein kinase. Molec. Endocr. 4:465- 475, 1990. 3 A c

GAM47 269 PRKACG Foss, K. B.; Berube, D.; Simard, J.; Beebe, S. J.; Sandberg, M.;Grzeschik, K.- H.; Gagne, R.; Hansson, V.; Jahnsen, T.: Localizationof the catalytic subunit C- gamma of cAMP- dependent protein kinaseon human chromosome 9q13. (Abstract) Cytogenet. Cell Genet. 58:1937- 1938, 1991. 3 A c

GAM47 269 PRKACG Foss, K. B.; Simard, J.; Berube, D.; Beebe, S. J.; Sandberg, M.;Grzeschik, K.- H.; Gagne, R.; Hansson, V.; Jahnsen, T.: Localizationof the catalytic subunit C- gamma of the cAMP- dependent protein kinasegene (PRKACG) to human chromosome region 9q13. Cytogenet. Cell Genet. 60:22- 25, 1992. 3 A c

GAM47 269 PRKACG Reinton, N.; Haugen, T. B.; Orstavik, S.; Skalhegg, B. S.; Hansson,V.; Jahnsen, T.; Tasken, K.: The gene encoding the C gamma catalyticsubunit of cAMP- dependent protein kinase is a transcribed retroposon. Genomics49: 290-297, 1998. 3 A c

GAM47 269 PSCD4 Ogasawara, M.; Kim, S.- C.; Adamik, R.; Togawa, A.; Ferrans, V.J.; Takeda, K.; Kirby, M.; Moss, J.; Vaughan, M.: Similarities infunction and gene structure of cytohesin- 4 and cytohesin- 1, guaninenucleotide- exchange 3 A c

proteins for ADP- ribosylation factors. J. Biol.Chem. 275: 3221- 3230, 2000.

GAM47 269 PTHLH Albright, F.: Case records of the Massachusetts General Hospital(case 27461). New Eng. J. Med. 225: 789- 791, 1941. 3 A c

GAM47 269 PTHLH Bakre, M. M.; Zhu, Y.; Yin, H.; Burton, D. W.; Terkeltaub, R.;Deftos, L. J.; Varner, J. A.: Parathyroid hormone- related peptideis a naturally occurring, protein kinase A- dependent angiogenesisinhibitor. Nature Med. 8: 995- 1003, 2002. 3 A c

GAM47 269 PTHLH Broadus, A. E.; Mangin, M.; Ikeda, K.; Insogna, K. L.; Weir, E.C.; Burtis, W. J.; Stewart, A. F.: Humoral hypercalcemia of cancer:identification of a novel parathyroid hormone- like peptide. New Eng.J. Med. 319: 556- 563, 1988. 3 A c

GAM47 269 PTHLH Hammonds, R. G., Jr.; McKay, P.; Winslow, G. A.; Diefenbach- Jagger,H.; Grill, V.; Glatz, J.; Rodda, C. P.; Moseley, J. M.; Wood, W. I.;Martin, T. J.: Purification and characterization of recombinant humanparathyroid hormone- related protein. J. Biol. Chem. 264: 14806- 14811,1989. 3 A c

GAM47 269 PTHLH Hendy, G. N.; Sakaguchi, A. Y.; Lalley, P. A.; Martinez, L.; Yasuda,T.; Banville, D.; Goltzman, D.: Gene for parathyroid hormone- likepeptide is on mouse chromosome 6. (Abstract) Cytogenet. Cell Genet. 51:1003 only, 1989. 3 A c

GAM47 269 PTHLH Hendy, G. N.; Sakaguchi, A. Y.; Lalley, P. A.; Martinez, L.; Yasuda,T.; Banville, D.; Goltzman, D.: Gene for parathyroid hormone- likepeptide is on mouse chromosome 6. Cytogenet. Cell Genet. 53: 80- 82,1990. 3 A c

GAM47 269 PTHLH Henry, J. G.; Mitnick, M.; Dann, P. R.; Stewart, A. F.: Parathyroidhormone- related protein- (1- 36) is biologically active when administeredsubcutaneously to humans. J. Clin. Endocr. Metab. 82: 900- 906, 1997. 3 A c

GAM47 269 PTHLH Holick, M. F.; Ray, S.; Chen, T. C.; Tian, X.; Persons, K. S.:A parathyroid hormone antagonist stimulates epidermal proliferationand hair growth in mice. Proc. Nat. Acad. Sci. 91: 8014- 8016, 1994. 3 A c

GAM47 269 PTHLH Karaplis, A. C.; Luz, A.; Glowacki, J.; Bronson, R. T.; Tybulewicz,V. L. J.; Kronenberg, H. M.; Mulligan, R. C.: Lethal skeletal dysplasiafrom targeted disruption of the parathyroid hormone- related peptidegene. Genes Dev. 8: 277- 289, 1994. 3 A c

GAM47 269 PTHLH Lanske, B.; Amling, M.; Neff, L.; Guiducci, J.; Baron, R.; Kronenberg,H. M.: Ablation of the PTHrP gene or the PTH/PTHrP receptor geneleads to distinct abnormalities in bone development. J. Clin. Invest. 104:399- 407, 1999. 3 A c

GAM47 269 PTHLH Lanske, B.; Karaplis, A. C.; Lee, K.; Luz, A.; Vortkamp, A.; Pirro,A.; Karperien, M.; Defize, L. H. K.; Ho, C.; Mulligan, R. C.; Abou- Samra,A.-B.; Juppner, H.; Segre, G. V.; Kronenberg, H. M.: PTH/PTHrP receptorin early development and Indian hedgehog- regulated bone growth. Science 273:663-666, 1996. 3 A c

GAM47 269 PTHLH Mangin, M.; Ikeda, K.; Dreyer, B. E.; Broadus, A. E.: Isolationand characterization of the human parathyroid hormone- like peptidegene. Proc. Nat. Acad. Sci. 86: 2408- 2412, 1989. 3 A c

GAM47 269 PTHLH Mangin, M.; Webb, A. C.; Dreyer, B. E.; Posillico, J. T.; Ikeda,K.; Weir, E. C.; Stewart, A. F.; Bander, N. H.; Milstone, L.; Barton,D. E.; Francke, U.; Broadus, A. E.: Identification of a cDNA encodinga parathyroid hormone- like peptide from a human tumor associated withhumoral hypercalcemia of malignancy. Proc. Nat. Acad. Sci. 85: 597- 601,1988. 3 A c

GAM47 269 PTHLH Miao, D.; He, B.; Karaplis, A. C.; Goltzman, D.: Parathyroidhormone is essential for normal fetal bone formation. J. Clin. Invest. 109:1173- 1182, 3 A c

2002.

GAM47 269 PTHLH Moseley, J. M.; Kubota, M.; Diefenbach- Jagger, H.; Wettenhall,R. E. H.; Kemp, B. E.; Suva, L. J.; Rodda, C. P.; Ebeling, P. R.;Hudson, P. J.; Zajac, J. D.; Martin, T. J.: Parathyroid hormone- relatedprotein purified from a human lung cancer cell line. Proc. Nat. Acad.Sci. 84: 5048- 5052, 1987. 3 A c

GAM47 269 PTHLH Philbrick, W. M.; Dreyer, B. E.; Nakchbandi, I. A.; Karaplis,A. C.: Parathyroid hormone- related protein is required for tootheruption. Proc. Nat. Acad. Sci. 95: 11846- 11851, 1998. 3 A c

GAM47 269 PTHLH Strewler, G. J.: The physiology of parathyroid hormone- relatedprotein. New Eng. J. Med. 342: 177- 185, 2000. 3 A c

GAM47 269 PTHLH Suva, L. J.; Winslow, G. A.; Wettenhall, R. E. H.; Hammonds, R.G.; Moseley, J. M.; Diefenbach- Jagger, H.; Rodda, C. P.; Kemp, B.E.; Rodriguez, H.; Chen, E. Y.; Hudson, P. J.; Martin, T. J.; Wood,W. I.: A parathyroid hormone- related protein implicated in malignanthypercalcemia: cloning and expression. Science 237: 893- 896, 1987. 3 A c

GAM47 269 PTHLH Vortkamp, A.; Lee, K.; Lanske, B.; Segre, G. V.; Kronenberg, H.M.; Tabin, C. J.: Regulation of rate of cartilage differentiationby Indian hedgehog and PTH- related protein. Science 273: 613- 622,1996. 3 A c

GAM47 269 PTHLH Wysolmerski, J. J.; Cormier, S.; Philbrick, W. M.; Dann, P.; Zhang,J.- P.; Roume, J.; Delezoide, A.- L.; Silve, C.: Absence of functionaltype 1 parathyroid hormone (PTH)/PTH- related protein receptors inhumans is associated with abnormal breast development and tooth impaction. J.Clin. Endocr. Metab. 86: 1788- 1794, 2001. 3 A c

GAM47 269 PTHLH Wysolmerski, J. J.; Philbrick, W. M.; Dunbar, M. E.; Lanske, B.;Kronenberg, H.; Broadus, A. E.: Rescue of the parathyroid hormone- relatedprotein knockout mouse demonstrates that parathyroid hormone- relatedprotein is essential for mammary gland development. Development 125:1285- 1294, 1998. 3 A c

GAM47 269 PTHLH Yasuda, T.; Banville, D.; Hendy, G. N.; Goltzman, D.: Characterizationof the human parathyroid hormone- like peptide gene: functional andevolutionary aspects. J. Biol. Chem. 264: 7720- 7725, 1989. 3 A c

GAM47 269 PVR Gromeier, M.; Solecki, D.; Patel, D. D.; Wimmer, E.: Expressionof the human poliovirus receptor/CD155 gene during development ofthe central nervous system: implications for the pathogenesis of poliomyelitis. Virology 273:248- 257, 2000. 3 A c

GAM47 269 PVR He, Y.; Bowman, V. D.; Mueller, S.; Bator, C. M.; Bella, J.; Peng,X.; Baker, T. S.; Wimmer, E.; Kuhn, R. J.; Rossmann, M. G.: Interactionof the poliovirus receptor with poliovirus. Proc. Nat. Acad. Sci. 97:79- 84, 2000. 3 A c

GAM47 269 PVR Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka,N.; Takeuchi, K.; Takegami, T.; Nomoto, A.: The poliovirus receptorprotein is produced both as membrane- bound and secreted forms. EMBOJ. 9: 3217- 3224, 1990. 3 A c

GAM47 269 PVR Koike, S.; Taya, C.; Kurata, T.; Abe, S.; Ise, I.; Yonekawa, H.;Nomoto, A.: Transgenic mice susceptible to poliovirus. Proc. Nat.Acad. Sci. 88: 951- 955, 1991. 3 A c

GAM47 269 PVR Mendelsohn, C. L.; Wimmer, E.; Racaniello, V. R.: Cellular receptorfor poliovirus: molecular cloning, nucleotide sequence, and expressionof a new member of the immunoglobulin superfamily. Cell 56: 855- 865,1989. 3 A c

GAM47 269 PVR Mendelsohn, C.; Johnson, B.; Lionetti, K. A.; Nobis, P.; Wimmer,E.; Racaniello, V. R.: Transformation of a human poliovirus receptorgene into mouse cells. Proc. Nat. Acad. Sci. 83: 7845- 7849, 1986. 3 A c

GAM47 269 PVR Miller, D. A.; Miller, O. J.; Dev, V. G.; Hashmi, S.; Tantravahi,R. R.; 3 A c

Medrano, L.; Green, H.: Human chromosome 19 carries a poliovirusreceptor gene. Cell 1: 167- 174, 1974.

GAM47 269 PVR Schonk, D.; van Dijk, P.; Riegmann, P.; Trapman, J.; Holm, C.;Willcocks, T. 3 A c C.; Sillekens, P.; van Venrooij, W.; Wimmer, E.; Geurtsvan Kessel, A.; Ropers, H.- H.; Wieringa, B.: Assignment of sevengenes to distinct intervals on the midportion of human chromosome19q surrounding the myotonic dystrophy gene region. Cytogenet. CellGenet. 54: 15- 19, 1990.

GAM47 269 PVR Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal 3 A c mouse chromosome 9 linkage map that further defines linkagegroups homologous with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685, 1991.

GAM47 269 PVR Shepley, M. P.; Sherry, B.; Weiner, H. L.: Monoclonal antibodyidentification 3 A c of a 100- kDa membrane protein in HeLa cells and humanspinal cord involved in poliovirus attachment. Proc. Nat. Acad. Sci. 85:7743- 7747, 1988.

GAM47 269 PVR Siddique, T.; Bartlett, R. J.; McKinney, R.; Hung, W.- Y.; Bruns,G.; 3 A c Wilfert, C.; Roses, A. D.: The poliovirus sensitivity (PVS) ison chromosome 19q13- qter. (Abstract) Cytogenet. Cell Genet. 40:745 only, 1985.

GAM47 269 PVR Siddique, T.; McKinney, R.; Hung, W.- Y.; Bartlett, R. J.; Bruns,G.; 3 A c Mohandas, T. K.; Ropers, H.- H.; Wilfert, C.; Roses, A. D.: Thepoliovirus sensitivity (PVS) gene is on chromosome 19q12- q13.2. Genomics 3:156- 160, 1988.

GAM47 269 PVR Solecki, D. J.; Gromeier, M.; Mueller, S.; Bernhardt, G.; Wimmer,E.: 3 A c Expression of the human poliovirus receptor/CD155 gene is activatedby Sonic hedgehog. J. Biol. Chem. 277: 25697- 25702, 2002.

GAM47 269 PVR Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 A c Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993.

GAM47 269 PXN Fernandez- Valle, C.; Tang, Y.; Ricard, J.; Rodenas- Ruano, A.; Taylor,A.; 3 A c Hackler, E.; Biggerstaff, J.; Iacovelli, J.: Paxillin binds schwannominand regulates its density- dependent localization and effect on cellmorphology. Nature Genet. 31: 354- 362, 2002.

GAM47 269 PXN Glenney, J. R., Jr.; Zokas, L.: Novel tyrosine kinase substratesfrom Rous 3 A c sarcoma virus- transformed cells are present in the membraneskeleton. J. Cell Biol. 108: 2401- 2408, 1989.

GAM47 269 PXN Horikoshi, N.; Cong, J.; Kley, N.; Shenk, T.: Isolation of 3 A c differentiallyexpressed cDNAs from p53- dependent apoptotic cells: activation ofthe human homologue of the Drosophila peroxidasin gene. Biochem.Biophys. Res. Commun. 261: 864- 869, 1999.

GAM47 269 PXN Mazaki, Y.; Hashimoto, S.; Sabe, H.: Monocyte cells and cancercells express 3 A c novel paxillin isoforms with different binding propertiesto focal adhesion proteins. J. Biol. Chem. 272: 7437- 7444, 1997.

GAM47 269 PXN Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; 3 A c Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM47 269 PXN Salgia, R.; Li, J.- L.; Lo, S. H.; Brunkhorst, B.; Kansas, G. S.;Sobhany, E. 3 A c S.; Sun, Y.; Pisick, E.; Hallek, M.; Ernst, T.; Tantravahi,R.; Chen, L. B.;

Griffin, J. D.: Molecular cloning of human paxillin,a focal adhesion protein phosphorylated by P210(BCR/ABL). J. Biol.Chem. 270: 5039- 5047, 1995.

GAM47 269 PXN Turner, C. E.; Glenney, J. R., Jr.; Burridge, K.: Paxillin: anew vinculin- 3 A c
binding protein present in focal adhesions. J. CellBiol. 111: 1059- 1068, 1990.

GAM47 269 PXN Weiler, S. R.; Taylor, S. M.; Deans, R. J.; Kan- Mitchell, J.; Mitchell,M. 3 A c
S.; Trent, J. M.: Assignment of a human melanoma associated geneMG50 (D2S448) to chromosome 2p25.3 by fluorescence in situ hybridization. Genomics 22:243- 244, 1994.

GAM47 269 RBM8A Conklin, D. C.; Rixon, M. W.; Kuestner, R. E.; Maurer, M. F.; Whitmore,T. 3 A c
E.; Millar, R. P.: Cloning and gene expression of a novel humanribonucleoprotein. Biochim. Biophys. Acta 1492: 465- 469, 2000.

GAM47 269 RBM8A Kataoka, N.; Yong, J.; Kim, V. N.; Velazquez, F.; Perkinson, R.A.; Wang, F.; 3 A c
Dreyfuss, G.: Pre- mRNA splicing imprints mRNA in thenucleus with a novel RNA- binding protein that persists in the cytoplasm. Molec.Cell 6: 673- 682, 2000.

GAM47 269 RBM8A Salicioni, A. M.; Xi. M.; Vanderveer, L. A.; Balsara, B.; Testa,J. R.; 3 A c
Dunbrack, R. L., Jr.; Godwin, A. K.: Identification and structuralanalysis of human RBM8A and RBM8B: two highly conserved RNA- bindingmotif proteins that interact with OVCA1, a candidate tumor suppressor. Genomics 69:54- 62, 2000.

GAM47 269 RBM8A Zhao, X.- F.; Nowak, N. J.; Shows, T. B.; Aplan, P. D.: MAGOH interactswith 3 A c
a novel RNA- binding protein. Genomics 63: 145- 148, 2000.

GAM47 269 RERE Amler, L. C.; Bauer, A.; Corvi, R.; Dihlmann, S.; Praml, C.; Cavenee,W. K.; 3 A c
Schwab, M.; Hampton, G. M.: Identification and characterizationof novel genes located at the t(1;15)(p36.2;q24) translocation breakpointin the neuroblastoma cell line NGP. Genomics 64: 195- 202, 2000.

GAM47 269 RERE Yanagisawa, H.; Bundo, M.; Miyashita, T.; Okamura- Oho, Y.; Tadokoro,K.; 3 A c
Tokunaga, K.; Yamada, M.: Protein binding of a DRPLA family througharginine-glutamic acid dipeptide repeats is enhanced by extended polyglutamine. Hum.Molec. Genet. 9: 1433- 1442, 2000.

GAM47 269 REST Abderrahmani, A.; Steinmann, M.; Plaisance, V.; Niederhauser, G.;Haefliger, 3 A c
J.- A.; Mooser, V.; Bonny, C.; Nicod, P.; Waeber, G.: Thetranscriptional repressor REST determines the cell- specific expressionof the human MAPK8IP1 gene encoding IB1 (JIP- 1). Molec. Cell. Biol. 21:7256- 7627, 2001.

GAM47 269 REST Chen, Z.- F.; Paquette, A. J.; Anderson, D. J.: NRSF/REST is requiredin vivo 3 A c
for repression of multiple neuronal target genes during embryogenesis. NatureGenet. 20: 136- 142, 1998.

GAM47 269 REST Palm, K.; Metsis, M.; Timmusk, T.: Neuron- specific splicing ofzinc finger 3 A c
transcription factor REST/NRSF/XBR is frequent in neuroblastomasand conserved in human, mouse and rat. Molec. Brain Res. 72: 30- 39,1999.

GAM47 269 REST Schoenherr, C. J.; Anderson, D. J.: The neuron- restrictive silencerfactor 3 A c
(NRSF): a coordinate repressor of multiple neuron- specificgenes. Science 267: 1360- 1363, 1995.

GAM47 269 REST Thiel, G.; Lietz, M.; Cramer, M.: Biological activity and modulatorstructure 3 A c
of RE- 1- silencing transcription factor (REST), a repressorof neuronal genes. J. Biol. Chem. 273: 26891- 26899, 1998.

GAM47 269 RET Amiel, J.; Salomon, R.; Attie, T.; Pelet, A.; Trang, H.; Mokhtari,M.; 3 A c
Gaultier, C.; Munnich, A.; Lyonnet, S.: Mutations of the RET- GDNFsignaling pathway in Ondine's curse. (Letter) Am. J. Hum. Genet. 62:715- 717, 1998.

GAM47 269 RET Angrist, M.; Bolk, S.; Thiel, B.; Puffenberger, E. G.; Hofstra,R. M.; Buys, C. H. C. M.; Cass, D. T.; Chakravarti, A.: Mutationanalysis of the RET receptor tyrosine kinase in Hirschsprung disease. Hum.Molec. Genet. 4: 821-830, 1995. 3 A c

GAM47 269 RET Antinolo, G.; Marcos, I.; Fernandez, R. M.; Romero, M.; Borrego,S.: A novel germline point mutation, c.2304G(T, in codon 768 of theRET proto- oncogene in a patient with medullary thyroid carcinoma.(Letter) Am. J. Med. Genet. 110: 85- 87, 2002. 3 A c

GAM47 269 RET Attie, T.; Pelet, A.; Edery, P.; Eng, C.; Mulligan, L. M.; Amiel,J.; Boutrand, L.; Beldjord, C.; Nihoul- Fekete, C.; Munnich, A.; Ponder,B. A. J.; Lyonnet, S.: Diversity of RET proto- oncogene mutationsin familial and sporadic Hirschsprung disease. Hum. Molec. Genet. 4:1381- 1386, 1995. 3 A c

GAM47 269 RET Attie- Bitach, T.; Abitbol, M.; Gerard, M.; Delezoide, A.- L.; Auge,J.; Pelet, A.; Amiel, J.; Pachnis, V.; Munnich, A.; Lyonnet, S.; Vekemans,M.: Expression of the RET proto- oncogene in human embryos. Am. J.Med. Genet. 80: 481- 486, 1998. 3 A c

GAM47 269 RET Auricchio, A.; Griseri, P.; Carpentieri, M. L.; Betsos, N.; Staiano,A.; Tozzi, A.; Priolo, M.; Thompson, H.; Bocciardi, R.; Romeo, G.;Ballabio, A.; Ceccherini, I.: Double heterozygosity for a RET substitutioninterfering with splicing and an EDNRB missense mutation in Hirschsprungdisease. (Letter) Am. J. Hum. Genet. 64: 1216- 1221, 1999. 3 A c

GAM47 269 RET Batourina, E.; Choi, C.; Paragas, N.; Bello, N.; Hensle, T.; Costantini,F. D.; Schuchardt, A.; Bacallao, R. L.; Mendelsohn, C. L.: Distalureter morphogenesis depends on epithelial cell remodeling mediatedby vitamin A and Ret. Nature Genet. 32: 109- 115, 2002. Note: Erratum:Nature Genet. 32: 331 only, 2002. 3 A c

GAM47 269 RET Batourina, E.; et al; et al: Vitamin A controls epithelial/mesenchymalinteractions through Ret expression. Nature Genet. 27: 74- 78, 2001. 3 A c

GAM47 269 RET Berndt, I.; Reuter, M.; Saller, B.; Frank- Raue, K.; Groth, P.:Grubendorf, M.; Raue, F.; Ritter, M. M.; Hoppner, W.: A new hot spotfor mutations in the ret protooncogene causing familial medullarythyroid carcinoma and multiple endocrine neoplasia type 2A. J. Clin.Endocr. Metab. 83: 770- 774, 1998. 3 A c

GAM47 269 RET Boccia, L. M.; Green, J. S.; Joyce, C.; Eng, C.; Taylor, S. A.M.; Mulligan, L. M.: Mutation of RET codon 768 is associated withthe FMTC phenotype. Clin. Genet. 51: 81- 85, 1997. 3 A c

GAM47 269 RET Bolino, A.; Schuffenecker, I.; Luo, Y.; Seri, M.; Silengo, M.;Tocco, T.; Chabrier, G.; Houdent, C.; Murat, A.; Schlumberger, M.;Tourniaire, J.; Lenoir, G. M.; Romeo, G.: RET mutations in exons13 and 14 of FMTC patients. Oncogene 10: 2415- 2419, 1995. 3 A c

GAM47 269 RET Bolk Gabriel, S.; Salomon, R.; Pelet, A.; Angrist, M.; Amiel,J.; Fornage, M.; Attie- Bitach, T.; Olson, J. M.; Hofstra, R.; Buys,C.; Steffann, J.; Munnich, A.; Lyonnet, S.; Chakravarti, A.: Segregationat three loci explains familial and population risk in Hirschsprungdisease. Nature Genet. 31: 89-93, 2002. 3 A c

GAM47 269 RET Bolk, S.; Angrist, M.; Schwartz, S.; Silvestri, J. M.; Weese- Mayer,D. E.; Chakravarti, A.: Congenital central hypoventilation syndrome:mutation analysis of the receptor tyrosine kinase RET. Am. J. Med.Genet. 63: 603-609, 1996. 3 A c

GAM47 269 RET Bongarzone, I.; Vigano, E.; Alberti, L.; Borrello, M. G.; Pasini,B.; Greco, 3 A c

A.; Mondellini, P.; Smith, D. P.; Ponder, B. A. J.; Romeo,G.; Pierotti, M. A.: Full activation of MEN2B mutant RET by an additionalMEN2A mutation or by ligand GDNF stimulation. Oncogene 16: 2295- 2301,1998.

GAM47 269 RET Borrego, S.; Ruiz, A.; Saez, M. E.; Gimm, O.; Gao, X.; Lopez- Alonso,M.; Hernandez, A.; Wright, F. A.; Antinolo, G.; Eng, C.: RET genotypescomprising specific haplotypes of polymorphic variants predisposeto isolated Hirschsprung disease. J. Med. Genet. 37: 572- 578, 2000. 3 A c

GAM47 269 RET Borrego, S.; Saez, M. E.; Ruiz, A.; Gimm, O.; Lopez- Alonso, M.;Antinolo, G.; Eng, C.: Specific polymorphisms in the RET proto- oncogeneare over-represented in patients with Hirschsprung disease and mayrepresent loci modifying phenotypic expression. J. Med. Genet. 36:771- 774, 1999. 3 A c

GAM47 269 RET Carlson, K. M.; Bracamontes, J.; Jackson, C. E.; Clark, R.; Lacroix,A.; Wells, S. A., Jr.; Goodfellow, P. J.: Parent- of- origin effectsin multiple endocrine neoplasia type 2B. Am. J. Hum. Genet. 55:1076- 1082, 1994. 3 A c

GAM47 269 RET Carlson, K. M.; Dou, S.; Chi, D.; Scavarda, N.; Toshima, K.; Jackson,C. E.; Wells, S. A., Jr.; Goodfellow, P. J.; Donis- Keller, H.: Singlemissense mutation in the tyrosine kinase catalytic domain of the RETprotooncogene is associated with multiple endocrine neoplasia type2B. Proc. Nat. Acad. Sci. 91: 1579- 1583, 1994. 3 A c

GAM47 269 RET Carrasquillo, M. M.; McCallion, A. S.; Puffenberger, E. G.; Kashuk,C. S.; Nouri, N.; Chakravarti, A.: Genome- wide association studyand mouse model identify interaction between RET and EDNRB pathwaysin Hirschsprung disease. Nature Genet. 32: 237- 244, 2002. 3 A c

GAM47 269 RET Ceccherini, I.; Hofstra, R. M.; Luo, Y.; Stulp, R. P.; Barone,V.; Stelwagen, T.; Bocciardi, R.; Nijveen, H.; Bolino, A.; Seri, M.;Ronchetto, P.; Pasini, B.; Bozzano, M.; Buys, C. H. C. M.; Romeo,G.: DNA polymorphisms and conditions for SSCP analysis of the 20exons of the Ret proto- oncogene. Oncogene 9: 3025- 3029, 1994. 3 A c

GAM47 269 RET Ceccherini, I.; Romei, C.; Barone, V.; Pacini, F.; Martino, E.;Loviselli, A.; Pinchera, A.; Romeo, G.: Identification of the cys634- to- tyrmutation of the RET proto- oncogene in a pedigree with multiple endocrineneoplasia type 2A and localized cutaneous lichen amyloidosis. J.Endocr. Invest. 17: 201- 204, 1994. 3 A c

GAM47 269 RET Cetta, F.; Chiappetta, G.; Melillo, R. M.; Petracci, M.; Montalto,G.; Santoro, M.; Fusco, A.: The ret/ptc1 oncogene is activated infamilial adenomatous polyposis- associated thyroid papillary carcinomas. J.Clin. Endocr. Metab. 83: 1003- 1006, 1998. 3 A c

GAM47 269 RET Decker, R. A.; Peacock, M. L.; Watson, P.: Hirschsprung diseasein MEN 2A: increased spectrum of RET exon 10 genotypes and stronggenotype- phenotype correlation. Hum. Molec. Genet. 7: 129- 134, 1998. 3 A c

GAM47 269 RET Donis- Keller, H.; Dou, S.; Chi, D.; Carlson, K. M.; Toshima, K.;Lairmore, T. C.; Howe, J. R.; Moley, J. F.; Goodfellow, P.; Wells,S. A., Jr.: Mutations in the RET proto- oncogene are associated withMEN 2A and FMTC. Hum. Molec. Genet. 2: 851- 856, 1993. 3 A c

GAM47 269 RET Doray, B.; Salomon, R.; Amiel, J.; Pelet, A.; Touraine, R.; Billaud,M.; Attie, T.; Bachy, B.; Munnich, A.; Lyonnet, S.: Mutation of theRET ligand, neurturin, supports multigenic inheritance in Hirschsprungdisease. Hum. Molec. Genet. 7: 1449- 1452, 1998. 3 A c

GAM47 269 RET Edery, P.; Lyonnet, S.; Mulligan, L. M.; Pelet, A.; Dow, E.; Abel,L.; Holder, S.; Nihoul- Fekete, C.; Ponder, B. A. J.; Munnich, A.:Mutations of 3 A c

the RET proto- oncogene in Hirschsprung's disease. Nature 367:378- 380, 1994.

GAM47 269 RET Eng, C.: The RET proto- oncogene in multiple endocrine neoplasiatype 2 and 3 A c
Hirschsprung's disease. New Eng. J. Med. 335: 943- 951,1996.

GAM47 269 RET Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; 3 A c
Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P.
A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-
oncogene and the von Hippel- Lindau disease tumoursuppressor gene in
sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937,
1995.

GAM47 269 RET Eng, C.; Mulligan, L. M.: Mutations of the RET proto- oncogenein the 3 A c
multiple endocrine neoplasia type 2 syndromes, related sporadictumours, and
Hirschsprung disease. Hum. Mutat. 9: 97- 109, 1997.

GAM47 269 RET Eng, C.; Mulligan, L. M.; Smith, D. P.; Healey, C. S.; Frilling,A.; Raue, 3 A c
F.; Neumann, H. P. H.; Pfragner, R.; Behmel, A.; Lorenzo,M. J.; Stonehouse,
T. J.; Ponder, M. A.; Ponder, B. A. J.: Mutationof the RET protooncogene in
sporadic medullary thyroid carcinoma. GenesChromosomes Cancer 12: 209- 212,
1995.

GAM47 269 RET Eng, C.; Smith, D. P.; Mulligan, L. M.; Healey, C. S.; Zvelebil,M. J.; 3 A c
Stonehouse, T. J.; Ponder, M. A.; Jackson, C. E.; Waterfield,M. D.; Ponder,
B. A. J.: A novel point mutation in the tyrosine kinasedomain of the RET
proto- oncogene in sporadic medullary thyroid carcinomaand in a family with
FMTC. Oncogene 10: 509- 513, 1995.

GAM47 269 RET Eng, C.; Smith, D. P.; Mulligan, L. M.; Nagai, M. A.; Healey,C. S.; Ponder, 3 A c
M. A.; Gardner, E.; Scheumann, G. F. W.; Jackson, C.E.; Tunnacliffe, A.;
Ponder, B. A. J.: Point mutation within thetyrosine kinase domain of the RET
proto- oncogene in multiple endocrineneoplasia type 2B and related sporadic
tumors. Hum. Molec. Genet. 3:237- 241, 1994.

GAM47 269 RET Farndon, J. R.; Leight, G. S.; Dilley, W. G.; Baylin, S. B.; Smallridge,R. 3 A c
C.; Harrison, T. S.; Wells, S. A., Jr.: Familial medullary thyroidcarcinoma
without associated endocrinopathies: a distinct clinicalentity. Brit. J.
Surg. 73: 278- 281, 1986.

GAM47 269 RET Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of 3 A c
cancer. Science 278: 1043- 1050, 1997.

GAM47 269 RET Fitze, G.; Schreiber, M.; Kuhlisch, E.; Schackert, H. K.; Roesner,D.: 3 A c
Association of RET protooncogene codon 45 polymorphism with
Hirschsprungdisease. (Letter) Am. J. Hum. Genet. 65: 1469- 1473, 1999.

GAM47 269 RET Gardner, E.; Mulligan, L. M.; Eng, C.; Healey, C. S.; Kwok, J.B. J.; Ponder, 3 A c
M. A.; Ponder, B. A. J.: Haplotype analysis of MEN2 mutations. Hum. Molec.
Genet. 3: 1771- 1774, 1994.

GAM47 269 RET Grieco, M.; Santoro, M.; Berlingieri, M. T.; Melillo, R. M.; Donghi,R.; 3 A c
Bongarzone, I.; Pierotti, M. A.; Della Porta, G.; Fusco, A.; Vecchio,G.: PTC
is a novel rearranged form of the ret proto- oncogene andis frequently
detected in vivo in human thyroid papillary carcinomas. Cell 60:557- 563,
1990.

GAM47 269 RET Hofstra, R. M. W.; Landsvater, R. M.; Ceccherini, I.; Stulp, R.P.; 3 A c
Stelwagen, T.; Luo, Y.; Pasini, B.; Hoppener, J. W. M.; Ploosvan Amstel, H.
K.; Romeo, G.; Lips, C. J. M.; Buys, C. H. C. M.:A mutation in the RET
proto- oncogene associated with multiple endocrineneoplasia type 2B and
sporadic medullary thyroid carcinoma. Nature 367:375- 376, 1994.

GAM47 269 RET Hofstra, R. M. W.; Sijmons, R. H.; Stelwagen, T.; Stulp, R. P.;Kousseff, B. G.; Lips, C. J. M.; Steijlen, P. M.; Van Voorst Vader,P. C.; Buys, C. H. C. M.: RET mutation screening in familial cutaneouslichen amyloidosis and in skin amyloidosis associated with multipleendocrine neoplasia. J. Invest. Derm. 107: 215- 218, 1996. 3 A c

GAM47 269 RET Hoppener, J. W. M.; Lips, C. J. M.: RET receptor tyrosine kinasegene mutations: molecular biological, physiological and clinical aspects. Europ.J. Clin. Invest. 26: 613- 624, 1996. 3 A c

GAM47 269 RET Hoppner, W.; Ritter, M. M.: A duplication of 12 bp in the criticalcysteine rich domain of the RET proto- oncogene results in a distinctphenotype of multiple endocrine neoplasia type 2A. Hum. Molec. Genet. 6:587- 590, 1997. 3 A c

GAM47 269 RET Ikeda, I.; Ishizaka, Y.; Tahira, T.; Suzuki, T.; Onda, M.; Sugimura,T.; Nagao, M.: Specific expression of the ret proto- oncogene in humanneuroblastoma cell lines. Oncogene 5: 1291- 1296, 1990. 3 A c

GAM47 269 RET Ishizaka, Y.; Itoh, F.; Tahira, T.; Ikeda, I.; Sugimura, T.; Tucker,J.; Fertitta, A.; Carrano, A. V.; Nagao, M.: Human ret proto- oncogenemapped to chromosome 10q11.2. Oncogene 4: 1519- 1521, 1989. 3 A c

GAM47 269 RET Iwashita, T.; Murakami, H.; Asai, N.; Takahashi, M.: Mechanismof Ret dysfunction by Hirschsprung mutations affecting its extracellulardomain. Hum. Molec. Genet. 5: 1577- 1580, 1996. 3 A c

GAM47 269 RET Japon, M. A.; Urbano, A. G.; Saez, C.; Segura, D. I.; Cerro, A.L.; Dieguez, C.; Alvarez, C. V.: Glial- derived neurotropic factorand RET gene expression in normal human anterior pituitary cell typesand in pituitary tumors. J. Clin. Endocr. Metab. 87: 1879- 1884,2002. 3 A c

GAM47 269 RET Julies, M. G.; Moore, S. W.; Kotze, M. J.; du Plessis, L.: NovelRET mutations in Hirschsprung's disease patients from the diverseSouth African population. Europ. J. Hum. Genet. 9: 419- 423, 2001. 3 A c

GAM47 269 RET Klugbauer, S.; Demidchik, E. P.; Lengfelder, E.; Rabes, H. M.: Detection of a novel type of RET rearrangement (PTC5) in thyroidcarcinomas after Chernobyl and analysis of the involved RET- fusedgene RFG5. Cancer Res. 58: 198- 203, 1998. 3 A c

GAM47 269 RET Klugbauer, S.; Rabes, H. M.: The transcription coactivator HTIF1and a related protein are fused to the RET receptor tyrosine kinasein childhood papillary thyroid carcinomas. Oncogene 18: 4388- 4393,1999. 3 A c

GAM47 269 RET Lairmore, T. C.; Dou, S.; Howe, J. R.; Chi, D.; Carlson, K.; Veile,R.; Mishra, S. K.; Wells, S. A., Jr.; Donis- Keller, H.: A 1.5- megabaseyeast artificial chromosome contig from human chromosome 10q11.2 connectingthree genetic loci (RET, D10S94, and D10S102) closely linked to theMEN2A locus. Proc. Nat. Acad. Sci. 90: 492- 496, 1993. 3 A c

GAM47 269 RET Lombardo, F.; Baudin, E.; Chiefari, E.; Arturi, F.; Bardet, S.;Caillou, B.; Conte, C.; Dallapiccola, B.; Giuffrida, D.; Bidart, J.- M.;Schlumberger, M.; Filetti, S.: Familial medullary thyroid carcinoma:clinical variability and low aggressiveness associated with RET mutationat codon 804. J. Clin. Endocr. Metab. 87: 1674- 1680, 2002. 3 A c

GAM47 269 RET Lore, F.; Di Cairano, G.; Talidis, F.: Unilateral renal agenesisin a family with medullary thyroid carcinoma. (Letter) New Eng. J.Med. 342: 1218- 1219, 2000. 3 A c

GAM47 269 RET Machens, A.; Gimm, O.; Hinze, R.; Hoppner, W.; Boehm, B. O.; Dralle,H.: Genotype- phenotype correlations in hereditary medullary thyroidcarcinoma: oncological features and biochemical properties. J. Clin.Endocr. Metab. 86: 3 A c

1104- 1109, 2001.

GAM47 269 RET Mendelsohn, C.; et al; et al: Function of the retinoic acid receptors(RARs) 3 A c during development (II). Multiple abnormalities at variousstages of organogenesis in RAR double mutants. Development 120:2749- 2771, 1994.

GAM47 269 RET Menko, F. H.; van der Luijt, R. B.; de Valk, I. A. J.; Toorians,A. W. F. T.; 3 A c Sepers, J. M.; van Diest, P. J.; Lips, C. J. M.: AtypicalMEN type 2B associated with two germline RET mutations on the sameallele not involving codon 918. J. Clin. Endocr. Metab. 87: 393- 397,2002.

GAM47 269 RET Mulligan, L. M.; Eng, C.; Healey, C. S.; Clayton, D.; Kwok, J.B. J.; 3 A c Gardner, E.; Ponder, M. A.; Frilling, A.; Jackson, C. E.; Lehnert,H.; Neumann, H. P. H.; Thibodeau, S. N.; Ponder, B. A. J.: Specificmutations of the RET proto- oncogene are related to disease phenotypein MEN 2A and FMTC. Nature Genet. 6: 70- 74, 1994.

GAM47 269 RET Mulligan, L. M.; Kwok, J. B. J.; Healey, C. S.; Elsdon, M. J.;Eng, C.; 3 A c Gardner, E.; Love, D. R.; Mole, S. E.; Moore, J. K.; Papi,L.; Ponder, M. A.; Telenius, H.; Tunnacliffe, A.; Ponder, B. A. J.: Germ- line mutations of the RET proto- oncogene in multiple endocrineneoplasia type 2A. Nature 363: 458- 460, 1993.

GAM47 269 RET Munnes, M.; Fanaei, S.; Schmitz, B.; Muiznieks, I.; Holschneider,A. M.; 3 A c Doerfler, W.: Familial form of Hirschsprung disease: nucleotidesequence studies reveal point mutations in the RET proto- oncogenein two of six families but not in other candidate genes. Am. J. Med.Genet. 94: 19- 27, 2000.

GAM47 269 RET Nakata, T.; Kitamura, Y.; Shimizu, K.; Tanaka, S.; Fujimori, M.;Yokoyama, 3 A c S.; Ito, K.; Emi, M.: Fusion of a novel gene, ELKS, toRET due to translocation t(10;12)(q11;p13) in a papillary thyroidcarcinoma. Genes Chromosomes Cancer 25: 97- 103, 1999.

GAM47 269 RET Niccoli- Sire, P.; Murat, A.; Rohmer, V.; Franc, S.; Chabrier,G.; Baldet, 3 A c L.; Maes, B.; Savagner, F.; Giraud, S.; Bezieau, S.; Kottler,M.- L.; Morange, S.; Conte- Devolx, B.: The French Calcitonin TumorsStudy Group (GETC).: Familial medullary thyroid carcinoma with noncysteineRET mutations: phenotype- genotype relationship in a large series ofpatients. J. Clin. Endocr. Metab. 86: 3746- 3753, 2001.

GAM47 269 RET Pachnis, V.; Mankoo, B.; Costantini, F.: Expression of the c- retproto- 3 A c oncogene during mouse embryogenesis. Development 119: 1005- 1017,1993.

GAM47 269 RET Pasini, B.; Hofstra, R. M. W.; Yin, L.; Bocciardi, R.; Santamaria,G.; 3 A c Grootscholten, P. M.; Ceccherini, I.; Patrone, G.; Priolo, M.;Buys, C. H. C. M.; Romeo, G.: The physical map of the human RET proto- oncogene. Oncogene 11:1737- 1743, 1995.

GAM47 269 RET Pelet, A.; Geneste, O.; Edery, P.; Pasini, A.; Chappuis, S.; Attie,T.; 3 A c Munnich, A.; Lenoir, G.; Lyonnet, S.; Billaud, M.: Various mechanismscause RET- mediated signaling defects in Hirschsprung's disease. J.Clin. Invest. 101: 1415- 1423, 1998.

GAM47 269 RET Pierotti, M. A.; Santoro, M.; Jenkins, R. B.; Sozzi, G.; Bongarzone,I.; 3 A c Grieco, M.; Monzini, N.; Miozzo, M.; Herrmann, M. A.; Fusco, A.;Hay, I. D.; Della Porta, G.; Vecchio, G.: Characterization of aninversion on the long arm of chromosome 10 juxtaposing D10S170 andRET and creating the oncogenic sequence RET/PTC. Proc. Nat. Acad.Sci. 89: 1616- 1620, 1992.

GAM47 269 RET Pigny, P.; Bauters, C.; Wemeau, J.- L.; Houcke, M. L.; Crepin,M.; Caron, P.; 3 A c Giraud, S.; Calender, A.; Buisine, M.- P.; Kerckaert,J.- P.; Porchet, N.: A

novel 9- base pair duplication in RET exon 8in familial medullary thyroid carcinoma. J. Clin. Endocr. Metab. 84:1700- 1704, 1999.

GAM47 269 RET Puffenberger, E. G.; Hosoda, K.; Washington, S. S.; Nakao, K.;deWit, D.; Yanagisawa, M.; Chakravarti, A.: A missense mutation ofthe endothelin- B receptor gene in multigenic Hirschsprung's disease. Cell 79:1257- 1266, 1994. 3 A c

GAM47 269 RET Robinson, M. F.; Cote, G. J.; Nunziata, V.; Brandi, M. L.; Ferrer,J. P.; Martins Bugalho, M. J. G.; Almeida Ruas, M. M.; Chik, C.; Colantuoni,V.; Gagel, R. F.: Mutation of a specific codon of the RET proto- oncogenein the multiple endocrine neoplasia type 2A/cutaneous lichen amyloidosissyndrome. (Abstract) Fifth International Workshop on Multiple EndocrineNeoplasia, Stockholm, Archipelago , 1994. 3 A c

GAM47 269 RET Rodrigues, G. A.; Park, M.: Dimerization mediated through a leucinezipper activates the oncogenic potential of the met receptor tyrosinekinase. Molec. Cell. Biol. 13: 6711- 6722, 1993. 3 A c

GAM47 269 RET Romeo, G.; Ronchetto, P.; Luo, Y.; Barone, V.; Seri, M.; Ceccherini,I.; Pasini, B.; Bocciardi, R.; Lerone, M.; Kaariainen, H.; Martucciello,G.: Point mutations affecting the tyrosine kinase domain of the RETproto- oncogene in Hirschsprung's disease. Nature 367: 377- 378, 1994. 3 A c

GAM47 269 RET Salvatore, D.; Barone, M. V.; Salvatore, G.; Melillo, R. M.; Chiappetta,G.; Mineo, A.; Fenzi, G.; Vecchio, G.; Fusco, A.; Santoro, M.: Tyrosines1015 and 1062 are in vivo autophosphorylation sites in Ret and Ret- derivedoncoproteins. J. Clin. Endocr. Metab. 85: 3898- 3907, 2000. 3 A c

GAM47 269 RET Santoro, M.; Carlomagno, F.; Hay, I. D.; Herrmann, M. A.; Grieco,M.; Melillo, R.; Pierotti, M. A.; Bongarzone, I.; Della Porta, G.;Berger, N.; Peix, J. L.; Paulin, C.; Fabien, N.; Vecchio, G.; Jenkins,R. B.; Fusco, A.: Ret oncogene activation in human thyroid neoplasmsis restricted to the papillary cancer subtype. J. Clin. Invest. 89:1517- 1522, 1992. 3 A c

GAM47 269 RET Santoro, M.; Carlomagno, F.; Romano, A.; Bottaro, D. P.; Dathan,N. A.; Grieco, M.; Fusco, A.; Vecchio, G.; Matoskova, B.; Kraus, M.H.; Di Fiore, P. P.: Activation of RET as a dominant transforminggene by germline mutations of MEN2A and MEN2B. Science 267: 381- 383,1995. 3 A c

GAM47 269 RET Schuchardt, A.; D'Agati, V.; Larsson- Blomberg, L.; Costantini,F.; Pachnis, V.: Defects in the kidney and enteric nervous systemof mice lacking the tyrosine kinase receptor Ret. Nature 367: 380- 383,1994. 3 A c

GAM47 269 RET Seri, M.; Celli, I.; Betsos, N.; Claudiani, F.; Camera, G.; Romeo,G.: A cys634gly substitution of the RET proto- oncogene in a familywith recurrence of multiple endocrine neoplasia type 2A and cutaneouslichen amyloidosis. Clin. Genet. 51: 86- 90, 1997. 3 A c

GAM47 269 RET Seri, M.; Yin, L.; Barone, A.; Bolino, A.; Celli, I.; Bocciardi,R.; Pasini, B.; Ceccherini, I.; Lerone, M.; Kristoffersson, U.; Larsson,L. T.; Casasa, J. M.; Cass, D. T.; Abramowicz, M. J.; Vanderwinden,J.- M.; Kravcenkiene, I.; Baric, I.; Silengo, M.; Martucciello, G.;Romeo, G.: Frequency of RET mutations in long- and short- segmentHirschsprung disease. Hum. Mutat. 9: 243- 249, 1997. 3 A c

GAM47 269 RET Shirahama, S.; Ogura, K.; Takami, H.; Ito, K.; Tohsen, T.; Miyauchi,A.; Nakamura, Y.: Mutational analysis of the RET proto- oncogene in71 Japanese patients with medullary thyroid carcinoma. J. Hum. Genet. 43:101- 106, 1998. 3 A c

GAM47 269 RET Svensson, P.- J.; Anvret, M.; Molander, M.- L.; Nordenskjold, A.: Phenotypic variation in a family with mutations in two Hirschsprung- relatedgenes (RET 3 A c

and endothelin receptor B). Hum. Genet. 103: 145- 148,1998.

GAM47 269 RET Takahashi, M.; Buma, Y.; Hiai, H.: Isolation of ret proto- oncogenecDNA with an amino- terminal signal sequence. Oncogene 4: 805- 806,1989. 3 A c

GAM47 269 RET Takahashi, M.; Buma, Y.; Iwamoto, T.; Inaguma, Y.; Ikeda, H.;Hiai, H.: Cloning and expression of the ret proto- oncogene encodinga tyrosine kinase with two potential transmembrane domains. Oncogene 3:571- 578, 1988. 3 A c

GAM47 269 RET Takahashi, M.; Ritz, J.; Cooper, G. M.: Activation of a novelhuman transforming gene, ret, by DNA rearrangement. Cell 42: 581- 588,1985. 3 A c

GAM47 269 RET Tessitore, A.; Sinisi, A. A.; Pasquali, D.; Cardone, M.; Vitale,D.; Bellastella, A.; Colantuoni, V.: A novel case of multiple endocrineneoplasia type 2A associated with two de novo mutations of the RETprotooncogene. J. Clin. Endocr. Metab. 84: 3522- 3527, 1999. 3 A c

GAM47 269 RET van Heyningen, V.: One gene- - four syndromes. Nature 367: 319- 320,1994. 3 A c

GAM47 269 RET Xue, F.; Yu, H.; Maurer, L. H.; Memoli, V. A.; Nutile- McMenemey,N.; Schuster, M. K.; Bowden, D. W.; Mao, J.; Noll, W. W.: GermlineRET mutations in MEN 2A and FMTC and their detection by simple DNAdiagnostic tests. Hum. Molec. Genet. 3: 635- 638, 1994. 3 A c

GAM47 269 RET Yin, L.; Ceccherini, I.; Pasini, B.; Matera, I.; Bicocchi, M.P.; Barone, V.; Bocciardi, R.; Kaariainen, H.; Weber, D.; Devoto,M.; Romeo, G.: Close linkage with the RET protooncogene and boundariesof deletion mutations in autosomal dominant Hirschsprung disease. Hum.Molec. Genet. 2: 1803- 1808, 1993. 3 A c

GAM47 269 SDC1 Ala- Kapee, M.; Nevanlinna, H.; Mali, M.; Jalkanen, M.; Schroder,J.: Localization of gene for human syndecan, an integral membraneproteoglycan and a matrix receptor, to chromosome 2. Somat. CellMolec. Genet. 16: 501- 505, 1990. 3 A c

GAM47 269 SDC1 Alexander, C. M.; Reichsman, F.; Hinkes, M. T.; Lincecum, J.; Becker,K. A.; Cumberledge, S.; Bernfield, M.: Syndecan- 1 is required forWnt- 1- induced mammary tumorigenesis in mice. Nature Genet. 25: 329- 332,2000. 3 A c

GAM47 269 SDC1 Mali, M.; Jaakkola, P.; Arvilommi, A.- M.; Jalkanen, M.: Sequenceof human syndecan indicates a novel gene family of integral membraneproteoglycans. J. Biol. Chem. 265: 6884- 6889, 1990. 3 A c

GAM47 269 SDC1 Oettinger, H. F.; Streeter, H.; Lose, E.; Copeland, N. G.; Gilbert,D. J.; Justice, M. J.; Jenkins, N. A.; Mohandas, T.; Bernfield, M.: Chromosome mapping of the murine syndecan gene. Genomics 11: 334- 338,1991. 3 A c

GAM47 269 SDC1 Reizes, O.; Lincecum, J.; Wang, Z.; Goldberger, O.; Huang, L.;Kaksonen, M.; Ahima, R.; Hinkes, M. T.; Barsh, G. S.; Rauvala, H.;Bernfield, M.: Transgenic expression of syndecan- 1 uncovers a physiologicalcontrol of feeding behavior by syndecan- 3. Cell 106: 105- 116, 2001. 3 A c

GAM47 269 SDC1 Sanderson, R. D.; Lalor, P.; Bernfield, M.: B lymphocytes expressand lose syndecan at specific stages of differentiation. Cell Regulation 1:27- 35, 1989. 3 A c

GAM47 269 SDC1 Spring, J.; Goldberger, O. A.; Jenkins, N. A.; Gilbert, D. J.;Copeland, N. G.; Bernfield, M.: Mapping of the syndecan genes inthe mouse: linkage with members of the Myc gene family. Genomics 21:597- 601, 1994. 3 A c

GAM47 269 SDC1 Westman, P.; Hsieh, C.- L.; Mali, M.; Jalkanen, M.; Francke, U.;Schroder, J.: Assignment of the human syndecan (SDC) gene to shortarm of chromosome 2. (Abstract) Cytogenet. Cell Genet. 58: 1873- 1874,1991. 3 A c

GAM47 269 SFRP2 Chang, J. T.; Esumi, N.; Moore, K.; Li, Y.; Zhang, S.; Chew, C.;Goodman, B.; Rattner, A.; Moody, S.; Stetten, G.; Campochiaro, P.A.; Zack, D. J.: Cloning 3 A c

and characterization of a secreted frizzled- relatedprotein that is expressed by the retinal pigment epithelium. Hum.Molec. Genet. 8: 575- 583, 1999.

GAM47 269 SFRP2 Melkonyan, H. S.; Chang, W. C.; Shapiro, J. P.; Mahadevappa, M.;Fitzpatrick, 3 A c
P. A.; Kiefer, M. C.; Tomei, L. D.; Umansky, S. R.:SARPs: a family of secreted apoptosis- related proteins. Proc. Nat.Acad. Sci. 94: 13636- 13641, 1997.

GAM47 269 SFRP2 Rattner, A.; Hsieh, J.- C.; Smallwood, P. M.; Gilbert, D. J.; Copeland,N. 3 A c
G.; Jenkins, N. A.; Nathans, J.: A family of secreted proteinscontains homology to the cysteine- rich ligand- binding domain of frizzledreceptors. Proc. Nat. Acad. Sci. 94: 2859- 2863, 1997.

GAM47 269 SHFM3 Gurrieri, F.; Genuardi, M.; Chiurazzi, P.; Gillessen- Kaesbach,G.; Neri, G.: 3 A c
Exclusion of linkage between autosomal dominant splithand/split foot and markers from chromosome 7q: further evidence forgenetic heterogeneity. (Letter) Am. J. Hum. Genet. 55: 853- 855,1994.

GAM47 269 SHFM3 Gurrieri, F.; Prinos, P.; Tackels, D.; Kilpatrick, M. W.; Allanson,J.; 3 A c
Genuardi, M.; Vuckov, A.; Nanni, L.; Sangiorgi, E.; Garofalo,G.; Nunes, M. E.; Neri, G.; Schwartz, C.; Tsipouras, P.: A splithand- split foot (SHFM3) gene is located at 10q24- q25. Am. J. Med.Genet. 62: 427- 436, 1996.

GAM47 269 SHFM3 Ianakiev, P.; Kilpatrick, M. W.; Dealy, C.; Kosher, R.; Korenberg,J. R.; 3 A c
Chen, X.- N.; Tsipouras, P.: A novel human gene encoding anF- box/WD40 containing protein maps in the SHFM3 critical region on10q24. Biochem. Biophys. Res. Commun. 261: 64- 70, 1999.

GAM47 269 SHFM3 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 A c
and expression analysis of new members of the mammalianF- box protein family. Genomics 67: 40- 47, 2000.

GAM47 269 SHFM3 Johnson, K. R.; Lane, P. W.; Ward- Bailey, P.; Davisson, M. T.:Mapping the 3 A c
mouse dactylaplasia mutation, Dac, and a gene that controlsits expression, mdac. Genomics 29: 457- 464, 1995.

GAM47 269 SHFM3 Nunes, M. E.; Schutt, G.; Kapur, R. P.; Luthardt, F.; Kukolich,M.; Byers, 3 A c
P.; Evans, J. P.: A second autosomal split hand/foot locusmaps to chromosome 10q24- q25. Hum. Molec. Genet. 4: 2165- 2170, 1995.

GAM47 269 SHFM3 Ozen, R. S.; Baysal, B. E.; Devlin, B.; Farr, J. E.; Gorry, M.;Ehrlich, G. 3 A c
D.; Richard, C. W., III: Fine mapping of the split- hand/split- footlocus (SHFM3) at 10q24: evidence for anticipation and segregationdistortion. Am. J. Hum. Genet. 64: 1646- 1654, 1999.

GAM47 269 SHFM3 Palmer, S. E.; Scherer, S. W.; Kukolich, M.; Wijsman, E. M.; Tsui,L.- C.; 3 A c
Stephens, K.; Evans, J. P.: Evidence for locus heterogeneityin human autosomal dominant split hand/split foot malformation. Am.J. Hum. Genet. 55: 21- 26, 1994.

GAM47 269 SHFM3 Raas- Rothschild, A.; Manouvrier, S.; Gonzales, M.; Farriaux, J.P.; Lyonnet, 3 A c
S.; Munnich, A.: Refined mapping of a gene for splithand- split foot malformation (SHFM3) on chromosome 10q25. J. Med.Genet. 33: 996- 1001, 1996.

GAM47 269 SHFM3 Sidow, A.; Bulotsky, M. S.; Kerrebrock, A. W.; Birren, B. W.;Altshuler, D; 3 A c
Jaenisch, R.; Johnson, K. R.; Lander, E. S.: A novelmember of the F- box/WD40 gene family, encoding dactylin, is disruptedin the mouse dactylaplasia mutant. Nature Genet. 23: 104- 107, 1999.

GAM47 269 SOD3 Adachi, T.; Ohta, H.; Yamada, H.; Futenma, A.; Kato, K.; Hirano,K.: 3 A c
Quantitative analysis of extracellular- superoxide dismutase inserum and urine by ELISA with monoclonal antibody. Clin. Chim. Acta 212:89- 102, 1992.

GAM47 269 SOD3 Folz, R. J.; Crapo, J. D.: Extracellular superoxide dismutase(SOD3): tissue- 3 A c
specific expression, genomic characterization, andcomputer- assisted
sequence analysis of the human EC SOD gene. Genomics 22:162- 171, 1994.
GAM47 269 SOD3 Hendrickson, D. J.; Fisher, J. H.; Jones, C.; Ho, Y.- S.: 3 A c
Regionallocalization of human extracellular superoxide dismutase gene to
4pter- q21.Genomics 8: 736- 738, 1990.
GAM47 269 SOD3 Hjalmarsson, K.; Marklund, S. L.; Engstrom, A.; Edlund, T.: Isolationand 3 A c
sequence of complementary DNA encoding human extracellular
superoxidedismutase. Proc. Nat. Acad. Sci. 84: 6340- 6344, 1987.
GAM47 269 SOD3 Marklund, S. L.: Extracellular superoxide dismutase in human tissuesand 3 A c
human cell lines. J. Clin. Invest. 74: 1398- 1403, 1984.
GAM47 269 SOD3 Sandstrom, J.; Nilsson, P.; Karlsson, K.; Marklund, S. L.: 10- foldincrease 3 A c
in human plasma extracellular superoxide dismutase contentcaused by a
mutation in heparin- binding domain. J. Biol. Chem. 269:19163- 19166, 1994.
GAM47 269 SOD3 Yamada, H.; Yamada, Y.; Adachi, T.; Goto, H.; Ogasawara, N.; Futenma,A.; 3 A c
Kitano, M.; Hirano, K.; Kato, K.: Molecular analysis of extracellular-
superoxidedismutase gene associated with high level in serum. Jpn. J.
Hum.Genet. 40: 177- 184, 1995.
GAM47 269 SPARC Findlay, D. M.; Fisher, L. W.; McQuillan, C. I.; Termine, J. D.;Young, M. 3 A c
F.: Isolation of the osteonectin gene: evidence that avariable region of the
osteonectin molecule is encoded within oneexon. Biochemistry 27: 1483- 1489,
1988.
GAM47 269 SPARC Gilmour, D. T.; Lyon, G. J.; Carlton, M. B. L.; Sanes, J. R.; Cunningham,J. 3 A c
M.; Anderson, J. R.; Hogan, B. L. M.; Evans, M. J.; Colledge, W.H.: Mice
deficient for the secreted glycoprotein SPARC/osteonectin/BM40develop
normally but show severe age- onset cataract formation anddisruption of the
lens. EMBO J. 17: 1860- 1870, 1998.
GAM47 269 SPARC Goldblum, S. E.; Ding, X.; Funk, S. E.; Sage, E. H.: SPARC (secretedprotein 3 A c
acidic and rich in cysteine) regulates endothelial cell shapeand barrier
function. Proc. Nat. Acad. Sci. 91: 3448- 3452, 1994.
GAM47 269 SPARC Le Beau, M. M.; Espinosa, R., III; Neuman, W. L.; Stock, W.; Roulston,D.; 3 A c
Larson, R. A.; Keinanen, M.; Westbrook, C. A.: Cytogenetic andmolecular
delineation of the smallest commonly deleted region of chromosome5 in
malignant myeloid diseases. Proc. Nat. Acad. Sci. 90: 5484- 5488,1993.
GAM47 269 SPARC Mason, I. J.; Murphy, D.; Munke, M.; Francke, U.; Elliott, R. W.;Hogan, B. 3 A c
L. M.: Developmental and transformation- sensitive expressionof the SPARC
gene on mouse chromosome 11. EMBO J. 5: 1831- 1837,1986.
GAM47 269 SPARC Mason, I. J.; Taylor, A.; Williams, J. G.; Sage, H.; Hogan, B.L. M.: 3 A c
Evidence from molecular cloning that SPARC, a major productof mouse embryo
parietal endoderm, is related to an endothelial cell'culture shock'
glycoprotein of Mr 43,000. EMBO J. 5: 1465- 1472,1986.
GAM47 269 SPARC Naylor, S. L.; Helen- Davis, D.; Villarreal, X. C.; Long, G. L.: The human 3 A c
osteonectin gene on chromosome 5 is polymorphic. (Abstract) Cytogenet.Cell
Genet. 51: 1051 only, 1989.
GAM47 269 SPARC Schwartz, R. C.; Young, M. F.; Tsipouras, P.: Two RFLPs in the5- prime end 3 A c
of the human osteonectin (ON) gene. Nucleic Acids Res. 16:9076 only, 1988.
GAM47 269 SPARC Stenner, D. D.; Tracy, R. P.; Riggs, B. L.; Mann, K. G.: Humanplatelets 3 A c
contain and secrete osteonectin, a major protein of mineralizedbone. Proc.
Nat. Acad. Sci. 83: 6892- 6896, 1986.
GAM47 269 SPARC Swaroop, A.; Francke, U.: Molecular cloning, cDNA sequence, andexpression of 3 A c

human SPARC (osteonectin). (Abstract) Am. J. Hum. Genet. 41:A240 only, 1987.

GAM47 269 SPARC Swaroop, A.; Hogan, B. L. M.; Francke, U.: Molecular analysisof the cDNA for 3 A c
human SPARC/osteonectin/BM- 40: sequence, expression,and localization of the
gene to chromosome 5q31- q33. Genomics 2:37- 47, 1988.

GAM47 269 SPARC Termine, J. D.; Kleinman, H. K.; Whitson, S. W.; Conn, K. M.;McGarvey, M. 3 A c
L.; Martin, G. R.: Osteonectin, a bone- specific proteinlinking mineral to
collagen. Cell 26: 99- 105, 1981.

GAM47 269 SQSTM1 Gong, J.; Xu, J.; Bezanilla, M.; van Huizen, R.; Derin, R.; Li,M.: 3 A c
Differential stimulation of PKC phosphorylation of potassiumchannels by ZIP1
and ZIP2. Science 285: 1565- 1569, 1999.

GAM47 269 SQSTM1 Joung, I.; Strominger, J. L.; Shin, J.: Molecular cloning of 3 A c
aphosphotyrosine- independent ligand of the p56- lck SH2 domain. Proc.Nat.
Acad. Sci. 93: 5991- 5995, 1996.

GAM47 269 SQSTM1 Laurin, N.; Brown, J. P.; Morissette, J.; Raymond, V.: Recurrentmutation of 3 A c
the gene encoding sequestosome 1 (SQSTM1/p62) in Pagetdisease of bone. Am.
J. Hum. Genet. 70: 1582- 1588, 2002.

GAM47 269 SQSTM1 Park, I.; Chung, J.; Walsh, C. T.; Yun, Y.; Strominger, J. L.;Shin, J.: 3 A c
Phosphotyrosine- independent binding of a 62- kDa proteinto the src homology
2 (SH2) domain of p56- lck and its regulation byphosphorylation of ser- 59
in the lck unique N- terminal region. Proc.Nat. Acad. Sci. 92: 12338- 12342,
1995.

GAM47 269 SQSTM1 Vadlamudi, R. K.; Joung, I.; Strominger, J. L.; Shin, J.: p62,a 3 A c
phosphotyrosine- independent ligand of the SH2 domain of p56- lck,belongs to
a new class of ubiquitin- binding proteins. J. Biol. Chem. 271:20235- 20237,
1996.

GAM47 269 STAT3 Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.- J.; Wei, S.; Matsusaka,T.; 3 A c
Yoshida, K.; Sudo, T.; Naruto, M.; Kishimoto, T.: Molecular cloningof APRF,
a novel IFN- stimulated gene factor 3 p91- related transcriptionfactor
involved in the gp130- mediated signaling pathway. Cell 77:63- 71, 1994.

GAM47 269 STAT3 Bromberg, J. F.; Wrzeszczynska, M. H.; Devgan, G.; Zhao, Y.; Pestell,R. G.; 3 A c
Albanese, C.; Darnell, J. E., Jr.: Stat3 as an oncogene. Cell 98:295- 303,
1999.

GAM47 269 STAT3 Caldenhoven, E.; van Dijk, T. B.; Solari, R.; Armstrong, J.; Raaijmakers,J. 3 A c
A. M.; Lammers, J.- W. J.; Koenderman, L.; de Groot, R. P.: STAT3- beta,a
splice variant of transcription factor STAT3, is a dominant
negativeregulator of transcription. J. Biol. Chem. 271: 13221- 13227, 1996.

GAM47 269 STAT3 Choi, J. Y.; Li, W. L.; Kouri, R. E.; Yu, J.; Kao, F. T.; Ruano,G.: 3 A c
Assignment of the acute phase response factor (APRF) gene to17q21 by
microdissection clone sequencing and fluorescence in situhybridization of a
p1 clone. Genomics 37: 264- 265, 1996.

GAM47 269 STAT3 Chung, C. D.; Liao, J.; Liu, B.; Rao, X.; Jay, P.; Berta, P.; Shuai,K.: 3 A c
Specific inhibition of Stat3 signal transduction by PIAS3. Science 278:1803-
1805, 1997.

GAM47 269 STAT3 Foley, H. A.; Ofori- Acquah, S. F.; Yoshimura, A.; Critz, S.; Baliga,B. S.; 3 A c
Pace, B. S.: Stat- 3 beta inhibits gamma- globin gene expressionin erythroid
cells. J. Biol. Chem. 277: 16211- 16219, 2002.

GAM47 269 STAT3 Lutticken, C.; Wegenka, U. M.; Yuan, J.; Buschmann, J.; Schindler,C.; 3 A c
Ziemiecki, A.; Harpur, A. G.; Wilks, A. F.; Yasukawa, K.; Taga,T.;
Kishimoto, T.; Barbieri, G.; Pellegrini, S.; Sendtner, M.; Heinrich,P. C.;
Horn, F.: Association of transcription factor APRF and proteinkinase Jak1

with the interleukin- 6 signal transducer gp130. Science 263:89- 92, 1994.

GAM47 269 STAT3 Nakashima, K.; Yanagisawa, M.; Arakawa, H.; Kimura, N.; Hisatsune,T.; 3 A c
Kawabata, M.; Miyazono, K.; Taga, T.: Synergistic signaling infetal brain by
STAT3- Smad1 complex bridged by p300. Science 284:479- 482, 1999.

GAM47 269 STAT3 Pfeffer, L. M.; Mullersman, J. E.; Pfeffer, S. R.; Murti, A.; Shi,W.; Yang, 3 A c
C. H.: STAT3 as an adapter to couple phosphatidylinositol3- kinase to the
IFNAR1 chain of the type I interferon receptor. Science 276:1418- 1420,
1997.

GAM47 269 STAT3 Ram, P. T.; Horvath, C. M.; Iyengar, R.: Stat3- mediated transformationof 3 A c
NIH- 3T3 cells by the constitutively active Q205L G- alpha(O) protein.
Science 287:142- 144, 2000.

GAM47 269 STAT3 Simon, A. R.; Vikis, H. G.; Stewart, S.; Fanburg, B. L.; Cochran,B. H.; 3 A c
Guan, K.- L.: Regulation of STAT3 by direct binding to theRac1 GTPase.
Science 290: 144- 147, 2000.

GAM47 269 STAT3 Vaisse, C.; Halaas, J. L.; Horvath, C. M.; Darnell, J. E., Jr.;Stoffel, M.; 3 A c
Friedman, J. M.: Leptin activation of Stat3 in the hypothalamusof wildtype
and ob/ob mice but not in db/db mice. Nature Genet. 14:95- 100, 1996.

GAM47 269 STAT3 Yoo, J.- Y.; Huso, D. L.; Nathans, D.; Desiderio, S.: Specificablation of 3 A c
Stat3- beta distorts the pattern of Stat3- responsive geneexpression and
impairs recovery from endotoxic shock. Cell 108:331- 344, 2002.

GAM47 269 SUV39H1 Aagaard, L.; Laible, G.; Selenko, P.; Schmid, M.; Dorn, R.; Schotta,G.; 3 A c
Kuhfittig, S.; Wolf, A.; Lebersorger, A.; Singh, P. B.; Reuter,G.; Jenuwein,
T.: Functional mammalian homologues of the DrosophilaPEV- modifier Su(var)3-
9 encode centromere- associated proteins whichcomplex with the
heterochromatin component M31. EMBO J. 18: 1923- 1938,1999.

GAM47 269 SUV39H1 Bannister, A. J.; Zegerman, P.; Partridge, J. F.; Miska, E. A.;Thomas, J. 3 A c
O.; Allshire, R. C.; Kouzarides, T.: Selective recognitionof methylated
lysine 9 on histone H3 by the HP1 chromo domain. Nature 410:120- 124, 2001.

GAM47 269 SUV39H1 Lachner, M.; O'Carroll, D.; Rea, S.; Mechtler, K.; Jenuwein, T.: Methylation 3 A c
of histone H3 lysine 9 creates a binding site for HP1proteins. Nature 410:
116- 120, 2001.

GAM47 269 SUV39H1 Melcher, M.; Schmid, M.; Aagaard, L.; Selenko, P.; Laible, G.;Jenuwein, T.: 3 A c
Structure- function analysis of SUV39H1 reveals a dominantrole in
heterochromatin organization, chromosome segregation, andmitotic
progression. Molec. Cell Biol. 20: 3728- 3841, 2000.

GAM47 269 SUV39H1 Nielsen, S. J.; Schneider, R.; Bauer, U.- M.; Bannister, A. J.;Morrison, A.; 3 A c
O'Carroll, D.; Firestein, R.; Cleary, M.; Jenuwein,T.; Herrera, R. E.;
Kouzarides, T.: Rb targets histone H3 methylationand HP1 to promoters.
Nature 412: 561- 565, 2001.

GAM47 269 SUV39H1 Peters, A. H. F. M.; O'Carroll, D.; Scherthan, H.; Mechtler, K.;Sauer, S.; 3 A c
Schofer, C.; Weipoltshammer, K.; Pagani, M.; Lachner, M.;Kohlmaier, A.;
Opravil, S.; Doyle, M.; Sibilia, M.; Jenuwein, T.:Loss of the Suv39h histone
methyltransferases impairs mammalian heterochromatinand genome stability.
Cell 107: 323- 337, 2001.

GAM47 269 SUV39H1 Rea, S.; Eisenhaber, F.; O'Carroll, D.; Strahl, B. D.; Sun, Z.- W.;Schmid, 3 A c
M.; Opravil, S.; Mechtler, K.; Ponting, C. P.; Allis, C. D.;Jenuwein, T.:
Regulation of chromatin structure by site- specifichistone H3
methyltransferases. Nature 406: 593- 599, 2000.

GAM47 269 SUV39H1 Scott, A. F.: Personal Communication. Baltimore, Md. 8/7/2000. 3 A c

GAM47 269 TCFL4 Billin, A. N.; Eilers, A. L.; Queva, C.; Ayer, D. E.: Mlx, a novelMax- like 3 A c

BHLHZip protein that interacts with the Max network of transcriptionfactors. J. Biol. Chem. 274: 36344- 36350, 1999.

GAM47 269 TCFL4 Bjerknes, M.; Cheng, H.: TCFL4: a gene at 17q21.1 encoding a putativebasic 3 A c helix- loop- helix leucine- zipper transcription factor. Gene 181:7- 11, 1996.

GAM47 269 TCFL4 Cairo, S.; Merla, G.; Urbinati, F.; Ballabio, A.; Reymond, A.:WBSCR14, a 3 A c gene mapping to the Williams- Beuren syndrome deleted region,is a new member of the Mlx transcription factor network. Hum. Molec.Genet. 10: 617- 627, 2001.

GAM47 269 TCL1B Hallas, C.; Pekarsky, Y.; Itoyama, T.; Varnum, J.; Bichi, R.; Rothstein,J. 3 A c L.; Croce, C. M.: Genomic analysis of human and mouse TCL1 locireveals a complex of tightly clustered genes. Proc. Nat. Acad. Sci. 96:14418- 14423, 1999.

GAM47 269 TCL1B Pekarsky, Y.; Hallas, C.; Isobe, M.; Russo, G.; Croce, C. M.:Abnormalities 3 A c at 14q32.1 in T cell malignancies involve two oncogenes. Proc.Nat. Acad. Sci. 96: 2949- 2951, 1999.

GAM47 269 TFDP2 Zhang, Y.; Chellappan, S. P.: Cloning and characterization ofhuman DP2, a 3 A c novel dimerization partner of E2F. Oncogene 10: 2085- 2093,1995.

GAM47 269 TFDP2 Zhang, Y.; Venkatraj, V. S.; Fischer, S. G.; Warburton, D.; Chellappan,S. 3 A c P.: Genomic cloning and chromosomal assignment of the E2F dimerizationpartner TFDP gene family. Genomics 39: 95- 98, 1997.

GAM47 269 TGFBR3 Brown, C. B.; Boyer, A. S.; Runyan, R. B.; Barnett, J. V.: Requirementof 3 A c type III TGF- beta receptor for endocardial cell transformationin the heart. Science 283: 2080- 2082, 1999.

GAM47 269 TGFBR3 Johnson, D. W.; Qumsiyeh, M.; Benkhalifa, M.; Marchuk, D. A.:Assignment of 3 A c human transforming growth factor- beta type I and typeIII receptor genes (TGFBR1 and TGFBR3) to 9q33- q34 and 1p32- p33, respectively. Genomics 28:356- 357, 1995.

GAM47 269 TGFBR3 Lewis, K. A.; Gray, P. C.; Blount, A. L.; MacConell, L. A.; Wiater,E.; 3 A c Bilezikjian, L. M.; Vale, W.: Betaglycan binds inhibin and canmediate functional antagonism of activin signalling. Nature 404:411- 414, 2000.

GAM47 269 TM6SF2 Carim- Todd, L.; Escarceller, M.; Estivill, X.; Sumoy, L.: Cloningof the 3 A c novel gene TM6SF1 reveals conservation of clusters of paralogousgenes between human chromosomes 15q24- q26 and 19p13.3- p12. Cytogenet.Cell Genet. 90: 255- 260, 2000.

GAM47 269 TM6SF2 Nagase, T.; Kikuno, R.; Ohara, O.: Prediction of the coding sequencesof 3 A c unidentified human genes. XXI. The complete sequences of 60 newcDNA clones from brain which code for large proteins. DNA Res. 8:179- 187, 2001.

GAM47 269 USP4 Di Fruscio, M.; Gilchrist, C. A.; Baker, R. T.; Gray, D. A.: 3 A c Genomicstructure of Unp, a murine gene encoding a ubiquitin- specific protease. Biochim.Biophys. Acta 1398: 9- 17, 1998.

GAM47 269 USP4 Frederick, A.; Rolfe, M.; Chiu, M. I.: The human UNP locus at3p21.31 encodes 3 A c two tissue- selective, cytoplasmic isoforms with deubiquitinatingactivity that have reduced expression in small cell lung carcinomacell lines. Oncogene 16: 153- 165, 1998.

GAM47 269 USP4 Gray, D. A.; Inazawa, J.; Gupta, K.; Wong, A.; Ueda, R.; Takahashi,T.: 3 A c Elevated expression of Unph, a proto- oncogene at 3p21.3, in humanlung tumors. Oncogene 10: 2179- 2183, 1995.

GAM47 269 USP4 Gupta, K.; Chevrette, M.; Gray, D. A.: The Unp proto- oncogeneencodes a 3 A c nuclear protein. Oncogene 9: 1729- 1731, 1994.

GAM47 269 USP4 Gupta, K.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Gray,D. A.: Unp, 3 A c
a mouse gene related to the tre oncogene. Oncogene 8:2307- 2310, 1993.

GAM47 269 VANGL2 Doudney, K.; Murdoch, J. N.; Paternotte, C.; Bentley, L.; Gregory,S.; Copp, 3 A c
A. J.; Stanier, P.: Comparative physical and transcriptmaps of approximately
1 Mb around loop- tail, a gene for severe neuraltube defects on distal mouse
chromosome 1 and human chromosome 1q22- q23. Genomics 72:180- 192, 2001.

GAM47 269 VANGL2 Kibar, Z.; Vogan, K. J.; Groulx, N.; Justice, M. J.; Underhill,D. A.; Gros, 3 A c
P.: Ltap, a mammalian homolog of Drosophila Strabismus/VanGogh, is altered
in the mouse neural tube mutant loop- tail. NatureGenet. 28: 251- 255, 2001.

GAM47 269 VANGL2 Mullick, A.; Trasler, D.; Gros, P.: High- resolution linkage mapin the 3 A c
vicinity of the Lp locus. Genomics 26: 479- 488, 1995.

GAM47 269 VANGL2 Murdoch, J. N.; Doudney, K.; Paternotte, C.; Copp, A. J.; Stanier,P.: Severe 3 A c
neural tube defects in the loop- tail mouse result frommutation of Lpp1, a
novel gene involved in floor plate specification. Hum.Molec. Genet. 10:
2593- 2601, 2001.

GAM47 269 VANGL2 Stanier, P.; Henson, J. N.; Eddleston, J.; Moore, G. E.; Copp,A. J.: Genetic 3 A c
basis of neural tube defects: the mouse gene loop- tailmaps to a region of
chromosome 1 syntenic with human 1q21- q23. Genomics 26:473- 478, 1995.

GAM47 269 VEGFB Bellomo, D.; Headrick, J. P.; Silins, G. U.; Paterson, C. A.; Thomas,P. S.; 3 A c
Gartside, M.; Mould, A.; Cahill, M. M.; Tonks, I. D.; Grimmond,S. M.;
Townson, S.; Wells, C.; Little, M.; Cummings, M. C.; Hayward,N. K.; Kay, G.
F.: Mice lacking the vascular endothelial growth factor- Bgene (Vegfb) have
smaller hearts, dysfunctional coronary vasculature,and impaired recovery
from cardiac ischemia. Circ. Res. 86: e29- e35,2000.

GAM47 269 VEGFB Gerace, L; Cirenei, N.; Cappelletti, M.; Petraroli, R.; Sebastiani,F.; 3 A c
Marziliano, N.: Assignment of the mouse Vegfb gene to mouse chromosome19B by
in situ hybridization. Cytogenet. Cell Genet. 95: 242- 243,2001.

GAM47 269 VEGFB Grimmond, S.; Lagercrantz, J.; Drinkwater, C.; Silins, G.; Townson,S.; 3 A c
Pollock, P.; Gotley, D.; Carson, E.; Rakar, S.; Nordenskjold,M.; Ward, L.;
Hayward, N.; Weber, G.: Cloning and characterizationof a novel human gene
related to vascular endothelial growth factor. GenomeRes. 6: 124- 131, 1996.

GAM47 269 VEGFB Olofsson, B.; Pajusola, K.; Kaipainen, A.; von Euler, G.; Joukov,V.; 3 A c
Saksela, O.; Orpana, A.; Pettersson, R. F.; Alitalo, K.; Eriksson,U.:
Vascular endothelial growth factor B, a novel growth factor forendothelial
cells. Proc. Nat. Acad. Sci. 93: 2576- 2581, 1996.

GAM47 269 VEGFB Olofsson, B.; Pajusola, K.; von Euler, G.; Chilov, D.; Alitalo,K.; Eriksson, 3 A c
U.: Genomic organization of the mouse and human genesfor vascular
endothelial growth factor B (VEGF- B) and characterizationof a second splice
isoform. J. Biol. Chem. 271: 19310- 19317, 1996.

GAM47 269 VIPR1 Couvineau, A.; Rouyer- Fessard, C.; Darmoul, D.; Maoret, J.- J.;Carrero, I.; 3 A c
Ogier- Denis, E.; Laburthe, M.: Human intestinal VIPreceptor: cloning and
functional expression of two cDNA encoding proteinswith different N-
terminal domains. Biochem. Biophys. Res. Commun. 200:769- 776, 1994.

GAM47 269 VIPR1 Hashimoto, H.; Nishino, A.; Shintani, N.; Hagihara, N.; Copeland,N. G.; 3 A c
Jenkins, N. A.; Yamamoto, K.; Matsuda, T.; Ishihara, T.; Nagata,S.; Baba,
A.: Genomic organization and chromosomal location of themouse vasoactive
intestinal polypeptide 1 (VPAC- 1) receptor. Genomics 58:90- 93, 1999.

GAM47 269 VIPR1 Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 A c
M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor,
and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991.

GAM47 269 VIPR1 Sreedharan, S. P.; Huang, J.- X.; Cheung, M.- C.; Goetzl, E. J.:Structure, 3 A c
expression, and chromosomal localization of the type Ihuman vasoactive
intestinal peptide receptor gene. Proc. Nat. Acad.Sci. 92: 2939- 2943, 1995.

GAM47 269 VIPR1 Sreedharan, S. P.; Patel, D. R.; Huang, J.- X.; Goetzl, E. J.:Cloning and 3 A c
functional expression of a human neuroendocrine vasoactiveintestinal peptide
receptor. Biochem. Biophys. Res. Commun. 193:546- 553, 1993.

GAM47 269 VIPR1 Sreedharan, S. P.; Robichon, A.; Peterson, K. E.; Goetzl, E. J.: Cloning and 3 A c
expression of the human vasoactive intestinal peptidereceptor. Proc. Nat.
Acad. Sci. 88: 4986- 4990, 1991.

GAM47 269 VIPR1 Vassart, G.: Personal Communication. Brussels, Belgium 1/15/1992. 3 A c

GAM47 269 VIPR1 Wenger, G. D.: Personal Communication. Columbus, Ohio 8/3/1993. 3 A c

GAM47 269 WBSCR1 Osborne, L. R.; Martindale, D.; Scherer, S. W.; Shi, X.- M.; Huizenga,J.; 3 A c
Heng, H. H. Q.; Costa, T.; Pober, B.; Lew, L.; Brinkman, J.; Rommens,J.;
Koop, B.; Tsui, L.- C.: Identification of genes from a 500- kbregion at
7q11.23 that is commonly deleted in Williams syndrome patients. Genomics
36:328- 336, 1996.

GAM47 269 WBSCR1 Richter- Cook, N. J.; Dever, T. E.; Hensold, J. O.; Merrick, W.C.: 3 A c
Purification and characterization of a new eukaryotic proteintranslation
factor: eukaryotic initiation factor 4H. J. Biol. Chem. 273:7579- 7587,
1998.

GAM47 269 ZNF142 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; 3 A c
Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding
sequences of unidentified human genes. VI. The codingsequences of 80 new
genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line
KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM47 269 ZNF142 Tommerup, N.; Aagaard, L.; Lund, C. L.; Boel, E.; Baxendale, S.;Bates, G. 3 A c
P.; Lehrach, H.; Vissing, H.: A zinc- finger gene ZNF141mapping at
4p16.3/D4S90 is a candidate gene for the Wolf- Hirschhorn(4p-) syndrome.
Hum. Molec. Genet. 2: 1571- 1575, 1993.

GAM47 269 ZNF142 Tommerup, N.; Vissing, H.: Isolation and fine mapping of 16 novelhuman zinc 3 A c
finger- encoding cDNAs identify putative candidate genesfor developmental
and malignant disorders. Genomics 27: 259- 264,1995.

GAM49 338 FGF18 Hu, M. C.- T.; Qiu, W. R.; Wang, Y.- P.; Hill, D.; Ring, B. D.; Scully,S.; 3 C c
Bolon, B.; DeRose, M.; Luethy, R.; Simonet, W. S.; Arakawa, T.;Danilenko, D.
M.: FGF- 18, a novel member of the fibroblast growthfactor family,
stimulates hepatic and intestinal proliferation. Molec.Cell. Biol. 18: 6063-
6074, 1998.

GAM49 338 FGF18 Ohbayashi, N.; Hoshikawa, M.; Kimura, S.; Yamasaki, M.; Fukui,S.; Itoh, N.: 3 C c
Structure and expression of the mRNA encoding a novelfibroblast growth
factor, FGF- 18. J. Biol. Chem. 273: 18161- 18164,1998.

GAM49 338 FGF18 Whitmore, T. E.; Maurer, M. F.; Sexson, S.; Raymond, F.; Conklin,D.; 3 C c
Deisher, T. A.: Assignment of fibroblast growth factor 18 (FGF18)to human
chromosome 5q34 by use of radiation hybrid mapping and fluorescencein situ
hybridization. Cytogenet. Cell Genet. 90: 231- 233, 2000.

GAM49 338 S100B Allore, R. J.; Friend, W. C.; O'Hanlon, D.; Neilson, K. M.; Baumal,R.; Dunn, 3 C c
R. J.; Marks, A.: Cloning and expression of the human S100- betagene. J.
Biol. Chem. 265: 15537- 15543, 1990.

GAM49 338 S100B Allore, R.; O'Hanlon, D.; Price, R.; Neilson, K.; Willard, H. F.;Cox, D. R.; 3 C c
Marks, A.; Dunn, R. J.: Gene encoding the beta- subunitof S100 protein is on
chromosome 21: implications for Down syndrome. Science 239:1311- 1313, 1988.

GAM49 338 S100B Duncan, A. M. V.; Higgins, J.; Dunn, R. J.; Allore, R.; Marks,A.: Refined sublocalization of the human gene encoding the beta subunitof the S100 protein (S100B) and confirmation of a subtle t(9;21) translocationusing in situ hybridization. Cytogenet. Cell Genet. 50: 234- 235,1989. 3 C c

GAM49 338 S100B Morii, K.; Tanaka, R.; Takahashi, Y.; Minoshima, S.; Fukuyama,R.; Shimizu, N.; Kuwano, R.: Structure and chromosome assignmentof human S100 alpha and beta subunit genes. Biochem. Biophys. Res.Commun. 175: 185- 191, 1991. 3 C c

GAM49 338 S100B Reeves, R. H.; Yao, J.; Crowley, M. R.; Buck, S.; Zhang, X.; Yarowsky,P.; Gearhart, J. D.; Hilt, D. C.: Astrocytosis and axonal proliferationin the hippocampus of S100b transgenic mice. Proc. Nat. Acad. Sci. 91:5359- 5363, 1994. 3 C c

GAM49 338 S100B Shimizu, A.; Sakai, Y.; Ohno, K.; Masaki, S.; Kuwano, R.; Takahashi,Y.; Miyashita, N.; Watanabe, T.: A molecular genetic linkage mapof mouse chromosome 10, including the Myb, S100b, Pah, Sl, and Ifggenes. Biochem. Genet. 30: 529- 535, 1992. 3 C c

GAM49 338 TNFRSF6B Bai, C.; Connolly, B.; Metzker, M. L.; Hilliard, C. A.; Liu, X.;Sandig, V.; Soderman, A.; Galloway, S. M.; Liu, Q.; Austin, C. P.;Caskey, C. T.: Overexpression of M68/DCR3 in human gastrointestinaltract tumors independent of gene amplification and its location ina four- gene cluster. Proc. Nat. Acad. Sci. 97: 1230- 1235, 2000. 3 C c

GAM49 338 TNFRSF6B Pitti, R. M.; Marsters, S. A.; Lawrence, D. A.; Roy, M.; Kischkel,F. C.; Dowd, P.; Huang, A.; Donahue, C. J.; Sherwood, S. W.; Baldwin,D. T.; Godowski, P. J.; Wood, W. I.; Gurney, A. L.; Hillan, K. J.;Cohen, R. L.; Goddard, A. D.; Botstein, D.; Ashkenazi, A.: Genomicamplification of a decoy receptor for Fas ligand in lung and coloncancer. Nature 396: 699- 703, 1998. 3 C c

GAM51 201 ABCD4 Holzinger, A.; Kammerer, S.; Roscher, A. A.: Primary structureof human PMP69, a putative peroxisomal ABC- transporter. Biochem.Biophys. Res. Commun. 237: 152- 157, 1997. 3 C c

GAM51 201 ABCD4 Holzinger, A.; Roscher, A. A.; Landgraf, P.; Lichtner, P.; Kammerer,S.: Genomic organization and chromosomal localization of the humanperoxisomal membrane protein- 1- like protein (PXMP1- L) gene encodinga peroxisomal ABC transporter. FEBS Lett. 426: 238- 242, 1998. 3 C c

GAM51 201 ABCD4 Shani, N.; Jimenez- Sanchez, G.; Steel, G.; Dean, M.; Valle, D.: Identification of a fourth half ABC transporter in the human peroxisomalmembrane. Hum. Molec. Genet. 6: 1925- 1931, 1997. 3 C c

GAM51 201 ACAD8 Andresen, B. S.; Christensen, E.; Corydon, T. J.; Bross, P.; Pilgaard,B.; Wanders, R. J. A.; Ruiter, J. P. N.; Simonsen, H.; Winter, V.;Knudsen, I.; Schroeder, L. D.; Gregersen, N.; Skovby, F.: Isolated2-methylbutyrylglycinuria caused by short/branched- chain acyl-CoAdehydrogenase deficiency: identification of a new enzyme defect, resolutionof its molecular basis, and evidence for distinct acyl- CoA dehydrogenasesin isoleucine and valine metabolism. Am. J. Hum. Genet. 67: 1095- 1103,2000. 3 C c

GAM51 201 ACAD8 Telford, E. A. R.; Moynihan, L. M.; Markham, A. F.; Lench, N. J.: Isolation and characterisation of a cDNA encoding the precursorfor a novel member of the acyl- CoA dehydrogenase gene family. Biochim.Biophys. Acta 1446: 371-376, 1999. 3 C c

GAM51 201 ANP32A Fink, T. M.; Vaesen, M.; Kratzin, H. D.; Lichter, P.; Zimmer, M.: Localization of the gene encoding the putative human HLA class IIassociated protein (PHAPI) to chromosome 15q22.3- q23 by fluorescencein situ 3 C c

hybridization. Genomics 29: 309- 310, 1995.

GAM51 201 ANP32A Li, M.; Makkinje, A.; Damuni, Z.: Molecular identification ofI- 1(PP2A), a 3 C c
novel potent heat- stable inhibitor protein of proteinphosphatase 2A.
Biochemistry 35: 6998- 7002, 1996.

GAM51 201 ANP32A Matilla, A.; Koshy, B. T.; Cummings, C. J.; Isobe, T.; Orr, H.T.; Zoghbi, H. 3 C c
Y.: The cerebellar leucine- rich acidic nuclear proteininteracts with
ataxin- 1. Nature 389: 974- 978, 1997. Note: Erratum:Nature 391: 818 only,
1998.

GAM51 201 ANP32A Sandberg, A. A.; Morgan, R.; McCallister, J. A.; Kaiser- McCaw,B.; Hecht, 3 C c
F.: Acute myeloblastic leukemia (AML) with t(6;9)(p23;q34):a specific
subgroup of AML? Cancer Genet. Cytogenet. 10: 139- 142,1983.

GAM51 201 ANP32A Vaesen, M.; Barnikol- Watanabe, S.; Gotz, H.; Awni, L. A.; Cole,T.; 3 C c
Zimmermann, B; Kratzin, H. D.; Hilschmann, N.: Purification
andcharacterization of two putative HLA class II associated proteins:PHAPI
and PHAPII. Biol. Chem. Hoppe- Seyler 375: 113- 126, 1994.

GAM51 201 ANP32A von Lindern, M.; Fornerod, M.; van Baal, S.; Jaegle, M.; de Wit,T.; Buijs, 3 C c
A.; Grosveld, G.: The translocation (6;9), associatedwith a specific subtype
of acute myeloid leukemia, results in thefusion of two genes, dek and can,
and the expression of a chimeric,leukemia- specific dek- can mRNA. Molec.
Cell. Biol. 12: 1687- 1697,1992.

GAM51 201 ANP32A von Lindern, M.; Poustka, A.; Lehrach, H.; Grosveld, G.: The (6;9)chromosome 3 C c
translocation, associated with a specific subtype of acutenonlymphocytic
leukemia, leads to aberrant transcription of a targetgene on 9q34. Molec.
Cell. Biol. 10: 4016- 4026, 1990.

GAM51 201 ANP32A von Lindern, M.; van Baal, S.; Wiegant, J.; Raap, A.; Hagemeijer,A.; 3 C c
Grosveld, G.: Can, a putative oncogene associated with myeloidleukemogenesis
may be activated by fusion of its 3- prime half to differentgenes:
characterization of the set gene. Molec. Cell Biol. 12: 3346- 3355,1992.

GAM51 201 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene 3 C c
structure of a novel water channel expressed exclusively in humankidney:
evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics
35: 543- 550, 1996.

GAM51 201 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem 3 C c
arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at
chromosome locus 12q13. Genomics 43: 387- 389, 1997.

GAM51 201 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: 3 C c
an intracellular vesicle water channel protein in renalepithelia. Proc. Nat.
Acad. Sci. 96: 5808- 5813, 1999.

GAM51 201 BMP1 Amano, S.; Scott, I. C.; Takahara, K.; Koch, M.; Champliaud, M.- F.;Gerecke, 3 C c
D. R.; Keene, D. R.; Hudson, D. L.; Nishiyama, T.; Lee, S.;Greenspan, D. S.;
Burgeson, R. E.: Bone morphogenetic protein 1 isan extracellular processing
enzyme of the laminin 5 gamma- 2 chain. J.Biol. Chem. 275: 22728- 22735,
2000.

GAM51 201 BMP1 Bond, J. S.; Beynon, R. J.: The astacin family of metalloendopeptidases. 3 C c
ProteinSci. 4: 1247- 1261, 1995.

GAM51 201 BMP1 Ceci, J. D.; Kingsley, D. M.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: 3 C c
An interspecific backcross linkage map of the proximal halfof mouse
chromosome 14. Genomics 6: 673- 678, 1990.

GAM51 201 BMP1 Kessler, E.; Takahara, K.; Biniaminov, L.; Brusel, M.; Greenspan,D.: Bone 3 C c
morphogenic protein- 1: the type I procollagen C- proteinase. Science

271:360- 362, 1996.

GAM51 201 BMP1 Reddi, A. H.: BMP- 1: resurrection as procollagen C- proteinase. Science 3 C c
271:5- 6, 1996.

GAM51 201 BMP1 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; 3 C c
Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.;
Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases,
including novel family member mammalian Tolloid- like2, have differential
enzymatic activities and distributions of expressionrelevant to patterning
and skeletogenesis. Dev. Biol. 213: 283- 300,1999.

GAM51 201 BMP1 Tabas, J. A.; Zasloff, M.; Wasmuth, J. J.; Emanuel, B. S.; Altherr,M. R.; 3 C c
McPherson, J. D.; Wozney, J. M.; Kaplan, F. S.: Bone morphogeneticprotein:
chromosomal localization of human genes for BMP1, BMP2A,and BMP3. Genomics
9: 283- 289, 1991.

GAM51 201 BMP1 Takahara, K.; Lee, S.; Wood, S.; Greenspan, D. S.: Structuralorganization 3 C c
and genetic localization of the human bone morphogeneticprotein 1/mammalian
tolloid gene. Genomics 29: 9- 15, 1995.

GAM51 201 BMP1 Takahara, K.; Lyons, G. E.; Greenspan, D. S.: Bone morphogeneticprotein- 1 3 C c
and a mammalian tolloid homologue (mTld) are encoded byalternatively spliced
transcripts which are differentially expressedin some tissues. J. Biol.
Chem. 269: 32572- 32578, 1994.

GAM51 201 BMP1 Wozney, J. M.; Rosen, V.; Celeste, A. J.; Mitsock, L. M.; Whitters,M. J.; 3 C c
Kriz, R. W.; Hewick, R. M.; Wang, E. A.: Novel regulatorsof bone formation:
molecular clones and activities. Science 242:1528- 1534, 1988.

GAM51 201 BMP1 Yoshiura, K.; Tamura, T.; Hong, H.- S.; Ohta, T.; Soejima, H.;Kishino, T.; 3 C c
Jinno, Y.; Niikawa, N.: Mapping of the bone morphogeneticprotein 1 gene
(BMP1) to 8p21: removal of BMP1 from candidacy forthe bone disorder in
Langer- Giedion syndrome. Cytogenet. Cell Genet. 64:208- 209, 1993.

GAM51 201 CENTD2 Miura, K.; Jacques, K. M.; Stauffer, S.; Kubosaki, A.; Zhu, K.;Hirsch, D. 3 C c
S.; Resau, J.; Zheng, Y.; Randazzo, P. A.: ARAP1: a pointof convergence for
Arf and Rho signaling. Molec. Cell 9: 109- 119,2002.

GAM51 201 CENTD2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; 3 C c
Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of
unidentified human genes. XI. The complete sequencesof 100 new cDNA clones
from brain which code for large proteins invitro. DNA Res. 5: 277- 286,
1998.

GAM51 201 CRHR2 Bale, T. L.; Contarino, A.; Smith, G. W.; Chan, R.; Gold, L. H.;Sawchenko, 3 C c
P. E.; Koob, G. F.; Vale, W. W.; Lee, K.- F.: Mice deficientfor
corticotropin- releasing hormone receptor- 2 display anxiety- likebehaviour
and are hypersensitive to stress. Nature Genet. 24: 410- 414,2000.

GAM51 201 CRHR2 Coste, S. C.; Kesterson, R. A.; Heldwein, K. A.; Stevens, S. L.;Heard, A. 3 C c
D.; Hollis, J. H.; Murray, S. E.; Hill, J. K.; Pantely,G. A.; Hohimer, A.
R.; Hatton, D. C.; Phillips, T. J.; Finn, D. A.;Low, M. J.; Rittenberg, M.
B.; Stenzel, P.; Stenzel- Poore, M. P.:Abnormal adaptations to stress and
impaired cardiovascular functionin mice lacking corticotropin- releasing
hormone receptor- 2. NatureGenet. 24: 403- 409, 2000.

GAM51 201 CRHR2 Hsu, S. Y.; Hsueh, A. J. W.: Human stresscopin and stresscopin- 3 C c
relatedpeptide are selective ligands for the type 2 corticotropin-
releasinghormone receptor. Nature Med. 7: 605- 611, 2001.

GAM51 201 CRHR2 Kishimoto, T.; Radulovic, J.; Radulovic, M.; Lin, C. R.; Schrick,C.; 3 C c
Hooshmand, F.; Hermanson, O.; Rosenfeld, M. G.; Spiess, J.: Deletionof Crhr2

reveals an anxiolytic role for corticotropin- releasing hormonereceptor- 2. Nature Genet. 24: 415- 419, 2000.

GAM51 201 CRHR2 Kostich, W. A.; Chen, A.; Sperle, K.; Largent, B. L.: 3 C c
Molecularidentification and analysis of a novel human corticotropin-releasingfactor (CRF) receptor: the CRF2- gamma receptor. Molec. Endocr. 12:1077- 1085, 1998.

GAM51 201 CRHR2 Lesh, J. S.; Burrows, H. L.; Seasholtz, A. F.; Camper, S. A.:Mapping of the 3 C c
mouse corticotropin- releasing hormone receptor 2 gene(Crhr2) to chromosome 6. Mammalian Genome 8: 944- 945, 1997.

GAM51 201 CRHR2 Liaw, C. W.; Grigoriadis, D. E.; Lovenberg, T. W.; De Souza, E.B.; Maki, R. 3 C c
A.: Localization of ligand- binding domains of humancorticotropin- releasing factor receptor: a chimeric receptor approach. Molec.Endocr. 11: 980- 985, 1997.

GAM51 201 CRHR2 Liaw, C. W.; Lovenberg, T. W.; Barry, G.; Oltersdorf, T.; Grigoriadis,D. E.; 3 C c
De Souza, E. B.: Cloning and characterization of the humancorticotropin-releasing factor- 2 receptor complementary deoxyribonucleicacid. Endocrinology 137: 72- 77, 1996.

GAM51 201 CRHR2 Meyer, A. H.; Ullmer, C.; Schmuck, K.; Morel, C.; Wishart, W.;Lubbert, H.; 3 C c
Engels, P.: Localization of the human CRF2 receptorto 7p21- p15 by radiation hybrid mapping and FISH analysis. Genomics 40:189- 190, 1997.

GAM51 201 HNRPK Dejgaard, K.; Leffers, H.; Rasmussen, H. H.; Madsen, P.; Kruse,T. A.; 3 C c
Gesser, B.; Nielsen, H.; Celis, J. E.: Identification, molecularcloning, expression and chromosome mapping of a family of transformationupregulated hnRNP- K proteins derived by alternative splicing. J.Molec. Biol. 236: 33-48, 1994.

GAM51 201 HNRPK Tommerup, N.; Leffers, H.: Assignment of human KH- box- containinggenes by 3 C c
in situ hybridization: HNRNPK maps to 9q21.32- q21.33, PCBP1to 2p12- p13, and PCBP2 to 12q13.12- q13.13, distal to FRA12A. Genomics 32:297- 298, 1996.

GAM51 201 HOXD4 Mavilio, F.; Simeone, A.; Giampaolo, A.; Faiella, A.; Zappavigna,V.; 3 C c
Acampora, D.; Poiana, G.; Russo, G.; Peschle, C.; Boncinelli,E.: Differential and stage- related expression in embryonic tissuesof a new human homoeobox gene. Nature 324: 664- 668, 1986.

GAM51 201 HOXD4 Oliver, G.; Sidell, N.; Fiske, W.; Heinzmann, C.; Mohandas, T.;Sparkes, R. 3 C c
S.; De Robertis, E. M.: Complementary homeo protein gradientsin developing limb buds. Genes Dev. 3: 641- 650, 1989.

GAM51 201 HOXD4 Zakany, J.; Duboule, D.: Hox genes and the making of sphincters. Nature 3 C c
401:761- 762, 1999.

GAM51 201 ITGAM Arnaout, M. A.; Gupta, S. K.; Pierce, M. W.; Tenen, D. G.: Aminoacid 3 C c
sequence of the alpha subunit of human leukocyte adhesion receptorMo1 (complement receptor type 3). J. Cell Biol. 106: 2153- 2158,1988.

GAM51 201 ITGAM Arnaout, M. A.; Remold- O'Donnell, E.; Pierce, M. W.; Harris, P.;Tenen, D. 3 C c
G.: Molecular cloning of the alpha- subunit of human andguinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localizationand homology to the alpha- subunits of integrins. Proc. Nat. Acad.Sci. 85: 2776- 2780, 1988.

GAM51 201 ITGAM Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; 3 C c
Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P. G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome 16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991.

GAM51 201 ITGAM Corbi, A. L.; Kishimoto, T. K.; Miller, L. J.; Springer, T. A.: The human 3 C c
leukocyte adhesion glycoprotein Mac- 1 (complement receptortype 3, CD11b)

alpha subunit: cloning, primary structure, and relationto the integrins, von Willebrand factor and factor B. J. Biol. Chem. 263:12403- 12411, 1988.

GAM51 201 ITGAM Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. C.: Chromosomal location of the genes encoding the leukocyteadhesion receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988. 3 C c

GAM51 201 ITGAM Pierce, M. W.; Remold- O'Donnell, E.; Todd, R. F., III; Arnaout,M. A.: N-terminal sequence of human leukocyte glycoprotein Mo1: conservationacross species and homology to platelet IIb/IIIa. Biochim. Biophys.Acta 874: 368-371, 1986. 3 C c

GAM51 201 ITGAM Simon, D. I.; Chen, Z.; Seifert, P.; Edelman, E. R.; Ballantyne,C. M.; Rogers, C.: Decreased neointimal formation in Mac- 1 - /- micereveals a role for inflammation in vascular repair after angioplasty. J.Clin. Invest. 105: 293- 300, 2000. 3 C c

GAM51 201 ITGAM Springer, T. A.; Teplow, D. B.; Dreyer, W. J.: Sequence homologyof the LFA- 1 and Mac- 1 leukocyte adhesion glycoproteins and unexpectedrelation to leukocyte interferon. Nature 314: 540- 542, 1985. 3 C c

GAM51 201 JRKL Toth, M.; Grimsby, J.; Buzsaki, G.; Donovan, G. P.: Epilepticseizures caused by inactivation of a novel gene, jerky, related tocentromere binding protein- B in transgenic mice. Nature Genet. 11:71- 75, 1995. Note: Erratum: Nature Genet. 12: 110 only, 1996. 3 C c

GAM51 201 JRKL Zeng, Z.; Kyaw, H.; Gakenheimer, K. R.; Augustus, M.; Fan, P.;Zhang, X.; Su, K.; Carter, K. C.; Li, Y.: Cloning, mapping, and tissuedistribution of a human homologue of the mouse jerky gene product. Biochem.Biophys. Res. Commun. 236: 389- 395, 1997. 3 C c

GAM51 201 LTA Aggarwal, B. B.; Eessalu, T. E.; Hass, P. E.: Characterizationof receptors for human tumour necrosis factor and their regulationby gamma- interferon. Nature 318: 665- 667, 1985. 3 C c

GAM51 201 LTA Evans, A. M.; Petersen, J. W.; Sekhon, G. S.; DeMars, R.: Mappingof prolactin and tumor necrosis factor- beta genes on human chromosome6p using lymphoblastoid cell deletion mutants. Somat. Cell Molec.Genet. 15: 203- 213, 1989. 3 C c

GAM51 201 LTA Gray, P. W.; Aggarwal, B. B.; Benton, C. V.; Bringman, T. S.; Henzel,W. J.; Jarrett, J. A.; Leung, D. W.; Moffat, B.; Ng, P.; Svedersky,L. P.; Palladino, M. A.; Nedwin, G. E.: Cloning and expression ofcDNA for human lymphotoxin, a lymphokine with tumour necrosis activity. Nature 312:721-724, 1984. 3 C c

GAM51 201 LTA Jongeneel, C. V.; Briant, L.; Udalova, I. A.; Sevin, A.; Nedospasov,S. A.; Cambon- Thomsen, A.: Extensive genetic polymorphism in thehuman tumor necrosis factor region and relation to extended HLA haplotypes. Proc.Nat. Acad. Sci. 88: 9717- 9721, 1991. 3 C c

GAM51 201 LTA Koss, K.; Satsangi, J.; Fanning, G. C.; Welsh, K. I.; Jewell, D.P.: Cytokine (TNF- alpha, LT- alpha, and IL- 10) polymorphisms in inflammatorybowel diseases and normal controls: differential effects on productionand allele frequencies. Genes Immun. 1: 185- 190, 2000. 3 C c

GAM51 201 LTA Spies, T.; Blanck, G.; Bresnahan, M.; Sands, J.; Strominger, J.L.: A new cluster of genes within the human major histocompatibilitycomplex. Science 243: 214- 217, 1989. 3 C c

GAM51 201 OTOF Adato, A.; Raskin, L.; Petit, C.; Bonne- Tamir, B.: Deafness heterogeneityin a Druze isolate from the Middle East: novel OTOF and PDS mutations,low 3 C c

prevalence of GJB2 35delG mutation and indication for a new DFNBlocus. Europ. J. Hum. Genet. 8: 437- 442, 2000.

GAM51 201 OTOF Yasunaga, S.; Grati, M.; Chardenoux, S.; Smith, T. N.; Friedman,T. B.; Lalwani, A. K.; Wilcox, E. R.; Petit, C.: OTOF encodes multiplelong and short isoforms: genetic evidence that the long ones underlierecessive deafness DFNB9. Am. J. Hum. Genet. 67: 591- 600, 2000. 3 C c

GAM51 201 OTOF Yasunaga, S.; Grati, M.; Cohen- Salmon, M.; El- Amraoui, A.; Mustapha,M.; Salem, N.; El- Zir, E.; Loiselet, J.; Petit, C.: A mutation inOTOF, encoding otoferlin, a FER- 1- like protein, causes DFNB9, a nonsyndromicform of deafness. Nature Genet. 21: 363- 369, 1999. 3 C c

GAM51 201 OTOF Yasunaga, S.; Petit, C.: Physical map of the region surroundingthe OTOFERLIN locus on chromosome 2p22- p23. Genomics 66: 110- 112,2000. 3 C c

GAM51 201 RGL Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999. 3 C c

GAM51 201 RGL Sood, R.; Makalowska, I.; Carpten, J. D.; Robbins, C. M.; Stephan,D. A.; Connors, T. D.; Morgenbesser, S. D.; Su, K.; Pinkett, H. W.;Graham, C. L.; Quesenberry, M. I.; Baxevanis, A. D.; Klinger, K. W.;Trent, J. M.; Bonner, T. I.: The human RGL (RalGDS- like) gene: cloning,expression analysis and genomic organization. Biochim. Biophys. Acta 1491:285- 288, 2000. 3 C c

GAM51 201 UBE2I Bernier- Villamor, V.; Sampson, D. A.; Matunis, M. J.; Lima, C.D.: Structural basis for E2- mediated SUMO conjugation revealed bya complex between ubiquitin- conjugating enzyme Ubc9 and RanGAP1. Cell 108:345- 356, 2002. 3 C c

GAM51 201 UBE2I Hoege, C.; Pfander, B.; Moldovan, G.- L.; Pyrowolakis, G.; Jentsch,S.: RAD6- dependent DNA repair is linked to modification of PCNA byubiquitin and SUMO. Nature 419: 135- 141, 2002. 3 C c

GAM51 201 UBE2I Shi, Y.; Zou, M.; Farid, N. R.; Paterson, M. C.: Association ofFHIT (fragile histidine triad), a candidate tumour suppressor gene,with the ubiquitin-conjugating enzyme hUBC9. Biochem. J. 352: 443- 448,2000. 3 C c

GAM51 201 UBE2I Tachibana, M.; Iwata, N.; Watanabe, A.; Nobukuni, Y.; Ploplis,B.; Kajigaya, S.: Assignment of the gene for a ubiquitin- conjugatingenzyme (UBE2I) to human chromosome band 16p13.3 by in situ hybridization. Cytogenet.Cell Genet. 75: 222- 223, 1996. 3 C c

GAM51 201 UBE2I Wang, Z.- Y.; Qiu, Q.- Q.; Seufert, W.; Taguchi, T.; Testa, J. R.;Whitmore, S. A.; Callen, D. F.; Welsh, D.; Shenk, T.; Deuel, T. F.: Molecular cloning of the cDNA and chromosome localization of thegene for human ubiquitin-conjugating enzyme 9. J. Biol. Chem. 271:24811- 24816, 1996. 3 C c

GAM51 201 UBE2I Watanabe, T. K.; Fujiwara, T.; Kawai, A.; Shimizu, F.; Takami,S.; Hirano, H.; Okuno, S.; Ozaki, K.; Takeda, S.; Shimada, Y.; Nagata,M.; Takaichi, A.; Takahashi, E.; Nakamura, Y.; Shin, S.: Cloning,expression, and mapping of UBE2I, a novel gene encoding a human homologueof yeast ubiquitin-conjugating enzymes which are critical for regulatingthe cell cycle. Cytogenet. Cell Genet. 72: 86- 89, 1996. 3 C c

GAM51 201 UBE2I Yasugi, T.; Howley, P. M.: Identification of the structural andfunctional human homolog of the yeast ubiquitin conjugating enzymeUBC9. Nucleic Acids Res. 24: 2005- 2010, 1996. 3 C c

GAM52 373 GJA5 Gelb, B. D.; Zhang, J.; Cotter, P. D.; Gershin, I. F.; Desnick,R. J.: 3 C c

Physical mapping of the human connexin 40 (GJA5) flavin-containingmonooxygenase 5, and natriuretic peptide receptor A genes on 1q21. Genomics 39:409- 411, 1997.

GAM52 373 GJA5 Kanter, H. L.; Saffitz, J. E.; Beyer, E. C.: Cardiac myocytesexpress multiple gap junction proteins. Circ. Res. 70: 438- 444,1992. 3 C c

GAM52 373 GJA5 Kanter, H. L.; Saffitz, J. E.; Beyer, E. C.: Molecular cloningof two human cardiac gap junction proteins, connexin40 and connexin45. J.Molec. Cell. Cardiol. 26: 861- 868, 1994. 3 C c

GAM52 373 GJA5 Oviedo- Orta, E.; Hoy, T.; Evans, W. H.: Intercellular communicationin the immune system: differential expression of connexin40 and 43,and perturbation of gap junction channel functions in peripheral bloodand tonsil human lymphocyte subpopulations. Immunology 99: 578- 590,2000. 3 C c

GAM52 373 GJA5 Seul, K. H.; Tadros, P. N.; Beyer, E. C.: Mouse connexin40: genestructure and promoter analysis. Genomics 46: 120- 126, 1997. 3 C c

GAM52 373 GJA5 Willecke, K.; Jungbluth, S.; Dahl, E.; Hennemann, H.; Heynkes,R.; Grzeschik, K.- H.: Six genes of the human connexin gene familycoding for gap junctional proteins are assigned to four differenthuman chromosomes. Europ. J. Cell Biol. 53: 275- 280, 1990. 3 C c

GAM53 359 FOSB Bibb, J. A.; Chen, J.; Taylor, J. R.; Svenningsson, P.; Nishi,A.; Snyder, G. L.; Yan, Z.; Sagawa, Z. K.; Ouimet, C. C.; Nairn, A.C.; Nestler, E. J.; Greengard, P.: Effects of chronic exposure tococaine are regulated by the neuronal protein Cdk5. Nature 410:376- 380, 2001. 3 C c

GAM53 359 FOSB Brown, J. R.; Ye, H.; Bronson, R. T.; Dikkes, P.; Greenberg, M.E.: A defect in nurturing in mice lacking the immediate early genefosB. Cell 86: 297-309, 1996. 3 C c

GAM53 359 FOSB Forsdyke, D.: Personal Communication. Kingston, Ontario, Canada 6/8/1992. 3 C c

GAM53 359 FOSB Kelz, M. B.; Chen, J.; Carlezon, W. A., Jr.; Whisler, K.; Gilden,L.; Beckmann, A. M.; Steffen, C.; Zhang, Y.- J.; Marotti, L.; Self,D. W.; Tkatch, T.; Baranauskas, G.; Surmeier, D. J.; Neve, R. L.;Duman, R. S.; Picciotto, M. R.; Nestler, E. J.: Expression of thetranscription factor delta- FosB in the brain controls sensitivityto cocaine. Nature 401: 272-276, 1999. 3 C c

GAM53 359 FOSB Lazo, P. S.; Dorfman, K.; Noguchi, T.; Mattei, M. G.; Bravo, R.: Structure and mapping of the fosB gene: FosB downregulates the activityof the fosB promoter. Nucleic Acids Res. 20: 343- 350, 1992. 3 C c

GAM53 359 FOSB Martin- Gallardo, A.; McCombie, W. R.; Gocayne, J. D.; FitzGerald,M. G.; Wallace, S.; Lee, B. M. B.; Lamerdin, J.; Trapp, S.; Kelley,J. M.; Liu, L.-I.; Dubnick, M.; Johnston- Dow, L. A.; Kerlavage, A.R.; de Jong, P.; Carrano, A.; Fields, C.; Venter, J. C.: AutomatedDNA sequencing and analysis of 106 kilobases from human chromosome19q13.3. Nature Genet. 1: 34- 39, 1992. 3 C c

GAM53 359 FOSB Nakabeppu, Y.; Nathans, D.: A naturally occurring truncated formof FosB that inhibits Fos/Jun transcriptional activity. Cell 64:751- 759, 1991. 3 C c

GAM53 359 FOSB Siderovski, D. P.; Blum, S.; Forsdyke, R. E.; Forsdyke, D. R.:A set of human putative lymphocyte G0/G1 switch genes includes geneshomologous to rodent cytokine and zinc finger protein- encoding genes. DNACell Biol. 9: 579- 587, 1990. 3 C c

GAM54 275 AKAP13 Carr, D. W.; Hausken, Z. E.; Fraser, I. D.; Stofko- Hahn, R. E.;Scott, J. D: Association of the type II cAMP- dependent protein kinasewith a human thyroid RII- anchoring protein: cloning and characterizationof the RII- 3 C c

binding domain. J. Biol. Chem. 267: 13376- 13382, 1992.

GAM54 275 AKAP13 Carr, D. W.; Stofko- Hahn, R. E.; Fraser, I. D.; Bishop, S. M.;Acott, T. S.; 3 C c
Brennan, R. G.; Scott, J. D.: Interaction of the regulatorysubunit (RII) of
cAMP- dependent protein kinase with RII- anchoringproteins occurs through an
amphipathic helix binding motif. J. Biol.Chem. 266: 14188- 14192, 1991.

GAM54 275 AKAP13 Rubino, D.; Driggers, P.; Arbit, D.; Kemp, L.; Miller, B.; Coso,O.; Pagliai, 3 C c
K.; Gray, K.; Gutkind, S.; Segars, J.: Characterizationof Brx, a novel Dbl
family member that modulates estrogen receptoraction. Oncogene 16: 2513-
2526, 1998.

GAM54 275 AKAP13 Sterpetti, P.; Hack, A. A.; Bashar, M. P.; Park, B.; Cheng, S.- D.;Knoll, J. 3 C c
H. M.; Urano, T.; Feig, L. A.; Toksoz, D.: Activation ofthe Lbc Rho exchange
factor proto- oncogene by truncation of an extendedC terminus that regulates
transformation and targeting. Molec. Cell.Biol. 19: 1334- 1345, 1999.

GAM54 275 AKAP13 Toksoz, D.; Williams, D. A.: Novel human oncogene lbc detectedby 3 C c
transfection with distinct homology regions to signal transductionproducts.
Oncogene 9: 621- 628, 1994.

GAM54 275 BN51T Greco, A.; Ittmann, M.; Barletta, C.; Basilico, C.; Croce, C. M.;Cannizzaro, 3 C c
L. A.; Huebner, K.: Chromosomal localization of humangenes required for G(1)
progression in mammalian cells. Genomics 4:240- 245, 1989.

GAM54 275 BN51T Ittmann, M.; Greco, A.; Basilico, C.: Isolation of the human genethat 3 C c
complements a temperature- sensitive cell cycle mutation in BHKcells. Molec.
Cell. Biol. 7: 3386- 3393, 1987.

GAM54 275 FCGRT Ahouse, J. J.; Hagerman, C. L.; Mittal, P.; Gilbert, D. J.; Copeland,N. G.; 3 C b
Jenkins, N. A.; Simister, N. E.: Mouse MHC class I- like Fcreceptor encoded
outside the MHC. J. Immun. 151: 6076- 6088, 1993.

GAM54 275 FCGRT Junghans, R. P.; Anderson, C. L.: The protection receptor forIgG catabolism 3 C b
is the beta- 2- microglobulin- containing neonatal intestinaltransport
receptor. Proc. Nat. Acad. Sci. 93: 5512- 5516, 1996.

GAM54 275 FCGRT Junghans, R. P.; Ebralidze, A.; Tiwari, B.: Does (CUG)n repeatin DMPK mRNA 3 C b
'paint' chromosome 19 to suppress distant genes to createthe diverse
phenotype of myotonic dystrophy? A new hypothesis of long- rangecis
autosomal inactivation. Neurogenetics 3: 59- 67, 2001.

GAM54 275 FCGRT Kandil, E.; Egashira, M.; Miyosi, O.; Niikawa, N.; Ishibashi, T.;Kasahara, 3 C b
M.: The human gene encoding the heavy chain of the majorhistocompatibility
complex class I- like Fc receptor (FCGRT) maps to19q13.3. Cytogenet. Cell
Genet. 73: 97- 98, 1996.

GAM54 275 FCGRT Story, C. M.; Mikulska, J. E.; Simister, N. E.: A major 3 C b
histocompatibilitycomplex class I- like Fc receptor cloned from human
placenta: possiblerole in transfer of immunoglobulin G from mother to fetus.
J. Exp.Med. 180: 2377- 2381, 1994.

GAM54 275 FCGRT Waldmann, T. A.; Strober, W.: Metabolism of immunoglobulins. Prog.Allergy 3 C b
13: 1- 110, 1969.

GAM54 275 MATN1 Deak, F.; Piecha, D.; Bachrati, C.; Paulsson, M.; Kiss, I.: Primarystructure 3 C c
and expression of matrilin- 2, the closest relative of cartilagematrix
protein within the von Willebrand factor type A- like modulesuperfamily. J.
Biol. Chem. 272: 9268- 9274, 1997.

GAM54 275 MATN1 Deak, F.; Wagener, R.; Kiss, I.; Paulsson, M.: The matrilins:a novel family 3 C c
of oligomeric extracellular matrix proteins. MatrixBiol. 18: 55- 64, 1999.

GAM54 275 MATN1 Hansson, A.- S.; Heinegard, D.; Holmdahl, R.: A new animal modelfor 3 C c
relapsing polychondritis, induced by cartilage matrix protein(matrilin- 1).

J. Clin. Invest. 104: 589- 598, 1999.

GAM54 275 MATN1 Jenkins, R. N.; Osborne- Lawrence, S. L.; Sinclair, A. K.; Eddy,R. L., Jr.; 3 C c
Byers, M. G.; Shows, T. B.; Duby, A. D.: Structure andchromosomal location
of the human gene encoding cartilage matrix protein. J.Biol. Chem. 265:
19624- 19631, 1990.

GAM54 275 MATN1 Lang, B.; Rothenfusser, A.; Lanchbury, J. S.; Rauh, G.; Breedveld,F. C.; 3 C c
Urlacher, A.; Albert, E. D.; Peter, H.- H.; Melchers, I.: Susceptibilityto
relapsing polychondritis is associated with HLA- DR4. ArthritisRheum. 36:
660- 664, 1993.

GAM54 275 MATN1 Loughlin, J.; Irven, C.; Sykes, B.: Exclusion of the cartilagelink protein 3 C c
and the cartilage matrix protein genes as the mutantloci in several
heritable chondrodysplasias. Hum. Genet. 94: 698- 700,1994.

GAM54 275 MATN1 Muratoglu, S.; Krysan, K.; Balazs, M.; Sheng, H.; Zakany, R.; Modis,L.; 3 C c
Kiss, I.; Deak, F.: Primary structure of human matrilin- 2,
chromosomelocation of the MATN2 gene and conservation of an AT- AC intron
inmatrilin genes. Cytogenet. Cell Genet. 90: 323- 327, 2000.

GAM54 275 MATN1 Wagener, R.; Kobbe, B.; Paulsson, M.: Primary structure of matrilin- 3,a new 3 C c
member of a family of extracellular matrix proteins relatedto cartilage
matrix protein (matrilin- 1) and von Willebrand factor. FEBSLett. 413: 129-
134, 1997.

GAM54 275 MATN1 Zeuner, M.; Straub, R. H.; Rauh, G.; Albert, E. D.; Scholmerich,J.; Lang, 3 C c
B.: Relapsing polychondritis: clinical and immunogeneticanalysis of 62
patients. J. Rheum. 24: 96- 101, 1997.

GAM54 275 NDUFV3 Berry, A.; Scott, H. S.; Kudoh, J.; Talior, I.; Korostishevsky,M.; 3 C c
Wattenhofer, M.; Guipponi, M.; Barras, C.; Rossier, C.; Shibuya,K.; Wang,
J.; Kawasaki, K.; Asakawa, S.; Minoshima, S.; Shimizu, N.;Antonarakis, S.;
Bonne- Tamir, B.: Refined localization of autosomalrecessive nonsyndromic
deafness DFNB10 locus using 34 novel microsatellitemarkers, genomic
structure, and exclusion of six known genes in theregion. Genomics 68: 22-
29, 2000.

GAM54 275 NDUFV3 de Coo, R. F. M.; Buddiger, P.; Smeets, H. J. M.; van Oost, B.A.: Molecular 3 C c
cloning and characterization of the human mitochondrialNADH:oxidoreductase
10- kDa gene (NDUFV3). Genomics 45: 434- 437,1997.

GAM54 275 PAX8 Koseki, H.; Zachgo, J.; Mizutani, Y.; Simon- Chazottes, D.; Guenet,J.- L.; 3 C c
Balling, R.; Gossler, A.: Fine genetic mapping of the proximalpart of mouse
chromosome 2 excludes Pax- 8 as a candidate gene forDanforth's short tail
(Sd). Mammalian Genome 4: 324- 327, 1993.

GAM54 275 PAX8 Kroll, T. G.; Sarraf, P.; Pecciarini, L.; Chen, C.- J.; Mueller,E.; 3 C c
Splegelman, B. M.; Fletcher, J. A.: PAX8- PPAR- gamma- 1 fusionin oncogene
human thyroid carcinoma. Science 289: 1357- 1360, 2000.

GAM54 275 PAX8 Macchia, P. E.; Lapi, P.; Krude, H.; Pirro, M. T.; Missero, C.;Chiovato, L.; 3 C c
Souabni, A.; Baserga, M.; Tassi, V.; Pinchera, A.; Fenzi,G.; Gruters, A.;
Busslinger, M.; Di Lauro, R.: PAX8 mutations associatedwith congenital
hypothyroidism caused by thyroid dysgenesis. NatureGenet. 19: 83- 86, 1998.

GAM54 275 PAX8 Mansouri, A.; Chowdhury, K.; Gruss, P.: Follicular cells of thethyroid gland 3 C c
require Pax8 gene function. Nature Genet. 19: 87- 90,1998.

GAM54 275 PAX8 Mansouri, A.; St- Onge, L.; Gruss, P.: Role of Pax genes in endoderm- 3 C c
derivedorgans. Trends Endocr. Metab. 10: 164- 167, 1999.

GAM54 275 PAX8 Pasca di Magliano, M.; Di Lauro, R.; Zannini, M.: Pax8 has a keyrole in 3 C c
thyroid cell differentiation. Proc. Nat. Acad. Sci. 97:13144- 13149, 2000.

GAM54 275 PAX8 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman 3 C c
homologs of the murine paired- box- containing genes. MammalianGenome 4: 78-
82, 1993.

GAM54 275 PAX8 Plachov, D.; Chowdhury, K.; Walther, C.; Simon, D.; Guenet, J.- L.;Gruss, 3 C c
P.: Pax- 8, a murine paired box gene expressed in the developingexcretory
system and thyroid gland. Development 110: 643- 651, 1990.

GAM54 275 PAX8 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: 3 C c
Chromosomal localization of seven PAX genes and cloning of anovel family
member, PAX- 9. Nature Genet. 3: 292- 298, 1993.

GAM54 275 PAX8 Tell, G.; Pellizzari, L.; Esposito, G.; Pucillo, C.; Macchia,P. E.; Di 3 C c
Lauro, R.; Damante, G.: Structural defects of a Pax8 mutantthat give rise to
congenital hypothyroidism. Biochem. J. 341: 89- 93,1999.

GAM54 275 PAX8 Torban, E.; Pelletier, J.; Goodyer, P.: F329L polymorphism inthe human PAX8 3 C c
gene. Am. J. Med. Genet. 72: 186- 187, 1997.

GAM54 275 PAX8 Vilain, C.; Rydlewski, C.; Duprez, L.; Heinrichs, C.; Abramowicz,M.; 3 C c
Malvaux, P.; Renneboog, B.; Parma, J.; Costagliola, S.; Vassart,G.:
Autosomal dominant transmission of congenital thyroid hypoplasiadue to loss-
of- function mutation of PAX8. J. Clin. Endocr. Metab. 86:234- 238, 2001.

GAM54 275 PAX8 Walther, C.; Guenet, J.- L.; Simon, D.; Deutsch, U.; Jostes, B.;Goulding, 3 C c
M.; Plachov, D.; Balling, R.; Gruss, P.: Pax: a murinemultigene family of
paired box- containing genes. Genomics 11: 424- 434,1991.

GAM55 387 AP2B1 Druck, T.; Gu, Y.; Prabhala. G.; Cannizzaro, L. A.; Park, S.- H.;Huebner, 1 B c
K.; Keen, J. H.: Chromosome localization of human genesfor clathrin adaptor
polypeptides AP2- beta and AP50 and the clathrin- bindingprotein, VCP.
Genomics 30: 94- 97, 1995.

GAM55 387 AP2B1 Ponnambalam, S.; Robinson, M. S.; Jackson, A. P.; Peiperl, L.;Parham, P.: 1 B c
Conservation and diversity in families of coated vesicleadaptins. J. Biol.
Chem. 265: 4814- 4820, 1990.

GAM55 387 CAV2 Engelman, J. A.; Zhang, X. L.; Galbiati, F.; Lisanti, M. P.: 1 B c
Chromosomallocalization, genomic organization, and developmental expression
ofthe murine caveolin gene family (Cav- 1, - 2, and - 3): Cav- 1 and Cav-
2genes map to a known tumor suppressor locus (6- A2/7q31). FEBS Lett.
429:330- 336, 1998.

GAM55 387 CAV2 Engelman, J. A.; Zhang, X. L.; Lisanti, M. P.: Genes encodinghuman caveolin- 1 B c
1 and - 2 are co- localized to the D7S522 locus (7q31.1),a known fragile
site (FRA7G) that is frequently deleted in human cancers. FEBSLett. 436:
403- 410, 1998.

GAM55 387 CAV2 Engelman, J. A.; Zhang, X.; Galbiati, F.; Volonte, D.; Sotgia,F.; Pestell, 1 B c
R. G.; Minetti, C.; Scherer, P. E.; Okamoto, T.; Lisanti,M. P.: Molecular
genetics of the caveolin gene family: implicationsfor human cancers,
diabetes, Alzheimer disease, and muscular dystrophy. Am.J. Hum. Genet. 63:
1578- 1587, 1998.

GAM55 387 CAV2 Galbiati, F.; Volonte, D.; Gil, O.; Zanazzi, G.; Salzer, J. L.;Sargiacomo, 1 B c
M.; Scherer, P. E.; Engelman, J. A.; Schlegel, A.; Parenti,M.; Okamoto, T.;
Lisanti, M. P.: Expression of caveolin- 1 and - 2in differentiating PC12
cells and dorsal root ganglion neurons: caveolin- 2is up- regulated in
response to cell injury. Proc. Nat. Acad. Sci. 95:10257- 10262, 1998.

GAM55 387 CAV2 Scherer, P. E.; Okamoto, T.; Chun, M.; Nishimoto, I.; Lodish, H.F.; Lisanti, 1 B c
M. P.: Identification, sequence, and expression of caveolin- 2defines a
caveolin gene family. Proc. Nat. Acad. Sci. 93: 131- 135,1996.

GAM55 387 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a member of a multigene family. Genomics 52: 332- 341, 1998. 1 B b

GAM55 387 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a new member of the MTG8/ETO gene family, maps on 20q11region and is deleted in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998. 1 B b

GAM55 387 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic fusion protein forms a complex with a novel member of theMTG8(ETO/CDR) family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998. 1 B b

GAM55 387 CRMP1 Hamajima, N.; Matsuda, K.; Sakata, S.; Tamaki, N.; Sasaki, M.;Nonaka, M.: A novel gene family defined by human dihydropyrimidinaseand three related proteins with differential tissue distribution. Gene 180:157- 163, 1996. 1 B c

GAM55 387 CRMP1 Ruiz- Perez, V. L.; Ide, S. E.; Strom, T. M.; Lorenz, B.; Wilson,D.; Woods, K.; King, L.; Francomano, C.; Freisinger, P.; Spranger,S.; Marino, B.; Dallapiccola, B.; Wright, M.; Meitinger, T.; Polymeropoulos,M. H.; Goodship, J.: Mutations in a new gene in Ellis- van Creveldsyndrome and Weyers acrodental dysostosis. Nature Genet. 24: 283- 286,2000. Note: Erratum: Nature Genet. 25: 125 only, 2000. 1 B c

GAM55 387 CRMP1 Torres, R.; Polymeropoulos, M. H.: Genomic organization and localizationof the human CRMP- 1 gene. DNA Res. 5: 393- 395, 1998. 1 B c

GAM55 387 CUL3 Du, M.; Sansores- Garcia, L.; Zu, Z.; Wu, K. K.: Cloning and expressionanalysis of a novel salicylate suppressible gene, Hs- CUL- 3, a memberof cullin/Cdc53 family. J. Biol. Chem. 273: 24289- 24292, 1998. 1 B c

GAM55 387 CUL3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 1 B c

GAM55 387 CUL3 Kipreos, E. T.; Lander, L. E.; Wing, J. P.; He, W. W.; Hedgecock,E. M.: cul- 1 is required for cell cycle exit in C. elegans and identifiesa novel gene family. Cell 85: 829- 839, 1996. 1 B c

GAM55 387 CUL3 Michel, J. J.; Xiong, Y.: Human CUL- 1, but not other cullin familymembers, selectively interacts with SKP1 to form a complex with SKP2and cyclin A. Cell Growth Differ. 9: 435- 449, 1998. 1 B c

GAM55 387 EPHB6 Matsuoka, H.; Iwata, N.; Ito, M.; Shimoyama, M.; Nagata, A.; Chihara,K.; Takai, S.; Matsui, T.: Expression of a kinase- defective Eph- likereceptor in the normal human brain. Biochem. Biophys. Res. Commun. 235:487- 492, 1997. 1 B c

GAM55 387 EPHB6 Tang, X. X.; Zhao, H.; Robinson, M. E.; Cohen, B.; Cnaan, A.; London,W.; Cohn, S. L.; Cheung, N.- K. V.; Brodeur, G. M.; Evans, A. E.; Ikegaki,N.: Implications of EPHB6, EFNB2, and EFNB3 expressions in humanneuroblastoma. Proc. Nat. Acad. Sci. 97: 10936- 10941, 2000. 1 B c

GAM55 387 HAT1 Dutnall, R. N.; Tafrov, S. T.; Sternglanz, R.; Ramakrishnan, V.: Structure of the histone acetyltransferase Hat1: a paradigm forthe GCN5- related N-acetyltransferase superfamily. Cell 94: 427- 438,1998. 1 B c

GAM55 387 HAT1 Verreault, A.; Kaufman, P. D.; Kobayashi, R.; Stillman, B.: NucleosomalDNA regulates the core- histone- binding subunit of the human Hat1 acetyltransferase. Curr.Biol. 8: 96- 108, 1998. 1 B c

GAM55 387 KRT6A Bowden, P. E.; Haley, J. L.; Kansky, A.; Rothnagel, J. A.; Jones,D. O.; Turner, R. J.: Mutation of a type II keratin gene (K6a) inpachyonychia congenita. Nature Genet. 10: 363- 365, 1995. 1 B c

GAM55 387 KRT6A Rosenberg, M.; Fuchs, E.; Le Beau, M. M.; Eddy, R. L.; Shows, T.B.: Three epidermal and one simple epithelial type II keratin genesmap to human chromosome 12. Cytogenet. Cell Genet. 57: 33- 38, 1991. 1 B c

GAM55 387 KRT6A Takahashi, K.; Paladini, R. D.; Coulombe, P. A.: Cloning and characterizationof multiple human genes and cDNAs encoding highly related type IIkeratin 6 isoforms. J. Biol. Chem. 270: 18581- 18592, 1995. 1 B c

GAM55 387 KRT6A Tyner, A.; Eichman, M.; Fuchs, E.: The sequence of a type II keratingene expressed in human skin: conservation of structure among allintermediate filament genes. Proc. Nat. Acad. Sci. 82: 4683- 4687,1985. 1 B c

GAM55 387 KRT6A Wong, P.; Colucci- Guyon, E.; Takahashi, K.; Gu, C.; Babinet, C.;Coulombe, P. A.: Introducing a null mutation in the mouse K6- alphaand K6- beta genes reveals their essential structural role in the oralmucosa. J. Cell Biol. 150: 921- 928, 2000. 1 B c

GAM55 387 MAP3K8 Aoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima,K.: The human cot proto- oncogene encodes two protein serine/threoninekinases with different transforming activities by alternative initiationof translation. J. Biol. Chem. 268: 22723- 22732, 1993. 1 B c

GAM55 387 MAP3K8 Chan, A. M.- L.; Chedid, M.; McGovern, E. S.; Popescu, N. C.; Miki,T.; Aaronson, S. A.: Expression cDNA cloning of a serine kinase transforminggene. Oncogene 8: 1329- 1333, 1993. 1 B c

GAM55 387 MAP3K8 Miyoshi, J.; Higashi, T.; Mukai, H.; Ohuchi, T.; Kakunaga, T.:Structure and transforming potential of the human cot oncogene encodinga putative protein kinase. Molec. Cell. Biol. 11: 4088- 4096, 1991. 1 B c

GAM55 387 MAP3K8 Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.: The murine cotproto- oncogene: genome structure and tissue- specific expression. Jpn.J. Cancer Res. 84: 518- 525, 1993. 1 B c

GAM55 387 NPM1 Chan, W.- Y.; Liu, Q.- R.; Borjigin, J.; Busch, H.; Rennert, O. M.;Tease, L. A.; Chan, P.- K.: Characterization of the cDNA encodinghuman nucleophosmin and studies of its role in normal and abnormalgrowth. Biochemistry 28: 1033- 1039, 1989. 1 B c

GAM55 387 NPM1 Cheng, G.- X.; Zhu, X.- H.; Men, X.- Q.; Wang, L.; Huang, Q.- H.; Jin,X. L.; Xiong, S.- M.; Zhu, J.; Guo, W.- M.; Chen, J.- Q.; Xu, S.- F.;So, E.; Chan, L.- C.; Waxman, S.; Zelent, A.; Chen, G.- Q.; Dong, S.;Liu, J.- X.; Chen, S.- J.: Distinct leukemia phenotypes in transgenicmice and different corepressor interactions generated by promyelocyticleukemia variant fusion genes PLZF- RAR- alpha and NPM- RAR- alpha. Proc.Nat. Acad. Sci. 96: 6318- 6323, 1999. 1 B c

GAM55 387 NPM1 Dutta, S.; Akey, I. V.; Dingwall, C.; Hartman, K. L.; Laue, T.;Nolte, R. T.; Head, J. F.; Akey, C. W.: The crystal structure ofnucleoplasmin- core: implications for histone binding and nucleosomeassembly. Molec. Cell 8: 841- 853, 2001. 1 B c

GAM55 387 NPM1 Morris, S. W.; Kirstein, M. N.; Valentine, M. B.; Dittmer, K. G.;Shapiro, D. N.; Saltman, D. L.; Look, A. T.: Fusion of a kinase gene,ALK, to a nucleolar protein gene, NPM, in non- Hodgkin's lymphoma. Science 263:1281- 1284, 1994. 1 B c

GAM55 387 NPM1 Okuda, M.; Horn, H. F.; Tarapore, P.; Tokuyama, Y.; Smulian, A.G.; Chan, P.- K.; Knudsen, E. S.; Hofmann, I. A.; Snyder, J. D.; Bove,K. E.; Fukasawa, K.: Nucleophosmin/B23 is a target of CDK2/cyclinE in centrosome duplication. Cell 103: 127- 140, 2000. 1 B c

GAM55 387 NPM1 Redner, R. L.; Rush, E. A.; Faas, S.; Rudert, W. A.; Corey, S.J.: The t(5;17) variant of acute promyelocytic leukemia expressesa nucleophosmin- 1 B c

retinoic acid receptor fusion. Blood 87: 882- 886,1996.

GAM55 387 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C. Genomics 47: 323- 324, 1998. 1 B c

GAM55 387 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to human chromosome 21q22.3. Genomics 41: 193- 200,1997. 1 B c

GAM55 387 PSMA1 Bey, F.; Silva Pereira, I.; Coux, O.; Viegas- Pequignot, E.; RecillasTarga, F.; Nothwang, H. G.; Dutrillaux, B.; Scherrer, K.: The prosomalRNA- binding protein p27K is a member of the alpha- type human prosomalgene family. Molec. Gen. Genet. 237: 193- 205, 1993. 1 B b

GAM55 387 PSMA1 Coux, O.; Tanaka, K.; Goldberg, A. L.: Structure and functionsof the 20S and 26S proteasomes. Ann. Rev. Biochem. 65: 801- 847,1996. 1 B b

GAM55 387 PSMA1 DeMartino, G. N.; Orth, K.; McCullough, M. L.; Lee, L. W.; Munn,T. Z.; Moomaw, C. R.; Dawson, P. A.; Slaughter, C. A.: The primarystructures of four subunits of the human, high molecular weight proteinase,macropain (proteasome), are distinct but homologous. Biochim. Biophys.Acta 1079: 29- 38, 1991. 1 B b

GAM55 387 PTER Alimova- Kost, M. V.; Imreh, S.; Buchman, V. L.; Ninkina, N. N.: Assignment of phosphotriesterase- related gene (PTER) to human chromosomeband 10p12 by in situ hybridization. Cytogenet. Cell Genet. 83:16- 17, 1998. 1 B c

GAM55 387 PTER Davies, J. A.; Buchman, V. L.; Krylova, O.; Ninkina, N. N.: Molecularcloning and expression pattern of rpr- 1, a resiniferatoxin- binding,phosphotriesterase- related protein, expressed in rat kidney tubules. FEBSLett. 410: 378- 382, 1997. 1 B c

GAM55 387 TXNRD2 Gasdaska, P. Y.; Berggren, M. M.; Berry, M. J.; Powis, G.: Cloning,sequencing, and functional expression of a novel human thioredoxinreductase. FEBS Lett. 442: 105- 111, 1999. 1 B c

GAM55 387 TXNRD2 Kawai, H.; Ota, T.; Suzuki, F.; Tatsuka, M.: Molecular cloningof mouse thioredoxin reductases. Gene 242: 321- 330, 2000. 1 B c

GAM55 387 TXNRD2 Lescure, A.; Gautheret, D.; Carbon, P.; Krol, A.: Novel selenoproteinsidentified in silico and in vivo by using a conserved RNA structuralmotif. J. Biol. Chem. 274: 38147- 38154, 1999. 1 B c

GAM55 387 TXNRD2 Miranda- Vizuete, A.; Damdimopoulos, A. E.; Spyrou, G.: cDNA cloning,expression and chromosomal localization of the mouse mitochondrialthioredoxin reductase gene. Biochim. Biophys. Acta 1447: 113- 118,1999. 1 B c

GAM55 387 TXNRD2 Miranda- Vizuette, A.; Damdimopoulos, A. E.; Pedrajas, J. R.; Gustafsson,J.- A.; Spyrou, G.: Human mitochondrial thioredoxin reductase: cDNAcloning, expression, and genomic organization. Europ. J. Biochem. 261:405- 412, 1999. 1 B c

GAM55 387 TXNRD2 Sun, Q.- A.; Wu, Y.; Zappacosta, F.; Jeang, K.- T.; Lee, B. J.; Hatfield,D. L.; Gladyshev, V. N.: Redox regulation of cell signaling by selenocysteinein mammalian thioredoxin reductases. J. Biol. Chem. 274: 24522- 24530,1999. 1 B c

GAM59 377 PITX1 Crawford, M. J.; Lanctot, C.; Tremblay, J. J.; Jenkins, N.; Gilbert,D.; Copeland, N.; Beatty, B.; Drouin, J.: Human and murine PTX1/Ptx1gene maps to the region for Treacher Collins syndrome. MammalianGenome 8: 841- 845, 1997. 3 C c

GAM59 377 PITX1 Lamonerie, T.; Tremblay, J. J.; Lanctot, C.; Thierrien, M.; Gauthier,Y.; Drouin, J.: Ptx1, a bicoid- related homeo box transcription factorinvolved in transcription of the pro- opiomelanocortin gene. GenesDev. 10: 1284- 3 C c

1295, 1996.

GAM59 377 PITX1 Logan, M.; Tabin, C. J.: Role of Pitx1 upstream of Tbx4 in specificationof 3 C c
hindlimb identity. Science 283: 1736- 1739, 1999.

GAM59 377 PITX1 Pellegrini- Bouiller, I.; Manrique, C.; Gunz, G.; Grino, M.; Zamora,A. J.; 3 C c
Figarella- Branger, D.; Grisoli, F.; Jaquet, P.; Enjalbert,A.: Expression of
the members of the Ptx family of transcriptionfactors in human pituitary
adenomas. J. Clin. Endocr. Metab. 84:2212- 2220, 1999.

GAM59 377 PITX1 Shang, J.; Li, X.; Ring, H. Z.; Clayton, D. A.; Francke, U.: Backfoot,a 3 C c
novel homeobox gene, maps to human chromosome 5 (BFT) and mousechromosome 13
(Bft). Genomics 40: 108- 113, 1997.

GAM59 377 PITX1 Skelly, R. H.; Korbonits, M.; Grossman, A.; Besser, G. M.; Monson,J. P.; 3 C c
Geddes, J. F.; Burrin, J. M.: Expression of the pituitarytranscription
factor Ptx- 1, but not that of the trans- activating factorProp- 1, is
reduced in human corticotroph adenomas and is associatedwith decreased
alpha- subunit secretion. J. Clin. Endocr. Metab. 85:2537- 2542, 2000.

GAM59 377 PITX1 Szeto, D. P.; Rodriguez- Esteban, C.; Ryan, A. K.; O'Connell, S.M.; Liu, F.; 3 C c
Kioussi, C.; Gleiberman, A. S.; Izpisua- Belmonte, J.C.; Rosenfeld, M. G.:
Role of the Bicoid- related homeodomain factorPitx1 in specifying hindlimb
morphogenesis and pituitary development. GenesDev. 13: 484- 494, 1999.

GAM59 377 TBX6 Chapman, D. L.; Agulnik, I.; Hancock, S.; Silver, L. M.; Papaioannou,V. E.: 3 C c
Tbx6, a mouse T- box gene implicated in paraxial mesoderm formationat
gastrulation. Dev. Biol. 180: 534- 542, 1996.

GAM59 377 TBX6 Chapman, D. L.; Papaioannou, V. E.: Three neural tubes in mouseembryos with 3 C c
mutations in the T- box gene Tbx6. Nature 391: 695- 697,1998.

GAM59 377 TBX6 Papapetrou, C.; Putt, W.; Fox, M.; Edwards, Y. H.: The human TBX6gene: 3 C c
cloning and assignment to chromosome 16p11.2. Genomics 55:238- 241, 1999.

GAM60 381 BARD1 Irminger- Finger, I.; Leung, W.- C.; Li, J.; Dubois- Dauphin, M.;Harb, J.; 3 C c
Feki, A.; Jefford, C. E.; Soriano, J. V.; Jaconi, M.; Montesano,R.; Krause,
K.- H.: Identification of BARD1 as mediator between proapoptoticstress and
p53- dependent apoptosis. Molec. Cell 8: 1255- 1266, 2001.

GAM60 381 BARD1 Jin, Y.; Xu, X. L.; Yang, M.- C. W.; Wei, F.; Ayi, T.- C.; Bowcock,A. M.; 3 C c
Baer, R.: Cell cycle- dependent colocalization of BARD1 andBRCA1 proteins in
discrete nuclear domains. Proc. Nat. Acad. Sci. 94:12075- 12080, 1997.

GAM60 381 BARD1 Kleiman, F. E.; Manley, J. L.: Functional interaction of BRCA1- 3 C c
associatedBARD1 with polyadenylation factor CstF- 50. Science 285: 1576-
1579,1999.

GAM60 381 BARD1 Wu, L. C.; Wang, Z. W.; Tsan, J. T.; Spillman, M. A.; Phung, A.;Xu, X. L.; 3 C c
Yang, M.- C. W.; Hwang, L.- Y.; Bowcock, A. M.; Baer, R.: Identification of
a RING protein that can interact in vivo withthe BRCA1 gene product. Nature
Genet. 14: 430- 440, 1996.

GAM63 348 ACP1 Arnaud, J.; Vavrusa, B.; Sevin, J.; Constans, J.: Human red- cellacid 4 A c
phosphatase (ACP1): a new mutant (ACP1*KUK) detected by isoelectricfocusing,
kinetics of thermostability and substrate activity. Hum.Hered. 39: 288- 293,
1989.

GAM63 348 ACP1 Arnaud, J.; Vavrusa, B.; Wiederanders, G.; Constans, J.: Humanred- cell acid 4 A c
phosphatase (ACP1): kinetic and thermodynamic characterizationof the KUK
variant. Hum. Hered. 42: 140- 142, 1992.

GAM63 348 ACP1 Beemer, F. A.; van der Heiden, C.; Van Hemel, J. O.; Jansen, M.: Letter to 4 A c
the editors. (Letter) Clin. Genet. 24: 151, 1983.

GAM63 348 ACP1 Berg, K.: Close linkage between APOB and ACP1 excluded. (Abstract) 4 A c

Cytogenet.Cell Genet. 46: 580, 1987.

GAM63 348 ACP1 Bottini, E.; Carapella, E.; Orzalesi, M.; Lucarelli, P.; Pascone,R.; Gloria- 4 A c
Bottini, F.; Coccia, M.: Is there a role of erythrocyteacid phosphatase
polymorphism in intrauterine development? (Letter) Am.J. Hum. Genet. 32:
764- 767, 1980.

GAM63 348 ACP1 Bryson, G. L. M.; Massa, H.; Trask, B. J.; Van Etten, R. L.: Genestructure, 4 A c
sequence, and chromosomal localization of the human redcell- type low
molecular weight acid phosphotyrosyl phosphatase gene,ACP1. Genomics 30:
133- 140, 1995.

GAM63 348 ACP1 Chautard- Freire- Maia, E. A.: Linkage relationships between 22autosomal 4 A c
markers. Ann. Hum. Genet. 38: 191- 198, 1974.

GAM63 348 ACP1 Chu, E. H. Y.; Chang, C. C.; Sun, N. C.: Synteny of the humangenes for gal- 4 A c
1- PT, ACP- 1, MDH- 1, and gal- plus- activator and assignmentto chromosome
2. Birth Defects Orig. Art. Ser. XI(3): 103- 106, 1975.Note: Alternate:
Cytogenet. Cell Genet. 14: 273- 276, 1975...

GAM63 348 ACP1 Dissing, J.; Johnsen, A. H.: Human red cell acid phosphatase (ACP1):the 4 A c
primary structure of the two pairs of isozymes encoded by theACP1*A and
ACP1*C alleles. Biochim. Biophys. Acta 1121: 261- 268,1992.

GAM63 348 ACP1 Dissing, J.; Johnsen, A. H.; Sensabaugh, G. F.: Human red cellacid 4 A c
phosphatase (ACP1): the amino acid sequence of the two isozymesBf and Bs
encoded by the ACP1*B allele. J. Biol. Chem. 266: 20619- 20625,1991.

GAM63 348 ACP1 Emanuel, B. S.; Zackai, E. H.; Van Dyke, D. C.; Swallow, D. M.;Allen, F. H.; 4 A c
Mellman, W. J.: Deletion mapping: further evidencefor the location of acid
phosphatase (ACP- 1) within 2p23. Am. J.Med. Genet. 4: 167- 172, 1979.

GAM63 348 ACP1 Ferguson- Smith, M. A.; Newman, B. F.; Ellis, P. M.; Thomson, D.M. G.; 4 A c
Riley, I. D.: Assignment by deletion of human red cell acidphosphatase gene
locus to the short arm of chromosome 2. Nature 243:271- 273, 1973.

GAM63 348 ACP1 Fisher, R. A.; Harris, H.: Studies on the separate isoenzymesof red cell 4 A c
acid phosphatase phenotypes A and B: chromatographic separationof the
isoenzymes. Ann. Hum. Genet. 34: 431- 438, 1971.

GAM63 348 ACP1 Fuhrmann, W.; Lichte, K. H.: Human red cell acid phosphatasepolymorphism: a 4 A c
study on gene frequency and forensic use of the systemin cases of disputed
paternity. Humangenetik 3: 121- 126, 1966.

GAM63 348 ACP1 Giblett, E. R.; Scott, N. M.: Red cell acid phosphatase: racialdistribution 4 A c
and report of a new phenotype. Am. J. Hum. Genet. 17:425- 432, 1965.

GAM63 348 ACP1 Hamerton, J. L.; Mohandas, T.; McAlpine, P. J.; Douglas, G. R.: Localization 4 A c
of human gene loci using spontaneous chromosome rearrangementsin human-
Chinese hamster somatic cell hybrids. Am. J. Hum. Genet. 27:595- 608, 1975.

GAM63 348 ACP1 Herbich, J.; Fisher, R. A.; Hopkinson, D. A.: Atypical segregationof human 4 A c
red cell acid phosphatase phenotypes: evidence for a rare'silent' allele
P(O). Ann. Hum. Genet. 34: 145- 152, 1970.

GAM63 348 ACP1 Herbich, J.; Meinhart, K.: The rare 'silent' allele P(O) or P(V)(P Vienna) 4 A c
of human red cell acid phosphatase, typed in a second family. Humangenetik
15:345- 348, 1972.

GAM63 348 ACP1 Hopkinson, D. A.; Spencer, N.; Harris, H.: Red cell acid 4 A c
phosphatasevariants: a new human polymorphism. Nature 199: 969- 971, 1963.

GAM63 348 ACP1 Hulten, M.; Lindsten, J.; Pen- Ming, L. M.; Fraccaro, M.; Mannini,A.; 4 A c
Tiepolo, L.; Robson, E. B.; Heiken, A.; Tillinger, K. G.:
Possiblelocalization of the genes for the Kidd blood group on an
autosomeinvolved in a reciprocal translocation. Nature 211: 1067- 1068,

1966.

GAM63 348 ACP1 Junien, C.; Kaplan, J.- C.; Bernheim, A.; Berger, R.: Regionalassignment of 4 A c
red cell acid phosphatase locus to band 2p25. Hum.Genet. 48: 17- 21, 1979.

GAM63 348 ACP1 Karp, G. W., Jr.; Sutton, H. E.: Some new phenotypes of humanred cell acid 4 A c
phosphatase. Am. J. Hum. Genet. 19: 54- 62, 1967.

GAM63 348 ACP1 Larson, L. M.; Bruce, A. W.; Saumur, J. H.; Wasdahl, W. A.: Furtherevidence 4 A c
by gene dosage for the regional assignment of erythrocyteacid phosphatase
(ACP1) and malate dehydrogenase (MDH1) loci on chromosome2p. Clin. Genet.
22: 220- 225, 1982.

GAM63 348 ACP1 Lothe, R. A.; Gedde- Dahl, T.; Olaisen, B.; Bakker, E.; Pearson,P.: Very 4 A c
close linkage between D2S1 and ACP1 on chromosome 2p. Ann.Hum. Genet. 50:
361- 367, 1986.

GAM63 348 ACP1 Mace, M. A.; Cook, P. J. L.; Robson, E. B.: Linkage data on redcell acid 4 A c
phosphatase from family studies. Ann. Hum. Genet. 38:471- 477, 1975.

GAM63 348 ACP1 Mace, M. A.; Robson, E. B.: Linkage data on ACP- 1 and MNSs. Cytogenet.Cell 4 A c
Genet. 13: 123- 125, 1974.

GAM63 348 ACP1 Magenis, R. E.; Koler, R. D.; Lovrien, E. W.; Bigley, R. H.; Duval,M. C.; 4 A c
Overton, K. M.: Gene dosage: evidence for assignment of erythrocyteacid
phosphatase locus to chromosome 2. Proc. Nat. Acad. Sci. 72:4526- 4530,
1975.

GAM63 348 ACP1 Mayr, W. R.: No close linkage between MNSs and red cell acidphosphatase. 4 A c
Hum. Hered. 26: 1- 3, 1976.

GAM63 348 ACP1 Miller, S. A.; Nelson, M. S.; Dykes, D. D.; Polesky, H. F.: Comparisonof 4 A c
acid phosphatase ACP1 variants by isoelectric focusing and
conventionalelectrophoresis: identification of three new alleles, ACP1*N,
ACP1*Pand ACP1*S. Hum. Hered. 37: 371- 375, 1987.

GAM63 348 ACP1 Mohrenweiser, H. W.; Novotny, J. E.: ACP- 1- GUA- 1: a low- activityvariant 4 A c
of human erythrocyte acid phosphatase: association with increasedglutathione
reductase activity. Am. J. Hum. Genet. 34: 425- 433,1982.

GAM63 348 ACP1 Nezbeda, P.: Occurrence of the ACP- 1 null allele in Czechoslovakia. 4 A c
Hum.Genet. 46: 227- 229, 1979.

GAM63 348 ACP1 Palmarino, R.; Agostino, R.; Gloria, F.; Lucarelli, P.; Businco,L.; 4 A c
Antognoni, G.; Maggioni, G.; Workman, P. L.; Bottini, E.: Redcell acid
phosphatase: another polymorphism correlated with malaria? Am.J. Phys.
Anthrop. 43: 177- 186, 1975.

GAM63 348 ACP1 Povey, S.; Swallow, D. M.; Bobrow, M.; Craig, I.; Van Heyningen,V.: Probable 4 A c
assignment of the locus determining human red cell acidphosphatase ACP(1) to
chromosome 2 using somatic cell hybrids. Ann.Hum. Genet. 38: 1- 5, 1974.

GAM63 348 ACP1 Renwick, J. H.: Assignment and map- positioning of human lociusing 4 A c
chromosomal variation. Ann. Hum. Genet. 35: 79- 97, 1971.

GAM63 348 ACP1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 4 A c
New York: Oxford Univ. Press (pub.) 1988.

GAM63 348 ACP1 Sensabaugh, G. F.; Golden, V. L.: Phenotype dependence in theinhibition of 4 A c
red cell acid phosphatase (ACP) by folates. Am. J.Hum. Genet. 30: 553- 560,
1978.

GAM63 348 ACP1 Siciliano, M. J.; Bachinski, L.; Dolf, G.; Carrano, A. V.; Thompson,L. H.: 4 A c
Chromosomal assignments of human DNA repair genes that complementChinese
hamster ovary (CHO) cell mutants. (Abstract) Cytogenet. CellGenet. 46: 691-
692, 1987.

GAM63 348 ACP1 Swallow, D. M.; Povey, S.; Harris, H.: Activity of the 'red cell'acid 4 A c

phosphatase locus in other tissues. Ann. Hum. Genet. 37: 31- 38,1973.

GAM63 348 ACP1 Thompson, L. H.; Carrano, A. V.; Sato, K.; Salazar, E. P.; White,B. F.; 4 A c
Stewart, S. A.; Minkler, J. L.; Siciliano, M. J.: Identificationof
nucleotide- excision- repair genes on human chromosomes 2 and 13by
functional complementation in hamster- human hybrids. Somat. CellMolec.
Genet. 13: 539- 551, 1987.

GAM63 348 ACP1 Van Cong, N.; Moullec, J.: Linkage probable entre les groupesde phosphatase 4 A c
acide des globules rouges et le systeme Lewis. Ann.Genet. 14: 121- 125,
1971.

GAM63 348 ACP1 Wakita, Y.; Narahara, K.; Takahashi, Y.; Kikkawa, K.; Kimura,S.; Oda, M.; 4 A c
Kimoto, H.: Duplication of 2p25: confirmation of theassignment of soluble
acid phosphatase (ACP1) locus to 2p25. Hum.Genet. 71: 259- 260, 1985.

GAM63 348 ACP1 Weitkamp, L. R.; Janzen, M. K.; Guttormsen, S. A.; Gershowitz,H.: Inherited 4 A c
pericentric inversion of chromosome number two: a linkagestudy. Ann. Hum.
Genet. 33: 53- 59, 1969.

GAM63 348 ACP1 Weitkamp, L. R.; Lovrien, E. W.; Olaisen, B.; Fenger, K.; Gedde- Dahl,T., 4 A c
Jr.; Sorensen, S. A.; Conneally, P. M.; Bias, W. B.; Ott, J.:Linkage
relations of the loci for the MN blood group and red cellphosphate. Birth
Defects Orig. Art. Ser. 11(3): 276- 280, 1975. Note:Alternate: Cytogenet.
Cell Genet. 14: 446- 450, 1975...

GAM63 348 ACP1 Wo, Y.- Y. P.; McCormack, A. L.; Shabanowitz, J.; Hunt, D. F.;Davis, J. P.; 4 A c
Mitchell, G. L.; Van Etten, R. L.: Sequencing, cloning,and expression of
human red cell- type acid phosphatase, a cytoplasmicphosphotyrosyl protein
phosphatase. J. Biol. Chem. 267: 10856- 10865,1992.

GAM63 348 ACP1 Yoshihara, C. M.; Mohrenweiser, H. W.: Characterization of ACP1(TIC- 1),an 4 A c
electrophoretic variant of erythrocyte acid phosphatase restrictedto the
Ticuna Indians of Central Amazonas. Am. J. Hum. Genet. 32:898- 907, 1980.

GAM63 348 ADAM10 Hattori, M.; Osterfield, M.; Flanagan, J. G.: Regulated cleavageof a 4 A c
contact- mediated axon repellent. Science 289: 1360- 1365, 2000.

GAM63 348 ADAM10 Lunn, C. A.; Fan, X.; Dalie, B.; Miller, K.; Zavodny, P. J.; Narula,S. K.; 4 A c
Lundell, D.: Purification of ADAM 10 from bovine spleen asa TNFalpha
convertase. FEBS Lett. 400: 333- 335, 1997.

GAM63 348 ADAM10 Wolfsberg, T. G.; Primakoff, P.; Myles, D. G.; White, J. M.: ADAM,a novel 4 A c
family of membrane proteins containing a disintegrin and
metalloproteasedomain: multipotential functions in cell- cell and cell-
matrix interactions. J.Cell Biol. 131: 275- 278, 1995.

GAM63 348 ADAM10 Yamazaki, K.; Mizui, Y.; Tanaka, I.: Radiation hybrid mappingof human ADAM10 4 A c
gene to chromosome 15. Genomics 45: 457- 459, 1997.

GAM63 348 ADAM33 Shapiro, S. D.; Owen, C. A.: ADAM- 33 surfaces as an asthma gene.(Letter) 4 A c
New Eng. J. Med. 347: 936- 938, 2002.

GAM63 348 ADAM33 Van Eerdewegh, P.; Little, R. D.; Dupuis, J.; Del Mastro, R. G.;Falls, K.; 4 A c
Simon, J.; Torrey, D.; Pandit, S.; McKenny, J.; Braunschweiger,K.; Walsh,
A.; Liu, Z.; and 26 others: Association of the ADAM33gene with asthma and
bronchial hyperresponsiveness. Nature 418:426- 430, 2002.

GAM63 348 ADAM33 Yoshinaka, T.; Nishii, K.; Yamada, K.; Sawada, H.; Nishiwaki, E.;Smith, K.; 4 A c
Yoshino, K.; Ishiguro, H.; Higashiyama, S.: Identificationand
characterization of novel mouse and human ADAM33s with
potentialmetalloprotease activity. Gene 282: 227- 236, 2002.

GAM63 348 ALOX12B Boeglin, W. E.; Kim, R. B.; Brash, A. R.: A 12R- lipoxygenase inhuman skin: 4 A c
mechanistic evidence, molecular cloning, and expression. Proc.Nat. Acad.

Sci. 95: 6744- 6749, 1998.

GAM63 348 ALOX12B Jobard, F.; Lefevre, C.; Karaduman, A.; Blanchet- Bardon, C.; Emre,S.; Weissenbach, J.; Ozguc, M.; Lathrop, M.; Prud'homme, J.- F.; Fischer,J.: Lipoxygenase- 3 (ALOXE3) and 12(R)- lipoxygenase (ALOX12B) aremutated in non- bullous congenital ichthyosiform erythroderma (NCIE)linked to chromosome 17p13.1. Hum. Molec. Genet. 11: 107- 113, 2002. 4 A c

GAM63 348 ALOX12B Sun, D.; McDonnell, M.; Chen, X.- S.; Lakkis, M. M.; Li, H.; Isaacs,S. N.; Elsea, S. H.; Patel, P. I.; Funk, C. D.: Human 12(R)- lipoxygenaseand the mouse ortholog: molecular cloning, expression, and gene chromosomalassignment. J. Biol. Chem. 273: 33540- 33547, 1998. 4 A c

GAM63 348 AMFR Hirono, Y.; Fushida, S.; Yonemura, Y.; Yamamoto, H.; Watanabe,H.; Raz, A.: Expression of autocrine motility factor receptor correlateswith disease progression in human gastric cancer. Brit. J. Cancer 74:2003- 2007, 1996. 4 A c

GAM63 348 AMFR Huang, B.; Xie, Y.; Raz, A.: Identification of an upstream regionthat controls the transcription of the human autocrine motility factorreceptor. Biochem. Biophys. Res. Commun. 212: 727- 742, 1995. 4 A c

GAM63 348 AMFR Silletti, S.; Yao, J.; Sanford, J.; Mohammed, A. N.; Otto, T.;Wolman, S. R.; Raz, A.: Autocrine motility factor receptor in humanbladder carcinoma: gene expression, loss of cell- contact regulationand chromosomal mapping. Int. J. Oncol. 3: 801- 807, 1993. 4 A c

GAM63 348 AMFR Watanabe, H.; Carmi, P.; Hogan, V.; Raz, T.; Silletti, S.; Nabi,I. R.; Raz, A.: Purification of human tumor cell autocrine motilityfactor and molecular cloning of its receptor. J. Biol. Chem. 266:13442- 13448, 1991. 4 A c

GAM63 348 AP1B1 Arinami, T.; Kondo, I.; Hamaguchi, H.; Nakajima, S.: Multifocalmeningiomas in a patient with a constitutional ring chromosome 22. J.Med. Genet. 23: 178- 180, 1986. 4 A c

GAM63 348 AP1B1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 4 A c

GAM63 348 AP1B1 Petrella, R.; Levine, S.; Wilmot, P. L.; Ashar, K. D.; Casamassima,A. C.; Shapiro, L. R.: Multiple meningiomas in a patient with constitutionalring chromosome 22. Am. J. Med. Genet. 47: 184- 186, 1993. 4 A c

GAM63 348 AP1B1 Peyrard, M.; Fransson, I.; Xie, Y.- G.; Han, F.- Y.; Ruttledge, M.H.; Swahn, S.; Collins, J. E.; Dunham, I.; Collins, V. P.; Dumanski,J. P.: Characterization of a new member of the human beta- adaptingene family from chromosome 22q12, a candidate meningioma gene. Hum.Molec. Genet. 3: 1393- 1399, 1994. 4 A c

GAM63 348 AP1B1 Peyrard, M.; Pan, H.- Q.; Kedra, D.; Fransson, I.; Swahn, S.; Hartman,K.; Clifton, S. W.; Roe, B. A.; Dumanski, J. P.: Structure of thepromoter and genomic organization of the human beta- prime- adaptingene (BAM22) from chromosome 22q12. Genomics 36: 112- 117, 1996. 4 A c

GAM63 348 AP1B1 Zankl, H.; Zang, K. D.: Correlations between clinical and cytogeneticaldata in 180 human meningiomas. Cancer Genet. Cytogenet. 1: 351- 356,1980. 4 A c

GAM63 348 BAPX1 Tribioli, C.; Frasch, M.; Lufkin, T.: Bapx1: an evolutionary conservedhomologue of the Drosophila bagpipe homeobox gene is expressed insplanchnic mesoderm and the embryonic skeleton. Mech. Dev. 65: 145- 162,1997. 4 A c

GAM63 348 BAPX1 Tribioli, C.; Lufkin, T.: Molecular cloning, chromosomal mappingand developmental expression of BAPX1, a novel human homeobox- containinggene homologous to Drosophila bagpipe. Gene 203: 225- 233, 1997. 4 A c

GAM63 348 BAPX1 Yoshiura, K.- I.; Murray, J. C.: Sequence and chromosomal assignmentof human 4 A c
BAPX1, a bagpipe- related gene, to 4p16.1: a candidate genefor skeletal
dysplasia. Genomics 45: 425- 428, 1997.

GAM63 348 BMP1 Amano, S.; Scott, I. C.; Takahara, K.; Koch, M.; Champliaud, M.- F.;Gerecke, 4 A c
D. R.; Keene, D. R.; Hudson, D. L.; Nishiyama, T.; Lee, S.;Greenspan, D. S.;
Burgeson, R. E.: Bone morphogenetic protein 1 isan extracellular processing
enzyme of the laminin 5 gamma- 2 chain. J.Biol. Chem. 275: 22728- 22735,
2000.

GAM63 348 BMP1 Bond, J. S.; Beynon, R. J.: The astacin family of metalloendopeptidases. 4 A c
ProteinSci. 4: 1247- 1261, 1995.

GAM63 348 BMP1 Ceci, J. D.; Kingsley, D. M.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: 4 A c
An interspecific backcross linkage map of the proximal halfof mouse
chromosome 14. Genomics 6: 673- 678, 1990.

GAM63 348 BMP1 Kessler, E.; Takahara, K.; Biniaminov, L.; Brusel, M.; Greenspan,D.: Bone 4 A c
morphogenic protein- 1: the type I procollagen C- proteinase. Science
271:360- 362, 1996.

GAM63 348 BMP1 Reddi, A. H.: BMP- 1: resurrection as procollagen C- proteinase. Science 4 A c
271:5- 6, 1996.

GAM63 348 BMP1 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; 4 A c
Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.;
Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases,
including novel family member mammalian Tolloid- like2, have differential
enzymatic activities and distributions of expressionrelevant to patterning
and skeletogenesis. Dev. Biol. 213: 283- 300,1999.

GAM63 348 BMP1 Tabas, J. A.; Zasloff, M.; Wasmuth, J. J.; Emanuel, B. S.; Altherr,M. R.; 4 A c
McPherson, J. D.; Wozney, J. M.; Kaplan, F. S.: Bone morphogeneticprotein:
chromosomal localization of human genes for BMP1, BMP2A,and BMP3. Genomics
9: 283- 289, 1991.

GAM63 348 BMP1 Takahara, K.; Lee, S.; Wood, S.; Greenspan, D. S.: Structuralorganization 4 A c
and genetic localization of the human bone morphogeneticprotein 1/mammalian
tolloid gene. Genomics 29: 9- 15, 1995.

GAM63 348 BMP1 Takahara, K.; Lyons, G. E.; Greenspan, D. S.: Bone morphogeneticprotein- 1 4 A c
and a mammalian tolloid homologue (mTld) are encoded byalternatively spliced
transcripts which are differentially expressedin some tissues. J. Biol.
Chem. 269: 32572- 32578, 1994.

GAM63 348 BMP1 Wozney, J. M.; Rosen, V.; Celeste, A. J.; Mitsock, L. M.; Whitters,M. J.; 4 A c
Kriz, R. W.; Hewick, R. M.; Wang, E. A.: Novel regulatorsof bone formation:
molecular clones and activities. Science 242:1528- 1534, 1988.

GAM63 348 BMP1 Yoshiura, K.; Tamura, T.; Hong, H.- S.; Ohta, T.; Soejima, H.;Kishino, T.; 4 A c
Jinno, Y.; Niikawa, N.: Mapping of the bone morphogeneticprotein 1 gene
(BMP1) to 8p21: removal of BMP1 from candidacy forthe bone disorder in
Langer- Giedion syndrome. Cytogenet. Cell Genet. 64:208- 209, 1993.

GAM63 348 C1orf6 Davidson, J. D.; Riley, B.; Burright, E.N.; Duvick, L.A.; Zoghbi,H.Y.; Orr, 4 A c
H. T.: Identification and characterization of an ataxin- 1-
interactingprotein: A1Up, a ubiquitin- like nuclear protein. Hum. Molec.
Genet. 9:2305- 2312, 2000.

GAM63 348 C1orf6 Fogli, A.; Giglio, S.; Arrigo, G.; Lo Nigro, C.; Zollo, M.; Viggiano,L.; 4 A c
Rocchi, M.; Archidiacono, N.; Zuffardi, O.; Carrozzo, R.: Identificationof
two paralogous regions mapping to the short and long arms of humanchromosome
2 comprising LIS1 pseudogenes. Cytogenet. Cell Genet. 86:225- 232, 1999.

GAM63 348 CACNG6 Burgess, D. L.; Gefrides, L. A.; Foreman, P. J.; Noebels, J. L.: A cluster 4 A c
of three novel Ca(2+) channel gamma subunit genes on chromosome19q13.4:
evolution and expression profile of the gamma subunit genefamily. Genomics
71: 339- 350, 2001.

GAM63 348 CACNG6 Chu, P.- J.; Robertson, H. M.; Best, P. M.: Calcium channel gammasubunits 4 A c
provide insights into the evolution of this gene family. Gene 280:37- 48,
2001.

GAM63 348 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 4 A c
member of a multigene family. Genomics 52: 332- 341, 1998.

GAM63 348 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 4 A c
new member of the MTG8/ETO gene family, maps on 20q11region and is deleted
in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM63 348 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 4 A c
Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic
fusion protein forms a complex with a novel member of theMTG8(ETO/CDR)
family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM63 348 CCNH Akoulitchev, S.; Chuikov, S.; Reinberg, D.: TFIIH is negativelyregulated by 4 A c
cdk8- containing mediator complexes. Nature 407: 102- 106,2000.

GAM63 348 CCNH Andersen, G.; Poterszman, A.; Egly, J. M.; Moras, D.; Thierry,J.- C: The 4 A c
crystal structure of human cyclin H. FEBS Lett. 397:65- 69, 1996.

GAM63 348 CCNH Eki, T.; Okumura, K.; Abe, M.; Kagotani, K.; Taguchi, H.; Murakami,Y.; Pan, 4 A c
Z.- Q.; Hanaoka, F.: Mapping of the human genes encodingcyclin H (CCNH) and
the CDK- activating kinase (CAK) assembly factorMAT1 (MNAT1) to chromosome
bands 5q13.3- q14 and 14q23, respectively. Genomics 47:115- 120, 1998.

GAM63 348 CCNH Fisher, R. P.; Morgan, D. O.: A novel cyclin associates with MO15/CDK7to 4 A c
form the CDK- activating kinase. Cell 78: 713- 724, 1994.

GAM63 348 CCNH Shiekhattar, R.; Mermelstein, F.; Fisher, R. P.; Drapkin, R.; Dynlacht,B.; 4 A c
Wessling, H. C.; Morgan, D. O.; Reinberg, D.: Cdk- activatingkinase complex
is a component of human transcription factor TFIIH. Nature 374:283- 287,
1995.

GAM63 348 CD2AP Dustin, M. L.; Olszowy, M. W.; Holdorf, A. D.; Li, J.; Bromley,S.; Desai, 4 A c
N.; Widder, P.; Rosenberger, F.; van der Merwe, P. A.;Allen, P. M.; Shaw, A.
S.: A novel adaptor protein orchestrates receptorpatterning and cytoskeletal
polarity in T- cell contacts. Cell 94:667- 677, 1998.

GAM63 348 CD2AP Kirsch, K. H.; Georgescu, M.- M.; Ishimaru, S.; Hanafusa, H.: CMS:an adapter 4 A c
molecule involved in cytoskeletal rearrangements. Proc.Nat. Acad. Sci. 96:
6211- 6216, 1999.

GAM63 348 CD2AP Shih, N.- Y.; Li, J.; Karpitskii, V.; Nguyen, A.; Dustin, M. L.;Kanagawa, 4 A c
O.; Miner, J. H.; Shaw, A. S.: Congenital nephrotic syndromein mice lacking
CD2- associated protein. Science 286: 312- 315, 1999.

GAM63 348 CD37 Knobeloch, K.- P.; Wright, M. D.; Ochsenbein, A. F.; Liesenfeld,O.; Lohler, 4 A c
J.; Zinkernagel, R. M.; Horak, I.; Orinska, Z.: Targetedinactivation of the
tetraspanin CD37 impairs T- cell- dependent B- cellresponse under suboptimal
costimulatory conditions. Molec. Cell.Biol. 20: 5363- 5369, 2000.

GAM63 348 CD37 Virtaneva, K. I.; Angelisova, P.; Baumruker, T.; Horejsi, V.; Nevanlinna,H.; 4 A c
Schroder, J.: The genes for CD37, CD53, and R2, all members ofa novel gene
family, are located on different chromosomes. Immunogenetics 37:461- 465,
1993.

GAM63 348 CELSR2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; 4 A c
Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding

sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM63 348 CELSR2 Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara,O.: 4 A c
Identification of high- molecular- weight proteins with multipleEGF- like motifs by motif- trap screening. Genomics 51: 27- 34, 1998.

GAM63 348 CENPB Earnshaw, W. C.; Sullivan, K. F.; Machlin, P. S.; Cooke, C. A.;Kaiser, D. 4 A c
A.; Pollard, T. D.; Rothfield, N. F.; Cleveland, D. W.: Molecular cloning of cDNA for CENP- B, the major human centromereautoantigen. J. Cell Biol. 104: 817- 829, 1987.

GAM63 348 CENPB Seki, N.; Saito, T.; Kitagawa, K.; Masumoto, H.; Okazaki, T.; Hori,T.- A.: 4 A c
Mapping of the human centromere protein B gene (CENPB) tochromosome 20p13 by fluorescence in situ hybridization. Genomics 24:187- 188, 1994.

GAM63 348 CENPB Sugimoto, K.; Yata, H.; Himeno, M.: Mapping of the human CENP- Bgene to 4 A c
chromosome 20 and the CENP- C gene to chromosome 12 by a rapidcycle DNA amplification procedure. Genomics 17: 240- 242, 1993.

GAM63 348 CHC1 Bischoff, F. R.; Maier, G.; Tilz, G.; Ponstingl, H.: A 47- kDahuman nuclear 4 A c
protein recognized by antikinetochore autoimmune serais homologous with the protein encoded by RCC1, a gene implicatedin onset of chromosome condensation. Proc. Nat. Acad. Sci. 87: 8617- 8621,1990.

GAM63 348 CHC1 Carazo- Salas, R. E.; Guarguaglini, G.; Gruss, O. J.; Segref, A.;Karsenti, 4 A c
E.; Mattaj, I. W.: Generation of GTP- bound Ran by RCC1is required for chromatin- induced mitotic spindle formation. Nature 400:178- 181, 1999.

GAM63 348 CHC1 Furuno, N.; Nakagawa, K.; Eguchi, U.; Ohtubo, M.; Nishimoto, T.;Soeda, E.: 4 A c
Complete nucleotide sequence of the human RCC1 gene involvedin coupling between DNA replication and mitosis. Genomics 11: 459- 461,1991.

GAM63 348 CHC1 Hayashi, N.; Yokoyama, N.; Seki, T.; Azuma, Y.; Ohba, T.; Nishimoto,T.: 4 A c
RanBP1, a Ras- like nuclear G protein binding to Ran/TC4, inhibitsRCC1 via Ran/TC4. Molec. Gen. Genet. 247: 661- 669, 1995.

GAM63 348 CHC1 Kai, R.; Ohtsubo, M.; Sekiguchi, M.; Nishimoto, T.: Molecularcloning of a 4 A c
human gene that regulates chromosome condensation andis essential for cell proliferation. Molec. Cell. Biol. 6: 2027- 2032,1986.

GAM63 348 CHC1 McAlpine, P. J.: Personal Communication. Winnipeg, Manitoba,Canada 4 A c
6/22/1988.

GAM63 348 CHC1 Nemergut, M. E.; Mizzen, C. A.; Stukenberg, T.; Allis, C. D.; Macara,I. G.: 4 A c
Chromatin docking and exchange activity enhancement of RCC1by histones H2A and H2B. Science 292: 1540- 1543, 2001.

GAM63 348 CHC1 Nishimoto, T.; Seino, H.; Seki, N.; Hori, T.- A.: The human CHC1gene 4 A c
encoding RCC1 (regulator of chromosome condensation) (CHC1) islocalized to human chromosome 1p36.1. Genomics 23: 719- 721, 1994.

GAM63 348 CHC1 Ohba, T.; Nakamura, M.; Nishitani, H.; Nishimoto, T.: Self- organizationof 4 A c
microtubule asters induced in Xenopus egg extracts by GTP- boundRan. Science 284: 1356- 1358, 1999.

GAM63 348 CHC1 Ohtsubo, M.; Kai, R.; Furuno, N.; Sekiguchi, T.; Sekiguchi, M.;Hayashida, 4 A c
H.; Kuma, K.; Miyata, T.; Fukushige, S.; Murotsu, T.; Matsubara,K.; Nishimoto, T.: Isolation and characterization of the active cDNAof the human cell cycle gene (RCC1) involved in the regulation ofonset of chromosome condensation. Genes Dev. 1: 585- 593, 1987.

GAM63 348 CHD4 Seelig, H. P.; Moosbrugger, I.; Ehrfeld, H.; Fink, T.; Renz, M.;Genth, E.: 4 A c
The major dermatomyositis- specific Mi- 2 autoantigen isa presumed helicase

involved in transcriptional activation. ArthritisRheum. 38: 1389- 1399, 1995.

GAM63 348 CHD4 Seelig, H. P.; Renz, M.; Targoff, I. N.; Ge, Q.; Frank, M. B.:Two forms of the major antigenic protein of the dermatomyositis- specificMi- 2 autoantigen. (Letter) Arthritis Rheum. 39: 1769- 1771, 1996. 4 A c

GAM63 348 CHD4 Wade, P. A.; Gegonne, A.; Jones, P. L.; Ballestar, E.; Aubry, F.;Wolffe, A. P.: Mi- 2 complex couples DNA methylation to chromatinremodelling and histone deacetylation. Nature Genet. 23: 62- 66,1999. 4 A c

GAM63 348 CHD4 Zhang, Y.; LeRoy, G.; Seelig, H.- P.; Lane, W. S.; Reinberg, D.: The dermatomyositis- specific autoantigen Mi2 is a component of acomplex containing histone deacetylase and nucleosome remodeling activities. Cell 95:279- 289, 1998. 4 A c

GAM63 348 CHD4 Zhang, Y.; Ng, H.- H.; Erdjument- Bromage, H.; Tempst, P.; Bird,A.; Reinberg, D.: Analysis of the NuRD subunits reveals a histonedeacetylase core complex and a connection with DNA methylation. GenesDev. 13: 1924- 1935, 1999. 4 A c

GAM63 348 CHRNB2 Anand, R.; Lindstrom, J.: Chromosomal localization of seven neuronalnicotinic acetylcholine receptor subunit genes in humans. Genomics 13:962- 967, 1992. 4 A c

GAM63 348 CHRNB2 Anand, R.; Lindstrom, J.: Nucleotide sequence of the human nicotinicacetylcholine receptor beta- 2 subunit gene. Nucleic Acids Res. 18:4272, 1990. 4 A c

GAM63 348 CHRNB2 Bessis, A.; Simon- Chazottes, D.; Devillers- Thiery, A.; Guenet,J.- L.; Changeux, J.- P.: Chromosomal localization of the mouse genescoding for alpha- 2, alpha- 3, alpha- 4 and beta- 2 subunits of neuronalnicotinic acetylcholine receptor. FEBS Lett. 264: 48- 52, 1990. 4 A c

GAM63 348 CHRNB2 De Fusco, M.; Becchetti, A.; Patrignani, A.; Annesi, G.; Gambardella,A.; Quattrone, A.; Ballabio, A.; Wanke, E.; Casari, G.: The nicotinicreceptor beta- 2 subunit is mutant in nocturnal frontal lobe epilepsy. NatureGenet. 26: 275- 276, 2000. 4 A c

GAM63 348 CHRNB2 Elliott, K. J.; Ellis, S. B.; Berckhan, K. J.; Urrutia, A.; Chavez-Noriega,L. E.; Johnson, E. C.; Velicelebi, G.; Harpold, M. M.: Comparativestructure of human neuronal alpha(2)- alpha(7) and beta(2)- beta(4)nicotinic acetylcholine receptor subunits and functional expressionof the alpha(2), alpha(3), alpha(4), alpha(7), beta(2), and beta(4)subunits. J. Molec. Neurosci. 7: 217- 228, 1996. 4 A c

GAM63 348 CHRNB2 Groot Kormelink, P. J.; Luyten, W. H. M. L.: Cloning and sequenceof full- length cDNAs encoding the human neuronal nicotinic acetylcholinereceptor (nAChR) subunits beta- 3 and beta- 4 and expression of sevennAChR subunits in the human neuroblastoma cell line SH- SY5Y and/orIMR- 32. FEBS Lett. 400: 309- 314, 1997. 4 A c

GAM63 348 CHRNB2 Lueders, K. K.; Elliott, R. W.; Marenholz, I.; Mischke, D.; DuPree,M.; Hamer, D.: Genomic organization and mapping of the human andmouse neuronal beta- 1- nicotinic acetylcholine receptor genes. MammalianGenome 10: 900- 905, 1999. 4 A c

GAM63 348 CHRNB2 Marubio, L. M.; del Mar Arroyo- Jimenez, M.; Cordero- Erausquin,M.; Lena, C.; Le Novere, N.; de Kerchove d'Exaerde, A.; Huchet, M.;Damaj, M. I.; Changeux, J.- P.: Reduced antinociception in mice lackingneuronal nicotinic receptor subunits. Nature 398: 805- 810, 1999. 4 A c

GAM63 348 CHRNB2 Phillips, H. A.; Favre, I.; Kirkpatrick, M.; Zuberi, S. M.; Goudie,D.; 4 A c

Heron, S. E.; Scheffer, I. E.; Sutherland, G. R.; Berkovic, S.F.; Bertrand, D.; Mulley, J. C.: CHRNB2 is the second acetylcholinereceptor subunit associated with autosomal dominant nocturnal frontallobe epilepsy. Am. J. Hum. Genet. 68: 225- 231, 2001.

GAM63 348 CHRNB2 Picciotto, M. R.; Zoli, M.; Lena, C.; Bessis, A.; Lallemand, Y.;LeNovere, 4 A c
N.; Vincent, P.; Pich, E. M.; Brulet, P.; Changeux, J.- P.: Abnormal avoidance learning in mice lacking functional high- affinitynicotine receptor in the brain. Nature 374: 65- 67, 1995.

GAM63 348 CHRNB2 Rempel, N.; Heyers, S.; Engels, H.; Sleegers, E.; Steinlein, O.K.: The 4 A c
structures of the human neuronal nicotinic acetylcholinereceptor beta- 2- and alpha- 3- subunit genes (CHRNB2 and CHRNA3). Hum.Genet. 103: 645- 653, 1998.

GAM63 348 CHRNB2 Zoli, M.; Picciotto, M. R.; Ferrari, R.; Cocchi, D.; Changeux,J.- P.: 4 A c
Increased neurodegeneration during ageing in mice lackinghigh- affinity nicotine receptors. EMBO J. 18: 1235- 1244, 1999.

GAM63 348 CHST1 Fukuta, M.; Inazawa, J.; Torii, T.; Tsuzuki, K.; Shimada, E.; Habuchi,O.: 4 A c
Molecular cloning and characterization of human keratan sulfategal- 6- sulfotransferase. J. Biol. Chem. 272: 32321- 32328, 1997.

GAM63 348 CHST1 Iida, A.; Saito, S.; Sekine, A.; Mishima, C.; Kitamura, Y.; Kondo,K.; 4 A c
Harigae, S.; Osawa, S.; Nakamura, Y.: Catalog of 77 single- nucleotidepolymorphisms (SNPs) in the carbohydrate sulfotransferase 1 (CHST1)and carbohydrate sulfotransferase 3 (CHST3) genes. J. Hum. Genet. 47:14- 19, 2002.

GAM63 348 CHST1 Mazany, K. D.; Peng, T.; Watson, C. E.; Tabas, I.; Williams, K.J.: Human 4 A c
chondroitin 6- sulfotransferase: cloning, gene structure,and chromosomal localization. Biochim. Biophys. Acta 1407: 92- 97,1998.

GAM63 348 CKMT1 Bark, C. J.: Mitochondrial creatine kinase: a poor prognosticsign. J.A.M.A. 4 A c
243: 2058- 2060, 1980.

GAM63 348 CKMT1 Stallings, R. L.; Olson, E.; Strauss, A. W.; Thompson, L. H.; Bachinski,L. 4 A c
L.; Siciliano, M. J.: Human creatine kinase genes on chromosomes15 and 19, and proximity of the gene for the muscle form to the genesfor apolipoprotein C2 and excision repair. Am. J. Hum. Genet. 43:144- 151, 1988.

GAM63 348 CKMT1 Steeghs, K.; Merkx, G.; Wieringa, B.: The ubiquitous mitochondrialcreatine 4 A c
kinase gene maps to a conserved region on human chromosome15q15 and mouse chromosome 2 bands F1- F3. Genomics 24: 193- 195,1994.

GAM63 348 CLCN6 Brandt, S.; Jentsch, T. J.: ClC- 6 and ClC- 7 are two novel broadlyexpressed 4 A c
members of the CLC chloride channel family. FEBS Lett. 377:15- 20, 1995.

GAM63 348 CLCN6 Eggermont, J.; Buyse, G.; Voets, T.; Tytgat, J.; De Smedt, H.;Droogmans, G.: 4 A c
Alternative splicing of ClC- 6 (a member of the ClCchloride- channel family) transcripts generates three truncated isoformsone of which, ClC- 6c, is kidney- specific. Biochem. J. 325: 269- 276,1997.

GAM63 348 CLCN6 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 4 A c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM63 348 CPLX2 McMahon, H. T.; Missler, M.; Li, C.; Sudhof, T. C.: Complexins:cytosolic 4 A c
proteins that regulate SNAP receptor function. Cell 83:111- 119, 1995.

GAM63 348 CPLX2 Reim, K.; Mansour, M.; Varoqueaux, F.; McMahon, H. T.; Sudhof,T. C.; Brose, 4 A c
N.; Rosenmund, C.: Complexins regulate a late stepin Ca(2+)- dependent

neurotransmitter release. Cell 104: 71- 81, 2001.

GAM63 348 CPLX2 Tokumaru, H.; Umayahara, K.; Pellegrini, L. L.; Ishizuka, T.; Saisu,H.; 4 A c
Betz, H.; Augustine, G. J.; Abe, T.: SNARE complex oligomerizationby
synaphin/complexin is essential for synaptic vesicle exocytosis. Cell
104:421- 432, 2001.

GAM63 348 CUL3 Du, M.; Sansores- Garcia, L.; Zu, Z.; Wu, K. K.: Cloning and 4 A c
expressionanalysis of a novel salicylate suppressible gene, Hs- CUL- 3, a
memberof cullin/Cdc53 family. J. Biol. Chem. 273: 24289- 24292, 1998.

GAM63 348 CUL3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 4 A c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM63 348 CUL3 Kipreos, E. T.; Lander, L. E.; Wing, J. P.; He, W. W.; Hedgecock,E. M.: cul- 4 A c
1 is required for cell cycle exit in C. elegans and identifiesa novel gene
family. Cell 85: 829- 839, 1996.

GAM63 348 CUL3 Michel, J. J.; Xiong, Y.: Human CUL- 1, but not other cullin familymembers, 4 A c
selectively interacts with SKP1 to form a complex with SKP2and cyclin A.
Cell Growth Differ. 9: 435- 449, 1998.

GAM63 348 DAG1 Arahata, K.; Hayashi, Y. K.; Mizuno, Y.; Yoshida, M.; Ozawa, E.: Dystrophin- 4 A c
associated glycoprotein and dystrophin co- localisationat sarcolemma in
Fukuyama congenital muscular dystrophy. (Letter) Lancet 342:623- 624, 1993.

GAM63 348 DAG1 Campanelli, J. T.; Roberds, S. L.; Campbell, K. P.; Scheller, R.H.: A role 4 A c
for dystrophin- associated glycoproteins and utrophin inagrin- induced AChR
clustering. Cell 77: 663- 674, 1994.

GAM63 348 DAG1 Cao, W.; Henry, M. D.; Borrow, P.; Yamada, H.; Elder, J. H.; Ravkov,E. V.; 4 A c
Nichol, S. T.; Compans, R. W.; Campbell, K. P.; Oldstone, M.B. A.:
Identification of alpha- dystroglycan as a receptor for
lymphocyticchoriomeningitis virus and Lassa fever virus. Science 282: 2079-
2081,1998.

GAM63 348 DAG1 Cohn, R. D.; Henry, M. D.; Michele, D. E.; Barresi, R.; Saito,F.; Moore, S. 4 A c
A.; Flanagan, J. D.; Skwarchuk, M. W.; Robbins, M. E.;Mendell, J. R.;
Williamson, R. A.; Campbell, K. P.: Disruption ofDag1 in differentiated
skeletal muscle reveals a role for dystroglycanin muscle regeneration. Cell
110: 639- 648, 2002.

GAM63 348 DAG1 Cote, P. D.; Moukhles, H.; Lindenbaum, M.; Carbonetto, S.: Chimaericmice 4 A c
deficient in dystroglycans develop muscular dystrophy and havedisrupted
myoneural synapses. Nature Genet. 23: 338- 342, 1999.

GAM63 348 DAG1 Gee, S. H.; Montanaro, F.; Lindenbaum, M. H.; Carbonetto, S.:Dystroglycan- 4 A c
alpha, a dystrophin- associated glycoprotein, is a functionalagrin receptor.
Cell 77: 675- 686, 1994.

GAM63 348 DAG1 Gorecki, D. C.; Derry, J. M. J.; Barnard, E. A.: Dystroglycan:brain 4 A c
localisation and chromosome mapping in the mouse. Hum. Molec.Genet. 3: 1589-
1597, 1994.

GAM63 348 DAG1 Hayashi, Y. K.; Ogawa, M.; Tagawa, K.; Noguchi, S.; Ishihara, T.;Nonaka, I.; 4 A c
Arahata, K.: Selective deficiency of alpha- dystroglycanin Fukuyama- type
congenital muscular dystrophy. Neurology 57: 115- 121,2001.

GAM63 348 DAG1 Henry, M. D.; Campbell, K. P.: A role for dystroglycan in basementmembrane 4 A c
assembly. Cell 95: 859- 970, 1998.

GAM63 348 DAG1 Ibraghimov- Beskrovnaya, O.; Ervasti, J. M.; Leveille, C. J.; Slaughter,C. 4 A c
A.; Sernett, S. W.; Campbell, K. P.: Primary structure of dystrophin-

associatedglycoproteins linking dystrophin to the extracellular matrix. Nature 355:696- 702, 1992.

GAM63 348 DAG1 Ibraghimov- Beskrovnaya, O.; Milatovich, A.; Ozcelik, T.; Yang,B.; Francke, U.; Campbell, K. P.: Dystroglycan: tissue distribution,human muscle cDNA, genomic structure and chromosome mapping. (Abstract) Am.J. Hum. Genet. 51 (suppl.): A130 only, 1992. 4 A c

GAM63 348 DAG1 Ibraghimov- Beskrovnaya, O.; Milatovich, A.; Ozcelik, T.; Yang,B.; Koepnick, K.; Francke, U.; Campbell, K. P.: Human dystroglycan:skeletal muscle cDNA, genomic structure, origin of tissue specificisoforms and chromosomal localization. Hum. Molec. Genet. 2: 1651- 1657,1993. 4 A c

GAM63 348 DAG1 Ma, J.; Nastuk, M. A.; McKechnie, B. A.; Fallon, J. R.: The agrinreceptor: localization in the postsynaptic membrane, interaction withagrin, and relationship to the acetylcholine receptor. J. Biol. Chem. 268:25108- 25117, 1993. 4 A c

GAM63 348 DAG1 Matsumura, K.; Nonaka, I.; Campbell, K. P.: Abnormal expressionof dystrophin- associated proteins in Fukuyama- type congenital musculardystrophy. Lancet 341: 521- 522, 1993. 4 A c

GAM63 348 DAG1 Matsumura, K.; Tome, F. M. S.; Collin, H.; Azibi, K.; Chaouch,M.; Kaplan, J.- C.; Fardeau, M.; Campbell, K. P.: Deficiency of the50K dystrophin- associated glycoprotein in severe childhood autosomalrecessive muscular dystrophy. Nature 359: 320- 322, 1992. 4 A c

GAM63 348 DAG1 Matsumura, K.; Tome, F. M. S.; Ionasescu, V.; Ervasti, J. M.;Anderson, R. D.; Romero, N. B.; Simon, D.; Recan, D.; Kaplan, J.- C.;Fardeau, M.; Campbell, K. P.: Deficiency of dystrophin- associatedproteins in Duchenne muscular dystrophy patients lacking COOH- terminaldomains of dystrophin. J. Clin. Invest. 92: 866- 871, 1993. 4 A c

GAM63 348 DAG1 Michele, D. E.; Barresi, R.; Kanagawa, M.; Saito, F.; Cohn, R.D.; Satz, J. S.; Dollar, J.; Nishino, I.; Kelley, R. I.; Somer, H.;Straub, V.; Mathews, K. D.; Moore, S. A.; Campbell, K. P.: Post- translationaldisruption of dystroglycan- ligand interactions in congenital musculardystrophies. Nature 418: 417- 422, 2002. 4 A c

GAM63 348 DAG1 Moore, S. A.; Saito, F.; Chen, J.; Michele, D. E.; Henry, M. D.;Messing, A.; Cohn, R. D.; Ross- Barta, S. E.; Westra, S.; Williamson,R. A.; Hoshi, T.; Campbell, K. P.: Deletion of brain dystroglycanrecapitulates aspects of congenital muscular dystrophy. Nature 418:422- 425, 2002. 4 A c

GAM63 348 DAG1 Rambukkana, A.; Yamada, H.; Zanazzi, G.; Mathus, T.; Salzer, J.L.; Yurchenco, P. D.; Campbell, K. P.; Fischetti, V. A.: Role ofalpha- dystroglycan as a Schwann cell receptor for Mycobacterium leprae. Science 282:2076- 2078, 1998. 4 A c

GAM63 348 DAG1 Sealock, R.; Froehner, S. C.: Dystrophin- associated proteinsand synapse formation: is alpha- dystroglycan the agrin receptor? Cell 77:617- 619, 1994. 4 A c

GAM63 348 DAG1 Spear, P. G.: A welcome mat for leprosy and Lassa fever. Science 282:1999- 2000, 1998. 4 A c

GAM63 348 DAG1 Tinsley, J. M.; Blake, D. J.; Zuellig, R. A.; Davies, K. E.:Increasing complexity of the dystrophin- associated protein complex. Proc.Nat. Acad. Sci. 91: 8307- 8313, 1994. 4 A c

GAM63 348 DAG1 Williamson, R. A.; Henry, M. D.; Daniels, K. J.; Hrstka, R. F.;Lee, J. C.; Sunada, Y.; Ibraghimov- Beskrovnaya, O.; Campbell, K. P.: Dystroglycan is essential for early embryonic development: disruptionof Reichert's membrane 4 A c

in Dag1- null mice. Hum. Molec. Genet. 6:831- 841, 1997.

GAM63 348 DAG1 Yamada, H.; Denzer, A. J.; Hori, H.; Tanaka, T.; Anderson, L.V. B.; Fujita, 4 A c
S.; Fukuta- Ohi, H.; Shimizu, T.; Ruegg, M. A.; Matsumura,K.: Dystroglycan
is a dual receptor for agrin and laminin- 2 in Schwanncell membrane. J.
Biol. Chem. 271: 23418- 23423, 1996.

GAM63 348 DAG1 Yamada, H.; Saito, F.; Fukuta- Ohi, H.; Zhong, D.; Hase, A.; Arai,K.; 4 A c
Okuyama, A.; Maekawa, R.; Shimizu, T.; Matsumura, K.: Processingof beta-
dystroglycan by matrix metalloproteinase disrupts the linkbetween the
extracellular matrix and cell membrane via the dystroglycancomplex. Hum.
Molec. Genet. 10: 1563- 1569, 2001.

GAM63 348 DDX11 Amann, J.; Kidd, V. J.; Lahti, J. M.: Characterization of putativehuman 4 A c
homologues of the yeast chromosome transmission fidelity gene,CHL1. J. Biol.
Chem. 272: 3823- 3832, 1997.

GAM63 348 DDX11 Amann, J.; Valentine, M.; Kidd, V. J.; Lahti, J. M.: Localizationof Chl1- 4 A c
related helicase genes to human chromosome regions 12p11 and12p13:
similarity between parts of these genes and conserved humantelomeric-
associated DNA. Genomics 32: 260- 265, 1996.

GAM63 348 DDX11 Frank, S.; Werner, S.: The human homologue of the yeast CHL1 geneis a novel 4 A c
keratinocyte growth factor- regulated gene. J. Biol. Chem. 271:24337- 24340,
1996.

GAM63 348 DVL3 Bui, T. D.; Beier, D. R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; 4 A c
Kaklamanis, L.; Kearney, L.; Regan, R.; Sussman, D. J.; Harris,A. L.: cDNA
cloning of a human dishevelled DVL- 3 gene, mapping to3q27, and expression
in human breast and colon carcinomas. Biochem.Biophys. Res. Commun. 239:
510- 516, 1997.

GAM63 348 DVL3 Klingensmith, J.; Nusse, R.; Perrimon, N.: The Drosophila segmentpolarity 4 A c
gene dishevelled encodes a novel protein required for responseto wingless
signal. Genes Dev. 8: 118- 130, 1994.

GAM63 348 DVL3 Pizzuti, A.; Amati, F.; Calabrese, G.; Mari, A.; Colosimo, A; Silani,V.; 4 A c
Giardino, L.; Ratti, A.; Penso, D.; Calza, L.; Palka, G.; Scarlato,G.;
Novelli, G.; Dallapicolla, B.: cDNA characterization and chromosomalmapping
of two human homologs of the Drosophila dishevelled polaritygene. Hum.
Molec. Genet. 5: 953- 958, 1996.

GAM63 348 DVL3 Semenov, M. V.; Snyder, M.: Human dishevelled genes constitutea DHR- 4 A c
containing multigene family. Genomics 42: 302- 310, 1997.

GAM63 348 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; 4 A c
Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.:
Neurodevelopmental delay, motor abnormalities and cognitive deficitsin
transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's
syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001.

GAM63 348 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the 4 A c
Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262-
265, 1997.

GAM63 348 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A 4 A c
potassium channel mutation in weaver mice implicates membraneexcitability in
granule cell differentiation. Nature Genet. 11:126- 129, 1995.

GAM63 348 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; 4 A c
Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk
gene from 'the Down syndrome critical region' of chromosome 21.
Biochem.Biophys. Res. Commun. 225: 92- 99, 1996.

GAM63 348 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.; Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in transgenic mice implicates minibrain in learningdefects associated with Down syndrome. Nature Genet. 16: 28- 36,1997. 4 A c

GAM63 348 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to chromosome 16, localizes to the nucleus, and can form multimers. Biochem.Biophys. Res. Commun. 231: 640- 644, 1997. 4 A c

GAM63 348 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.; Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the Drosophila minibrain gene: human homologue maps to 21q22.2in the Down syndrome 'critical region.' Genomics 38: 331- 339, 1996. 4 A c

GAM63 348 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein kinase family involved in postembryonic neurogenesisin Drosophila. Neuron 14: 287- 301, 1995. 4 A c

GAM63 348 DYRK1B Leder, S.; Weber, Y.; Altafaj, X.; Estivill, X.; Joost, H.- G.;Becker, W.: Cloning and characterization of DYRK1B, a novel memberof the DYRK family of protein kinases. Biochem. Biophys. Res. Commun. 254:474- 479, 1999. 4 A c

GAM63 348 DYRK1B Lee, K.; Deng, X.; Friedman, E.: Mirk protein kinase is a mitogen- activatedprotein kinase substrate that mediates survival of colon cancer cells. CancerRes. 60: 3631- 3637, 2000. 4 A c

GAM63 348 EGR3 Morris, M. E.; Viswanathan, N.; Kuhlman, S.; Davis, F. C.; Weitz,C. J.: A screen for genes induced in the suprachiasmatic nucleusby light. Science 279: 1544- 1547, 1998. 4 A c

GAM63 348 EGR3 Patwardhan, S.; Gashler, A.; Siegel, M. G.; Chang, L. C.; Joseph,L. J.; Shows, T. B.; Le Beau, M. M.; Sukhatme, V. P.: EGR3, a novelmember of the Egr family of genes encoding immediate- early transcriptionfactors. Oncogene 6: 917- 928, 1991. 4 A c

GAM63 348 EGR3 Tourtellotte, W. G.; Milbrandt, J.: Sensory ataxia and musclespindle agenesis in mice lacking the transcription factor Egr3. NatureGenet. 20: 87- 91, 1998. 4 A c

GAM63 348 ENO2 Craig, S. P.; Day, I. N. M.; Thompson, R. J.; Craig, I. W.: Localisationof neurone- specific enolase (ENO2) to 12p13. Cytogenet. Cell Genet. 54:71- 73, 1990. 4 A c

GAM63 348 ENO2 Craig, S. P.; Day, I. N. M.; Thompson, R. J.; Craig, I. W.: Localizationof human neurone- specific enolase to chromosome 12p13. (Abstract) Cytogenet.Cell Genet. 51: 980 only, 1989. 4 A c

GAM63 348 ENO2 Feo, S.; Oliva, D.; Barbieri, G.; Xu, W.; Fried, M.; Giallongo,A.: The gene for the muscle- specific enolase is on the short armof human chromosome 17. Genomics 6: 192- 194, 1990. 4 A c

GAM63 348 ENO2 Grzeschik, K.- H.: Assignment of human genes: beta- glucuronidaseto chromosome 7, adenylate kinase- 1 to 9, a second enzyme with enolaseactivity to 12, and mitochondrial IDH to 15. Cytogenet. Cell Genet. 16:142- 148, 1976. Note: Alternate: Birth Defects Orig. Art. Ser. 12(7):142- 148, 1976. 4 A c

GAM63 348 ENO2 Herbschleb- Voogt, E.; Monteba- van Heuvel, M.; Wijnen, L. M. M.;Westerveld, A.; Pearson, P. L.; Meera Khan, P.: Chromosomal assignmentand regional localization of CS, ENO- 2, GAPDH, LDH- B, PEP- B and TPIin man- rodent cell hybrids. Cytogenet. Cell Genet. 22: 482- 486,1978. 4 A c

GAM63 348 ENO2 Hinks, L. J.; Day, I. N. M.: Further studies of enolase loci.(Abstract) 4 A c
Cytogenet. Cell Genet. 58: 1854 only, 1991.

GAM63 348 ENO2 Law, M. L.; Kao, F.: Regional mapping of the gene coding for enolase- 2on 4 A c
human chromosome 12. J. Cell Sci. 53: 245- 254, 1982.

GAM63 348 ENO2 Mattei, J. F.; Baeteman, M. A.; Mattei, M. G.; Ardissonne, J. P.;Giraud, F.: 4 A c
Regional assignments of CS and ENO2 on chromosome 12.(Abstract) Cytogenet.
Cell Genet. 32: 297 only, 1982.

GAM63 348 ENO2 Oliva, D.; Cali, L.; Feo, S.; Giallongo, A.: Complete structureof the human 4 A c
gene encoding neuron- specific enolase. Genomics 10:157- 165, 1991.

GAM63 348 ERBB3 Carraway, K. L., III; Sliwkowski, M. X.; Akita, R.; Platko, J.V.; Guy, P. 4 A c
M.; Nuijens, A.; Diamonti, A. J.; Vandlen, R. L.; Cantley,L. C.; Cerione, R.
A.: The erbB3 gene product is a receptor for heregulin. J.Biol. Chem. 269:
14303- 14306, 1994.

GAM63 348 ERBB3 Cho, H.- S.; Leahy, D. J.: Structure of the extracellular regionof HER3 4 A c
reveals an interdomain tether. Science 297: 1330- 1333, 2002.

GAM63 348 ERBB3 Kraus, M. H.; Issing, W.; Miki, T.; Popescu, N. C.; Aaronson, S.A.: 4 A c
Isolation and characterization of ERBB3, a third member of theERBB/epidermal
growth factor receptor family: evidence for overexpressionin a subset of
human mammary tumors. Proc. Nat. Acad. Sci. 86: 9193- 9197,1989.

GAM63 348 ERBB3 Plowman, G. D.; Whitney, G. S.; Neubauer, M. G.; Green, J. M.;McDonald, V. 4 A c
L.; Todaro, G. J.; Shoyab, M.: Molecular cloning andexpression of an
additional epidermal growth factor receptor- relatedgene. Proc. Nat. Acad.
Sci. 87: 4905- 4909, 1990.

GAM63 348 FTL Aguilar- Martinez, P.; Biron, C.; Masmejean, C.; Jeanjean, P.; Schved,J.- 4 A c
F.: A novel mutation in the iron responsive element of ferritinL- subunit
gene as a cause for hereditary hyperferritinemia- cataractsyndrome. (Letter)
Blood 88: 1895- 1903, 1996.

GAM63 348 FTL Beaumont, C.; Leneuve, P.; Devaux, I.; Scoazec, J.- Y.; Berthier,M.; 4 A c
Loiseau, M.- N.; Grandchamp, B.; Bonneau, D.: Mutation in theiron responsive
element of the L ferritin mRNA in a family with dominanthyperferritinaemia
and cataract. Nature Genet. 11: 444- 446, 1995.

GAM63 348 FTL Brown, A. J. P.; Leibold, E. A.; Munro, H. N.: Isolation of cDNAclones for 4 A c
the light subunit of rat liver ferritin: evidence thatthe light subunit is
encoded by a multigene family. Proc. Nat. Acad.Sci. 80: 1265- 1269, 1983.

GAM63 348 FTL Camaschella, C.; Zecchina, G.; Lockitch, G.; Roetto, A.; Campanella,A.; 4 A c
Arosio, P.; Levi, S.: A new mutation (G51C) in the iron- responsiveelement
(IRE) of L- ferritin associated with hyperferritinaemia- cataractsyndrome
decreases the binding affinity of the mutated IRE for iron-
regulatoryproteins. Brit. J. Haemat. 108: 480- 482, 2000.

GAM63 348 FTL Caskey, J. H.; Jones, C.; Miller, Y. E.; Seligman, P. A.: Humanferritin gene 4 A c
is assigned to chromosome 19. Proc. Nat. Acad. Sci. 80:482- 486, 1983.

GAM63 348 FTL Cazzola, M.; Bergamaschi, G.; Tonon, L.; Arbustini, E.; Grasso,M.; Vercesi, 4 A c
E.; Barosi, G.; Bianchi, P. E.; Cairo, G.; Arosio, P.: Hereditary
hyperferritinemia- cataract syndrome: relationship betweenphenotypes and
specific mutations in the iron- responsive element offerritin light- chain
mRNA. Blood 90: 814- 821, 1997.

GAM63 348 FTL Cazzola, M.; Foglieni, B.; Bergamaschi, G.; Levi, S.; Lazzarino,M.; Arosio, 4 A c
P.: A novel deletion of the L- ferritin iron- responsiveelement responsible
for severe hereditary hyperferritinaemia- cataractsyndrome. Brit. J. Haemat.
116: 667- 670, 2002.

GAM63 348 FTL Curtis, A. R. J.; Fey, C.; Morris, C. M.; Bindoff, L. A.; Ince,P. G.; Chinnery, P. F.; Coulthard, A.; Jackson, M. J.; Jackson, A.P.; McHale, D. P.; Hay, D.; Barker, W. A.; Markham, A. F.; Bates,D.; Curtis, A.; Burn, J.: Mutation in the gene encoding ferritinlight polypeptide causes dominant adult- onset basal ganglia disease. NatureGenet. 28: 350- 354, 2001. 4 A c

GAM63 348 FTL Dorner, M. H.; Salfeld, J.; Will, H.; Leibold, E. A.; Vass, J.K.; Munro, H. N.: Structure of human ferritin light subunit messengerRNA: comparison with heavy subunit message and functional implications. Proc.Nat. Acad. Sci. 82: 3139- 3143, 1985. 4 A c

GAM63 348 FTL Filie, J. D.; Buckler, C. E.; Kozak, C. A.: Genetic mapping ofthe mouse ferritin light chain gene and 11 pseudogenes on 11 mousechromosomes. Mammalian Genome 9: 111- 113, 1998. 4 A c

GAM63 348 FTL Girelli, D.; Bozzini, C.; Zecchina, G.; Tinazzi, E.; Bosio, S.;Piperno, A.; Ramenghi, U.; Peters, J.; Levi, S.; Camaschella, C.;Corrocher, R.: Clinical, biochemical and molecular findings in aseries of families with hereditary hyperferritinaemia- cataract syndrome. Brit.J. Haemat. 115: 334- 340, 2001. 4 A c

GAM63 348 FTL Girelli, D.; Corrocher, R.; Bisceglia, L.; Olivieri, O.; De Franceschi,L.; Zelante, L.; Gasparini, P.: Molecular basis for the recentlydescribed hereditary hyperferritinemia- cataract syndrome: A mutationin the iron-responsive element of ferritin L- subunit gene (the 'Veronamutation'). Blood 86: 4050- 453, 1995. 4 A c

GAM63 348 FTL Girelli, D.; Corrocher, R.; Bisceglia, L.; Olivieri, O.; Zelante,L.; Panozzo, G.; Gasparini, P.: Hereditary hyperferritinemia- cataractsyndrome caused by a 29- base pair deletion in the iron responsiveelement of ferritin L- subunit gene. Blood 90: 2084- 2088, 1997. 4 A c

GAM63 348 FTL Girelli, D.; Olivieri, O.; De Franceschi, L.; Corrocher, R.; Bergamaschi,G.; Cazzola, M.: A linkage between hereditary hyperferritinaemianot related to iron overload and autosomal dominant congenital cataract. Brit.J. Haemat. 90: 931- 934, 1995. 4 A c

GAM63 348 FTL Hentze, M. W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi,W.; Drysdale, J.; Leonard, W. J.; Harford, J. B.; Klausner, R. D.: Cloning, characterization, expression, and chromosomal localizationof a human ferritin heavy- chain gene. Proc. Nat. Acad. Sci. 83:7226- 7230, 1986. 4 A c

GAM63 348 FTL Lebo, R. V.; Kan, Y. W.; Cheung, M.- C.; Jain, S. K.; Drysdale,J.: Human ferritin light chain gene sequences mapped to several sortedchromosomes. Hum. Genet. 71: 325- 328, 1985. 4 A c

GAM63 348 FTL Martin, M. E.; Fargion, S.; Brissot, P.; Pellat, B.; Beaumont,C.: A point mutation in the bulge of the iron- responsive elementof the L ferritin gene in two families with the hereditary hyperferritinemia- cataractsyndrome. Blood 91: 319- 323, 1998. 4 A c

GAM63 348 FTL McGill, J. R.; Boyd, D.; Barrett, K. J.; Drysdale, J. W.; Moore,C. M.: Localization of human ferritin H (heavy) and L (light) subunitsby in situ hybridization. (Abstract) Am. J. Hum. Genet. 36: 146S,1984. 4 A c

GAM63 348 FTL McLeod, J. L.; Craig, J.; Gumley, S.; Roberts, S.; Kirkland, M.A.: Mutation spectrum in Australian pedigrees with hereditary hyperferritinaemia-cataractsyndrome reveals novel and de novo mutations. Brit. J. Haemat. 118:1179- 1182, 2002. 4 A c

GAM63 348 FTL Mumford, A. D.; Vulliamy, T.; Lindsay, J.; Watson, A.: Hereditaryhyperferritinemia- cataract syndrome: two novel mutations in the L- ferritiniron- responsive element. (Letter) Blood 91: 367- 368, 1998. 4 A c

GAM63 348 FTL Munro, H. N.; Aziz, N.; Leibold, E. A.; Murray, M.; Rogers, J.;Vass, J. K.; 4 A c
White, K.: The ferritin genes: structure, expression,and regulation. Ann.
N.Y. Acad. Sci. 526: 113- 123, 1988.

GAM63 348 FTL Santoro, C.; Marone, M.; Ferrone, M.; Costanzo, F.; Colombo, M.;Minganti, 4 A c
C.; Cortese, R.; Silengo, L.: Cloning of the gene codingfor human L
apoferritin. Nucleic Acids Res. 14: 2863- 2876, 1986.

GAM63 348 FTL Watanabe, N.; Drysdale, J. W.: Evidence for distinct mRNAs forferritin 4 A c
subunits. Biochem. Biophys. Res. Commun. 98: 507- 511, 1981.

GAM63 348 FTL Worwood, M.; Brook, J. D.; Cragg, S. J.; Hellkuhl, B.; Jones,B. M.; Perera, 4 A c
P.; Roberts, S. H.; Shaw, D. J.: Assignment of humanferritin genes to
chromosomes 11 and 19q13.3- 19qter. Hum. Genet. 69:371- 374, 1985.

GAM63 348 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, 4 A c
J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2
in the allergic response. Nature 412: 186- 190,2001.

GAM63 348 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 4 A c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM63 348 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; 4 A c
Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab-
family adapter proteins act downstream of cytokine and growthfactor
receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999.

GAM63 348 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH 4 A c
mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell
Genet. 94: 39- 42, 2001.

GAM63 348 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology 4 A c
domain- containing adapter protein, acts to uncouple signalingfrom ERK
kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999.

GAM63 348 GATA4 Arceci, R. J.; King, A. A.; Simon, M. C.; Orkin, S. H.; Wilson,D. B.: Mouse 4 A c
GATA- 4: a retinoic acid- inducible GATA- binding transcriptionfactor
expressed in endodermally derived tissues and heart. Molec.Cell. Biol. 13:
2235- 2246, 1993.

GAM63 348 GATA4 Cirillo, L. A.; Lin, F. R.; Cuesta, I.; Friedman, D.; Jarnik, M.;Zaret, K. 4 A c
S.: Opening of compacted chromatin by early developmentaltranscription
factors HNF3(FoxA) and GATA- 4. Molec. Cell 9: 279- 289,2002.

GAM63 348 GATA4 Crispino, J. D.; Lodish, M. B.; Thurberg, B. L.; Litovsky, S. H.;Collins, 4 A c
T.; Molkentin, J. D.; Orkin, S. H.: Proper coronary vasculardevelopment and
heart morphogenesis depend on interaction of GATA- 4with FOG cofactors.
Genes Dev. 15: 839- 844, 2001.

GAM63 348 GATA4 Evans, T.; Reitman, M.; Felsenfeld, G.: An erythrocyte- specificDNA- binding 4 A c
factor recognizes a regulatory sequence common to allchicken globin genes.
Proc. Nat. Acad. Sci. 85: 5976- 5980, 1988.

GAM63 348 GATA4 Hasegawa, K.; Lee, S. J.; Jobe, S. M.; Markham, B. E.; Kitsis,R. N.: cis- 4 A c
acting sequences that mediate induction of beta- myosinheavy chain gene
expression during left ventricular hypertrophy dueto aortic constriction.
Circulation 96: 3943- 3953, 1997.

GAM63 348 GATA4 Herzig, T. C.; Jobe, S. M.; Aoki, H.; Molkentin, J. D.; Cowley,A. W., Jr.; 4 A c
Izumo, S.; Markham, B. E.: Angiotensin II type- 1a receptorgene expression
in the heart: AP- 1 and GATA- 4 participate in the responseto pressure
overload. Proc. Nat. Acad. Sci. 94: 7543- 7548, 1997.

GAM63 348 GATA4 Huang, W.- Y.; Cukerman, E.; Liew, C.- C.: Identification of a GATAmotif in the cardiac alpha- myosin heavy- chain- encoding gene and isolationof a human GATA- 4 cDNA. Gene 155: 219- 223, 1995. 4 A c

GAM63 348 GATA4 Huang, W.- Y.; Heng, H. H. Q.; Liew, C.- C.: Assignment of the humanGATA4 gene to 8p23.1- p22 using fluorescence in situ hybridizationanalysis. Cytogenet. Cell Genet. 72: 217- 218, 1996. 4 A c

GAM63 348 GATA4 Kennedy, S. J.; Teebi, A. S.; Adatia, I.; Teshima, I.: Inheritedduplication, dup(8)(p23.1p23.1)Pat, in a father and daughter withcongenital heart defects. (Letter) Am. J. Med. Genet. 104: 79- 80,2001. 4 A c

GAM63 348 GATA4 Ketola, I.; Pentikainen, V.; Vaskivuo, T.; Ilvesmaki, V.; Herva,R.; Dunkel, L.; Tapanainen, J. S.; Toppari, J.; Heikinheimo, M.:Expression of transcription factor GATA- 4 during human testiculardevelopment and disease. J. Clin. Endocr. Metab. 85: 3925- 3931,2000. 4 A c

GAM63 348 GATA4 Laitinen, M. P. E.; Anttonen, M.; Ketola, I.; Wilson, D. B.; Ritvos,O.; Butzow, R.; Heikinheimo, M.: Transcription factors GATA- 4 andGATA- 6 and a GATA family cofactor, FOG- 2, are expressed in human ovaryand sex cord-derived ovarian tumors. J. Clin. Endocr. Metab. 85:3476- 3483, 2000. 4 A c

GAM63 348 GATA4 Molkentin, J. D.; Kalvakolanu, D. V.; Markham, B. E.: Transcriptionfactor GATA- 4 regulates cardiac muscle- specific expression of thealpha- myosin heavy- chain gene. Molec. Cell. Biol. 14: 4947- 4957,1994. 4 A c

GAM63 348 GATA4 Pehlivan, T.; Pober, B. R.; Brueckner, M.; Garrett, S.; Slaugh,R.; Van Rheeden, R.; Wilson, D. B.; Watson, M. S.; Hing, A. V.: GATA4haploinsufficiency in patients with interstitial deletion of chromosomeregion 8p23.1 and congenital heart disease. Am. J. Med. Genet. 83:201- 206, 1999. 4 A c

GAM63 348 GATA4 Vaskivuo, T. E.; Anttonen, M.; Herva, R.; Billig, H.; Dorland,M.; Te Velde, E. R.; Stenback, F.; Heikinheimo, M.; Tapanainen, J.S.: Survival of human ovarian follicles from fetal to adult life:apoptosis, apoptosis- related proteins, and transcription factor GATA- 4. J.Clin. Endocr. Metab. 86: 3421-3429, 2001. 4 A c

GAM63 348 GATA4 White, R. A.; Dowler, L. L.; Pasztor, L. M.; Gatson, L. L.; Adkison,L. R.; Angeloni, S. V.; Wilson, D. B.: Assignment of the transcriptionfactor GATA4 gene to human chromosome 8 and mouse chromosome 14: Gata4is a candidate gene for Ds (disorganization). Genomics 27: 20- 26,1995. 4 A c

GAM63 348 GBF1 Mansour, S. J.; Herbrick, J.- A.; Scherer, S. W.; Melancon, P.:Human GBF1 is a ubiquitously expressed gene of the Sec7 domain familymapping to 10q24. Genomics 54: 323- 327, 1998. 4 A c

GAM63 348 GBF1 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 4 A c

GAM63 348 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a novel secretin- like human G- protein- coupledreceptor gene. Genomics 55: 296- 305, 1999. 4 A c

GAM63 348 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected with mRNA differential display using human melanoma celllines with different metastatic potential. FEBS Lett. 446: 292- 298,1999. 4 A c

GAM63 348 GYS1 Browner, M. F.; Nakano, K.; Bang, A. G.; Fletterick, R. J.: Humanmuscle glycogen synthase cDNA sequence: a negatively charged proteinwith an asymmetric charge distribution. Proc. Nat. Acad. Sci. 86:1443- 1447, 1989. 4 A c

GAM63 348 GYS1 Groop, L. C.; Kankuri, M.; Schalin- Jantti, C.; Ekstrand, A.; Nikula- ljas,P.; Widen, E.; Kuismanen, E.; Eriksson, J.; Franssila- Kallunki, A.;Saloranta, C.; Koskimies, S.: Association between polymorphism ofthe glycogen synthase gene and non- insulin- dependent diabetes mellitus. NewEng. J. Med. 328: 10- 14, 1993. 4 A c

GAM63 348 GYS1 Huang, X.; Vaag, A.; Hansson, M.; Weng, J.; Laurila, E.; Groop,L.: Impaired insulin- stimulated expression of the glycogen synthasegene in skeletal muscle of type 2 diabetic patients is acquired ratherthan inherited. J. Clin. Endocr. Metab. 85: 1584- 1590, 2000. 4 A c

GAM63 348 GYS1 Kadowaki, T.; Kadowaki, H.; Yazaki, Y.: Polymorphism of the glycogensynthase gene and non- insulin- dependent diabetes mellitus. (Letter) NewEng. J. Med. 328: 1569, 1993. 4 A c

GAM63 348 GYS1 Lehto, M.; Stoffel, M.; Groop, L.; Espinosa, R., III; Le Beau,M. M.; Bell, G. I.: Assignment of the gene encoding glycogen synthase(GYS) to human chromosome 19, band q13.3. Genomics 15: 460- 461,1993. 4 A c

GAM63 348 GYS1 Seldin, M. F.; Mott, D.; Bhat, D.; Petro, A.; Kuhn, C. M.; Kingsmore,S. F.; Bogardus, C.; Opara, E.; Feinglos, M. N.; Surwit, R. S.: Glycogensynthase: a putative locus for diet- induced hyperglycemia. J. Clin.Invest. 94: 269- 276, 1994. 4 A c

GAM63 348 GYS1 Zouali, H.; Velho, G.; Froguel, P.: Polymorphism of the glycogensynthase gene and non- insulin- dependent diabetes mellitus. (Letter) NewEng. J. Med. 328: 1568, 1993. 4 A c

GAM63 348 HIVEP3 Hicar, M. D.; Liu, Y.; Allen, C. E.; Wu, L.- C.: Structure of thehuman zinc finger protein HIVEP3: molecular cloning, expression, exon- intronstructure, and comparison with paralogous genes HIVEP1 and HIVEP2. Genomics 71:89- 100, 2001. 4 A c

GAM63 348 HIVEP3 Oukka, M.; Kim, S. T.; Lugo, G.; Sun, J.; Wu, L.- C.; Glimcher,L. H.: A mammalian homolog of Drosophila schnurri, KRC, regulatesTNF receptor- driven responses and interacts with TRAF2. Molec. Cell 9:121- 131, 2002. 4 A c

GAM63 348 HNRPDL Doi, A.; Shiosaka, T.; Takaoka, Y.; Yanagisawa, K.; Fujita, S.: Molecular cloning of the cDNA encoding A+U- rich element RNA bindingfactor. Biochim. Biophys. Acta 1396: 51- 56, 1998. 4 A c

GAM63 348 HNRPDL Kamei, D.; Tsuchiya, N.; Yamazaki, M.; Meguro, H.; Yamada, M.:Two forms of expression and genomic structure of the human heterogeneousnuclear ribonucleoprotein D- like JKTBP gene (HNRPDL). Gene 228:13- 22, 1999. 4 A c

GAM63 348 HNRPDL Tsuchiya, N.; Kamei, D.; Takano, A.; Matsui, T.; Yamada, M.: Cloningand characterization of a cDNA encoding a novel heterogeneous nuclearribonucleoprotein- like protein and its expression in myeloid leukemiacells. J. Biochem. 123: 499- 507, 1998. 4 A c

GAM63 348 IDH3G Brenner, V.; Nyakatura, G.; Rosenthal, A.; Platzer, M.: Genomicorganization of two novel genes on human Xq28: compact head to headarrangement of IDH-gamma and TRAP- delta is conserved in rat and mouse. Genomics 44:8- 14, 1997. 4 A c

GAM63 348 IDH3G Fink, J. M.; Dobyns, W. B.; Guerrini, R.; Hirsch, B. A.: Identificationof a duplication of Xq28 associated with bilateral periventricularnodular heterotopia. Am. J. Hum. Genet. 61: 379- 387, 1997. 4 A c

GAM63 348 IDH3G Fox, J. W.; Lamperti, E. D.; Eksioglu, Y. Z.; Hong, S. E.; Feng,Y.; Graham, 4 A c

D. A.; Scheffer, I. E.; Dobyns, W. B.; Hirsch, B. A.;Radtke, R. A.; Berkovic, S. F.; Huttenlocher, P. R.; Walsh, C. A.: Mutations in filamin 1 prevent migration of cerebral cortical neuronsin human periventricular heterotopia. Neuron 21: 1315- 1325, 1998.

GAM63 348 IL17B Li, H.; Chen, J.; Huang, A.; Stinson, J.; Heldens, S.; Foster,J.; Dowd, P.; Gurney, A. L.; Wood, W. I.: Cloning and characterizationof IL- 17B and IL- 17C, two new members of the IL- 17 cytokine family. Proc.Nat. Acad. Sci. 97: 773- 778, 2000. 4 A c

GAM63 348 IL17B Shi, Y.; Ullrich, S. J.; Zhang, J.; Connolly, K.; Grzegorzewski,K. J.; Barber, M. C.; Wang, W.; Wathen, K.; Hodge, V.; Fisher, C.L.; Olsen, H.; Ruben, S. M.; Knyazev, I.; Cho, Y. H.; Kao, V.; Wilkinson,K. A.; Carrell, J. A.; Ebner, R.: A novel cytokine receptor- ligandpair: identification, molecular characterization, and in vivo immunomodulatoryactivity. J. Biol. Chem. 275: 19167- 19176, 2000. 4 A c

GAM63 348 IRF2 Harada, H.; Kitagawa, M.; Tanaka, N.; Yamamoto, H.; Harada, K.;Ishihara, M.; Taniguchi, T.: Anti- oncogenic and oncogenic potentialsof interferon regulatory factors- 1 and - 2. Science 259: 971- 974,1993. 4 A c

GAM63 348 IRF2 Harada, H.; Takahashi, E.- I.; Itoh, S.; Harada, K.; Hori, T.- A.;Taniguchi, T.: Structure and regulation of the human interferon regulatoryfactor 1 (IRF- 1) and IRF- 2 genes: implications for a gene networkin the interferon system. Molec. Cell. Biol. 14: 1500- 1509, 1994. 4 A c

GAM63 348 IRF2 Hida, S.; Ogasawara, K.; Sato, K.; Abe, M.; Takayanagi, H.; Yokochi,T.; Sato, T.; Hirose, S.; Shirai, T.; Taki, S.; Taniguchi, T.: CD8+T cell-mediated skin disease in mice lacking IRF- 2, the transcriptionalattenuator of interferon- alpha/beta signaling. Immunity 13: 643- 655,2000. 4 A c

GAM63 348 IRF2 Ko, J.; Gendron- Fitzpatrick, A.; Splitter, G. A.: Susceptibilityof IFN regulatory factor- 1 and IFN consensus sequence binding protein-deficientmice to brucellosis. J. Immun. 168: 2433- 2440, 2002. 4 A c

GAM63 348 IRF2 Nishio, Y.; Noguchi, E.; Ito, S.; Ichikawa, E.; Umebayashi, Y.;Otsuka, F.; Arinami, T.: Mutation and association analysis of theinterferon regulatory factor 2 gene (IRF2) with atopic dermatitis. J.Hum. Genet. 46: 664- 667, 2001. 4 A c

GAM63 348 ITIH1 Bost, F.; Bourguignon, J.; Martin, J.- P.; Sesboue, R.; Thiberville,L.; Diarra- Mehrpour, M.: Isolation and characterization of the humaninter-alpha- trypsin inhibitor heavy- chain H1 gene. Europ. J. Biochem. 218:283-291, 1993. 4 A b

GAM63 348 ITIH1 Diarra- Mehrpour, M.; Bourguignon, J.; Bost, F.; Sesboue, R.; Muschio,F.; Sarafan, N.; Martin, J.- P.: Human inter- alpha- trypsin inhibitor:full-length cDNA sequence of the heavy chain H1. Biochim. Biophys.Acta 1132: 114-118, 1992. 4 A b

GAM63 348 ITIH1 Diarra- Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesboue,R.; Muschio- Bonnet, F.; Martin, J.- P.: Tandem orientation of theinter- alpha-trypsin inhibitor heavy chain H1 and H3 genes. Biochim.Biophys. Acta 1219: 551- 554, 1994. 4 A b

GAM63 348 ITIH1 Diarra- Mehrpour, M.; Bourguignon, J.; Sesboue, R.; Mattei, M.- G.;Passage, E.; Salier, J.- P.; Martin, J.- P.: Human plasma inter- alpha-trypsininhibitor is encoded by four genes on three chromosomes. Europ. J.Biochem. 179: 147- 154, 1989. 4 A b

GAM63 348 ITIH1 Diarra- Mehrpour, M.; Sarafan, N.; Bourguignon, J.; Bonnet, F.;Bost, F.; Martin, J.- P.: Human inter- alpha- trypsin inhibitor heavychain H3 gene: 4 A b

genomic organization, promoter analysis, and gene linkage. J.Biol. Chem. 273: 26809- 26819, 1998.

GAM63 348 ITIH1 Ding, M.; Umetsu, K.; Yuasa, I.; Sato, M.; Harada, A.; Suzuki,T.: Molecular basis of inter- alpha- trypsin inhibitor heavy chainH1 (ITIH1) polymorphism. Hum. Genet. 95: 435- 436, 1995. 4 A b

GAM63 348 ITIH1 Leveillard, T.; Salier, J. P.; Sesboue, R.; Bourguignon, J.; Diarra-Mehrpour,M.; Martin, J. P.: Sst I RFLP in the human inter- alpha- trypsin inhibitorheavy chain gene ITIH1. Nucleic Acids Res. 16: 11852 only, 1988. 4 A b

GAM63 348 ITIH1 Salier, J. P.; Diarra- Mehrpour, M.; Sesboue, R.; Bourguignon, J.;Benarous, R.; Ohkubo, I.; Kurachi, S.; Kurachi, K.; Martin, J. P.: Isolation and characterization of cDNAs encoding the heavy chainof human inter- alpha-trypsin inhibitor (IATI): unambiguous evidencefor multipolypeptide chain structure of IATI. Proc. Nat. Acad. Sci. 84:8272- 8276, 1987. 4 A b

GAM63 348 ITIH1 Vogt, U.; Cleve, H.: A 'new' genetic polymorphism of a human serumprotein: inter- alpha- trypsin- inhibitor. Hum. Genet. 84: 151- 154,1990. 4 A b

GAM63 348 ITIH1 Vogt, U.; Sesboue, R.; Bourguignon, J.; Diarra- Mehrpour, M.; Martin,J.- P.; Cleve, H.: The polymorphism of the plasma inter- alpha- trypsininhibitor (ITI) and its relationship to the heavy chain H1 subunitgene (ITIH1) at 3p211- 212. Hum. Genet. 94: 39- 44, 1994. 4 A b

GAM63 348 ITPKB Erneux, C.; Roeckel, N.; Takazawa, K.; Mailleux, P.; Vassart, G.;Mattei, M. G.: Localization of the genes for human inositol 1,4,5- trisphosphate3-kinase A (ITPKA) and B (ITPKB) to chromosome regions 15q14- q21 and1q41-q43, respectively, by in situ hybridization. Genomics 14:546- 547, 1992. 4 A c

GAM63 348 ITPKB Takazawa, K.; Perret, J.; Dumont, J. E.; Erneux, C.: Molecularcloning and expression of a new putative inositol 1,4,5- trisphosphate3- kinase isoenzyme. Biochem. J. 278: 883- 886, 1991. 4 A c

GAM63 348 KCNA6 Albrecht, B.; Weber, K.; Pongs, O.: Characterization of a voltage-activatedK- channel gene cluster on human chromosome 12p13. Receptors Channels 3:213- 220, 1995. 4 A c

GAM63 348 KCNA6 Grupe, A.; Schroter, K. H.; Ruppersberg, J. P.; Stocker, M.; Drewes,T.; Beckh, S.; Pongs, O.: Cloning and expression of a human voltage-gatedpotassium channel: a novel member of the RCK potassium channel family. EMBOJ. 9: 1749- 1756, 1990. 4 A c

GAM63 348 KCNA6 Klocke, R.; Roberds, S. L.; Tamkun, M. M.; Gronemeier, M.; Augustin,A.; Albrecht, B.; Pongs, O.; Jockusch, H.: Chromosomal mapping inthe mouse of eight K(+)- channel genes representing the four Shaker- likesubfamilies Shaker, Shab, Shaw, and Shal. Genomics 18: 568- 574,1993. 4 A c

GAM63 348 KPNA1 Ayala- Madrigal, M. L.; Doerr, S.; Ramirez- Duenas, M. L.; Hansmann,I.: Assignment of karyopherin alpha 1 (KPNA1) to human chromosomeband 3q21 by in situ hybridization. Cytogenet. Cell Genet. 90: 58- 59,2000. 4 A c

GAM63 348 KPNA1 Conti, E.; Uy, M.; Leighton, L.; Blobel, G.; Kuriyan, J.: Crystallographicanalysis of the recognition of a nuclear localization signal by thenuclear import factor karyopherin alpha. Cell 94: 193- 204, 1998. 4 A c

GAM63 348 KPNA1 Cortes, P.; Ye, Z.- S.; Baltimore, D.: RAG- 1 interacts with therepeated amino acid motif of the human homologue of the yeast proteinSRP1. Proc. Nat. Acad. Sci. 91: 7633- 7637, 1994. 4 A c

GAM63 348 KPNB2 Bonifaci, N.; Moroianu, J.; Radu, A.; Blobel, G.: Karyopherinbeta- 2 mediates nuclear import of a mRNA binding protein. Proc. Nat.Acad. Sci. 94: 5055- 5060, 1997. 4 A c

GAM63 348 KPNB2 Michael, W. M.; Choi, M.; Dreyfuss, G.: A nuclear export signalin hnRNP A1: 4 A c

a signal- mediated, temperature- dependent nuclear proteinexport pathway. Cell 83: 415- 422, 1995.

GAM63 348 KPNB2 Pollard, V. W.; Michael, W. M.; Nakielny, S.; Siomi, M. C.; Wang,F.; Dreyfuss, G.: A novel receptor- mediated nuclear protein importpathway. Cell 86: 985- 994, 1996. 4 A c

GAM63 348 LAMB1 Bonneau, D.; Huret, J. L.; Godeau, G.; Couet, D.; Putterman, M.;Tanzer, J.; Babin, P.; Larregue, M.: Recurrent ctb(7)(q31.3) andpossible laminin involvement in a neonatal cutis laxa with a Marfanphenotype. Hum. Genet. 87: 317- 319, 1991. 4 A c

GAM63 348 LAMB1 Buchanan, R.; Wyatt, G. P.: Marfan's syndrome presenting as anintrapartum death. Arch. Dis. Child. 60: 1074- 1076, 1985. 4 A c

GAM63 348 LAMB1 Burgeson, R. E.; Chiquet, M.; Deutzmann, R.; Ekblom, P.; Engel,J.; Kleinman, H.; Martin, G. R.; Meneguzzi, G.; Paulsson, M.; Sanes,J.; Timpl, R.; Tryggvason, K.; Yamada, Y.; Yurchenco, P. D.: A newnomenclature for the laminins. Matrix Biol. 14: 209- 211, 1994. 4 A c

GAM63 348 LAMB1 Day, D. L.; Burke, B. A.: Pulmonary emphysema in a neonate withMarfan syndrome. Pediat. Radiol. 16: 518- 521, 1986. 4 A c

GAM63 348 LAMB1 Elliott, R. W.; Barlow, D.; Hogan, B. L. M.: Linkage of genesfor laminin B1 and B2 subunits on chromosome 1 in mouse. In VitroCell Dev. Biol. 21: 477- 484, 1985. 4 A c

GAM63 348 LAMB1 Gross, D. M.; Robinson, L. K.; Smith, L. T.; Glass, N.; Rosenberg,H.; Duvic, M.: Severe perinatal Marfan syndrome. Pediatrics 84:83- 89, 1989. 4 A c

GAM63 348 LAMB1 Hohn, A. R.; Webb, H. M.: Cardiac studies of infant twins withMarfan's syndrome. Am. J. Dis. Child. 122: 526- 528, 1971. 4 A c

GAM63 348 LAMB1 Hopker, V. H.; Shewan, D.; Tessier- Lavigne, M.; Poo, M.; Holt,C.: Growth- cone attraction to netrin- 1 is converted to repulsionby laminin- 1. Nature 401: 69- 73, 1999. 4 A c

GAM63 348 LAMB1 Huret, J.; Bonneau, D.; Godeau, G.; Leheup, B.; Larregue, M.:Neonatal cutis laxa with Marfan habitus: this syndrome maps with B1laminin at the junction 7q31.3- q32. (Abstract) Cytogenet. Cell Genet. 58:1922 only, 1991. 4 A c

GAM63 348 LAMB1 Iwamoto, Y.; Robey, F. A.; Graf, J.; Sasaki, M.; Kleinman, H.K.; Yamada, Y.; Martin, G. R.: YIGSR, a synthetic laminin pentapeptide,inhibits experimental metastasis formation. Science 238: 1132- 1134,1987. 4 A c

GAM63 348 LAMB1 Jaye, M.; Modi, W. S.; Ricca, G. A.; Mudd, R.; Chiu, I.- M.; O'Brien,S. J.; Drohan, W. N.: Isolation of a cDNA clone for the human laminin- B1chain and its gene localization. Am. J. Hum. Genet. 41: 605- 615,1987. 4 A c

GAM63 348 LAMB1 Kleinman, H. K.: Personal Communication. Bethesda, Md. 1/7/1982. 4 A c

GAM63 348 LAMB1 Lababidi, Z.; Monzon, C.: Early cardiac manifestations of Marfan'ssyndrome in the newborn. Am. Heart J. 102: 943- 945, 1981. 4 A c

GAM63 348 LAMB1 Modi, W. S.; Jaye, M.; O'Brien, S. J.: Chromosomal localizationof a cDNA clone for the human B1 laminin chain. (Abstract) Cytogenet.Cell Genet. 46: 663 only, 1987. 4 A c

GAM63 348 LAMB1 Neimann, N.; Rauber, G.; Marchal, C.; Vidailhet, M.; Fall, M.: Maladie de Marfan chez un nouveau- ne avec atteintes polyviscerales:etude anatomo- clinique. Ann. Paediat. 15: 619- 624, 1968. 4 A c

GAM63 348 LAMB1 Pikkarainen, T.; Eddy, R.; Fukushima, Y.; Byers, M.; Shows, T.;Pihlajaniemi, T.; Saraste, M.; Tryggvason, K.: Human laminin B1 chain:a multidomain protein with gene (LAMB1) locus in the q22 region ofchromosome 7. J. Biol. Chem. 262: 10454- 10462, 1987. 4 A c

GAM63 348 LAMB1 Pikkarainen, T.; Savolainen, E.- R.; Tryggvason, K.: Nhe I andHinc II 4 A c

polymorphisms in the human laminin B1 chain gene on 7q22. NucleicAcids Res. 17: 4424 only, 1989.

GAM63 348 LAMB1 Sasaki, M.; Kato, S.; Kohno, K.; Martin, G. R.; Yamada, Y.: Sequenceof the cDNA encoding the laminin B1 chain reveals a multidomain proteincontaining cysteine- rich repeats. Proc. Nat. Acad. Sci. 84: 935- 939,1987. 4 A c

GAM63 348 LAMB1 Vuolteenaho, R.; Chow, L. T.; Tryggvason, K.: Structure of thehuman laminin B1 chain gene. J. Biol. Chem. 265: 15611- 15616, 1990. 4 A c

GAM63 348 MCP Bora, N. S.; Lublin, D. M.; Kumar, B. V.; Hockett, R. D.; Holers,V. M.; Atkinson, J. P.: Structural gene for human membrane cofactorprotein (MCP) of complement maps to within 100 kb of the 3- prime endof the C3b/C4b receptor gene. J. Exp. Med. 169: 597- 602, 1989. 4 A c

GAM63 348 MCP Cui, W.; Hourcade, D.; Post, T.; Greenlund, A. C.; Atkinson, J.P.; Kumar, V.: Characterization of the promoter region of the membranecofactor protein (CD46) gene of the human complement system and comparisonto a membrane cofactor protein- like genetic element. J. Immun. 151:4137- 4146, 1993. 4 A c

GAM63 348 MCP Dorig, R. E.; Marcil, A.; Chopra, A.; Richardson, C. D.: The humanCD46 molecule is a receptor for measles virus (Edmonston strain). Cell 75:295-305, 1993. 4 A c

GAM63 348 MCP Kallstrom, H.; Gill, D. B.; Albiger, B.; Liszewski, M. K.; Atkinson,J. P.; Jonsson, A.- B.: Attachment of Neisseria gonorrhoeae to thecellular pilus receptor CD46: identification of domains importantfor bacterial adherence. Cell. Microbiol. 3: 133- 143, 2001. 4 A c

GAM63 348 MCP Lublin, D. M.; Liszewski, M. K.; Post, T. W.; Arce, M. A.; LeBeau,M. M.; Rebentisch, M. B.; Lemons, R. S.; Seya, T.; Atkinson, J. P.: Molecular cloning and chromosomal localization of human complementmembrane cofactor protein (MCP): evidence for inclusion in the multigenefamily of complement-regulatory proteins. J. Exp. Med. 168: 181- 194,1988. 4 A c

GAM63 348 MCP Marie, J. C.; Astier, A. L.; Rivailler, P.; Rabourdin- Combe, C.;Wild, T. F.; Horvat, B.: Linking innate and acquired immunity: divergentrole of CD46 cytoplasmic domains in T cell- induced inflammation. NatureImmun. 3: 659-666, 2002. 4 A c

GAM63 348 MCP Post, T. W.; Liszewski, M. K.; Adams, E. M.; Tedja, I.; Miller,E. A.; Atkinson, J. P.: Membrane cofactor protein of the complementsystem: alternative splicing of serine/threonine/proline- rich exonsand cytoplasmic tails produces multiple isoforms that correlate withprotein phenotype. J. Exp. Med. 174: 93- 102, 1991. 4 A c

GAM63 348 MCP Purcell, D. F. J.; Johnstone, R. W.; McKenzie, I. F. C.: Identificationof four different CD46 (MCP) molecules with anti- peptide antibodies. Biochem.Biophys. Res. Commun. 180: 1091- 1097, 1991. 4 A c

GAM63 348 MCP Santoro, F.; Kennedy, P. E.; Locatelli, G.; Malnati, M. S.; Berger,E. A.; Lusso, P.: CD46 is a cellular receptor for human herpesvirus6. Cell 99: 817-827, 1999. 4 A c

GAM63 348 MCP Tatsuo, H.; Ono, N.; Tanaka, K.; Yanagi, Y.: SLAM (CDw150) isa cellular receptor for measles virus. Nature 406: 893- 897, 2000. 4 A c

GAM63 348 MGA Naim, H. Y.; Sterchi, E. E.; Lentze, M. J.: Structure, biosynthesis,and glycosylation of human small intestinal maltase- glucoamylase. J.Biol. Chem. 263: 19709- 19717, 1988. 4 A c

GAM63 348 MGA Nichols, B. L.; Eldering, J.; Avery, S.; Hahn, D.; Quaroni, A.;Sterchi, E.: Human small intestinal maltase- glucoamylase cDNA cloning:homology to sucrase- isomaltase. J. Biol. Chem. 273: 3076- 3081, 1998. 4 A c

GAM63 348 MGA Schuler, G. D.; Boguski, M. S.; Stewart, E. A.; Stein, L. D.; Gyapay,G.; 4 A c
Rice, K.; White, R. E.; Rodriguez- Tome, P.; Aggarwal, A.; Bajorek,E.;
Bentolila, S.; Birren, B. B.; Butler, A.; Castle, A. B.; Chiannilkulchai,N.;
Chu, A.; Clee, C.; Cowles, S.; Day, P. J. R.; Dibling, T.; and84 others: A
gene map of the human genome. Science 274: 540- 546,1996.

GAM63 348 MME Barker, P. E.; Shipp, M. A.; D'Adamio, L.; Masteller, E. L.; Reinherz,E. L.: 4 A c
The common acute lymphoblastic leukemia antigen gene mapsto chromosomal
region 3(q21- q27). J. Immun. 142: 283- 287, 1989.

GAM63 348 MME D'Adamio, L.; Shipp, M. A.; Masteller, E. L.; Reinherz, E. L.:Organization 4 A c
of the gene encoding common acute lymphoblastic leukemiaantigen (neutral
endopeptidase 24.11): multiple miniexons and separate5- prime untranslated
regions. Proc. Nat. Acad. Sci. 86: 7103- 7107,1989.

GAM63 348 MME Debiec, H.; Guigonis, V.; Mougenot, B.; Decobert, F.; Haymann,J.- P.; 4 A c
Bensman, A.; Deschenes, G.; Ronco, P. M.: Antenatal
membranousglomerulonephritis due to anti- neutral endopeptidase antibodies.
NewEng. J. Med. 346: 2053- 2060, 2002.

GAM63 348 MME Iwata, N.; Tsubuki, S.; Takaki, Y.; Shirotani, K.; Lu, B.; Gerard,N. P.; 4 A c
Gerard, C.; Hama, E.; Lee, H.- J.; Saido, T. C.: Metabolicregulation of
brain A- beta by neprilysin. Science 292: 1550- 1552,2001.

GAM63 348 MME Letarte, M.; Vera, S.; Tran, R.; Addis, J. B. L.; Onizuka, R. 4 A c
J.;Quackenbush, E. J.; Jongeneel, C. V.; McInnes, R. R.: Common
acutelymphocytic leukemia antigen is identical to neutral endopeptidase.
J.Exp. Med. 168: 1247- 1253, 1988.

GAM63 348 MME Shipp, M. A.; Vijayaraghavan, J.; Schmidt, E. V.; Masteller, E.L.; D'Adamio, 4 A c
L.; Hersh, L. B.; Reinherz, E. L.: Common acute lymphoblasticleukemia
antigen (CALLA) is active neutral endopeptidase 24.11
('enkephalinase'):direct evidence by cDNA transfection analysis. Proc. Nat.
Acad. Sci. 86:297- 301, 1989.

GAM63 348 MME Tran- Paterson, R.; Willard, H. F.; Letarte, M.: The common 4 A c
acutelymphoblastic leukemia antigen (neutral endopeptidase- - 3.4.24.11)gene
is located on human chromosome 3. Cancer Genet. Cytogenet. 42:129- 134,
1989.

GAM63 348 MS4A2 Folster- Holst, R.; Moises, H. W.; Yang, L.; Fritsch, W.; Weissenbach,J.; 4 A c
Christophers, E.: Linkage between atopy and the IgE high- affinityreceptor
gene at 11q13 in atopic dermatitis families. Hum. Genet. 102:236- 239, 1998.

GAM63 348 MS4A2 Hill, M. R.; Cookson, W. O. C. M.: A new variant of the beta subunitof the 4 A c
high- affinity receptor for immunoglobulin E (Fc- epsilon- RI- betaE237G):
associations with measures of atopy and bronchial hyper- responsiveness.
Hum.Molec. Genet. 5: 959- 962, 1996.

GAM63 348 MS4A2 Hizawa, N.; Yamaguchi, E.; Furuya, K.; Ohnuma, N.; Kodama, N.;Kojima, J.; 4 A c
Ohe, M.; Kawakami, Y.: Association between high serumtotal IgE levels and
D11S97 on chromosome 11q13 in Japanese subjects. J.Med. Genet. 32: 363- 369,
1995.

GAM63 348 MS4A2 Hupp, K.; Siwarski, D.; Mock, B. A.; Kinet, J.- P.: Gene mappingof the three 4 A c
subunits of the high affinity FcR for IgE to mouse chromosomes1 and 19. J.
Immun. 143: 3787- 3791, 1989.

GAM63 348 MS4A2 Kuster, H.; Zhang, L.; Brini, A. T.; MacGlashan, D. W. J.; Kinet,J.- P.: The 4 A c
gene and cDNA for the human high affinity immunoglobulinE receptor beta
chain and expression of the complete human receptor. J.Biol. Chem. 267:
12782- 12787, 1992.

GAM63 348 MS4A2 Nagata, H.; Mutoh, H.; Kumahara, K.; Arimoto, Y.; Tomemori, T.;Sakurai, D.; 4 A c
Arase, K.; Ohno, K.; Yamakoshi, T.; Nakano, K.; Okawa,T.; Numata, T.; Konno,
A.: Association between nasal allergy anda coding variant of the Fc-
epsilon- RI- beta gene Glu237Gly in a Japanesepopulation. Hum. Genet. 109:
262- 266, 2001.

GAM63 348 MS4A2 Sandford, A. J.; Shirakawa, T.; Moffatt, M. F.; Daniels, S. E.;Ra, C.; Faux, 4 A c
J. A.; Young, R. P.; Nakamura, Y.; Lathrop, G. M.; Cookson,W. O. C. M.;
Hopkin, J. M.: Localisation of atopy and beta subunitof high- affinity IgE
receptor (FCER1) on chromosome 11q. Lancet 341:332- 334, 1993.

GAM63 348 MS4A2 Shirakawa, T.; Li, A.; Dubowitz, M.; Dekker, J. W.; Shaw, A. E.;Faux, J. A.; 4 A c
Ra, C.; Cookson, W. O. C. M.; Hopkin, J. M.: Associationbetween atopy and
variants of the beta subunit of the high- affinityimmunoglobulin E receptor.
Nature Genet. 7: 125- 130, 1994.

GAM63 348 MS4A2 Shirakawa, T.; Mao, X.- Q.; Sasaki, S.; Enomoto, T.; Kawai, M.;Morimoto, K.; 4 A c
Hopkin, J.: Association between atopic asthma and acoding variant of Fc-
epsilon- RI- beta in a Japanese population. Hum.Molec. Genet. 5: 1129- 1130,
1996.

GAM63 348 MS4A2 Szepetowski, P.; Gaudray, P.: FCER1B, a candidate gene for atopy,is located 4 A c
in 11q13 between CD20 and TCN1. Genomics 19: 399- 400,1994.

GAM63 348 MUC3B Fox, M. F.; Lahbib, F.; Pratt, W.; Attwood, J.; Gum, J.; Kim, Y.;Swallow, D. 4 A c
M.: Regional localization of the intestinal mucin geneMUC3 to chromosome
7q22. Ann. Hum. Genet. 56: 281- 287, 1992.

GAM63 348 MUC3B Kyo, K.; Muto, T.; Nagawa, H.; Lathrop, G. M.; Nakamura, Y.: Associationsof 4 A c
distinct variants of the intestinal mucin gene MUC3A with ulcerativecolitis
and Crohn's disease. J. Hum. Genet. 46: 5- 20, 2001.

GAM63 348 MUC3B Pratt, W. S.; Crawley, S.; Hicks, J.; Ho, J.; Nash, M.; Kim, Y.S.; Gum, J. 4 A c
R.; Swallow, D. M.: Multiple transcripts of MUC3: evidencefor two genes,
MUC3A and MUC3B. Biochem. Biophys. Res. Commun. 275:916- 923, 2000.

GAM63 348 NEK6 Kimura, M.; Okano, Y.: Identification and assignment of the humanNIMA- 4 A c
related protein kinase 7 gene (NEK7) to human chromosome 1q31.3.
Cytogenet.Cell Genet. 94: 33- 38, 2001.

GAM63 348 NEK6 Li, M. Z.; Yu, L.; Liu, Q.; Chu, J. Y.; Zhao, S. Y.: Assignmentof NEK6, a 4 A c
NIMA- related gene, to human chromosome 9q33.3- q34.11 byradiation hybrid
mapping. Cytogenet. Cell Genet. 87: 271- 272, 1999.

GAM63 348 NRXN1 Geppert, M.; Khvotchev, M.; Krasnoperov, V.; Goda, Y.; Missler,M.; Hammer, 4 A c
R. E.; Ichtchenko, K.; Petrenko, A. G.; Sudhof, T. C.: Neurexin I- alpha is
a major alpha- latrotoxin receptor that cooperatesin alpha- latrotoxin
action. J. Biol. Chem. 273: 1705- 1710, 1998.

GAM63 348 NRXN1 Ichtchenko, K.; Hata, Y.; Nguyen, T.; Ullrich, B.; Missler, M.;Moomaw, C.; 4 A c
Sudhof, T. C.: Neuroligin 1: a splice site- specific ligandfor beta-
neurexins. Cell 81: 435- 443, 1995.

GAM63 348 NRXN1 Kleiderlein, J. J.; Nisson, P. E.; Jessee, J.; Li, W.- B.; Becker,K. G.; 4 A c
Derby, M. L.; Ross, C. A.; Margolis, R. L.: CCG repeats incDNAs from human
brain. Hum. Genet. 103: 666- 673, 1998. Note: Erratum:Hum. Genet. 104: 113
only, 1999.

GAM63 348 NRXN1 Margolis, R.: Personal Communication. Baltimore, Md. 3/29/2000. 4 A c

GAM63 348 NRXN1 Missler, M.; Sudhof, T. C.: Neurexins: three genes and 1001 products. 4 A c
TrendsGenet. 14: 20- 26, 1998.

GAM63 348 NRXN1 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 4 A c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.

IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM63 348 NRXN1 Rowen, L.; Young, J.; Birditt, B.; Kaur, A.; Madan, A.; Philipps,D. L.; Qin, 4 A c
S.; Minx, P.; Wilson, R. K.; Hood, L.; Graveley, B. R.: Analysis of the human neurexin genes: alternative splicing and thegeneration of protein diversity. Genomics 79: 587- 597, 2002.

GAM63 348 NRXN1 Tabuchi, K.; Sudhof, T. C.: Structure and evolution of neurexingenes: 4 A c
insight into the mechanism of alternative splicing. Genomics 79:849- 859, 2002.

GAM63 348 NRXN1 Ullrich, B.; Ushkaryov, Y. A.; Sudhof, T. C.: Cartography of neurexins:more 4 A c
than 1000 isoforms generated by alternative splicing and expressedin distinct subsets of neurons. Neuron 14: 497- 507, 1995.

GAM63 348 NRXN1 Ushkaryov, Y. A.; Petrenko, A. G.; Geppert, M.; Sudhof, T. C.: Neurexins: 4 A c
synaptic cell surface proteins related to the alpha- latrotoxinreceptor and laminin. Science 257: 50- 56, 1992.

GAM63 348 OAS3 Hovanessian, A. G.; Laurent, A. G.; Chebath, J.; Galabru, J.; Robert,N.; 4 A c
Svab, J.: Identification of 69- kd and 100- kd forms of 2- 5A synthetasein interferon- treated human cells by specific monoclonal antibodies. EMBOJ. 6: 1273- 1280, 1987.

GAM63 348 OAS3 Hovnanian, A.; Rebouillat, D.; Mattei, M.- G.; Levy, E. R.; Marie,I.; 4 A c
Monaco, A. P.; Hovanessian, A. G.: The human 2- prime,5- prime-oligoadenylatesynthetase locus is composed of three distinct genes clustered onchromosome 12q24.2 encoding the 100- , 69- , and 40- kDa forms. Genomics 52:267- 277, 1998.

GAM63 348 OGG1 Aburatani, H.; Hippo, Y.; Ishida, T.; Takashima, R.; Matsuba, C.;Kodama, T.; 4 A c
Takao, M.; Yasui, A.; Yamamoto, K.; Asano, M.; Fukasawa,K.; Yoshinari, T.; Inoue, H.; Ohtsuka, E.; Nishimura, S.: Cloningand characterization of mammalian 8- hydroxyguanine- specific DNA glycosylase/apurinic,apyrimidinic lyase, a functional mutM homologue. Cancer Res. 57:2151- 2156, 1997.

GAM63 348 OGG1 Arai, K.; Morishita, K.; Shinmura, K.; Kohno, T.; Kim, S.- R.; Nohmi,T.; 4 A c
Taniwaki, M.; Ohwada, S.; Yokota, J.: Cloning of a human homologof the yeast OGG1 gene that is involved in the repair of oxidativeDNA damage. Oncogene 14: 2857- 2861, 1997.

GAM63 348 OGG1 Audebert, M.; Chevillard, S.; Levalois, C.; Gyapay, G.; Vieillefond,A.; 4 A c
Klijanienko, J.; Vielh, P.; El Naggar, A. K.; Oudard, S.; Boiteux,S.; Radicella, J. P.: Alterations of the DNA repair gene OGG1 inhuman clear cell carcinomas of the kidney. Cancer Res. 60: 4740- 4744,2000.

GAM63 348 OGG1 Bjoras, M.; Luna, L.; Johnsen, B.; Hoff, E.; Haug, T.; Rognes,T.; Seeberg, 4 A c
E.: Opposite base- dependent reactions of a human baseexcision repair enzyme on DNA containing 7,8- dihydro- 8- oxoguanineand abasic sites. EMBO J. 16: 6314- 6322, 1997.

GAM63 348 OGG1 Ishida, T.; Hippo, Y.; Nakahori, Y.; Matsushita, I.; Kodama, T.;Nishimura, 4 A c
S.; Aburatani, H.: Structure and chromosome location ofhuman OGG1. Cytogenet. Cell Genet. 85: 232- 236, 1999.

GAM63 348 OGG1 Kohno, T.; Shinmura, K.; Tosaka, M.; Tani, M.; Kim, S.- R.; Sugimura,H.; 4 A c
Nohmi, T.; Kasai, H.; Yokota, J.: Genetic polymorphisms and alternativesplicing of the hOGG1 gene, that is involved in the repair of 8-hydroxyguaninein damaged DNA. Oncogene 16: 3219- 3225, 1998.

GAM63 348 OGG1 Kuo, F. C.; Sklar, J.: Augmented expression of a human gene for8- oxoguanine 4 A c
DNA glycosylase (MutM) in B lymphocytes of the dark zonein lymph node

germinal centers. J. Exp. Med. 186: 1547- 1556, 1997.

GAM63 348 OGG1 Lu, R.; Nash, H. M.; Verdine, G. L.: A mammalian DNA repair enzymethat 4 A c
excises oxidatively damaged guanines maps to a locus frequentlylost in lung
cancer. Curr. Biol. 7: 397- 407, 1997.

GAM63 348 OGG1 Radicella, J. P.; Dherin, C.; Desmaze, C.; Fox, M. S.; Boiteux,S.: Cloning 4 A c
and characterization of hOGG1, a human homolog of theOGG1 gene of
Saccharomyces cerevisiae. Proc. Nat. Acad. Sci. 94:8010- 8015, 1997.

GAM63 348 OGG1 Roldan- Arjona, T.; Wei, Y.- F.; Carter, K. C.; Klungland, A.; Anselmino,C.; 4 A c
Wang, R.- P.; Augustus, M.; Lindahl, T.: Molecular cloning andfunctional
expression of a human cDNA encoding the antimutator enzyme8- hydroxyguanine-
DNA glycosylase. Proc. Nat. Acad. Sci. 94: 8016- 8020,1997.

GAM63 348 OGG1 Rosenquist, T. A.; Zharkov, D. O.; Grollman, A. P.: Cloning 4 A c
andcharacterization of a mammalian 8- oxoguanine DNA glycosylase. Proc.Nat.
Acad. Sci. 94: 7429- 7434, 1997.

GAM63 348 OGG1 Tani, M.; Shinmura, K.; Kohno, T.; Shiroishi, T.; Wakama, S.;Kim, S.- R.; 4 A c
Nohmi, T.; Kasai, H.; Takenoshita, S.; Nagamachi, Y.;Yokota, J.: Genomic
structure and chromosomal localization of themouse Ogg1 gene that is
involved in the repair of 8- hydroxyguaninein DNA damage. Mammalian Genome
9: 32- 37, 1998.

GAM63 348 p100 Callebaut, I.; Mornon, J. P.: The human EBNA- 2 coactivator p100:multidomain 4 A c
organization and relationship to the staphylococcal nucleasefold and to the
tudor protein involved in Drosophila melanogasterdevelopment. Biochem. J.
321: 125- 132, 1997.

GAM63 348 p100 Heidebrecht, H. J.; Buck, F.; Steinmann, J.; Sprenger, R.; Wacker,H. H.; 4 A c
Parwaresch, R.: p100: a novel proliferation- associated nuclearprotein
specifically restricted to cell cycle phases S, G2, and M. Blood 90:226-
233, 1997.

GAM63 348 p100 Lienard, P.; Riviere, M.; Van Vooren, P.; Szpirer, C.; Szpirer,J.: 4 A c
Assignment of SND1, the gene encoding coactivator p100, to humanchromosome
7q31.3 and rat chromosome 4q23 by in situ hybridization. Cytogenet.Cell
Genet. 90: 253- 254, 2000.

GAM63 348 p100 Manda, R.; Kohno, T.; Matsuno, Y.; Takenoshita, S.; Kuwano, H.;Yokota, J.: 4 A c
Identification of genes (SPON2 and C20orf2) differentiallyexpressed between
cancerous and noncancerous lung cells by mRNA differentialdisplay. Genomics
61: 5- 14, 1999.

GAM63 348 p100 Tong, X.; Drapkin, R.; Yalamanchili, R.; Mosialos, G.; Kieff, E.: The 4 A c
Epstein- Barr virus nuclear protein 2 acidic domain forms a complexwith a
novel cellular coactivator that can interact with TFIIE. Molec.Cell. Biol.
15: 4735- 4744, 1995.

GAM63 348 p100 Zhang, Y.; Heidebrecht, H.- J.; Rott, A.; Schlegelberger, B.; Parwaresch,R.: 4 A c
Assignment of human proliferation associated p100 gene (C20orf1)to human
chromosome band 20q11.2 by in situ hybridization. Cytogenet.Cell Genet. 84:
182- 183, 1999.

GAM63 348 PACE4 Kiefer, M. C.; Tucker, J. E.; Joh, R.; Landsberg, K. E.; Saltman,D.; Barr, 4 A c
P. J.: Identification of a second human subtilisin- likeprotease gene in the
fes/fps region of chromosome 15. DNA Cell Biol. 10:757- 769, 1991.

GAM63 348 PACE4 Mbikay, M.; Seidah, N. G.; Chretien, M.; Simpson, E. M.: 4 A c
Chromosomalassignment of the genes for proprotein convertases PC4, PC5, and
PACE4 in mouse and human. Genomics 26: 123- 129, 1995.

GAM63 348 PCDH12 Ludwig, D.; Lorenz, J.; Dejana, E.; Bohlen, P.; Hicklin, D. J.;Witte, L.; 4 A c

Pytowski, B.: cDNA cloning, chromosomal mapping, and expressionanalysis of human VE- cadherin- 2. Mammalian Genome 11: 1030- 1033,2000.

GAM63 348 PCDH12 Telo, P.; Breviario, F.; Huber, P.; Panzeri, C.; Dejana, E.: 4 A c Identificationof a novel cadherin (vascular endothelial cadherin- 2) located at intercellularjunctions in endothelial cells. J. Biol. Chem. 273: 17565- 17572,1998.

GAM63 348 PCDH12 Wu, Q.; Maniatis, T.: Large exons encoding multiple ectodomainsare a 4 A c characteristic feature of protocadherin genes. Proc. Nat. Acad.Sci. 97: 3124- 3129, 2000.

GAM63 348 PFKL Bernardi, G.: Personal Communication. Paris, France 5/13/1992. 4 A c

GAM63 348 PFKL Boulard, M. R.; Bois, M.; Reviron, M.; Najean, Y.: Red- cell 4 A c phosphofructokinasedeficiency. New Eng. J. Med. 291: 978- 979, 1974.

GAM63 348 PFKL Chadefaux, B.; Rethore, M. O.; Allard, D.: Regional mapping ofliver type 6- 4 A c phosphofructokinase isoenzyme on chromosome 21. Hum.Genet. 68: 136- 137, 1984.

GAM63 348 PFKL Cox, D. R.; Kawashima, H.; Vora, S.; Epstein, C. J.: Regionalmapping of SOD- 4 A c 1, PRGS, and PFK- L on human chromosome 21. (Abstract) Cytogenet.Cell Genet. 37: 441- 442, 1984.

GAM63 348 PFKL Elson, A.; Levanon, D.; Brandeis, M.; Dafni, N.; Bernstein, Y.;Danciger, E.; 4 A c Groner, Y.: The structure of the human liver- type phosphofructokinasegene. Genomics 7: 47- 56, 1990.

GAM63 348 PFKL Etiemble, J.; Kahn, A.; Boivin, P.; Bernard, J. F.; Goudemand,M.: Hereditary 4 A c hemolytic anemia with erythrocyte phosphofructokinasedeficiency. Hum. Genet. 31: 83- 91, 1976.

GAM63 348 PFKL Etiemble, J.; Picat, C.; Simeon, J.; Blatrix, C.; Boivin, P.:Inherited 4 A c erythrocyte phosphofructokinase deficiency: molecular mechanism. Hum.Genet. 55: 383- 390, 1980.

GAM63 348 PFKL Gehnrich, S. C.; Gekakis, N.; Sul, H. S.: Liver (B- type) 4 A c phosphofructokinasemRNA: cloning, structure, and expression. J. Biol. Chem. 263: 11755- 11759,1988.

GAM63 348 PFKL Kahn, A.; Etiemble, J.; Meienhofer, M. C.; Boivin, P.: 4 A c Erythrocytephosphofructokinase deficiency associated with an unstable variantof muscle phosphofructokinase. Clin. Chim. Acta 61: 415- 419, 1975.

GAM63 348 PFKL Levanon, D.; Danciger, E.; Dafni, N.; Groner, Y.: Genomic clonesof the human 4 A c liver- type phosphofructokinase. Biochem. Biophys. Res.Commun. 141: 374- 380, 1986.

GAM63 348 PFKL Miwa, S.; Sato, T.; Murao, H.; Kozuru, M.; Ibayashi, H.: A newtype of 4 A c phosphofructokinase deficiency: hereditary nonspherocytichemolytic anemia. Acta Haemat. Jpn. 35: 113- 118, 1972.

GAM63 348 PFKL Pantelakis, S. N.; Karaklis, A. G.; Alexiou, D.; Vardas, E.; Valaes,T.: Red 4 A c cell enzymes in trisomy 21. Am. J. Hum. Genet. 22: 184- 193,1970.

GAM63 348 PFKL Petersen, M. B.; Slaugenhaupt, S. A.; Lewis, J. G.; Warren, A.C.; 4 A c Chakravarti, A.; Antonarakis, S. E.: A genetic linkage map of27 markers on human chromosome 21. Genomics 9: 407- 419, 1991.

GAM63 348 PFKL Van Keuren, M.; Drabkin, H.; Hart, I.; Harker, D.; Patterson,D.; Vora, S.: 4 A c Regional assignment of human liver- type 6- phosphofructokinaseto chromosome 21q22.3 by using somatic cell hybrids and a monoclonalanti- L antibody. Hum. Genet. 74: 34- 40, 1986.

GAM63 348 PFKL Vora, S.; Davidson, M.; Seaman, C.; Miranda, A. F.; Noble, N.A.; Tanaka, K. 4 A c R.; Frenkel, E. P.; DiMauro, S.: Heterogeneity ofthe molecular lesions in

inherited phosphofructokinase deficiency. J.Clin. Invest. 72: 1995- 2006, 1983.

GAM63 348 PFKL Vora, S.; Durham, S.; de Martinville, B.; Francke, U.: Assignmentof the genes for liver type phosphofructokinase (PFKL) to chromosome21 and for muscle type (PFKM) to region p32- q32 of chromosome 1. (Abstract) Cytogenet.Cell Genet. 32: 324 only, 1982. 4 A c

GAM63 348 PFKL Vora, S.; Francke, U.: Assignment of the human gene for liver- type6- phosphofructokinase isozyme (PFKL) to chromosome 21 by using somaticcell hybrids and monoclonal anti- L antibody. Proc. Nat. Acad. Sci. 78:3738- 3742, 1981. 4 A c

GAM63 348 PFKL Vora, S.; Francke, U.: Assignment of the human gene for livertype phosphofructokinase isozyme to chromosome 21 using somatic cellhybrids. (Abstract) Pediat. Res. 15: 570 only, 1981. 4 A c

GAM63 348 PFKL Vora, S.; Seaman, C.; Durham, S.; Piomelli, S.: Isozymes of humanphosphofructokinase: identification and subunit structural characterizationof a new system. Proc. Nat. Acad. Sci. 77: 62- 66, 1980. 4 A c

GAM63 348 PFKL Wang, D.; Fang, H.; Cantor, C. R.; Smith, C. L.: A contiguousNotI restriction map of band q22.3 of human chromosome 21. Proc.Nat. Acad. Sci. 89: 3222- 3226, 1992. 4 A c

GAM63 348 PLEK Cmarik, J. L.; Hegamyer, G.; Gerrard, B.; Dean, M.; Colburn, N.H.: cDNA cloning and mapping of mouse pleckstrin (Plek), a gene upregulatedin transformation- resistant cells. Genomics 66: 204- 212, 2000. 4 A c

GAM63 348 PLEK Tyers, M.; Haslam, R. J.; Rachubinski, R. A.; Harley, C. B.: Molecularanalysis of pleckstrin: the major protein kinase C substrate of platelets. J.Cell. Biochem. 40: 133- 145, 1989. 4 A c

GAM63 348 PLEK Tyers, M.; Rachubinski, R. A.; Stewart, M. I.; Varrichio, A. M.;Shorr, R. G. L.; Haslam, R. J.; Harley, C. B.: Molecular cloningand expression of the major protein kinase C substrate of platelets. Nature 333:470- 473, 1988. 4 A c

GAM63 348 PPT2 Gupta, P.; Soyombo, A. A.; Atashband, A.; Wisniewski, K. E.; Shelton,J. M.; Richardson, J. A.; Hammer, R. E.; Hofmann, S. L.: Disruptionof PPT1 or PPT2 causes neuronal ceroid lipofuscinosis in knockoutmice. Proc. Nat. Acad. Sci. 98: 13566- 13571, 2001. 4 A c

GAM63 348 PPT2 Soyombo, A. A.; Hofmann, S. L.: Molecular cloning and expressionof palmitoyl- protein thioesterase 2 (PPT2), a homolog of lysosomalpalmitoyl- protein thioesterase with a distinct substrate specificity. J.Biol. Chem. 272: 27456- 27463, 1997. 4 A c

GAM63 348 PRLR Arden, K. C.; Boutin, J.- M.; Djiane, J.; Kelly, P. A.; Cavenee,W. K.: The receptors for prolactin and growth hormone are localizedin the same region of human chromosome 5. Cytogenet. Cell Genet. 53:161- 165, 1990. 4 A c

GAM63 348 PRLR Arden, K. C.; Cavenee, W. K.; Boutin, J.- M.; Kelly, P. A.: Thegenes encoding the receptors for prolactin and growth hormone mapto human chromosome 5. (Abstract) Am. J. Hum. Genet. 45 (suppl.):A129 only, 1989. 4 A c

GAM63 348 PRLR Boutin, J.- M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur,L.; Ali, S.; Gould, D.; Djiane, J.; Kelly, P. A.: Identificationof a cDNA encoding a long form of prolactin receptor in human hepatomaand breast cancer cells. Molec. Endocr. 3: 1455- 1461, 1989. 4 A c

GAM63 348 PRLR Cunningham, B. C.; Bass, S.; Fuh, G.; Wells, J. A.: Zinc mediationof the binding of human growth hormone to the human prolactin receptor. Science 250:1709- 1712, 1990. 4 A c

GAM63 348 PRLR Glasow, A.; Horn, L.- C.; Taymans, S. E.; Stratakis, C. A.; Kelly,P. A.; 4 A c

Kohler, U.; Gillespie, J.; Vonderhaar, B. K.; Bornstein, S.R.: Mutational analysis of the PRL receptor gene in human breasttumors with differential PRL receptor protein expression. J. Clin.Endocr. Metab. 86: 3826- 3832, 2001.

GAM63 348 PRLR Hu, Z.- Z.; Zhuang, L.; Meng, J.; Leondires, M.; Dufau, M. L.:The human prolactin receptor gene structure and alternative promoterutilization: the generic promoter hPIII and a novel human promoterhP(N). J. Clin. Endocr. Metab. 84: 1153- 1156, 1999. 4 A c

GAM63 348 PRLR Ormandy, C. J.; Camus, A.; Barra, J.; Damotte, D.; Lucas, B.; Buteau,H.; Edery, M.; Brousse, N.; Babinet, C.; Binart, N.; Kelly, P. A.: Null mutation of the prolactin receptor gene produces multiple reproductivedefects in the mouse. Genes Dev. 11: 167- 178, 1997. 4 A c

GAM63 348 PRLR Perrot- Applanat, M.; Gualillo, O.; Pezet, A.; Vincent, V.; Edery,M.; Kelly, P. A.: Dominant negative and cooperative effects of mutantforms of prolactin receptor. Molec. Endocr. 11: 1020- 1032, 1997. 4 A c

GAM63 348 PROCR Franchi, F.; Biguzzi, E.; Cetin, I.; Facchetti, F.; Radaelli, T.;Bozzo, M.; Pardi, G.; Faioni, E. M.: Mutations in the thrombomodulinand endothelial protein C receptor genes in women with late fetalloss. Brit. J. Haemat. 114: 641- 646, 2001. 4 A c

GAM63 348 PROCR Fukudome, K.; Esmon, C. T.: Identification, cloning, and regulationof a novel endothelial cell protein C/activated protein C receptor. J.Biol. Chem. 269: 26486- 26491, 1994. 4 A c

GAM63 348 PROCR Hayashi, T.; Nakamura, H.; Okada, A.; Takebayashi, S.; Wakita,T.; Yuasa, H.; Okumura, K.; Suzuki, K.: Organization and chromosomallocalization of the human endothelial protein C receptor gene. Gene 238:367- 373, 1999. 4 A c

GAM63 348 PROCR Mincheva, A.; Rothbarth, K.; Werner, D.; Lichter, P.: Assignmentof the gene encoding centrosome- associated protein CCD41 to mousechromosome 2H. Mammalian Genome 6: 444 only, 1995. 4 A c

GAM63 348 PROCR Riewald, M.; Petrovan, R. J.; Donner, A.; Mueller, B. M.; Ruf,W.: Activation of endothelial cell protease activated receptor 1by the protein C pathway. Science 296: 1880- 1882, 2002. 4 A c

GAM63 348 PROCR Rothbarth, K.; Dabaghian, A. R. H.; Stammer, H.; Werner, D.: Onesingle mRNA encodes the centrosomal protein CCD41 and the endothelialcell protein C receptor (EPCR). FEBS Lett. 458: 77- 80, 1999. 4 A c

GAM63 348 PROCR Rothbarth, K.; Petzelt, C.; Lu, X.; Todorov, I. T.; Joswig, G.;Pepperkok, R.; Ansorge, W.; Werner, D.: cDNA- derived molecular characteristicsand antibodies to a new centrosome- associated and G2/M phase- prevalentprotein. J. Cell Sci. 104: 19- 30, 1993. 4 A c

GAM63 348 PROCR Simmonds, R. E.; Lane, D. A.: Structural and functional implicationsof the intron/exon organization of the human endothelial cell proteinC/activated protein C receptor (EPCR) gene: comparison with the structureof CD1/major histocompatibility complex alpha- 1 and alpha- 2 domains. Blood 94:632- 641, 1999. 4 A c

GAM63 348 PROCR Ye, X.; Fukudome, K.; Tsuneyoshi, N.; Satoh, T.; Tokunaga, O.;Sugawara, K.; Mizokami, H.; Kimoto, M.: The endothelial cell proteinC receptor (EPCR) functions as a primary receptor for protein C activationon endothelial cells in arteries, veins, and capillaries. Biochem.Biophys. Res. Commun. 259: 671- 677, 1999. 4 A c

GAM63 348 PSG7 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; 4 A c

Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999.

GAM63 348 PSG7 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. 4 A c
W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by fluorescence in situ hybridization. Genomics 12:773- 779, 1992.

GAM63 348 PSG7 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.; Georgescu,A.; 4 A c
Carrano, A.; Hammarstrom, S.: Gene organization of the pregnancy-specificglycoprotein region on human chromosome 19: assembly and analysisof a 700- kb cosmid contig spanning the region. Genomics 23: 659- 668,1994.

GAM63 348 PSG7 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The 4 A c
pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19: fine structure of the 11 PSG genes and identificationof 6 new genes forming a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics 23: 669- 684, 1994.

GAM63 348 PSG7 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, 4 A c
H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.; Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly linked on the long arm of chromosome 19 and arecoordinately expressed. Biochem. Biophys. Res. Commun. 167: 848- 859,1990.

GAM63 348 PSG7 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades- 4 A c
Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan, K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772, 1992.

GAM63 348 PSG7 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 4 A c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993.

GAM63 348 PSG7 Tynan, K.; Olsen, A.; Trask, B.; de Jong, P.; Thompson, J.; Zimmermann,W.; 4 A c
Carrano, A.; Mohrenweiser, H.: Assembly and analysis of cosmidcontigs in the CEA- gene family region of human chromosome 19. NucleicAcids Res. 20: 1629- 1636, 1992.

GAM63 348 PSMC3 DeMartino, G. N.; Proske, R. J.; Moomaw, C. R.; Strong, A. A.;Song, X.; 4 A c
Hisamatsu, H.; Tanaka, K.; Slaughter, C. A.: Identification,purification, and characterization of a PA700- dependent activatorof the proteasome. J. Biol. Chem. 271: 3112- 3118, 1996.

GAM63 348 PSMC3 Hoyle, J.; Tan, K. H.; Fisher, E. M. C.: Localization of genesencoding two 4 A c
human one- domain members of the AAA family: PSMC5 (thethyroid hormone receptor- interacting protein, TRIP1) and PSMC3 (theTat- binding protein, TBP1). Hum. Genet. 99: 285- 288, 1997.

GAM63 348 PSMC3 Nelbock, P.; Dillon, P. J.; Perkins, A.; Rosen, C. A.: A cDNAfor a protein 4 A c
that interacts with the human immunodeficiency virusTat transactivator. Science 248: 1650- 1653, 1990.

GAM63 348 PSMC3 Ohana, B.; Moore, P. A.; Ruben, S. M.; Southgate, C. D.; Green,M. R.; Rosen, 4 A c
C. A.: The type 1 human immunodeficiency virus Tatbinding protein is a transcriptional activator belonging to an additionalfamily of evolutionarily conserved genes. Proc. Nat. Acad. Sci. 90:138- 142, 1993.

GAM63 348 PSMC3 Sakao, Y.; Kawai, T.; Takeuchi, O.; Copeland, N. G.; Gilbert, D.J.; Jenkins, 4 A c

N. A.; Takeda, K.; Akira, S.: Mouse proteasomal ATPasesPsmc3 and Psmc4: genomic organization and gene targeting. Genomics 67:1- 7, 2000.

GAM63 348 PSMC3 Tanahashi, N.; Suzuki, M.; Fujiwara, T.; Takahashi, E.; Shimbara,N.; Chung, C. H.; Tanaka, K.: Chromosomal localization and immunologicalanalysis of a family of human 26S proteasomal ATPases. Biochem. Biophys.Res. Commun. 243: 229- 232, 1998. 4 A c

GAM63 348 RABIF Muller- Pillasch, F.; Zimmerhackl, F.; Lacher, U.; Schultz, N.;Hameister, H.; Varga, G.; Friess, H.; Buchler, M.; Adler, G.; Gress,T. M.: Cloning of novel transcripts of the human guanine- nucleotide- exchangefactor Mss4: in situ chromosomal mapping and expression in pancreaticcancer. Genomics 46: 389- 396, 1997. 4 A c

GAM63 348 RABIF Yu, H.; Schreiber, S. L.: Cloning, Zn(2+) binding, and structuralcharacterization of the guanine nucleotide exchange factor human Mss4. Biochemistry 34:9103- 9110, 1995. 4 A c

GAM63 348 RAI14 Kutty, R. K.; Kutty, G.; Samuel, W.; Duncan, T.; Bridges, C. C.;El-Sherbeeny, A.; Nagineni, C. N.; Smith, S. B.; Wiggert, B.: Molecularcharacterization and developmental expression of NORPEG, a novel geneinduced by retinoic acid. J. Biol. Chem. 276: 2831- 2840, 2001. 4 A c

GAM63 348 RAI14 Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of the coding sequences of unidentified human genes. XVI.The complete sequences of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 65- 73, 2000. 4 A c

GAM63 348 REGL Gharib, B.; Fox, M. F.; Bartoli, C.; Giorgi, D.; Sansonetti, A.;Swallow, D. M.; Dagorn, J. C.; Berge- Lefranc, J. L.: Human regenerationprotein/lithostathine genes map to chromosome 2p12. Ann. Hum. Genet. 57:9- 16, 1993. 4 A c

GAM63 348 REGL Miyashita, H.; Nakagawara, K.; Mori, M.; Narushima, Y.; Noguchi,N.; Moriizumi, S.; Takasawa, S.; Yonekura, H.; Takeuchi, T.; Okamoto,H.: Human REG family genes are tandemly ordered in a 95- kilobaseregion of chromosome 2p12. FEBS Lett. 377: 429- 433, 1995. 4 A c

GAM63 348 REGL Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki,Y.; Miyashita, H.; Yonekura, H.; Okamoto, H.: Isolation, structuraldetermination and expression of a novel reg gene, human regI- beta. Biochim.Biophys. Acta 1217: 199- 202, 1994. 4 A c

GAM63 348 RFX1 Doyle, J.; Hoffman, S.; Ucla, C.; Reith, W.; Mach, B.; Stubbs,L.: Locations of human and mouse genes encoding the RFX1 and RFX2transcription factor proteins. Genomics 35: 227- 230, 1996. 4 A c

GAM63 348 RFX1 Emery, P.; Durand, B.; Mach, B.; Reith, W.: RFX proteins, a novelfamily of DNA binding proteins conserved in the eukaryotic kingdom. NucleicAcids Res. 24: 803- 807, 1996. 4 A c

GAM63 348 RFX1 Mach, B.; Steimle, V.; Reith, W.: MHC class II- deficient combinedimmunodeficiency: a disease of gene regulation. Immun. Rev. 138:207- 221, 1994. 4 A c

GAM63 348 RFX1 Pugliati, L.; Reith, W.; Fey, S.; Mach, B.: Mapping the RF- X gene,encoding a DNA- binding protein controlling HLA class II gene expression,to 19p13.(Abstract) Cytogenet. Cell Genet. 51: 1061 only, 1989. 4 A c

GAM63 348 RFX1 Pugliatti, L.; Derre, J.; Berger, R.; Ucla, C.; Reith, W.; Mach,B.: The genes for MHC class II regulatory factors RFX1 and RFX2 arelocated on the short arm of chromosome 19. Genomics 13: 1307- 1310,1992. 4 A c

GAM63 348 RFX1 Reith, W.: Personal Communication. Geneva, Switzerland 5/30/1997. 4 A c

GAM63 348 RFX1 Reith, W.; Ucla, C.; Barras, E.; Gaud, A.; Durand, B.; Herrero- Sanchez,C.; 4 A c
Kobr, M.; Mach, B.: RFX1, a transactivator of hepatitis B virusenhancer I,
belongs to a novel family of homodimeric and heterodimericDNA- binding
proteins. Molec. Cell. Biol. 14: 1230- 1244, 1994.

GAM63 348 RGL Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 4 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XIII. The completesequences of 100
new cDNA clones from brain which code for large proteinsin vitro. DNA Res.
6: 63- 70, 1999.

GAM63 348 RGL Sood, R.; Makalowska, I.; Carpten, J. D.; Robbins, C. M.; Stephan,D. A.; 4 A c
Connors, T. D.; Morgenbesser, S. D.; Su, K.; Pinkett, H. W.;Graham, C. L.;
Quesenberry, M. I.; Baxevanis, A. D.; Klinger, K. W.;Trent, J. M.; Bonner,
T. I.: The human RGL (RalGDS- like) gene: cloning,expression analysis and
genomic organization. Biochim. Biophys. Acta 1491:285- 288, 2000.

GAM63 348 RNF3 Beck, S.; Hanson, I.; Kelly, A.; Pappin, D. J.; Trowsdale, J.:A homologue of 4 A c
the Drosophila female sterile homeotic (fsh) gene inthe class II region of
the human MHC. DNA Sequence 2: 203- 210, 1992.

GAM63 348 RNF3 Denis, G. V.; Green, M. R.: A novel, mitogen- activated nuclearkinase is 4 A c
related to a Drosophila developmental regulator. GenesDev. 10: 261- 271,
1996.

GAM63 348 RNF3 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 4 A c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. II. The codingsequences of 40 new
genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell
line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM63 348 RNF3 Okamoto, N.; Ando, A.; Kawai, J.; Yoshiwara, T.; Tsuji, K.; Inoko,H.: 4 A c
Orientation of HLA- DNA gene and identification of a CpG island-
associatedgene adjacent to DNA in human major histocompatibility complex
classII region. Hum. Immun. 32: 221- 228, 1991.

GAM63 348 RNF3 Thorpe, K. L.; Abdulla, S.; Kaufman, J.; Trowsdale, J.; Beck, S.: Phylogeny 4 A c
and structure of the RING3 gene. Immunogenetics 44:391- 396, 1996.

GAM63 348 RNTRE Lanzetti, L.; Rybin, V.; Malabarba, M. G.; Christoforidis, S.;Scita, G.; 4 A c
Zerial, M.; Di Fiore, P. P.: The Eps8 protein coordinatesEGF receptor
signalling through Rac and trafficking through Rab5. Nature 408:374- 377,
2000.

GAM63 348 RNTRE Matoskova, B.; Wong, W. T.; Nomura, N.; Robbins, K. C.; Di Fiore,P. P.: RN- 4 A c
tre specifically binds to the SH3 domain of eps8 with highaffinity and
confers growth advantage to NIH3T3 upon carboxy- terminaltruncation.
Oncogene 12: 2679- 2688, 1996.

GAM63 348 RNTRE Matoskova, B.; Wong, W. T.; Seki, N.; Nagase, T.; Nomura, N.; Robbins,K. C.; 4 A c
Di Fiore, P. P.: RN- tre identifies a family of tre- relatedproteins
displaying a novel potential protein binding domain. Oncogene 12:2563- 2571,
1996.

GAM63 348 RNTRE Nomura, N.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Kawarabayasi,Y.; Sato, S.; 4 A c
Nagase, T.; Seki, N.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. I. The codingsequences of 40 new
genes (KIAA0001- KIAA0040) deduced by analysisof randomly samples cDNA
clones from human immature myeloid cell lineKG- 1. DNA Res. 1: 27- 35, 1994.

GAM63 348 SCN8A Burgess, D. L.; Kohrman, D. C.; Galt, J.; Plummer, N. W.; Jones,J. M.; 4 A c
Spear, B.; Meisler, M. H.: Mutation of a new sodium channelgene, Scn8a, in

the mouse mutant 'motor endplate disease'. NatureGenet. 10: 461- 465, 1995.

GAM63 348 SCN8A DeRepentigny, Y.; Cote, P. D.; Pool, M.; Bernier, G.; Girard, S.;Vidal, S. 4 A c
M.; Kothary, R.: Pathological and genetic analysis of thedegenerating muscle
(dmu) mouse: a new allele of Scn8a. Hum. Molec.Genet. 10: 1819- 1827, 2001.

GAM63 348 SCN8A Kohrman, D. C.; Harris, J. B.; Meisler, M. H.: Mutation detectionin the med 4 A c
and med(J) alleles of the sodium channel Scn8a: unusualsplicing due to a
minor class AT- AC intron. J. Biol. Chem. 271:17576- 17581, 1996.

GAM63 348 SCN8A Kohrman, D. C.; Plummer, N. W.; Schuster, T.; Jones, J. M.; Jang,W.; 4 A c
Burgess, D. L.; Galt, J.; Spear, B. T.; Meisler, M. H.: Insertionalmutation
of the motor endplate disease (med) locus on mouse chromosome15. Genomics
26: 171- 177, 1995.

GAM63 348 SCN8A Kohrman, D. C.; Smith, M. R.; Goldin, A. L.; Harris, J.; Meisler,M. H.: A 4 A c
missense mutation in the sodium channel Scn8a is responsiblefor cerebellar
ataxia in the mouse mutant jolting. J. Neurosci. 16:5993- 5999, 1996.

GAM63 348 SCN8A Meisler, M. H.; Sprunger, L. K.; Plummer, N. W.; Escayg, A.; Jones,J. M.: 4 A c
Ion channel mutations in mouse models of inherited neurologicaldisease. Ann.
Med. 29: 569- 574, 1997.

GAM63 348 SCN8A Plummer, N. W.; Galt, J.; Jones, J. M.; Burgess, D. L.; Sprunger,L. K.; 4 A c
Kohrman, D. C.; Meisler, M. H.: Exon organization, codingsequence, physical
mapping, and polymorphic intragenic markers forthe human neuronal sodium
channel gene SCN8A. Genomics 54: 287- 296,1998.

GAM63 348 SCN8A Plummer, N. W.; McBurney, M. W.; Meisler, M. H.: Alternative splicingof the 4 A c
sodium channel SCN8A predicts a truncated two- domain proteinin fetal brain
and non- neuronal cells. J. Biol. Chem. 272: 24008- 24015,1997.

GAM63 348 SCN8A Reid, E.; Escayg, A.; Dearlove, A. M.; Lee, D. D.; Meisler, M.H.; 4 A c
Rubinsztein, D. C.: The spastic paraplegia SPG10 locus: narrowingof critical
region and exclusion of sodium channel gene SCN8A as acandidate. J. Med.
Genet. 38: 65- 67, 2001.

GAM63 348 SCN8A Sprunger, L. K.; Escayg, A.; Tallaksen- Greene, S.; Albin, R. L.;Meisler, M. 4 A c
H.: Dystonia associated with mutation of the neuronalsodium channel Scn8a
and identification of the modifier locus Scnm1on mouse chromosome 3. Hum.
Molec. Genet. 8: 471- 479, 1999.

GAM63 348 SERPINB5 Futscher, B. W.; Oshiro, M. M.; Wozniak, R. J.; Holtan, N.; Hanigan,C. L.; 4 A c
Duan, H.; Domann, F. E.: Role for DNA methylation in the controlof cell
type- specific maspin expression. Nature Genet. 31: 175- 179,2002.

GAM63 348 SERPINB5 Ngamkitidechakul, C.; Burke, J. M.; O'Brien, W. J.; Twining, S.S.: Maspin: 4 A c
synthesis by human cornea and regulation of in vitrostromal cell adhesion to
extracellular matrix. Invest. Ophthal. Vis.Sci. 42: 3135- 3141, 2001.

GAM63 348 SERPINB5 Schneider, S. S.; Schick, C.; Fish, K. E.; Miller, E.; Pena, J.C.; Treter, 4 A c
S. D.; Hui, S. M.; Silverman, G. A.: A serine proteinaseinhibitor locus at
18q21.3 contains a tandem duplication of the humansquamous cell carcinoma
antigen gene. Proc. Nat. Acad. Sci. 92:3147- 3151, 1995.

GAM63 348 SERPINB5 Zou, Z.; Anisowicz, A.; Hendrix, M. J. C.; Thor, A.; Neveu, M.;Sheng, S.; 4 A c
Rafidi, K.; Seftor, E.; Sager, R.: Maspin, a serpin withtumor- suppressing
activity in human mammary epithelial cells. Science 263:526- 529, 1994.

GAM63 348 SIAT1 Grundmann, U.; Nerlich, C.; Rein, T.; Zettlmeissl, G.: CompletecDNA sequence 4 A c
encoding human beta- galactoside alpha- 2,6- sialyltransferase. NucleicAcids
Res. 18: 667 only, 1990.

GAM63 348 SIAT1 Wang, X.; Vertino, A.; Eddy, R. L.; Byers, M. G.; Jani- Sait, S.N.; Shows, 4 A c
T. B.; Lau, J. T. Y.: Chromosome mapping and organizationof the human beta-

galactoside alpha- 2,6- sialyltransferase gene: differentialand cell- type specific usage of upstream exon sequences in B- lymphoblastoidcells. J. Biol. Chem. 268: 4355- 4361, 1993.

GAM63 348 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 4 A c

GAM63 348 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 4 A c

GAM63 348 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 4 A c

GAM63 348 SLA Angrist, M.; Wells, D. E.; Chakravarti, A.; Pandey, A.: Chromosomallocalization of the mouse Src- like adapter protein (Slap) gene andits putative human homolog SLA. Genomics 30: 623- 625, 1995. 4 A c

GAM63 348 SLA Holland, S. J.; Liao, X. C.; Mendenhall, M. K.; Zhou, X.; Pardo,J.; Chu, P.; Spencer, C.; Fu, A.; Sheng, N.; Yu, P.; Pali, E.; Nagin,A.; and 14 others: Functional cloning of Src- like adapter protein- 2(SLAP- 2), a novel inhibitor of antigen receptor signaling. J. Exp.Med. 194: 1263- 1276, 2001. 4 A c

GAM63 348 SLA Kratchmarova, I.; Sosinowski, T.; Weiss, A.; Witter, K.; Vincenz,C.; Pandey, A.: Characterization of promoter region and genomic structureof the murine and human genes encoding Src like adapter protein. Gene 262:267- 273, 2001. 4 A c

GAM63 348 SLA Meijerink, P. H. S.; Yanakiev, P.; Zorn, I.; Grierson, A. J.; Bikker,H.; Dye, D.; Kalaydjieva, L.; Baas, F.: The gene for the human Src- likeadaptor protein (hSLAP) is located within the 64- kb intron of thethyroglobulin gene. Europ. J. Biochem. 254: 297- 303, 1998. 4 A c

GAM63 348 SLA Pandey, A.; Lindberg, R. A.; Dixit, V. M.: Receptor orphans finda family. Curr. Biol. 5: 986- 989, 1995. 4 A c

GAM63 348 SLA Sosinowski, T.; Pandey, A.; Dixit, V. M.; Weiss, A.: Src- likeadaptor protein (SLAP) is a negative regulator of T cell receptorsignaling. J. Exp. Med. 191: 463- 474, 2000. 4 A c

GAM63 348 SLC21A3 Kullak- Ublick, G. A.; Hagenbuch, B.; Stieger, B.; Schteingart,C. D.; Hofmann, A. F.; Wolkoff, A. W.; Meier, P. J.: Molecular andfunctional characterization of an organic anion transporting polypeptidecloned from human liver. :Gastroenterology 109: 1274- 1282, 1995. 4 A c

GAM63 348 SLC21A3 Kullak- Ublick, G.- A.; Beuers, U.; Meier, P. J.; Domdey, H.; Paumgartner,G.: Assignment of the human organic anion transporting polypeptide(OATP) gene to chromosome 12p12 by fluorescence in situ hybridization. J.Hepatol. 25: 985- 987, 1996. 4 A c

GAM63 348 SLC39A4 Kury, S.; Dreno, B.; Bezieau, S.; Giraudet, S.; Kharfi, M.; Kamoun,R.; Moisan, J.- P.: Identification of SLC39A4, a gene involved inacrodermatitis enteropathica. Nature Genet. 31: 239- 240, 2002. 4 A c

GAM63 348 SLC39A4 Rogers, E. E.; Eide, D. J.; Guerinot, M. L.: Altered selectivityin an Arabidopsis metal transporter. Proc. Nat. Acad. Sci. 97: 12356- 12360,2000. 4 A c

GAM63 348 SLC39A4 Wang, K.; Pugh, E. W.; Griffen, S.; Doheny, K. F.; Mostafa, W.Z.; al-Aboosi, M. M.; el- Shanti, H.; Gitschier, J.: Homozygositymapping places the acrodermatitis enteropathica gene on chromosomalregion 8q24.3. Am. J. Hum. Genet. 68: 1055- 1060, 2001. 4 A c

GAM63 348 SLC39A4 Wang, K.; Zhou, B.; Kuo, Y.- M.; Zemansky, J.; Gitschier, J.: Anovel member of a zinc transporter family is defective in acrodermatitisenteropathica. Am. J. Hum. Genet. 71: 66- 73, 2002. 4 A c

GAM63 348 SLC6A2 Bruss, M.; Kunz, J.; Lingen, B.; Bonisch, H.: Chromosomal mappingof the human gene for the tricyclic antidepressant- sensitive noradrenalinetransporter. Hum. Genet. 91: 278- 280, 1993. 4 A c

GAM63 348 SLC6A2 Esler, M.; Jennings, G.; Lambert, G.; Meredith, I.; Horne, M.;Eisenhofer, G.: Overflow of catecholamine neurotransmitters to thecirculation: source, fate, and functions. Physiol. Rev. 70: 963- 985,1990. 4 A c

GAM63 348 SLC6A2 Fritz, J. D.; Jayanthi, L. D.; Thoreson, M. A.; Blakely, R. D.: Cloning and chromosomal mapping of the murine norepinephrine transporter. J.Neurochem. 70: 2241- 2251, 1998. 4 A c

GAM63 348 SLC6A2 Gelernter, J.; Kruger, S.; Kidd, K. K.; Amara, S.: TaqI RFLP atnorepinephrine transporter protein (NET) locus. Hum. Molec. Genet. 2:820 only, 1993. 4 A c

GAM63 348 SLC6A2 Gelernter, J.; Kruger, S.; Pakstis, A. J.; Pacholczyk, T.; Sparkes,R. S.; Kidd, K. K.; Amara, S.: Assignment of the norepinephrine transporterprotein (NET1) locus to chromosome 16. Genomics 18: 690- 692, 1993. 4 A c

GAM63 348 SLC6A2 Kaye, W. H.; Jimerson, D. C.; Lake, C. R.; Ebert, M. H.: Alterednorepinephrine metabolism following long- term weight recovery in patientswith anorexia nervosa. Psychiat. Res. 14: 333- 342, 1985. 4 A c

GAM63 348 SLC6A2 Pacholczyk, T.; Blakely, R. D.; Amara, S. G.: Expression cloningof a cocaine- and antidepressant- sensitive human noradrenaline transporter. Nature 350:350- 354, 1991. 4 A c

GAM63 348 SLC6A2 Paczkowski, F. A.; Bonisch, H.; Bryan- Lluka, L. J.: Pharmacologicalproperties of the naturally occurring ala457pro variant of the humannorepinephrine transporter. Pharmacogenetics 12: 165- 173, 2002. 4 A c

GAM63 348 SLC6A2 Pirke, K. M.; Kellner, M.; Philipp, E.; Laessle, R.; Krieg, J.C.; Fichter, M. M.: Plasma norepinephrine after a standardized testmeal in acute and remitted patients with anorexia nervosa and in healthycontrols. Biol. Psychiat. 31: 1074- 1077, 1992. 4 A c

GAM63 348 SLC6A2 Porzgen, P.; Bonisch, H.; Bruss, M.: Molecular cloning and organizationof the coding region of the human norepinephrine transporter gene. Biochem.Biophys. Res. Commun. 215: 1145- 1150, 1995. Notes: Erratum: Biochem.Biophys. Res. Commun. 227: 642- 643, 1996. 4 A c

GAM63 348 SLC6A2 Shannon, J. R.; Flattem, N. L.; Jordan, J.; Jacob, G.; Black,B. K.; Biaggioni, I.; Blakely, R. D.; Robertson, D.: Orthostaticintolerance and tachycardia associated with norepinephrine- transporterdeficiency. New Eng. J. Med. 342: 541- 549, 2000. 4 A c

GAM63 348 SLC6A2 Urwin, R. E.; Bennetts, B.; Wilcken, B.; Lampropoulos, B.; Beumont,P.; Clarke, S.; Russell, J.; Tanner, S.; Nunn, K. P.: Anorexia nervosa(restrictive subtype) is associated with a polymorphism in the novelnorepinephrine transporter gene promoter polymorphic region. Molec.Psychiat. 7: 652- 657, 2002. 4 A c

GAM63 348 SLC9A1 Denker, S. P.; Huang, D. C.; Orlowski, J.; Furthmayr, H.; Barber,D. L.: Direct binding of the Na- H exchanger NHE1 to ERM proteinsregulates the cortical cytoskeleton and cell shape independently ofH(+) translocation. Molec. Cell 6: 1425- 1436, 2000. 4 A c

GAM63 348 SLC9A1 Dudley, C. R. K.; Giuffra, L. A.; Tippett, P.; Kidd, K. K.; Reeders,S. T.: The Na+/H+ antiporter: a 'melt' polymorphism allows regionalmapping to the 4 A c

short arm of chromosome 1. Hum. Genet. 86: 79- 83,1990.

GAM63 348 SLC9A1 Franchi, A.; Perucca- Lostanlen, D.; Pouyssegur, J.: Functionalexpression of 4 A c
a human Na+/H+ antiporter gene transfected into antiporter- deficientmouse L
cells. Proc. Nat. Acad. Sci. 83: 9388- 9392, 1986.

GAM63 348 SLC9A1 Lifton, R. P.; Sardet, C.; Pouyssegur, J.; Lalouel, J.- M.: Cloningof the 4 A c
human genomic amiloride- sensitive Na+/H+ antiporter gene, identificationof
genetic polymorphisms, and localization on the genetic map of chromosome1p.
Genomics 7: 131- 135, 1990.

GAM63 348 SLC9A1 Mattei, M.- G.; Galloni, M.; Sardet, C.; Franchi, A.; Counillon,L.; Passage, 4 A c
E.; Pouyssegur, J.: Localization of the antiporter gene(APNH) and
chromosomal homology between human 1p, mouse 4 and Chinesehamster 2q.
(Abstract) Cytogenet. Cell Genet. 51: 1041, 1989.

GAM63 348 SLC9A1 Mattei, M.- G.; Sardet, C.; Franchi, A.; Pouyssegur, J.: Chromosomalmapping 4 A c
of the amiloride- sensitive Na+/H+ antiporter gene. (Abstract)
Cytogenet.Cell Genet. 46: 658- 659, 1987.

GAM63 348 SLC9A1 Mattei, M.- G.; Sardet, C.; Franchi, A.; Pouyssegur, J.: The humanamiloride- 4 A c
sensitive Na+/H+ antiporter: localization to chromosome1 by in situ
hybridization. Cytogenet. Cell Genet. 48: 6- 8, 1988.

GAM63 348 SLC9A1 Mendoza, S. A.: The Na+/H+ antiport is a mediator of cell proliferation. 4 A c
ActaPaediat. Scand. 76: 545- 547, 1987.

GAM63 348 SLC9A1 Morahan, G.; Rakar, S.: Localization of the mouse Na+/H+ exchangergene on 4 A c
distal chromosome 4. Genomics 15: 231- 232, 1993.

GAM63 348 SLC9A1 Sardet, C.; Franchi, A.; Pouyssegur, J.: Molecular cloning, 4 A c
primarystructure, and expression of the human growth factor- activatable
Na(+)/H(+)antiporter. Cell 56: 271- 280, 1989.

GAM63 348 SLC9A3R1 Bonilha, V. L.; Rodriguez- Boulan, E.: Polarity and developmentalregulation 4 A c
of two PDZ proteins in the retinal pigment epithelium. Invest.Ophthal. Vis.
Sci. 42: 3274- 3282, 2001.

GAM63 348 SLC9A3R1 Murthy, A.; Gonzalez- Agosti, C.; Cordero, E.; Pinney, D.; Candia,C.; 4 A c
Solomon, F.; Gusella, J.; Ramesh, V.: NHE- RF, a regulatory cofactorfor
Na(+)- H(+) exchange, is a common interactor for merlin and ERM(MERM)
proteins. J. Biol. Chem. 273: 1273- 1276, 1998.

GAM63 348 SLC9A3R1 Reczek, D.; Berryman, M.; Bretscher, A.: Identification of EBP50:a PDZ- 4 A c
containing phosphoprotein that associates with members of theezrin- radixin-
moesin family. J. Cell Biol. 139: 169- 179, 1997.

GAM63 348 SLC9A3R1 Shenolikar, S.; Voltz, J. W.; Minkoff, C. M.; Wade, J. B.; Weinman,E. J.: 4 A c
Targeted disruption of the mouse NHERF- 1 gene promotes internalizationof
proximal tubule sodium- phosphate cotransporter type IIa and renalphosphate
wasting. Proc. Nat. Acad. Sci. 99: 11470- 11475, 2002.

GAM63 348 SMARCD1 Ring, H. Z.; Vameghi- Meyers, V.; Wang, W.; Crabtree, G. R.; Francke,U.: 4 A c
Five SWI/SNF- related, matrix- associated, actin- dependent regulatorof
chromatin (SMARC) genes are dispersed in the human genome. Genomics 51:140-
143, 1998.

GAM63 348 SMARCD1 Wang, W.; Xue, Y.; Zhou, S.; Kuo, A.; Cairns, B. R.; Crabtree,G. R.: 4 A c
Diversity and specialization of mammalian SWI/SNF complexes. GenesDev. 10:
2117- 2130, 1996.

GAM63 348 SMCX Agulnik, A. I.; Mitchell, M. J.; Lerner, J. L.; Woods, D. R.; Bishop,C. E.: 4 A c
A mouse Y chromosome gene encoded by a region essential forspermatogenesis
and expression of male- specific minor histocompatibilityantigens. Hum.
Molec. Genet. 3: 873- 878, 1994.

GAM63 348 SMCX Agulnik, A. I.; Mitchell, M. J.; Mattei, M.- G.; Borsani, G.; Avner,P. A.; 4 A c
Lerner, J. L.; Bishop, C. E.: A novel X gene with a widelytranscribed Y-
linked homologue escapes X- inactivation in mouse andhuman. Hum. Molec.
Genet. 3: 879- 884, 1994.

GAM63 348 SMCX Brown, C. J.; Miller, A. P.; Carrel, L.; Rupert, J. L.; Davies,K. E.; 4 A c
Willard, H. F.: The DXS423E gene in Xp11.21 escapes X
chromosomeinactivation. Hum. Molec. Genet. 4: 251- 255, 1995.

GAM63 348 SMCX Lingenfelter, P. A.; Adler, D. A.; Poslinski, D.; Thomas, S.; Elliott,R. W.; 4 A c
Chapman, V. M.; Disteche, C. M.: Escape from X inactivationof Smcx is
preceded by silencing during mouse development. NatureGenet. 18: 212- 213,
1998.

GAM63 348 SMCX Wu, J.; Ellison, J.; Salido, E.; Yen, P.; Mohandas, T.; Shapiro,L. J.: 4 A c
Isolation and characterization of XE169, a novel human genethat escapes X-
inactivation. Hum. Molec. Genet. 3: 153- 160, 1994.

GAM63 348 SMCX Wu, J.; Salido, E. C.; Yen, P. H.; Mohandas, T. K.; Heng, H. H.Q.; Tsui, L.- 4 A c
C.; Park, J.; Chapman, V. M.; Shapiro, L. J.: The murineXe169 gene escapes
X- inactivation like its human homologue. NatureGenet. 7: 491- 496, 1994.

GAM63 348 SOX9 Angle, C. R.: Congenital bowing and angulation of the long bones. Pediatrics 4 A c
13:257- 268, 1954.

GAM63 348 SOX9 Bain, A. D.; Barrett, H. S.: Congenital bowing of the long bones:report of a 4 A c
case. Arch. Dis. Child. 34: 516- 524, 1959.

GAM63 348 SOX9 Bell, D. M.; Leung, K. K. H.; Wheatley, S. C.; Ng, L. J.; Zhou,S.; Ling, K. 4 A c
W.; Sham, M. H.; Koopman, P.; Tam, P. P. L.; Cheah, K.S. E.: SOX9 directly
regulates the type- II collagen gene. NatureGenet. 16: 174- 178, 1997.

GAM63 348 SOX9 Bi, W.; Huang, W.; Whitworth, D. J.; Deng, J. M.; Zhang, Z.; Behringer,R. 4 A c
R.; de Crombrugghe, B.: Haploinsufficiency of Sox9 results indefective
cartilage primordia and premature skeletal mineralization. Proc.Nat. Acad.
Sci. 98: 6698- 6703, 2001.

GAM63 348 SOX9 Bishop, C. E.; Whitworth, D. J.; Qin, Y.; Agoulnik, A. I.; Agoulnik,I. U.; 4 A c
Harrison, W. R.; Behringer, R. R.; Overbeek, P. A.: A transgenicinsertion
upstream of Sox9 is associated with dominant XX sex reversalin the mouse.
Nature Genet. 26: 490- 494, 2000.

GAM63 348 SOX9 Caffey, J. P.: Prenatal bowing and thickening of tubular bones,with multiple 4 A c
cutaneous dimples in arms and legs: a congenital syndromeof mechanical
origin. Am. J. Dis. Child. 74: 543- 562, 1947.

GAM63 348 SOX9 Cameron, F. J.; Hageman, R. M.; Cooke- Yarborough, C.; Kwok, C.;Goodwin, L. 4 A c
L.; Sillence, D. O.; Sinclair, A. H.: A novel germ linemutation in SOX9
causes familial campomelic dysplasia and sex reversal. Hum.Molec. Genet. 5:
1625- 1630, 1996.

GAM63 348 SOX9 Cameron, F. J.; Sinclair, A. H.: Mutations in SRY and SOX9: testis- 4 A c
determininggenes. Hum. Mutat. 9: 388- 395, 1997.

GAM63 348 SOX9 Cooke, C. T.; Mulcahy, M. T.; Cullity, G. J.; Watson, M.; Sprague,P.: 4 A c
Campomelic dysplasia with sex reversal: morphological and cytogeneticstudies
of a case. Pathology 17: 526- 529, 1985.

GAM63 348 SOX9 Cremin, B. J.; Orsmond, G.; Beighton, P.: Autosomal recessiveinheritance in 4 A c
camptomelic dwarfism.(Letter) Lancet I: 488- 489,1973.

GAM63 348 SOX9 Dagna Bricarelli, F.; Fraccaro, M.; Lindsten, J.; Muller, U.;Baggio, P.; 4 A c
Carbone, L. D. L.; Hjerpe, A.; Lindgren, F.; Mayerova,A.; Ringertz, H.;
Ritzen, E. M.; Rovetta, D. C.; Sicchero, C.; Wolf,U.: Sex- reversed XY
females with campomelic dysplasia are H- Y negative. Hum.Genet. 57: 15- 22,

1981.

GAM63 348 SOX9 Ebensperger, C.; Jager, R. J.; Lattermann, U.; Dagna Bricarelli,F.; Keutel, J.; Lindsten, J.; Rehder, H.; Muller, U.; Wolf, U.: Noevidence of mutations in four candidate genes for male sex determination/differentiationin sex-reversed XY females with campomelic dysplasia. Ann. Genet. 34:233- 238, 1991. 4 A c

GAM63 348 SOX9 Fontaine, G.; Walbaum, R.; Farriaux, J. P.; Tilmont, P.; Peuzin,F.; Delecour, M.: Le conseil genetique dans la dysplasie campomelique(a propos de deux observations). J. Genet. Hum. 28: 267- 279, 1980. 4 A c

GAM63 348 SOX9 Foster, J. W.; Dominguez- Steglich, M. A.; Guioli, S.; Kwok, C.;Weller, P. A.; Stevanovic, M.; Weissenbach, J.; Mansour, S.; Young,I. D.; Goodfellow, P. N.; Brook, J. D.; Schafer, A. J.: Campomelicdysplasia and autosomal sex reversal caused by mutations in an SRY- relatedgene. Nature 372: 525- 530, 1994. 4 A c

GAM63 348 SOX9 Friedrich, U.; Schaefer, E.; Meinecke, P.: Campomelic dysplasiawithout overt campomelia. Clin. Dysmorph. 1: 172- 178, 1992. 4 A c

GAM63 348 SOX9 Fryns, J. P.; van den Berghe, K.; van Assche, A.; van den Berghe,H.: Prenatal diagnosis of campomelic dwarfism. Clin. Genet. 19:199- 201, 1981. 4 A c

GAM63 348 SOX9 Gasca, S.; Canizares, J.; de Santa Barbara, P.; Mejean, C.; Poulat,F.; Berta, P.; Boizet- Bonhoure, B.: A nuclear export signal withinthe high mobility group domain regulates the nucleocytoplasmic translocationof SOX9 during sexual determination. Proc. Nat. Acad. Sci. 99: 11199- 11204,2002. 4 A c

GAM63 348 SOX9 Glass, R. B. J.; Rosenbaum, K. N.: Acampomelic campomelic dysplasia:further radiographic variations. Am. J. Med. Genet. 69: 29- 32, 1997. 4 A c

GAM63 348 SOX9 Hall, B.; Spranger, J. W.: Campomelic dysplasia: further elucidationof a distinct entity. Am. J. Dis. Child. 134: 285- 289, 1980. 4 A c

GAM63 348 SOX9 Hoefnagel, D.; Wurster- Hill, D. H.; Dupree, W. B.; Benirschke,K.; Fuld, G. L.: Camptomelic dwarfism associated with XY- gonadaldysgenesis and chromosome anomalies. Clin. Genet. 13: 489- 499, 1978. 4 A c

GAM63 348 SOX9 Houston, C. S.; Opitz, J. M.; Spranger, J. W.; Macpherson, R.I.; Reed, M. H.; Gilbert, E. F.; Herrmann, J.; Schinzel, A.: Thecampomelic syndrome: review, report of 17 cases, and follow- up onthe currently 17- year- old boy first reported by Maroteaux et al in1971. Am. J. Med. Genet. 15: 3- 28, 1983. 4 A c

GAM63 348 SOX9 Hovmoller, M. L.; Osuna, A.; Eklof, O.; Fredga, K.; Hjerpe, A.;Lindsten, J.; Ritzen, M.; Stanescu, V.; Svenningsen, N.: Camptomelicdwarfism. A genetically determined mesenchymal disorder combined withsex reversal. Hereditas 86: 51- 62, 1977. 4 A c

GAM63 348 SOX9 Huang, W.; Chung, U.; Kronenberg, H. M.; de Crombrugghe, B.:The chondrogenic transcription factor Sox9 is a target of signalingby the parathyroid hormone- related peptide in the growth plate ofendochondral bones. Proc. Nat. Acad. Sci. 98: 160- 165, 2001. 4 A c

GAM63 348 SOX9 Kanai, Y.; Koopman, P.: Structural and functional characterizationof the mouse Sox9 promoter: implications for campomelic dysplasia. Hum.Molec. Genet. 8: 691- 696, 1999. 4 A c

GAM63 348 SOX9 Lahn, B. T.; Page, D. C.: Four evolutionary strata on the humanX chromosome. Science 286: 964- 967, 1999. 4 A c

GAM63 348 SOX9 Lahn, B. T.; Page, D. C.: Functional coherence of the human Ychromosome. Science 278: 675- 680, 1997. 4 A c

GAM63 348 SOX9 Lee, F. A.; Issacs, H.; Strauss, J.: The 'camptomelic' syndrome.Short life- 4 A c

span dwarfism with respiratory distress, hypotonia, peculiarfacies, and multiple skeletal and cartilaginous deformities. Am.J. Dis. Child. 124: 485-496, 1972.

GAM63 348 SOX9 Lynch, S. A.; Gaunt, M. L.; Minford, A. M. B.: Campomelic dysplasia:evidence of autosomal dominant inheritance. J. Med. Genet. 30: 683- 686,1993. 4 A c

GAM63 348 SOX9 Macpherson, R. I.; Skinner, S. A.; Donnenfeld, A. E.: Acampomeliccampomelic dysplasia. Pediat. Radiol. 20: 90- 93, 1989. 4 A c

GAM63 348 SOX9 Mansour, S.; Hall, C. M.; Pembrey, M. E.; Young, I. D.: A clinicaland genetic study of campomelic dysplasia. J. Med. Genet. 32: 415- 420,1995. 4 A c

GAM63 348 SOX9 Maraia, R.; Saal, H. M.; Wangsa, D.: A chromosome 17q de novoparacentric inversion in a patient with campomelic dysplasia; casereport and etiologic hypothesis. Clin. Genet. 39: 401- 408, 1991. 4 A c

GAM63 348 SOX9 Maroteaux, P.; Spranger, J. W.; Opitz, J. M.; Kucera, J.; Lowry,R. B.; Schimke, R. N.; Kagan, S. M.: Le syndrome campomelique. PresseMed. 22: 1157-1162, 1971. 4 A c

GAM63 348 SOX9 Mellows, H. J.; Pryse- Davies, J.; Bennett, M. J.; Carter, C. O.: The camptomelic syndrome in two female siblings. Clin. Genet. 18:137- 141, 1980. 4 A c

GAM63 348 SOX9 Meyer, J.; Sudbeck, P.; Held, M.; Wagner, T.; Schmitz, M. L.;Bricarelli, F. D.; Eggermont, E.; Friedrich, U.; Haas, O. A.; Kobelt,A.; Leroy, J. G.; van Maldergem, L.; Michel, E.; Mitulla, B.; Pfeiffer,R. A.; Schinzel, A.; Schmidt, H.; Scherer, G.: Mutational analysisof the SOX9 gene in campomelic dysplasia and autosomal sex reversal:lack of genotype/phenotype correlations. Hum. Molec. Genet. 6: 91- 98,1997. 4 A c

GAM63 348 SOX9 Moedjono, S. J.; Crandall, B. F.; Sparkes, R. S.; Feldman, G.M.; Austin, G. E.; Perry, S.: The campomelic syndrome in a singletonand monozygotic twins. Clin. Genet. 18: 397- 401, 1980. 4 A c

GAM63 348 SOX9 Moog, U.; Jansen, N. J. G.; Scherer, G.; Schrander- Stumpel, C.T. R. M.: Acampomelic campomelic syndrome. Am. J. Med. Genet. 104:239- 245, 2001. 4 A c

GAM63 348 SOX9 Morais da Silva, S.; Hacker, A.; Harley, V.; Goodfellow, P.; Swain,A.; Lovell- Badge, R.: Sox9 expression during gonadal developmentimplies a conserved role for the gene in testis differentiation inmammals and birds. Nature Genet. 14: 62- 68, 1996. 4 A c

GAM63 348 SOX9 Murakami, S.; Kan, M.; McKeehan, W. L.; de Crombrugghe, B.: Up- regulationof the chondrogenic Sox9 gene by fibroblast growth factors is mediatedby the mitogen- activated protein kinase pathway. Proc. Nat. Acad.Sci. 97: 1113-1118, 2000. 4 A c

GAM63 348 SOX9 Ninomiya, S.; Isomura, M.; Narahara, K.; Seino, Y.; Nakamura,Y.: Isolation of a testis- specific cDNA on chromosome 17q from aregion adjacent to the breakpoint of t(12;17) observed in a patientwith acampomelic campomelic dysplasia and sex reversal. Hum. Molec.Genet. 5: 69- 72, 1996. 4 A c

GAM63 348 SOX9 Ninomiya, S.; Yokoyama, Y.; Teraoka, M.; Mori, R.; Inoue, C.;Yamashita, S.; Tamai, H.; Funato, M.; Seino, Y.: A novel mutation(296 del G) of the SOX9 gene in a patient with campomelic syndromeand sex reversal. Clin. Genet. 58: 224- 227, 2000. 4 A c

GAM63 348 SOX9 Olney, P. N.; Kean, L. S.; Graham, D.; Elsas, L. J.; May, K. M.: Campomelic syndrome and deletion of SOX9. Am. J. Med. Genet. 84:20- 24, 1999. 4 A c

GAM63 348 SOX9 Ozkilic, A.; Seven, M.; Yuksel, A.: A case of acampomelic campomelicdysplasia. Genet. Counsel. 13: 23- 28, 2002. 4 A c

GAM63 348 SOX9 Patel, M.; Dorman, K. S.; Zhang, Y.- H.; Huang, B.- L.; Arnold,A. P.; Sinsheimer, J. S.; Vilain, E.; McCabe, E. R. B.: Primate DAX1,SRY, and SOX9: 4 A c

evolutionary stratification of sex- determination pathway. Am.J. Hum. Genet. 68: 275- 280, 2001.

GAM63 348 SOX9 Pfeifer, D.; Kist, R.; Dewar, K.; Devon, K.; Lander, E. S.; Birren,B.; Korniszewski, L.; Back, E.; Scherer, G.: Campomelic dysplasiatranslocation breakpoints are scattered over 1 Mb proximal to SOX9:evidence for an extended control region. Am. J. Hum. Genet. 65:111- 124, 1999. 4 A c

GAM63 348 SOX9 Puck, S. M.; Haseltine, F. P.; Francke, U.: Absence of H- Y antigenin an XY female with campomelic dysplasia. Hum. Genet. 57: 23- 27,1981. 4 A c

GAM63 348 SOX9 Rimoin, D. L.: Personal Communication. Torrance, Calif. 8/12/1976. 4 A c

GAM63 348 SOX9 Rodriguez, J. I.: Vascular anomalies in campomelic syndrome. Am.J. Med. Genet. 46: 185- 192, 1993. 4 A c

GAM63 348 SOX9 Savarirayan, R.; Bankier, A.: Acampomelic campomelic dysplasiawith de novo 5q;17q reciprocal translocation and severe phenotype. J.Med. Genet. 35: 597- 599, 1998. 4 A c

GAM63 348 SOX9 Schimke, R. N.: XY sex- reversed campomelia- - possibly an X- linkeddisorder? (Letter) Clin. Genet. 16: 62- 63, 1979. 4 A c

GAM63 348 SOX9 Schmickel, R. D.: Contiguous gene syndromes: a component of recognizablesyndromes. J. Pediat. 109: 231- 241, 1986. 4 A c

GAM63 348 SOX9 Shafai, T.; Schwartz, L.: Camptomelic syndrome in siblings. J.Pediat. 89: 512- 513, 1976. 4 A c

GAM63 348 SOX9 Spranger, J.: Advances in bone dysplasias. (Abstract) SixthInt. Cong. Hum. Genet. Jerusalem , 1981. 4 A c

GAM63 348 SOX9 Stuve, A.; Wiedemann, H.- R.: Congenital bowing of the long bonesin two sisters. (Letter) Lancet I: 495, 1971. 4 A c

GAM63 348 SOX9 Sudbeck, P.; Schmitz, M. L.; Baeuerle, P. A.; Scherer, G.: Sexreversal by loss of the C- terminal transactivation domain of humanSOX9. Nature Genet. 13: 230- 232, 1996. 4 A c

GAM63 348 SOX9 Thong, M.- K.; Scherer, G.; Kozlowski, K.; Haan, E.; Morris, L.: Acampomelic campomelic dysplasia with SOX9 mutation. Am. J. Med.Genet. 93: 421- 425, 2000. 4 A c

GAM63 348 SOX9 Thurmon, T. F.; De Fraites, E. B.; Anderson, E. E.: Familialcampomelic dwarfism. J. Pediat. 83: 841- 843, 1973. 4 A c

GAM63 348 SOX9 Tommerup, N.; Schempp, W.; Meinecke, P.; Pedersen, S.; Bolund,L.; Brandt, C.; Goodpasture, C.; Guldberg, P.; Held, K.; Reinwein,H.; Saugstad, O. D.; Scherer, G.; Skjeldal, O.; Toder, R.; Westvik,J.; van der Hagen, C. B.; Wolf, U.: Assignment of an autosomal sexreversal locus (SRA1) and campomelic dysplasia (CMPD1) to 17q24.3- q25.1. NatureGenet. 4: 170- 174, 1993. 4 A c

GAM63 348 SOX9 Vidal, V. P. I.; Chaboissier, M.- C.; de Rooij, D. G.; Schedl,A.: Sox9 induces testis development in XX transgenic mice. NatureGenet. 28: 216- 217, 2001. 4 A c

GAM63 348 SOX9 Wagner, T.; Wirth, J.; Meyer, J.; Zabel, B.; Held, M.; Zimmer,J.; Pasantes, J.; Dagna Bricarelli, F.; Keutel, J.; Hustert, E.; Wolf,U.; Tommerup, N.; Schempp, W.; Scherer, G.: Autosomal sex reversaland campomelic dysplasia are caused by mutations in and around theSRY- related gene SOX9. Cell 79: 1111- 1120, 1994. 4 A c

GAM63 348 SOX9 Weller, S. D. V.: Hypophosphatasia with congenital dimples. Proc.Roy. Soc. Med. 52: 637, 1959. 4 A c

GAM63 348 SOX9 Wirth, J.; Wagner, T.; Meyer, J.; Pfeiffer, R. A.; Tietze, H.- U.;Schempp, W.; Scherer, G.: Translocation breakpoints in three patientswith campomelic dysplasia and autosomal sex reversal map more than130 kb from SOX9. Hum. 4 A c

Genet. 97: 186- 193, 1996.

GAM63 348 SOX9 Wright, E.; Hargrave, M. R.; Christiansen, J.; Cooper, L.; Kun,J.; Evans, T.; Gangadharan, U.; Greenfield, A.; Koopman, P.: TheSry- related gene Sox9 is expressed during chondrogenesis in mouseembryos. Nature Genet. 9: 15- 20, 1995. 4 A c

GAM63 348 SOX9 Wunderle, V. M.; Critcher, R.; Hastie, N.; Goodfellow, P. N.;Schedl, A.: Deletion of long- range regulatory elements upstream ofSOX9 causes campomelic dysplasia. Proc. Nat. Acad. Sci. 95: 10649- 10654,1998. 4 A c

GAM63 348 SOX9 Young, I. D.; Zuccollo, J. M.; Maltby, E. L.; Broderick, N. J.: Campomelic dysplasia associated with a de novo 2q;17q reciprocaltranslocation. J. Med. Genet. 29: 251- 252, 1992. 4 A c

GAM63 348 SSX1 Cannizzaro, L. A.; Dal Cin, P.; Mendez, M. J.; Sandberg, A. A.: Sublocalization of Xp breakpoint in the X;18 chromosome translocationof synovial sarcoma. (Abstract) Cytogenet. Cell Genet. 51: 974,1989. 4 A c

GAM63 348 SSX1 Chand, A.; Clark, J.; Cooper, C. S.; Craig, I. W.: Long- rangeorganization of reiterated sequences, including the SSX1 cDNA, atthe OATL1 cluster in Xp11.23. Genomics 30: 545- 552, 1995. 4 A c

GAM63 348 SSX1 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994. 4 A c

GAM63 348 SSX1 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995. 4 A c

GAM63 348 SSX1 Enzinger, F. M.; Weiss, S. W.: Soft Tissue Tumors. St. Louis:C. V. Mosby (pub.) 1983. Pp. 519- 549. 4 A c

GAM63 348 SSX1 Gilgenkrantz, S.; Mujica, P.; Chery, M.; Gregoire, M.- J.; Leotard,B.; Mandel, J.- L.: Mapping the breakpoint at Xp11.2 in synovial sarcoma.(Abstract) Cytogenet. Cell Genet. 51: 1004, 1989. 4 A c

GAM63 348 SSX1 Griffin, C. A.; Emanuel, B. S.: Translocation (X;18) in a synovialsarcoma. (Letter) Cancer Genet. Cytogenet. 26: 181- 183, 1987. 4 A c

GAM63 348 SSX1 Karakousis, C. P.; Dal Cin, P.; Turc- Carel, C.; Limon, J.; Sandberg,A. A.: Chromosomal changes in soft- tissue sarcomas: a new diagnosticparameter. Arch. Surg. 122: 1257- 1260, 1987. 4 A c

GAM63 348 SSX1 Knight, J. C.; Martin, C. A.; Warren, W.; Smith, S.; Westbury,G.; Fisher, C.; Gusterson, B. A.; Cooper, C. S.; Reeves, B. R.: Mappingthe translocation t(X;18)(p11.2;q11.2) in human synovial sarcoma.(Abstract) Cytogenet. Cell Genet. 51: 1023, 1989. 4 A c

GAM63 348 SSX1 Knight, J. C.; Reeves, B. R.; Kearney, L.; Monaco, A. P.; Lehrach,H.; Cooper, C. S.: Localization of the synovial sarcoma t(X;18)(p11.2;q11.2)breakpoint by fluorescence in situ hybridization. Hum. Molec. Genet. 1:633- 637, 1992. 4 A c

GAM63 348 SSX1 Miozzo, M.; Sozzi, G.; Cariani, C. T.; Di Palma, S.; Luksch, R.;Azzarelli, A.; Pierotti, M. A.; Della Porta, G.: A synovial sarcomawith t(X;18)(p11;q11) in a patient with Turner's syndrome. GenesChromosomes Cancer 4: 192- 193, 1992. 4 A c

GAM63 348 SSX1 Sinke, R. J.; de Leeuw, B.; Janssen, H. A. P.; Olde Weghuis, D.;Suijkerbuijk, R. F.; Meloni, A. M.; Gilgenkrantz, S.; Berger, W.;Ropers, H. H.; Sandberg, A. A.; Geurts van Kessel, A.: Localizationof X chromosome 4 A c

short arm markers relative to synovial sarcoma- andrenal adenocarcinoma-associated translocation breakpoints. Hum. Genet. 92:305- 308, 1993.

GAM63 348 SSX1 Smith, S.; Reeves, B. R.; Wong, L.; Fisher, C.: A consistentchromosome translocation in synovial sarcoma. (Letter) Cancer Genet.Cytogenet. 26: 179-180, 1987. 4 A c

GAM63 348 SSX1 Turc- Carel, C.; Dal Cin, P.; Limon, J.; Rao, U.; Li, F. P.; Corson,J. M.; Zimmerman, R.; Parry, D. M.; Cowan, J. M.; Sandberg, A. A.: Involvement of chromosome X in primary cytogenetic change in humanneoplasia: nonrandom translocation in synovial sarcoma. Proc. Nat.Acad. Sci. 84: 1981- 1985, 1987. 4 A c

GAM63 348 SSX1 Ueda, T.; Aozasa, K.; Tsujimoto, M.; Uchida, A.; Taniwaki, M.;Abe, T.: Translocation X;18 and insertion 15;11 in a case of synovialsarcoma. Cancer Genet. Cytogenet. 30: 183- 185, 1988. 4 A c

GAM63 348 SSX1 Wang- Wuu, S.; Soukup, S. W.; Lange, B. J.: Another synovial sarcomawith t(X;18). Cancer Genet. Cytogenet. 29: 179- 181, 1987. 4 A c

GAM63 348 SYNGR1 Janz, R.; Sudhof, T. C.; Hammer, R. E.; Unni, V.; Siegelbaum, S.A.; Bolshakov, V. Y.: Essential roles in synaptic plasticity forsynaptogyrin I and synaptophysin I. Neuron 24: 687- 700, 1999. 4 A c

GAM63 348 SYNGR1 Kedra, D.; Pan, H.- Q.; Seroussi, E.; Fransson, I.; Guilbaud, C.;Collins, J. E.; Dunham, I.; Blennow, E.; Roe, B. A.; Piehl, F.; Dumanski,J. P.: Characterization of the human synaptogyrin gene family. Hum.Genet. 103: 131-141, 1998. 4 A c

GAM63 348 SYNGR1 McMahon, H. T.; Bolshakov, V. Y.; Janz, R.; Hammer, R. E.; Siegelbaum,S. A.; Sudhof, T. C.: Synaptophysin, a major synaptic vesicle protein,is not essential for neurotransmitter release. Proc. Nat. Acad. Sci. 93:4760- 4764, 1996. 4 A c

GAM63 348 TEM7 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in mice and humans. Cancer Res. 61: 6649- 6655, 2001. 4 A c

GAM63 348 TEM7 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.; Kinzler, K. W.: Genes expressed in human tumor endothelium. Science 289:1197- 1202, 2000. 4 A c

GAM63 348 THPO Bartley, T. D.; Bogenberger, J.; Hunt, P.; Li, Y.- S.; Lu, H. S.;Martin, F.; Chang, M.- S.; Samal, B.; Nichol, J. L.; Swift, S.; Johnson,M. J.; Hsu, R.-Y.; and 41 others: Identification and cloning ofa megakaryocyte growth and development factor that is a ligand forthe cytokine receptor Mpl. Cell 77: 1117- 1124, 1994. 4 A c

GAM63 348 THPO Chang, M.- S.; Hsu, R.- Y.; McNinch, J.; Copeland, N. G.; Jenkins,N. A.: The gene for murine megakaryocyte growth and development factor(thrombopoietin, Thpo) is located on mouse chromosome 16. Genomics 26:636- 637, 1995. 4 A c

GAM63 348 THPO Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.; Perkins,C.; Mar, V.; Suggs, S.; Welcher, A.; Li, L.; Lu, H.; Bartley, T.;Hunt, P.; Martin, F.; Samal, B.; Bogenberger, J.: Cloning and characterizationof the human megakaryocyte growth and development factor (MGDF) gene. J.Biol. Chem. 270: 511- 514, 1995. 4 A c

GAM63 348 THPO de Sauvage, F. J.; Hass, P. E.; Spencer, S. D.; Malloy, B. E.;Gurney, A. L.; Spencer, S. A.; Darbonne, W. C.; Henzel, W. J.; Wong,S. C.; Kuang, W.- J.; Oles, K. J.; Hultgren, B.; Solberg, L. A., Jr.;Goeddel, D. V.; Eaton, D. L.: Stimulation of megakaryocytopoiesisand thrombopoiesis by the c- Mpl ligand. 4 A c

Nature 369: 533- 538, 1994.

GAM63 348 THPO Farese, A. M.; Hunt, P.; Grab, L. B.; MacVittie, T. J.: 4 A c
Combinedadministration of recombinant human megakaryocyte growth and developmentfactor and granulocyte colony- stimulating factor enhances multilineagehematopoietic reconstitution in nonhuman primates after radiation- inducedmarrow aplasia. J. Clin. Invest. 97: 2145- 2151, 1996.

GAM63 348 THPO Foster, D. C.; Sprecher, C. A.; Grant, F. J.; Kramer, J. M.; Kuijper,J. L.; 4 A c
Holly, R. D.; Whitmore, T. E.; Heipel, M. D.; Bell, L. A.;Ching, A. F. T.; McGrane, V.; Hart, C.; O'Hara, P. J.; Lok, S.: Humanthrombopoietin: gene structure, cDNA sequence, expression, and chromosomallocalization. Proc. Nat. Acad. Sci. 91: 13023- 13027, 1994.

GAM63 348 THPO Ghilardi, N.; Wiestner, A.; Kikuchi, M.; Ohsaka, A.; Skoda, R.C.: Hereditary 4 A c
thrombocythaemia in a Japanese family is caused bya novel point mutation in the thrombopoietin gene. Brit. J. Haemat. 107:310- 316, 1999.

GAM63 348 THPO Kaushansky, K.; Lok, S.; Holly, R. D.; Broudy, V. C.; Lin, N.;Bailey, M. C.; 4 A c
Forstrom, J. W.; Buddle, M. M.; Oort, P. J.; Hagen,F. S.; Roth, G. J.; Papayannopoulou, T.; Foster, D. C.: Promotionof megakaryocyte progenitor expansion and differentiation by the c- Mplligand thrombopoietin. Nature 369: 568- 571, 1994.

GAM63 348 THPO Kikuchi, M.; Tayama, T.; Hayakawa, H.; Takahashi, I.; Hoshino,H.; Ohsaka, 4 A c
A.: Familial thrombocytosis. Brit. J. Haemat. 89: 900- 902,1995.

GAM63 348 THPO Kondo, T.; Okabe, M.; Sanada, M.; Kurosawa, M.; Suzuki, S.; Kobayashi,M.; 4 A c
Hosokawa, M.; Asaka, M.: Familial essential thrombocythemia associatedwith one- base deletion in the 5- prime- untranslated region of the thrombopoietingene. Blood 92: 1091- 1096, 1998.

GAM63 348 THPO Li, J.; Yang, C.; Xia, Y.; Bertino, A.; Glaspy, J.; Roberts, M.;Kuter, D. 4 A c
J.: Thrombocytopenia caused by the development of antibodiesto thrombopoietin. Blood 98: 3241- 3248, 2001.

GAM63 348 THPO Lok, S.; Kaushansky, K.; Holly, R. D.; Kuijper, J. L.; Lofton- Day,C. E.; 4 A c
Oort, P. J.; Grant, F. J.; Heipel, M. D.; Burkhead, S. K.;Kramer, J. M.; Bell, L. A.; Sprecher, C. A.; Blumberg, H.; Johnson,R.; Prunkard, D.; Ching, A. F. T.; Mathewes, S. L.; Bailey, M. C.;Forstrom, J. W.; Buddle, M. M.; Osborn, S. G.; Evans, S. J.; Sheppard,P. O.; Presnell, S. R.; O'Hara, P. J.; Hagen, F. S.; Roth, G. J.;Foster, D. C.: Cloning and expression of murine thrombopoietin cDNAand stimulation of platelet production in vivo. Nature 369: 565- 568,1994.

GAM63 348 THPO Metcalf, D.: Thrombopoietin: at last. Nature 369: 519- 520,1994. 4 A c

GAM63 348 THPO Methia, N.; Louache, F.; Vainchenker, W.; Wendling, F.: 4 A c
Oligodeoxynucleotidesantisense to the proto- oncogene c- mpl specifically inhibit in vitromegakaryocytopoiesis. Blood 82: 1395- 1401, 1993.

GAM63 348 THPO Ratajczak, M. Z.; Ratajczak, J.; Marlicz, W.; Pletcher, C. H.,Jr.; 4 A c
Machalinski, B.; Moore, J.; Hung, H.; Gewirtz, A. M.: Recombinanthuman thrombopoietin (TPO) stimulates erythropoiesis by inhibitingerythroid progenitor cell apoptosis. Brit. J. Haemat. 98: 8- 17,1997.

GAM63 348 THPO Sohma, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.;Shimada, Y.; 4 A c
Kawamura, K.; Miyazaki, H.: Molecular cloning and chromosomallocalization of the human thrombopoietin gene. FEBS Lett. 353: 57- 61,1994.

GAM63 348 THPO Vigon, I.; Mornon, J.- P.; Cocault, L.; Mitjavila, M.- T.; Tambourin,P.; 4 A c
Gisselbrecht, S.; Souyri, M.: Molecular cloning and characterizationof MPL, the human homolog of the v- mpl oncogene: identification ofa member of the

hematopoietic growth factor receptor superfamily. Proc.Nat. Acad. Sci. 89: 5640- 5644, 1992.

GAM63 348 THPO Wendling, F.; Maraskovsky, E.; Debili, N.; Florindo, C.; Teepe,M.; Titeux, M.; Methia, N.; Breton- Gorius, J.; Cosman, D.; Vainchenker,W.: c- Mpl ligand is a humoral regulator of megakaryocytopoiesis. Nature 369:571- 574, 1994. 4 A c

GAM63 348 THPO Wiestner, A.; Schlemper, R. J.; van der Maas, A. P. C.; Skoda,R. C.: An activating splice donor mutation in the thrombopoietingene causes hereditary thrombocythaemia. Nature Genet. 18: 49- 52,1998. 4 A c

GAM63 348 TMOD2 Cox, P. R.; Zoghbi, H. Y.: Sequencing, expression analysis, andmapping of three unique human tropomodulin genes and their mouse orthologs. Genomics 63:97- 107, 2000. 4 A c

GAM63 348 TMOD2 Watakabe, A.; Kobayashi, R.; Helfman, D. M.: N- tropomodulin: anovel isoform of tropomodulin identified as the major binding proteinto brain tropomyosin. J. Cell Sci. 109: 2299- 2310, 1996. 4 A c

GAM63 348 B TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999. 4 A c

GAM63 348 B TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997. 4 A c

GAM63 348 B TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997. 4 A c

GAM63 348 B TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998. 4 A c

GAM63 348 B TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997. 4 A c

GAM63 348 B TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997. 4 A c

GAM63 348 B TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997. 4 A c

GAM63 348 B TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997. 4 A c

GAM63 348 B TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997. 4 A c

GAM63 348 B TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA 4 A c

damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141-
143, 1997.

GAM63 348 TNFRSF8 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, 4 A c
H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor-
associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF-
kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997.

GAM63 348 TNFRSF8 Durkop, H.; Latza, U.; Hummel, M.; Eitelbach, F.; Seed, B.; Stein,H.: 4 A c
Molecular cloning and expression of a new member of the nervegrowth factor
receptor family that is characteristic for Hodgkin'sdisease. Cell 68: 421-
427, 1992.

GAM63 348 TNFRSF8 Fonatsch, C.; Latza, U.; Durkop, H.; Rieder, H.; Stein, H.: Assignmentof the 4 A c
human CD30 (Ki- 1) gene to 1p36. Genomics 14: 825- 826, 1992.

GAM63 348 TNFRSF8 Kurts, C.; Carbone, F. R.; Krummel, M. F.; Koch, K. M.; Miller,J. F. A. P.; 4 A c
Heath, W. R.: Signalling through CD30 protects againstautoimmune diabetes
mediated by CD8 T cells. Nature 398: 341- 344,1999.

GAM63 348 TNFRSF8 McClive, P. J.; Morahan, G.: Assignment of the mouse homologuesof 6 loci 4 A c
from HSA1p to chromosomes 3 and 4. Genomics 23: 243- 246,1994.

GAM63 348 TNFRSF8 Stein, H.; Gerdes, J.; Schwab, U.; Lemke, H.; Mason, D. Y.; Ziegler,A.; 4 A c
Schienle, W.; Diehl, V.: Identification of Hodgkin and Sternberg- Reedcells
as a unique cell type derived from a newly detected small cellpopulation.
Int. J. Cancer 30: 445- 449, 1982.

GAM63 348 TPX1 Kasahara, M.; Figueroa, F.; Klein, J.: Random cloning of genesfrom mouse 4 A c
chromosome 17. Proc. Nat. Acad. Sci. 84: 3325- 3328, 1987.

GAM63 348 TPX1 Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.: Cloning 4 A c
and mapping of a testis- specific gene with sequence similarityto a sperm-
coating glycoprotein gene. Genomics 5: 527- 534, 1989.

GAM63 348 TPX1 Kasahara, M.; Passmore, H. C.; Klein, J.: A testis- specific geneTpx- 1 maps 4 A c
between Pgk- 2 and Mep- 1 on mouse chromosome 17. Immunogenetics 29:61- 63,
1989.

GAM63 348 TRPC6 D'Esposito, M.; Strazzullo, M.; Cuccurese, M.; Spalluto, C.; Rocchi,M.; 4 A c
D'Urso, M.; Ciccodicola, A.: Identification and assignment ofthe human
transient receptor potential channel 6 gene TRPC6 to chromosome11q21- q22.
Cytogenet. Cell Genet. 83: 46- 47, 1998.

GAM63 348 TRPC6 Hofmann, T.; Obukhov, A. G.; Schaefer, M.; Harteneck, C.; Gudermann,T.; 4 A c
Schultz, G.: Direct activation of human TRPC6 and TRPC3 channelsby
diacylglycerol. Nature 397: 259- 263, 1999.

GAM63 348 UBE2V1 Deng, L.; Wang, C.; Spencer, E.; Yang, L.; Braun, A.; You, J.;Slaughter, C.; 4 A c
Pickart, C.; Chen, Z. J.: Activation of the I- kappa- Bcomplex by TRAF6
requires a dimeric ubiquitin- conjugating enzyme complexand a unique
polyubiquitin chain. Cell 103: 351- 361, 2000.

GAM63 348 UBE2V1 Hofmann, R. M.; Pickart, C. M.: Noncanonical MMS2- encoded ubiquitin- 4 A c
conjugatingenzyme functions in assembly of novel polyubiquitin chains for
DNArepair. Cell 96: 645- 653, 1999.

GAM63 348 UBE2V1 Rothofsky, M. L.; Lin, S. L.: CROC- 1 encodes a protein which 4 A c
mediatestranscriptional activation of the human FOS promoter. Gene 195:141-
149, 1997.

GAM63 348 UBE2V1 Sancho, E.; Vila, M. R.; Sanchez- Pulido, L.; Lozano, J. J.; Paciucci,R.; 4 A c
Nadal, M.; Fox, M.; Harvey, C.; Bercovich, B.; Loukili, N.; Ciechanover,A.;
Lin, S. L.; Sanz, F.; Estivill, X.; Valencia, A.; Thomson, T.M.: Role of
UEV- 1, an inactive variant of the E2 ubiquitin- conjugatingenzymes, in in

vitro differentiation and cell cycle behavior of HT- 29- M6intestinal mucosecretory cells. Molec. Cell. Biol. 18: 576- 589,1998.

GAM63 348 UNC119 Higashide, T.; Inana, G.: Characterization of the gene for HRG4(UNC119), a novel photoreceptor synaptic protein homologous to unc- 119. Genomics 57:446- 450, 1999. 4 A c

GAM63 348 UNC119 Higashide, T.; McLaren, M. J.; Inana, G.: Localization of HRG4,a photoreceptor protein homologous to unc- 119, in ribbon synapse. Invest.Ophthal. Vis. Sci. 39: 690- 698, 1998. 4 A c

GAM63 348 UNC119 Higashide, T.; Murakami, A.; McLaren, M. J.; Inana, G.: Cloningof the cDNA for a novel photoreceptor protein. J. Biol. Chem. 271:1797- 1804, 1996. 4 A c

GAM63 348 UNC119 Swanson, D. A.; Chang, J. T.; Campochiaro, P. A.; Zack, D. J.;Valle, D.: Mammalian orthologs of C. elegans unc- 119 highly expressedin photoreceptors. Invest. Ophthal. Vis. Sci. 39: 2085- 2094, 1998. 4 A c

GAM63 348 ZNF179 Kimura, T.; Arakawa, Y.; Inoue, S.; Fukushima, Y.; Kondo, I.; Koyama,K.; Hosoi, T.; Orimo, A.; Muramatsu, M.; Nakamura, Y.; Abe, T.; Inazawa,J.: The brain finger protein gene (ZNF179), a member of the RINGfinger family, maps within the Smith- Magenis syndrome region at 17p11.2. Am.J. Med. Genet. 69: 320- 324, 1997. 4 A c

GAM63 348 ZNF179 Matsuda, Y.; Inue, S.; Seki, N.; Hosoi, T.; Orimo, A.; Muramatsu,M.; Hori, T.: Chromosome mapping of human (ZNF179), mouse, and ratgenes for brain finger protein (bfp), a member of the RING fingerfamily. Genomics 33: 325- 327, 1996. 4 A c

GAM64 239 BAPX1 Tribioli, C.; Frasch, M.; Lufkin, T.: Bapx1: an evolutionary conservedhomologue of the Drosophila bagpipe homeobox gene is expressed insplanchnic mesoderm and the embryonic skeleton. Mech. Dev. 65: 145- 162,1997. 3 C c

GAM64 239 BAPX1 Tribioli, C.; Lufkin, T.: Molecular cloning, chromosomal mappingand developmental expression of BAPX1, a novel human homeobox- containinggene homologous to Drosophila bagpipe. Gene 203: 225- 233, 1997. 3 C c

GAM64 239 BAPX1 Yoshiura, K.- I.; Murray, J. C.: Sequence and chromosomal assignmentof human BAPX1, a bagpipe- related gene, to 4p16.1: a candidate genefor skeletal dysplasia. Genomics 45: 425- 428, 1997. 3 C c

GAM64 239 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. W.: Chromosomal localization and racial distributionof the polymorphic human dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352, 1988. 3 C c

GAM64 239 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies three RFLPs. Nucleic Acids Res. 15: 5501 only,1987. 3 C c

GAM64 239 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: Chromosomal localization and racial distribution of the polymorphichDHFR- psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985. 3 C c

GAM64 239 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; Nienhuis, A. W.: Chromosomal organization of the human dihydrofolatereductase genes: dispersion, selective amplification and a novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984. 3 C c

GAM64 239 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in dihydrofolatereductase that confer resistance to methotrexate: potential for clinicalapplication. Hum. Mutat. 11: 259- 263, 1998. 3 C c

GAM64 239 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: 3 C c

Intronless human dihydrofolate reductase genes are derivedfrom processed RNA molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982.

GAM64 239 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association 3 C c
with variation in protein structure. Science 220: 1125- 1129,1983.

GAM64 239 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 3 C c
757 and 807- 812, 1975.

GAM64 239 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the 3 C c
human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5.
Molec. Cell. Biol. 4: 2010- 2016, 1984.

GAM64 239 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater- 3 C c
Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed
ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med.
310: 789- 790, 1984.

GAM64 239 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment 3 C c
of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus
musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986.

GAM64 239 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: 3 C c
Human dihydrofolate reductase gene is located in chromosome 5and is unlinked
to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984.

GAM64 239 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human 3 C c
dihydrofolate reductase gene to band q23 of chromosome 5and of related
pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85,
1985.

GAM64 239 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; 3 C c
Attardi, G.: Chromosomal location of the normal human DHFRgene and of its
amplified copies in methotrexate resistant cell variants.(Abstract)
Cytogenet. Cell Genet. 37: 534 only, 1984.

GAM64 239 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 3 C c
10/7/1983.

GAM64 239 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: 3 C c
Amplification of the human dihydrofolate reductase gene viadouble minutes is
initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000.

GAM64 239 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. 3 C c
A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing
megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976.

GAM64 239 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)- 3 C c
formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967.

GAM64 239 GFRA1 Eng, C.; Myers, S. M.; Kogon, M. D.; Sanicola, M.; Hession, C.;Cate, R. L.; 3 C c
Mulligan, L. M.: Genomic structure and chromosomal localizationof the human
GDNFR- alpha gene. Oncogene 16: 597- 601, 1998.

GAM64 239 GFRA1 GFR- alpha Nomenclature Committee: Nomenclature of GPI- linkedreceptors for 3 C c
the GDNF ligand family. Neuron 19: 485 only, 1997.

GAM64 239 GFRA1 Gorodinsky, A.; Zimonjic, D. B.; Popescu, N. C.; Milbrandt, J.: Assignment 3 C c
of the GDNF family receptor alpha- 1 (GFRA1) to humanchromosome band 10q26
by in situ hybridization. Cytogenet. Cell Genet. 78:289- 290, 1997.

GAM64 239 GFRA1 Jing, S.; Wen, D.; Yu, Y.; Holst, P. L.; Luo, Y.; Fang, M.; Tamir,R.; 3 C c
Antonio, L.; Hu, Z.; Cupples, R.; Louis, J.- C.; Hu, S.; Altrock,B. W.; Fox,
G. M.: GDNF- induced activation of the Ret protein tyrosinekinase is
mediated by GDNFR- alpha, a novel receptor for GDNF. Cell 85:1113- 1124,
1996.

GAM64 239 GFRA1 Paratcha, G.; Ledda, F.; Baars, L.; Coulpier, M.; Besset, V.; Anders,J.; 3 C c
Scott, R.; Ibanez, C. F.: Released GFR- alpha- 1 potentiates
downstreamsignaling, neuronal survival, and differentiation via a novel
mechanismof recruitment of c- Ret to lipid rafts. Neuron 29: 171- 184, 2001.

GAM64 239 GFRA1 Puliti, A.; Cinti, R.; Seri, M.; Ceccherini, I.; Romeo, G.: Assignmentof 3 C c
mouse Gfra1, the homologue of a new human HSCR candidate gene,to the
telomeric region of mouse chromosome 19. Cytogenet. Cell Genet. 78:291- 294,
1997.

GAM64 239 GFRA1 Shefelbine, S. E.; Khorana, S.; Schultz, P. N.; Huang, E.; Thobe,N.; Hu, Z. 3 C c
J.; Fox, G. M.; Jing, S.; Cote, G. J.; Gagel, R. F.: Mutationalanalysis of
the GDNF/RET- GDNFR- alpha signaling complex in a kindredwith vesicoureteral
reflux. Hum. Genet. 102: 474- 478, 1998.

GAM64 239 RAD50 Carney, J. P.; Maser, R. S.; Olivares, H.; Davis, E. M.; Le Beau,M.; Yates, 3 C c
J. R., III; Hays, L.; Morgan, W. F.; Petrini, J. H. J.: The hMre11/hRad50
protein complex and Nijmegen breakage syndrome:linkage of double- strand
break repair to the cellular DNA damage response. Cell 93:477- 486, 1998.

GAM64 239 RAD50 Dolganov, G. M.; Maser, R. S.; Novikov, A.; Tosto, L.; Chong, S.;Bressan, D. 3 C c
A.; Petrini, J. H. J.: Human Rad50 is physically associatedwith human Mre11:
identification of a conserved multiprotein complexiimplicated in
recombinational DNA repair. Molec. Cell Biol. 16:4832- 4841, 1996.

GAM64 239 RAD50 Hopfner, K.- P.; Craig, L.; Moncalian, G.; Zinkel, R. A.; Usui,T.; Owen, B. 3 C c
A. L.; Karcher, A.; Henderson, B.; Bodmer, J.- L.; McMurray,C. T.; Carney,
J. P.; Petrini, J. H. J.; Tainer, J. A.: The Rad50zinc- hook is a structure
joining Mre11 complexes in DNA recombinationand repair. Nature 418: 562-
566, 2002.

GAM64 239 RAD50 Hopfner, K.- P.; Karcher, A.; Craig, L.; Woo, T. T.; Carney, J.P.; Tainer, 3 C c
J. A.: Structural biochemistry and interaction architectureof the DNA
double- strand break repair Mre11 nuclease and Rad50- ATPase. Cell 105:473-
485, 2001.

GAM64 239 RAD50 Luo, G.; Yao, M. S.; Bender, C. F.; Mills, M.; Bladl, A. R.; Bradley,A.; 3 C c
Petrini, J. H. J.: Disruption of mRad50 causes embryonic stemcell lethality,
abnormal embryonic development, and sensitivity toionizing radiation. Proc.
Nat. Acad. Sci. 96: 7376- 7381, 1999.

GAM64 239 RAD50 Stracker, T. H.; Carson, C. T.; Weitzman, M. D.: Adenovirus 3 C c
oncoproteinsinactivate the Mre11- Rad50- NBS1 DNA repair complex. Nature
418:348- 352, 2002.

GAM64 239 RAD50 Trujillo, K. M.; Yuan, S.- S. F.; Lee, E. Y.- H. P.; Sung, P.: 3 C c
Nucleaseactivities in a complex of human recombination and DNA repair
factorsRad50, Mre11, and p95. J. Biol. Chem. 273: 21447- 21450, 1998.

GAM64 239 RAD50 Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin,J.: BASC, a 3 C c
super complex of BRCA1- associated proteins involved inthe recognition and
repair of aberrant DNA structures. Genes Dev. 14:927- 939, 2000.

GAM64 239 RAD50 Zhong, Q.; Chen, C.- F.; Li, S.; Chen, Y.; Wang, C.- C.; Xiao, J.;Chen, P.- 3 C c
L.; Sharp, Z. D.; Lee, W.- H.: Association of BRCA1 withthe hRad50- hMre11-
p95 complex and the DNA damage response. Science 285:747- 750, 1999.

GAM64 239 RAD50 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 C c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human
telomeres. Nature Genet. 25: 347- 352, 2000.

GAM64 239 REPS2 Ikeda, M.; Ishida, O.; Hinoi, T.; Kishida, S.; Kikuchi, A.: 3 C c
Identificationand characterization of a novel protein interacting with Ral-

bindingprotein 1, a putative effector protein of Ral. J. Biol. Chem. 273:814- 821, 1998.

GAM64 239 REPS2 Koshiba, S.; Kigawa, T.; Iwahara, J.; Kikuchi, A.; Yokoyama, S.: Solution structure of the Eps15 homology domain of a human POB1(partner of RalBP1). FEBS Lett. 442: 138- 142, 1999. 3 C c

GAM65 272 BYSL Pack, S. D.; Pak, E.; Tanigami, A.; Ledbetter, D. H.; Fukuda, M.N.: Assignment of the bystin gene BYSL to human chromosome band 6p21.1by in situ hybridization. Cytogenet. Cell Genet. 83: 76- 77, 1998. 3 B c

GAM65 272 BYSL Suzuki, N.; Nakayama, J.; Shih, I. M.; Aoki, D.; Nozawa, S.; Fukuda,M. N.: Expression of trophinin, tastin, and bystin by trophoblastand endometrial cells in human placenta. Biol. Reprod. 60: 621- 627,1999. 3 B c

GAM65 272 BYSL Suzuki, N.; Zara, J.; Sato, T.; Ong, E.; Bakhiet, N.; Oshima, R.G.; Watson, K. L.; Fukuda, M. N.: A cytoplasmic protein, bystin,interacts with trophinin, tastin, and cytokeratin and may be involvedin trophinin- mediated cell adhesion between trophoblast and endometrialepithelial cells. Proc. Nat. Acad. Sci. 95: 5027- 5032, 1998. 3 B c

GAM65 272 CA3 Beechey, C.; Tweedie, S.; Spurr, N.; Ball, S.; Peters, J.; Edwards,Y.: Mapping of mouse carbonic anhydrase- 3, Car- 3: another locus inthe homologous region of mouse chromosome 3 and human chromosome 8. Genomics 6:692- 696, 1990. 3 B c

GAM65 272 CA3 Carter, N.; Jeffery, S.; Shiels, A.; Edwards, Y.; Tipler, T.; Hopkinson,D. A.: Characterization of human carbonic anhydrase III from skeletalmuscle. Biochem. Genet. 17: 837- 854, 1979. 3 B c

GAM65 272 CA3 Edwards, Y. H.; Lloyd, J. C.; Parkar, M.; Povey, S.: The genefor human muscle specific carbonic anhydrase (CAIII) is assigned tochromosome 8. Ann. Hum. Genet. 50: 41- 47, 1986. 3 B c

GAM65 272 CA3 Edwards, Y. H.; Lloyd, J.; Parkar, M.; Povey, S.: Human musclespecific carbonic anhydrase, CA3, is on chromosome 8. (Abstract) Cytogenet.Cell Genet. 40: 621 only, 1985. 3 B c

GAM65 272 CA3 Heath, R.; Carter, N. D.; Jeffery, S.; Edwards, R. J.; Watts, D.C.; Watts, R. L.: Evaluation of carrier detection of Duchenne musculardystrophy using carbonic anhydrase III and creatine kinase. Am. J.Med. Genet. 21: 291- 296, 1985. 3 B c

GAM65 272 CA3 Lloyd, J. C.; Isenberg, H.; Hopkinson, D. A.; Edwards, Y. H.:Isolation of a cDNA clone for the human muscle specific carbonic anhydrase,CA III. Ann. Hum. Genet. 49: 241- 251, 1985. 3 B c

GAM65 272 CA3 Lloyd, J.; Brownson, C.; Tweedie, S.; Charlton, J.; Edwards, Y.H.: Human muscle carbonic anhydrase: gene structure and DNA methylationpatterns in fetal and adult tissues. Genes Dev. 1: 594- 602, 1987. 3 B c

GAM65 272 CA3 Lloyd, J.; McMillan, S.; Hopkinson, D.; Edwards, Y. H.: Nucleotidesequence and derived amino acid sequence of a cDNA encoding humanmuscle carbonic anhydrase. Gene 41: 233- 239, 1986. 3 B c

GAM65 272 CA3 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: World Distribution. New York: Oxford Univ. Press (pub.) 1988. 3 B c

GAM65 272 CA3 Wade, R.; Gunning, P.; Eddy, R.; Shows, T.; Kedes, L.: Nucleotidesequence, tissue- specific expression, and chromosome location of humancarbonic anhydrase III: the human CAIII gene is located on the samechromosome as the closely linked CAI and CAII genes. Proc. Nat. Acad.Sci. 83: 9571- 9575, 1986. 3 B c

GAM65 272 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 B c

member of a multigene family. Genomics 52: 332- 341, 1998.

GAM65 272 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a new member of the MTG8/ETO gene family, maps on 20q11region and is deleted in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998. 3 B c

GAM65 272 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic fusion protein forms a complex with a novel member of theMTG8(ETO/CDR) family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998. 3 B c

GAM65 272 CD8A Amrani, A.; Verdaguer, J.; Serra, P.; Tafuro, S.; Tan, R.; Santamaria,P.: Progression of autoimmune diabetes driven by avidity maturationof a T- cell population. Nature 406: 739- 742, 2000. 3 B c

GAM65 272 CD8A Bowcock, A. M.; Kavathas, P.; Margolskee, R. F.; Herzenberg, L.;Cavalli-Sforza, L. L.: An RFLP associated with pcDLeu2- 14, a humanT- cell differentiation antigen CD8 (Leu2) cDNA mapped to 2p12. NucleicAcids Res. 14: 7817 only, 1986. 3 B c

GAM65 272 CD8A Bruns, G.; Kavathas, P.; Shiloh, Y.; Sakai, K.; Schwaber, J.; Latt,S. A.; Herzenberg, L. A.: The human T cell antigen Leu- 2 (T8) isencoded on chromosome 2. Hum. Genet. 70: 311- 314, 1985. 3 B c

GAM65 272 CD8A Giblin, P.; Ledbetter, J. A.; Kavathas, P.: A secreted form ofthe human lymphocyte cell surface molecule CD8 arises from alternativesplicing. Proc. Nat. Acad. Sci. 86: 998- 1002, 1989. 3 B c

GAM65 272 CD8A Kavathas, P.; Sukhatme, V. P.; Herzenberg, L. A.; Parnes, J. R.: Isolation of the gene encoding the human T- lymphocyte differentiationantigen Leu- 2 (T8) by gene transfer and cDNA subtraction. Proc. Nat.Acad. Sci. 81: 7688- 7692, 1984. 3 B c

GAM65 272 CD8A Ledbetter, J. A.; Evans, R. L.; Lipinski, M.; Cunningham- Rundles,C.; Good, R. A.; Herzenberg, L. A.: Evolutionary conservation ofsurface molecules that distinguish T lymphocyte helper- inducer andcytotoxic- suppressor subpopulations in mouse and man. J. Exp. Med. 153:310- 323, 1981. 3 B c

GAM65 272 CD8A Ledbetter, J. A.; Seaman, W. E.; Tsu, T. T.; Herzenberg, L. A.: Lyt- 2 and Lyt- 3 antigens are on two different polypeptide subunitslinked by disulfide bonds: relationship of subunits to T cell cytolyticactivity. J. Exp. Med. 153: 1503- 1516, 1981. 3 B c

GAM65 272 CD8A Leishman, A. J.; Naidenko, O. V.; Attinger, A.; Koning, F.; Lena,C. J.; Xiong, Y.; Chang, H.- C.; Reinherz, E.; Kronenberg, M.; Cheroutre,H.: T cell responses modulated through interaction between CD8- alpha- alphaand the nonclassical MHC class I molecule, TL. Science 294: 1936- 1939,2001. 3 B c

GAM65 272 CD8A Littman, D. R.: The structure of the CD4 and CD8 genes. Annu.Rev. Immun. 5: 561- 584, 1987. 3 B c

GAM65 272 CD8A Littman, D. R.; Thomas, Y.; Maddon, P. J.; Chess, L.; Axel, R.: The isolation and sequence of the gene encoding T8: a molecule definingfunctional classes of T lymphocytes. Cell 40: 237- 246, 1985. 3 B c

GAM65 272 CD8A Mecucci, C.; Van Den Berghe, H.: OKT8- positive T- cell lymphomaassociated with a chromosome rearrangement t(2;17) possibly involvingthe T8 locus. (Letter) New Eng. J. Med. 313: 185- 186, 1985. 3 B c

GAM65 272 CD8A Nakauchi, H.; Nolan, G. P.; Hsu, C.; Huang, H. S.; Kavathas, P.;Herzenberg, L. A.: Molecular cloning of Lyt- 2, a membrane glycoproteinmarking a subset of mouse T lymphocytes: molecular homology to itshuman counterpart, Leu-2/T8, and to immunoglobulin variable regions. Proc.Nat. Acad. Sci. 82: 5126- 5130, 1985. 3 B c

GAM65 272 CD8A Sukhatme, V. P.; Sizer, K. C.; Vollmer, A. C.; Hunkapiller, T.;Parnes, J. R.: The T cell differentiation antigen leu- 2/T8 is homologousto immunoglobulin and T cell receptor variable regions. Cell 40:591- 597, 1985. 3 B c

GAM65 272 CD8A Sukhatme, V. P.; Vollmer, A. C.; Erikson, J.; Isobe, M.; Croce,C.; Parnes, J. R.: Gene for the human T cell differentiation antigenLeu- 2/T8 is closely linked to the kappa light chain locus on chromosome2. J. Exp. Med. 161: 429- 434, 1985. 3 B c

GAM65 272 CD8A Traver, D.; Akashi, K.; Manz, M.; Merad, M.; Miyamoto, T.; Engleman,E. G.; Weissman, I. L.: Development of CD8- alpha- positive dendriticcells from a common myeloid progenitor. Science 290: 2152- 2154,2000. 3 B c

GAM65 272 CD8A Weichhold, G. M.; Huber, C.; Parnes, J. R.; Zachau, H. G.: TheCD8- alpha locus is located on the telomere side of the immunoglobulin- kappalocus at a distance of 2 Mb. Genomics 16: 512- 514, 1993. 3 B c

GAM65 272 DBY Foresta, C.; Ferlin, A.; Moro, E.: Deletion and expression analysisof AZFa genes on the human Y chromosome revealed a major role forDBY in male infertility. Hum. Molec. Genet. 9: 1161- 1169, 2000. 3 B c

GAM65 272 DBY Lahn, B. T.; Page, D. C.: Functional coherence of the human Ychromosome. Science 278: 675- 680, 1997. 3 B c

GAM65 272 DBY Scott, D.; Addey, C.; Ellis, P; James, E.; Mitchell, M. J.; Saut,N.; Jurcevic, S.; Simpson, E.: Dendritic cells permit identificationof genes encoding MHC class II- restricted epitopes of transplantationantigens. Immunity 12: 711- 720, 2000. 3 B c

GAM65 272 DBY Shen, P.; Wang, F.; Underhill, P. A.; Franco, C.; Yang, W.- H.;Roxas, A.; Sung, R.; Lin, A. A.; Hyman, R. W.; Vollrath, D.; Davis,R. W.; Cavalli-Sforza, L. L.; Oefner, P. J.: Population genetic implicationsfrom sequence variation in four Y chromosome genes. Proc. Nat. Acad.Sci. 97: 7354- 7359, 2000. 3 B c

GAM65 272 EHD1 Di Fiore, P. P.; Pelicci, P. G.; Sorkin, A.: EH: a novel protein-proteininteraction domain potentially involved in intracellular sorting. TrendsBiochem. Sci. 22: 411- 413, 1997. 3 B c

GAM65 272 EHD1 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.; Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.; Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the 2.8- Mb region containing the multiple endocrineneoplasia type 1 locus. Genome Res. 7: 725- 735, 1997. 3 B c

GAM65 272 EHD1 Haider, N. B.; Searby, C.; Galperin, E.; Mintz, L.; Horowitz, M.;Stone, E. M.; Sheffield, V. C.: Evaluation and molecular characterizationof EHD1, a candidate gene for Bardet- Biedl syndrome 1 (BBS1). Gene 240:227- 232, 1999. 3 B c

GAM65 272 EHD1 Mintz, L.; Galperin, E.; Pasmanik- Chor, M.; Tulzinsky, S.; Bromberg,Y.; Kozak, C. A.; Joyner, A.; Fein, A.; Horowitz, M.: EHD1- - an EH- domain-containingprotein with a specific expression pattern. Genomics 59: 66-76,1999. 3 B c

GAM65 272 EHD1 Rotem- Yehudar, R.; Galperin, E.; Horowitz, M.: Association ofinsulin- like growth factor 1 receptor with EHD1 and SNAP29. J. Biol.Chem. 276: 33054-33060, 2001. 3 B c

GAM65 272 GABRE Davies, P. A.; Hanna, M. C.; Hales, T. G.; Kirkness, E. F.: Insensitivityto anaesthetic agents conferred by a class of GABA(A) receptor subunit. Nature 385:820- 823, 1997. 3 B b

GAM65 272 GABRE Sinkkonen, S. T.; Hanna, M. C.; Kirkness, E. F.; Korpi, E. R.:GABA- A 3 B b

receptor epsilon and theta subunits display unusual structuralvariation between species and are enriched in the rat locus ceruleus. J.Neurosci. 20: 3588- 3595, 2000.

GAM65 272 GABRE Wilke, K.; Gaul, R.; Klauck, S. M.; Poustka, A.: A gene in humanchromosome band Xq28 (GABRE) defines a putative new subunit classof the GABA(A) neurotransmitter receptor. Genomics 45: 1- 10, 1997. 3 B b

GAM65 272 ITGAV Bader, B. L.; Rayburn, H.; Crowley, D.; Hynes, R. O.: Extensivevasculogenesis, angiogenesis, and organogenesis precede lethalityin mice lacking all alpha- V integrins. Cell 95: 507- 519, 1998. 3 B c

GAM65 272 ITGAV Fernandez- Ruiz, E.; de Villena, F. P.- M.; Rodriguez de Cordoba,S.; Sanchez- Madrid, F.: Regional localization of the human vitronectinreceptor alpha- subunit gene (VNRA) to chromosome 2q31- q32. Cytogenet.Cell Genet. 62: 26- 28, 1993. 3 B c

GAM65 272 ITGAV Fitzgerald, L. A.; Poncz, M.; Steiner, B.; Rall, S. C., Jr.; Bennett,J. S.; Phillips, D. R.: Comparison of cDNA- derived protein sequencesof the human fibronectin and vitronectin receptor alpha- subunits andplatelet glycoprotein IIb. Biochemistry 26: 8158- 8165, 1987. 3 B c

GAM65 272 ITGAV Sims, M. A.; Field, S. D.; Barnes, M. R.; Shaikh, N.; Ellington,K.; Murphy, K. E.; Spurr, N.; Campbell, D. A.: Cloning and characterisationof ITGAV, the genomic sequence for human cell adhesion protein (vitronectin)receptor alpha subunit, CD51. Cytogenet. Cell Genet. 89: 268- 271,2000. 3 B c

GAM65 272 ITGAV Sosnoski, D.; Emanuel, B. S.; Hawkins, A. L.; van Tuinen, P.; Ledbetter,D. H.; Nussbaum, R. L.; Kaos, F.- T.; Schwartz, E.; Phillips, D.; Bennett,J. S.; Fitzgerald, L. A.; Poncz, M.: Chromosomal localization ofthe genes for the vitronectin and fibronectin receptors alpha- subunitsand for platelet glycoproteins IIb and IIIa. J. Clin. Invest. 81:1993- 1998, 1988. 3 B c

GAM65 272 ITGAV Spurr, N. K.; Rooke, L.: Confirmation of the assignment of thevitronectin (VNRA) and fibronectin (FNRA) receptor alpha- subunits. Ann.Hum. Genet. 55: 217- 223, 1991. 3 B c

GAM65 272 ITGAV Suzuki, S.; Argraves, W. S.; Pytela, R.; Arai, H.; Krusius, T.;Pierschbacher, M. D.; Ruoslahti, E.: cDNA and amino acid sequencesof the cell adhesion protein receptor recognizing vitronectin reveala transmembrane domain and homologies with other adhesion proteinreceptors. Proc. Nat. Acad. Sci. 83: 8614- 8618, 1986. 3 B c

GAM65 272 ITGAV Xiong, J.- P.; Stehle, T.; Diefenbach, B.; Zhang, R.; Dunker, R.;Scott, D. L.; Joachimiak, A.; Goodman, S. L.; Arnaout, M. A.: Crystalstructure of the extracellular segment of integrin alpha- V- beta- 3. Science 294:339- 345, 2001. 3 B c

GAM65 272 ITGAV Xiong, J.- P.; Stehle, T.; Zhang, R.; Joachimiak, A.; Frech, M.;Goodman, S. L.; Arnaout, M. A.: Crystal structure of the extracellularsegment of integrin alpha- V- beta- 3 in complex with an Arg- Gly- Aspligand. Science 296: 151- 155, 2002. 3 B c

GAM65 272 MAML1 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. V. The codingsequences of 40 new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 3: 17- 24, 1996. 3 B c

GAM65 272 MAML1 Wu, L.; Aster, J. C.; Blacklow, S. C.; Lake, R.; Artavanis- Tsakonas,S.; Griffin, J. D.: MAML1, a human homologue of Drosophila mastermind,is a transcriptional co- activator for NOTCH receptors. Nature Genet. 26:484- 489, 2000. 3 B c

GAM65 272 MCL1 Bae, J.; Leo, C. P.; Hsu, S. Y.; Hsueh, A. J. W.: MCL- 1S, a splicingvariant of the antiapoptotic BCL- 2 family member MCL- 1, encodes aproapoptotic protein possessing only the BH3 domain. J. Biol. Chem. 275:25255- 25261, 2000. 3 B c

GAM65 272 MCL1 Craig, R. W.; Jabs, E. W.; Zhou, P.; Kozopas, K. M.; Hawkins, A.L.; Rochelle, J. M.; Seldin, M. F.; Griffin, C. A.: Human and mousechromosomal mapping of the myeloid cell leukemia- 1 gene: MCL1 mapsto human chromosome 1q21, a region that is frequently altered in preneoplasticand neoplastic disease. Genomics 23: 457- 463, 1994. 3 B c

GAM65 272 MCL1 Kozopas, K. M.; Yang, T.; Buchan, H. L.; Zhou, P.; Craig, R. W.: MCL1, a gene expressed in programmed myeloid cell differentiation,has sequence similarity to BCL2. Proc. Nat. Acad. Sci. 90: 3516- 3520,1993. 3 B c

GAM65 272 MCL1 Rinkenberger, J. L.; Horning, S.; Klocke, B.; Roth, K.; Korsmeyer,S. J.: Mcl- 1 deficiency results in peri- implantation embryonic lethality. GenesDev. 14: 23- 27, 2000. 3 B c

GAM65 272 PDE4C Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.;Rodgers, L.; Riggs, M.; Wigler, M.; Ferguson, K.: A family of humanphosphodiesterases homologous to the dunce learning and memory geneproduct of Drosophila melanogaster are potential targets for antidepressantdrugs. Molec. Cell. Biol. 13: 6558- 6571, 1993. 3 B c

GAM65 272 PDE4C Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994. 3 B c

GAM65 272 PDE4C Sullivan, M.; Olsen, A. S.; Houslay, M. D.: Genomic organisationof the human cyclic AMP- specific phosphodiesterase PDE4C gene andits chromosomal localisation to 19p13.1, between RAB3A and JUND. Cell.Signal. 11: 735- 742, 1999. 3 B c

GAM65 272 PLCG1 Bristol, A.; Hall, S. M.; Kriz, R. W.; Stahl, M. L.; Fan, Y. S.;Byers, M. G.; Eddy, R. L.; Shows, T. B.; Knopf, J. L.: PhospholipaseC- 148: chromosomal location and deletion mapping of functional domains. ColdSpring Harbor Symp. Quant. Biol. 53: 915- 920, 1988. 3 B c

GAM65 272 PLCG1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 3 B c

GAM65 272 PLCG1 Nelson, K. K.; Knopf, J. L.; Siracusa, L. D.: Localization ofphospholipase C- gamma 1 to mouse chromosome 2. Mammalian Genome 3:597- 600, 1992. 3 B c

GAM65 272 PLCG1 Rothschild, C. B.; Akots, G.; Fajans, S. S.; Bowden, D. W.: Amicrosatellite polymorphism associated with the PLC1 (phospholipaseC) locus: identification, mapping, and linkage to the MODY locus onchromosome 20. Genomics 13: 560- 564, 1992. 3 B c

GAM65 272 PLCG1 Stahl, M. L.; Ferenz, C. R.; Kelleher, K. L.; Kriz, R. W.; Knopf,J. L.: Sequence similarity of phospholipase C with the non- catalyticregion of src. Nature 332: 269- 272, 1988. 3 B c

GAM65 272 PLCG1 Ye, K.; Aghdasi, B.; Luo, H. R.; Moriarity, J. L.; Wu, F. Y.; Hong,J. J.; Hurt, K. J.; Bae, S. S.; Suh, P.- G.; Snyder, S. H.: PhospholipaseC- gamma- 1 is a physiological guanine nucleotide exchange factor forthe nuclear GTPase PIKE. Nature 415: 541- 544, 2002. 3 B c

GAM65 272 PLXNA2 Maestrini, E.; Tamagnone, L.; Longati, P.; Cremona, O.; Gulisano,M.; Bione, S.; Tamanini, F.; Neel, B. G.; Toniolo, D.; Comoglio, P.M.: A family of 3 B c

transmembrane proteins with homology to the MET- hepatocytegrowth factor receptor. Proc. Nat. Acad. Sci. 93: 674- 678, 1996.

GAM65 272 PLXNA2 Tamagnone, L.; Artigiani, S.; Chen, H.; He, Z.; Ming, G.; Song,H.; Chedotal, 3 B c
A.; Winberg, M. L.; Goodman, C. S.; Poo, M.; Tessier- Lavigne,M.; Comoglio,
P. M.: Plexins are a large family of receptors fortransmembrane, secreted,
and GPI- anchored semaphorins in vertebrates. Cell 99:71- 80, 1999.

GAM65 272 RAD21 Hakimi, M.- A.; Bochar, D. A.; Schmiesing, J. A.; Dong, Y.; Barak,O. G.; 3 B c
Speicher, D. W.; Yokomori, K.; Shiekhattar, R.: A chromatinremodelling
complex that loads cohesin onto human chromosomes. Nature 418:994- 998,
2002.

GAM65 272 RAD21 Hauf, S.; Waizenegger, I. C.; Peters, J.- M.: Cohesin cleavageby separase 3 B c
required for anaphase and cytokinesis in human cells. Science 293:1320-
1323, 2001.

GAM65 272 RAD21 Hoque, M. T.; Ishikawa, F.: Human chromatid cohesin componenthRad21 is 3 B c
phosphorylated in M phase and associated with metaphasecentromeres. J. Biol.
Chem. 276: 5059- 5067, 2001.

GAM65 272 RAD21 McKay, M. J.; Troelstra, C.; van der Spek, P.; Kanaar, R.; Smit,B.; 3 B c
Hagemeijer, A.; Bootsma, D.; Hoeijmakers, J. H. J.: Sequenceconservation of
the rad21 Schizosaccharomyces pombe DNA double- strandbreak repair gene in
human and mouse. Genomics 36: 305- 315, 1996.

GAM65 272 RAD21 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 B c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. II. The codingsequences of 40 new
genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell
line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM65 272 RAD21 Sadano, H.; Sugimoto, H.; Sakai, F.; Nomura, N.; Osumi, T.: NXP- 1,a human 3 B c
protein related to Rad21/Scc1/Mcd1, is a component of thenuclear matrix.
Biochem. Biophys. Res. Commun. 267: 418- 422, 2000.

GAM65 272 RAD21 Sumara, I.; Vorlaufer, E.; Gieffers, C.; Peters, B. H.; Peters,J.- M.: 3 B c
Characterization of vertebrate cohesin complexes and theirregulation in
prophase. J. Cell Biol. 151: 749- 761, 2000.

GAM65 272 SLA Angrist, M.; Wells, D. E.; Chakravarti, A.; Pandey, A.: 3 B c
Chromosomallocalization of the mouse Src- like adapter protein (Slap) gene
andits putative human homolog SLA. Genomics 30: 623- 625, 1995.

GAM65 272 SLA Holland, S. J.; Liao, X. C.; Mendenhall, M. K.; Zhou, X.; Pardo,J.; Chu, P.; 3 B c
Spencer, C.; Fu, A.; Sheng, N.; Yu, P.; Pali, E.; Nagin,A.; and 14 others:
Functional cloning of Src- like adapter protein- 2(SLAP- 2), a novel
inhibitor of antigen receptor signaling. J. Exp.Med. 194: 1263- 1276, 2001.

GAM65 272 SLA Kratchmarova, I.; Sosinowski, T.; Weiss, A.; Witter, K.; Vincenz,C.; Pandey, 3 B c
A.: Characterization of promoter region and genomic structureof the murine
and human genes encoding Src like adapter protein. Gene 262:267- 273, 2001.

GAM65 272 SLA Meijerink, P. H. S.; Yanakiev, P.; Zorn, I.; Grierson, A. J.; Bikker,H.; 3 B c
Dye, D.; Kalaydjieva, L.; Baas, F.: The gene for the human Src- likeadaptor
protein (hSLAP) is located within the 64- kb intron of thethyroglobulin
gene. Europ. J. Biochem. 254: 297- 303, 1998.

GAM65 272 SLA Pandey, A.; Lindberg, R. A.; Dixit, V. M.: Receptor orphans finda family. 3 B c
Curr. Biol. 5: 986- 989, 1995.

GAM65 272 SLA Sosinowski, T.; Pandey, A.; Dixit, V. M.; Weiss, A.: Src- likeadaptor 3 B c
protein (SLAP) is a negative regulator of T cell receptorsignaling. J. Exp.
Med. 191: 463- 474, 2000.

GAM65 272 TRPM7 Nadler, M. J. S.; Hermosura, M. C.; Inabe, K.; Perraud, A.- L.;Zhu, Q.; 3 B c
Stokes, A. J.; Kurosaki, T.; Kinet, J.- P.; Penner, R.; Scharenberg,A. M.;
Fleig, A.: LTRPC7 is a Mg- ATP- regulated divalent cation channelrequired
for cell viability. Nature 411: 590- 595, 2001. Note: Erratum Nature 412:660
only, 2001.

GAM65 272 TRPM7 Runnels, L. W.; Yue, L.; Clapham, D. E.: The TRPM7 channel isinactivated by 3 B c
PIP(2) hydrolysis. Nature Cell Biol. 4: 329- 336,2002.

GAM65 272 TRPM7 Runnels, L. W.; Yue, L.; Clapham, D. E.: TRP- PLIK, a bifunctionalprotein 3 B c
with kinase and ion channel activities. Science 291: 1043- 1047,2001.

GAM65 272 TRPM7 Scott, A. F.: Personal Communication. Baltimore, Md. 3/8/2001. 3 B c

GAM65 272 VNN1 Aurrand- Lions, M.; Galland, F.; Bazin, H.; Zakharyev, V. M.; Imhof,B. A.; 3 B c
Naquet, P.: Vanin- 1, a novel GPI- linked perivascular moleculeinvolved in
thymus homing. Immunity 5: 391- 405, 1996.

GAM65 272 VNN1 Galland, F.; Malergue, F.; Bazin, H.; Mattei, M. G.; Aurrand- Lions,M.; 3 B c
Theillet, C.; Naquet, P.: Two human genes related to murine vanin- 1are
located on the long arm of human chromosome 6. Genomics 53:203- 213, 1998.

GAM65 272 VNN1 Grimmond, S.; Van Hateren, N.; Siggers, P.; Arkell, R.; Larder,R.; Soares, 3 B c
M. B.; de Fatima Bonaldo, M.; Smith, L.; Tymowska- Lalanne,Z.; Wells, C.;
Greenfield, A.: Sexually dimorphic expression of proteasenexin- 1 and vanin-
1 in the developing mouse gonad prior to overt differentiationsuggests a
role in mammalian sexual development. Hum. Molec. Genet. 9:1553- 1560, 2000.

GAM65 272 VNN1 Martin, F.; Malergue, F.; Pitari, G.; Philippe, J. M.; Philips,S.; Chabret, 3 B c
C.; Granjeaud, S.; Mattei, M. G.; Mungall, A. J.; Naquet,P.; Galland, F.:
Vanin genes are clustered (human 6q22- 24 and mouse10A2B1) and encode
isoforms of pantetheinase ectoenzymes. Immunogenetics 53:296- 306, 2001.

GAM65 272 VNN1 Pitari, G.; Malergue, F.; Martin, F.; Philippe, J. M.; Massucci,M. T.; 3 B c
Chabret, C.; Maras, B.; Dupre, S.; Naquet, P.; Galland, F.: Pantetheinase
activity of membrane- bound vanin- 1: lack of free cysteaminein tissues of
vanin- 1 deficient mice. FEBS Lett. 483: 149- 154, 2000.

GAM66 238 C5R1 Bao, L.; Gerard, N. P.; Eddy, R. L., Jr.; Shows, T. B.; Gerard,C.: Mapping 1 B c
of genes for the human C5a receptor (C5AR), human FMLPreceptor (FPR), and
two FMLP receptor homologue orphan receptors (FPRH1,FPRH2) to chromosome 19.
Genomics 13: 437- 440, 1992.

GAM66 238 C5R1 Collaborative Study on the Genetics of Asthma: A genome- widesearch for 1 B c
asthma susceptibility loci in ethnically diverse populations. NatureGenet.
15: 389- 392, 1997.

GAM66 238 C5R1 Gavett, S. H.; O'Hearn, D. J.; Li, X.; Huang, S. K.; Finkelman,F. D.; Wills- 1 B c
Karp, M.: Interleukin 12 inhibits antigen- induced
airwayhyperresponsiveness, inflammation, and Th2 cytokine expression inmice.
J. Exp. Med. 182: 1527- 1536, 1995.

GAM66 238 C5R1 Hopken, U. E.; Lu, D.; Gerard, N. P.; Gerard, C.: The C5a 1 B c
chemoattractantreceptor mediates mucosal defense to infection. Nature 383:
86- 89,1996.

GAM66 238 C5R1 Karp, C. L.; Grupe, A.; Schadt, E.; Ewart, S. L.; Keane- Moore,M.; Cuomo, P. 1 B c
J.; Kohl, J.; Wahl, L.; Kuperman, D.; Germer, S.; Aud,D.; Peltz, G.; Wills-
Karp, M.: Identification of complement factor5 as a susceptibility locus for
experimental allergic asthma. NatureImmun. 1: 221- 226, 2000.

GAM66 238 C5R1 Ober, C.; Cox, N. J.; Abney, M.; Di Rienzo, A.; Lander, E. S.;Changyaleket, 1 B c
B.; Gidley, H.; Kurtz, B.; Lee, J.; Nance, M.; Pettersson,A.; Prescott, J.;
Richardson, A.; Schlenker, E.; Summerhill, E.; Willadsen,S.; Parry, R.;

Collaborative Study on the Genetics of Asthma: Genome- widesearch for asthma susceptibility loci in a founder population. Hum.Molec. Genet. 7: 1393-1398, 1998.

GAM66 238 C5R1 Wjst, M.; Fischer, G.; Immervoll, T.; Jung, M.; Saar, K.; Rueschendorf,F.; Reis, A.; Ulbrecht, M.; Gomolka, M.; Weiss, E. H.; Jaeger, L.;Nickel, R.; and 14 others: A genome- wide search for linkage toasthma. Genomics 58: 1-8, 1999. 1 B c

GAM66 238 CCND2 Inaba, T.; Matsushime, H.; Valentine, M.; Roussel, M. F.; Sherr,C. J.; Look, A. T.: Genomic organization, chromosomal localization,and independent expression of human cyclin D genes. Genomics 13:565- 574, 1992. 1 B c

GAM66 238 CCND2 Kim, H. A.; Pomeroy, S. L.; Whoriskey, W.; Pawlitzky, I.; Benowitz,L. I.; Sicinski, P.; Stiles, C. D.; Roberts, T. M.: A developmentallyregulated switch directs regenerative growth of Schwann cells throughcyclin D1. Neuron 26: 405- 416, 2000. 1 B c

GAM66 238 CCND2 Xiong, Y.; Menninger, J.; Beach, D.; Ward, D. C.: Molecular cloningand chromosomal mapping of CCND genes encoding human D- type cyclins. Genomics 13:575- 584, 1992. 1 B c

GAM66 238 CRYZ Garland, D.; Rao, P. V.; Del Corso, A.; Mura, U.; Zigler, J. S.,Jr.: Zeta-crystallin is a major protein in the lens of Camelus dromedarius.Arch. Biochem. Biophys. 285: 134- 136, 1991. 1 B c

GAM66 238 CRYZ Gonzalez, P.; Rao, P. V.; Zigler, J. S., Jr.: Organization ofthe human zeta-crystallin/quinone reductase gene (CRYZ). Genomics 21:317- 324, 1994. 1 B c

GAM66 238 CRYZ Heinzmann, C.; Kojis, T. L.; Gonzalez, P.; Rao, P. V.; Zigler,J. S., Jr.; Polymeropoulos, M. H.; Klisak, I.; Sparkes, R. S.; Mohandas,T.; Bateman, J. B.: Assignment of the zeta- crystallin gene (CRYZ)to human chromosome 1p22-p31 and identification of restriction fragmentlength polymorphisms. Genomics 23: 403- 407, 1994. 1 B c

GAM66 238 CRYZ Huang, Q.- L.; Russell, P.; Stone, S. H.; Zigler, J. S., Jr.: Zeta-crystallin,a novel lens protein from the guinea pig. Curr. Eye Res. 6: 725-732,1987. 1 B c

GAM66 238 CRYZ Rodriguez, I. R.; Gonzalez, P.; Zigler, J. S., Jr.; Borras, T.: A guinea-pig hereditary cataract contains a splice site deletionin a crystallin gene. Biochim. Biophys. Acta 1180: 44- 52, 1992. 1 B c

GAM66 238 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila-relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997. 1 B c

GAM66 238 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998. 1 B c

GAM66 238 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994. 1 B c

GAM66 238 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997. 1 B c

GAM66 238 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993. 1 B c

GAM66 238 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; 1 B c
Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X
chromosome breakpoints associated with premature ovarianfailure (POF) map to
a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997.

GAM66 238 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, 1 B c
sequence, expression, and processing of the interleukin 16precursor. Proc.
Nat. Acad. Sci. 94: 5273- 5277, 1997.

GAM66 238 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 1 B c
381: 30 only, 1996.

GAM66 238 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 1 B c
16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics
49:704- 706, 1999.

GAM66 238 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. 1 B c
C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte
chemoattractant factor: association of biologic functionwith CD4 expression.
Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994.

GAM66 238 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human 1 B c
lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128:
2569- 2574, 1982.

GAM66 238 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS 1 B c
human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311-
314, 1993.

GAM66 238 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; 1 B c
Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M.
E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945-
1954, 1995.

GAM66 238 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; 1 B c
Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure
and function between human and murine IL- 16. J. Immun. 160:5945- 5954,
1998.

GAM66 238 RAD50 Carney, J. P.; Maser, R. S.; Olivares, H.; Davis, E. M.; Le Beau,M.; Yates, 1 B c
J. R., III; Hays, L.; Morgan, W. F.; Petrini, J. H. J.: The hMre11/hRad50
protein complex and Nijmegen breakage syndrome:linkage of double- strand
break repair to the cellular DNA damage response. Cell 93:477- 486, 1998.

GAM66 238 RAD50 Dolganov, G. M.; Maser, R. S.; Novikov, A.; Tosto, L.; Chong, S.;Bressan, D. 1 B c
A.; Petrini, J. H. J.: Human Rad50 is physically associatedwith human Mre11:
identification of a conserved multiprotein complexim plicated in
recombinational DNA repair. Molec. Cell Biol. 16:4832- 4841, 1996.

GAM66 238 RAD50 Hopfner, K.- P.; Craig, L.; Moncalian, G.; Zinkel, R. A.; Usui,T.; Owen, B. 1 B c
A. L.; Karcher, A.; Henderson, B.; Bodmer, J.- L.; McMurray,C. T.; Carney,
J. P.; Petrini, J. H. J.; Tainer, J. A.: The Rad50zinc- hook is a structure
joining Mre11 complexes in DNA recombinationand repair. Nature 418: 562-
566, 2002.

GAM66 238 RAD50 Hopfner, K.- P.; Karcher, A.; Craig, L.; Woo, T. T.; Carney, J.P.; Tainer, 1 B c
J. A.: Structural biochemistry and interaction architectureof the DNA
double- strand break repair Mre11 nuclease and Rad50- ATPase. Cell 105:473-
485, 2001.

GAM66 238 RAD50 Luo, G.; Yao, M. S.; Bender, C. F.; Mills, M.; Bladl, A. R.; Bradley,A.; 1 B c
Petrini, J. H. J.: Disruption of mRad50 causes embryonic stemcell lethality,
abnormal embryonic development, and sensitivity toionizing radiation. Proc.

Nat. Acad. Sci. 96: 7376- 7381, 1999.

GAM66 238 RAD50 Stracker, T. H.; Carson, C. T.; Weitzman, M. D.: Adenovirus 1 B c
oncoproteinsinactivate the Mre11- Rad50- NBS1 DNA repair complex. Nature
418:348- 352, 2002.

GAM66 238 RAD50 Trujillo, K. M.; Yuan, S.- S. F.; Lee, E. Y.- H. P.; Sung, P.: 1 B c
Nucleaseactivities in a complex of human recombination and DNA repair
factorsRad50, Mre11, and p95. J. Biol. Chem. 273: 21447- 21450, 1998.

GAM66 238 RAD50 Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin,J.: BASC, a 1 B c
super complex of BRCA1- associated proteins involved inthe recognition and
repair of aberrant DNA structures. Genes Dev. 14:927- 939, 2000.

GAM66 238 RAD50 Zhong, Q.; Chen, C.- F.; Li, S.; Chen, Y.; Wang, C.- C.; Xiao, J.;Chen, P.- 1 B c
L.; Sharp, Z. D.; Lee, W.- H.: Association of BRCA1 withthe hRad50- hMre11-
p95 complex and the DNA damage response. Science 285:747- 750, 1999.

GAM66 238 RAD50 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 1 B c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human
telomeres. Nature Genet. 25: 347- 352, 2000.

GAM66 238 SMCY Agulnik, A. I.; Bishop, C. E.; Lerner, J. L.; Agulnik, S. I.; Solovyev,V. 1 B c
V.: Analysis of mutation rates in the SMCY/SMCX genes shows thatmammalian
evolution is male driven. Mammalian Genome 8: 134- 138,1997.

GAM66 238 SMCY Agulnik, A. I.; Mitchell, M. J.; Lerner, J. L.; Woods, D. R.; Bishop,C. E.: 1 B c
A mouse Y chromosome gene encoded by a region essential forspermatogenesis
and expression of male- specific minor histocompatibilityantigens. Hum.
Molec. Genet. 3: 873- 878, 1994.

GAM66 238 SMCY Agulnik, A. I.; Mitchell, M. J.; Mattei, M.- G.; Borsani, G.; Avner,P. A.; 1 B c
Lerner, J. L.; Bishop, C. E.: A novel X gene with a widelytranscribed Y-
linked homologue escapes X- inactivation in mouse andhuman. Hum. Molec.
Genet. 3: 879- 884, 1994.

GAM66 238 SMCY Burgoyne, P. S.; Levy, E. R.; McLaren, A.: Spermatogenic failurein male mice 1 B c
lacking H- Y antigen. Nature 320: 170- 172, 1986.

GAM66 238 SMCY Eichwald, E. J.; Silmser, C. R.: Skin. Transplant. Bull. 2:148- 149, 1955. 1 B c

GAM66 238 SMCY Gasser, D. L.; Silvers, W. K.: Genetics and immunology of sex- 1 B c
linkedantigens. Adv. Immun. 15: 215- 247, 1972.

GAM66 238 SMCY Kent- First, M. G.; Maffitt, M.; Muallem, A.; Brisco, P.; Shultz,J.; 1 B c
Ekenberg, S.; Agulnik, A. I.; Agulnik, I.; Shramm, D.; Bavister,B.; Abdul-
Mawgood, A.; VandeBerg, J.: Gene sequence and evolutionaryconservation of
human SMCY. (Letter) Nature Genet. 14: 128- 129,1996.

GAM66 238 SMCY Scott, D. M.; Ehrmann, I. E.; Ellis, P. S.; Bishop, C. E.; Agulnik,A. I.; 1 B c
Simpson, E.; Mitchell, M. J.: Identification of a mouse male-
specifictransplantation antigen, H- Y. Nature 376: 695- 698, 1995.

GAM66 238 SMCY Shen, P.; Wang, F.; Underhill, P. A.; Franco, C.; Yang, W.- H.;Roxas, A.; 1 B c
Sung, R.; Lin, A. A.; Hyman, R. W.; Vollrath, D.; Davis,R. W.; Cavalli-
Sforza, L. L.; Oefner, P. J.: Population genetic implicationsfrom sequence
variation in four Y chromosome genes. Proc. Nat. Acad.Sci. 97: 7354- 7359,
2000.

GAM66 238 SMCY Simpson, E.: The H- Y antigen and sex reversal. Cell 44: 813- 814,1986. 1 B c

GAM66 238 SMCY Simpson, E.; Chandler, P.; Goulmy, E.; Disteche, C. M.; Ferguson- Smith,M. 1 B c
A.; Page, D. C.: Separation of the genetic loci for the H- Y antigenand for
testis determination on human Y chromosome. Nature 326:876- 878, 1987.

GAM66 238 SMCY Simpson, E.; Chandler, P.; Goulmy, E.; Ma, K.; Hargreave, T. B.;Chandley, A. 1 B c
C.: Loss of the 'azoospermia factor' (AZF) on Yq inman is not associated

with loss of HYA. Hum. Molec. Genet. 2: 469- 471,1993.

GAM66 238 SMCY Wachtel, S. S.; Koo, G. C.; Breg, W. R.; Elias, S.; Boyse, E.A.; Miller, O. 1 B c
J.: Expression of H- Y antigen in human males withtwo Y chromosomes. New
Eng. J. Med. 293: 1070- 1072, 1975.

GAM66 238 SMCY Wachtel, S. S.; Koo, G. C.; Zuckerman, E. E.; Hammerling, U.;Scheid, M. P.; 1 B c
Boyse, E. A.: Serological crossreactivity betweenH- Y (male) antigens of
mouse and man. Proc. Nat. Acad. Sci. 71:1215- 1218, 1974.

GAM66 238 SMCY Wang, W.; Meadows, L. R.; den Haan, J. M. M.; Sherman, N. E.;Chen, Y.; 1 B c
Blokland, E.; Shabanowitz, J.; Agulnik, A. I.; Hendrickson,R. C.; Bishop, C.
E.; Hunt, D. F.; Goulmy, E.; Engelhard, V. H.:Human H- Y: a male- specific
histocompatibility antigen derived fromthe SMCY protein. Science 269: 1588-
1590, 1995.

GAM66 238 ST5 Klinger, H. P.: Suppression of tumorigenicity in somatic cellhybrids. I. 1 B c
Suppression and reexpression of tumorigenicity in diploidhuman x D98/AH2
hybrids and independent segregation of tumorigenicityfrom other cell
phenotypes. Cytogenet. Cell Genet. 27: 254- 266,1980.

GAM66 238 ST5 Lichy, J. H.; Modi, W. S.; Seuanez, H. N.; Howley, P. M.: Identificationof a 1 B c
human chromosome 11 gene which is differentially regulated intumorigenic and
nontumorigenic somatic cell hybrids of HeLa cells. CellGrowth Differ. 3:
541- 548, 1992.

GAM66 238 ST5 Stanbridge, E. J.: Suppression of malignancy in human cells. Nature 260:17- 1 B c
20, 1976.

GAM66 238 XT3 Nash, S. R.; Giros, B.; Kingsmore, S. F.; Kim, K. M.; El- Mestikawy,S.; 1 B c
Dong, Q.; Fumagalli, F.; Seldin, M. F.; Caron, M. G.: Cloning,gene structure
and genomic localization of an orphan transporter frommouse kidney with six
alternatively- spliced isoforms. Receptors Channels 6:113- 128, 1998.

GAM66 238 XT3 Scott, A. F.: Personal Communication. Baltimore, Md. 2/5/2001. 1 B c

GAM67 282 ARNT2 Hirose, K.; Morita, M.; Ema, M.; Mimura, J.; Hamada, H.; Fujii,H.; Saijo, 1 B c
Y.; Gotoh, O.; Sogawa, K.; Fujii- Kuriyama, Y.: cDNA cloningand tissue-
specific expression of a novel basic helix- loop- helix/PASfactor (Arnt2)
with close sequence similarity to the aryl hydrocarbonreceptor nuclear
translocator (Arnt). Molec. Cell. Biol. 16: 1706- 1713,1996.

GAM67 282 ARNT2 Keith, B.; Adelman, D. M.; Simon, M. C.: Targeted mutation ofthe murine 1 B c
arylhydrocarbon receptor nuclear translocator 2 (Arnt2)gene reveals partial
redundancy with Arnt. Proc. Nat. Acad. Sci. 98:6692- 6697, 2001.

GAM67 282 ARNT2 Michaud, J. L.; DeRossi, C.; May, N. R.; Holdener, B. C.; Fan,C.- M.: ARNT2 1 B c
acts as the dimerization partner of SIM1 for the developmentof the
hypothalamus. Mech. Dev. 90: 253- 261, 2000.

GAM67 282 ARNT2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 1 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM67 282 CDC25A Demetrick, D. J.; Beach, D. H.: Chromosome mapping of human CDC25Aand CDC25B 1 B c
phosphatases. Genomics 18: 144- 147, 1993.

GAM67 282 CDC25A Falck, J.; Mailand, N.; Syljuasen, R. G.; Bartek, J.; Lukas, J.: The ATM- 1 B c
Chk2- Cdc25A checkpoint pathway guards against radioresistantDNA synthesis.
Nature 410: 842- 847, 2001.

GAM67 282 CDC25A Falck, J.; Petrini, J. H. J.; Williams, B. R.; Lukas, J.; Bartek,J.: The DNA 1 B c

damage- dependent intra- S phase checkpoint is regulatedby parallel pathways. Nature Genet. 30: 290- 294, 2002.

GAM67 282 CDC25A Fauman, E. B.; Cogswell, J. P.; Lovejoy, B.; Rocque, W. J.; Holmes,W.; Montana, V. G.; Piwnica- Worms, H.; Rink, M. J.; Saper, M. A.:Crystal structure of the catalytic domain of the human cell cyclecontrol phosphatase, Cdc25A. Cell 93: 617- 625, 1998. 1 B c

GAM67 282 CDC25A Galaktionov, K.; Lee, A. K.; Eckstein, J.; Draetta, G.; Meckler,J.; Loda, M.; Beach, D.: CDC25 phosphatases as potential human oncogenes. Science 269:1575- 1577, 1995. 1 B c

GAM67 282 CDC25A Mailand, N.; Falck, J.; Lukas, C.; Syljuasen, R. G.; Welcker, M.;Bartek, J.; Lukas, J.: Rapid destruction of human Cdc25A in responseto DNA damage. Science 288: 1425- 1429, 2000. 1 B c

GAM67 282 COL4A2 Boyd, C. D.; Toth- Fejel, S.; Gadi, I. K.; Litt, M.; Condon, M.R.; Kolbe, M.; Hagen, I. K.; Kurkinen, M.; Mackenzie, J. W.; Magenis,E.: The genes coding for human pro alpha- 1(IV) collagen and pro alpha- 2(IV)collagen are both located at the end of the long arm of chromosome13. Am. J. Hum. Genet. 42: 309- 314, 1988. 1 B c

GAM67 282 COL4A2 Brazel, D.; Pollner, R.; Oberbaumer, I.; Kuhn, K.: Human basementmembrane collagen (type IV): the amino acid sequence of the alpha- 2(IV)chain and its comparison with the alpha- 1(IV) chain reveals deletionsin the alpha- 1(IV) chain. Europ. J. Biochem. 172: 35- 42, 1988. 1 B c

GAM67 282 COL4A2 Griffin, C. A.; Emanuel, B. S.; Hansen, J. R.; Cavenee, W. K.;Myers, J. C.: Human collagen genes encoding basement membrane alpha- 1(IV)and alpha- 2(IV) chains map to the distal long arm of chromosome 13. Proc.Nat. Acad. Sci. 84: 512- 516, 1987. 1 B c

GAM67 282 COL4A2 Haniel, A.; Welge- Lussen, U.; Kuhn, K.; Poschl, E.: Identificationand characterization of a novel transcriptional silencer in the humancollagen type IV gene COL4A2. J. Biol. Chem. 270: 11209- 11215, 1995. 1 B c

GAM67 282 COL4A2 Killen, P. D.; Francomano, C. A.; Yamada, Y.; Modi, W. S.; O'Brien,S. J.: Partial structure of the human alpha- 2(IV) collagen chainand chromosomal localization of the gene (COL4A2). Hum. Genet. 77:318- 324, 1987. 1 B c

GAM67 282 COL4A2 Koizumi, T.; Hendel, E.; Lalley, P. A.; Tchetgen, M.- B. N.; Nadeau,J. H.: Homologs of genes and anonymous loci on human chromosome 13map to mouse chromosomes 8 and 14. Mammalian Genome 6: 263- 268,1995. 1 B c

GAM67 282 COL4A2 Solomon, E.; Hall, V.; Kurkinen, M.: The human alpha- 2(IV) collagengene, COL4A2, is syntenic with the alpha- 1(IV) gene, COL4A1, on chromosome13. Ann. Hum. Genet. 51: 125- 127, 1987. 1 B c

GAM67 282 CUL3 Du, M.; Sansores- Garcia, L.; Zu, Z.; Wu, K. K.: Cloning and expressionanalysis of a novel salicylate suppressible gene, Hs- CUL- 3, a memberof cullin/Cdc53 family. J. Biol. Chem. 273: 24289- 24292, 1998. 1 B c

GAM67 282 CUL3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 1 B c

GAM67 282 CUL3 Kipreos, E. T.; Lander, L. E.; Wing, J. P.; He, W. W.; Hedgecock,E. M.: cul- 1 is required for cell cycle exit in C. elegans and identifiesa novel gene family. Cell 85: 829- 839, 1996. 1 B c

GAM67 282 CUL3 Michel, J. J.; Xiong, Y.: Human CUL- 1, but not other cullin familymembers, selectively interacts with SKP1 to form a complex with SKP2and cyclin A. Cell Growth Differ. 9: 435- 449, 1998. 1 B c

GAM67 282 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; 1 B c
Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene:
molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230,
1998.

GAM67 282 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii- 1 B c
Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in
humanpolymorphonuclear leukocytes: cDNA cloning and expression of
leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993.

GAM67 282 E2F3 Cloud, J. E.; Rogers, C.; Reza, T. L.; Ziebold, U.; Stone, J. R.;Picard, M. 1 B c
H.; Caron, A. M.; Bronson, R. T.; Lees, J. A.: Mutantmouse models reveal the
relative roles of E2F1 and E2F3 in vivo. Molec.Cell. Biol. 22: 2663- 2672,
2002.

GAM67 282 E2F3 He, Y.; Armanious, M. K.; Thomas, M. J.; Cress, W. D.: Identificationof E2F- 1 B c
3B, an alternative form of E2F- 3 lacking a conserved N- terminalregion.
Oncogene 19: 3422- 3433, 2000.

GAM67 282 E2F3 Lees, J. A.; Saito, M.; Vidal, M.; Valentine, M.; Look, T.; Harlow,E.; 1 B c
Dyson, N.; Helin, K.: The retinoblastoma protein binds to a familyof E2F
transcription factors. Molec. Cell. Biol. 13: 7813- 7825,1993.

GAM67 282 E2F3 Leone, G.; Sears, R.; Huang, E.; Rempel, R.; Nuckolls, F.; Park,C.- H.; 1 B c
Giangrande, P.; Wu, L.; Saavedra, H. I.; Field, S. J.; Thompson,M. A.; Yang,
H.; Fujiwara, Y.; Greenberg, M. E.; Orkin, S.; Smith,C.; Nevins, J. R.: Myc
requires distinct E2F activities to induceS phase and apoptosis. Molec. Cell
8: 105- 113, 2001.

GAM67 282 E2F3 Wu, L.; Timmers, C.; Maiti, B.; Saavedra, H. I.; Sang, L.; Chong,G. T.; 1 B c
Nuckolls, F.; Giangrande, P.; Wright, F. A.; Field, S. J.;Greenberg, M. E.;
Orkin, S.; Nevins, J. R.; Robinson, M. L.; Leone,G.: The E2F1- 3
transcription factors are essential for cellular proliferation. Nature
414:457- 462, 2001.

GAM67 282 FZD4 Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.;Hirai, M.; 1 B c
Katoh, M.: Molecular cloning and characterization of humanfrizzled- 4 on
chromosome 11q14- q21. Biochem. Biophys. Res. Commun. 264:955- 961, 1999.

GAM67 282 FZD4 Robitaille, J.; MacDonald, M. L. E.; Kaykas, A.; Sheldahl, L. C.;Zeisler, 1 B c
J.; Dube, M.- P.; Zhang, L.- H.; Singaraja, R. R.; Guernsey,D. L.; Zhang,
B.; Siebert, L. F.; Hoskin- Mott, A.; Trese, M. T.; Pimstone,S. N.; Shastry,
B. S.; Moon, R. T.; Hayden, M. R.; Goldberg, Y. P.;Samuels, M. E.: Mutant
frizzled- 4 disrupts retinal angiogenesis infamilial exudative
vitreoretinopathy. Nature Genet. 32: 326- 330,2002.

GAM67 282 KCNS2 Banfi, S.; Borsani, G.; Rossi, E.; Bernard, L.; Guffanti, A.; Rubboli,F.; 1 B c
Marchitiello, A.; Giglio, S.; Coluccia, E.; Zollo, M.; Zuffardi,O.;
Ballabio, A.: Identification and mapping of human cDNAs homologousto
Drosophila mutant genes through EST database searching. NatureGenet. 13:
167- 174, 1996.

GAM67 282 KCNS2 Salinas, M.; Duprat, F.; Heurteaux, C.; Hugnot, J.- P.; Lazdunski,M.: New 1 B c
modulatory alpha subunits for mammalian Shab K(+) channels. J.Biol. Chem.
272: 24371- 24379, 1997.

GAM67 282 KPNA3 Kohler, M.; Ansieau, S.; Prehn, S.; Leutz, A.; Haller, H.; Hartmann,E.: 1 B c
Cloning of two novel human importin- alpha subunits and analysisof the
expression pattern of the importin- alpha protein family. FEBSLett. 417:
104- 108, 1997.

GAM67 282 KPNA3 Moore, M. S.; Blobel, G.: The two steps of nuclear import, targetingto the 1 B c

nuclear envelope and translocation through the nuclear pore,require different cytosolic factors. Cell 69: 939- 950, 1992.

GAM67 282 KPNA3 Takeda, S.; Fujiwara, T.; Shimizu, F.; Kawai, A.; Shinomiya, K.;Okuno, S.; 1 B c
Ozaki, K.; Katagiri, T.; Shimada, Y.; Nagata, M.; Watanabe,T.; Takaichi, A.; Kuga, Y.; Suzuki, M.; Hishigaki, H.; Takahashi,E.; Shin, S.; Nakamura, Y.; Hirai, Y.: Isolation and mapping of karyopherinalpha- 3 (KPNA3), a human gene that is highly homologous to genes encodingXenopus importin, yeast SRP1 and human RCH1. Cytogenet. Cell Genet. 76:87- 93, 1997.

GAM67 282 RABIF Muller- Pillasch, F.; Zimmerhackl, F.; Lacher, U.; Schultz, N.;Hameister, 1 B c
H.; Varga, G.; Friess, H.; Buchler, M.; Adler, G.; Gress,T. M.: Cloning of novel transcripts of the human guanine- nucleotide- exchangefactor Mss4: in situ chromosomal mapping and expression in pancreaticcancer. Genomics 46: 389- 396, 1997.

GAM67 282 RABIF Yu, H.; Schreiber, S. L.: Cloning, Zn(2+) binding, and 1 B c
structuralcharacterization of the guanine nucleotide exchange factor human Mss4. Biochemistry 34:9103- 9110, 1995.

GAM67 282 SREBF1 DeBose- Boyd, R. A.; Brown, M. S.; Li, W.- P.; Nohturfft, A.; Goldstein,J. 1 B c
L.; Espenshade, P. J.: Transport- dependent proteolysis of SREBP:relocation of Site- 1 protease from Golgi to ER obviates the need forSREBP transport to Golgi. Cell 99: 703- 712, 1999.

GAM67 282 SREBF1 Hua, X.; Wu, J.; Goldstein, J. L.; Brown, M. S.; Hobbs, H. H.:Structure of 1 B c
the human gene encoding sterol regulatory element bindingprotein- 1 (SREBF1) and localization of SREBF1 and SREBF2 to chromosomes17p11.2 and 22q13. Genomics 25: 667- 673, 1995.

GAM67 282 SREBF1 Lloyd, D. J.; Trembath, R. C.; Shackleton, S.: A novel interactionbetween 1 B c
lamin A and SREBP1: implications for partial lipodystrophyand other laminopathies. Hum. Molec. Genet. 11: 769- 777, 2002.

GAM67 282 SREBF1 Osborne, T. F.: CREating a SCAP- less liver keeps SREBPs pinnedin the ER 1 B c
membrane and prevents increased lipid synthesis in responseto low cholesterol and high insulin. Genes Dev. 15: 1873- 1878, 2001.

GAM67 282 SREBF1 Shimano, H.; Shimomura, I.; Hammer, R. E.; Herz, J.; Goldstein,J. L.; Brown, 1 B c
M. S.; Horton, J. D.: Elevated levels of SREBP- 2 andcholesterol synthesis in livers of mice homozygous for a targeteddisruption of the SREBP- 1 gene. J. Clin. Invest. 100: 2115- 2124,1997.

GAM67 282 SREBF1 Shimomura, I.; Hammer, R. E.; Richardson, J. A.; Ikemoto, S.; Bashmakov,Y.; 1 B c
Goldstein, J. L.; Brown, M. S.: Insulin resistance and diabetesmellitus in transgenic mice expressing nuclear SREBP- 1c in adiposetissue: model for congenital generalized lipodystrophy. Genes Dev. 12:3182- 3194, 1998.

GAM67 282 SREBF1 Shimomura, I.; Matsuda, M.; Hammer, R. E.; Bashmakov, Y.; Brown,M. S.; 1 B c
Goldstein, J. L.: Decreased IRS- 2 and increased SREBP- 1c leadto mixed insulin resistance and sensitivity in livers of lipodystrophicand ob/ob mice. Molec. Cell 6: 77- 86, 2000.

GAM67 282 SREBF1 Tobe, K.; Suzuki, R.; Aoyama, M.; Yamauchi, T.; Kamon, J.; Kubota,N.; 1 B c
Terauchi, Y.; Matsui, J.; Akanuma, Y.; Kimura, S.; Tanaka, J.;Abe, M.; Ohsumi, J.; Nagai, R.; Kadowaki, T.: Increased expressionof the sterol regulatory element- binding protein- 1 gene in insulinreceptor substrate- 2 - /- mouse liver. J. Biol. Chem. 276: 38337- 38340,2001.

GAM67 282 SREBF1 Wang, X.; Sato, R.; Brown, M. S.; Hua, X.; Goldstein, J. L.: SREBP- 1,a 1 B c
membrane- bound transcription factor released by sterol-regulatedproteolysis. Cell 77: 53- 62, 1994.

GAM67 282 SREBF1 Yokoyama, C.; Wang, X.; Briggs, M. R.; Admon, A.; Wu, J.; Hua,X.; Goldstein, 1 B c
J. L.; Brown, M. S.: SREBP- 1, a basic- helix- loop- helix- leucinezipper
protein that controls transcription of the low density lipoproteinreceptor
gene. Cell 75: 187- 197, 1993.

GAM67 282 TAF4 Dunah, A. W.; Jeong, H.; Griffin, A.; Kim, Y.- M.; Standaert, D.G.; Hersch, 1 B c
S. M.; Mouradian, M. M.; Young, A. B.; Tanese, N.; Krainc,D.: Sp1 and
TAFII130 transcriptional activity disrupted in earlyHuntington's disease.
Science 296: 2238- 2243, 2002.

GAM67 282 TAF4 Mengus, G.; May, M.; Carre, L.; Chambon, P.; Davidson, I.: HumanTAF(II)135 1 B c
potentiates transcriptional activation by the AF- 2s ofthe retinoic acid,
vitamin D3, and thyroid hormone receptors in mammaliancells. Genes Dev. 11:
1381- 1395, 1997.

GAM67 282 TAF4 Shimohata, T.; Nakajima, T.; Yamada, M.; Uchida, C.; Onodera, O.;Naruse, S.; 1 B c
Kimura, T.; Koide, R.; Nozaki, K.; Sano, Y.; Ishiguro,H.; Sakoe, K.; and 16
others: Expanded polyglutamine stretchesinteract with TAF(II)130,
interfering with CREB- dependent transcription. NatureGenet. 26: 29- 36,
2000.

GAM67 282 TAF4 Tanese, N.; Saluja, D.; Vassallo, M. F.; Chen, J.- L.; Admon, A.: Molecular 1 B c
cloning and analysis of two subunits of the human TFIIDcomplex: hTAFII130
and hTAFII100. Proc. Nat. Acad. Sci. 93: 13611- 13616,1996.

GAM67 282 UPF3B Kim, V. N.; Kataoka, N.; Dreyfuss, G.: Role of the nonsense- mediateddecay 1 B c
factor hUpf3 in the splicing- dependent exon- exon junction complex. Science
293:1832- 1836, 2001.

GAM67 282 UPF3B Lykke- Andersen, J.; Shu, M.- D.; Steitz, J. A.: Human Upf proteinstarget an 1 B c
mRNA for nonsense- mediated decay when bound downstream ofa termination
codon. Cell 103: 1121- 1131, 2000.

GAM67 282 UPF3B Scott, A. F.: Personal Communication. Baltimore, Md. 2/9/2001. 1 B c

GAM67 282 UPF3B Serin, G.; Gersappe, A.; Black, J. D.; Aronoff, R.; Maquat, L.E.: 1 B c
Identification and characterization of human orthologues to
Saccharomycescerevisiae Upf2 protein and Upf3 protein (Caenorhabditis
elegans SMG- 4). Molec.Cell. Biol. 21: 209- 223, 2001.

GAM68 251 GRLF1 LeClerc, S.; Palaniswami, R.; Xie, B.; Govdan, M. V.: Molecularcloning and 3 C c
characterization of a factor that binds the human glucocorticoidreceptor
gene and represses its expression. J. Biol. Chem. 266:17333- 17340, 1991.

GAM68 251 GRLF1 Tikoo, A.; Czekay, S.; Viars, C.; White, S.; Heath, J. K.; Arden,K.; Maruta, 3 C c
H.: p190- A, a human tumor suppressor gene, maps to thechromosomal region
19q13.3 that is reportedly deleted in some gliomas. Gene 257:23- 31, 2000.

GAM69 258 ADCY8 Parma, J.; Stengel, D.; Gannage, M.- H.; Poyard, M.; Barouki, R.;Hanoune, 3 B c
J.: Sequence of a human brain adenylyl cyclase partial cDNA:evidence for a
consensus cyclase domain. Biochem. Biophys. Res. Commun. 179:455- 462, 1991.

GAM69 258 ADCY8 Stengel, D.; Parma, J.; Gannage, M.- H.; Roeckel, N.; Mattei, M.- 3 B c
G.;Barouki, R.; Hanoune, J.: Different chromosomal localization of
twoadenylyl cyclase genes expressed in human brain. Hum. Genet. 90:126- 130,
1992.

GAM69 258 ADD2 Bianchi, G.; Tripodi, G.; Casari, G.; Salardi, S.; Barber, B. R.;Garcia, R.; 3 B c
Leoni, P.; Torielli, L.; Cusi, D.; Ferrandi, M.; Pinna,L. A.; Baralle, F.
E.; Ferrari, P.: Two point mutations within theadducin genes are involved in
blood pressure variation. Proc. Nat.Acad. Sci. 91: 3999- 4003, 1994.

GAM69 258 ADD2 Gilligan, D. M.; Lieman, J.; Bennett, V.: Assignment of the humanbeta- 3 B c
adducin gene (ADD2) to 2p13- p14 by in situ hybridization. Genomics 28:610-

612, 1995.

GAM69 258 ADD2 Gilligan, D. M.; Lozovatsky, L.; Gwynn, B.; Brugnara, C.; Mohandas,N.; Peters, L. L.: Targeted disruption of the beta adducin gene (Add2)causes red blood cell spherocytosis in mice. Proc. Nat. Acad. Sci. 96:10717- 10722, 1999. 3 B c

GAM69 258 ADD2 Joshi, R.; Gilligan, D. M.; Otto, E.; McLaughlin, T.; Bennett,V.: Primary structure and domain organization of human alpha andbeta adducin. J. Cell Biol. 115: 665- 675, 1991. 3 B c

GAM69 258 ADD2 Muro, A. F.; Marro, M. L.; Gajovic, S.; Porro, F.; Luzzatto, L.;Baralle, F. E.: Mild spherocytic hereditary elliptocytosis and alteredlevels of alpha- and gamma- adducins in beta- adducin- deficient mice. Blood 95:3978- 3985, 2000. 3 B c

GAM69 258 ADD2 Tisminetzky, S.; Devescovi, G.; Tripodi, G.; Muro, A.; Bianchi,G.; Colombi, M.; Moro, L.; Barlati, S.; Tuteja, R.; Baralle, F. E.: Genomic organisation and chromosomal localisation of the gene encodinghuman beta adducin. Gene 167: 313- 316, 1995. 3 B c

GAM69 258 ADD2 White, R. A.; Angeloni, S. V.; Pasztor, L. M.: Chromosomal localizationof the beta- adducin gene to mouse chromosome 6 and human chromosome2. Mammalian Genome 6: 741- 743, 1995. 3 B c

GAM69 258 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 B c

GAM69 258 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 B c

GAM69 258 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 B c

GAM69 258 CCNB1 Brandeis, M.; Rosewell, I.; Carrington, M.; Crompton, T.; Jacobs,M. A.; Kirk, J.; Gannon, J.; Hunt, T.: Cyclin B2- null mice developnormally and are fertile whereas cyclin B1- null mice die in utero. Proc.Nat. Acad. Sci. 95: 4344- 4349, 1998. 3 B c

GAM69 258 CCNB1 Lock, L. F.; Pines, J.; Hunter, T.; Gilbert, D. J.; Gopalan, G.;Jenkins, N. A.; Copeland, N. G.; Donovan, P. J.: A single cyclinA gene and multiple cyclin B1- related sequences are dispersed in themouse genome. Genomics 13: 415- 424, 1992. 3 B c

GAM69 258 CCNB1 Milatovich, A.; Francke, U.: Human cyclin B1 gene (CCNB1) assignedto chromosome 5 (q13- qter). Somat. Cell Molec. Genet. 18: 303- 307,1992. 3 B c

GAM69 258 CCNB1 Pines, J.; Hunter, T.: Isolation of a human cyclin cDNA: evidencefor cyclin mRNA and protein regulation in the cell cycle and for interactionwith p34(cdc2). Cell 58: 833- 846, 1989. 3 B c

GAM69 258 CCNB1 Sartor, H.; Ehlert, F.; Grzeschik, K.- H.; Muller, R.; Adolph, S.: Assignment of two human cell cycle genes, CDC25C and CCNB1, to 5q31and 5q12, respectively. Genomics 13: 911- 912, 1992. 3 B c

GAM69 258 CCNB1 Toyoshima- Morimoto, F.; Taniguchi, E.; Shinya, N.; Iwamatsu, A.;Nishida, E.: Polo- like kinase 1 phosphorylates cyclin B1 and targetsit to the nucleus during prophase. Nature 410: 215- 220, 2001. Note:Erratum: Nature 410: 847 only, 2001. 3 B c

GAM69 258 CNN1 Maguchi, M.; Nishida, W.; Kohara, K.; Kuwano, A.; Kondo, I.; Hiwada,K.: 3 B c

Molecular cloning and gene mapping of human basic and acidiccalponins. Biochem. Biophys. Res. Commun. 217: 238- 244, 1995.

GAM69 258 CNN1 Miano, J. M.; Krahe, R.; Garcia, E.; Elliott, J. M.; Olson, E.N.: 3 B c
Expression, genomic structure and high resolution mapping to19p13.2 of the human smooth muscle cell calponin gene. Gene 197:215- 224, 1997.

GAM69 258 CNN1 Miano, J. M.; Thomas, S.; Disteche, C. M.: Expression and chromosomalmapping 3 B c
of the mouse smooth muscle calponin gene. Mammalian Genome 12:187- 191, 2001.

GAM69 258 CNN1 Strasser, P.; Gimona, M.; Moessler, H.; Herzog, M.; Small, J. V.: Mammalian 3 B c
calponin: identification and expression of genetic variants. FEBSLett. 330: 13- 18, 1993.

GAM69 258 CYP21A2 Amor, M.; Parker, K. L.; Globerman, H.; New, M. I.; White, P. C.: Mutation 3 B b
in the CYP21B gene (ile172- to- asn) causes steroid 21- hydroxylasedeficiency. Proc. Nat. Acad. Sci. 85: 1600- 1604, 1988.

GAM69 258 CYP21A2 Araujo, M.; Sanches, M. R.; Suzuki, L. A.; Guerra, G., Jr.; Farah,S. B.; De 3 B b
Mello, M. P.: Molecular analysis of CYP21 and C4 genesin Brazilian families with the classical form of steroid 21- hydroxylasedeficiency. Braz. J. Med. Biol. Res. 29: 1- 13, 1996.

GAM69 258 CYP21A2 Aston, C. E.; Sherman, S. L.; Morton, N. E.; Speiser, P. W.; New,M. I.: 3 B b
Genetic mapping of the 21- hydroxylase locus: estimation ofsmall recombination frequencies. Am. J. Hum. Genet. 43: 304- 310,1988.

GAM69 258 CYP21A2 Bachega, T. A. S. S.; Billerbeck, A. E. C.; Madureira, G.; Marcondes,J. A. 3 B b
M.; Longui, C. A.; Leite, M. V.; Arnhold, I. J. P.; Mendonca,B. B.: Molecular genotyping in Brazilian patients with the classicaland nonclassical forms of 21- hydroxylase deficiency. J. Clin. Endocr.Metab. 83: 4416- 4419, 1998.

GAM69 258 CYP21A2 Bachega, T. A. S. S.; Brenlha, E. M. L.; Billerbeck, A. E. C.;Marcondes, J. 3 B b
A. M.; Madureira, G.; Arnhold, I. J. P.; Mendonca, B.B.: Variable ACTH- stimulated 17- hydroxyprogesterone values in 21- hydroxylasedeficiency carriers are not related to the different CYP21 gene mutations. J.Clin. Endocr. Metab. 87: 786- 790, 2002.

GAM69 258 CYP21A2 Baumgartner- Parzer, S. M.; Schulze, E.; Waldhausl, W.; Pauschenwein,S.; 3 B b
Rondot, S.; Nowotny, P.; Meyer, K.; Frisch, H.; Waldhauser, F.;Vierhapper, H.: Mutational spectrum of the steroid 21- hydroxylasegene in Austria: identification of a novel missense mutation. J.Clin. Endocr. Metab. 86: 4771- 4775, 2001.

GAM69 258 CYP21A2 Beuschlein, F.; Schulze, E.; Mora, P.; Gensheimer, H.- P.; Maser- Gluth,C.; 3 B b
Allolio, B.; Reincke, M.: Steroid 21- hydroxylase mutations and21- hydroxylase messenger ribonucleic acid expression in human adrenocorticaltumors. J. Clin. Endocr. Metab. 83: 2585- 2588, 1998.

GAM69 258 CYP21A2 Bias, W. B.; Urban, M. D.; Migeon, C. J.; Hsu, S. H.; Lee, P. A.: Intra- HLA 3 B b
recombinations localizing the 21- hydroxylase deficiencygene within the HLA complex. Hum. Immun. 2: 139- 145, 1981.

GAM69 258 CYP21A2 Billerbeck, A. E. C.; Bachega, T. A. S. S.; Frazzatto, E. T.; Nishi,M. Y.; 3 B b
Goldberg, A. C.; Marin, M. L. C.; Madureira, G.; Monte, O.;Arnhold, I. J. P.; Mendonca, B. B.: A novel missense mutation, GLY424SER,in Brazilian patients with 21- hydroxylase deficiency. J. Clin. Endocr.Metab. 84: 2870- 2872, 1999.

GAM69 258 CYP21A2 Blankstein, J.; Faiman, C.; Reyes, F. I.; Schroeder, M. L.; Winter,J. S. D.: 3 B b
Adult- onset familial adrenal 21- hydroxylase deficiency. Am.J. Med. 68:

441- 448, 1980.

GAM69 258 CYP21A2 Bongiovanni, A. M.: Disorders of adrenocortical steroid biogenesis.In:Stanbury, J. B.; Wyngaarden, J. B.; Fredrickson, D. S.: The MetabolicBasis of Inherited Disease. New York: McGraw- Hill (pub.) (3rded.): 1972. Pp. 857- 885. 3 B b

GAM69 258 CYP21A2 Bongiovanni, A. M.; Root, A. W.: The adrenogenital syndrome. NewEng. J. Med. 268: 1283- 1289; 1342- 1351; 1391- 1399, 1963. 3 B b

GAM69 258 CYP21A2 Boudreaux, D.; Waisman, J.; Skinner, D. G.; Low, R.: Giant adrenalmyelolipoma and testicular interstitial cell tumor in a man with congenital21- hydroxylase deficiency. Am. J. Surg. Path. 3: 109- 123, 1979. 3 B b

GAM69 258 CYP21A2 Carroll, M. C.; Campbell, R. D.; Porter, R. R.: Mapping of steroid21- hydroxylase genes adjacent to complement component C4 genes inHLA, the major histocompatibility complex in man. Proc. Nat. Acad.Sci. 82: 521- 525, 1985. 3 B b

GAM69 258 CYP21A2 Chaplin, D. D.; Galbraith, L. J.; Seidman, J. G.; White, P. C.;Parker, K. L.: Nucleotide sequence analysis of murine 21- hydroxylasegene: mutations affecting gene expression. Proc. Nat. Acad. Sci. 83:9601- 9605, 1986. 3 B b

GAM69 258 CYP21A2 Charmandari, E.; Hindmarsh, P. C.; Johnston, A.; Brook, C. G.D.: Congenital adrenal hyperplasia due to 21- hydroxylase deficiency:alterations in cortisol pharmacokinetics at puberty. J. Clin. Endocr.Metab. 86: 2701- 2708, 2001. 3 B b

GAM69 258 CYP21A2 Childs, B.; Grumbach, M. M.; Van Wyk, J. J.: Virilizing adrenalhyperplasia: genetic and hormonal studies. J. Clin. Invest. 35:213- 222, 1956. 3 B b

GAM69 258 CYP21A2 Chiou, S.- H.; Hu, M.- C.; Chung, B.: A missense mutation at ile172- to- asnor arg356- to- trp causes steroid 21- hydroxylase deficiency. J. Biol.Chem. 265: 3549- 3552, 1990. 3 B b

GAM69 258 CYP21A2 Chrousos, G. P.; Loriaux, D. L.; Mann, D. L.; Cutler, G. B., Jr.: Late- onset 21- hydroxylase deficiency mimicking idiopathic hirsutismor polycystic ovarian disease: an allelic variant of congenital virilizingadrenal hyperplasia with a milder enzymatic defect. Ann. Intern.Med. 96: 143- 148, 1982. 3 B b

GAM69 258 CYP21A2 Collier, S.; Tassabehji, M.; Strachan, T.: A de novo pathologicalpoint mutation at the 21- hydroxylase locus: implications for geneconversion in the human genome. Nature Genet. 3: 260- 265, 1993. 3 B b

GAM69 258 CYP21A2 Cooper, D. Y.; Levin, S.; Narasimhulu, S.; Rosenthal, O.; Estabrook,R. W.: Photochemical action spectrum of the terminal oxidase of mixedfunction oxidase systems. Science 147: 400- 402, 1965. 3 B b

GAM69 258 CYP21A2 Cornean, R. E.; Hindmarsh, P. C.; Brook, C. G. D.: Obesity in21- hydroxylase deficient patients. Arch. Dis. Child. 78: 261- 263,1998. 3 B b

GAM69 258 CYP21A2 Couillin, P.; Kottler- Missonnier, M. L.; Grisard, M. C.; Hors,J.; Feingold, J.; Boue, J.; Boue, A.: HLA- A, B, C, DR alleles incongenital adrenal hyperplasia. Hum. Genet. 53: 389- 392, 1980. 3 B b

GAM69 258 CYP21A2 Cutfield, R. G.; Bateman, J. M.; Odell, W. D.: Infertility causedby bilateral testicular masses secondary to congenital adrenal hyperplasia(21- hydroxylase deficiency). Fertil. Steril. 40: 809- 814, 1983. 3 B b

GAM69 258 CYP21A2 Cutler, G. B., Jr.; Laue, L.: Congenital adrenal hyperplasiadue to 21- hydroxylase deficiency. New Eng. J. Med. 323: 1806- 1813,1990. 3 B b

GAM69 258 CYP21A2 Dacou- Voutetakis, C.; Dracopoulou, M.: High incidence of moleculardefects of the CYP21 gene in patients with premature adrenarche. J.Clin. Endocr. Metab. 84: 1570- 1574, 1999. 3 B b

GAM69 258 CYP21A2 Day, D. J.; Speiser, P. W.; Schulze, E.; Bettendorf, M.; Fitness,J.; Barany, 3 B b
F.; White, P. C.: Identification of non- amplifying CYP21genes when using
PCR- based diagnosis of 21- hydroxylase deficiencyin congenital adrenal
hyperplasia (CAH) affected pedigrees. Hum.Molec. Genet. 5: 2039- 2048, 1996.

GAM69 258 CYP21A2 Deneux, C.; Tardy, V.; Dib, A.; Mornet, E.; Billaud, L.; Charron,D.; Morel, 3 B b
Y.; Kuttenn, F.: Phenotype- genotype correlation in 56women with
nonclassical congenital adrenal hyperplasia due to 21-
hydroxylasedeficiency. J. Clin. Endocr. Metab. 86: 207- 213, 2001.

GAM69 258 CYP21A2 Donohoue, P. A.; Jospe, N.; Migeon, C. J.; Van Dop, C.: Two distinctareas of 3 B b
unequal crossingover within the steroid 21- hydroxylase genesproduce absence
of CYP21B. Genomics 5: 397- 406, 1989.

GAM69 258 CYP21A2 Dracopoulou- Vabouli, M.; Maniati- Christidi, M.; Dacou- Voutetakis,C.: The 3 B b
spectrum of molecular defects of the CYP21 gene in the Hellenicpopulation:
variable concordance between genotype and phenotype inthe different forms of
congenital adrenal hyperplasia. J. Clin. Endocr.Metab. 86: 2845- 2848, 2001.

GAM69 258 CYP21A2 Duck, S. C.: Malignancy associated with congenital adrenal hyperplasia. 3 B b
J.Pediat. 99: 423- 424, 1981.

GAM69 258 CYP21A2 Dumic, M.; Brkljacic, L.; Mardesic, D.; Plavsic, V.; Lukenda,M.; Kastelan, 3 B b
A.: 'Cryptic' form of congenital adrenal hyperplasiadue to 21- hydroxylase
deficiency in the Yugoslav population. ActaEndocr. 109: 386- 392, 1985.

GAM69 258 CYP21A2 Dupont, B.; Smithwick, E. M.; Oberfield, S. E.; Lee, T. D.; Levine,L. S.: 3 B b
Close genetic linkage between HLA and congenital adrenal hyperplasia(21-
hydroxylase deficiency). Lancet II: 1309- 1312, 1977.

GAM69 258 CYP21A2 Ezquieta, B.; Oliver, A.; Gracia, R.; Gancedo, P. G.: Analysisof steroid 21- 3 B b
hydroxylase gene mutations in the Spanish population. Hum.Genet. 96: 198-
204, 1995.

GAM69 258 CYP21A2 Ferenczi, A.; Garami, M.; Kiss, E.; Pek, M.; Sasvari- Szekely,M.; Barta, C.; 3 B b
Staub, M.; Solyom, J.; Fekete, G.: Screening for mutationsof 21- hydroxylase
gene in Hungarian patients with congenital adrenalhyperplasia. J. Clin.
Endocr. Metab. 84: 2369- 2372, 1999.

GAM69 258 CYP21A2 Fitness, J.; Dixit, N.; Webster, D.; Torresani, T.; Pergolizzi,R.; Speiser, 3 B b
P. W.; Day, D. J.: Genotyping of CYP21, linked chromosome6p markers, and a
sex- specific gene in neonatal screening for congenitaladrenal hyperplasia.
J. Clin. Endocr. Metab. 84: 960- 966, 1999.

GAM69 258 CYP21A2 Fleischnick, E.; Awdeh, Z. L.; Raum, D.; Granados, J.; Alosco,S. M.; 3 B b
Crigler, J. F., Jr.; Gerald, P. S.; Giles, C. M.; Yunis, E.J.; Alper, C. A.:
Extended MHC haplotypes in 21- hydroxylase- deficiencycongenital adrenal
hyperplasia: shared genotypes in unrelated patients. Lancet I:152- 156,
1983.

GAM69 258 CYP21A2 Flori, J.; Tongio, M. M.; Kurtz, F.; Mayer, S.; Juif, J. G.:Liaison entre le 3 B b
gene responsible de l'hyperplasie surrenalienne pardeficit en 21 hydroxylase
et les marqueurs du bras court du chromosome6. J. Genet. Hum. 28: 185- 193,
1980.

GAM69 258 CYP21A2 Forest, M. G.; Betuel, H.; David, M.: Prenatal treatment in 3 B b
congenitaladrenal hyperplasia due to 21- hydroxylase deficiency: up- date 88
ofthe French multicentric study. Endocr. Res. 15: 277- 301, 1989.

GAM69 258 CYP21A2 Galal, O. M.; Rudd, B. T.; Drayer, N. M.: Evaluation of deficiencyof 21- 3 B b
hydroxylation in patients with congenital adrenal hyperplasia. Arch.Dis.
Child. 43: 410- 414, 1968.

GAM69 258 CYP21A2 Ghanem, N.; Lobaccaro, J. M.; Buresi, C.; Abbal, M.; Halaby, G.;Sultan, C.; 3 B b

Lefranc, G.: Defective, deleted or converted CYP21B geneand negative association with a rare restriction fragment length polymorphismallele of the factor B gene in congenital adrenal hyperplasia. Hum.Genet. 86: 117-125, 1990.

GAM69 258 CYP21A2 Ghizzoni, L.; Mastorakos, G.; Street, M. E.; Vottero, A.; Mazzardo,G.; Vanelli, M.; Chrousos, G. P.; Bernasconi, S.: Spontaneous thyrotropinand cortisol secretion interactions in patients with nonclassical21- hydroxylase deficiency and control children. J. Clin. Endocr.Metab. 82: 3677- 3683, 1997. 3 B b

GAM69 258 CYP21A2 Globerman, H.; Amor, H.; Parker, K. L.; New, M. I.; White, P.C.: A nonsense mutation causing steroid 21- hydroxylase deficiency. J.Clin. Invest. 82: 139- 144, 1988. 3 B b

GAM69 258 CYP21A2 Gordon, M. T.; Conway, D. I.; Anderson, D. C.; Harris, R.: Geneticsand biochemical variability of variants of 21 hydroxylase deficiency. J.Med. Genet. 22: 354- 360, 1985. 3 B b

GAM69 258 CYP21A2 Gotoh, H.; Sagai, T.; Hata, J.- I.; Shiroishi, T.; Moriwaki, K.: Steroid 21- hydroxylase deficiency in mice. Endocrinology 123:1923- 1927, 1988. 3 B b

GAM69 258 CYP21A2 Grosse- Wilde, H.; Weil, J.; Albert, E.; Scholz, S.; Bidlingmaier,F.; Sippel, W. G.; Knorr, D.: Genetic linkage studies between congenitaladrenal hyperplasia and the HLA blood group system. Immunogenetics 8:41- 49, 1979. 3 B b

GAM69 258 CYP21A2 Gueux, B.; Fiet, J.; Couillin, P.; Raux- Demay, M.- C.; Mornet,E.; Galons, H.; Villette, J.- M.; Boue, J.; Dreux, C.: Prenatal diagnosisof 21-hydroxylase deficiency congenital adrenal hyperplasia by simultaneousradioimmunoassay of 21- deoxycortisol and 17-hydroxyprogesterone inamniotic fluid. J. Clin. Endocr. Metab. 66: 534- 537, 1988. 3 B b

GAM69 258 CYP21A2 Gutai, J. P.; Lee, P. A.; Johnsonbaugh, R. E.; Gareis, F.; Urban,M. D.; Migeon, C. J.: Detection of the heterozygous state in siblingsof patients with congenital adrenal hyperplasia due to 21- hydroxylasedeficiency. J. Pediat. 94: 770- 772, 1979. 3 B b

GAM69 258 CYP21A2 Haglund- Stengler, B.; Ritzen, E. M.; Gustafsson, J.; Luthman,H.: Haplotypes of the steroid 21- hydroxylase gene region encodingmild steroid 21-hydroxylase deficiency. Proc. Nat. Acad. Sci. 88:8352- 8356, 1991. 3 B b

GAM69 258 CYP21A2 Harada, F.; Kimura, A.; Iwanaga, T.; Shimozawa, K.; Yata, J.;Sasazuki, T.: Gene conversion- like events cause steroid 21- hydroxylasedeficiency in congenital adrenal hyperplasia. Proc. Nat. Acad. Sci. 84:8091- 8094, 1987. 3 B b

GAM69 258 CYP21A2 Helmberg, A.; Tusie- Luna, M. T.; Tabarelli, M.; Kofler, R.; White,P. C.: R339H and P453S: CYP21 mutations associated with nonclassicsteroid 21-hydroxylase deficiency that are not apparent gene conversions. Molec.Endocr. 6: 1318- 1322, 1992. 3 B b

GAM69 258 CYP21A2 Higashi, Y.; Tanae, A.; Inoue, H.; Fujii- Kuriyama, Y.: Evidencefor frequent gene conversion in the steroid 21- hydroxylase P- 450(C21)gene: implications for steroid 21- hydroxylase deficiency. Am. J.Hum. Genet. 42: 17- 25, 1988. 3 B b

GAM69 258 CYP21A2 Higashi, Y.; Tanae, A.; Inoue, H.; Hiromasa, T.; Fujii- Kuriyama,Y.: Aberrant splicing and missense mutations cause steroid 21- hydroxylase(P-450[C21]) deficiency in humans: possible gene conversion products. Proc.Nat. Acad. Sci. 85: 7486- 7490, 1988. 3 B b

GAM69 258 CYP21A2 Higashi, Y.; Yoshioka, H.; Yamane, M.; Gotoh, O.; Fujii- Kuriyama,Y.: Complete nucleotide sequence of two steroid 21- hydroxylase genestandemly arranged in human chromosome: a pseudogene and a genuinegene. Proc. Nat. 3 B b

Acad. Sci. 83: 2841- 2845, 1986.

GAM69 258 CYP21A2 Hirschfeld, A. J.; Fleshman, J. K.: An unusually high incidenceof salt- losing congenital adrenal hyperplasia in the Alaskan Eskimo. J.Pediat. 75: 492- 494, 1969. 3 B b

GAM69 258 CYP21A2 Holler, W.; Scholz, S.; Knorr, D.; Bidlingmaier, F.; Keller, E.;Albert, E. D.: Genetic differences between the salt- wasting, simplevirilizing, and nonclassical types of congenital adrenal hyperplasia. J.Clin. Endocr. Metab. 60: 757- 763, 1985. 3 B b

GAM69 258 CYP21A2 Hughes, I. A.; Dyas, J.; Riad- Fahmy, D.; Laurence, K. M.: Prenataldiagnosis of congenital adrenal hyperplasia: reliability of amnioticfluid steroid analysis. J. Med. Genet. 24: 344- 347, 1987. 3 B b

GAM69 258 CYP21A2 Jaaskelainen, J.; Levo, A.; Voutilainen, R.; Partanen, J.: Population- wideevaluation of disease manifestation in relation to molecular genotypein steroid 21- hydroxylase (CYP21) deficiency: good correlation ina well defined population. J. Clin. Endocr. Metab. 82: 3293- 3297,1997. 3 B b

GAM69 258 CYP21A2 Jaresch, S.; Kornely, E.; Kley, H.- K.; Schlaghecke, R.: Adrenalincidentaloma and patients with homozygous or heterozygous congenitaladrenal hyperplasia. J. Clin. Endocr. Metab. 74: 685- 689, 1992. 3 B b

GAM69 258 CYP21A2 Jones, H. W., Jr.: Personal Communication. Baltimore, Md. 2/10/1978. 3 B b

GAM69 258 CYP21A2 Jospe, N.; Donohoue, P. A.; Van Dop, C.; McLean, R. H.; Bias,W. B.; Migeon, C. J.: Prevalence of polymorphic 21- hydroxylase gene(CA21HB) mutations in salt- losing congenital adrenal hyperplasia. Biochem.Biophys. Res. Commun. 142: 798- 804, 1987. 3 B b

GAM69 258 CYP21A2 Kadair, R. G.; Block, M. B.; Katz, F. H.; Hofeldt, F. D.: 'Masked'21- hydroxylase deficiency of the adrenal presenting with gynecomastiaand bilateral testicular masses. Am. J. Med. 62: 278- 282, 1977. 3 B b

GAM69 258 CYP21A2 Kawaguchi, H.; O'hUigin, C.; Klein, J.: Evolutionary origin ofmutations in the primate cytochrome P450c21 gene. Am. J. Hum. Genet. 50:766- 780, 1992. 3 B b

GAM69 258 CYP21A2 Kayes- Wandover, K.; White, P. C.: Steroidogenic enzyme gene expressionin the human heart. J. Clin. Endocr. Metab. 85: 2519- 2525, 2000. 3 B b

GAM69 258 CYP21A2 Kirby- Keyser, L.; Porter, C. C.; Donohoue, P. A.: E380D: a novelpoint mutation of CYP21 in an HLA- homozygous patient with salt- losingcongenital adrenal hyperplasia due to 21- hydroxylase deficiency. Hum.Mutat. 9: 181- 182, 1997. 3 B b

GAM69 258 CYP21A2 Kirkland, R. T.; Kirkland, J. L.; Keenan, B. S.; Bongiovanni,A. M.; Rosenberg, H. S.; Clayton, G. W.: Bilateral testicular tumorsin congenital adrenal hyperplasia. J. Clin. Endocr. Metab. 44: 369- 378,1977. 3 B b

GAM69 258 CYP21A2 Klouda, P. T.; Harris, R.; Price, D. A.: Linkage and associationbetween HLA and 21- hydroxylase deficiency. J. Med. Genet. 17: 337- 341,1980. 3 B b

GAM69 258 CYP21A2 Knochenhauer, E. S.; Cortet- Rudelli, C.; Cunningham, R. D.; Conway- Myers,B. A.; Dewailly, D.; Azziz, R.: Carriers of 21- hydroxylase deficiencyare not at increased risk for hyperandrogenism. J. Clin. Endocr.Metab. 82: 479- 485, 1997. 3 B b

GAM69 258 CYP21A2 Krone, N.; Braun, A.; Roscher, A. A.; Knorr, D.; Schwarz, H. P.: Predicting phenotype in steroid 21- hydroxylase deficiency? Comprehensivegenotyping in 155 unrelated, well defined patients from Southern Germany. J.Clin. Endocr. Metab. 85: 1059- 1065, 2000. 3 B b

GAM69 258 CYP21A2 Kuttenn, F.; Couillin, P.; Girard, F.; Billaud, L.; Vincens, M.;Boucekkine, C.; Thalabard, J.- C.; Maudelonde, T.; Spritzer, P.; Mowszowicz,I.; Boue, A.; Mauvais- Jarvis, P.: Late- onset adrenal hyperplasiain hirsutism. New 3 B b

Eng. J. Med. 313: 224- 231, 1985.

GAM69 258 CYP21A2 Kuttenn, F.; Mowszowicz, I.; Schaison, G.; Mauvais- Jarvis, P.: Androgen 3 B b
production and skin metabolism in hirsutism. J. Endocr. 75:83- 91, 1977.

GAM69 258 CYP21A2 L'Allemand, D.; Tardy, V.; Gruters, A.; Schnabel, D.; Krude, H.;Morel, Y.: 3 B b
How a patient homozygous for a 30- kb deletion of the C4- CYP21 genomic
region can have a nonclassic form of 21- hydroxylase deficiency. J.Clin.
Endocr. Metab. 85: 4562- 4567, 2000.

GAM69 258 CYP21A2 Lako, M.; Ramsden, S.; Campbell, R. D.; Strachan, T.: Mutationscreening in 3 B b
British 21- hydroxylase deficiency families and developmentof novel
microsatellite based approaches to prenatal diagnosis. J.Med. Genet. 36:
119- 124, 1999.

GAM69 258 CYP21A2 Lau, I. F.; Soardi, F. C.; Lemos- Marini, S. H. V.; Guerra, G.,Jr.; 3 B b
Baptista, M. T. M.; De Mello, M. P.: H28+C insertion in theCYP21 gene: a
novel frameshift mutation in a Brazilian patient withthe classical form of
21- hydroxylase deficiency. J. Clin. Endocr.Metab. 86: 5877- 5880, 2001.

GAM69 258 CYP21A2 Laue, L.; Merke, D. P.; Jones, J. V.; Barnes, K. M.; Hill, S.;Cutler, G. B.: 3 B b
A preliminary study of flutamide, testolactone, andreduced hydrocortisone
dose in the treatment of congenital adrenalhyperplasia. J. Clin. Endocr.
Metab. 81: 3535- 3539, 1996.

GAM69 258 CYP21A2 Layrisse, A.; White, C.; Gunczler, P.; Gafaro Valera, L.; Arias,S.; Yunis, 3 B b
E. J.; Alper, C. A.; Awdeh, Z. L.: Sharing of MHC haplotypesamong apparently
unrelated patients with congenital adrenal hyperplasiadue to 21- hydroxylase
deficiency. Immunogenetics 25: 99- 103, 1987.

GAM69 258 CYP21A2 Lee, H.- H.; Chao, H.- T.; Ng, H.- T.; Choo, K.- B.: Direct 3 B b
moleculardiagnosis of CYP21 mutations in congenital adrenal hyperplasia.
J.Med. Genet. 33: 371- 375, 1996.

GAM69 258 CYP21A2 Levine, L. S.; Dupont, B.; Lorenzen, F.; Pang, S.; Pollack, M.;Oberfield, S. 3 B b
E.; Kohn, B.; Lerner, A.; Cacciari, E.; Mantero, F.;Cassio, A.; Scaroni, C.;
Chiumello, G.; Rondanini, G. F.; Gargantini,L.; Giovannelli, G.; Virdis, R.;
Bartolotta, E.; Migliori, C.; Pintor,C.; Tato, L.; Barboni, F.; New, M. I.:
Genetic and hormonal characterizationof cryptic 21- hydroxylase deficiency.
J. Clin. Endocr. Metab. 53:1193- 1198, 1981.

GAM69 258 CYP21A2 Levine, L. S.; Dupont, B.; Lorenzen, F.; Pang, S.; Pollack, M.;Oberfield, 3 B b
S.; Kohn, B.; Lerner, A.; Cacciari, E.; Mantero, F.; Cassio,A.; Scaroni, C.;
Chiumello, G.; Rondanini, G. F.; Gargantini, L.;Giovannelli, G.; Virdis, R.;
Bartolotta, E.; Migliori, C.; Pintor,C.; Tato, L.; Barboni, F.; New, M. I.:
Cryptic 21- hydroxylase deficiencyin families of patients with classical
congenital adrenal hyperplasia. J.Clin. Endocr. Metab. 51: 1316- 1324, 1980.

GAM69 258 CYP21A2 Levine, L. S.; Pang, S.; Dupont, B.; Pollack, M.; Lorenzen, F.;New, M. I.: 3 B b
Detection of heterozygote of 21- hydroxylase deficiency.(Letter) Lancet I:
603- 604, 1980.

GAM69 258 CYP21A2 Levine, L. S.; Zachmann, M.; New, M. I.; Prader, A.; Pollack,M. S.; O'Neill, 3 B b
G. J.; Yang, S. Y.; Oberfield, S. E.; Dupont, B.:Genetic mapping of the 21-
hydroxylase- deficiency gene within the HLAlinkage group. New Eng. J. Med.
299: 911- 915, 1978.

GAM69 258 CYP21A2 Levo, A.; Partanen, J.: Mutation- haplotype analysis of steroid21- 3 B b
hydroxylase (CYP21) deficiency in Finland. Implications for thepopulation
history of defective alleles. Hum. Genet. 99: 488- 497,1997.

GAM69 258 CYP21A2 Lewis, V. G.; Money, J.; Epstein, R.: Concordance of verbal andnonverbal 3 B b
ability in the adrenogenital syndrome. Johns Hopkins Med.J. 122: 192- 195,

1968.

GAM69 258 CYP21A2 Libber, S. M.; Migeon, C. J.; Bias, W. B.: Ascertainment of 21- hydroxylasedeficiency in individuals with HLA- B14 haplotype. J. Clin. Endocr.Metab. 60: 727- 730, 1985. 3 B b

GAM69 258 CYP21A2 Lo, J. C.; Schwitzgebel, V. M.; Tyrrell, J. B.; Fitzgerald, P.A.; Kaplan, S. L.; Conte, F. A.; Grumbach, M. M.: Normal female infantsborn of mothers with classic congenital adrenal hyperplasia due to21- hydroxylase deficiency. J. Clin. Endocr. Metab. 84: 930- 936,1999. 3 B b

GAM69 258 CYP21A2 Lopez- Gutierrez, A. U.; Riba, L.; Ordonez- Sanchez, M. L.; Ramirez-Jimenez,S.; Cerrillo- Hinojosa, M.; Tusie- Luna, M. T.: Uniparental disomyfor chromosome 6 results in steroid 21- hydroxylase deficiency: evidenceof different genetic mechanisms involved in the production of thedisease. J. Med. Genet. 35: 1014- 1019, 1998. 3 B b

GAM69 258 CYP21A2 Lorenzen, F.; Pang, S.; New, M. I.; Dupont, B.; Pollack, M.; Chow,D. M.; Levine, L. S.: Hormonal phenotype and HLA- genotype in familiesof patients with congenital adrenal hyperplasia (21- hydroxylase deficiency). Pediat.Res. 13: 1356- 1360, 1979. 3 B b

GAM69 258 CYP21A2 Lorenzen, F.; Pang, S.; New, M. I.; Oberfield, S.; Dupont, B.;Chow, D.; Schneider, B.; Levine, L.: Studies of the C- 21 and C- 19steroids and HLA genotyping in siblings and parents of patients withcongenital adrenal hyperplasia due to 21- hydroxylase deficiency. J.Clin. Endocr. Metab. 50: 572- 577, 1980. 3 B b

GAM69 258 CYP21A2 Lubani, M. M.; Issa, A.- R. A.; Bushnaq, R.; Al- Saleh, Q. A.; Dudin,K. I.; Reavey, P. C.; El- Khalifa, M. Y.; Manandhar, D. S.; Abdul Al,Y. K.; Ismail, E. A.; Teebi, A. S.: Prevalence of congenital adrenalhyperplasia in Kuwait. Europ. J. Pediat. 149: 391- 392, 1990. 3 B b

GAM69 258 CYP21A2 Matteson, K. J.; Phillips, J. A., III; Miller, W. L.; Chung, B.- C.;Orlando, P. J.; Frisch, H.; Ferrandez, A.; Burr, I. M.: P450XXI (steroid21-hydroxylase) gene deletions are not found in family studies ofcongenital adrenal hyperplasia. Proc. Nat. Acad. Sci. 84: 5858- 5862,1987. 3 B b

GAM69 258 CYP21A2 McAlpine, P. J.: Personal Communication. Winnipeg, Manitoba,Canada 2/26/1988. 3 B b

GAM69 258 CYP21A2 McGuire, L. S.; Omenn, G. S.: Congenital adrenal hyperplasia.I. Family studies of IQ. Behav. Genet. 5: 165- 173, 1975. 3 B b

GAM69 258 CYP21A2 Merkatz, I. R.; New, M. I.; Peterson, R. E.; Seaman, M. P.: Prenataldiagnosis of adrenogenital syndrome by amniocentesis. J. Pediat. 75:977- 982, 1969. 3 B b

GAM69 258 CYP21A2 Merke, D. P.; Chrousos, G. P.; Eisenhofer, G.; Weise, M.; Keil,M. F.; Rogol, A. D.; Van Wyk, J. J.; Bornstein, S. R.: Adrenomedullarydysplasia and hypofunction in patients with classic 21- hydroxylasedeficiency. New Eng. J. Med. 343: 1362- 1368, 2000. 3 B b

GAM69 258 CYP21A2 Merke, D. P.; Keil, M. F.; Jones, J. V.; Fields, J.; Hill, S.;Cutler, G. B., Jr.: Flutamide, testolactone, and reduced hydrocortisonedose maintain normal growth velocity and bone maturation despite elevatedandrogen levels in children with congenital adrenal hyperplasia. J.Clin. Endocr. Metab. 85: 1114- 1120, 2000. 3 B b

GAM69 258 CYP21A2 Meyer- Bahlburg, H. F. L.: What causes low rates of child- bearingin congenital adrenal hyperplasia? J. Clin. Endocr. Metab. 84: 1844- 1847,1999. 3 B b

GAM69 258 CYP21A2 Miller, W. L.: Gene conversions, deletions and polymorphismsin congenital adrenal hyperplasia. Am. J. Hum. Genet. 42: 4- 7, 1988. 3 B b

GAM69 258 CYP21A2 Miller, W. L.: Personal Communication. San Francisco, Calif. 1/3/1996. 3 B b

GAM69 258 DMN Mizuno, Y.; Thompson, T. G.; Guyon, J. R.; Lidov, H. G. W.; Brosius,M.; Imamura, M.; Ozawa, E.; Watkins, S. C.; Kunkel, L. M.: Desmuslin,an intermediate filament protein that interacts with alpha- dystrobrevinand desmin. Proc. Nat. Acad. Sci. 98: 6156- 6161, 2001. 3 B c

GAM69 258 DMN Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B c

GAM69 258 FGF18 Hu, M. C.- T.; Qiu, W. R.; Wang, Y.- P.; Hill, D.; Ring, B. D.; Scully,S.; Bolon, B.; DeRose, M.; Luethy, R.; Simonet, W. S.; Arakawa, T.;Danilenko, D. M.: FGF- 18, a novel member of the fibroblast growthfactor family, stimulates hepatic and intestinal proliferation. Molec.Cell. Biol. 18: 6063- 6074, 1998. 3 B c

GAM69 258 FGF18 Ohbayashi, N.; Hoshikawa, M.; Kimura, S.; Yamasaki, M.; Fukui,S.; Itoh, N.: Structure and expression of the mRNA encoding a novelfibroblast growth factor, FGF- 18. J. Biol. Chem. 273: 18161- 18164,1998. 3 B c

GAM69 258 FGF18 Whitmore, T. E.; Maurer, M. F.; Sexson, S.; Raymond, F.; Conklin,D.; Deisher, T. A.: Assignment of fibroblast growth factor 18 (FGF18)to human chromosome 5q34 by use of radiation hybrid mapping and fluorescencein situ hybridization. Cytogenet. Cell Genet. 90: 231- 233, 2000. 3 B c

GAM69 258 HNF4A Aguilar- Salinas, C. A.; Reyes- Rodriguez, E.; Ordonez- Sanchez, M.L.; Torres, M. A.; Ramirez- Jimenez, S.; Dominguez- Lopez, A.; Martinez- Francois,J. R.; Velasco- Perez, M. L.; Alpizar, M.; Garcia- Garcia, E.; Gomez- Perez,F.; Rull, J.; Tusie- Luna, M. T.: Early- onset type 2 diabetes: metabolicand genetic characterization in the Mexican population. J. Clin.Endocr. Metab. 86: 220- 226, 2001. 3 B c

GAM69 258 HNF4A Argyrokastritis, A.; Kamakari, S.; Kapsetaki, M.; Kritis, A.; Talianidis,I.; Moschonas, N. K.: Human hepatocyte nuclear factor- 4 (hHNF- 4)gene maps to 20q12- q13.1 between PLCG1 and D20S17. Hum. Genet. 99:233- 236, 1997. 3 B c

GAM69 258 HNF4A Avraham, K. B.; Prezioso, V. R.; Chen, W. S.; Lai, E.; Sladek,F. M.; Zhong, W.; Darnell, J. E., Jr.; Jenkins, N. A.; Copeland, N.G.: Murine chromosomal location of four hepatocyte- enriched transcriptionfactors: HNF- 3- alpha, HNF3- beta, HNF- 3- gamma, and HFN- 4. Genomics 13:264- 268, 1992. 3 B c

GAM69 258 HNF4A Chartier, F. L.; Bossu, J.- P.; Laudet, V.; Fruchart, J.- C.: Cloningand sequencing of cDNAs encoding the human hepatocyte nuclear factor4 indicate the presence of two isoforms in human liver. Gene 147:269- 272, 1994. 3 B c

GAM69 258 HNF4A Eeckhoute, J.; Formstecher, P.; Laine, B.: Maturity- onset diabetesof the young type 1 (MODY1)- associated mutations R154X and E276Q inhepatocyte nuclear factor 4- alpha (HNF4- alpha) gene impair recruitmentof p300, a key transcriptional coactivator. Molec. Endocr. 15: 1200- 1210,2001. 3 B c

GAM69 258 HNF4A Fajans, S. S.: Maturity- onset diabetes of the young (MODY). DiabetesMetab. Rev. 5: 579- 606, 1989. 3 B c

GAM69 258 HNF4A Fajans, S. S.; Bell, G. I.; Polonsky, K. S.: Molecular mechanismsand clinical pathophysiology of maturity- onset diabetes of the young. NewEng. J. Med. 345: 971- 980, 2001. 3 B c

GAM69 258 HNF4A Furuta, H.; Iwasaki, N.; Oda, N.; Hinokio, Y.; Horikawa, Y.; Yamagata,K.; Yano, N.; Sugahiro, J.; Ogata, M.; Ohgawara, H.; Omori, Y.; Iwamoto,Y.; Bell, G. I.: Organization and partial sequence of the hepatocytenuclear 3 B c

factor- 4- alpha/MODY1 gene and identification of a missensemutation, R127W, in a Japanese family with MODY. Diabetes 46: 1652- 1657,1997.

GAM69 258 HNF4A Hani, E. H.; Suaud, L.; Boutin, P.; Chevre, J.- C.; Durand, E.;Philippi, A.; 3 B c
Demenais, F.; Vionnet, N.; Furuta, H.; Velho, G.; Bell,G. I.; Laine, B.;
Froguel, P.: A missense mutation in hepatocytenuclear factor- 4- alpha,
resulting in a reduced transactivation activity,in human late- onset non-
insulin- dependent diabetes mellitus. J. Clin.Invest. 101: 521- 526, 1998.

GAM69 258 HNF4A Lausen, J.; Thomas, H.; Lemm, I.; Bulman, M.; Borgschulze, M.;Lingott, A.; 3 B c
Hattersley, A. T.; Ryffel, G. U.: Naturally occurringmutations in the human
HNF4- alpha gene impair the function of thetranscription factor to a varying
degree. Nucleic Acids Res. 28:430- 437, 2000.

GAM69 258 HNF4A Li, J.; Ning, G.; Duncan, S. A.: Mammalian hepatocyte 3 B c
differentiationrequires the transcription factor HNF- 4- alpha. Genes Dev.
14: 464- 474,2000.

GAM69 258 HNF4A Lindner, T.; Gragnoli, C.; Furuta, H.; Cockburn, B. N.; Petzold,C.; 3 B c
Rietzsch, H.; Weiss, U.; Schulze, J.; Bell, G. I.: Hepatic functionin a
family with a nonsense mutation (R154X) in the hepatocyte nuclearfactor- 4-
alpha/MODY1 gene. J. Clin. Invest. 100: 1400- 1405, 1997.

GAM69 258 HNF4A Moller, A. M.; Dalgaard, L. T.; Ambye, L.; Hansen, L.; Schmitz,O.; Hansen, 3 B c
T.; Pedersen, O.: A novel Phe75fsdelT mutation in thehepatocyte nuclear
factor- 4- alpha gene in a Danish pedigree with maturity- onsetdiabetes of
the young. J. Clin. Endocr. Metab. 84: 367- 369, 1999.

GAM69 258 HNF4A Stoffel, M.; Duncan, S. A.: The maturity- onset diabetes of theyoung (MODY1) 3 B c
transcription factor HNF4- alpha regulates expressionof genes required for
glucose transport and metabolism. Proc. Nat.Acad. Sci. 94: 13209- 13214,
1997.

GAM69 258 HNF4A Thomas, H.; Jaschkowitz, K.; Bulman, M.; Frayling, T. M.; Mitchell,S. M. S.; 3 B c
Roosen, S.; Lingott- Frieg, A.; Tack, C. J.; Ellard, S.;Ryffel, G. U.;
Hattersley, A. T.: A distant upstream promoter ofthe HNF- 4- alpha gene
connects the transcription factors involved inmaturity- onset diabetes of
the young. Hum. Molec. Genet. 10: 2089- 2097,2001.

GAM69 258 HNF4A Yamagata, K.; Furuta, H.; Oda, N.; Kaisaki, P. J.; Menzel, S.;Cox, N. J.; 3 B c
Fajans, S. S.; Signorini, S.; Stoffel, M.; Bell, G. I.: Mutations in the
hepatocyte nuclear factor- 4- alpha gene in maturity- onsetdiabetes of the
young (MODY1). Nature 384: 458- 460, 1996.

GAM69 258 HNF4A Zouali, H.; Hani, E. H.; Philippi, A.; Vionnet, N.; Beckmann,J. S.; 3 B c
Demenais, F.; Froguel, P.: A susceptibility locus for early- onsetnon-
insulin dependent (type 2) diabetes mellitus maps to chromosome20q, proximal
to the phosphoenolpyruvate carboxykinase gene. Hum.Molec. Genet. 6: 1401-
1408, 1997.

GAM69 258 HOXB6 Apiou, F.; Flagiello, D.; Cillo, C.; Malfoy, B.; Poupon, M.- F.;Dutrillaux, 3 B c
B.: Fine mapping of human HOX gene clusters. Cytogenet.Cell Genet. 73: 114-
115, 1996.

GAM69 258 HOXB6 Kaur, S.; Singh, G.; Stock, J. L.; Schreiner, C. M.; Kier, A. B.;Yager, K. 3 B c
L.; Mucenski, M. L.; Scott, W. J., Jr.; Potter, S. S.:Dominant mutation of
the murine Hox- 2.2 gene results in developmentalabnormalities. J. Exp.
Zool. 264: 323- 336, 1992.

GAM69 258 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 B c
M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like
growth factor- I and cognitive function inhealthy older men. J. Clin.

Endocr. Metab. 84: 471- 475, 1999.

GAM69 258 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- 3 B c
like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993.

GAM69 258 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and 3 B c
absence of association with stature among African Pygmies. Hum.Genet. 85:
349- 354, 1990.

GAM69 258 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for 3 B c
insulin- like growth factors I and II and for epidermalgrowth factor in man.
(Abstract) Am. J. Hum. Genet. 36: 133S only,1984.

GAM69 258 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of 3 B c
genes for insulin- like growth factors I and II and epidermalgrowth factor.
Nature 310: 781- 784, 1984.

GAM69 258 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, 3 B c
A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of
recombinant human insulin- like growth factor I(IGF- I) therapy on the
growth hormone- IGF system of a patient witha partial IGF- I gene deletion.
J. Clin. Endocr. Metab. 84: 1611- 1616,1999.

GAM69 258 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; 3 B c
Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of
the growth hormone receptor in children with idiopathicshort stature. New
Eng. J. Med. 333: 1093- 1098, 1995.

GAM69 258 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; 3 B c
Froesch, E. R.: Small stature and insulin- like growth factors:prolonged
treatment of mini- poodles with recombinant human insulin- likegrowth factor
I. Acta Endocr. 121: 456- 464, 1989.

GAM69 258 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. 3 B c
S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating
concentrations of insulin- like growth factor- I and riskof breast cancer.
Lancet 351: 1393- 1396, 1998.

GAM69 258 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: 3 B c
Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding
protein- 3, and prostate- specific antigen as predictorsof clinical prostate
cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000.

GAM69 258 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; 3 B c
Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith,
D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival
signaling in retinal endothelial cells: direct correlationwith clinical
retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001.

GAM69 258 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer 3 B c
prevention. Lancet 351: 1373- 1375, 1998.

GAM69 258 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; 3 B c
Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J.
S.: The human gene encoding insulin- like growthfactor I is located on
chromosome 12. Hum. Genet. 69: 157- 160, 1985.

GAM69 258 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, 3 B c
J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic
linkage map of mouse chromosome 10: localizationof eighteen molecular
markers using a single interspecific backcross. Genetics 125:855- 866, 1990.

GAM69 258 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete 3 B c
characterization of the human IGF- I nucleotide sequenceisolated from a

newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986.

GAM69 258 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; 3 B c
Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated
blood pressure and enhanced myocardial contractilityin mice with severe IGF-
1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996.

GAM69 258 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: 3 B c
Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat.
Acad. Sci. 80: 2216- 2220, 1983.

GAM69 258 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; 3 B c
Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand
implications for cell type- specific growth. Nature 364: 208- 213,1993.

GAM69 258 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: 3 B c
Mice carrying null mutations of the genes encoding insulin- likegrowth
factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993.

GAM69 258 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like 3 B c
growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83:
9343- 9347, 1986.

GAM69 258 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human 3 B c
genes for insulin- like growth factors I and II and epidermalgrowth factor
are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively.
Cytogenet.Cell Genet. 41: 245- 249, 1986.

GAM69 258 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 3 B c
1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2
(IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985.

GAM69 258 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. 3 B c
D.: Growth characteristics and response to growth hormonetherapy in patients
with hypochondroplasia: genetic linkage of theinsulin- like growth factor I
gene at chromosome 12q23 to the diseasein a subgroup of these patients.
Clin. Endocr. 34: 265- 274, 1991.

GAM69 258 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: 3 B c
IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin
association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999.

GAM69 258 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, 3 B c
M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene
expression sustains hypertrophy and regeneration insenescent skeletal
muscle. Nature Genet. 27: 195- 200, 2001.

GAM69 258 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like 3 B c
growth factor 1 regulates the location, stability,and transcriptional
activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000.

GAM69 258 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, 3 B c
S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal
embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993.

GAM69 258 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the 3 B c
protein which binds insulin- like growth factor in human serum. Europ.J.
Biochem. 172: 421- 425, 1988.

GAM69 258 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; 3 B c
Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith,
R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the
insulin- like growth factor I receptor and its ligandin relation to type 2
diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000.

GAM69 258 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed 3 B c
in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986.

GAM69 258 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; 3 B c
Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I)
reduces hyperglycaemia in patients with extremeinsulin resistance.
Diabetologia 34: 675- 679, 1991.

GAM69 258 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; 3 B c
Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a
Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999.

GAM69 258 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. 3 B c
E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma:
chemical and biological properties, partial sequenceanalysis, and
relationship to other somatomedins. Biochemistry 19:790- 797, 1980.

GAM69 258 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like 3 B c
growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58,
1991.

GAM69 258 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- 3 B c
like growth factor genes: chromosome organization andassociation with
disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984.

GAM69 258 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: 3 B c
Localization of insulin- like growth factor genes to human chromosomes11 and
12. Nature 310: 784- 786, 1984.

GAM69 258 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of 3 B c
the human insulin- like growth factor I gene using asingle synthetic DNA
probe. EMBO J. 3: 361- 364, 1984.

GAM69 258 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; 3 B c
Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-
resistantdiabetic ketoacidosis with insulin- like growth factor I in an
adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-
857,1992.

GAM69 258 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; 3 B c
Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic
variation in the gene for insulin- like growth factor- 1and low birthweight.
Lancet 359: 1036- 1037, 2002.

GAM69 258 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand 3 B c
assays that somatomedin- C and insulin- like growth factor- Iare similar to
each other and different from other somatomedins. J.Clin. Endocr. Metab. 50:
206- 208, 1980.

GAM69 258 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish 3 B c
Osteoporosis Prevention Study: Effect of sex hormone replacementon the
insulin- like growth factor system and bone mineral: a cross- sectionaland
longitudinal study in 595 perimenopausal women participating inthe Danish
osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999.

GAM69 258 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. 3 B c
L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy
on body composition and insulin resistance in IGF- Igene deletion. J. Clin.
Endocr. Metab. 85: 1407- 1411, 2000.

GAM69 258 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 3 B c
Intrauterine growth retardation and postnatal growth failureassociated with
deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335:

1363- 1367, 1996.

GAM69 258 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 3 B c
regional localization of human genes for insulin- like growthfactors I
(IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell
Genet. 40: 782 only, 1985.

GAM69 258 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 3 B c
growth factors and bone mineral density in African Americanand white girls.
J. Pediat. 137: 826- 832, 2000.

GAM69 258 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 3 B c
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM69 258 NQO2 Jaiswal, A. K.; Bell, D. W.; Radjendirane, V.; Testa, J. R.: Localizationof 3 B c
human NQO1 gene to chromosome 16q22 and NQO2- 6p25 and
associatedpolymorphisms. Pharmacogenetics 9: 413- 418, 1999.

GAM69 258 NQO2 Jaiswal, A. K.; Burnett, P.; Adesnik, M.; McBride, O. W.: Nucleotideand 3 B c
deduced amino acid sequence of a human cDNA (NQO2) correspondingto a second
member of the NAD(P)H:quinone oxidoreductase gene family:extensive
polymorphism at the NQO2 gene locus on chromosome 6. (Abstract) Biochemistry
29:1899- 1906, 1990.

GAM69 258 NQO2 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- 3 B c
inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and
localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578,
1988.

GAM69 258 NR3C2 Arriza, J. L.; Weinberger, C.; Cerelli, G.; Glaser, T. M.; Handelin,B. L.; 3 B c
Housman, D. E.; Evans, R. M.: Cloning of human mineralocorticoidreceptor
complementary DNA: structural and functional kinship withthe glucocorticoid
receptor. Science 237: 268- 275, 1987.

GAM69 258 NR3C2 Berger, S.; Bleich, M.; Schmid, W.; Cole, T. J.; Peters, J.; Watanabe,H.; 3 B c
Kriz, W.; Warth, R.; Greger, R.; Schutz, G.: Mineralocorticoidreceptor
knockout mice: pathophysiology of Na+ metabolism. Proc.Nat. Acad. Sci. 95:
9424- 9429, 1998.

GAM69 258 NR3C2 Chung, E.; Hanukoglu, A.; Rees, M.; Thompson, R.; Dillon, M.; Hanukoglu,I.; 3 B c
Bistritzer, T.; Kuhnle, U.; Seckl, J.; Gardiner, R. M.: Exclusionof the
locus for autosomal recessive pseudohypoaldosteronism type1 from the
mineralocorticoid receptor gene region on human chromosome4q by linkage
analysis. J. Clin. Endocr. Metab. 80: 3341- 3345, 1995.

GAM69 258 NR3C2 Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Nowak, N. 3 B c
J.; Shows, T. B.: The human mineralocorticoid receptorgene (MLR) is located
on chromosome 4 at q31.2. Cytogenet. Cell Genet. 52:83- 84, 1989.

GAM69 258 NR3C2 Geller, D. S.; Farhi, A.; Pinkerton, N.; Fradley, M.; Moritz, M.;Spitzer, 3 B c
A.; Meinke, G.; Tsai, F. T. F.; Sigler, P. B.; Lifton, R.P.: Activating
mineralocorticoid receptor mutation in hypertensionexacerbated by pregnancy.
Science 289: 119- 123, 2000.

GAM69 258 NR3C2 Geller, D. S.; Rodriguez- Soriano, J.; Vallo Boado, A.; Schifter,S.; Bayer, 3 B c
M.; Chang, S. S.; Lifton, R. P.: Mutations in the mineralocorticoidreceptor
gene cause autosomal dominant pseudohypoaldosteronism typeI. Nature Genet.
19: 279- 281, 1998.

GAM69 258 NR3C2 Hellal- Levy, C.; Fagart, J.; Souque, A.; Wurtz, J.- M.; Moras, D.;Rafestin- 3 B c
Oblin, M.- E.: Crucial role of the H11- H12 loop in stabilizingthe active
conformation of the human mineralocorticoid receptor. Molec.Endocr. 14:
1210- 1221, 2000.

GAM69 258 NR3C2 Le Menuet, D.; Isnard, R.; Bichara, M.; Viengchareun, S.; Muffat- Joly,M.; 3 B c
Walker, F.; Zennaro, M.- C.; Lombes, M.: Alteration of cardiacand renal
functions in transgenic mice overexpressing human mineralocorticoidreceptor.
J. Biol. Chem. 276: 38911- 38920, 2001.

GAM69 258 NR3C2 Morrison, N.; Harrap, S. B.; Arriza, J. L.; Boyd, E.; Connor, J.M.: Regional 3 B c
chromosomal assignment of the human mineralocorticoidreceptor gene to
4q31.1. Hum. Genet. 85: 130- 132, 1990.

GAM69 258 NR3C2 Morrison, N.; Harrap, S. B.; Arriza, J. L.; Boyd, E.; Connor,J. M.: Regional 3 B c
chromosomal assignment of the human mineralocorticoidreceptor gene to
4q31.1. (Abstract) Cytogenet. Cell Genet. 51: 1048,1989.

GAM69 258 NR3C2 Tajima, T.; Kitagawa, H.; Yokoya, S.; Tachibana, K.; Adachi, M.;Nakae, J.; 3 B c
Suwa, S; Katoh, S.; Fujieda, K.: A novel missense mutationof
mineralocorticoid receptor gene in one Japanese family with a renalform of
pseudohypoaldosteronism type 1. J. Clin. Endocr. Metab. 85:4690- 4694, 2000.

GAM69 258 NR3C2 Viemann, M.; Peter, M.; Lopez- Siguero, J. P.; Simic- Schleicher,G.; 3 B c
Sippell, W. G.: Evidence for genetic heterogeneity of
pseudohypoaldosteronismtype 1: identification of a novel mutation in the
human mineralocorticoidreceptor in one sporadic case and no mutations in two
autosomal dominantkindreds. J. Clin. Endocr. Metab. 86: 2056- 2059, 2001.

GAM69 258 p100 Callebaut, I.; Mornon, J. P.: The human EBNA- 2 coactivator p100:multidomain 3 B c
organization and relationship to the staphylococcal nucleasefold and to the
tudor protein involved in Drosophila melanogasterdevelopment. Biochem. J.
321: 125- 132, 1997.

GAM69 258 p100 Heidebrecht, H. J.; Buck, F.; Steinmann, J.; Sprenger, R.; Wacker,H. H.; 3 B c
Parwaresch, R.: p100: a novel proliferation- associated nuclearprotein
specifically restricted to cell cycle phases S, G2, and M. Blood 90:226-
233, 1997.

GAM69 258 p100 Lienard, P.; Riviere, M.; Van Vooren, P.; Szpirer, C.; Szpirer,J.: 3 B c
Assignment of SND1, the gene encoding coactivator p100, to humanchromosome
7q31.3 and rat chromosome 4q23 by in situ hybridization. Cytogenet.Cell
Genet. 90: 253- 254, 2000.

GAM69 258 p100 Manda, R.; Kohno, T.; Matsuno, Y.; Takenoshita, S.; Kuwano, H.;Yokota, J.: 3 B c
Identification of genes (SPON2 and C20orf2) differentiallyexpressed between
cancerous and noncancerous lung cells by mRNA differentialdisplay. Genomics
61: 5- 14, 1999.

GAM69 258 p100 Tong, X.; Drapkin, R.; Yalamanchili, R.; Mosialos, G.; Kieff, E.: The 3 B c
Epstein- Barr virus nuclear protein 2 acidic domain forms a complexwith a
novel cellular coactivator that can interact with TFIIE. Molec.Cell. Biol.
15: 4735- 4744, 1995.

GAM69 258 p100 Zhang, Y.; Heidebrecht, H.- J.; Rott, A.; Schlegelberger, B.; Parwaresch,R.: 3 B c
Assignment of human proliferation associated p100 gene (C20orf1)to human
chromosome band 20q11.2 by in situ hybridization. Cytogenet.Cell Genet. 84:
182- 183, 1999.

GAM69 258 PAK1 Amano, M.; Mukai, H.; Ono, Y.; Chihara, K.; Matsui, T.; Hamajima,Y.; Okawa, 3 B c
K.; Iwamatsu, A.; Kaibuchi, K.: Identification of a putativetarget for rho
as the serine- threonine kinase protein kinase N. Science 271:648- 651,
1996.

GAM69 258 PAK1 Bartsch, J. W.; Mukai, H.; Takahashi, N.; Ronsiek, M.; Fuchs, S.;Jockusch, 3 B c
H.; Ono, Y.: The protein kinase N (PKN) gene PRKCL1/Prkcl1maps to human
chromosome 19p12- p13.1 and mouse chromosome 8 with closelinkage to the

myodystrophy (myd) mutation. Genomics 49: 129- 132,1998.

GAM69 258 PAK1 Bekri, S.; Adelaide, J.; Merscher, S.; Grosgeorge, J.; Caroli- Bosc,F.; Perucca- Lostanlen, D.; Kelley, P. M.; Pebusque, M.- J.; Theillet,C.; Birnbaum, D.; Gaudray, P.: Detailed map of a region commonlyamplified at 11q13- q14 in human breast carcinoma. Cytogenet. CellGenet. 79: 125- 131, 1997. 3 B c

GAM69 258 PAK1 Brown, J. L.; Stowers, L.; Baer, M.; Trejo, J.; Coughlin, S.; Chant,J.: Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinasepathway. Curr. Biol. 6: 598- 605, 1996. 3 B c

GAM69 258 PAK1 Knaus, U. G.; Morris, S.; Dong, H.- J.; Chernoff, J.; Bokoch, G.M.: Regulation of human leukocyte p21- activated kinases through Gprotein-coupled receptors. Science 269: 221- 223, 1995. 3 B c

GAM69 258 PAK1 Lei, M.; Lu, W.; Meng, W.; Parrini, M.- C.; Eck, M. J.; Mayer, B.J.; Harrison, S. C.: Structure of PAK1 in an autoinhibited conformationreveals a multistage activation switch. Cell 102: 387- 397, 2000. 3 B c

GAM69 258 PAK1 Mukai, H.; Ono, Y.: A novel protein kinase with leucine zipper-likesequences: its catalytic domain is highly homologous to that of proteinkinase C. Biochem. Biophys. Res. Commun. 199: 897- 904, 1994. 3 B c

GAM69 258 PAK1 Palmer, R. H.; Ridden, J.; Parker, P. J.: Cloning and expressionspatterns of two members of a novel protein- kinase- C- related kinasefamily. Europ. J. Biochem. 227: 344- 351, 1995. 3 B c

GAM69 258 PAK1 Palmer, R. H.; Ridden, J.; Parker, P. J.: Identification of multiple,novel, protein kinase C- related gene products. FEBS Lett. 356: 5- 8,1994. 3 B c

GAM69 258 PAK1 Parrini, M. C.; Lei, M.; Harrison, S. C.; Mayer, B. J.: Pak1 kinasehomodimers are autoinhibited in trans and dissociated upon activationby Cdc42 and Rac1. Molec. Cell 9: 73- 83, 2002. 3 B c

GAM69 258 PAK1 Ridley, A. J.; Hall, A.: The small GTP- binding protein rho regulatesthe assembly of focal adhesions and actin stress fibers in responseto growth factors. Cell 70: 389- 399, 1992. 3 B c

GAM69 258 PAK1 Sanders, L. C.; Matsumura, F.; Bokoch, G. M.; de Lanerolle, P.: Inhibition of myosin light chain kinase by p21- activated kinase. Science 283:2083-2085, 1999. 3 B c

GAM69 258 PAK1 Vadlamudi, R. K.; Li, F.; Adam, L.; Nguyen, D.; Ohta, Y.; Stossel,T. P.; Kumar, R.: Filamin is essential in actin cytoskeletal assemblymediated by p21- activated kinase 1. Nature Cell Biol. 4: 681- 690,2002. 3 B c

GAM69 258 PAK1 Yu, W.; Liu, J.; Morrice, N. A.; Wettenhall, R. E. H.: Isolationand characterization of a structural homologue of human PRK2 fromrat liver. J. Biol. Chem. 272: 10030- 10034, 1997. 3 B c

GAM69 258 PDGFB Aurias, A.; Rimbaut, C.; Buffe, D.; Dubousset, J.; Mazabraud, A.: Chromosomal translocations in Ewing's sarcoma. (Letter) New Eng.J. Med. 309: 496- 497, 1983. 3 B c

GAM69 258 PDGFB Bartram, C. R.; de Klein, A.; Hagemeijer, A.; Grosveld, G.; Heisterkamp,N.; Groffen, J.: Localization of the human c- sis oncogene in Ph- 1- positiveand Ph- 1- negative chronic myelocytic leukemia by in situ hybridization. Blood 63:223- 225, 1984. 3 B c

GAM69 258 PDGFB Bechet, J.- M.; Bornkamm, G.; Freese, U.- K.; Lenoir, G. M.: Thec- sis oncogene is not activated in Ewing's sarcoma. (Letter) NewEng. J. Med. 310: 393 only, 1984. 3 B c

GAM69 258 PDGFB Bishop, J. M.: Enemies within: the genesis of retrovirus oncogenes. Cell 23:5- 6, 1981. 3 B c

GAM69 258 PDGFB Bolger, G. B.; Stamberg, J.; Kirsch, I. R.; Hollis, G. F.; Schwarz,D. F.; 3 B c
Thomas, G. H.: Chromosomal translocation t(14;22) and oncogene(c- sis)
variant in a pedigree with familial meningioma. New Eng.J. Med. 312: 564-
567, 1985.

GAM69 258 PDGFB Cohen, J. B.; Levinson, A. D.: A point mutation in the last 3 B c
intronresponsible for increased expression and transforming activity ofthe
c- Ha- ras oncogene. Nature 334: 119- 124, 1988.

GAM69 258 PDGFB Collins, T.; Ginsburg, D.; Boss, J. M.; Orkin, S. H.; Pober, J.S.: Cultured 3 B c
human endothelial cells express platelet- derived growthfactor B chain: cDNA
cloning and structural analysis. Nature 316:748- 750, 1985.

GAM69 258 PDGFB Dalla- Favera, R.; Gallo, R. C.; Giallongo, A.; Croce, C.: 3 B c
Chromosomallocalization of the human homolog (c- sis) of the simian sarcoma
virusonc gene. Science 218: 686- 688, 1982.

GAM69 258 PDGFB Dalla- Favera, R.; Gelmann, E. P.; Gallo, R. C.; Wong- Staal, F.: A human 3 B c
onc gene homologous to the transforming gene (v- sis) ofsimian sarcoma
virus. Nature 292: 31- 35, 1981.

GAM69 258 PDGFB Deuel, T. F.; Huang, J. S.; Huang, S. S.; Stroobant, P.; Waterfield,M. D.: 3 B c
Expression of a platelet- derived growth factor- like proteinin simian
sarcoma virus transformed cells. Science 221: 1348- 1350,1983.

GAM69 258 PDGFB Devare, S. G.; Reddy, E. P.; Law, J. D.; Robbins, K. C.; Aaronson,S. A.: 3 B c
Nucleotide sequence of the simian sarcoma virus genome: demonstrationthat
its acquired cellular sequences encode the transforming geneproduct p28-
sis. Proc. Nat. Acad. Sci. 80: 731- 735, 1983.

GAM69 258 PDGFB Doolittle, R. F.; Hunkapiller, M. W.; Hood, L. E.; Devare, S.G.; Robbins, K. 3 B c
C.; Aaronson, S. A.; Antoniades, H. N.: Simian sarcomavirus onc gene, v-
sis, is derived from the gene (or genes) encodinga platelet- derived growth
factor. Science 221: 275- 277, 1983.

GAM69 258 PDGFB Gardner, T. L.; Elston, D. M.; Wotowic, P. J.: A familial 3 B c
dermatofibrosarcomaprotuberans. J. Am. Acad. Derm. 39: 504- 505, 1998.

GAM69 258 PDGFB Groffen, J.; Heisterkamp, N.; Stephenson, J. R.; Geurts van Kessel,A.; de 3 B c
Klein, A.; Grosveld, G.; Bootsma, D.: c- sis is translocatedfrom chromosome
22 to chromosome 9 in chronic myelocytic leukemia. J.Exp. Med. 158: 9- 15,
1983.

GAM69 258 PDGFB Hermansson, M.; Nister, M.; Betsholtz, C.; Heldin, C.- H.; Westermark,B.; 3 B c
Funa, K.: Endothelial cell hyperplasia in human glioblastoma:coexpression of
mRNA for platelet- derived growth factor (PDGF) B chainand PDGF receptor
suggests autocrine growth stimulation. Proc. Nat.Acad. Sci. 85: 7748- 7752,
1988.

GAM69 258 PDGFB Jhanwar, S. C.; Neel, B. G.; Hayward, W. S.; Chaganti, R. S. K.: 3 B c
Localization of the cellular oncogenes ABL, SIS, and FES on humangerm- line
chromosomes. Cytogenet. Cell Genet. 38: 73- 75, 1984.

GAM69 258 PDGFB Josephs, S. F.; Dalla- Favera, R.; Gelmann, E. P.; Gallo, R. C.;Wong- Staal, 3 B c
F.: 5- prime viral and human cellular sequences correspondingto the
transforming gene of simian sarcoma virus. Science 219: 503- 505,1983.

GAM69 258 PDGFB Josephs, S. F.; Guo, C.; Ratner, L.; Wong- Staal, F.: Human proto- 3 B c
oncogenenucleotide sequences corresponding to the transforming region of
simiansarcoma virus. Science 223: 487- 491, 1984.

GAM69 258 PDGFB Josephs, S. F.; Ratner, L.; Clarke, M. F.; Westin, E. H.; Reitz,M. S.; Wong- 3 B c
Staal, F.: Transforming potential of human c- sis nucleotidesequences
encoding platelet- derived growth factor. Science 225:636- 639, 1984.

GAM69 258 PDGFB Julier, C.; Lathrop, M.; Lalouel, J. M.; Kaplan, J. C.: Use ofmultilocus tests of gene order: example for chromosome 22. (Abstract) Cytogenet.Cell Genet. 40: 663- 664, 1985. 3 B c

GAM69 258 PDGFB Julier, C.; Lathrop, M.; Lalouel, J. M.; Reghis, A.; Szajnert,M. F.; Kaplan, J. C.: New restriction fragment length polymorphismson human chromosome 22 at loci SIS, MB and IGLV. (Abstract) Cytogenet.Cell Genet. 40: 664 only, 1985. 3 B c

GAM69 258 PDGFB Julier, C.; Reghis, A.; Szajnert, M. F.; Kaplan, J. C.; Lathrop,G. M.; Lalouel, J. M.: A preliminary linkage map of human chromosome22. (Abstract) Cytogenet. Cell Genet. 40: 665 only, 1985. 3 B c

GAM69 258 PDGFB Kelly, J. D.; Raines, E. W.; Ross, R.; Murray, M. J.: The B chainof PDGF alone is sufficient for mitogenesis. EMBO J. 4: 3399- 3405,1985. 3 B c

GAM69 258 PDGFB Kiuru- Kuhlefelt, S.; El- Rifai, W.; Fanburg- Smith, J.; Kere, J.;Miettinen, M.; Knuutila, S.: Concomitant DNA copy number amplificationat 17q and 22q in dermatofibrosarcoma protuberans. Cytogenet. CellGenet. 92: 192- 195, 2001. 3 B c

GAM69 258 PDGFB Kozak, C. A.; Sears, J. F.; Hoggan, M. D.: Genetic mapping ofthe mouse proto- oncogene c- sis to chromosome 15. Science 221: 867- 869,1983. 3 B c

GAM69 258 PDGFB Leal, F.; Williams, L. T.; Robbins, K. C.; Aaronson, S. A.: Evidencethat the v- sis gene product transforms by interaction with the receptorfor platelet-derived growth factor. Science 230: 327- 330, 1985. 3 B c

GAM69 258 PDGFB Lindahl, P.; Johansson, B. R.; Leveen, P.; Betsholtz, C.: Pericyteloss and microaneurysm formation in PDGF- B- deficient mice. Science 277:242- 245, 1997. 3 B c

GAM69 258 PDGFB Owen, A. J.; Pantazis, P.; Antoniades, H. N.: Simian sarcomavirus-transformed cells secrete a mitogen identical to platelet- derivedgrowth factor. Science 225: 54- 56, 1984. 3 B c

GAM69 258 PDGFB Rao, C. D.; Igarashi, H.; Chiu, I.- M.; Robbins, K. C.; Aaronson,S. A.: Structure and sequence of the human c- sis/platelet- derivedgrowth factor 2 (SIS/PDGF2) transcriptional unit. Proc. Nat. Acad.Sci. 83: 2392- 2396, 1986. 3 B c

GAM69 258 PDGFB Robbins, K. C.; Antoniades, H. N.; Devare, S. G.; Hunkapiller,M. W.; Aaronson, S. A.: Structural and immunological similaritiesbetween simian sarcoma virus gene product(s) and human platelet- derivedgrowth factor. Nature 305: 605- 608, 1983. 3 B c

GAM69 258 PDGFB Robbins, K. C.; Devare, S. G.; Reddy, E. P.; Aaronson, S. A.:In vivo identification of the transforming gene product of simiansarcoma virus. Science 218: 1131- 1133, 1982. 3 B c

GAM69 258 PDGFB Romashkova, J. A.; Makarov, S. S.: NF- kappa- B is a target ofAKT in anti-apoptotic PDGF signalling. Nature 401: 86- 90, 1999. 3 B c

GAM69 258 PDGFB Shimizu, A.; O'Brien, K. P.; Sjoblom, T.; Pietras, K.; Buchdunger,E.; Collins, V. P.; Heldin, C.- H.; Dumanski, J. P.; Ostman, A.: Thedermatofibrosarcoma protuberans- associated collagen type I- alpha-1/platelet- derivedgrowth factor (PDGF) beta- chain fusion gene generates a transformingprotein that is processed to functional PDGF- BB. Cancer Res. 59:3719- 3723, 1999. 3 B c

GAM69 258 PDGFB Simon, M.- P.; Navarro, M.; Roux, D.; Pouyssegur, J.: Structuraland functional analysis of a chimeric protein COL1A1- PDGFB generatedby the translocation t(17;22)(q22;q13.1) in dermatofibrosarcoma protuberans(DP). Oncogene 20: 2965- 2975, 2001. 3 B c

GAM69 258 PDGFB Simon, M.- P.; Pedeutour, F.; Sirvent, N.; Grosgeorge, J.; Minoletti,F.; Coindre, J.- M.; Terrier- Lacombe, M.- J.; Mandahl, N.; Craver, R.D.; Blin, 3 B c

N.; Sozzi, G.; Turc- Carel, C.; O'Brien, K. P.; Kedra, D.;Fransson, I.; Guilbaud, C.; Dumanski, J. P.: Deregulation of theplatelet- derived growth factor B- chain gene via fusion with collagengene COL1A1 in dermatofibrosarcoma protuberans and giant- cell fibroblastoma. NatureGenet. 15: 95- 98, 1997.

GAM69 258 PDGFB Smidt, M.; Kirsch, I.; Ratner, L.: Deletion of Alu sequencesin the fifth c- sis intron in individuals with meningiomas. J. Clin.Invest. 86: 1151- 1157, 1990. 3 B c

GAM69 258 PDGFB Swan, D. C.; McBride, O. W.; Robbins, K. C.; Keithley, D. A.;Reddy, E. P.; Aaronson, S. A.: Chromosomal mapping of the simiansarcoma virus onc gene analogue in human cells. Proc. Nat. Acad.Sci. 79: 4691- 4695, 1982. 3 B c

GAM69 258 PDGFB Turc- Carel, C.; Philip, I.; Berger, M. P.; Philip, T.; Lenoir,G. M.: Chromosomal translocations in Ewing's sarcoma. (Letter) NewEng. J. Med. 309: 497- 498, 1983. 3 B c

GAM69 258 PDGFB Waterfield, M. D.; Scrace, G. T.; Whittle, N.; Stroobant, P.;Johnsson, A.; Wasteson, A.; Westermark, B.; Heldin, C.- H.; Huang,J. S.; Deuel, T. F.: Platelet- derived growth factor is structurallyrelated to the putative transforming protein p28(sis) of simian sarcomavirus. Nature 304: 35- 39, 1983. 3 B c

GAM69 258 PDGFB Wong- Staal, F.; Dalla- Favera, R.; Franchini, G.; Gelmann, E. P.;Gallo, R. C.: Three distinct genes in human DNA related to the transforminggenes of mammalian sarcoma retroviruses. Science 213: 226- 228, 1981. 3 B c

GAM69 258 PTK7 Banga, S. S.; Ozer, H. L.; Park, S.- K.; Lee, S.- T.: Assignmentof PTK7 encoding a receptor protein tyrosine kinase- like moleculeto human chromosome 6p21.1- p12.2 by fluorescence in situ hybridization. Cytogenet.Cell Genet. 76: 43- 44, 1997. 3 B c

GAM69 258 PTK7 Lee, S.- T.; Strunk, K. M.; Spritz, R. A.: A survey of proteintyrosine kinase mRNAs expressed in normal human melanocytes. Oncogene 8:3403- 3410, 1993. 3 B c

GAM69 258 PTK7 Mossie, K.; Jallal, B.; Alves, F.; Sures, I.; Plowman, G. D.; Ullrich,A.: Colon carcinoma kinase- 4 defines a new subclass of the receptortyrosine kinase family. Oncogene 11: 2179- 2184, 1995. 3 B c

GAM69 258 PTK7 Park, S.- K.; Lee, H.- S.; Lee, S.- T.: Characterization of the humanfull- length PTK7 cDNA encoding a receptor protein tyrosine kinase- likemolecule closely related to chick KLG. J. Biochem. 119: 235- 239,1996. 3 B c

GAM69 258 RNF3 Beck, S.; Hanson, I.; Kelly, A.; Pappin, D. J.; Trowsdale, J.:A homologue of the Drosophila female sterile homeotic (fsh) gene inthe class II region of the human MHC. DNA Sequence 2: 203- 210, 1992. 3 B c

GAM69 258 RNF3 Denis, G. V.; Green, M. R.: A novel, mitogen- activated nuclearkinase is related to a Drosophila developmental regulator. GenesDev. 10: 261- 271, 1996. 3 B c

GAM69 258 RNF3 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994. 3 B c

GAM69 258 RNF3 Okamoto, N.; Ando, A.; Kawai, J.; Yoshiwara, T.; Tsuji, K.; Inoko,H.: Orientation of HLA- DNA gene and identification of a CpG island- associatedgene adjacent to DNA in human major histocompatibility complex classII region. Hum. Immun. 32: 221- 228, 1991. 3 B c

GAM69 258 RNF3 Thorpe, K. L.; Abdulla, S.; Kaufman, J.; Trowsdale, J.; Beck, S.: Phylogeny and structure of the RING3 gene. Immunogenetics 44:391- 396, 1996. 3 B c

GAM69 258 USP9Y Brown, G. M.; Furlong, R. A.; Sargent, C. A.; Erickson, R. P.;Longepied, G.; Mitchell, M.; Jones, M. H.; Hargreave, T. B.; Cooke,H. J.; Affara, N. A.: Characterisation of the coding sequence andfine mapping of the human DFFRY gene and comparative expression analysisand mapping to the Sxr- b interval of the mouse Y chromosome of theDffry gene. Hum. Molec. Genet. 7: 97- 107, 1998. 3 B c

GAM69 258 USP9Y Ferlin, A.; Moro, E.; Garolla, A.; Foresta, C.: Human male infertilityand Y chromosome deletions: role of the AZF- candidate genes DAZ, RBMand DFFRY. Hum. Reprod. 14: 1710- 1716, 1999. 3 B c

GAM69 258 USP9Y Foresta, C.; Ferlin, A.; Moro, E.: Deletion and expression analysisof AZFa genes on the human Y chromosome revealed a major role forDBY in male infertility. Hum. Molec. Genet. 9: 1161- 1169, 2000. 3 B c

GAM69 258 USP9Y Jones, M. H.; Furlong, R. A.; Burkin, H.; Chalmers, I. J.; Brown,G. M.; Khwaja, O.; Affara, N. A.: The Drosophila developmental genefat facets has a human homologue in Xp11.4 which escapes X- inactivationand has related sequences on Yq11.2. Hum. Molec. Genet. 5: 1695- 1701,1996. 3 B c

GAM69 258 USP9Y Sargent, C. A..; Boucher, C. A.; Kirsch, S.; Brown, G.; Weiss,B.; Trundley, A.; Burgoyne, P.; Saut, N.; Durand, C.; Levy, N.; Terriou,P.; Hargreave, T.; Cooke, H.; Mitchell, M.; Rappold, G. A.; Affara,N. A.: The critical region of overlap defining the AZFa male infertilityinterval of proximal Yq contains three transcribed sequences. J.Med. Genet. 36: 670- 677, 1999. 3 B c

GAM69 258 USP9Y Shen, P.; Wang, F.; Underhill, P. A.; Franco, C.; Yang, W.- H.;Roxas, A.; Sung, R.; Lin, A. A.; Hyman, R. W.; Vollrath, D.; Davis,R. W.; Cavalli-Sforza, L. L.; Oefner, P. J.: Population genetic implicationsfrom sequence variation in four Y chromosome genes. Proc. Nat. Acad.Sci. 97: 7354- 7359, 2000. 3 B c

GAM69 258 USP9Y Sun, C.; Skaletsky, H.; Birren, B.; Devon, K.; Tang, Z.; Silber,S.; Oates, R.; Page, D. C.: An azoospermic man with a de novo pointmutation in the Y-chromosomal gene USP9Y. Nature Genet. 23: 429- 432,1999. 3 B c

GAM69 258 USP9Y Thomson, R.; Pritchard, J. K.; Shen, P.; Oefner, P. J.; Feldman,M. W.: Recent common ancestry of human Y chromosomes: evidence fromDNA sequence data. Proc. Nat. Acad. Sci. 97: 7360- 7365, 2000. 3 B c

GAM71 257 ABCD4 Holzinger, A.; Kammerer, S.; Roscher, A. A.: Primary structureof human PMP69, a putative peroxisomal ABC- transporter. Biochem.Biophys. Res. Commun. 237: 152- 157, 1997. 3 C c

GAM71 257 ABCD4 Holzinger, A.; Roscher, A. A.; Landgraf, P.; Lichtner, P.; Kammerer,S.: Genomic organization and chromosomal localization of the humanperoxisomal membrane protein- 1- like protein (PXMP1- L) gene encodinga peroxisomal ABC transporter. FEBS Lett. 426: 238- 242, 1998. 3 C c

GAM71 257 ABCD4 Shani, N.; Jimenez- Sanchez, G.; Steel, G.; Dean, M.; Valle, D.: Identification of a fourth half ABC transporter in the human peroxisomalmembrane. Hum. Molec. Genet. 6: 1925- 1931, 1997. 3 C c

GAM71 257 ADAMTS13 Bianchi, V.; Robles, R.; Alberio, L.; Furlan, M.; Lammle, B.:Von Willebrand factor- cleaving protease (ADAMTS13) in thrombocytopenicdisorders: a severely deficient activity is specific for thromboticthrombocytopenic purpura. Blood 100: 710- 713, 2002. 3 C c

GAM71 257 ADAMTS13 Fujikawa, K.; Suzuki, H.; McMullen, B.; Chung, D.: Purificationof human von Willebrand factor- cleaving protease and its identificationas a new member 3 C c

of the metalloproteinase family. Blood 98: 1662- 1666,2001.

GAM71 257 ADAMTS13 Furlan, M.; Robles, R.; Galbusera, M.; Remuzzi, G.; Kyrle, P. A.;Brenner, 3 C c
B.; Krause, M.; Scharrer, I.; Aumann, V.; Mittler, U.; Solenthaler,M.;
Lammle, B.: Von Willebrand factor- cleaving protease in
thromboticthrombocytopenic purpura and the hemolytic- uremic syndrome. New
Eng.J. Med. 339: 1578- 1584, 1998.

GAM71 257 ADAMTS13 Furlan, M.; Robles, R.; Lammle, B.: Partial purification and 3 C c
characterizationof a protease from human plasma cleaving von Willebrand
factor tofragments produced by in vivo proteolysis. Blood 87: 4223-
4234,1996.

GAM71 257 ADAMTS13 Furlan, M.; Robles, R.; Solenthaler, M.; Wassmer, M.; Sandoz, Pl;Lammle, B.: 3 C c
Deficient activity of von Willebrand factor- cleavingprotease in chronic
relapsing thrombotic thrombocytopenic purpura. Blood 89:3097- 3103, 1997.

GAM71 257 ADAMTS13 Gerritsen, H. E.; Robles, R.; Lammle, B.; Furlan, M.: Partialamino acid 3 C c
sequence of purified von Willebrand factor- cleaving protease. Blood
98:1654- 1661, 2001.

GAM71 257 ADAMTS13 Kokame, K.; Matsumoto, M.; Soejima, K.; Yagi, H.; Ishizashi, H.;Funato, M.; 3 C c
Tamai, H.; Konno, M.; Kamide, K.; Kawano, Y.; Miyata,T.; Fujimura, Y.:
Mutations and common polymorphisms in ADAMTS13gene responsible for von
Willebrand factor- cleaving protease activity. Proc.Nat. Acad. Sci. 99:
11902- 11907, 2002.

GAM71 257 ADAMTS13 Levy, G. G.; Nichols, W. C.; Lian, E. C.; Foroud, T.; McClintick,J. N.; 3 C c
McGee, B. M.; Yang, A. Y.; Slemieniak, D. R.; Stark, K. R.;Gruppo, R.;
Sarode, R.; Shurin, S. B.; Chandrasekaran, V.; Stabler,S. P.; Sabio, H.;
Bouhassira, E. E.; Upshaw, J. D., Jr.; Ginsburg,D.; Tsai, H.- M.: Mutations
in a member of the ADAMTS gene familycause thrombotic thrombocytopenic
purpura. Nature 413: 488- 494,2001.

GAM71 257 ADAMTS13 Tsai, H.- M.: Physiologic cleavage of von Willebrand factor bya plasma 3 C c
protease is dependent on its conformation and requires calciumion. Blood 87:
4235- 4244, 1996.

GAM71 257 ADAMTS13 Tsai, H.- M.; Lian, E. C.- Y.: Antibodies to von Willebrand factor- 3 C c
cleavingprotease in acute thrombotic thrombocytopenic purpura. New Eng.
J.Med. 339: 1585- 1594, 1998.

GAM71 257 BACE Cai, H.; Wang, Y.; McCarthy, D.; Wen, H.; Borchelt, D. R.; Price,D. L.; 3 C c
Wong, P. C.: BACE1 is the major beta- secretase for generationof A- beta
peptides by neurons. Nature Neurosci. 4: 233- 234, 2001.

GAM71 257 BACE De Strooper, B.; Konig, G.: A firm base for drug development. Nature 3 C c
402:471- 472, 1999.

GAM71 257 BACE Fan, W.; Bennett, B. D.; Babu- Khan, S.; Luo, Y.; Louis, J.- C.;McCaleb, M.; 3 C c
Citron, M.; Vassar, R.; Richards, W. G.: Response toSaunders et al. (1999).
Science 286: 1255a, 1999. Note: ElectronicPublication.

GAM71 257 BACE Haniu, M.; Denis, P.; Young, Y.; Mendiaz, E. A.; Fuller, J.; Hui,J. O.; 3 C c
Bennett, B. D.; Kahn, S.; Ross, S.; Burgess, T.; Katta, V.;Rogers, G.;
Vassar, R.; Citron, M.: Characterization of Alzheimer'sbeta- secretase
protein BACE: a pepsin family member with unusual properties. J.Biol. Chem.
275: 21099- 21106, 2000.

GAM71 257 BACE Hong, L.; Koelsch, G.; Lin, X.; Wu, S.; Terzyan, S.; Ghosh, A.K.; Zhang, X. 3 C c
C.; Tang, J.: Structure of the protease domain of memapsin2 (beta-
secretase) complexed with inhibitor. Science 290: 150- 153,2000.

GAM71 257 BACE Hussain, I.; Powell, D.; Howlett, D. R.; Tew, D. G.; Meek, T. D.;Chapman, 3 C c

C.; Gloger, I. S.; Murphy, K. E.; Southan, C. D.; Ryan, D.M.; Smith, T. S.; Simmons, D. L.; Walsh, F. S.; Dingwall, C.; Christie,G.: Identification of a novel aspartic protease (asp2) as beta- secretase Molec.Cell Neurosci. 14: 419- 427, 1999.

GAM71 257 BACE Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, 3 C c
L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643- 648, 2001.

GAM71 257 BACE Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.- H.; Goldstein, L. S.: Axonal 3 C c
transport of amyloid precursor protein is mediated by directbinding to the kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000.

GAM71 257 BACE Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis,P.; Fan, 3 C c
W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.;Yan, Q.; Richards, W. G.; Citron, M.; Vassar, R.: Mice deficientin BACE1, the Alzheimer's beta- secretase, have normal phenotype andabolished beta- amyloid generation. Nature Neurosci. 4: 231- 232,2001.

GAM71 257 BACE Nicolaou, M.; Song, Y.- Q.; Sato, C. A.; Orlacchio, A.; Kawarai,T.; 3 C c
Medeiros, H.; Liang, Y.; Sorbi, S.; Richard, E.; Rogaev, E. I.;Moliaka, Y.; Bruni, A. C.; Jorge, R.; Percy, M.; Duara, R.; Farrer,L. A.; St George- Hyslop, P.; Rogaeva, E. A.: Mutations in the openreading frame of the beta- site APP cleaving enzyme (BACE) locus arenot a common cause of Alzheimer's disease. Neurogenetics 3: 203- 206,2001.

GAM71 257 BACE Roberds, S. L.; Anderson, J.; Basi, G.; Bienkowski, M. J.; Branstetter,D. 3 C c
G.; Chen, K. S.; Freedman, S. B.; Frigon, N. L.; Games, D.; Hu,K.; Johnson- Wood, K.; Kappenman, K. E.; and 20 others: BACE knockoutmice are healthy despite lacking the primary beta- secretase activityin brain: implications for Alzheimer's disease therapeutics. Hum.Molec. Genet. 10: 1317- 1324, 2001.

GAM71 257 BACE Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a 3 C c
BACE homolog, BACE2, reside in the obligate Down syndromeregion of chromosome 21. Science 286: 1255a, 1999. Note: ElectronicPublication.

GAM71 257 BACE Sinha, S.; Anderson, J. P.; Barbour, R.; Basi, G. S.; Caccavello,R.; Davis, 3 C c
D.; Doan, M.; Dovey, H. F.; Frigon, N.; Hong, J.; Jacobson- Croak,K.; Jewett, N.; and 15 others: Purification and cloning of amyloidprecursor protein beta- secretase from human brain. Nature 402: 537- 540,1999.

GAM71 257 BACE Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz,E. A.; Dents, 3 C c
P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff,R.; Luo, Y.; Fisher, S.; and 12 others: Beta- secretase cleavageof Alzheimer's amyloid precursor protein by the transmembrane asparticprotease BACE. Science 286: 735- 741, 1999.

GAM71 257 BACE Yan, R.; Bienkowski, M. J.; Shuck, M. E.; Miao, H.; Tory, M. C.;Pauley, A. 3 C c
M.; Brashler, J. R.; Stratman, N. C.; Mathews, W. R.; Buhl,A. E.; Carter, D. B.; Tomasselli, A. G.; Parodi, L. A.; Heinrikson,R. L.; Gurney, M. E.: Membrane- anchored aspartyl protease with Alzheimer'sdisease beta- secretase activity. Nature 402: 533- 536, 1999.

GAM71 257 CSRP1 Alli, C.; Consalez, G. G.: Linkage mapping of Csrp to proximalmouse 3 C c
chromosome 3. Mammalian Genome 9: 172 only, 1998.

GAM71 257 CSRP1 Erdel, M.; Weiskirchen, R.: Assignment of CSRP1 encoding the LIMdomain 3 C c
protein CRP1, to human chromosome 1q32 by fluorescence in situhybridization. Cytogenet. Cell Genet. 83: 10- 11, 1998.

GAM71 257 CSRP1 Liebhaber, S. A.; Emery, J. G.; Urbanek, M.; Wang, X.; Cooke, N.E.: 3 C c
Characterization of a human cDNA encoding a widely expressedand highly
conserved cysteine- rich protein with an unusual zinc- fingermotif. Nucleic
Acids Res. 18: 3871- 3879, 1990.

GAM71 257 CSRP1 Wang, X.; Lee, G.; Liebhaber, S. A.; Cooke, N. E.: Human cysteine- 3 C c
richprotein: a member of the LIM/double- finger family displaying
coordinateserum induction with c- myc. J. Biol. Chem. 267: 9176- 9184, 1992.

GAM71 257 CSRP1 Wang, X.; Ray, K.; Szpirer, J.; Levan, G.; Liebhaber, S. A.; Cooke,N. E.: 3 C c
Analysis of the human cysteine- rich protein gene (CSRP), assignmentto
chromosome 1q24- 1q32, and identification of an associated MspIpolymorphism.
Genomics 14: 391- 397, 1992.

GAM71 257 CSRP1 Weiskirchen, R.; Pino, J. D.; Macalma, T.; Bister, K.; Beckerle,M. C.: The 3 C c
cysteine- rich protein family of highly related LIM domainproteins. J. Biol.
Chem. 270: 28946- 28954, 1995.

GAM71 257 DAG1 Arahata, K.; Hayashi, Y. K.; Mizuno, Y.; Yoshida, M.; Ozawa, E.: Dystrophin- 3 C c
associated glycoprotein and dystrophin co- localisationat sarcolemma in
Fukuyama congenital muscular dystrophy. (Letter) Lancet 342:623- 624, 1993.

GAM71 257 DAG1 Campanelli, J. T.; Roberds, S. L.; Campbell, K. P.; Scheller, R.H.: A role 3 C c
for dystrophin- associated glycoproteins and utrophin inagrin- induced AChR
clustering. Cell 77: 663- 674, 1994.

GAM71 257 DAG1 Cao, W.; Henry, M. D.; Borrow, P.; Yamada, H.; Elder, J. H.; Ravkov,E. V.; 3 C c
Nichol, S. T.; Compans, R. W.; Campbell, K. P.; Oldstone, M.B. A.:
Identification of alpha- dystroglycan as a receptor for
lymphocyticchoriomeningitis virus and Lassa fever virus. Science 282: 2079-
2081,1998.

GAM71 257 DAG1 Cohn, R. D.; Henry, M. D.; Michele, D. E.; Barresi, R.; Saito,F.; Moore, S. 3 C c
A.; Flanagan, J. D.; Skwarchuk, M. W.; Robbins, M. E.;Mendell, J. R.;
Williamson, R. A.; Campbell, K. P.: Disruption ofDag1 in differentiated
skeletal muscle reveals a role for dystroglycanin muscle regeneration. Cell
110: 639- 648, 2002.

GAM71 257 DAG1 Cote, P. D.; Moukhles, H.; Lindenbaum, M.; Carbonetto, S.: Chimaericmice 3 C c
deficient in dystroglycans develop muscular dystrophy and havedisrupted
myoneural synapses. Nature Genet. 23: 338- 342, 1999.

GAM71 257 DAG1 Gee, S. H.; Montanaro, F.; Lindenbaum, M. H.; Carbonetto, S.:Dystroglycan- 3 C c
alpha, a dystrophin- associated glycoprotein, is a functionalagrin receptor.
Cell 77: 675- 686, 1994.

GAM71 257 DAG1 Gorecki, D. C.; Derry, J. M. J.; Barnard, E. A.: Dystroglycan:brain 3 C c
localisation and chromosome mapping in the mouse. Hum. Molec.Genet. 3: 1589-
1597, 1994.

GAM71 257 DAG1 Hayashi, Y. K.; Ogawa, M.; Tagawa, K.; Noguchi, S.; Ishihara, T.;Nonaka, I.; 3 C c
Arahata, K.: Selective deficiency of alpha- dystroglycanin Fukuyama- type
congenital muscular dystrophy. Neurology 57: 115- 121,2001.

GAM71 257 DAG1 Henry, M. D.; Campbell, K. P.: A role for dystroglycan in basementmembrane 3 C c
assembly. Cell 95: 859- 970, 1998.

GAM71 257 DAG1 Ibraghimov- Beskrovnaya, O.; Ervasti, J. M.; Leveille, C. J.; Slaughter,C. 3 C c
A.; Sernett, S. W.; Campbell, K. P.: Primary structure of dystrophin-
associatedglycoproteins linking dystrophin to the extracellular matrix.
Nature 355:696- 702, 1992.

GAM71 257 DAG1 Ibraghimov- Beskrovnaya, O.; Milatovich, A.; Ozcelik, T.; Yang,B.; Francke, 3 C c
U.; Campbell, K. P.: Dystroglycan: tissue distribution,human muscle cDNA,

genomic structure and chromosome mapping. (Abstract) Am.J. Hum. Genet. 51 (suppl.): A130 only, 1992.

GAM71 257 DAG1 Ibraghimov- Beskrovnaya, O.; Milatovich, A.; Ozcelik, T.; Yang,B.; Koepnick, 3 C c
K.; Francke, U.; Campbell, K. P.: Human dystroglycan:skeletal muscle cDNA, genomic structure, origin of tissue specificisoforms and chromosomal localization. Hum. Molec. Genet. 2: 1651- 1657,1993.

GAM71 257 DAG1 Ma, J.; Nastuk, M. A.; McKechnie, B. A.; Fallon, J. R.: The agrinreceptor: 3 C c
localization in the postsynaptic membrane, interaction withagrin, and relationship to the acetylcholine receptor. J. Biol. Chem. 268:25108- 25117, 1993.

GAM71 257 DAG1 Matsumura, K.; Nonaka, I.; Campbell, K. P.: Abnormal expressionof 3 C c
dystrophin- associated proteins in Fukuyama- type congenital musculardystrophy. Lancet 341: 521- 522, 1993.

GAM71 257 DAG1 Matsumura, K.; Tome, F. M. S.; Collin, H.; Azibi, K.; Chaouch,M.; Kaplan, 3 C c
J.- C.; Fardeau, M.; Campbell, K. P.: Deficiency of the50K dystrophin- associated glycoprotein in severe childhood autosomalrecessive muscular dystrophy. Nature 359: 320- 322, 1992.

GAM71 257 DAG1 Matsumura, K.; Tome, F. M. S.; Ionasescu, V.; Ervasti, J. M.;Anderson, R. 3 C c
D.; Romero, N. B.; Simon, D.; Recan, D.; Kaplan, J.- C.;Fardeau, M.; Campbell, K. P.: Deficiency of dystrophin- associatedproteins in Duchenne muscular dystrophy patients lacking COOH- terminaldomains of dystrophin. J. Clin. Invest. 92: 866- 871, 1993.

GAM71 257 DAG1 Michele, D. E.; Barresi, R.; Kanagawa, M.; Saito, F.; Cohn, R.D.; Satz, J. 3 C c
S.; Dollar, J.; Nishino, I.; Kelley, R. I.; Somer, H.;Straub, V.; Mathews, K. D.; Moore, S. A.; Campbell, K. P.: Post- translationaldisruption of dystroglycan- ligand interactions in congenital musculardystrophies. Nature 418: 417- 422, 2002.

GAM71 257 DAG1 Moore, S. A.; Saito, F.; Chen, J.; Michele, D. E.; Henry, M. D.;Messing, A.; 3 C c
Cohn, R. D.; Ross- Barta, S. E.; Westra, S.; Williamson,R. A.; Hoshi, T.; Campbell, K. P.: Deletion of brain dystroglycanrecapitulates aspects of congenital muscular dystrophy. Nature 418:422- 425, 2002.

GAM71 257 DAG1 Rambukkana, A.; Yamada, H.; Zanazzi, G.; Mathus, T.; Salzer, J.L.; 3 C c
Yurchenco, P. D.; Campbell, K. P.; Fischetti, V. A.: Role ofalpha- dystroglycan as a Schwann cell receptor for Mycobacterium leprae. Science 282:2076- 2078, 1998.

GAM71 257 DAG1 Sealock, R.; Froehner, S. C.: Dystrophin- associated proteinsand synapse 3 C c
formation: is alpha- dystroglycan the agrin receptor? Cell 77:617- 619, 1994.

GAM71 257 DAG1 Spear, P. G.: A welcome mat for leprosy and Lassa fever. Science 282:1999- 3 C c
2000, 1998.

GAM71 257 DAG1 Tinsley, J. M.; Blake, D. J.; Zuellig, R. A.; Davies, K. E.:Increasing 3 C c
complexity of the dystrophin- associated protein complex. Proc.Nat. Acad. Sci. 91: 8307- 8313, 1994.

GAM71 257 DAG1 Williamson, R. A.; Henry, M. D.; Daniels, K. J.; Hrstka, R. F.;Lee, J. C.; 3 C c
Sunada, Y.; Ibraghimov- Beskrovnaya, O.; Campbell, K. P.: Dystroglycan is essential for early embryonic development: disruptionof Reichert's membrane in Dag1- null mice. Hum. Molec. Genet. 6:831- 841, 1997.

GAM71 257 DAG1 Yamada, H.; Denzer, A. J.; Hori, H.; Tanaka, T.; Anderson, L.V. B.; Fujita, 3 C c
S.; Fukuta- Ohi, H.; Shimizu, T.; Ruegg, M. A.; Matsumura,K.: Dystroglycan is a dual receptor for agrin and laminin- 2 in Schwanncell membrane. J.

Biol. Chem. 271: 23418- 23423, 1996.

GAM71 257 DAG1 Yamada, H.; Saito, F.; Fukuta- Ohi, H.; Zhong, D.; Hase, A.; Arai,K.; Okuyama, A.; Maekawa, R.; Shimizu, T.; Matsumura, K.: Processingof beta-dystroglycan by matrix metalloproteinase disrupts the linkbetween the extracellular matrix and cell membrane via the dystroglycancomplex. Hum. Molec. Genet. 10: 1563- 1569, 2001. 3 C c

GAM71 257 DUSP7 Groom, L. A.; Sneddon, A. A.; Alessi, D. R.; Dowd, S.; Keyse, S.M.: Differential regulation of the MAP, SAP and RK/p38 kinases byPyst1, a novel cytosolic dual- specificity phosphatase. EMBO J. 15:3621- 3632, 1996. 3 C c

GAM71 257 DUSP7 Muda, M.; Boschert, U.; Dickinson, R.; Martinou, J.- C.; Martinou,I.; Camps, M.; Schlegel, W.; Arkinstall, S.: MKP- 3, a novel cytosolicprotein- tyrosine phosphatase that exemplifies a new class of mitogen- activatedprotein kinase phosphatase. J. Biol. Chem. 271: 4319- 4326, 1996. 3 C c

GAM71 257 DUSP7 Smith, A.; Price, C.; Cullen, M.; Muda, M.; King, A.; Ozanne, B.;Arkinstall, S.; Ahsworth, A.: Chromosomal localization of three humandual specificity phosphatase genes (DUSP4, DUSP6, and DUSP7). Genomics 42:524- 527, 1997. 3 C c

GAM71 257 EGLN2 Bruick, R. K.; McKnight, S. L.: A conserved family of prolyl- 4-hydroxylasesthat modify HIF. Science 294: 1337- 1340, 2001. 3 C c

GAM71 257 EGLN2 Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell 107:43- 54, 2001. 3 C c

GAM71 257 EMP1 Ben Porath, I.; Kozak, C. A.; Benvenisty, N.: Chromosomal mappingof Tmp (Emp1), Xmp (Emp2), and Ymp (Emp3), genes encoding membraneproteins related to Pmp22. Genomics 49: 443- 447, 1998. 3 C c

GAM71 257 EMP1 Ben- Porath, I.; Benvenisty, N.: Characterization of a tumor-associatedgene, a member of a novel family of genes encoding membrane glycoproteins. Gene 183:69- 75, 1996. 3 C c

GAM71 257 EMP1 Chen, Y.; Medvedev, A.; Ruzanov, P.; Marvin, K. W.; Jetten, A.M.: cDNA cloning, genomic structure, and chromosome mapping of thehuman epithelial membrane protein CL- 20 gene (EMP1), a member of thePMP22 family. Genomics 41: 40- 48, 1997. 3 C c

GAM71 257 EMP1 Liehr, T.; Kuhlenbaumer, G.; Wulf, P.; Taylor, V.; Suter, U.; VanBroeckhoven, C.; Lupski, J. R.; Claussen, U.; Rautenstrauss, B.:Regional localization of the human epithelial membrane protein genes1, 2, and 3 (EMP1, EMP2, EMP3) to 12p12.3, 16p13.2, and 19q13.3. Genomics 58:106- 108, 1999. 3 C c

GAM71 257 EMP1 Marvin, K. W.; Fujimoto, W.; Jetten, A. M.: Identification andcharacterization of a novel squamous cell- associated gene relatedto PMP22. J. Biol. Chem. 270: 28910- 28916, 1995. 3 C c

GAM71 257 EMP1 Ruegg, C. L.; Wu, H.; Fagnoni, F. F.; Engleman, E. G.; Laus, R.: B4B, a novel growth- arrest gene, is expressed by a subset of progenitor/pre-Blymphocytes negative for cytoplasmic mu- chain. J. Immun. 157: 72- 80,1996. 3 C c

GAM71 257 FCER2 Delespesse, G.; Sarfati, M.; Peleman, R.: Influence of recombinantIL- 4, IFN- alpha, and IFN- gamma on the production of human IgE- bindingfactor (soluble CD23). J. Immun. 142: 134- 138, 1989. 3 C c

GAM71 257 FCER2 Ludin, C.; Hofstetter, H.; Sarfati, M.; Levy, C. A.; Suter, U.;Alaimo, D.; Kilchherr, E.; Frost, H.; Delespesse, G.: Cloning andexpression of the cDNA 3 C c

coding for a human lymphocyte IgE receptor.EMBO J. 6: 109- 114, 1987.

GAM71 257 FCER2 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 C c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM71 257 FCER2 Wendel- Hansen, V.; Riviere, M.; Uno, M.; Jansson, I.; Szpirer,J.; Islam, M. 3 C c
Q.; Levan, G.; Klein, G.; Yodoi, J.; Rosen, A.; Szpirer,C.: The gene
encoding CD23 leukocyte antigen (FCE2) is located onhuman chromosome 19.
Somat. Cell Molec. Genet. 16: 283- 286, 1990.

GAM71 257 GNAI2 Blatt, C.; Eversole- Cire, P.; Cohn, V. H.; Zollman, S.; Fournier,R. E. K.; 3 C c
Mohandas, L. T.; Nesbitt, M.; Lugo, T.; Jones, D. T.; Reed,R. R.; Weiner, L.
P.; Sparkes, R. S.; Simon, M. I.: Chromosomal localizationof genes encoding
guanine nucleotide- binding protein subunits in mouseand human. Proc. Nat.
Acad. Sci. 85: 7642- 7646, 1988.

GAM71 257 GNAI2 Hermouet, S.; Merendino, J. J., Jr.; Gutkind, J. S.; Spiegel, A.M.: 3 C c
Activating and inactivating mutations of the alpha subunit ofG(i2) protein
have opposite effects on proliferation of NIH 3T3 cells. Proc.Nat. Acad.
Sci. 88: 10455- 10459, 1991.

GAM71 257 GNAI2 Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.;Kaziro, Y.: 3 C c
Presence of three distinct molecular species of G(i)protein alpha subunit:
structure of rat cDNAs and human genomic DNAs. J.Biol. Chem. 263: 6656-
6664, 1988.

GAM71 257 GNAI2 Lerman, B. B.; Dong, B.; Stein, K. M.; Markowitz, S. M.; Linden,J.; 3 C c
Catanzaro, D. F.: Right ventricular outflow tract tachycardiadue to a
somatic cell mutation in G protein subunit- alpha- i2. J.Clin. Invest. 101:
2862- 2868, 1998.

GAM71 257 GNAI2 Lyons, J.; Landis, C. A.; Harsh, G.; Vallar, L.; Grunewald, K.;Feichtinger, 3 C c
H.; Duh, Q.- Y.; Clark, O. H.; Kawasaki, E.; Bourne, H.R.; McCormick, F.:
Two G protein oncogenes in human endocrine tumors. Science 249:655- 659,
1990.

GAM71 257 GNAI2 Magovcevic, I.; Ang, S.- L.; Seidman, J. G.; Tolman, C. J.; Neer,E. J.; 3 C c
Morton, C. C.: Regional localization of the human G proteinalpha(i2) (GNAI2)
gene: assignment to 3p21 and a related sequence(GNAI2L) to 12p12- p13.
Genomics 12: 125- 129, 1992.

GAM71 257 GNAI2 Rudolph, U.; Finegold, M. J.; Rich, S. S.; Harriman, G. R.; Srinivasan,Y.; 3 C c
Brabet, P.; Boulay, G.; Bradley, A.; Birnbaumer, L.: Ulcerativecolitis and
adenocarcinoma of the colon in G alpha(i2)- deficient mice. NatureGenet. 10:
143- 150, 1995.

GAM71 257 GNAI2 Sparkes, R. S.; Cohn, V. H.; Cire- Eversole, P.; Blatt, C.; Amatruda,T. T.; 3 C c
Weiner, L. P.; Nesbitt, M.; Reed, R. R.; Lochrie, M. A.; Fournier,R. E. K.;
Simon, M. I.: Mapping of genes encoding the subunits ofguanine nucleotide-
binding proteins (G- proteins) in the mouse. (Abstract) Cytogenet.Cell
Genet. 46: 696 only, 1987.

GAM71 257 GNAI2 Sparkes, R. S.; Cohn, V. H.; Mohandas, T.; Zollman, S.; Cire- Eversole,P.; 3 C c
Amatruda, T. T.; Reed, R. R.; Lochrie, M. A.; Simon, M. I.: Mappingof genes
encoding the subunits of guanine nucleotide- binding protein(G- proteins) in
humans. (Abstract) Cytogenet. Cell Genet. 46: 696only, 1987.

GAM71 257 GNAI2 Wilkie, T. M.; Gilbert, D. J.; Olsen, A. S.; Chen, X.- N.; Amatruda,T. T.; 3 C c
Korenberg, J. R.; Trask, B. J.; de Jong, P.; Reed, R. R.; Simon,M. I.;

Jenkins, N. A.; Copeland, N. G.: Evolution of the mammalianG protein alpha subunit multigene family. Nature Genet. 1: 85- 91,1992.

GAM71 257 GNAI2 Williamson, E. A.; Ince, P. G.; Harrison, D.; Kendall- Taylor,P.; Harris, P. E.: G- protein mutations in human pituitary adrenocorticotrophichormone-secreting adenomas. Europ. J. Clin. Invest. 25: 128- 131,1995. 3 C c

GAM71 257 HIRA Halford, S.; Wilson, D. I.; Daw, S. C. M.; Roberts, C.; Wadey,R.; Kamath, S.; Wickremasinghe, A.; Burn, J.; Goodship, J.; Mattei,M.- G.; Moorman, A. F. M.; Scambler, P. J.: Isolation of a gene expressedduring early embryogenesis from the region of 22q11 commonly deletedin DiGeorge syndrome.. Hum. Molec. Genet. 2: 1577- 1582, 1993. 3 C c

GAM71 257 HIRA Lamour, V.; Lecluse, Y.; Desmaze, C.; Spector, M.; Bodescot, M.;Aurias, A.; Osley, M. A.; Lipinski, M.: A human homolog of the S.cerevisiae HIR1 and HIR2 transcriptional repressors cloned from theDiGeorge syndrome critical region. Hum. Molec. Genet. 4: 791- 799,1995. 3 C c

GAM71 257 HIRA Llevadot, R.; Scambler, P.; Estivill, X.; Pritchard, M.: Genomicorganization of TUPLE1/HIRA: a gene implicated in DiGeorge syndrome. MammalianGenome 7: 911- 914, 1996. 3 C c

GAM71 257 HIRA Lorain, S.; Quivy, J.- P.; Monier- Gavelle, F.; Scamps, C.; Lecluse,Y.; Almouzni, G.; Lipinski, M.: Core histones and HIRIP3, a novelhistone-binding protein, directly interact with WD repeat proteinHIRA. Molec. Cell. Biol. 18: 5546- 5556, 1998. 3 C c

GAM71 257 HIRA Magnaghi, P.; Roberts, C.; Lorain, S.; Lipinski, M.; Scambler,P. J.: HIRA, a mammalian homologue of Saccharomyces cerevisiae transcriptionalco-repressors, interacts with Pax3. Nature Genet. 20: 74- 77, 1998. 3 C c

GAM71 257 HIRA Mattei, M.- G.; Halford, S.; Scambler, P. J.: Mapping of the Tuple1gene to mouse chromosome 16A- B1. Genomics 23: 717- 718, 1994. 3 C c

GAM71 257 HIRA Roberts, C.; Daw, S. C. M.; Halford, S.; Scambler, P. J.: Cloningand developmental expression analysis of chick Hira (Chira), a candidategene for DiGeorge syndrome. Hum. Molec. Genet. 6: 237- 245, 1997. 3 C c

GAM71 257 HIRA Wilming, L. G.; Snoeren, C. A. S.; van Rijswijk, A.; Grosveld,F.; Meijers, C.: The murine homologue of HIRA, a DiGeorge syndromecandidate gene, is expressed in embryonic structures affected in humanCATCH22 patients. Hum. Molec. Genet. 6: 247- 258, 1997. 3 C c

GAM71 257 ID4 Pagliuca, A.; Bartoli, P. C.; Saccone, S.; Valle, G. D.; Lania,L.: Molecular cloning of ID4, a novel dominant negative helix- loop- helixhuman gene on chromosome 6p21.3- p22. Genomics 27: 200- 203, 1995. 3 C c

GAM71 257 ID4 Rigolet, M.; Rich, T.; Gross- Morand, M.- S.; Molina- Gomes, D.; Viegas-Pequignot,E.; Junien, C.: cDNA cloning, tissue distribution and chromosomallocalization of the human ID4 gene. DNA Res. 5: 309- 313, 1998. 3 C c

GAM71 257 LOXL2 Jourdan- Le Saux, C.; Le Saux, O.; Donlon, T.; Boyd, C. D.; Csiszar,K.: The human lysyl oxidase- related gene (LOXL2) maps between markersD8S280 and D8S278 on chromosome 8p21.2- p21.3. Genomics 51: 305- 307,1998. 3 C c

GAM71 257 LOXL2 Jourdan- Le Saux, C.; Tronecker, H.; Bogic, L.; Bryant- Greenwood,G. D.; Boyd, C. D.; Csiszar, K.: The LOXL2 gene encodes a new lysyloxidase- like protein and is expressed at high levels in reproductivetissues. J. Biol. Chem. 274: 12939- 12944, 1999. 3 C c

GAM71 257 LOXL2 Murano, S.; Thweatt, R.; Reis, R. J. S.; Jones, R. A.; Moerman,E. J.; Goldstein, S.: Diverse gene sequences are overexpressed inWerner syndrome fibroblasts undergoing premature replicative senescence. Molec.Cell. Biol. 11: 3905- 3914, 1991. 3 C c

GAM71 257 LOXL2 Saito, H.; Papaconstantinou, J.; Sato, H.; Goldstein, S.: Regulationof a novel gene encoding a lysyl oxidase- related protein in cellularadhesion and senescence. J. Biol. Chem. 272: 8157- 8160, 1997. 3 C c

GAM71 257 MLN Daikh, D. I.; Douglass, J. O.; Adelman, J. P.: Structure and expressionof the human motilin gene. DNA 8: 615- 621, 1989. 3 C c

GAM71 257 MLN Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Yano, H.; Seino, Y.; Fujita, J.; Yamada, Y.; Inagaki, N.; Takeda,J.; Imura, H.; Bell, G. I.; Shows, T. B.: Localization of the humanmotilin gene (MLN) to chromosome 6p21.2. (Abstract) Cytogenet. CellGenet. 51: 977 only, 1989. 3 C c

GAM71 257 MLN Feighner, S. D.; Tan, C. P.; McKee, K. K.; Palyha, O. C.; Hreniuk,D. L.; Pong, S.- S.; Austin, C. P.; Figueroa, D.; MacNeil, D.; Cascieri,M. A.; Nargund, R.; Bakshi, R.; Abramovitz, M.; Stocco, R.; Kargman,S.; O'Neill, G.; Van Der Ploeg, L. H. T.; Evans, J.; Patchett, A.A.; Smith, R. G.; Howard, A. D.: Receptor for motilin identifiedin the human gastrointestinal system. Science 284: 2184- 2188, 1999. 3 C c

GAM71 257 MLN Gasparini, P.; Grifa, A.; Savasta, S.; Merlo, I.; Bisceglia, L.;Totaro, A.; Zelante, L.: The motilin gene: subregional localisation,tissue expression, DNA polymorphisms and exclusion as a candidategene for the HLA- associated immotile cilia syndrome. Hum. Genet. 94:671- 674, 1994. 3 C c

GAM71 257 MSF Bahabri, S. A.; Suwairi, W. M.; Laxer, R. M.; Polinkovsky, A.;Dalaan, A. A.; Warman, M. L.: The camptodactyly- arthropathy- coxavara- pericarditis syndrome: clinical features and genetic mappingto human chromosome 1. Arthritis Rheum. 41: 730- 735, 1998. 3 C c

GAM71 257 MSF Flannery, C. R.; Hughes, C. E.; Schumacher, B. L.; Tudor, D.; Aydelotte,M. B.; Kuettner, K. E.; Caterson, B.: Articular cartilage superficialzone protein (SZP) is homologous to megakaryocyte stimulating factorprecursor and is a multifunctional proteoglycan with potential growth-promoting,cytoprotective, and lubricating properties in cartilage metabolism. Biochem.Biophys. Res. Commun. 254: 535- 541, 1999. 3 C c

GAM71 257 MSF Ikegawa, S.; Sano, M.; Koshizuka, Y.; Nakamura, Y.: Isolation,characterization and mapping of the mouse and human PRG4 (proteoglycan4) genes. Cytogenet. Cell Genet. 90: 291- 297, 2000. 3 C c

GAM71 257 MSF Marcelino, J.; Carpten, J. D.; Suwairi, W. M.; Gutierrez, O. M.;Schwartz, S.; Robbins, C.; Sood, R.; Makalowska, I.; Baxevanis, A.;Johnstone, B.; Laxer, R. M.; Zemel, L.; and 13 others: CACP, encodinga secreted proteoglycan, is mutated in camptodactyly- arthropathy- coxavara-pericarditis syndrome. Nature Genet. 23: 319- 322, 1999. 3 C c

GAM71 257 MSF McIlhatton, M. A.; Burrows, J. F.; Donaghy, P. G.; Chanduloy, S.;Johnston, P. G.; Russell, S. E. H.: Genomic organization, complexsplicing pattern and expression of a human septin gene on chromosome17q25.3. Oncogene 20: 5930-5939, 2001. 3 C c

GAM71 257 MSF Merberg, D. M.; Fitz, L. J.; Temple, P.; Giannotti, J.; Murtha,P.; Fitzgerald, M.; Scaltreto, H.; Kelleher, K.; Preissner, K.; Kriz,R.; Jacobs, K.; Turner, K.: In: Preissner, K. T.; Rosenblatt, S.;Kost, C.; Wegerhoff, J.; Mosher, D. F. (eds.): Biology of Vitronectinsand Their Receptors. Elsevier Science, B.V. 1993. Pp. 45- 53. 3 C c

GAM71 257 MSF Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 3 C c

6: 63- 70, 1999.

GAM71 257 MSF Osaka, M.; Rowley, J. D.; Zeleznik- Le, N. J.: MSF (MLL septin- likefusion), 3 C c
a fusion partner gene of MLL, in a therapy- related acutemyeloid leukemia
with a t(11;17)(q23;q25). Proc. Nat. Acad. Sci. 96:6428- 6433, 1999.

GAM71 257 MSF Russell, S. E. H.; McIlhatton, M. A.; Burrows, J. F.; Donaghy,P. G.; 3 C c
Chanduloy, S.; Petty, E. M.; Kalikin, L. M.; Church, S. W.;McIlroy, S.;
Harkin, D. P.; Keilty, G. W.; Cranston, A. N.; Weissenbach,J.; Hickey, I.;
Johnston, P. G.: Isolation and mapping of a humanseptin gene to a region on
chromosome 17q, commonly deleted in sporadicepithelial ovarian tumors.
Cancer Res. 60: 4729- 4734, 2000.

GAM71 257 MSF Schumacher, B. L.; Block, J. A.; Schmid, T. M.; Aydelotte, M. B.;Kuettner, 3 C c
K. E.: A novel proteoglycan synthesized and secreted bychondrocytes of the
superficial zone of articular cartilage. Arch.Biochem. Biophys. 15: 144-
152, 1994.

GAM71 257 PBX2 Aguado, B.; Campbell, R. D.: The novel gene G17, located in thehuman major 3 C c
histocompatibility complex, encodes PBX2, a homeodomain- containingprotein.
Genomics 25: 650- 659, 1995.

GAM71 257 PBX2 Katsanis, N.; Fitzgibbon, J.; Fisher, E. M. C.: Paralogy 3 C c
mapping:identification of a region in the human MHC triplicated onto
humanchromosomes 1 and 9 allows the prediction and isolation of novel PBXand
NOTCH loci. Genomics 35: 101- 108, 1996.

GAM71 257 PBX2 Monica, K.; Galili, N.; Nourse, J.; Saltman, D.; Cleary, M. L.: PBX2 and 3 C c
PBX3, new homeobox genes with extensive homology to thehuman proto- oncogene
PBX1. Molec. Cell. Biol. 11: 6149- 6157, 1991.

GAM71 257 PBX2 Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.;Ando, A.; 3 C c
Inoko, H.; Ikemura, T.: Three genes in the human MHC classIII region near
the junction with the class II: gene for receptorof advanced glycosylation
end products, PBX2 homeobox gene and a Notchhomolog, human counterpart of
mouse mammary tumor gene int- 3. Genomics 23:408- 419, 1994.

GAM71 257 PTPN1 Ahmad, F.; Azevedo, J. L., Jr.; Cortright, R.; Dohm, G. L.; Goldstein,B. J.: 3 C c
Alternations in skeletal muscle protein- tyrosine phosphataseactivity and
expression in insulin- resistant human obesity and diabetes. J.Clin. Invest.
100: 449- 458, 1997.

GAM71 257 PTPN1 Brown- Shimer, S.; Johnson, K. A.; Lawrence, J. B.; Johnson, C.;Bruskin, A.; 3 C c
Green, N. R.; Hill, D. E.: Molecular cloning and chromosomemapping of the
human gene encoding protein phosphotyrosyl phosphatase1B. Proc. Nat. Acad.
Sci. 87: 5148- 5152, 1990.

GAM71 257 PTPN1 Charbonneau, H.; Tonks, N. K.; Kumar, S.; Diltz, C. D.; Harrylock,M.; Cool, 3 C c
D. E.; Krebs, E. G.; Fischer, E. H.; Walsh, K. A.: Humanplacenta protein-
tyrosine- phosphatase: amino acid sequence and relationshipto a family of
receptor- like proteins. Proc. Nat. Acad. Sci. 86:5252- 5256, 1989.

GAM71 257 PTPN1 Chernoff, J.; Schievella, A. R.; Jost, C. A.; Erikson, R. L.; Neel,B. G.: 3 C c
Cloning of a cDNA for a major human protein- tyrosine- phosphatase.
Proc.Nat. Acad. Sci. 87: 2735- 2739, 1990.

GAM71 257 PTPN1 Di Paola, R.; Frittitta, L.; Miscio, G.; Bozzali, M.; Baratta,R.; Centra, 3 C c
M.; Spampinato, D.; Santagati, M. G.; Ercolino, T.; Cisternino,C.; Soccio,
T. Mastroianno, S.; Tassi, V.; Almgren, P.; Pizzuti, A.;Vigneri, R.;
Trischitta, V.: A variation in 3- prime UTR of hPTP1Bincreases specific gene
expression and associates with insulin resistance. Am.J. Hum. Genet. 70:
806- 812, 2002.

GAM71 257 PTPN1 Elchebly, M.; Payette, P.; Michaliszyn, E.; Cromlish, W.; Collins,S.; Loy, A. L.; Normandin, D.; Cheng, A.; Himms- Hagen, J.; Chan, C.-C.;Ramachandran, C.; Gresser, M. J.; Tremblay, M. L.; Kennedy, B. P.: Increased insulin sensitivity and obesity resistance in mice lackingthe protein tyrosine phosphatase- 1B gene. Science 283: 1544- 1548,1999. 3 C c

GAM71 257 PTPN1 Forsell, P. K. A. L.; Boie, Y.; Montalibet, J.; Collins, S.; Kennedy,B. P.: Genomic characterization of the human and mouse protein tyrosinephosphatase-1B genes. Gene 260: 145- 153, 2000. 3 C c

GAM71 257 PTPN1 Gu, H. F.; Almgren, P.; Lindholm, E.; Frittitta, L.; Pizzuti, A.;Trischitta, V.; Groop, L. C.: Association between the human glycoproteinPC- 1 gene and elevated glucose and insulin levels in paired- siblinganalysis. Diabetes 49: 1601- 1603, 2000. 3 C c

GAM71 257 PTPN1 Haj, F. G.; Verveer, P. J.; Squire, A.; Neel, B. G.; Bastiaens,P. I. H.: Imaging sites of receptor dephosphorylation by PTP1B onthe surface of the endoplasmic reticulum. Science 295: 1708- 1711,2002. 3 C c

GAM71 257 PTPN1 Jia, Z.; Barford, D.; Flint, A. J.; Tonks, N. K.: Structuralbasis for phosphotyrosine peptide recognition by protein tyrosinephosphatase 1B. Science 268: 1754- 1758, 1995. 3 C c

GAM71 257 PTPN1 Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Howk, R.; Ravera,M.; Ricca, G.; Jaye, M.; Schlessinger, J.: Cloning of three humantyrosine phosphatases reveals a multigene family of receptor- linkedprotein- tyrosine-phosphatases expressed in brain. Proc. Nat. Acad.Sci. 87: 7000- 7004, 1990. 3 C c

GAM71 257 PTPN1 Kennedy, B. P.; Ramachandran, C.: Protein tyrosine phosphatase- 1Bin diabetes. Biochem. Pharm. 60: 877- 883, 2000. 3 C c

GAM71 257 PTPN1 Mok, A.; Cao, H.; Zinman, B.; Hanley, A. J. G.; Harris, S. B.;Kennedy, B. P.; Hegele, R. A.: A single nucleotide polymorphism inprotein tyrosine phosphatase PTP- 1B is associated with protectionfrom diabetes or impaired glucose tolerance in Oji- Cree. J. Clin.Endocr. Metab. 87: 724- 727, 2002. 3 C c

GAM71 257 PTPN1 Salmeen, A.; Andersen, J. N.; Myers, M. P.; Tonks, N. K.; Barford,D.: Molecular basis for the dephosphorylation of the activation segmentof the insulin receptor by protein tyrosine phosphatase 1B. Molec.Cell 6: 1401-1412, 2000. 3 C c

GAM71 257 PTPN1 Tonks, N. K.; Diltz, C. D.; Fischer, E. H.: Purification of themajor protein- tyrosine- phosphatases of human placenta. J. Biol. Chem. 263:6722-6730, 1988. 3 C c

GAM71 257 RNPEP Aurich- Costa, J.; Cadel, S.; Gouzy, C.; Foulon, T.; Cherif, D.;Cohen, P.: Assignment of the aminopeptidase B gene (RNPEP) to humanchromosome 1 band q32 by in situ hybridization. Cytogenet. Cell Genet. 79:143- 144, 1997. 3 C c

GAM71 257 RNPEP Cadel, S.; Foulon, T.; Viron, A.; Balogh, A.; Midol- Monnet, S.;Noel, N.; Cohen, P.: Aminopeptidase B from the rat testis is a bifunctionalenzyme structurally related to leukotriene- A4 hydrolase. Proc. Nat.Acad. Sci. 94: 2963- 2968, 1997. 3 C c

GAM71 257 RNPEP Cadel, S.; Pierotti, A. R.; Foulton, T.; Creminon, C.; Barre, N.;Segretain, D.; Cohen, P.: Aminopeptidase- B in the rat testes: isolation,functional properties and cellular localization in the seminiferoustubules. Molec. Cell. Endocr. 110: 149- 160, 1995. 3 C c

GAM71 257 RNPEP Hopsu, V. K.; Kantonen, U. M.; Glenner, G. G.: A peptidase fromrat tissues selectively hydrolyzing N- terminal arginine and lysineresidues. Life Sci. 3: 1449- 1453, 1964. 3 C c

GAM71 257 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human 3 C c

intestine:biology and function. Gastroenterology 113: 332- 340, 1997.

GAM71 257 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563- 566, 1994. 3 C c

GAM71 257 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 3 C c

GAM71 257 SLC21A9 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5: 355- 364, 1998. 3 C c

GAM71 257 SLC21A9 St- Pierre, M. V.; Hagenbuch, B.; Ugele, B.; Meier, P. J.; Stallmach,T.: Characterization of an organic anion- transporting polypeptide(OATP- B) in human placenta. J. Clin. Endocr. Metab. 87: 1856- 1863,2002. 3 C c

GAM71 257 SLC6A2 Bruss, M.; Kunz, J.; Lingen, B.; Bonisch, H.: Chromosomal mappingof the human gene for the tricyclic antidepressant- sensitive noradrenalinetransporter. Hum. Genet. 91: 278- 280, 1993. 3 C c

GAM71 257 SLC6A2 Esler, M.; Jennings, G.; Lambert, G.; Meredith, I.; Horne, M.;Eisenhofer, G.: Overflow of catecholamine neurotransmitters to thecirculation: source, fate, and functions. Physiol. Rev. 70: 963- 985,1990. 3 C c

GAM71 257 SLC6A2 Fritz, J. D.; Jayanthi, L. D.; Thoreson, M. A.; Blakely, R. D.: Cloning and chromosomal mapping of the murine norepinephrine transporter. J.Neurochem. 70: 2241- 2251, 1998. 3 C c

GAM71 257 SLC6A2 Gelernter, J.; Kruger, S.; Kidd, K. K.; Amara, S.: TaqI RFLP atnorepinephrine transporter protein (NET) locus. Hum. Molec. Genet. 2:820 only, 1993. 3 C c

GAM71 257 SLC6A2 Gelernter, J.; Kruger, S.; Pakstis, A. J.; Pacholczyk, T.; Sparkes,R. S.; Kidd, K. K.; Amara, S.: Assignment of the norepinephrine transporterprotein (NET1) locus to chromosome 16. Genomics 18: 690- 692, 1993. 3 C c

GAM71 257 SLC6A2 Kaye, W. H.; Jimerson, D. C.; Lake, C. R.; Ebert, M. H.: Alterednorepinephrine metabolism following long- term weight recovery in patientswith anorexia nervosa. Psychiat. Res. 14: 333- 342, 1985. 3 C c

GAM71 257 SLC6A2 Pacholczyk, T.; Blakely, R. D.; Amara, S. G.: Expression cloningof a cocaine- and antidepressant- sensitive human noradrenaline transporter. Nature 350:350- 354, 1991. 3 C c

GAM71 257 SLC6A2 Paczkowski, F. A.; Bonisch, H.; Bryan- Lluka, L. J.: Pharmacologicalproperties of the naturally occurring ala457pro variant of the humannorepinephrine transporter. Pharmacogenetics 12: 165- 173, 2002. 3 C c

GAM71 257 SLC6A2 Pirke, K. M.; Kellner, M.; Philipp, E.; Laessle, R.; Krieg, J.C.; Fichter, M. M.: Plasma norepinephrine after a standardized testmeal in acute and remitted patients with anorexia nervosa and in healthycontrols. Biol. Psychiat. 31: 1074- 1077, 1992. 3 C c

GAM71 257 SLC6A2 Porzgen, P.; Bonisch, H.; Bruss, M.: Molecular cloning and organizationof the coding region of the human norepinephrine transporter gene. Biochem.Biophys. Res. Commun. 215: 1145- 1150, 1995. Notes: Erratum: Biochem.Biophys. Res. Commun. 227: 642- 643, 1996. 3 C c

GAM71 257 SLC6A2 Shannon, J. R.; Flattem, N. L.; Jordan, J.; Jacob, G.; Black,B. K.; 3 C c

Biaggioni, I.; Blakely, R. D.; Robertson, D.: Orthostaticintolerance and tachycardia associated with norepinephrine- transporterdeficiency. New Eng. J. Med. 342: 541- 549, 2000.

GAM71 257 SLC6A2 Urwin, R. E.; Bennetts, B.; Wilcken, B.; Lampropoulos, B.; Beumont,P.; Clarke, S.; Russell, J.; Tanner, S.; Nunn, K. P.: Anorexia nervosa(restrictive subtype) is associated with a polymorphism in the novelnorepinephrine transporter gene promoter polymorphic region. Molec.Psychiat. 7: 652- 657, 2002. 3 C c

GAM71 257 SLC9A3R2 Hall, R. A.; Ostedgaard, L. S.; Premont, R. T.; Blitzer, J. T.;Rahman, N.; Welsh, M. J.; Lefkowitz, R. J.: A C- terminal motif foundin the beta- 2-adrenergic receptor, P2Y1 receptor and cystic fibrosistransmembrane conductance regulator determines binding to the Na(+)/H(+)exchanger regulatory factor family of PDZ proteins. Proc. Nat. Acad.Sci. 95: 8496-8501, 1998. 3 C b

GAM71 257 SLC9A3R2 Imai, K.; Sarker, A. H.; Akiyama, K.; Ikeda, S.; Yao, M.; Tsutsui,K.; Shohmori, T.; Seki, S.: Genomic structure and sequence of a humanhomologue (NTHL1/NTH1) of Escherichia coli endonuclease III with thoseof the adjacent parts of TSC2 and SLC9A3R2 genes. Gene 222: 287- 295,1998. 3 C b

GAM71 257 SLC9A3R2 Mahon, M. J.; Donowitz, M.; Yun, C. C.; Segre, G. V.: Na+/H+ exchangerregulatory factor 2 directs parathyroid hormone 1 receptor signalling. Nature 417:858- 861, 2002. 3 C b

GAM71 257 SLC9A3R2 Poulat, F.; de Santa Barbara, P.; Desclozeaux, M.; Soullier, S.;Moniot, B.; Bonneaud, N.; Boizet, B.; Berta, P. The human testisdetermining factor SRY binds a nuclear factor containing PDZ proteininteraction domains. J. Biol. Chem. 272: 7167- 7172, 1997. 3 C b

GAM71 257 SLC9A3R2 Reczek, D.; Berryman, M.; Bretscher, A.: Identification of EBP50:a PDZ-containing phosphoprotein that associates with members of theezrin- radixin-moesin family. J. Cell Biol. 139: 169- 179, 1997. 3 C b

GAM71 257 SLC9A3R2 Yun, C. H. C.; Oh, S.; Zizak, M.; Steplock, D.; Tsao, S.; Tse,C.- M.; Weinman, E. J.; Donowitz, M.: cAMP- mediated inhibition ofthe epithelial brush border Na(+)/H(+) exchanger, NHE3, requires anassociated regulatory protein. Proc. Nat. Acad. Sci. 94: 3010- 3015,1997. 3 C b

GAM71 257 SLC9A3R2 Yun, C.- H. C.; Lamprecht, G.; Forster, D. V.; Sidor, A.: NHE3kinase A regulatory protein E3KARP binds the epithelial brush borderNa(+)/H(+) exchanger NHE3 and the cytoskeletal protein ezrin. J.Biol. Chem. 273: 25856-25863, 1998. 3 C b

GAM71 257 STK10 Kuramochi, S.; Matsuda, Y.; Okamoto, M.; Kitamura, F.; Yonekawa,H.; Karasuyama, H.: Molecular cloning of the human gene STK10 encodinglymphocyte- oriented kinase, and comparative chromosomal mapping ofthe human, mouse, and rat homologues. Immunogenetics 49: 369- 375,1999. 3 C c

GAM71 257 STK10 Kuramochi, S.; Moriguchi, T.; Kuida, K.; Endo, J.; Semba, K.; Nishida,E.; Karasuyama, H.: LOK is a novel mouse STE20- like protein kinasethat is expressed predominantly in lymphocytes. J. Biol. Chem. 272:22679- 22684, 1997. 3 C c

GAM71 257 SYNGR1 Janz, R.; Sudhof, T. C.; Hammer, R. E.; Unni, V.; Siegelbaum, S.A.; Bolshakov, V. Y.: Essential roles in synaptic plasticity forsynaptogyrin I and synaptophysin I. Neuron 24: 687- 700, 1999. 3 C c

GAM71 257 SYNGR1 Kedra, D.; Pan, H.- Q.; Seroussi, E.; Fransson, I.; Guilbaud, C.;Collins, J. E.; Dunham, I.; Blennow, E.; Roe, B. A.; Piehl, F.; Dumanski,J. P.: Characterization of the human synaptogyrin gene family. Hum.Genet. 103: 131- 3 C c

141, 1998.

GAM71 257 SYNGR1 McMahon, H. T.; Bolshakov, V. Y.; Janz, R.; Hammer, R. E.; Siegelbaum,S. A.; 3 C c
Sudhof, T. C.: Synaptophysin, a major synaptic vesicle protein,is not
essential for neurotransmitter release. Proc. Nat. Acad. Sci. 93:4760- 4764,
1996.

GAM71 257 TFAP4 Hu, Y.- F.; Luscher, B.; Admon, A.; Mermod, N.; Tjian, R.: 3 C c
Transcriptionfactor AP- 4 contains multiple dimerization domains that
regulate dimerspecificity. Genes Dev. 4: 1741- 1752, 1990.

GAM71 257 TFAP4 Mermod, N.; Williams, T. J.; Tjian, R.: Enhancer binding factorsAP- 4 and 3 C c
AP- 1 act in concert to activate SV40 late transcription invitro. Nature
332: 557- 561, 1988.

GAM71 257 TFAP4 Steingrimsson, E.; Sawadogo, M.; Gilbert, D. J.; Zervos, A. S.;Brent, R.; 3 C c
Blanar, M. A.; Fisher, D. E.; Copeland, N. G.; Jenkins,N. A.: Murine
chromosomal location of five bHLH- Zip transcriptionfactor genes. Genomics
28: 179- 183, 1995.

GAM71 257 UCP3 Argyropoulos, G.; Brown, A. M.; Willi, S. M.; Zhu, J.; He, Y.;Reitman, M.; 3 C c
Gevao, S. M.; Spruill, I.; Garvey, W. T.: Effects ofmutations in the human
uncoupling protein 3 gene on the respiratoryquotient and fat oxidation in
severe obesity and type 2 diabetes. J.Clin. Invest. 102: 1345- 1351, 1998.

GAM71 257 UCP3 Boss, O.; Giacobino, J.- P.; Muzzin, P.: Genomic structure of 3 C c
uncouplingprotein- 3 (UCP3) and its assignment to chromosome 11q13. Genomics
47:425- 426, 1998.

GAM71 257 UCP3 Boss, O.; Samec, S.; Paoloni- Giacobino, A.; Rossier, C.; Dulloo,A.; 3 C c
Seydoux, J.; Muzzin, P.; Giacobino, J.- P.: Uncoupling protein- 3:a new
member of the mitochondrial carrier family with tissue- specificexpression.
FEBS Lett. 408: 39- 42, 1997.

GAM71 257 UCP3 Bouchard, C.; Perusse, L.; Chagnon, Y. C.; Warden, C.; Ricquier,D.: Linkage 3 C c
between markers in the vicinity of the uncoupling protein2 gene and resting
metabolic rate in humans. Hum. Molec. Genet. 6:1887- 1889, 1997.

GAM71 257 UCP3 Brown, A. M.; Dolan, J. W.; Willi, S. M.; Garvey, W. T.; Argyropoulos,G.: 3 C c
Endogenous mutations in human uncoupling protein 3 alter itsfunctional
properties. FEBS Lett. 464: 189- 193, 1999.

GAM71 257 UCP3 Brown, A. M.; Willi, S. M.; Argyropoulos, G.; Garvey, W. T.: Anovel missense 3 C c
mutation, R70W, in the human uncoupling protein 3 genein a family with type
2 diabetes. (Abstract) Hum. Mutat. 13: 508only, 1999. Note: Full article
online.

GAM71 257 UCP3 Clapham, J. C.; Arch, J. R. S.; Chapman, H.; Haynes, A.; Lister,C.; Moore, 3 C c
G. B. T.; Piercy, V.; Carter, S. A.; Lehner, I.; Smith,S. A.; Beeley, L. J.;
Godden, R. J.; and 15 others: Mice overexpressinghuman uncoupling protein- 3
in skeletal muscle are hyperphagic andlean. Nature 406: 415- 418, 2000.

GAM71 257 UCP3 Dalgaard, L. T.; Sorensen, T. I. A.; Drivsholm, T.; Borch- Johnsen,K.; 3 C c
Andersen, T.; Hansen, T.; Pedersen, O.: A prevalent polymorphismin the
promoter of the UCP3 gene and its relationship to body massindex and long
term body weight change in the Danish population. J.Clin. Endocr. Metab. 86:
1398- 1402, 2001.

GAM71 257 UCP3 Echtay, K. S.; Roussel, D.; St- Pierre, J.; Jekabsons, M. B.; Cadenas,S.; 3 C c
Stuart, J. A.; Harper, J. A.; Roebuck, S. J.; Morrison, A.; Pickering,S.;
Clapham, J. C.; Brand, M. D.: Superoxide activates mitochondrialuncoupling
proteins. Nature 415: 96- 99, 2002.

GAM71 257 UCP3 Fleury, C.; Neverova, M.; Collins, S.; Raimbault, S.; Champigny,O.; Levi- 3 C c

Meyrueis, C.; Bouillaud, F.; Seldin, M. F.; Surwit, R. S.;Ricquier, D.; Warden, C. H.: Uncoupling protein- 2: a novel gene linkedto obesity and hyperinsulinemia. Nature Genet. 15: 269- 272, 1997.

GAM71 257 UCP3 Gong, D.- W.; Monemdjou, S.; Gavrilova, O.; Leon, L. R.; Marcus- Samuels,B.; 3 C c
Chou, C. J.; Everett, C.; Kozak, L. P.; Li, C.; Deng, C.; Harper,M.- E.; Reitman, M. L.: Lack of obesity and normal response to fastingand thyroid hormone in mice lacking uncoupling protein- 3. J. Biol.Chem. 275: 16251- 16257, 2000.

GAM71 257 UCP3 Millet, L.; Vidal, H.; Andreelli, F.; Larrouy, D.; Riou, J.- P.;Ricquier, 3 C c
D.; Laville, M.; Langin, D.: Increased uncoupling protein- 2and - 3 mRNA expression during fasting in obese and lean humans. J.Clin. Invest. 100: 2665- 2670, 1997.

GAM71 257 UCP3 Vidal- Puig, A. J.; Grujic, D.; Zhang, C.- Y.; Hagen, T.; Boss,O.; Ido, Y.; 3 C c
Szczepanik, A.; Wade, J.; Mootha, V.; Cortright, R.;Muoio, D. M.; Lowell, B. B.: Energy metabolism in uncoupling protein3 gene knockout mice. J. Biol. Chem. 275: 16258- 16266, 2000.

GAM71 257 UCP3 Vidal- Puig, A.; Solanes, G.; Grujic, D.; Flier, J. S.; Lowell,B. B.: UCP3: 3 C c
an uncoupling protein homologue expressed preferentiallyand abundantly in skeletal muscle and brown adipose tissue. Biochem.Biophys. Res. Commun. 235: 79- 82, 1997.

GAM71 257 UCP3 Walder, K.; Norman, R. A.; Hanson, R. L.; Schrauwen, P.; Neverova,M.; 3 C c
Jenkinson, C. P.; Easlick, J.; Warden, C. H.; Pecqueur, C.; Raimbault,S.; Ricquier, D.; Harper, M.; Silver, K.; Shuldiner, A. R.; Solanes,G.; Lowell, B. B.; Chung, W. K.; Leibel, R. L.; Pratley, R.; Ravussin,E.: Association between uncoupling protein polymorphisms (UCP2- UCP3)and energy metabolism/obesity in Pima Indians. Hum. Molec. Genet. 7:1431- 1435, 1998.

GAM72 342 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: 3 C b
Apolipoprotein L gene family: tissue- specific expression,splicing, promoter regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001.

GAM72 342 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya- 3 C b
Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a new human high density lipoprotein apolipoproteinexpressed by the pancreas: identification, cloning, characterization,and plasma distribution of apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997.

GAM72 342 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. 3 C b
L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.; Bahn, S.: Gene expression analysis in schizophrenia:reproducible up- regulation of several members of the apolipoproteinL family located in a high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat. Acad. Sci. 99: 4680- 4685, 2002.

GAM72 342 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The 3 C b
apolipoprotein L gene cluster has emerged recently in evolutionand is expressed in human vascular tissue. Genomics 79: 539- 546,2002.

GAM72 342 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman 3 C b
apolipoprotein L gene cluster: identification, classification,and sites of distribution. Genomics 74: 71- 78, 2001.

GAM72 342 ARSD Franco, B.; Meroni, G.; Parenti, G.; Levilliers, J.; Bernard, L.;Gebbia, M.; 3 C b
Cox, L.; Maroteaux, P.; Sheffield, L.; Rappold, G. A.;Andria, G.; Petit, C.; Ballabio, A.: A cluster of sulfatase geneson Xp22.3: mutations in chondrodysplasia punctata (CDPX) and implicationsfor warfarin embryopathy.

Cell 81: 1- 20, 1995.

GAM72 342 ARSD Meroni, G.; Franco, B.; Archidiacono, N.; Messali, S.; Andolfi,G.; Rocchi, M.; Ballabio, A.: Characterization of a cluster of sulfatasegenes on Xp22.3 suggests gene duplications in an ancestral pseudoautosomalregion. Hum. Molec. Genet. 5: 423- 431, 1996. 3 C b

GAM72 342 BPHL Puente, X. S.; Lopez- Otin, C.: Cloning and expression analysisof a novel human serine hydrolase with sequence similarity to prokaryoticenzymes involved in the degradation of aromatic compounds. J. Biol.Chem. 270: 12926- 12932, 1995. 3 C c

GAM72 342 BPHL Puente, X. S.; Pendas, A. M.; Lopez- Otin, C.: Structural characterizationand chromosomal localization of the gene encoding human biphenyl hydrolase- relatedprotein (BPHL). Genomics 51: 459- 462, 1998. 3 C c

GAM72 342 CASP10 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.; Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a novel human apoptotic cysteine protease containingtwo FADD- like domains. Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996. 3 C b

GAM72 342 CASP10 Park, W. S.; Lee, J. H.; Shin, M. S.; Park, J. Y.; Kim, H. S.;Lee, J. H.; Kim, Y. S.; Lee, S. N.; Xiao, W.; Park, C. H.; Lee, S.H.; Yoo, N. J.; Lee, J. Y.: Inactivating mutations of the caspase- 10gene in gastric cancer. Oncogene 21: 2919- 2925, 2002. 3 C b

GAM72 342 CASP10 Shin, M. S.; Kim, H. S.; Kang, C. S.; Park, W. S.; Kim, S. Y.;Lee, S. N.; Lee, J. H.; Park, J. Y.; Jang, J. J.; Kim, C. W.; Kim,S. H.; Lee, J. Y.; Yoo, N. J.; Lee, S. H.: Inactivating mutationsof CASP10 gene in non- Hodgkin lymphomas. Blood 99: 4094- 4099, 2002. 3 C b

GAM72 342 CASP10 Vincenz, C.; Dixit, V. M.: Fas- associated death domain proteininterleukin- 1- beta- converting enzyme 2 (FLICE2), an ICE/Ced- 3 homologue,is proximally involved in CD95- and p55- mediated death signaling. J.Biol. Chem. 272: 6578- 6583, 1997. 3 C b

GAM72 342 CASP10 Wang, J.; Chun, H. J.; Wong, W.; Spencer, D. M.; Lenardo, M. J.: Caspase- 10 is an initiator caspase in death receptor signaling. Proc.Nat. Acad. Sci. 98: 13884- 13888, 2001. 3 C b

GAM72 342 CASP10 Wang, J.; Zheng, L.; Lobito, A.; Chan, F. K.; Dale, J.; Sneller,M.; Yao, X.; Puck, J. M.; Straus, S. E.; Lenardo, M. J.: Inheritedhuman caspase 10 mutations underlie defective lymphocyte and dendriticcell apoptosis in autoimmune lymphoproliferative syndrome type II. Cell 98:47- 58, 1999. 3 C b

GAM72 342 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T. P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte activation caused by caspase- 8 mutations lead to humanimmunodeficiency. Nature 419: 395- 399, 2002. 3 C b

GAM72 342 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.; Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a novel human apoptotic cysteine protease containingtwo FADD- like domains. Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996. 3 C b

GAM72 342 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager, V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a 3 C b

novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM72 342 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 C b
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM72 342 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 C b
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell
death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM72 342 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 C b
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM72 342 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 C b
Caspase- 8 is required for cell death induced by expanded
polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM72 342 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 C b
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM72 342 CNGB1 Ardell, M. D.; Aragon, I.; Oliveira, L.; Porche, G. E.; Burke,E.; Pittler, 3 C b
S. J.: The beta subunit of human rod photoreceptor cGMP- gatedcation channel
is generated from a complex transcription unit. FEBSLett. 389: 213- 218,
1996.

GAM72 342 CNGB1 Ardell, M. D.; Makhija, A. K.; Oliveira, L.; Miniou, P.; Viegas- 3 C b
Pequignot,E.; Pittler, S. J.: cDNA, gene structure, and chromosomal
localizationof human GAR1 (CNCG3L), a homolog of the third subunit of bovine
photoreceptorcGMP- gated channel. Genomics 28: 32- 38, 1995.

GAM72 342 CNGB1 Bareil, C.; Hamel, C. P.; Delague, V.; Arnaud, B.; Demaille, J.;Claustres, 3 C b
M.: Segregation of a mutation in CNGB1 encoding the beta- subunitof the rod
cGMP- gated channel in a family with autosomal recessiveretinitis
pigmentosa. Hum. Genet. 108: 328- 334, 2001.

GAM72 342 CNGB1 Bird, A. C.: Retinal photoreceptor dystrophies. LI. Edward JacksonMemorial 3 C b
Lecture. Am. J. Ophthal. 119: 543- 562, 1995.

GAM72 342 CNGB1 Chen, T. Y.; Peng, Y. W.; Dhallan, R. S.; Ahamed, B.; Reed, R.R.; Yau, K. 3 C b
W.: A new subunit of the cyclic nucleotide- gated cationchannel in retinal
rods. Nature 362: 764- 767, 1993.

GAM72 342 CNGB1 Chen, T.- Y.; Illing, M.; Molday, L. L.; Hsu, Y.- T.; Yau, K.- W.;Molday, R. 3 C b
S.: Subunit 2 (or beta) of retinal rod cGMP- gated cationchannel is a
component of the 240- kDa channel- associated protein andmediates Ca(2+)-
calmodulin modulation. Proc. Nat. Acad. Sci. 91:11757- 11761, 1994.

GAM72 342 CNGB1 Korschen, H. G.; Beyermann, M.; Muller, F.; Heck, M.; Vantler,M.; Koch, K.- 3 C b
W.; Kellner, R.; Wolfrum, U.; Bode, C.; Hofmann, K. P.;Kaupp, U. B.:
Interaction of glutamic- acid- rich proteins with thecGMP signalling pathway
in rod photoreceptors. Nature 400: 761- 766,1999.

GAM72 342 CNGB1 Sugimoto, Y.; Yatsunami, K.; Tsujimoto, M.; Khorana, H. G.; Ichikawa,A.: The 3 C b
amino acid sequence of a glutamic acid- rich protein frombovine retina as
deduced from the cDNA sequence. Proc. Nat. Acad.Sci. 88: 3116- 3119, 1991.

GAM72 342 CPM Kas, K.; Schoenmakers, E. F. P. M.; Van de Ven, W. J. M.: Physicalmap 3 C b
location of the human carboxypeptidase M gene (CPM) distal toD12S375 and
proximal to D12S8 at chromosome 12q15. Genomics 30:403- 405, 1995.

GAM72 342 CPM Rehli, M.; Krause, S. W.; Kreutz, M.; Andreesen, R.: CarboxypeptidaseM is 3 C b
identical to the MAX.1 antigen and its expression is associatedwith monocyte
to macrophage differentiation. J. Biol. Chem. 270:15644- 15649, 1995.

GAM72 342 CPM Tan, F.; Chan, S. J.; Steiner, D. F.; Schilling, J. W.; Skidgel,R. A.: 3 C b
Molecular cloning and sequencing of the cDNA for human membrane-
boundcarboxypeptidase M: comparison with carboxypeptidases A, B, H, andN. J.
Biol. Chem. 264: 13165- 13170, 1989.

GAM72 342 CROT Ferdinandusse, S.; Mulders, J.; IJlst, L.; Denis, S.; Dacremont,G.; 3 C b
Waterham, H. R.; Wanders, R. J. A.: Molecular cloning and expressionof human
carnitine octanoyltransferase: evidence for its role in theperoxisomal beta-
oxidation of branched- chain fatty acids. Biochem.Biophys. Res. Commun. 263:
213- 218, 1999.

GAM72 342 CROT van der Leij, F. R.; Huijkman, N. C. A.; Boomsma, C.; Kuipers,J. R. G.; 3 C b
Bartelds, B.: Genomics of the human carnitine acyltransferasegenes. Molec.
Genet. Metab. 71: 139- 153, 2000.

GAM72 342 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; 3 C b
Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H,
L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245,
1997.

GAM72 342 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; 3 C b
Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S
controls the trafficking and maturation of MHC class IImolecules in
dendritic cells. J. Cell Biol. 147: 775- 790, 1999.

GAM72 342 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. 3 C b
J.; Chapman, H. A.: Structure and chromosomal assignmentof the human
cathepsin K gene. Genomics 41: 258- 262, 1997.

GAM72 342 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; 3 C b
Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.;
Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell
selection and maturation by cathepsin S. Immunity 15:909- 919, 2001.

GAM72 342 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: 3 C b
Molecular cloning and expression of human alveolar macrophagecathepsin S, an
elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992.

GAM72 342 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; 3 C b
Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization,
gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536,
1994.

GAM72 342 CYP3A4 Brooks, B. A.; McBride, O. W.; Dolphin, C. T.; Farrall, M.; Scambler,P. J.; 3 C b
Gonzalez, F. J.; Idle, J. R.: The gene CYP3 encoding P450PCN1(nifedipine
oxidase) is tightly linked to the gene COL1A2 encodingcollagen type 1 alpha
on 7q21- q22.1. Am. J. Hum. Genet. 43: 280- 284,1988.

GAM72 342 CYP3A4 Chen, H.; Sandler, D. P.; Taylor, J. A.; Shore, D. L.; Liu, E.;Bloomfield, 3 C b
C. D.; Bell, D. A.: Increased risk for myelodysplasticsyndromes in
individuals with glutathione transferase theta 1 (GSTT1)gene defect. Lancet
347: 295- 297, 1996.

GAM72 342 CYP3A4 Daly, A. K.; Salh, B. S.; Bilton, D.; Allen, J.; Knight, A. D.;Webb, A. K.; 3 C b
Braganza, J. M.; Idle, J. R.: Deficient nifedipine oxidation:a rare
inherited trait associated with cystic fibrosis kindreds. Pharmacogenetics
2:19- 24, 1992.

GAM72 342 CYP3A4 Elshourbagy, N. A.; Guzelian, P. S.: Separation, purification,and 3 C b

characterization of a novel form of hepatic cytochrome P- 450 fromrats treated with pregnenolone- 16- alpha- carbonitrile. J. Biol. Chem. 255:1279-1285, 1980.

GAM72 342 CYP3A4 Felix, C. A.; Walker, A. H.; Lange, B. J.; Williams, T. M.; Winick,N. J.; Cheung, N.- K. V.; Lovett, B. D.; Nowell, P. C.; Blair, I. A.;Rebbeck, T. R.: Association of CYP3A4 genotype with treatment- relatedleukemia. Proc. Nat. Acad. Sci. 95: 13176- 13181, 1998. 3 C b

GAM72 342 CYP3A4 Forrester, L. M.; Neal, G. E.; Judah, D. J.; Glancey, M. J.; Wolf,C. R.: Evidence for involvement of multiple forms of cytochrome P- 450in aflatoxin B(1) metabolism in human liver. Proc. Nat. Acad. Sci. 87:8306- 8310, 1990. 3 C b

GAM72 342 CYP3A4 Gonzalez, F. J.; Schmid, B. J.; Umeno, M.; McBride, O. W.; Hardwick,J. P.; Meyer, U. A.; Gelboin, H. V.; Idle, J. R.: Human P450PCN1:sequence, chromosome localization, and direct evidence through cDNAexpression that P450PCN1 is nifedipine oxidase. DNA 7: 79- 86, 1988. 3 C b

GAM72 342 CYP3A4 Hoyo- Vadillo, C.; Castaneda- Hernandez, G.; Herrera, J. E.; Vidal-Garate,J.; Moreno- Ramos, A.; Chavez, F.; Hong, E.: Pharmacokinetics of nifedipineslow release tablet in Mexican subjects: further evidence for an oxidationpolymorphism. J. Clin. Pharm. 29: 816- 820, 1989. 3 C b

GAM72 342 CYP3A4 Inoue, K.; Inazawa, J.; Nakagawa, H.; Shimada, T.; Yamazaki, H.;Guengerich, F. P.; Abe, T.: Assignment of the human cytochrome P- 450nifedipine oxidase gene (CYP3A4) to chromosome 7 at band q22.1 byfluorescence in situ hybridization. Jpn. J. Hum. Genet. 37: 133- 138,1992. 3 C b

GAM72 342 CYP3A4 Kittles, R. A.; Chen, W.; Panguluri, R. K.; Ahaghotu, C.; Jackson,A.; Adebamowo, C. A.; Griffin, R.; Williams, T.; Ukoli, F.; Adams- Campbell,L.; Kwagyan, J.; Isaacs, W.; Freeman, V.; Dunston, G. M.: CYP3A4- Vand prostate cancer in African Americans: causal or confounding associationbecause of population stratification? Hum. Genet. 110: 553- 560,2002. 3 C b

GAM72 342 CYP3A4 Kleinbloesem, C. H.; van Brummelen, P.; Faber, H.; Danhof, M.;Vermeulen, N. P. E.; Breimer, D. D.: Variability in nifedipine pharmacokineticsand dynamics: a new oxidation polymorphism in man. Biochem. Pharm. 33:3721-3724, 1984. 3 C b

GAM72 342 CYP3A4 Lehmann, J. M.; McKee, D. D.; Watson, M. A.; Willson, T. M.; Moore,J. T.; Kliewer, S. A.: The human orphan nuclear receptor PXR is activatedby compounds that regulate CYP3A4 gene expression and cause drug interactions. J.Clin. Invest. 102: 1016- 1023, 1998. 3 C b

GAM72 342 CYP3A4 Lown, K. S.; Bailey, D. G.; Fontana, R. J.; Janardan, S. K.; Adair,C. H.; Fortlage, L. A.; Brown, M. B.; Guo, W.; Watkins, P. B.: Grapefruitjuice increases felodipine oral availability in humans by decreasingintestinal CYP3A protein expression. J. Clin. Invest. 99: 2545- 2553,1997. 3 C b

GAM72 342 CYP3A4 Molowa, D. T.; Schuetz, E. G.; Wrighton, S. A.; Watkins, P. B.;Kremers, P.; Mendez- Picon, G.; Parker, G. A.; Guzelian, P. S.: CompletecDNA sequence of a cytochrome P- 450 inducible by glucocorticoids inhuman liver. Proc. Nat. Acad. Sci. 83: 5311- 5315, 1986. 3 C b

GAM72 342 CYP3A4 Nebert, D. W.; Gonzalez, F. J.: P450 genes: structure, evolution,and regulation. Annu. Rev. Biochem. 56: 945- 993, 1987. 3 C b

GAM72 342 CYP3A4 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 3 C b

GAM72 342 CYP3A4 Paris, P. L.; Kupelian, P. A.; Hall, J. M.; Williams, T. L.; Levin,H.; Klein, E. A.; Casey, G.; Witte, J. S.: Association between aCYP3A4 genetic 3 C b

variant and clinical presentation in African- Americanprostate cancer patients. Cancer Epidemiol. Biomarkers Prev. 8:901- 905, 1999.

GAM72 342 CYP3A4 Rebbeck, T. R.; Jaffe, J. M.; Walker, A. H.; Wein, A. J.; Malkowicz,S. B.: 3 C b Modification of clinical presentation of prostate tumors bya novel genetic variant in CYP3A4. J. Nat. Cancer Inst. 90: 1225- 1229,1998.

GAM72 342 CYP3A4 Renwick, A. G.; Robertson, D. R. C.; Macklin, B.; Challenor, V.;Waller, D. 3 C b G.; George, C. F.: The pharmacokinetics of oral nifedipine- - apopulation study. Brit. J. Clin. Pharm. 25: 701- 708, 1988.

GAM72 342 CYP3A4 Riddell, D. C.; Wang, H.; Umbenhauer, D. R.; Beaume, P. H.; Guengerich,F. 3 C b P.; Hamerton, J. L.: Regional assignment for the genes encodinghuman P450IIIA3 (CYP3) and P450IIC9 (CYP2C). (Abstract) Cytogenet.Cell Genet. 46: 682, 1987.

GAM72 342 CYP3A4 Schellens, J. H. M.; Soons, P. A.; Breimer, D. D.: Lack of bimodalityin 3 C b nifedipine plasma kinetics in a large population of healthy subjects. Biochem.Pharm. 37: 2507- 2510, 1988.

GAM72 342 CYP3A4 Shet, M. S.; Fisher, C. W.; Holmans, P. L.; Estabrook, R. W.:Human 3 C b cytochrome P450 3A4: enzymatic properties of a purified recombinantfusion protein containing NADPH- P450 reductase. Proc. Nat. Acad.Sci. 90: 11748- 11752, 1993.

GAM72 342 CYP3A4 Shimada, T.; Guengerich, F. P.: Evidence for cytochrome P- 450(NF),the 3 C b nifedipine oxidase, being the principal enzyme involved in thebioactivation of aflatoxins in human liver. Proc. Nat. Acad. Sci. 86:462- 465, 1989.

GAM72 342 CYP3A4 Spurr, N. K.; Gough, A. C.; Stevenson, K.; Wolf, C. R.: The humancytochrome 3 C b P450 CYP3 locus: assignment to chromosome 7q22- qter. Hum.Genet. 81: 171- 174, 1989.

GAM72 342 CYP3A4 Walker, A. H.; Jaffe, J. M.; Gunasegaram, S.; Cummings, S. A.;Huang, C.- S.; 3 C b Chern, H.- D.; Olopade, O. I.; Weber, B. L.; Rebbeck,T. R.: Characterization of an allelic variant in the nifedipine- specificelement of CYP3A4: ethnic distribution and implications for prostatecancer risk. Hum. Mutat. 12: 289- 293, 1998.

GAM72 342 CYP3A4 Watkins, P. B.; Wrighton, S. A.; Maurel, P.; Schuetz, E. G.; Mendez- 3 C b Picon,G.; Parker, G. A.; Guzelian, P. S.: Identification of an inducibleform of cytochrome P- 450 in human liver. Proc. Nat. Acad. Sci. 82:6310- 6314, 1985.

GAM72 342 CYP3A4 Wolf, C. R.; Smith, C. A. D.; Gough, A. C.; Moss, J. E.; Vallis,K. A.; 3 C b Howard, G.; Carey, F. J.; Mills, K.; McNee, W.; Carmichael,J.; Spurr, N. K.: Relationship between the debrisoquine hydroxylasepolymorphism and cancer susceptibility. Carcinogenesis 13: 1035- 1038,1992.

GAM72 342 CYP3A4 Wrighton, S. A.; Stevens, J. C.: The human hepatic cytochromesP450 involved 3 C b in drug metabolism. Crit. Rev. Toxicol. 22: 1- 21,1992.

GAM72 342 CYP3A4 Wrighton, S. A.; Vandenbranden, M.: Isolation and characterizationof human 3 C b fetal liver cytochrome P450HLp2: a third member of the P450IIIgene family. Arch. Biochem. Biophys. 268: 144- 151, 1989.

GAM72 342 CYP3A4 Xie, W.; Barwick, J. L.; Downes, M.; Blumberg, B.; Simon, C. M.;Nelson, M. 3 C b C.; Neuschwander- Tetri, B. A.; Brunt, E. M.; Guzelian,P. S.; Evans, R. M.: Humanized xenobiotic response in mice expressingnuclear receptor SXR. Nature 406: 435- 439, 2000.

GAM72 342 DAPP1 Dowler, S.; Currie, R. A.; Downes, C. P.; Alessi, D. R.: DAPP1:a dual 3 C b adaptor for phosphotyrosine and 3- phosphoinositides. Biochem.J. 342: 7- 12, 1999.

GAM72 342 DAPP1 Marshall, A. J.; Niiro, H.; Lerner, C. G.; Yun, T. J.; Thomas,S.; Disteche, 3 C b
C. M.; Clark, E. A.: A novel B lymphocyte- associatedadaptor protein, Bam32,
regulates antigen receptor signaling downstreamof phosphatidylinositol 3-
kinase. J. Exp. Med. 191: 1319- 1331, 2000.

GAM72 342 DCLRE1C Ma, Y.; Pannicke, U.; Schwarz, K.; Lieber, M. R.: Hairpin openingand 3 C c
overhang processing by an Artemis/DNA- dependent protein kinasecomplex in
nonhomologous end joining and V(D)J recombination. Cell 108:781- 794, 2002.

GAM72 342 DCLRE1C Moshous, D.; Callebaut, I.; de Chasseval, R.; Corneo, B.; Cavazzana- 3 C c
Calvo,M.; Le Deist, F.; Tezcan, I.; Sanal, O.; Bertrand, Y.; Philippe,
N.;Fischer, A.; de Villartay, J.- P.: Artemis, a novel DNA double-
strandbreak repair/V(D)J recombination protein, is mutated in human
severecombined immune deficiency. Cell 105: 177- 186, 2001.

GAM72 342 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. 3 C b
W.: Chromosomal localization and racial distributionof the polymorphic human
dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352,
1988.

GAM72 342 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel 3 C b
form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies
three RFLPs. Nucleic Acids Res. 15: 5501 only,1987.

GAM72 342 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: 3 C b
Chromosomal localization and racial distribution of the polymorphichDHFR-
psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985.

GAM72 342 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; 3 C b
Nienhuis, A. W.: Chromosomal organization of the human
dihydrofolatereductase genes: dispersion, selective amplification and a
novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984.

GAM72 342 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in 3 C b
dihydrofolatereductase that confer resistance to methotrexate: potential for
clinicalapplication. Hum. Mutat. 11: 259- 263, 1998.

GAM72 342 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: 3 C b
Intronless human dihydrofolate reductase genes are derivedfrom processed RNA
molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982.

GAM72 342 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association 3 C b
with variation in protein structure. Science 220: 1125- 1129,1983.

GAM72 342 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 3 C b
757 and 807- 812, 1975.

GAM72 342 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the 3 C b
human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5.
Molec. Cell. Biol. 4: 2010- 2016, 1984.

GAM72 342 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater- 3 C b
Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed
ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med.
310: 789- 790, 1984.

GAM72 342 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment 3 C b
of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus
musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986.

GAM72 342 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: 3 C b
Human dihydrofolate reductase gene is located in chromosome 5and is unlinked
to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984.

GAM72 342 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human 3 C b

dihydrofolate reductase gene to band q23 of chromosome 5and of related pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85, 1985.

GAM72 342 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; 3 C b Attardi, G.: Chromosomal location of the normal human DHFRgene and of its amplified copies in methotrexate resistant cell variants.(Abstract) Cytogenet. Cell Genet. 37: 534 only, 1984.

GAM72 342 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 3 C b 10/7/1983.

GAM72 342 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: 3 C b Amplification of the human dihydrofolate reductase gene viadouble minutes is initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000.

GAM72 342 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. 3 C b A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976.

GAM72 342 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)- 3 C b formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967.

GAM72 342 DNASE2 Brook, J. D.; Shaw, D. J.; Meredith, A. L.; Bruns, G. A. P.; Harper,P. S.: 3 C b Localisation of genetic markers and orientation of the linkagegroup on chromosome 19. Hum. Genet. 68: 282- 285, 1984.

GAM72 342 DNASE2 Bruns, G. A. P.; Regina, V. M.; Gerald, P. S.: Lysosomal DNaseand chromosome 3 C b

19.(Abstract) J. Cell Biol. 83: 444a only, 1979.

GAM72 342 DNASE2 Kawane, K.; Fukuyama, H.; Kondoh, G.; Takeda, J.; Ohsawa, Y.; Uchiyama,Y.; 3 C b Nagata, S.: Requirement of DNase II for definitive erythropoiesisin the mouse fetal liver. Science 292: 1546- 1549, 2001.

GAM72 342 DNASE2 Yasuda, T.; Nadano, D.; Sawazaki, K.; Kishi, K.: Genetic polymorphismof 3 C b human deoxyribonuclease II (DNase II): low activity levels in urineand leukocytes are due to an autosomal recessive allele. Ann. Hum.Genet. 56: 1- 10, 1992.

GAM72 342 DNASE2 Yasuda, T.; Takeshita, H.; Iida, R.; Nakajima, T.; Hosomi, O.;Nakashima, Y.; 3 C b Kishi, K.: Molecular cloning of the cDNA encodinghuman deoxyribonuclease II. J. Biol. Chem. 273: 2610- 2616, 1998.

GAM72 342 DNASE2 Yasuda, T.; Takeshita, H.; Iida, R.; Nakajima, T.; Hosomi, O.;Nakashima, Y.; 3 C b Mogi, K.; Kishi, K.: Chromosomal localization of ahuman deoxyribonuclease II gene (DNASE2) to 19p13.2- p13.1 using boththe polymerase chain reaction and fluorescence in situ hybridizationanalysis. Biochem. Biophys. Res. Commun. 244: 815- 818, 1998.

GAM72 342 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 C b Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998.

GAM72 342 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 C b M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000.

GAM72 342 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 C b Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001.

GAM72 342 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; 3 C b Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad.

Sci. 95: 6642- 6646, 1998.

GAM72 342 FGF2 Abraham, J. A.; Mergia, A.; Whang, J. L.; Tumolo, A.; Friedman,J.; Hjerild, 3 C c
K. A.; Gospodarowicz, D.; Fiddes, J. C.: Nucleotidesequence of a bovine
clone encoding the angiogenic protein, basicfibroblast growth factor.
Science 233: 545- 548, 1986.

GAM72 342 FGF2 Abraham, J. A.; Whang, J. L.; Tumolo, A.; Mergia, A.; Friedman,J.; 3 C c
Gospodarowicz, D.; Fiddes, J. C.: Human basic fibroblast growthfactor:
nucleotide sequence and genomic organization. EMBO J. 5:2523- 2528, 1986.

GAM72 342 FGF2 Doniach, T.: Basic FGF as an inducer of anteroposterior neuralpattern. Cell 3 C c
83: 1067- 1070, 1995.

GAM72 342 FGF2 Dono, R.; Texido, G.; Dussel, R.; Ehmke, H.; Zeller, R.: Impairedcerebral 3 C c
cortex development and blood pressure regulation in FGF2- deficientmice.
EMBO J. 17: 4213- 4225, 1998.

GAM72 342 FGF2 Eckenstein, F. P.: Fibroblast growth factors in the nervous system. 3 C c
J.Neurobiol. 25: 1467- 1480, 1994.

GAM72 342 FGF2 Fukushima, Y.; Byers, M. G.; Fiddes, J. C.; Shows, T. B.: Thehuman basic 3 C c
fibroblast growth factor gene (FGFB) is assigned to chromosome4q25.
Cytogenet. Cell Genet. 54: 159- 160, 1990.

GAM72 342 FGF2 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; 3 C c
Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast
growth factor homologous factor 2 (FHF2): gene structure,expression and
mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated
by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63,
1999.

GAM72 342 FGF2 Gritti, A.; Parati, E. A.; Cova, L.; Frolichsthal, P.; Galli, R.;Wanke, E.; 3 C c
Faravelli, L.; Morassutti, D. J.; Roisen, F.; Nickel, D.D.; Vescovi, A. L.:
Multipotential stem cells from the adult mousebrain proliferate and self-
renew in response to basic fibroblast growthfactor. J. Neurosci. 16: 1091-
1100, 1996.

GAM72 342 FGF2 Johnson, R. L.; Tabin, C. J.: Molecular models for vertebratelimb 3 C c
development. Cell 90: 979- 990, 1997.

GAM72 342 FGF2 Jung, J.; Zheng, M.; Goldfarb, M.; Zaret, K. S.: Initiation ofmammalian 3 C c
liver development from endoderm by fibroblast growth factors. Science
284:1998- 2003, 1999.

GAM72 342 FGF2 Kawaguchi, H.; Nakamura, K.; Tabata, Y.; Ikada, Y.; Aoyama, I.;Anzai, J.; 3 C c
Nakamura, T.; Hiyama, Y.; Tamura, M.: Acceleration offracture healing in
nonhuman primates by fibroblast growth factor- 2. J.Clin. Endocr. Metab. 86:
875- 880, 2001.

GAM72 342 FGF2 Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.: Cloning andexpression of 3 C c
cDNA encoding human basic fibroblast growth factor. FEBSLett. 213: 189- 194,
1987.

GAM72 342 FGF2 Lafage- Pochitaloff, M.; Galland, F.; Simonetti, J.; Prats, H.;Mattei, M.- 3 C c
G.; Birnbaum, D.: The human basic fibroblast growth factorgene is located on
the long arm of chromosome 4 at bands q26- q27. OncogeneRes. 5: 241- 244,
1990.

GAM72 342 FGF2 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; 3 C c
Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21
by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997.

GAM72 342 FGF2 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 3 C c
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM72 342 FGF2 Mergia, A.; Eddy, R.; Abraham, J. A.; Fiddes, J. C.; Shows, T.B.: The genes for basic and acidic fibroblast growth factors areon different human chromosomes. Biochem. Biophys. Res. Commun. 138:644- 651, 1986. 3 C c

GAM72 342 FGF2 Montero, A.; Okada, Y.; Tomita, M.; Ito, M.; Tsurukami, H.; Nakamura,T.; Doetschman, T.; Coffin, J. D.; Hurley, M. M.: Disruption of thefibroblast growth factor- 2 gene results in decreased bone mass andbone formation. J. Clin. Invest. 105: 1085- 1093, 2000. 3 C c

GAM72 342 FGF2 Ortega, S.; Ittmann, M.; Tsang, S. H.; Ehrlich, M.; Basilico,C.: Neuronal defects and delayed wound healing in mice lacking fibroblastgrowth factor 2. Proc. Nat. Acad. Sci. 95: 5672- 5677, 1998. 3 C c

GAM72 342 FGF2 Plotnikov, A. N.; Hubbard, S. R.; Schlessinger, J.; Mohammadi,M.: Crystal structures of two FGF- FGFR complexes reveal the determinantsof ligand-receptor specificity. Cell 101: 413- 424, 2000. 3 C c

GAM72 342 FGF2 Plotnikov, A. N.; Schlessinger, J.; Hubbard, S. R.; Mohammadi,M.: Structural basis for FGF receptor dimerization and activation. Cell 98:641- 650, 1999. 3 C c

GAM72 342 FGF2 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast growth factor (FGF) homologous factors: new membersof the FGF family implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850-9857, 1996. 3 C c

GAM72 342 FLRT2 Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VIII. 78 new cDNAclones from brain which code for large proteins in vitro. DNA Res. 4:307- 313, 1997. 3 C c

GAM72 342 FLRT2 Lacy, S. E.; Bonnemann, C. G.; Buzney, E. A.; Kunkel, L. M.: Identificationof FLRT1, FLRT2, and FLRT3: a novel family of transmembrane leucine- richrepeat proteins. Genomics 62: 417- 426, 1999. 3 C c

GAM72 342 GALNT3 Bennett, E. P.; Hassan, H,.; Clausen, H.: cDNA cloning and expressionof a novel human UDP- N- acetyl- alpha- D- galactosamine. J. Biol. Chem. 271:17006- 17012, 1996. 3 C b

GAM72 342 GALNT3 Bennett, E. P.; Weghuis, D. O.; Merkx, G.; Geurts van Kessel, A.;Eiberg, H.; Clausen, H.: Genomic organization and chromosomal localizationof three members of the UDP- N- acetylgalactosamine:polypeptide N-acetylgalactosaminyltransferasefamily. Glycobiology 8: 547- 555, 1998. 3 C b

GAM72 342 GALNT3 Zara, J.; Hagen, F. K.; Ten Hagen, K. G.; Van Wuyckhuyse, B. C.;Tabak, L. A.: Cloning and expression of mouse UDP- GalNAc:polypeptideN-acetylgalactosaminyltransferase- T3. Biochem. Biophys. Res. Commun. 228:38-44, 1996. 3 C b

GAM72 342 GAS7 Ju, Y.- T.; Chang, A. C. Y.; She, B.- R.; Tsaur, M.- L.; Hwang, H.- M.;Chao, C. C.- K.; Cohen, S. N.; Lin- Chao, S.: Gas7: a gene expressedpreferentially in growth- arrested fibroblasts and terminally differentiatedPurkinje neurons affects neurite formation. Proc. Nat. Acad. Sci. 95:11423- 11428, 1998. 3 C b

GAM72 342 GAS7 Kurtz, A.; Zimmer, A.: Interspecies fluorescence in situ hybridizationfurther defines synteny homology between mouse chromosome 11 and humanchromosome 17. Mammalian Genome 6: 379- 380, 1995. 3 C b

GAM72 342 GAS7 Megonigal, M. D.; Cheung, N.- K. V.; Rappaport, E. F.; Nowell, P.C.; Wilson, R. B.; Jones, D. H.; Addya, K.; Leonard, D. G. B.; Kushner,B. H.; Williams, T. M.; Lange, B. J.; Felix, C. A.: Detection ofleukemia- associated MLL-GAS7 translocation early during chemotherapywith DNA topoisomerase II 3 C b

inhibitors. Proc. Nat. Acad. Sci. 97:2814- 2819, 2000.

GAM72 342 GPRK7 Chen, C.- K.; Zhang, K.; Church- Kopish, J.; Huang, W.; Zhang, H.;Chen, Y.- 3 C b
J.; Frederick, J. M.; Baehr, W.: Characterization of humanGRK7 as a
potential cone opsin kinase. Molec. Vision 7: 305- 313,2001.

GAM72 342 GPRK7 Haribabu, B.; Snyderman, R.: Identification of additional membersof human G- 3 C b
protein- coupled receptor kinase multigene family. Proc.Nat. Acad. Sci. 90:
9398- 9402, 1993.

GAM72 342 GPRK7 Slentz- Kesler, K.; Moore, J. T.; Lombard, M.; Zhang, J.; Hollingsworth,R.; 3 C b
Weiner, M. P.: Identification of the human Mnk2 gene (MKNK2)through protein
interaction with estrogen receptor beta. Genomics 69:63- 71, 2000.

GAM72 342 GPRK7 Waskiewicz, A. J.; Flynn, A.; Proud, C. G.; Cooper, J. A.: Mitogen- 3 C b
activatedprotein kinases activate the serine/threonine kinases Mnk1 and
Mnk2. EMBOJ. 16: 1909- 1920, 1997.

GAM72 342 GPRK7 Weiss, E. R.; Ducceschi, M. H.; Horner, T. J.; Li, A.; Craft, C.M.; Osawa, 3 C b
S.: Species- specific differences in expression of G- protein-
coupledreceptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor
cells:implications for cone cell phototransduction. J. Neurosci. 21: 9175-
9184,2001.

GAM72 342 HIP1 Chopra, V. S.; Metzler, M.; Rasper, D. M.; Engqvist- Goldstein,A. E. Y.; 3 C b
Singaraja, R.; Gan, L.; Fichter, K. M.; McCutcheon, K.;Drubin, D.;
Nicholson, D. W.; Hayden, M. R.: HIP12 is a non- proapoptoticmember of a
gene family including HIP1, an interacting protein withhuntingtin. Mammalian
Genome 11: 1006- 1015, 2000.

GAM72 342 HIP1 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 C b
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM72 342 HIP1 Hackam, A. S.; Yassa, A. S.; Singaraja, R.; Metzler, M.; Gutekunst,C.- A.; 3 C b
Gan, L.; Warby, S.; Wellington, C. L.; Vaillancourt, J.; Chen,N.; Gervais,
F. G.; Raymond, L.; Nicholson, D. W.; Hayden, M. R.:Huntingtin interacting
protein 1 induces apoptosis via a novel caspase- dependentdeath effector
domain. J. Biol. Chem. 275: 41299- 41308, 2000.

GAM72 342 HIP1 Himmelbauer, H.; Wedemeyer, N.; Haaf, T.; Wanker, E. E.; Schalkwyk,L. C.; 3 C b
Lehrach, H.: IRS- PCR- based genetic mapping of the huntingtininteracting
protein gene (HIP1) on mouse chromosome 5. MammalianGenome 9: 26- 31, 1998.

GAM72 342 HIP1 Kalchman, M. A.; Koide, H. B.; McCutcheon, K.; Graham, R. K.; Nichol,K.; 3 C b
Nishiyama, K.; Kazemi- Esfarjani, P.; Lynn, F. C.; Wellington,C.; Metzler,
M.; Goldberg, Y. P.; Kanazawa, I.; Gietz, R. D.; Hayden,M. R.: HIP1, a human
homologue of S. cerevisiae Slap2, interactswith membrane- associated
huntingtin in the brain. Nature Genet. 16:44- 53, 1997.

GAM72 342 HIP1 Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof 3 C b
Huntingtin interacting protein 1 to platelet- derived growth factor-
betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with
t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998.

GAM72 342 HIP1 Waelter, S.; Scherzinger, E.; Hasenbank, R.; Nordhoff, E.; Lurz,R.; Goehler, 3 C b
H.; Gauss, C.; Sathasivam, K.; Bates, G. P.; Lehrach,H.; Wanker, E. E.: The
huntingtin interacting protein HIP1 is a clathrinand alpha- adaptin- binding
protein involved in receptor- mediated endocytosis. Hum.Molec. Genet. 10:
1807- 1817, 2001.

GAM72 342 HIP1 Wanker, E. E.; Rovira, C.; Scherzinger, E.; Hasenbank, R.; Walter,S.; Tait, 3 C b
D.; Colicelli, J.; Lehrach, H.: HIP- I: a huntingtin interactingprotein
isolated by the yeast two- hybrid system. Hum. Molec. Genet. 6:487- 495,
1997.

GAM72 342 HIP1 Wedemeyer, N.; Peoples, R.; Himmelbauer, H.; Lehrach, H.; Francke,U.; 3 C b
Wanker, E. E.: Localization of the human HIP1 gene close to theelastin (ELN)
locus on 7q11.23. Genomics 46: 313- 315, 1997.

GAM72 342 HLA-E Braud, V. M.; Allan, D. S. J.; O'Callaghan, C. A.; Soderstrom,K.; D'Andrea, 3 C b
A.; Ogg, G. S.; Lazetic, S.; Young, N. T.; Bell, J.I.; Phillips, J. H.;
Lanier, L. L.; McMichael, A. J.: HLA- E bindsto natural killer cell
receptors CD94/NKG2A, B and C. Nature 391:795- 799, 1998.

GAM72 342 HLA-E Carroll, M. C.; Katzman, P.; Alicot, E. M.; Koller, B. H.; Geraghty,D. E.; 3 C b
Orr, H. T.; Strominger, J. L.; Spies, T.: Linkage map of thehuman major
histocompatibility complex including the tumor necrosisfactor genes. Proc.
Nat. Acad. Sci. 84: 8535- 8539, 1987.

GAM72 342 HLA-E O'Callaghan, C. A.; Tormo, J.; Willcox, B. E.; Braud, V. M.; Jakobsen,B. K.; 3 C b
Stuart, D. I.; McMichael, A. J.; Bell, J. I.; Jones, E. Y.: Structural
features impose tight peptide binding specificity inthe nonclassical MHC
molecule HLA- E. Molec. Cell 1: 531- 541, 1998.

GAM72 342 HLA-E Ohya, K.; Kondo, K.; Mizuno, S.: Polymorphism in the human classl MHC locus 3 C b
HLA- E in Japanese. Immunogenetics 32: 205- 209, 1990.

GAM72 342 HLA-E Orr, H. T.: Personal Communication. Minneapolis, Minn. 1/30/1988. 3 C b

GAM72 342 HSPA5 Hendershot, L. M.; Valentine, V. A.; Lee, A. S.; Morris, S. W.;Shapiro, D. 3 C c
N.: Localization of the gene encoding human BiP/GRP78,the endoplasmic
reticulum cognate of the HSP70 family, to chromosome9q34. Genomics 20: 281-
284, 1994.

GAM72 342 HSPA5 Law, M. L.; Seeliger, M. B.; Lee, A. S.; Kao, F. T.: Genetic mappingof the 3 C c
structural gene coding for a glucose- regulated protein (GRP78)of 78k-
dalton to the long arm of human chromosome 9. (Abstract) Cytogenet.Cell
Genet. 37: 518- 519, 1984.

GAM72 342 HSPA5 Lee, A. S.; Delegeane, A. M.; Baker, V.; Chow, P. C.: 3 C c
Transcriptionalregulation of two genes specifically induced by glucose
starvationin hamster mutant fibroblast cell line. J. Biol. Chem. 258: 597-
603,1983.

GAM72 342 HSPA5 Lee, A. S.; Delegeane, A.; Scharff, D.: Highly conserved glucose- 3 C c
regulatedprotein in hamster and chicken cells: preliminary
characterizationof its cDNA clone. Proc. Nat. Acad. Sci. 78: 4922- 4925,
1981.

GAM72 342 HSPA5 Muresan, Z.; Arvan, P.: Enhanced binding to the molecular chaperoneBiP slows 3 C c
thyroglobulin export from the endoplasmic reticulum. Molec.Endocr. 12: 458-
467, 1998.

GAM72 342 HSPA5 Womack, J. E.: Personal Communication. College Station, Texas 2/26/1990. 3 C c

GAM72 342 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 C b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM72 342 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 C b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM72 342 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 C b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814-
819, 1992.

GAM72 342 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 C b

R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang, Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell-derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87: 7512- 7516, 1990.

GAM72 342 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract) Cytogenet.Cell Genet. 58: 2027 only, 1991. 3 C b

GAM72 342 IL13RA1 Aman, M. J.; Tayebi, N.; Obiri, N. I.; Puri, R. K.; Modi, W. S.;Leonard, W. J.: cDNA cloning and characterization of the human interleukin13 receptor alpha chain. J. Biol. Chem. 271: 29265- 29270, 1996. 3 C c

GAM72 342 IL13RA1 Guo, J.; Apiou , F.; Mellerin, M.- P.; Lebeau, B.; Jacques, Y.;Minvielle, S.: Chromosome mapping and expression of the human interleukin- 13receptor. Genomics 42: 141- 5, 1997. 3 C c

GAM72 342 IL13RA1 Heinzmann, H.; Mao, X.- Q.; Akaiwa, M.; Kreomer, R. T.; Gao, P.- S.;Ohshima, K.; Umeshita, R.; Abe, Y.; Braun, S.; Yamashita, T.; Roberts,M. H.; Sugimoto, R.; and 20 others: Genetic variants of IL- 13 signallingand human asthma and atopy. Hum. Molec. Genet. 9: 549- 559, 2000. 3 C c

GAM72 342 IL13RA1 Hilton, D. J.; Zhang, J.- G.; Metcalf, D.; Alexander, W. S.; Nicola,N. A.; Willson, T. A.: Cloning and characterization of a bindingsubunit of the interleukin 13 receptor that is also a component ofthe interleukin 4 receptor. Proc. Nat. Acad. Sci. 93: 497- 501, 1996. 3 C c

GAM72 342 IL13RA1 Zurawski, S. M.; Vega, F., Jr.; Huyghe, B.; Zurawski, G.: Receptorsfor interleukin- 13 and interleukin- 4 are complex and share a novelcomponent that functions in signal transduction. EMBO J. 12: 2663- 2670,1993. 3 C c

GAM72 342 IL18 Corbaz, A.; ten Hove, T.; Herren, S.; Graber, P.; Schwartsburd,B.; Belzer, I.; Harrison, J.; Plitz, T.; Kosco- Vilbois, M. H.; Kim,S.- H.; Dinarello, C. A.; Novick, D.; van Deventer, S.; Chvatchko,Y.: IL- 18- binding protein expression by endothelial cells and macrophagesis up- regulated during active Crohn's disease. J. Immun. 168: 3608- 3616,2002. 3 C b

GAM72 342 IL18 Konishi, H.; Tsutsui, H.; Murakami, T.; Yumikura- Futatsugi, S.;Yamanaka, K.; Tanaka, M.; Iwakura, Y.; Suzuki, N.; Takeda, K.; Akira,S.; Nakanishi, K.; Mizutani, H.: IL- 18 contributes to the spontaneousdevelopment of atopic dermatitis- like inflammatory skin lesion independentlyof IgE/stat6 under specific pathogen- free conditions. Proc. Nat.Acad. Sci. 99: 11340- 11345, 2002. 3 C b

GAM72 342 IL18 Nolan, K. F.; Greaves, D. R.; Waldmann, H.: The human interleukin18 gene IL18 maps to 11q22.2- q22.3, closely linked to the DRD2 genelocus and distinct from mapped IDDM loci. Genomics 51: 161- 163,1998. 3 C b

GAM72 342 IL18 Okamoto, I.; Kohno, K.; Tanimoto, T.; Iwaki, K.; Ishihara, T.;Akamatsu, S.; Ikegami, H.; Kurimoto, M.: IL- 18 prevents the developmentof chronic graft-versus- host disease in mice. J. Immun. 164: 6067- 6074,2000. 3 C b

GAM72 342 IL18 Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.;Tanimoto, T.; Torigoe, K.; Okura, T.; Nukada, Y.; Hattori, K.; Akita,K.; Namba, M.; Tanabe, F.; Konishi, K.; Fukuda, S.; Kurimoto, M.:Cloning of a new cytokine that induces IFN- gamma production by T cells. Nature 378:88- 91, 1995. 3 C b

GAM72 342 IL18 Pizarro, T. T.; Michie, M. H.; Bentz, M.; Woraratanadharm, J.;Smith, M. F., Jr.; Foley, E.; Moskaluk, C. A.; Bickston, S. J.; Cominelli,F.: IL- 18, a novel immunoregulatory cytokine, is up- regulated inCrohn's disease: expression and localization in intestinal mucosalcells. J. Immun. 162: 6829-6835, 1999. 3 C b

GAM72 342 IL18 Reddy, P.; Teshima, T.; Kukuruga, M.; Ordemann, R.; Liu, C.; Lowler,K.; 3 C b
Ferrara, J. L. M.: Interleukin- 18 regulates acute graft- versus-
hostdisease by enhancing Fas- mediated donor T cell apoptosis. J. Exp.Med.
194: 1433- 1440, 2001.

GAM72 342 IL18 Rothe, H.; Jenkins, N. A.; Copeland, N. G.; Kolb, H.: Active stageof 3 C b
autoimmune diabetes is associated with the expression of a novelcytokine,
IGIF, which is located near Idd2. J. Clin. Invest. 99:469- 474, 1997.

GAM72 342 IL18 Sarvetnick, N.: IFN- gamma, IGIF, and IDDM. (Editorial) J. Clin.Invest. 99: 3 C b
371- 372, 1997.

GAM72 342 IL18 Shida, K.; Shiratori, I.; Matsumoto, M.; Fukumori, Y.; Matsuhisa,A.; 3 C b
Kikkawa, S.; Tsuji, S.; Okamura, H.; Toyoshima, K.; Seya, T.:An alternative
form of IL- 18 in human blood plasma: complex formationwith IgM defined by
monoclonal antibodies. J. Immun. 166: 6671- 6679,2001.

GAM72 342 IL18 Sugawara, S.; Uehara, A.; Nochi, T.; Yamaguchi, T.; Ueda, H.;Sugiyama, A.; 3 C b
Hanzawa, K.; Kumagai, K.; Okamura, H.; Takada, H.:Neutrophil proteinase 3-
mediated induction of bioactive IL- 18 secretionby human oral epithelial
cells. J. Immun. 167: 6568- 6575, 2001.

GAM72 342 IL18 ten Hove, T.; Corbaz, A.; Amitai, H.; Aloni, S.; Belzer, I.; Graber,P.; 3 C b
Drillenburg, P.; van Deventer, S. J.; Chvatchko, Y.; Te Velde,A. A.:
Blockade of endogenous IL- 18 ameliorates TNBS- induced colitisby decreasing
local TNF- alpha production in mice. Gastroenterology 121:1372- 1379, 2001.

GAM72 342 IL18 Vidal- Vanaclocha, F.; Fantuzzi, G.; Mendoza, L.; Fuentes, A. M.;Anasagasti, 3 C b
M. J.; Martin, J.; Carrascal, T.; Walsh, P.; Reznikov,L. L.; Kim, S.- H.;
Novick, D.; Rubinstein, M.; Dinarello, C. A.:IL- 18 regulates IL- 1- beta-
dependent hepatic melanoma metastasis viavascular cell adhesion molecule- 1.
Proc. Nat. Acad. Sci. 97: 734- 739,2000.

GAM72 342 IPP Chang- Yeh, A.; Jabs, E. W.; Li, X.; Dracopoli, N. C.; Huang, R.C. C.: The 3 C b
IPP gene is assigned to human chromosome 1p32- 1p22. Genomics 15:239- 241,
1993.

GAM72 342 IPP Chang- Yeh, A.; Mold, D. E.; Brilliant, M. H.; Huang, R. C. C.:The mouse 3 C b
intracisternal A particle- promoted placental gene retrotranspositionis
mouse- strain- specific. Proc. Nat. Acad. Sci. 90: 292- 296, 1993.

GAM72 342 IPP Chang- Yeh, A.; Mold, D. E.; Huang, R. C. C.: Identification ofa novel 3 C b
murine IAP- promoted placenta- expressed gene. Nucleic AcidsRes. 19: 3667-
3672, 1991.

GAM72 342 IPP Mold, D. E.; Chang- Yeh, A.; Huang, R. C. C.: Cell lineage- 3 C b
specificexpression of the MIPP gene. Biochem. Biophys. Res. Commun.
177:1062- 1067, 1991.

GAM72 342 IRAK4 Li, S.; Strelow, A.; Fontana, E. J.; Wesche, H.: IRAK- 4: a novelmember of 3 C b
the IRAK family with the properties of an IRAK- kinase. Proc.Nat. Acad. Sci.
99: 5567- 5572, 2002.

GAM72 342 IRAK4 Scanlan, M. J.; Gordon, J. D.; Williamson, B.; Stockert, E.; Bander,N. H.; 3 C b
Jongeneel, V.; Gure, A. O.; Jager, D.; Jager, E.; Knuth, A.;Chen, Y.- T.;
Old, L. J.: Antigens recognized by autologous antibodyin patients with
renal- cell carcinoma. Int. J. Cancer 83: 456- 464,1999.

GAM72 342 IRAK4 Scott, A. F.: Personal Communication. Baltimore, Md. 4/25/2002. 3 C b

GAM72 342 IRAK4 Suzuki, N.; Suzuki, S.; Duncan, G. S.; Millar, D. G.; Wada, T.;Mirtsos, C.; 3 C b
Takada, H.; Wakeham, A.; Itie, A.; Li, S.; Penninger,J. M.; Wesche, H.;
Ohashi, P. S.; Mak, T. W.; Yeh, W.- C.: Severeimpairment of interleukin- 1
and Toll- like receptor signalling in micelacking IRAK- 4. Nature 416: 750-

754, 2002.

GAM72 342 ITCH Chen, X.; Wen, S.; Fukuda, M. N.; Gavva, N. R.; Hsu, D.; Akama,T. O.; Yang- 3 C c
Feng, T.; Shen, C. K. J.: Human ITCH is a coregulatorof the hematopoietic
transcription factor NF- E2. Genomics 73: 238- 241,2001.

GAM72 342 ITCH D'Andrea, A. D.; Serhan, C. N.: Relieving the Itch. Nature Genet. 18:97- 99, 3 C c
1998.

GAM72 342 ITCH Perry, W. L.; Hustad, C. M.; Swing, D. A.; O'Sullivan, T. N.; Jenkins,N. A.; 3 C c
Copeland, N. G.: The itchy locus encodes a novel ubiquitinprotein ligase
that is disrupted in a18H mice. Nature Genet. 18:143- 146, 1998.

GAM72 342 ITCH Qiu, L.; Joazeiro, C.; Fang, N.; Wang, H.- Y.; Elly, C.; Altman,Y.; Fang, 3 C c
D.; Hunter, T.; Liu, Y.- C.: Recognition and ubiquitinationof Notch by Itch,
a Hect- type E3 ubiquitin ligase. J. Biol. Chem. 275:35734- 35737, 2000.

GAM72 342 ITCH Winberg, G.; Matskova, L.; Chen, F.; Plant, P.; Rotin, D.; Gish,G.; Ingham, 3 C c
R.; Ernberg, I.; Pawson, T.: Latent membrane protein2A of Epstein- Barr
virus binds WW domain E3 protein- ubiquitin ligasesthat ubiquitinate B- cell
tyrosine kinases. Molec. Cell. Biol. 20:8526- 8535, 2000.

GAM72 342 ITCH Wood, J. D.; Yuan, J.; Margolis, R. L.; Colomer, V.; Duan, K.;Kushi, J.; 3 C c
Kaminsky, Z.; Kleiderlein, J. J., Jr.; Sharp, A. H.; Ross,C. A.: Atrophin-
1, the DRPLA gene product, interacts with two familiesof WW domain-
containing proteins. Molec. Cell. Neurosci. 11: 149- 160,1998.

GAM72 342 KCNA7 Bardien- Kruger, S.; Wulff, H.; Arieff, Z.; Brink, P.; Chandy, K.G.; 3 C b
Corfield, V.: Characterisation of the human voltage- gated potassiumchannel
gene, KCNA7, a candidate gene for inherited cardiac disorders,and its
exclusion as cause of progressive familial heart block I (PFHBI). Europ.J.
Hum. Genet. 10: 36- 43, 2002.

GAM72 342 KCNA7 Kalman, K.; Nguyen, A.; Tseng- Crank, J.; Dukes, I. D.; Chandy,G.; Hustad, 3 C b
C. M.; Copeland, N. G.; Jenkins, N. A.; Mohrenweiser,H.; Brandriff, B.;
Cahalan, M.; Gutman, G. A.; Chandy, K. G.: Genomicorganization, chromosomal
localization, tissue distribution, and biophysicalcharacterization of a
novel mammalian Shaker- related voltage- gatedpotassium channel, Kv1.7. J.
Biol. Chem. 273: 5851- 5857, 1998.

GAM72 342 KCNA7 McPherson, J. D.; Wasmuth, J. J.; Chandy, K. G.; Swanson, R.; Dethlefs,B.; 3 C b
Chandy, G.; Wymore, R.; Ghanshani, S.: Chromosomal localizationof 7
potassium channel genes. (Abstract) Cytogenet. Cell Genet. 58:1979 only,
1991.

GAM72 342 KCNJ5 Ashford, M. L. J.; Bond, C. T.; Blair, T. A.; Adelman, J. P.:Cloning and 3 C b
functional expression of a rat heart KATP channel. Nature 370:456- 459,
1994.

GAM72 342 KCNJ5 Bond, C. T.; Pessia, M.; Xia, X.- M.; Lagrutta, A.; Kavanaugh, M.P.; 3 C b
Adelman, J. P.: Cloning and expression of a family of inwardrectifier
potassium channels. Receptors Channels 2: 183- 191, 1994.

GAM72 342 KCNJ5 Tucker, S. J.; James, M. R.; Adelman, J. P.: Assignment of K(ATP)- 1,the 3 C b
cardiac ATP- sensitive potassium channel gene (KCNJ5), to humanchromosome
11q24. Genomics 28: 127- 128, 1995.

GAM72 342 KCNJ5 Wickman, K.; Seldin, M. F.; Gendler, S. J.; Clapham, D. E.: 3 C b
Partialstructure, chromosome localization, and expression of the mouse
Girk4gene. Genomics 40: 395- 401, 1997.

GAM72 342 KCNK6 Chavez, R. A.; Gray, A. T.; Zhao, B. B.; Kindler, C. H.; Mazurek,M. J.; 3 C c
Mehta, Y.; Forsayeth, J. R.; Yost, C. S.: TWIK- 2, a new weakinward
rectifying member of the tandem pore domain potassium channelfamily. J.

Biol. Chem. 274: 7887- 7892, 1999.

GAM72 342 KCNK6 Gray, A. T.; Kindler, C. H.; Sampson, E. R.; Yost, C. S.: Assignmentof KCNK6 3 C c encoding the human weak inward rectifier potassium channelTWIK- 2 to chromosome band 19q13.1 by radiation hybrid mapping. Cytogenet.Cell Genet. 84: 190- 191, 1999.

GAM72 342 KCNK6 Pountney, D. J.; Gulkarov, I.; Vega- Saenz de Miera, E.; Holmes,D.; Saganich, M.; Rudy, B.; Artman, M.; Coetzee, W. A.: Identificationand cloning of TWIK- originated similarity sequence (TOSS): a novelhuman 2- pore K(+) channel principal subunit. FEBS Lett. 450: 191- 196,1999. 3 C c

GAM72 342 KCNK6 Salinas, M.; Reyes, R.; Lesage, F.; Fosset, M.; Heurteaux, C.;Romey, G.; Lazdunski, M.: Cloning of a new mouse two- P domain channelsubunit and a human homologue with a unique pore structure. J. Biol.Chem. 274: 11751- 11760, 1999. 3 C c

GAM72 342 KIF1B Gong, T.- W. L.; Burmeister, M.; Lomax, M. I.: The novel gene D4Mil1emaps to mouse chromosome 4 and human chromosome 1p36. Mammalian Genome 7:790- 791, 1996. 3 C c

GAM72 342 KIF1B Nangaku, M.; Sato- Yoshitake, R.; Okada, Y.; Noda, Y.; Takemura,R.; Yamazaki, H.; Hirokawa, N.: KIF1B, a novel microtubule plus end- directedmonomeric motor protein for transport of mitochondria. Cell 79:1209- 1220, 1994. 3 C c

GAM72 342 KIF1B Saito, M.; Hayashi, Y.; Suzuki, T.; Tanaka, H.; Hozumi, I.; Tsuji,S.: Linkage mapping of the gene for Charcot- Marie- Tooth disease type2 to chromosome 1p (CMT2A) and the clinical features of CMT2A. Neurology 49:1630- 1635, 1997. 3 C c

GAM72 342 KIF1B Yang, H. W.; Chen, Y. Z.; Takita, J.; Soeda, E.; Piao, H. Y.; Hayashi,Y.: Genomic structure and mutational analysis of the human KIF1Bgene which is homozygously deleted in neuroblastoma at chromosome1p36.2. Oncogene 20: 5075- 5083, 2001. 3 C c

GAM72 342 KIF1B Zhao, C.; Takita, J.; Tanaka, Y.; Setou, M.; Nakagawa, T.; Takeda,S.; Yang, H. W.; Terada, S.; Nakata, T.; Takei, Y.; Saito, M.; Tsuji,S.; Hayashi, Y.; Hirokawa, N.: Charcot- Marie- Tooth disease type 2Acaused by mutation in a microtubule motor KIF1B- beta. Cell 105:587- 597, 2001. 3 C c

GAM72 342 KIF3B Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C b

GAM72 342 KIF3B Nonaka, S.; Tanaka, Y.; Okada, Y.; Takeda, S.; Harada, A.; Kanai,Y.; Kido, M.; Hirokawa, N.: Randomization of left- right asymmetrydue to loss of nodal cilia generating leftward flow of extraembryonicfluid in mice lacking KIF3B motor protein. Cell 95: 829- 837, 1998. 3 C b

GAM72 342 KIF3B Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.: KIF3A/B: aheterodimeric kinesin superfamily protein that works as a microtubuleplus end- directed motor for membrane organelle transport. J. CellBiol. 130: 1387- 1399, 1995. 3 C b

GAM72 342 MASP1 Dahl, M. R.; Thiel, S.; Matsushita, M.; Fujita, T.; Willis, A.C.; Christensen, T.; Vorup- Jensen, T.; Jensenius, J. C.: MASP- 3 andits association with distinct complexes of the mannan- binding lectincomplement activation pathway. Immunity 15: 127- 135, 2001. 3 C c

GAM72 342 MASP1 Endo, Y.; Sato, T.; Matsushita, M.; Fujita, T.: Exon structureof the gene encoding the human mannose- binding protein- associatedserine protease light 3 C c

chain: comparison with complement C1r and C1sgenes. Int. Immun. 8: 1355-
1358, 1996.

GAM72 342 MASP1 Matsushita, M.; Thiel, S.; Jensenius, J. C.; Terai, I.; Fujita,T.: 3 C c
Proteolytic activities of two types of mannose- binding lectin-
associatedserine protease. J. Immun. 165: 2637- 2642, 2000.

GAM72 342 MASP1 Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.: Molecular characterizationof 3 C c
a novel serine protease involved in activation of the complementsystem by
mannose- binding protein. Int. Immun. 6: 665- 669, 1994.

GAM72 342 MASP1 Takada, F.; Seki, N.; Matsuda, Y.; Takayama, Y.; Kawakami, M.:Localization 3 C c
of the genes for the 100- kDa complement- activating componentsof Ra-
reactive factor (CRARF and Crarf) to human 3q27- q28 and mouse16B2- B3.
Genomics 25: 757- 759, 1995.

GAM72 342 MASP1 Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M.: A new memberof the C1s 3 C c
family of complement proteins found in a bactericidal factor,Ra- reactive
factor, in human serum. Biochem. Biophys. Res. Commun. 196:1003- 1009, 1993.

GAM72 342 MASP1 Takayama, Y.; Takada, F.; Nowatari, M.; Kawakami, M.; Matsu- ura,N.: Gene 3 C c
structure of the P100 serine- protease component of the humanRa- reactive
factor. Molec. Immun. 36: 505- 514, 1999.

GAM72 342 MIR16 Loftus, B. J.; Kim, U.- J.; Sneddon, V. P.; Kalush, F.; Brandon,R.; 3 C c
Fuhrmann, J.; Mason, T.; Crosby, M. L.; Barnstead, M.; Cronin,L.; Mays, A.
D.; Cao, Y.; Xu, R. X.; Kang, H.- L.; Mitchell, S.; Eichler,E. E.; Harris,
P. C.; Venter, J. C.; Adams, M. D.: Genome duplicationsand other features in
12 Mb of DNA sequence from human chromosome16p and 16q. Genomics 60: 295-
308, 1999.

GAM72 342 MIR16 Zheng, B.; Chen, D.; Farquhar, M. G.: MIR16, a putative 3 C c
membraneglycerophosphodiester phosphodiesterase, interacts with RGS16.
Proc.Nat. Acad. Sci. 97: 3999- 4004, 2000.

GAM72 342 MLLT4 Prasad, R.; Gu, Y.; Alder, H.; Nakamura, T.; Canaani, O.; Saito,H.; Huebner, 3 C b
K.; Gale, R. P.; Nowell, P. C.; Kuriyama, K.; Miyazaki,Y.; Croce, C. M.;
Canaani, E.: Cloning of the ALL- 1 fusion partner,the AF- 6 gene, involved
in acute myeloid leukemias with the t(6;11)chromosome translocation. Cancer
Res. 53: 5624- 5628, 1993.

GAM72 342 MLLT4 Saha, V.; Lillington, D. M.; Shelling, A. N.; Chaplin, T.; Yaspo,M.- L.; 3 C b
Ganesan, T. S.; Young, B. D.: AF6 gene on chromosome band6q27 maps distal to
the minimal region of deletion in epithelial ovariancancer. Genes
Chromosomes Cancer 14: 220- 222, 1995.

GAM72 342 Nrap Luo, G.; Leroy, E.; Kozak, C. A.; Polymeropoulos, M. H.; Horowits,R.: 3 C b
Mapping of the gene (NRAP) encoding N- RAP in the mouse and humangenomes.
Genomics 45: 229- 232, 1997.

GAM72 342 Nrap Luo, G.; Zhang, J. Q.; Nguyen, T.- P.; Herrera, A. H.; Paterson,B.; 3 C b
Horowits, R.: Complete cDNA sequence and tissue localizationof N- RAP, a
novel nebulin- related protein of striated muscle. CellMotil. Cytoskeleton
38: 75- 90, 1997.

GAM72 342 OASL Hartmann, R.; Olsen, H. S.; Widder, S.; Jorgensen, R.; Justesen,J.: p59OASL, 3 C c
a 2- prime- 5- prime oligoadenylate synthetase like protein:a novel human
gene related to the 2- prime- 5- prime oligoadenylate synthetasefamily.
Nucleic Acids Res. 26: 4121- 4127, 1998.

GAM72 342 OASL Lee, J. W.; Choi, H.- S.; Gyuris, J.; Brent, R.; Moore, D. D.:Two classes of 3 C c
proteins dependent on either the presence or absenceof thyroid hormone for

interaction with the thyroid hormone receptor. Molec.Endocr. 9: 243- 254, 1995.

GAM72 342 P2RX7 Buell, G. N.; Talabot, F.; Gos, A.; Lorenz, J.; Lai, E.; Morris,M. A.; Antonarakis, S. E.: Gene structure and chromosomal localizationof the human P2X7 receptor. Receptors Channels 5: 347- 354, 1998. 3 C b

GAM72 342 P2RX7 Gu, B. J.; Zhang, W.; Worthington, R. A.; Sluyter, R.; Dao- Ung,P.; Petrou, S.; Barden, J. A.; Wiley, J. S.: A glu- 496 to ala polymorphismleads to loss of function of the human P2X(7) receptor. J. Biol.Chem. 276: 11135- 11142, 2001. 3 C b

GAM72 342 P2RX7 Rassendren, F.; Buell, G. N.; Virginio, C.; Collo, G.; North, R.A.; Surprenant, A.: The permeabilizing ATP receptor, P2X(7). J.Biol. Chem. 272: 5482- 5486, 1997. 3 C b

GAM72 342 P2RX7 Solle, M.; Labasi, J.; Perregaux, D. G.; Stam, E.; Petrushova,N.; Koller, B. H.; Griffiths, R. J.; Gabel, C. A.: Altered cytokineproduction in mice lacking P2X7 receptors. J. Biol. Chem. 276: 125- 132,2001. 3 C b

GAM72 342 P2RX7 Wiley, J. S.; Dao- Ung, L. P.; Gu, B. J.; Sluyter, R.; Shemon, A.N.; Li, C.; Taper, J.; Gallo, J.; Manoharan, A.: A loss- of- functionpolymorphic mutation in the cytolytic P2X7 receptor gene and chroniclymphocyte leukaemia: a molecular study. Lancet 359: 1114- 1119,2002. 3 C b

GAM72 342 P2RX7 Worthington, R. A.; Smart, M. L.; Gu, B. J.; Williams, D. A.; Petrou,S.; Wiley, J. S.; Barden, J. A.: Point mutations confer loss of ATP- inducedhuman P2X(7) receptor function. FEBS Lett. 512: 43- 46, 2002. 3 C b

GAM72 342 P2RY6 Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.: Molecular cloningand functional analysis of a novel P2 nucleotide receptor. J. Biol.Chem. 270: 26152- 26158, 1995. 3 C c

GAM72 342 P2RY6 Communi, D.; Parmentier, M.; Boeynaems, J.- M.: Cloning, functionalexpression and tissue distribution of the human P2Y6 receptor. Biochem.Biophys. Res. Commun. 222: 303- 308, 1996. 3 C c

GAM72 342 P2RY6 Maier, R.; Glatz, A.; Mosbacher, J.; Bilbe, G.: Cloning of P2Y6cDNAs and identification of a pseudogene: comparison of P2Y receptorsubtype expression in bone and brain tissues. Biochem. Biophys. Res.Commun. 237: 297- 302, 1997. 3 C c

GAM72 342 P2RY6 Pidlaoan, L. V.; Jin, J.; Sandhu, A. K.; Athwal, R. S.; Kunapuli,S. P.: Colocalization of P2Y2 and P2Y6 receptor genes at human chromosome11q13.3- 14.1. Somat. Cell Molec. Genet. 23: 291- 296, 1997. 3 C c

GAM72 342 P2RY6 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127- 130, 1997. 3 C c

GAM72 342 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine protocadherin- beta one- exon gene families show high evolutionaryconservation, despite the difference in gene number. FEBS Lett. 495:120- 125, 2001. 3 C b

GAM72 342 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C b

GAM72 342 PDE4C Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.;Rodgers, L.; Riggs, M.; Wigler, M.; Ferguson, K.: A family of humanphosphodiesterases homologous to the dunce learning and memory geneproduct of Drosophila 3 C b

melanogaster are potential targets for antidepressantdrugs. Molec. Cell. Biol. 13: 6558- 6571, 1993.

GAM72 342 PDE4C Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 3 C b
Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM72 342 PDE4C Sullivan, M.; Olsen, A. S.; Houslay, M. D.: Genomic organisationof the human 3 C b
cyclic AMP- specific phosphodiesterase PDE4C gene andits chromosomal localisation to 19p13.1, between RAB3A and JUND. Cell.Signal. 11: 735- 742, 1999.

GAM72 342 PLA2G2D Ishizaki, J.; Suzuki, N.; Higashino, K.; Yokota, Y.; Ono, T.; Kawamoto,K.; 3 C b
Fujii, N.; Arita, H.; Hanasaki, K.: Cloning and characterizationof novel mouse and human secretory phospholipase A(2)s. J. Biol.Chem. 274: 24973- 24979, 1999.

GAM72 342 PLA2G2D Shakhov, A. N.; Rubtsov, A. V.; Lyakhov, I. G.; Tumanov, A. V.;Nedospasov, 3 C b
S. A.: SPLASH (PLA(2)IID), a novel member of phospholipaseA2 family, is associated with lymphotoxin- deficiency. Genes Immun. 1:191- 199, 2000.

GAM72 342 POLK Gerlach, V. L.; Aravind, L.; Gotway, G.; Schultz, R. A.; Koonin,E. V.; 3 C c
Friedberg, E. C.: Human and mouse homologs of Escherichiacoli DinB (DNA polymerase IV), members of the UmuC/DinB superfamily. Proc.Nat. Acad. Sci. 96: 11922- 11927, 1999.

GAM72 342 POLK Johnson, R. E.; Prakash, S.; Prakash, L.: The human DINB1 geneencodes the 3 C c
DNA polymerase Pol- theta. Proc. Nat. Acad. Sci. 97:3838- 3843, 2000.

GAM72 342 POLK Ogi, T.; Kato, T., Jr.; Kato, T.; Ohmori, H.: Mutation enhancementby DINB1, 3 C c
a mammalian homologue of the Escherichia coli mutagenesisprotein dinB. Genes Cells 4: 607- 618, 1999.

GAM72 342 POLK Ohashi, E.; Ogi, T.; Kusumoto, R.; Iwai, S.; Masutani, C.; Hanaoka,F.; 3 C c
Ohmori, H.: Error- prone bypass of certain DNA lesions by thehuman DNA polymerase kappa. Genes Dev. 14: 1589- 1594, 2000.

GAM72 342 POLK Walowsky, C.; Fitzhugh, D. J.; Castano, I. B.; Ju, J. Y.; Levin,N. A.; 3 C c
Christman, M. F.: The topoisomerase- related function geneTRF4 affects cellular sensitivity to the antitumor agent camptothecin. J.Biol. Chem. 274: 7302- 7308, 1999.

GAM72 342 POLK Wang, Z.; Castano, I. B.; De Las Penas, A.; Adams, C.; Christman,M. F.: Pol 3 C c
kappa: a DNA polymerase required for sister chromatidcohesion. Science 289: 774- 779, 2000.

GAM72 342 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 3 C b
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM72 342 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 3 C b
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY) to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet. 76: 49- 52, 1997.

GAM72 342 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 3 C b
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM72 342 PSD Chardin, P.; Paris, S.; Antonny, B.; Robineau, S.; Beraud- Dufour,S.; 3 C c
Jackson, C. L.; Chabre, M.: A human exchange factor for ARF containsSec7- and pleckstrin- homology domains. Nature 384: 481- 484, 1996.

GAM72 342 PSD Kolanus, W.; Nagel, W.; Schiller, B.; Zeitlmann, L.; Godar, S.;Stockinger, H.; Seed, B.: Alpha- L- beta- 2 integrin/LFA- 1 binding toICAM- 1 induced by cytohesin- 1, a cytoplasmic regulatory molecule. Cell 86:233- 242, 1996. 3 C c

GAM72 342 PSD Perletti, L.; Talarico, D.; Trecca, D.; Ronchetti, D.; Fracchiolla,N. S.; Maiolo, A. T.; Neri, A.: Identification of a novel gene, PSD,adjacent to NFKB2/lyt- 10, which contains Sec7 and pleckstrin- homologydomains. Genomics 46: 251- 259, 1997. 3 C c

GAM72 342 RAD18 Hoege, C.; Pfander, B.; Moldovan, G.- L.; Pyrowolakis, G.; Jentsch,S.: RAD6- dependent DNA repair is linked to modification of PCNA byubiquitin and SUMO. Nature 419: 135- 141, 2002. 3 C c

GAM72 342 RAD18 Tateishi, S.; Sakuraba, Y.; Masuyama, S.; Inoue, H.; Yamaizumi,M.: Dysfunction of human Rad18 results in defective postreplicationrepair and hypersensitivity to multiple mutagens. Proc. Nat. Acad.Sci. 97: 7927- 7932, 2000. 3 C c

GAM72 342 RAD51L1 Albala, J. S.; Thelen, M. P.; Prange, C.; Fan, W.; Christensen,M.; Thompson, L. H.; Lennon, G. G.: Identification of a novel humanRAD51 homolog, RAD51B. Genomics 46: 476- 479, 1997. 3 C b

GAM72 342 RAD51L1 Cartwright, R.; Dunn, A. M.; Simpson, P. J.; Tambini, C. E.; Thacker,J.: Isolation of novel human and mouse genes of the recA/RAD51 recombination- repairgene family. Nucleic Acids Res. 26: 1653- 1659, 1998. 3 C b

GAM72 342 RAD51L1 Heim, S.; Nilbert, M.; Vanni, R.; Floderus, U.- M.; Mandahl, N.;Liedgren, S.; Lecca, U.; Mitelman, F.: A specific translocation,t(12;14)(q14- 15;q23- 24), characterizes a subgroup of uterine leiomyomas. CancerGenet. Cytogenet. 32: 13- 17, 1988. 3 C b

GAM72 342 RAD51L1 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 C b

GAM72 342 RAD51L1 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 C b

GAM72 342 RAD51L1 Rice, M. C.; Smith, S. T.; Bullrich, F.; Havre, P.; Kmiec, E. B.: Isolation of human and mouse genes based on homology to REC2, arecombinational repair gene from the fungus Ustilago maydis. Proc.Nat. Acad. Sci. 94: 7417- 7422, 1997. 3 C b

GAM72 342 RAD51L1 Schoenmakers, E. F. P. M.; Huysmans, C.; Van de Ven, W. J. M.:Allelic knockout of novel splice variants of human recombination repairgene RAD51B in t(12;14) uterine leiomyomas. Cancer Res. 59: 19- 23,1999. 3 C b

GAM72 342 RBL1 Chen, C.- R.; Kang, Y.; Siegel, P. M.; Massague, J.: E2F4/5 andp107 as Smad cofactors linking the TGF- beta receptor to c- myc repression. Cell 110:19- 32, 2002. 3 C c

GAM72 342 RBL1 Ewen, M. E.; Xing, Y.; Lawrence, J. B.; Livingston, D. M.: Molecularcloning, chromosomal mapping, and expression of the cDNA for p107,a retinoblastoma gene product- related protein. Cell 66: 1155- 1164,1991. 3 C c

GAM72 342 RBL1 Huppi, K.; Siwarski, D.; Mock, B. A.; Dosik, J.; Hamel, P. A.:Molecular cloning, chromosomal mapping, and expression of the mousep107 gene. Mammalian Genome 7: 353- 355, 1996. 3 C c

GAM72 342 RBL1 Kim, K. K.; Soonpaa, M. H.; Wang, H.; Field, L. J.: Developmentalexpression of p107 mRNA and evidence for alternative splicing of thep107 (RBL1) gene product. Genomics 28: 520- 529, 1995. 3 C c

GAM72 342 RBL1 LeCouter, J. E.; Kablar, B.; Hardy, W. R.; Ying, C.; Megeney, L.A.; May, L. 3 C c
L.; Rudnicki, M. A.: Strain- dependent myeloid hyperplasia,growth
deficiency, and accelerated cell cycle in mice lacking theRb- related p107
gene. Molec. Cell. Biol. 18: 7455- 7465, 1998.

GAM72 342 SFRS2IP Tanner, S.; Stagljar, I.; Georgiev, O.; Schaffner, W.; Bourquin,J.- P.: A 3 C c
novel SR- related protein specifically interacts with thecarboxy- terminal
domain (CTD) of RNA polymerase II through a conservedinteraction domain.
Biol. Chem. 378: 565- 571, 1997.

GAM72 342 SFRS2IP Zhang, W.- J.; Wu, J. Y.: Sip1, a novel RS domain- containing 3 C c
proteinessential for pre- mRNA splicing. Molec. Cell. Biol. 18: 676-
684,1998.

GAM72 342 TBX6 Chapman, D. L.; Agulnik, I.; Hancock, S.; Silver, L. M.; Papaioannou,V. E.: 3 C c
Tbx6, a mouse T- box gene implicated in paraxial mesoderm formationat
gastrulation. Dev. Biol. 180: 534- 542, 1996.

GAM72 342 TBX6 Chapman, D. L.; Papaioannou, V. E.: Three neural tubes in mouseembryos with 3 C c
mutations in the T- box gene Tbx6. Nature 391: 695- 697,1998.

GAM72 342 TBX6 Papapetrou, C.; Putt, W.; Fox, M.; Edwards, Y. H.: The human TBX6gene: 3 C c
cloning and assignment to chromosome 16p11.2. Genomics 55:238- 241, 1999.

GAM72 342 TDG Barrett, T. E.; Savva, R.; Panayotou, G.; Barlow, T.; Brown, T.;Jiricny, J.; 3 C c
Pearl, L. H.: Crystal structure of a G:T/U mismatch- specificDNA
glycosylase: mismatch recognition by complementary- strand interactions.
Cell 92:117- 129, 1998.

GAM72 342 TDG De Gregorio, L.; Gallinari, P.; Gariboldi, M.; Manenti, G.; Pierotti,M. A.; 3 C c
Jiricny, J.; Dragani, T. A.: Genetic mapping of thymine DNAglycosylase (Tdg)
gene and of one pseudogene in the mouse. MammalianGenome 7: 909- 910, 1996.

GAM72 342 TDG Lindahl, T.: DNA repair enzymes. Ann. Rev. Biochem. 51: 61- 87,1982. 3 C c

GAM72 342 TDG Neddermann, P.; Gallinari, P.; Lettieri, T.; Schmid, D.; Truong,O.; Hsuan, 3 C c
J. J.; Wiebauer, K.; Jiricny, J.: Cloning and expressionof human G/T
mismatch- specific thymine- DNA glycosylase. J. Biol.Chem. 271: 12767-
12774, 1996.

GAM72 342 TDG Sard, L.; Tornielli, S.; Gallinari, P.; Minoletti, F.; Jiricny,J.; Lettieri, 3 C c
T.; Pierotti, M. A.; Sozzi, G.; Radice, P.: Chromosomallocalizations and
molecular analysis of TDG gene- related sequences. Genomics 44:222- 226,
1997.

GAM72 342 TDG Tini, M.; Benecke, A.; Um, S.- J.; Torchia, J.; Evans, R. M.; Chambon,P.: 3 C c
Association of CBP/p300 acetylase and thymine DNA glycosylaselinks DNA
repair and transcription. Molec. Cell 9: 265- 277, 2002.

GAM72 342 TEP1 Harrington, L.; McPhail, T.; Mar, V.; Zhou, W.; Oulton, R.; Bass,M. B.; 3 C b
Arruda, I.; Robinson, M. O.: A mammalian telomerase- associatedprotein.
Science 275: 973- 976, 1997.

GAM72 342 TEP1 Saito, T.; Matsuda, Y.; Suzuki, T.; Hayashi, A.; Yuan, X.; Saito,M.; 3 C b
Nakayama, J.; Hori, T.; Ishikawa, F.: Comparative gene mappingof the human
and mouse TEP1 genes, which encode one protein componentof telomerases.
Genomics 46: 46- 50, 1997.

GAM72 342 TES Tatarelli, C.; Linnenbach, A.; Mimori, K.; Croce, C. M.: Characterizationof 3 C c
the human TESTIN gene localized in the FRA7G region at 7q31.2. Genomics
68:1- 12, 2000.

GAM72 342 TES Tobias, E. S.; Hurlstone, A. F. L.; MacKenzie, E.; McFarlane, R.;Black, D. 3 C c
M.: The TES gene at 7q31.1 is methylated in tumours andencodes a novel
growth- suppressing LIM domain protein. Oncogene 20:2844- 2853, 2001.

GAM72 342 TNFRSF1B Baker, E.; Chen, L. Z.; Smith, C. A.; Callen, D. F.; Goodwin, R.;Sutherland, 3 C b
G. R.: Chromosomal location of the human tumor necrosisfactor receptor
genes. Cytogenet. Cell Genet. 57: 117- 118, 1991.

GAM72 342 TNFRSF1B Beltinger, C. P.; White, P. S.; Maris, J. M.; Sulman, E. P.; Jensen,S. J.; 3 C b
LePaslier, D.; Stallard, B. J.; Goeddel, D. V.; de Sauvage,F. J.; Brodeur,
G. M.: Physical mapping and genomic structure ofthe human TNFR2 gene.
Genomics 35: 94- 100, 1996.

GAM72 342 TNFRSF1B Bruce, A. J.; Boling, W.; Kindy, M. S.; Peschon, J.; Kraemer, P.J.; 3 C b
Carpenter, M. K.; Holtsberg, F. W.; Mattson, M. P.: Altered neuronaland
microglial responses to excitotoxic and ischemic brain injuryin mice lacking
TNF receptors. Nature Med. 2: 788- 794, 1996.

GAM72 342 TNFRSF1B Chan, F. K.- M.; Chun, H. J.; Zheng, L.; Siegel, R. M.; Bui, K.L.; Lenardo, 3 C b
M. J.: A domain in TNF receptors that mediates ligand- independentreceptor
assembly and signaling. Science 288: 2351- 2354, 2000.

GAM72 342 TNFRSF1B Geurts, J. M. W.; Janssen, R. G. J. H.; van Greevenbroek, M. M.J.; van der 3 C b
Kallen, C. J. H.; Cantor, R. M.; Bu, X.; Aouizerat, B.E.; Allayee, H.;
Rotter, J. I.; de Bruin, T. W. A.: Identificationof TNFRSF1B as a novel
modifier gene in familial combined hyperlipidemia. Hum.Molec. Genet. 9:
2067- 2074, 2000.

GAM72 342 TNFRSF1B Glenn, C. L.; Wang, W. Y. S.; Benjafield, A. V.; Morris, B. J.: Linkage and 3 C b
association of tumor necrosis factor receptor 2 locuswith hypertension,
hypercholesterolemia and plasma shed receptor. Hum.Molec. Genet. 9: 1943-
1949, 2000.

GAM72 342 TNFRSF1B Kaufman, B. A.; White, P. S.; Steinbrueck, T.; Donis- Keller, H.;Brodeur, G. 3 C b
M.: Linkage mapping of the tumor necrosis factor receptor2 (TNFR2) gene to
1p36.2 using the single- strand conformation polymorphismtechnique. Hum.
Genet. 94: 418- 422, 1994.

GAM72 342 TNFRSF1B Kemper, O.; Derre, J.; Cherif, D.; Engelmann, H.; Wallach, D.;Berger, R.: 3 C b
The gene for the type II (p75) tumor necrosis factorreceptor (TNF- RII) is
localized on band 1p36.2- p36.3. Hum. Genet. 87:623- 624, 1991.

GAM72 342 TNFRSF1B Li, X.; Yang, Y.; Ashwell, J. D.: TNF- RII and c- IAP1 mediate 3 C b
ubiquitinationand degradation of TRAF2. Nature 416: 345- 349, 2002.

GAM72 342 TNFRSF1B Milatovich, A.; Song, K.; Heller, R. A.; Francke, U.: Tumor necrosisfactor 3 C b
receptor genes, TNFR1 and TNFR2, on human chromosomes 12 and1. Somat. Cell
Molec. Genet. 17: 519- 523, 1991.

GAM72 342 TNFRSF1B Santee, S. M.; Owen- Schaub, L. B.: Human tumor necrosis factorreceptor 3 C b
p75/80 (CD120b) gene structure and promoter characterization. J.Biol. Chem.
271: 21151- 21159, 1996.

GAM72 342 TNFRSF1B Sashio, H.; Tamura, K.; Ito, R.; Yamamoto, Y.; Bamba, H.; Kosaka,T.; Fukui, 3 C b
S.; Sawada, K.; Fukuda, Y.; Tamura, K.; Satomi, M.; Shimoyama,T.; Furuyama,
J.: Polymorphisms of the TNF gene and the TNF receptorsuperfamily member 1B
gene are associated with susceptibility to ulcerativecolitis and Crohn's
disease, respectively. Immunogenetics 53: 1020- 1027,2002.

GAM72 342 TNFRSF1B Schall, T. J.; Lewis, M.; Koller, K. J.; Lee, A.; Rice, G. C.;Wong, G. H. 3 C b
W.; Gatanaga, T.; Granger, G. A.; Lentz, R.; Raab, H.;Kohr, W. J.; Goeddel,
D. V.: Molecular cloning and expression ofa receptor for human tumor
necrosis factor. Cell 61: 361- 370, 1990.

GAM72 342 TNFRSF1B Van Ostade, X.; Vandenabeele, P.; Everaerdt, B.; Loetscher, H.;Gentz, R.; 3 C b
Brockhaus, M.; Lesslauer, W.; Tavernier, J.; Brouckaert,P.; Fiers, W.: Human
TNF mutants with selective activity on the p55receptor. Nature 361: 266-

269, 1993.

GAM72 342 TNFRSF1B White, P. S.; Maris, J. M.; Beltinger, C.; Sulman, E.; Marshall,H. N.; Fujimori, M.; Kaufman, B. A.; Biegel, J. A.; Allen, C.; Hilliard,C.; Valentine, M. B.; Look, A. T.; Enomoto, H.; Sakiyama, S.; Brodeur,G. M.: A region of consistent deletion in neuroblastoma maps withinhuman chromosome 1p36.2- 36.3. Proc. Nat. Acad. Sci. 92: 5520- 5524,1995. 3 C b

GAM72 342 TNFSF10 Cretney, E.; Takeda, K.; Yagita, H.; Glaccum, M.; Peschon, J. J.;Smyth, M. J.: Increased susceptibility to tumor initiation and metastasisin TNF-related apoptosis- inducing ligand- deficient mice. J. Immun. 168:1356-1361, 2002. 3 C c

GAM72 342 TNFSF10 Degli- Esposti, M. A.; Dougall, W. C.; Smolak, P. J.; Waugh, J.Y.; Smith, C. A.; Goodwin, R. G.: The novel receptor TRAIL- R4 inducesNF- kappa- B and protects against TRAIL- mediated apoptosis, yet retainsan incomplete death domain. Immunity 7: 813- 820, 1997. 3 C c

GAM72 342 TNFSF10 Gong, B.; Almasan, A.: Genomic organization and transcriptionalregulation of human Apo2/TRAIL gene. Biochem. Biophys. Res. Commun. 278:747- 752, 2000. 3 C c

GAM72 342 TNFSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999. 3 C c

GAM72 342 TNFSF10 Nitsch, R.; Bechmann, I.; Deisz, R. A.; Haas, D.; Lehmann, T. N.;Wendling, U.; Zipp, F.: Human brain- cell death induced by tumour- necrosis- factor-relatedapoptosis- inducing ligand (TRAIL). Lancet 356: 827- 828, 2000. 3 C c

GAM72 342 TNFSF10 Pitti, R. M.; Marsters, S. A.; Ruppert, S.; Donahue, C. J.; Moore,A.; Ashkenazi, A.: Induction of apoptosis by Apo- 2 ligand, a newmember of the tumor necrosis factor cytokine family. J. Biol. Chem. 271:12687- 12690, 1996. 3 C c

GAM72 342 TNFSF10 Raftery, M. J.; Schwab, M.; Eibert, S. M.; Samstag, Y.; Walczak,H.; Schonrich, G.: Targeting the function of mature dendritic cellsby human cytomegalovirus: a multilayered viral defense strategy. Immunity 15:997-1009, 2001. 3 C c

GAM72 342 TNFSF10 Wiley, S. R.; Schooley, K.; Smolak, P. J.; Din, W. S.; Huang, C.-P.;Nicholl, J. K.; Sutherland, G. R.; Smith, T. D.; Rauch, C.; Smith,C. A.; Goodwin, R. G.: Identification and characterization of a newmember of the TNF family that induces apoptosis. Immunity 3: 673- 682,1995. 3 C c

GAM72 342 TPM4 Laing, N. G.; Wilton, S. D.; Akkari, P. A.; Dorosz, S.; Boundy,K.; Kneebone, C.; Blumbergs, P.; White, S.; Watkins, H.; Love, D.R.; Haan, E.: A mutation in the alpha tropomyosin gene TPM3 associatedwith autosomal dominant nemaline myopathy. Nature Genet. 9: 75- 79,1995. 3 C c

GAM72 342 TPM4 Wilton, S. D.; Lim, L.; Dorosz, S. D.; Gunn, H. C.; Eyre, H. J.;Callen, D. F.; Laing, N. G.: Assignment of the human alpha- tropomyosingene TPM4 to band 19p13.1 by fluorescence in situ hybridization. Cytogenet.Cell Genet. 72: 294- 296, 1996. 3 C c

GAM72 342 TRIM9 Li, Y.; Chin, L.- S.; Weigel, C.; Li, L.: Spring, a novel RINGfinger protein that regulates synaptic vesicle exocytosis. J. Biol.Chem. 276: 40824- 40833, 2001. 3 C c

GAM72 342 TRIM9 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci, S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell compartments. EMBO J. 20: 2140- 2151, 2001. 3 C c

GAM72 342 TSN Aoki, K.; Inazawa, J.; Takahashi, T.; Nakahara, K.; Kasai, M.:Genomic structure and chromosomal localization of the gene encodingtranslin, a recombination hotspot binding protein. Genomics 43:237- 241, 1997. 3 C c

GAM72 342 TSN Aoki, K.; Nakahara, K.; Ikegawa, C.; Seto, M.; Takahashi, T.; Minowada,J.; Strominger, J. L.; Maziarz, R. T.; Kasai, M.: Nuclear proteinsbinding to a novel target sequence within the recombination hotspotregions of Bcl- 2 and the immunoglobulin D(H) gene family. Oncogene 9:1109- 1115, 1994. 3 C c

GAM72 342 TSN Aoki, K.; Suzuki, K.; Sugano, T.; Tasaka, T.; Nakahara, K.; Kuge,O.; Omori, A.; Kasai, M.: A novel gene, 'Translin,' encodes a recombinationhotspot binding protein associated with chromosomal translocations. NatureGenet. 10: 167- 174, 1995. 3 C c

GAM72 342 TSN Badge, R. M.; Yardley, J.; Jeffreys, A. J.; Armour, J. A. L.:Crossover breakpoint mapping identifies a subtelomeric hotspot formale meiotic recombination. Hum. Molec. Genet. 9: 1239- 1244, 2000. 3 C c

GAM72 342 TSN Hosaka, T.; Kanoe, H.; Nakayama, T.; Murakami, H.; Yamamoto, H.;Nakamata, T.; Tsuboyama, T.; Oka, M.; Kasai, M.; Sasaki, M. S.; Nakamura,T.; Toguchida, J.: Translin binds to the sequences adjacent to thebreakpoints of the TLS and CHOP genes in liposarcomas with translocationt(12;16). Oncogene 19: 5821- 5825, 2000. 3 C c

GAM72 342 TSN Kasai, M.; Aoki, K.; Matsuo, Y.; Minowada, J.; Maziarz, R. T.;Strominger, J. L.: Recombination hotspot associated factors specificallyrecognize novel target sequences at the site of interchromosomal rearrangementsin T- ALL patients with t(8;14)(q24;q11)and (t(1;14)(p32;q11). Int.Immun. 6: 1017- 1025, 1994. 3 C c

GAM72 342 UBE2B Hoege, C.; Pfander, B.; Moldovan, G.- L.; Pyrowolakis, G.; Jentsch,S.: RAD6- dependent DNA repair is linked to modification of PCNA byubiquitin and SUMO. Nature 419: 135- 141, 2002. 3 C c

GAM72 342 UBE2B Koken, M. H. M.; Smit, E. M. E.; Jaspers- Dekker, I.; Oostra, B.A.; Hagemeijer, A.; Bootsma, D.; Hoeijmakers, J. H. J.: Localizationof two human homologs, HHR6A and HHR6B, of the yeast DNA repair geneRAD6 to chromosomes Xq24- q25 and 5q23- q31. Genomics 12: 447- 453,1992. 3 C c

GAM72 342 UBE2B Lench, N. J.; Thompson, J.; Markham, A. F.; Robinson, P. A.: (CGG)trinucleotide repeat polymorphism in the 5- prime region of the HHR6Bgene: the human homolog of the yeast DNA repair gene RAD6. Hum. Genet. 96:369- 370, 1995. 3 C c

GAM72 342 UBE2B Roest, H. P.; van Klaveren, J.; de Wit, J.; van Gurp, C. G.; Koken,M. H. M.; Vermey, M.; van Roijen, J. H.; Hoogerbrugge, J. W.; Vreeburg,J. T. M.; Baarends, W. M.; Bootsma, D.; Grootegoed, J. A.; Hoeijmakers,J. H. J.: Inactivation of the HR6B ubiquitin- conjugating DNA repairenzyme in mice causes male sterility associated with chromatin modification. Cell 86:799- 810, 1996. 3 C c

GAM72 342 UBE2B Roller, M. L.; Lossie, A. C.; Koken, M. H. M.; Smit, E. M. E.;Hagemeijer, A.; Camper, S. A.: Localization of sequences relatedto the human RAD6 DNA repair gene on mouse chromosomes 11 and 13. MammalianGenome 6: 305- 306, 1995. 3 C c

GAM72 342 UBE2G2 Katsanis, N.; Fisher, E. M. C.: Identification, expression, andchromosomal localization of ubiquitin conjugating enzyme 7 (UBE2G2),a human homologue of the Saccharomyces cerevisiae Ubc7 gene. Genomics 51:128- 131, 1998. 3 C b

GAM72 342 UBE2G2 Rose, S. A.; Leek, J. P.; Moynihan, T. P.; Ardley, H. C.; Markham,A. F.; Robinson, P. A.: Assignment of the ubiquitin conjugating enzymegene, UBE2G2, 3 C b

to human chromosome band 21q22.3 by in situ hybridization. Cytogenet.Cell Genet. 83: 98- 99, 1998.

GAM72 342 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 C c

GAM72 342 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 C c

GAM72 342 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 C c

GAM72 342 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 C c

GAM72 342 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000. 3 C c

GAM72 342 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938. 3 C c

GAM72 342 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999. 3 C c

GAM72 342 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence for a founder effect. Hum. Genet. 95: 551- 556,1995. 3 C c

GAM72 342 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. Arch.Neurol. 28: 67- 68, 1973. 3 C c

GAM72 342 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942. 3 C c

GAM72 342 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures of phaeochromocytoma. Lancet I: 492- 494, 1970. 3 C c

GAM72 342 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962. 3 C c

GAM72 342 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell, J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.; Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the von Hippel- Lindau disease tumorsuppressor gene: correlations with phenotype. Hum. Mutat. 5: 66- 75,1995. 3 C c

GAM72 342 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: Genotype- phenotype correlation in von Hippel- Lindaudisease: identification of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996. 3 C c

GAM72 342 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's disease. J.A.M.A. 178: 280- 282, 1961. 3 C c

GAM72 342 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with peculiar vascular new growth, probably primarily retinal,affecting both eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894. 3 C c

GAM72 342 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994. 3 C c

GAM72 342 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E. R.: Identification of intragenic mutations in thevon Hippel- Lindau disease tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994. 3 C c

GAM72 342 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928. 3 C c

GAM72 342 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994. 3 C c

GAM72 342 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988. 3 C c

GAM72 342 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459- 6463, 1995. 3 C c

GAM72 342 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995. 3 C c

GAM72 342 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001. 3 C c

GAM72 342 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto- oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995. 3 C c

GAM72 342 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell107: 43- 54, 2001. 3 C c

GAM72 342 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 C c

GAM72 342 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 3 C c

GAM72 342 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin TRiC. Molec. Cell 1051- 1061, 1999. 3 C c

GAM72 342 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof von Hippel- Lindau disease. Radiology 133: 289- 295, 1979. 3 C c

GAM72 342 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331, 1979. 3 C c

GAM72 342 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001. 3 C c

GAM72 342 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with hydrocephalus as a complication of cerebellar hemangioblastoma:identification of pro157leu mutation in the VHL gene. J. Hum. Genet. 45:47- 51, 2000. 3 C c

GAM72 342 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C Thomas (pub.) 1946. 3 C c

GAM72 342 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989. 3 C c

GAM72 342 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg. Path. 18: 1254- 1260, 1994. 3 C c

GAM72 342 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.; Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999. 3 C c

GAM72 342 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 C c

GAM72 342 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 C c

GAM72 342 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 C c

GAM72 342 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 C c

GAM72 342 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991. 3 C c

GAM72 342 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. 3 C c

J.A.M.A. 267: 1226- 1231, 1992.

GAM72 342 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; 3 C c
Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston
Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in
VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997.

GAM72 342 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: 3 C c
Segregation and linkage analyses of von Hippel Lindau diseaseamong 220
descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984.

GAM72 342 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: 3 C c
histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66:
693- 705,1968.

GAM72 342 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 C c

GAM72 342 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a 3 C c
Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986.

GAM72 342 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid 3 C c
tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour,
phaeochromocytoma and the von Hippel- Lindau complex:two distinctive
neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987.

GAM72 342 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: 3 C c
Familial pheochromocytoma associated with a novel mutation inthe von Hippel-
Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996.

GAM72 342 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; 3 C c
Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam:
North Holland (pub.) 14: 1972. Pp. 241- 259.

GAM72 342 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors 3 C c
in livers with targeted inactivation of the von Hippel- Lindautumor
suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001.

GAM72 342 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 3 C c
retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022-
1034, 1971.

GAM72 342 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 3 C c
hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8:
601- 606,1967.

GAM72 342 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, 3 C c
D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing
of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas.
Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994.

GAM72 342 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; 3 C c
McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.;
Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von
Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma
only. J. Med. Genet. 37: 939- 943,2000.

GAM72 342 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 3 C c
Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips,
C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in
families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet.
106: 425- 431, 2000.

GAM72 342 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 C c
von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve
the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM72 342 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002. 3 C c

GAM72 342 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989. 3 C c

GAM72 342 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976. 3 C c

GAM72 342 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990. 3 C c

GAM72 342 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982. 3 C c

GAM72 342 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986. 3 C c

GAM72 342 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995. 3 C c

GAM72 342 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996. 3 C c

GAM72 342 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 3 C c

GAM72 342 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL- mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001. 3 C c

GAM72 342 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel- Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 3 C c

GAM72 342 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)- regulated prolyl hydroxylation. Science 292: 468- 472, 2001. 3 C c

GAM72 342 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 C c

GAM72 342 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 3 C c

GAM72 342 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 C c

GAM72 342 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 C c

GAM72 342 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 C c

GAM72 342 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 C c

GAM72 342 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 C c

GAM72 342 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 C c

GAM72 342 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-581, 1995. 3 C c

GAM72 342 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 C c

GAM72 342 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 C c

GAM72 342 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel-Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 C c

GAM72 342 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 C c

GAM72 342 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 C c

GAM72 342 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel-Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 C c

GAM72 342 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 C c

GAM72 342 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 C c

GAM72 342 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317-1320, 1993. 3 C c

GAM72 342 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 C c

GAM72 342 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 C c

GAM72 342 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 C c

GAM72 342 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 C c

GAM72 342 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002. 3 C c

GAM72 342 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 C c

GAM72 342 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 3 C c

GAM72 342 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 C c

GAM72 342 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 C c

GAM72 342 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 C c

GAM72 342 WW45 Tapon, N.; Harvey, K. F.; Bell, D. W.; Wahrer, D. C. R.; Schiripo,T. A.; Haber, D. A.; Hariharan, I. K.: salvador promotes both cellcycle exit and apoptosis in Drosophila and is mutated in human cancercell lines. Cell 110: 467- 478, 2002. 3 C b

GAM72 342 WW45 Valverde, P.: Cloning, expression, and mapping of hWW45, a novelhuman WW domain- containing gene. Biochem. Biophys. Res. Commun. 276:990- 998, 2000. 3 C b

GAM72 342 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 3 C b

GAM72 342 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 C b

GAM72 342 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- 3 C b

ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987.

GAM72 342 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the 3 C b XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995.

GAM72 342 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, 3 C b T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002.

GAM72 342 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in 3 C b two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002.

GAM72 342 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; 3 C b McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001.

GAM72 342 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; 3 C b Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997.

GAM72 342 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: 3 C b Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995.

GAM73 264 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, 3 C c J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2 in the allergic response. Nature 412: 186- 190,2001.

GAM73 264 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 C c Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM73 264 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; 3 C c Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab- family adapter proteins act downstream of cytokine and growthfactor receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999.

GAM73 264 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH 3 C c mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell Genet. 94: 39- 42, 2001.

GAM73 264 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology 3 C c domain- containing adapter protein, acts to uncouple signalingfrom ERK kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999.

GAM73 264 MSN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, 3 C c J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM- dependent movement of CD43 defines a novelprotein complex distal to the immunological synapse. Immunity 15:739- 750, 2001.

GAM73 264 MSN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe 3 C c immunological synapse is mediated by phosphorylation- regulatedrelocation of the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001.

GAM73 264 MSN Lankes, W. T.; Furthmayr, H.: Moesin: a member of the protein4.1- talin- 3 C c ezrin family of proteins. Proc. Nat. Acad. Sci. 88: 8297- 8301,1991.

GAM73 264 MSN Lankes, W.; Griesmacher, A.; Grunwald, J.; Schwartz- Albiez, R.;Keller, R.: 3 C c A heparin- binding protein involved in inhibition of smooth- musclecell

proliferation. Biochem. J. 251: 831- 842, 1988.

GAM73 264 MSN Shcherbina, A.; Bretscher, A.; Rosen, F. S.; Kenney, D. M.; Remold- 3 C c
O'Donnell,E.: The cytoskeletal linker protein moesin: decreased levels in
Wiskott- Aldrichsyndrome platelets and identification of a cleavage pathway
in normalplatelets. Brit. J. Haemat. 106: 216- 223, 1999.

GAM73 264 MSN Wilgenbus, K. K.; Hsieh, C.- L.; Lankes, W. T.; Milatovich, A.;Francke, U.; 3 C c
Furthmayr, H.: Structure and localization on the X chromosomeof the gene
coding for the human filopodial protein moesin (MSN). Genomics 19:326- 333,
1994.

GAM74 254 LTBR Crowe, P. D.; VanArsdale, T. L.; Walter, B. N.; Ware, C. F.; Hession,C.; 3 C c
Ehrenfels, B.; Browning, J. L.; Din, W. S.; Goodwin, R. G; Smith,C. A.: A
lymphotoxin- beta- specific receptor. Science 264: 707- 710,1994.

GAM74 254 LTBR Nakamura, T.; Tashiro, K.; Nazarea, M.; Nakano, T.; Sasayama, S.;Honjo, T.: 3 C c
The murine lymphotoxin- beta receptor cDNA: isolation bythe signal sequence
trap and chromosomal mapping. Genomics 30: 312- 319,1995.

GAM74 254 LTBR Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo,T.: 3 C c
Signal sequence trap: a cloning strategy for secreted proteinsand type I
membrane proteins. Science 261: 600- 603, 1993.

GAM74 254 SLC7A6 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; 3 C c
Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding
sequences of unidentified human genes. VI. The codingsequences of 80 new
genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line
KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM74 254 SLC7A6 Torrents, D.; Estevez, R.; Pineda, M.; Fernandez, E.; Lloberas,J.; Shi, Y.- 3 C c
B.; Zorzano, A.; Palacin, M.: Identification and characterizationof a
membrane protein (y(+)L amino acid transporter- 1) that associateswith 4F2hc
to encode the amino acid transport activity y(+)L: a candidategene for
lysinuric protein intolerance. J. Biol. Chem. 273: 32437- 32445,1998.

GAM74 254 THY1 Ades, E. W.; Zwerner, R. K.; Acton, R. T.; Balch, C. M.: Isolationand 3 C c
partial characterisation of the human homologue of Thy- 1. J.Exp. Med. 151:
400- 406, 1980.

GAM74 254 THY1 Bonewald, L.; Ades, E. W.; Tung, E.; Marchalonis, J. J.; Wang,A. C.: 3 C c
Biochemical characterization of human Thy- 1. J. Immunogenet. 11:283- 296,
1984.

GAM74 254 THY1 Gatti, R. A.; Lathrop, G. M.; Salser, W.; Silver, J.; Lalouel,J. M.; White, 3 C c
R.: Location of Thy- 1 with respect to a primary linkagemap of chromosome
11q. (Abstract) Cytogenet. Cell Genet. 46: 618only, 1987.

GAM74 254 THY1 Gatti, R. A.; Shaked, R.; Wei, S.; Koyama, M.; Salser, W.; Silver,J.: DNA 3 C c
polymorphism in the human Thy- 1 gene. Hum. Immun. 22:145- 150, 1988.

GAM74 254 THY1 Greenspan, R. J.; O'Brien, M. C.: Genetic evidence for the roleof Thy- 1 in 3 C c
neurite outgrowth in the mouse. J. Neurogenet. 5: 25- 36,1989.

GAM74 254 THY1 Grzeschik, K.- H.; Kazazian, H. H.: Report of the committee onthe genetic 3 C c
constitution of chromosomes 10, 11, and 12. Cytogenet.Cell Genet. 40: 179-
205, 1985.

GAM74 254 THY1 Hood, L.; Kronenberg, M.; Hunkapiller, T.: T cell antigen receptorsand the 3 C c
immunoglobulin supergene family. Cell 40: 225- 229, 1985.

GAM74 254 THY1 Letarte- Muirhead, M.; Barclay, A. N.; Williams, A. F.: Purificationof the 3 C c
Thy- 1 molecule, a major cell surface glycoprotein of rat
thymocytes.Biochem. J. 151: 685- 697, 1975.

GAM74 254 THY1 Mansour, M. H.; Negm, H. I.; Cooper, E. L.: Thy- 1 evolution. Dev.Comp. 3 C c

Immun. 11: 3- 15, 1987.

GAM74 254 THY1 McKenzie, J. L.; Fabre, J. W.: Human Thy- 1: unusual localizationand possible functional significance in lymphoid tissues. J. Immun. 126:843-850, 1981. 3 C c

GAM74 254 THY1 Morris, R.: Thy- 1 in developing nervous tissue. Dev. Neurosci. 7:133- 160, 1985. 3 C c

GAM74 254 THY1 Raff, M. C.: Surface antigenic markers for distinguishing T andB lymphocytes in mice. Transplant. Rev. 6: 52- 80, 1971. 3 C c

GAM74 254 THY1 Rettig, W. J.; Dracopoli, N. C.; Chesa, P. G.; Spengler, B. A.;Beresford, H. R.; Davies, P.; Biedler, J. L.; Old, L. J.: Role ofhuman chromosome 11 in determining surface antigenic phenotype ofnormal and malignant cells: somatic cell genetic analysis of eightantigens, including putative human Thy- 1. J. Exp. Med. 162: 1603- 1619,1985. 3 C c

GAM74 254 THY1 Rettig, W. J.; Dracopoli, N. C.; Silver, J.; Old, L. J.: HumanTHY- 1: regional mapping on chromosome 11 and comparison with otherchromosome 11-encoded cell surface glycoproteins. (Abstract) Cytogenet.Cell Genet. 40: 731 only, 1985. 3 C c

GAM74 254 THY1 Rettig, W. J.; Dracopoli, N. C.; Spengler, B. A.; Biedler, J.L.; Old, L. J.: Somatic cell genetic analysis of human cell surfaceantigens, including putative human Thy- 1: eight distinct antigenicsystems controlled by chromosome 11. (Abstract) Cytogenet. CellGenet. 40: 732 only, 1985. 3 C c

GAM74 254 THY1 Seki, T.; Spurr, N.; Obata, F.; Goyert, S.; Goodfellow, P.; Silver,J.: The human Thy- 1 gene: structure and chromosomal location. Proc.Nat. Acad. Sci. 82: 6657- 6661, 1985. 3 C c

GAM74 254 THY1 Tse, A. G. D.; Barclay, A. N.; Watts, A.; Williams, A. F.: Aglycophospholipid tail at the carboxyl terminus of the Thy- 1 glycoproteinof neurons and thymocytes. Science 230: 1003- 1008, 1985. 3 C c

GAM74 254 THY1 Tunnacliffe, A.; McGuire, R. S.: A physical linkage group inhuman chromosome band 11q23 covering a region implicated in leukocyteneoplasia. Genomics 8: 447- 453, 1990. 3 C c

GAM74 254 THY1 van den Elsen, P.; Bruns, G.; Gerhard, D. S.; Pravtcheva, D.;Jones, C.; Housman, D.; Ruddle, F. A.; Orkin, S.; Terhorst, C.: Assignmentof the gene coding for the T3- delta subunit of the T3- - T- cell receptorcomplex to the long arm of human chromosome 11 and to mouse chromosome9. Proc. Nat. Acad. Sci. 82: 2920- 2924, 1985. 3 C c

GAM74 254 THY1 van Rijs, J.; Giguere, V.; Hurst, J.; van Agthoven, T.; Geurtsvan Kessel, A.; Goyert, S.; Grosveld, F.: Chromosomal localizationof the human Thy- 1 gene. Proc. Nat. Acad. Sci. 82: 5832- 5835, 1985. 3 C c

GAM74 254 THY1 Williams, A. F.; Gagnon, J.: Neuronal cell Thy- 1 glycoprotein:homology with immunoglobulin. Science 216: 696- 703, 1982. 3 C c

GAM74 254 UBTF Bell, S. P.; Learned, R. M.; Jantzen, H.- M.; Tjian, R.: Functionalcooperativity between transcription factors UBF1 and SL1 mediateshuman ribosomal RNA synthesis. Science 241: 1192- 1197, 1988. 3 C c

GAM74 254 UBTF Chan, E. K. L.; Imai, H.; Hamel, J. C.; Tan, E. M.: Human autoantibodyto RNA polymerase I transcription factor hUBF: molecular identityof nucleolus organizer region autoantigen NOR- 90 and ribosomal RNAtranscription upstream binding factor. J. Exp. Med. 174: 1239- 1244,1991. 3 C c

GAM74 254 UBTF Hisatake, K.; Nishimura, T.; Maeda, Y.; Hanada, K.; Song, C.- Z.;Muramatsu, M.: Cloning and structural analysis of cDNA and the genefor mouse transcription factor UBF. Nuc. Acids Res. 19: 4631- 4637,1991. 3 C c

GAM74 254 UBTF Jantzen, H.- M.; Admon, A.; Bell, S. P.; Tjian, R.: Nucleolar 3 C c
transcriptionfactor hUBF contains a DNA- binding motif with homology to HMG
proteins. Nature 344:830- 836, 1990.

GAM74 254 UBTF Jones, K. A.; Black, D. M.; Griffiths, B. L.; Solomon, E.: Localizationof 3 C c
the human RNA polymerase I transcription factor gene (UBTF) tothe S17S183
locus on chromosome 17q21 and construction of a long- rangerestriction map
of the region. Genomics 30: 602- 604, 1995.

GAM74 254 UBTF Matera, A. G.; Wu, W.; Imai, H.; O'Keefe, C. L.; Chan, E. K. L.: Molecular 3 C c
cloning of the RNA polymerase I transcription factor hUBF/NOR- 90(UBTF) gene
and localization to 17q21.3 by fluorescence in situ hybridizationand
radiation hybrid mapping. Genomics 41: 135- 138, 1997.

GAM74 254 UBTF O'Mahony, D. J.; Rothblum, L. I.: Identification of two formsof the RNA 3 C c
polymerase I transcription factor UBF. Proc. Nat. Acad.Sci. 88: 3180- 3184,
1991.

GAM75 210 ADCY7 Hellevuo, K.; Berry, R.; Sikela, J. M.; Tabakoff, B.: Localizationof the 3 C c
gene for a novel human adenylyl cyclase (ADCY7) to chromosome16. Hum. Genet.
95: 197- 200, 1995.

GAM75 210 ADCY7 Hellevuo, K.; Yoshimura, M.; Kao, M.; Hoffman, P. L.; Cooper, D.M. F.; 3 C c
Tabakoff, B.: A novel adenylyl cyclase sequence cloned fromthe human
erythroleukemia cell line. Biochem. Biophys. Res. Commun. 192:311- 318,
1993.

GAM75 210 GCK Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 3 C c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.;
Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.;
Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the
2.8- Mb region containing the multiple endocrineneoplasia type 1 locus.
Genome Res. 7: 725- 735, 1997.

GAM75 210 GCK Katz, P.; Whalen, G.; Kehrl, J. H.: Differential expression ofa novel 3 C c
protein kinase in human B lymphocytes: preferential localizationin the
germinal center. J. Biol. Chem. 269: 16802- 16809, 1994.

GAM75 210 GCK Pombo, C. M.; Kehrl, J. H.; Sanchez, I.; Katz, P.; Avruch, J.;Zon, L. I.; 3 C c
Woodgett, J. R.; Force, T.; Kyriakis, J. M.: Activationof the SAPK pathway
by the human STE20 homologue germinal centre kinase. Nature 377:750- 754,
1995.

GAM75 210 GCK Ren, M.; Zeng, J.; De Lemos- Chiarandini, C.; Rosenfeld, M.; Adesnik,M.; 3 C c
Sabatini, D. D.: In its active form, the GTP- binding proteinrab8 interacts
with a stress- activated protein kinase. Proc. Nat.Acad. Sci. 93: 5151-
5155, 1996.

GAM75 210 GORASP1 Barr, F. A.; Nakamura, N.; Warren, G.: Mapping the interactionbetween 3 C c
GRASP65 and GM130, components of a protein complex involvedin the stacking
of Golgi cisternae. EMBO J. 17: 3258- 3268, 1998.

GAM75 210 GORASP1 Lane, J. D; Lucocq, J.; Pryde, J.; Barr, F. A.; Woodman, P. G.;Allan, V. J.; 3 C c
Lowe, M.: Caspase- mediated cleavage of the stackingprotein GRASP65 is
required for Golgi fragmentation during apoptosis. J.Cell Biol. 156: 495-
509, 2002.

GAM75 210 GORASP1 Sutterlin, C.; Hsu, P.; Mallabiabarrena, A.; Malhotra, V.: Fragmentationand 3 C c
dispersal of the pericentriolar Golgi complex is required forentry into
mitosis in mammalian cells. Cell 109: 359- 369, 2002.

GAM76 292 ARHGEF5 Chan, A. M- L.; McGovern, E. S.; Catalano, G.; Fleming, T. P.; Miki,T.: 3 C c
Expression cDNA cloning of a novel oncogene with sequence similarityto

regulators of small GTP- binding proteins. Oncogene 9: 1057- 1063,1994.

GAM76 292 ARHGEF5 Miki, T.; Fleming, T. P.; Crescenzi, M.; Molloy, C. J.; Blam, S.B.; 3 C c
Reynolds, S. H.; Aaronson, S. A.: Development of a highly
efficientexpression cDNA cloning system: application to oncogene isolation.
Proc.Nat. Acad. Sci. 88: 5167- 5171, 1991.

GAM76 292 ARHGEF5 Takai, S.; Chan, A. M.- L.; Yamada, K.; Miki, T.: Assignment ofthe human TIM 3 C c
proto- oncogene to 7q33- q35. Cancer Genet. Cytogenet. 83:87- 89, 1995.

GAM76 292 CHRNB4 Elliott, K. J.; Ellis, S. B.; Berckhan, K. J.; Urrutia, A.; Chavez- 3 C c
Noriega,L. E.; Johnson, E. C.; Velicelebi, G.; Harpold, M. M.:
Comparativestructure of human neuronal alpha(2)- alpha(7) and beta(2)-
beta(4)nicotinic acetylcholine receptor subunits and functional expressionof
the alpha(2), alpha(3), alpha(4), alpha(7), beta(2), and beta(4)subunits. J.
Molec. Neurosci. 7: 217- 228, 1996.

GAM76 292 CHRNB4 Groot Kormelink, P. J.; Luyten, W. H. M. L.: Cloning and sequenceof full- 3 C c
length cDNAs encoding the human neuronal nicotinic acetylcholinereceptor
(nAChR) subunits beta- 3 and beta- 4 and expression of sevennAChR subunits
in the human neuroblastoma cell line SH- SY5Y and/orIMR- 32. FEBS Lett. 400:
309- 314, 1997.

GAM76 292 CHRNB4 Khakh, B. S.; Zhou, X.; Sydes, J.; Galligan, J. J.; Lester, H.A.: State- 3 C c
dependent cross- inhibition between transmitter- gated cationchannels.
Nature 406: 405- 410, 2000.

GAM76 292 CHRNB4 Raimondi, E.; Rubboli, F.; Moralli, D.; Chini, B.; Fornasari, D.;Tarroni, 3 C c
P.; De Carli, L.; Clementi, F.: Chromosomal localizationand physical linkage
of the genes encoding the human alpha- 3, alpha- 5,and beta- 4 neuronal
nicotinic receptor subunits. Genomics 12: 849- 850,1992.

GAM76 292 CHRNB4 Tarroni, P.; Rubboli, F.; Chini, B.; Zwart, R.; Oortgiesen, M.;Sher, E.; 3 C c
Clementi, F.: Neuronal- type nicotinic receptors in humanneuroblastoma and
small- cell lung carcinoma cell lines. FEBS Lett. 312:66- 70, 1992.

GAM76 292 PRTN3 Belaaouaj, A.; Walsh, B. C.; Jenkins, N. A.; Copeland, N. G.; Shapiro,S. D.: 3 C c
Characterization of the mouse neutrophil elastase gene andlocalization to
chromosome 10. Mammalian Genome 8: 5- 8, 1997.

GAM76 292 PRTN3 Campanelli, D.; Melchior, M.; Fu, Y.; Nakata, M.; Shuman, H.; Nathan,C.; 3 C c
Gabay, J. E.: Cloning of cDNA for proteinase 3: a serine
protease,antibiotic, and autoantigen from human neutrophils. J. Exp. Med.
172:1709- 1715, 1990.

GAM76 292 PRTN3 Davies, D. J.; Moran, J. E.; Niall, J. F.; Ryan, G. B.: Segmentalnecrotising 3 C c
glomerulonephritis with antineutrophil antibody: possiblearbovirus
aetiology. Brit. Med. J. 285: 606 only, 1982.

GAM76 292 PRTN3 Gupta, S. K.; Niles, J. L.; McCluskey, R. T.; Arnaout, M. A.:Identity of 3 C c
Wegener's autoantigen (P29) with proteinase 3 and myeloblastin.(Letter)
Blood 76: 2162 only, 1990.

GAM76 292 PRTN3 Jenne, D. E.; Tschopp, J.; Ludemann, J.; Utecht, B.; Gross, W.L.: Wegener's 3 C c
autoantigen decoded. (Letter) Nature 346: 520 only,1990.

GAM76 292 PRTN3 Kao, R. C.; Wehner, N. G.; Skubitz, K. M.; Gray, B. H.; Hoidal,J. R.: 3 C c
Proteinase 3: a distinct human polymorphonuclear leukocyteproteinase that
produces emphysema in hamsters. J. Clin. Invest. 82:1963- 1973, 1988.

GAM76 292 PRTN3 Ludemann, J.; Utecht, B.; Gross, W. L.: Anti- neutrophil cytoplasmantibodies 3 C c
in Wegener's granulomatosis recognize an elastinolyticenzyme. J. Exp. Med.
171: 357- 362, 1990.

GAM76 292 PRTN3 Lutz, P. G.; Moog- Lutz, C.; Coumau- Gatbois, E.; Kobari, L.; DiGioia, Y.; 3 C c

Cayre, Y. E.: Myeloblastin is a granulocyte colony- stimulatingfactor-responsive gene conferring factor- independent growth to hematopoieticcells. Proc. Nat. Acad. Sci. 97: 1601- 1606, 2000.

GAM76 292 PRTN3 Niles, J. L.; McCluskey, R. T.; Ahmad, M. F.; Arnaout, M. A.:Wegener's granulomatosis autoantigen is a novel neutrophil serineproteinase. Blood 74: 1888- 1893, 1989. 3 C c

GAM76 292 PRTN3 Sturrock, A. B.; Espinosa, R., III; Hoidal, J. R.; Le Beau, M.M.: Localization of the gene encoding proteinase- 3 (the Wegener'sgranulomatosis autoantigen) to human chromosome band 19p13.3. Cytogenet.Cell Genet. 64: 33-34, 1993. 3 C c

GAM76 292 PRTN3 Sturrock, A. B.; Franklin, K. F.; Rao, G.; Marshall, B. C.; Rebentisch,M. B.; Lemons, R. S.; Hoidal, J. R.: Structure, chromosomal assignment,and expression of the gene for proteinase- 3: the Wegener's granulomatosisautoantigen. J. Biol. Chem. 267: 21193- 21199, 1992. 3 C c

GAM76 292 PRTN3 Sugawara, S.; Uehara, A.; Nochi, T.; Yamaguchi, T.; Ueda, H.;Sugiyama, A.; Hanzawa, K.; Kumagai, K.; Okamura, H.; Takada, H.:Neutrophil proteinase 3-mediated induction of bioactive IL- 18 secretionby human oral epithelial cells. J. Immun. 167: 6568- 6575, 2001. 3 C c

GAM76 292 PRTN3 Zimmer, M.; Medcalf, R. L.; Fink, T. M.; Mattmann, C.; Lichter,P.; Jenne, D. E.: Three human elastase- like genes coordinately expressedin the myelomonocyte lineage are organized as a single genetic locuson 19pter. Proc. Nat. Acad. Sci. 89: 8215- 8219, 1992. 3 C c

GAM76 292 SMTN Engelen, J. J. M.; Esterling, L. E.; Albrechts, J. C. M.; Detera-Wadleigh,S. D.; van Eys, G. J. J. M.: Assignment of the human gene for smoothelin(SMTN) to chromosome 22q12 by fluorescence in situ hybridization andradiation hybrid mapping. Genomics 43: 245- 247, 1997. 3 C c

GAM76 292 SMTN Rensen, S.; Merkx, G.; Doevendans, P.; Geurts van Kessel, A.; vanEys, G.: Structure and chromosome location of Smtn, the mouse smoothelingene. Cytogenet. Cell Genet. 89: 225- 229, 2000. 3 C c

GAM76 292 SMTN van der Loop, F. T. L.; Schaart, G.; Timmer, E. D. J.; Ramaekers,F. C. S.; van Eys, G. J. J. M.: Smoothelin, a novel cytoskeletalprotein specific for smooth muscle cells. J. Cell Biol. 134: 401- 411,1996. 3 C c

GAM78 277 GOSR2 Bui, T. D.; Levy, E. R.; Subramaniam, V. N.; Lowe, S. L.; Hong,W.: cDNA characterization and chromosomal mapping of human GolgiSNARE GS27 and GS28 to chromosome 17. Genomics 57: 285- 288, 1999. 3 C c

GAM78 277 GOSR2 Hay, J. C.; Chao, D. S.; Kuo, C. S.; Scheller, R. H.: Proteininteractions regulating vesicle transport between the endoplasmicreticulum and Golgi apparatus in mammalian cells. Cell 89: 149- 158,1997. 3 C c

GAM78 277 GOSR2 Lowe, S. L.; Peter, F.; Subramaniam, V. N.; Wong, S. H.; Hong,W.: A SNARE involved in protein transport through the Golgi apparatus. Nature 389:881-884, 1997. 3 C c

GAM80 362 SYK Colucci, F.; Schweighoffer, E.; Tomasello, E.; Turner, M.; Ortaldo,J. R.; Vivier, E.; Tybulewicz, V. L. J.; Di Santo, J. P.: Naturalcytotoxicity uncoupled from the Syk and ZAP- 70 intracellular kinases. NatureImmun. 3: 288- 294, 2002. 3 C c

GAM80 362 SYK Coopman, P. J. P.; Do, M. T. H.; Barth, M.; Bowden, E. T.; Hayes,A. J.; Basyuk, E.; Blancato, J. K.; Vezza, P. R.; McLeskey, S. W.;Mangeat, P. H.; Mueller, S. C.: The Syk tyrosine kinase suppressesmalignant growth of human breast cancer cells. Nature 406: 742- 747,2000. 3 C c

GAM80 362 SYK Inatome, R.; Yanagi, S.; Takano, T.; Yamamura, H.: A criticalrole for Syk in 3 C c

endothelial cell proliferation and migration. Biochem.Biophys. Res. Commun. 286: 195- 199, 2001.

GAM80 362 SYK Ku, G.; Malissen, B.; Mattei, M.- G.: Chromosomal location of theSyk and ZAP- 70 tyrosine kinase genes in mice and humans. Immunogenetics 40:300- 302, 1994. 3 C c

GAM80 362 SYK Mocsai, A.; Zhou, M.; Meng, F.; Tybulewicz, V. L.; Lowell, C. A.: Syk is required for integrin signaling in neutrophils. Immunity 16:547- 558, 2002. 3 C c

GAM80 362 SYK Muller, B.; Cooper, L.; Terhorst, C.: Molecular cloning of thehuman homologue to the pig protein- tyrosine kinase syk. Immunogenetics 39:359- 362, 1994. 3 C c

GAM80 362 SYK Taniguchi, T.; Kobayashi, T.; Kondo, J.; Takahashi, K.; Nakamura,H.; Suzuki, J.; Nagai, K.; Yamada, T.; Nakamura, S.; Yamamura, H.: Molecular cloning of a porcine gene syk that encodes a 72- kDa protein- tyrosinekinase showing high susceptibility to proteolysis. J. Biol. Chem. 266:15790- 15796, 1991. 3 C c

GAM80 362 SYK Toyabe, S.- I.; Watanabe, A.; Harada, W.; Karasawa, T.; Uchiyama,M.: Specific immunoglobulin E responses in ZAP- 70- deficient patientsare mediated by Syk- dependent T- cell receptor signalling. Immunology 103:164- 171, 2001. 3 C c

GAM80 362 SYK Zioncheck, T. F.; Harrison, M. L.; Isaacson, C. C.; Geahlen, R.L.: Generation of an active protein- tyrosine kinase from lymphocytesby proteolysis. J. Biol. Chem. 263: 19195- 19202, 1988. 3 C c

GAM81 256 CNTFR Davis, S.; Aldrich, T. H.; Valenzuela, D. M.; Wong, V.; Furth,M. E.; Squinto, S. P.; Yancopoulos, G. D.: The receptor for ciliaryneurotrophic factor. Science 253: 59- 63, 1991. 3 C c

GAM81 256 CNTFR DeChiara, T. M.; Vejsada, R.; Poueymirou, W. T.; Acheson, A.; Suri,C.; Conover, J. C. Friedman, B.; McClain, J.; Pan, L.; Stahl, N.;Ip, N. Y.; Kato, A.; Yancopoulos, G. D.: Mice lacking the CNTF receptor,unlike mice lacking CNTF, exhibit profound motor neuron deficits atbirth. Cell 83: 313- 322, 1995. 3 C c

GAM81 256 CNTFR Donaldson, D. H.; Britt, D. E.; Jones, C.; Jackson, C. L.; Patterson,D.: Localization of the gene for the ciliary neurotrophic factorreceptor (CNTFR) to human chromosome 9. Genomics 17: 782- 784, 1993. 3 C c

GAM81 256 CNTFR Pilz, A.; Woodward, K.; Povey, S.; Abbott, C.: Comparative mappingof 50 human chromosome 9 loci in the laboratory mouse. Genomics 25:139- 149, 1995. 3 C c

GAM81 256 CNTFR Valenzuela, D. M.; Rojas, E.; Le Beau, M. M.; Espinosa, R., III;Brannan, C. I.; McClain, J.; Masiakowski, P.; Ip, N. Y.; Copeland,N. G.; Jenkins, N. A.; Yancopoulos, G. D.: Genomic organization andchromosomal localization of the human and mouse genes encoding thealpha receptor component for ciliary neurotrophic factor. Genomics 25:157- 163, 1995. 3 C c

GAM81 256 SLC25A11 Iacobazzi, V.; Palmieri, F.; Runswick, M. J.; Walker, J. E.: Sequencesof the human and bovine genes for the mitochondrial 2- oxoglutaratecarrier. DNA Seq. 3: 79- 88, 1992. 3 C c

GAM81 256 SLC25A11 Piccininni, S.; Iacobazzi, V.; Lauria, G.; Rocchi, M.; Palmieri,F.: Assignment of the oxoglutarate carrier gene (SLC20A4) to humanchromosome 17p13.3. Cytogenet. Cell Genet. 83: 256- 257, 1998. 3 C c

GAM82 333 ADAMTS5 Abbaszade, I.; Liu, R.- Q.; Yang, F.; Rosenfeld, S. A.; Ross, O.H.; Link, J. R.; Ellis, D. M.; Tortorella, M. D.; Pratta, M. A.; Hollis,J. M.; Wynn, R.; Duke, J. L.; and 15 others: Cloning and characterizationof ADAMTS11, an aggrecanase from the ADAMTS family. J. Biol. Chem. 274:23443- 23450, 1999. 3 C c

GAM82 333 ADAMTS5 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- 3 C c

TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.

GAM82 333 CSNK2A1 Boldyreff, B.; Klett, C.; Gottert, E.; Geurts van Kessel, A.; Hameister,H.; Issinger, O.- G.: Assignment of casein kinase 2 alpha sequencesto two different human chromosomes. Hum. Genet. 89: 79- 82, 1992. 3 C c

GAM82 333 CSNK2A1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 3 C c

GAM82 333 CSNK2A1 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine 392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292, 2001. 3 C c

GAM82 333 CSNK2A1 Meisner, H.; Heller- Harrison, R.; Buxton, J.; Czech, M. P.: Molecularcloning of the human casein kinase II alpha subunit. Biochemistry 28:4072- 4076, 1989. 3 C c

GAM82 333 CSNK2A1 Wirkner, U.; Voss, H.; Lichter, P.; Ansorge, W.; Pyerin, W.: Thehuman gene (CSNK2A1) coding for the casein kinase II subunit alphais located on chromosome 20 and contains tandemly arranged Alu repeats. Genomics 19:257- 265, 1994. 3 C c

GAM82 333 CSNK2A1 Wirkner, U.; Voss, H.; Lichter, P.; Weitz, S.; Ansorge, W.; Pyerin,W.: Human casein kinase II subunit alpha: sequence of a processed(pseudo)gene and its localization on chromosome 11. Biochim. Biophys.Acta 1131: 220- 222, 1992. 3 C c

GAM82 333 CSNK2A1 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping of the human casein kinase II catalytic subunit genes: twoloci carrying the homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125- 7129, 1991. 3 C c

GAM83 287 ACE Amant, C.; Bauters, C.; Bodart, J.- C.; Lablanche, J.- M.; Grollier,G.; Danchin, N.; Hamon, M.; Richard, F.; Helbecque, N.; McFadden,E. P.; Amouyel, P.; Bertrand, M. E.: D allele of the angiotensinI- converting enzyme is a major risk factor for restenosis after coronarystenting. Circulation 96: 56- 60, 1997. 1 A c

GAM83 287 ACE Arbustini, E.; Grasso, M.; Fasani, R.; Klersy, C.; Diegoli, M.;Porcu, E.; Banchieri, N.; Fortina, P.; Danesino, C.; Specchia, G.: Angiotensin converting enzyme gene deletion allele is independentlyand strongly associated with coronary atherosclerosis and myocardialinfarction. Brit. Heart J. 74: 584- 591, 1995. 1 A c

GAM83 287 ACE Berge, K. E.; Berg, K.: No effect of insertion/deletion polymorphismat the ACE locus on normal blood pressure level or variability. Clin.Genet. 45: 169- 174, 1994. 1 A c

GAM83 287 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: Insertion/deletion(I/D) polymorphism at the locus for angiotensin I- converting enzymeand myocardial infarction. Clin. Genet. 44: 292- 297, 1993. 1 A c

GAM83 287 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: Insertion/deletion(I/D) polymorphism at the locus for angiotensin I- converting enzymeand parental history of myocardial infarction. Clin. Genet. 44:298- 301, 1993. 1 A c

GAM83 287 ACE Brown, N. J.; Ray, W. A.; Snowden, M.; Griffin, M. R.: Black Americanshave an increased rate of angiotensin converting enzyme inhibitor- associatedangioedema. Clin. Pharmacol. Therapeutics 60: 8- 13, 1996. 1 A c

GAM83 287 ACE Cambien, F.; Alhenc- Gelas, F.; Herbeth, B.; Andre, J. L.; Rakotovao,R.; 1 A c
Gonzales, M. F.; Allegrini, J.; Bloch, C.: Familial resemblanceof plasma
angiotensin- converting enzyme level: the Nancy study. Am.J. Hum. Genet. 43:
774- 780, 1988.

GAM83 287 ACE Cambien, F.; Poirier, O.; Lecerf, L.; Evans, A.; Cambou, J.- P.;Arveiler, 1 A c
D.; Luc, G.; Bard, J.- M.; Bara, L.; Ricard, S.; Tiret, L.;Amouyel, P.;
Alhenc- Gelas, F.; Soubrier, F.: Deletion polymorphismin the gene for
angiotensin- converting enzyme is a potent risk factorfor myocardial
infarction. Nature 359: 641- 644, 1992.

GAM83 287 ACE Doria, A.; Warram, J. H.; Krolewski, A. S.: Genetic predispositionto 1 A c
diabetic nephropathy: evidence for a role of the angiotensin I-
convertingenzyme gene. Diabetes 43: 690- 695, 1994.

GAM83 287 ACE Ehlers, M. R. W.; Fox, E. A.; Strydom, D. J.; Riordan, J. F.:Molecular 1 A c
cloning of human testicular angiotensin- converting enzyme:the testis
isozyme is identical to the C- terminal half of endothelialangiotensin-
converting enzyme. Proc. Nat. Acad. Sci. 86: 7741- 7745,1989.

GAM83 287 ACE Esther, C. R., Jr.; Marino, E. M.; Howard, T. E.; Machaud, A.;Corvol, P.; 1 A c
Capecchi, M. R.; Bernstein, K. E.: The critical roleof tissue angiotensin-
converting enzyme as revealed by gene targetingin mice. J. Clin. Invest. 99:
2375- 2385, 1997.

GAM83 287 ACE Evans, A. E.; Poirier, O.; Kee, F.; Lecerf, L.; McCrum, E.; Falconer,T.; 1 A c
Crane, J.; O'Rourke, D. F.; Cambien, F.: Polymorphisms of theangiotensin-
converting- enzyme gene in subjects who die from coronaryheart disease.
Quart. J. Med. 87: 211- 214, 1994.

GAM83 287 ACE Exner, D. V.; Dries, D. L.; Domanski, M. J.; Cohn, J. N.: Lesserresponse to 1 A c
angiotensin- converting- enzyme inhibitor therapy in blackas compared with
white patients with left ventricular dysfunction. NewEng. J. Med. 344: 1351-
1357, 2001.

GAM83 287 ACE Gardemann, A.; Fink, M.; Stricker, J.; Nguyen, Q. D.; Humme, J.;Katz, N.; 1 A c
Tillmanns, H.; Hehrlein, F. W.; Rau, M.; Haberbosch, W.: ACE I/D gene
polymorphism: presence of the ACE D allele increasesthe risk of coronary
artery disease in younger individuals. Atherosclerosis 139:153- 159, 1998.

GAM83 287 ACE Gayagay, G.; Yu, B.; Hambly, B.; Boston, T.; Hahn, A.; Celermajer,D. S.; 1 A c
Trent, R. J.: Elite endurance athletes and the ACE I allele:the role of
genes in athletic performance. Hum. Genet. 103: 48- 50,1998.

GAM83 287 ACE Hagaman, J. R.; Moyer, J. S.; Bachman, E. S.; Sibony, M.; Magyar,P. L.; 1 A c
Welch, J. E.; Smithies, O.; Krege, J. H.; O'Brien, D. A.:Angiotensin-
converting enzyme and male fertility. Proc. Nat. Acad.Sci. 95: 2552- 2557,
1998.

GAM83 287 ACE Hamdi, H. K.; Reznik, J.; Castellon, R.; Atilano, S. R.; Ong,J. M.; Udar, 1 A c
N.; Tavis, J. H.; Aoki, A. M.; Nesburn, A. B.; Boyer,D. S.; Small, K. W.;
Brown, D. J.; Kenney, M. C.: Alu DNA polymorphismin ACE gene is protective
for age- related macular degeneration. Biochem.Biophys. Res. Commun. 295:
668- 672, 2002.

GAM83 287 ACE Howard, T. E.; Shai, S. Y.; Langford, K. G.; Martin, B. M.; Bernstein,K. E.: 1 A c
Transcription of testicular angiotensin- converting enzyme(ACE) is initiated
within the 12th intron of the somatic ACE gene. Molec.Cell. Biol. 10: 4294-
4302, 1990.

GAM83 287 ACE Huang, W.; Gallois, Y.; Bouby, N.; Bruneval, P.; Heudes, D.; Belair,M.- F.; 1 A c
Krege, J. H.; Menteton, P.; Marre, M.; Smithies, O.; Alhenc- Gelas,F.:

Genetically increased angiotensin I- converting enzyme level andrenal complications in the diabetic mouse. Proc. Nat. Acad. Sci. 98:13330- 13334, 2001.

GAM83 287 ACE Jeffery, S.; Malik, A. K. S.; Crosby, A.; Bland, M.; Eastwood,J. B.; Amoah- 1 A c
Danquah, J.; Acheampong, J. W.; Plange- Rhule, J.: Adominant relationship between the ACE D allele and serum ACE levelsin a Ghanaian population. (Letter) J. Med. Genet. 36: 869- 870, 1999.

GAM83 287 ACE Jeunemaitre, X.; Lifton, R. P.; Hunt, S. C.; Williams, R. R.;Lalouel, J.- 1 A c
M.: Absence of linkage between the angiotensin convertingenzyme locus and human essential hypertension. Nature Genet. 1:72- 75, 1992.

GAM83 287 ACE Julier, C.; Delepine, M.; Keavney, B.; Terwilliger, J.; Davis,S.; Weeks, D. 1 A c
E.; Bui, T.; Jeunemaitre, X.; Velho, G.; Froguel, P.;Ratcliffe, P.; Corvol, P.; Soubrier, F.; Lathrop, G. M.: Geneticsusceptibility for human familial essential hypertension in a regionof homology with blood pressure linkage on rat chromosome 10. Hum.Molec. Genet. 6: 2077- 2085, 1997.

GAM83 287 ACE Keavney, B.; McKenzie, C.; Parish, S.; Palmer, A.; Clark, S.;Youngman, L.; 1 A c
Delepine, M.; Lathrop, M.; Peto, R.; Collins, R.: Large- scaletest of hypothesized associations between the angiotensin- converting- enzymeinsertion/deletion polymorphism and myocardial infarction in about5000 cases and 6000 controls. Lancet 355: 434- 442, 2000.

GAM83 287 ACE Kehoe, P. G.; Russ, C.; McIlroy, S.; Williams, H.; Holmans, P.;Holmes, C.; 1 A c
Liolitsa, D.; Vahidassr, D.; Powell, J.; McGleenon, B.;Liddell, M.; Plomin, R.; and 9 others: Variation in DCP1, encodingACE, is associated with susceptibility to Alzheimer disease. (Letter) NatureGenet. 21: 71- 72, 1999.

GAM83 287 ACE Keramatipour, M.; McConnell, R. S.; Kirkpatrick, P.; Tebbs, S.;Furlong, R. 1 A c
A.; Rubinsztein, D. C.: The ACE I allele is associatedwith increased risk for ruptured intracranial aneurysms. J. Med.Genet. 37: 498- 500, 2000.

GAM83 287 ACE Krege, J. H.; John, S. W. M.; Langenbach, L. L.; Hodgin, J. B.;Hagaman, J. 1 A c
R.; Bachman, E. S.; Jennette, J. C.; O'Brien, D. A.; Smithies,O.: Male- female differences in fertility and blood pressure in ACE- deficientmice. Nature 375: 146- 148, 1995.

GAM83 287 ACE Kurtz, T. W.: The ACE of hearts. Nature 359: 588- 589, 1992. 1 A c

GAM83 287 ACE Lindpaintner, K.; Lee, M.; Larson, M. G.; Rao, V. S; Pfeffer,M. A.; Ordovas, 1 A c
J. M.; Schaefer, E. J.; Wilson, A. F.; Wilson, P.W. F.; Vasan, R. S.; Myers, R. H.; Levy, D.: Absence of associationor genetic linkage between the angiotensin- converting- enzyme geneand left ventricular mass. New Eng. J. Med. 334: 1023- 1028, 1996.

GAM83 287 ACE Lindpaintner, K.; Pfeffer, M. A.; Kreutz, R.; Stampfer, M. J.;Grodstein, F.; 1 A c
LaMotte, F.; Buring, J.; Hennekens, C. H.: A prospectiveevaluation of an angiotensin- converting- enzyme gene polymorphism andthe risk of ischemic heart disease. New Eng. J. Med. 332: 706- 711,1995.

GAM83 287 ACE Marre, M.; Bernadet, P.; Gallois, Y.; Savagner, F.; Guyene, T.- T.;Hallab, 1 A c
M.; Cambien, F.; Passa, P.; Alhenc- Gelas, F.: Relationshipsbetween angiotensin I converting enzyme gene polymorphism, plasmalevels, and diabetic retinal and renal complications. Diabetes 43:384- 388, 1994.

GAM83 287 ACE Marre, M.; Jeunemaitre, X.; Gallois, Y.; Rodier, M.; Chatellier,G.; Sert, 1 A c
C.; Dusselier, L.; Kahal, Z.; Chaillous, L.; Halimi, S.;Muller, A.; Sackmann, H.; Bauduceau, B.; Bled, F.; Passa, P.; Alhenc- Gelas,F.: Contribution of genetic polymorphism in the renin- angiotensinsystem to the development of renal complications in insulin- dependentdiabetes. J. Clin.

Invest. 99: 1585- 1595, 1997.

GAM83 287 ACE Mattei, M.- G.; Hubert, C.; Alhenc- Gelas, F.; Roeckel, N.; Corvol,P.; Soubrier, F.: Angiotensin- I converting enzyme gene is on chromosome17. (Abstract) Cytogenet. Cell Genet. 51: 1041, 1989. 1 A c

GAM83 287 ACE Montgomery, H. E.; Clarkson, P.; Dollery, C. M.; Prasad, K.; Losi,M.- A.; Hemingway, H.; Statters, D.; Jubb, M.; Girvain, M.; Varnava,A.; World, M.; Deanfield, J.; Talmud, P.; McEwan, J. R.; McKenna,W. J.; Humphries, S.: Association of angiotensin- converting enzymegene I/D polymorphism with change in left ventricular mass in responseto physical training. Circulation 96: 741- 747, 1997. 1 A c

GAM83 287 ACE Montgomery, H. E.; Marshall, R.; Hemingway, H.; Myerson, S.; Clarkson,P.; Dollery, C.; Hayward, M.; Holliman, D. E.; Jubb, M.; World, M.;Thomas, E. L.; Brynes, A. E.; Saeed, N.; Barnard, M.; Bell, J. D.;Prasad, K.; Rayson, M.; Talmud, P. J.; Humphries, S. E.: Human genefor physical performance. (Letter) Nature 393: 221- 222, 1998. 1 A c

GAM83 287 ACE Ohishi, M.; Fujii, K.; Minamino, T.; Hagaki, J.; Kamitani, A.;Rakugi, H.; Zhao, Y.; Mikami, H.; Miki, T.; Ogihara, T.: A potentgenetic risk factor for restenosis. (Letter) Nature Genet. 5: 324- 325,1993. 1 A c

GAM83 287 ACE Oike, Y.; Hata, A.; Ogata, Y.; Numata, Y.; Shido, K.; Kondo, K.: Angiotensin converting enzyme as a genetic risk factor for coronaryartery spasm: implication in the pathogenesis of myocardial infarction. J.Clin. Invest. 96: 2975- 2979, 1995. 1 A c

GAM83 287 ACE Okabe, T.; Fusisawa, M.; Yotsumoto, M.; Takaru, F.; Lanzillo,J. J.; Fanburg, B. L.: Familial elevation of serum angiotensin- convertingenzyme. Quart. J. Med. 216: 55- 61, 1985. 1 A c

GAM83 287 ACE Pfeffer, M. A.; Braunwald, E.; Moye, L. A.; Basta, L.; Brown,E. J., Jr.; Cuddy, T. E.; Davis, B. R.; Geltman, E. M.; Goldman, S.;Flaker, G. C.; Klein, M.; Lamas, G. A.; Packer, M.; Rouleau, J.; Rouleau,J. L.; Rutherford, J.; Wertheimer, J. H.; Hawkins, C. M.: Effectof captopril on mortality and morbidity in patients with left ventriculardysfunction after myocardial infarction: results of the survival andventricular enlargement trial. New Eng. J. Med. 327: 669- 677, 1992. 1 A c

GAM83 287 ACE Ramaraj, P.; Kessler, S. P.; Colmenares, C.; Sen, G. C.: Selectiverestoration of male fertility in mice lacking angiotensin-convertingenzymes by sperm- specific expression of the testicular isozyme. J.Clin. Invest. 102: 371- 378, 1998. 1 A c

GAM83 287 ACE Rigat, B.; Hubert, C.; Alhenc- Gelas, F.; Cambien, F.; Corvol,P.; Soubrier, F.: An insertion/deletion polymorphism in the angiotensinI- converting enzyme gene accounting for half the variance of serumenzyme levels. J. Clin. Invest. 86: 1343- 1346, 1990. 1 A c

GAM83 287 ACE Rigat, B.; Hubert, C.; Corvol, P.; Soubrier, F.: PCR detectionof the insertion/deletion polymorphism of the human angiotensin convertingenzyme gene (DCP1) (dipeptidylcarboxypeptidase 1). Nucleic AcidsRes. 20: 1433, 1992. 1 A c

GAM83 287 ACE Ruiz, J.; Blanche, H.; Cohen, N.; Velho, G.; Cambien, F.; Cohen,D.; Passa, P.; Froguel, P.: Insertion/deletion polymorphism of theangiotensin-converting enzyme gene is strongly associated with coronaryheart disease in non- insulin- dependent diabetes mellitus. Proc. Nat.Acad. Sci. 91: 3662-3665, 1994. 1 A c

GAM83 287 ACE Schachter, F.; Faure- Delanef, L.; Guenot, F.; Rouger, H.; Froguel,P.; 1 A c

Lesueur- Ginot, L.; Cohen, D.: Genetic associations with humanlongevity at the APOE and ACE loci. Nature Genet. 6: 29- 32, 1994.

GAM83 287 ACE Schmidt, S.; Schone, N.; Ritz, E.; Giesel, R.; Bergis, K.; Strojek,K.; Greszczak, W.; Schroter, W.; Willms, B. H. L.; Petzold, R.; Henrichs,H. R.; Rambausek, M.; Schwarzbeck, A.; Kohr, B.; Schneider, P.; Bosch,A.: Association of ACE gene polymorphism and diabetic nephropathy? KidneyInt. 47: 1176- 1181, 1995. 1 A c

GAM83 287 ACE Schunkert, H.; Hense, H.- W.; Holmer, S. R.; Stender, M.; Perz,S.; Keil, U.; Lorell, B. H.; Riegger, G. A. J.: Association betweena deletion polymorphism of the angiotensin- converting- enzyme geneand left ventricular hypertrophy. New Eng. J. Med. 330: 1634- 1638,1994. 1 A c

GAM83 287 ACE Singer, D. R. J.; Missouris, C. G.; Jeffery, S.: Angiotensin-convertingenzyme gene polymorphism: what to do about all the confusion? (Editorial) Circulation 94:236- 239, 1996. 1 A c

GAM83 287 ACE Soubrier, F.; Alhenc- Gelas, F.; Hubert, C.; Allegrini, J.; John,M.; Tregear, G.; Corvol, P.: Two putative active centers in humanangiotensin I-converting enzyme revealed by molecular cloning. Proc.Nat. Acad. Sci. 85: 9386- 9390, 1988. 1 A c

GAM83 287 ACE Tarnow, L.; Cambien, F.; Rossing, P.; Nielsen, F. S.; Hansen,B. V.; Lecerf, L.; Poirier, O.; Danilov, S.; Parving, H.- H.: Lackof relationship between an insertion/deletion polymorphism in theangiotensin I- converting enzyme gene and diabetic nephropathy andproliferative retinopathy in IDDM patients. Diabetes 44: 489- 494,1995. 1 A c

GAM83 287 ACE Tiret, L.; Rigat, B.; Visvikis, S.; Breda, C.; Corvol, P.; Cambien,F.; Soubrier, F.: Evidence, from combined segregation and linkageanalysis, that a variant of the angiotensin I- converting enzyme (ACE)gene controls plasma ACE levels. Am. J. Hum. Genet. 51: 197- 205,1992. 1 A c

GAM83 287 ACE Vleming, L. J.; van der Pijl, J. W.; Lemkes, H. H. P. J.; Westendorp,R. G. J.; Maassen, J. A.; Daha, M. R.; van Es, L. A.; van Kooten,C.: The DD genotype of the ACE gene polymorphism is associated withprogression of diabetic nephropathy to end stage renal failure inIDDM. Clin. Nephrol. 51: 133- 140, 1999. 1 A c

GAM83 287 ACE Williams, A. G.; Rayson, M. P.; Jubb, M.; World, M.; Woods, D.R.; Hayward, M.; Martin, J.; Humphries, S. E.; Montgomery, H. E.:The ACE gene and muscle performance. Nature 403: 614 only, 2000. 1 A c

GAM83 287 ACE Winkelmann, B. R.; Nauck, M.; Klein, B.; Russ, A. P.; Bohm, B.O.; Siekmeier, R.; Ihnken, K.; Verho, M.; Gross, W.; Marz, W.: Deletionpolymorphism of the angiotensin I- converting enzyme gene is associatedwith increased plasma angiotensin- converting enzyme activity but notwith increased risk for myocardial infarction and coronary arterydisease. Ann. Intern. Med. 125: 19-25, 1996. 1 A c

GAM83 287 ACE Woods, D.; Onambele, G.; Woledge, R.; Skelton, D.; Bruce, S.;Humphries, S. E.; Montgomery, H.: Angiotensin- I converting enzymegenotype- dependent benefit from hormone replacement therapy in isometricmuscle strength and bone mineral density. J. Clin. Endocr. Metab. 86:2200- 2204, 2001. 1 A c

GAM83 287 ACE Yoshida, H.; Mitarai, T.; Kawamura, T.; Kitajima, T.; Miyazaki,Y.; Nagasawa, R.; Kawaguchi, Y.; Kubo, H.; Ichikawa, I.; Sakai, O.: Role of the deletion polymorphism of the angiotensin convertingenzyme gene in the progression and therapeutic responsiveness of IgAnephropathy. J. Clin. Invest. 96: 2162-2169, 1995. 1 A c

GAM83 287 ACE Yoshioka, T.; Xu, Y.; Yoshida, H.; Shiraga, H.; Muraki, T.; Ito,K.: Deletion 1 A c
polymorphism of the angiotensin converting enzyme genepredicts persistent
proteinuria in Henoch- Schonlein purpura nephritis. Arch.Dis. Child. 79:
394- 399, 1998.

GAM83 287 ACE Zhu, X.; Bouzekri, N.; Southam, L.; Cooper, R. S.; Adeyemo, A.;McKenzie, C. 1 A c
A.; Luke, A.; Chen, G.; Elston, R. C.; Ward, R.: Linkageand association
analysis of angiotensin I- converting enzyme (ACE)- genepolymorphisms with
ACE concentration and blood pressure. Am. J. Hum.Genet. 68: 1139- 1148,
2001.

GAM83 287 ACE Zhu, X.; McKenzie, C. A.; Forrester, T.; Nickerson, D. A.; Broeckel,U.; 1 A c
Schunkert, H.; Doering, A.; Jacob, H. J.; Cooper, R. S.; Rieder,M. J.:
Localization of a small genomic region associated with elevatedACE. Am. J.
Hum. Genet. 67: 1144- 1153, 2000. Note: Erratum: Am.J. Hum. Genet. 67: 1365
only, 2000.

GAM83 287 ASPH Jia, S.; VanDusen, W. J.; Diehl, R. E.; Kohl, N. E.; Dixon, R.A. F.; 1 A c
Elliston, K. O.; Stern, A. M.; Friedman, P. A.: cDNA cloningand expression
of bovine aspartyl (asparaginyl) beta- hydroxylase. J.Biol. Chem. 267:
14322- 14327, 1992.

GAM83 287 ASPH Korioth, F.; Gieffers, C.; Frey, J.: Cloning and characterizationof the 1 A c
human gene encoding aspartyl beta- hydroxylase. Gene 150:395- 399, 1994.

GAM83 287 ASPH Lavaissiere, L.; Jia, S.; Nishiyama, M.; de la Monte, S.; Stern,A. M.; 1 A c
Wands, J. R.; Friedman, P. A.: Overexpression of human
aspartyl(asparaginyl)- beta- hydroxylasein hepatocellular carcinoma and
cholangiocarcinoma. J. Clin. Invest. 98:1313- 1323, 1996.

GAM83 287 ASPH Lim, K. Y.; Hong, C.- S.; Kim, D. H.: cDNA cloning and characterizationof 1 A c
human cardiac junctin. Gene 255: 35- 42, 2000.

GAM83 287 ASPH Scott, A. F.: Personal Communication. Baltimore, Md. 2/19/2001. 1 A c

GAM83 287 ASPH Treves, S.; Feriotto, G.; Moccagatta, L.; Gambari, R.; Zorzato,F.: Molecular 1 A c
cloning, expression, functional characterization, chromosomallocalization,
and gene structure of junctate, a novel integral calciumbinding protein of
sarco(endo)plasmic reticulum membrane. J. Biol.Chem. 275: 39555- 39568,
2000.

GAM83 287 ASPH Wetzel, G. T.; Ding, S.; Chen, F.: Molecular cloning of junctinfrom human 1 A c
and developing rabbit heart. Molec. Genet. Metab. 69:252- 258, 2000.

GAM83 287 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 1 A c
Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.:
Identification of Bach2 as a B- cell- specific partner for smallMaf proteins
that negatively regulate the immunoglobulin heavy chaingene 3- prime
enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM83 287 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 1 A c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-
basic leucine zipper transcription factors that interact withMafK and
regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-
6095, 1996.

GAM83 287 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, 1 A c
A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.;
Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B
cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene
19: 3739- 3749, 2000.

GAM83 287 CASP10 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 1 A c

Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.; Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a novel human apoptotic cysteine protease containingtwo FADD- like domains. Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM83 287 CASP10 Park, W. S.; Lee, J. H.; Shin, M. S.; Park, J. Y.; Kim, H. S.;Lee, J. H.; Kim, Y. S.; Lee, S. N.; Xiao, W.; Park, C. H.; Lee, S.H.; Yoo, N. J.; Lee, J. Y.: Inactivating mutations of the caspase- 10gene in gastric cancer. Oncogene 21: 2919- 2925, 2002. 1 A c

GAM83 287 CASP10 Shin, M. S.; Kim, H. S.; Kang, C. S.; Park, W. S.; Kim, S. Y.;Lee, S. N.; Lee, J. H.; Park, J. Y.; Jang, J. J.; Kim, C. W.; Kim,S. H.; Lee, J. Y.; Yoo, N. J.; Lee, S. H.: Inactivating mutationsof CASP10 gene in non- Hodgkin lymphomas. Blood 99: 4094- 4099, 2002. 1 A c

GAM83 287 CASP10 Vincenz, C.; Dixit, V. M.: Fas- associated death domain proteininterleukin- 1- beta- converting enzyme 2 (FLICE2), an ICE/Ced- 3 homologue,is proximally involved in CD95- and p55- mediated death signaling. J.Biol. Chem. 272: 6578- 6583, 1997. 1 A c

GAM83 287 CASP10 Wang, J.; Chun, H. J.; Wong, W.; Spencer, D. M.; Lenardo, M. J.: Caspase- 10 is an initiator caspase in death receptor signaling. Proc.Nat. Acad. Sci. 98: 13884- 13888, 2001. 1 A c

GAM83 287 CASP10 Wang, J.; Zheng, L.; Lobito, A.; Chan, F. K.; Dale, J.; Sneller,M.; Yao, X.; Puck, J. M.; Straus, S. E.; Lenardo, M. J.: Inheritedhuman caspase 10 mutations underlie defective lymphocyte and dendriticcell apoptosis in autoimmune lymphoproliferative syndrome type II. Cell 98:47- 58, 1999. 1 A c

GAM83 287 CCKBR Beinborn, M.; Lee, Y.- M.; McBride, E. W.; Quinn, S. M.; Kopin,A. S.: A single amino acid of the cholecystokinin- B/gastrin receptordetermines specificity for non- peptide antagonists. Nature 362:348- 350, 1993. 1 A b

GAM83 287 CCKBR Huppi, K.; Siwarski, D.; Pisegna, J. R.; Wank, S.: Chromosomallocalization of the gastric and brain receptors for cholecystokinin(CCKAR and CCKBR) in human and mouse. Genomics 25: 727- 729, 1995. 1 A b

GAM83 287 CCKBR Lee, Y.- M.; Beinborn, M.; McBride, E. W.; Lu, M.; Kolakowski, L.F., Jr.; Kopin, A. S.: The human brain cholecystokinin- B/gastrinreceptor: cloning and characterization. J. Biol. Chem. 268: 8164- 8169,1993. 1 A b

GAM83 287 CCKBR Pisegna, J. R.; de Weerth, A.; Huppi, K.; Wank, S. A.: Molecularcloning of the human brain and gastric cholecystokinin receptor: structure,functional expression and chromosomal localization. Biochem. Biophys.Res. Commun. 189: 296- 303, 1992. 1 A b

GAM83 287 CCKBR Samuelson, L. C.; Isakoff, M. S.; Lacourse, K. A.: Localizationof the murine cholecystokinin A and B receptor genes. MammalianGenome 6: 242- 246, 1995. 1 A b

GAM83 287 CCKBR Zimonjic, D. B.; Popescu, N. C.; Matsui, T.; Ito, M.; Chihara,K.: Localization of the human cholecystokinin- B/gastrin receptorgene (CCKBR) to chromosome 11p15.5- p15.4 by fluorescence in situ hybridization.Cytogenet. Cell Genet. 65: 184- 185, 1994. 1 A b

GAM83 287 CX3CR1 Faure, S.; Meyer, L.; Costagliola, D.; Vaneensberghe, C.; Genin,E.; Autran, B.; French ALT and IMMUNOCO Study Groups; Delfraisay,J.- F.; SEROCO Study Group; McDermott, D. H.; Murphy, P. M.; Debre,P.; Theodorou, I.; Cambadiere, C.: Rapid progression to AIDS in HIV+individuals with a structural variant of the chemokine receptor CX(3)CR1. Science 287:2274- 2277, 2000. 1 A c

GAM83 287 CX3CR1 Imai, T.; Hieshima, K.; Haskell, C.; Baba, M.; Nagira, M.; Nishimura,M.; Kakizaki, M.; Takagi, S.; Nomiyama, H.; Schall, T. J.; Yoshie,O.: Identification and molecular characterization of fractalkinereceptor CX3CR1, 1 A c

which mediates both leukocyte migration and adhesion. Cell 91:521- 530, 1997.

GAM83 287 CX3CR1 Maho, A.; Bensimon, A.; Vassart, G.; Parmentier, M.: Mapping ofthe CCXCR1, 1 A c CX3CR1, CCBP2 and CCR9 genes to the CCR cluster withinthe 3p21.3 region of the human genome. Cytogenet. Cell Genet. 87:265- 268, 1999.

GAM83 287 CX3CR1 Moatti, D.; Faure, S.; Fumeron, F.; Amara, M. E. W.; Seknadji,P.; McDermott, 1 A c D. H.; Debre, P.; Aumont, M. C.; Murphy, P. M.; deProst, D.; Combadiere, C.: Polymorphism in the fractalkine receptorCX3CR1 as a genetic risk factor for coronary artery disease. Blood 97:1925- 1928, 2001.

GAM83 287 CX3CR1 Raport, C. J.; Schweickart, V. L.; Eddy, R. L., Jr.; Shows, T.B.; Gray, P. 1 A c W.: The orphan G- protein- coupled receptor- encoding geneV28 is closely related to genes for chemokine receptors and is expressedin lymphoid and neural tissues. Gene 163: 295- 299, 1995.

GAM83 287 CX3CR1 Tripp, R. A.; Jones, L. P.; Haynes, L. M.; Zheng, H.; Murphy, P.M.; 1 A c Anderson, L. J.: CX3C chemokine mimicry by respiratory syncytialvirus G glycoprotein. Nature Immun. 2: 732- 738, 2001.

GAM83 287 DHCR24 Greeve, I.; Hermans- Borgmeyer, I.; Brellinger, C.; Kasper, D.;Gomez- Isla, 1 A c T.; Behl, C.; Levkau, B.; Nitsch, R. M.: The human DIMINUTO/DWARF1homolog seladin- 1 confers resistance to Alzheimer's disease- associatedneurodegeneration and oxidative stress. J. Neurosci. 20: 7345- 7352,2000.

GAM83 287 DHCR24 Nomura, N.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Kawarabayasi,Y.; Sato, S.; 1 A c Nagase, T.; Seki, N.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. I. The codingsequences of 40 new genes (KIAA0001- KIAA0040) deduced by analysisof randomly sampled cDNA clones from human immature myeloid cell lineKG- 1. DNA Res. 1: 27- 35, 1994.

GAM83 287 DHCR24 Sarkar, D.; Imai, T.; Kambe, F.; Shibata, A.; Ohmori, S.; Siddiq,A.; 1 A c Hayasaka, S.; Funahashi, H.; Seo, H.: The human homolog of Diminuto/Dwarf1gene (hDiminuto): a novel ACTH- responsive gene overexpressed in benigncortisol- producing adrenocortical adenomas. J. Clin. Endocr. Metab. 86:5130- 5137, 2001.

GAM83 287 DHCR24 Waterham, H. R.; Koster, J.; Romeijn, G. J.; Hennekam, R. C. M.;Vreken, P.; 1 A c Andersson, H. C.; FitzPatrick, D. R.; Kelley, R. I.; Wanders,R. J. A.: Mutations in the 3- beta- hydroxysterol delta- 24- reductasegene cause desmosterolosis, an autosomal recessive disorder of cholesterolbiosynthesis. Am. J. Hum. Genet. 69: 685- 694, 2001.

GAM83 287 E2F3 Cloud, J. E.; Rogers, C.; Reza, T. L.; Ziebold, U.; Stone, J. R.;Picard, M. 1 A c H.; Caron, A. M.; Bronson, R. T.; Lees, J. A.: Mutantmouse models reveal the relative roles of E2F1 and E2F3 in vivo. Molec.Cell. Biol. 22: 2663- 2672, 2002.

GAM83 287 E2F3 He, Y.; Armanious, M. K.; Thomas, M. J.; Cress, W. D.: Identificationof E2F- 1 A c 3B, an alternative form of E2F- 3 lacking a conserved N- terminalregion. Oncogene 19: 3422- 3433, 2000.

GAM83 287 E2F3 Lees, J. A.; Saito, M.; Vidal, M.; Valentine, M.; Look, T.; Harlow,E.; 1 A c Dyson, N.; Helin, K.: The retinoblastoma protein binds to a familyof E2F transcription factors. Molec. Cell. Biol. 13: 7813- 7825,1993.

GAM83 287 E2F3 Leone, G.; Sears, R.; Huang, E.; Rempel, R.; Nuckolls, F.; Park,C.- H.; 1 A c Giangrande, P.; Wu, L.; Saavedra, H. I.; Field, S. J.; Thompson,M. A.; Yang, H.; Fujiwara, Y.; Greenberg, M. E.; Orkin, S.; Smith,C.; Nevins, J. R.: Myc requires distinct E2F activities to induceS phase and apoptosis. Molec. Cell

8: 105- 113, 2001.

GAM83 287 E2F3 Wu, L.; Timmers, C.; Maiti, B.; Saavedra, H. I.; Sang, L.; Chong,G. T.; 1 A c
Nuckolls, F.; Giangrande, P.; Wright, F. A.; Field, S. J.;Greenberg, M. E.;
Orkin, S.; Nevins, J. R.; Robinson, M. L.; Leone,G.: The E2F1- 3
transcription factors are essential for cellular proliferation. Nature
414:457- 462, 2001.

GAM83 287 FKBP2 Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.;Forbes, S. A.; 1 A c
Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B.T.; Farnebo, F.;
Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud,S.; Zhang, C. X.; Salandre,
J.; Calender, A.: Definition of the minimalMEN1 candidate area based on a 5-
Mb integrated map of proximal 11q13. Genomics 37:354- 365, 1996.

GAM83 287 FKBP2 DiLella, A. G.; Hawkins, A.; Craig, R. J.; Schreiber, S. L.; Griffin,C. A.: 1 A c
Chromosomal band assignments of the genes encoding human FKBP12and FKBP13.
Biochem. Biophys. Res. Commun. 189: 819- 823, 1992.

GAM83 287 FKBP2 Jin, Y. J.; Albers, M. W.; Lane, W. S.; Bierer, B. E.; Schreiber,S. L.; 1 A c
Burakoff, S. J.: Molecular cloning of a membrane- associatedhuman FK506-
and rapamycin- binding protein, FKBP- 13. Proc. Nat. Acad.Sci. 88: 6677-
6681, 1991.

GAM83 287 GPLD1 LeBoeuf, R. C.; Caldwell, M.; Guo, Y.; Metz, C.; Davitz, M. A.;Olson, L. K.; 1 A c
Deeg, M. A.: Mouse glycosylphosphatidylinositol- specificphospholipase D
(Gpld1) characterization. Mammalian Genome 9: 710- 714,1998.

GAM83 287 GPLD1 Scallon, B. J.; Fung, W.- J. C.; Tsang, T. C.; Li, S.; Kado- Fong,H.; Huang, 1 A c
K.- S.; Kochan, J. P.: Primary structure and functionalactivity of a
phosphatidylinositol- glycan- specific phospholipase D. Science 252:446-
448, 1991.

GAM83 287 GPLD1 Schofield, J. N.; Rademacher, T. W.: Structure and expressionof the human 1 A c
glycosylphosphatidylinositol phospholipase D1 (GPLD1)gene. Biochim. Biophys.
Acta 1494: 189- 194, 2000.

GAM83 287 GPLD1 Tsang, T. C.; Fung, W.- J.; Levine, J.; Metz, C. N.; Davitz, M.A.; Burns, D. 1 A c
K.; Huang, K.- S.; Kochan, J. P.: Isolation and expressionof two human
glycosylphosphatidylinositol phospholipase D (GPI- PLD)cDNAs. (Abstract)
FASEB J. (supp.) 6: A1922 only, 1992.

GAM83 287 HOXB7 Acampora, D.; D'Esposito, M.; Faiella, A.; Pannese, M.; Migliaccio,E.; 1 A c
Morelli, F.; Stornaiuolo, A.; Nigro, V.; Simeone, A.; Boncinelli,E.: The
human HOX gene family. Nucleic Acids Res. 17: 10385- 10402,1989.

GAM83 287 HOXB7 Lill, M. C.; Fuller, J. F.; Herzig, R.; Crooks, G. M.; Gasson,J. C.: The 1 A c
role of the homeobox gene, HOX B7, in human myelomonocyticdifferentiation.
Blood 85: 692- 697, 1995.

GAM83 287 HOXB7 Simeone, A.; Mavilio, F.; Acampora, D.; Giampaolo, A.; Faiella,A.; 1 A c
Zappavigna, V.; D'Esposito, M.; Pannese, M.; Russo, G.; Boncinelli,E.;
Peschle, C.: Two human homeobox genes, c1 and c8: structure analysisand
expression in embryonic development. Proc. Nat. Acad. Sci. 84:4914- 4918,
1987.

GAM83 287 HOXB7 Yaron, Y.; McAdara, J. K.; Lynch, M.; Hughes, E.; Gasson, J. C.: 1 A c
Identification of novel functional regions important for the activityof
HOXB7 in mammalian cells. J. Immun. 166: 5058- 5067, 2001.

GAM83 287 IGF2R Acquati, F.; Malgaretti, N.; Hauptschein, R.; Rao, P.; Gaidano,G.; 1 A c
Taramelli, R.: A 2- Mb YAC contig linking the plasminogen- apoprotein(a)gene
family to the insulin- like growth factor 2 receptor (IGF2R) geneon the
telomeric region of chromosome 6 (6q26- q27). Genomics 22:664- 666, 1994.

GAM83 287 IGF2R Barlow, D. P.; Stoger, R.; Herrmann, B. G.; Saito, K.; Schweifer,N.: The mouse insulin- like growth factor type- 2 receptor is imprintedand closely linked to the Tme locus. Nature 349: 84- 87, 1991. 1 A c

GAM83 287 IGF2R De Souza, A. T.; Hankins, G. R.; Washington, M. K.; Fine, R. L.;Orton, T. C.; Jirtle, R. L.: Frequent loss of heterozygosity on 6qat the mannose 6-phosphate/insulin- like growth factor II receptorlocus in human hepatocellular tumors. Oncogene 10: 1725- 1729, 1995. 1 A c

GAM83 287 IGF2R De Souza, A. T.; Hankins, G. R.; Washington, M. K.; Orton, T. C.;Jirtle, R. L.: M6P/IGF2R gene is mutated in human hepatocellularcarcinomas with loss of heterozygosity. Nature Genet. 11: 447- 449,1995. 1 A c

GAM83 287 IGF2R DeChiara, T. M.; Robertson, E. J.; Efstratiadis, A.: Parentalimprinting of the mouse insulin- like growth factor II gene. Cell 64:849- 859, 1991. 1 A c

GAM83 287 IGF2R Feinberg, A. P.: Genomic imprinting and gene activation in cancer. NatureGenet. 4: 110- 113, 1993. 1 A c

GAM83 287 IGF2R Haig, D.; Graham, C.: Genomic imprinting and the strange caseof the insulin- like growth factor II receptor. Cell 64: 1045- 1046,1991. 1 A c

GAM83 287 IGF2R Haig, D.; Westoby, M.: Parent- specific gene expression and thetriploid endosperm. Am. Nat. 134: 147- 155, 1989. 1 A c

GAM83 287 IGF2R Kalscheuer, V. M.; Mariman, E. C.; Schepens, M. T.; Rehder, H.;Ropers, H.-H.: The insulin- like- growth factor type- 2 receptor geneis imprinted in the mouse but not in humans. Nature Genet. 5: 74- 78,1993. 1 A c

GAM83 287 IGF2R Kiess, W.; Blickenstaff, G. D.; Sklar, M. M.; Thomas, C. L.; Nissley,S. P.; Sahagian, G. G.: Biochemical evidence that the type II insulin- likegrowth factor receptor is identical to the cation- independent mannose6- phosphate receptor. J. Biol. Chem. 263: 9339- 9344, 1988. 1 A c

GAM83 287 IGF2R Killian, J. K.; Oka, Y.; Jang, H.- S.; Fu, X.; Waterland, R. A.;Sohda, T.; Sakaguchi, S.; Jirtle, R. L.: Mannose 6- phosphate/insulin- likegrowth factor 2 receptor (M6P/IGF2R) variants in American and Japanesepopulations. Hum. Mutat. 18: 25- 31, 2001. 1 A c

GAM83 287 IGF2R Kornfeld, S.; Mellman, I.: The biogenesis of lysosomes. Annu.Rev. Cell Biol. 5: 483- 525, 1989. 1 A c

GAM83 287 IGF2R Lau, M. M. H.; Stewart, C. E. H.; Liu, Z.; Bhatt, H.; Rotwein,P.; Stewart, C. L.: Loss of the imprinted IGF2/cation- independentmannose 6- phosphate receptor results in fetal overgrowth and perinatallethality. Genes Dev. 8: 2953- 2963, 1994. 1 A c

GAM83 287 IGF2R Laureys, G.; Barton, D. E.; Ullrich, A.; Francke, U.: Chromosomalmapping of the gene for the type II insulin- like growth factor receptor/cation-independentmannose 6- phosphate receptor in man and mouse. Genomics 3: 224-229,1988. 1 A c

GAM83 287 IGF2R MacDonald, R. G.; Pfeffer, S. R.; Coussens, L.; Tepper, M. A.;Brocklebank, C. M.; Mole, J. E.; Anderson, J. K.: A single receptorbinds both insulin-like growth factor II and mannose- 6- phosphate. Science 239:1134- 1137, 1988. 1 A c

GAM83 287 IGF2R Morgan, D. O.; Edman, J. D.; Standring, D. N.; Fried, V. A.; Smith,M. C.; Roth, R. A.; Rutter, W. J.: Insulin- like growth factor IIreceptor as a multifunctional binding protein. Nature 329: 301- 307,1987. 1 A c

GAM83 287 IGF2R Motyka, B.; Korbutt, G.; Pinkoski, M. J.; Heibein, J. A.; Caputo,A.; Hobman, M.; Barry, M.; Shostak, I.; Sawchuk, T.; Holmes, C. F.B.; Gauldie, J.; Bleackley, R. C.: Mannose 6- phosphate/insulin- likegrowth factor II receptor is a death receptor for granzyme B duringcytotoxic T cell- induced 1 A c

apoptosis. Cell 103: 491- 500, 2000.

GAM83 287 IGF2R Ogawa, O.; McNoe, L. A.; Eccles, M. R.; Morison, I. M.; Reeve,A. E.: Human 1 A c
insulin- like growth factor type I and type II receptorsare not imprinted.
Hum. Molec. Genet. 2: 2163- 2165, 1993.

GAM83 287 IGF2R Oshima, A.; Nolan, C. M.; Kyle, J. W.; Grubb, J. H.; Sly, W. S.: The human 1 A c
cation- independent mannose 6- phosphate receptor: cloningand sequence of
the full- length cDNA and expression of functionalreceptor in COS cells. J.
Biol. Chem. 263: 2553- 2562, 1988.

GAM83 287 IGF2R Puertollano, R.; Aguilar, R. C.; Gorshkova, I.; Crouch, R. J.;Bonifacino, J. 1 A c
S.: Sorting of mannose 6- phosphate receptors mediatedby the GGAs. Science
292: 1712- 1716, 2001.

GAM83 287 IGF2R Rao, P. H.; Murty, V. V. V. S.; Gaidano, G.; Hauptschein, R.;Dalla- Favera, 1 A c
R.; Chaganti, R. S. K.: Subregional mapping of 8 singlecopy loci to
chromosome 6 by fluorescence in situ hybridization. Cytogenet.Cell Genet.
66: 272- 273, 1994.

GAM83 287 IGF2R Roth, R. A.: Structure of the receptor for insulin- like growthfactor II: 1 A c
the puzzle amplified. Science 239: 1269- 1271, 1988.

GAM83 287 IGF2R Sleutels, F.; Zwart, R.; Barlow, D. P.: The non- coding Air RNAis required 1 A c
for silencing autosomal imprinted genes. Nature 415:810- 813, 2002.

GAM83 287 IGF2R Souza, R. F.; Appel, R.; Yin, J.; Wang, S.; Smolinski, K. N.;Abraham, J. M.; 1 A c
Zou, T.- T.; Shi, Y.- Q.; Lei, J.; Cottrell, J.; Cymes,K.; Biden, K.; Simms,
L.; Leggett, B.; Lynch, P. M.; Frazier, M.;Powell, S. M.; Harpaz, N.;
Sugimura, H.; Young, J.; Meltzer, S. J.: Microsatellite instability in the
insulin- like growth factor IIreceptor gene in gastrointestinal tumours.
(Letter) Nature Genet. 14:255- 257, 1996.

GAM83 287 IGF2R Szebeny, G.; Rotwein, P.: The mouse insulin- like growth factorII/cation- 1 A c
independent mannose 6- phosphate (IGF- II/MPR) receptor gene:molecular
cloning and genomic organization. Genomics 19: 120- 129,1994.

GAM83 287 IGF2R Tong, P. Y.; Tollefsen, S. E.; Kornfeld, S.: The cation- independentmannose 1 A c
6- phosphate receptor binds insulin- like growth factor II. J.Biol. Chem.
263: 2585- 2588, 1988.

GAM83 287 IGF2R Waheed, A.; Braulke, T.; Junghans, U.; von Figura, K.: Mannose6- 1 A c
phosphate/insulin like growth factor II receptor: the two typesof ligands
bind simultaneously to one receptor at different sites. Biochem.Biophys.
Res. Commun. 152: 1248- 1254, 1988.

GAM83 287 IGF2R Xu, Y.; Goodyer, C. G.; Deal, C.; Polychronakos, C.: Functionalpolymorphism 1 A c
in the parental imprinting of the human IGF2R gene. Biochem.Biophys. Res.
Commun. 197: 747- 754, 1993.

GAM83 287 IGF2R Young, L. E.; Fernandes, K.; McEvoy, T. G.; Butterwith, S. C.;Gutierrez, C. 1 A c
G.; Carolan, C.; Broadbent, P. J.; Robinson, J. J.;Wilmut, I.; Sinclair, K.
D.: Epigenetic change in IGF2R is associatedwith fetal overgrowth after
sheep embryo culture. Nature Genet. 27:153- 154, 2001.

GAM83 287 IGF2R Zhu, Y.; Doray, B.; Poussu, A.; Lehto, V.- P.; Kornfeld, S.: Bindingof GGA2 1 A c
to the lysosomal enzyme sorting motif of the mannose 6- phosphatereceptor.
Science 292: 1716- 1718, 2001.

GAM83 287 IMMP2L Boghosian- Sell, L.; Comings, D. E.; Overhauser, J.: Tourette syndromein a 1 A c
pedigree with a 7;18 translocation: identification of a YAC spanningthe
translocation breakpoint at 18q22.3. Am. J. Hum. Genet. 59:999- 1005, 1996.

GAM83 287 IMMP2L Petek, E.; Windpassinger, C.; Vincent, J. B.; Cheung, J.; Boright,A. P.; 1 A c
Scherer, S. W.; Kroisel, P. M.; Wagner, K.: Disruption ofa novel gene

(IMMP2L) by a breakpoint in 7q31 associated with Tourettesyndrome. Am. J. Hum. Genet. 848- 858, 2001.

GAM83 287 ITK Cheng, G.; Ye, Z.- S.; Baltimore, D.: Binding of Bruton's tyrosinekinase to Fyn, Lyn, or Hck through a Src homology 3 domain- mediatedinteraction. Proc. Nat. Acad. Sci. 91: 8152- 8155, 1994. 1 A c

GAM83 287 ITK Gibson, S.; Leung, B.; Squire, J. A.; Hill, M.; Arima, N.; Goss,P.; Hogg, D.; Mills, G. B.: Identification, cloning, and characterizationof a novel human T- cell- specific tyrosine kinase located at the hematopoietincomplex on chromosome 5q. Blood 82: 1561- 1572, 1993. 1 A c

GAM83 287 ITK Janis, E. M.; Siliciano, J. D.; Isaac, D. D.; Griffin, C. A.; Hawkins,A. L.; Kozak, C. A.; Desiderio, S.: Mapping of the gene for the tyrosinekinase Itk to a region of conserved synteny between mouse chromosome11 and human chromosome 5q. Genomics 23: 269- 271, 1994. 1 A c

GAM83 287 ITK Schaeffer, E. M.; Debnath, J.; Yap, G.; McVicar, D.; Liao, X. C.;Littman, D. R.; Sher, A.; Varmus, H. E.; Lenardo, M. J.; Schwartzberg,P. L.: Requirement for Tec kinases Rlk and Itk in T cell receptorsignaling and immunity. Science 284: 638- 641, 1999. 1 A c

GAM83 287 ITK Woods, M. L.; Kivens, W. J.; Adelsman, M. A.; Qiu, Y.; August,A.; Shimizu, Y.: A novel function for the Tec family tyrosine kinaseItk in activation of beta- 1 integrins by the T- cell receptor. EMBOJ. 20: 1232- 1244, 2001. 1 A c

GAM83 287 LARGE Grewal, P. K.; Holzfeind, P. J.; Bittner, R. E.; Hewitt, J. E.: Mutant glycosyltransferase and altered glycosylation of alpha- dystroglycanin the myodystrophy mouse. Nature Genet. 28: 151- 154, 2001. 1 A c

GAM83 287 LARGE Michele, D. E.; Barresi, R.; Kanagawa, M.; Saito, F.; Cohn, R.D.; Satz, J. S.; Dollar, J.; Nishino, I.; Kelley, R. I.; Somer, H.;Straub, V.; Mathews, K. D.; Moore, S. A.; Campbell, K. P.: Post- translationaldisruption of dystroglycan- ligand interactions in congenital musculardystrophies. Nature 418: 417- 422, 2002. 1 A c

GAM83 287 LARGE Peyrard, M.; Seroussi, E.; Sandberg- Nordqvist, A.- C.; Xie, Y.- G.;Han, F.- Y.; Fransson, I.; Collins, J.; Dunham, I.; Kost- Alimova, M.;Imreh, S.; Dumanski, J. P.: The human LARGE gene from 22q12.3- q13.1is a new, distinct member of the glycosyltransferase gene family. Proc.Nat. Acad. Sci. 96: 598- 603, 1999. 1 A c

GAM83 287 LTA Aggarwal, B. B.; Eessalu, T. E.; Hass, P. E.: Characterizationof receptors for human tumour necrosis factor and their regulationby gamma- interferon. Nature 318: 665- 667, 1985. 1 A c

GAM83 287 LTA Evans, A. M.; Petersen, J. W.; Sekhon, G. S.; DeMars, R.: Mappingof prolactin and tumor necrosis factor- beta genes on human chromosome6p using lymphoblastoid cell deletion mutants. Somat. Cell Molec.Genet. 15: 203- 213, 1989. 1 A c

GAM83 287 LTA Gray, P. W.; Aggarwal, B. B.; Benton, C. V.; Bringman, T. S.; Henzel,W. J.; Jarrett, J. A.; Leung, D. W.; Moffat, B.; Ng, P.; Svedersky,L. P.; Palladino, M. A.; Nedwin, G. E.: Cloning and expression ofcDNA for human lymphotoxin, a lymphokine with tumour necrosis activity. Nature 312:721- 724, 1984. 1 A c

GAM83 287 LTA Jongeneel, C. V.; Briant, L.; Udalova, I. A.; Sevin, A.; Nedospasov,S. A.; Cambon- Thomsen, A.: Extensive genetic polymorphism in thehuman tumor necrosis factor region and relation to extended HLA haplotypes. Proc.Nat. Acad. Sci. 88: 9717- 9721, 1991. 1 A c

GAM83 287 LTA Koss, K.; Satsangi, J.; Fanning, G. C.; Welsh, K. I.; Jewell, D.P.: Cytokine 1 A c

(TNF- alpha, LT- alpha, and IL- 10) polymorphisms in inflammatorybowel diseases and normal controls: differential effects on productionand allele frequencies. Genes Immun. 1: 185- 190, 2000.

GAM83 287 LTA Spies, T.; Blanck, G.; Bresnahan, M.; Sands, J.; Strominger, J.L.: A new cluster of genes within the human major histocompatibilitycomplex. Science 243: 214- 217, 1989. 1 A c

GAM83 287 MEIS1 Mercader, N.; Leonardo, E.; Azpiazu, N.; Serrano, A.; Morata, G.;Martinez- A, C.; Torres, M.: Conserved regulation of proximodistallimb axis development by Meis1/Hth. Nature 402: 425- 429, 1999. 1 A c

GAM83 287 MEIS1 Moskow, J. J.; Bullrich, F.; Huebner, K.; Daar, I. O.; Buchberg,A. M.: Meis1, a PBX1- related homeobox gene involved in myeloid leukemiain BXH- 2 mice. Molec. Cell. Biol. 15: 5434- 5443, 1995. 1 A c

GAM83 287 MEIS1 Steelman, S.; Moskow, J. J.; Muzynski, K.; North, C.; Druck, T.;Montgomery, J. C.; Huebner, K.; Daar, I. O.; Buchberg, A. M.: Identificationof a conserved family of Meis1- related homeobox genes. Genome Res. 7:142- 156, 1997. 1 A c

GAM83 287 MEIS1 Thorsteinsdottir, U.; Kroon, E.; Jerome, L.; Blasi, F.; Sauvageau,G.: Defining roles for HOX and MEIS1 genes in induction of acutemyeloid leukemia. Molec. Cell. Biol. 21: 224- 234, 2001. 1 A c

GAM83 287 MFAP2 Chen, Y.; Faraco, J.; Yin, W.; Germiller, J.; Francke, U.; Bonadio,J.: Structure, chromosomal localization, and expression pattern ofthe murine Magp gene. J. Biol. Chem. 268: 27381- 27389, 1993. 1 A c

GAM83 287 MFAP2 Faraco, J.; Bashir, M.; Rosenbloom, J.; Francke, U.: Characterizationof the human gene for microfibril- associated glycoprotein (MFAP2),assignment to chromosome 1p36.1- p35, and linkage to D1S170. Genomics 25:630- 637, 1995. 1 A c

GAM83 287 MFAP2 Gibson, M. A.; Hughes, J. L.; Fanning, J. C.; Cleary, E. G.: Themajor antigen of elastin- associated microfibrils is a 31- kDa glycoprotein.J. Biol. Chem. 261: 11429- 11436, 1986. 1 A c

GAM83 287 MFAP2 Low, F. N.: Microfibrils: fine filamentous components of the tissuespace. Anat. Rec. 142: 131- 137, 1962. 1 A c

GAM83 287 NEK6 Kimura, M.; Okano, Y.: Identification and assignment of the humanNIMA- related protein kinase 7 gene (NEK7) to human chromosome 1q31.3. Cytogenet.Cell Genet. 94: 33- 38, 2001. 1 A c

GAM83 287 NEK6 Li, M. Z.; Yu, L.; Liu, Q.; Chu, J. Y.; Zhao, S. Y.: Assignmentof NEK6, a NIMA- related gene, to human chromosome 9q33.3- q34.11 byradiation hybrid mapping. Cytogenet. Cell Genet. 87: 271- 272, 1999. 1 A c

GAM83 287 PDE5A Loughney, K.; Hill, T. R.; Florio, V. A.; Uher, L.; Rosman, G.J.; Wolda, S. L.; Jones, B. A.; Howard, M. L.; McAllister- Lucas, L.M.; Sonnenburg, W. K.; Francis, S. H.; Corbin, J. D.; Beavo, J. A.;Ferguson, K.: Isolation and characterization of cDNAs encoding PDE5A,a human cGMP- binding, cGMP- specific 3- prime,5- prime- cyclic nucleotidephosphodiesterase. Gene 216: 139- 147, 1998. 1 A c

GAM83 287 PDE5A Stacey, P.; Rulten, S.; Dapling, A.; Phillips, S. C.: Molecularcloning and expression of human cGMP- binding cGMP- specific phosphodiesterase(PDE5). Biochem. Biophys. Res. Commun. 247: 249- 254, 1998. 1 A c

GAM83 287 PDE5A Yanaka, N.; Kotera, J.; Ohtsuka, A.; Akatsuka, H.; Imai, Y.; Michibata,H.; Fujishige, K.; Kawai, E.; Takebayashi, S.- I.; Okumura, K.; Omori,K.: Expression, structure and chromosomal localization of the humancGMP- binding cGMP- specific phosphodiesterase PDE5A gene. Eur. J.Biochem. 255: 391- 399, 1998. 1 A c

GAM83 287 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 1 A c
Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J
recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585,
2002.

GAM83 287 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 1 A c
cell coactivator of octamer- binding transcription factors. Nature 373:360-
362, 1995.

GAM83 287 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 1 A c
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-
specific coactivator of octamer- binding transcription factors1 and 2, to
11q23.1 by somatic cell hybridization and in situ hybridization. Genomics
33:143- 145, 1996.

GAM83 287 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 1 A c
of action of the B- cell- specific transcriptional activatorOCA- B. Molec.
Cell. Biol. 15: 4115- 4124, 1995.

GAM83 287 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 1 A c
Matthias, P.: B cell development and immunoglobulin gene transcriptionin the
absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM83 287 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 1 A c
Immun. 9: 373- 398, 1991.

GAM83 287 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 1 A c
specificcoactivator that stimulates immunoglobulin promoter activity
throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM83 287 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 1 A c
Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B,
BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-
864, 2000.

GAM83 287 PPP1R3A Chen, Y. H.; Hansen, L.; Chen, M. X.; Bjorbaek, C.; Vestergaard,H.; Hansen, 1 A c
T.; Cohen, P. T. W.; Pedersen, O.: Sequence of the humanglycogen- associated
regulatory subunit of type 1 protein phosphataseand analysis of its coding
region and mRNA level in muscle from patientswith NIDDM. Diabetes 43: 1234-
1241, 1994.

GAM83 287 PPP1R3A Hansen, L.; Hansen, T.; Vestergaard, H.; Bjorbaek, C.; Echwald,S. M.; 1 A c
Clausen, J. O.; Chen, Y. H.; Chen, M. X.; Cohen, P. T. W.;Pedersen, O.: A
widespread amino acid polymorphism at codon 905 ofthe glycogen- associated
regulatory subunit of protein phosphatase- 1is associated with insulin
resistance and hypersecretion of insulin. Hum.Molec. Genet. 4: 1313- 1320,
1995.

GAM83 287 PPP1R3A Hegele, R. A.; Harris, S. B.; Zinman, B.; Wang, J.; Cao, H.; Hanley,A. J. 1 A c
G.; Tsui, L.- C.; Scherer, S. W.: Variation in the AU(AT)- richelement
within the 3- prime- untranslated region of PPP1R3 is associatedwith
variation in plasma glucose in aboriginal Canadians. J. Clin.Endocr. Metab.
83: 3980- 3983, 1998.

GAM83 287 PPP1R3A Savage, D. B.; Agostini, M.; Barroso, I.; Gurnell, M.; Luan, J.;Meirhaeghe, 1 A c
A.; Harding, A.- H.; Ihrke, G.; Rajanayagam, O.; Soos,M. A.; George, S.;
Berger, D.; and 9 others: Digenic inheritanceof severe insulin resistance in
a human pedigree. Nature Genet. 31:379- 384, 2002.

GAM83 287 PPP1R3A Tang, P. M.; Bondor, J. A.; Swiderek, K. M.; DePaoli- Roach, A.A.: Molecular 1 A c
cloning and expression of the regulatory (RG1) subunitof the glycogen-
associated protein phosphatase. J. Biol. Chem. 266:15782- 15789, 1991.

GAM83 287 PRDM2 Buyse, I. M.; Shao, G.; Huang, S.: The retinoblastoma proteinbinds to RIZ, a 1 A c
zinc- finger protein that shares an epitope with theadenovirus E1A protein.
Proc. Nat. Acad. Sci. 92: 4467- 4471, 1995.

GAM83 287 PRDM2 Buyse, I. M.; Takahashi, E.; Huang, S.: Physical mapping of 1 A c
theretinoblastoma interacting zinc finger gene RIZ to D1S228 on
chromosome1p36. Genomics 34: 119- 121, 1996.

GAM83 287 PRDM2 Chadwick, R. B.; Jiang, G.- L.; Bennington, G. A.; Yuan, B.; Johnson,C. K.; 1 A c
Stevens, M. W.; Niemann, T. H.; Peltomaki, P.; Huang, S.; dela Chapelle, A.:
Candidate tumor suppressor RIZ is frequently involvedin colorectal
carcinogenesis. Proc. Nat. Acad. Sci. 97: 2662- 2667,2000.

GAM83 287 PRDM2 Mock, B. A.; Coleman, M. P.; Huang, S.: Riz maps to distal chromosome4 near 1 A c
genes involved in tumorigenesis and nerve degeneration. MammalianGenome 7:
637 only, 1996.

GAM83 287 PRDM2 Poetsch, M.; Dittberner, T.; Woenckhaus, C.: Frameshift mutationsof RIZ, but 1 A c
no point mutations in RIZ1 exons in malignant melanomaswith deletions in
1p36. Oncogene 21: 3038- 3042, 2002.

GAM83 287 PYCR1 Dougherty, K. M.; Brandriss, M. C.; Valle, D.: Cloning human pyrroline- 5- 1 A c
carboxylatereductase cDNA by complementation in Saccharomyces cerevisiae.
J.Biol. Chem. 267: 871- 875, 1992.

GAM83 287 PYCR1 Merrill, M. J.; Yeh, G. C.; Phang, J. M.: Purified human 1 A c
erythrocytepyrroline- 5- carboxylate reductase: preferential oxidation of
NADPH. J.Biol. Chem. 264: 9352- 9358, 1989.

GAM83 287 RASGRP2 Kawasaki, H.; Springett, G. M.; Toki, S.; Canales, J. J.; Harlan,P.; 1 A c
Blumenstiel, J. P.; Chen, E. J.; Bany, I. A.; Mochizuki, N.; Ashbacher,A.;
Matsuda, M.; Housman, D. E.; Graybiel, A. M.: A Rap guanine
nucleotideexchange factor enriched highly in the basal ganglia. Proc.
Nat.Acad. Sci. 95: 13278- 13283, 1998.

GAM83 287 RASGRP2 Kedra, D.; Seroussi, E.; Fransson, I.; Trifunovic, J.; Clark, 1 A c
M.;Lagercrantz, J.; Blennow, E.; Mehlin, H.; Dumanski, J.: The
germinalcenter kinase gene and a novel CDC25- like gene are located in
thevicinity of the PYGM gene on 11q13. Hum. Genet. 100: 611- 619, 1997.

GAM83 287 RING1 Kikuti, Y. Y.; Tamiya, G.; Ando, A.; Chen, L.; Kimura, M.; Ferreira,E.; 1 A c
Tsuji, K.; Trowsdale, J.; Inoko, H.: Physical mapping 220 kbcentromeric of
the human MHC and DNA sequence analysis of the 43- kbsegment including the
RING1, HKE6, and HKE4 genes. Genomics 42:422- 435, 1997.

GAM83 287 RING1 Lovering, R.; Hanson, I. M.; Borden, K. L. B.; Martin, S.; O'Reilly,N. J.; 1 A c
Evan, G. I.; Rahman, D.; Pappin, D. J. C.; Trowsdale, J.; Freemont,P. S.:
Identification and preliminary characterization of a proteinmotif related to
the zinc finger. Proc. Nat. Acad. Sci. 90: 2112- 2116,1993.

GAM83 287 RING1 Satijn, D. P. E.; Gunster, M. J.; van der Vlag, J.; Hamer, K. M.;Schul, W.; 1 A c
Alkema, M. J.; Saurin, A. J.; Freemont, P. S.; van Driel,R.; Otte, A. P.:
RING1 is associated with the polycomb group proteincomplex and acts as a
transcriptional repressor. Molec. Cell. Biol. 17:4105- 4113, 1997.

GAM83 287 SFRS2IP Tanner, S.; Stagljar, I.; Georgiev, O.; Schaffner, W.; Bourquin,J.- P.: A 1 A c
novel SR- related protein specifically interacts with thecarboxy- terminal
domain (CTD) of RNA polymerase II through a conservedinteraction domain.
Biol. Chem. 378: 565- 571, 1997.

GAM83 287 SFRS2IP Zhang, W.- J.; Wu, J. Y.: Sip1, a novel RS domain- containing 1 A c
proteinessential for pre- mRNA splicing. Molec. Cell. Biol. 18: 676-
684,1998.

GAM83 287 SOX4 Critcher, R.; Stitson, R. N. M.; Wade- Martins, R.; Easty, D. J.;Farr, C. J.: Assignment of Sox4 to mouse chromosome 13 bands A3- A5by fluorescence in situ hybridization; refinement of the human SOX4location to 6p22.3 and of SOX20 to chromosome 17p12.3. Cytogenet.Cell Genet. 81: 294- 295, 1998. 1 A c

GAM83 287 SOX4 Denny, P.; Swift, S.; Connor, F.; Ashworth, A.: An SRY- relatedgene expressed during spermatogenesis in the mouse encodes a sequence-specificDNA- binding protein. EMBO J. 11: 3705- 3712, 1992. 1 A c

GAM83 287 SOX4 Farr, C. J.; Easty, D. J.; Ragoussis, J.; Collignon, J.; Lovell- Badge,R.; Goodfellow, P. N.: Characterization and mapping of the humanSOX4 gene. Mammalian Genome 4: 577- 584, 1993. 1 A c

GAM83 287 SOX4 Geijsen, N.; Uings, I. J.; Pals, C.; Armstrong, J.; McKinnon, M.;Raaijmakers, J. A. M.; Lammers, J.- W. J.; Koenderman, L.; Coffer,P. J.: Cytokine- specific transcriptional regulation through an IL- 5R-alphainteracting protein. Science 293: 1136- 1138, 2001. 1 A c

GAM83 287 SOX4 Hansen, G. M.; Skapura, D.; Justice, M. J.: Genetic profile ofinsertion mutations in mouse leukemias and lymphomas. Genome Res. 10:237- 243, 2000. 1 A c

GAM83 287 SOX4 Li, J.; et al; et al: Leukaemia disease genes: large- scale cloningand pathway predictions. Nature Genet. 23: 348- 353, 1999. 1 A c

GAM83 287 SOX4 Lund, A. H.; Turner, G.; Trubetskoy, A.; Verhoeven, E.; Wientjens,E.; Hulsman, D.; Russell, R.; DePinho, R. A.; Lenz, J.; van Lohuizen,M.: Genome-wide retroviral insertional tagging of genes involvedin cancer in Cdkn2a-deficient mice. Nature Genet. 32: 160- 165, 2002. 1 A c

GAM83 287 SOX4 Suzuki, T.; Shen, H.; Akagi, K.; Morse, H. C., III; Malley, J.D.; Naiman, D. Q.; Jenkins, N. A.; Copeland, N. G.: New genes involvedin cancer identified by retroviral tagging. Nature Genet. 32: 166- 174,2002. Note: Erratum: Nature Genet. 32: 331 only, 2002. 1 A c

GAM83 287 SOX4 van de Wetering, M.; Oosterwegel, M.; van Norren, K.; Clevers,H.: Sox- 4, an Sry- like HMG box protein, is a transcriptional activatoris lymphocytes. EMBO J. 12: 3847- 3854, 1993. 1 A c

GAM83 287 SSA1 Frank, M. B.; Itoh, K.; Fujisaku, A.; Pontarotti, P.; Mattei, M.- G.;Neas, B. R.: The mapping of the human 52- kD Ro/SSA autoantigen geneto human chromosome 11, and its polymorphisms. Am. J. Hum. Genet. 52:183- 191, 1993. 1 A c

GAM83 287 SSA1 Frank, M. B.; Mattei, M.- G.: Mapping of the human 60000 M(r) Ro/SSAlocus: the genes for three Ro/SSA autoantigens are located on separatechromosomes. Immunogenetics 39: 428- 431, 1994. 1 A c

GAM83 287 SSA1 Itoh, K.; Itoh, Y.; Frank, M. B.: Protein heterogeneity in thehuman Ro/SSA ribonucleoproteins: the 52- and 60- kD Ro/SSA autoantigensare encoded by separate genes. J. Clin. Invest. 87: 177- 186, 1991. 1 A c

GAM83 287 SSA1 Schoenlebe, J.; Buyon, J. P.; Zitelli, B. J.; Friedman, D.; Greco,M. A.; Knisely, A. S.: Neonatal hemochromatosis associated with maternalautoantibodies against Ro/SS- A and La/SS- B ribonucleoproteins. Am.J. Dis. Child. 147: 1072- 1075, 1993. 1 A c

GAM83 287 STAT1 Chen, X.; Vinkemeier, U.; Zhao, Y.; Jeruzalmi, D.; Darnell, J.E., Jr.; Kuriyan, J.: Crystal structure of a tyrosine phosphorylatedSTAT- 1 dimer bound to DNA. Cell 93: 827- 839, 1998. 1 A c

GAM83 287 STAT1 Copeland, N. G.; Gilbert, D. J.; Schindler, C.; Zhong, Z.; Wen,Z.; Darnell, J. E., Jr.; Mui, A. L.- F.; Miyajima, A.; Quelle, F. W.;Ihle, J. N.; Jenkins, N. A.: Distribution of the mammalian Stat genefamily in mouse chromosomes. Genomics 29: 225- 228, 1995. 1 A c

GAM83 287 STAT1 Darnell, J. E., Jr.; Kerr, I. M.; Stark, G. M.: Jak- STAT pathwaysand 1 A c

transcriptional activation in response to IFNs and other extracellularsignaling proteins. Science 264: 1415- 1421, 1994.

GAM83 287 STAT1 Dupuis, S.; Dargemont, C.; Fieschi, C.; Thomassin, N.; Rosenzweig,S.; Harris, J.; Holland, S. M.; Schreiber, R. D.; Casanova, J.- L.: Impairment of mycobacterial but not viral immunity by a germlinehuman STAT1 mutation. Science 293: 300- 303, 2001. 1 A c

GAM83 287 STAT1 Durbin, J. E.; Hackenmiller, R.; Simon, M. C.; Levy, D. E.: Targeteddisruption of the mouse Stat1 gene results in compromised innate immunityto viral disease. Cell 84: 443- 450, 1996. 1 A c

GAM83 287 STAT1 Haddad, B.; Pabon- Pena, C. R.; Young, H.; Sun, W. H.: Assignmentof STAT1 to human chromosome 2q32 by FISH and radiation hybrids. Cytogenet.Cell Genet. 83: 58- 59, 1998. 1 A c

GAM83 287 STAT1 Ihle, J. N.: Cytokine receptor signalling. Nature 377: 591- 594,1995. 1 A c

GAM83 287 STAT1 Ihle, J. N.: STATs: signal transducers and activators of transcription. Cell 84:331- 334, 1996. 1 A c

GAM83 287 STAT1 Ihle, J. N.; Kerr, I. M.: Jaks and Stats in signaling by the cytokinereceptor superfamily. Trends Genet. 11: 69- 74, 1995. 1 A c

GAM83 287 STAT1 Kaplan, D. H.; Shankaran, V.; Dighe, A. S.; Stockert, E.; Aguet,M.; Old, L. J.; Schreiber, R. D.: Demonstration of an interferongamma- dependent tumor surveillance system in immunocompetent mice. Proc.Nat. Acad. Sci. 95: 7556- 7561, 1998. 1 A c

GAM83 287 STAT1 Meraz, M. A.; White, J. M.; Sheehan, K. C. F.; Bach, E. A.; Rodig,S. J.; Dighe, A. S.; Kaplan, D. H.; Riley, J. K.; Greenlund, A. C.Campbell, D.; Carver- Moore, K.; DuBois, R. N.; Clark, R.; Aguet, M.;Schreiber, R. D.: Targeted disruption of the Stat1 gene in mice revealsunexpected physiologic specificity in the JAK- STAT signaling pathway. Cell 84:431- 442, 1996. 1 A c

GAM83 287 STAT1 Mowen, K. A.; Tang, J.; Zhu, W.; Schurter, B. T.; Shuai, K.; Herschman,H. R.; David, M.: Arginine methylation of STAT1 modulates IFN- alpha/beta- inducedtranscription. Cell 104: 731- 741, 2001. 1 A c

GAM83 287 STAT1 Ramana, C. V.; Chatterjee- Kishore, M.; Nguyen, H.; Stark, G. R.: Complex roles of Stat1 in regulating gene expression. Oncogene 19:2619- 2627, 2000. 1 A c

GAM83 287 STAT1 Schindler, C.; Fu, X.- Y.; Improta, T.; Aebersold, R.; Darnell,J. E., Jr.: Proteins of transcription factor ISGF- 3: one gene encodesthe 91- and 84- kDa ISGF- 3 proteins that are activated by interferonalpha. Proc. Nat. Acad. Sci. 89: 7836- 7839, 1992. 1 A c

GAM83 287 STAT1 Shankaran, V.; Ikeda, H.; Bruce, A. T.; White, J. M.; Swanson,P. E.; Old, L. J.; Schreiber, R. D.: IFN- gamma and lymphocytes preventprimary tumour development and shape tumour immunogenicity. Nature 410:1107- 1111, 2001. 1 A c

GAM83 287 STAT1 Yamamoto, K.; Kobayashi, H.; Arai, A.; Miura, O.; Hirosawa, S.;Miyasaka, N.: cDNA cloning, expression and chromosome mapping ofthe human STAT4 gene: both STAT4 and STAT1 genes are mapped to 2q32.2- q32.3. Cytogenet.Cell Genet. 77: 207- 210, 1997. 1 A c

GAM83 287 SVIL Pope, R. K.; Pestonjamasp, K. N.; Smith, K. P.; Wulfkuhle, J. D.;Strassel, C. P.; Lawrence, J. B.; Luna, E. J.: Cloning, characterization,and chromosomal localization of human supervillin (SVIL). Genomics 52:342- 351, 1998. 1 A c

GAM83 287 SVIL Ting, H.- J.; Yeh, S.; Nishimura, K.; Chang, C.: Supervillin associateswith androgen receptor and modulates its transcriptional activity. Proc.Nat. Acad. Sci. 99: 661- 666, 2002. 1 A c

GAM83 287 TUBA3 Cowan, N. J.; Dobner, P. R.; Fuchs, E. V.; Cleveland, D. W.: Expressionof 1 A c

human alpha- tubulin genes: interspecies conservation of 3-primeuntranslated regions. Molec. Cell. Biol. 3: 1738- 1745, 1983.

GAM83 287 TUBA3 Gerhard, D. S.; Dobner, P. R.; Bruns, G.: Testis specific alpha- tubulinis on chromosome 2q. (Abstract) Cytogenet. Cell Genet. 40: 639- 640,1985. 1 A c

GAM83 287 TUBA3 Hall, J. L.; Cowan, N. J.: Structural features and restrictedexpression of a human alpha- tubulin gene. Nucleic Acids Res. 13:207- 223, 1985. 1 A c

GAM83 287 TUBA3 Lewis, S. A.; Cowan, N. J.: Tubulin genes: structure, expression,and regulation.In: Avila, J. (ed.): Microtubule proteins. BocaRaton: CRC Press, Inc. 1990. Pp. 37- 66. 1 A c

GAM83 287 TUBA3 Miller, F. D.; Naus, C. C. G.; Durand, M.; Bloom, F. E.; Milner,R. J.: Isotypes of alpha- tubulin are differentially regulated duringneuronal maturation. J. Cell Biol. 105: 3065- 3073, 1987. 1 A c

GAM83 287 TUBA3 Rasooly, R. S.: Personal Communication. Baltimore, Md. 2/1998. 1 A c

GAM83 287 TUBA3 Scott, A. F.: Personal Communication. Baltimore, Md. 10/3/2001. 1 A c

GAM83 287 TUBA3 Todd, S.; Naylor, S. L.: Dinucleotide repeat polymorphism in thehuman tubulin alpha 1 (testis specific) gene (TUBA1). Nucleic AcidsRes. 19: 3755 only, 1991. 1 A c

GAM83 287 UBE2V1 Deng, L.; Wang, C.; Spencer, E.; Yang, L.; Braun, A.; You, J.;Slaughter, C.; Pickart, C.; Chen, Z. J.: Activation of the I- kappa- Bcomplex by TRAF6 requires a dimeric ubiquitin- conjugating enzyme complexand a unique polyubiquitin chain. Cell 103: 351- 361, 2000. 1 A c

GAM83 287 UBE2V1 Hofmann, R. M.; Pickart, C. M.: Noncanonical MMS2- encoded ubiquitin-conjugatingenzyme functions in assembly of novel polyubiquitin chains for DNArepair. Cell 96: 645- 653, 1999. 1 A c

GAM83 287 UBE2V1 Rothofsky, M. L.; Lin, S. L.: CROC- 1 encodes a protein which mediatestranscriptional activation of the human FOS promoter. Gene 195:141-149, 1997. 1 A c

GAM83 287 UBE2V1 Sancho, E.; Vila, M. R.; Sanchez- Pulido, L.; Lozano, J. J.; Paciucci,R.; Nadal, M.; Fox, M.; Harvey, C.; Bercovich, B.; Loukili, N.; Ciechanover,A.; Lin, S. L.; Sanz, F.; Estivill, X.; Valencia, A.; Thomson, T.M.: Role of UEV- 1, an inactive variant of the E2 ubiquitin- conjugatingenzymes, in in vitro differentiation and cell cycle behavior of HT- 29- M6intestinal mucosecretory cells. Molec. Cell. Biol. 18: 576- 589,1998. 1 A c

GAM83 287 YWHAG Autieri, M. V.; Carbone, C. J.: 14- 3- 3- Gamma interacts with andis phosphorylated by multiple protein kinase C isoforms in PDGF-stimulatedhuman vascular smooth muscle cells. DNA Cell Biol. 18: 555-564,1999. 1 A c

GAM83 287 YWHAG Autieri, M. V.; Feuerstein, G. Z.; Yue, T.- L.; Ohlstein, E. H.;Douglas, S. A.: Use of differential display to identify differentiallyexpressed mRNAs induced by rat carotid artery balloon angioplasty. Lab.Invest. 72: 656- 661, 1995. 1 A c

GAM83 287 YWHAG Autieri, M. V.; Haines, D. S.; Romanic, A. M.; Ohlstein, E. H.: Expression of 14- 3- 3- gamma in injured arteries and growth factor- and cytokine-stimulated human vascular smooth muscle cells. CellGrowth Diff. 7: 1453-1460, 1996. 1 A c

GAM83 287 YWHAG Horie, M.; Suzuki, M.; Takahashi, E.; Tanigami, A.: Cloning, expression,and chromosomal mapping of the human 14- 3- 3gamma gene (YWHAG) to 7q11.23. Genomics 60:241- 243, 1999. 1 A c

GAM83 287 YWHAG Morrison, D.: 14- 3- 3: modulators of signaling proteins? Science 266:56-57, 1994. 1 A c

GAM84 204 DGCR2 Augusseau, S.; Jouk, S.; Jalbert, P.; Prieur, M.: DiGeorge syndromeand 22q11 3 C c
rearrangements. (Letter) Hum. Genet. 74: 206 only, 1986.

GAM84 204 DGCR2 Bartsch, O.; Wagner, A.; Hinkel, G. K.; Lichtner, P.; Murken, 3 C c
J.;Schuffenhauer, S.: No evidence for chromosomal microdeletions atthe
second DiGeorge syndrome locus on 10p near D10S585. (Letter) Am.J. Med.
Genet. 83: 425- 426, 1999.

GAM84 204 DGCR2 Daw, S. C. M.; Taylor, C.; Kraman, M.; Call, K.; Mao, J.; Schuffenhauer,S.; 3 C c
Meitinger, T.; Lipson, T.; Goodship, J.; Scambler, P.: A commonregion of 10p
deleted in DiGeorge and velocardiofacial syndromes. NatureGenet. 13: 458-
461, 1996.

GAM84 204 DGCR2 Demczuk, S.; Aledo, R.; Zucman, J.; Delattre, O.; Desmaze, C.;Dauphinot, L.; 3 C c
Jalbert, P.; Rouleau, G. A.; Thomas, G.; Aurias, A.: Cloning of a balanced
translocation breakpoint in the DiGeorge syndromecritical region and
isolation of a novel potential adhesion receptorgene in its vicinity. Hum.
Molec. Genet. 4: 551- 558, 1995.

GAM84 204 DGCR2 Hasegawa, T.; Hasegawa, Y.; Aso, T.; Koto, S.; Nagai, T.; Tsuchiya,Y.; Kim, 3 C c
K. C.; Ohashi, H.; Wakui, K.; Fukushima, Y.: HDR
syndrome(hypoparathyroidism, sensorineural deafness, renal dysplasia)
associatedwith del(10)(p13). Am. J. Med. Genet. 73: 416- 418, 1997.

GAM84 204 DGCR2 Lichtner, P.; Konig, R.; Hasegawa, T.; Van Esch, H.; Meitinger,T.; 3 C c
Schuffenhauer, S.: An HDR (hypoparathyroidism, deafness, renaldysplasia)
syndrome locus maps distal to the DiGeorge syndrome regionon 10p13/14. J.
Med. Genet. 37: 33- 37, 2000.

GAM84 204 DGCR2 Schuffenhauer, S.; Lichtner, P.; Peykar- Derakhshandeh, P.; Murken,J.; Haas, 3 C c
O. A.; Back, E.; Wolff, G.; Zabel, B.; Barisic, I.; Rauch,A.; Borochowitz,
Z.; Dallapiccola, B.; Ross, M.; Meitinger, T.: Deletionmapping on chromosome
10p and definition of a critical region forthe second DiGeorge syndrome
locus (DGS2). Europ. J. Hum. Genet. 6:213- 225, 1998.

GAM84 204 DGCR2 Van Esch, H.; Groenen, P.; Daw, S.; Poffyn, A.; Holvoet, M.; Scambler,P.; 3 C c
Fryns, J.- P.; Van de Ven, W.; Devriendt, K.: Partial DiGeorgesyndrome in
two patients with a 10p rearrangement. Clin. Genet. 55:269- 276, 1999.

GAM84 204 DGCR2 Wadey, R.; Daw, S.; Taylor, C.; Atif, U.; Kamath, S.; Halford,S.; O'Donnell, 3 C c
H.; Wilson, D.; Goodship, J.; Burn, J.; Scambler, P.: Isolation of a gene
encoding an integral membrane protein from thevicinity of a balanced
translocation breakpoint associated with DiGeorgesyndrome. Hum. Molec.
Genet. 4: 1027- 1033, 1995.

GAM88 310 C18orf1 Yoshikawa, T.; Sanders, A. R.; Esterling, L. E.; Detera- Wadleigh,S. D.: 3 B c
Multiple transcriptional variants and RNA editing in C18orf1,a novel gene
with LDLRA and transmembrane domains on 18p11.2. Genomics 47:246- 257, 1998.

GAM88 310 C18orf1 Yoshikawa, T.; Sanders, A. R.; Esterling, L. E.; Overharser, J.;Garnes, J. 3 B c
A.; Lennon, G.; Grewal, R.; Detera- Wadleigh, S. D.: Isolationof chromosome
18- specific brain transcripts as positional candidatesfor bipolar disorder.
Am. J. Med. Genet. (Neuropsych. Genet.) 74:140- 149, 1997.

GAM88 310 NCYM Armstrong, B. C.; Krystal, G. W.: Isolation and characterizationof 3 B c
complementary DNA for N- cym, a gene encoded by the DNA strand oppositeto N-
myc. Cell Growth Differ. 3: 385- 390, 1992.

GAM88 310 NCYM Krystal, G. W.; Armstrong, B. C.; Battey, J. F.: N- myc mRNA formsan RNA- 3 B c
RNA duplex with endogenous antisense transcripts. Molec. Cell.Biol. 10:
4180- 4191, 1990.

GAM88 310 SAS Jankowski, S. A.; De Jong, P.; Meltzer, P. S.: Genomic structureof SAS, a 3 B c

member of the transmembrane 4 superfamily amplified in humansarcomas. Genomics 25: 501- 506, 1995.

GAM88 310 SAS Meltzer, P. S.; Jankowski, S. A.; Dal Cin, P.; Sandberg, A. A.;Paz, I. B.; 3 B c
Coccia, M. A.; Smith, S. H.: Identification and cloningof a novel amplified DNA sequence in human malignant fibrous histiocytomaderived from a region of chromosome 12 frequently rearranged in softtissue tumors. (Abstract) Cytogenet. Cell Genet. 58: 1979 only,1991.

GAM88 310 SOX9 Angle, C. R.: Congenital bowing and angulation of the long bones. Pediatrics 3 B c
13:257- 268, 1954.

GAM88 310 SOX9 Bain, A. D.; Barrett, H. S.: Congenital bowing of the long bones:report of a 3 B c
case. Arch. Dis. Child. 34: 516- 524, 1959.

GAM88 310 SOX9 Bell, D. M.; Leung, K. K. H.; Wheatley, S. C.; Ng, L. J.; Zhou,S.; Ling, K. 3 B c
W.; Sham, M. H.; Koopman, P.; Tam, P. P. L.; Cheah, K.S. E.: SOX9 directly regulates the type- II collagen gene. NatureGenet. 16: 174- 178, 1997.

GAM88 310 SOX9 Bi, W.; Huang, W.; Whitworth, D. J.; Deng, J. M.; Zhang, Z.; Behringer,R. 3 B c
R.; de Crombrugghe, B.: Haploinsufficiency of Sox9 results indefective cartilage primordia and premature skeletal mineralization. Proc.Nat. Acad. Sci. 98: 6698- 6703, 2001.

GAM88 310 SOX9 Bishop, C. E.; Whitworth, D. J.; Qin, Y.; Agoulnik, A. I.; Agoulnik,I. U.; 3 B c
Harrison, W. R.; Behringer, R. R.; Overbeek, P. A.: A transgenicinsertion upstream of Sox9 is associated with dominant XX sex reversalin the mouse. Nature Genet. 26: 490- 494, 2000.

GAM88 310 SOX9 Caffey, J. P.: Prenatal bowing and thickening of tubular bones,with multiple 3 B c
cutaneous dimples in arms and legs: a congenital syndromeof mechanical origin. Am. J. Dis. Child. 74: 543- 562, 1947.

GAM88 310 SOX9 Cameron, F. J.; Hageman, R. M.; Cooke- Yarborough, C.; Kwok, C.;Goodwin, L. 3 B c
L.; Sillence, D. O.; Sinclair, A. H.: A novel germ linemutation in SOX9 causes familial campomelic dysplasia and sex reversal. Hum.Molec. Genet. 5: 1625- 1630, 1996.

GAM88 310 SOX9 Cameron, F. J.; Sinclair, A. H.: Mutations in SRY and SOX9: testis- 3 B c
determininggenes. Hum. Mutat. 9: 388- 395, 1997.

GAM88 310 SOX9 Cooke, C. T.; Mulcahy, M. T.; Cullity, G. J.; Watson, M.; Sprague,P.: 3 B c
Campomelic dysplasia with sex reversal: morphological and cytogeneticstudies of a case. Pathology 17: 526- 529, 1985.

GAM88 310 SOX9 Cremin, B. J.; Orsmond, G.; Beighton, P.: Autosomal recessiveinheritance in 3 B c
camptomelic dwarfism.(Letter) Lancet I: 488- 489,1973.

GAM88 310 SOX9 Dagna Bricarelli, F.; Fraccaro, M.; Lindsten, J.; Muller, U.;Baggio, P.; 3 B c
Carbone, L. D. L.; Hjerpe, A.; Lindgren, F.; Mayerova,A.; Ringertz, H.; Ritzen, E. M.; Rovetta, D. C.; Sicchero, C.; Wolf,U.: Sex- reversed XY females with campomelic dysplasia are H- Y negative. Hum.Genet. 57: 15- 22, 1981.

GAM88 310 SOX9 Ebensperger, C.; Jager, R. J.; Lattermann, U.; Dagna Bricarelli,F.; Keutel, 3 B c
J.; Lindsten, J.; Rehder, H.; Muller, U.; Wolf, U.: Noevidence of mutations in four candidate genes for male sex determination/differentiationin sex-reversed XY females with campomelic dysplasia. Ann. Genet. 34:233- 238, 1991.

GAM88 310 SOX9 Fontaine, G.; Walbaum, R.; Farriaux, J. P.; Tilmont, P.; Peuzin,F.; 3 B c
Delecour, M.: Le conseil genetique dans la dysplasie campomelique(a propos de deux observations). J. Genet. Hum. 28: 267- 279, 1980.

GAM88 310 SOX9 Foster, J. W.; Dominguez- Steglich, M. A.; Guioli, S.; Kwok, C.;Weller, P. 3 B c

A.; Stevanovic, M.; Weissenbach, J.; Mansour, S.; Young,I. D.; Goodfellow, P. N.; Brook, J. D.; Schafer, A. J.: Campomelicdysplasia and autosomal sex reversal caused by mutations in an SRY- relatedgene. Nature 372: 525- 530, 1994.

GAM88 310 SOX9 Friedrich, U.; Schaefer, E.; Meinecke, P.: Campomelic dysplasiawithout overt campomelia. Clin. Dysmorph. 1: 172- 178, 1992. 3 B c

GAM88 310 SOX9 Fryns, J. P.; van den Berghe, K.; van Assche, A.; van den Berghe,H.: Prenatal diagnosis of campomelic dwarfism. Clin. Genet. 19:199- 201, 1981. 3 B c

GAM88 310 SOX9 Gasca, S.; Canizares, J.; de Santa Barbara, P.; Mejean, C.; Poulat,F.; Berta, P.; Boizet- Bonhoure, B.: A nuclear export signal withinthe high mobility group domain regulates the nucleocytoplasmic translocationof SOX9 during sexual determination. Proc. Nat. Acad. Sci. 99: 11199- 11204,2002. 3 B c

GAM88 310 SOX9 Glass, R. B. J.; Rosenbaum, K. N.: Acampomelic campomelic dysplasia:further radiographic variations. Am. J. Med. Genet. 69: 29- 32, 1997. 3 B c

GAM88 310 SOX9 Hall, B.; Spranger, J. W.: Campomelic dysplasia: further elucidationof a distinct entity. Am. J. Dis. Child. 134: 285- 289, 1980. 3 B c

GAM88 310 SOX9 Hoefnagel, D.; Wurster- Hill, D. H.; Dupree, W. B.; Benirschke,K.; Fuld, G. L.: Camptomelic dwarfism associated with XY- gonadaldysgenesis and chromosome anomalies. Clin. Genet. 13: 489- 499, 1978. 3 B c

GAM88 310 SOX9 Houston, C. S.; Opitz, J. M.; Spranger, J. W.; Macpherson, R.I.; Reed, M. H.; Gilbert, E. F.; Herrmann, J.; Schinzel, A.: Thecampomelic syndrome: review, report of 17 cases, and follow- up onthe currently 17- year- old boy first reported by Maroteaux et al in1971. Am. J. Med. Genet. 15: 3- 28, 1983. 3 B c

GAM88 310 SOX9 Hovmoller, M. L.; Osuna, A.; Eklof, O.; Fredga, K.; Hjerpe, A.;Lindsten, J.; Ritzen, M.; Stanescu, V.; Svenningsen, N.: Camptomelicdwarfism. A genetically determined mesenchymal disorder combined withsex reversal. Hereditas 86: 51- 62, 1977. 3 B c

GAM88 310 SOX9 Huang, W.; Chung, U.; Kronenberg, H. M.; de Crombrugghe, B.:The chondrogenic transcription factor Sox9 is a target of signalingby the parathyroid hormone- related peptide in the growth plate ofendochondral bones. Proc. Nat. Acad. Sci. 98: 160- 165, 2001. 3 B c

GAM88 310 SOX9 Kanai, Y.; Koopman, P.: Structural and functional characterizationof the mouse Sox9 promoter: implications for campomelic dysplasia. Hum.Molec. Genet. 8: 691- 696, 1999. 3 B c

GAM88 310 SOX9 Lahn, B. T.; Page, D. C.: Four evolutionary strata on the humanX chromosome. Science 286: 964- 967, 1999. 3 B c

GAM88 310 SOX9 Lahn, B. T.; Page, D. C.: Functional coherence of the human Ychromosome. Science 278: 675- 680, 1997. 3 B c

GAM88 310 SOX9 Lee, F. A.; Issacs, H.; Strauss, J.: The 'camptomelic' syndrome.Short life- span dwarfism with respiratory distress, hypotonia, peculiarfacies, and multiple skeletal and cartilaginous deformities. Am.J. Dis. Child. 124: 485- 496, 1972. 3 B c

GAM88 310 SOX9 Lynch, S. A.; Gaunt, M. L.; Minford, A. M. B.: Campomelic dysplasia:evidence of autosomal dominant inheritance. J. Med. Genet. 30: 683- 686,1993. 3 B c

GAM88 310 SOX9 Macpherson, R. I.; Skinner, S. A.; Donnenfeld, A. E.: Acampomeliccampomelic dysplasia. Pediat. Radiol. 20: 90- 93, 1989. 3 B c

GAM88 310 SOX9 Mansour, S.; Hall, C. M.; Pembrey, M. E.; Young, I. D.: A clinicaland genetic study of campomelic dysplasia. J. Med. Genet. 32: 415- 420,1995. 3 B c

GAM88 310 SOX9 Maraia, R.; Saal, H. M.; Wangsa, D.: A chromosome 17q de novoparacentric 3 B c

inversion in a patient with campomelic dysplasia; casereport and etiologic hypothesis. Clin. Genet. 39: 401- 408, 1991.

GAM88 310 SOX9 Maroteaux, P.; Spranger, J. W.; Opitz, J. M.; Kucera, J.; Lowry,R. B.; Schimke, R. N.; Kagan, S. M.: Le syndrome campomelique. PresseMed. 22: 1157-1162, 1971. 3 B c

GAM88 310 SOX9 Mellows, H. J.; Pryse- Davies, J.; Bennett, M. J.; Carter, C. O.: The camptomelic syndrome in two female siblings. Clin. Genet. 18:137- 141, 1980. 3 B c

GAM88 310 SOX9 Meyer, J.; Sudbeck, P.; Held, M.; Wagner, T.; Schmitz, M. L.;Bricarelli, F. D.; Eggermont, E.; Friedrich, U.; Haas, O. A.; Kobelt,A.; Leroy, J. G.; van Maldergem, L.; Michel, E.; Mitulla, B.; Pfeiffer,R. A.; Schinzel, A.; Schmidt, H.; Scherer, G.: Mutational analysisof the SOX9 gene in campomelic dysplasia and autosomal sex reversal:lack of genotype/phenotype correlations. Hum. Molec. Genet. 6: 91- 98,1997. 3 B c

GAM88 310 SOX9 Moedjono, S. J.; Crandall, B. F.; Sparkes, R. S.; Feldman, G.M.; Austin, G. E.; Perry, S.: The campomelic syndrome in a singletonand monozygotic twins. Clin. Genet. 18: 397- 401, 1980. 3 B c

GAM88 310 SOX9 Moog, U.; Jansen, N. J. G.; Scherer, G.; Schrander- Stumpel, C.T. R. M.: Acampomelic campomelic syndrome. Am. J. Med. Genet. 104:239- 245, 2001. 3 B c

GAM88 310 SOX9 Morais da Silva, S.; Hacker, A.; Harley, V.; Goodfellow, P.; Swain,A.; Lovell- Badge, R.: Sox9 expression during gonadal developmentimplies a conserved role for the gene in testis differentiation inmammals and birds. Nature Genet. 14: 62- 68, 1996. 3 B c

GAM88 310 SOX9 Murakami, S.; Kan, M.; McKeehan, W. L.; de Crombrugghe, B.: Up- regulationof the chondrogenic Sox9 gene by fibroblast growth factors is mediatedby the mitogen- activated protein kinase pathway. Proc. Nat. Acad.Sci. 97: 1113-1118, 2000. 3 B c

GAM88 310 SOX9 Ninomiya, S.; Isomura, M.; Narahara, K.; Seino, Y.; Nakamura,Y.: Isolation of a testis- specific cDNA on chromosome 17q from aregion adjacent to the breakpoint of t(12;17) observed in a patientwith acampomelic campomelic dysplasia and sex reversal. Hum. Molec.Genet. 5: 69- 72, 1996. 3 B c

GAM88 310 SOX9 Ninomiya, S.; Yokoyama, Y.; Teraoka, M.; Mori, R.; Inoue, C.;Yamashita, S.; Tamai, H.; Funato, M.; Seino, Y.: A novel mutation(296 del G) of the SOX9 gene in a patient with campomelic syndromeand sex reversal. Clin. Genet. 58: 224- 227, 2000. 3 B c

GAM88 310 SOX9 Olney, P. N.; Kean, L. S.; Graham, D.; Elsas, L. J.; May, K. M.: Campomelic syndrome and deletion of SOX9. Am. J. Med. Genet. 84:20- 24, 1999. 3 B c

GAM88 310 SOX9 Ozkilic, A.; Seven, M.; Yuksel, A.: A case of acampomelic campomelicdysplasia. Genet. Counsel. 13: 23- 28, 2002. 3 B c

GAM88 310 SOX9 Patel, M.; Dorman, K. S.; Zhang, Y.- H.; Huang, B.- L.; Arnold,A. P.; Sinsheimer, J. S.; Vilain, E.; McCabe, E. R. B.: Primate DAX1,SRY, and SOX9: evolutionary stratification of sex- determination pathway. Am.J. Hum. Genet. 68: 275- 280, 2001. 3 B c

GAM88 310 SOX9 Pfeifer, D.; Kist, R.; Dewar, K.; Devon, K.; Lander, E. S.; Birren,B.; Korniszewski, L.; Back, E.; Scherer, G.: Campomelic dysplasiatranslocation breakpoints are scattered over 1 Mb proximal to SOX9:evidence for an extended control region. Am. J. Hum. Genet. 65:111- 124, 1999. 3 B c

GAM88 310 SOX9 Puck, S. M.; Haseltine, F. P.; Francke, U.: Absence of H- Y antigenin an XY female with campomelic dysplasia. Hum. Genet. 57: 23- 27,1981. 3 B c

GAM88 310 SOX9 Rimoin, D. L.: Personal Communication. Torrance, Calif. 8/12/1976. 3 B c

GAM88 310 SOX9 Rodriguez, J. I.: Vascular anomalies in campomelic syndrome. Am.J. Med. 3 B c

Genet. 46: 185- 192, 1993.

GAM88 310 SOX9 Savarirayan, R.; Bankier, A.: Acampomelic campomelic dysplasiawith de novo 5q;17q reciprocal translocation and severe phenotype. J.Med. Genet. 35: 597- 599, 1998. 3 B c

GAM88 310 SOX9 Schimke, R. N.: XY sex- reversed campomelia- - possibly an X- linkeddisorder? (Letter) Clin. Genet. 16: 62- 63, 1979. 3 B c

GAM88 310 SOX9 Schmickel, R. D.: Contiguous gene syndromes: a component of recognizablesyndromes. J. Pediat. 109: 231- 241, 1986. 3 B c

GAM88 310 SOX9 Shafai, T.; Schwartz, L.: Camptomelic syndrome in siblings. J.Pediat. 89: 512- 513, 1976. 3 B c

GAM88 310 SOX9 Spranger, J.: Advances in bone dysplasias. (Abstract) SixthInt. Cong. Hum. Genet. Jerusalem , 1981. 3 B c

GAM88 310 SOX9 Stuve, A.; Wiedemann, H.- R.: Congenital bowing of the long bonesin two sisters. (Letter) Lancet I: 495, 1971. 3 B c

GAM88 310 SOX9 Sudbeck, P.; Schmitz, M. L.; Baeuerle, P. A.; Scherer, G.: Sexreversal by loss of the C- terminal transactivation domain of humanSOX9. Nature Genet. 13: 230- 232, 1996. 3 B c

GAM88 310 SOX9 Thong, M.- K.; Scherer, G.; Kozlowski, K.; Haan, E.; Morris, L.: Acampomelic campomelic dysplasia with SOX9 mutation. Am. J. Med.Genet. 93: 421- 425, 2000. 3 B c

GAM88 310 SOX9 Thurmon, T. F.; De Fraites, E. B.; Anderson, E. E.: Familialcampomelic dwarfism. J. Pediat. 83: 841- 843, 1973. 3 B c

GAM88 310 SOX9 Tommerup, N.; Schempp, W.; Meinecke, P.; Pedersen, S.; Bolund,L.; Brandt, C.; Goodpasture, C.; Guldberg, P.; Held, K.; Reinwein,H.; Saugstad, O. D.; Scherer, G.; Skjeldal, O.; Toder, R.; Westvik,J.; van der Hagen, C. B.; Wolf, U.: Assignment of an autosomal sexreversal locus (SRA1) and campomelic dysplasia (CMPD1) to 17q24.3- q25.1. NatureGenet. 4: 170- 174, 1993. 3 B c

GAM88 310 SOX9 Vidal, V. P. I.; Chaboissier, M.- C.; de Rooij, D. G.; Schedl,A.: Sox9 induces testis development in XX transgenic mice. NatureGenet. 28: 216- 217, 2001. 3 B c

GAM88 310 SOX9 Wagner, T.; Wirth, J.; Meyer, J.; Zabel, B.; Held, M.; Zimmer,J.; Pasantes, J.; Dagna Bricarelli, F.; Keutel, J.; Hustert, E.; Wolf,U.; Tommerup, N.; Schempp, W.; Scherer, G.: Autosomal sex reversaland campomelic dysplasia are caused by mutations in and around theSRY- related gene SOX9. Cell 79: 1111- 1120, 1994. 3 B c

GAM88 310 SOX9 Weller, S. D. V.: Hypophosphatasia with congenital dimples. Proc.Roy. Soc. Med. 52: 637, 1959. 3 B c

GAM88 310 SOX9 Wirth, J.; Wagner, T.; Meyer, J.; Pfeiffer, R. A.; Tietze, H.- U.;Schempp, W.; Scherer, G.: Translocation breakpoints in three patientswith campomelic dysplasia and autosomal sex reversal map more than130 kb from SOX9. Hum. Genet. 97: 186- 193, 1996. 3 B c

GAM88 310 SOX9 Wright, E.; Hargrave, M. R.; Christiansen, J.; Cooper, L.; Kun,J.; Evans, T.; Gangadharan, U.; Greenfield, A.; Koopman, P.: TheSry- related gene Sox9 is expressed during chondrogenesis in mouseembryos. Nature Genet. 9: 15- 20, 1995. 3 B c

GAM88 310 SOX9 Wunderle, V. M.; Critcher, R.; Hastie, N.; Goodfellow, P. N.;Schedl, A.: Deletion of long- range regulatory elements upstream ofSOX9 causes campomelic dysplasia. Proc. Nat. Acad. Sci. 95: 10649- 10654,1998. 3 B c

GAM88 310 SOX9 Young, I. D.; Zuccollo, J. M.; Maltby, E. L.; Broderick, N. J.: Campomelic dysplasia associated with a de novo 2q;17q reciprocaltranslocation. J. Med. 3 B c

Genet. 29: 251- 252, 1992.

GAM90 374 BCL6 Akasaka, T.; Miura, I.; Takahashi, N.; Akasaka, H.; Yonetani, N.;Ohno, H.; 3 C c Fukuhara, S.; Okuma, M.: A recurring translocation, t(3;6)(q27;p21),in non-Hodgkin's lymphoma results in replacement of the 5- prime regulatoryregion of BCL6 with a novel H4 histone gene. Cancer Res. 57: 7- 12,1997.

GAM90 374 BCL6 Baron, B. W.; Nucifora, G.; McCabe, N.; Espinosa, R., III; Le Beau,M. M.; 3 C c McKeithan, T. W.: Identification of the gene associated withthe recurring chromosomal translocations t(3;14)(q27;q32) and t(3;22)(q27;q11)in B- cell lymphomas. Proc. Nat. Acad. Sci. 90: 5262- 5266, 1993.

GAM90 374 BCL6 Capello, D.; Carbone, A.; Pastore, C.; Gloghini, A.; Saglio, G.;Gaidano, G.: 3 C c Point mutations of the BCL- 6 gene in Burkitt's syndrome. Brit.J. Haemat. 99: 168- 170, 1997.

GAM90 374 BCL6 Cattoretti, G.; Chang, C.- C.; Cechova, K.; Zhang, J.; Ye, B. H.;Falini, B.; 3 C c Louie, D. C.; Offit, K.; Chaganti, R. S. K.; Dalla- Favera,R.: BCL- 6 protein is expressed in germinal- center B cells. Blood 86:45- 53, 1995.

GAM90 374 BCL6 Cesarman, E.; Chadburn, A.; Liu, Y.- F.; Migliazza, A.; Dalla- Favera,R.; 3 C c Knowles, D. M.: BCL- 6 gene mutations in posttransplantation lymphoproliferativedisorders predict response to therapy and clinical outcome. Blood 92:2294- 2302, 1998.

GAM90 374 BCL6 Chaganti, S. R.; Chen, W.; Parsa, N.; Offit, K.; Louie, D. C.;Dalla- Favera, 3 C c R.; Chaganti, R. S. K.: Involvement of BCL6 in chromosomalaberrations affecting band 3q27 in B- cell non- Hodgkin lymphoma. GenesChromosomes Cancer 23: 323- 327, 1998.

GAM90 374 BCL6 Chaganti, S. R.; Rao, P. H.; Chen, W.; Dyomin, V.; Jhanwar, S.C.; Parsa, N. 3 C c Z.; Dalla- Favera, R.; Chaganti, R. S. K.: Deregulationof BCL6 in non-Hodgkin lymphoma by insertion of IGH sequences in complextranslocations involving band 3q27. Genes Chromosomes Cancer 23:328- 336, 1998.

GAM90 374 BCL6 Chang, C.- C.; Ye, B. H.; Chaganti, R. S. K.; Dalla- Favera, R.:BCL- 6, a 3 C c POZ/zinc- finger protein, is a sequence- specific transcriptionalrepressor. Proc. Nat. Acad. Sci. 93: 6947- 6952, 1996.

GAM90 374 BCL6 Dhordain, P.; Albagli, O.; Honore, N.; Guidez, F.; Lantoine, D.;Schmid, M.; 3 C c De The, H.; Zelent, A.; Koken, M. H. M.: Colocalizationand heteromerization between the two human oncogene POZ/zinc fingerproteins, LAZ3 (BCL6) and PLZF. Oncogene 19: 6240- 6250, 2000.

GAM90 374 BCL6 Gaidano, G.; Capello, D.; Gloghini, A.; Fassone, L.; Vivenza,D.; Ariatti, 3 C c C.; Migliazza, A.; Saglio, G.; Carbone, A.: Frequentmutation of bcl- 6 proto- oncogene in high grade, but not low grade,MALT lymphomas of the gastrointestinal tract. Haematologica 84:582- 588, 1999.

GAM90 374 BCL6 Galiegue- Zouitina, S.; Quief, S.; Hildebrand, M.- P.; Denis, 3 C c C.;Detourmignies, L.; Lai, J.- L.; Kerckaert, J.- P.: Nonrandom fusionof L-plastin (LCP1) and LAZ3 (BCL6) genes by t(3;13)(q27;q14) chromosometranslocation in two cases of B- cell non- Hodgkin lymphoma. GenesChromosomes Cancer 26: 97- 105, 1999.

GAM90 374 BCL6 Hamblin, T. J.; Davis, Z.; Gardiner, A.; Oscier, D. G.; Stevenson,F. K.: 3 C c Unmutated Ig V(H) genes are associated with a more aggressiveform of chronic lymphocytic leukemia. Blood 94: 1848- 1854, 1999.

GAM90 374 BCL6 Hosokawa, Y.; Maeda, Y.; Ichinohasama, R.; Miura, I.; Taniwaki,M.; Seto, M.: 3 C c The Ikaros gene, a central regulator of lymphoid differentiation,fuses to the BCL6 gene as a result of t(3;7)(q27;p12) translocationin a patient with diffuse large B- cell lymphoma. Blood 95: 2719- 2721,2000.

GAM90 374 BCL6 Ichii, H.; Sakamoto, A.; Hatano, M.; Okada, S.; Toyama, H.; Taki,S.; Arima, M.; Kuroda, Y.; Tokuhisa, T.: Role of Bcl- 6 in the generationand maintenance of memory CD8+ T cells. Nature Immun. 3: 558- 563,2002. 3 C c

GAM90 374 BCL6 Ichinohasama, R.; Miura, I.; Funato, T.; Sato, I.; Suzuki, C.;Saito, Y.; Decoteau, J. F.; Myers, J. B.; Kadin, M. E.; Sawai, T.;Ooya, K.: A recurrent nonrandom translocation (3;7)(q27;p12) associatedwith BCL- 6 gene rearrangement in B- cell diffuse large cell lymphoma. CancerGenet. Cytogenet. 104: 19- 27, 1998. 3 C c

GAM90 374 BCL6 Kerckaert, J.- P.; Deweindt, C.; Tilly, H.; Quief, S.; Lecocq,G.; Bastard, C.: LAZ3, a novel zinc- finger encoding gene, is disruptedby recurring chromosome 3q27 translocations in human lymphomas. NatureGenet. 5: 66- 70, 1993. 3 C c

GAM90 374 BCL6 Liao, X.; Gilbert, D. J.; Dent, A.; Staudt, L. M.; Jenkins, N.A.; Copeland, N. G.: Mapping of the mouse Bcl6 gene to chromosome16. Mammalian Genome 7: 621- 622, 1996. 3 C c

GAM90 374 BCL6 Migliazza, A.; Martinotti, S.; Chen, W.; Fusco, C.; Ye, B. H.;Knowles, D. M.; Offit, K.; Changanti, R. S. K.; Dalla- Favera, R.:Frequent somatic hypermutation of the 5- prime noncoding region ofthe BCL6 gene in B- cell lymphoma. Proc. Nat. Acad. Sci. 92: 12520- 12524,1995. 3 C c

GAM90 374 BCL6 Miki, T.; Kawamata, N.; Arai, A.; Ohashi, K.; Nakamura, Y.; Kato,A.; Hirosawa, S.; Aoki, N.: Molecular cloning of the breakpoint for3q27 translocation in B- cell lymphomas and leukemias. Blood 83:217- 222, 1994. 3 C c

GAM90 374 BCL6 Miki, T.; Kawamata, N.; Hirosawa, S.; Aoki, N.: Gene involvedin the 3q27 translocation associated with B- cell lymphoma, BCL5, encodesa Kruppel- like zinc- finger protein. Blood 83: 26- 32, 1994. 3 C c

GAM90 374 BCL6 Sahota, S. S.; Davis, Z.; Hamblin, T. J.; Stevenson, F. K.: Somaticmutation of bcl- 6 genes can occur in the absence of V- H mutationsin chronic lymphocytic leukemia. Blood 95: 3534- 3540, 2000. 3 C c

GAM90 374 BCL6 Shaffer, A. L.; Yu, X.; He, Y.; Boldrick, J.; Chan, E. P.; Staudt,L. M.: BCL- 6 represses genes that function in lymphocyte differentiation,inflammation, and cell cycle control. Immunity 13: 199- 212, 2000. 3 C c

GAM90 374 BCL6 Shen, H. M.; Peters, A.; Baron, B.; Zhu, X.; Storb, U.: Mutationof BCL- 6 gene in normal B cells by the process of somatic hypermutationof Ig genes. Science 280: 1750- 1752, 1998. 3 C c

GAM90 374 BCL6 Ueda, C.; Akasaka, T.; Kurata, M.; Maesako, Y.; Nishikori, M.;Ichinohasama, R.; Imada, K.; Uchiyama, T.; Ohno, H.: The gene forinterleukin- 21 receptor is the partner of BCL6 in t(13;16)(q27;p11),which is recurrently observed in diffuse large B- cell lymphoma. Oncogene 21:368- 376, 2002. 3 C c

GAM90 374 BCL6 Ye, B. H.; Cattoretti, G.; Shen, Q.; Zhang, J.; Hawe, N.; de Waard,R.; Leung, C.; Nouri- Shirazi, M.; Orazi, A.; Chaganti, R. S. K.; Rothman,P.; Stall, A. M.; Pandolfi, P.- P.; Dalla- Favera, R.: The BCL- 6 proto- oncogenecontrols germinal- centre formation and Th2- type inflammation. NatureGenet. 16: 161- 170, 1997. 3 C c

GAM90 374 BCL6 Ye, B. H.; Lista, F.; Lo Coco, F.; Knowles, D. M.; Offit, K.;Chaganti, R. S. K.; Dalla- Favera, R.: Alterations of a zinc finger- encodinggene, BCL- 6, in diffuse large- cell lymphoma. Science 262: 747- 750,1993. 3 C c

GAM90 374 BCL6 Ye, B. H.; Rao, P. H.; Chaganti, R. S. K.; Dalla- Favera, R.:Cloning of bcl- 6, the locus involved in chromosome translocationsaffecting band 3q27 in B- cell lymphoma. Cancer Res. 53: 2732- 2735,1993. 3 C c

GAM90 374 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, 3 C c
G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.;
Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.;
Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for
Muckle- Wells syndrome and familial cold urticaria:a novel mutation
underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002.

GAM90 374 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, 3 C c
E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile
neurological cutaneous and articular syndromeis caused by mutations in
CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes.
Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM90 374 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. 3 C c
D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes
familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature
Genet. 29: 301- 305, 2001.

GAM90 374 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 C c
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM90 374 EBAG9 Ikeda, K.; Sato, M.; Tsutsumi, O.; Tsuchiya, F.; Tsuneizumi, M.;Emi, M.; 3 C c
Imoto, I.; Inazawa, J.; Muramatsu, M.; Inoue, S.: Promoteranalysis and
chromosomal mapping of human EBAG9 gene. Biochem. Biophys.Res. Commun. 273:
654- 660, 2000.

GAM90 374 EBAG9 Nakashima, M.; Sonoda, K.; Watanabe, T.: Inhibition of cell growthand 3 C c
induction of apoptotic cell death by the human tumor- associatedantigen
RCAS1. Nature Med. 5: 938- 942, 1999.

GAM90 374 EBAG9 Watanabe, T.; Inoue, S.; Hiroi, H.; Orimo, A.; Kawashima, H.; Muramatsu,M.: 3 C c
Isolation of estrogen- responsive genes with a CpG island library.
Molec.Cell. Biol. 18: 442- 449, 1998.

GAM90 374 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, 3 C c
J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2
in the allergic response. Nature 412: 186- 190,2001.

GAM90 374 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 C c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM90 374 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; 3 C c
Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab-
family adapter proteins act downstream of cytokine and growthfactor
receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999.

GAM90 374 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH 3 C c
mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell
Genet. 94: 39- 42, 2001.

GAM90 374 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology 3 C c
domain- containing adapter protein, acts to uncouple signalingfrom ERK
kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999.

GAM90 374 IRF1 Buckwalter, M. S.; Lossie, A. C.; Scarlett, L. M.; Camper, S. A.: 3 C c
Localization of the human chromosome 5q genes Gabra- 1, Gabrg- 2,I1- 4, I1-

5, and Irf- 1 on mouse chromosome 11. Mammalian Genome 3:604- 607, 1992.

GAM90 374 IRF1 Eason, D. D.; Shepherd, A. T.; Blanck, G.: Interferon regulatoryfactor 1 3 C c
tryptophan 11 to arginine point mutation abolishes DNA binding.
Biochim.Biophys. Acta 1446: 140- 144, 1999.

GAM90 374 IRF1 Harada, H.; Fujita, T.; Miyamoto, M.; Kimura, Y.; Maruyama, M.;Furia, A.; 3 C c
Miyata, T.; Taniguchi, T.: Structurally similar but functionallydistinct
factors, IRF- 1 and IRF- 2, bind to the same regulatory elementsof IFN and
IFN- inducible genes. Cell 58: 729- 739, 1989.

GAM90 374 IRF1 Harada, H.; Kondo, T.; Ogawa, S.; Tamura, T.; Kitagawa, M.; Tanaka,N.; 3 C c
Lamphier, M. S.; Hirai, H.; Taniguchi, T.: Accelerated exon skippingof IRF-
1 mRNA in human myelodysplasia/leukemia: a possible mechanismof tumor
suppressor inactivation Oncogene 9: 3313- 3320, 1994.

GAM90 374 IRF1 Harada, H.; Willison, K.; Sakakibara, J.; Miyamoto, M.; Fujita,T.; 3 C c
Taniguchi, T.: Absence of the type I IFN system in EC cells:transcriptional
activator (IRF- 1) and repressor (IRF- 2) genes aredevelopmentally
regulated. Cell 63: 303- 312, 1990.

GAM90 374 IRF1 Itoh, S.; Harada, H.; Nakamura, Y.; White, R.; Taniguchi, T.:Assignment of 3 C c
the human interferon regulatory factor- 1 (IRF1) geneto chromosome 5q23-
q31. Genomics 10: 1097- 1099, 1991.

GAM90 374 IRF1 Ko, J.; Gendron- Fitzpatrick, A.; Splitter, G. A.: Susceptibilityof IFN 3 C c
regulatory factor- 1 and IFN consensus sequence binding protein-
deficientmice to brucellosis. J. Immun. 168: 2433- 2440, 2002.

GAM90 374 IRF1 Miyamoto, M.; Fujita, T.; Kimura, Y.; Maruyama, M.; Harada, H.;Sudo, Y.; 3 C c
Miyata, T.; Taniguchi, T.: Regulated expression of a geneencoding a nuclear
factor, IRF- 1, that specifically binds to IFN- betagene regulatory
elements. Cell 54: 903- 913, 1988.

GAM90 374 IRF1 Nozawa, H.; Oda, E.; Ueda, S.; Tamura, G.; Maesawa, C.; Muto, T.;Taniguchi, 3 C c
T.; Tanaka, N.: Functionally inactivating point mutationin the tumor-
suppressor IRF- 1 gene identified in human gastric cancer. Int.J. Cancer 77:
522- 527, 1998.

GAM90 374 IRF1 Tamura, G.; Sakata, K.; Nishizuka, S.; Maesawa, C.; Suzuki, Y.;Terashima, 3 C c
M.; Eda, Y.; Satodate, R.: Allelotype of adenoma and
differentiatedadenocarcinoma of the stomach. J. Path. 180: 371- 377, 1996.

GAM90 374 IRF1 Willman, C. L.; Sever, C. E.; Pallavicini, M. G.; Harada, H.;Tanaka, N.; 3 C c
Slovak, M. L.; Yamamoto, H.; Harada, K.; Meeker, T. C.;List, A. F.;
Taniguchi, T.: Deletion of IRF- 1, mapping to chromosome5q31.1, in human
leukemia and preleukemic myelodysplasia. Science 259:968- 971, 1993.

GAM90 374 IRF1 Yamada, G.; Ogawa, M.; Akagi, K.; Miyamoto, H.; Nakano, N.; Itoh,S.; 3 C c
Miyazaki, J.; Nishikawa, S.; Yamamura, K.; Taniguchi, T.: Specificdepletion
of the B- cell population induced by aberrant expressionof human interferon
regulatory factor 1 gene in transgenic mice. Proc.Nat. Acad. Sci. 88: 532-
536, 1991.

GAM90 374 MIR16 Loftus, B. J.; Kim, U.- J.; Sneddon, V. P.; Kalush, F.; Brandon,R.; 3 C a
Fuhrmann, J.; Mason, T.; Crosby, M. L.; Barnstead, M.; Cronin,L.; Mays, A.
D.; Cao, Y.; Xu, R. X.; Kang, H.- L.; Mitchell, S.; Eichler,E. E.; Harris,
P. C.; Venter, J. C.; Adams, M. D.: Genome duplicationsand other features in
12 Mb of DNA sequence from human chromosome16p and 16q. Genomics 60: 295-
308, 1999.

GAM90 374 MIR16 Zheng, B.; Chen, D.; Farquhar, M. G.: MIR16, a putative 3 C a
membraneglycerophosphodiester phosphodiesterase, interacts with RGS16.

Proc.Nat. Acad. Sci. 97: 3999- 4004, 2000.

GAM90 374 NFE2L1 Chan, J. Y.; Cheung, M.- C.; Moi, P.; Chan, K.; Kan, Y. W.: 3 C c
Chromosomallocalization of the human NF- E2 family of bZIP transcription
factorsby fluorescence in situ hybridization. Hum. Genet. 95: 265- 269,1995.

GAM90 374 NFE2L1 Chan, J. Y.; Han, X.- L.; Kan, Y. W.: Cloning of Nrf1, an NF- E2- 3 C c
relatedtranscription factor, by genetic selection in yeast. Proc. Nat.
Acad.Sci. 90: 11371- 11375, 1993.

GAM90 374 NFE2L1 Chan, J. Y.; Kwong, M.; Lu, R.; Chang, J.; Wang, B.; Yen, T. S.B.; Kan, Y. 3 C c
W.: Targeted disruption of the ubiquitous CNC- bZIP transcriptionfactor,
Nrf- 1, results in anemia and embryonic lethality in mice. EMBOJ. 17: 1779-
1787, 1998.

GAM90 374 NFE2L1 Luna, L.; Johnsen, O.; Skartlien, A. H.; Pedeutour, F.; Turc- Carel,C.; 3 C c
Prydz, H.; Kolsto, A.- B.: Molecular cloning of a putative novelhuman bZIP
transcription factor on chromosome 17q22. Genomics 22:553- 562, 1994.

GAM90 374 NFE2L1 Luna, L.; Johnsen, O.; Skartlien, A.; Pedeutour, F.; Turc- Carel,C.; Prydz, 3 C c
H.; Kolsto, A.- B.: Molecular cloning of a putative novelhuman bZIP
transcription factor on chromosome 17q22. Genomics 22:553- 562, 1994.

GAM90 374 NFE2L1 McKie, J.; Johnstone, K.; Mattei, M.- G.; Scambler, P.: Cloningand mapping 3 C c
of murine Nfe2l1. Genomics 25: 716- 719, 1995.

GAM90 374 NFE2L1 McKie, J.; Scambler, P. J.: The Nfe2l1 gene maps to distal mousechromosome 3 C c
11. Mammalian Genome 7: 89- 90, 1996.

GAM90 374 NLGN1 Ichtchenko, K.; Hata, Y.; Nguyen, T.; Ullrich, B.; Missler, M.;Moomaw, C.; 3 C c
Sudhof, T. C.: Neuroligin 1: a splice site- specific ligandfor beta-
neurexins. Cell 81: 435- 443, 1995.

GAM90 374 NLGN1 Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirosawa, M.; Miyajima, N.;Tanaka, A.; 3 C c
Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of
unidentified human genes. XIV. The complete sequencesof 100 new cDNA clones
from brain which code for large proteins invitro. DNA Res. 6: 197- 205,
1999.

GAM90 374 NLGN1 Scheiffele, P.; Fan, J.; Choih, J.; Fetter, R.; Serafini, T.:Neuroligin 3 C c
expressed in nonneuronal cells triggers presynaptic developmentin contacting
axons. Cell 101: 657- 669, 2000.

GAM90 374 NRXN2 Bergman, L.; Silins, G.; Grimmond, S.; Hummerich, H.; Stewart,C.; Little, 3 C c
P.; Hayward, N.: A 500- kb sequence- ready cosmid contigand transcript map
of the MEN1 region on 11q13. Genomics 55: 49- 56,1999.

GAM90 374 NRXN2 Missler, M.; Sudhof, T. C.: Neurexins: three genes and 1001 products. 3 C c
TrendsGenet. 14: 20- 26, 1998.

GAM90 374 NRXN2 Rowen, L.; Young, J.; Birditt, B.; Kaur, A.; Madan, A.; Philipps,D. L.; Qin, 3 C c
S.; Minx, P.; Wilson, R. K.; Hood, L.; Graveley, B. R.: Analysis of the
human neurexin genes: alternative splicing and thegeneration of protein
diversity. Genomics 79: 587- 597, 2002.

GAM90 374 NRXN2 Tabuchi, K.; Sudhof, T. C.: Structure and evolution of neurexingenes: 3 C c
insight into the mechanism of alternative splicing. Genomics 79:849- 859,
2002.

GAM90 374 NRXN2 Ushkaryov, Y. A.; Petrenko, A. G.; Geppert, M.; Sudhof, T. C.:Neurexins: 3 C c
synaptic cell surface proteins related to the alpha- latrotoxinreceptor and
laminin. Science 257: 50- 56, 1992.

GAM90 374 NUMB Salcini, A. E.; Confalonieri, S.; Doria, M.; Santolini, E.; Tassi,E.; 3 C c
Minenkova, O.; Cesareni, G.; Pelicci, P. G.; Di Fiore, P. P.:Binding
specificity and in vivo targets of the EH domain, a novelprotein- protein

interaction module. Genes Dev. 11: 2239- 2249, 1997.

GAM90 374 NUMB Sherrington, R.; Rogaev, E. I.; Liang, Y.; Rogaeva, E. A.; Levesque,G.; Ikeda, M.; Chi, H.; Lin, C.; Li, G.; Holman, K.; Tsuda, T.; Mar.;and 21 others: Cloning of a gene bearing missense mutations inearly- onset familial Alzheimer's disease. Nature 375: 754- 760, 1995. 3 C c

GAM90 374 NUMB Verdi, J. M.; Bashirullah, A.; Goldhawk, D. E.; Kubu, C. J.; Jamali,M.; Meakin, S. O.; Lipshitz, H. D.: Distinct human NUMB isoformsregulate differentiation vs. proliferation in the neuronal lineage. Proc.Nat. Acad. Sci. 96: 10472- 10476, 1999. 3 C c

GAM90 374 NUMB Zhong, W.; Feder, J. N.; Jiang, M.- M.; Jan, L. Y.; Jan, Y. N.:Asymmetric localization of a mammalian Numb homolog during mouse corticalneurogenesis. Neuron 17: 43- 53, 1996. 3 C c

GAM90 374 ROCK2 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 C c

GAM90 374 ROCK2 Nakamura, M.; Nagano, T.; Chikama, T.; Nishida, T.: Role of thesmall GTP- binding protein Rho in epithelial cell migration in therabbit cornea. Invest. Ophthal. Vis. Sci. 42: 941- 947, 2001. 3 C c

GAM90 374 ROCK2 Rao, P. V.; Deng, P.- F.; Kumar, J.; Epstein, D. L.: Modulationof aqueous humor outflow facility by the Rho kinase- specific inhibitorY- 27632. Invest. Ophthal. Vis. Sci. 42: 1029- 1037, 2001. 3 C c

GAM90 374 ROCK2 Takahashi, N.; Tuiki, H.; Saya, H.; Kaibuchi, K.: Localizationof the gene coding for ROCK II/Rho kinase on human chromosome 2p24. Genomics 55:235- 237, 1999. 3 C c

GAM90 374 WNT10B Bui, T. D.; Rankin, J.; Smith, K.; Huguet, E. L.; Ruben, S.; Strachan,T.; Harris, A. L.; Lindsay, S.: A novel human Wnt gene, WNT10B, mapsto 12q13 and is expressed in human breast carcinomas. Oncogene 14:1249- 1253, 1997. 3 C c

GAM90 374 WNT10B Hardiman, G.; Kastelein, R. A.; Bazan, J. F.: Isolation, characterizationand chromosomal localization of human WNT10B. Cytogenet. Cell Genet. 77:278- 282, 1997. 3 C c

GAM90 374 WNT10B Kirikoshi, H.; Sekihara, H.; Katoh, M.: WNT10A and WNT6, clusteredin human chromosome 2q35 region with head- to- tail manner, are stronglycoexpressed in SW480 cells. Biochem. Biophys. Res. Commun. 283:798- 805, 2001. 3 C c

GAM90 374 WNT10B Ross, S. E.; Hemati, N.; Longo, K. A.; Bennett, C. N.; Lucas, P.C.; Erickson, R. L.; MacDougald, O. A.: Inhibition of adipogenesisby Wnt signaling. Science 289: 950- 953, 2000. 3 C c

GAM91 336 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 C c

GAM91 336 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 C c

GAM91 336 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 C c

GAM93 397 PKP2 Bonne, S.; van Hengel, J.; van Roy, F.: Chromosomal mapping ofhuman armadillo genes belonging to the p120(ctn)/plakophilin subfamily. Genomics 51:452- 454, 1998. 3 C b

GAM93 397 PKP2 Bonne, S.; van Hengel, J; van Roy, F.: Assignment of the plakophilin- 2gene 3 C b
(PKP2) and a plakophilin- 2 pseudogene (PKP2P1) to human chromosomebands
12p11 and 12p13, respectively, by in situ hybridization. Cytogenet.Cell
Genet. 88: 286- 287, 2000.

GAM93 397 PKP2 Mertens, C.; Kuhn, C.; Franke, W. W.: Plakophilins 2a and 2b:constitutive 3 C b
proteins of dual location in the karyoplasm and the desmosomalplaque. J.
Cell Biol. 135: 1009- 1025, 1996.

GAM93 397 PKP2 Schmidt, A; Langbein, L.; Pratzel, S.; Rode, M.; Rackwitz, H.- R.;Franke, W. 3 C b
W.: Plakophilin 3- - a novel cell- type- specific desmosomalplaque protein.
Differentiation 64: 291- 306, 1999.

GAM94 332 ABCA1 Becq, F.; Hamon, Y.; Bajetto, A.; Gola, M.; Verrier, B.; Chimini,G.: ABC1, 3 B c
an ATP binding cassette transporter required for phagocytosisof apoptotic
cells, generates a regulated anion flux after expressionin Xenopus laevis
oocytes. J. Biol. Chem. 272: 2695- 2699, 1997.

GAM94 332 ABCA1 Bodzioch, M.; Orso, E.; Klucken, J.; Langmann, T.; Bottcher, A.;Diederich, 3 B c
W.; Drobnik, W.; Barlage, S.; Buchler, C.; Porsch- Ozcurumez,M.; Kaminski,
W. E.; Hahmann, H. W.; Oette, K.; Rothe, G.; Aslanidis,C.; Lackner, K. J.;
Schmitz, G.: The gene encoding ATP- binding cassettetransporter 1 is mutated
in Tangier disease. Nature Genet. 22: 347- 351,1999.

GAM94 332 ABCA1 Brooks- Wilson, A.; Marcil, M.; Clee, S. M.; Zhang, L.- H.; Roomp,K.; van 3 B c
Dam, M.; Yu, L.; Brewer, C.; Collins, J. A.; Molhuizen, H.O. F.; Loubser,
O.; Ouelette, B. F. F.; and 14 others: Mutationsin ABC1 in Tangier disease
and familial high- density lipoprotein deficiency. NatureGenet. 22: 336-
345, 1999.

GAM94 332 ABCA1 Decottignies, A.; Goffeau, A.: Complete inventory of the yeastABC proteins. 3 B c
Nature Genet. 15: 137- 145, 1997.

GAM94 332 ABCA1 Goossens, M.; Brauner, R.; Czernichow, P.; Duquesnoy, P.; Rappaport,R.: 3 B c
Isolated growth hormone (GH) deficiency type 1A associated witha double
deletion in the human GH gene cluster. J. Clin. Endocr.Metab. 62: 712- 716,
1986.

GAM94 332 ABCA1 Guo, Z.; Inazu, A.; Yu, W.; Suzumura, T.; Okamoto, M.; Nohara,A.; 3 B c
Higashikata, T.; Sano, R.; Wakasugi, K.; Hayakawa, T.; Yoshida,K.; Suehiro,
T.; Schmitz, G.; Mabuchi, H.: Double deletions and missensemutations in the
first nucleotide- binding fold of the ATP- bindingcassette transporter A1
(ABCA1) gene in Japanese patients with Tangierdisease. J. Hum. Genet. 47:
325- 329, 2002.

GAM94 332 ABCA1 Hong, S. H.; Rhyne, J.; Zeller, K.; Miller, M.: Novel ABCA1 compoundvariant 3 B c
associated with HDL cholesterol deficiency. Biochim. Biophys.Acta 1587: 60-
64, 2002.

GAM94 332 ABCA1 Hoop, R. C.; Russo, L. S.; Riconda, D. L.; Schwartz, L. S.; Hoffman,E. P.: 3 B c
Restoration of half the normal dystrophin sequence in a double-
deletionDuchenne muscular dystrophy family. Am. J. Med. Genet. 49: 323-
327,1994.

GAM94 332 ABCA1 Huang, W.; Moriyama, K.; Koga, T.; Hua, H.; Ageta, M.; Kawabata,S.; 3 B c
Mawatari, K.; Imamura, T.; Eto, T.; Kawamura, M.; Teramoto, T.;Sasaki, J.:
Novel mutations in ABCA1 gene in Japanese patients withTangier disease and
familial high density lipoprotein deficiency withcoronary heart disease.
Biochim. Biophys. Acta 1537: 71- 78, 2001.

GAM94 332 ABCA1 Ishii, J.; Nagano, M.; Kujiraoka, T.; Ishihara, M.; Egashira,T.; Takada, D.; 3 B c
Tsuji, M.; Hattori, H.; Emi, M.: Clinical variantof Tangier disease in

Japan: mutation of the ABCA1 gene in hypoalphalipoproteinemiawith corneal lipidosis. J. Hum. Genet. 47: 366- 369, 2002.

GAM94 332 ABCA1 Jennings, M. W.; Jones, R. W.; Wood, W. G.; Weatherall, D. J.: Analysis of an inversion within the human beta globin gene cluster. NucleicAcids Res. 13: 2897- 2906, 1985. 3 B c

GAM94 332 ABCA1 Kulozik, A. E.; Bellan- Koch, A.; Kohne, E.; Kleihauer, E.: Adeletion/inversion rearrangement of the beta- globin gene cluster ina Turkish family with delta- beta(0)- thalassemia intermedia. Blood 79:2455- 2459, 1992. 3 B c

GAM94 332 ABCA1 Langmann, T.; Klucken, J.; Reil, M.; Liebisch, G.; Luciani, M.- F.;Chimini, G.; Kaminski, W. E.; Schmitz, G.: Molecular cloning of thehuman ATP- binding cassette transporter 1 (hABC1): evidence for sterol- dependentregulation in macrophages. Biochem. Biophys. Res. Commun. 257: 29- 33,1999. 3 B c

GAM94 332 ABCA1 Lapicka- Bodzioch, K.; Bodzioch, M.; Krull, M.; Kielar, D.; Probst,M.; Kiec, B.; Andrikovics, H.; Bottcher, A.; Hubacek, J.; Aslanidis,C.; Suttorp, N.; Schmitz, G.: Homogeneous assay based on 52 primersets to scan for mutations of the ABCA1 gene and its application ingenetic analysis of a new patient with familial high- density lipoproteindeficiency syndrome. Biochim. Biophys. Acta 1537: 42- 48, 2001. 3 B c

GAM94 332 ABCA1 Lawn, R. M.; Wade, D. P.; Garvin, M. R.; Wang, X.; Schwartz, K.;Porter, J. G.; Seilhamer, J. J.; Vaughan, A. M.; Oram, J. F.: TheTangier disease gene product ABC1 controls the cellular apolipoprotein- mediatedlipid removal pathway. J. Clin. Invest. 104: R25- R31, 1999. 3 B c

GAM94 332 ABCA1 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000. 3 B c

GAM94 332 ABCA1 Luciani, M. F.; Denizot, F.; Savary, S.; Mattei, M. G.; Chimini,G.: Cloning of two novel ABC transporters mapping on human chromosome9. Genomics 21: 150- 159, 1994. 3 B c

GAM94 332 ABCA1 Marcil, M.; Boucher, B.; Krimbou, L.; Solymoss, B. C.; Davignon,J.; Frohlich, J.; Genest, J., Jr.: Severe familial HDL deficiencyin French-Canadian kindreds: clinical, biochemical, and molecularcharacterization. Arterioscler. Thromb. Vasc. Biol. 15: 1015- 1024,1995. 3 B c

GAM94 332 ABCA1 Marcil, M.; Yu, L.; Krimbou, L.; Boucher, B.; Oram, J. F.; Cohn,J. S.; Genest, J., Jr.: Cellular cholesterol transport and effluxin fibroblasts are abnormal in subjects with familial HDL deficiency. Arterioscler.Thromb. Vasc. Biol. 19: 159- 169, 1999. 3 B c

GAM94 332 ABCA1 McNeish, J.; Aiello, R. J.; Guyot, D.; Turi, T.; Gabel, C.; Aldinger,C.; Hoppe, K. L.; Roach, M. L.; Royer, L. J.; de Wet, J.; Broccardo,C.; Chimini, G.; Francone, O. L.: High density lipoprotein deficiencyand foam cell accumulation in mice with targeted disruption of ATP- bindingcassette transporter- 1. Proc. Nat. Acad. Sci. 97: 4245- 4250, 2000. 3 B c

GAM94 332 ABCA1 Orso, E.; Broccardo, C.; Kaminski, W. E.; Bottcher, A.; Liebisch,G.; Drobnik, W.; Gotz, A.; Chambenoit, O.; Diederich, W.; Langmann,T.; Spruss, T.; Luciani, M.- F.; Rothe, G.; Lackner, K. J.; Chimini,G.; Schmitz, G.: Transport of lipids from Golgi to plasma membraneis defective in Tangier disease patients and Abc1- deficient mice. NatureGenet. 24: 192- 196, 2000. 3 B c

GAM94 332 ABCA1 Pullinger, C. R.; Hakamata, H.; Duchateau, P. N.; Eng, C.; Aouizerat,B. E.; Cho, M. H.; Fielding, C. J.; Kane, J. P.: Analysis of hABC1gene 5- prime end: additional peptide sequence, promoter region, andfour polymorphisms. 3 B c

Biochem. Biophys. Res. Commun. 271: 451- 455,2000.

GAM94 332 ABCA1 Remaley, A. T.; Rust, S.; Rosier, M.; Knapper, C.; Naudin, L.;Broccardo, C.; 3 B c
Peterson, K. M.; Koch, C.; Arnould, I.; Prades, C.;Duverger, N.; Funke, H.;
Assman, G.; Dinger, M.; Dean, M.; Chimini,G.; Santamarina- Fojo, S.;
Fredrickson, D. S.; Denefle, P. Brewer,H. B., Jr.: Human ATP- binding
cassette transporter 1 (ABC1): genomicorganization and identification of the
genetic defect in the originalTangier disease kindred. Proc. Nat. Acad. Sci.
96: 12685- 12690,1999.

GAM94 332 ABCA1 Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, 3 B c
K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation
of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers.
Science 289: 1524- 1529, 2000.

GAM94 332 ABCA1 Rust, S.; Rosier, M.; Funke, H.; Real, J.; Amoura, Z.; Piette,J.- C.; 3 B c
Deleuze, J.- F.; Brewer, H. B.; Duverger, N.; Denefle, P.; Assmann,G.:
Tangier disease is caused by mutations in the gene encoding ATP-
bindingcassette transporter 1. Nature Genet. 22: 352- 355, 1999.

GAM94 332 ABCA1 Santamarina- Fojo, S.; Peterson, K.; Knapper, C.; Qiu, Y.; Freeman,L.; 3 B c
Cheng, J.- F.; Osorio, J.; Remaley, A.; Yang, X.- P.; Haudenschild,C.;
Prades, C.; Chimini, G.; Blackmon, E.; Francois, T.; Duverger,N.; Rubin, E.
M.; Rosier, M.; Denefle, P.; Fredrickson, D. S.; Brewer,H. B., Jr.: Complete
genomic sequence of the human ABCA1 gene: analysisof the human and mouse
ATP- binding cassette A promoter. Proc. Nat.Acad. Sci. 97: 7987- 7992, 2000.
Note: Erratum: Proc. Nat. Acad. Sci.99: 1098 only, 2002.

GAM94 332 ABCA1 Szakacs, G.; Langmann, T.; Ozvegy, C.; Orso, E.; Schmitz, G.;Varadi, A.; 3 B c
Sarkadi, B.: Characterization of the ATPase cycle ofhuman ABCA1:
implications for its function as a regulator rather thanan active
transporter. Biochem. Biophys. Res. Commun. 288: 1258- 1264,2001.

GAM94 332 ABCA1 Tanaka, A. R.; Ikeda, Y.; Abe- Dohmae, S.; Arakawa, R.; Sadanami,K.; Kidera, 3 B c
A.; Nakagawa, S.; Nagase, T.; Aoki, R.; Kioka, N.; Amachi,T.; Yokoyama, S.;
Ueda, K.: Human ABCA1 contains a large amino terminalextracellular domain
homologous to an epitope of Sjogren's syndrome. Biochem.Biophys. Res.
Commun. 283: 1019- 1025, 2001.

GAM94 332 ABCA1 Utech, M.; Hobbel, G.; Rust, S.; Reinecke, H.; Assmann, G.; Walter,M.: 3 B c
Accumulation of RhoA, RhoB, RhoG, and Rac1 in fibroblasts fromTangier
disease subjects suggests a regulatory role of Rho familyproteins in
cholesterol efflux. Biochem. Biophys. Res. Commun. 280:229- 236, 2001.

GAM94 332 ABCA1 Young, S. G.; Fielding, C. J.: The ABCs of cholesterol efflux. NatureGenet. 3 B c
22: 316- 318, 1999.

GAM94 332 ABCA1 Zhao, L.- X.; Zhou, C.- J.; Tanaka, A.; Nakata, M.; Hirabayashi,T.; Amachi, 3 B c
T.; Shioda, S.; Ueda, K.; Inagaki, N.: Cloning, characterizationand tissue
distribution of the rat ATP- binding cassette (ABC) transporterABC2/ABCA2.
Biochem J. 350: 865- 872, 2000.

GAM94 332 ABCA1 Zwarts, K. Y.; Clee, S. M.; Zwinderman, A. H.; Engert, J. C.;Singaraja, R.; 3 B c
Loubser, O.; James, E.; Roomp, K.; Hudson, T. J.; Jukema,J. W.; Kastelein,
J. J. P.; Hayden, M. R.: ABCA1 regulatory variantsinfluence coronary artery
disease independent of effects on plasmalipid levels. Clin. Genet. 61: 115-
125, 2002.

GAM94 332 ABR Heisterkamp, N.; Kaartinen, V.; van Soest, S.; Bokoch, G. M.; Groffen,J.: 3 B c
Human ABR encodes a protein with GAP- rac activity and homologyto the DBL
nucleotide exchange factor domain. J. Biol. Chem. 268:16903- 16906, 1993.

GAM94 332 ABR Heisterkamp, N.; Morris, C.; Groffen, J.: ABR, an active BCR- relatedgene. 3 B c
Nucleic Acids Res. 17: 8821- 8831, 1989.

GAM94 332 ABR McDonald, J. D.; Daneshvar, L.; Willert, J. R.; Matsumura, K.;Waldman, F.; 3 B c
Cogen, P. H.: Physical mapping of chromosome 17p13.3in the region of a
putative tumor suppressor gene important in medulloblastoma. Genomics
23:229- 232, 1994.

GAM94 332 ACE Amant, C.; Bauters, C.; Bodart, J.- C.; Lablanche, J.- M.; Grollier,G.; 3 B c
Danchin, N.; Hamon, M.; Richard, F.; Helbecque, N.; McFadden,E. P.; Amouyel,
P.; Bertrand, M. E.: D allele of the angiotensinI- converting enzyme is a
major risk factor for restenosis after coronarystenting. Circulation 96: 56-
60, 1997.

GAM94 332 ACE Arbustini, E.; Grasso, M.; Fasani, R.; Klersy, C.; Diegoli, M.;Porcu, E.; 3 B c
Banchieri, N.; Fortina, P.; Danesino, C.; Specchia, G.: Angiotensin
converting enzyme gene deletion allele is independentlyand strongly
associated with coronary atherosclerosis and myocardialinfarction. Brit.
Heart J. 74: 584- 591, 1995.

GAM94 332 ACE Berge, K. E.; Berg, K.: No effect of insertion/deletion polymorphismat the 3 B c
ACE locus on normal blood pressure level or variability. Clin.Genet. 45:
169- 174, 1994.

GAM94 332 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: 3 B c
Insertion/deletion(I/D) polymorphism at the locus for angiotensin I-
converting enzymeand myocardial infarction. Clin. Genet. 44: 292- 297, 1993.

GAM94 332 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: 3 B c
Insertion/deletion(I/D) polymorphism at the locus for angiotensin I-
converting enzymeand parental history of myocardial infarction. Clin. Genet.
44:298- 301, 1993.

GAM94 332 ACE Brown, N. J.; Ray, W. A.; Snowden, M.; Griffin, M. R.: Black Americanshave 3 B c
an increased rate of angiotensin converting enzyme inhibitor-
associatedangioedema. Clin. Pharmacol. Therapeutics 60: 8- 13, 1996.

GAM94 332 ACE Cambien, F.; Alhenc- Gelas, F.; Herbeth, B.; Andre, J. L.; Rakotovao,R.; 3 B c
Gonzales, M. F.; Allegrini, J.; Bloch, C.: Familial resemblanceof plasma
angiotensin- converting enzyme level: the Nancy study. Am.J. Hum. Genet. 43:
774- 780, 1988.

GAM94 332 ACE Cambien, F.; Poirier, O.; Lecerf, L.; Evans, A.; Cambou, J.- P.;Arveiler, 3 B c
D.; Luc, G.; Bard, J.- M.; Bara, L.; Ricard, S.; Tiret, L.;Amouyel, P.;
Alhenc- Gelas, F.; Soubrier, F.: Deletion polymorphismin the gene for
angiotensin- converting enzyme is a potent risk factorfor myocardial
infarction. Nature 359: 641- 644, 1992.

GAM94 332 ACE Doria, A.; Warram, J. H.; Krolewski, A. S.: Genetic predispositionto 3 B c
diabetic nephropathy: evidence for a role of the angiotensin I-
convertingenzyme gene. Diabetes 43: 690- 695, 1994.

GAM94 332 ACE Ehlers, M. R. W.; Fox, E. A.; Strydom, D. J.; Riordan, J. F.:Molecular 3 B c
cloning of human testicular angiotensin- converting enzyme:the testis
isozyme is identical to the C- terminal half of endothelialangiotensin-
converting enzyme. Proc. Nat. Acad. Sci. 86: 7741- 7745,1989.

GAM94 332 ACE Esther, C. R., Jr.; Marino, E. M.; Howard, T. E.; Machaud, A.;Corvol, P.; 3 B c
Capecchi, M. R.; Bernstein, K. E.: The critical roleof tissue angiotensin-
converting enzyme as revealed by gene targetingin mice. J. Clin. Invest. 99:
2375- 2385, 1997.

GAM94 332 ACE Evans, A. E.; Poirier, O.; Kee, F.; Lecerf, L.; McCrum, E.; Falconer,T.; 3 B c

Crane, J.; O'Rourke, D. F.; Cambien, F.: Polymorphisms of theangiotensin-converting- enzyme gene in subjects who die from coronaryheart disease. Quart. J. Med. 87: 211- 214, 1994.

GAM94 332 ACE Exner, D. V.; Dries, D. L.; Domanski, M. J.; Cohn, J. N.: Lesserresponse to angiotensin- converting- enzyme inhibitor therapy in blackas compared with white patients with left ventricular dysfunction. NewEng. J. Med. 344: 1351-1357, 2001. 3 B c

GAM94 332 ACE Gardemann, A.; Fink, M.; Stricker, J.; Nguyen, Q. D.; Humme, J.;Katz, N.; Tillmanns, H.; Hehrlein, F. W.; Rau, M.; Haberbosch, W.: ACE I/D gene polymorphism: presence of the ACE D allele increasesthe risk of coronary artery disease in younger individuals. Atherosclerosis 139:153- 159, 1998. 3 B c

GAM94 332 ACE Gayagay, G.; Yu, B.; Hambly, B.; Boston, T.; Hahn, A.; Celermajer,D. S.; Trent, R. J.: Elite endurance athletes and the ACE I allele:the role of genes in athletic performance. Hum. Genet. 103: 48- 50,1998. 3 B c

GAM94 332 ACE Hagaman, J. R.; Moyer, J. S.; Bachman, E. S.; Sibony, M.; Magyar,P. L.; Welch, J. E.; Smithies, O.; Krege, J. H.; O'Brien, D. A.:Angiotensin-converting enzyme and male fertility. Proc. Nat. Acad.Sci. 95: 2552- 2557, 1998. 3 B c

GAM94 332 ACE Hamdi, H. K.; Reznik, J.; Castellon, R.; Atilano, S. R.; Ong,J. M.; Udar, N.; Tavis, J. H.; Aoki, A. M.; Nesburn, A. B.; Boyer,D. S.; Small, K. W.; Brown, D. J.; Kenney, M. C.: Alu DNA polymorphismin ACE gene is protective for age- related macular degeneration. Biochem.Biophys. Res. Commun. 295: 668- 672, 2002. 3 B c

GAM94 332 ACE Howard, T. E.; Shai, S. Y.; Langford, K. G.; Martin, B. M.; Bernstein,K. E.: Transcription of testicular angiotensin- converting enzyme(ACE) is initiated within the 12th intron of the somatic ACE gene. Molec.Cell. Biol. 10: 4294-4302, 1990. 3 B c

GAM94 332 ACE Huang, W.; Gallois, Y.; Bouby, N.; Bruneval, P.; Heudes, D.; Belair,M.- F.; Krege, J. H.; Menteton, P.; Marre, M.; Smithies, O.; Alhenc- Gelas,F.: Genetically increased angiotensin I- converting enzyme level andrenal complications in the diabetic mouse. Proc. Nat. Acad. Sci. 98:13330- 13334, 2001. 3 B c

GAM94 332 ACE Jeffery, S.; Malik, A. K. S.; Crosby, A.; Bland, M.; Eastwood,J. B.; Amoah-Danquah, J.; Acheampong, J. W.; Plange- Rhule, J.: Adominant relationship between the ACE D allele and serum ACE levelsin a Ghanaian population. (Letter) J. Med. Genet. 36: 869- 870, 1999. 3 B c

GAM94 332 ACE Jeunemaitre, X.; Lifton, R. P.; Hunt, S. C.; Williams, R. R.;Lalouel, J.-M.: Absence of linkage between the angiotensin convertingenzyme locus and human essential hypertension. Nature Genet. 1:72- 75, 1992. 3 B c

GAM94 332 ACE Julier, C.; Delepine, M.; Keavney, B.; Terwilliger, J.; Davis,S.; Weeks, D. E.; Bui, T.; Jeunemaitre, X.; Velho, G.; Froguel, P.;Ratcliffe, P.; Corvol, P.; Soubrier, F.; Lathrop, G. M.: Geneticsusceptibility for human familial essential hypertension in a regionof homology with blood pressure linkage on rat chromosome 10. Hum.Molec. Genet. 6: 2077- 2085, 1997. 3 B c

GAM94 332 ACE Keavney, B.; McKenzie, C.; Parish, S.; Palmer, A.; Clark, S.;Youngman, L.; Delepine, M.; Lathrop, M.; Peto, R.; Collins, R.: Large- scaletest of hypothesized associations between the angiotensin- converting-enzymeinsertion/deletion polymorphism and myocardial infarction in about5000 cases and 6000 controls. Lancet 355: 434- 442, 2000. 3 B c

GAM94 332 ACE Kehoe, P. G.; Russ, C.; McIlroy, S.; Williams, H.; Holmans, P.;Holmes, C.; 3 B c

Liolitsa, D.; Vahidassr, D.; Powell, J.; McGleenon, B.;Liddell, M.; Plomin, R.; and 9 others: Variation in DCP1, encodingACE, is associated with susceptibility to Alzheimer disease. (Letter) NatureGenet. 21: 71- 72, 1999.

GAM94 332 ACE Keramatipour, M.; McConnell, R. S.; Kirkpatrick, P.; Tebbs, S.;Furlong, R. A.; Rubinsztein, D. C.: The ACE I allele is associatedwith increased risk for ruptured intracranial aneurysms. J. Med.Genet. 37: 498- 500, 2000. 3 B c

GAM94 332 ACE Krege, J. H.; John, S. W. M.; Langenbach, L. L.; Hodgin, J. B.;Hagaman, J. R.; Bachman, E. S.; Jennette, J. C.; O'Brien, D. A.; Smithies,O.: Male-female differences in fertility and blood pressure in ACE- deficientmice. Nature 375: 146- 148, 1995. 3 B c

GAM94 332 ACE Kurtz, T. W.: The ACE of hearts. Nature 359: 588- 589, 1992. 3 B c

GAM94 332 ACE Lindpaintner, K.; Lee, M.; Larson, M. G.; Rao, V. S; Pfeffer,M. A.; Ordovas, J. M.; Schaefer, E. J.; Wilson, A. F.; Wilson, P.W. F.; Vasan, R. S.; Myers, R. H.; Levy, D.: Absence of associationor genetic linkage between the angiotensin- converting- enzyme geneand left ventricular mass. New Eng. J. Med. 334: 1023- 1028, 1996. 3 B c

GAM94 332 ACE Lindpaintner, K.; Pfeffer, M. A.; Kreutz, R.; Stampfer, M. J.;Grodstein, F.; LaMotte, F.; Buring, J.; Hennekens, C. H.: A prospectiveevaluation of an angiotensin- converting- enzyme gene polymorphism andthe risk of ischemic heart disease. New Eng. J. Med. 332: 706- 711,1995. 3 B c

GAM94 332 ACE Marre, M.; Bernadet, P.; Gallois, Y.; Savagner, F.; Guyene, T.- T.;Hallab, M.; Cambien, F.; Passa, P.; Alhenc- Gelas, F.: Relationshipsbetween angiotensin I converting enzyme gene polymorphism, plasmalevels, and diabetic retinal and renal complications. Diabetes 43:384- 388, 1994. 3 B c

GAM94 332 ACE Marre, M.; Jeunemaitre, X.; Gallois, Y.; Rodier, M.; Chatellier,G.; Sert, C.; Dusselier, L.; Kahal, Z.; Chaillous, L.; Halimi, S.;Muller, A.; Sackmann, H.; Bauduceau, B.; Bled, F.; Passa, P.; Alhenc- Gelas,F.: Contribution of genetic polymorphism in the renin- angiotensinsystem to the development of renal complications in insulin- dependentdiabetes. J. Clin. Invest. 99: 1585- 1595, 1997. 3 B c

GAM94 332 ACE Mattei, M.- G.; Hubert, C.; Alhenc- Gelas, F.; Roeckel, N.; Corvol,P.; Soubrier, F.: Angiotensin- I converting enzyme gene is on chromosome17. (Abstract) Cytogenet. Cell Genet. 51: 1041, 1989. 3 B c

GAM94 332 ACE Montgomery, H. E.; Clarkson, P.; Dollery, C. M.; Prasad, K.; Losi,M.- A.; Hemingway, H.; Statters, D.; Jubb, M.; Girvain, M.; Varnava,A.; World, M.; Deanfield, J.; Talmud, P.; McEwan, J. R.; McKenna,W. J.; Humphries, S.: Association of angiotensin- converting enzymegene I/D polymorphism with change in left ventricular mass in responseto physical training. Circulation 96: 741- 747, 1997. 3 B c

GAM94 332 ACE Montgomery, H. E.; Marshall, R.; Hemingway, H.; Myerson, S.; Clarkson,P.; Dollery, C.; Hayward, M.; Holliman, D. E.; Jubb, M.; World, M.;Thomas, E. L.; Brynes, A. E.; Saeed, N.; Barnard, M.; Bell, J. D.;Prasad, K.; Rayson, M.; Talmud, P. J.; Humphries, S. E.: Human genefor physical performance. (Letter) Nature 393: 221- 222, 1998. 3 B c

GAM94 332 ACE Ohishi, M.; Fujii, K.; Minamino, T.; Hagaki, J.; Kamitani, A.;Rakugi, H.; Zhao, Y.; Mikami, H.; Miki, T.; Ogihara, T.: A potentgenetic risk factor for restenosis. (Letter) Nature Genet. 5: 324- 325,1993. 3 B c

GAM94 332 ACE Oike, Y.; Hata, A.; Ogata, Y.; Numata, Y.; Shido, K.; Kondo, K.: Angiotensin converting enzyme as a genetic risk factor for coronaryartery spasm: implication in the pathogenesis of myocardial infarction. J.Clin. Invest. 3 B c

96: 2975- 2979, 1995.

GAM94 332 ACE Okabe, T.; Fusisawa, M.; Yotsumoto, M.; Takaru, F.; Lanzillo,J. J.; Fanburg, 3 B c
B. L.: Familial elevation of serum angiotensin- convertingenzyme. Quart. J.
Med. 216: 55- 61, 1985.

GAM94 332 ACE Pfeffer, M. A.; Braunwald, E.; Moye, L. A.; Basta, L.; Brown,E. J., Jr.; 3 B c
Cuddy, T. E.; Davis, B. R.; Geltman, E. M.; Goldman, S.;Flaker, G. C.;
Klein, M.; Lamas, G. A.; Packer, M.; Rouleau, J.; Rouleau,J. L.; Rutherford,
J.; Wertheimer, J. H.; Hawkins, C. M.: Effectof captopril on mortality and
morbidity in patients with left ventricular dysfunction after myocardial
infarction: results of the survival andventricular enlargement trial. New
Eng. J. Med. 327: 669- 677, 1992.

GAM94 332 ACE Ramaraj, P.; Kessler, S. P.; Colmenares, C.; Sen, G. C.: 3 B c
Selectiverestoration of male fertility in mice lacking angiotensin-
convertingenzymes by sperm- specific expression of the testicular isozyme.
J.Clin. Invest. 102: 371- 378, 1998.

GAM94 332 ACE Rigat, B.; Hubert, C.; Alhenc- Gelas, F.; Cambien, F.; Corvol,P.; Soubrier, 3 B c
F.: An insertion/deletion polymorphism in the angiotensinI- converting
enzyme gene accounting for half the variance of serumenzyme levels. J. Clin.
Invest. 86: 1343- 1346, 1990.

GAM94 332 ACE Rigat, B.; Hubert, C.; Corvol, P.; Soubrier, F.: PCR detectionof the 3 B c
insertion/deletion polymorphism of the human angiotensin convertingenzyme
gene (DCP1) (dipeptidylcarboxypeptidase 1). Nucleic AcidsRes. 20: 1433,
1992.

GAM94 332 ACE Ruiz, J.; Blanche, H.; Cohen, N.; Velho, G.; Cambien, F.; Cohen,D.; Passa, 3 B c
P.; Froguel, P.: Insertion/deletion polymorphism of theangiotensin-
converting enzyme gene is strongly associated with coronaryheart disease in
non- insulin- dependent diabetes mellitus. Proc. Nat.Acad. Sci. 91: 3662-
3665, 1994.

GAM94 332 ACE Schachter, F.; Faure- Delanef, L.; Guenot, F.; Rouger, H.; Froguel,P.; 3 B c
Lesueur- Ginot, L.; Cohen, D.: Genetic associations with humanlongevity at
the APOE and ACE loci. Nature Genet. 6: 29- 32, 1994.

GAM94 332 ACE Schmidt, S.; Schone, N.; Ritz, E.; Giesel, R.; Bergis, K.; Strojek,K.; 3 B c
Greszczak, W.; Schroter, W.; Willms, B. H. L.; Petzold, R.; Henrichs,H. R.;
Rambausek, M.; Schwarzbeck, A.; Kohr, B.; Schneider, P.; Bosch,A.:
Association of ACE gene polymorphism and diabetic nephropathy? KidneyInt.
47: 1176- 1181, 1995.

GAM94 332 ACE Schunkert, H.; Hense, H.- W.; Holmer, S. R.; Stender, M.; Perz,S.; Keil, U.; 3 B c
Lorell, B. H.; Riegger, G. A. J.: Association betweena deletion polymorphism
of the angiotensin- converting- enzyme geneand left ventricular hypertrophy.
New Eng. J. Med. 330: 1634- 1638,1994.

GAM94 332 ACE Singer, D. R. J.; Missouris, C. G.; Jeffery, S.: Angiotensin- 3 B c
convertingenzyme gene polymorphism: what to do about all the confusion?
(Editorial) Circulation 94:236- 239, 1996.

GAM94 332 ACE Soubrier, F.; Alhenc- Gelas, F.; Hubert, C.; Allegrini, J.; John,M.; 3 B c
Tregear, G.; Corvol, P.: Two putative active centers in humanangiotensin I-
converting enzyme revealed by molecular cloning. Proc.Nat. Acad. Sci. 85:
9386- 9390, 1988.

GAM94 332 ACE Tarnow, L.; Cambien, F.; Rossing, P.; Nielsen, F. S.; Hansen,B. V.; Lecerf, 3 B c
L.; Poirier, O.; Danilov, S.; Parving, H.- H.: Lackof relationship between
an insertion/deletion polymorphism in theangiotensin I- converting enzyme

gene and diabetic nephropathy andproliferative retinopathy in IDDM patients. Diabetes 44: 489- 494,1995.

GAM94 332 ACE Tiret, L.; Rigat, B.; Visvikis, S.; Breda, C.; Corvol, P.; Cambien,F.; Soubrier, F.: Evidence, from combined segregation and linkageanalysis, that a variant of the angiotensin I- converting enzyme (ACE)gene controls plasma ACE levels. Am. J. Hum. Genet. 51: 197- 205,1992. 3 B c

GAM94 332 ACE Vleming, L. J.; van der Pijl, J. W.; Lemkes, H. H. P. J.; Westendorp,R. G. J.; Maassen, J. A.; Daha, M. R.; van Es, L. A.; van Kooten,C.: The DD genotype of the ACE gene polymorphism is associated withprogression of diabetic nephropathy to end stage renal failure inIDDM. Clin. Nephrol. 51: 133- 140, 1999. 3 B c

GAM94 332 ACE Williams, A. G.; Rayson, M. P.; Jubb, M.; World, M.; Woods, D.R.; Hayward, M.; Martin, J.; Humphries, S. E.; Montgomery, H. E.:The ACE gene and muscle performance. Nature 403: 614 only, 2000. 3 B c

GAM94 332 ACE Winkelmann, B. R.; Nauck, M.; Klein, B.; Russ, A. P.; Bohm, B.O.; Siekmeier, R.; Ihnken, K.; Verho, M.; Gross, W.; Marz, W.: Deletionpolymorphism of the angiotensin I- converting enzyme gene is associatedwith increased plasma angiotensin- converting enzyme activity but notwith increased risk for myocardial infarction and coronary arterydisease. Ann. Intern. Med. 125: 19- 25, 1996. 3 B c

GAM94 332 ACE Woods, D.; Onambele, G.; Woledge, R.; Skelton, D.; Bruce, S.;Humphries, S. E.; Montgomery, H.: Angiotensin- I converting enzymegenotype- dependent benefit from hormone replacement therapy in isometricmuscle strength and bone mineral density. J. Clin. Endocr. Metab. 86:2200- 2204, 2001. 3 B c

GAM94 332 ACE Yoshida, H.; Mitarai, T.; Kawamura, T.; Kitajima, T.; Miyazaki,Y.; Nagasawa, R.; Kawaguchi, Y.; Kubo, H.; Ichikawa, I.; Sakai, O.: Role of the deletion polymorphism of the angiotensin convertingenzyme gene in the progression and therapeutic responsiveness of IgAnephropathy. J. Clin. Invest. 96: 2162- 2169, 1995. 3 B c

GAM94 332 ACE Yoshioka, T.; Xu, Y.; Yoshida, H.; Shiraga, H.; Muraki, T.; Ito,K.: Deletion polymorphism of the angiotensin converting enzyme genepredicts persistent proteinuria in Henoch- Schonlein purpura nephritis. Arch.Dis. Child. 79: 394- 399, 1998. 3 B c

GAM94 332 ACE Zhu, X.; Bouzekri, N.; Southam, L.; Cooper, R. S.; Adeyemo, A.;McKenzie, C. A.; Luke, A.; Chen, G.; Elston, R. C.; Ward, R.: Linkageand association analysis of angiotensin I- converting enzyme (ACE)- genepolymorphisms with ACE concentration and blood pressure. Am. J. Hum.Genet. 68: 1139- 1148, 2001. 3 B c

GAM94 332 ACE Zhu, X.; McKenzie, C. A.; Forrester, T.; Nickerson, D. A.; Broeckel,U.; Schunkert, H.; Doering, A.; Jacob, H. J.; Cooper, R. S.; Rieder,M. J.: Localization of a small genomic region associated with elevatedACE. Am. J. Hum. Genet. 67: 1144- 1153, 2000. Note: Erratum: Am.J. Hum. Genet. 67: 1365 only, 2000. 3 B c

GAM94 332 ADAM10 Hattori, M.; Osterfield, M.; Flanagan, J. G.: Regulated cleavageof a contact- mediated axon repellent. Science 289: 1360- 1365, 2000. 3 B c

GAM94 332 ADAM10 Lunn, C. A.; Fan, X.; Dalie, B.; Miller, K.; Zavodny, P. J.; Narula,S. K.; Lundell, D.: Purification of ADAM 10 from bovine spleen asa TNFalpha convertase. FEBS Lett. 400: 333- 335, 1997. 3 B c

GAM94 332 ADAM10 Wolfsberg, T. G.; Primakoff, P.; Myles, D. G.; White, J. M.: ADAM,a novel family of membrane proteins containing a disintegrin and 3 B c

metalloproteasedomain: multipotential functions in cell- cell and cell-matrix interactions. J.Cell Biol. 131: 275- 278, 1995.

GAM94 332 ADAM10 Yamazaki, K.; Mizui, Y.; Tanaka, I.: Radiation hybrid mappingof human ADAM10 gene to chromosome 15. Genomics 45: 457- 459, 1997. 3 B c

GAM94 332 ADAMTS8 Georgiadis, K. E.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS8,a novel metalloprotease of the ADAM- TS family located on mouse chromosome9 and human chromosome 11. Genomics 62: 312- 315, 1999. 3 B c

GAM94 332 ADAMTS8 Vazquez, F.; Hastings, G.; Ortega, M.- A.; Lane, T. F.; Oikemus,S.; Lombardo, M.; Iruela- Arispe, M. L.: METH- 1, a human orthologof ADAMTS- 1, and METH- 2 are members of a new family of proteins withangio- inhibitory activity. J. Biol. Chem. 274: 23349- 23357, 1999. 3 B c

GAM94 332 AKAP2 Dong, F.; Feldmesser, M.; Casadevall, A.; Rubin, C. S.: Molecularcharacterization of a cDNA that encodes six isoforms of a novel murineA kinase anchor protein. J. Biol. Chem. 273: 6533- 6541, 1998. 3 B c

GAM94 332 AKAP2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999. 3 B c

GAM94 332 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and Drosophila. Genomics 26: 101- 106, 1995. 3 B c

GAM94 332 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer protein delta- COP, encoded by the archain gene, is conservedacross diverse eukaryotes. Mammalian Genome 7: 784- 786, 1996. 3 B c

GAM94 332 BACE Cai, H.; Wang, Y.; McCarthy, D.; Wen, H.; Borchelt, D. R.; Price,D. L.; Wong, P. C.: BACE1 is the major beta- secretase for generationof A- beta peptides by neurons. Nature Neurosci. 4: 233- 234, 2001. 3 B c

GAM94 332 BACE De Strooper, B.; Konig, G.: A firm base for drug development. Nature 402:471- 472, 1999. 3 B c

GAM94 332 BACE Fan, W.; Bennett, B. D.; Babu- Khan, S.; Luo, Y.; Louis, J.- C.;McCaleb, M.; Citron, M.; Vassar, R.; Richards, W. G.: Response toSaunders et al. (1999). Science 286: 1255a, 1999. Note: ElectronicPublication. 3 B c

GAM94 332 BACE Haniu, M.; Denis, P.; Young, Y.; Mendiaz, E. A.; Fuller, J.; Hui,J. O.; Bennett, B. D.; Kahn, S.; Ross, S.; Burgess, T.; Katta, V.;Rogers, G.; Vassar, R.; Citron, M.: Characterization of Alzheimer'sbeta- secretase protein BACE: a pepsin family member with unusual properties. J.Biol. Chem. 275: 21099- 21106, 2000. 3 B c

GAM94 332 BACE Hong, L.; Koelsch, G.; Lin, X.; Wu, S.; Terzyan, S.; Ghosh, A.K.; Zhang, X. C.; Tang, J.: Structure of the protease domain of memapsin2 (beta-secretase) complexed with inhibitor. Science 290: 150- 153,2000. 3 B c

GAM94 332 BACE Hussain, I.; Powell, D.; Howlett, D. R.; Tew, D. G.; Meek, T. D.;Chapman, C.; Gloger, I. S.; Murphy, K. E.; Southan, C. D.; Ryan, D.M.; Smith, T. S.; Simmons, D. L.; Walsh, F. S.; Dingwall, C.; Christie,G.: Identification of a novel aspartic protease (asp2) as beta- secretase Molec.Cell Neurosci. 14: 419- 427, 1999. 3 B c

GAM94 332 BACE Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643-648, 2001. 3 B c

GAM94 332 BACE Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.- H.; Goldstein, L. S.: Axonal 3 B c
transport of amyloid precursor protein is mediated by directbinding to the
kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000.

GAM94 332 BACE Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis,P.; Fan, 3 B c
W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.;Yan, Q.;
Richards, W. G.; Citron, M.; Vassar, R.: Mice deficientin BACE1, the
Alzheimer's beta- secretase, have normal phenotype andabolished beta-
amyloid generation. Nature Neurosci. 4: 231- 232,2001.

GAM94 332 BACE Nicolaou, M.; Song, Y.- Q.; Sato, C. A.; Orlacchio, A.; Kawarai,T.; 3 B c
Medeiros, H.; Liang, Y.; Sorbi, S.; Richard, E.; Rogaev, E. I.;Moliaka, Y.;
Bruni, A. C.; Jorge, R.; Percy, M.; Duara, R.; Farrer,L. A.; St George-
Hyslop, P.; Rogaeva, E. A.: Mutations in the openreading frame of the beta-
site APP cleaving enzyme (BACE) locus arenot a common cause of Alzheimer's
disease. Neurogenetics 3: 203- 206,2001.

GAM94 332 BACE Roberds, S. L.; Anderson, J.; Basi, G.; Bienkowski, M. J.; Branstetter,D. 3 B c
G.; Chen, K. S.; Freedman, S. B.; Frigon, N. L.; Games, D.; Hu,K.; Johnson-
Wood, K.; Kappenman, K. E.; and 20 others: BACE knockoutmice are healthy
despite lacking the primary beta- secretase activityin brain: implications
for Alzheimer's disease therapeutics. Hum.Molec. Genet. 10: 1317- 1324,
2001.

GAM94 332 BACE Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a 3 B c
BACE homolog, BACE2, reside in the obligate Down syndromeregion of
chromosome 21. Science 286: 1255a, 1999. Note: ElectronicPublication.

GAM94 332 BACE Sinha, S.; Anderson, J. P.; Barbour, R.; Basi, G. S.; Caccavello,R.; Davis, 3 B c
D.; Doan, M.; Dovey, H. F.; Frigon, N.; Hong, J.; Jacobson- Croak,K.;
Jewett, N.; and 15 others: Purification and cloning of amyloidprecursor
protein beta- secretase from human brain. Nature 402: 537- 540,1999.

GAM94 332 BACE Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz,E. A.; Dents, 3 B c
P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff,R.; Luo, Y.; Fisher, S.;
and 12 others: Beta- secretase cleavageof Alzheimer's amyloid precursor
protein by the transmembrane asparticprotease BACE. Science 286: 735- 741,
1999.

GAM94 332 BACE Yan, R.; Bienkowski, M. J.; Shuck, M. E.; Miao, H.; Tory, M. C.;Pauley, A. 3 B c
M.; Brashler, J. R.; Stratman, N. C.; Mathews, W. R.; Buhl,A. E.; Carter, D.
B.; Tomasselli, A. G.; Parodi, L. A.; Heinrikson,R. L.; Gurney, M. E.:
Membrane- anchored aspartyl protease with Alzheimer'sdisease beta- secretase
activity. Nature 402: 533- 536, 1999.

GAM94 332 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 3 B c
Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.:
Identification of Bach2 as a B- cell- specific partner for smallMaf proteins
that negatively regulate the immunoglobulin heavy chaingene 3- prime
enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM94 332 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 3 B c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-
basic leucine zipper transcription factors that interact withMafK and
regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-
6095, 1996.

GAM94 332 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, 3 B c
A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.;
Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B

cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene 19: 3739- 3749, 2000.

GAM94 332 BDKRB2 AbdAlla, S.; Lother, H.; Quitterer, U.: AT(1)- receptor heterodimersshow enhanced G- protein activation and altered receptor sequestration. Nature 407:94- 98, 2000. 3 B c

GAM94 332 BDKRB2 Braun, A.; Kammerer, S.; Bohme, E.; Muller, B.; Roscher, A. A.: Identification of polymorphic sites of the human bradykinin B(2)receptor gene. Biochem. Biophys. Res. Commun. 211: 234- 240, 1995. 3 B c

GAM94 332 BDKRB2 Erdmann, J.; Hegemann, N.; Weidemann, A.; Kallisch, H.; Hummel,M.; Hetzer, R.; Fleck, E.; Regitz- Zagrosek, V.: Screening the humanbradykinin B2 receptor gene in patients with cardiovascular diseases:identification of a functional mutation in the promoter and a newcoding variant (T21M). Am. J. Med. Genet. 80: 521- 525, 1998. 3 B c

GAM94 332 BDKRB2 Hess, J. F.; Borkowski, J. A.; Young, G. S.; Strader, C. D.; Ransom,R. W.: Cloning and pharmacological characterization of a human bradykinin(BK- 2) receptor. Biochem. Biophys. Res. Commun. 184: 260- 268, 1992. 3 B c

GAM94 332 BDKRB2 Kammerer, S.; Braun, A.; Arnold, N.; Roscher, A. A.: The humanbradykinin B(2) receptor gene: full length cDNA, genomic organizationand identification of the regulatory region. Biochem. Biophys. Res.Commun. 211: 226- 233, 1995. 3 B c

GAM94 332 BDKRB2 Ma, J.; Wang, D.; Ward, D. C.; Chen, L.; Dessai, T.; Chao, J.;Chao, L.: Structure and chromosomal localization of the gene (BDKRB2)encoding human bradykinin B2 receptor. Genomics 23: 362- 369, 1994. 3 B c

GAM94 332 BDKRB2 Powell, S. J.; Slynn, G.; Thomas, C.; Hopkins, B.; Briggs, I.;Graham, A.: Human bradykinin B2 receptor: nucleotide sequence analysisand assignment to chromosome 14. Genomics 15: 435- 438, 1993. 3 B c

GAM94 332 BDKRB2 Taketo, M.; Yokoyama, S.; Rochelle, J.; Kimura, S.; Higashida,H.; Taketo, M.; Seldin, M. F.: Mouse B2 bradykinin receptor genemaps to distal chromosome 12. Genomics 27: 222- 223, 1995. 3 B c

GAM94 332 BMP4 Connor, J. M.: Fibrodysplasia ossificans progressiva: lessonsfrom rare maladies. (Editorial) New Eng. J. Med. 335: 591- 593, 1996. 3 B b

GAM94 332 BMP4 Dickinson, M. E.; Kobrin, M. S.; Silan, C. M.; Kingsley, D. M.;Justice, M. J.; Miller, D. A.; Ceci, J. D.; Lock, L. F.; Lee, A.;Buchberg, A. M.; Siracusa, L. D.; Lyons, K. M.; Derynck, R.; Hogan,B. L. M.; Copeland, N. G.; Jenkins, N. A.: Chromosomal localizationof seven members of the murine TGF-beta superfamily suggests closelinkage to several morphogenetic mutant loci. Genomics 6: 505- 520,1990. 3 B b

GAM94 332 BMP4 Dooley, C. A.; Attia, G. R.; Rainey, W. E.; Moore, D. R.; Carr,B. R.: Bone morphogenetic protein inhibits ovarian androgen production. J.Clin. Endocr. Metab. 85: 3331- 3337, 2000. 3 B b

GAM94 332 BMP4 McAlpine, P. J.: Personal Communication. Winnipeg, Manitoba,Canada 7/15/1992. 3 B b

GAM94 332 BMP4 Monsoro- Burq, A.- H.; le Douarin, N. M.: BMP4 plays a key rolein left- right patterning in chick embryos by maintaining Sonic Hedgehogasymmetry. Molec. Cell 7: 789- 799, 2001. 3 B b

GAM94 332 BMP4 Shafritz, A. B.; Shore, E. M.; Gannon, F. H.; Zasloff, M. A.; Taub,R.; Muenke, M.; Kaplan, F. S.: Overexpression of an osteogenic morphogenin fibrodysplasia ossificans progressiva. New Eng. J. Med. 335:555- 561, 1996. 3 B b

GAM94 332 BMP4 Tabas, J. A.; Hahn, G. V.; Cohen, R. B.; Seaunez, H. N.; Modi,W. S.; Wozney, J. M.; Zasloff, M.; Kaplan, F. S.: Chromosomal assignmentof the human gene for bone morphogenetic protein 4. Clin. Orthop.Rel. Res. 293: 310- 316, 3 B b

1993.

GAM94 332 BMP4 Tucker, A. S.; Matthews, K. L.; Sharpe, P. T.: Transformationof tooth type 3 B b
induced by inhibition of BMP signaling. Science 282:1136- 1138, 1998.

GAM94 332 BMP4 van den Wijngaard, A.; Olde Weghuis, D.; Boersma, C. J. C.; vanZoelen, E. J. 3 B b
J.; Geurts van Kessel, A.; Olijve, W.: Fine mappingof the human bone
morphogenetic protein- 4 gene (BMP4) to chromosome14q22- q23 by in situ
hybridization. Genomics 27: 559- 560, 1995.

GAM94 332 BMP4 van den Wijngaard, A.; van Kraay, M.; van Zoelen, E. J. J.; Olijve,W.; 3 B b
Boersma, C. J. C.: Genomic organization of the human bone
morphogeneticprotein- 4 gene: molecular basis for multiple transcripts.
Biochem.Biophys. Res. Commun. 219: 789- 794, 1996.

GAM94 332 CALCR Christopoulos, G.; Perry, K. J.; Morfis, M.; Tilakaratne, N.; Gao,Y.; 3 B c
Fraser, N. J.; Main, M. J.; Foord, S. M.; Sexton, P. M.: Multipleamylin
receptors arise from receptor activity- modifying protein interactionwith
the calcitonin receptor gene product. Molec. Pharm. 56: 235- 242,1999.

GAM94 332 CALCR de Vernejoul, M.- C.: Personal Communication. Paris, France 1/19/1999. 3 B c

GAM94 332 CALCR Gorn, A. H.; Lin, H. Y.; Yamin, M.; Auron, P. E.; Flannery, M.R.; Tapp, D. 3 B c
R.; Manning, C. A.; Lodish, H. F.; Krane, S. M.; Goldring,S. R.: Cloning,
characterization, and expression of a human calcitoninreceptor from an
ovarian carcinoma cell line. J. Clin. Invest. 90:1726- 1735, 1992.

GAM94 332 CALCR Gorn, A. H.; Rudolph, S. M.; Flannery, M. R.; Morton, C. C.; Weremowicz,S.; 3 B c
Wang, J.- T.; Krane, S. M.; Goldring, S. R.: Expression of twohuman skeletal
calcitonin receptor isoforms cloned from a giant celltumor of bone. J. Clin.
Invest. 95: 2680- 2691, 1995.

GAM94 332 CALCR Masi, L.; Becherini, L.; Colli, E.; Gennari, L.; Mansani, R.; Falchetti,A.; 3 B c
Becorpi, A. M.; Cepollaro, C.; Gonnelli, S.; Tanini, A.; Brandi,M. L.:
Polymorphisms of the calcitonin receptor gene are associatedwith bone
mineral density in postmenopausal Italian women. Biochem.Biophys. Res.
Commun. 248: 190- 195, 1998.

GAM94 332 CALCR Masi, L.; Becherini, L.; Gennari, L.; Colli, E.; Mansani, R.; Falchetti,A.; 3 B c
Cepollaro, C.; Gonnelli, S.; Tanini, A.; Brandi, M. L.: Allelicvariants of
human calcitonin receptor: distribution and associationwith bone mass in
postmenopausal Italian women. Biochem. Biophys.Res. Commun. 245: 622- 626,
1998.

GAM94 332 CALCR Nakamura, M.; Zhang, Z. Q.; Shan, L.; Hisa, T.; Sasaki, M.; Tsukino,R.; 3 B c
Yokoi, T.; Kaname, A.; Kakudo, K.: Allelic variants of humancalcitonin
receptor in the Japanese population. Hum. Genet. 99:38- 41, 1997.

GAM94 332 CALCR Perez Jurado, L. A.; Li, X.; Francke, U.: The human calcitoninreceptor gene 3 B c
(CALCR) at 7q21.3 is outside the deletion associatedwith the Williams
syndrome. Cytogenet. Cell Genet. 70: 246- 249,1995.

GAM94 332 CALCR Taboulet, J.; Frendo, J. L.; Delage- Murroux, R.; Pichaud, F.; deVernejoul, 3 B c
M. C.; Jullienne, A.: Evidence for 2 allelic forms ofcalcitonin receptor
gene: distribution in normal and osteoporoticwomen. (Abstract) J. Bone
Miner. Res. 11 (suppl. 1): S204, 1996.

GAM94 332 CALCR Taboulet, J.; Frenkian, M.; Frendo, J. L.; Feingold, N.; Jullienne,A.; de 3 B c
Vernejoul, M. C.: Calcitonin receptor polymorphism is associatedwith a
decreased fracture risk in post- menopausal women. Hum. Molec.Genet. 7:
2129- 2133, 1998.

GAM94 332 CASK Cohen, A. R.; Wood, D. F.; Marfatia, S. M.; Walther, Z.; Chishti,A. H.; 3 B c
Anderson, J. M.: Human CASK/LIN- 2 binds syndecan- 2 and protein4.1 and

localizes to the basolateral membrane of epithelial cells. J.Cell Biol. 142: 129- 138, 1998.

GAM94 332 CASK Dimitratos, S. D.; Stathakis, D. G.; Nelson, C. A.; Woods, D. F.;Bryant, P. 3 B c J.: The location of human CASK at Xp11.4 identifies thisgene as a candidate for X- linked optic atrophy. Genomics 51: 308- 309,1998.

GAM94 332 CASK Hsueh, Y.- P.; Wang, T.- F.; Yang, F.- C.; Sheng, M.: Nuclear 3 B c transcriptionand transcription regulation by the membrane- associated guanylatekinase CASK/LIN- 2. Nature 404: 298- 302, 2000.

GAM94 332 CASK Setou, M.; Nakagawa, T.; Seog, D.- H.; Hirokawa, N.: Kinesin 3 B c superfamilymotor protein KIF17 and mLin- 10 in NMDA receptor- containing vesicletransport. Science 288: 1796- 1802, 2000.

GAM94 332 CASK Stevenson, D.; Laverty, H. G.; Wenwieser, S.; Douglas, M.; Wilson,J. B.: 3 B c Mapping and expression analysis of the human CASK gene. MammalianGenome 11: 934- 937, 2000.

GAM94 332 CCRL1 Gosling, J.; Dairaghi, D. J.; Wang, Y.; Hanley, M.; Talbot, D.;Miao, Z.; 3 B c Schall, T. J.: Cutting edge: identification of a novelchemokine receptor that binds dendritic cell- and T cell- active chemokinesincluding ELC, SLC, and TECK. J. Immun. 164: 2851- 2856, 2000.

GAM94 332 CCRL1 Khoja, H.; Wang, G.; Ng, C.- T. L.; Tucker, J.; Brown, T.; Shyamala,V.: 3 B c Cloning of CCRL1, an orphan seven transmembrane receptor relatedto chemokine receptors, expressed abundantly in the heart. Gene 246:229- 238, 2000.

GAM94 332 CCRL1 Schweickart, V. L.; Epp, A.; Raport, C. J.; Gray, P. W.: CCR11is a 3 B c functional receptor for the monocyte chemoattractant proteinfamily of chemokines. J. Biol. Chem. 275: 9550- 9556, 2000. Note:Erratum: J. Biol. Chem. 276: 856 only, 2001.

GAM94 332 CD28 Aruffo, A.; Seed, B.: Molecular cloning of a CD28 cDNA by a high- 3 B c efficiencyCOS cell expression system. Proc. Nat. Acad. Sci. 84: 8573- 8577,1987.

GAM94 332 CD28 Buonavista, N.; Balzano, C.; Pontarotti, P.; Le Paslier, D.; Golstein,P.: 3 B c Molecular linkage of the human CTLA4 and CD28 Ig- superfamilygenes in yeast artificial chromosomes. Genomics 13: 856- 861, 1992.

GAM94 332 CD28 Howard, T. A.; Rochelle, J. M.; Seldin, M. F.: Cd28 and Ctla- 4,two related 3 B c members of the Ig supergene family, are tightly linkedon proximal mouse chromosome 1. Immunogenetics 33: 74- 76, 1991.

GAM94 332 CD28 Lafage- Pochitaloff, M.; Costello, R.; Couez, D.; Simonetti, J.;Mannoni, P.; 3 B c Mawas, C.; Olive, D.: Human CD28 and CTLA- 4 Ig superfamilygenes are located on chromosome 2 at bands q33- q34. Immunogenetics 31:198- 201, 1990.

GAM94 332 CD28 Lee, K. P.; Taylor, C.; Petryniak, B.; Turka, L. A.; June, C. H.;Thompson, 3 B c C. B.: The genomic organization of the CD28 gene: implicationsfor the regulation of CD28 mRNA expression and heterogeneity. J.Immun. 145: 344- 352, 1990.

GAM94 332 CD28 Lesslauer, W.; Gmunder, H.; Bohlen, P.: Purification and N- terminalamino 3 B c acid sequence of the human T90/44 (CD28) antigen. Immunogenetics 27:388- 391, 1988.

GAM94 332 CD28 Okkenhaug, K.; Wu, L.; Garza, K. M.; La Rose, J.; Khoo, W.; Odermatt,B.; 3 B c Mak, T. W.; Ohashi, P. S.; Rottapel, R.: A point mutation inCD28 distinguishes proliferative signals from survival signals. NatureImmun. 2: 325- 332, 2001.

GAM94 332 CDC25A Demetrick, D. J.; Beach, D. H.: Chromosome mapping of human CDC25Aand CDC25B 3 B c

phosphatases. Genomics 18: 144- 147, 1993.

GAM94 332 CDC25A Falck, J.; Mailand, N.; Syljuasen, R. G.; Bartek, J.; Lukas, J.: The ATM- 3 B c
Chk2- Cdc25A checkpoint pathway guards against radioresistantDNA synthesis.
Nature 410: 842- 847, 2001.

GAM94 332 CDC25A Falck, J.; Petrini, J. H. J.; Williams, B. R.; Lukas, J.; Bartek,J.: The DNA 3 B c
damage- dependent intra- S phase checkpoint is regulatedby parallel
pathways. Nature Genet. 30: 290- 294, 2002.

GAM94 332 CDC25A Fauman, E. B.; Cogswell, J. P.; Lovejoy, B.; Rocque, W. J.; Holmes,W.; 3 B c
Montana, V. G.; Piwnica- Worms, H.; Rink, M. J.; Saper, M. A.:Crystal
structure of the catalytic domain of the human cell cyclecontrol
phosphatase, Cdc25A. Cell 93: 617- 625, 1998.

GAM94 332 CDC25A Galaktionov, K.; Lee, A. K.; Eckstein, J.; Draetta, G.; Meckler,J.; Loda, 3 B c
M.; Beach, D.: CDC25 phosphatases as potential human oncogenes. Science
269:1575- 1577, 1995.

GAM94 332 CDC25A Mailand, N.; Falck, J.; Lukas, C.; Syljuasen, R. G.; Welcker, M.;Bartek, J.; 3 B c
Lukas, J.: Rapid destruction of human Cdc25A in responseto DNA damage.
Science 288: 1425- 1429, 2000.

GAM94 332 CDC2L1 Bunnell, B.; Heath, L. S.; Adams, D. E.; Lahti, J. M.; Kidd, V.J.: Elevated 3 B c
expression of a p58 protein kinase leads to changesin the CHO cell cycle.
Proc. Nat. Acad. Sci. 87: 7467- 7471, 1990.

GAM94 332 CDC2L1 Cornelis, S.; Bruynooghe, Y.; Denecker, G.; Van Huffel, S.; Tinton,S.; 3 B c
Beyaert, R.: Identification and characterization of a novel cellcycle-
regulated internal ribosome entry site. Molec. Cell 5: 597- 605,2000.

GAM94 332 CDC2L1 Eipers, P. G.; Barnoski, B. L.; Han, J.; Carroll, A. J.; Kidd,V. J.: 3 B c
Localization of the expressed human p58 protein kinase chromosomalgene to
chromosome 1p36 and a highly related sequence to chromosome15. Genomics 11:
621- 629, 1991.

GAM94 332 CDC2L1 Eipers, P. G.; Lahti, J. M.; Kidd, V. J.: Structure and expressionof the 3 B c
human p58(clk- 1) protein kinase chromosomal gene. Genomics 13:613- 621,
1992.

GAM94 332 CDC2L1 Gururajan, R.; Lahti, J. M.; Grenet, J.; Easton, J.; Gruber, I.;Ambros, P. 3 B c
F.; Kidd, V. J.: Duplication of a genomic region containingthe Cdc2L1- 2 and
MMP21- 22 genes on human chromosome 1p36.3 and theirlinkage to D1Z2. Genome
Res. 8: 929- 939, 1998.

GAM94 332 CDC2L1 Lahti, J. M.; Valentine, M.; Xiang, J.; Jones, B.; Amann, J.; Grenet,J.; 3 B c
Richmond, G.; Look, A. T.; Kidd, V. J.: Alterations in the PITSLREprotein
kinase gene complex on chromosome 1p36 in childhood neuroblastoma.
NatureGenet. 7: 370- 375, 1994.

GAM94 332 CDC2L1 White, P. S.; Maris, J. M.; Beltinger, C.; Sulman, E.; Marshall,H. N.; 3 B c
Fujimori, M.; Kaufman, B. A.; Biegel, J. A.; Allen, C.; Hilliard,C.;
Valentine, M. B.; Look, A. T.; Enomoto, H.; Sakiyama, S.; Brodeur,G. M.: A
region of consistent deletion in neuroblastoma maps withinhuman chromosome
1p36.2- 36.3. Proc. Nat. Acad. Sci. 92: 5520- 5524,1995.

GAM94 332 CDC2L1 Xiang, J.; Lahti, J. M.; Grenet, J.; Easton, J.; Kidd, V. J.:Molecular 3 B c
cloning and expression of alternatively spliced PITSLREprotein kinase
isoforms. J. Biol. Chem. 269: 15786- 15794, 1994.

GAM94 332 CDH18 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene 3 B c
cluster to a region of chromosome 5 subject to frequent allelicloss in
carcinoma. Genomics 57: 160- 163, 1999.

GAM94 332 CDH18 Shibata, T.; Shimoyama, Y.; Gotoh, M.; Hirohashi, S.: Identificationof human 3 B c

cadherin- 14, a novel neurally specific type II cadherin,by protein interaction cloning. J. Biol. Chem. 272: 5236- 5240, 1997.

GAM94 332 CDKN2C Blais, A.; Labrie, Y.; Pouliot, F.; Lachance, Y.; Labrie, C.:Structure of the gene encoding the human cyclin- dependent kinase inhibitorp18 and mutational analysis in breast cancer. Biochem. Biophys. Res.Commun. 247: 146- 153, 1998. 3 B c

GAM94 332 CDKN2C Guan, K.- L.; Jenkins, C. W.; Li, Y.; Nichols, M. A.; Wu, X.; O'Keefe,C. L.; Matera, A. G.; Xiong, Y.: Growth suppression by p18, a p16(INK4/MTS1)- and p14(INK4B/MTS2)- related CDK6 inhibitor, correlates with wild- typepRb function. Genes Dev. 8: 2939- 2952, 1994. 3 B c

GAM94 332 CDKN2C Lapointe, J.; Lachance, Y.; Labrie, Y.; Labrie, C.: A p18 mutantdefective in CDK6 binding in human breast cancer cells. Cancer Res. 56:4586- 4589, 1996. 3 B c

GAM94 332 CHRNB2 Anand, R.; Lindstrom, J.: Chromosomal localization of seven neuronalnicotinic acetylcholine receptor subunit genes in humans. Genomics 13:962- 967, 1992. 3 B c

GAM94 332 CHRNB2 Anand, R.; Lindstrom, J.: Nucleotide sequence of the human nicotinicacetylcholine receptor beta- 2 subunit gene. Nucleic Acids Res. 18:4272, 1990. 3 B c

GAM94 332 CHRNB2 Bessis, A.; Simon- Chazottes, D.; Devillers- Thiery, A.; Guenet,J.- L.; Changeux, J.- P.: Chromosomal localization of the mouse genescoding for alpha- 2, alpha- 3, alpha- 4 and beta- 2 subunits of neuronalnicotinic acetylcholine receptor. FEBS Lett. 264: 48- 52, 1990. 3 B c

GAM94 332 CHRNB2 De Fusco, M.; Becchetti, A.; Patrignani, A.; Annesi, G.; Gambardella,A.; Quattrone, A.; Ballabio, A.; Wanke, E.; Casari, G.: The nicotinicreceptor beta- 2 subunit is mutant in nocturnal frontal lobe epilepsy. NatureGenet. 26: 275- 276, 2000. 3 B c

GAM94 332 CHRNB2 Elliott, K. J.; Ellis, S. B.; Berckhan, K. J.; Urrutia, A.; Chavez-Noriega,L. E.; Johnson, E. C.; Velicelebi, G.; Harpold, M. M.: Comparativestructure of human neuronal alpha(2)- alpha(7) and beta(2)- beta(4)nicotinic acetylcholine receptor subunits and functional expressionof the alpha(2), alpha(3), alpha(4), alpha(7), beta(2), and beta(4)subunits. J. Molec. Neurosci. 7: 217- 228, 1996. 3 B c

GAM94 332 CHRNB2 Groot Kormelink, P. J.; Luyten, W. H. M. L.: Cloning and sequenceof full-length cDNAs encoding the human neuronal nicotinic acetylcholinereceptor (nAChR) subunits beta- 3 and beta- 4 and expression of sevennAChR subunits in the human neuroblastoma cell line SH- SY5Y and/orIMR- 32. FEBS Lett. 400: 309- 314, 1997. 3 B c

GAM94 332 CHRNB2 Lueders, K. K.; Elliott, R. W.; Marenholz, I.; Mischke, D.; DuPree,M.; Hamer, D.: Genomic organization and mapping of the human andmouse neuronal beta- 1- nicotinic acetylcholine receptor genes. MammalianGenome 10: 900- 905, 1999. 3 B c

GAM94 332 CHRNB2 Marubio, L. M.; del Mar Arroyo- Jimenez, M.; Cordero- Erausquin,M.; Lena, C.; Le Novere, N.; de Kerchove d'Exaerde, A.; Huchet, M.;Damaj, M. I.; Changeux, J.- P.: Reduced antinociception in mice lackingneuronal nicotinic receptor subunits. Nature 398: 805- 810, 1999. 3 B c

GAM94 332 CHRNB2 Phillips, H. A.; Favre, I.; Kirkpatrick, M.; Zuberi, S. M.; Goudie,D.; Heron, S. E.; Scheffer, I. E.; Sutherland, G. R.; Berkovic, S.F.; Bertrand, D.; Mulley, J. C.: CHRNB2 is the second acetylcholinereceptor subunit associated with autosomal dominant nocturnal frontallobe epilepsy. Am. J. Hum. Genet. 68: 225- 231, 2001. 3 B c

GAM94 332 CHRNB2 Picciotto, M. R.; Zoli, M.; Lena, C.; Bessis, A.; Lallemand, Y.;LeNovere, N.; Vincent, P.; Pich, E. M.; Brulet, P.; Changeux, J.- P.: Abnormal avoidance learning in mice lacking functional high- affinitynicotine receptor in the brain. Nature 374: 65- 67, 1995. 3 B c

GAM94 332 CHRNB2 Rempel, N.; Heyers, S.; Engels, H.; Sleegers, E.; Steinlein, O.K.: The structures of the human neuronal nicotinic acetylcholinereceptor beta- 2- and alpha- 3- subunit genes (CHRNB2 and CHRNA3). Hum.Genet. 103: 645- 653, 1998. 3 B c

GAM94 332 CHRNB2 Zoli, M.; Picciotto, M. R.; Ferrari, R.; Cocchi, D.; Changeux,J.- P.: Increased neurodegeneration during ageing in mice lackinghigh- affinity nicotine receptors. EMBO J. 18: 1235- 1244, 1999. 3 B c

GAM94 332 CHST1 Fukuta, M.; Inazawa, J.; Torii, T.; Tsuzuki, K.; Shimada, E.; Habuchi,O.: Molecular cloning and characterization of human keratan sulfategal- 6- sulfotransferase. J. Biol. Chem. 272: 32321- 32328, 1997. 3 B c

GAM94 332 CHST1 Iida, A.; Saito, S.; Sekine, A.; Mishima, C.; Kitamura, Y.; Kondo,K.; Harigae, S.; Osawa, S.; Nakamura, Y.: Catalog of 77 single- nucleotidepolymorphisms (SNPs) in the carbohydrate sulfotransferase 1 (CHST1)and carbohydrate sulfotransferase 3 (CHST3) genes. J. Hum. Genet. 47:14- 19, 2002. 3 B c

GAM94 332 CHST1 Mazany, K. D.; Peng, T.; Watson, C. E.; Tabas, I.; Williams, K.J.: Human chondroitin 6- sulfotransferase: cloning, gene structure,and chromosomal localization. Biochim. Biophys. Acta 1407: 92- 97,1998. 3 B c

GAM94 332 CLCN4 Disteche, C. M.; Brannan, C. I.; Larsen, A.; Adler, D. A.; Schorderet,D. F.; Gearing, D.; Copeland, N. G.; Jenkins, N. A.; Park, L. S.:The human pseudoautosomal GM- CSF receptor alpha subunit gene is autosomalin mouse. Nature Genet. 1: 333- 336, 1992. 3 B c

GAM94 332 CLCN4 Ellis, N. A.: Ecce Ohno. Nature Genet. 10: 373- 375, 1995. 3 B c

GAM94 332 CLCN4 Haldane, J. B. S.: Sex ratio and unisexual sterility in hybridanimals. J. Genet. 12: 101- 109, 1922. 3 B c

GAM94 332 CLCN4 Milatovich, A.; Kitamura, T.; Miyajima, A.; Francke, U.: Genefor the alpha- subunit of the human interleukin- 3 receptor (IL3RA)localized to the X- Y pseudoautosomal region. Am. J. Hum. Genet. 53:1146- 1153, 1993. 3 B c

GAM94 332 CLCN4 Ohno, S.: Sex Chromosomes and Sex- linked Genes. Berlin and NewYork: Springer (pub.) 1967. 3 B c

GAM94 332 CLCN4 Palmer, S.; Perry, J.; Ashworth, A.: A contravention of Ohno'slaw in mice. Nature Genet. 10: 472- 476, 1995. 3 B c

GAM94 332 CLCN4 Rugarli, E. I.; Adler, D. A.; Borsani, G.; Tsuchiya, K.; Franco,B.; Hauge, X.; Disteche, C.; Chapman, V.; Ballabio, A.: Differentchromosomal localization of the Clcn4 gene in Mus spretus and C57BL/6Jmice. Nature Genet. 10: 466- 471, 1995. 3 B c

GAM94 332 CLCN4 Schnur, R. E.; Wick, P. A.: Intragenic TaqI restriction fragmentlength polymorphism (RFLP) in CLCN4, between the loci for X- linkedocular albinism (OA1) and microphthalmia with linear skin defectssyndrome (MLS). Hum. Genet. 95: 594- 595, 1995. 3 B c

GAM94 332 CLCN4 van Slegtenhorst, M. A.; Bassi, M. T.; Borsani, G.; Wapenaar, M.C.; Ferrero, G. B.; de Conciliis, L.; Rugarli, E. I.; Grillo, A.;Franco, B.; Zoghbi, H. Y.; Ballabio, A.: A gene from the Xp22.3 regionshares homology with voltage- gated chloride channels. Hum. Molec.Genet. 3: 547- 552, 1994. 3 B c

GAM94 332 CLDN14 Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.;Park, H.- S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.- K.; Groner,Y.; Soeda, E.; 3 B c

and 52 others: The DNA sequence of human chromosome21. Nature 405: 311- 319, 2000. Note: Erratum: Nature: 407: 110 only,2000.

GAM94 332 CLDN14 Wilcox, E. R.; Burton, Q. L.; Naz, S.; Riazuddin, S.; Smith, T.N.; Ploplis, 3 B c B.; Belyatseva, I.; Ben- Yosef, T.; Liburd, N. A.; Morell,R. J.; Kachar, B.; Wu, D. K.; Griffith, A. J.; Riazuddin, S.; Friedman,T. B.: Mutations in the gene encoding tight junction claudin- 14 causerecessive deafness DFNB29. Cell 104: 165- 172, 2001.

GAM94 332 COL19A1 Gerecke, D. R.; Olson, P. F.; Koch, M.; Knoll, J. H. M.; Taylor,R.; Hudson, 3 B c D. L.; Champliaud, M.- F.; Olsen, B. R.; Burgeson, R. E.: Complete primary structure of two splice variants of collagen XII,and assignment of alpha- 1(XII) collagen (COL12A1), alpha- 1(IX) collagen(COL9A1), and alpha- 1(XIX) collagen (COL19A1) to human chromosome6q12- q13. Genomics 41: 236- 242, 1997.

GAM94 332 COL19A1 Inoguchi, K.; Yoshioka, H.; Khaleduzzaman, M.; Ninomiya, Y.: ThemRNA for 3 B c alpha- 1(XIX) collagen chain, a new member of FACITs, containsa long unusual 3- prime untranslated region and displays many uniquesplicing variants. J. Biochem. 117: 137- 146, 1995.

GAM94 332 COL19A1 Khaleduzzaman, M.; Sumiyoshi, H.; Ueki, Y.; Inoguchi, K.; Ninomiya,Y.; 3 B c Yoshioka, H.: Structure of the human type XIX collagen (COL19A1)gene, which suggests it has arisen from an ancestor gene of the FACITfamily. Genomics 45: 304- 312, 1997.

GAM94 332 COL19A1 Myers, J. C.; Sun, M. J.; D'Ippolito, J. A.; Jabs, E. W.; Neilson,E. G.; 3 B c Dion, A. S.: Human cDNA clones transcribed from an unusuallyhigh molecular weight RNA encode a new collagen chain. Gene 123:211- 217, 1993.

GAM94 332 COL19A1 Yoshioka, H.; Zhang, H.; Ramirez, F.; Mattei, M.- G.; Moradi- Ameli,M.; van 3 B c der Rest, M.; Gordon, M. K.: Synteny between the loci fora novel FACIT- like collagen (D6S228E) and alpha 1(IX) collagen (COL9A1)on 6q12- q14 in humans. Genomics 13: 884- 886, 1992.

GAM94 332 CSF1R Benz- Lemoine, E.; Brizard, A.; Huret, J.- L.; Babin, P.; Guilhot,F.; Couet, 3 B c D.; Tanzer, J.: Malignant histiocytosis: a specific t(2;5)(p23;q35)translocation? Review of the literature. Blood 72: 1045- 1047, 1988.

GAM94 332 CSF1R Boultwood, J.; Rack, K.; Kelly, S.; Madden, J.; Sakaguchi, A. Y.;Wang, L.- 3 B c M.; Oscier, D. G.; Buckle, V. J.; Wainscoat, J. S.: Lossof both CSF1R (FMS) alleles in patients with myelodysplasia and achromosome 5 deletion. Proc. Nat. Acad. Sci. 88: 6176- 6180, 1991.

GAM94 332 CSF1R De Qi Xu; Guilhot, S.; Galibert, F.: Restriction fragment lengthpolymorphism 3 B c of the human c- fms gene. Proc. Nat. Acad. Sci. 82:2862- 2865, 1985.

GAM94 332 CSF1R Eccles, M. R.: Genes encoding the platelet- derived growth factor(PDGF) 3 B c receptor and colony- stimulating factor 1 (CSF- 1) receptor arephysically associated in mice as in humans. Gene 108: 285- 288, 1991.

GAM94 332 CSF1R Gisselbrecht, S.; Fichelson, S.; Sola, B.; Bordereaux, D.; Hampe,A.; Andre, 3 B c C.; Galibert, F.; Tambourin, P. E.: Frequent c- fms activationby proviral insertion in mouse myeloblastic leukaemias. Nature 329:259- 261, 1987.

GAM94 332 CSF1R Groffen, J.; Heisterkamp, N.; Spurr, N. K.; Dana, S. L.; Wasmuth,J. J.; 3 B c Stephenson, J. R.: Regional assignment of the human c- fmsoncogene to band q34 of chromosome 5. (Abstract) Cytogenet. CellGenet. 37: 484 only, 1984.

GAM94 332 CSF1R Hampe, A.; Gobet, M.; Sherr, C. J.; Galibert, F.: Nucleotide sequenceof the 3 B c feline retroviral oncogene v- fms shows unexpected homologywith oncogenes encoding tyrosine- specific protein kinases. Proc.Nat. Acad. Sci. 81: 85-

89, 1984.

GAM94 332 CSF1R Hampe, A.; Shamoon, B.- M.; Gobet, M.; Sherr, C. J.; Galibert, F.: 3 B c
Nucleotide sequence and structural organization of the human FMSproto-
oncogene. Oncogene Res. 4: 9- 17, 1989.

GAM94 332 CSF1R How, G.- F.; Venkatesh, B.; Brenner, S.: Conserved linkage betweenthe puffer 3 B c
fish (Fugu rubripes) and human genes for platelet- derivedgrowth factor
receptor and macrophage colony- stimulating factor receptor. GenomeRes. 6:
1185- 1191, 1996.

GAM94 332 CSF1R Kondo, M.; Scherer, D. C.; Miyamoto, T.; King, A. G.; Akashi,K.; Sugamura, 3 B c
K.; Weissman, I. L.: Cell- fate conversion of lymphoid- committedprogenitors
by instructive actions of cytokines. Nature 407: 383- 386,2000.

GAM94 332 CSF1R Le Beau, M. M.; Westbrook, C. A.; Diaz, M. O.; Larson, R. A.;Rowley, J. D.; 3 B c
Gasson, J. C.; Golde, D. W.; Sherr, C. J.: Evidencefor the involvement of
GM- CSF and FMS in the deletion (5q) in myeloiddisorders. Science 231: 984-
987, 1986.

GAM94 332 CSF1R Morgan, R.; Hecht, B. K.; Sandberg, A. A.; Hecht, F.; Smith, S.D.: 3 B c
Chromosome 5q35 breakpoint in malignant histiocytosis. (Letter) NewEng. J.
Med. 314: 1322 only, 1986.

GAM94 332 CSF1R Ridge, S. A.; Worwood, M.; Oscier, D.; Jacobs, A.; Padua, R. A.: FMS 3 B c
mutations in myelodysplastic, leukemic, and normal subjects. Proc.Nat. Acad.
Sci. 87: 1377- 1380, 1990.

GAM94 332 CSF1R Roberts, W. M.; Look, A. T.; Roussel, M. F.; Sherr, C. J.: Tandemlinkage of 3 B c
human CSF- 1 receptor (c- fms) and PDGF receptor genes. Cell 55:655- 661,
1988.

GAM94 332 CSF1R Sapi, E.; Flick, M. B.; Kacinski, B. M.: The first intron ofhuman c- fms 3 B c
proto- oncogene contains a processed pseudogene (RPL7P)for ribosomal protein
L7. Genomics 22: 641- 645, 1994.

GAM94 332 CSF1R Verbeek, J. S.; Roebroek, A. J. M.; van den Ouweland, A. M. W.;Bloemers, H. 3 B c
P. J.; Van de Ven, W. J. M.: Human c- fms proto- oncogene:comparative
analysis with an abnormal allele. Molec. Cell. Biol. 5:422- 426, 1985.

GAM94 332 CSF1R Verbeek, J. S.; van Heerikhuizen, H.; de Pauw, B. E.; Haanen,C.; Bloemers, 3 B c
H. P. J.; Van de Ven, W. J. M.: A hereditary abnormalc- fms proto- oncogene
in a patient with acute lymphocytic leukaemiaand congenital hypothyroidism.
Brit. J. Haemat. 61: 135- 138, 1985.

GAM94 332 CSF1R Yarden, Y.; Ullrich, A.: Growth factor receptor tyrosine kinases. Ann.Rev. 3 B c
Biochem. 57: 443- 478, 1988.

GAM94 332 CSPG3 Masternak, K.; Barras, E.; Zufferey, M.; Conrad, B.; Corthals,G.; Aebersold, 3 B c
R.; Sanchez, J.- C.; Hochstrasser, D. F.; Mach, B.;Reith, W.: A gene
encoding a novel RFX- associated transactivatoris mutated in the majority of
MHC class II deficiency patients. NatureGenet. 20: 273- 277, 1998.

GAM94 332 CSPG3 Prange, C. K.; Pennacchio, L. A.; Lieuallen, K.; Fan, W.; Lennon,G. G.: 3 B c
Characterization of the human neurocan gene, CSPG3. Gene 221:199- 205, 1998.

GAM94 332 CSPG3 Rauch, U.; Grimpe, B.; Kulbe, G.; Arnold- Ammer, I.; Beier, D. R.;Fassler, 3 B c
R.: Structure and chromosomal localization of the mouseneurocan gene.
Genomics 28: 405- 410, 1995.

GAM94 332 CSPG3 Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R. U.; Margolis,R. K.: 3 B c
Cloning and primary structure of neurocan, a developmentallyregulated,
aggregating chondroitin sulfate proteoglycan of brain. J.Biol. Chem. 267:
19536- 19547, 1992.

GAM94 332 CXCL1 Anisowicz, A.; Bardwell, L.; Sager, R.: Constitutive overexpressionof a 3 B c

growth- regulated gene in transformed Chinese hamster and humancells. Proc. Nat. Acad. Sci. 84: 7188- 7192, 1987.

GAM94 332 CXCL1 Anisowicz, A.; Zajchowski, D.; Stenman, G.; Sager, R.: Functionaldiversity 3 B c
of GRO gene expression in human fibroblasts and mammaryepithelial cells. Proc. Nat. Acad. Sci. 85: 9645- 9649, 1988.

GAM94 332 CXCL1 Horuk, R.; Yansura, D. G.; Reilly, D.; Spencer, S.; Bourell, J.;Henzel, W.; 3 B c
Rice, G.; Unemori, E.: Purification, receptor bindinganalysis, and biological characterization of human melanoma growthstimulating activity (MGSA): evidence for a novel MGSA receptor. J.Biol. Chem. 268: 541- 546, 1993.

GAM94 332 CXCL1 O'Donovan, N.; Galvin, M.; Morgan, J. G.: Physical mapping ofthe CXC 3 B c
chemokine locus on human chromosome 4. Cytogenet. Cell Genet. 84:39- 42, 1999.

GAM94 332 CXCL1 Richmond, A.; Balentien, E.; Thomas, H. G.; Flaggs, G.; Barton,D. E.; 3 B c
Spiess, J.; Bordoni, R.; Francke, U.; Derynck, R.: Molecularcharacterization and chromosomal mapping of melanoma growth stimulatoryactivity, a growth factor structurally related to beta- thromboglobulin. EMBOJ. 7: 2025- 2033, 1988.

GAM94 332 CXCL1 Sakaguchi, A. Y.; Lalley, P. A.; Ghosh Choudhury, G.; Martinez,L.; Han, E. 3 B c
S.; Killary, A. M.; Naylor, S. L.; Wang, L.- M.: Mousemelanoma growth stimulatory activity gene (Mgsa) is polymorphic andsyntenic with the W, Patch, Rumpwhite, and recessive spotting locion chromosome 5. Genomics 5: 629- 632, 1989.

GAM94 332 CXCL1 Tsai, H.- H.; Frost, E.; To, V.; Robinson, S.; ffrench- Constant,C.; 3 B c
Geertman, R.; Ransohoff, R. M.; Miller, R. H.: The chemokinereceptor CXCR2 controls positioning of oligodendrocyte precursorsin developing spinal cord by arresting their migration. Cell 110:373- 383, 2002.

GAM94 332 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; 3 B c
Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene: molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230, 1998.

GAM94 332 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii- 3 B c
Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in humanpolymorphonuclear leukocytes: cDNA cloning and expression of leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993.

GAM94 332 CYP7B1 Li- Hawkins, J.; Lund, E. G.; Turley, S. D.; Russell, D. W.: Disruptionof 3 B c
the oxysterol 7- alpha- hydroxylase gene in mice. J. Biol. Chem. 275:16536- 16542, 2000.

GAM94 332 CYP7B1 Setchell, K. D. R.; Schwarz, M.; O'Connell, N. C.; Lund, E. G.;Davis, D. L.; 3 B c
Lathe, R.; Thompson, H. R.; Tyson, R. W.; Sokol, R.J.; Russell, D. W.: Identification of a new inborn error in bileacid synthesis: mutation of the oxysterol 7- alpha- hydroxylase genecauses severe neonatal liver disease. J. Clin. Invest. 102: 1690- 1703,1998.

GAM94 332 DCT Bouchard, B.; Del Marmol, V.; Jackson, I. J.; Cherif, D.; Dubertret,L.: 3 B c
Molecular characterization of a human tyrosinase- related- protein- 2cDNA: patterns of expression in melanocytic cells. Europ. J. Biochem. 219:127- 134, 1994.

GAM94 332 DCT Budd, P. S.; Jackson, I. J.: Structure of the mouse tyrosinase- 3 B c
relatedprotein- 2/dopachrome tautomerase (Tyrp2/Dct) gene and sequence oftwo novel slaty alleles. Genomics 29: 35- 43, 1995.

GAM94 332 DCT Cassady, J. L.; Sturm, R. A.: Sequence of the human dopachrometautomerase- 3 B c
encoding TRP- 2 cDNA. Gene 143: 295- 298, 1994.

GAM94 332 DCT Jackson, I. J.; Chambers, D. M.; Tsukamoto, K.; Copeland, N. G.;Gilbert, D. 3 B c
J.; Jenkins, N. A.; Hearing, V.: A second tyrosinase- relatedprotein, TRP-
2, maps to and is mutated at the mouse slaty locus. EMBOJ. 11: 527- 535,
1992.

GAM94 332 DCT Khong, H. T.; Rosenberg, S. A.: Pre- existing immunity to tyrosinase- 3 B c
relatedprotein (TRP)- 2, a new TRP- 2 isoform, and the NY- ESO- 1 melanoma
antigenin a patient with a dramatic response to immunotherapy. J. Immun.
168:951- 956, 2002.

GAM94 332 DCT Kwon, B. S.: Pigmentation genes: the tyrosinase gene family andthe pmel 17 3 B c
gene family. J. Invest. Derm. 100: 134S- 140S, 1993.

GAM94 332 DCT Sturm, R. A.; Baker, E.; Sutherland, G. R.: Assignment of thetyrosinase- 3 B c
related protein- 2 gene (TYRP2) to human chromosome 13q31- q32by
fluorescence in situ hybridization: extended synteny with mousechromosome
14. Genomics 21: 293- 296, 1994.

GAM94 332 DCT Sturm, R. A.; O'Sullivan B. J.; Box, N. F.; Smith, A. G.; Smit,S. E.; 3 B c
Puttick, E. R. J.; Parsons, P. G.; Dunn, I. S.: Chromosomalstructure of the
human TYRP1 and TYRP2 loci and comparison of thetyrosinase- related protein
gene family. Genomics 29: 24- 34, 1995.

GAM94 332 DDX11 Amann, J.; Kidd, V. J.; Lahti, J. M.: Characterization of putativehuman 3 B c
homologues of the yeast chromosome transmission fidelity gene,CHL1. J. Biol.
Chem. 272: 3823- 3832, 1997.

GAM94 332 DDX11 Amann, J.; Valentine, M.; Kidd, V. J.; Lahti, J. M.: Localizationof Chl1- 3 B c
related helicase genes to human chromosome regions 12p11 and12p13:
similarity between parts of these genes and conserved humantelomeric-
associated DNA. Genomics 32: 260- 265, 1996.

GAM94 332 DDX11 Frank, S.; Werner, S.: The human homologue of the yeast CHL1 geneis a novel 3 B c
keratinocyte growth factor- regulated gene. J. Biol. Chem. 271:24337- 24340,
1996.

GAM94 332 DMD Abbs, S.; Roberts, R. G.; Mathew, C. G.; Bentley, D. R.; Bobrow,M.: Accurate 3 B c
assessment of intragenic recombination frequency withinthe Duchenne muscular
dystrophy gene. Genomics 7: 602- 606, 1990.

GAM94 332 DMD Ahn, A. H.; Kunkel, L. M.: The structural and functional diversityof 3 B c
dystrophin. Nature Genet. 3: 283- 291, 1993.

GAM94 332 DMD Alwine, J. C.; Kemp, D. J.; Stark, G. R.: Method for detectionof specific 3 B c
RNAs in agarose gels by transfer to diazobenzyloxymethyl- paperand by
hybridization with DNA probes. Proc. Nat. Acad. Sci. 74:5350- 5354, 1977.

GAM94 332 DMD Angelini, C.; Beggs, A. H.; Hoffman, E. P.; Fanin, M.; Kunkel,L. M.: 3 B c
Enormous dystrophin in a patient with Becker muscular dystrophy. Neurology
40:808- 812, 1990.

GAM94 332 DMD Badorff, C.; Berkely, N.; Mehrotra, S.; Talhouk, J. W.; Rhoads,R. E.; 3 B c
Knowlton, K. U.: Enteroviral protease 2A directly cleavesdystrophin and is
inhibited by a dystrophin- based substrate analogue. J.Biol. Chem. 275:
11191- 11197, 2000.

GAM94 332 DMD Badorff, C.; Lee, G.- H.; Lamphear, B. J.; Martone, M. E.; Campbell,K. P.; 3 B c
Rhoads, R. E.; Knowlton, K. U.: Enteroviral protease 2A cleavesdystrophin:
evidence of cytoskeletal disruption in an acquired cardiomyopathy.
NatureMed. 5: 320- 326, 1999.

GAM94 332 DMD Bakker, E.; Hofker, M. H.; Goor, N.; Mandel, J. L.; Wrogemann,K.; Davies, K. 3 B c

E.; Kunkel, L. M.; Willard, H. F.; Fenton, W. A.; Sandkuyl,L.; Majoor-Krakauer, D.; van Essen, A. J.; Jahoda, M. G. J.; Sachs,E. S.; van Ommen, G. J. B.; Pearson, P. L.: Prenatal diagnosis andcarrier detection of Duchenne muscular dystrophy with closely linkedRFLPs. Lancet I: 655- 658, 1985.

GAM94 332 DMD Bakker, E.; Pearson, P. L.: Mutation of the Duchenne musculardystrophy gene associated with meiotic recombination. (Letter) Clin.Genet. 30: 347- 349, 1986. 3 B c

GAM94 332 DMD Bakker, E.; Van Broeckhoven, C.; Bonten, E. J.; van de Vooren,M. J.; Veenema, H.; Van Hul, W.; Van Ommen, G. J. B.; Vandenberghe,A.; Pearson, P. L.: Germline mosaicism and Duchenne muscular dystrophymutations. Nature 329: 554- 556, 1987. 3 B c

GAM94 332 DMD Bar, S.; Barnea, E.; Levy, Z.; Neuman, S.; Yaffe, D.; Nudel, U.: A novel product of the Duchenne muscular dystrophy gene which greatlydiffers from the known isoforms in its structure and tissue distribution. Biochem.J. 272: 557- 560, 1990. 3 B c

GAM94 332 DMD Barbieri, A. M.; Soriani, N.; Tubiello, G. M.; Ferrari, M.; Carrera,P.: A nonsense mutation (gln- 673- term) in exon 17 of the human dystrophingene detected by heteroduplex analysis. Hum. Genet. 96: 343- 344,1995. 3 B c

GAM94 332 DMD Bartlett, R. J.; Pericak- Vance, M. A.; Koh, J.; Yamaoka, L. H.;Chen, J. C.; Hung, W.- Y.; Speer, M. C.; Wapenaar, M. C.; Van Ommen,G. J. B.; Bakker, E.; Pearson, P. L.; Kandt, R. S.; Siddique, T.;Gilbert, J. R.; Lee, J. E.; Sirotkin- Roses, M. J.; Roses, A. D.:Duchenne muscular dystrophy: high frequency of deletions. Neurology 38:1- 4, 1988. 3 B c

GAM94 332 DMD Barton- Davis, E. R.; Cordier, L.; Shoturma, D. I.; Leland, S.E.; Sweeney, H. L.: Aminoglycoside antibiotics restore dystrophinfunction to skeletal muscles of mdx mice. J. Clin. Invest. 104:375- 381, 1999. 3 B c

GAM94 332 DMD Bastianutto, C.; Bestard, J. A.; Lahnakoski, K.; Broere, D.; DeVisser, M.; Zaccolo, M.; Pozzan, T.; Ferlini, A.; Muntoni, F.; Patarnello,T.; Klamut, H. J.: Dystrophin muscle enhancer 1 is implicated inthe activation of non-muscle isoforms in the skeletal muscle of patientswith X- linked dilated cardiomyopathy. Hum. Molec. Genet. 10: 2627- 2635,2001. 3 B c

GAM94 332 DMD Baumbach, L. L.; Chamberlain, J. S.; Ward, P. A.; Farwell, N.J.; Caskey, C. T.: Molecular and clinical correlation of deletionleading to Duchenne and Becker muscular dystrophies. Neurology 39:465- 474, 1989. 3 B c

GAM94 332 DMD Baumbach, L. L.; Ward, P. A.; Fenwick, R.; Caskey, C. T.: Analysisof mutations at the Duchenne muscular dystrophy locus provides noevidence for illegitimate recombination in deletion formation. (Abstract) Am.J. Hum. Genet. 45 (suppl.): A173, 1989. 3 B c

GAM94 332 DMD Becker, P. E.: Eine neue X- chromosomale Muskeldystrophie. ActaPsychiat. Neurol. Scand. 193: 427, 1955. 3 B c

GAM94 332 DMD Becker, P. E.: Neue Ergebnisse der Genetik der Muskeldystrophien. ActaGenet. Statist. Med. 7: 303- 310, 1957. 3 B c

GAM94 332 DMD Becker, P. E.: Two new families of benign sex- linked recessivemuscular dystrophy. Rev. Canad. Biol. 21: 551- 566, 1962. 3 B c

GAM94 332 DMD Beggs, A. H.; Koenig, M.; Boyce, F. M.; Kunkel, L. M.: Detectionof 98% of DMD/BMD gene deletions by polymerase chain reaction. Hum.Genet. 86: 45- 48, 1990. 3 B c

GAM94 332 DMD Berko, B. A.; Swift, M.: X- linked dilated cardiomyopathy. NewEng. J. Med. 316: 1186- 1191, 1987. 3 B c

GAM94 332 DMD Bettecken, T.; Muller, C. R.: Identification of a 220- kb insertioninto the 3 B c

Duchenne gene in a family with an atypical course of musculardystrophy. Genomics 4: 592- 596, 1989.

GAM94 332 DMD Bies, R. D.: X- linked dilated cardiomyopathy. (Letter) New Eng.J. Med. 330: 3 B c 368- 369, 1994.

GAM94 332 DMD Bies, R. D.; Caskey, C. T.; Fenwick, R.: An intact cysteine- richdomain is 3 B c required for dystrophin function. J. Clin. Invest. 90:666- 672, 1992.

GAM94 332 DMD Bittner, R. E.; Streubel, B.; Shorny, S.; Schaden, G.; Voit, T.;Hoger, H.: 3 B c Coisogenic all- plus- one immunization: a model for identifyingmissing proteins in null- mutant conditions. Antibodies to dystrophinin mdx mouse after transplantation of muscle from normal coisogenicdonor. Neuropediatrics 25: 176- 182, 1994.

GAM94 332 DMD Blake, D. J.; Love, D. R.; Tinsley, J.; Morris, G. E.; Turley,H.; Gatter, 3 B c K.; Dickson, G.; Edwards, Y. H.; Davies, K. E.: Characterizationof a 4.8kb transcript from the Duchenne muscular dystrophy locus expressedin schwannoma cells. Hum. Molec. Genet. 1: 103- 109, 1992.

GAM94 332 DMD Bodrug, S. E.; Ray, P. N.; Gonzalez, I. L.; Schmickel, R. D.;Sylvester, J. 3 B c E.; Worton, R. G.: Molecular analysis of a constitutionalX- autosome translocation in a female with muscular dystrophy. Science 237:1620- 1624, 1987.

GAM94 332 DMD Boyce, F. M.; Beggs, A. H.; Feener, C.; Kunkel, L. M.: Dystrophinis 3 B c transcribed in brain from a distant upstream promoter. Proc. Nat.Acad. Sci. 88: 1276- 1280, 1991.

GAM94 332 DMD Boyd, Y.; Buckle, V. J.: Cytogenetic heterogeneity of 3 B c translocationsassociated with Duchenne muscular dystrophy. Clin. Genet. 29: 108- 115,1986.

GAM94 332 DMD Bulman, D. E.; Gangopadhyay, S. B.; Bebchuck, K. G.; Worton, R.G.; Ray, P. 3 B c N.: Point mutation in the human dystrophin gene: identificationthrough Western blot analysis. Genomics 10: 457- 460, 1991.

GAM94 332 DMD Burke, J. F.; Mogg, A. E.: Suppression of a nonsense mutationin mammalian 3 B c cells in vivo by the aminoglycoside antibiotics G- 418and paromomycin. Nucleic Acids Res. 13: 6265- 6272, 1985.

GAM94 332 DMD Burnette, W. N.: 'Western blotting': electrophoretic transferof proteins 3 B c from sodium dodecyl sulfate- polyacrylamide gels to unmodifiednitrocellulose and radiographic detection with antibody and radioiodinatedprotein A. Anal. Biochem. 112: 195- 203, 1981.

GAM94 332 DMD Bushby, K. M. D.; Cleghorn, N. J.; Curtis, A.; Haggerty, I. D.;Nicholson, L. 3 B c V. B.; Johnson, M. A.; Harris, J. B.; Bhattacharya,S. S.: Identification of a mutation in the promoter region of thedystrophin gene in a patient with atypical Becker muscular dystrophy. Hum.Genet. 88: 195- 199, 1991.

GAM94 332 DMD Chamberlain, J. S.; Pearlman, J. A.; Muzny, D. M.; Gibbs, R. A.;Ranier, J. 3 B c E.; Reeves, A. A.; Caskey, C. T.: Expression of the murineDuchenne muscular dystrophy gene in muscle and brain. Science 239:1416- 1418, 1988.

GAM94 332 DMD Chelly, J.; Concordet, J.- P.; Kaplan, J.- C.; Kahn, A.: 3 B c Illegitimatetranscription: transcription of any gene in any cell type. Proc.Nat. Acad. Sci. 86: 2617- 2621, 1989.

GAM94 332 DMD Chelly, J.; Gilgenkrantz, H.; Hugnot, J. P.; Hamard, G.; Lambert,M.; Recan, 3 B c D.; Akli, S.; Cometto, M.; Kahn, A.; Kaplan, J. C.: Illegitimatetranscription: application to the analysis of truncated transcriptsof the dystrophin gene in nonmuscle cultured cells from Duchenne andBecker patients. J. Clin. Invest. 88: 1161- 1166, 1991.

GAM94 332 DMD Chelly, J.; Hamard, G.; Koulakoff, A.; Kaplan, J.- C.; Kahn, A.;Berwald- 3 B c
Netter, Y.: Dystrophin gene transcribed from different promotersin neuronal
and glial cells. Nature 344: 64- 65, 1990.

GAM94 332 DMD Chelly, J.; Kaplan, J.- C.; Maire, P.; Gautron, S.; Kahn, A.:Transcription 3 B c
of the dystrophin gene in human muscle and non- muscletissues. Nature 333:
858- 860, 1988.

GAM94 332 DMD Clemens, P. R.; Ward, P. A.; Caskey, C. T.; Bulman, D. E.; Fenwick,R. G.: 3 B c
Premature chain termination mutation causing Duchenne musculardystrophy.
Neurology 42: 1775- 1782, 1992.

GAM94 332 DMD Comi, G. P.; Ciafaloni, E.; de Silva, H. A. R.; Prelle, A.; Bardoni,A.; 3 B c
Rigoletto, C.; Robotti, M.; Bresolin, N.; Moggio, M.; Fortunato,F.; Ciscato,
P.; Turconi, A.; Rose, A. D.; Scarlato, G.: A G(+1)- to- Atransversion at
the 5- prime splice site of intron 69 of the dystrophingene causing the
absence of peripheral nerve Dp116 and severe clinicalinvolvement in a DMD
patient. Hum. Molec. Genet. 4: 2171- 2174, 1995.

GAM94 332 DMD Cooper, B. J.; Valentine, B. A.; Wilson, S.; Patterson, D. F.;Concannon, P. 3 B c
W.: Canine muscular dystrophy: confirmation of X- linkedinheritance. J.
Hered. 79: 405- 408, 1988.

GAM94 332 DMD Covone, A. E.; Lerone, M.; Romeo, G.: Genotype- phenotype correlationand 3 B c
germline mosaicism in DMD/BMD patients with deletions of the dystrophingene.
Hum. Genet. 87: 353- 360, 1991.

GAM94 332 DMD Cox, G. A.; Cole, N. M.; Matsumura, K.; Phelps, S. F.; Hauschka,S. D.; 3 B c
Campbell, K. P.; Faulkner, J. A.; Chamberlain, J. S.: Overexpressionof
dystrophin in transgenic mdx mice eliminates dystrophic symptomswithout
toxicity. Nature 364: 725- 729, 1993.

GAM94 332 DMD Cox, G. A.; Sunada, Y.; Campbell, K. P.; Chamberlain, J. S.:Dp71 can restore 3 B c
the dystrophin- associated glycoprotein complex inmuscle but fails to
prevent dystrophy. Nature Genet. 8: 333- 339,1994.

GAM94 332 DMD Crawford, G. E.; Lu, Q. L.; Partridge, T. A.; Chamberlain, J.S.: Suppression 3 B c
of revertant fibers in mdx mice by expression ofa functional dystrophin.
Hum. Molec. Genet. 10: 2745- 2750, 2001.

GAM94 332 DMD Darras, B. T.; Blattner, P.; Harper, J. F.; Spiro, A. J.; Alter,S.; Francke, 3 B c
U.: Intragenic deletions in 21 Duchenne muscular dystrophy(DMD)/Becker
muscular dystrophy (BMD) families studied with the dystrophincDNA: location
of breakpoints on HindIII and BglII exon- containingfragment maps, meiotic
and mitotic origin of the mutations. Am. J.Hum. Genet. 43: 620- 629, 1988.

GAM94 332 DMD Darras, B. T.; Francke, U.: A partial deletion of the musculardystrophy gene 3 B c
transmitted twice by an unaffected male. Nature 329:556- 558, 1987.

GAM94 332 DMD Darras, B. T.; Francke, U.: Normal human genomic restriction- 3 B c
fragmentpatterns and polymorphisms revealed by hybridization with the
entiredystrophin cDNA. Am. J. Hum. Genet. 43: 612- 619, 1988.

GAM94 332 DMD Davies, K. E.; Smith, T. J.; Bundey, S.; Read, A. P.; Flint, T.;Bell, M.; 3 B c
Speer, A.: Mild and severe muscular dystrophy associatedwith deletions in
Xp21 of the human X chromosome. J. Med. Genet. 25:9- 13, 1988.

GAM94 332 DMD De Angelis, F. G.; Sthandier, O.; Berarducci, B.; Toso, S.; Galluzzi,G.; 3 B c
Ricci, E.; Cossu, G.; Bozzoni, I.: Chimeric snRNA molecules
carryingantisense sequences against the splice junctions of exon 51 of
thedystrophin pre- mRNA induce exon skipping and restoration of a
dystrophinsynthesis in delta- 48- 50 DMD cells. Proc Nat. Acad. Sci. 99:
9456- 9461,2002.

GAM94 332 DMD den Dunnen, J. T.; Bakker, E.; Klein Breteler, E. G.; Pearson,P. L.; van Ommen, G. J. B.: Direct mutation of more than 50% of theDuchenne muscular dystrophy mutations by field inversion gels. Nature 329:640- 642, 1987. 3 B c

GAM94 332 DMD den Dunnen, J. T.; Grootscholten, P. M.; Bakker, E.; Blonden,L. A. J.; Ginjaar, H. B.; Wapenaar, M. C.; van Paassen, H. M. B.;van Broeckhoven, C.; Pearson, P. L.; van Ommen, G. J. B.: Topographyof the Duchenne muscular dystrophy (DMD) gene: FIGE and cDNA analysisof 194 cases reveals 115 deletions and 13 duplications. Am. J. Hum.Genet. 45: 835- 847, 1989. 3 B c

GAM94 332 DMD Dickson, G.; Pizzey, J. A.; Elsom, V. E.; Love, D.; Davies, K.E.; Walsh, F. S.: Distinct dystrophin mRNA species are expressedin embryonic and adult mouse skeletal muscle. FEBS Lett. 242: 47- 52,1988. 3 B c

GAM94 332 DMD Dominguez- Steglich, M.; Meng, G.; Bettecken, T.; Muller, C. R.;Schmid, M.: The dystrophin gene is autosomally located on a microchromosomein chicken. Genomics 8: 536- 540, 1990. 3 B c

GAM94 332 DMD Doolittle, R. F.: Similar amino acid sequences: chance or commonancestry? Science 214: 149- 159, 1981. 3 B c

GAM94 332 DMD Doriguzzi, C.; Palmucci, L.; Mongini, T.; Chiado- Piat, L.; Restagno,G.; Ferrone, M.: Exercise intolerance and recurrent myoglobinuriaas the only expression of Xp21 Becker type muscular dystrophy. J.Neurol. 240: 269- 271, 1993. 3 B c

GAM94 332 DMD Dubrovsky, A. L.; Taratuto, A. L.; Sevlever, G.; Schultz, M.;Pegoraro, E.; Hoop, R. C.; Hoffman, E. P.: Duchenne muscular dystrophyand myotonic dystrophy in the same patient. Am. J. Med. Genet. 55:342- 348, 1995. 3 B c

GAM94 332 DMD Emery, A. E. H.: Duchenne Muscular Dystrophy. Oxford, UK: OxfordUniversity Press (pub.) (2nd ed.): 1993. 3 B c

GAM94 332 DMD England, S. B.; Nicholson, L. V. B.; Johnson, M. A.; Forrest,S. M.; Love, D. R.; Zubrzycka- Gaarn, E. E.; Bulman, D. E.; Harris,J. B.; Davies, K. E.: Very mild muscular dystrophy associated withthe deletion of 46% dystrophin. Nature 343: 180- 182, 1990. 3 B c

GAM94 332 DMD Fabb, S. A.; Wells, D. J.; Serpente, P.; Dickson, G.: Adeno- associatedvirus vector gene transfer and sarcolemmal expression of a 144 kDamicro-dystrophin effectively restores the dystrophin- associated proteincomplex and inhibits myofibre degeneration in nude/mdx mice. Hum.Molec. Genet. 11: 733- 741, 2002. 3 B c

GAM94 332 DMD Feener, C. A.; Boyce, F. M.; Kunkel, L. M.: Rapid detection ofCA polymorphisms in cloned DNA: application to the 5- prime regionof the dystrophin gene. Am. J. Hum. Genet. 48: 621- 627, 1991. 3 B c

GAM94 332 DMD Ferlini, A.; Galie, N.; Merlini, L.; Sewry, C.; Branzi, A.; Muntoni,F.: A novel Alu- like element rearranged in the dystrophin gene causesa splicing mutation in a family with X- linked dilated cardiomyopathy. Am.J. Hum. Genet. 63: 436- 446, 1998. 3 B c

GAM94 332 DMD Finnegan, D. J.: Eukaryotic transposable elements and genomeevolution. Trends Genet. 5: 103- 107, 1989. 3 B c

GAM94 332 DMD Forrest, S. M.; Cross, G. S.; Speer, A.; Gardner- Medwin, D.; Burn,J.; Davies, K. E.: Preferential deletion of exons in Duchenne andBecker muscular dystrophies. Nature 329: 638- 640, 1987. 3 B c

GAM94 332 DMD Francke, U.; Ochs, H. D.; de Martinville, B.; Giacalone, J.; Lindgren,V.; Disteche, C.; Pagon, R. A.; Hofker, M. H.; van Ommen, G.- J. B.;Pearson, P. L.; Wedgwood, R. J.: Minor Xp21 chromosome deletion ina male associated with expression of Duchenne muscular dystrophy,chronic granulomatous disease, 3 B c

retinitis pigmentosa, and McLeod syndrome. Am.J. Hum. Genet. 37: 250- 267, 1985.

GAM94 332 DMD Furst, D.; Nave, R.; Osborn, M.; Weber, K.; Bardosi, A.; Archidiacono,N.; 3 B c
Ferro, M.; Romano, V.; Romeo, G.: Nebulin and titin expressionin Duchenne muscular dystrophy appears normal. FEBS Lett. 224: 49- 53,1987.

GAM94 332 DMD Giacalone, J. P.; Francke, U.: Common sequence motifs at therearrangement 3 B c
sites of a constitutional X/autosome translocation andassociated deletion. Am. J. Hum. Genet. 50: 725- 741, 1992.

GAM94 332 DMD Gillard, E. F.; Chamberlain, J. S.; Murphy, E. G.; Duff, C. L.;Smith, B.; 3 B c
Burghes, A. H. M.; Thompson, M. W.; Sutherland, J.; Oss,I.; Bodrug, S. E.; Klamut, H. J.; Ray, P. N.; Worton, R. G.: Molecularand phenotypic analysis of patients with deletions within the deletion- richregion of the Duchenne muscular dystrophy (DMD) gene. Am. J. Hum.Genet. 45: 507- 520, 1989.

GAM94 332 DMD Ginjaar, I. B.; Kneppers, A. L. J.; Meulen, J.- D. M.; Anderson,L. V. B.; 3 B c
Bremmer- Bout, M.; van Deutekom, J. C. T.; Weegenaar, J.;den Dunnen, J. T.; Bakker, E.: Dystrophin nonsense mutation inducesdifferent levels of exon 29 skipping and leads to variable phenotypeswithin one BMD family. Europ. J. Hum. Genet. 8: 793- 796, 2000.

GAM94 332 DMD Gospe, S. M., Jr.; Lazaro, R. P.; Lava, N. S.; Grootscholten,P. M.; Scott, 3 B c
M. O.; Fischbeck, K. H.: Familial X- linked myalgiaand cramps: a nonprogressive myopathy associated with a deletion inthe dystrophin gene. Neurology 39: 1277- 1280, 1989.

GAM94 332 DMD Greenberg, D. S.; Sunada, Y.; Campbell, K. P.; Yaffe, D.; Nudel,U.: 3 B c
Exogenous Dp71 restores the levels of dystrophin associated proteinsbut does not alleviate muscle damage in mdx mice. Nature Genet. 8:340- 344, 1994.

GAM94 332 DMD Gussoni, E.; Soneoka, Y.; Strickland, C. D.; Buzney, E. A.; Khan,M. K.; 3 B c
Flint, A. F.; Kunkel, L. M.; Mulligan, R. C.: Dystrophin expressionin the mdx mouse restored by stem cell transplantation. Nature 401:390- 394, 1999.

GAM94 332 DMD Hagiwara, Y.; Mizuno, Y.; Takemitsu, M.; Matsuzaki, T.; Nonaka,I.; Ozawa, 3 B c
E.: Dystrophin- positive muscle fibers following C2 myoblasttransplantation into mdx nude mice. Acta Neuropath. 90: 592- 600,1995.

GAM94 332 DMD Hagiwara, Y.; Nishio, H.; Kitoh, Y.; Takeshima, Y.; Narita, N.;Wada, H.; 3 B c
Yokoyama, M.; Nakamura, H.; Matsuo, M.: A novel point mutation(G(- 1) to T) in a 5- prime splice donor site of intron 13 of the dystrophingene results in exon skipping and is responsible for Becker musculardystrophy. Am. J. Hum. Genet. 54: 53- 61, 1994.

GAM94 332 DMD Hammonds, R. G., Jr.: Protein sequence of DMD gene is relatedto actin- 3 B c
binding domain of alpha- actinin. (Letter) Cell 51: 1, 1987.

GAM94 332 DMD Harper, S. Q.; Hauser, M. A.; DelloRusso, C.; Duan, D.; Crawford,R. W.; 3 B c
Phelps, S. F.; Harper, H. A.; Robinson, A. S.; Engelhardt,J. F.; Brooks, S. V.; Chamberlain, J. S.: Modular flexibility ofdystrophin: implications for gene therapy of Duchenne muscular dystrophy. NatureMed. 8: 253- 261, 2002.

GAM94 332 DMD Hart, K. A.; Hodgson, S.; Walker, A.; Cole, C. G.; Johnson, L.;Dubowitz, V.; 3 B c
Bobrow, M.: DNA deletions in mild and severe Beckermuscular dystrophy. Hum. Genet. 75: 281- 285, 1987.

GAM94 332 DMD Hodgson, S. V.; Abbs, S.; Clark, S.; Manzur, A.; Heckmatt, J.Z. H.; 3 B c
Dubowitz, V.; Bobrow, M.: Correlation of clinical and deletiondata in Duchenne and Becker muscular dystrophy, with special referenceto mental ability. Neuromusc. Disord. 2: 269- 276, 1992.

GAM94 332 DMD Hoffman, E. P.; Brown, R. H., Jr.; Kunkel, L. M.: The proteinproduct of the 3 B c

Duchenne muscular dystrophy locus. Cell 51: 919- 928,1987.

GAM94 332 DMD Hoffman, E. P.; Fischbeck, K. H.; Brown, R. H.; Johnson, M.; Medori,R.; Loike, J. D.; Harris, J. B.; Waterston, R.; Brooke, M.; Specht,L.; Kupsky, W.; Chamberlain, J.; Caskey, C. T.; Shapiro, F.; Kunkel,L. M.: Characterization of dystrophin in muscle- biopsy specimensfrom patients with Duchenne's or Becker's muscular dystrophy. NewEng. J. Med. 318: 1363- 1368, 1988. 3 B c

GAM94 332 DMD Hoffman, E. P.; Knudson, C. M.; Campbell, K. P.; Kunkel, L. M.: Subcellular fractionation of dystrophin to the triads of skeletalmuscle. Nature 330: 754- 758, 1987. 3 B c

GAM94 332 DMD Hoffman, E. P.; Monaco, A. P.; Feener, C. C.; Kunkel, L. M.:Conservation of the Duchenne muscular dystrophy gene in mice and humans. Science 238:347- 350, 1987. 3 B c

GAM94 332 DMD Hoop, R. C.; Russo, L. S.; Riconda, D. L.; Schwartz, L. S.; Hoffman,E. P.: Restoration of half the normal dystrophin sequence in a double- deletionDuchenne muscular dystrophy family. Am. J. Med. Genet. 49: 323- 327,1994. 3 B c

GAM94 332 DMD Howard, P. L.; Dally, G. Y.; Wong, M. H.; Ho, A.; Weleber, R.G.; Pillers, D.- A. M.; Ray, P. N.: Localization of dystrophin isoformDp71 to the inner limiting membrane of the retina suggests a uniquefunctional contribution of Dp71 in the retina. Hum. Molec. Genet. 7:1385- 1391, 1998. 3 B c

GAM94 332 DMD Hu, X.; Burghes, A. H. M.; Bulman, D. E.; Ray, P. N.; Worton,R. G.: Evidence for mutation by unequal sister chromatid exchangein the Duchenne muscular dystrophy gene. Am. J. Hum. Genet. 44:855- 863, 1989. 3 B c

GAM94 332 DMD Hu, X.; Burghes, A. H. M.; Ray, P. N.; Thompson, M. W.; Murphy,E. G.; Worton, R. G.: Partial gene duplication in Duchenne and Beckermuscular dystrophies. J. Med. Genet. 25: 369- 376, 1988. 3 B c

GAM94 332 DMD Hu, X.; Ray, P. N.; Murphy, E. G.; Thompson, M. W.; Worton, R.G.: Duplicational mutation at the Duchenne muscular dystrophy locus:its frequency, distribution, origin, and phenotype- genotype correlation. Am.J. Hum. Genet. 46: 682- 695, 1990. 3 B c

GAM94 332 DMD Hu, X.; Ray, P. N.; Worton, R. G.: Mechanisms of tandem duplicationin the Duchenne muscular dystrophy gene include both homologous andnonhomologous intrachromosomal recombination. EMBO J. 10: 2471- 2477,1991. 3 B c

GAM94 332 DMD Hu, X.; Worton, R. G.: Partial gene duplication as a cause ofhuman disease. Hum. Mutat. 1: 3- 12, 1992. 3 B c

GAM94 332 DMD Ingram, V. M.: Gene evolution and the haemoglobins. Nature 189:704- 708, 1961. 3 B c

GAM94 332 DMD Itagaki, Y.; Saida, K.; Iwamura, K.: Regenerative capacity ofmdx mouse muscles after repeated applications of myo- necrotic bupivacaine. ActaNeuropath. 89: 380- 384, 1995. 3 B c

GAM94 332 DMD Kaplan, J.- C.; Kahn, A.; Chelly, J.: Illegitimate transcription:its use in the study of inherited disease. Hum. Mutat. 1: 357- 360,1992. 3 B c

GAM94 332 DMD Kavaslar, G. N.; Telatar, M.; Serdaroglu, P.; Deymeer, F.; Ozdemir,C.; Tolun, A.: Identification of a one- basepair deletion in exon6 of the dystrophin gene. Hum. Mutat. 6: 85- 86, 1995. 3 B c

GAM94 332 DMD Kilimann, M. W.; Pizzuti, A.; Grompe, M.; Caskey, C. T.: Pointmutations and polymorphisms in the human dystrophin gene identifiedin genomic DNA sequences amplified by multiplex PCR. Hum. Genet. 89:253- 258, 1992. 3 B c

GAM94 332 DMD Kim, T.- W.; Wu, K.; Black, I. B.: Deficiency of brain synapticdystrophin in 3 B c

human Duchenne muscular dystrophy. Ann. Neurol. 38:446- 449, 1995.

GAM94 332 DMD Kingston, H. M.; Sarfarazi, M.; Thomas, N. S. T.; Harper, P. S.: 3 B c
Localisation of the Becker muscular dystrophy gene on the shortarm of the X chromosome by linkage to cloned DNA sequences. Hum.Genet. 67: 6- 17, 1984.

GAM94 332 DMD Kingston, H. M.; Thomas, N. S. T.; Pearson, P. L.; Sarfarazi,M.; Harper, P. 3 B c
S.: Genetic linkage between Becker muscular dystrophyand a polymorphic DNA sequence on the short arm of the X chromosome. J.Med. Genet. 20: 255- 258, 1983.

GAM94 332 DMD Kneppers, A. L. J.; Deutz- Terlouw, P. P.; van Ommen, G. J. B.;Bakker, E.: 3 B c
Point mutation screening for Duchenne muscular dystrophy(DMD) by SSCP-analysis of multiplex PCR products by use of the PhastSystem(TM). Am. J. Hum. Genet. Suppl. 53: Abstract- 1493, 1993.

GAM94 332 DPYSL3 Byk, T.; Dobransky, T.; Cifuentes- Diaz, C.; Sobel, A.: Identificationand 3 B c
molecular characterization of Unc- 33- like phosphoprotein (Ulip),a putative mammalian homolog of the axonal guidance- associated unc- 33gene product. J. Neurosci. 16: 688- 701, 1996.

GAM94 332 DPYSL3 Gaetano, C; Matsuo, T.; Thiele, C. J.: Identification and characterizationof 3 B c
a retinoic acid- regulated human homologue of the unc- 33- like phosphoproteingene (hUlip) from neuroblastoma cells. J. Biol. Chem. 272: 12195- 12201,1997.

GAM94 332 DPYSL3 Hamajima, N.; Matsuda, K.; Sakata, S.; Tamaki, N.; Sasaki, M.;Nonaka, M.: A 3 B c
novel gene family defined by human dihydropyrimidinaseand three related proteins with differential tissue distribution. Gene 180:157- 163, 1996.

GAM94 332 DPYSL3 Matsuo, T.; Stauffer, J. K.; Walker, R. L.; Meltzer, P.; Thiele,C. J.: 3 B c
Structure and promoter analysis of the human unc- 33- like phosphoproteingene: E- box required for maximal expression in neuroblastoma and myoblasts. J.Biol. Chem. 275: 16560- 16568, 2000.

GAM94 332 DRD3 Accili, D.; Fishburn, C. S.; Drago, J.; Steiner, H.; Lachowicz,J. E.; Park, 3 B c
B.- H.; Gauda, E. B.; Lee, E. J.; Cool, M. H.; Sibley,D. R.; Gerfen, C. R.; Westphal, H.; Fuchs, S.: A targeted mutationof the D3 dopamine receptor gene is associated with hyperactivityin mice. Proc. Nat. Acad. Sci. 93: 1945-1949, 1996.

GAM94 332 DRD3 Asico, L. D.; Ladines, C.; Fuchs, S.; Accili, D.; Carey, R. M.;Semeraro, C.; 3 B c
Pocchiari, F.; Felder, R. A.; Eisner, G. M.; Jose, P.A.: Disruption of the dopamine D3 receptor gene produces renin- dependenthypertension. J. Clin. Invest. 102: 493- 498, 1998.

GAM94 332 DRD3 Crocq, M.- A.; Mant, R.; Asherson, P.; Williams, J.; Hode, Y.; Mayerova,A.; 3 B c
Collier, D.; Lannfelt, L.; Sokoloff, P.; Schwartz, J.- C.; Gill,M.; Macher, J.- P.; McGuffin, P.; Owen, M. J.: Association betweenschizophrenia and homozygosity at the dopamine D3 receptor gene. J.Med. Genet. 29: 858- 860, 1992.

GAM94 332 DRD3 Guillin, O.; Diaz, J.; Carroll, P.; Griffon, N.; Schwartz, J.- C.;Sokoloff, 3 B c
P.: BDNF controls dopamine D3 receptor expression and triggersbehavioural sensitization. Nature 411: 86- 89, 2001.

GAM94 332 DRD3 Ilani, T.; Ben- Shachar, D.; Strous, R. D.; Mazor, M.; Sheinkman,A.; Kotler, 3 B c
M.; Fuchs, S.: A peripheral marker for schizophrenia:increased levels of D3 dopamine receptor mRNA in blood lymphocytes. Proc.Nat. Acad. Sci. 98: 625-628, 2001.

GAM94 332 DRD3 Le Coniat, M.; Sokoloff, P.; Hillion, J.; Martres, M.- P.; Giros,B.; Pilon, 3 B c
C.; Schwartz, J.- C.; Berger, R.: Chromosomal localizationof the human D- 3

dopamine receptor gene. Hum. Genet. 87: 618- 620,1991.

GAM94 332 DRD3 Nanko, S.; Sasaki, T.; Fukuda, R.; Hattori, M.; Dai, X. Y.; Kazamatsuri,H.; 3 B c
Kuwata, S.; Juji, T.; Gill, M.: A study of the association
betweenschizophrenia and the dopamine D3 receptor gene. Hum. Genet. 92:336-
338, 1993.

GAM94 332 DRD3 Nothen, M. M.; Cichon, S.; Propping, P.; Fimmers, R.; Schwab, S.G.; 3 B c
Wildenauer, D. B.: Excess of homozygosity at the dopamine D3receptor gene in
schizophrenia not confirmed. (Letter) J. Med. Genet. 30:708- 712, 1993.

GAM94 332 DRD3 Pilla, M.; Perachon, S.; Sautel, F.; Garrido, F.; Mann, A.; Wermuth,C. G.; 3 B c
Schwartz, J.- C.; Everitt, B. J.; Sokoloff, P.: Selective inhibitionof
cocaine- seeking behaviour by a partial dopamine D3 receptor agonist. Nature
400:371- 375, 1999.

GAM94 332 DRD3 Shaikh, S.; Ball, D.; Craddock, N.; Castle, D.; Hunt, N.; Mant,R.; Owen, M.; 3 B c
Collier, D.; Gill, M.: The dopamine D3 receptor gene:no association with
bipolar affective disorder. J. Med. Genet. 30:308- 309, 1993.

GAM94 332 DRD3 Sokoloff, P.; Giros, B.; Martres, M.- P.; Bouthenet, M.- L.; Schwartz,J.- 3 B c
C.: Molecular cloning and characterization of a novel dopaminereceptor (D-
3) as a target for neuroleptics. Nature 347: 146- 151,1990.

GAM94 332 DRD3 Spurlock, G.; Williams, J.; McGuffin, P.; Aschauer, H. N.; Lenzinger,E.; 3 B c
Fuchs, K.; Sieghart, W. C.; Meszaros, K.; Fathi, N.; Laurent,C.; Mallet, J.;
Macciardi, F.; Pedrini, S.; Gill, M.; Hawi, Z.; Gibson,S.; Jazin, E. E.;
Yang, H.- T.; Adolfsson, R.; Pato, C. N.; Dourado,A. M.; Owen, M. J.:
European Multicentre Association Study of Schizophrenia:a study of the DRD2
ser311- to- cys and DRD3 ser9- to- gly polymorphisms. Am.J. Med. Genet. 81:
24- 28, 1998.

GAM94 332 EIF5A Koettnitz, K.; Kappel, B.; Baumruker, T.; Hauber, J.; Bevec, D.: The genomic 3 B c
structure encoding human initiation factor eIF- 5A. Gene 144:249- 252, 1994.

GAM94 332 EIF5A Koettnitz, K.; Wohl, T.; Kappel, B.; Lottspeich, F.; Hauber, J.;Bevec, D.: 3 B c
Identification of a new member of the human eIF- 5A genefamily. Gene 159:
283- 284, 1995.

GAM94 332 EIF5A Steinkasserer, A.; Jones, T.; Sheer, D.; Koettnitz, K.; Hauber,J.; Bevec, 3 B c
D.: The eukaryotic cofactor for the human immunodeficiencyvirus type 1 (HIV-
1) rev protein, eIF- 5A, maps to chromosome 17p12- p13:three eIF- 5A
pseudogenes map to 10q23.3, 17q25, and 19q13.2. Genomics 25:749- 752, 1995.

GAM94 332 FGF13 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; 3 B c
Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast
growth factor homologous factor 2 (FHF2): gene structure,expression and
mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated
by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63,
1999.

GAM94 332 FGF13 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; 3 B c
Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21
by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997.

GAM94 332 FGF13 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. 3 B c
C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast
growth factor (FGF) homologous factors: new membersof the FGF family
implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850-
9857, 1996.

GAM94 332 FKBP10 Patterson, C. E.; Gao, J.; Rooney, A. P.; Davis, E. C.: Genomicorganization 3 B b
of mouse and human 65 kDa FK506- binding protein genesand evolution of the

FKBP multigene family. Genomics 79: 881- 889,2002.

GAM94 332 FKBP10 Patterson, C. E.; Schaub, T.; Coleman, E. J.; Davis, E. C.: 3 B b
Developmentalregulation of FKBP65: an ER localized extracellular matrix-
bindingprotein. Molec. Biol. Cell 11: 3925- 3935, 2000.

GAM94 332 FLT4 Aprelikova, O.; Pajusola, K.; Partanen, J.; Armstrong, E.; Alitalo,R.; 3 B c
Bailey, S. K.; McMahon, J.; Wasmuth, J.; Huebner, K.; Alitalo,K.: FLT4, a
novel class III receptor tyrosine kinase in chromosome5q33- qter. Cancer
Res. 52: 746- 748, 1992.

GAM94 332 FLT4 Dumont, D. J.; Jussila, L.; Taipale, J.; Lymboussaki, A.; Mustonen,T.; 3 B c
Pajusola, K.; Breitman, M.; Alitalo, K.: Cardiovascular failurein mouse
embryos deficient in VEGF receptor- 3. Science 282: 946- 949,1998.

GAM94 332 FLT4 Evans, A. L.; Brice, G.; Sotirova, V.; Mortimer, P.; Beninson,J.; Burnand, 3 B c
K.; Rosbotham, J.; Child, A.; Sarfarazi, M.: Mappingof primary congenital
lymphedema to the 5q35.3 region. Am. J. Hum.Genet. 64: 547- 555, 1999.

GAM94 332 FLT4 Ferrell, R. E.; Levinson, K. L.; Esman, J. H.; Kimak, M. A.; Lawrence,E. C.; 3 B c
Barmada, M. M.; Finegold, D. N.: Hereditary lymphedema: evidencefor linkage
and genetic heterogeneity. Hum. Molec. Genet. 7: 2073- 2078,1998.

GAM94 332 FLT4 Galland, F.; Karamysheva, A.; Mattei, M.- G.; Rosnet, O.; Marchetto,S.; 3 B c
Birnbaum, D.: Chromosomal localization of FLT4, a novel receptor-
typetyrosine kinase gene. Genomics 13: 475- 478, 1992.

GAM94 332 FLT4 Irrthum, A.; Karkkainen, M. J.; Devriendt, K.; Alitalo, K.; Vikkula,M.: 3 B c
Congenital hereditary lymphedema caused by a mutation that inactivatesVEGFR3
tyrosine kinase. Am. J. Hum. Genet. 67: 295- 301, 2000.

GAM94 332 FLT4 Kaipainen, A.; Korhonen, J.; Mustonen, T.; van Hinsbergh, V. W.M.; Fang, G.- 3 B c
H.; Dumont, D.; Breitman, M.; Alitalo, K.: Expressionof the fms- like
tyrosine kinase 4 gene becomes restricted to lymphaticendothelium during
development. Proc. Nat. Acad. Sci. 92: 3566- 3570,1995.

GAM94 332 FLT4 Karkkainen, M. J.; Ferrell, R. E.; Lawrence, E. C.; Kimak, M. A.;Levinson, 3 B c
K. L.; McTigue, M. A.; Alitalo, K.; Finegold, D. N.: Missensemutations
interfere with VEGFR- 3 signalling in primary lymphoedema. NatureGenet. 25:
153- 159, 2000.

GAM94 332 FLT4 Karkkainen, M. J.; Saaristo, A.; Jussila, L.; Karila, K. A.; Lawrence,E. C.; 3 B c
Pajusola, K.; Bueler, H.; Eichmann, A.; Kauppinen, R.; Kettunen,M. I.; Yla-
Herttuala, S.; Finegold, D. N.; Ferrell, R. E.; Alitalo,K.: A model for gene
therapy of human hereditary lymphedema. Proc.Nat. Acad. Sci. 98: 12677-
12682, 2001.

GAM94 332 FLT4 Lee, J.; Gray, A.; Yuan, J.; Luoh, S.- M.; Avraham, H.; Wood, W.I.: Vascular 3 B c
endothelial growth factor- related protein: a ligandand specific activator
of the tyrosine kinase receptor Flt4. Proc.Nat. Acad. Sci. 93: 1988- 1992,
1996.

GAM94 332 FLT4 Lyon, M. F.; Glenister, P. H.: Gene order of Chy- vt- Re on chromosome11. 3 B c
Mouse Newsletter 74: 96 only, 1986.

GAM94 332 FLT4 Lyon, M. F.; Glenister, P. H.: New Mutants. Mouse Newsletter 71:26 only, 3 B c
1984.

GAM94 332 FLT4 Milroy, W. F.: An undescribed variety of hereditary oedema. NewYork Med. J. 3 B c
56: 505- 508, 1892.

GAM94 332 FLT4 Offori, T. W.; Platt, C. C.; Stephens, M.; Hopkinson, G. B.:Angiosarcoma in 3 B c
congenital hereditary lymphoedema (Milroy's disease):diagnostic beacons and
a review of the literature. Clin. Exp. Derm. 18:174- 177, 1993.

GAM94 332 FLT4 Pajusola, K.; Aprelikova, O.; Korhonen, J.; Kaipainen, A.; Pertovaara,L.; 3 B c

Alitalo, R.; Alitalo, K.: FLT4 receptor tyrosine kinase containsseven immunoglobulin- like loops and is expressed in multiple humantissues and cell lines. Cancer Res. 52: 5738- 5743, 1992.

GAM94 332 FLT4 Pajusola, K.; Aprelikova, O.; Pelicci, G.; Weich, H.; Claesson- Welsh,L.; 3 B c
Alitalo, K.: Signalling properties of FLT4, a proteolyticallyprocessed receptor tyrosine kinase related to two VEGF receptors. Oncogene 9:3545-3555, 1994.

GAM94 332 FLT4 Walter, J. W.; North, P. E.; Waner, M.; Mizeracki, A.; Blei, F.;Walker, J. 3 B c
W. T.; Reinisch, J. F.; Marchuk, D. A.: Somatic mutationof vascular endothelial growth factor receptors in juvenile hemangioma. GenesChromosomes Cancer 33: 295- 303, 2002.

GAM94 332 FLT4 Warrington, J. A.; Bailey, S. K.; Armstrong, E.; Aprelikova, O.;Alitalo, K.; 3 B c
Dolganov, G. M.; Wilcox, A. S.; Sikela, J. M.; Wolfe,S. F.; Lovett, M.; Wasmuth, J. J.: A radiation hybrid map of 18 growthfactor, growth factor receptor, hormone receptor, or neurotransmitterreceptor genes on the distal region of the long arm of chromosome5. Genomics 13: 803- 808, 1992.

GAM94 332 FOSB Bibb, J. A.; Chen, J.; Taylor, J. R.; Svenningsson, P.; Nishi,A.; Snyder, G. 3 B c
L.; Yan, Z.; Sagawa, Z. K.; Ouimet, C. C.; Nairn, A.C.; Nestler, E. J.; Greengard, P.: Effects of chronic exposure tococaine are regulated by the neuronal protein Cdk5. Nature 410:376- 380, 2001.

GAM94 332 FOSB Brown, J. R.; Ye, H.; Bronson, R. T.; Dikkes, P.; Greenberg, M.E.: A defect 3 B c
in nurturing in mice lacking the immediate early genefosB. Cell 86: 297-309, 1996.

GAM94 332 FOSB Forsdyke, D.: Personal Communication. Kingston, Ontario, Canada 6/8/1992. 3 B c

GAM94 332 FOSB Kelz, M. B.; Chen, J.; Carlezon, W. A., Jr.; Whisler, K.; Gilden,L.; 3 B c
Beckmann, A. M.; Steffen, C.; Zhang, Y.- J.; Marotti, L.; Self,D. W.; Tkatch, T.; Baranauskas, G.; Surmeier, D. J.; Neve, R. L.;Duman, R. S.; Picciotto, M. R.; Nestler, E. J.: Expression of thetranscription factor delta- FosB in the brain controls sensitivityto cocaine. Nature 401: 272-276, 1999.

GAM94 332 FOSB Lazo, P. S.; Dorfman, K.; Noguchi, T.; Mattei, M. G.; Bravo, R.: Structure 3 B c
and mapping of the fosB gene: FosB downregulates the activityof the fosB promoter. Nucleic Acids Res. 20: 343- 350, 1992.

GAM94 332 FOSB Martin- Gallardo, A.; McCombie, W. R.; Gocayne, J. D.; FitzGerald,M. G.; 3 B c
Wallace, S.; Lee, B. M. B.; Lamerdin, J.; Trapp, S.; Kelley,J. M.; Liu, L.-I.; Dubnick, M.; Johnston- Dow, L. A.; Kerlavage, A.R.; de Jong, P.; Carrano, A.; Fields, C.; Venter, J. C.: AutomatedDNA sequencing and analysis of 106 kilobases from human chromosome19q13.3. Nature Genet. 1: 34- 39, 1992.

GAM94 332 FOSB Nakabeppu, Y.; Nathans, D.: A naturally occurring truncated formof FosB that 3 B c
inhibits Fos/Jun transcriptional activity. Cell 64:751- 759, 1991.

GAM94 332 FOSB Siderovski, D. P.; Blum, S.; Forsdyke, R. E.; Forsdyke, D. R.:A set of human 3 B c
putative lymphocyte G0/G1 switch genes includes geneshomologous to rodent cytokine and zinc finger protein- encoding genes. DNACell Biol. 9: 579- 587, 1990.

GAM94 332 FZD1 Liu, T.; DeCostanzo, A. J.; Liu, X.; Wang, H.; Hallagan, S.; Moon,R. T.; 3 B b
Malbon, C. C.: G protein signaling from activated rat frizzled- 1to the beta- catenin- Lef- Tcf pathway. Science 292: 1718- 1722, 2001.

GAM94 332 FZD1 Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.: Molecularcloning, 3 B b
differential expression, and chromosomal localization ofhuman frizzled- 1,

frizzled- 2, and frizzled- 7. Biochem. Biophys. Res.Commun. 252: 117- 122, 1998.

GAM94 332 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2 in the allergic response. Nature 412: 186- 190,2001. 3 B c

GAM94 332 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998. 3 B c

GAM94 332 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab-family adapter proteins act downstream of cytokine and growthfactor receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999. 3 B c

GAM94 332 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell Genet. 94: 39- 42, 2001. 3 B c

GAM94 332 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology domain- containing adapter protein, acts to uncouple signalingfrom ERK kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999. 3 B c

GAM94 332 GNGT2 Ong, O. C.; Hu, K.; Rong, H.; Lee, R. H.; Fung, B. K.- K.: Genestructure and chromosome localization of the G- gamma- c subunit ofhuman cone G- protein (GNGT2). Genomics 44: 101- 109, 1997. 3 B c

GAM94 332 GNGT2 Ong, O. C.; Yamane, H. K.; Phan, K. B.; Fong, H. K.; Bok, D.; Lee,R. H.; Fung, B. K.- K.: Molecular cloning and characterization ofthe G protein gamma subunit of cone photoreceptors. J. Biol. Chem. 270:8495- 8500, 1995. 3 B c

GAM94 332 GPM6B Narayanan, V.; Olinsky, S.; Dahle, E.; Naidu, S.; Zoghbi, H. Y.: Mutation analysis of the M6b gene in patients with Rett syndrome. Am.J. Med. Genet. 78: 165- 168, 1998. 3 B b

GAM94 332 GPM6B Olinsky, S.; Loop, B. T.; DeKosky, A.; Ripepi, B.; Weng, W.; Cummins,J.; Wenger, S. L.; Yan, Y.; Lagenaur, C.; Narayanan, V.: Chromosomalmapping of the human M6 genes. Genomics 33: 532- 536, 1996. 3 B b

GAM94 332 GPM6B Yan, Y.; Lagenaur, C.; Narayanan, V.: Molecular cloning of M6:identification of a PLP/DM20 gene family. Neuron 11: 423- 431, 1993. 3 B b

GAM94 332 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a novel secretin- like human G- protein- coupledreceptor gene. Genomics 55: 296- 305, 1999. 3 B c

GAM94 332 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected with mRNA differential display using human melanoma celllines with different metastatic potential. FEBS Lett. 446: 292- 298,1999. 3 B c

GAM94 332 HMGB2 Shirakawa, H.; Yoshida, M.: Structure of a gene coding for humanHMG2 protein. J. Biol. Chem. 267: 6641- 6645, 1992. 3 B c

GAM94 332 HMGB2 Wanschura, S.; Schoenmakers, E. F. P. M.; Huysmans, C.; Bartnitzke,S.; Van de Ven, W. J. M.; Bullerdiek, J.: Mapping of the human HMG2gene to 4q31. Genomics 31: 264- 265, 1996. 3 B c

GAM94 332 HOXB5 Acampora, D.; D'Esposito, M.; Faiella, A.; Pannese, M.; Migliaccio,E.; Morelli, F.; Stornaiuolo, A.; Nigro, V.; Simeone, A.; Boncinelli,E.: The human HOX gene family. Nucleic Acids Res. 17: 10385- 10402,1989. 3 B b

GAM94 332 HOXB5 Comings, D. E.: Evidence for ancient tetraploidy and conservationof linkage 3 B b

groups in mammalian chromosomes. Nature 238: 455- 467,1972.

GAM94 332 HOXB5 Deol, M. S.: Genetical studies on the skeleton of the mouse. XXVIII.Tail- 3 B b
short. Proc. Roy. Soc. Ser. B. 155: 78- 95, 1961.

GAM94 332 HOXB5 Hart, C. P.; Awgulewitsch, A.; Fainsod, A.; McGinnis, W.; Ruddle,F. H.: 3 B b
Homeo box gene complex on mouse chromosome 11: molecular cloning,expression
in embryogenesis, and homology to a human homeo box locus. Cell 43:9- 18,
1985.

GAM94 332 HOXB5 Hauser, C. A.; Joyner, A. L.; Klein, R. D.; Learned, T. K.; Martin,G. R.; 3 B b
Tjian, R.: Expression of homologous homeo- box- containing genesin
differentiated human teratocarcinoma cells and mouse embryos. Cell 43:19-
28, 1985.

GAM94 332 HOXB5 Joyner, A. L.; Lebo, R. V.; Kan, Y. W.; Tjian, R.; Cox, D. R.;Martin, G. R.: 3 B b
Comparative chromosome mapping of a conserved homoeobox region in mouse and
human. Nature 314: 173- 175, 1985.

GAM94 332 HOXB5 Levine, M.; Rubin, G. M.; Tjian, R.: Human DNA sequences homologousto a 3 B b
protein coding region conserved between homeotic genes of Drosophila. Cell
38:667- 673, 1984.

GAM94 332 HOXB5 Manley, J. L.; Levine, M. S.: The homeo box and mammalian development. Cell 3 B b
43:1- 2, 1985.

GAM94 332 HOXB5 Meijlink, F.; de Laaf, R.; Verrijzer, P.; Destree, O.; Kroezen,V.; Hilkens, 3 B b
J.; Deschamps, J.: A mouse homeobox containing geneon chromosome 11:
sequence and tissue- specific expression. NucleicAcids Res. 15: 6773- 6786,
1987.

GAM94 332 HOXB5 Miki, T.; Murphy, P. D.; Pletcher, B. A.; Kidd, J. R.; Ferguson- Smith,A. 3 B b
C.; Ruddle, F. H.; Kidd, K. K.: HOX2 maps to 17q near PPY andNGFR.
(Abstract) Cytogenet. Cell Genet. 46: 662 only, 1987.

GAM94 332 HOXB5 Munke, M.; Cox, D. R.; Jackson, I. J.; Hogan, B. L. M.; Francke,U.: The 3 B b
murine Hox- 2 cluster of homeo box containing genes maps distalon chromosome
11 near the tail- short (Ts) locus. Cytogenet. CellGenet. 42: 236- 240,
1986.

GAM94 332 HOXB5 Rabin, M.; Ferguson- Smith, A.; Hart, C. P.; Ruddle, F. H.: Cognatehomeo- 3 B b
box loci mapped on homologous human and mouse chromosomes. Proc.Nat. Acad.
Sci. 83: 9104- 9108, 1986.

GAM94 332 HOXB5 Rabin, M.; Hart, C. P.; Ferguson- Smith, A.; McGinnis, W.; Levine,M.; 3 B b
Ruddle, F. H.: Two homoeo box loci mapped in evolutionarily relatedmouse and
human chromosomes. Nature 314: 175- 178, 1985.

GAM94 332 HOXB5 Ruddle, F. H.: Personal Communication. New Haven, Conn. 1985. 3 B b

GAM94 332 HOXB5 Ruddle, F. H.: Personal Communication. New Haven, Conn. 1987. 3 B b

GAM94 332 HOXB5 Schughart, K.; Utset, M. F.; Awgulewitsch, A.; Ruddle, F. H.:Structure and 3 B b
expression of Hox- 2.2, a murine homeobox- containinggene. Proc. Nat. Acad.
Sci. 85: 5582- 5586, 1988.

GAM94 332 HOXB5 Trainor, P. A.; Ariza- McNaughton, L.; Krumlauf, R.: Role of theisthmus and 3 B b
FGFs in resolving the paradox of neural crest plasticityand prepatterning.
Science 295: 1288- 1291, 2002.

GAM94 332 HOXB5 Xu, W.; Gorman, P. A.; Rider, S. H.; Hedge, P. J.; Moore, G.;Prichard, C.; 3 B b
Sheer, D.; Solomon, E.: Construction of a genetic mapof human chromosome 17
by use of chromosome- mediated gene transfer. Proc.Nat. Acad. Sci. 85: 8563-
8567, 1988.

GAM94 332 HOXB6 Apiou, F.; Flagiello, D.; Cillo, C.; Malfoy, B.; Poupon, M.- F.;Dutrillaux, 3 B b
B.: Fine mapping of human HOX gene clusters. Cytogenet.Cell Genet. 73: 114-

115, 1996.

GAM94 332 HOXB6 Kaur, S.; Singh, G.; Stock, J. L.; Schreiner, C. M.; Kier, A. B.;Yager, K. 3 B b
L.; Mucenski, M. L.; Scott, W. J., Jr.; Potter, S. S.:Dominant mutation of
the murine Hox- 2.2 gene results in developmentalabnormalities. J. Exp.
Zool. 264: 323- 336, 1992.

GAM94 332 HOXC4 Apiou, F.; Flagiello, D.; Cillo, C.; Malfoy, B.; Poupon, M.- F.;Dutrillaux, 3 B c
B.: Fine mapping of human HOX gene clusters. Cytogenet.Cell Genet. 73: 114-
115, 1996.

GAM94 332 HOXC6 Chariot, A.; Castronovo, V.; Le, P.; Gillet, C.; Sobel, M. E.;Gielen, J.: 3 B c
Cloning and expression of a new HOXC6 transcript encodinga repressing
protein. Biochem. J. 319: 91- 97, 1996.

GAM94 332 HOXC6 Simeone, A.; Mavilio, F.; Acampora, D.; Giampaolo, A.; Faiella,A.; 3 B c
Zappavigna, V.; D'Esposito, M.; Pannese, M.; Russo, G.; Boncinelli,E.;
Peschle, C.: Two human homeobox genes, c1 and c8: structure analysisand
expression in embryonic development. Proc. Nat. Acad. Sci. 84:4914- 4918,
1987.

GAM94 332 ICA1 Gaedigk, R.; Duncan, A. M. V.; Miyazaki, I.; Robinson, B. H.; Dosch,H.- M.: 3 B c
ICA1 encoding p69, a protein linked to the development oftype 1 diabetes,
maps to human chromosome 7p22. Cytogenet. Cell Genet. 66:274- 276, 1994.

GAM94 332 ICA1 Gaedigk, R.; Karges, W.; Hui, M. F.; Scherer, S. W.; Dosch, H.- M.: Genomic 3 B c
organization and transcript analysis of ICAp69, a targetantigen in diabetic
autoimmunity. Genomics 38: 382- 391, 1996.

GAM94 332 ICA1 Pietropaolo, M.; Castano, L.; Babu, S.; Buelow, R.; Kuo, Y.- L.S.; Martin, 3 B c
S.; Martin, A.; Powers, A. C.; Prochazka, M.; Naggert,J.; Leiter, E. H.;
Eisenbarth, G. S.: Islet cell autoantigen 69 kD(ICA69): molecular cloning
and characterization of a novel diabetes- associatedautoantigen. J. Clin.
Invest. 92: 359- 371, 1993.

GAM94 332 IFNAR2 Croze, E.; Russell- Harde, D.; Wagner, T. C.; Pu, H.; Pfeffer, L.M.; Perez, 3 B c
H. D.: The human type I interferon receptor: identificationof the interferon
beta- specific receptor- associated phosphoprotein. J.Biol. Chem. 271:
33165- 33168, 1996.

GAM94 332 IFNAR2 Croze, E.; Usacheva, A.; Asarnow, D.; Minshall, R.D.; Perez, 3 B c
H.D.;Colamonici, O.: Receptor for activated C- kinase (RACK- 1), a WD motif-
containingprotein, specifically associates with the human type I IFN
receptor. J.Immun. 165: 5127- 5132, 2000.

GAM94 332 IFNAR2 Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.;Pitha, P.; 3 B c
Colamonici, O. R.: Cloning and expression of a long formof the beta subunit
of the interferon alpha/beta receptor that isrequired for signaling. J.
Biol. Chem. 270: 21606- 21611, 1995.

GAM94 332 IFNAR2 Lutfalla, G.; Holland, S. J.; Cinato, E.; Monneron, D.; Reboul,J.; Rogers, 3 B c
N. C.; Smith, J. M.; Stark, G. R.; Gardiner, K.; Mogensen,K. E.; Kerr, I.
M.; Uze, G.: Mutant U5A cells are complemented byan interferon- alpha/beta
receptor subunit generated by alternativeprocessing of a new member of a
cytokine receptor gene cluster. EMBOJ. 14: 5100- 5108, 1995.

GAM94 332 IFNAR2 Novick, D.; Cohen, B.; Rubinstein, M.: The human interferon 3 B c
alpha/betareceptor: characterization and molecular cloning. Cell 77: 391-
400,1994.

GAM94 332 IFNAR2 Platanias, L. C.; Uddin, S.; Domanski, P.; Colamonici, O. R.:Differences in 3 B c
interferon alpha and beta signaling: interferon betaselectively induces the
interaction of the alpha and beta(L) subunitsof the type I interferon

receptor. J. Biol. Chem. 271: 23630- 23633,1996.

GAM94 332 IFNAR2 Raz, R.; Cheung, K.; Ling, L.; Levy, D. E.: Three distinct locion human 3 B c
chromosome 21 contribute to interferon- alpha/beta responsiveness.
Somat.Cell Molec. Genet. 21: 139- 145, 1995.

GAM94 332 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 B c
M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like
growth factor- I and cognitive function inhealthy older men. J. Clin.
Endocr. Metab. 84: 471- 475, 1999.

GAM94 332 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- 3 B c
like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993.

GAM94 332 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and 3 B c
absence of association with stature among African Pygmies. Hum.Genet. 85:
349- 354, 1990.

GAM94 332 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for 3 B c
insulin- like growth factors I and II and for epidermalgrowth factor in man.
(Abstract) Am. J. Hum. Genet. 36: 133S only,1984.

GAM94 332 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of 3 B c
genes for insulin- like growth factors I and II and epidermalgrowth factor.
Nature 310: 781- 784, 1984.

GAM94 332 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, 3 B c
A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of
recombinant human insulin- like growth factor I(IGF- I) therapy on the
growth hormone- IGF system of a patient witha partial IGF- I gene deletion.
J. Clin. Endocr. Metab. 84: 1611- 1616,1999.

GAM94 332 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; 3 B c
Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of
the growth hormone receptor in children with idiopathicshort stature. New
Eng. J. Med. 333: 1093- 1098, 1995.

GAM94 332 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; 3 B c
Froesch, E. R.: Small stature and insulin- like growth factors:prolonged
treatment of mini- poodles with recombinant human insulin- likegrowth factor
I. Acta Endocr. 121: 456- 464, 1989.

GAM94 332 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. 3 B c
S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating
concentrations of insulin- like growth factor- I and riskof breast cancer.
Lancet 351: 1393- 1396, 1998.

GAM94 332 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: 3 B c
Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding
protein- 3, and prostate- specific antigen as predictorsof clinical prostate
cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000.

GAM94 332 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; 3 B c
Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith,
D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival
signaling in retinal endothelial cells: direct correlationwith clinical
retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001.

GAM94 332 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer 3 B c
prevention. Lancet 351: 1373- 1375, 1998.

GAM94 332 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; 3 B c
Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J.
S.: The human gene encoding insulin- like growthfactor I is located on

chromosome 12. Hum. Genet. 69: 157- 160, 1985.

GAM94 332 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990. 3 B c

GAM94 332 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986. 3 B c

GAM94 332 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF- 1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996. 3 B c

GAM94 332 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat. Acad. Sci. 80: 2216- 2220, 1983. 3 B c

GAM94 332 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand implications for cell type- specific growth. Nature 364: 208- 213,1993. 3 B c

GAM94 332 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: Mice carrying null mutations of the genes encoding insulin- likegrowth factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993. 3 B c

GAM94 332 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83: 9343- 9347, 1986. 3 B c

GAM94 332 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human genes for insulin- like growth factors I and II and epidermalgrowth factor are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively. Cytogenet.Cell Genet. 41: 245- 249, 1986. 3 B c

GAM94 332 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2 (IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985. 3 B c

GAM94 332 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. D.: Growth characteristics and response to growth hormonetherapy in patients with hypochondroplasia: genetic linkage of theinsulin- like growth factor I gene at chromosome 12q23 to the diseasein a subgroup of these patients. Clin. Endocr. 34: 265- 274, 1991. 3 B c

GAM94 332 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999. 3 B c

GAM94 332 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene expression sustains hypertrophy and regeneration insenescent skeletal muscle. Nature Genet. 27: 195- 200, 2001. 3 B c

GAM94 332 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like growth factor 1 regulates the location, stability,and transcriptional activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000. 3 B c

GAM94 332 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993. 3 B c

GAM94 332 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the 3 B c

protein which binds insulin- like growth factor in human serum. Europ.J. Biochem. 172: 421- 425, 1988.

GAM94 332 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith, R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the insulin- like growth factor I receptor and its ligandin relation to type 2 diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000. 3 B c

GAM94 332 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986. 3 B c

GAM94 332 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I) reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991. 3 B c

GAM94 332 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999. 3 B c

GAM94 332 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980. 3 B c

GAM94 332 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 1991. 3 B c

GAM94 332 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984. 3 B c

GAM94 332 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984. 3 B c

GAM94 332 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984. 3 B c

GAM94 332 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853- 857,1992. 3 B c

GAM94 332 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002. 3 B c

GAM94 332 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980. 3 B c

GAM94 332 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999. 3 B c

GAM94 332 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. 3 B c
L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy
on body composition and insulin resistance in IGF- Igene deletion. J. Clin.
Endocr. Metab. 85: 1407- 1411, 2000.

GAM94 332 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 3 B c
Intrauterine growth retardation and postnatal growth failureassociated with
deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335:
1363- 1367, 1996.

GAM94 332 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 3 B c
regional localization of human genes for insulin- like growthfactors I
(IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell
Genet. 40: 782 only, 1985.

GAM94 332 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 3 B c
growth factors and bone mineral density in African Americanand white girls.
J. Pediat. 137: 826- 832, 2000.

GAM94 332 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 3 B c
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM94 332 IL15RA Anderson, D. M.; Kumaki, S.; Ahdieh, M.; Bertles, J.; Tometsko,M.; Loomis, 3 B c
A.; Giri, J.; Copeland, N. G.; Gilbert, D. J.; Jenkins,N. A.; Valentine, V.;
Shapiro, D. N.; Morris, S. W.; Park, L. S.;Cosman, D.: Functional
characterization of the human interleukin- 15receptor alpha chain and close
linkage of IL15RA and IL2RA genes. J.Biol. Chem. 270: 29862- 29869, 1995.

GAM94 332 IL15RA Giri, J. G.; Kumaki, S.; Ahdieh, M.; Friend, D. J.; Loomis, A.;Shanebeck, 3 B c
K.; DuBose, R.; Cosman, D.; Park, L. S.; Anderson, D. M.: Identification and
cloning of a novel IL- 15 binding protein thatis structurally related to the
alpha of the IL- 2 receptor. EMBO J. 14:3654- 3663, 1995.

GAM94 332 IL19 Blumberg, H.; Conklin, D.; Xu, W.; Grossmann, A.; Brender, T.;Carollo, S.; 3 B c
Eagan, M.; Foster, D.; Haldeman, B. A.; Hammond, A.;Haugen, H.; Jelinek, L.;
and 14 others: Interleukin 20: discovery,receptor identification, and role
in epidermal function. Cell 104:9- 19, 2001.

GAM94 332 IL19 Gallagher, G.; Dickensheets, H.; Eskdale, J.; Izotova, L. S.; 3 B c
Mirochnitchenko,O. V.; Peat, J. D.; Vazquez, N.; Pestka, S.; Donnelly, R.
P.; Kotenko,S. V.: Cloning, expression and initial characterisation of
interleukin- 19(IL- 19), a novel homologue of human interleukin- 10 (IL-
10). GenesImmunity 1: 442- 450, 2000.

GAM94 332 IL1RL1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 3 B c
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp)
on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM94 332 IL1RL1 Kumar, S.; Tzimas, M. N.; Griswold, D. E.; Young, P. R.: Expressionof ST2, 3 B c
an interleukin- 1 receptor homologue, is induced by proinflammatorystimuli.
Biochem. Biophys. Res. Commun. 235: 474- 478, 1997.

GAM94 332 IL1RL1 Sims, J. E.; Painter, S. L.; Gow, I. R.: Genomic organizationof the type I 3 B c
and type II IL- 1 receptors. Cytokine 7: 483- 490, 1995.

GAM94 332 IL1RL1 Tago, K.; Noda, T.; Hayakawa, M.; Iwahana, H.; Yanagisawa, K.;Yashiro, T.; 3 B c
Tominaga, S.: Tissue distribution and subcellular localizationof a variant
form of the human ST2 gene product, ST2V. Biochem. Biophys.Res. Commun. 285:
1377- 1383, 2001.

GAM94 332 IL1RL1 Tominaga, S.: A putative protein of a growth specific cDNA fromBALB/c- 3T3 3 B c
cells is highly similar to the extracellular portion ofmouse interleukin 1
receptor. FEBS Lett. 258: 301- 304, 1989.

GAM94 332 IL1RL1 Tominaga, S.; Inazawa, J.; Tsuji, S.: Assignment of the humanST2 gene to chromosome 2 at q11.2. Hum. Genet. 97: 561- 563, 1996. 3 B c

GAM94 332 IL1RL1 Tominaga, S.; Yokota, T.; Yanagisawa, K.; Tsukamoto, T.; Takagi,T.; Tetsuka, T.: Nucleotide sequence of a complementary DNA for humanST2. Biochim. Biophys. Acta 1171: 215- 218, 1992. 3 B c

GAM94 332 IL2 Cantrell, D. A.; Smith, K. A.: The interleukin- 2 T- cell system:a new cell growth model. Science 224: 1312- 1316, 1984. 3 B c

GAM94 332 IL2 Clark, S. C.; Arya, S. K.; Wong- Staal, F.; Matsumoto- Kobayashi,M.; Kay, M.; Kaufman, R. J.; Brown, E. L.; Shoemaker, C.; Copeland,T.; Oroszlan, S.; Smith, K.; Sarngadharan, M. G.; Lindner, S. G.;Gallo, R. C.: Human T- cell growth factor: partial amino acid sequence,cDNA cloning, and organization and expression in normal and leukemiccells. Proc. Nat. Acad. Sci. 81: 2543- 2547, 1984. 3 B c

GAM94 332 IL2 Degrave, W.; Tavernier, J.; Duerinck, F.; Plaetinck, G.; Devos,R.; Fiers, W.: Cloning and structure of the human interleukin 2 chromosomalgene. EMBO J. 2: 2349- 2353, 1983. 3 B c

GAM94 332 IL2 Depper, J. M.; Leonard, W. J.; Drogula, C.; Kronke, M.; Waldmann,T. A.; Greene, W. C.: Interleukin 2 (IL- 2) augments transcriptionof the IL- 2 receptor gene. Proc. Nat. Acad. Sci. 82: 4230- 4234,1985. 3 B c

GAM94 332 IL2 Fiorentino, L.; Austen, D.; Pravtcheva, D.; Ruddle, F. H.; Brownell,E.: Assignment of the interleukin- 2 locus to mouse chromosome 3. Genomics 5:651- 653, 1989. 3 B c

GAM94 332 IL2 Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.: Structureof the human interleukin 2 gene. Proc. Nat. Acad. Sci. 80: 7437- 7441,1983. 3 B c

GAM94 332 IL2 Greene, W. C.; Leonard, W. J.: The human interleukin- 2 receptor. Annu.Rev. Immun. 4: 69- 95, 1986. 3 B c

GAM94 332 IL2 Holbrook, N. J.; Smith, K. A.; Fornace, A. J., Jr.; Comeau, C.M.; Wiskocil, R. L.; Crabtree, G. R.: T- cell growth factor: completenucleotide sequence and organization of the gene in normal and malignantcells. Proc. Nat. Acad. Sci. 81: 1634- 1638, 1984. 3 B c

GAM94 332 IL2 Hollander, G. A.; Zuklys, S.; Morel, C.; Mizoguchi, E.; Mobisson,K.; Simpson, S.; Terhorst, C.; Wishart, W.; Golan, D. E.; Bhan, A.K.; Burakoff, S. J.: Monoallelic expression of the interleukin- 2locus. Science 279: 2118- 2121, 1998. 3 B c

GAM94 332 IL2 Ku, C. C.; Murakami, M.; Sakamoto, A.; Kappler, J.; Marrack, P.: Control of homeostasis of CD8+ memory T cells by opposing cytokines. Science 288:675- 678, 2000. 3 B c

GAM94 332 IL2 Leonard, W. J.; Donlon, T. A.; Lebo, R. V.; Greene, W. C.: Localizationof the gene encoding the human interleukin- 2 receptor on chromosome10. Science 228: 1547- 1549, 1985. 3 B c

GAM94 332 IL2 Lowenthal, J. W.; Zubler, R. H.; Nabholz, M.; MacDonald, H. R.: Similarities between interleukin- 2 receptor number and affinityon activated B and T lymphocytes. Nature 315: 669- 672, 1985. 3 B c

GAM94 332 IL2 Rosenberg, S. A.; Grimm, E. A.; McGrogan, M.; Doyle, M.; Kawasaki,E.; Koths, K.; Mark, D. F.: Biological activity of recombinant humaninterleukin- 2 produced in Escherichia coli. Science 223: 1412- 1415,1984. 3 B c

GAM94 332 IL2 Seigel, L. J.; Harper, M. E.; Wong- Staal, F.; Gallo, R. C.; Nash,W. G.; O'Brien, S. J.: Gene for T- cell growth factor: location onhuman chromosome 4q and feline chromosome B1. Science 223: 175- 178,1984. 3 B c

GAM94 332 IL2 Shows, T.; Eddy, R.; Haley, L.; Byers, M.; Henry, M.; Fujita,T.; Matsui, H.; 3 B c

Taniguchi, T.: Interleukin 2 (IL2) is assigned tohuman chromosome 4. Somat. Cell Molec. Genet. 10: 315- 318, 1984.

GAM94 332 IL2 Smith, K. A.: Interleukin- 2: inception, impact, and implications. Science 3 B c 240:1169- 1176, 1988.

GAM94 332 IL2 Smith, K. A.; Cantrell, D. A.: Interleukin 2 regulates its ownreceptors. 3 B c Proc. Nat. Acad. Sci. 82: 864- 868, 1985.

GAM94 332 IL2 Stern, A. S.; Pan, Y.- C. E.; Urdal, D. L.; Mochizuki, D. Y.; DeChiara,S.; 3 B c Blacher, R.; Wideman, J.; Gillis, S.: Purification to homogeneityand partial characterization of interleukin 2 from a human T- cellleukemia. Proc. Nat. Acad. Sci. 81: 871- 875, 1984.

GAM94 332 IL2 Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.;Yoshimoto, 3 B c R.; Hamuro, J.: Structure and expression of a cloned cDNAfor human interleukin- 2. Nature 302: 305- 310, 1983.

GAM94 332 IL2 Webb, G. C.; Campbell, H. D.; Lee, J. S.; Young, I. G.: Mappingthe gene for 3 B c murine T- cell growth factor, Il- 2, to bands B- C on chromosome3 and for the alpha chain of the IL2- receptor, Il- 2ra, to bands A2- A3on chromosome 2. Cytogenet. Cell Genet. 54: 164- 168, 1990.

GAM94 332 IL2 Weinberg, K.; Parkman, R.: Severe combined immunodeficiency dueto a specific 3 B c defect in the production of interleukin- 2. New Eng.J. Med. 322: 1718- 1723, 1990.

GAM94 332 IL2 Yang, J.; Patil, R. V.; Yu, H.; Gordon, M.; Wax, M. B.: T cellsubsets and 3 B c sIL- 2R/IL- 2 levels in patients with glaucoma. Am. J.Ophthal. 131: 421- 426, 2001.

GAM94 332 IL6R Kluck, P. M. C.; Wiegant, J.; Jansen, R. P. M.; Bolk, M. W. J.;Raap, A. K.; 3 B c Willemze, R.; Landegent, J. E.: The human interleukin- 6receptor alpha- chain gene is localized on chromosome 1 band q21. Hum.Genet. 90: 542- 544, 1993.

GAM94 332 IL6R Szpirer, J.; Szpirer, C.; Riviere, M.; Houart, C.; Baumann, M.;Fey, G. H.; 3 B c Poli, V.; Cortese, R.; Islam, M. Q.; Levan, G.: The interleukin- 6- dependentDNA- binding protein gene (transcription factor 5: TCF5) maps to humanchromosome 20 and rat chromosome 3, the IL6 receptor locus (IL6R)to human chromosome 1 and rat chromosome 2, and the rat IL6 gene torat chromosome 4. Genomics 10: 539- 546, 1991.

GAM94 332 IL6R Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.;Seed, B.; 3 B c Taniguchi, T.; Hirano, T.; Kishimoto, T.: Cloning and expressionof the human interleukin- 6 (BSF- 2/IFN- beta- 2) receptor. Science 241:825- 828, 1988.

GAM94 332 JAK2 Campbell, G. S.; Argetsinger, L. S.; Ihle, J. N.; Kelly, P. A.;Rillema, J. 3 B c A.; Carter- Su, C.: Activation of JAK2 tyrosine kinaseby prolactin receptors in Nb2 cells and mouse mammary gland explants. Proc.Nat. Acad. Sci. 91: 5232- 5236, 1994.

GAM94 332 JAK2 Digicaylioglu, M.; Lipton, S. A.: Erythropoietin- mediated 3 B c neuroprotectioninvolves cross- talk between Jak2 and NF- kappa- B signalling cascades. Nature 412:641- 647, 2001.

GAM94 332 JAK2 Gough, N. M.; Rakar, S.; Harpur, A.; Wilks, A. F.: Localizationof genes for 3 B c two members of the JAK family of protein tyrosine kinasesto murine chromosomes 4 and 19. Mammalian Genome 6: 247- 248, 1995.

GAM94 332 JAK2 Huang, L. J.; Constantinescu, S. N.; Lodish, H. F.: The N- terminaldomain of 3 B c Janus kinase 2 is required for Golgi processing and cellsurface expression of erythropoietin receptor. Molec. Cell 8: 1327- 1338,2001.

GAM94 332 JAK2 Neubauer, H.; Cumano, A.; Muller, M.; Wu, H.; Huffstadt, U.; Pfeffer,K.: 3 B c

Jak2 deficiency defines an essential developmental checkpointin definitive hematopoiesis. Cell 93: 397- 409, 1998.

GAM94 332 JAK2 Parganas, E.; Wang, D.; Stravopodis, D.; Topham, D. J.; Marine,J.- C.; 3 B c
Teglund, S.; Vanin, E. F.; Bodner, S.; Colamonici, O. R.; vanDeursen, J. M.;
Grosveld, G.; Ihle, J. N.: Jak2 is essential forsignaling through a variety
of cytokine receptors. Cell 93: 385- 395,1998.

GAM94 332 JAK2 Pritchard, M. A.; Baker, E.; Callen, D. F.; Sutherland, G. R.;Wilks, A. F.: 3 B c
Two members of the JAK family of protein tyrosine kinasesmap to chromosomes
1p31.3 and 9p24. Mammalian Genome 3: 36- 38, 1992.

GAM94 332 JAK2 Saltzman, A.; Stone, M.; Franks, C.; Searfoss, G.; Munro, R.; Jaye,M.; 3 B c
Ivashchenko, Y.: Cloning and characterization of human Jak- 2kinase: high
mRNA expression in immune cells and muscle tissue. Biochem.Biophys. Res.
Commun. 246: 627- 633, 1998.

GAM94 332 JAK2 Schwaller, J.; Parganas, E.; Wang, D.; Cain, D.; Aster, J. C.;Williams, I. 3 B c
R.; Lee, C.- K.; Gerthner, R.; Kitamura, T.; Frantsve,J.; Anastasiadou, E.;
Loh, M. L.; Levy, D. E.; Ihle, J. N.; Gilliland,D. G.: Stat5 is essential
for the myelo- and lymphoproliferativedisease induced by TEL/JAK2. Molec.
Cell 6: 693- 704, 2000.

GAM94 332 JAK2 Watling, D.; Guschin, D.; Muller, M.; Silvennoinen, O.; Witthuhn,B. A.; 3 B c
Quelle, F. W.; Rogers, N. C.; Schindler, C.; Stark, G. R.;Ihle, J. N.; Kerr,
I. M.: Complementation by the protein tyrosinekinase JAK2 of a mutant cell
line defective in the interferon- gammasignal transduction pathway. Nature
366: 166- 170, 1993.

GAM94 332 KCNA4 Gessler, M.; Grupe, A.; Grzeschik, K.- H.; Pongs, O.: The potassiumchannel 3 B c
gene HK1 maps to human chromosome 11p14.1, close to the FSHBgene. Hum.
Genet. 90: 319- 321, 1992.

GAM94 332 KCNA4 Grandy, D.; Mathew, M. K.; Ramaswami, M.; Tanouye, M.; Sheffield,V.; Jones, 3 B c
C. A.; Al- Dhalimi, M.; Zhang, Y.; Saez, C.; Litt, M.:A human voltage- gated
potassium channel gene, HuKII, maps to chromosome11p14- p13. (Abstract) Am.
J. Hum. Genet. 51 (suppl.): A396 only,1992.

GAM94 332 KCNA4 Klocke, R.; Roberds, S. L.; Tamkun, M. M.; Gronemeier, M.; Augustin,A.; 3 B c
Albrecht, B.; Pongs, O.; Jockusch, H.: Chromosomal mapping inthe mouse of
eight K(+)- channel genes representing the four Shaker- likesubfamilies
Shaker, Shab, Shaw, and Shal. Genomics 18: 568- 574,1993.

GAM94 332 KCNA4 Philipson, L. H.; Eddy, R. L.; Shows, T. B.; Bell, G. I.: Assignmentof human 3 B c
potassium channel gene KCNA4 (Kv1.4, PCN2) to chromosome11q13.4- q14.1.
Genomics 15: 463- 464, 1993.

GAM94 332 KCNA4 Philipson, L. H.; Hice, R. E.; Schaefer, K.; LaMendola, J.; Bell,G. I.; 3 B c
Neldon, D. J.; Steiner, D. F.: Sequence and functional expressionin Xenopus
oocytes of a human insulinoma and islet potassium channel. Proc.Nat. Acad.
Sci. 88: 53- 57, 1991.

GAM94 332 KCNA4 Philipson, L. H.; Schaefer, K.; LaMendola, J.; Bell, G. I.; Steiner,D. F.: 3 B c
Sequence of a human fetal skeletal muscle potassium channelcDNA related to
RCK4. Nucleic Acids Res. 18: 7160 only, 1990.

GAM94 332 KCNA4 Stuehmer, W.; Ruppersberg, J. P.; Schroter, K. H.; Sakmann, B.;Stocker, M.; 3 B c
Giese, K. P.; Perschke, A.; Baumann, A.; Pongs, O.:Molecular basis of
functional diversity of voltage- gated potassiumchannels in mammalian brain.
EMBO J. 8: 3235- 3244, 1989.

GAM94 332 KCNA4 Tamkun, M. M.; Knoth, K. M.; Walbridge, J. A.; Kroemer, H.; Roden,D. M.; 3 B c
Glover, D. M.: Molecular cloning and characterization of twovoltage- gated

K+ channel cDNAs from human ventricle. FASEB J. 5:331- 337, 1991.

GAM94 332 KCNK6 Chavez, R. A.; Gray, A. T.; Zhao, B. B.; Kindler, C. H.; Mazurek,M. J.; 3 B c
Mehta, Y.; Forsayeth, J. R.; Yost, C. S.: TWIK- 2, a new weakinward
rectifying member of the tandem pore domain potassium channelfamily. J.
Biol. Chem. 274: 7887- 7892, 1999.

GAM94 332 KCNK6 Gray, A. T.; Kindler, C. H.; Sampson, E. R.; Yost, C. S.: Assignmentof KCNK6 3 B c
encoding the human weak inward rectifier potassium channelTWIK- 2 to
chromosome band 19q13.1 by radiation hybrid mapping. Cytogenet.Cell Genet.
84: 190- 191, 1999.

GAM94 332 KCNK6 Pountney, D. J.; Gulkarov, I.; Vega- Saenz de Miera, E.; Holmes,D.; 3 B c
Saganich, M.; Rudy, B.; Artman, M.; Coetzee, W. A.: Identificationand
cloning of TWIK- originated similarity sequence (TOSS): a novelhuman 2- pore
K(+) channel principal subunit. FEBS Lett. 450: 191- 196,1999.

GAM94 332 KCNK6 Salinas, M.; Reyes, R.; Lesage, F.; Fosset, M.; Heurteaux, C.;Romey, G.; 3 B c
Lazdunski, M.: Cloning of a new mouse two- P domain channelsubunit and a
human homologue with a unique pore structure. J. Biol.Chem. 274: 11751-
11760, 1999.

GAM94 332 KCNMB3 Behrens, R.; Nolting, A.; Reimann, F.; Schwarz, M.; Waldschutz,R.; Pongs, 3 B c
O.: hKCNMB3 and hKCNMB4, cloning and characterizationof two members of the
large- conductance calcium- activated potassiumchannel beta subunit family.
FEBS Lett. 474: 99- 106, 2000.

GAM94 332 KCNMB3 Brenner, R.; Jegla, T. J.; Wickenden, A.; Liu, Y.; Aldrich, R.W.: Cloning 3 B c
and functional characterization of novel large conductancecalcium- activated
potassium channel beta subunits, hKCNMB3 and hKCNMB4. J.Biol. Chem. 275:
6453- 6461, 2000.

GAM94 332 KCNMB3 Riazi, M. A.; Brinkman- Mills, P.; Johnson, A.; Naylor, S. L.; Minoshima,S.; 3 B c
Shimizu, N.; Baldini, A.; McDermid, H. E.: Identification ofa putative
regulatory subunit of a calcium- activated potassium channelin the dup(3q)
syndrome region and a related sequence on 22q11.2. Genomics 62:90- 94, 1999.

GAM94 332 KCNMB3 Uebele, V. N.; Lagrutta, A.; Wade, T.; Figueroa, D. J.; Liu, Y.;McKenna, E.; 3 B c
Austin, C. P.; Bennett, P. B.; Swanson, R.: Cloningand functional expression
of two families of beta- subunits of thelarge conductance calcium- activated
K(+) channel. J. Biol. Chem. 275:23211- 23218, 2000.

GAM94 332 KCNN3 Austin, C. P.; Holder, D. J.; Ma, L.; Mixson, L. A.; Caskey, C.T.: Mapping 3 B c
of hKCa3 to chromosome 1q21 and investigation of linkageof CAG repeat
polymorphism to schizophrenia. Molec. Psychiat. 4:261- 266, 1999.

GAM94 332 KCNN3 Bond, C. T.; Sprengel, R.; Bissonnette, J. M.; Kaufmann, W. A.;Pribnow, D.; 3 B c
Neelands, T.; Storck, T.; Baetscher, M.; Jerecic, J.;Maylie, J.; Knaus, H.-
G.; Seeburg, P. H.; Adelman, J. P.: Respirationand parturition affected by
conditional overexpression of the Ca(2+)- activatedK(+) channel subunit,
SK3. Science 289: 1942- 1946, 2000.

GAM94 332 KCNN3 Chandy, K. G.; Fantino, E.; Wittekindt, O.; Kalman, K.; Tong, L.- L.;Ho, T.- 3 B c
H.; Gutman, G. A.; Crocq, M.- A.; Ganguli, R.; Nimgaonkar, V.;Morris-
Rosendahl, D. J.; Gargus, J. J.: Isolation of a novel potassiumchannel gene
hSKCa3 containing a polymorphic CAG repeat: a candidatefor schizophrenia and
bipolar disorder? Molec. Psychiat. 3: 32- 37,1998.

GAM94 332 KCNN3 Frebourg, T.; Bonnet- Brilhault, F.; Laurent, C.; Campion, D.; Thibaut,F.; 3 B c
Deleuze, J. F.; Petit, M.; Mallet, J.: No evidence for the involvementof the
hSKCa3 potassium channel gene in familial and sporadic casesof
schizophrenia. (Abstract) Am. J. Hum. Genet. (suppl.) 63: A326only, 1998.

GAM94 332 KCNN3 Kohler, M.; Hirschberg, B.; Bond, C. T.; Kinzie, J. M.; Marrion,N. V.; 3 B c
Maylie, J.; Adelman, J. P.: Small- conductance, calcium- activatedpotassium
channels from mammalian brain. Science 273: 1709- 1714,1996.

GAM94 332 KCNN3 Navon, R.; Shamir, E.; Dror, V.; Ghanshani, S.; Litmanovitch, T.;Kimchi, R.; 3 B c
Swartz, M.; Barak, Y.; Fantino, E.; Kalman, K.; Jones,E. G.; Avivi, L.;
Chandy, K. G.; Gargus, J. J.; Gutman, G. A.: Strongassociation between
schizophrenia and long CAG repeats in the hKCa3/KCNN3gene, mapped to 1q21,
among Israeli Jews. (Abstract) Am. J. Hum.Genet. 63 (suppl.): A337 only,
1998.

GAM94 332 KCNN3 Sun, G.; Tomita, H.; Shakkottai, V. G.; Gargus, J. J.: Genomicorganization 3 B c
and promoter analysis of human KCNN3 gene. J. Hum. Genet. 46:463- 470, 2001.

GAM94 332 KCNN3 Wittekindt, O.; Jauch, A.; Burgert, E.; Scharer, L.; Holtgreve- Grez,H.; 3 B c
Yvert, G.; Imbert, G.; Zimmer, J.; Hoehe, M. R.; Macher, J.- P.;Chiaroni,
P.; van Calker, D.; Crocq, M.- A.; Morris- Rosendahl, D. J.: The human small
conductance calcium- regulated potassium channelgene (hSKCa3) contains two
CAG repeats in exon 1, is on chromosome1q21.3, and shows a possible
association with schizophrenia. Neurogenetics 1:259- 265, 1998.

GAM94 332 KCNS2 Banfi, S.; Borsani, G.; Rossi, E.; Bernard, L.; Guffanti, A.; Rubboli,F.; 3 B c
Marchitiello, A.; Giglio, S.; Coluccia, E.; Zollo, M.; Zuffardi,O.;
Ballabio, A.: Identification and mapping of human cDNAs homologousto
Drosophila mutant genes through EST database searching. NatureGenet. 13:
167- 174, 1996.

GAM94 332 KCNS2 Salinas, M.; Duprat, F.; Heurteaux, C.; Hugnot, J.- P.; Lazdunski,M.: New 3 B c
modulatory alpha subunits for mammalian Shab K(+) channels. J.Biol. Chem.
272: 24371- 24379, 1997.

GAM94 332 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; 3 B c
Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.;
Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2
purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363-
18367,1996.

GAM94 332 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof 3 B c
leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature
372: 179- 182, 1994.

GAM94 332 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; 3 B c
Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol.
Nature 384: 39- 43, 1996.

GAM94 332 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 3 B c
specifictranscriptional regulation of human leukotriene B4 receptor gene.
J.Exp. Med. 192: 413- 420, 2000.

GAM94 332 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 3 B c
chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM94 332 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 3 B c
Leukotrienes and lipoxins: structures, biosynthesis,and biological effects.
Science 237: 1171- 1176, 1987.

GAM94 332 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 B c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene
and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-
130, 1997.

GAM94 332 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 3 B c
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature

387:620- 624, 1997.

GAM94 332 MAGEA8 De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J. J.; Szikora,J.- P.; De Smet, C.; Brasseur, F.; van der Bruggen, P.; Lethe, B.;Lurquin, C.; Brasseur, R.; Chomez, P.; De Backer, O.; Cavenee, W.;Boon, T.: Structure, chromosomal localization, and expression of12 genes of the MAGE family. Immunogenetics 40: 360- 369, 1994. 3 B c

GAM94 332 MAGEA8 De Plaen, E.; De Backer, O.; Arnaud, D.; Bonjean, B.; Chomez, P.;Martelange, V.; Avner, P.; Baldacci, P.; Babinet, C.; Hwang, S.- Y.;Knowles, B.; Boon, T.: A new family of mouse genes homologous tothe human MAGE genes. Genomics 55: 176- 184, 1999. 3 B c

GAM94 332 MAGEA8 Rogner, U. C.; Wilke, K.; Steck, E.; Korn, B.; Poustka, A.: Themelanoma antigen gene (MAGE) family is clustered in the chromosomalband Xq28. Genomics 29: 725- 731, 1995. 3 B c

GAM94 332 MAP1B Edelmann, W.; Zervas, M.; Costello, P.; Roback. L.; Fischer, I.;Hammarback, J. A.; Cowan, N.; Davies, P.; Wainer, B.; Kucherlapati,R.: Neuronal abnormalities in microtubule- associated protein 1B mutantmice. Proc. Nat. Acad. Sci. 93: 1270- 1275, 1996. 3 B c

GAM94 332 MAP1B Hammarback, J. A.; Obar, R. A.; Hughes, S. M.; Vallee, R. B.:MAP1B is encoded as a polyprotein that is processed to form a complexN- terminal microtubule- binding domain. Neuron 7: 129- 139, 1991. 3 B c

GAM94 332 MAP1B Lien, L. L.; Boyce, F. M.; Kleyn, P.; Brzustowicz, L. M.; Menninger,J.; Ward, D. C.; Gilliam, T. C.; Kunkel, L. M.: Mapping of humanmicrotubule-associated protein 1B in proximity to the spinal muscularatrophy locus at 5q13. Proc. Nat. Acad. Sci. 88: 7873- 7876, 1991. 3 B c

GAM94 332 MAP1B Lien, L. L.; Feener, C. A.; Fischbach, N.; Kunkel, L. M.: Cloningof human microtubule- associated protein 1B and the identificationof a related gene on chromosome 15. Genomics 22: 273- 280, 1994. 3 B c

GAM94 332 MAP1B Wirth, B.; Voosen, B.; Rohrig, D.; Knapp, M.; Piechaczek, B.; Rudnik-Schoneborn,S.; Zerres, K.: Fine mapping and narrowing of the genetic intervalof the spinal muscular atrophy region by linkage studies. Genomics 15:113- 118, 1993. 3 B c

GAM94 332 MAP1B Zhang, Y. Q.; Bailey, A. M.; Matthies, H. J. G.; Renden, R. B.;Smith, M. A.; Speese, S. D.; Rubin, G. M.; Broadie, K.: Drosophilafragile X- related gene regulates the MAP1B homolog Futsch to controlsynaptic structure and function. Cell 107: 591- 603, 2001. 3 B c

GAM94 332 MEF2C Breitbart, R. E.; Liang, C.; Smoot, L. B.; Laheru, D. A.; Mahdavi,V.; Nadal-Ginard, B.: A fourth human MEF2 transcription factor, hMEF2D,is an early marker of the myogenic lineage. Development 118: 1095- 1106,1993. 3 B c

GAM94 332 MEF2C Chen, S. L.; Dowhan, D. H.; Hosking, B. M.; Muscat, G. E. O.:The steroid receptor coactivator, GRIP- 1, is necessary for MEF- 2C- dependentgene expression and skeletal muscle differentiation. Genes Dev. 14:1209- 1228, 2000. 3 B c

GAM94 332 MEF2C Krainc, D.; Haas, M.; Ward, D. C.; Lipton, S. A.; Bruns, G.; Leifer,D.: Assignment of human myocyte- specific enhancer binding factor2C (hMEF2C) to human chromosome 5q14 and evidence that MEF2C is evolutionarilyconserved. Genomics 29: 809- 811, 1995. 3 B c

GAM94 332 MEF2C Leifer, D.; Krainc, D.; Yu, Y.- T.; McDermott, J.; Breitbart, R.E.; Heng, J.; Neve, R. L.; Kosofsky, B.; Nadal- Ginard, B.; Lipton,S. A.: MEF2C, a MADS/MEF2- family transcription factor expressed ina laminar distribution in cerebral cortex. Proc. Nat. Acad. Sci. 90:1546- 1550, 1993. 3 B c

GAM94 332 MEF2C Lin, Q.; Schwarz, J.; Bucana, C.; Olson, E. N.: Control of mousecardiac morphogenesis and myogenesis by transcription factor MEF2C. Science 276:1404- 1407, 1997. 3 B c

GAM94 332 MEF2C Mao, Z.; Bonni, A.; Xia, F.; Nadal- Vicans, M.; Greenberg, M. E.: Neuronal activity- dependent cell survival mediated by transcriptionfactor MEF2. Science 286: 785- 790, 1999. 3 B c

GAM94 332 MEF2C Martin, J. F.; Miano, J. M.; Hustad, C. M.; Copeland, N. G.; Jenkins,N. A.; Olson, E. N.: A Mef2 gene that generates a muscle- specificisoform via alternative mRNA splicing. Molec. Cell. Biol. 14: 1647- 1656,1994. 3 B c

GAM94 332 MEF2C McDermott, J. C.; Cardoso, M. C.; Yu, Y.- T.; Andres, V.; Leifer,D.; Krainc, D.; Lipton, S. A.; Nadal- Ginard, B.: hMEF2C gene encodesskeletal muscle- and brain- specific transcription factors. Molec.Cell. Biol. 13: 2564- 2577, 1993. 3 B c

GAM94 332 MEIS2 Capdevila, J.; Tsukui, T.; Esteban, C. R.; Zappavigna, V.; Belmonte,J. C. I.: Control of vertebrate limb outgrowth by the proximal factorMeis2 and distal antagonism of BMPs by Gremlin. Molec. Cell 4: 839- 849,1999. 3 B c

GAM94 332 MEIS2 Mercader, N.; Leonardo, E.; Azpiazu, N.; Serrano, A.; Morata, G.;Martinez- A, C.; Torres, M.: Conserved regulation of proximodistallimb axis development by Meis1/Hth. Nature 402: 425- 429, 1999. 3 B c

GAM94 332 MEIS2 Nakamura, T.; Jenkins, N. A.; Copeland, N. G.: Identificationof a new family of Pbx- related homeobox genes. Oncogene 13: 2235- 2242,1996. 3 B c

GAM94 332 MEIS2 Smith, J. E., Jr.; Bollekens, J. A.; Inghirami, G.; Takeshita,K.: Cloning and mapping of the MEIS1 gene, the human homolog of amurine leukemogenic gene. Genomics 43: 99- 103, 1997. 3 B c

GAM94 332 MEIS2 Smith, J. E.; Afonja, O.; Yee, H. T.; Inghirami, G.; Takeshita,K.: Chromosomal mapping to 15q14 and expression analysis of the humanMEIS2 homeobox gene. Mammalian Genome 8: 951- 952, 1997. 3 B c

GAM94 332 MEIS2 Steelman, S.; Moskow, J. J.; Muzynski, K.; North, C.; Druck, T.;Montgomery, J. C.; Huebner, K.; Daar, I. O.; Buchberg, A. M.: Identificationof a conserved family of Meis1- related homeobox genes. Genome Res. 7:142- 156, 1997. 3 B c

GAM94 332 MSF Bahabri, S. A.; Suwairi, W. M.; Laxer, R. M.; Polinkovsky, A.;Dalaan, A. A.; Warman, M. L.: The camptodactyly- arthropathy- coxavara- pericarditis syndrome: clinical features and genetic mappingto human chromosome 1. Arthritis Rheum. 41: 730- 735, 1998. 3 B c

GAM94 332 MSF Flannery, C. R.; Hughes, C. E.; Schumacher, B. L.; Tudor, D.; Aydelotte,M. B.; Kuettner, K. E.; Caterson, B.: Articular cartilage superficialzone protein (SZP) is homologous to megakaryocyte stimulating factorprecursor and is a multifunctional proteoglycan with potential growth- promoting,cytoprotective, and lubricating properties in cartilage metabolism. Biochem.Biophys. Res. Commun. 254: 535- 541, 1999. 3 B c

GAM94 332 MSF Ikegawa, S.; Sano, M.; Koshizuka, Y.; Nakamura, Y.: Isolation,characterization and mapping of the mouse and human PRG4 (proteoglycan4) genes. Cytogenet. Cell Genet. 90: 291- 297, 2000. 3 B c

GAM94 332 MSF Marcelino, J.; Carpten, J. D.; Suwairi, W. M.; Gutierrez, O. M.;Schwartz, S.; Robbins, C.; Sood, R.; Makalowska, I.; Baxevanis, A.;Johnstone, B.; Laxer, R. M.; Zemel, L.; and 13 others: CACP, encodinga secreted proteoglycan, is mutated in camptodactyly- arthropathy- coxavara- pericarditis syndrome. Nature Genet. 23: 319- 322, 1999. 3 B c

GAM94 332 MSF McIlhatton, M. A.; Burrows, J. F.; Donaghy, P. G.; Chanduloy, S.;Johnston, 3 B c

P. G.; Russell, S. E. H.: Genomic organization, complexsplicing pattern and expression of a human septin gene on chromosome17q25.3. Oncogene 20: 5930-5939, 2001.

GAM94 332 MSF Merberg, D. M.; Fitz, L. J.; Temple, P.; Giannotti, J.; Murtha,P.; 3 B c
Fitzgerald, M.; Scaltreto, H.; Kelleher, K.; Preissner, K.; Kriz,R.; Jacobs, K.; Turner, K.: In: Preissner, K. T.; Rosenblatt, S.;Kost, C.; Wegerhoff, J.; Mosher, D. F. (eds.): Biology of Vitronectinsand Their Receptors. Elsevier Science, B.V. 1993. Pp. 45- 53.

GAM94 332 MSF Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999.

GAM94 332 MSF Osaka, M.; Rowley, J. D.; Zeleznik- Le, N. J.: MSF (MLL septin- likefusion), 3 B c
a fusion partner gene of MLL, in a therapy- related acutemyeloid leukemia with a t(11;17)(q23;q25). Proc. Nat. Acad. Sci. 96:6428- 6433, 1999.

GAM94 332 MSF Russell, S. E. H.; McIlhatton, M. A.; Burrows, J. F.; Donaghy,P. G.; 3 B c
Chanduloy, S.; Petty, E. M.; Kalikin, L. M.; Church, S. W.;McIlroy, S.; Harkin, D. P.; Keilty, G. W.; Cranston, A. N.; Weissenbach,J.; Hickey, I.; Johnston, P. G.: Isolation and mapping of a humanseptin gene to a region on chromosome 17q, commonly deleted in sporadicepithelial ovarian tumors. Cancer Res. 60: 4729- 4734, 2000.

GAM94 332 MSF Schumacher, B. L.; Block, J. A.; Schmid, T. M.; Aydelotte, M. B.;Kuettner, 3 B c
K. E.: A novel proteoglycan synthesized and secreted bychondrocytes of the superficial zone of articular cartilage. Arch.Biochem. Biophys. 15: 144-152, 1994.

GAM94 332 MXI1 Albarosa, R.; DiDonato, S.; Finocchiaro, G.: Redefinition of thecoding 3 B c
sequence of the MXI1 gene and identification of a polymorphicrepeat in the 3- prime non- coding region that allows the detectionof loss of heterozygosity of chromosome 10q25 in glioblastomas. Hum.Genet. 95: 709-711, 1995.

GAM94 332 MXI1 Eagle, L. R.; Yin, X.; Brothman, A. R.; Williams, B. J.; Atkin,N. B.; 3 B c
Prochownik, E. V.: Mutation of the MXI1 gene in prostate cancer. NatureGenet. 9: 249- 255, 1995.

GAM94 332 MXI1 Edelhoff, S.; Ayer, D. E.; Zervos, A. S.; Steingrimsson, E.; Jenkins,N. A.; 3 B c
Copeland, N. G.; Eisenman, R. N.; Brent, R.; Disteche, C. M.: Mapping of two genes encoding members of a distinct subfamily ofMAX interacting proteins: MAD to human chromosome 2 and mouse chromosome6, and MXI1 to chromosome 10 and mouse chromosome 19. Oncogene 9:665- 668, 1994.

GAM94 332 MXI1 Li, X.- J.; Wang, D.- Y.; Zhu, Y.; Guo, R.- J.; Wang, X.- D.; Lubomir,K.; 3 B c
Mukai, K.; Sasaki, H.; Yoshida, H.; Oka, T.; Machinami, R.; Shinmura,K.; Tanaka, M.; Sugimura, H.: Mxi1 mutations in human neurofibrosarcomas. Jpn.J. Cancer Res. 90: 740- 746, 1999.

GAM94 332 MXI1 Prochownik, E. V.; Grove, L. E.; Deubler, D.; Zhu, X. L.; Stephenson,R. A.; 3 B c
Rohr, L. R.; Yin, X.; Brothman, A. R.: Commonly occurringloss and mutation of the MXI1 gene in prostate cancer. Genes ChromosomesCancer 22: 295- 304, 1998.

GAM94 332 MXI1 Schreiber- Agus, N.; Meng, Y.; Hoang, T.; Hou, H., Jr.; Chen, K.;Greenberg, 3 B c
R.; Cordon- Cardo, C.; Lee, H.- W.; DePinho, R. A.: Roleof Mxi1 in ageing organ systems and the regulation of normal and neoplasticgrowth. Nature 393:

483- 487, 1998.

GAM94 332 MXI1 Shapiro, D. N.; Valentine, V.; Eagle, L.; Yin, X.; Morris, S. W.;Prochownik, 3 B c
E. V.: Assignment of the human MAD and MXI1 genes tochromosomes 2p12- p13
and 10q24- q25. Genomics 23: 282- 285, 1994.

GAM94 332 MXI1 Steingrimsson, E.; Sawadogo, M.; Gilbert, D. J.; Zervos, A. S.;Brent, R.; 3 B c
Blanar, M. A.; Fisher, D. E.; Copeland, N. G.; Jenkins,N. A.: Murine
chromosomal location of five bHLH- Zip transcriptionfactor genes. Genomics
28: 179- 183, 1995.

GAM94 332 MXI1 Wechsler, D. S.; Hawkins, A. L.; Li, X.; Jabs, E. W.; Griffin,C. A.; Dang, 3 B c
C. V.: Localization of the human Mxi1 transcriptionfactor gene (MXI1) to
chromosome 10q24- q25. Genomics 21: 669- 672,1994.

GAM94 332 MXI1 Wechsler, D. S.; Shelly, C. A.; Dang, C. V.: Genomic organizationof human 3 B c
MXI1, a putative tumor suppressor gene. Genomics 32: 466- 470,1996.

GAM94 332 MXI1 Zervos, A. S.; Gyuris, J.; Brent, R.: Mxi1, a protein that 3 B c
specificallyinteracts with Max to bind Myc- Max recognition sites. Cell 72:
223- 232,1993. Note: Erratum: Cell 79: 389 only, 1994.

GAM94 332 MYLK Garcia, J. G.; Lazar, V.; Gilbert- McClain, L. I.; Gallagher, P.J.; Verin, 3 B c
A. D.: Myosin light chain kinase in endothelium: molecularcloning and
regulation. Am. J. Resp. Cell Molec. Biol. 16: 489- 494,1997.

GAM94 332 MYLK Giorgi, D.; Brand- Arpon, V.; Rouquier, S.: The functional myosinlight chain 3 B c
kinase (MYLK) gene localizes with marker D3S3552 on humanchromosome 3q21 in
a greater than 5- Mb yeast artificial chromosomeregion and is not linked to
olfactory receptor genes. Cytogenet.Cell Genet. 92: 85- 88, 2001.

GAM94 332 MYLK Lazar, V.; Garcia, J. G. N.: A single human myosin light chainkinase gene 3 B c
(MLCK; MYLK) transcribes multiple nonmuscle isoforms. Genomics 57:256- 267,
1999.

GAM94 332 MYLK Potier, M.- C.; Chelot, E.; Pekarsky, Y.; Gardiner, K.; Rossier,J.; Turnell, 3 B c
W. G.: The human myosin light chain kinase (MLCK) fromhippocampus: cloning,
sequencing, expression, and localization to3cen- q21. Genomics 29: 562- 570,
1995.

GAM94 332 MYLK Walker, L. A.; MacDonald, J. A.; Liu, X.; Nakamoto, R. K.; Haystead,T. A. 3 B c
J.; Somlyo, A. V.; Somlyo, A. P.: Site- specific phosphorylationand point
mutations of telokin modulate its Ca(2+)- desensitizing effectin smooth
muscle. J. Biol. Chem. 276: 24519- 24524, 2001.

GAM94 332 MYLK Watterson, D. M.; Schavocky, J. P.; Guo, L.; Weiss, C.; Chlenski,A.; 3 B c
Shirinsky, V. P.; Van Eldik, L. J.; Haiech, J.: Analysis of thekinase-
related protein gene found at human chromosome 3q21 in a multi- genecluster:
organization, expression, alternative splicing, and polymorphicmarker. J.
Cell. Biochem. 75: 481- 491, 1999.

GAM94 332 NEFH Al- Chalabi, A.; Andersen, P. M.; Nilsson, P.; Chioza, B.; Andersson,J. L.; 3 B c
Russ, C.; Shaw, C. E.; Powell, J. F.; Leigh, P. N.: Deletionsof the heavy
neurofilament subunit tail in amyotrophic lateral sclerosis. Hum.Molec.
Genet. 8: 157- 164, 1999.

GAM94 332 NEFH Bucan, M.; Gatalica, B.; Nolan, P.; Chung, A.; Leroux, A.; Grossman,M. H.; 3 B c
Nadeau, J. H.; Emanuel, B. S.; Budarf, M.: Comparative mappingof 9 human
chromosome 22q loci in the laboratory mouse. Hum. Molec.Genet. 2: 1245-
1252, 1993.

GAM94 332 NEFH Collard, J.- F.; Cote, F.; Julien, J.- P.: Defective axonal transportin a 3 B c
transgenic mouse model of amyotrophic lateral sclerosis. Nature 375:61- 64,
1995.

GAM94 332 NEFH Figlewicz, D. A.; Krizus, A.; Martinoli, M. G.; Meininger, V.;Dib, M.; 3 B c
Rouleau, G. A.; Julien, J.- P.: Variants of the heavy neurofilamentsubunit
are associated with the development of amyotrophic lateralsclerosis. Hum.
Molec. Genet. 3: 1757- 1761, 1994.

GAM94 332 NEFH Lees, J. F.; Shneidman, P. S.; Skuntz, S. F.; Carden, M. J.; Lazzarini,R. 3 B c
A.: The structure and organization of the human heavy neurofilamentsubunit
(NF- H) and the gene encoding it. EMBO J. 7: 1947- 1955, 1988.

GAM94 332 NEFH Mattei, M.- G.; Dautigny, A.; Pham- Dinh, D.; Passage, E.; Mattei,J.- F.; 3 B c
Jolles, P.: The gene encoding the large human neurofilamentsubunit (NF- H)
maps to the q121- q131 region on human chromosome 22. Hum.Genet. 80: 293-
295, 1988.

GAM94 332 NEFH Rooke, K.; Figlewicz, D. A.; Han, F.; Rouleau, G. A.: Analysisof the KSP 3 B c
repeat of the neurofilament heavy subunit in familial amyotrophiclateral
sclerosis. Neurology 46: 789- 790, 1996.

GAM94 332 NEFH Rouleau, G. A.; Merel, P.; Lutchman, M.; Sanson, M.; Zucman, J.;Marineau, 3 B c
C.; Hoang- Xuan, K.; Demczuk, S.; Desmaze, C.; Plougastel,B.; Pulst, S. M.;
Lenoir, G.; Bijlsma, E.; Fashold, R.; Dumanski,J.; de Jong, P.; Parry, D.;
Eldrige, R.; Aurias, A.; Delattre, O.;Thomas, G.: Alteration in a new gene
encoding a putative membrane- organizingprotein causes neuro- fibromatosis
type 2. Nature 363: 515- 521, 1993.

GAM94 332 NEFH Tomkins, J.; Usher, P.; Slade, J. Y.; Ince, P. G.; Curtis, A.;Bushby, K.; 3 B c
Shaw, P. J.: Novel insertion in the KSP region of theneurofilament heavy
gene in amyotrophic lateral sclerosis. Neuroreport 9:3967- 3970, 1998.

GAM94 332 NEFH Vechio, J. D.; Bruijn, L. I.; Xu, Z.; Brown, R. H., Jr.; Cleveland,D. W.: 3 B c
Sequence variants in human neurofilament proteins: absenceof linkage to
familial amyotrophic lateral sclerosis. Ann. Neurol. 40:603- 610, 1996.

GAM94 332 NEFH Watson, C. J.; Gaunt, L.; Evans, G.; Patel, K.; Harris, R.; Strachan,T.: A 3 B c
disease- associated germline deletion maps the type 2 neurofibromatosis(NF2)
gene between the Ewing sarcoma region and the leukaemia inhibitoryfactor
locus. Hum. Molec. Genet. 2: 701- 704, 1993.

GAM94 332 NFE2 Bannerman, R. M.; Edwards, J. A.; Kreimer- Birnbaum, M.; McFarland,E.; 3 B c
Russell, E. S.: Hereditary microcytic anaemia in the mouse; studiesin iron
distribution and metabolism. Brit. J. Haemat. 23: 235- 245,1972.

GAM94 332 NFE2 Chan, J. Y.; Cheung, M.- C.; Moi, P.; Chan, K.; Kan, Y. W.: 3 B c
Chromosomallocalization of the human NF- E2 family of bZIP transcription
factorsby fluorescence in situ hybridization. Hum. Genet. 95: 265- 269,1995.

GAM94 332 NFE2 Chan, J. Y.; Han, X.- L.; Kan, Y. W.: Isolation of cDNA encodingthe human 3 B c
NF- E2 protein. Proc. Nat. Acad. Sci. 90: 11366- 11370,1993.

GAM94 332 NFE2 Peters, L. L.; Andrews, N. C.; Eicher, E. M.; Davidson, M. B.;Orkin, S. H.; 3 B c
Lux, S. E.: Mouse microcytic anaemia caused by a defectin the gene encoding
the globin enhancer- binding protein NF- E2. Nature 362:768- 770, 1993.

GAM94 332 NFE2 Peters, L. L.; Bishop, T. R.; Andrews, N. C.: Globin- enhancerbinding factor 3 B c
NF- E2 is implicated in the regulation of heme biosynthesisand iron uptake
in mk/mk mice. (Abstract) Blood 82 (suppl. 1): 179a,1993.

GAM94 332 NFE2 Shivdasani, R. A.; Orkin, S. H.: Erythropoiesis and globin geneexpression in 3 B c
mice lacking the transcription factor NF- E2. Proc.Nat. Acad. Sci. 92: 8690-
8694, 1995.

GAM94 332 NFE2 Shivdasani, R. A.; Rosenblatt, M. F.; Zucker- Franklin, D.; Jackson,C. W.; 3 B c
Hunt, P.; Saris, C. J. M.; Orkin, S. H.: Transcription factorNF- E2 is
required for platelet formation independent of the actionsof

thrombopoietin/MGDF in megakaryocyte development. Cell 81: 695- 704,1995.

GAM94 332 NFE2 Weremowicz, S.; Andrews, N. C.; Orkin, S. H.; Morton, C. C.: Mappingthe p45 3 B c
subunit of human NFE2 to 12q13. (Abstract) Human Genome MappingWorkshop 93
25, 1993.

GAM94 332 NFIB Geurts, J. M. W.; Schoenmakers, E. F. P. M.; Roijer, E.; Astrom,A.- K.; 3 B c
Stenman, G.; van de Ven, W. J. M.: Identification of NFIBas recurrent
translocation partner gene of HMGIC in pleomorphic adenomas. Oncogene
16:865- 872, 1998.

GAM94 332 NFIB Qian, F.; Kruse, U.; Lichter, P.; Sippel, A. E.: Chromosomal localizationof 3 B c
the four genes (NFIA, B, C, and X) for the human transcriptionfactor nuclear
factor I by FISH. Genomics 28: 66- 73, 1995.

GAM94 332 NOL3 Koseki, T.; Inohara, N.; Chen, S.; Nunez, G.: ARC, an inhibitorof apoptosis 3 B c
expressed in skeletal muscle and heart that interactsselectively with
caspases. Proc. Nat. Acad. Sci. 95: 5156- 5160,1998.

GAM94 332 NOL3 Li, P.- F.; Li, J.; Muller, E.- C.; Otto, A.; Dietz, R.; von Harsdorf,R.: 3 B c
Phosphorylation by protein kinase CK2: a signaling switch forthe caspase-
inhibiting protein ARC. Molec. Cell 10: 247- 258, 2002.

GAM94 332 NOL3 Stoss, O.; Schwaiger, F.- W.; Cooper, T. A.; Stamm, S.: Alternativesplicing 3 B c
determines the intracellular localization of the novel nuclearprotein Nop30
and its interaction with the splicing factor SRp30c. J.Biol. Chem. 274:
10951- 10962, 1999.

GAM94 332 NR1H2 Janowski, B. A.; Grogan, M. J.; Jones, S. A.; Wisely, G. B.; Kliewer,S. A.; 3 B c
Corey, E. J.; Mangelsdorf, D. J.: Structural requirementsof ligands for the
oxysterol liver X receptors LXR- alpha and LXR- beta. Proc.Nat. Acad. Sci.
96: 266- 271, 1999.

GAM94 332 NR1H2 Le Beau, M. M.; Song, C.; Davis, E. M.; Hiipakka, R. A.; Kokontis,J. M.; 3 B c
Liao, S.: Assignment of the human ubiquitous receptor gene(UNR) to 19q13.3
using fluorescence in situ hybridization. Genomics 26:166- 168, 1995.

GAM94 332 NR1H2 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, 3 B c
J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid
synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000.

GAM94 332 NR1H2 Repa, J. J.; Berge, K. E.; Pomajzl, C.; Richardson, J. A.; Hobbs,H.; 3 B c
Mangelsdorf, D. J.: Regulation of ATP- binding cassette steroltransporters
ABCG5 and ABCG8 by the liver X receptors alpha and beta. J.Biol. Chem. 277:
18793- 18800, 2002.

GAM94 332 NR1H2 Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, 3 B c
K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation
of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers.
Science 289: 1524- 1529, 2000.

GAM94 332 NR1H2 Shinar, D. M.; Endo, N.; Rutledge, S. J.; Vogel, R.; Rodan, G.A.; Schmidt, 3 B c
A.: NER, a new member of the gene family encoding thehuman steroid hormone
nuclear receptor. Gene 147: 273- 276, 1994.

GAM94 332 NR1H2 Song, C.; Hiipakka, R. A.; Kokontis, J. M.; Liao, S.: Ubiquitousreceptor: 3 B c
structures, immunocytochemical localization, and modulationof gene
activation by receptors for retinoic acids and thyroid hormones. Ann.N.Y.
Acad. Sci. 761: 38- 49, 1995.

GAM94 332 NR1H2 Tangirala, R. K.; Bischoff, E. D.; Joseph, S. B.; Wagner, B. L.;Walczak, R.; 3 B c
Laffitte, B. A.; Daige, C. L.; Thomas, D.; Heyman, R.A.; Mangelsdorf, D. J.;
Wang, X.; Lusis, A. J.; Tontonoz, P.; Schulman,I. G.: Identification of
macrophage liver X receptors as inhibitorsof atherosclerosis. Proc. Nat.

Acad. Sci. 99: 11896- 11901, 2002.

GAM94 332 NYX Bech- Hansen, N. T.; Naylor, M. J.; Maybaum, T. A.; Sparkes, R.L.; Koop, B.; 3 B c
Birch, D. G.; Bergen, A. A. B.; Prinsen, C. F. M.; Polomeno,R. C.; Gal, A.;
Drack, A. V.; Musarella, M. A.; Jacobson, S. G.; Young,R. S. L.; Weleber, R.
G.: Mutations in NYX, encoding the leucine- richproteoglycan nyctalopin,
cause X- linked complete congenital stationarynight blindness. Nature Genet.
26: 319- 323, 2000.

GAM94 332 NYX Pusch, C. M.; Zeitz, C.; Brandau, O.; Pesch, K.; Achatz, H.; Feil,S.; 3 B c
Scharfe, C.; Maurer, J.; Jacobi, F. K.; Pinckers, A.; Andreasson,S.;
Hardcastle, A.; Wissinger, B.; Berger, W.; Meindl, A.: The completeform of
X- linked congenital stationary night blindness is caused bymutations in a
gene encoding a leucine- rich repeat protein. NatureGenet. 26: 324- 327,
2000.

GAM94 332 OTX1 Acampora, D.; Mazan, S.; Avantaggiato, V.; Barone, P.; Tuorto,F.; Lallemand, 3 B c
Y.; Brulet, P.; Simeone, A.: Epilepsy and brain abnormalitiesin mice lacking
the Otx1 gene. Nature Genet. 14: 218- 222, 1996.

GAM94 332 OTX1 Boncinelli, E.; Gulisano, M.; Broccoli, V.: Emx and Otx homeoboxgenes in the 3 B c
developing mouse brain. J. Neurobiol. 24: 1356- 1366,1993.

GAM94 332 OTX1 Frantz, G. D.; Weimann, J. M.; Levin, M. E.; McConnell, S. K.:Otx1 and Otx2 3 B c
define layers and regions in developing cerebral cortexand cerebellum. J.
Neurosci. 14: 5725- 5740, 1994.

GAM94 332 OTX1 Kastury, K.; Druck, T.; Huebner, K.; Barletta, C.; Acampora, D.;Simeone, A.; 3 B c
Faiella, A.; Boncinelli, E.: Chromosome locations ofhuman EMX and OTX genes.
Genomics 22: 41- 45, 1994.

GAM94 332 OTX1 Simeone, A.; Acampora, D.; Gulisano, M.; Stornaiuolo, A.; Boncinelli,E.: 3 B c
Nested expression domains of four homeobox genes in developingrostral brain.
Nature 358: 687- 690, 1992.

GAM94 332 PAX2 Amiel, J.; Audollent, S.; Joly, D.; Dureau, P.; Salomon, R.; Tellier,A.- L.; 3 B c
Auge, J.; Bouissou, F.; Antignac, C.; Gubler, M.- C.; Eccles,M. R.; Munnich,
A.; Vekemans, M.; Lyonnet, S.; Attie- Bitach, T.:PAX2 mutations in renal-
coloboma syndrome: mutational hotspot andgermline mosaicism. Europ. J. Hum.
Genet. 8: 820- 826, 2000.

GAM94 332 PAX2 Dehbi, M.; Ghahremani, M.; Lechner, M.; Dressler, G.; Pelletier,J.: The 3 B c
paired- box transcription factor, PAX2, positively modulatesexpression of
the Wilms' tumor suppressor gene. Oncogene 13: 447- 453,1996.

GAM94 332 PAX2 Devriendt, K.; Matthijs, G.; Van Damme, B.; Van Caesbroeck, D.;Eccles, M.; 3 B c
Vanrenterghem, Y.; Fryns, J.- P.; Leys, A.: Missense mutationand
hexanucleotide duplication in the PAX2 gene in two unrelated familieswith
renal- coloboma syndrome (MIM 120330). Hum. Genet. 103: 149- 153,1998.

GAM94 332 PAX2 Dressler, G. R.; Deutsch, U.; Chowdhury, K.; Nornes, H. O.; Gruss,P.: Pax2, 3 B c
a new murine paired- box- containing gene and its expressionin the
developing excretory system. Development 109: 787- 795, 1990.

GAM94 332 PAX2 Favor, J.; Sandulache, R.; Neuhauser- Klaus, A.; Pretsch, W.; Chatterjee,B.; 3 B c
Senft, E.; Wurst, W.; Blanquet, V.; Grimes, P.; Sporle, R.; Schughart,K.:
The mouse Pax2(1Neu) mutation is identical to a human PAX2 mutationin a
family with renal- coloboma syndrome and results in developmentaldefects of
the brain, ear, eye, and kidney. Proc. Nat. Acad. Sci. 93:13870- 13875,
1996.

GAM94 332 PAX2 Ford, B.; Rupps, R.; Lirenman, D.; Van Allen, M. I.; Farquharson,D.; Lyons, 3 B c
C.; Friedman, J. M.: Renal- coloboma syndrome: prenataldetection and

clinical spectrum in a large family. Am. J. Med. Genet. 99:137- 141, 2001.

GAM94 332 PAX2 Keller, S. A.; Jones, J. M.; Boyle, A.; Barrow, L. L.; Killen,P. D.; Green, D. G.; Kapousta, N. V.; Hitchcock, P. F.; Swank, R.T.; Meisler, M. H.: Kidney and retinal defects (Krd), a transgene- inducedmutation with a deletion of mouse chromosome 19 that includes thePax2 locus. Genomics 23: 309- 320, 1994. 3 B c

GAM94 332 PAX2 Narahara, K.; Baker, E.; Ito, S.; Yokoyama, Y.; Yu, S.; Hewitt,D.; Sutherland, G. R.; Eccles, M. R.; Richards, R. I.: Localisationof a 10q breakpoint within the PAX2 gene in a patient with a de novot(10;13) translocation and optic nerve coloboma- renal disease. J.Med. Genet. 34: 213- 216, 1997. 3 B c

GAM94 332 PAX2 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman homologs of the murine paired- box- containing genes. MammalianGenome 4: 78- 82, 1993. 3 B c

GAM94 332 PAX2 Porteous, S.; Torban, E.; Cho, N.- P.; Cunliffe, H.; Chua, L.;McNoe, L.; Ward, T.; Souza, C.; Gus, P.; Giugliani, R.; Sato, T.;Yun, K.; Favor, J.; Sicotte, M.; Goodyer, P.; Eccles, M.: Primaryrenal hypoplasia in humans and mice with PAX2 mutations: evidenceof increased apoptosis in fetal kidneys of Pax2(1Neu) +/- mutant mice. Hum.Molec. Genet. 9: 1- 11, 2000. 3 B c

GAM94 332 PAX2 Sanyanusin, P.; McNoe, L. A.; Sullivan, M. J.; Weaver, R. G.;Eccles, M. R.: Mutation of PAX2 in two siblings with renal- colobomasyndrome. Hum. Molec. Genet. 4: 2183- 2184, 1995. 3 B c

GAM94 332 PAX2 Sanyanusin, P.; Norrish, J. H.; Ward, T. A.; Nebel, A.; McNoe,L. A.; Eccles, M. R.: Genomic structure of the human PAX2 gene. Genomics 35:258- 261, 1996. 3 B c

GAM94 332 PAX2 Sanyanusin, P.; Schimmenti, L. A.; McNoe, L. A.; Ward, T. A.;Pierpont, M. E. M.; Sullivan, M. J.; Dobyns, W. B.; Eccles, M. R.: Mutation of the PAX2 gene in a family with optic nerve colobomas,renal anomalies and vesicoureteral reflux. Nature Genet. 9: 358- 364,1995. 3 B c

GAM94 332 PAX2 Schimmenti, L. A.; Cunliffe, H. E.; McNoe, L. A.; Ward, T. A.;French, M. C.; Shim, H. H.; Zhang, Y.- H.; Proesmans, W.; Leys, A.;Byerly, K. A.; Braddock, S. R.; Masuno, M.; Imaizumi, K.; Devriendt,K.; Eccles, M. R.: Further delineation of renal- coloboma syndromein patients with extreme variability of phenotype and identical PAX2mutations. Am. J. Hum. Genet. 60: 869- 878, 1997. 3 B c

GAM94 332 PAX2 Schimmenti, L. A.; Pierpont, M. E.; Carpenter, B. L. M.; Kashtan,C. E.; Johnson, M. R.; Dobyns, W. B.: Autosomal dominant optic nervecolobomas, vesicoureteral reflux, and renal anomalies. Am. J. Med.Genet. 59: 204- 208, 1995. 3 B c

GAM94 332 PAX2 Schimmenti, L. A.; Shim, H. H.; Wirtschafter, J. D.; Panzarino,V. A.; Kashtan, C. E.; Kirkpatrick, S. J.; Wargowski, D. S.; France,T. D.; Michel, E.; Dobyns, W. B.: Homonucleotide expansion and contractionmutations of PAX2 and inclusion of Chiari 1 malformation as part ofrenal- coloboma syndrome. Hum. Mutat. 14: 369- 376, 1999. 3 B c

GAM94 332 PAX2 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: Chromosomal localization of seven PAX genes and cloning of anovel family member, PAX- 9. Nature Genet. 3: 292- 298, 1993. 3 B c

GAM94 332 PAX2 Tellier, A.- L.; Amiel, J.; Delezoide, A.- L.; Audollent, S.; Auge,J.; Esnault, D.; Encha- Razavi, F.; Munnich, A.; Lyonnet, S.; Vekemans,M.; Attie- Bitach, T.: Expression of the PAX2 gene in human embryosand exclusion in the CHARGE syndrome. Am. J. Med. Genet. 93: 85- 88,2000. 3 B c

GAM94 332 PAX2 Tellier, A.- L.; Amiel, J.; Salomon, R.; Jolly, D.; Delezoide,A.- L.; Auge, 3 B c
J.; Gubler, M.- C.; Munnich, A.; Lyonnet, S.; Antignac,C.; Vekemans, M.;
Broyer, M.; Attie- Bitach, T.: PAX2 expression duringearly human development
and its mutations in renal hypoplasia withor without coloboma. (Abstract)
Am. J. Hum. Genet. 63 (suppl.):A7 only, 1998.

GAM94 332 PAX2 Ward, T. A.; Nebel, A.; Reeve, A. E.; Eccles, M. R.: Alternativemessenger 3 B c
RNA forms and open reading frames within an additional conservedregion of
the human PAX- 2 gene. Cell Growth Differ. 5: 1015- 1021,1994.

GAM94 332 PAX2 Weaver, R. G.; Cashwell, L. F.; Lorentz, W.; Whiteman, D.; Geisinger,K. R.; 3 B c
Ball, M.: Optic nerve coloboma associated with renal disease. Am.J. Med.
Genet. 29: 597- 605, 1988.

GAM94 332 PAX7 Barr, F. G.; Nauta, L. E.; Davis, R. J.; Schafer, B. W.; Nycum,L. M.; 3 B c
Biegel, J. A.: In vivo amplification of the PAX3- FKHR andPAX7- FKHR fusion
genes in alveolar rhabdomyosarcoma. Hum. Molec.Genet. 5: 15- 21, 1996.

GAM94 332 PAX7 Burri, M.; Tromvoukis, Y.; Bopp, D.; Frigerio, G.; Noll, M.: Conservationof 3 B c
the paired domain in metazoans and its structure in three isolatedhuman
genes. EMBO J. 8: 1183- 1190, 1989.

GAM94 332 PAX7 Gruss, P.; Walther, C.: Pax in development. Cell 69: 719- 722,1992. 3 B c

GAM94 332 PAX7 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman 3 B c
homologs of the murine paired- box- containing genes. MammalianGenome 4: 78-
82, 1993.

GAM94 332 PAX7 Schafer, B. W.; Mattei, M. G.: The human paired domain gene PAX7(Hup1) maps 3 B c
to chromosome 1p35- 1p36.2. Genomics 17: 249- 251, 1993.

GAM94 332 PAX7 Seale, P.; Sabourin, L. A.; Girgis- Gabardo, A.; Mansouri, A.; Gruss,P.; 3 B c
Rudnicki, M. A.: Pax7 is required for the specification of myogenicsatellite
cells. Cell 102: 777- 786, 2000.

GAM94 332 PAX7 Shapiro, D. N.; Sublett, J. E.; Li, B.; Valentine, M. B.; Morris,S. W.; 3 B c
Noll, M.: The gene for PAX7, a member of the paired- box- containinggenes,
is localized on human chromosome arm 1p36. Genomics 17: 767- 769,1993.

GAM94 332 PAX7 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: 3 B c
Chromosomal localization of seven PAX genes and cloning of anovel family
member, PAX- 9. Nature Genet. 3: 292- 298, 1993.

GAM94 332 PAX7 Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: 3 B c
Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes
Cancer 5: 299- 310, 1992.

GAM94 332 PDE4B Huston, E.; Lumb, S.; Russell, A.; Catterall, C.; Ross, A. H.;Steele, M. R.; 3 B c
Bolger, G. B.; Perry, M. J.; Owens, R. J.; Houslay,M. D.: Molecular cloning
and transient expression in COS7 cells ofa novel human PDE4B cAMP- specific
phosphodiesterase, HSPDE4B3. Biochem.J. 328: 549- 558, 1997.

GAM94 332 PDE4B Livi, G. P.; Kmetz, P.; McHale, M. M.; Cieslinski, L. B.; Sathe,G. M.; 3 B c
Taylor, D. P.; Davis, R. L.; Torphy, T. J.; Balcarek, J. M.: Cloning and
expression of cDNA for a human low- K(m), rolipram- sensitivecyclic AMP
phosphodiesterase. Molec. Cell. Biol. 10: 2678- 2686,1990.

GAM94 332 PDE4B Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 3 B c
Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases
inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM94 332 PDE4B Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins,M.; 3 B c
Jarnagin, K.; Shelton, E. R.: The cDNA of a human lymphocytecyclic- AMP
phosphodiesterase (PDE IV) reveals a multigene family. Gene 129:239- 247,
1993.

GAM94 332 PDE4B Szpirer, C.; Szpirer, J.; Riviere, M.; Swinnen, J.; Vicini, E.;Conti, M.: 3 B c
Chromosomal localization of the human and rat genes (PDE4Dand PDE4B)
encoding the cAMP- specific phosphodiesterases 3 and 4. Cytogenet.Cell
Genet. 69: 11- 14, 1995.

GAM94 332 PDE4B Xu, R. X.; Hassell, A. M.; Vanderwall, D.; Lambert, M. H.; Holmes,W. D.; 3 B c
Luther, M. A.; Rocque, W. J.; Milburn, M. V.; Zhao, Y.; Ke,H.; Nolte, R. T.:
Atomic structure of PDE4: insights into phosphodiesterasemechanism and
specificity. Science 288: 1822- 1825, 2000.

GAM94 332 PDE4C Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.;Rodgers, 3 B c
L.; Riggs, M.; Wigler, M.; Ferguson, K.: A family of humanphosphodiesterases
homologous to the dunce learning and memory geneproduct of Drosophila
melanogaster are potential targets for antidepressantdrugs. Molec. Cell.
Biol. 13: 6558- 6571, 1993.

GAM94 332 PDE4C Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 3 B c
Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases
inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM94 332 PDE4C Sullivan, M.; Olsen, A. S.; Houslay, M. D.: Genomic organisationof the human 3 B c
cyclic AMP- specific phosphodiesterase PDE4C gene andits chromosomal
localisation to 19p13.1, between RAB3A and JUND. Cell.Signal. 11: 735- 742,
1999.

GAM94 332 PHEMX Hu, R.- J.; Lee, M. P.; Connors, T. D.; Johnson, L. A.; Burn, T.C.; Su, K.; 3 B c
Landes, G. M.; Feinberg, A. P.: A 2.5- Mb transcript mapof a tumor-
suppressing subchromosomal transferable fragment from 11p15.5,and isolation
and sequence analysis of three novel genes. Genomics 46:9- 17, 1997.

GAM94 332 PHEMX Koi, M.; Johnson, L. A.; Kalikin, L. M.; Little, P. F. R.; Nakamura,Y.; 3 B c
Feinberg, A. P.: Tumor cell growth arrest caused by
subchromosomaltransferable DNA fragments from chromosome 11. Science 260:
361- 364,1993.

GAM94 332 PHEMX Lee, M. P.; Brandenburg, S.; Landes, G. M.; Adams, M.; Miller,G.; Feinberg, 3 B c
A. P.: Two novel genes in the center of the 11p15 imprinteddomain escape
genomic imprinting. Hum. Molec. Genet. 8: 683- 690,1999.

GAM94 332 PIP5K1B Campuzano, V.; Montermini, L.; Molto, M. D.; Pianese, L.; Cossee,M.; 3 B c
Cavalcanti, F.; Monros, E.; Rodius, F.; Duclos, F.; Monticelli,A.; Zara, F.;
Canizares, J.; Koutnikova, H.; Bidichandani, S. I.;Gellera, C.; Brice, A.;
Trouillas, P.; De Michele, G.; Filla, A.;De Frutos, R.; Palau, F.; Patel, P.
I.; Di Donato, S.; Mandel, J.- L.; Cocozza, S.; Koenig, M.; Pandolfo, M.:
Friedreich's ataxia:autosomal recessive disease caused by an intronic GAA
triplet repeatexpansion. Science 271: 1423- 1427, 1996.

GAM94 332 PIP5K1B Carvajal, J. J.; Pook, M. A.; dos Santos, M.; Doudney, K.; Hillermann,R.; 3 B c
Minogue, S.; Williamson, R.; Hsuan, J. J.; Chamberlain, S.: TheFriedreich's
ataxia gene encodes a novel phosphatidylinositol- 4- phosphate5- kinase.
Nature Genet. 14: 157- 162, 1996.

GAM94 332 PIP5K1B Carvajal, J. J.; Pook, M. A.; Doudney, K.; Hillermann, R.; Wilkes,D.; Al- 3 B c
Mahdawi, S.; Williamson, R.; Chamberlain, S.: Friedreich'sataxia: a defect
in signal transduction? Hum. Molec. Genet. 4: 1411- 1419,1995.

GAM94 332 PIP5K1B Pook, M. A.; Carvajal, J. J; Doudney, K.; Hillermann, R.; Chamberlain,S.: 3 B c
Exon- intron structure of a 2.7- kb transcript of the STM7 genewith
phosphatidylinositol- 4- phosphate 5- kinase activity. Genomics 42:170- 172,
1997.

GAM94 332 PLXNA2 Maestrini, E.; Tamagnone, L.; Longati, P.; Cremona, O.; Gulisano,M.; Bione, 3 B c

S.; Tamanini, F.; Neel, B. G.; Toniolo, D.; Comoglio, P.M.: A family of transmembrane proteins with homology to the MET- hepatocytegrowth factor receptor. Proc. Nat. Acad. Sci. 93: 674- 678, 1996.

GAM94 332 PLXNA2 Tamagnone, L.; Artigiani, S.; Chen, H.; He, Z.; Ming, G.; Song,H.; Chedotal, 3 B c
A.; Winberg, M. L.; Goodman, C. S.; Poo, M.; Tessier- Lavigne,M.; Comoglio, P. M.: Plexins are a large family of receptors fortransmembrane, secreted, and GPI- anchored semaphorins in vertebrates. Cell 99:71- 80, 1999.

GAM94 332 PLXNB2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM94 332 PLXNB2 Shinoura, N.; Shamraj, O. I.; Hugenholz, H.; Zhu, J. G.; McBlack,P.; 3 B c
Warnick, R.; Tew, J. J.; Wani, M. A.; Menon, A. G.: Identificationand partial sequence of a cDNA that is differentially expressed inhuman brain tumors. Cancer Lett. 89: 215- 221, 1995.

GAM94 332 PLXNB2 Tamagnone, L.; Artigiani, S.; Chen, H.; He, Z.; Ming, G.; Song,H.; Chedotal, 3 B c
A.; Winberg, M. L.; Goodman, C. S.; Poo, M.; Tessier- Lavigne,M.; Comoglio, P. M.: Plexins are a large family of receptors fortransmembrane, secreted, and GPI- anchored semaphorins in vertebrates. Cell 99:71- 80, 1999.

GAM94 332 POLK Gerlach, V. L.; Aravind, L.; Gotway, G.; Schultz, R. A.; Koonin,E. V.; 3 B c
Friedberg, E. C.: Human and mouse homologs of Escherichiacoli DinB (DNA polymerase IV), members of the UmuC/DinB superfamily. Proc.Nat. Acad. Sci. 96: 11922- 11927, 1999.

GAM94 332 POLK Johnson, R. E.; Prakash, S.; Prakash, L.: The human DINB1 geneencodes the 3 B c
DNA polymerase Pol- theta. Proc. Nat. Acad. Sci. 97:3838- 3843, 2000.

GAM94 332 POLK Ogi, T.; Kato, T., Jr.; Kato, T.; Ohmori, H.: Mutation enhancementby DINB1, 3 B c
a mammalian homologue of the Escherichia coli mutagenesisprotein dinB. Genes Cells 4: 607- 618, 1999.

GAM94 332 POLK Ohashi, E.; Ogi, T.; Kusumoto, R.; Iwai, S.; Masutani, C.; Hanaoka,F.; 3 B c
Ohmori, H.: Error- prone bypass of certain DNA lesions by thehuman DNA polymerase kappa. Genes Dev. 14: 1589- 1594, 2000.

GAM94 332 POLK Walowsky, C.; Fitzhugh, D. J.; Castano, I. B.; Ju, J. Y.; Levin,N. A.; 3 B c
Christman, M. F.: The topoisomerase- related function geneTRF4 affects cellular sensitivity to the antitumor agent camptothecin. J.Biol. Chem. 274: 7302- 7308, 1999.

GAM94 332 POLK Wang, Z.; Castano, I. B.; De Las Penas, A.; Adams, C.; Christman,M. F.: Pol 3 B c
kappa: a DNA polymerase required for sister chromatidcohesion. Science 289: 774- 779, 2000.

GAM94 332 POU3F2 Atanasoski, S.; Toldo, S. S.; Malipiero, U.; Schreiber, E.; Fries,R.; 3 B c
Fontana, A.: Isolation of the human genomic brain- 2/N- Oct 3 gene(POUF3) and assignment to chromosome 6q16. Genomics 26: 272- 280,1995.

GAM94 332 POU3F2 Schreiber, E.; Tobler, A.; Malipiero, U.; Schaffner, W.; Fontana,A.: cDNA 3 B c
cloning of human N- Oct 3, a nervous- system specific POUdomain transcription factor binding to the octamer DNA motif. NucleicAcids Res. 21: 253- 258, 1993.

GAM94 332 POU3F2 Xia, Y.- R.; Andersen, B.; Mehrabian, M.; Diep, A. T.; Warden, C.H.; 3 B c
Mohandas, T.; McEvilly, R. J.; Rosenfeld, M. G.; Lusis, A. J.: Chromosomal organization of mammalian POU domain factors. Genomics 18:126- 130, 1993.

GAM94 332 PPP1R11 Amadou, C.; Ribouchon, M. T.; Mattei, M. G.; Jenkins, N. A.; Gilbert,D. J.; 3 B c

Copeland, N. G.; Avoustin, P.; Pontarotti, P.: Localizationof new genes and markers to the distal part of the human major histocompatibilitycomplex (MHC) region and comparison with the mouse: new insights intothe evolution of mammalian genomes. Genomics 26: 9- 20, 1995.

GAM94 332 PPP1R11 El Kahloun, A.; Chauvel, B.; Mauvieux, V.; Dorval, I.; Jouanolle,A.- M.; 3 B c
Gicquel, I.; Le Gall, J.- Y.; David, V.: Localization of sevennew genes around the HLA- A locus. Hum. Molec. Genet. 2: 55- 60, 1993.

GAM94 332 PPP1R11 Giffon, T.; Lepourcelet, M.; Pichon, L.; Jezequel, P.; Bouric,P.; Carn, G.; 3 B c
Pontarotti, P.; Le Gall, J.- Y.; David, V.: Cloningof a human homologue of the mouse Tctex- 5 gene within the MHC classI region. Immunogenetics 44: 331- 339, 1996.

GAM94 332 PPP1R11 Lepourcelet, M.; Andrieux, N.; Giffon, T.; Pichon, L.; Hampe, A.;Galibert, 3 B c
F.; Mosser, J.: Systematic sequencing of the human HLA- A/HLA- Fregion: establishment of a cosmid contig and identification of a newgene cluster within 37 kb of sequence. Genomics 37: 316- 326, 1996.

GAM94 332 PPP1R11 Zhang, J.; Zhang, L.; Zhao, S.; Lee, E. Y. C.: Identificationand 3 B c
characterization of the human HCG V gene product as a novel inhibitorof protein phosphatase- 1. Biochemistry 37: 16728- 16734, 1998.

GAM94 332 PPP2R1B Arai, Y.; Hosoda, F.; Nakayama, K.; Ohki, M.: A yeast artificialchromosome 3 B c
contig and NotI restriction map that spans the tumor suppressorgene(s) locus, 11q.22.2- q23.3. Genomics 35: 196- 206, 1996.

GAM94 332 PPP2R1B Hemmer, S.; Wasenius, V.- M.; Haglund, C.; Zhu, Y.; Knuutila, S.;Franssila, 3 B c
K.; Joensuu, H.: Alterations in the suppressor gene PPP2R1Bin parathyroid hyperplasias and adenomas. Cancer Genet. Cytogenet. 134:13- 17, 2002.

GAM94 332 PPP2R1B Walter, G.; Mumby, M.: Protein serine/threonine phosphatases andcell 3 B c
transformation. Biochim. Biophys. Acta 1155: 207- 226, 1993.

GAM94 332 PPP2R1B Wang, S. S.; Esplin, E. D.; Li, J. L.; Huang, L.; Gazdar, A.; Minna,J.; 3 B c
Evans, G. A.: Alterations of the PPP2R1B gene in human lung andcolon cancer. Science 282: 284- 287, 1998.

GAM94 332 PSG1 Barnett, T. R.; Pickle, W., II; Rae, P. M. M.; Hart, J.; Kamarck,M.; Elting, 3 B c
J.: Human pregnancy- specific beta(1)- glycoproteins arecoded within chromosome 19. Am. J. Hum. Genet. 44: 890- 893, 1989.

GAM94 332 PSG1 Barnett, T.; Pickle, W., II; Rae, P. M. M.; Hart, J.; Kamarck,M.; Elting, 3 B c
J.: Pregnancy- specific beta- 1- glycoproteins are relatedto carcinoembryonic antigens and map to chromosome 19. (Abstract) Cytogenet.Cell Genet. 51: 958, 1989.

GAM94 332 PSG1 Bartels, I.; Lindemann, A.: Maternal levels of pregnancy- specificbeta- 1- 3 B c
glycoprotein (SP- 1) are elevated in pregnancies affected byDown's syndrome. Hum. Genet. 80: 46- 48, 1988.

GAM94 332 PSG1 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, 3 B c
F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999.

GAM94 332 PSG1 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. 3 B c
W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by fluorescence in situ hybridization. Genomics 12:773- 779, 1992.

GAM94 332 PSG1 Chan, W.- Y.; Qiu, W.- R.: Human pregnancy- specific beta- 1 glycoproteinis 3 B c
encoded by multiple genes localized on two chromosomes. Am. J.Hum. Genet. 43: 152- 159, 1988.

GAM94 332 PSG1 Khan, W. N.; Teglund, S.; Bremer, K.; Hammarstrom, S.: The pregnancy- 3 B c
specificglycoprotein family of the immunoglobulin superfamily:
identificationof new members and estimation of family size. Genomics 12:
780- 787,1992.

GAM94 332 PSG1 Niemann, S. C.; Flake, A.; Bohn, H.; Bartels, I.: Pregnancy- specificbeta- 3 B c
1- glycoprotein: cDNA cloning, tissue expression, and speciesspecificity of
one member of the PSBG family. Hum. Genet. 82: 239- 243,1989.

GAM94 332 PSG1 Niemann, S. C.; Schonk, D.; van Dijk, P. E.; Grzeschik, K.- H.;Bartels, I.: 3 B c
Chromosomal assignment of a cDNA clone encoding pregnancy- specificbeta- 1-
glycoprotein to chromosome 19. (Abstract) Cytogenet. CellGenet. 51: 1053,
1989.

GAM94 332 PSG1 Niemann, S. C.; Schonk, D.; van Dijk, P.; Wieringa, B.; Grzeschik,K.- H.; 3 B c
Bartels, I.: Regional localization of the gene encoding pregnancyspecific
beta- 1- glycoprotein 1 (PSBG1) to human chromosome 19q13.1. Cytogenet.Cell
Genet. 52: 95- 97, 1989.

GAM94 332 PSG1 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.;Georgescu, A.; 3 B c
Carrano, A.; Hammarstrom, S.: Gene organization ofthe pregnancy- specific
glycoprotein region on human chromosome 19:assembly and analysis of a 700-
kb cosmid contig spanning the region. Genomics 23:659- 668, 1994.

GAM94 332 PSG1 Streydio, C.; Swillens, S.; Georges, M.; Szpirer, C.; Vassart,G.: Structure, 3 B c
evolution and chromosomal localization of the humanpregnancy- specific beta-
1 glycoprotein gene family. Genomics 6:579- 592, 1990. Note: Erratum:
Genomics 7: 661- 662, 1990.

GAM94 332 PSG1 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The 3 B c
pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19:
fine structure of the 11 PSG genes and identificationof 6 new genes forming
a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics
23: 669- 684, 1994.

GAM94 332 PSG1 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, 3 B c
H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.;
Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly
linked on the long arm of chromosome 19 and arecoordinately expressed.
Biochem. Biophys. Res. Commun. 167: 848- 859,1990.

GAM94 332 PSG1 Watanabe, S.; Chou, J. Y.: Isolation and characterization ofcomplementary 3 B c
DNAs encoding human pregnancy- specific beta- 1- glycoprotein. J.Biol. Chem.
263: 2049- 2054, 1988.

GAM94 332 PTGFRN Charrin, S.; Le Naour, F.; Oualid, M.; Billard, M.; Faure, G.,Hanash, S. M.; 3 B c
Boucheix, C.; Rubinstein, E.: The major CD9 and CD81molecular partner:
identification and characterization of the complexes. J.Biol. Chem. 276:
14329- 14337, 2001.

GAM94 332 PTGFRN Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of 3 B c
the coding sequences of unidentified human genes. XVI.The complete sequences
of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA
Res. 7: 65- 73, 2000.

GAM94 332 PTGFRN Orlicky, D. J.; Berry, R.; Sikela, J. M.: Human chromosome 1 localizationof 3 B c
the gene for a prostaglandin F- 2- alpha receptor negative
regulatoryprotein. Hum. Genet. 97: 655- 658, 1996.

GAM94 332 PTGFRN Stipp, C. S.; Orlicky, D.; Hemler, M. E.: FPRP, a major, 3 B c
highlystoichiometric, highly specific CD81- and CD9- associated protein.
J.Biol. Chem. 276: 4853- 4862, 2001.

GAM94 332 PTK2 Andre, E.; Becker- Andre, M.: Expression of an N- terminally truncatedform 3 B c
of human focal adhesion kinase in brain. Biochem. Biophys. Res.Commun. 190:
140- 147, 1993.

GAM94 332 PTK2 Fiedorek, F. T., Jr.; Kay, E. S.: Mapping of the focal adhesionkinase (Fadk) 3 B c
gene to mouse chromosome 15 and human chromosome 8. MammalianGenome 6: 123-
126, 1995.

GAM94 332 PTK2 Polte, T. R.; Hanks, S. K.: Interaction between focal adhesionkinase and 3 B c
Crk- associated tyrosine kinase substrate p130- Cas. Proc.Nat. Acad. Sci.
92: 10678- 10682, 1995.

GAM94 332 PTK2 Schaller, M. D.; Borgman, C.; Cobb, B. S.; Vines, R. R.; Reynolds,A. B.; 3 B c
Parsons, J. T.: pp125(FAK), a structurally distinctive protein-
tyrosinekinase associated with focal adhesions. Proc. Nat. Acad. Sci.
89:5192- 5196, 1992.

GAM94 332 PTPN6 Banville, D.; Stocco, R.; Shen, S.- H.: Human protein tyrosinephosphatase 1C 3 B c
(PTPN6) gene structure: alternate promoter usage andexon skipping generate
multiple transcripts. Genomics 27: 165- 173,1995.

GAM94 332 PTPN6 Beghini, A.; Ripamonti, C. B.; Peterlongo, P.; Roversi, G.; Cairoli,R.; 3 B c
Morra, E.; Larizza, L.: RNA hyperediting and alternative splicingof
hematopoietic cell phosphatase (PTPN6) gene in acute myeloid leukemia.
Hum.Molec. Genet. 9: 2297- 2304, 2000.

GAM94 332 PTPN6 Matthews, R. J.; Bowne, D. B.; Flores, E.; Thomas, M. L.: Characterizationof 3 B c
hematopoietic intracellular protein tyrosine phosphatases: descriptionof a
phosphatase containing an SH2 domain and another enriched inproline- ,
glutamic acid- , serine- , and threonine- rich sequences. Molec.Cell. Biol.
12: 2396- 2405, 1992.

GAM94 332 PTPN6 Plutzky, J.; Neel, B. G.; Rosenberg, R. D.; Eddy, R. L.; Byers,M. G.; Jani- 3 B c
Sait, S.; Shows, T. B.: Chromosomal localization of anSH2- containing
tyrosine phosphatase (PTPN6). Genomics 13: 869- 872,1992.

GAM94 332 PTPN6 Shen, S.- H.; Bastien, L.; Posner, B. I.; Chretien, P.: A protein- 3 B c
tyrosinephosphatase with sequence similarity to the SH2 domain of the
protein- tyrosinekinases. Nature 352: 736- 739, 1991.

GAM94 332 PTPN6 Shultz, L. D.; Schweitzer, P. A.; Rajan, T. V.; Yi, T.; Ihle, J.N.; 3 B c
Matthews, R. J.; Thomas, M. L.; Beier, D. R.: Mutations at themurine
motheaten locus are within the hematopoietic cell protein-
tyrosinephosphatase (Hcph) gene. Cell 73: 1445- 1454, 1993.

GAM94 332 PTPN6 Tsui, H. W.; Siminovitch, K. A.; de Souza, L.; Tsui, F. W. L.:Motheaten and 3 B c
viable motheaten mice have mutations in the haematopoieticcell phosphatase
gene. Nature Genet. 4: 124- 129, 1993.

GAM94 332 PTPN6 Yi, T.; Cleveland, J. L.; Ihle, J. N.: Identification of novelprotein 3 B c
tyrosine phosphatases of hematopoietic cells by PCR amplification. Blood
78:2222- 2228, 1991.

GAM94 332 PTPN6 Yi, T.; Cleveland, J. L.; Ihle, J. N.: Protein tyrosine 3 B c
phosphatasecontaining SH2 domains: characterization, preferential
expressionin hematopoietic cells, and localization to human chromosome
12p12- p13. Molec.Cell. Biol. 12: 836- 846, 1992.

GAM94 332 PTPN6 Yi, T.; Gilbert, D. J.; Jenkins, N. A.; Copeland, N. G.; Ihle,J. N.: 3 B c
Assignment of a novel protein tyrosine phosphatase gene (Hcph)to mouse
chromosome 6. Genomics 14: 793- 795, 1992.

GAM94 332 PWP2H Lafreniere, R. G.; Rochefort, D. L.; Chretien, N.; Neville, C.E.; Korneluk, 3 B c
R. G.; Zuo, L.; Wei, Y.; Lichter, J.; Rouleau, G. A.: Isolation and genomic

structure of a human homolog of the yeastperiodic tryptophan protein 2 (PWP2) gene mapping to 21q22.3. GenomeRes. 6: 1216- 1226, 1996.

GAM94 332 PWP2H Lalioti, M. D.; Chen, H.; Rossier, C.; Shafaatian, R.; Reid, J.D.; 3 B c
Antonarakis, S. E.: Cloning the cDNA of human PWP2, which encodesa protein with WD repeats and maps to 21q22.3. Genomics 35: 321- 327,1996.

GAM94 332 PWP2H Yamakawa, K.; Gao, D.- Q.; Korenberg, J. R.: A periodic tryptophanprotein 2 3 B c
gene homologue (PWP2H) in the candidate region of progressivemyoclonus epilepsy on 21q22.3. Cytogenet. Cell Genet. 74: 140- 145,1996.

GAM94 332 RAB13 Leek, J. P.; Hamlin, P. J.; Wilton, J.; Lench, N. J.: Assignmentof the Rab13 3 B c
gene (RAB13) to human chromosome band 12q13 by in situhybridization. Cytogenet. Cell Genet. 79: 210- 211, 1997.

GAM94 332 RAB13 Novick, P.; Zerial, M.: The diversity of Rab proteins in vesicletransport. 3 B c
Curr. Opin. Cell Biol. 9: 496- 504, 1997.

GAM94 332 RAB13 Salminen, A.; Novick, P. J.: A ras- like protein is required fora post- 3 B c
Golgi event in yeast secretion. Cell 49: 527- 538, 1987.

GAM94 332 RAB13 Zahraoui, A.; Joberty, G.; Arpin, M.; Fontaine, J. J.; Hellio,R.; Tavitian, 3 B c
A.; Louvard, D.: A small rab GTPase is distributedin cytoplasmic vesicles in nonpolarized cells but colocalizes withthe tight junction marker ZO- 1 in polarized epithelial cells. J.Cell. Biol. 124: 101- 115, 1994.

GAM94 332 RAB5A Bucci, C.; Parton, R. G.; Mather, I. H.; Stunnenberg, H.; Simons,K.; 3 B c
Hoflack, B.; Zerial, M.: The small GTPase rab5 functions as aregulatory factor in the early endocytic pathway. Cell 70: 715- 728,1992.

GAM94 332 RAB5A Lanzetti, L.; Rybin, V.; Malabarba, M. G.; Christoforidis, S.;Scita, G.; 3 B c
Zerial, M.; Di Fiore, P. P.: The Eps8 protein coordinatesEGF receptor signalling through Rac and trafficking through Rab5. Nature 408:374- 377, 2000.

GAM94 332 RAB5A Rousseau- Merck, M. F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: 3 B c
Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350- 354, 1991.

GAM94 332 RAB5A Stenmark, H.; Vitale, G.; Ullrich, O.; Zerial, M.: Rabaptin- 5is a direct 3 B c
effector of the small GTPase Rab5 in endocytic membranefusion. Cell 83: 423- 432, 1995.

GAM94 332 RAB5A Xiao, G.- H.; Shoarinejad, F.; Jin, F.; Golemis, E. A.; Yeung, R.S.: The 3 B c
tuberous sclerosis 2 gene product, tuberin, functions asa Rab5 GTPase activating protein (GAP) in modulating endocytosis. J.Biol. Chem. 272: 6097- 6100, 1997.

GAM94 332 RAB5A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes 3 B c
encode a family of GTP- binding proteins related to yeastYPT1 and SEC4 products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989.

GAM94 332 RAD54B Hiramoto, T.; Nakanishi, T.; Sumiyoshi, T.; Fukuda, T.; Matsuura,S.; Tauchi, 3 B c
H.; Komatsu, K.; Shibasaki, Y.; Inui, H.; Watatani, M.;Yasutomi, M.; Sumii, K.; Kajiyama, G.; Kamada, N.; Miyagawa, K.; Kamiya,K.: Mutations of a novel human RAD54 homologue, RAD54B, in primarycancer. Oncogene 18: 3422- 3426, 1999.

GAM94 332 RAD54B Miyagawa, K.; Tsuruga, T.; Kinomura, A.; Usui, K.; Katsura, M.;Tashiro, S.; 3 B c
Mishima, H.; Tanaka, K.: A role for RAD54B in homologousrecombination in human cells. EMBO J. 21: 175- 180, 2002.

GAM94 332 RAD54B Tanaka, K.; Hiramoto, T.; Fukuda, T.; Miyagawa, K.: A novel humanRad54 3 B c
homologue, Rad54B, associates with Rad51. J. Biol. Chem. 275:26316- 26321, 2000.

GAM94 332 RBL1 Chen, C.- R.; Kang, Y.; Siegel, P. M.; Massague, J.: E2F4/5 andp107 as Smad 3 B c
cofactors linking the TGF- beta receptor to c- myc repression. Cell 110:19-
32, 2002.

GAM94 332 RBL1 Ewen, M. E.; Xing, Y.; Lawrence, J. B.; Livingston, D. M.: Molecularcloning, 3 B c
chromosomal mapping, and expression of the cDNA for p107,a retinoblastoma
gene product- related protein. Cell 66: 1155- 1164,1991.

GAM94 332 RBL1 Huppi, K.; Siwarski, D.; Mock, B. A.; Dosik, J.; Hamel, P. A.:Molecular 3 B c
cloning, chromosomal mapping, and expression of the mousep107 gene.
Mammalian Genome 7: 353- 355, 1996.

GAM94 332 RBL1 Kim, K. K.; Soonpaa, M. H.; Wang, H.; Field, L. J.: Developmentalexpression 3 B c
of p107 mRNA and evidence for alternative splicing of thep107 (RBL1) gene
product. Genomics 28: 520- 529, 1995.

GAM94 332 RBL1 LeCouter, J. E.; Kablar, B.; Hardy, W. R.; Ying, C.; Megeney, L.A.; May, L. 3 B c
L.; Rudnicki, M. A.: Strain- dependent myeloid hyperplasia,growth
deficiency, and accelerated cell cycle in mice lacking theRb- related p107
gene. Molec. Cell. Biol. 18: 7455- 7465, 1998.

GAM94 332 RORA Becker- Andre, M.; Andre, E.; DeLamarter, J. F.: Identificationof nuclear 3 B c
receptor mRNAs by RT- PCR amplification of conserved zinc- fingermotif
sequences. Biochem. Biophys. Res. Commun. 194: 1371- 1379,1993.

GAM94 332 RORA Carlberg, C.; Hooft van Huijsduijnen, R.; Staple, J. K.; DeLamarter,J. F.; 3 B c
Becker- Andre, M.: RZRs, a new family of retinoid- related orphanreceptors
that function as both monomers and homodimers. Molec. Endocr. 8:757- 770,
1994.

GAM94 332 RORA Coste, H.; Rodriguez, J. C.: Orphan nuclear hormone receptor Rev- erb- 3 B c
alpharegulates the human apolipoprotein CIII promoter. J. Biol. Chem.
277:27120- 27129, 2002.

GAM94 332 RORA Giguere, V.; Beatty, B.; Squire, J.; Copeland, N. G.; Jenkins,N. A.: The 3 B c
orphan nuclear receptor ROR- alpha (RORA) maps to a conservedregion of
homology on human chromosome 15q21- q22 and mouse chromosome9. Genomics 28:
596- 598, 1995.

GAM94 332 RORA Giguere, V.; Tini, M.; Flock, G.; Ong, E.; Evans, R. M.; Otulakowski,G.: 3 B c
Isoform- specific amino- terminal domains dictate DNA- binding propertiesof
ROR- alpha, a novel family of orphan hormone nuclear receptors. GenesDev. 8:
538- 553, 1994.

GAM94 332 RORA Hamilton, B. A.; Frankel, W. N.; Kerrebrock, A. W.; Hawkins, T.L.; FitzHugh, 3 B c
W.; Kusumi, K.; Russell, L. B.; Mueller, K. L.; vanBerkel, V.; Birren, B.
W.; Kruglyak, L.; Lander, E. S.: Disruptionof the nuclear hormone receptor
ROR- alpha in staggerer mice. Nature 379:736- 739, 1996.

GAM94 332 RORA Matysiak- Scholze, U.; Nehls, M.: The structural integrity of ROR- 3 B c
alphaisoforms is mutated in staggerer mice: cerebellar coexpression ofROR-
alpha- 1 and ROR- alpha- 4. Genomics 43: 78- 84, 1997.

GAM94 332 RORA Meyer, T.; Kneissel, M.; Mariani, J.; Fournier, B.: In vitro andin vivo 3 B c
evidence for orphan nuclear receptor ROR- alpha function inbone metabolism.
Proc. Nat. Acad. Sci. 97: 9197- 9202, 2000.

GAM94 332 RORA Ueda, H. R.; Chen, W.; Adachi, A.; Wakamatsu, H.; Hayashi, S.;Takasugi, T.; 3 B c
Nagano, M.; Nakahama, K.; Suzuki, Y.; Sugano, S.; Iino,M.; Shigeyoshi, Y.;
Hashimoto, S.: A transcription factor responseelement for gene expression
during circadian night. Nature 418:534- 539, 2002.

GAM94 332 RORA Zanjani, H. S.; Herrup, K.; Guastavino, J.- M.; Delhaye- Bouchaud,N.; 3 B c
Mariani, J.: Developmental studies of the inferior olivary nucleusin

staggerer mutant mice. Develop. Brain Res. 82: 18- 28, 1994.

GAM94 332 RPL22 Nucifora, G.; Begy, C. R.; Erickson, R.; Drabkin, H. A.; Rowley,J. D.: The 3 B c
3;21 translocation in myelodysplasia results in a fusiontranscript between
the AML1 gene and the gene for EAP, a highly conservedprotein associated
with the Epstein- Barr virus small RNA EBER 1. Proc.Nat. Acad. Sci. 90:
7784- 7788, 1993.

GAM94 332 RPL22 Nucifora, G.; Rowley, J. D.: AML1 and the 8;21 and 3;21 translocationsin 3 B c
acute and chronic myeloid leukemia. Blood 86: 1- 14, 1995.

GAM94 332 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; 3 B c
Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The
granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic
cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001.

GAM94 332 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the 3 B c
gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25
by fluorescence in situ hybridization. Genomics 37:406- 408, 1996.

GAM94 332 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen 3 B c
responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a
cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec.
Endocr. 15: 1971- 1982, 2001.

GAM94 332 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, 3 B c
S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial
characterization of two novel members of the ovalbuminfamily of serine
proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995.

GAM94 332 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. 3 B c
A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to
the viral apoptotic regulator cytokine responsemodifier A is present in
cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996.

GAM94 332 SIGLEC5 Cornish, A. L.; Freeman, S.; Forbes, G.; Ni, J.; Zhang, M.; Cepeda,M.; 3 B c
Gentz, R.; Augustus, M.; Carter, K. C.; Crocker, P. R.: Characterizationof
siglec- 5, a novel glycoprotein expressed on myeloid cells relatedto CD33.
Blood 92: 2123- 2132, 1998.

GAM94 332 SIGLEC5 Kim, H.- S.: Assignment of the human OB binding protein- 2 gene(CD33L2) to 3 B c
chromosome 19q13.3 by radiation hybrid mapping. Cytogenet.Cell Genet. 84: 96
only, 1999.

GAM94 332 SIGLEC5 Patel, N.; Brinkman- Van der Linden, E. C. M.; Altmann, S. W.; Gish,K.; 3 B c
Balasubramanian, S.; Timans, J. C.; Peterson, D.; Bell, M. P.;Bazan, J. F.;
Varki, A.; Kastelein, R. A.: OB- BP1/Siglec- 6: a leptin- and sialic acid-
binding protein of the immunoglobulin superfamily. J.Biol. Chem. 274: 22729-
22738, 1999.

GAM94 332 SIX2 Boucher, C. A.; Winchester, C. L.; Hamilton, G. M.; Winter, A.D.; Johnson, 3 B c
K. J.; Bailey, M. E. S.: Structure, mapping and expressionof the human gene
encoding the homeodomain protein, SIX2. Gene 247:145- 151, 2000.

GAM94 332 SIX2 Oliver, G.; Wehr, R.; Jenkins, N. A.; Copeland, N. G.; Cheyette,B. N. R.; 3 B c
Hartenstein, V.; Zipursky, S. L.; Gruss, P.: Homeobox genesand connective
tissue patterning. Development 121: 693- 705, 1995.

GAM94 332 SLC14A1 Barbosa, J.; Rich, S.; Dunsworth, T.; Swanson, J.: Linkage 3 B c
disequilibriumbetween insulin- dependent diabetes and the Kidd blood group
Jk(b)allele. J. Clin. Endocr. Metab. 55: 193- 195, 1982.

GAM94 332 SLC14A1 Field, L. L.; Marazita, M. L.; Spence, M. A.; Crandall, B. F.;Sparkes, R. 3 B c
S.: Is JK linked to IGK on chromosome 2? (Abstract) Cytogenet.Cell Genet.

40: 628- 629, 1985.

GAM94 332 SLC14A1 Gedde- Dahl, T.: Personal Communication. Oslo, Norway 9/26/1986. 3 B c

GAM94 332 SLC14A1 Geitvik, G. A.; Hoyheim, B.; Gedde- Dahl, T.; Grzeschik, K. H.;Lothe, R.; Tomter, H.; Olaisen, B.: The Kidd (JK) blood group locusassigned to chromosome 18 by close linkage to a DNA- RFLP. Hum. Genet. 77:205- 209, 1987. 3 B c

GAM94 332 SLC14A1 Hodge, S. E.; Anderson, C. E.; Neiswanger, K.; Field, L. L.; Spence,M. A.; Sparkes, R. S.; Sparkes, M. C.; Crist, M.; Terasaki, P. I.;Rimoin, D. L.; Rotter, J. I.: Close genetic linkage between diabetesmellitus and Kidd blood group. Lancet II: 893- 895, 1981. 3 B c

GAM94 332 SLC14A1 Hulten, M.; Lindsten, J.; Pen- Ming, L. M.; Fraccaro, M.; Mannini,A.; Trepolo, L.; Robson, E. B.; Heiken, A.; Tellingen, K. G.: Possiblelocalization of the genes for the Kidd blood group on an autosomeinvolved in a reciprocal translocation. Nature 211: 1067- 1068, 1968. 3 B c

GAM94 332 SLC14A1 Keats, B. J. B.; Morton, N. E.; Rao, D. C.: Likely linkage: InVwith Jk. Hum. Genet. 39: 157- 159, 1977. 3 B c

GAM94 332 SLC14A1 Keats, B. J. B.; Morton, N. E.; Rao, D. C.: Possible linkages(lod score over 1.5) and a tentative map of the Jk- Km linkage group. Cytogenet.Cell Genet. 22: 304- 308, 1978. 3 B c

GAM94 332 SLC14A1 Leppert, M.; Ferrell, R.; Kamboh, M. I.; Beasley, J.; O'Connell,P.; Lathrop, M.; Lalouel, J.- M.; White, R.: Linkage of the polymorphicprotein markers F13B, C1S, C1R, and blood group antigen Kidd in CEPHreference families. (Abstract) Cytogenet. Cell Genet. 46: 647, 1987. 3 B c

GAM94 332 SLC14A1 Lucien, N.; Chiaroni, J.; Cartron, J.- P.; Bailly, P.: Partialdeletion in the JK locus causing a Jk(null) phenotype. Blood 99:1079- 1081, 2002. 3 B c

GAM94 332 SLC14A1 Lucien, N.; Sidoux- Walter, F.; Olives, B.; Moulds, J.; Le Pennec,P.- Y.; Cartron, J.- P.; Bailly, P.: Characterization of the gene encodingthe human Kidd blood group/urea transporter protein: evidence forsplice site mutations in Jk- null individuals. J. Biol. Chem. 273:12973- 12980, 1998. 3 B c

GAM94 332 SLC14A1 Mace, M. A.; Robson, E. B.: Linkage data on ACP- 1 and MNSs. Cytogenet.Cell Genet. 13: 123- 125, 1974. 3 B c

GAM94 332 SLC14A1 Mohr, J.; Eiberg, H.: Colton blood groups: indication of linkagewith the Kidd (Jk) system as support for assignment to chromosome7. Clin. Genet. 11: 372- 374, 1977. 3 B c

GAM94 332 SLC14A1 Olives, B.; Mattei, M.- G.; Huet, M.; Neau, P.; Martial, S.; Cartron,J.- P.; Bailly, P.: Kidd blood group and urea transport function ofhuman erythrocytes are carried by the same protein. J. Biol. Chem. 270:15607- 15610, 1995. 3 B c

GAM94 332 SLC14A1 Olives, B.; Merriman, M.; Bailly, P.; Bain, S.; Barnett, A.; Todd,J.; Cartron, J.- P.; Merriman, T.: The molecular basis of the Kiddblood group polymorphism and its lack of association with type 1 diabetessusceptibility. Hum. Molec. Genet. 6: 1017- 1020, 1997. 3 B c

GAM94 332 SLC14A1 Olives, B.; Neau, P.; Bailly, P.; Hediger, M. A.; Rousselet, G.;Cartron, J.- P.; Ripoche, P.: Cloning and functional expression ofa urea transporter from human bone marrow cells. J. Biol. Chem. 269:31649- 31652, 1994. 3 B c

GAM94 332 SLC14A1 Pausch, V.; Mayr, W. R.: Analysis of the linkage JK- IGK, MNS- GCand of two other possible linkage groups. Hum. Hered. 37: 260- 262,1987. 3 B c

GAM94 332 SLC14A1 Promeneur, D.; Rousselet, G.; Bankir, L.; et al: Evidence fordistinct vascular and tubular urea transporters in the rat kidney. J.Am. Soc. 3 B c

Nephrol. 7: 852- 860, 1996.

GAM94 332 SLC14A1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 B c
New York: Oxford Univ. Press (pub.) 1988.

GAM94 332 SLC14A1 Sands, J. M.; Gargus, J. J.; Frohlich, O.; Gunn, R. B.; Kokko,J. P.: Urinary 3 B c
concentrating ability in patients with Jk(a/b) bloodtype who lack carrier-
mediated urea transport. J. Am. Soc. Nephrol. 2:1689- 1696, 1992.

GAM94 332 SLC14A1 Sherman, S. L.; Simpson, S. P.: Evidence for the location ofJK and CO on 3 B c
chromosome 2 based on family studies. (Abstract) Cytogenet.Cell Genet. 40:
743, 1985.

GAM94 332 SLC14A1 Shokeir, M. H. K.; Ying, K. L.; Pabello, P.: Deletion of thelong arm of 3 B c
chromosome no. 7: tentative assignment of the Kidd (Jk)locus. Clin. Genet.
4: 360- 368, 1973.

GAM94 332 SLC14A1 Sidoux- Walter, F.; Lucien, N.; Nissinen, R.; Sistonen, P.; Henry,S.; 3 B c
Moulds, J.; Cartron, J.- P.; Bailly, P.: Molecular heterogeneityof the Jk-
null phenotype: expression analysis of the Jk(S291P) mutationfound in Finns.
Blood 96: 1566- 1573, 2000.

GAM94 332 SLC14A1 Tsukaguchi, H.; Shayakul, C.; Berger, U. V.; Tokui, T.; Brown,D.; Hediger, 3 B c
M. A.: Cloning and characterization of the urea transportationUT3:
localization in rat kidney and testis. J. Clin. Invest. 99:1506- 1515, 1997.

GAM94 332 SLC14A1 Xu, Y.; Olives, B.; Bailly, P.; et al: Endothelial cells of thekidney vasa 3 B c
recta express the urea transporter HUT11. Kidney Int. 51:138- 146, 1997.

GAM94 332 SLC38A3 Chaudhry, F. A.; Reimer, R. J.; Krizaj, D.; Barber, D.; Storm- Mathisen,J.; 3 B c
Copenhagen, D. R.; Edwards, R. H.: Molecular analysis of systemN suggests
novel physiological roles in nitrogen metabolism and synaptictransmission.
Cell 99: 769- 780, 1999.

GAM94 332 SLC38A3 Lerman, M. I.; Minna, J. D.: The 630- kb lung cancer homozygousdeletion 3 B c
region on human chromosome 3p21.3: identification and evaluationof the
resident candidate tumor suppressor genes. Cancer Res. 60:6116- 6133, 2000.

GAM94 332 SMARCA5 Aihara, T.; Miyoshi, Y.; Koyama, K.; Suzuki, M.; Takahashi, E.;Monden, M.; 3 B c
Nakamura, Y.: Cloning and mapping of SMARCA5 encodinghSNF2H, a novel human
homologue of Drosophila ISWI. Cytogenet. CellGenet. 81: 191- 193, 1998.

GAM94 332 SMARCA5 Bochar, D. A.; Savard, J.; Wang, W.; Lafleur, D. W.; Moore, P.;Cote, J.; 3 B c
Shiekhattar, R.: A family of chromatin remodeling factorsrelated to Williams
syndrome transcription factor. Proc. Nat. Acad.Sci. 97: 1038- 1043, 2000.

GAM94 332 SMARCA5 Bozhenok, L.; Wade, P. A.; Varga- Weisz, P.: WSTF- ISWI chromatinremodeling 3 B c
complex targets heterochromatic replication foci. EMBOJ. 21: 2231- 2241,
2002.

GAM94 332 SMARCA5 Lazzaro, M. A.; Picketts, D. J.: Cloning and characterizationof the murine 3 B c
Imitation Switch (ISWI) genes: differential expressionpatterns suggest
distinct developmental roles for Snf2h and Snf2l. J.Neurochem. 77: 1145-
1156, 2001.

GAM94 332 SMARCA5 LeRoy, G.; Orphanides, G.; Lane, W. S.; Reinberg, D.: Requirementof RSF and 3 B c
FACT for transcription of chromatin templates in vitro. Science 282:1900-
1904, 1998.

GAM94 332 SMARCA5 Poot, R. A.; Dellaire, G.; Hulsmann, B. B.; Grimaldi, M. A.; Corona,D. F. 3 B c
V.; Becker, P. B.; Bickmore, W. A.; Varga- Weisz, P. D.: HuCHRAC,a human
ISWI chromatin remodelling complex contains hACF1 and twonovel histone- fold
proteins. EMBO J. 19: 3377- 3387, 2000.

GAM94 332 SOX9 Angle, C. R.: Congenital bowing and angulation of the long bones. Pediatrics 3 B c
13:257- 268, 1954.

GAM94 332 SOX9 Bain, A. D.; Barrett, H. S.: Congenital bowing of the long bones:report of a 3 B c
case. Arch. Dis. Child. 34: 516- 524, 1959.

GAM94 332 SOX9 Bell, D. M.; Leung, K. K. H.; Wheatley, S. C.; Ng, L. J.; Zhou,S.; Ling, K. 3 B c
W.; Sham, M. H.; Koopman, P.; Tam, P. P. L.; Cheah, K.S. E.: SOX9 directly
regulates the type- II collagen gene. NatureGenet. 16: 174- 178, 1997.

GAM94 332 SOX9 Bi, W.; Huang, W.; Whitworth, D. J.; Deng, J. M.; Zhang, Z.; Behringer,R. 3 B c
R.; de Crombrugghe, B.: Haploinsufficiency of Sox9 results indefective
cartilage primordia and premature skeletal mineralization. Proc.Nat. Acad.
Sci. 98: 6698- 6703, 2001.

GAM94 332 SOX9 Bishop, C. E.; Whitworth, D. J.; Qin, Y.; Agoulnik, A. I.; Agoulnik,I. U.; 3 B c
Harrison, W. R.; Behringer, R. R.; Overbeek, P. A.: A transgenicinsertion
upstream of Sox9 is associated with dominant XX sex reversalin the mouse.
Nature Genet. 26: 490- 494, 2000.

GAM94 332 SOX9 Caffey, J. P.: Prenatal bowing and thickening of tubular bones,with multiple 3 B c
cutaneous dimples in arms and legs: a congenital syndromeof mechanical
origin. Am. J. Dis. Child. 74: 543- 562, 1947.

GAM94 332 SOX9 Cameron, F. J.; Hageman, R. M.; Cooke- Yarborough, C.; Kwok, C.;Goodwin, L. 3 B c
L.; Sillence, D. O.; Sinclair, A. H.: A novel germ linemutation in SOX9
causes familial campomelic dysplasia and sex reversal. Hum.Molec. Genet. 5:
1625- 1630, 1996.

GAM94 332 SOX9 Cameron, F. J.; Sinclair, A. H.: Mutations in SRY and SOX9: testis- 3 B c
determininggenes. Hum. Mutat. 9: 388- 395, 1997.

GAM94 332 SOX9 Cooke, C. T.; Mulcahy, M. T.; Cullity, G. J.; Watson, M.; Sprague,P.: 3 B c
Campomelic dysplasia with sex reversal: morphological and cytogeneticstudies
of a case. Pathology 17: 526- 529, 1985.

GAM94 332 SOX9 Cremin, B. J.; Orsmond, G.; Beighton, P.: Autosomal recessiveinheritance in 3 B c
camptomelic dwarfism.(Letter) Lancet I: 488- 489,1973.

GAM94 332 SOX9 Dagna Bricarelli, F.; Fraccaro, M.; Lindsten, J.; Muller, U.;Baggio, P.; 3 B c
Carbone, L. D. L.; Hjerpe, A.; Lindgren, F.; Mayerova,A.; Ringertz, H.;
Ritzen, E. M.; Rovetta, D. C.; Sicchero, C.; Wolf,U.: Sex- reversed XY
females with campomelic dysplasia are H- Y negative. Hum.Genet. 57: 15- 22,
1981.

GAM94 332 SOX9 Ebensperger, C.; Jager, R. J.; Lattermann, U.; Dagna Bricarelli,F.; Keutel, 3 B c
J.; Lindsten, J.; Rehder, H.; Muller, U.; Wolf, U.: Noevidence of mutations
in four candidate genes for male sex determination/differentiationin sex-
reversed XY females with campomelic dysplasia. Ann. Genet. 34:233- 238,
1991.

GAM94 332 SOX9 Fontaine, G.; Walbaum, R.; Farriaux, J. P.; Tilmont, P.; Peuzin,F.; 3 B c
Delecour, M.: Le conseil genetique dans la dysplasie campomelique(a propos
de deux observations). J. Genet. Hum. 28: 267- 279, 1980.

GAM94 332 SOX9 Foster, J. W.; Dominguez- Steglich, M. A.; Guioli, S.; Kwok, C.;Weller, P. 3 B c
A.; Stevanovic, M.; Weissenbach, J.; Mansour, S.; Young,I. D.; Goodfellow,
P. N.; Brook, J. D.; Schafer, A. J.: Campomelicdysplasia and autosomal sex
reversal caused by mutations in an SRY- relatedgene. Nature 372: 525- 530,
1994.

GAM94 332 SOX9 Friedrich, U.; Schaefer, E.; Meinecke, P.: Campomelic dysplasiawithout overt 3 B c
campomelia. Clin. Dysmorph. 1: 172- 178, 1992.

GAM94 332 SOX9 Fryns, J. P.; van den Berghe, K.; van Assche, A.; van den Berghe,H.: 3 B c

Prenatal diagnosis of campomelic dwarfism. Clin. Genet. 19:199- 201, 1981.

GAM94 332 SOX9 Gasca, S.; Canizares, J.; de Santa Barbara, P.; Mejean, C.; Poulat,F.; Berta, P.; Boizet- Bonhoure, B.: A nuclear export signal withinthe high mobility group domain regulates the nucleocytoplasmic translocationof SOX9 during sexual determination. Proc. Nat. Acad. Sci. 99: 11199- 11204,2002. 3 B c

GAM94 332 SOX9 Glass, R. B. J.; Rosenbaum, K. N.: Acampomelic campomelic dysplasia:further radiographic variations. Am. J. Med. Genet. 69: 29- 32, 1997. 3 B c

GAM94 332 SOX9 Hall, B.; Spranger, J. W.: Campomelic dysplasia: further elucidationof a distinct entity. Am. J. Dis. Child. 134: 285- 289, 1980. 3 B c

GAM94 332 SOX9 Hoefnagel, D.; Wurster- Hill, D. H.; Dupree, W. B.; Benirschke,K.; Fuld, G. L.: Camptomelic dwarfism associated with XY- gonadaldysgenesis and chromosome anomalies. Clin. Genet. 13: 489- 499, 1978. 3 B c

GAM94 332 SOX9 Houston, C. S.; Opitz, J. M.; Spranger, J. W.; Macpherson, R.I.; Reed, M. H.; Gilbert, E. F.; Herrmann, J.; Schinzel, A.: Thecampomelic syndrome: review, report of 17 cases, and follow- up onthe currently 17- year- old boy first reported by Maroteaux et al in1971. Am. J. Med. Genet. 15: 3- 28, 1983. 3 B c

GAM94 332 SOX9 Hovmoller, M. L.; Osuna, A.; Eklof, O.; Fredga, K.; Hjerpe, A.;Lindsten, J.; Ritzen, M.; Stanescu, V.; Svenningsen, N.: Camptomelicdwarfism. A genetically determined mesenchymal disorder combined withsex reversal. Hereditas 86: 51- 62, 1977. 3 B c

GAM94 332 SOX9 Huang, W.; Chung, U.; Kronenberg, H. M.; de Crombrugghe, B.:The chondrogenic transcription factor Sox9 is a target of signalingby the parathyroid hormone- related peptide in the growth plate ofendochondral bones. Proc. Nat. Acad. Sci. 98: 160- 165, 2001. 3 B c

GAM94 332 SOX9 Kanai, Y.; Koopman, P.: Structural and functional characterizationof the mouse Sox9 promoter: implications for campomelic dysplasia. Hum.Molec. Genet. 8: 691- 696, 1999. 3 B c

GAM94 332 SOX9 Lahn, B. T.; Page, D. C.: Four evolutionary strata on the humanX chromosome. Science 286: 964- 967, 1999. 3 B c

GAM94 332 SOX9 Lahn, B. T.; Page, D. C.: Functional coherence of the human Ychromosome. Science 278: 675- 680, 1997. 3 B c

GAM94 332 SOX9 Lee, F. A.; Issacs, H.; Strauss, J.: The 'camptomelic' syndrome.Short life- span dwarfism with respiratory distress, hypotonia, peculiarfacies, and multiple skeletal and cartilaginous deformities. Am.J. Dis. Child. 124: 485- 496, 1972. 3 B c

GAM94 332 SOX9 Lynch, S. A.; Gaunt, M. L.; Minford, A. M. B.: Campomelic dysplasia:evidence of autosomal dominant inheritance. J. Med. Genet. 30: 683- 686,1993. 3 B c

GAM94 332 SOX9 Macpherson, R. I.; Skinner, S. A.; Donnenfeld, A. E.: Acampomeliccampomelic dysplasia. Pediat. Radiol. 20: 90- 93, 1989. 3 B c

GAM94 332 SOX9 Mansour, S.; Hall, C. M.; Pembrey, M. E.; Young, I. D.: A clinicaland genetic study of campomelic dysplasia. J. Med. Genet. 32: 415- 420,1995. 3 B c

GAM94 332 SOX9 Maraia, R.; Saal, H. M.; Wangsa, D.: A chromosome 17q de novoparacentric inversion in a patient with campomelic dysplasia; casereport and etiologic hypothesis. Clin. Genet. 39: 401- 408, 1991. 3 B c

GAM94 332 SOX9 Maroteaux, P.; Spranger, J. W.; Opitz, J. M.; Kucera, J.; Lowry,R. B.; Schimke, R. N.; Kagan, S. M.: Le syndrome campomelique. PresseMed. 22: 1157- 1162, 1971. 3 B c

GAM94 332 SOX9 Mellows, H. J.; Pryse- Davies, J.; Bennett, M. J.; Carter, C. O.: The camptomelic syndrome in two female siblings. Clin. Genet. 18:137- 141, 1980. 3 B c

GAM94 332 SOX9 Meyer, J.; Sudbeck, P.; Held, M.; Wagner, T.; Schmitz, M. L.;Bricarelli, F. 3 B c
D.; Eggermont, E.; Friedrich, U.; Haas, O. A.; Kobelt,A.; Leroy, J. G.; van
Maldergem, L.; Michel, E.; Mitulla, B.; Pfeiffer,R. A.; Schinzel, A.;
Schmidt, H.; Scherer, G.: Mutational analysisof the SOX9 gene in campomelic
dysplasia and autosomal sex reversal:lack of genotype/phenotype
correlations. Hum. Molec. Genet. 6: 91- 98,1997.

GAM94 332 SOX9 Moedjono, S. J.; Crandall, B. F.; Sparkes, R. S.; Feldman, G.M.; Austin, G. 3 B c
E.; Perry, S.: The campomelic syndrome in a singletonand monozygotic twins.
Clin. Genet. 18: 397- 401, 1980.

GAM94 332 SOX9 Moog, U.; Jansen, N. J. G.; Scherer, G.; Schrander- Stumpel, C.T. R. M.: 3 B c
Acampomelic campomelic syndrome. Am. J. Med. Genet. 104:239- 245, 2001.

GAM94 332 SOX9 Morais da Silva, S.; Hacker, A.; Harley, V.; Goodfellow, P.; Swain,A.; 3 B c
Lovell- Badge, R.: Sox9 expression during gonadal developmentimplies a
conserved role for the gene in testis differentiation inmammals and birds.
Nature Genet. 14: 62- 68, 1996.

GAM94 332 SOX9 Murakami, S.; Kan, M.; McKeehan, W. L.; de Crombrugghe, B.: Up- regulationof 3 B c
the chondrogenic Sox9 gene by fibroblast growth factors is mediatedby the
mitogen- activated protein kinase pathway. Proc. Nat. Acad.Sci. 97: 1113-
1118, 2000.

GAM94 332 SOX9 Ninomiya, S.; Isomura, M.; Narahara, K.; Seino, Y.; Nakamura,Y.: Isolation 3 B c
of a testis- specific cDNA on chromosome 17q from aregion adjacent to the
breakpoint of t(12;17) observed in a patientwith acampomelic campomelic
dysplasia and sex reversal. Hum. Molec.Genet. 5: 69- 72, 1996.

GAM94 332 SOX9 Ninomiya, S.; Yokoyama, Y.; Teraoka, M.; Mori, R.; Inoue, C.;Yamashita, S.; 3 B c
Tamai, H.; Funato, M.; Seino, Y.: A novel mutation(296 del G) of the SOX9
gene in a patient with campomelic syndromeand sex reversal. Clin. Genet. 58:
224- 227, 2000.

GAM94 332 SOX9 Olney, P. N.; Kean, L. S.; Graham, D.; Elsas, L. J.; May, K. M.: Campomelic 3 B c
syndrome and deletion of SOX9. Am. J. Med. Genet. 84:20- 24, 1999.

GAM94 332 SOX9 Ozkilic, A.; Seven, M.; Yuksel, A.: A case of acampomelic 3 B c
campomelicdysplasia. Genet. Counsel. 13: 23- 28, 2002.

GAM94 332 SOX9 Patel, M.; Dorman, K. S.; Zhang, Y.- H.; Huang, B.- L.; Arnold,A. P.; 3 B c
Sinsheimer, J. S.; Vilain, E.; McCabe, E. R. B.: Primate DAX1,SRY, and SOX9:
evolutionary stratification of sex- determination pathway. Am.J. Hum. Genet.
68: 275- 280, 2001.

GAM94 332 SOX9 Pfeifer, D.; Kist, R.; Dewar, K.; Devon, K.; Lander, E. S.; Birren,B.; 3 B c
Korniszewski, L.; Back, E.; Scherer, G.: Campomelic dysplasiatranslocation
breakpoints are scattered over 1 Mb proximal to SOX9:evidence for an
extended control region. Am. J. Hum. Genet. 65:111- 124, 1999.

GAM94 332 SOX9 Puck, S. M.; Haseltine, F. P.; Francke, U.: Absence of H- Y antigenin an XY 3 B c
female with campomelic dysplasia. Hum. Genet. 57: 23- 27,1981.

GAM94 332 SOX9 Rimoin, D. L.: Personal Communication. Torrance, Calif. 8/12/1976. 3 B c

GAM94 332 SOX9 Rodriguez, J. I.: Vascular anomalies in campomelic syndrome. Am.J. Med. 3 B c
Genet. 46: 185- 192, 1993.

GAM94 332 SOX9 Savarirayan, R.; Bankier, A.: Acampomelic campomelic dysplasiawith de novo 3 B c
5q;17q reciprocal translocation and severe phenotype. J.Med. Genet. 35: 597-
599, 1998.

GAM94 332 SOX9 Schimke, R. N.: XY sex- reversed campomelia- - possibly an X- 3 B c
linkeddisorder? (Letter) Clin. Genet. 16: 62- 63, 1979.

GAM94 332 SOX9 Schmickel, R. D.: Contiguous gene syndromes: a component of 3 B c

recognizablesyndromes. J. Pediat. 109: 231- 241, 1986.

GAM94 332 SOX9 Shafai, T.; Schwartz, L.: Camptomelic syndrome in siblings. J.Pediat. 89: 512- 513, 1976. 3 B c

GAM94 332 SOX9 Spranger, J.: Advances in bone dysplasias. (Abstract) SixthInt. Cong. Hum. Genet. Jerusalem , 1981. 3 B c

GAM94 332 SOX9 Stuve, A.; Wiedemann, H.- R.: Congenital bowing of the long bonesin two sisters. (Letter) Lancet I: 495, 1971. 3 B c

GAM94 332 SOX9 Sudbeck, P.; Schmitz, M. L.; Baeuerle, P. A.; Scherer, G.: Sexreversal by loss of the C- terminal transactivation domain of humanSOX9. Nature Genet. 13: 230- 232, 1996. 3 B c

GAM94 332 SOX9 Thong, M.- K.; Scherer, G.; Kozlowski, K.; Haan, E.; Morris, L.: Acampomelic campomelic dysplasia with SOX9 mutation. Am. J. Med.Genet. 93: 421- 425, 2000. 3 B c

GAM94 332 SOX9 Thurmon, T. F.; De Fraites, E. B.; Anderson, E. E.: Familialcampomelic dwarfism. J. Pediat. 83: 841- 843, 1973. 3 B c

GAM94 332 SOX9 Tommerup, N.; Schempp, W.; Meinecke, P.; Pedersen, S.; Bolund,L.; Brandt, C.; Goodpasture, C.; Guldberg, P.; Held, K.; Reinwein,H.; Saugstad, O. D.; Scherer, G.; Skjeldal, O.; Toder, R.; Westvik,J.; van der Hagen, C. B.; Wolf, U.: Assignment of an autosomal sexreversal locus (SRA1) and campomelic dysplasia (CMPD1) to 17q24.3- q25.1. NatureGenet. 4: 170- 174, 1993. 3 B c

GAM94 332 SOX9 Vidal, V. P. I.; Chaboissier, M.- C.; de Rooij, D. G.; Schedl,A.: Sox9 induces testis development in XX transgenic mice. NatureGenet. 28: 216- 217, 2001. 3 B c

GAM94 332 SOX9 Wagner, T.; Wirth, J.; Meyer, J.; Zabel, B.; Held, M.; Zimmer,J.; Pasantes, J.; Dagna Bricarelli, F.; Keutel, J.; Hustert, E.; Wolf,U.; Tommerup, N.; Schempp, W.; Scherer, G.: Autosomal sex reversaland campomelic dysplasia are caused by mutations in and around theSRY- related gene SOX9. Cell 79: 1111- 1120, 1994. 3 B c

GAM94 332 SOX9 Weller, S. D. V.: Hypophosphatasia with congenital dimples. Proc.Roy. Soc. Med. 52: 637, 1959. 3 B c

GAM94 332 SOX9 Wirth, J.; Wagner, T.; Meyer, J.; Pfeiffer, R. A.; Tietze, H.- U.;Schempp, W.; Scherer, G.: Translocation breakpoints in three patientswith campomelic dysplasia and autosomal sex reversal map more than130 kb from SOX9. Hum. Genet. 97: 186- 193, 1996. 3 B c

GAM94 332 SOX9 Wright, E.; Hargrave, M. R.; Christiansen, J.; Cooper, L.; Kun,J.; Evans, T.; Gangadharan, U.; Greenfield, A.; Koopman, P.: TheSry- related gene Sox9 is expressed during chondrogenesis in mouseembryos. Nature Genet. 9: 15- 20, 1995. 3 B c

GAM94 332 SOX9 Wunderle, V. M.; Critcher, R.; Hastie, N.; Goodfellow, P. N.;Schedl, A.: Deletion of long- range regulatory elements upstream ofSOX9 causes campomelic dysplasia. Proc. Nat. Acad. Sci. 95: 10649- 10654,1998. 3 B c

GAM94 332 SOX9 Young, I. D.; Zuccollo, J. M.; Maltby, E. L.; Broderick, N. J.: Campomelic dysplasia associated with a de novo 2q;17q reciprocaltranslocation. J. Med. Genet. 29: 251- 252, 1992. 3 B c

GAM94 332 SYNGR1 Janz, R.; Sudhof, T. C.; Hammer, R. E.; Unni, V.; Siegelbaum, S.A.; Bolshakov, V. Y.: Essential roles in synaptic plasticity forsynaptogyrin I and synaptophysin I. Neuron 24: 687- 700, 1999. 3 B c

GAM94 332 SYNGR1 Kedra, D.; Pan, H.- Q.; Seroussi, E.; Fransson, I.; Guilbaud, C.;Collins, J. E.; Dunham, I.; Blennow, E.; Roe, B. A.; Piehl, F.; Dumanski,J. P.: Characterization of the human synaptogyrin gene family. Hum.Genet. 103: 131- 3 B c

141, 1998.

GAM94 332 SYNGR1 McMahon, H. T.; Bolshakov, V. Y.; Janz, R.; Hammer, R. E.; Siegelbaum,S. A.; 3 B c
Sudhof, T. C.: Synaptophysin, a major synaptic vesicle protein,is not
essential for neurotransmitter release. Proc. Nat. Acad. Sci. 93:4760- 4764,
1996.

GAM94 332 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; 3 B c
Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.;
Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1
are associated with human left- right lateralitydefects. Nature Genet. 26:
365- 369, 2000.

GAM94 332 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: 3 B c
Molecular characterization of a gene of the 'EGF family' expressedin
undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991,
1989.

GAM94 332 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, 3 B c
A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation
in the CFC domain of TDGF1 is associated with human forebraindefects. Hum.
Genet. 110: 422- 428, 2002.

GAM94 332 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; 3 B c
Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene
and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991.

GAM94 332 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. 3 B c
A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes.
Mammalian Genome 8: 502- 505, 1997.

GAM94 332 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; 3 B c
Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and
Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996.

GAM94 332 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, 3 B c
G.: Regional localization of the human EGF- like growthfactor CRIPTO gene
(TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995.

GAM94 332 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in 3 B c
vertebratedevelopment. Trends Genet. 16: 303- 309, 2000.

GAM94 332 TEM8 Bradley, K. A.; Mogridge, J.; Mourez, M.; Collier, R. J.; Young,J. A. T.: 3 B c
Identification of the cellular receptor for anthrax toxin. Nature 414:160-
161, 2001.

GAM94 332 TEM8 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. 3 B c
W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in
mice and humans. Cancer Res. 61: 6649- 6655, 2001.

GAM94 332 TEM8 Scott, A. F.: Personal Communication. Baltimore, Md. 10/23/2001. 3 B c

GAM94 332 TEM8 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; 3 B c
Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.;
Kinzler, K. W.: Genes expressed in human tumor endothelium. Science
289:1197- 1202, 2000.

GAM94 332 TGFA Brissenden, J. E.; Derynck, R.; Francke, U.: Transforming growthfactor alpha 3 B c
gene (TGFA) maps to human chromosome 2 close to the breakpointof the t(2;8)
variant translocation in Burkitt lymphoma. (Abstract) Cytogenet.Cell Genet.
40: 589 only, 1985.

GAM94 332 TGFA Collin, G. B.; Marshall, J. D.; Naggert, J. K.; Nishina, P. M.: TGFA: exon- 3 B c
intron structure and evaluation as a candidate gene forAlstrom syndrome.
(Letter) Clin. Genet. 55: 61- 62, 1999.

GAM94 332 TGFA Ellis, D. L.; Kafka, S. P.; Chow, J. C.; Nanney, L. B.; Inman,W. H.; 3 B c
McCadden, M. E.; King, L. E., Jr.: Melanoma, growth factors,acanthosis
nigricans, the sign of Leser- Trelat, and multiple acrochordons:a possible
role for alpha- transforming growth factor in cutaneousparaneoplastic
syndromes. New Eng. J. Med. 317: 1582- 1587, 1987.

GAM94 332 TGFA Fernandez- Larrea, J.; Merlos- Suarez, A.; Urena, J. M.; Baselga,J.; 3 B c
Arribas, J.: A role for a PDZ protein in the early secretorypathway for the
targeting of proTGF- alpha to the cell surface. Molec.Cell 3: 423- 433,
1999.

GAM94 332 TGFA Fowler, K. J.; Mann, G. B.; Dunn, A. R.: Linkage of the murinetransforming 3 B c
growth factor- alpha gene with Igk, Ly- 2, and Fabp1 onchromosome 6.
Genomics 16: 782- 784, 1993.

GAM94 332 TGFA Kramer, A.; Yang, F.- C.; Snodgrass, P.; Li, X.; Scammell, T. E.;Davis, F. 3 B c
C.; Weitz, C. J.: Regulation of daily locomotor activityand sleep by
hypothalamic EGF receptor signaling. Science 294: 2511- 2515,2001.

GAM94 332 TGFA Tam, J. P.; Scheikh, M. A.; Solomon, D. S.; Ossowski, L.: Efficientsynthesis 3 B c
of human type alpha transforming growth factor: its physicaland biological
characterization. Proc. Nat. Acad. Sci. 83: 8082- 8086,1986.

GAM94 332 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. 3 B c
B.: Assignment of the gene coding for human TGF- alphato chromosome 2p13.
(Abstract) Cytogenet. Cell Genet. 40: 762 only,1985.

GAM94 332 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. 3 B c
B.: The gene for human transforming growth factor alphais on the short arm
of chromosome 2. Cytogenet. Cell Genet. 42:94- 98, 1986.

GAM94 332 TGM3 Kim, I.- G.; Gorman, J. J.; Park, S.- C.; Chung, S.- I.; Steinert,P. M.: The 3 B c
deduced sequence of the novel protransglutaminase E (TGase3)of human and
mouse. J. Biol. Chem. 268: 12682- 12690, 1993.

GAM94 332 TGM3 Kim, I.- G.; Lee, S.- C.; Lee, J.- H.; Yang, J.- M.; Chung, S.- I.;Steinert, 3 B c
P. M.: Structure and organization of the human transglutaminase3 gene:
evolutionary relationship to the transglutaminase family. J.Invest. Derm.
103: 137- 142, 1994.

GAM94 332 TGM3 Wang, M.; Kim, I.- G.; Steinert, P. M.; McBride, O. W.: Assignmentof the 3 B c
human transglutaminase 2 (TGM2) and transglutaminase 3 (TGM3)genes to
chromosome 20q11.2. Genomics 23: 721- 722, 1994.

GAM94 332 TLE1 Imai, Y.; Kurokawa, M.; Tanaka, K.; Friedman, A. D.; Ogawa, S.;Mitani, K.; 3 B c
Yazaki, Y.; Hirai, H.: TLE, the human homolog of groucho,interacts with AML1
and acts as a repressor of AML1- induced transactivation. Biochem.Biophys.
Res. Commun. 252: 582- 589, 1998.

GAM94 332 TLE1 Liu, Y.; Dehni, G.; Purcell, K. J.; Sokolow, J.; Carcangiu, M.L.; Artavanis- 3 B c
Tsakonas, S.; Stifani, S.: Epithelial expression andchromosomal location of
human TLE genes: implications for Notch signalingand neoplasia. Genomics 31:
58- 64, 1996.

GAM94 332 TLE1 Miyasaka, H.; Choudhury, B. K.; Hou, E. W.; Li, S. S.- L.: Molecularcloning 3 B c
and expression of mouse and human cDNA encoding AES and ESGproteins with
strong similarity to Drosophila enhancer of split grouchoprotein. Europ. J.
Biochem. 216: 343- 352, 1993.

GAM94 332 TLE1 Stifani, S.; Blaumueller, C. M.; Redhead, N. J.; Hill, R. E.; Artavanis- 3 B c
Tsakonas,S.: Human homologs of a Drosophila enhancer of split gene
productdefine a novel family of nuclear proteins. Nature Genet. 2: 119-
127,1992.

GAM94 332 TRPM1 Duncan, L. M.; Deeds, J.; Hunter, J.; Shao, J.; Holmgren, L. M.;Woolf, E. A.; Tepper, R. I.; Shyjan, A. W.: Down- regulation of thenovel gene melastatin correlates with potential for melanoma metastasis. CancerRes. 58: 1515- 1520, 1998. 3 B c

GAM94 332 TRPM1 Fang, D.; Setaluri, V.: Expression and up- regulation of alternativelyspliced transcripts of melastatin, a melanoma metastasis- related gene,in human melanoma cells. Biochem. Biophys. Res. Commun. 279: 53- 61,2000. 3 B c

GAM94 332 TRPM1 Hunter, J. J.; Shao, J.; Smutko, J. S.; Dussault, B. J.; Nagle,D. L.; Woolf, E. A.; Holmgren, L. M.; Moore, K. J.; Shyjan, A. W.: Chromosomal localization and genomic characterization of the mousemelastatin gene (Mlsn1). Genomics 54: 116- 123, 1998. 3 B c

GAM94 332 TRPM1 Xu, X. Z.; Moebius, F.; Gill, D. L.; Montell, C.: Regulation ofmelastatin, a TRP- related protein, through interaction with a cytoplasmicisoform. Proc. Nat. Acad. Sci. 98: 10692- 10697, 2001. 3 B c

GAM94 332 TXK Haire, R. N.; Litman, G. W.: The murine form of TXK, a novel TECkinase expressed in thymus maps to chromosome 5. Mammalian Genome 6:476- 480, 1995. 3 B c

GAM94 332 TXK Haire, R. N.; Ohta, Y.; Lewis, J. E.; Fu, S. M.; Kroisel, P.; Litman,G. W.: TXK, a novel human tyrosine kinase expressed in T cells sharessequence identity with Tec family kinases and maps to 4p12. Hum.Molec. Genet. 3: 897- 901, 1994. 3 B c

GAM94 332 TXK Schaeffer, E. M.; Debnath, J.; Yap, G.; McVicar, D.; Liao, X. C.;Littman, D. R.; Sher, A.; Varmus, H. E.; Lenardo, M. J.; Schwartzberg,P. L.: Requirement for Tec kinases Rlk and Itk in T cell receptorsignaling and immunity. Science 284: 638- 641, 1999. 3 B c

GAM94 332 TXK Schneider, H.; Schwartzberg, P. L.; Rudd, C. E.: Resting lymphocytekinase (Rlk/Txk) phosphorylates the YVKM motif and regulates PI 3- kinasebinding to T- cell antigen CTLA- 4. Biochem. Biophys. Res. Commun. 252:14- 19, 1998. 3 B c

GAM94 332 TXK Takeba, Y.; Nagafuchi, H.; Takeno, M.; Kashiwakura, J.; Suzuki,N.: Txk, a member of nonreceptor tyrosine kinase of Tec family, actsas a Th1 cell- specific transcription factor and regulates IFN- gammagene transcription. J. Immun. 168: 2365- 2370, 2002. 3 B c

GAM94 332 USF1 Gregor, P. D.; Sawadogo, M.; Roeder, R. G.: The adenovirus majorlate transcription factor USF is a member of the helix- loop- helixgroup of regulatory proteins and binds to DNA as a dimer. Genes Dev. 4:1730- 1740, 1990. 3 B c

GAM94 332 USF1 Henrion, A. A.; Martinez, A.; Mattei, M.- G.; Kahn, A.; Raymondjean,M.: Structure, sequence, and chromosomal location of the gene forUSF2 transcription factors in mouse. Genomics 25: 36- 43, 1995. 3 B c

GAM94 332 USF1 Roy, A. L.; Du, H.; Gregor, P. D.; Novina, C. D.; Martinez, E.;Roeder, R. G.: Cloning of an Inr- and E- box binding protein, TFII- I,that interacts physically and functionally with USF1. EMBO J. 16:7091- 7104, 1997. 3 B c

GAM94 332 USF1 Shieh, B.- H.; Sparkes, R. S.; Gaynor, R. B.; Lusis, A. J.: Localizationof the gene- encoding upstream stimulatory factor (USF) to human chromosome1q22- q23. Genomics 16: 266- 268, 1993. 3 B c

GAM94 332 USF1 Steingrimsson, E.; Sawadogo, M.; Gilbert, D. J.; Zervos, A. S.;Brent, R.; Blanar, M. A.; Fisher, D. E.; Copeland, N. G.; Jenkins,N. A.: Murine chromosomal location of five bHLH- Zip transcriptionfactor genes. Genomics 28: 179- 183, 1995. 3 B c

GAM94 332 USF1 Zhong, G.; Fan, P.; Ji, H.; Dong, F.; Huang, Y.: Identificationof a 3 B c

chlamydial protease- like activity factor responsible for thedegradation of host transcription factors. J. Exp. Med. 193: 935- 942,2001.

GAM94 332 USP14 Deshpande, K. L.; Seubert, P. H.; Tillman, D. M.; Farkas, W. R.;Katze, J. 3 B c R.: Cloning and characterization of cDNA encoding the rabbittRNA- guanine transglycosylase 60- kilodalton subunit. Arch. Biochem.Biophys. 326: 1- 7, 1996.

GAM94 332 USP14 Wilson, S. M.; Bhattacharyya, B.; Rachel, R. A.; Coppola, V.; Tessarollo,L.; 3 B c Householder, D. B.; Fletcher, C. F.; Miller, R. J.; Copeland,N. G.; Jenkins, N. A.: Synaptic defects in ataxia mice result froma mutation in Usp14, encoding a ubiquitin- specific protease. NatureGenet. 7Oct, 2002. Note: Advance Electronic Publication.

GAM94 332 VEGFB Bellomo, D.; Headrick, J. P.; Silins, G. U.; Paterson, C. A.; Thomas,P. S.; 3 B c Gartside, M.; Mould, A.; Cahill, M. M.; Tonks, I. D.; Grimmond,S. M.; Townson, S.; Wells, C.; Little, M.; Cummings, M. C.; Hayward,N. K.; Kay, G. F.: Mice lacking the vascular endothelial growth factor- Bgene (Vegfb) have smaller hearts, dysfunctional coronary vasculature,and impaired recovery from cardiac ischemia. Circ. Res. 86: e29- e35,2000.

GAM94 332 VEGFB Gerace, L; Cirenei, N.; Cappelletti, M.; Petraroli, R.; Sebastiani,F.; 3 B c Marziliano, N.: Assignment of the mouse Vegfb gene to mouse chromosome19B by in situ hybridization. Cytogenet. Cell Genet. 95: 242- 243,2001.

GAM94 332 VEGFB Grimmond, S.; Lagercrantz, J.; Drinkwater, C.; Silins, G.; Townson,S.; 3 B c Pollock, P.; Gotley, D.; Carson, E.; Rakar, S.; Nordenskjold,M.; Ward, L.; Hayward, N.; Weber, G.: Cloning and characterizationof a novel human gene related to vascular endothelial growth factor. GenomeRes. 6: 124- 131, 1996.

GAM94 332 VEGFB Olofsson, B.; Pajusola, K.; Kaipainen, A.; von Euler, G.; Joukov,V.; 3 B c Saksela, O.; Orpana, A.; Pettersson, R. F.; Alitalo, K.; Eriksson,U.: Vascular endothelial growth factor B, a novel growth factor forendothelial cells. Proc. Nat. Acad. Sci. 93: 2576- 2581, 1996.

GAM94 332 VEGFB Olofsson, B.; Pajusola, K.; von Euler, G.; Chilov, D.; Alitalo,K.; Eriksson, 3 B c U.: Genomic organization of the mouse and human genesfor vascular endothelial growth factor B (VEGF- B) and characterizationof a second splice isoform. J. Biol. Chem. 271: 19310- 19317, 1996.

GAM94 332 VNN1 Aurrand- Lions, M.; Galland, F.; Bazin, H.; Zakharyev, V. M.; Imhof,B. A.; 3 B c Naquet, P.: Vanin- 1, a novel GPI- linked perivascular moleculeinvolved in thymus homing. Immunity 5: 391- 405, 1996.

GAM94 332 VNN1 Galland, F.; Malergue, F.; Bazin, H.; Mattei, M. G.; Aurrand- Lions,M.; 3 B c Theillet, C.; Naquet, P.: Two human genes related to murine vanin- 1are located on the long arm of human chromosome 6. Genomics 53:203- 213, 1998.

GAM94 332 VNN1 Grimmond, S.; Van Hateren, N.; Siggers, P.; Arkell, R.; Larder,R.; Soares, 3 B c M. B.; de Fatima Bonaldo, M.; Smith, L.; Tymowska- Lalanne,Z.; Wells, C.; Greenfield, A.: Sexually dimorphic expression of proteasenexin- 1 and vanin- 1 in the developing mouse gonad prior to overt differentiationsuggests a role in mammalian sexual development. Hum. Molec. Genet. 9:1553- 1560, 2000.

GAM94 332 VNN1 Martin, F.; Malergue, F.; Pitari, G.; Philippe, J. M.; Philips,S.; Chabret, 3 B c C.; Granjeaud, S.; Mattei, M. G.; Mungall, A. J.; Naquet,P.; Galland, F.: Vanin genes are clustered (human 6q22- 24 and mouse10A2B1) and encode isoforms of pantetheinase ectoenzymes. Immunogenetics 53:296- 306, 2001.

GAM94 332 VNN1 Pitari, G.; Malergue, F.; Martin, F.; Philippe, J. M.; Massucci,M. T.; 3 B c Chabret, C.; Maras, B.; Dupre, S.; Naquet, P.; Galland, F.: Pantetheinase activity of membrane- bound vanin- 1: lack of free cysteaminein tissues of

vanin- 1 deficient mice. FEBS Lett. 483: 149- 154, 2000.

GAM96 394 ABCA1 Becq, F.; Hamon, Y.; Bajetto, A.; Gola, M.; Verrier, B.; Chimini,G.: ABC1, 1 A c
an ATP binding cassette transporter required for phagocytosisof apoptotic
cells, generates a regulated anion flux after expressionin Xenopus laevis
oocytes. J. Biol. Chem. 272: 2695- 2699, 1997.

GAM96 394 ABCA1 Bodzioch, M.; Orso, E.; Klucken, J.; Langmann, T.; Bottcher, A.;Diederich, 1 A c
W.; Drobnik, W.; Barlage, S.; Buchler, C.; Porsch- Ozcurumez,M.; Kaminski,
W. E.; Hahmann, H. W.; Oette, K.; Rothe, G.; Aslanidis,C.; Lackner, K. J.;
Schmitz, G.: The gene encoding ATP- binding cassettetransporter 1 is mutated
in Tangier disease. Nature Genet. 22: 347- 351,1999.

GAM96 394 ABCA1 Brooks- Wilson, A.; Marcil, M.; Clee, S. M.; Zhang, L.- H.; Roomp,K.; van 1 A c
Dam, M.; Yu, L.; Brewer, C.; Collins, J. A.; Molhuizen, H.O. F.; Loubser,
O.; Ouelette, B. F. F.; and 14 others: Mutationsin ABC1 in Tangier disease
and familial high- density lipoprotein deficiency. NatureGenet. 22: 336-
345, 1999.

GAM96 394 ABCA1 Decottignies, A.; Goffeau, A.: Complete inventory of the yeastABC proteins. 1 A c
Nature Genet. 15: 137- 145, 1997.

GAM96 394 ABCA1 Goossens, M.; Brauner, R.; Czernichow, P.; Duquesnoy, P.; Rappaport,R.: 1 A c
Isolated growth hormone (GH) deficiency type 1A associated witha double
deletion in the human GH gene cluster. J. Clin. Endocr.Metab. 62: 712- 716,
1986.

GAM96 394 ABCA1 Guo, Z.; Inazu, A.; Yu, W.; Suzumura, T.; Okamoto, M.; Nohara,A.; 1 A c
Higashikata, T.; Sano, R.; Wakasugi, K.; Hayakawa, T.; Yoshida,K.; Suehiro,
T.; Schmitz, G.; Mabuchi, H.: Double deletions and missensemutations in the
first nucleotide- binding fold of the ATP- bindingcassette transporter A1
(ABCA1) gene in Japanese patients with Tangierdisease. J. Hum. Genet. 47:
325- 329, 2002.

GAM96 394 ABCA1 Hong, S. H.; Rhyne, J.; Zeller, K.; Miller, M.: Novel ABCA1 compoundvariant 1 A c
associated with HDL cholesterol deficiency. Biochim. Biophys.Acta 1587: 60-
64, 2002.

GAM96 394 ABCA1 Hoop, R. C.; Russo, L. S.; Riconda, D. L.; Schwartz, L. S.; Hoffman,E. P.: 1 A c
Restoration of half the normal dystrophin sequence in a double-
deletionDuchenne muscular dystrophy family. Am. J. Med. Genet. 49: 323-
327,1994.

GAM96 394 ABCA1 Huang, W.; Moriyama, K.; Koga, T.; Hua, H.; Ageta, M.; Kawabata,S.; 1 A c
Mawatari, K.; Imamura, T.; Eto, T.; Kawamura, M.; Teramoto, T.;Sasaki, J.:
Novel mutations in ABCA1 gene in Japanese patients withTangier disease and
familial high density lipoprotein deficiency withcoronary heart disease.
Biochim. Biophys. Acta 1537: 71- 78, 2001.

GAM96 394 ABCA1 Ishii, J.; Nagano, M.; Kujiraoka, T.; Ishihara, M.; Egashira,T.; Takada, D.; 1 A c
Tsuji, M.; Hattori, H.; Emi, M.: Clinical variantof Tangier disease in
Japan: mutation of the ABCA1 gene in hypoalphalipoproteinemiawith corneal
lipidosis. J. Hum. Genet. 47: 366- 369, 2002.

GAM96 394 ABCA1 Jennings, M. W.; Jones, R. W.; Wood, W. G.; Weatherall, D. J.: Analysis of 1 A c
an inversion within the human beta globin gene cluster. NucleicAcids Res.
13: 2897- 2906, 1985.

GAM96 394 ABCA1 Kulozik, A. E.; Bellan- Koch, A.; Kohne, E.; Kleihauer, E.: 1 A c
Adeletion/inversion rearrangement of the beta- globin gene cluster ina
Turkish family with delta- beta(0)- thalassemia intermedia. Blood 79:2455-
2459, 1992.

GAM96 394 ABCA1 Langmann, T.; Klucken, J.; Reil, M.; Liebisch, G.; Luciani, M.- F.;Chimini, 1 A c
G.; Kaminski, W. E.; Schmitz, G.: Molecular cloning of thehuman ATP- binding
cassette transporter 1 (hABC1): evidence for sterol- dependentregulation in
macrophages. Biochem. Biophys. Res. Commun. 257: 29- 33,1999.

GAM96 394 ABCA1 Lapicka- Bodzioch, K.; Bodzioch, M.; Krull, M.; Kielar, D.; Probst,M.; Kiec, 1 A c
B.; Andrikovics, H.; Bottcher, A.; Hubacek, J.; Aslanidis,C.; Suttorp, N.;
Schmitz, G.: Homogeneous assay based on 52 primersets to scan for mutations
of the ABCA1 gene and its application ingenetic analysis of a new patient
with familial high- density lipoproteindeficiency syndrome. Biochim.
Biophys. Acta 1537: 42- 48, 2001.

GAM96 394 ABCA1 Lawn, R. M.; Wade, D. P.; Garvin, M. R.; Wang, X.; Schwartz, K.;Porter, J. 1 A c
G.; Seilhamer, J. J.; Vaughan, A. M.; Oram, J. F.: TheTangier disease gene
product ABC1 controls the cellular apolipoprotein- mediatedlipid removal
pathway. J. Clin. Invest. 104: R25- R31, 1999.

GAM96 394 ABCA1 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, 1 A c
J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid
synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000.

GAM96 394 ABCA1 Luciani, M. F.; Denizot, F.; Savary, S.; Mattei, M. G.; Chimini,G.: Cloning 1 A c
of two novel ABC transporters mapping on human chromosome9. Genomics 21:
150- 159, 1994.

GAM96 394 ABCA1 Marcil, M.; Boucher, B.; Krimbou, L.; Solymoss, B. C.; Davignon,J.; 1 A c
Frohlich, J.; Genest, J., Jr.: Severe familial HDL deficiencyin French-
Canadian kindreds: clinical, biochemical, and molecularcharacterization.
Arterioscler. Thromb. Vasc. Biol. 15: 1015- 1024,1995.

GAM96 394 ABCA1 Marcil, M.; Yu, L.; Krimbou, L.; Boucher, B.; Oram, J. F.; Cohn,J. S.; 1 A c
Genest, J., Jr.: Cellular cholesterol transport and effluxin fibroblasts are
abnormal in subjects with familial HDL deficiency. Arterioscler.Thromb.
Vasc. Biol. 19: 159- 169, 1999.

GAM96 394 ABCA1 McNeish, J.; Aiello, R. J.; Guyot, D.; Turi, T.; Gabel, C.; Aldinger,C.; 1 A c
Hoppe, K. L.; Roach, M. L.; Royer, L. J.; de Wet, J.; Broccardo,C.; Chimini,
G.; Francone, O. L.: High density lipoprotein deficiencyand foam cell
accumulation in mice with targeted disruption of ATP- bindingcassette
transporter- 1. Proc. Nat. Acad. Sci. 97: 4245- 4250, 2000.

GAM96 394 ABCA1 Orso, E.; Broccardo, C.; Kaminski, W. E.; Bottcher, A.; Liebisch,G.; 1 A c
Drobnik, W.; Gotz, A.; Chambenoit, O.; Diederich, W.; Langmann,T.; Spruss,
T.; Luciani, M.- F.; Rothe, G.; Lackner, K. J.; Chimini,G.; Schmitz, G.:
Transport of lipids from Golgi to plasma membraneis defective in Tangier
disease patients and Abc1- deficient mice. NatureGenet. 24: 192- 196, 2000.

GAM96 394 ABCA1 Pullinger, C. R.; Hakamata, H.; Duchateau, P. N.; Eng, C.; Aouizerat,B. E.; 1 A c
Cho, M. H.; Fielding, C. J.; Kane, J. P.: Analysis of hABC1gene 5- prime
end: additional peptide sequence, promoter region, andfour polymorphisms.
Biochem. Biophys. Res. Commun. 271: 451- 455,2000.

GAM96 394 ABCA1 Remaley, A. T.; Rust, S.; Rosier, M.; Knapper, C.; Naudin, L.;Broccardo, C.; 1 A c
Peterson, K. M.; Koch, C.; Arnould, I.; Prades, C.;Duverger, N.; Funke, H.;
Assman, G.; Dinger, M.; Dean, M.; Chimini,G.; Santamarina- Fojo, S.;
Fredrickson, D. S.; Denefle, P. Brewer,H. B., Jr.: Human ATP- binding
cassette transporter 1 (ABC1): genomicorganization and identification of the
genetic defect in the originalTangier disease kindred. Proc. Nat. Acad. Sci.
96: 12685- 12690,1999.

GAM96 394 ABCA1 Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, 1 A c

K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers. Science 289: 1524- 1529, 2000.

GAM96 394 ABCA1 Rust, S.; Rosier, M.; Funke, H.; Real, J.; Amoura, Z.; Piette,J.- C.; Deleuze, J.- F.; Brewer, H. B.; Duverger, N.; Denefle, P.; Assmann,G.: Tangier disease is caused by mutations in the gene encoding ATP- bindingcassette transporter 1. Nature Genet. 22: 352- 355, 1999. 1 A c

GAM96 394 ABCA1 Santamarina- Fojo, S.; Peterson, K.; Knapper, C.; Qiu, Y.; Freeman,L.; Cheng, J.- F.; Osorio, J.; Remaley, A.; Yang, X.- P.; Haudenschild,C.; Prades, C.; Chimini, G.; Blackmon, E.; Francois, T.; Duverger,N.; Rubin, E. M.; Rosier, M.; Denefle, P.; Fredrickson, D. S.; Brewer,H. B., Jr.: Complete genomic sequence of the human ABCA1 gene: analysisof the human and mouse ATP- binding cassette A promoter. Proc. Nat.Acad. Sci. 97: 7987- 7992, 2000. Note: Erratum: Proc. Nat. Acad. Sci.99: 1098 only, 2002. 1 A c

GAM96 394 ABCA1 Szakacs, G.; Langmann, T.; Ozvegy, C.; Orso, E.; Schmitz, G.;Varadi, A.; Sarkadi, B.: Characterization of the ATPase cycle ofhuman ABCA1: implications for its function as a regulator rather thanan active transporter. Biochem. Biophys. Res. Commun. 288: 1258- 1264,2001. 1 A c

GAM96 394 ABCA1 Tanaka, A. R.; Ikeda, Y.; Abe- Dohmae, S.; Arakawa, R.; Sadanami,K.; Kidera, A.; Nakagawa, S.; Nagase, T.; Aoki, R.; Kioka, N.; Amachi,T.; Yokoyama, S.; Ueda, K.: Human ABCA1 contains a large amino terminalextracellular domain homologous to an epitope of Sjogren's syndrome. Biochem.Biophys. Res. Commun. 283: 1019- 1025, 2001. 1 A c

GAM96 394 ABCA1 Utech, M.; Hobbel, G.; Rust, S.; Reinecke, H.; Assmann, G.; Walter,M.: Accumulation of RhoA, RhoB, RhoG, and Rac1 in fibroblasts fromTangier disease subjects suggests a regulatory role of Rho familyproteins in cholesterol efflux. Biochem. Biophys. Res. Commun. 280:229- 236, 2001. 1 A c

GAM96 394 ABCA1 Young, S. G.; Fielding, C. J.: The ABCs of cholesterol efflux. NatureGenet. 22: 316- 318, 1999. 1 A c

GAM96 394 ABCA1 Zhao, L.- X.; Zhou, C.- J.; Tanaka, A.; Nakata, M.; Hirabayashi,T.; Amachi, T.; Shioda, S.; Ueda, K.; Inagaki, N.: Cloning, characterizationand tissue distribution of the rat ATP- binding cassette (ABC) transporterABC2/ABCA2. Biochem J. 350: 865- 872, 2000. 1 A c

GAM96 394 ABCA1 Zwarts, K. Y.; Clee, S. M.; Zwinderman, A. H.; Engert, J. C.;Singaraja, R.; Loubser, O.; James, E.; Roomp, K.; Hudson, T. J.; Jukema,J. W.; Kastelein, J. J. P.; Hayden, M. R.: ABCA1 regulatory variantsinfluence coronary artery disease independent of effects on plasmalipid levels. Clin. Genet. 61: 115- 125, 2002. 1 A c

GAM96 394 ABCC1 Cole, S. P. C.; Bhardwaj, G.; Gerlach, J. H.; Mackie, J. E.; Grant,C. E.; Almquist, K. C.; Stewart, A. J.; Kurz, E. U.; Duncan, A. M.V.; Deeley, R. G.: Overexpression of a transporter gene in a multidrug- resistanthuman lung cancer cell line. Science 258: 1650- 1654, 1992. 1 A c

GAM96 394 ABCC1 Conrad, S.; Kauffmann, H.- M.; Ito, K.; Deeley, R. G.; Cole, S.P. C.; Schrenk, D.: Identification of human multidrug resistanceprotein 1 (MRP1) mutations and characterization of a G671V substitution. J.Hum. Genet. 46: 656- 663, 2001. 1 A c

GAM96 394 ABCC1 Grant, C. E.; Kurz, E. U.; Cole, S. P. C.; Deeley, R. G.: Analysisof the intron- exon organization of the human multidrug- resistanceprotein gene (MRP) and alternative splicing of its mRNA. Genomics 45:368- 378, 1997. 1 A c

GAM96 394 ABCC1 Lorico, A.; Bertola, A.; Baum, C.; Fodstad, O.; Rappa, G.: Roleof multidrug 1 A c

resistance protein 1 in protection from heavy metal oxyanions:investigations in vitro and in Mrp1- deficient mice. Biochem. Biophys.Res. Commun. 291: 617- 622, 2002.

GAM96 394 ABCC1 Robbiani, D. F.; Finch, R. A.; Jager, D.; Muller, W. A.; Sartorelli,A. C.; 1 A c Randolph, G. J.: The leukotriene C4 transporter MRP1 regulatesCCL19 (MIP- 3-beta, ELC)- dependent mobilization of dendritic cellsto lymph nodes. Cell 103: 757- 768, 2000.

GAM96 394 ABCC1 Schultz, M. J.; Wijnholds, J.; Peppelenbosch, M. P.; Vervoordeldonk,M. J. B. 1 A c M.; Speelman, P.; van Deventer, S. J. H.; Borst, P.; vander Poll, T.: Mice lacking the multidrug resistance protein 1 areresistant to Streptococcus pneumoniae- induced pneumonia. J. Immun. 166:4059- 4064, 2001.

GAM96 394 ABCC1 Zaman, G. J. R.; Flens, M. J.; van Leusden, M. R.; de Haas, M.;Mulder, H. 1 A c S.; Lankelma, J.; Pinedo, H. M.; Scheper, R. J.; Baas,F.; Broxterman, H. J.; Borst, P.: The human multidrug resistance- associatedprotein MRP is a plasma membrane drug- efflux pump. Proc. Nat. Acad.Sci. 91: 8822- 8826, 1994.

GAM96 394 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 1 A c adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995.

GAM96 394 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 1 A c members are randomly located on different chromosomes. Hum.Genet. 94: 527-529, 1994.

GAM96 394 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: 1 A c Chromosomal mapping of human adenylyl cyclase genestype III, type V and type VI. Hum. Genet. 94: 69- 73, 1994.

GAM96 394 AKAP13 Carr, D. W.; Hausken, Z. E.; Fraser, I. D.; Stofko- Hahn, R. E.;Scott, J. D: 1 A c Association of the type II cAMP- dependent protein kinasewith a human thyroid RII- anchoring protein: cloning and characterizationof the RII-binding domain. J. Biol. Chem. 267: 13376- 13382, 1992.

GAM96 394 AKAP13 Carr, D. W.; Stofko- Hahn, R. E.; Fraser, I. D.; Bishop, S. M.;Acott, T. S.; 1 A c Brennan, R. G.; Scott, J. D.: Interaction of the regulatorysubunit (RII) of cAMP- dependent protein kinase with RII- anchoringproteins occurs through an amphipathic helix binding motif. J. Biol.Chem. 266: 14188- 14192, 1991.

GAM96 394 AKAP13 Rubino, D.; Driggers, P.; Arbit, D.; Kemp, L.; Miller, B.; Coso,O.; Pagliai, 1 A c K.; Gray, K.; Gutkind, S.; Segars, J.: Characterizationof Brx, a novel Dbl family member that modulates estrogen receptoraction. Oncogene 16: 2513-2526, 1998.

GAM96 394 AKAP13 Sterpetti, P.; Hack, A. A.; Bashar, M. P.; Park, B.; Cheng, S.- D.;Knoll, J. 1 A c H. M.; Urano, T.; Feig, L. A.; Toksoz, D.: Activation ofthe Lbc Rho exchange factor proto- oncogene by truncation of an extendedC terminus that regulates transformation and targeting. Molec. Cell.Biol. 19: 1334- 1345, 1999.

GAM96 394 AKAP13 Toksoz, D.; Williams, D. A.: Novel human oncogene lbc detectedby 1 A c transfection with distinct homology regions to signal transductionproducts. Oncogene 9: 621- 628, 1994.

GAM96 394 ALDH1A3 Grun, F.; Hirose, Y.; Kawauchi, S.; Ogura, T.; Umesono, K.: 1 A c Aldehydedehydrogenase 6, a cytosolic retinaldehyde dehydrogenase prominentlyexpressed in sensory neuroepithelia during development. J. Biol.Chem. 275: 41210- 41218, 2000.

GAM96 394 ALDH1A3 Hsu, L. C.; Chang, W.- C.; Hiraoka, L.; Hsieh, C.- L.: Molecularcloning, 1 A c genomic organization, and chromosomal localization of anadditional human aldehyde dehydrogenase gene, ALDH6. Genomics 24:333- 341, 1994.

GAM96 394 ASH1 Ahmad, I.: Mash- 1 is expressed during ROD photoreceptor differentiationand binds an E- box, E(opsin- 1), in the rat opsin gene. Brain Res.Dev. Brain Res. 90: 184- 189, 1995. 1 A c

GAM96 394 ASH1 Ball, D. W.; Azzoli, C. G.; Baylin, S. B.; Chi, D.; Dou, S.; Donis-Keller,H.; Cumaraswamy, A.; Borges, M.; Nelkin, B. D.: Identification ofa human achaete- scute homolog highly expressed in neuroendocrine tumors. Proc.Nat. Acad. Sci. 90: 5648- 5652, 1993. 1 A c

GAM96 394 ASH1 Guillemot, F.; Lo, L.- C.; Johnson, J. E.; Auerbach, A.; Anderson,D. J.; Joyner, A. L.: Mammalian achaete- scute homolog 1 is requiredfor the early development of olfactory and autonomic neurons. Cell 75:463- 476, 1993. 1 A c

GAM96 394 ASH1 Letinic, K.; Zoncu, R.; Rakic, P.: Origin of GABAergic neuronsin the human neocortex. Nature 417: 645- 649, 2002. 1 A c

GAM96 394 ASH1 Renault, B.; Lieman, J.; Ward, D.; Krauter, K.; Kucherlapati, R.: Localization of the human achaete- scute homolog gene (ASCL1) distalto phenylalanine hydroxylase (PAH) and proximal to tumor rejectionantigen (TRA1) on chromosome 12q22- q23. Genomics 30: 81- 83, 1995. 1 A c

GAM96 394 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.: Identification of Bach2 as a B- cell- specific partner for smallMaf proteins that negatively regulate the immunoglobulin heavy chaingene 3- prime enhancer. EMBO J. 17: 5734- 5743, 1998. 1 A c

GAM96 394 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-basic leucine zipper transcription factors that interact withMafK and regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-6095, 1996. 1 A c

GAM96 394 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.; Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene 19: 3739- 3749, 2000. 1 A c

GAM96 394 BGLAP Celeste, A. J.; Rosen, V.; Buecker, J. L.; Kriz, R.; Wang, E. A.;Wozney, J. M.: Isolation of the human gene for bone gla protein utilizingmouse and rat cDNA clones. EMBO J. 5: 1885- 1890, 1986. 1 A c

GAM96 394 BGLAP Desbois, C.; Seldin, M. F.; Karsenty, G.: Localization of theosteocalcin gene cluster on mouse chromosome 3. Mammalian Genome 5:321- 322, 1994. 1 A c

GAM96 394 BGLAP Ducy, P.; Karsenty, G.: Two distinct osteoblast- specific cis-actingelements control expression of a mouse osteocalcin gene. Molec. Cell.Biol. 15: 1858- 1869, 1995. 1 A c

GAM96 394 BGLAP Ducy, P.; Zhang, R.; Geoffroy, V.; Ridall, A. L.; Karsenty, G.: Osf2/Cbfa1: a transcriptional activator of osteoblast differentiation. Cell 89:747- 754, 1997. 1 A c

GAM96 394 BGLAP Johnson, T. L.; Sakaguchi, A. Y.; Lalley, P. A.; Leach, R. J.:Chromosomal assignment in mouse of matrix GLA protein and bone GLAprotein genes. Genomics 11: 770- 772, 1991. 1 A c

GAM96 394 BGLAP Kaplan, F. S.; Tabas, J. A.; Zasloff, M. A.: Fibrodysplasia ossificansprogressiva: a clue from the fly? Calcif. Tissue Int. 47: 117-125,1990. 1 A c

GAM96 394 BGLAP Kerner, S. A.; Scott, R. A.; Pike, J. W.: Sequence elements inthe human osteocalcin gene confer basal activation and inducible responseto hormonal 1 A c

vitamin D(3). Proc. Nat. Acad. Sci. 86: 4455- 4459, 1989.

GAM96 394 BGLAP Mitchell, B. D.; Cole, S. A.; Bauer, R. L.; Iturria, S. J.; Rodriguez,E. A.; 1 A c
Blangero, J.; MacCluer, J. W.; Hixson, J. E.: Genes influencingvariation in
serum osteocalcin concentrations are linked to markerson chromosomes 16q and
20q. J. Clin. Endocr. Metab. 85: 1362- 1366,2000.

GAM96 394 BGLAP Morrison, N. A.; Yeoman, R.; Kelly, P. J.; Eisman, J. A.: Contributionof 1 A c
trans- acting factor alleles to normal physiological variability:vitamin D
receptor gene polymorphisms and circulating osteocalcin. Proc.Nat. Acad.
Sci. 89: 6665- 6669, 1992.

GAM96 394 BGLAP Pan, L. C.; Price, P. A.: The propeptide of rat bone gamma- 1 A c
carboxyglutamicacid protein shares homology with other vitamin K- dependent
proteinprecursors. Proc. Nat. Acad. Sci. 82: 6109- 6113, 1985.

GAM96 394 BGLAP Puchacz, E.; Lian, J. B.; Stein, G. S.; Wozney, J.; Huebner, K.;Croce, C.: 1 A c
Chromosomal localization of the human osteocalcin gene. Endocrinology
124:2648- 2650, 1989.

GAM96 394 BGLAP Staal, A.; van Wijnen, A. J.; Birkenhager, J. C.; Pols, H. A.P.; Prahl, J.; 1 A c
DeLuca, H.; Gaub, M.- P.; Lian, J. B.; Stein, G. S.;van Leeuwen, J. P. T.
M.; Stein, J. L.: Distinct conformations ofvitamin D receptor/retinoid X
receptor- alpha heterodimers are specifiedby dinucleotide differences in the
vitamin D- responsive elements ofthe osteocalcin and osteopontin genes.
Molec. Endocr. 10: 1444- 1456,1996.

GAM96 394 BGLAP Tabas, J. A.; Zasloff, M.; Wasmuth, J. J.; Emanuel, B. S.; Altherr,M. R.; 1 A c
McPherson, J. D.; Wozney, J. M.; Kaplan, F. S.: Bone morphogeneticprotein:
chromosomal localization of human genes for BMP1, BMP2A,and BMP3. Genomics
9: 283- 289, 1991.

GAM96 394 CADPS Ann, K.; Kowalchyk, J. A.; Loyet, K. M.; Martin, T. F. J.: NovelCa(2+)- 1 A c
binding protein (CAPS) related to UNC- 31 required for Ca(2+)-
activatedexocytosis. J. Biol. Chem. 272: 19637- 19640, 1997.

GAM96 394 CADPS Berwin, B.; Floor, E.; Martin, T. F. J.: CAPS (mammalian UNC- 31)protein 1 A c
localizes to membranes involved in dense- core vesicle exocytosis. Neuron
21:137- 145, 1998.

GAM96 394 CADPS Hirosawa, M.; Nagase, T.; Ishikawa, K.; Kikuno, R.; Nomura, N.;Ohara, O.: 1 A c
Characterization of cDNA clones selected by the GeneMarkanalysis from size-
fractionated cDNA libraries from human brain. DNARes. 6: 329- 336, 1999.

GAM96 394 CADPS Walent, J. H.; Porter, B. W.; Martin, T. F. J.: A novel 145 kdbrain 1 A c
cytosolic protein reconstitutes Ca(2+)- regulated secretion inpermeable
neuroendocrine cells. Cell 70: 765- 775, 1992.

GAM96 394 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 1 A c
membrane- associated C- type lectin that exhibits CD4- independentbinding of
human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad.
Sci. 89: 8356- 8360, 1992.

GAM96 394 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 1 A c
for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR.
Science 294: 2163- 2166, 2001.

GAM96 394 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 1 A c
Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S.
L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-
SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-
infection of T cells. Cell 100: 587- 597,2000.

GAM96 394 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 1 A c

F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000.

GAM96 394 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000. 1 A c

GAM96 394 CLNS1A Anguita, J.; Chalfant, M. L.; Civan, M. M.; Coca- Prados, M.: Molecularcloning of the human volume- sensitive chloride conductance regulatoryprotein, pI(Cln), from ocular ciliary epithelium. Biochem. Biophys.Res. Commun. 208: 89- 95, 1995. 1 A c

GAM96 394 CLNS1A Buyse, G.; De Greef, C.; Raeymaekers, L.; Droogmans, G.; Nilius,B.; Eggermont, J.: The ubiquitously expressed pI(Cln) protein formshomomeric complexes in vitro. Biochem. Biophys. Res. Commun. 218:822- 827, 1996. 1 A c

GAM96 394 CLNS1A Nagl, U. O.; Erdel, M.; Schmarda, A.; Seri, M.; Pinggera, G. M.;Gschwentner, M.; Duba, C.; Galietta, L. J. V.; Deetjen, P.; Utermann,G.; Paulmichl, M.: Chromosomal localization of the genes (CLNS1Aand CLNS1B) coding for the swelling- dependent chloride channel I(Cln). Genomics 38:438- 441, 1996. 1 A c

GAM96 394 CLNS1A Schwartz, R. S.; Rybicki, A. C.; Nagel, R. L.: Molecular cloningand expression of a chloride channel- associated protein pI(Cln) inhuman young red blood cells: association with actin. Biochem. J. 327:609- 616, 1997. 1 A c

GAM96 394 CPT1B Britton, C. H.; Mackey, D. W.; Esser, V.; Foster, D. W.; Burns,D. K.; Yarnall, D. P.; Froguel, P.; McGarry, J. D.: Fine chromosomemapping of the genes for human liver and muscle carnitine palmitoyltransferasel (CPT1A and CPT1B). Genomics 40: 209- 211, 1997. 1 A c

GAM96 394 CPT1B van der Leij, F. R.; Takens, J.; van der Veen, A. Y.; Terpstra,P.; Kuipers, J. R. G.: Localization and intron usage analysis ofthe human CPT1B gene for muscle type carnitine palmitoyltransferasel. Biochim. Biophys. Acta 1352: 123- 128, 1997. 1 A c

GAM96 394 CPT1B Yamazaki, N.; Shinohara, Y.; Shima, A.; Yamanaka, Y.; Terada, H.: Isolation and characterization of cDNA and genomic clones encodinghuman muscle type carnitine palmitoyltransferase I. Biochim. Biophys.Acta 1307: 157- 161, 1996. 1 A c

GAM96 394 CPT1B Yamazaki, N.; Yamanaka, Y.; Hashimoto, Y.; Shinohara, Y.; Shima,A.; Terada, H.: Structural features of the gene encoding human muscletype carnitine palmitoyltransferase I. FEBS Lett. 409: 401- 406,1997. 1 A c

GAM96 394 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. W.: Chromosomal localization and racial distributionof the polymorphic human dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352, 1988. 1 A c

GAM96 394 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies three RFLPs. Nucleic Acids Res. 15: 5501 only,1987. 1 A c

GAM96 394 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: Chromosomal localization and racial distribution of the polymorphichDHFR- psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985. 1 A c

GAM96 394 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; Nienhuis, A. W.: Chromosomal organization of the human dihydrofolatereductase genes: dispersion, selective amplification and a novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984. 1 A c

GAM96 394 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in 1 A c

dihydrofolatereductase that confer resistance to methotrexate: potential for clinicalapplication. Hum. Mutat. 11: 259- 263, 1998.

GAM96 394 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: 1 A c
Intronless human dihydrofolate reductase genes are derivedfrom processed RNA molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982.

GAM96 394 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association 1 A c
with variation in protein structure. Science 220: 1125- 1129,1983.

GAM96 394 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 1 A c
757 and 807- 812, 1975.

GAM96 394 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the 1 A c
human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5. Molec. Cell. Biol. 4: 2010- 2016, 1984.

GAM96 394 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater- 1 A c
Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med. 310: 789- 790, 1984.

GAM96 394 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment 1 A c
of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986.

GAM96 394 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: 1 A c
Human dihydrofolate reductase gene is located in chromosome 5and is unlinked to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984.

GAM96 394 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human 1 A c
dihydrofolate reductase gene to band q23 of chromosome 5and of related pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85, 1985.

GAM96 394 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; 1 A c
Attardi, G.: Chromosomal location of the normal human DHFRgene and of its amplified copies in methotrexate resistant cell variants.(Abstract) Cytogenet. Cell Genet. 37: 534 only, 1984.

GAM96 394 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 1 A c
10/7/1983.

GAM96 394 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: 1 A c
Amplification of the human dihydrofolate reductase gene viadouble minutes is initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000.

GAM96 394 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. 1 A c
A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976.

GAM96 394 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)- 1 A c
formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967.

GAM96 394 DSCR1 Fuentes, J. J.; Genesca, L.; Kingsbury, T. J.; Cunningham, K. W.;Perez- 1 A c
Riba, M.; Estivill, X.; de la Luna, S.: DSCR1, overexpressedin Down syndrome, is an inhibitor of calcineurin- mediated signalingpathways. Hum. Molec. Genet. 9: 1681- 1690, 2000.

GAM96 394 DSCR1 Fuentes, J. J.; Pritchard, M. A.; Estivill, X.: Genomic 1 A c
organization,alternative splicing, and expression patterns of the DSCR1 (Down syndromecandidate region 1) gene. Genomics 44: 358- 361, 1997.

GAM96 394 DSCR1 Fuentes, J.- J.; Pritchard, M. A.; Planas, A. M.; Bosch, A.; Ferrer,I.; 1 A c
Estivill, X.: A new human gene from the Down syndrome criticalregion encodes a proline- rich protein highly expressed in fetal brainand heart. Hum.

Molec. Genet. 4: 1935- 1944, 1995.

GAM96 394 DSCR1 Kingsbury, T. J.; Cunningham, K. W.: A conserved family of calcineurinregulators. Genes Dev. 14: 1595- 1604, 2000. 1 A c

GAM96 394 DSCR1 Rothermel, B.; Vega, R. B.; Yang, J.; Wu, H.; Bassel- Duby, R.;Williams, R. S.: A protein encoded within the Down syndrome criticalregion is enriched in striated muscles and inhibits calcineurin signaling. J.Biol. Chem. 275: 8719- 8725, 2000. 1 A c

GAM96 394 DSCR1 Strippoli, P.; Petrini, M.; Lenzi, L.; Carinci, P.; Zannotti, M.: The murine DSCR1- like (Down syndrome candidate region 1) gene family:conserved synteny with the human orthologous genes. Gene 257: 223- 232,2000. 1 A c

GAM96 394 DSCR1 Yang, J.; Rothermel, B.; Vega, R. B.; Frey, N.; McKinsey, T. A.;Olson, E. N.; Bassel- Duby, R.; Williams, R. S.: Independent signalscontrol expression of the calcineurin inhibitory proteins MCIP1 andMCIP2 in striated muscles. Circ. Res. 87: 61e- 68e, 2000. 1 A c

GAM96 394 EPAC de Rooij, J.; Zwartkruis, F. J. T.; Verheijen, M. H. G.; Cool,R. H.; Nijman, S. M. B.; Wittinghofer, A.; Bos, J. L.: Epac is aRap1 guanine- nucleotide- exchange factor directly activated by cyclicAMP. Nature 396: 474- 477, 1998. 1 A c

GAM96 394 EPAC Kawasaki, H.; Springett, G. M.; Mochizuki, N.; Toki, S.; Nakaya,M.; Matsuda, M.; Housman, D. E.; Graybiel, A. M.: A family of cAMP- bindingproteins that directly activate Rap1. Science 282: 2275- 2279, 1998. 1 A c

GAM96 394 EPHB1 Contractor, A.; Rogers, C.; Maron, C.; Henkemeyer, M.; Swanson,G. T.; Heinemann, S. F.: Trans- synaptic Eph receptor- ephrin signalingin hippocampal mossy fiber LTP. Science 296: 1864- 1869, 2002. 1 A c

GAM96 394 EPHB1 Cowan, C. A.; Yokoyama, N.; Bianchi, L. M.; Henkemeyer, M.; Fritzsch,B.: EphB2 guides axons at the midline and is necessary for normalvestibular function. Neuron 26: 417- 430, 2000. 1 A c

GAM96 394 EPHB1 Tang, X. X.; Biegel, J. A.; Nycum, L. M.; Yoshioka, A.; Brodeur,G. M.; Pleasure, D. E.; Ikegaki, N.: cDNA cloning, molecular characterization,and chromosomal localization of NET (EPHT2), a human EPH- related receptorprotein- tyrosine kinase gene preferentially expressed in brain. :Genomics 29:426- 437, 1995. 1 A c

GAM96 394 FETUB Olivier, E.; Soury, E.; Risler, J. L.; Smith, F.; Schneider, K.;Lochner, K.; Jouzeau, J. Y.; Fey, G. H.; Salier, J. P.: A novel setof hepatic mRNAs preferentially expressed during an acute inflammationin rat represents mostly intracellular proteins. Genomics 57: 352- 364,1999. 1 A c

GAM96 394 FETUB Olivier, E.; Soury, E.; Ruminy, P.; Husson, A.; Parmentier, F.;Daveau, M.; Salier, J.- P.: Fetuin- B, a second member of the fetuinfamily in mammals. Biochem. J. 350: 589- 597, 2000. 1 A c

GAM96 394 GALNT2 Bennett, E. P.; Weghuis, D. O.; Merkx, G.; Geurts van Kessel, A.;Eiberg, H.; Clausen, H.: Genomic organization and chromosomal localizationof three members of the UDP- N- acetylgalactosamine:polypeptide N- acetylgalactosaminyltransferasefamily. Glycobiology 8: 547- 555, 1998. 1 A c

GAM96 394 GALNT2 White, T.; Bennett, E. P.; Takio, K.; Sorensen, T.; Bonding, N.;Clausen, H.: Purification and cDNA cloning of a human UDP- N- acetyl- alpha- D- galactosamine:polypeptideN- acetylgalactosaminyltransferase. J. Biol. Chem. 270: 24156- 24165,1995. 1 A c

GAM96 394 GNB5 Jones, J. M.; Huang, J.- D.; Mermall, V.; Hamilton, B. A.; Mooseker,M. S.; Escayg, A.; Copeland, N. G.; Jenkins, N. A.; Meisler, M. H.: The mouse neurological mutant flailer expresses a novel hybrid genederived by exon shuffling between Gnb5 and Myo5a. Hum. Molec. Genet. 9:821- 828, 2000. 1 A c

GAM96 394 GNB5 Jones, P. G.; Lombardi, S. J.; Cockett, M. I.: Cloning and tissuedistribution of the human G protein beta- 5 cDNA. Biochim. Biophys.Acta 1402: 288- 291, 1998. 1 A c

GAM96 394 GNB5 Watson, A. J.; Aragay, A. M.; Slepak, V. Z.; Simon, M. I.: A novelform of the G protein beta subunit G- beta- 5 is specifically expressedin the vertebrate retina. J. Biol. Chem. 271: 28154- 28160, 1996. 1 A c

GAM96 394 GNB5 Watson, A. J.; Katz, A.; Simon, M. I.: A fifth member of the mammalianG- protein beta subunit family: expression in brain and activationof the beta- 2 isotype of phospholipase C. J. Biol. Chem. 269: 22150- 22156,1994. 1 A c

GAM96 394 GOLGA4 Daigo, Y.; Isomura, M.; Nishiwaki, T.; Tamari, M.; Ishikawa, S.;Kai, M.; Murata, Y.; Takeuchi, K.; Yamane, Y.; Hayashi, R.; Minami,M.; Fujino, M. A.; Hojo, Y.; Uchiyama, I.; Takagi, T.; Nakamura, Y.: Characterization of a 1200- kb genomic segment of chromosome 3p22- p21.3. DNARes. 6: 37- 44, 1999. 1 A c

GAM96 394 GOLGA4 Erlich, R.; Gleeson, P. A.; Campbell, P.; Dietzsch, E.; Toh, B.- H.: Molecular characterization of trans- Golgi p230: a human peripheralmembrane protein encoded by a gene on chromosome 6p12- 22 containsextensive coiled-coil alpha- helical domains and a granin motif. J.Biol. Chem. 271: 8328- 8337, 1996. 1 A c

GAM96 394 GOLGA4 Fritzler, M. J.; Lung, C.- C.; Hamel, J. C.; Griffith, K. J.; Chan,E. K. L.: Molecular characterization of golgin- 245, a novel Golgicomplex protein containing a granin signature. J. Biol. Chem. 270:31262- 31268, 1995. 1 A c

GAM96 394 GOLGA4 Kooy, J.; Toh, B.- H.; Pettitt, J. M.; Erlich, R.; Gleeson, P. A.: Human autoantibodies as reagents to conserved Golgi components:characterization of a peripheral, 230- kDa compartment- specific Golgiprotein. J. Biol. Chem. 267: 20255- 20263, 1992. 1 A c

GAM96 394 GORASP1 Barr, F. A.; Nakamura, N.; Warren, G.: Mapping the interactionbetween GRASP65 and GM130, components of a protein complex involvedin the stacking of Golgi cisternae. EMBO J. 17: 3258- 3268, 1998. 1 A c

GAM96 394 GORASP1 Lane, J. D; Lucocq, J.; Pryde, J.; Barr, F. A.; Woodman, P. G.;Allan, V. J.; Lowe, M.: Caspase- mediated cleavage of the stackingprotein GRASP65 is required for Golgi fragmentation during apoptosis. J.Cell Biol. 156: 495- 509, 2002. 1 A c

GAM96 394 GORASP1 Sutterlin, C.; Hsu, P.; Mallabiabarrena, A.; Malhotra, V.: Fragmentationand dispersal of the pericentriolar Golgi complex is required forentry into mitosis in mammalian cells. Cell 109: 359- 369, 2002. 1 A c

GAM96 394 GPM6A Lagenaur, C.; Kunemund, V.; Fischer, G.; Fushiki, S.; Schachner,M.: Monoclonal M6 antibody interferes with neurite extension of culturedneurons. J. Neurobiol. 23: 71- 88, 1992. 1 A c

GAM96 394 GPM6A Olinsky, S.; Loop, B. T.; DeKosky, A.; Ripepi, B.; Weng, W.; Cummins,J.; Wenger, S. L.; Yan, Y.; Lagenaur, C.; Narayanan, V.: Chromosomalmapping of the human M6 genes. Genomics 33: 532- 536, 1996. 1 A c

GAM96 394 GPM6A Shimizu, F.; Watanabe, T. K.; Fujiwara, T.; Takahashi, E.; Nakamura,Y.; Maekawa, H.: Isolation and mapping of the human glycoproteinM6 gene (GPM6A) to 4q33- to- q34. Cytogenet. Cell Genet. 74: 138- 139,1996. 1 A c

GAM96 394 GPM6A Yan, Y.; Lagenaur, C.; Narayanan, V.: Molecular cloning of M6:identification of a PLP/DM20 gene family. Neuron 11: 423- 431, 1993. 1 A c

GAM96 394 GPR63 Kawasawa, Y.; Kume, K.; Izumi, T.; Shimizu, T.: Mammalian PSP24s(alpha and beta isoforms) are not responsive to lysophosphatidic acidin mammalian expression systems. Biochem. Biophys. Res. Commun. 276:957- 964, 2000. 1 A c

GAM96 394 GPR63 Kawasawa, Y.; Kume, K.; Nakade, S.; Haga, H.; Izumi, T.; Shimizu,T.: Brain- 1 A c

specific expression of novel G- protein- coupled receptors,with homologies to Xenopus PSP24 and human GPR45. Biochem. Biophys.Res. Commun. 276: 952-956, 2000.

GAM96 394 GPR63 Lee, D. K.; George, S. R.; Cheng, R.; Nguyen, T.; Liu, Y.; Brown,M.; Lynch, K. R.; O'Dowd, B. F.: Identification of four novel humanG protein- coupled receptors expressed in the brain. Molec. BrainRes. 86: 13- 22, 2001. 1 A c

GAM96 394 GPRK2L Ambrose, C.; James, M.; Barnes, G.; Lin, C.; Bates, G.; Altherr,M.; Duyao, M.; Groot, N.; Church, D.; Wasmuth, J. J.; Lehrach, H.;Housman, D.; Buckler, A.; Gusella, J. F.; MacDonald, M. E.: A novelG protein- coupled receptor kinase gene cloned from 4p16.3. Hum. Molec.Genet. 1: 697- 703, 1992. 1 A c

GAM96 394 GPRK2L Casari, G.; Barlassina, C.; Cusi, D.; Zagato, L.; Muirhead, R.;Righetti, M.; Nembri, P.; Amar, K.; Gatti, M.; Macciardi, F.; Binelli,G.; Bianchi, G.: Association of the alpha- adducin locus with essentialhypertension. Hypertension 25: 320- 326, 1995. 1 A c

GAM96 394 GPRK2L Felder, R. A.; Sanada, H.; Xu, J.; Yu, P.- Y.; Wang, Z.; Watanabe,H.; Asico, L. D.; Wang, W.; Zheng, S.; Yamaguchi, I.; Williams, S.M.; Gainer, J.; Brown, N. J.; Hazen- Martin, D.; Wong, L.- J. C.; Robillard,J. E.; Carey, R. M.; Eisner, G. M.; Jose, P. A.: G protein- coupledreceptor kinase 4 gene variants in human essential hypertension. Proc.Nat. Acad. Sci. 99: 3872-3877, 2002. 1 A c

GAM96 394 GPRK2L Grosson, C. L. S.; MacDonald, M. E.; Duyao, M. P.; Ambrose, C.M.; Roffler-Tarlov, S.; Gusella, J. F.: Synteny conservation of theHuntington's disease gene and surrounding loci on mouse chromosome 1 A c

GAM96 394 GPRK2L Mammalian Genome 5: 424- 428, 1994.5. Premont, R. T.; Macrae, A. D.; Stoffel, R. H.; Chung, N.; Pitcher,J. A.; Ambrose, C.; Inglese, J.; MacDonald, M. E.; Lefkowitz, R. J.: Characterization of the G protein-coupled receptor kinase GRK4:identification of four splice variants. J. Biol. Chem. 271: 6403- 6410,1996. 1 A c

GAM96 394 GPRK2L Sallese, M.; Mariggio, S.; Collodel, G.; Moretti, E.; Piomboni,P.; Baccetti, B.; De Blasi, A.: G protein- coupled receptor kinaseGRK4: molecular analysis of the four isoforms and ultrastructurallocalization in spermatozoa and germinal cells. J. Biol. Chem. 272:10188- 10195, 1997. 1 A c

GAM96 394 KARS Maas, S.; Kim, Y.- G.; Rich, A.: Genomic clustering of tRNA-specificadenosine deaminase ADAT1 and two tRNA synthetases. Mammalian Genome 12:387- 393, 2001. 1 A c

GAM96 394 KARS Nichols, R. C.; Blinder, J.; Pai, S. I.; Ge, Q.; Targoff, I. N.;Plotz, P. H.; Liu, P.: Assignment of two human autoantigen genes:isoleucyl- tRNA synthetase locates to 9q21 and lysyl- tRNA synthetaselocates to 16q23- q24. Genomics 36: 210- 213, 1996. 1 A c

GAM96 394 KARS Targoff, I. N.; Trieu, E. P.; Miller, F. W.: Reaction of anti-OJautoantibodies with components of the multi- enzyme complex of aminoacyl-tRNAsynthetases in addition to isoleucyl- tRNA synthetase. J. Clin. Invest. 91:2556- 2564, 1993. 1 A c

GAM96 394 KARS Tolkunova, E.; Park, H.; Xia, J.; King, M. P.; Davidson, E.: Thehuman lysyl-tRNA synthetase gene encodes both the cytoplasmic andmitochondrial enzymes by means of an unusual alternative splicingof the primary transcript. J. Biol. Chem. 275: 35063- 35069, 2000. 1 A c

GAM96 394 KCNA6 Albrecht, B.; Weber, K.; Pongs, O.: Characterization of a voltage-activatedK- channel gene cluster on human chromosome 12p13. Receptors Channels 3:213- 220, 1995. 1 A c

GAM96 394 KCNA6 Grupe, A.; Schroter, K. H.; Ruppersberg, J. P.; Stocker, M.; Drewes,T.; 1 A c
Beckh, S.; Pongs, O.: Cloning and expression of a human voltage-
gatedpotassium channel: a novel member of the RCK potassium channel family.
EMBOJ. 9: 1749- 1756, 1990.

GAM96 394 KCNA6 Klocke, R.; Roberds, S. L.; Tamkun, M. M.; Gronemeier, M.; Augustin,A.; 1 A c
Albrecht, B.; Pongs, O.; Jockusch, H.: Chromosomal mapping inthe mouse of
eight K(+)- channel genes representing the four Shaker- likesubfamilies
Shaker, Shab, Shaw, and Shal. Genomics 18: 568- 574,1993.

GAM96 394 KCNQ2 Berkovic, S. F.; Kennerson, M. L.; Howell, R. A.; Scheffer, I.E.; Hwang, P. 1 A c
A.; Nicholson, G. A.: Phenotypic expression of benignfamilial neonatal
convulsions linked to chromosome 20. Arch. Neurol. 51:1125- 1128, 1994.

GAM96 394 KCNQ2 Biervert, C.; Schroeder, B. C.; Kubisch, C.; Berkovic, S. F.; Propping,P.; 1 A c
Jentsch, T. J.; Steinlein, O. K.: A potassium channel mutationin neonatal
human epilepsy. Science 279: 406- 409, 1998.

GAM96 394 KCNQ2 Biervert, C.; Steinlein, O. K.: Structural and mutational analysisof KCNQ2, 1 A c
the major gene locus for benign familial neonatal convulsions. Hum.Genet.
104: 234- 240, 1999.

GAM96 394 KCNQ2 Cooper, E. C.; Aldape, K. D.; Abosch, A.; Barbaro, N. M.; Berger,M. S.; 1 A c
Peacock, W. S.; Jan, Y. N.; Jan, L. Y.: Colocalization andcoassembly of two
human brain M- type potassium channel subunits thatare mutated in epilepsy.
Proc. Nat. Acad. Sci. 97: 4914- 4919, 2000.

GAM96 394 KCNQ2 Dedek, K.; Kunath, B.; Kananura, C.; Reuner, U.; Jentsch, T. J.;Steinlein, 1 A c
O. K.: Myokymia and neonatal epilepsy caused by a mutationin the voltage
sensor of the KCNQ2 K(+) channel. Proc. Nat. Acad.Sci. 98: 12272- 12277,
2001.

GAM96 394 KCNQ2 del Giudice, E. M.; Coppola, G.; Scuccimarra, G.; Cirillo, G.;Bellini, G.; 1 A c
Pascotto, A.: Benign familial neonatal convulsions (BFNC)resulting from
mutation of the KCNQ2 voltage sensor. Europ. J. Hum.Genet. 8: 994- 997,
2000.

GAM96 394 KCNQ2 Singh, N. A.; Charlier, C.; Stauffer, D.; DuPont, B. R.; Leach,R. J.; Melis, 1 A c
R.; Ronen, G. M.; Bjerre, I.; Quattlebaum, T.; Murphy,J. V.; McHarg, M. L.;
Gagnon, D.; Rosales, T. O.; Peiffer, A.; Anderson,V. E.; Leppert, M.: A
novel potassium channel gene, KCNQ2, is mutatedin an inherited epilepsy of
newborns. Nature Genet. 18: 25- 29, 1998.

GAM96 394 KCNQ2 Wang, H.- S.; Pan, Z.; Shi, W.; Brown, B. S.; Wymore, R. S.; Cohen,I. S.; 1 A c
Dixon, J. E.; McKinnon, D.: KCNQ2 and KCNQ3 potassium channelsubunits:
molecular correlates of the M- channel. Science 282: 1890- 1893,1998.

GAM96 394 KCNQ2 Wang, Q.; Curren, M. E.; Splawski, I.; Burn, T. C.; Millholland,J. M.; 1 A c
VanRaay, T. J.; Shen, J.; Timothy, K. W.; Vincent, G. M.; deJager, T.;
Schwartz, P. J.; Towbin, J. A.; Moss, A. J.; Atkinson,D. L.; Landes, G. M.;
Connors, T. D.; Keating, M. T.: Positionalcloning of a novel potassium
channel gene: KVLQT1 mutations causecardiac arrhythmias. Nature Genet. 12:
17- 23, 1996.

GAM96 394 KCNQ2 Yang, W.- P.; Levesque, P. C.; Little, W. A.; Conder, M. L.; 1 A c
Ramakrishnan,P.; Neubauer, M. G.; Blanar, M. A.: Functional expression of
twoKvLQT1- related potassium channels responsible for an inherited
idiopathicepilepsy. J. Biol. Chem. 273: 19419- 19423, 1998.

GAM96 394 LANCL1 Bauer, H.; Mayer, H.; Marchler- Bauer, A.; Salzer, U.; Prohaska,R.: 1 A c
Characterization of p40/GPR69A as a peripheral membrane proteinrelated to
the lantibiotic synthetase component C. Biochem. Biophys.Res. Commun. 275:

69- 74, 2000.

GAM96 394 LANCL1 Mayer, H.; Bauer, H.; Prohaska, R.: Organization and chromosomallocalization of the human and mouse genes coding for LanC- like protein1 (LANCL1). Cytogenet. Cell Genet. 93: 100- 104, 2001. 1 A c

GAM96 394 LANCL1 Mayer, H.; Salzer, U.; Breuss, J.; Ziegler, S.; Marchler- Bauer,A.; Prohaska, R.: Isolation, molecular characterization, and tissue-specificexpression of a novel putative G protein- coupled receptor. Biochim.Biophys. Acta 1395: 301- 308, 1998. 1 A c

GAM96 394 MGA Naim, H. Y.; Sterchi, E. E.; Lentze, M. J.: Structure, biosynthesis,and glycosylation of human small intestinal maltase- glucoamylase. J.Biol. Chem. 263: 19709- 19717, 1988. 1 A c

GAM96 394 MGA Nichols, B. L.; Eldering, J.; Avery, S.; Hahn, D.; Quaroni, A.;Sterchi, E.: Human small intestinal maltase- glucoamylase cDNA cloning:homology to sucrase- isomaltase. J. Biol. Chem. 273: 3076- 3081, 1998. 1 A c

GAM96 394 MGA Schuler, G. D.; Boguski, M. S.; Stewart, E. A.; Stein, L. D.; Gyapay,G.; Rice, K.; White, R. E.; Rodriguez- Tome, P.; Aggarwal, A.; Bajorek,E.; Bentolila, S.; Birren, B. B.; Butler, A.; Castle, A. B.; Chiannilkulchai,N.; Chu, A.; Clee, C.; Cowles, S.; Day, P. J. R.; Dibling, T.; and84 others: A gene map of the human genome. Science 274: 540- 546,1996. 1 A c

GAM96 394 MLLT2 Domer, P. H.; Fakharzadeh, S. S.; Chen, C.- S.; Jockel, J.; Johansen,L.; Silverman, G. A.; Kersey, J. H.; Korsmeyer, S. J.: Acute mixed-lineageleukemia t(4;11)(q21;q23) generates an MLL- AF4 fusion product. Proc.Nat. Acad. Sci. 90: 7884- 7888, 1993. 1 A c

GAM96 394 MLLT2 Gu, Y.; Nakamura, T.; Alder, H.; Prasad, R.; Canaani, O.; Cimino,G.; Croce, C. M.; Canaani, E.: The t(4;11) chromosome translocationof human acute leukemias fuses the ALL- 1 gene, related to Drosophilatrithorax, to the AF-4 gene. Cell 71: 701- 708, 1992. 1 A c

GAM96 394 MLLT2 Isnard, P.; Depetris, D.; Mattei, M.- G.; Ferrier, P.; Djabali,M.: cDNA cloning, expression and chromosomal localization of themurine AF- 4 gene involved in human leukemia. Mammalian Genome 9:1065- 1068, 1998. 1 A c

GAM96 394 MLLT2 Lovett, B. D.; Lo Nigro, L.; Rappaport, E. F.; Blair, I. A.; Osheroff,N.; Zheng, N.; Megonigal, M. D.; Williams, W. R.; Nowell, P. C.; Felix,C. A.: Near- precise interchromosomal recombination and functionalDNA topoisomerase II cleavage sites at MLL and AF- 4 genomic breakpointsin treatment- related acute lymphoblastic leukemia with t(4;11) translocation. Proc.Nat. Acad. Sci. 98: 9802- 9807, 2001. 1 A c

GAM96 394 MLLT2 Nakamura, T.; Alder, H.; Gu, Y.; Prasad, R.; Canaani, O.; Kamada,N.; Gale, R. P.; Lange, B.; Crist, W. M.; Nowell, P. C.; Croce, C.M.; Canaani, E.: Genes on chromosomes 4, 9, and 19 involved in 11q23abnormalities in acute leukemia share sequence homology and/or commonmotifs. Proc. Nat. Acad. Sci. 90: 4631- 4635, 1993. 1 A c

GAM96 394 MLLT2 Uckun, F. M.; Herman- Hatten, K.; Crotty, M.- L.; Sensel, M. G.;Sather, H. N.; Tuel- Ahlgren, L.; Sarquis, M. B.; Bostrom, B.; Nachman,J. B.; Steinherz, P. G.; Gaynon, P. S.; Heerema, N.: Clinical significanceof MLL-AF4 fusion transcript expression in the absence of a cytogeneticallydetectable t(4;11)(q21;q23) chromosomal translocation. Blood 92:810- 821, 1998. 1 A c

GAM96 394 MRPS12 Johnson, D. F.; Hamon, M.; Fischel- Ghodsian, N.: Characterizationof the human mitochondrial ribosomal S12 gene. Genomics 52: 363- 368,1998. 1 A c

GAM96 394 MRPS12 Shah, Z. H.; Migliosi, V.; Miller, S. C. M.; Wang, A.; Friedman,T. B.; 1 A c

Jacobs, H. T.: Chromosomal locations of three human nucleargenes (RPSM12, TUFM, and AFG3L1) specifying putative components ofthe mitochondrial gene expression apparatus. Genomics 48: 384- 388,1998.

GAM96 394 NOX1 Banfi, B.; Maturana, A.; Jaconi, S.; Arnaudeau, S.; Laforge, T.;Sinha, S.; 1 A c
Ligeti, E.; Demaurex, N.; Krause, K.- H.: A mammalian H+channel generated through alternative splicing of the NADPH oxidasehomolog NOH- 1. Science 287: 138- 141, 2000.

GAM96 394 NOX1 Kikuchi, H.; Hikage, M.; Miyashita, H.; Fukumoto, M.: NADPH oxidasesubunit, 1 A c
gp9l- phox homologue, preferentially expressed in human colonepithelial cells. Gene 254: 237- 243, 2000.

GAM96 394 NOX1 Starace, D. M; Stefani, E.; Bezanilla, F.: Voltage- dependent 1 A c
protontransport by the voltage sensor of the Shaker K+ channel. Neuron 19:1319- 1327, 1997.

GAM96 394 NOX1 Suh, Y.- A.; Arnold, R. S.; Lassegue, B.; Shi, J.; Xu, X.; Sorescu,D.; 1 A c
Chung, A. B.; Griendling, K. K.; Lambeth, J. D.: Cell transformationby the superoxide- generating oxidase Mox1. Nature 401: 79- 82, 1999.

GAM96 394 OAS3 Hovanessian, A. G.; Laurent, A. G.; Chebath, J.; Galabru, J.; Robert,N.; 1 A c
Svab, J.: Identification of 69- kd and 100- kd forms of 2- 5A synthetasein interferon- treated human cells by specific monoclonal antibodies. EMBOJ. 6: 1273- 1280, 1987.

GAM96 394 OAS3 Hovnanian, A.; Rebouillat, D.; Mattei, M.- G.; Levy, E. R.; Marie,I.; 1 A c
Monaco, A. P.; Hovanessian, A. G.: The human 2- prime,5- prime- oligoadenylatesynthetase locus is composed of three distinct genes clustered onchromosome 12q24.2 encoding the 100- , 69- , and 40- kDa forms. Genomics 52:267- 277, 1998.

GAM96 394 P4HA1 Annunen, P.; Helaakoski, T.; Myllyharju, J.; Veijola, J.; Pihlajaniemi,T.; 1 A c
Kivirikko, K. I.: Cloning of the human prolyl 4- hydroxylase alphasubunit isoform alpha(II) and characterization of the type II enzymetetramer: the alpha(I) and alpha(II) subunits do not form a mixedalpha(I)alpha(II)beta2 tetramer. J. Biol. Chem. 272: 17342- 17348,1997.

GAM96 394 P4HA1 Friedman, L.; Higgin, J. J.; Moulder, G.; Barstead, R.; Raines,R. T.; 1 A c
Kimble, J.: Prolyl 4- hydroxylase is required for viabilityand morphogenesis in Caenorhabditis elegans. Proc. Nat. Acad. Sci. 97:4736- 4741, 2000.

GAM96 394 P4HA1 Helaakoski, T.; Annunen, P.; Vuori, K.; MacNeil, I. A.; Pihlajaniemi,T.; 1 A c
Kivirikko, K. I.: Cloning, baculovirus expression, and characterizationof a second mouse prolyl 4- hydroxylase alpha- subunit isoform: formationof an alpha(2)beta(2) tetramer with the protein disulfide- isomerase/betasubunit. Proc. Nat. Acad. Sci. 92: 4427- 4431, 1995.

GAM96 394 P4HA1 Helaakoski, T.; Veijola, J.; Vuori, K.; Rehn, M.; Chow, L. T.;Taillon- 1 A c
Miller, P.; Kivirikko, K. I.; Pihlajaniemi, T.: Structureand expression of the human gene for the alpha subunit of prolyl 4- hydroxylase:the two alternatively spliced types of mRNA correspond to two homologousexons the sequences of which are expressed in a variety of tissues. J.Biol. Chem. 269: 27847- 27854, 1994.

GAM96 394 P4HA1 Helaakoski, T.; Vuori, K.; Myllyla, R.; Kivirikko, K. I.; Pihlajaniemi,T.: 1 A c
Molecular cloning of the alpha- subunit of human prolyl 4- hydroxylase:the complete cDNA- derived amino acid sequence and evidence for alternativesplicing of RNA transcripts. Proc. Nat. Acad. Sci. 86: 4392- 4396,1989.

GAM96 394 P4HA1 Pajunen, L.; Jones, T. A.; Helaakoski, T.; Pihlajaniemi, T.; Solomon,E.; 1 A c

Sheer, D.; Kivirikko, K. I.: Assignment of the gene coding forthe alpha-subunit of prolyl 4- hydroxylase to human chromosome region10q21.3- 23.1. Am. J. Hum. Genet. 45: 829- 834, 1989.

GAM96 394 PABPC1 Afonina, E.; Stauber, R.; Pavlakis, G. N.: The human poly(A)- bindingprotein 1 A c 1 shuttles between the nucleus and the cytoplasm. J. Biol.Chem. 273: 13015-13021, 1998.

GAM96 394 PABPC1 Deo, R. C.; Bonanno, J. B.; Sonenberg, N.; Burley, S. K.: Recognitionof 1 A c polyadenylate RNA by the poly(A)- binding protein. Cell 98: 835- 845,1999.

GAM96 394 PABPC1 Feral, C.; Mattei, M. G.; Pawlak, A.; Guellaen, G.: Chromosomallocalization 1 A c of three human poly(A)- binding protein genes and fourrelated pseudogenes. Hum. Genet. 105: 347- 353, 1999.

GAM96 394 PABPC1 Gorlach, M.; Burd, C. G.; Dreyfuss, G.: The mRNA poly(A)- bindingprotein: 1 A c localization, abundance, and RNA- binding specificity. Exp.Cell Res. 211: 400- 407, 1994.

GAM96 394 PABPC1 Grange, T.; Martins de Sa, C.; Oddos, J.; Pictet, R.: Human 1 A c mRNApolyadenylate binding protein: evolutionary conservation of a nucleicacid binding motif. Nucleic Acids Res. 15: 4771- 4787, 1987.

GAM96 394 PABPC1 Laroia, G.; Cuesta, R.; Brewer, G.; Schneider, R. J.: Controlof mRNA decay 1 A c by heat shock- ubiquitin- proteasome pathway. Science 284:499- 502, 1999.

GAM96 394 PABPC1 Morris, C. M.; Bodger, M. P.: Localization of the human poly(A)- 1 A c bindingprotein gene (PAB1) to chromosomal regions 3q22- q25, 12q13- q14, and13q12- q13 by in situ hybridization. Genomics 15: 209- 211, 1993.

GAM96 394 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack 1 A c of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991.

GAM96 394 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; 1 A c Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine nucleotide synthesis on human chromosome 4 are closelylinked and divergently transcribed. J. Biol. Chem. 269: 5313- 5321,1994.

GAM96 394 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of 1 A c three human multifunctional de novo purine biosyntheticgenes by functional complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920, 1990.

GAM96 394 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 1 A c Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM96 394 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 1 A c Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM96 394 PFKFB4 Manzano, A.; Perez, J. X.; Nadal, M.; Estivill, X.; Lange, A.;Bartrons, R.: 1 A c Cloning, expression and chromosomal localization ofa human testis 6-phosphofructo- 2- kinase/fructose- 2,6- bisphosphatasegene. Gene 229: 83-89, 1999.

GAM96 394 PFKFB4 Sakai, A.; Kato, M.; Fukasawa, M.; Ishiguro, M.; Furuya, E.; Sakakibara,R.: 1 A c Cloning of cDNA encoding for a novel isozyme of fructose 6- phosphate,2-kinase/fructose2,6- bisphosphatase from human placenta. J. Biochem. 119: 506- 511,1996.

GAM96 394 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; 1 A c
Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx
activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C.
Genomics 47: 323- 324, 1998.

GAM96 394 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, 1 A c
S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to
human chromosome 21q22.3. Genomics 41: 193- 200,1997.

GAM96 394 PLA2G4A Dennis, E. A.: Diversity of group types, regulation, and functionof 1 A c
phospholipase A2. J. Biol. Chem. 269: 13057- 13060, 1994.

GAM96 394 PLA2G4A Dessen, A.; Tang, J.; Schmidt, H.; Stahl, M.; Clark, J. D.; Seehra,J.; 1 A c
Somers, W. S.: Crystal structure of human cytosolic phopholipaseA(2) reveals
a novel topology and catalytic mechanism. Cell 97:349- 360, 1999.

GAM96 394 PLA2G4A Seilhamer, J. J.; Plant, S.; Pruzanski, W.; Schilling, J.; Stefanski,E.; 1 A c
Vadas, P.; Johnson, L. K.: Multiple forms of phospholipase A(2)in arthritic
synovial fluid. J. Biochem. 106: 38- 42, 1989.

GAM96 394 PLA2G4A Sharp, J. D.; Pickard, R. T.; Chiou, X. G.; Manetta, J. V.; Kovacevic,S.; 1 A c
Miller, J. R.; Varshavsky, A. D.; Roberts, E. F.; Strifler, B.A.; Brems, D.
N.; Kramer, R. M.: Serine 228 is essential for catalyticactivities of 85-
kDa cytosolic phospholipase A2. J. Biol. Chem. 269:23250- 23254, 1994.

GAM96 394 PLA2G4A Sharp, J. D.; White, D. L.; Chiou, X. G.; Goodson, T.; Gamboa,G. C.; 1 A c
McClure, D.; Burgett, S.; Hoskins, J.; Skatrud, P. L.; Sportsman,J. R.;
Becker, G. W.; Kang, L. H.; Roberts, E. F.; Kramer, R. M.:Molecular cloning
and expression of human Ca(2+)- sensitive cytosolicphospholipase A2. J.
Biol. Chem. 266: 14850- 14853, 1991.

GAM96 394 PLA2G4A Sheridan, A. M.; Force, T.; Yoon, H.- J.; O'Leary, E.; Choukroun,G.; Taheri, 1 A c
M. R.; Bonventre, J. V.: PLIP, a novel splice variantof Tip60, interacts
with group IV cytosolic phospholipase A2, inducesapoptosis, and potentiates
prostaglandin production. Molec. Cell.Biol. 21: 4470- 4481, 2001.

GAM96 394 PLA2G4A Skorecki, K. L.: Personal Communication. Toronto, Canada 4/19/1995. 1 A c

GAM96 394 PLA2G4A Tay, A.; Simon, J. S.; Squire, J.; Hamel, K.; Jacob, H. J.; Skorecki,K.: 1 A c
Cytosolic phospholipase A2 gene in human and rat: chromosomallocalization
and polymorphic markers. Genomics 26: 138- 141, 1995.

GAM96 394 PLAGL1 Abdollahi, A.; Godwin, A. K.; Miller, P. D.; Getts, L. A.; Schultz,D. C.; 1 A c
Taguchi, T.; Testa, J. R.; Hamilton, T. C.: Identificationof a gene
containing zinc- finger motifs based on lost expression inmalignantly
transformed rat ovarian surface epithelial cells. CancerRes. 57: 2029- 2034,
1997.

GAM96 394 PLAGL1 Abdollahi, A.; Roberts, D.; Godwin, A. K.; Schultz, D. C.; Sonoda,G.; Testa, 1 A c
J. R.; Hamilton, T. C.: Identification of a zinc- fingergene at 6q25: a
chromosomal region implicated in development of manysolid tumors. Oncogene
14: 1973- 1979, 1997.

GAM96 394 PLAGL1 Arima, T.; Drewell, R. A.; Arney, K. L.; Inoue, J.; Makita, Y.;Hata, A.; 1 A c
Oshimura, M.; Wake, N.; Surani, M. A.: A conserved imprintingcontrol region
at the HYMAI/ZAC domain is implicated in transientneonatal diabetes
mellitus. Hum. Molec. Genet. 10: 1475- 1483, 2001.

GAM96 394 PLAGL1 Kamiya, M.; Judson, H.; Okazaki, Y.; Kusakabe, M.; Muramatsu, M.;Takada, S.; 1 A c
Takagi, N.; Arima, T.; Wake, N.; Kamimura, K.; Satomura,K.; Hermann, R.;
Bonthron, D. T.; Hayashizaki, Y.: The cell cyclecontrol gene ZAC/PLAGL1 is
imprinted: a strong candidate gene fortransient neonatal diabetes. Hum.
Molec. Genet. 9: 453- 460, 2000.

GAM96 394 PLAGL1 Mackay, D. J. G.; Coupe, A.- M.; Shield, J. P. H.; Storr, J. N.P.; Temple, 1 A c
I. K.; Robinson, D. O.: Relaxation of imprinted expressionof ZAC and HYMAI
in a patient with transient neonatal diabetes mellitus. Hum.Genet. 110: 139-
144, 2002.

GAM96 394 PLAGL1 Spengler, D.; Villalba, M.; Hoffmann, A.; Pantaloni, C.; Houssami,S.; 1 A c
Bockaert, J.; Journot, L.: Regulation of apoptosis and cell cyclearrest by
Zac1, a novel zinc finger protein expressed in the pituitarygland and the
brain. EMBO J. 16: 2814- 2825, 1997.

GAM96 394 PLAGL1 Temple, I. K.; Gardner, R. J.; Robinson, D. O.; Kibirige, M. S.;Ferguson, A. 1 A c
W.; Baum, J. D.; Barber, J. C. K.; James, R. S.; Shield,J. P. H.: Further
evidence for an imprinted gene for neonatal diabeteslocalised to chromosome
6q22- q23. Hum. Molec. Genet. 5: 1117- 1124,1996.

GAM96 394 PLAGL1 Temple, I. K.; James, R. S.; Crolla, J. A.; Sitch, F. L.; Jacobs,P. A.; 1 A c
Howell, W. M.; Betts, P.; Baum, J. D.; Shield, J. P. H.: Animprinted gene(s)
for diabetes? (Letter) Nature Genet. 9: 110- 112,1995.

GAM96 394 PLAGL1 Varrault, A.; Ciani, E.; Apiou, F.; Bilanges, B.; Hoffmann, A.;Pantaloni, 1 A c
C.; Bockaert, J.; Spengler, D.; Journot, L.: hZAC encodesa zinc finger
protein with antiproliferative properties and maps toa chromosomal region
frequently lost in cancer. Proc. Nat. Acad.Sci. 95: 8835- 8840, 1998.

GAM96 394 PMX1 Grueneberg, D. A.; Natesan, S.; Alexandre, C.; Gilman, M. Z.:Human and 1 A c
Drosophila homeodomain proteins that enhance the DNA- bindingactivity of
serum response factor. Science 257: 1089- 1095, 1992.

GAM96 394 PMX1 Kern, M. J.; Argao, E. A.; Birkenmeier, E. H.; Rowe, L. B.; Potter,S. S.: 1 A c
Genomic organization and chromosome localization of the murinehomeobox gene
Pmx. Genomics 19: 334- 340, 1994.

GAM96 394 PMX1 Nakamura, T.; Yamazaki, Y.; Hatano, Y.; Miura, I.: NUP98 is fusedto PMX1 1 A c
homeobox gene in human acute myelogenous leukemia with
chromosometranslocation t(1;11)(q23;p15). Blood 94: 741- 747, 1999.

GAM96 394 PMX1 Norris, R. A.; Scott, K. K.; Moore, C. S.; Stetten, G.; Brown,C. R.; Jabs, 1 A c
E. W.; Wulfsberg, E. A.; Yu, J.; Kern, M. J.: HumanPRRX1 and PRRX2 genes:
cloning, expression, genomic localization,and exclusion as disease genes for
Nager syndrome. Mammalian Genome 11:1000- 1005, 2000.

GAM96 394 PMX1 Riazuddin, S.; Castelein, C. M.; Ahmed, Z. M.; Lalwani, A. K.;Mastroianni, 1 A c
M. A.; Naz, S.; Smith, T. N.; Liburd, N. A.; Friedman,T. B.; Griffith, A.
J.; Riazuddin, S.; Wilcox, E. R.: Dominant modifierDFNM1 suppresses
recessive deafness DFNB26. Nature Genet. 26: 431- 434,2000.

GAM96 394 POLS Walowsky, C.; Fitzhugh, D. J.; Castano, I. B.; Ju, J. Y.; Levin,N. A.; 1 A c
Christman, M. F.: The topoisomerase- related function geneTRF4 affects
cellular sensitivity to the antitumor agent camptothecin. J.Biol. Chem. 274:
7302- 7308, 1999.

GAM96 394 POLS Wang, Z.; Castano, I. B.; De Las Penas, A.; Adams, C.; Christman,M. F.: Pol 1 A c
kappa: a DNA polymerase required for sister chromatidcohesion. Science 289:
774- 779, 2000.

GAM96 394 PPP2R5D McCright, B.; Brothman, A. R.; Virshup, D. M.: Assignment of humanprotein 1 A c
phosphatase 2A regulatory subunit genes B56- alpha, B56- beta,B56- gamma,
B56- delta, and B56- epsilon (PPP2R5A- - PPP2R5E), highly expressedin muscle
and brain, to chromosome regions 1q41, 11q12, 3p21, 6p21.1,and 7p11.2- to-
p12. Genomics 36: 168- 170, 1996.

GAM96 394 PPP2R5D McCright, B.; Rivers, A. M.; Audlin, S.; Virshup, D. M.: The B56family of 1 A c
protein phosphatase 2A (PP2A) regulatory subunits encodesdifferentiation-

induced phosphoproteins that target PP2A to both nucleusand cytoplasm. J. Biol. Chem. 271: 22081- 22089, 1996.

GAM96 394 PROK1 LeCouter, J.; Kowalski, J.; Foster, J.; Hass, P.; Zhang, Z.; Dillard- Telm,L.; Frantz, G.; Rangell, L.; DeGuzman, L.; Keller, G.- A.; Peale, F.;Gurney, P.; Hillan, K. J.; Ferrara, N.: Identification of an angiogenicmitogen selective for endocrine gland endothelium. Nature 412: 877- 884,2001. 1 A c

GAM96 394 PROK1 Li, M.; Bullock, C. M.; Knauer, D. J.; Ehlert, F. J.; Zhou, Q.Y.: Identification of two prokineticin cDNAs: recombinant proteinspotently contract gastrointestinal smooth muscle. Molec. Pharm. 59:692- 698, 2001. 1 A c

GAM96 394 PXF Braun, A.; Kammerer, S.; Weissenhorn, W.; Weiss, E. H.; Cleve,H.: Sequence of a putative human housekeeping gene (HK33) localizedon chromosome 1. Gene 146: 291- 295, 1994. 1 A c

GAM96 394 PXF Gotte, K.; Girzalsky, W.; Linkert, M.; Baumgart, E.; Kammerer,S.; Kunau, W.- H.; Erdmann, R.: Pex19p, a farnesylated protein essentialfor peroxisome biogenesis. Molec. Cell. Biol. 18: 616- 628, 1998. 1 A c

GAM96 394 PXF James, G. L.; Goldstein, J. L.; Pathak, R. K.; Anderson, R. G.W.; Brown, M. S.: PxF, a prenylated protein of peroxisomes J. Biol.Chem. 269: 14182- 14190, 1994. 1 A c

GAM96 394 PXF Kammerer, S.; Arnold, N.; Gutensohn, W.; Mewes, H.- W.; Kunau, W.- H.;Hofler, G.; Roscher, A. A.; Braun, A.: Genomic organization and molecularcharacterization of a gene encoding HsPXF, a human peroxisomal farnesylatedprotein. Genomics 45: 200- 210, 1997. 1 A c

GAM96 394 PXF Kinoshita, N.; Ghaedi, K.; Shimozawa, N.; Wanders, R. J. A.; Matsuzono,Y.; Imanaka, T.; Okumoto, K.; Suzuki, Y.; Kondo, N.; Fujiki, Y.:Newly identified Chinese hamster ovary cell mutants are defectivein biogenesis of peroxisomal membrane vesicles (peroxisomal ghosts),representing a novel complementation group in mammals J. Biol. Chem. 273:24122- 24130, 1998. 1 A c

GAM96 394 PXF Matsuzono, Y.; Kinoshita, N.; Tamura, S.; Shimozawa, N.; Hamasaki,M.; Ghaedi, K.; Wanders, R. J. A.; Suzuki, Y.; Kondo, N.; Fujiki,Y.: Human PEX19: cDNA cloning by functional complementation, mutationanalysis in a patient with Zellweger syndrome, and potential rolein peroxisomal membrane assembly. Proc. Nat. Acad. Sci. 96: 2116- 2121,1999. 1 A c

GAM96 394 RP42 Mas, C.; Bourgeois, F.; Bulfone, A.; Levacher, B.; Mugnier, C.;Simonneau, M.: Cloning and expression analysis of a novel gene, RP42,mapping to an autism susceptibility locus on 6q16. Genomics 65:70- 74, 2000. 1 A c

GAM96 394 SLC4A4 Abuladze, N.; Lee, I.; Newman, D.; Hwang, J.; Boorer, K.; Pushkin,A.; Kurtz, I.: Molecular cloning, chromosomal localization, tissuedistribution, and functional expression of the human pancreatic sodiumbicarbonate cotransporter. J. Biol. Chem. 273: 17689- 17695, 1998. 1 A c

GAM96 394 SLC4A4 Burnham, C. E.; Amlal, H.; Wang, Z.; Shull, G. E.; Soleimani, M.: Cloning and functional expression of a human kidney Na+:HCO3- cotransporter. J.Biol. Chem. 272: 19111- 19114, 1997. 1 A c

GAM96 394 SLC4A4 Choi, I.; Romero, M. F.; Khandoudi, N.; Bril, A.; Boron, W. F.: Cloning and characterization of a human electrogenic Na(+)- HCO(3-)cotransporter isoform (hhNBC). Am. J. Physiol. 276: C576- C584, 1999. 1 A c

GAM96 394 SLC4A4 Igarashi, T.; Inatomi, J.; Sekine, T.; Cha, S. H.; Kanai, Y.; Kunimi,M.; Tsukamoto, K.; Satoh, H.; Shimadzu, M.; Tozawa, F.; Mori, T.;Shiobara, M.; Seki, G.; Endou, H.: Mutations in SLC4A4 cause permanentisolated proximal renal tubular acidosis with ocular abnormalities.(Letter) Nature Genet. 23: 1 A c

264- 265, 1999.

GAM96 394 SLC4A4 Romero, M. F.; Boron, W. F.: Electrogenic Na(+)/HCO(3-) 1 A c
cotransporters:cloning and physiology. Annu. Rev. Physiol. 61: 699- 723,
1999.

GAM96 394 SLC4A4 Soleimani, M.; Burnham, C. E.: Physiologic and molecular aspectsof the 1 A c
Na(+):HCO(3-) cotransporter in health and disease processes. KidneyInt. 57:
371- 384, 2000.

GAM96 394 SLC4A4 Usui, T.; et al.; et al. :Pflugers Arch. 438: 458- 462, 1999. 1 A c

GAM96 394 SP3 Andersson, M.; Page, D. C.; Pettay, D.; Subrt, I.; Turleau, C.;de Grouchy, 1 A c
J.; de la Chapelle, A.: Y;autosome translocations andmosaicism in the
aetiology of 45,X maleness: assignment of fertilityfactor to distal Yq11.
Hum. Genet. 79: 2- 7, 1988.

GAM96 394 SP3 Chandley, A. C.; Gosden, J. R.; Hargreave, T. B.; Spowart, G.;Speed, R. M.; 1 A c
McBeath, S.: Deleted Yq in the sterile son of a manwith a satellited Y
chromosome (Yqs). J. Med. Genet. 26: 145- 153,1989.

GAM96 394 SP3 Foresta, C.; Bertella, A.; Moro, E.; Roverato, A.; Merico, M.;Ferlin, A.: 1 A c
Sertoli cell function in infertile patients with andwithout microdeletions
of the azoospermia factors on the Y chromosomelong arm. J. Clin. Endocr.
Metab. 86: 2414- 2419, 2001.

GAM96 394 SP3 Foresta, C.; Ferlin, A.; Moro, E.: Deletion and expression analysisof AZFa 1 A c
genes on the human Y chromosome revealed a major role forDBY in male
infertility. Hum. Molec. Genet. 9: 1161- 1169, 2000.

GAM96 394 SP3 Hagen, G.; Muller, S.; Beato, M.; Suske, G.: Cloning by recognitionsite 1 A c
screening of two novel GT box binding proteins: a family of Sp1related
genes. Nucleic Acids Res. 20: 5519- 5525, 1992.

GAM96 394 SP3 Hagen, G.; Muller, S.; Beato, M.; Suske, G.: Sp1- mediated 1 A c
transcriptionalactivation is repressed by Sp3. EMBO J. 13: 3843- 3851, 1994.

GAM96 394 SP3 Johnson, M. D.; Tho, S. P. T.; Behzadian, A.; McDonough, P. G.: Molecular 1 A c
scanning of Yq11 (interval 6) in men with Sertoli- cell- onlysyndrome. Am.
J. Obstet. Gynec. 161: 1732- 1737, 1989.

GAM96 394 SP3 Kalff- Suske, M.; Kunz, J.; Grzeschik, K.- H.; Suske, G.: HumanSp3 1 A c
transcriptional regulator gene (SP3) maps to chromosome 2q31. Genomics
37:410- 412, 1996.

GAM96 394 SP3 Kamp, C.; Hirschmann, P.; Voss, H.; Huellen, K.; Vogt, P. H.:Two long 1 A c
homologous retroviral sequence blocks in proximal Yq11 causeAZFa
microdeletions as a result of intrachromosomal recombinationevents. Hum.
Molec. Genet. 9: 2563- 2572, 2000.

GAM96 394 SP3 Kingsley, C.; Winoto, A.: Cloning of GT box- binding proteins:a novel Sp1 1 A c
multigene family regulating T- cell receptor gene expression. Molec.Cell.
Biol. 12: 4251- 44261, 1992.

GAM96 394 SP3 Kobayashi, K.; Mizuno, K.; Hida, A.; Komaki, R.; Tomita, K.; Matsushita,I.; 1 A c
Namiki, M.; Iwamoto, T.; Tamura, S.; Minowada, S.; Nakahori, Y.;Nakagome,
Y.: PCR analysis of the Y chromosome long arm in azoospermicpatients:
evidence for a second locus required for spermatogenesis. Hum.Molec. Genet.
3: 1965- 1967, 1994.

GAM96 394 SP3 Krausz, C.; Meyts, E. R.- D.; Frydelund- Larson, L.; Quintana- Murci,L.; 1 A c
McElreavey, K.; Skakkebaek, N. E.: Double- blind Y chromosomemicrodeletion
analysis in men with known sperm parameters and reproductivehormone
profiles: microdeletions are specific for spermatogenic failure. J.Clin.
Endocr. Metab. 86: 2638- 2642, 2001.

GAM96 394 SP3 Krausz, C.; Quintana- Murci, L.; Barbaux, S.; Siffroi, J.- P.; Rouba,H.; 1 A c
Delafontaine, D.; Souleyreau- Therville, N.; Arvis, G.; Antoine,J. M.;
Erdei, E.; Taar, J. P.; Tar, A.; Jeandidier, E.; Plessis, G.;Bourgeron, T.;
Dadoune, J.- P.; Fellous, M.; McElreavey, K.: A highfrequency of Y
chromosome deletions in males with nonidiopathic infertility. J.Clin.
Endocr. Metab. 84: 3606- 3612, 1999.

GAM96 394 SP3 Ma, K.; Inglis, J. D.; Sharkey, A.; Bickmore, W. A.; Hill, R.E.; Prosser, E. 1 A c
J.; Speed, R. M.; Thomson, E. J.; Jobling, M.; Taylor,K.; Wolfe, J.; Cooke,
H. J.; Hargreave, T. B.; Chandley, A. C.: AY chromosome gene family with
RNA- binding protein homology: candidatesfor the azoospermia factor AZF
controlling human spermatogenesis. Cell 75:1287- 1295, 1993.

GAM96 394 SP3 Ma, K.; Sharkey, A.; Kirsch, S.; Vogt, P.; Keil, R.; Hargreave,T. B.; 1 A c
McBeath, S.; Chandley, A. C.: Towards the molecular localisationof the AZF
locus: mapping of microdeletions in azoospermic men within14 subintervals of
interval 6 of the human Y chromosome. Hum. Molec.Genet. 1: 29- 33, 1992.

GAM96 394 SP3 Madgar, I.; Green, L.; Kent- First, M.; Weissenberg, R.; Gershoni- 1 A c
Baruch,R.; Goldman, B.; Friedman, E.: Genotyping of Israeli infertile
menwith idiopathic oligozoospermia. Clin. Genet. 62: 203- 207, 2002.

GAM96 394 SP3 Sargent, C. A..; Boucher, C. A.; Kirsch, S.; Brown, G.; Weiss,B.; Trundley, 1 A c
A.; Burgoyne, P.; Saut, N.; Durand, C.; Levy, N.; Terriou,P.; Hargreave, T.;
Cooke, H.; Mitchell, M.; Rappold, G. A.; Affara,N. A.: The critical region
of overlap defining the AZFa male infertilityinterval of proximal Yq
contains three transcribed sequences. J.Med. Genet. 36: 670- 677, 1999.

GAM96 394 SP3 Simpson, E.; Chandler, P.; Goulmy, E.; Ma, K.; Hargreave, T. B.;Chandley, A. 1 A c
C.: Loss of the 'azoospermia factor' (AZF) on Yq inman is not associated
with loss of HYA. Hum. Molec. Genet. 2: 469- 471,1993.

GAM96 394 SP3 Sun, C.; Skaletsky, H.; Rozen, S.; Gromoll, J.; Nieschlag, E.;Oates, R.; 1 A c
Page, D. C.: Deletion of azoospermia factor a (AZFa) regionof human Y
chromosome caused by recombination between HERV15 proviruses. Hum.Molec.
Genet. 9: 2291- 2296, 2000.

GAM96 394 SP3 Tiepolo, L.; Zuffardi, O.: Localization of factors 1 A c
controllingspermatogenesis in the nonfluorescent portion of the human Y
chromosomelong arm. Hum. Genet. 34: 119- 124, 1976.

GAM96 394 SP3 Vergnaud, G.; Page, D. C.; Simmler, M. C.; Brown, L.; Rouyer,F.; Noel, B.; 1 A c
Botstein, D.; de la Chapelle, A.; Weissenbach, J.:A deletion map of the
human Y chromosome based on DNA hybridization. Am.J. Hum. Genet. 38: 109-
124, 1986.

GAM96 394 SP3 Vogt, P. H.; Edelmann, A.; Kirsch, S.; Henegariu, O.; Hirschmann,P.; 1 A c
Kiesewetter, F.; Kohn, F. M.; Schill, W. B.; Farah, S.; Ramos,C.; Hartmann,
M.; Hartschuh, W.; Meschede, D.; Behre, H. M.; Castel,A.; Nieschlag, E.;
Weidner, W.; Grone, H.- J.; Jung, A.; Engel, W.;Haidl, G.: Human Y
chromosome azoospermia factors (AZF) mapped todifferent subregions in Yq11.
Hum. Molec. Genet. 5: 933- 943, 1996.

GAM96 394 SP3 Vogt, P.; Chandley, A. C.; Hargreave, T. B.; Keil, R.; Ma, K.;Sharkey, A.: 1 A c
Microdeletions in interval 6 of the Y chromosome ofmales with idiopathic
sterility point to disruption of AZF, a humanspermatogenesis gene. Hum.
Genet. 89: 491- 496, 1992.

GAM96 394 SRP Hsu, S. Y.; Hsueh, A. J. W.: Human stresscopin and stresscopin- 1 A c
relatedpeptide are selective ligands for the type 2 corticotropin-
releasinghormone receptor. Nature Med. 7: 605- 611, 2001.

GAM96 394 SRP Reyes, T. M.; Lewis, K.; Perrin, M. H.; Kunitake, K. S.; Vaughan,J.; Arias, 1 A c
C. A.; Hogenesch, J. B.; Gulyas, J.; Rivier, J.; Vale,W. W.; Sawchenko, P.
E.: Urocortin II: a member of the corticotropin- releasingfactor (CRF)
neuropeptide family that is selectively bound by type2 CRF receptors. Proc.
Nat. Acad. Sci. 98: 2843- 2848, 2001.

GAM96 394 UTX Greenfield, A. J.; Scott, D.; Pennisi, D.; Ehrmann, I.; Ellis,P.; Cooper, 1 A c
L.; Simpson, E.; Koopman, P.: An H- YDb epitope is encodedby a novel mouse Y
chromosome gene. Nature Genet. 14: 474- 478, 1996.

GAM96 394 UTX Greenfield, A.; Carrel, L.; Pennisi, D.; Philippe, C.; Quaderi,N.; Siggers, 1 A c
P.; Steiner, K.; Tam, P. P. L.; Monaco, A. P.; Willard,H. F.; Koopman, P.:
The UTX gene escapes X inactivation in mice andhumans. Hum. Molec. Genet. 7:
737- 742, 1998.

GAM96 394 VANGL2 Doudney, K.; Murdoch, J. N.; Paternotte, C.; Bentley, L.; Gregory,S.; Copp, 1 A c
A. J.; Stanier, P.: Comparative physical and transcriptmaps of approximately
1 Mb around loop- tail, a gene for severe neuraltube defects on distal mouse
chromosome 1 and human chromosome 1q22- q23. Genomics 72:180- 192, 2001.

GAM96 394 VANGL2 Kibar, Z.; Vogan, K. J.; Groulx, N.; Justice, M. J.; Underhill,D. A.; Gros, 1 A c
P.: Ltap, a mammalian homolog of Drosophila Strabismus/VanGogh, is altered
in the mouse neural tube mutant loop- tail. NatureGenet. 28: 251- 255, 2001.

GAM96 394 VANGL2 Mullick, A.; Trasler, D.; Gros, P.: High- resolution linkage mapin the 1 A c
vicinity of the Lp locus. Genomics 26: 479- 488, 1995.

GAM96 394 VANGL2 Murdoch, J. N.; Doudney, K.; Paternotte, C.; Copp, A. J.; Stanier,P.: Severe 1 A c
neural tube defects in the loop- tail mouse result frommutation of Lpp1, a
novel gene involved in floor plate specification. Hum.Molec. Genet. 10:
2593- 2601, 2001.

GAM96 394 VANGL2 Stanier, P.; Henson, J. N.; Eddleston, J.; Moore, G. E.; Copp,A. J.: Genetic 1 A c
basis of neural tube defects: the mouse gene loop- tailmaps to a region of
chromosome 1 syntenic with human 1q21- q23. Genomics 26:473- 478, 1995.

GAM97 274 F2R Bahou, W. F.; Nierman, W. C.; Durkin, A. S.; Potter, C. L.; Demetrick,D. J.: 3 C c
Chromosomal assignment of the human thrombin receptor gene:localization to
region q13 of chromosome 5. Blood 82: 1532- 1537,1993.

GAM97 274 F2R Coughlin, S. R.; Vu, T.- K. H.; Hung, D. T.; Wheaton, V. I.: 3 C c
Characterizationof a functional thrombin receptor: issues and opportunities.
J. Clin.Invest. 89: 351- 355, 1992.

GAM97 274 F2R Griffin, C. T.; Srinivasan, Y.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: A 3 C c
role for thrombin receptor signaling in endothelial cellsduring embryonic
development. Science 293: 1666- 1670, 2001.

GAM97 274 F2R Poirier, C.; O'Brien, E. P.; Bueno Brunialti, A. L.; Chambard,J.- C.; Swank, 3 C c
R. T.; Guenet, J.- L.: The gene encoding the thrombinreceptor (Cf2r) maps to
mouse chromosome 13. Mammalian Genome 7:322, 1996.

GAM97 274 F2R Riewald, M.; Petrovan, R. J.; Donner, A.; Mueller, B. M.; Ruf,W.: Activation 3 C c
of endothelial cell protease activated receptor 1by the protein C pathway.
Science 296: 1880- 1882, 2002.

GAM97 274 F2R Schmidt, V. A.; Nierman, W. C.; Feldblyum, T. V.; Maglott, D. R.;Bahou, W. 3 C c
F.: The human thrombin receptor and proteinase activatedreceptor- 2 genes
are tightly linked on chromosome 5q13. Brit. J.Haemat. 97: 523- 529, 1997.

GAM97 274 F2R Schmidt, V. A.; Vitale, E.; Bahou, W. F.: Genomic cloning 3 C c
andcharacterization of the human thrombin receptor gene: structural
similarityto the proteinase activated receptor- 2 gene. J. Biol. Chem.
271:9307- 9312, 1996.

GAM97 274 F2R Vu, T.- K. H.; Hung, D. T.; Wheaton, V. I.; Coughlin, S. R.: 3 C c
Molecularcloning of a functional thrombin receptor reveals a novel
proteolyticmechanism of receptor activation. Cell 64: 1057- 1068, 1991.

GAM97 274 FUT6 Brinkman- Van der Linden, E. C. M.; Mollicone, R.; Oriol, R.; Larson,G.; Van 3 C c
den Eijnden, D. H.; Van Dijk, W.: A missense mutation inthe FUT6 gene
results in total absence of alpha- 3- fucosylation ofhuman alpha- 1- acid
glycoprotein. J. Biol. Chem. 271: 14492- 14495,1996.

GAM97 274 FUT6 Cameron, H. S.; Szczepaniak, D.; Weston, B. W.: Expression ofhuman 3 C c
chromosome 19p alpha- (1,3)- fucosyltransferase genes in normaltissues:
alternative splicing, polyadenylation, and isoforms. J.Biol. Chem. 270:
20112- 20122, 1995.

GAM97 274 FUT6 Koszdin, K. L.; Bowen, B. R.: The cloning and expression of ahuman alpha- 3 C c
1,3 fucosyltransferase capable of forming the E- selectinligand. Biochem.
Biophys. Res. Commun. 187: 152- 157, 1992.

GAM97 274 FUT6 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. 3 C c
C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps
of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3
and 11q21. Genomics 26: 142- 146, 1995.

GAM97 274 FUT6 Mollicone, R.; Reguigne, I.; Fletcher, A.; Aziz, A.; Rustam, M.;Weston, B. 3 C c
W.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Molecular basisfor plasma
alpha(1,3)- fucosyltransferase gene deficiency (FUT6). J.Biol. Chem. 269:
12662- 12671, 1994.

GAM97 274 FUT6 Pang, H.; Koda, Y.; Soejima, M.; Schlaphoff, T.; Du Toit, E. D.;Kimura, H.: 3 C c
Allelic diversity of the human plasma alpha(1,3)fucosyltransferasegene
(FUT6). Ann. Hum. Genet. 63: 277- 284, 1999.

GAM97 274 FUT6 Schnyder- Candrian, S.; Borsig, L.; Moser, R.; Berger, E. G.: Localizationof 3 C c
alpha- 1,3- fucosyltransferase VI in Weibel- Palade bodies of
humanendothelial cells. Proc. Nat. Acad. Sci. 97: 8369- 8374, 2000.

GAM97 274 FUT6 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of 3 C c
a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple
homologous sequences that determine expressionof the Lewis x, sialyl Lewis
x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584,
1992.

GAM97 274 HIP1 Chopra, V. S.; Metzler, M.; Rasper, D. M.; Engqvist- Goldstein,A. E. Y.; 3 C c
Singaraja, R.; Gan, L.; Fichter, K. M.; McCutcheon, K.;Drubin, D.;
Nicholson, D. W.; Hayden, M. R.: HIP12 is a non- proapoptoticmember of a
gene family including HIP1, an interacting protein withhuntingtin. Mammalian
Genome 11: 1006- 1015, 2000.

GAM97 274 HIP1 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 C c
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM97 274 HIP1 Hackam, A. S.; Yassa, A. S.; Singaraja, R.; Metzler, M.; Gutekunst,C.- A.; 3 C c
Gan, L.; Warby, S.; Wellington, C. L.; Vaillancourt, J.; Chen,N.; Gervais,
F. G.; Raymond, L.; Nicholson, D. W.; Hayden, M. R.:Huntingtin interacting
protein 1 induces apoptosis via a novel caspase- dependentdeath effector
domain. J. Biol. Chem. 275: 41299- 41308, 2000.

GAM97 274 HIP1 Himmelbauer, H.; Wedemeyer, N.; Haaf, T.; Wanker, E. E.; Schalkwyk,L. C.; 3 C c
Lehrach, H.: IRS- PCR- based genetic mapping of the huntingtininteracting

protein gene (HIP1) on mouse chromosome 5. MammalianGenome 9: 26- 31, 1998.

GAM97 274 HIP1 Kalchman, M. A.; Koide, H. B.; McCutcheon, K.; Graham, R. K.; Nichol,K.; Nishiyama, K.; Kazemi- Esfarjani, P.; Lynn, F. C.; Wellington,C.; Metzler, M.; Goldberg, Y. P.; Kanazawa, I.; Gietz, R. D.; Hayden,M. R.: HIP1, a human homologue of S. cerevisiae Slap2, interactswith membrane- associated huntingtin in the brain. Nature Genet. 16:44- 53, 1997. 3 C c

GAM97 274 HIP1 Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof Huntingtin interacting protein 1 to platelet- derived growth factor- betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998. 3 C c

GAM97 274 HIP1 Waelter, S.; Scherzinger, E.; Hasenbank, R.; Nordhoff, E.; Lurz,R.; Goehler, H.; Gauss, C.; Sathasivam, K.; Bates, G. P.; Lehrach,H.; Wanker, E. E.: The huntingtin interacting protein HIP1 is a clathrinand alpha- adaptin- binding protein involved in receptor- mediated endocytosis. Hum.Molec. Genet. 10: 1807- 1817, 2001. 3 C c

GAM97 274 HIP1 Wanker, E. E.; Rovira, C.; Scherzinger, E.; Hasenbank, R.; Walter,S.; Tait, D.; Colicelli, J.; Lehrach, H.: HIP- I: a huntingtin interactingprotein isolated by the yeast two- hybrid system. Hum. Molec. Genet. 6:487- 495, 1997. 3 C c

GAM97 274 HIP1 Wedemeyer, N.; Peoples, R.; Himmelbauer, H.; Lehrach, H.; Francke,U.; Wanker, E. E.: Localization of the human HIP1 gene close to theelastin (ELN) locus on 7q11.23. Genomics 46: 313- 315, 1997. 3 C c

GAM97 274 IL18 Corbaz, A.; ten Hove, T.; Herren, S.; Graber, P.; Schwartsburd,B.; Belzer, I.; Harrison, J.; Plitz, T.; Kosco- Vilbois, M. H.; Kim,S.- H.; Dinarello, C. A.; Novick, D.; van Deventer, S.; Chvatchko,Y.: IL- 18- binding protein expression by endothelial cells and macrophagesis up- regulated during active Crohn's disease. J. Immun. 168: 3608- 3616,2002. 3 C b

GAM97 274 IL18 Konishi, H.; Tsutsui, H.; Murakami, T.; Yumikura- Futatsugi, S.;Yamanaka, K.; Tanaka, M.; Iwakura, Y.; Suzuki, N.; Takeda, K.; Akira,S.; Nakanishi, K.; Mizutani, H.: IL- 18 contributes to the spontaneousdevelopment of atopic dermatitis- like inflammatory skin lesion independentlyof IgE/stat6 under specific pathogen- free conditions. Proc. Nat.Acad. Sci. 99: 11340- 11345, 2002. 3 C b

GAM97 274 IL18 Nolan, K. F.; Greaves, D. R.; Waldmann, H.: The human interleukin18 gene IL18 maps to 11q22.2- q22.3, closely linked to the DRD2 genelocus and distinct from mapped IDDM loci. Genomics 51: 161- 163,1998. 3 C b

GAM97 274 IL18 Okamoto, I.; Kohno, K.; Tanimoto, T.; Iwaki, K.; Ishihara, T.;Akamatsu, S.; Ikegami, H.; Kurimoto, M.: IL- 18 prevents the developmentof chronic graft- versus- host disease in mice. J. Immun. 164: 6067- 6074,2000. 3 C b

GAM97 274 IL18 Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.;Tanimoto, T.; Torigoe, K.; Okura, T.; Nukada, Y.; Hattori, K.; Akita,K.; Namba, M.; Tanabe, F.; Konishi, K.; Fukuda, S.; Kurimoto, M.:Cloning of a new cytokine that induces IFN- gamma production by T cells. Nature 378:88- 91, 1995. 3 C b

GAM97 274 IL18 Pizarro, T. T.; Michie, M. H.; Bentz, M.; Woraratanadharm, J.;Smith, M. F., Jr.; Foley, E.; Moskaluk, C. A.; Bickston, S. J.; Cominelli,F.: IL- 18, a novel immunoregulatory cytokine, is up- regulated inCrohn's disease: expression and localization in intestinal mucosalcells. J. Immun. 162: 6829- 6835, 1999. 3 C b

GAM97 274 IL18 Reddy, P.; Teshima, T.; Kukuruga, M.; Ordemann, R.; Liu, C.; Lowler,K.; Ferrara, J. L. M.: Interleukin- 18 regulates acute graft- versus- 3 C b

hostdisease by enhancing Fas- mediated donor T cell apoptosis. J. Exp.Med. 194: 1433- 1440, 2001.

GAM97 274 IL18 Rothe, H.; Jenkins, N. A.; Copeland, N. G.; Kolb, H.: Active stageof 3 C b
autoimmune diabetes is associated with the expression of a novelcytokine, IGIF, which is located near Idd2. J. Clin. Invest. 99:469- 474, 1997.

GAM97 274 IL18 Sarvetnick, N.: IFN- gamma, IGIF, and IDDM. (Editorial) J. Clin.Invest. 99: 3 C b
371- 372, 1997.

GAM97 274 IL18 Shida, K.; Shiratori, I.; Matsumoto, M.; Fukumori, Y.; Matsuhisa,A.; 3 C b
Kikkawa, S.; Tsuji, S.; Okamura, H.; Toyoshima, K.; Seya, T.:An alternative form of IL- 18 in human blood plasma: complex formationwith IgM defined by monoclonal antibodies. J. Immun. 166: 6671- 6679,2001.

GAM97 274 IL18 Sugawara, S.; Uehara, A.; Nochi, T.; Yamaguchi, T.; Ueda, H.;Sugiyama, A.; 3 C b
Hanzawa, K.; Kumagai, K.; Okamura, H.; Takada, H.:Neutrophil proteinase 3- mediated induction of bioactive IL- 18 secretionby human oral epithelial cells. J. Immun. 167: 6568- 6575, 2001.

GAM97 274 IL18 ten Hove, T.; Corbaz, A.; Amitai, H.; Aloni, S.; Belzer, I.; Graber,P.; 3 C b
Drillenburg, P.; van Deventer, S. J.; Chvatchko, Y.; Te Velde,A. A.: Blockade of endogenous IL- 18 ameliorates TNBS- induced colitisby decreasing local TNF- alpha production in mice. Gastroenterology 121:1372- 1379, 2001.

GAM97 274 IL18 Vidal- Vanaclocha, F.; Fantuzzi, G.; Mendoza, L.; Fuentes, A. M.;Anasagasti, 3 C b
M. J.; Martin, J.; Carrascal, T.; Walsh, P.; Reznikov,L. L.; Kim, S.- H.; Novick, D.; Rubinstein, M.; Dinarello, C. A.:IL- 18 regulates IL- 1- beta- dependent hepatic melanoma metastasis viavascular cell adhesion molecule- 1. Proc. Nat. Acad. Sci. 97: 734- 739,2000.

GAM97 274 MASP1 Dahl, M. R.; Thiel, S.; Matsushita, M.; Fujita, T.; Willis, A.C.; 3 C c
Christensen, T.; Vorup- Jensen, T.; Jensenius, J. C.: MASP- 3 andits association with distinct complexes of the mannan- binding lectincomplement activation pathway. Immunity 15: 127- 135, 2001.

GAM97 274 MASP1 Endo, Y.; Sato, T.; Matsushita, M.; Fujita, T.: Exon structureof the gene 3 C c
encoding the human mannose- binding protein- associatedserine protease light chain: comparison with complement C1r and C1sgenes. Int. Immun. 8: 1355- 1358, 1996.

GAM97 274 MASP1 Matsushita, M.; Thiel, S.; Jensenius, J. C.; Terai, I.; Fujita,T.: 3 C c
Proteolytic activities of two types of mannose- binding lectin- associatedserine protease. J. Immun. 165: 2637- 2642, 2000.

GAM97 274 MASP1 Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.: Molecular characterizationof 3 C c
a novel serine protease involved in activation of the complementsystem by mannose- binding protein. Int. Immun. 6: 665- 669, 1994.

GAM97 274 MASP1 Takada, F.; Seki, N.; Matsuda, Y.; Takayama, Y.; Kawakami, M.:Localization 3 C c
of the genes for the 100- kDa complement- activating componentsof Ra- reactive factor (CRARF and Crarf) to human 3q27- q28 and mouse16B2- B3. Genomics 25: 757- 759, 1995.

GAM97 274 MASP1 Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M.: A new memberof the C1s 3 C c
family of complement proteins found in a bactericidal factor,Ra- reactive factor, in human serum. Biochem. Biophys. Res. Commun. 196:1003- 1009, 1993.

GAM97 274 MASP1 Takayama, Y.; Takada, F.; Nowatari, M.; Kawakami, M.; Matsu- ura,N.: Gene 3 C c
structure of the P100 serine- protease component of the humanRa- reactive factor. Molec. Immun. 36: 505- 514, 1999.

GAM97 274 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; 3 C b

Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.; Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998.

GAM97 274 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea transporter in the human kidney. FEBS Lett. 386: 156- 160,1996. 3 C b

GAM97 274 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.; Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2 is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157- 2164, 2001. 3 C b

GAM98 344 GAS7 Ju, Y.- T.; Chang, A. C. Y.; She, B.- R.; Tsaur, M.- L.; Hwang, H.- M.;Chao, C. C.- K.; Cohen, S. N.; Lin- Chao, S.: Gas7: a gene expressedpreferentially in growth- arrested fibroblasts and terminally differentiatedPurkinje neurons affects neurite formation. Proc. Nat. Acad. Sci. 95:11423- 11428, 1998. 3 C c

GAM98 344 GAS7 Kurtz, A.; Zimmer, A.: Interspecies fluorescence in situ hybridizationfurther defines synteny homology between mouse chromosome 11 and humanchromosome 17. Mammalian Genome 6: 379- 380, 1995. 3 C c

GAM98 344 GAS7 Megonigal, M. D.; Cheung, N.- K. V.; Rappaport, E. F.; Nowell, P.C.; Wilson, R. B.; Jones, D. H.; Addya, K.; Leonard, D. G. B.; Kushner,B. H.; Williams, T. M.; Lange, B. J.; Felix, C. A.: Detection ofleukemia- associated MLL-GAS7 translocation early during chemotherapywith DNA topoisomerase II inhibitors. Proc. Nat. Acad. Sci. 97:2814- 2819, 2000. 3 C c

GAM98 344 SLC7A5 Gaugitsch, H. W.; Prieschl, E. E.; Kalthoff, F.; Huber, N. E.;Baumruker, T.: A novel transiently expressed, integral membrane proteinlinked to cell activation: molecular cloning via the rapid degradationsignal AUUUA. J. Biol. Chem 267: 11267- 11273, 1992. 3 C c

GAM98 344 SLC7A5 Kanai, Y.; Segawa, H.; Miyamoto, K.; Uchino, H.; Takeda, H.; Endou,H.: Expression cloning and characterization of a transporter forlarge neutral amino acids activated by the heavy chain of 4F2 antigen(CD98). J. Biol. Chem. 273: 23629- 23632, 1998. 3 C c

GAM98 344 SLC7A5 Maglott, D. R.; Durkin, A. S.; Lane, S. A.; Callen, D. F.; Feldblyum,T. V.; Nierman, W. C.: The gene for membrane protein E16 (D16S469E)maps to human chromosome 16q24.3 and is expressed in human brain,thymus, and retina. Genomics 23: 303- 304, 1994. 3 C c

GAM98 344 SLC7A5 Mastroberardino, L.; Spindler, B.; Pfeiffer, R.; Skelly, P. J.;Loffing, J.; Shoemaker, C. B.; Verrey, F.: Amino- acid transport byheterodimers of 4F2hc/CD98 and members of a permease family. Nature 395:288- 291, 1998. 3 C c

GAM99 320 ACTC Buckingham, M.; Alonso, S.; Barton, P.; Cohen, A.; Daubas, P.;Garner, I.; Robert, B.; Weydert, A.: Actin and myosin multigene families:their expression during the formation and maturation of striated muscle. Am.J. Med. Genet. 25: 623- 634, 1986. 4 A c

GAM99 320 ACTC Crosby, J. L.; Phillips, S. J.; Nadeau, J. H.: The cardiac actinlocus (Actc- 1) is not on mouse chromosome 17 but is linked to beta- 2- microglobulinon chromosome 2. Genomics 5: 19- 23, 1989. 4 A c

GAM99 320 ACTC Czosnek, H.; Nudel, U.; Mayer, Y.; Barker, P. E.; Pravtcheva, D.D.; Ruddle, F. H.; Yaffe, D.: The genes coding for the cardiac muscleactin, the skeletal muscle actin and the cytoplasmic beta- actin arelocated on three different mouse chromosomes. EMBO J. 2: 1977- 1979,1983. 4 A c

GAM99 320 ACTC Elzinga, M.; Maron, B. J.; Adelstein, R. S.: Human heart and plateletactins 4 A c
are products of different genes. Science 191: 94- 95, 1976.
GAM99 320 ACTC Engel, J. N.; Gunning, P. W.; Kedes, L.: Isolation and characterizationof 4 A c
human actin genes. Proc. Nat. Acad. Sci. 78: 4674- 4678, 1981.
GAM99 320 ACTC Firtel, R. A.: Multigene families encoding actin and tubulin. Cell 24:6- 7, 4 A c
1981.
GAM99 320 ACTC Garner, I.; Minty, A. J.; Alonso, S.; Barton, P. J.; Buckingham,M. E.: A 5- 4 A c
prime duplication of the alpha- cardiac actin gene in BALB/cmice is
associated with abnormal levels of alpha- cardiac and alpha- skeletalactin
mRNAs in adult cardiac tissue. EMBO J. 5: 2559- 2567, 1986.
GAM99 320 ACTC Gunning, P.; Ponte, P.; Kedes, L.; Eddy, R.; Shows, T.: Chromosomallocation 4 A c
of the co- expressed human skeletal and cardiac actin genes. Proc.Nat. Acad.
Sci. 81: 1813- 1817, 1984.
GAM99 320 ACTC Hamada, H.; Petrino, M. G.; Kakunaga, T.: Molecular structureand 4 A c
evolutionary origin of human cardiac muscle actin gene. Proc.Nat. Acad. Sci.
79: 5901- 5905, 1982.
GAM99 320 ACTC Humphries, S. E.; Whittall, R.; Minty, A.; Buckingham, M.; Williamson,R.: 4 A c
There are approximately 20 actin genes in the human genome. NucleicAcids
Res. 9: 4895- 4908, 1981.
GAM99 320 ACTC Kramer, P. L.; Luty, J. A.; Litt, M.: Regional localization ofthe gene for 4 A c
cardiac muscle actin (ACTC) on chromosome 15q. Genomics 13:904- 905, 1992.
GAM99 320 ACTC Litt, M.; Luty, J. A.: A hypervariable microsatellite revealedby in vitro 4 A c
amplification of a dinucleotide repeat within the cardiacmuscle actin gene.
Am. J. Hum. Genet. 44: 397- 401, 1989.
GAM99 320 ACTC Mayosi, B. M.; Khogali, S. S.; Zhang, B.; Watkins, H.: Cardiacand skeletal 4 A c
actin gene mutations are not a common cause of dilatedcardiomyopathy. J.
Med. Genet. 36: 796- 797, 1999.
GAM99 320 ACTC Mogensen, J.; Klausen, I. C.; Pedersen, A. K.; Egeblad, H.; Bross,P.; Kruse, 4 A c
T. A.; Gregersen, N.; Hansen, P. S.; Baandrup, U.; Borglum,A. D.: Alpha-
cardiac actin is a novel disease gene in familial
hypertrophiccardiomyopathy. J. Clin. Invest. 103: R39- R43, 1999.
GAM99 320 ACTC Olson, T. M.; Michels, V. V.; Thibodeau, S. N.; Tai, Y.- S.; Keating,M. T.: 4 A c
Actin mutations in dilated cardiomyopathy, a heritable formof heart failure.
Science 280: 750- 752, 1998.
GAM99 320 ACTC Schwartz, K.; de la Bastie, D.; Bouveret, P.; Oliviero, P.; Alonso,S.; 4 A c
Buckingham, M.: Alpha- skeletal muscle actin mRNAs accumulatein
hypertrophied adult rat hearts. Circulation Res. 59: 551- 555,1986.
GAM99 320 ACTC Shows, T.; Eddy, R. L.; Haley, L.; Byers, M.; Henry, M.; Gunning,P.; Ponte, 4 A c
P.; Kedes, L.: The coexpressed genes for human alpha (ACTA)and cardiac actin
(ACTC) are on chromosomes 1 and 15, respectively.(Abstract) Cytogenet. Cell
Genet. 37: 583 only, 1984.
GAM99 320 ACTC Takai, E.; Akita, H.; Shiga, N.; Kanazawa, K.; Yamada, S.; Terashima,M.; 4 A c
Matsuda, Y.; Iwai, C.; Kawai, K.; Yokota, Y.; Yokoyama, M.:
Mutationalanalysis of the cardiac actin gene in familial and sporadic
dilatedcardiomyopathy. Am. J. Med. Genet. 86: 325- 327, 1999.
GAM99 320 ACTC Ueyama, H.; Inazawa, J.; Ariyama, T.; Nishino, H.; Ochiai, Y.;Ohkubo, I.; 4 A c
Miwa, T.: Reexamination of chromosomal loci of humanmuscle actin genes by
fluorescence in situ hybridization. Jpn. J.Hum. Genet. 40: 145- 148, 1995.
GAM99 320 ACTC Weber, J. L.; May, P. E.: Abundant class of human DNA polymorphismswhich can 4 A c
be typed using the polymerase chain reaction. Am. J. Hum.Genet. 44: 388-

396, 1989.

GAM99 320 ACTC Weydert, A.; Robert, B.; Alonso, S.; Caravatti, M.; Cohen, A.;Daubas, P.; 4 A c
Minty, A.; Buckingham, M.: Multigene families of contractileproteins: the
actins and myosins. (Abstract) Sixth Int. Cong. Hum.Genet., Jerusalem 39
only, 1981.

GAM99 320 AKAP2 Dong, F.; Feldmesser, M.; Casadevall, A.; Rubin, C. S.: 4 A c
Molecularcharacterization of a cDNA that encodes six isoforms of a novel
murineA kinase anchor protein. J. Biol. Chem. 273: 6533- 6541, 1998.

GAM99 320 AKAP2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 4 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XIII. The completesequences of 100
new cDNA clones from brain which code for large proteinsin vitro. DNA Res.
6: 63- 70, 1999.

GAM99 320 CPNE6 Nakayama, T.; Yaoi, T.; Kuwajima, G.: Localization and 4 A c
subcellulardistribution of N- copine in mouse brain. J. Neurochem. 72: 373-
379,1999.

GAM99 320 CPNE6 Nakayama, T.; Yaoi, Y.; Yasui, M.; Kuwajima, G.: N- copine: a noveltwo C2- 4 A c
domain- containing protein with neuronal activity- regulatedexpression. FEBS
Lett. 428: 80- 84, 1998.

GAM99 320 CPNE6 Scott, A. F.: Personal Communication. Baltimore, Md. 2001. 4 A c

GAM99 320 CPT1B Britton, C. H.; Mackey, D. W.; Esser, V.; Foster, D. W.; Burns,D. K.; 4 A c
Yarnall, D. P.; Froguel, P.; McGarry, J. D.: Fine chromosomemapping of the
genes for human liver and muscle carnitine palmitoyltransferasel (CPT1A and
CPT1B). Genomics 40: 209- 211, 1997.

GAM99 320 CPT1B van der Leij, F. R.; Takens, J.; van der Veen, A. Y.; Terpstra,P.; Kuipers, 4 A c
J. R. G.: Localization and intron usage analysis ofthe human CPT1B gene for
muscle type carnitine palmitoyltransferasel. Biochim. Biophys. Acta 1352:
123- 128, 1997.

GAM99 320 CPT1B Yamazaki, N.; Shinohara, Y.; Shima, A.; Yamanaka, Y.; Terada, H.: Isolation 4 A c
and characterization of cDNA and genomic clones encodinghuman muscle type
carnitine palmitoyltransferase I. Biochim. Biophys.Acta 1307: 157- 161,
1996.

GAM99 320 CPT1B Yamazaki, N.; Yamanaka, Y.; Hashimoto, Y.; Shinohara, Y.; Shima,A.; Terada, 4 A c
H.: Structural features of the gene encoding human muscletype carnitine
palmitoyltransferase I. FEBS Lett. 409: 401- 406,1997.

GAM99 320 CX3CR1 Faure, S.; Meyer, L.; Costagliola, D.; Vaneensberghe, C.; Genin,E.; Autran, 4 A c
B.; French ALT and IMMUNOCO Study Groups; Delfraisay,J.- F.; SEROCO Study
Group; McDermott, D. H.; Murphy, P. M.; Debre,P.; Theodorou, I.; Cambadiere,
C.: Rapid progression to AIDS in HIV+individuals with a structural variant
of the chemokine receptor CX(3)CR1. Science 287:2274- 2277, 2000.

GAM99 320 CX3CR1 Imai, T.; Hieshima, K.; Haskell, C.; Baba, M.; Nagira, M.; Nishimura,M.; 4 A c
Kakizaki, M.; Takagi, S.; Nomiyama, H.; Schall, T. J.; Yoshie,O.:
Identification and molecular characterization of fractalkinereceptor CX3CR1,
which mediates both leukocyte migration and adhesion. Cell 91:521- 530,
1997.

GAM99 320 CX3CR1 Maho, A.; Bensimon, A.; Vassart, G.; Parmentier, M.: Mapping ofthe CCXCR1, 4 A c
CX3CR1, CCBP2 and CCR9 genes to the CCR cluster withinthe 3p21.3 region of
the human genome. Cytogenet. Cell Genet. 87:265- 268, 1999.

GAM99 320 CX3CR1 Moatti, D.; Faure, S.; Fumeron, F.; Amara, M. E. W.; Seknadji,P.; McDermott, 4 A c
D. H.; Debre, P.; Aumont, M. C.; Murphy, P. M.; deProst, D.; Combadiere, C.:

Polymorphism in the fractalkine receptorCX3CR1 as a genetic risk factor for coronary artery disease. Blood 97:1925- 1928, 2001.

GAM99 320 CX3CR1 Raport, C. J.; Schweickart, V. L.; Eddy, R. L., Jr.; Shows, T.B.; Gray, P. W.: The orphan G- protein- coupled receptor- encoding geneV28 is closely related to genes for chemokine receptors and is expressedin lymphoid and neural tissues. Gene 163: 295- 299, 1995. 4 A c

GAM99 320 CX3CR1 Tripp, R. A.; Jones, L. P.; Haynes, L. M.; Zheng, H.; Murphy, P.M.; Anderson, L. J.: CX3C chemokine mimicry by respiratory syncytialvirus G glycoprotein. Nature Immun. 2: 732- 738, 2001. 4 A c

GAM99 320 DCTN1 Collin, G. B.; Nishina, P. M.; Marshall, J. D.; Naggert, J. K.: Human DCTN1: genomic structure and evaluation as a candidate forAlstrom syndrome. Genomics 53: 359- 364, 1998. 4 A c

GAM99 320 DCTN1 Holzbaur, E. L. F.; Tokito, M. K.: Localization of the DCTN1 geneencoding p150(Glued) to human chromosome 2p13 by fluorescence in situhybridization. Genomics 31: 398- 399, 1996. 4 A c

GAM99 320 DCTN1 Holzbaur, E. L. F.; Vallee, R. B.: Dyneins: molecular structureand cellular function. Ann. Rev. Cell Biol. 10: 339- 372, 1994. 4 A c

GAM99 320 DCTN1 Jang, W.; Weber, J. S.; Tokito, M. K.; Holzbaur, E. L. F.; Meisler,M. H.: Mouse p150(Glued) (dynactin 1) cDNA sequence and evaluationas a candidate for the neuromuscular disease mutation mnd2. Biochem.Biophys. Res. Commun. 231: 344- 347, 1997. 4 A c

GAM99 320 DCTN1 Korthaus, D.; Wedemeyer, N.; Lengeling, A.; Ronsiek, M.; Jockusch,H.; Schmitt- John, T.: Integrated radiation hybrid map of human chromosome2p13: possible involvement of dynactin in neuromuscular diseases. Genomics 43:242- 244, 1997. 4 A c

GAM99 320 DCTN1 Pushkin, A.; Abuladze, N.; Newman, D.; Tatishchev, S.; Kurtz, I.: Genomic organization of the DCTN1- SLC4A5 locus encoding both NBC4and p150(Glued). Cytogenet. Cell Genet. 95: 163- 168, 2001. 4 A c

GAM99 320 FAT2 Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara,O.: Identification of high- molecular- weight proteins with multipleEGF- like motifs by motif- trap screening. Genomics 51: 27- 34, 1998. 4 A c

GAM99 320 FAT2 Wu, Q.; Maniatis, T.: Large exons encoding multiple ectodomainsare a characteristic feature of protocadherin genes. Proc. Nat. Acad.Sci. 97: 3124- 3129, 2000. 4 A c

GAM99 320 FBXL5 Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol. 9: 1177- 1179, 1999. 4 A c

GAM99 320 FBXL5 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning and expression analysis of new members of the mammalianF- box protein family. Genomics 67: 40- 47, 2000. 4 A c

GAM99 320 FBXL5 Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999. 4 A c

GAM99 320 GC Baier, L. J.; Dobberfuhl, A. M.; Pratley, R. E.; Hanson, R. L.;Bogardus, C.: Variations in the vitamin D- binding protein (Gc locus)are associated with oral glucose tolerance in nondiabetic Pima Indians. J.Clin. Endocr. Metab. 83: 2993- 2996, 1998. 4 A c

GAM99 320 GC Baier, L.; The Pima Diabetes Genes Group: Suggestive linkageof genetic markers on chromosome 4q12 to NIDDM and insulin actionin Pima Indians: new evidence to extend associations reported in otherpopulations. (Abstract) Diabetes 45 (suppl. 2): 30A only, 1996. 4 A c

GAM99 320 GC Ball, S. P.; Cook, P. J. L.; Mars, M.; Buckton, K. E.: Linkagebetween 4 A c
dentinogenesis imperfecta and Gc. Ann. Hum. Genet. 46: 35- 40,1982.

GAM99 320 GC Bearn, A. G.; Bowman, B. H.; Kitchin, F. D.: Genetic and 4 A c
biochemicalconsideration of the serum group- specific component. Cold
SpringHarbor Symp. Quant. Biol. 29: 435- 442, 1964.

GAM99 320 GC Bowman, B. H.; Brune, J. L.; McCombs, J. L.; Moore, C. M.; Lum,J. B.; 4 A c
Wieder, K.; Barnett, D. R.; Yang, F.: Human group- specificcomponent: a
member of the albumin and alpha- fetoprotein gene family.(Abstract) Am. J.
Hum. Genet. 37: A145 only, 1985.

GAM99 320 GC Braun, A.; Bichlmaier, R.; Cleve, H.: Molecular analysis of thegene for the 4 A c
human vitamin- D- binding protein (group- specific component):allelic
differences of the common genetic GC types. Hum. Genet. 89:401- 406, 1992.

GAM99 320 GC Braun, A.; Kofler, A.; Morawietz, S.; Cleve, H.: Sequence andorganization of 4 A c
the human vitamin D- binding protein gene. Biochim.Biophys. Acta 1216: 385-
394, 1993.

GAM99 320 GC Chautard- Freire- Maia, E. A.: Concerning the linkage relationshipsof the Gc 4 A c
and MNSs loci (Hum. Genet. 43: 215- 220, 1978): disentanglingpart of the
data overlap. (Letter) Hum. Genet. 49: 115- 116, 1979.

GAM99 320 GC Cleve, H.; Kirk, R. L.; Gajdusek, D. C.; Guiart, J.: On the distributionof 4 A c
the Gc variant Gc Aborigine in Melanesian populations: determinationof Gc-
types in sera from Tongariki Island, New Hebrides. Acta Genet.Statist. Med.
17: 511- 517, 1967.

GAM99 320 GC Cleve, H.; Kirk, R. L.; Parker, W. C.; Bearn, A. G.; Schacht,L. E.; 4 A c
Kleinman, H.; Horsfall, W. R.: Two genetic variants of thegroup- specific
component of human serum: Gc Chippewa and Gc Aborigine. Am.J. Hum. Genet.
15: 368- 379, 1963.

GAM99 320 GC Cleve, H.; Patutschnick, W.: The vitamin D binding of the commonrare 4 A c
variants of the group- specific component (Gc): an autoradiographicstudy.
Hum. Genet. 38: 289- 296, 1977.

GAM99 320 GC Constans, J.; Cleve, H.; Dykes, D.; Fischer, M.; Kirk, R. L.;Papiha, S. S.; 4 A c
Scheffran, W.; Scherz, R.; Thymann, M.; Weber, W.:The polymorphism of the
vitamin D- binding protein (Gc); isoelectricfocusing in 3 M urea as
additional method for identification of geneticvariants. Hum. Genet. 65:
176- 180, 1983.

GAM99 320 GC Constans, J.; Viau, M.: Group- specific component: evidence fortwo subtypes 4 A c
of the Gc(1) gene. Science 198: 1070- 1071, 1977.

GAM99 320 GC Cooke, N. E.; David, E. V.: Serum vitamin D- binding protein isa third 4 A c
member of the albumin and alpha fetoprotein gene family. J.Clin. Invest. 76:
2420- 2424, 1985.

GAM99 320 GC Cooke, N. E.; Willard, H. F.; David, E. V.; George, D. L.: Directregional 4 A c
assignment of the gene for vitamin D binding protein (Gc- globulin)to human
chromosome 4q11- q13 and identification of an associated DNApolymorphism.
Hum. Genet. 73: 225- 229, 1986.

GAM99 320 GC Daiger, S. P.; Brewton, G. W.; Rios, A. A.; Mansell, P. W. A.;Reuben, J. M.: 4 A c
Genetic susceptibility to AIDS: absence of an associationwith group-
specific component (Gc). (Letter) New Eng. J. Med. 317:631- 632, 1987.

GAM99 320 GC Daiger, S. P.; Cavalli- Sforza, L. L.: Detection of genetic variationwith 4 A c
radioactive ligands. II. Genetic variants of vitamin D- labeledgroup-
specific component (Gc) proteins. Am. J. Hum. Genet. 29: 593- 604,1977.

GAM99 320 GC Daiger, S. P.; Miller, M.; Chakraborty, R.: Heritability of 4 A c

quantitativevariation at the group- specific component (Gc) locus. Am. J. Hum.Genet. 36: 663- 676, 1984.

GAM99 320 GC Daiger, S. P.; Schanfield, M. S.; Cavalli- Sforza, L. L.: Group- 4 A c
specificcomponent (Gc) proteins bind vitamin D and 25- hydroxyvitamin D. Proc.Nat. Acad. Sci. 72: 2076- 2080, 1975.

GAM99 320 GC Dykes, D. D.; Polesky, H. F.: Gc1C12: a new Gc variant. Hum.Hered. 32: 136- 4 A c
138, 1982.

GAM99 320 GC Dykes, D.; Copouls, B.; Polesky, H.: Description of six new Gcvariants. Hum. 4 A c
Genet. 63: 35- 37, 1983.

GAM99 320 GC Eales, L.- J.; Nye, K. E.; Parkin, J. M.; Weber, J. N.; Forster,S. M.; 4 A c
Harris, J. R. W.; Pinching, A. J.: Association of differentallelic forms of group specific component with susceptibility to andclinical manifestation of human immunodeficiency virus infection. Lancet I:999- 1002, 1987.

GAM99 320 GC Falk, C. T.; Martin, M. D.; Walker, M. E.; Chen, T.; Rubinstein,P.; Allen, 4 A c
F. H., Jr.: Family data suggesting a linkage between MNand Gc. (Abstract) Cytogenet. Cell Genet. 25: 152 only, 1979.

GAM99 320 GC German, J. L.; Walker, M. E.; Stiefel, F. H.; Allen, F. H., Jr.: 4 A c
Autoradiographic studies of human chromosomes. II. Data concerningthe position of the MN locus. Vox Sang. 16: 130- 145, 1969.

GAM99 320 GC Gilles, K.; Louie, L.; Newman, B.; Crandall, J.; King, M.- C.:Genetic 4 A c
susceptibility to AIDS: absence of an association with group- specificcomponent (Gc). (Letter) New Eng. J. Med. 317: 630- 631, 1987.

GAM99 320 GC Henningsen, K.; Jacobsen, P.; Mikkelsen, M.: B- F chromosome 4 A c
translocationassociated with father- child incompatibility within the Gc- system. Hum.Hered. 19: 283- 287, 1969.

GAM99 320 GC Hirschfeld, J.: Immune- electrophoretic demonstration of 4 A c
qualitativedifferences in human sera and their relation to the haptoglobins. ActaPath. Microbiol. Scand. 47: 160- 168, 1959.

GAM99 320 GC Hirschfeld, J.: The Gc- system: immuno- electrophoretic studiesof normal 4 A c
human sera with special reference to a new genetically determinedserum system (GC). Prog. Allergy 6: 155- 186, 1962.

GAM99 320 GC Johnson, A. M.; Cleve, H.; Alper, C. A.: Variants of the group- 4 A c
specifiedcomponent system as demonstrated by immunofixation electrophoresis:report of a new variant, Gc Boston (Gc B). Am. J. Hum. Genet. 27:728- 736, 1975.

GAM99 320 GC Karlsson, S.; Arnason, A.; Thordarson, G.; Olaisen, B.: Frequencyof Gc 4 A c
alleles and a variant Gc allele in Iceland. Hum. Hered. 30:119- 121, 1980.

GAM99 320 GC Kofler, A.; Braun, A.; Jenkins, T.; Serjeantson, S. W.; Cleve,H.: 4 A c
Characterization of mutants of the vitamin- D- binding protein/groupspecific component: GC Aborigine (1A1) from Australian Aboriginesand South African blacks, and 2A9 from South Germany. Vox Sang. 68:50- 54, 1995.

GAM99 320 GC Lee, W. M.; Galbraith, R. M.: The extracellular actin- scavengersystem and 4 A c
actin toxicity. New Eng. J. Med. 326: 1335- 1341, 1992.

GAM99 320 GC Magenis, R. E.; Eoff, J. S.; Toth- Fejel, S.; Lovrien, E.: Probablelinkage 4 A c
of GC to a chromosome 4 inversion and localization to 4q12.(Abstract) Cytogenet. Cell Genet. 40: 684 only, 1985.

GAM99 320 GC Mars, M.; Farrant, S.; Roberts, G. J.: Dentinogenesis imperfecta,report of a 4 A c
5- generation family. Brit. Dent. J. 140: 206- 209, 1976.

GAM99 320 GC McCombs, J. L.; Yang, F.; Bowman, B. H.; McGill, J. R.; Moore,C. M.: 4 A c
Chromosomal localization of group- specific component by insitu

hybridization. Cytogenet. Cell Genet. 42: 62- 64, 1986.

GAM99 320 GC Mikkelsen, M.; Jacobsen, P.; Henningsen, K.: Possible localizationof Gc- 4 A c
system on chromosome 4. Loss of long arm 4 material associatedwith father-
child incompatibility within the Gc- system. Hum. Hered. 27:105- 107, 1977.

GAM99 320 GC Mourant, A. E.; Tills, D.; Domaniewska- Sobczak, K.: Sunshineand the 4 A c
geographical distribution of the alleles of the Gc systemof plasma proteins.
Hum. Genet. 33: 307- 314, 1976.

GAM99 320 GC Parker, W. C.; Cleve, H.; Bearn, A. G.: Determination of phenotypesin the 4 A c
human group- specific component (Gc) system by starch gel electrophoresis.
Am.J. Hum. Genet. 15: 353- 367, 1963.

GAM99 320 GC Petrini, M.; Emerson, D. L.; Galbraith, R. M.: Linkage betweensurface 4 A c
immunoglobulin and cytoskeleton of B lymphocytes may involveGc protein.
Nature 306: 73- 74, 1983.

GAM99 320 GC Pierce, E. A.; Dame, M. C.; Bouillon, R.; Van Baelen, H.; DeLuca,H. F.: 4 A c
Monoclonal antibodies to human vitamin D- binding protein. Proc.Nat. Acad.
Sci. 82: 8429- 8433, 1985.

GAM99 320 GC Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 4 A c
New York: Oxford Univ. Press (pub.) 1988.

GAM99 320 GC Rucknagel, D. L.; Shreffler, D. C.; Halstead, S. B.: The Bangkokvariant of 4 A c
the serum group- specific component (Gc) and the frequencyof the Gc alleles
in Thailand. Am. J. Hum. Genet. 20: 478- 485, 1968.

GAM99 320 GC Schoentgen, F.; Metz- Boutigue, M.- H.; Jolles, J.; Constans, J.;Jolles, P.: 4 A c
Homology between the human vitamin D- binding protein(group specific
component), alpha- fetoprotein and serum albumin. FEBSLett. 185: 47- 50,
1985.

GAM99 320 GC Seppala, M.; Ruoslahti, E.; Makela, O.: Inheritance and geneticlinkage of Gc 4 A c
and TF groups. Acta Genet. Statist. Med. 17: 47- 54,1967.

GAM99 320 GC Shibata, T.; Abe, T.: Linkage between the loci for serum albuminand vitamin 4 A c
D binding protein (GC) in the Japanese quail. AnimalGenet. 27: 195- 197,
1996.

GAM99 320 GC Svasti, J.; Kurosky, A.; Bennett, A.; Bowman, B. H.: Molecularbasis for the 4 A c
three major forms of human serum vitamin D binding protein(group- specific
component). Biochemistry 18: 1611- 1617, 1979.

GAM99 320 GC Szathmary, E. J. E.: The effect of Gc genotype on fasting insulinlevel in 4 A c
Dogrib Indians. Hum. Genet. 75: 368- 372, 1987.

GAM99 320 GC Thymann, M.; Hjalmarsson, K.; Svensson, M.: Five new Gc variantsdetected by 4 A c
isoelectric focusing in agarose gel. Hum. Genet. 60:340- 343, 1982.

GAM99 320 GC Vavrusa, B.; Cleve, H.; Constans, J.: A deficiency mutant ofthe Gc system. 4 A c
Hum. Genet. 65: 102- 107, 1983.

GAM99 320 GC Weitkamp, L. R.: Comparative gene mapping: linkage between thealbumin and Gc 4 A c
loci in the horse. (Abstract) Am. J. Hum. Genet. 30:128A only, 1978.

GAM99 320 GC Weitkamp, L. R.: Concerning the linkage relationships of theGc and MNSs 4 A c
loci. Hum. Genet. 43: 215- 220, 1978.

GAM99 320 GC Weitkamp, L. R.; Rucknagel, D. L.; Gershowitz, H.: Genetic linkagebetween 4 A c
structural loci for albumin and group specific component (Gc). Am.J. Hum.
Genet. 18: 559- 571, 1966.

GAM99 320 GC Witke, F. W.; Gibbs, P. E. M.; Zielinski, R.; Yang, F.; Bowman,B. H.; 4 A c
Dugaiczyk, A.: Complete structure of the human Gc gene: differencesand
similarities between members of the albumin gene family. Genomics 16:751-
754, 1993.

GAM99 320 GC Yamamoto, N.; Homma, S.: Vitamin D- 3 binding protein (group- 4 A c
specificcomponent) is a precursor for the macrophage- activating signal
factorfrom lysophosphatidylcholine- treated lymphocytes. Proc. Nat.
Acad.Sci. 88: 8539- 8543, 1991.

GAM99 320 GC Yamamoto, Y.; Nishimoto, H.; Ikemoto, S.: Interstitial deletionof the 4 A c
proximal long arm of chromosome 4 associated with father-
childincompatibility within the Gc- system: probable reduced gene
dosageeffect and partial piebald trait. Am. J. Med. Genet. 32: 520-
523,1989.

GAM99 320 GC Yang, F.; Bergeron, J. M.; Linehan, L. A.; Lalley, P. A.; Sakaguchi,A. Y.; 4 A c
Bowman, B. H.: Mapping and conservation of the group- specificcomponent gene
in mouse. Genomics 7: 509- 516, 1990.

GAM99 320 GC Yang, F.; Brune, J. L.; Naylor, S. L.; Cupples, R. L.; Naberhaus,K. H.; 4 A c
Bowman, B. H.: Human group- specific component (Gc) is a memberof the
albumin family. Proc. Nat. Acad. Sci. 82: 7994- 7998, 1985.

GAM99 320 GC Yang, F.; Luna, V. J.; McAnelly, R. D.; Naberhaus, K. H.; Cupples,R. L.; 4 A c
Bowman, B. H.: Evolutionary and structural relationships amongthe group-
specific component, albumin and alpha- fetoprotein. NucleicAcids Res. 13:
8007- 8017, 1985.

GAM99 320 GC Yasuda, T.; Ikehara, Y.; Takagi, S.; Mizuta, K.; Kishi, K.: Ahereditary 4 A c
double double- banded variation in the vitamin D- bindingprotein (GC) system
analyzed by immunoblotting: duplication of the1F and 1A2 genes? Hum. Genet.
82: 89- 91, 1989.

GAM99 320 ICA1 Gaedigk, R.; Duncan, A. M. V.; Miyazaki, I.; Robinson, B. H.; Dosch,H.- M.: 4 A c
ICA1 encoding p69, a protein linked to the development oftype 1 diabetes,
maps to human chromosome 7p22. Cytogenet. Cell Genet. 66:274- 276, 1994.

GAM99 320 ICA1 Gaedigk, R.; Karges, W.; Hui, M. F.; Scherer, S. W.; Dosch, H.- M.: Genomic 4 A c
organization and transcript analysis of ICAp69, a targetantigen in diabetic
autoimmunity. Genomics 38: 382- 391, 1996.

GAM99 320 ICA1 Pietropaolo, M.; Castano, L.; Babu, S.; Buelow, R.; Kuo, Y.- L.S.; Martin, 4 A c
S.; Martin, A.; Powers, A. C.; Prochazka, M.; Naggert,J.; Leiter, E. H.;
Eisenbarth, G. S.: Islet cell autoantigen 69 kD(ICA69): molecular cloning
and characterization of a novel diabetes- associatedautoantigen. J. Clin.
Invest. 92: 359- 371, 1993.

GAM99 320 IREB2 Guo, B.; Yu, Y.; Leibold, E. A.: Iron regulates cytoplasmic levelsof a novel 4 A c
iron- responsive element- binding protein without aconitaseactivity. J.
Biol. Chem. 269: 24252- 24260, 1994.

GAM99 320 IREB2 Henderson, B. R.; Seiser, C.; Kuhn, L. C.: Characterization ofa second RNA- 4 A c
binding protein in rodents with specificity for iron- responsiveelements. J.
Biol. Chem. 268: 27327- 27334, 1993.

GAM99 320 IREB2 Hentze, M. W.; Kuhn, L. C.: Molecular control of vertebrate ironmetabolism: 4 A c
mRNA- based regulatory circuits operated by iron, nitricoxide, and oxidative
stress. Proc. Nat. Acad. Sci. 93: 8175- 8182,1996.

GAM99 320 IREB2 Iwai, K.; Klausner, R. D.; Rouault, T. A.: Requirements for iron- 4 A c
regulateddegradation of the RNA binding protein, iron regulatory protein 2.
EMBOJ. 14: 5350- 5357, 1995.

GAM99 320 IREB2 LaVaute, T.; Smith, S.; Cooperman, S.; Iwai, K.; Land, W.; Meyron- Holtz,E.; 4 A c
Drake, S. K.; Miller, G.; Abu- Asab, M.; Tsokos, M.; Switzer, R.,III;
Grinberg, A.; Love, P.; Tresser, N.; Rouault, T. A.: Targeteddeletion of the
gene encoding iron regulatory protein- 2 causes misregulationof iron

metabolism and neurodegenerative disease in mice. NatureGenet. 27: 209- 214, 2001.

GAM99 320 IREB2 Rouault, T. A.; Tang, C. K.; Kaptain, S.; Burgess, W. H.; Haile,D. J.; Samaniego, F.; McBride, O. W.; Harford, J. B.; Klausner, R.D.: Cloning of the cDNA encoding an RNA regulatory protein: the humaniron- responsive element- binding protein. Proc. Nat. Acad. Sci. 87:7958- 7962, 1990. 4 A c

GAM99 320 IREB2 Samaniego, F.; Chin, J.; Iwai, K.; Rouault, T. A.; Klausner, R.D.: Molecular characterization of a second iron- responsive elementbinding protein, iron regulatory protein 2: structure, function, andpost- translational regulation. J. Biol. Chem. 269: 30904- 30910,1994. 4 A c

GAM99 320 IREB2 Wu, K.- J.; Polack, A.; Dalla- Favera, R.: Coordinated regulationof iron- controlling genes, H- ferritin and IRP2, by c- MYC. Science 283:676- 679, 1999. 4 A c

GAM99 320 JUP Aberle, H.; Bierkamp, C.; Torchard, D.; Serova, O.; Wagner, T.;Natt, E.; Wirsching, J.; Heidkamper, C.; Montagna, M.; Lynch, H. T.;Lenoir, G. M.; Scherer, G.; Feunteun, J.; Kemler, R.: The human plakoglobingene localizes on chromosome 17q21 and is subjected to loss of heterozygosityin breast and ovarian cancers. Proc. Nat. Acad. Sci. 92: 6384- 6388,1995. 4 A c

GAM99 320 JUP Arnemann, J.; Spurr, N. K.; Wheeler, G. N.; Parker, A. E.; Buxton,R. S.: Chromosomal assignment of the human genes coding for the majorproteins of the desmosome junction, desmoglein DGI (DSG), desmocollinsDGII/III (DSC), desmoplakins DPI/II (DSP), and plakoglobin DPIII (JUP). Genomics 10:640- 645, 1991. 4 A c

GAM99 320 JUP Bierkamp, C.; Mclaughlin, K. J.; Schwarz, H.; Huber, O.; Kemler,R.: Embryonic heart and skin defects in mice lacking plakoglobin. Dev.Biol. 180: 780- 785, 1996. 4 A c

GAM99 320 JUP Cowley, C. M. E.; Simrak, D.; Spurr, N. K.; Arnemann, J.; Buxton,R. S.: The plakophilin 1 (PKP1) and plakoglobin (JUP) genes map tohuman chromosomes 1q and 17, respectively. Hum. Genet. 100: 486- 488,1997. 4 A c

GAM99 320 JUP Franke, W. W.; Goldschmidt, M. D.; Zimbelmann, R.; Mueller, H.M.; Schiller, D. L.; Cowin, P.: Molecular cloning and amino acidsequence of human plakoglobin, the common junctional plaque protein. Proc.Nat. Acad. Sci. 86: 4027- 4031, 1989. 4 A c

GAM99 320 JUP Guenet, J.- L.; Simon- Chazottes, D.; Ringwald, M.; Kemler, R.:The genes coding for alpha and beta catenin (Catna1 and Catnb) andplakoglobin (Jup) map to mouse chromosomes 18, 9, and 11, respectively. MammalianGenome 6: 363- 366, 1995. 4 A c

GAM99 320 JUP Knudsen, K. A.; Wheelock, M. J.: Plakoglobin, or an 83- kD homologuedistinct from beta- catenin, interacts with E- cadherin and N- cadherin. J.Cell Biol. 118: 671- 679, 1992. 4 A c

GAM99 320 JUP Kolligs, F. T.; Kolligs, B.; Hajra, K. M.; Hu, G.; Tani, M.; Cho,K. R.; Fearon, E. R.: Gamma- catenin is regulated by the APC tumorsuppressor and its oncogenic activity is distinct from that of beta- catenin. GenesDev. 14: 1319- 1331, 2000. 4 A c

GAM99 320 JUP Mathur, M.; Goodwin, L.; Cowin, P.: Interactions of the cytoplasmicdomain of the desmosomal cadherin Dsg1 with plakoglobin. J. Biol.Chem. 269: 14075- 14080, 1994. 4 A c

GAM99 320 JUP McKoy, G.; Protonotarios, N.; Crosby, A.; Tsatsopoulou, A.; Anastasakis,A.; Coonar, A.; Norman, M.; Baboonian, C.; Jeffery, S.; McKenna, W.J.: Identification of a deletion in plakoglobin in arrhythmogenicright 4 A c

ventricular cardiomyopathy with palmoplantar keratoderma andwoolly hair (Naxos disease). Lancet 355: 2119- 2124, 2000.

GAM99 320 JUP Ruiz, P.; Brinkmann, V.; Ledermann, B.; Behrend, M.; Grund, C.;Thalhammer, C.; Vogel, F.; Birchmeier, C.; Gunthert, U.; Franke, W.W.; Birchmeier, W.: Targeted mutation of plakoglobin in mice revealsessential functions of desmosomes in the embryonic heart. J. CellBiol. 135: 215- 225, 1996. 4 A c

GAM99 320 KIF1B Gong, T.- W. L.; Burmeister, M.; Lomax, M. I.: The novel gene D4Mil1emaps to mouse chromosome 4 and human chromosome 1p36. Mammalian Genome 7:790- 791, 1996. 4 A c

GAM99 320 KIF1B Nangaku, M.; Sato- Yoshitake, R.; Okada, Y.; Noda, Y.; Takemura,R.; Yamazaki, H.; Hirokawa, N.: KIF1B, a novel microtubule plus end-directedmonomeric motor protein for transport of mitochondria. Cell 79:1209-1220, 1994. 4 A c

GAM99 320 KIF1B Saito, M.; Hayashi, Y.; Suzuki, T.; Tanaka, H.; Hozumi, I.; Tsuji,S.: Linkage mapping of the gene for Charcot- Marie- Tooth disease type2 to chromosome 1p (CMT2A) and the clinical features of CMT2A. Neurology 49:1630-1635, 1997. 4 A c

GAM99 320 KIF1B Yang, H. W.; Chen, Y. Z.; Takita, J.; Soeda, E.; Piao, H. Y.; Hayashi,Y.: Genomic structure and mutational analysis of the human KIF1Bgene which is homozygously deleted in neuroblastoma at chromosome1p36.2. Oncogene 20: 5075- 5083, 2001. 4 A c

GAM99 320 KIF1B Zhao, C.; Takita, J.; Tanaka, Y.; Setou, M.; Nakagawa, T.; Takeda,S.; Yang, H. W.; Terada, S.; Nakata, T.; Takei, Y.; Saito, M.; Tsuji,S.; Hayashi, Y.; Hirokawa, N.: Charcot- Marie- Tooth disease type 2Acaused by mutation in a microtubule motor KIF1B- beta. Cell 105:587- 597, 2001. 4 A c

GAM99 320 KL Arking, D. E.; Krebsova, A.; Macek, M., Sr.; Macek, M., Jr.; Arking,A.; Mian, I. S.; Fried, L.; Hamosh, A.; Dey, S.; McIntosh, I.; Dietz,H. C.: Association of human aging with a functional variant of klotho. Proc.Nat. Acad. Sci. 99: 856- 861, 2002. 4 A c

GAM99 320 KL Koh, N.; Fujimori, T.; Nishiguchi, S.; Tamori, A.; Shiomi, S.;Nakatani, T.; Sugimura, K.; Kishimoto, T.; Kinoshita, S.; Kuroki,T.; Nabeshima, Y.: Severely reduced production of Klotho in humanchronic renal failure kidney. Biochem. Biophys. Res. Commun. 280:1015- 1020, 2001. 4 A c

GAM99 320 KL Kuro- o, M.; Matsumura, Y.; Aizawa, H.; Kawaguchi, H.; Suga, T.;Utsugi, T.; Ohyama, Y.; Kurabayashi, M.; Kaname, T.; Kume, E.; Iwasaki,H.; Iida, A.; Shiraki- Iida, T.; Nishikawa, S.; Nagai, R.; Nabeshima,Y.: Mutation of the mouse klotho gene leads to a syndrome resemblingageing. Nature 390: 45- 51, 1997. 4 A c

GAM99 320 KL Matsumura, Y.; Aizawa, H.; Shiraki- Iida, T.; Nagai, R.; Kuro- o,M.; Nabeshima, Y.: Identification of the human klotho gene and itstwo transcripts encoding membrane and secreted klotho protein. Biochem.Biophys. Res. Commun. 242: 626- 630, 1998. 4 A c

GAM99 320 KL Mori, K.; Yahata, K.; Mukoyama, M.; Suganami, T.; Makino, H.; Nagae,T.; Masuzaki, H.; Ogawa, Y.; Sugawara, A.; Nabeshima, Y.; Nakao, K.: Disruption of klotho gene causes an abnormal energy homeostasisin mice. Biochem. Biophys. Res. Commun. 278: 665- 670, 2000. 4 A c

GAM99 320 KL Saito, Y.; Nakamura, T.; Ohyama, Y; Suzuki, T.; Iida, A.; Shiraki- Iida,T.; Kuro- o, M.; Nabeshima, Y.; Kurabayashi, M.; Nagai, R.: In vivoklotho gene delivery protects against endothelial dysfunction in multiplerisk factor syndrome. Biochem. Biophys. Res. Commun. 276: 767- 772,2000. 4 A c

GAM99 320 KLK5 Brattsand, M.; Egelrud, T.: Purification, molecular cloning, andexpression 4 A c
of a human stratum corneum trypsin- like serine proteasewith possible
function in desquamation. J. Biol. Chem. 274: 30033- 30040,1999.

GAM99 320 KLK5 Harvey, T. J.; Hooper, J. D.; Myers, S. A.; Stephenson, S.- A.;Ashworth, L. 4 A c
K.; Clements, J. A.: Tissue- specific expression patternsand fine mapping of
the human kallikrein (KLK) locus on proximal 19q13.4. J.Biol. Chem. 275:
37397- 37406, 2000.

GAM99 320 KLK5 Kim, H.; Scorillas, A.; Katsaros, D.; Yousef, G. M.; Massobrio,M.; 4 A c
Fracchioli, S.; Piccinno, R.; Gordini, G.; Diamandis, E. P.:Human kallikrein
gene 5 (KLK5) expression is an indicator of poorprognosis in ovarian cancer.
Brit. J. Cancer 84: 643- 650, 2001.

GAM99 320 KLK5 Yousef, G. M.; Diamandis, E. P.: The new kallikrein- like gene,KLK- L2: 4 A c
molecular characterization, mapping, tissue expression, andhormonal
regulation. J. Biol. Chem. 274: 37511- 37516, 1999.

GAM99 320 LDLR Aalto- Setala, K.; Helve, E.; Kovanen, P. T.; Kontula, K.: Finnishtype of 4 A c
low density lipoprotein receptor gene mutation (FH- Helsinki)deletes exons
encoding the carboxy- terminal part of the receptor andcreates an
internalization- defective phenotype. J. Clin. Invest. 84:499- 505, 1989.

GAM99 320 LDLR Aalto- Setala, K.; Koivisto, U.- M.; Miettinen, T. A.; Gylling, 4 A c
H.;Kesaniemi, Y. A.; Savolainen, M.; Pyorala, K.; Ebeling, T.; Mononen,I.;
Turtola, H.; Viikari, J.; Kontula, K.: Prevalence and
geographicaldistribution of major LDL receptor gene rearrangements in
Finland. J.Intern. Med. 231: 227- 234, 1992.

GAM99 320 LDLR Agnello, V.; Abel, G.; Elfahal, M.; Knight, G. B.; Zhang, Q.- X.: Hepatitis 4 A c
C virus and other flaviviridae viruses enter cells vialow density
lipoprotein receptor. Proc. Nat. Acad. Sci. 96: 12766- 12771,1999.

GAM99 320 LDLR Allen, J. M.; Thompson, G. R.; Myant, N. B.; Steiner, R.; Oakley,C. M.: 4 A c
Cardiovascular complications of homozygous familial hypercholesterolaemia.
Brit.Heart J. 44: 361- 368, 1980.

GAM99 320 LDLR Benlian, P.; Amselem, S.; Loux, N.; Pastier, D.; Giraud, G.; deGennes, J. 4 A c
L.; Turpin, G.; Monnier, L.; Rieu, D.; Douste- Blazy, P.;Dastugue, B.;
Goossens, M.; Junien, C.: A LDL receptor gene homozygousmutation: PCR
amplification, direct genomic sequencing, associatedhaplotype, rapid
screening for frequency. Ann. Genet. 33: 65- 69,1990.

GAM99 320 LDLR Bertolini, S.; Lelli, N.; Coviello, D. A.; Ghisellini, M.; Masturzo,P.; 4 A c
Tiozzo, R.; Elicio, N.; Gaddi, A.; Calandra, S.: A large deletionin the LDL
receptor gene- - the cause of familial hypercholesterolemiain three Italian
families: a study that dates back to the 17th century(FH- Pavia). Am. J.
Hum. Genet. 51: 123- 134, 1992.

GAM99 320 LDLR Betard, C.; Kessling, A. M.; Roy, M.; Chamberland, A.; Lussier- Cacan,S.; 4 A c
Davignon, J.: Molecular genetic evidence for a founder effectin familial
hypercholesterolemia among French Canadians. Hum. Genet. 88:529- 536, 1992.

GAM99 320 LDLR Boehnke, M.; Arnheim, N.; Li, H.; Collins, F. S.: Fine- structuregenetic 4 A c
mapping of human chromosomes using the polymerase chain reactionon single
sperm: experimental design considerations. Am. J. Hum.Genet. 45: 21- 32,
1989.

GAM99 320 LDLR Brink, P. A.; Steyn, L. T.; Coetzee, G. A.; van der Westhuyzen,D. R.: 4 A c
Familial hypercholesterolemia in South African Afrikaners:PvuII and StuI DNA
polymorphisms in the LDL- receptor gene consistentwith a predominating
founder gene effect. Hum. Genet. 77: 32- 35,1987.

GAM99 320 LDLR Brown, M. S.; Goldstein, J. L.: Analysis of a mutant strain ofhuman 4 A c
fibroblasts with a defect in the internalization of receptor- boundlow
density lipoproteins. Cell 9: 663- 674, 1976.

GAM99 320 LDLR Brown, M. S.; Goldstein, J. L.: Familial hypercholesterolemia:defective 4 A c
binding of lipoproteins to cultured fibroblasts associatedwith impaired
regulation of 3- hydroxy- 3- methylglutaryl coenzyme atreductase activity.
Proc. Nat. Acad. Sci. 71: 788- 792, 1974.

GAM99 320 LDLR Brown, M. S.; Goldstein, J. L.: Receptor- mediated endocytosis:insights from 4 A c
the lipoprotein receptor system. Proc. Nat. Acad. Sci. 76:3330- 3337, 1979.

GAM99 320 LDLR Davis, C. G.; Lehrman, M. A.; Russell, D. W.; Anderson, R. G.W.; Brown, M. 4 A c
S.; Goldstein, J. L.: The J.D. mutation in familialhypercholesterolemia:
amino acid substitution in cytoplasmic domainimpedes internalization of LDL
receptors. Cell 45: 15- 24, 1986.

GAM99 320 LDLR De Braekeleer, M.: Hereditary disorders in Saguenay- Lac- St- Jean(Quebec, 4 A c
Canada). Hum. Hered. 41: 141- 146, 1991.

GAM99 320 LDLR Defesche, J. C.; Kastelein, J. J. P.: Molecular epidemiologyof familial 4 A c
hypercholesterolaemia. (Letter) Lancet 352: 1643- 1644,1998.

GAM99 320 LDLR Defesche, J. C.; van de Ree, M. A.; Kastelein, J. J. P.; van Diermen,D. E.; 4 A c
Janssens, N. W. E.; van Doormaal, J. J.; Hayden, M. R.: Detectionof the
pro664- to- leu mutation in the low- density lipoprotein receptorand its
relation to lipoprotein(a) levels in patients with
familialhypercholesterolemia of Dutch ancestry from The Netherlands and
Canada. Clin.Genet. 42: 273- 280, 1992.

GAM99 320 LDLR Defesche, J. C.; van Diermen, D. E.; Lansberg, P. J.; Lamping,R. J.; Reymer, 4 A c
P. W. A.; Hayden, M. R.; Kastelein, J. J. P.: SouthAfrican founder mutations
in the low- density lipoprotein receptorgene causing familial
hypercholesterolemia in the Dutch population. Hum.Genet. 92: 567- 570, 1993.

GAM99 320 LDLR Durst, R.; Colombo, R.; Shpitzen, S.; Ben Avi, L.; Friedlander,Y.; Wexler, 4 A c
R.; Raal, F. J.; Marais, D. A.; Defesche, J. C.; Mandelshtam,M. Y.; Kotze,
M. J.; Leitersdorf, E.; Meiner, V.: Recent origin andspread of a common
Lithuanian mutation, G197del LDLR, causing familialhypercholesterolemia:
positive selection is not always necessary toaccount for disease incidence
among Ashkenazi Jews. Am. J. Hum. Genet. 68:1172- 1188, 2001.

GAM99 320 LDLR Ekstrom, U.; Abrahamson, M.; Floren, C.- H.; Tollig, H.; Wettrell,G.; 4 A c
Nilsson, G.; Sun, X.- M.; Soutar, A. K.; Nilsson- Ehle, P.: Anindividual
with a healthy phenotype in spite of a pathogenic LDL receptormutation
(C240F). Clin. Genet. 55: 332- 339, 1999.

GAM99 320 LDLR Elston, R. C.; Namboodiri, K. K.; Go, R. C. P.; Siervogel, R.M.; Glueck, C. 4 A c
J.: Probable linkage between essential familial hypercholesterolemiaand
third complement component (C3). Cytogenet. Cell Genet. 16:294- 297, 1976.

GAM99 320 LDLR Esser, V.; Russell, D. W.: Transport- deficient mutations in thelow density 4 A c
lipoprotein receptor: alterations in the cysteine- richand cysteine- poor
regions of the protein block intracellular transport. J.Biol. Chem. 263:
13276- 13281, 1988.

GAM99 320 LDLR Feussner, G.; Dobmeyer, J.; Nissen, H.; Hansen, T. S.: UnusualXanthomas in a 4 A c
young patient with heterozygous familial hypercholesterolemiaand type III
hyperlipoproteinemia. Am. J. Med. Genet. 65: 149- 154,1996.

GAM99 320 LDLR Francke, U.; Brown, M. S.; Goldstein, J. L.: Assignment of thehuman gene for 4 A c
the low density lipoprotein receptor to chromosome19: synteny of a receptor,
a ligand, and a genetic disease. Proc.Nat. Acad. Sci. 81: 2826- 2830, 1984.

GAM99 320 LDLR Frank, S. L.; Taylor, B. A.; Lusis, A. J.: Linkage of the mouseLDL receptor gene on chromosome 9. Genomics 5: 646- 648, 1989. 4 A c

GAM99 320 LDLR Fumeron, F.; Grandchamp, B.; Fricker, J.; Krempf, M.; Wolf, L.- M.;Khayat, M.- C.; Boiffard, O.; Apfelbaum, M.: Presence of the FrenchCanadian deletion in a French patient with familial hypercholesterolemia.(Letter) New Eng. J. Med. 326: 69 only, 1992. 4 A c

GAM99 320 LDLR Gilbert, W.: Genes- in- pieces revisited. Science 228: 823- 824,1985. 4 A c

GAM99 320 LDLR Goldfarb, L. G.; Petersen, R. B.; Tabaton, M.; Brown, P.; LeBlanc,A. C.; Montagna, P.; Cortelli, P.; Julien, J.; Vital, C.; Pendelbury,W. W.; Haltia, M.; Wills, P. R.; and 9 others: Fatal familial insomniaand familial Creutzfeldt- Jakob disease: disease phenotype determinedby a DNA polymorphism. Science 258: 806- 808, 1992. 4 A c

GAM99 320 LDLR Goldstein, J. L.; Brown, M. S.; Stone, N. J.: Genetics of theLDL receptor: evidence that the mutations affecting binding and internalizationare allelic. Cell 12: 629- 641, 1977. 4 A c

GAM99 320 LDLR Goldstein, J. L.; Dana, S. E.; Brunschede, G. Y.; Brown, M. S.: Genetic heterogeneity in familial hypercholesterolemia: evidencefor two different mutations affecting functions of low- density lipoproteinreceptor. Proc. Nat. Acad. Sci. 72: 1092- 1096, 1975. 4 A c

GAM99 320 LDLR Graadt van Roggen, F.; van der Westhuyzen, D. R.; Marais, A. D.;Gevers, W.; Coetzee, G. A.: Low density lipoprotein receptor foundermutations in Afrikaner familial hypercholesterolaemic patients: acomparison of two geographical areas. Hum. Genet. 88: 204- 208, 1991. 4 A c

GAM99 320 LDLR Gudnason, V.; King- Underwood, L.; Seed, M.; Sun, X.- M.; Soutar,A. K.; Humphries, S. E.: Identification of recurrent and novel mutationsin exon 4 of the LDL receptor gene in patients with familial hypercholesterolemiain the United Kingdom. Arteriosclerosis Thromb. 13: 56- 63, 1993. 4 A c

GAM99 320 LDLR Gudnason, V.; Sigurdsson, G.; Nissen, H.; Humphries, S. E.: Commonfounder mutation in the LDL receptor gene causing familial hypercholesterolemiain the Icelandic population. Hum. Mutat. 10: 36- 44, 1997. 4 A c

GAM99 320 LDLR Henderson, H. E.; Berger, G. M. B.; Marais, A. D.: A new LDLreceptor gene deletion mutation in the South African population. Hum.Genet. 80: 371- 374, 1988. 4 A c

GAM99 320 LDLR Hobbs, H. H.: Personal Communication. Dallas, Tex. 12/1/1990. 4 A c

GAM99 320 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: Molecular geneticsof the LDL receptor gene in familial hypercholesterolemia. Hum. Mutat. 1:445- 466, 1992. 4 A c

GAM99 320 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.; Russell, D. W.:Deletion of exon encoding cysteine- rich repeat of low density lipoproteinreceptor alters its binding specificity in a subject with familialhypercholesterolemia. J. Biol. Chem. 261: 13114- 13120, 1986. 4 A c

GAM99 320 LDLR Hobbs, H. H.; Brown, M. S.; Russell, D. W.; Davignon, J.; Goldstein,J. L.: Deletion in the gene for the low- density- lipoprotein receptorin a majority of French Canadians with familial hypercholesterolemia. NewEng. J. Med. 317: 734- 737, 1987. 4 A c

GAM99 320 LDLR Hobbs, H. H.; Lehrman, M. A.; Yamamoto, T.; Russell, D. W.: Polymorphismand evolution of Alu sequences in the human low density lipoproteinreceptor gene. Proc. Nat. Acad. Sci. 82: 7651- 7655, 1985. 4 A c

GAM99 320 LDLR Hobbs, H. H.; Leitersdorf, E.; Goldstein, J. L.; Brown, M. S.;Russell, D. W.: Multiple CRM- mutations in familial hypercholesterolemia:evidence for 4 A c

13 alleles, including four deletions. J. Clin. Invest. 81:909- 917, 1988.

GAM99 320 LDLR Hobbs, H. H.; Leitersdorf, E.; Leffert, C. C.; Cryer, D. R.; Brown,M. S.; 4 A c
Goldstein, J. L.: Evidence for a dominant gene that
suppresseshypercholesterolemia in a family with defective low density
lipoproteinreceptors. J. Clin. Invest. 84: 656- 664, 1989.

GAM99 320 LDLR Hobbs, H. H.; Russell, D. W.; Brown, M. S.; Goldstein, J. L.:The LDL 4 A c
receptor locus in familial hypercholesterolemia: mutationalanalysis of a
membrane protein. Annu. Rev. Genet. 24: 133- 170, 1990.

GAM99 320 LDLR Horsthemke, B.; Beisiegel, U.; Dunning, A.; Havinga, J. R.; Williamson,R.; 4 A c
Humphries, S.: Unequal crossing- over between two Alu- repetitiveDNA
sequences in the low- density- lipoprotein- receptor gene: a
possiblemechanism for the defect in a patient with familial
hypercholesterolaemia. Europ.J. Biochem. 164: 77- 81, 1987.

GAM99 320 LDLR Horsthemke, B.; Dunning, A.; Humphries, S.: Identification ofdeletions in 4 A c
the human low density lipoprotein receptor gene. J.Med. Genet. 24: 144- 147,
1987.

GAM99 320 LDLR Horsthemke, B.; Kessling, A. M.; Seed, M.; Wynn, V.; Williamson,R.; 4 A c
Humphries, S. E.: Identification of a deletion in the low densitylipoprotein
(LDL) receptor gene in a patient with familial hypercholesterolaemia.
Hum.Genet. 71: 75- 78, 1985.

GAM99 320 LDLR Jensen, H. K.; Jensen, T. G.; Faergeman, O.; Jensen, L. G.; Andresen,B. S.; 4 A c
Corydon, M. J.; Andreasen, P. H.; Hansen, P. S.; Heath, F.;Bolund, L.;
Gregersen, N.: Two mutations in the same low- densitylipoprotein receptor
allele act in synergy to reduce receptor functionin heterozygous familial
hypercholesterolemia. Hum. Mutat. 9: 437- 444,1997.

GAM99 320 LDLR Jensen, J. M.; Kruse, T. A.; Brorholt- Petersen, J. U.; Christiansen,T. M.; 4 A c
Jensen, H. K.; Kolvraa, S.; Faergeman, O.: Linking genotypeto aorto-
coronary atherosclerosis: a model using familial hypercholesterolemiaand
aorto- coronary calcification. Ann. Hum. Genet. 63: 511- 520,1999.

GAM99 320 LDLR Kajinami, K.; Fujita, H.; Koizumi, J.; Mabuchi, H.; Takeda, R.;Ohta, M.: 4 A c
Genetically determined mild type of familial hypercholesterolemiaincluding
normocholesterolemic patients: FH- Tonami- 2. Circulation 80(suppl. 2): 278
only, 1989.

GAM99 320 LDLR Kajinami, K.; Mabuchi, H.; Itoh, H.; Michishita, I.; Takeda, M.;Wakasugi, 4 A c
T.; Koizumi, J.; Takeda, R.: New variant of low densitylipoprotein receptor
gene FH- Tonami. Arteriosclerosis 8: 187- 192,1988.

GAM99 320 LDLR Khachadurian, A. K.: The inheritance of essential familial 4 A c
hypercholesterolemia. Am.J. Med. 37: 402- 407, 1964.

GAM99 320 LDLR Kingsley, D. M.; Krieger, M.: Receptor- mediated endocytosis oflow density 4 A c
lipoprotein: somatic cell mutants define multiple genesrequired for
expression of surface- receptor activity. Proc. Nat.Acad. Sci. 81: 5454-
5458, 1984.

GAM99 320 LDLR Knight, B. L.; Gavigan, S. J. P.; Soutar, A. K.; Patel, D. D.: Defective 4 A c
processing and binding of low- density lipoprotein receptorsin fibroblasts
from a familial hypercholesterolaemic subject. Europ.J. Biochem. 179: 693-
698, 1989.

GAM99 320 LDLR Knoblauch, H.; Muller- Myhsok, B.; Busjahn, A.; Ben Avi, L.; Bahring,S.; 4 A c
Baron, H.; Heath, S. C.; Uhlmann, R.; Faulhaber, H.- D.; Shpitzen,S.; Aydin,
A.; Reshef, A.; and 11 others: A cholesterol- loweringgene maps to
chromosome 13q. Am. J. Hum. Genet. 66: 157- 166, 2000.

GAM99 320 LDLR Koivisto, U.- M.; Hubbard, A. L.; Mellman, I.: A novel cellularphenotype for 4 A c
familial hypercholesterolemia due to a defect in polarizedtargeting of LDL
receptor. Cell 105: 575- 585, 2001.

GAM99 320 LDLR Koivisto, U.- M.; Turtola, H.; Aalto- Setala, K.; Top, B.; Frants,R. R.; 4 A c
Kovanen, P. T.; Syvanen, A.- C.; Kontula, K.: The
familialhypercholesterolemia (FH)- North Karelia mutation of the low
densitylipoprotein receptor gene deletes seven nucleotides of exon 6 andis a
common cause of FH in Finland. J. Clin. Invest. 90: 219- 228,1992.

GAM99 320 LDLR Koivisto, U.- M.; Viikari, J. S.; Kontula, K.: Molecular characterizationof 4 A c
minor gene rearrangements in Finnish patients with heterozygousfamilial
hypercholesterolemia: identification of two common missensemutations
(Gly823- to- Asp and Leu380- to- His) and eight rare mutationsof the LDL
receptor gene. Am. J. Hum. Genet. 57: 789- 797, 1995.

GAM99 320 LDLR Komuro, I.; Kato, H.; Nakagawa, T.; Takahashi, K.; Mimori, A.;Takeuchi, F.; 4 A c
Nishida, Y.; Miyamoto, T.: Case report: the longest- livedpatient with
homozygous familial hypercholesterolemia secondary toa defect in
internalization of the LDL receptor. Am. J. Med. Sci. 294:341- 345, 1987.

GAM99 320 LDLR Kotze, M. J.; Langenhoven, E.; Retief, A. E.; Steyn, K.; Marais,M. P.; 4 A c
Grobbelaar, J. J.; Oosthuizen, C. J. J.; Weich, H. F. H.; Benade,A. J. S.:
Haplotype associations of three DNA polymorphisms at thehuman low density
lipoprotein receptor gene locus in familial hypercholesterolemia. J.Med.
Genet. 24: 750- 755, 1987.

GAM99 320 LDLR Kotze, M. J.; Langenhoven, E.; Warnich, L.; du Plessis, L.; Retief,A. E.: 4 A c
The molecular basis and diagnosis of familial hypercholesterolaemiain South
African Afrikaners. Ann. Hum. Genet. 55: 115- 121, 1991.

GAM99 320 LDLR Kotze, M. J.; Theart, L.; Peeters, A.; Langenhoven, E.: A denovo duplication 4 A c
in the low density lipoprotein receptor gene. Hum.Mutat. 6: 181- 183, 1995.

GAM99 320 LDLR Kotze, M. J.; Warnich, L.; Langenhoven, E.; du Plessis, L.; Retief,A. E.: An 4 A c
exon 4 mutation identified in the majority of South Africanfamilial
hypercholesterolaemics. J. Med. Genet. 27: 298- 302, 1990.

GAM99 320 LDLR Landsberger, D.; Meiner, V.; Reshef, A.; Levy, Y.; van der Westhuyzen,D. R.; 4 A c
Coetzee, G. A.; Leitersdorf, E.: A nonsense mutation in theLDL receptor gene
leads to familial hypercholesterolemia in the Druzesect. Am. J. Hum. Genet.
50: 427- 433, 1992.

GAM99 320 LDLR Langlois, S.: Personal Communication. Vancouver, British Columbia,Canada 4 A c
1989.

GAM99 320 LDLR Langlois, S.; Kastelein, J. J. P.; Hayden, M. R.: Characterizationof six 4 A c
partial deletions in the low- density- lipoprotein (LDL) receptorgene
causing familial hypercholesterolemia (FH). Am. J. Hum. Genet. 43:60- 68,
1988.

GAM99 320 LDLR Lee, W. K.; Haddad, L.; Macleod, M. J.; Dorrance, A. M.; Wilson,D. J.; 4 A c
Gaffney, D.; Dominiczak, M. H.; Packard, C. J.; Day, I. N.;Humphries, S. E.;
Dominiczak, A. F.: Identification of a common lowdensity lipoprotein
receptor mutation (C163Y) in the West of Scotland. J.Med. Genet. 35: 573-
578, 1998.

GAM99 320 LDLR Lehrman, M. A.; Goldstein, J. L.; Brown, M. S.; Russell, D. W.;Schneider, W. 4 A c
J.: Internalization- defective LDL receptors producedby genes with nonsense
and frameshift mutations that truncate thecytoplasmic domain. Cell 41: 735-
743, 1985.

GAM99 320 LDLR Lehrman, M. A.; Goldstein, J. L.; Russell, D. W.; Brown, M. S.: Duplication 4 A c

of seven exons in LDL receptor gene caused by Alu- Alurecombination in a subject with familial hypercholesterolemia. Cell 48:827- 835, 1987.

GAM99 320 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Alu- Alu 4 A c
recombination deletes splice acceptor sites and producessecreted low density lipoprotein receptor in a subject with familialhypercholesterolemia. J. Biol. Chem. 262: 3354- 3361, 1987.

GAM99 320 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Exon- Alu 4 A c
recombination deletes 5 kilobases from the low densitylipoprotein receptor gene, producing a null phenotype in familialhypercholesterolemia. Proc. Nat. Acad. Sci. 83: 3679- 3683, 1986.

GAM99 320 LDLR Lehrman, M. A.; Schneider, W. J.; Sudhof, T. C.; Brown, M. S.;Goldstein, J. 4 A c
L.; Russell, D. W.: Mutation in LDL receptor: Alu- Alurecombination deletes exons encoding transmembrane and cytoplasmicdomains. Science 227: 140- 146, 1985.

GAM99 320 LDLR Leitersdorf, E.; Hobbs, H. H.: Personal Communication. Dallas,Tex. 12/1990. 4 A c

GAM99 320 LDLR Leitersdorf, E.; Hobbs, H. H.; Fourie, A. M.; Jacobs, M.; vander Westhuyzen, 4 A c
D. R.; Coetzee, G. A.: Deletion in the first cysteine- richrepeat of low-density lipoprotein receptor impairs its transport butnot lipoprotein binding in fibroblasts from a subject with familialhypercholesterolemia. Proc. Nat. Acad. Sci. 85: 7912- 7916, 1988.

GAM99 320 LDLR Leitersdorf, E.; Tobin, E. J.; Davignon, J.; Hobbs, H. H.: Commonlow- 4 A c
density lipoprotein receptor mutations in the French Canadianpopulation. J. Clin. Invest. 85: 1014- 1023, 1990.

GAM99 320 LDLR Leitersdorf, E.; van der Westhuyzen, D. R.; Coetzee, G. A.; Hobbs,H. H.: Two 4 A c
common low density lipoprotein receptor gene mutationscause familial hypercholesterolemia in Afrikaners. J. Clin. Invest. 84:954- 961, 1989.

GAM99 320 LDLR Lelli, N.; Ghisellini, M.; Calandra, S.; Gaddi, A.; Ciarrocchi,A.; Coviello, 4 A c
D. A.; Bertolini, S.: Duplication of exons 13, 14 and15 of the LDL- receptor gene in a patient with heterozygous familialhypercholesterolemia. Hum. Genet. 86: 359- 362, 1991.

GAM99 320 LDLR Leren, T. P.; Solberg, K.; Rodningen, O. K.; Tonstad, S.; Ose,L.: Two 4 A c
founder mutations in the LDL receptor gene in Norwegian familialhypercholesterolemia subjects. Atherosclerosis 111: 175- 182, 1994.

GAM99 320 LDLR Li, H.; Gyllensten, U. B.; Cui, X.; Saiki, R. K.; Erlich, H. A.;Arnheim, N.: 4 A c
Amplification and analysis of DNA sequences in singlehuman sperm and diploid cells. Nature 335: 414- 417, 1988.

GAM99 320 LDLR Lindgren, V.; Luskey, K. L.; Russell, D. W.; Francke, U.: Humangenes 4 A c
involved in cholesterol metabolism: chromosomal mapping of theloci for the low density lipoprotein receptor and 3- hydroxy- 3- methylglutaryl-coenzymeA reductase with cDNA probes. Proc. Nat. Acad. Sci. 82: 8567-8571,1985.

GAM99 320 LDLR Loux, N.; Benlian, P.; Pastier, D.; Boileau, C.; Cambou, J. P.;Monnier, L.; 4 A c
Percheron, C.; Junien, C.: Recurrent mutation at aa792 in the LDL receptor gene in a French patient. Hum. Genet. 87:373- 375, 1991.

GAM99 320 LDLR Ma, Y. H.; Betard, C.; Roy, M.; Davignon, J.; Kessling, A. M.: 4 A c
Identification of a second 'French Canadian' LDL receptor gene deletionand development of a rapid method to detect both deletions. Clin.Genet. 36: 219-228, 1989.

GAM99 320 LDLR Maartmann- Moe, K.; Wang, H. S.; Donald, L. J.; Hamerton, J. L.;Berg, K.: 4 A c
Data from hybrid cell lines raise the possibility thatfactors controlling

the low density lipoprotein receptor activitymay reside on human chromosome 21, 5 or both. (Abstract) Cytogenet.Cell Genet. 32: 295- 296, 1982.

GAM99 320 LDLR Mandelshtam, M.; Chakir, K.; Shevtsov, S.; Golubkov, V.; Skobeleva,N.; Lipovetsky, B.; Konstantinov, V.; Denisenko, A.; Gaitskhoki, V.;Schwartz, E.: Prevalence of Lithuanian mutation among St. PetersburgJews with familial hypercholesterolemia. Hum. Mutat. 12: 255- 258,1998. 4 A c

GAM99 320 LDLR Meiner, V.; Landsberger, D.; Berkman, N.; Reshef, A.; Segal, P.;Seftel, H. C.; van der Westhuyzen, D. R.; Jeenah, M. S.; Coetzee,G. A.; Leitersdorf, E.: A common Lithuanian mutation causing familialhypercholesterolemia in Ashkenazi Jews. Am. J. Hum. Genet. 49: 443- 449,1991. 4 A c

GAM99 320 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamoto, A.: Analysisof a recycling- impaired mutant of low density lipoprotein receptorin familial hypercholesterolemia. J. Biol. Chem. 264: 16584- 16590,1989. 4 A c

GAM99 320 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamura, T.; Yamamoto,A.: A point mutation of low- density- lipoprotein receptor causingrapid degradation of the receptor. Europ. J. Biochem. 210: 1- 7,1992. 4 A c

GAM99 320 LDLR Moorjani, S.; Roy, M.; Torres, A.; Betard, C.; Gagne, C.; Lambert,M.; Brun, D.; Davignon, J.; Lupien, P.: Mutations of low- density- lipoprotein-receptorgene, variation in plasma cholesterol, and expression of coronaryheart disease in homozygous familial hypercholesterolaemia. Lancet 341:1303- 1306, 1993. 4 A c

GAM99 320 LDLR Oppenheim, A.; Friedlander, Y.; Dann, E. J.; Berkman, N.; Schwartz,S. P.; Leitersdorf, E.: Hypercholesterolemia in five Israeli Christian-Arabkindreds is caused by the 'Lebanese' allele at the low density lipoproteinreceptor gene locus and by an additional independent major factor. Hum.Genet. 88: 75- 84, 1991. 4 A c

GAM99 320 LDLR Pisciotta, L.; Cantafora, A.; De Stefano, F.; Langheim, S.; Calandra,S.; Bertolini, S.: A 'de novo' mutation of the LDL- receptor geneas the cause of familial hypercholesterolemia. Biochim. Biophys.Acta 1587: 7- 11, 2002. 4 A c

GAM99 320 LDLR Rodningen, O. K.; Rosby, O.; Tonstad, S.; Ose, L.; Berg, K.; Leren,T. P.: A 9.6 kilobase deletion in the low density lipoprotein receptorgene in Norwegian familial hypercholesterolemia subjects. Clin. Genet. 42:288- 295, 1992. 4 A c

GAM99 320 LDLR Rubinsztein, D. C.; Coetzee, G. A.; Marais, A. D.; Leitersdorf,E.; Seftel, H. C.; van der Westhuyzen, D. R.: Identification andproperties of the proline- 644- to- leucine mutant LDL receptor in SouthAfricans of Indian origin. J. Lipid Res. 33: 1647- 1655, 1992. 4 A c

GAM99 320 LDLR Rudiger, N. S.; Heinsvig, E. M.; Hansen, F. A.; Faergeman, O.;Bolund, L.; Gregersen, N.: DNA deletions in the low density lipoprotein(LDL) receptor gene in Danish families with familial hypercholesterolemia. Clin.Genet. 39: 451- 462, 1991. 4 A c

GAM99 320 LDLR Ruffner, D. E.; Sprung, C. N.; Minghetti, P. P.; Gibbs, P. E.M.; Dugaiczyk, A.: Invasion of the human albumin- alpha- fetoproteingene family by Alu, Kpn, and two novel repetitive DNA elements. Molec.Biol. Evol. 4: 1- 9, 1987. 4 A c

GAM99 320 LDLR Russell, D. W.; Lehrman, M. A.; Sudhof, T. C.; Yamamoto, T.; Davis,C. G.; Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: The LDL receptorin familial hypercholesterolemia: use of human mutations to dissecta membrane protein. Cold Spring Harbor Symp. Quant. Biol. 51: 811- 819,1986. 4 A c

GAM99 320 LDLR Russell, D. W.; Schneider, W. J.; Yamamoto, T.; Luskey, K. L.;Brown, M. S.; Goldstein, J. L.: Domain map of the LDL receptor: sequencehomology with the 4 A c

epidermal growth factor precursor. Cell 37: 577- 585,1984.

GAM99 320 LDLR Savov, A.; Angelicheva, D.; Balassopoulou, A.; Jordanova, A.;Noussia- 4 A c
Arvanitakis, S.; Kalaydjieva, L.: Double mutant alleles:are they rare? Hum.
Molec. Genet. 4: 1169- 1171, 1995.

GAM99 320 LDLR Schuster, H.; Manke, C.; Fischer, J.; Keller, C.; Wolfram, G.;Zollner, N.: 4 A c
Identification of the valine 408 to methionine mutationin the LDL receptor
in a Greek patient with homozygous familial hypercholesterolemia.
Clin.Genet. 48: 90- 92, 1995.

GAM99 320 LDLR Schuster, H.; Ostwald, P.; Keller, P.; Wolfram, G.; Keller, C.: 4 A c
Identification of the serine- 156 to leucine mutation in the low-
densitylipoprotein receptor in a German family with familial
hypercholesterolemia. Clin.Investig. 71: 172- 175, 1993.

GAM99 320 LDLR Seftel, H. C.; Baker, S. G.; Sandler, M. P.; Forman, M. B.; Joffe,B. I.; 4 A c
Mendelsohn, D.; Jenkins, T.; Mieny, C. J.: A host of
hypercholesterolaemichomozygotes in South Africa. Brit. Med. J. 281: 633-
636, 1980.

GAM99 320 MAGEA4 Chambost, H.; Van Baren, N.; Brasseur, F.; Godelaine, D.; Xerri,L.; Landi, 4 A c
S. J.; Theate, I.; Plumas, J.; Spagnoli, G. C.; Michel,G.; Coulie, P. G.;
Olive, D.: Expression of gene MAGE- A4 in Reed- Sternbergcells. Blood 95:
3530- 3533, 2000.

GAM99 320 MAGEA4 De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J. J.; Szikora,J.- P.; De 4 A c
Smet, C.; Brasseur, F.; van der Bruggen, P.; Lethe, B.;Lurquin, C.;
Brasseur, R.; Chomez, P.; De Backer, O.; Cavenee, W.;Boon, T.: Structure,
chromosomal localization, and expression of12 genes of the MAGE family.
Immunogenetics 40: 360- 369, 1994.

GAM99 320 MAGEA4 Rogner, U. C.; Wilke, K.; Steck, E.; Korn, B.; Poustka, A.: Themelanoma 4 A c
antigen gene (MAGE) family is clustered in the chromosomalband Xq28.
Genomics 29: 725- 731, 1995.

GAM99 320 MAP2K1 Brott, B. K.; Alessandrini, A.; Largaespada, D. A.; Copeland, N.G.; Jenkins, 4 A c
N. A.; Crews, C. M.; Erikson, R. L.: MEK2 is a kinaserelated to MEK1 and is
differentially expressed in murine tissues. CellGrowth Differ. 4: 921- 929,
1993.

GAM99 320 MAP2K1 Crews, C. M.; Alessandrini, A.; Erikson, R. L.: The primary structureof MEK, 4 A c
a protein kinase that phosphorylates the ERK gene product. Science 258:478-
480, 1992.

GAM99 320 MAP2K1 Favata, M. F.; Horiuchi, K. Y.; Manos, E. J.; Daulerio, A. J.;Stradley, D. 4 A c
A.; Feeser, W. S.; Van Dyk, D. E.; Pitts, W. J.; Earl,R. A.; Hobbs, F.;
Copeland, R. A.; Magolda, R. L.; Scherle, P. A.;Trzaskos, J. M.:
Identification of a novel inhibitor of mitogen- activatedprotein kinase
kinase. J. Biol. Chem. 273: 18623- 18632, 1998.

GAM99 320 MAP2K1 Meloche, S.; Gopalbhai, K.; Beatty, B. G.; Scherer, S. W.; Pellerin,J.: 4 A c
Chromosome mapping of the human genes encoding the MAP kinasekinase MEK1
(MAP2K1) to 15q21 and MEK2 (MAP2K2) to 7q32. Cytogenet.Cell Genet. 88: 249-
252, 2000.

GAM99 320 MAP2K1 Orth, K.; Palmer, L. E.; Bao, Z. Q.; Stewart, S.; Rudolph, A. E.;Bliska, J. 4 A c
B.; Dixon, J. E.: Inhibition of the mitogen- activatedprotein kinase kinase
superfamily by a Yersinia effector. Science 285:1920- 1923, 1999.

GAM99 320 MAP2K1 Perry, R. L. S.; Parker, M. H.; Rudnicki, M. A.: Activated MEK1binds the 4 A c
nuclear MyoD transcriptional complex to repress transactivation. Molec.Cell
8: 291- 301, 2001.

GAM99 320 MAP2K1 Pleschka, S.; Wolff, T.; Ehrhardt, C.; Hobom, G.; Planz, O.; Rapp,U. R.; Ludwig, S.: Influenza virus propagation is impaired by inhibitionof the Raf/MEK/ERK signalling cascade. Nature Cell Biol. 3: 301- 305,2001. 4 A c

GAM99 320 MAP2K1 Rampoldi, L.; Zimbello, R.; Bortoluzzi, S.; Tiso, N.; Valle, G.;Lanfranchi, G.; Danieli, G. A.: Chromosomal localization of fourMAPK signaling cascade genes: MEK1, MEK3, MEK4 and MEKK5. Cytogenet.Cell Genet. 78: 301- 303, 1997. 4 A c

GAM99 320 MAP2K1 Ryan, K. M.; Ernst, M. K.; Rice, N. R.; Vousden, K. H.: Role ofNF- kappa- B in p53- mediated programmed cell death. Nature 404: 892- 897,2000. 4 A c

GAM99 320 MAP2K1 Sebolt- Leopold, J. S.; Dudley, D. T.; Herrera, R.; Van Becelaere,K.; Wiland, A.; Gowan, R. C.; Tecle, H.; Barrett, S. D.; Bridges,A.; Przybranowski, S.; Leopold, W. R.; Saltiel, A. R.: Blockade ofthe MAP kinase pathway suppresses growth of colon tumors in vivo. NatureMed. 5: 810- 816, 1999. 4 A c

GAM99 320 MAP2K1 Seger, R.; Krebs, E. G.: The MAPK signaling cascade. FASEB J. 9:726- 735, 1995. 4 A c

GAM99 320 MAP2K1 Seger, R.; Seger, D.; Lozeman, F. J.; Ahn, N. G.; Graves, L. M.;Campbell, J. S.; Ericsson, L.; Harrylock, M.; Jensen, A. M.; Krebs,E. G.: Human T- cell mitogen- activated protein kinase kinases arerelated to yeast signal transduction kinases. J. Biol. Chem. 267:25628- 25631, 1992. 4 A c

GAM99 320 MAP2K1 Zheng, C. F.; Guan, K. L.: Cloning and characterization of twodistinct human extracellular signal- regulated kinase activator kinases,MEK1 and MEK2. J. Biol. Chem. 268: 11435- 11439, 1993. 4 A c

GAM99 320 MLLT2 Domer, P. H.; Fakharzadeh, S. S.; Chen, C.- S.; Jockel, J.; Johansen,L.; Silverman, G. A.; Kersey, J. H.; Korsmeyer, S. J.: Acute mixed-lineageleukemia t(4;11)(q21;q23) generates an MLL- AF4 fusion product. Proc.Nat. Acad. Sci. 90: 7884- 7888, 1993. 4 A c

GAM99 320 MLLT2 Gu, Y.; Nakamura, T.; Alder, H.; Prasad, R.; Canaani, O.; Cimino,G.; Croce, C. M.; Canaani, E.: The t(4;11) chromosome translocationof human acute leukemias fuses the ALL- 1 gene, related to Drosophilatrithorax, to the AF-4 gene. Cell 71: 701- 708, 1992. 4 A c

GAM99 320 MLLT2 Isnard, P.; Depetris, D.; Mattei, M.- G.; Ferrier, P.; Djabali,M.: cDNA cloning, expression and chromosomal localization of themurine AF- 4 gene involved in human leukemia. Mammalian Genome 9:1065- 1068, 1998. 4 A c

GAM99 320 MLLT2 Lovett, B. D.; Lo Nigro, L.; Rappaport, E. F.; Blair, I. A.; Osheroff,N.; Zheng, N.; Megonigal, M. D.; Williams, W. R.; Nowell, P. C.; Felix,C. A.: Near- precise interchromosomal recombination and functionalDNA topoisomerase II cleavage sites at MLL and AF- 4 genomic breakpointsin treatment- related acute lymphoblastic leukemia with t(4;11) translocation. Proc.Nat. Acad. Sci. 98: 9802- 9807, 2001. 4 A c

GAM99 320 MLLT2 Nakamura, T.; Alder, H.; Gu, Y.; Prasad, R.; Canaani, O.; Kamada,N.; Gale, R. P.; Lange, B.; Crist, W. M.; Nowell, P. C.; Croce, C.M.; Canaani, E.: Genes on chromosomes 4, 9, and 19 involved in 11q23abnormalities in acute leukemia share sequence homology and/or commonmotifs. Proc. Nat. Acad. Sci. 90: 4631- 4635, 1993. 4 A c

GAM99 320 MLLT2 Uckun, F. M.; Herman- Hatten, K.; Crotty, M.- L.; Sensel, M. G.;Sather, H. N.; Tuel- Ahlgren, L.; Sarquis, M. B.; Bostrom, B.; Nachman,J. B.; Steinherz, P. G.; Gaynon, P. S.; Heerema, N.: Clinical significanceof MLL-AF4 fusion transcript expression in the absence of a cytogeneticallydetectable t(4;11)(q21;q23) chromosomal translocation. Blood 92:810- 821, 1998. 4 A c

GAM99 320 OAS2 Hovanessian, A. G.; Laurent, A. G.; Chebath, J.; Galabru, J.; Robert,N.; 4 A c
Svab, J.: Identification of 69- kd and 100- kd forms of 2- 5A synthetasein
interferon- treated human cells by specific monoclonal antibodies. EMBOJ. 6:
1273- 1280, 1987.

GAM99 320 OAS2 Hovnanian, A.; Rebouillat, D.; Mattei, M.- G.; Levy, E. R.; Marie,I.; 4 A c
Monaco, A. P.; Hovanessian, A. G.: The human 2- prime,5- prime-
oligoadenylatesynthetase locus is composed of three distinct genes clustered
onchromosome 12q24.2 encoding the 100- , 69- , and 40- kDa forms. Genomics
52:267- 277, 1998.

GAM99 320 OAS2 Marie, I.; Galabru, J.; Svab, J.; Hovanessian, A. G.: Preparationand 4 A c
characterization of polyclonal antibodies specific for the 69and 100 k-
dalton forms of human 2- 5A synthetase. Biochem. Biophys.Res. Commun. 160:
580- 587, 1989.

GAM99 320 OAS2 Marie, I.; Hovanessian, A. G.: The 69- kDa 2- 5A synthetase is composedof 4 A c
two homologous and adjacent functional domains. J. Biol. Chem. 267:9933-
9939, 1992.

GAM99 320 PPP2R5C McCright, B.; Brothman, A. R.; Virshup, D. M.: Assignment of humanprotein 4 A c
phosphatase 2A regulatory subunit genes B56- alpha, B56- beta,B56- gamma,
B56- delta, and B56- epsilon (PPP2R5A- - PPP2R5E), highly expressedin muscle
and brain, to chromosome regions 1q41, 11q12, 3p21, 6p21.1,and 7p11.2- to-
p12. Genomics 36: 168- 170, 1996.

GAM99 320 PPP2R5C McCright, B.; Virshup, D. M.: Identification of a new family ofprotein 4 A c
phosphatase 2A regulatory subunits. J. Biol. Chem. 270:26123- 26128, 1995.

GAM99 320 PPP2R5C Muneer, S.; Ramalingam, V.; Wyatt, R.; Schultz, R. A.; Minna, J.D.; 4 A c
Kamibayashi, C.: Genomic organization and mapping of the geneencoding the
PP2A B56- gamma regulatory subunit. Genomics 79: 344- 348,2002.

GAM99 320 PRKCB1 Coussens, L.; Parker, P. J.; Rhee, L.; Yang- Feng, T. L.; Chen,E.; 4 A c
Waterfield, M. D.; Francke, U.; Ullrich, A.: Multiple, distinctforms of
bovine and human protein kinase C suggest diversity in cellularsignaling
pathways. Science 233: 859- 866, 1986.

GAM99 320 PRKCB1 Francke, U.; Darras, B. T.; Zander, N. F.; Kilimann, M. W.: Assignmentof 4 A c
human genes for phosphorylase kinase subunits alpha (PHKA) to Xq12- q13and
beta (PHKB) to 16q12- q13. Am. J. Hum. Genet. 45: 276- 282, 1989.

GAM99 320 PRKCB1 Greenham, J.; Adams, M.; Doggett, N.; Mole, S.: Elucidation ofthe exon- 4 A c
intron structure and size of the human protein kinase C betagene (PRKCB).
Hum. Genet. 103: 483- 487, 1998.

GAM99 320 PRKCB1 Leitges, M.; Schmedt, C.; Guinamard, R.; Davoust, J.; Schaal, S.;Stabel, S.; 4 A c
Tarakhovsky, A.: Immunodeficiency in protein kinase C- beta- deficientmice.
Science 273: 788- 791, 1996.

GAM99 320 PRKCB1 Su, T. T.; Guo, B.; Kawakami, Y.; Sommer, K.; Chae, K.; Humphries,L. A.; 4 A c
Kato, R. M.; Kang, S.; Patrone, L.; Wall, R.; Teitell, M.;Leitges, M.;
Kawakami, T.; Rawlings, D. J.: PKC- beta controls I- kappa- Bkinase lipid
raft recruitment and activation in response to BCR signaling. NatureImmun.
3: 780- 786, 2002.

GAM99 320 PSG1 Barnett, T. R.; Pickle, W., II; Rae, P. M. M.; Hart, J.; Kamarck,M.; Elting, 4 A c
J.: Human pregnancy- specific beta(1)- glycoproteins arecoded within
chromosome 19. Am. J. Hum. Genet. 44: 890- 893, 1989.

GAM99 320 PSG1 Barnett, T.; Pickle, W., II; Rae, P. M. M.; Hart, J.; Kamarck,M.; Elting, 4 A c
J.: Pregnancy- specific beta- 1- glycoproteins are relatedto
carcinoembryonic antigens and map to chromosome 19. (Abstract)

Cytogenet.Cell Genet. 51: 958, 1989.

GAM99 320 PSG1 Bartels, I.; Lindemann, A.: Maternal levels of pregnancy- specificbeta- 1- 4 A c
glycoprotein (SP- 1) are elevated in pregnancies affected byDown's syndrome.
Hum. Genet. 80: 46- 48, 1988.

GAM99 320 PSG1 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, 4 A c
F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.;
Lucka, L.; and 13 others: Redefined nomenclaturefor members of the
carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999.

GAM99 320 PSG1 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. 4 A c
W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances
among members of the carcinoembryonic antigen (CEA) genefamily determined by
fluorescence in situ hybridization. Genomics 12:773- 779, 1992.

GAM99 320 PSG1 Chan, W.- Y.; Qiu, W.- R.: Human pregnancy- specific beta- 1 glycoproteinis 4 A c
encoded by multiple genes localized on two chromosomes. Am. J.Hum. Genet.
43: 152- 159, 1988.

GAM99 320 PSG1 Khan, W. N.; Teglund, S.; Bremer, K.; Hammarstrom, S.: The pregnancy- 4 A c
specificglycoprotein family of the immunoglobulin superfamily:
identificationof new members and estimation of family size. Genomics 12:
780- 787,1992.

GAM99 320 PSG1 Niemann, S. C.; Flake, A.; Bohn, H.; Bartels, I.: Pregnancy- specificbeta- 4 A c
1- glycoprotein: cDNA cloning, tissue expression, and speciesspecificity of
one member of the PSBG family. Hum. Genet. 82: 239- 243,1989.

GAM99 320 PSG1 Niemann, S. C.; Schonk, D.; van Dijk, P. E.; Grzeschik, K.- H.;Bartels, I.: 4 A c
Chromosomal assignment of a cDNA clone encoding pregnancy- specificbeta- 1-
glycoprotein to chromosome 19. (Abstract) Cytogenet. CellGenet. 51: 1053,
1989.

GAM99 320 PSG1 Niemann, S. C.; Schonk, D.; van Dijk, P.; Wieringa, B.; Grzeschik,K.- H.; 4 A c
Bartels, I.: Regional localization of the gene encoding pregnancyspecific
beta- 1- glycoprotein 1 (PSBG1) to human chromosome 19q13.1. Cytogenet.Cell
Genet. 52: 95- 97, 1989.

GAM99 320 PSG1 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.;Georgescu, A.; 4 A c
Carrano, A.; Hammarstrom, S.: Gene organization ofthe pregnancy- specific
glycoprotein region on human chromosome 19:assembly and analysis of a 700-
kb cosmid contig spanning the region. Genomics 23:659- 668, 1994.

GAM99 320 PSG1 Streydio, C.; Swillens, S.; Georges, M.; Szpirer, C.; Vassart,G.: Structure, 4 A c
evolution and chromosomal localization of the humanpregnancy- specific beta-
1 glycoprotein gene family. Genomics 6:579- 592, 1990. Note: Erratum:
Genomics 7: 661- 662, 1990.

GAM99 320 PSG1 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The 4 A c
pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19:
fine structure of the 11 PSG genes and identificationof 6 new genes forming
a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics
23: 669- 684, 1994.

GAM99 320 PSG1 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, 4 A c
H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.;
Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly
linked on the long arm of chromosome 19 and arecoordinately expressed.
Biochem. Biophys. Res. Commun. 167: 848- 859,1990.

GAM99 320 PSG1 Watanabe, S.; Chou, J. Y.: Isolation and characterization ofcomplementary 4 A c
DNAs encoding human pregnancy- specific beta- 1- glycoprotein. J.Biol. Chem.

263: 2049- 2054, 1988.

GAM99 320 PSG4 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999. 4 A c

GAM99 320 PSG4 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by fluorescence in situ hybridization. Genomics 12:773- 779, 1992. 4 A c

GAM99 320 PSG4 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.; Georgescu,A.; Carrano, A.; Hammarstrom, S.: Gene organization of the pregnancy-specificglycoprotein region on human chromosome 19: assembly and analysisof a 700- kb cosmid contig spanning the region. Genomics 23: 659- 668,1994. 4 A c

GAM99 320 PSG4 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19: fine structure of the 11 PSG genes and identificationof 6 new genes forming a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics 23: 669- 684, 1994. 4 A c

GAM99 320 PSG4 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.; Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly linked on the long arm of chromosome 19 and arecoordinately expressed. Biochem. Biophys. Res. Commun. 167: 848- 859,1990. 4 A c

GAM99 320 PSG4 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades-Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan, K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772, 1992. 4 A c

GAM99 320 PSG4 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993. 4 A c

GAM99 320 PSG4 Tynan, K.; Olsen, A.; Trask, B.; de Jong, P.; Thompson, J.; Zimmermann,W.; Carrano, A.; Mohrenweiser, H.: Assembly and analysis of cosmidcontigs in the CEA- gene family region of human chromosome 19. NucleicAcids Res. 20: 1629-1636, 1992. 4 A c

GAM99 320 PTER Alimova- Kost, M. V.; Imreh, S.; Buchman, V. L.; Ninkina, N. N.: Assignment of phosphotriesterase- related gene (PTER) to human chromosomeband 10p12 by in situ hybridization. Cytogenet. Cell Genet. 83:16- 17, 1998. 4 A c

GAM99 320 PTER Davies, J. A.; Buchman, V. L.; Krylova, O.; Ninkina, N. N.: Molecularcloning and expression pattern of rpr- 1, a resiniferatoxin-binding,phosphotriesterase- related protein, expressed in rat kidney tubules. FEBSLett. 410: 378- 382, 1997. 4 A c

GAM99 320 SLC25A15 Camacho, J. A.; Obie, C.; Biery, B.; Goodman, B. K.; Hu, C.- A.;Almashanu, S.; Steel, G.; Casey, R.; Lambert, M.; Mitchell, G. A.;Valle, D.: Hyperornithinaemia- hyperammonaemia- homocitrullinuria syndromeis caused by mutations in a gene encoding a mitochondrial ornithinetransporter. Nature Genet. 22: 151- 158, 1999. 4 A c

GAM99 320 SLC25A15 Miyamoto, T.; Kanazawa, N.; Kato, S.; Kawakami, M.; Inoue, Y.;Kuhara, T.; 4 A c

Inoue, T.; Takeshita, K.; Tsujino, S.: Diagnosis of Japanesepatients with HHH syndrome by molecular genetic analysis: a commonmutation, R179X. J. Hum. Genet. 46: 260- 262, 2001.

GAM99 320 SLC25A15 Nakajima, M.; Ishii, S.; Mito, T.; Takeshita, K.; Takashima, S.;Takakura, H.; Inoue, I.; Saheki, T.; Akiyoshi, H.; Ichihara, K.:Clinical, biochemical and ultrastructural study on the pathogenesisof hyperornithinemia-hyperammonemia- homocitrullinuria syndrome. BrainDev. 10: 181- 185, 1988. 4 A c

GAM99 320 SLC25A15 Tsujino, S.; Kanazawa, N.; Ohashi, T.; Eto, Y.; Saito, T.; Kira,J.; Yamada, T.: Three novel mutations (G27E, insAAC, R179X) in theORNT1 gene of Japanese patients with hyperornithinemia, hyperammonemia,and homocitrullinuria syndrome. Ann. Neurol. 47: 625- 631, 2000. 4 A c

GAM99 320 SLC2A5 Burant, C. F.; Takeda, J.; Brot- Laroche, E.; Bell, G. I.; Davidson,N. O.: Fructose transporter in human spermatozoa and small intestineis GLUT5. J. Biol. Chem. 267: 14523- 14526, 1992. 4 A c

GAM99 320 SLC2A5 Davidson, N. O.; Hausman, A. M. L.; Ifkovits, C. A.; Buse, J. B.;Gould, G. W.; Burant, C. F.; Bell, G. I.: Human intestinal glucosetransporter expression and localization of GLUT5. Am. J. Physiol. 262:C795- C800, 1992. 4 A c

GAM99 320 SLC2A5 Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Kayano, T.; Shows, T. B.; Bell, G. I.: Assignment of genes encodingthree human glucose transporter/transporter- like proteins (GLUT4,GLUT5 and GLUT6) to chromosomes 17, 1 and 5, respectively. (Abstract) Cytogenet.Cell Genet. 51: 997 only, 1989. 4 A c

GAM99 320 SLC2A5 Kayano, T.; Burant, C. F.; Fukumoto, H.; Gould, G. W.; Fan, Y.S.; Eddy, R. L.; Byers, M. G.; Shows, T. B.; Seino, S.; Bell, G. I.: Human facilitative glucose transporters: isolation, functional characterization,and gene localization of cDNAs encoding an isoform (GLUT5) expressedin small intestine, kidney, muscle, and adipose tissue and an unusualglucose transporter pseudogene- like sequence (GLUT6). J. Biol. Chem. 265:13276-13282, 1990. 4 A c

GAM99 320 SLC2A5 White, P. S.; Jensen, S. J.; Rajalingam, V.; Stairs, D.; Sulman,E. P.; Maris, J. M.; Biegel, J. A.; Wooster, R.; Brodeur, G. M.:Physical mapping of the CA6, ENO1, and SLC2A5 (GLUT5) genes and reassignmentof SLC2A5 to 1p36.2. Cytogenet. Cell Genet. 81: 60- 64, 1998. 4 A c

GAM99 320 SORBS1 Baumann, C. A.; Ribon, V.; Kanzaki, M.; Thurmond, D. C.; Mora,S.; Shigematsu, S.; Bickel, P. E.; Pessin, J. E.; Saltiel, A. R.:CAP defines a second signalling pathway required for insulin- stimulatedglucose transport. Nature 407: 202- 207, 2000. 4 A c

GAM99 320 SORBS1 Chiang, S.- H.; Baumann, C. A.; Kanzaki, M.; Thurmond, D. C.; Watson,R. T.; Neudauer, C. L.; Macara, I. G.; Pessin, J. E.; Saltiel, A.R.: Insulin-stimulated GLUT4 translocation requires the CAP- dependentactivation of TC10. Nature 410: 944- 948, 2001. 4 A c

GAM99 320 SORBS1 Lebre, A.- S.; Jamot, L.; Takahashi, J.; Spasskey, N.; Leprince,C.; Ravise, N.; Zander, Fujigasaki, H.; Kussel- Andermann, P.; Duyckaerts,C.; Camonis, J. H.; Brice, A.: Ataxin- 7 interacts with a Cbl- associatedprotein that it recruits into neuronal intranuclear inclusions. Hum.Molec. Genet. 10: 10:-1201- 1213, 2001. 4 A c

GAM99 320 SORBS1 Lin, W.- H.; Chiu, K. C.; Chang, H.- M.; Lee, K.- C.; Tai, T.- Y.;Chuang, L.- M.: Molecular scanning of the human sorbin and SH3- domain- containing-1(SORBS1) gene: positive association of the T228A polymorphism withobesity and type 2 diabetes. Hum. Molec. Genet. 10: 1753- 1760, 2001. 4 A c

GAM99 320 SORBS1 Mastick, C. C.; Brady, M. J.; Saltiel, A. R.: Insulin stimulatesthe tyrosine 4 A c
phosphorylation of caveolin. J. Cell Biol. 129: 1523- 1531,1995.
GAM99 320 SORBS1 Ribon, V.; Printen, J. A.; Hoffman, N. G.; Kay, B. K.; Saltiel,A. R.: A 4 A c
novel, multifunctional c- Cbl binding protein in insulinreceptor signaling
in 3T3- L1 adipocytes. Molec. Cell. Biol. 18:872- 879, 1998.
GAM99 320 SORBS1 Scott, A. F.: Personal Communication. Baltimore, Md. 9/13/2000. 4 A c
GAM99 320 TLL2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 4 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XIII. The completesequences of 100
new cDNA clones from brain which code for large proteinsin vitro. DNA Res.
6: 63- 70, 1999.
GAM99 320 TLL2 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; 4 A c
Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.;
Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases,
including novel family member mammalian Tolloid- like2, have differential
enzymatic activities and distributions of expressionrelevant to patterning
and skeletogenesis. Dev. Biol. 213: 283- 300,1999.
GAM99 320 TLL2 Scott, I. C.; Clark, T. G.; Takahara, K.; Hoffman, G. G.; Eddy,R. L.; Haley, 4 A c
L. L.; Shows, T. B.; Greenspan, D. S.: Assignment ofTLL1 and TLL2, which
encode human BMP- 1/tolloid- related metalloproteases,to chromosomes 4q32-
q33 and 10q23- q24 and assignment of murine Tll2to chromosome 19. Cytogenet.
Cell Genet. 86: 64- 65, 1999.
GAM99 320 TNF Aggarwal, B. B.; Eessalu, T. E.; Hass, P. E.: Characterizationof receptors 4 A c
for human tumour necrosis factor and their regulationby gamma- interferon.
Nature 318: 665- 667, 1985.
GAM99 320 TNF Beattie, E. C.; Stellwagen, D.; Morishita, W.; Bresnahan, J. C.;Ha, B. K.; 4 A c
Von Zastrow, M.; Beattie, M. S.; Malenka, R. C.: Controlof synaptic strength
by glial TNF- alpha. Science 295: 2282- 2285,2002.
GAM99 320 TNF Beutler, B.; Krochin, N.; Milsark, I. W.; Luedke, C.; Cerami, A.: Control of 4 A c
cachectin (tumor necrosis factor) synthesis: mechanismsof endotoxin
resistance. Science 232: 977- 980, 1986.
GAM99 320 TNF Brenner, D. A.; O'Hara, M.; Angel, P.; Chojkier, M.; Karin, M.: Prolonged 4 A c
activation of JUN and collagenase genes by tumour necrosisfactor- alpha.
Nature 337: 661- 663, 1989.
GAM99 320 TNF Broudy, V. C.; Kaushansky, K.; Segal, G. M.; Harlan, J. M.; Adamson,J. W.: 4 A c
Tumor necrosis factor type alpha stimulates human endothelialcells to
produce granulocyte/macrophage colony- stimulating factor. Proc.Nat. Acad.
Sci. 83: 7467- 7471, 1986.
GAM99 320 TNF Bruce, A. J.; Boling, W.; Kindy, M. S.; Peschon, J.; Kraemer, P.J.; 4 A c
Carpenter, M. K.; Holtsberg, F. W.; Mattson, M. P.: Altered neuronaland
microglial responses to excitotoxic and ischemic brain injuryin mice lacking
TNF receptors. Nature Med. 2: 788- 794, 1996.
GAM99 320 TNF Cabrera, M.; Shaw, M. A.; Sharples, C.; Williams, H.; Castes, M.;Convit, J.; 4 A c
Blackwell, J. M.: Polymorphism in tumor necrosis factorgenes associated with
mucocutaneous leishmaniasis. J. Exp. Med. 182:1259- 1264, 1995.
GAM99 320 TNF Carroll, M. C.; Katzman, P.; Alicot, E. M.; Koller, B. H.; Geraghty,D. E.; 4 A c
Orr, H. T.; Strominger, J. L.; Spies, T.: Linkage map of thehuman major
histocompatibility complex including the tumor necrosisfactor genes. Proc.
Nat. Acad. Sci. 84: 8535- 8539, 1987.
GAM99 320 TNF Conway, D. J.; Holland, M. J.; Bailey, R. L.; Campbell, A. E.;Mahdi, O. S.; 4 A c

Jennings, R.; Mbena, E.; Mabey, D. C.: Scarring trachomais associated with polymorphism in the tumor necrosis factor alpha(TNF- alpha) gene promoter and with elevated TNF- alpha levels in tearfluid. Infect. Immun. 65: 1003- 1006, 1997.

GAM99 320 TNF D'Alfonso, S.; Richiardi, P. M.: A polymorphic variation in aputative 4 A c
regulation box of the TNFA promoter region. Immunogenetics 39:150- 154, 1994.

GAM99 320 TNF Davis, J. M.; Narachi, M. A.; Alton, N. K.; Arakawa, T.: Structureof human 4 A c
tumor necrosis factor alpha derived from recombinant DNA. Biochemistry 26:1322- 1326, 1987.

GAM99 320 TNF Escobar- Morreale, H. F.; Calvo, R. M.; Sancho, J.; San Millan,J. L.: TNF- 4 A c
alpha and hyperandrogenism: a clinical, biochemical, andmolecular genetic study. J. Clin. Endocr. Metab. 86: 3761- 3767,2001.

GAM99 320 TNF Franchimont, D.; Martens, H.; Hagelstein, M.- T.; Louis, E.; Dewe,W.; 4 A c
Chrousos, G. P.; Belaiche, J.; Geenen, V.: Tumor necrosis factoralpha decreases, and interleukin- 10 increases, the sensitivity ofhuman monocytes to dexamethasone: potential regulation of the glucocorticoidreceptor. J. Clin. Endocr. Metab. 84: 2834- 2839, 1999.

GAM99 320 TNF Galbraith, G. M. P.; Pandey, J. P.: Tumor necrosis factor alpha(TNF- alpha) 4 A c
gene polymorphism in alopecia areata. Hum. Genet. 96:433- 436, 1995.

GAM99 320 TNF Gorman, J. D.; Sack, K. E.; Davis, J. C., Jr.: Treatment of 4 A c
ankylosingspondylitis by inhibition of tumor necrosis factor- alpha. New Eng.J. Med. 346: 1349- 1356, 2002.

GAM99 320 TNF Herrmann, S.- M.; Ricard, S.; Nicaud, V.; Mallet, C.; Arveiler,D.; Evans, 4 A c
A.; Ruidavets, J.- B.; Luc, G.; Bara, L.; Parra, H.- J.;Poirier, O.; Cambien, F.: Polymorphisms of the tumour necrosis factor- alphagene, coronary heart disease and obesity. Europ. J. Clin. Invest. 28:59- 66, 1998.

GAM99 320 TNF Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. 4 A c
Phys. 111: 272- 277, 1999.

GAM99 320 TNF Inoko, H.; Trowsdale, J.: Linkage of TNF genes to the HLA- B locus. 4 A c
NucleicAcids Res. 15: 8957- 8962, 1987.

GAM99 320 TNF Knight, J. C.; Udalova, I.; Hill, A. V. S.; Greenwood, B. M.;Peshu, N.; 4 A c
Marsh, K.; Kwiatkowski, D.: A polymorphism that affectsOCT- 1 binding to the TNF promoter region is associated with severemalaria. Nature Genet. 22: 145- 150, 1999.

GAM99 320 TNF Koss, K.; Satsangi, J.; Fanning, G. C.; Welsh, K. I.; Jewell,D. P.: Cytokine 4 A c
(TNF- alpha, LT- alpha, and IL- 10) polymorphisms ininflammatory bowel diseases and normal controls: differential effectson production and allele frequencies. Genes Immun. 1: 185- 190, 2000.

GAM99 320 TNF Ma, J. J.; Nishimura, M.; Mine, H.; Kuroki, S.; Nukina, M.; Ohta,M.; Saji, 4 A c
H.; Obayashi, H.; Kawakami, H.; Saida, T.; Uchiyama, T.: Genetic contribution of the tumor necrosis factor region in Guillain- Barresyndrome. Ann. Neurol. 44: 815- 818, 1998.

GAM99 320 TNF Marino, M. W.; Dunn, A.; Grail, D.; Inglese, M.; Noguchi, Y.;Richards, E.; 4 A c
Jungbluth, A.; Wada, H.; Moore, M.; Williamson, B.;Basu, S.; Old, L. J.: Characterization of tumor necrosis factor- deficientmice. Proc. Nat. Acad. Sci. 94: 8093- 8098, 1997.

GAM99 320 TNF McCusker, S. M.; Curran, M. D.; Dynan, K. B.; McCullagh, C. D.;Urquhart, D. 4 A c
D.; Middleton, D.; Patterson, C. C.; McIlroy, S. P.;Passmore, A. P.: Association between polymorphism in regulatory regionof gene encoding tumour

necrosis factor- alpha and risk of Alzheimer'sdisease and vascular dementia: a case- control study. Lancet 357:436- 439, 2001.

GAM99 320 TNF McGuire, W.; Hill, A. V. S.; Allsopp, C. E. M.; Greenwood, B.M.; Kwiatkowski, D.: Variation in the TNF- alpha promoter region associatedwith susceptibility to cerebral malaria. Nature 371: 508- 511, 1994. 4 A c

GAM99 320 TNF Mira, J.- P.; Cariou, A.; Grall, F.; Delclaux, C.; Losser, M.- R.;Heshmati, F.; Cheval, C.; Monchi, M.; Teboul, J.- L.; Riche, F.; Leleu,G.; Arbibe, L.; Mignon, A.; Delpech, M.; Dhainaut, J.- F.: Associationof TNF2, a TNF- alpha promoter polymorphism, with septic shock susceptibilityand mortality: a multicenter study. J.A.M.A. 282: 561- 568, 1999. 4 A c

GAM99 320 TNF Moffatt, M. F.; Cookson, W. O. C. M.: Tumour necrosis factorhaplotypes and asthma. Hum. Molec. Genet. 6: 551- 554, 1997. 4 A c

GAM99 320 TNF Moraes, M. O.; Duppre, N. C.; Suffys, P. N.; Santos, A. R.; Almeida,A. S.; Nery, J. A. C.; Sampaio, E. P.; Sarno, E. N.: Tumor necrosisfactor- alpha promoter polymorphism TNF2 is associated with a strongerdelayed- type hypersensitivity reaction in the skin of borderline tuberculoidleprosy patients. Immunogenetics 53: 45- 47, 2001. 4 A c

GAM99 320 TNF Mulcahy, B.; Waldron- Lynch, F.; McDermott, M. F.; Adams, C.; Amos,C. I.; Zhu, D. K.; Ward, R. H.; Clegg, D. O.; Shanahan, F.; Molloy,M. G.; O'Gara, F.: Genetic variability in the tumor necrosis factor- lymphotoxinregion influences susceptibility to rheumatoid arthritis. Am. J.Hum. Genet. 59: 676- 683, 1996. 4 A c

GAM99 320 TNF Muller, U.; Jongeneel, C. V.; Nedospasov, S. A.; Lindahl, K. F.;Steinmetz, M.: Tumour necrosis factor and lymphotoxin genes map closeto H- 2D in the mouse major histocompatibility complex. Nature 325:265- 267, 1987. 4 A c

GAM99 320 TNF Nadel, S.; Newport, M. J.; Booy, R.; Levin, M.: Variation inthe tumor necrosis factor- alpha gene promoter region may be associatedwith death from meningococcal disease. J. Infect. Dis. 174: 878- 880,1996. 4 A c

GAM99 320 TNF Nedospasov, S. A.; Hirt, B.; Shakhov, A. N.; Dobrynin, V. N.;Kawashima, E.; Accolla, R. S.; Jongeneel, C. V.: The genes for tumornecrosis factor (TNR- alpha) and lymphotoxin (TNR- beta) are tandemlyarranged on chromosome 17 of the mouse. Nucleic Acids Res. 14: 7713- 7725,1986. 4 A c

GAM99 320 TNF Nedwin, G. E.; Naylor, S. L.; Sakaguchi, A. Y.; Smith, D.; Jarrett- Nedwin,J.; Pennica, D.; Goeddel, D. V.; Gray, P. W.: Human lymphotoxin andtumor necrosis factor genes: structure, homology and chromosomal localization. NucleicAcids Res. 13: 6361- 6373, 1985. 4 A c

GAM99 320 TNF Norman, R. A.; Bogardus, C.; Ravussin, E.: Linkage between obesityand a marker near the tumor necrosis factor- alpha locus in Pima Indians. J.Clin. Invest. 96: 158- 162, 1995. 4 A c

GAM99 320 TNF Obayashi, H.; Hasegawa, G.; Fukui, M.; Kamiuchi, K.; Kitamura,A.; Ogata, M.; Kanaitsuka, T.; Shigeta, H.; Kitagawa, Y.; Nakano,K.; Nishimura, M.; Ohta, M.; Nakamura, N.: Tumor necrosis factormicrosatellite polymorphism influences the development of insulindependency in adult- onset diabetes patients with the DRB1*1502- DQB1*0601allele and anti- glutamic acid decarboxylase antibodies. J. Clin.Endocr. Metab. 85: 3348- 3351, 2000. 4 A c

GAM99 320 TNF Old, L. J.: Tumor necrosis factor (TNF). Science 230: 630- 632,1985. 4 A c

GAM99 320 TNF Pennica, D.; Nedwin, G. E.; Hayflick, J. S.; Seeburg, P. H.; Derynck,R.; Palladino, M. A.; Kohr, W. J.; Aggarwal, B. B.; Goeddel, D. V.: Human tumour necrosis factor: precursor structure, expression andhomology to lymphotoxin. Nature 312: 724- 729, 1984. 4 A c

GAM99 320 TNF Ragoussis, J.; Bloemer, K.; Weiss, E. H.; Ziegler, A.: Localizationof the genes for tumor necrosis factor and lymphotoxin between theHLA class I and III regions by field inversion gel electrophoresis. Immunogenetics 27:66-69, 1988. 4 A c

GAM99 320 TNF Rasmussen, S. K.; Urhammer, S. A.; Jensen, J. N.; Hansen, T.;Borch- Johnsen, K.; Pedersen, O.: The - 238 and - 308 G6A polymorphismsof the tumor necrosis factor alpha gene promoter are not associatedwith features of the insulin resistance syndrome or altered birthweight in Danish Caucasians. J. Clin. Endocr. Metab. 85: 1731- 1734,2000. 4 A c

GAM99 320 TNF Rosmond, R.; Chagnon, M.; Bouchard, C.; Bjorntorp, P.: G- 308Apolymorphism of the tumor necrosis factor alpha gene promoter andsalivary cortisol secretion. J. Clin. Endocr. Metab. 86: 2178- 2180,2001. 4 A c

GAM99 320 TNF Roy, S.; McGuire, W.; Mascie- Taylor, C. G.; Saha, B.; Hazra, S.K.; Hill, A. V.; Kwiatkowski, D.: Tumor necrosis factor promoterpolymorphism and susceptibility to lepromatous leprosy. J. Infect.Dis. 176: 530- 532, 1997. 4 A c

GAM99 320 TNF Ruuls, S. R.; Sedgwick, J. D.: Unlinking tumor necrosis factorbiology from the major histocompatibility complex: lessons from humangenetics and animal models. Am. J. Hum. Genet. 65: 294- 301, 1999. 4 A c

GAM99 320 TNF Sashio, H.; Tamura, K.; Ito, R.; Yamamoto, Y.; Bamba, H.; Kosaka,T.; Fukui, S.; Sawada, K.; Fukuda, Y.; Tamura, K.; Satomi, M.; Shimoyama,T.; Furuyama, J.: Polymorphisms of the TNF gene and the TNF receptorsuperfamily member 1B gene are associated with susceptibility to ulcerativecolitis and Crohn's disease, respectively. Immunogenetics 53: 1020- 1027,2002. 4 A c

GAM99 320 TNF Spielman, R. S.; McGinnis, R. E.; Ewens, W. J.: Transmissiontest for linkage disequilibrium: the insulin gene region and insulin- dependentdiabetes mellitus (IDDM). Am. J. Hum. Genet. 52: 506- 516, 1993. 4 A c

GAM99 320 TNF Spies, T.; Morton, C. C.; Nedospasov, S. A.; Fiers, W.; Pious,D.; Strominger, J. L.: Genes for the tumor necrosis factors alphaand beta are linked to the human major histocompatibility complex. Proc.Nat. Acad. Sci. 83: 8699- 8702, 1986. 4 A c

GAM99 320 TNF van Hensbroek, M. B.; Palmer, A.; Onyiorah, E.; Schneider, G.;Jaffar, S.; Dolan, G.; Memming, H.; Frenkel, J.; Enwere, G.; Bennett,S.; Kwiatkowski, D.; Greenwood, B.: The effect of a monoclonal antibodyto tumor necrosis factor on survival from childhood cerebral malaria. J.Infect. Dis. 174: 1091- 1097, 1996. 4 A c

GAM99 320 TNF Van Ostade, X.; Vandenabeele, P.; Everaerdt, B.; Loetscher, H.;Gentz, R.; Brockhaus, M.; Lesslauer, W.; Tavernier, J.; Brouckaert,P.; Fiers, W.: Human TNF mutants with selective activity on the p55receptor. Nature 361: 266-269, 1993. 4 A c

GAM99 320 TNF Wang, A. M.; Creasey, A. A.; Ladner, M. B.; Lin, L. S.; Strickler,J.; Van Arsdell, J. N.; Yamamoto, R.; Mark, D. F.: Molecular cloningof the complementary DNA for human tumor necrosis factor. Science 228:149- 154, 1985. 4 A c

GAM99 320 TNF Wilson, A. G.; di Giovine, F. S.; Blakemore, A. I. F.; Duff, G.W.: Single base polymorphism in the human tumour necrosis factoralpha (TNF- alpha) gene detectable by NcoI restriction of PCR product. Hum.Molec. Genet. 1: 353 only, 1992. 4 A c

GAM99 320 TNF Wilson, A. G.; Symons, J. A.; McDowell, T. L.; et al: Effectsof a polymorphism in the human tumor necrosis factor alpha promoteron transcriptional activation. Proc. Nat. Acad. Sci. 94: 3195- 3199,1997. 4 A c

GAM99 320 TNF Winchester, E. C.; Millwood, I. Y.; Rand, L.; Penny, M. A.; Kessling,A. M.: 4 A c
Association of the TNF- alpha- 308 (G- A) polymorphism with self-
reportedhistory of childhood asthma. Hum. Genet. 107: 591- 596, 2000.

GAM99 320 TNF Witte, J. S.; Palmer, L. J.; O'Connor, R. D.; Hopkins, P. J.;Hall, J. M.: 4 A c
Relation between tumour necrosis factor polymorphismTNF- alpha- 308 and risk
of asthma. Europ. J. Hum. Genet. 10: 82- 85,2002.

GAM99 320 TNF Zinman, B.; Hanley, A. J. G.; Harris, S. B.; Kwan, J.; Fantus,I. G.: 4 A c
Circulating tumor necrosis factor- alpha concentrations ina Native Canadian
population with high rates of type 2 diabetes mellitus. J.Clin. Endocr.
Metab. 84: 272- 278, 1999.

GAM99 320 TRPC1 Berg, L.- P.; Shamsher, M. K.; El- Daher, S. S.; Kakkar, V. V.; Authi,K. S.: 4 A c
Expression of human TRPC genes in the megakaryocytic celllines MEG01, DAMI
and HEL. FEBS Lett. 403: 83- 86, 1997.

GAM99 320 TRPC1 Wes, P. D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten,G.; Montell, 4 A c
C.: TRPC1, a human homolog of a Drosophila store- operatedchannel. Proc.
Nat. Acad. Sci. 92: 9652- 9656, 1995.

GAM99 320 TRPC1 Xu, X.- Z. S.; Li, H.- S.; Guggino, W. B.; Montell, C.: Coassemblyof TRP and 4 A c
TRPL produces a distinct store- operated conductance. Cell 89:1155- 1164,
1997.

GAM99 320 TRPC1 Zhu, X.; Chu, P. B.; Peyton, M.; Birnbaumer, L.: Molecular cloningof a 4 A c
widely expressed human homologue for the Drosophila trp gene. FEBSLett. 373:
193- 198, 1995.

GAM99 320 TRPC1 Zhu, X.; Jiang, M.; Peyton, M.; Boulay, G.; Hurst, R.; Stefani,E.; 4 A c
Birnbaumer, L.: trp, a novel mammalian gene family essentialfor agonist-
activated capacitative Ca(2+) entry. Cell 85: 661- 671,1996.

GAM99 320 TRPC1 Zitt, C.; Zobel, A.; Obukhov, A. G.; Harteneck, C.; Kalkbrenner,F.; 4 A c
Luckhoff, A.; Schultz, G.: Cloning and functional expressionof a human
Ca(2+)- permeable cation channel activated by calcium storedepletion. Neuron
16: 1189- 1196, 1996.

GAM99 320 UBQLN1 Hanaoka, E.; Ozaki, T.; Ohira, M.; Nakamura, Y.; Suzuki, M.; Takahashi,E.; 4 A c
Moriya, H.; Nakagawara, A.; Sakiyama, S.: Molecular cloning andexpression
analysis of the human DA41 gene and its mapping to chromosome9q21.2- q21.3.
J. Hum. Genet. 45: 188- 191, 2000.

GAM99 320 UBQLN1 Kleijnen, M. F.; Shih, A. H.; Zhou, P.; Kumar, S.; Soccio, R. E.;Kedersha, 4 A c
N. L.; Gill, G.; Howley, P. M.: The hPLIC proteins mayprovide a link between
the ubiquitination machinery and the proteasome. Molec.Cell 6: 409- 419,
2000.

GAM99 320 UBQLN1 Ozaki, T.; Hishiki, T.; Toyama, Y.; Yuasa, S.; Nakagawara, A.;Sakiyama, S.: 4 A c
Identification of a new cellular protein that can interactspecifically with
DAN. DNA Cell Biol. 16: 985- 991, 1997.

GAM99 320 WASF3 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 4 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XII. The completesequences of 100 new
cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5:
355- 364, 1998.

GAM99 320 WASF3 Suetsugu, S.; Miki, H.; Takenawa, T.: Identification of two humanWAVE/SCAR 4 A c
homologues as general actin regulatory molecules which associatewith the
Arp2/3 complex. Biochem. Biophys. Res. Commun. 260: 296- 302,1999.

GAM100 243 AMD1 Maric, S. C.; Crozat, A.; Janne, O. A.: Structure and organizationof the 4 A c
human S- adenosylmethionine decarboxylase gene. J. Biol. Chem. 267:18915-

18923, 1992.

GAM100 243 AMD1 Maric, S. C.; Crozat, A.; Louhimo, J.; Knuutila, S.; Janne, O.A.: The human 4 A c
S- adenosylmethionine decarboxylase gene: nucleotidesequence of a pseudogene
and chromosomal localization of the activegene (AMD1) and the pseudogene
(AMD2). Cytogenet. Cell Genet. 70:195- 199, 1995.

GAM100 243 AMD1 Pulkka, A.; Ihalainen, R.; Suorsa, A.; Riviere, M.; Szpirer, J.;Pajunen, A.: 4 A c
Structures and chromosomal localizations of two ratgenes encoding S-
adenosylmethionine decarboxylase. Genomics 16:342- 349, 1993.

GAM100 243 AMD1 Radford, D. M.; Eddy, R.; Haley, L.; Henry, W. M.; Pegg, A. E.;Pajunen, A.; 4 A c
Shows, T. B.: Gene sequences coding for S- adenosylmethioninedecarboxylase
are present on human chromosome 6 and the X and arenot amplified in colon
neoplasia. Cytogenet. Cell Genet. 49: 285- 288,1989.

GAM100 243 AMD1 Radford, D. M.; Nakai, H.; Pegg, A. E.; Shows, T. B.: Mappinggenes for rate- 4 A c
limiting enzymes in polyamine biosynthesis. (Abstract) Am.J. Hum. Genet. 41:
A35 only, 1987.

GAM100 243 BACH1 Blouin, J.- L.; Sail, G. D.; Guipponi, M.; Rossier, C.; Pappasavas,M.- P.; 4 A c
Antonarakis, S. E.: Isolation of the human BACH1 transcriptionregulator
gene, which maps to chromosome 21q22.1. Hum. Genet. 102:282- 288, 1998.

GAM100 243 BACH1 Kanezaki, R.; Toki, T.; Yokoyama, M.; Yomogida, K.; Sugiyama, K.;Yamamoto, 4 A c
M.; Igarashi, K.; Ito, E.: Transcription factor BACH1 isrecruited to the
nucleus by its novel alternative spliced isoform. J.Biol. Chem. 276: 7278-
7284, 2001.

GAM100 243 BACH1 Ohira, M.; Seki, N.; Nagase, T.; Ishikawa, K.; Nomura, N.; Ohara,O.: 4 A c
Characterization of a human homolog (BACH1) of the mouse Bach1gene encoding
a BTB- basic leucine zipper transcription factor andits mapping to
chromosome 21q22.1. Genomics 47: 300- 306, 1998.

GAM100 243 BACH1 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 4 A c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-
basic leucine zipper transcription factors that interact withMafK and
regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-
6095, 1996.

GAM100 243 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 4 A c
Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.:
Identification of Bach2 as a B- cell- specific partner for smallMaf proteins
that negatively regulate the immunoglobulin heavy chaingene 3- prime
enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM100 243 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 4 A c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-
basic leucine zipper transcription factors that interact withMafK and
regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-
6095, 1996.

GAM100 243 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, 4 A c
A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.;
Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B
cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene
19: 3739- 3749, 2000.

GAM100 243 CCKBR Beinborn, M.; Lee, Y.- M.; McBride, E. W.; Quinn, S. M.; Kopin,A. S.: A 4 A c
single amino acid of the cholecystokinin- B/gastrin receptordetermines
specificity for non- peptide antagonists. Nature 362:348- 350, 1993.

GAM100 243 CCKBR Huppi, K.; Siwarski, D.; Pisegna, J. R.; Wank, S.: Chromosomallocalization 4 A c

of the gastric and brain receptors for cholecystokinin(CCKAR and CCKBR) in human and mouse. Genomics 25: 727- 729, 1995.

GAM100 243 CCKBR Lee, Y.- M.; Beinborn, M.; McBride, E. W.; Lu, M.; Kolakowski, L.F., Jr.; 4 A c
Kopin, A. S.: The human brain cholecystokinin- B/gastrinreceptor: cloning and characterization. J. Biol. Chem. 268: 8164- 8169,1993.

GAM100 243 CCKBR Pisegna, J. R.; de Weerth, A.; Huppi, K.; Wank, S. A.: Molecularcloning of 4 A c
the human brain and gastric cholecystokinin receptor: structure,functional expression and chromosomal localization. Biochem. Biophys.Res. Commun. 189: 296- 303, 1992.

GAM100 243 CCKBR Samuelson, L. C.; Isakoff, M. S.; Lacourse, K. A.: Localizationof the murine 4 A c
cholecystokinin A and B receptor genes. MammalianGenome 6: 242- 246, 1995.

GAM100 243 CCKBR Zimonjic, D. B.; Popescu, N. C.; Matsui, T.; Ito, M.; Chihara,K.: 4 A c
Localization of the human cholecystokinin- B/gastrin receptorgene (CCKBR) to chromosome 11p15.5- p15.4 by fluorescence in situ hybridization.Cytogenet. Cell Genet. 65: 184- 185, 1994.

GAM100 243 CCR9 Bonini, J. A.; Martin, S. K.; Dralyuk, F.; Roe, M. W.; Philipson,L. H.; 4 A c
Steiner, D. F.: Cloning, expression, and chromosomal mappingof a novel human CC- chemokine receptor (CCR10) that displays high- affinitybinding for MCP- 1 and MCP- 3. DNA Cell Biol. 16: 1249- 1256, 1997.

GAM100 243 CCR9 Maho, A.; Bensimon, A.; Vassart, G.; Parmentier, M.: Mapping ofthe CCXCR1, 4 A c
CX3CR1, CCBP2 and CCR9 genes to the CCR cluster withinthe 3p21.3 region of the human genome. Cytogenet. Cell Genet. 87:265- 268, 1999.

GAM100 243 CCR9 Nibbs, R. J. B.; Wylie, S. M.; Yang, J.; Landau, N. R.; Graham,G. J.: 4 A c
Cloning and characterization of a novel promiscuous humanbeta- chemokine receptor D6. J. Biol. Chem. 272: 32078- 32083, 1997.

GAM100 243 CYP7A1 Agellon, L. B.; Drover, V. A. B.; Cheema, S. K.; Gbaguidi, G. F.;Walsh, A.: 4 A c
Dietary cholesterol fails to stimulate the human cholesterol7- alpha- hydroxylase gene (CYP7A1) in transgenic mice. J. Biol. Chem. 277:20131- 20134, 2002.

GAM100 243 CYP7A1 Angelin, B.; Einarsson, K.; Hellstrom, K.; Leijd, B.: Bile acidkinetics in 4 A c
relation to endogenous triglyceride metabolism in varioustypes of hyperlipoproteinemia. J. Lipid Res. 19: 1004- 1016, 1978.

GAM100 243 CYP7A1 Angelin, B.; Hershon, K. S.; Brunzell, J. D.: Bile acid metabolismin 4 A c
hereditary forms of hypertriglyceridemia: evidence for an increasedsynthesis rate in monogenic familial hypertriglyceridemia. Proc.Nat. Acad. Sci. 84: 5434- 5438, 1987.

GAM100 243 CYP7A1 Cohen, J. C.; Cali, J. J.; Jelinek, D. F.; Mehrabian, M.; Sparkes,R. S.; 4 A c
Lusis, A. J.; Russell, D. W.; Hobbs, H. H.: Cloning of thehuman cholesterol 7- alpha- hydroxylase gene (CYP7) and localizationto chromosome 8q11- q12. Genomics 14: 153- 161, 1992.

GAM100 243 CYP7A1 Drover, V. A. B.; Wong, N. C. W.; Agellon, L. B.: A distinct thyroidhormone 4 A c
response element mediates repression of the human cholesterol7- alpha- hydroxylase (CYP7A1) gene promoter. Molec. Endocr. 16: 14- 23,2002.

GAM100 243 CYP7A1 Goodwin, B.; Jones, S. A.; Price, R. R.; Watson, M. A.; McKee,D. D.; Moore, 4 A c
L. B.; Galardi, C.; Wilson, J. G.; Lewis, M. C.; Roth,M. E.; Maloney, P. R.; Willson, T. M.; Kliewer, S. A.: A regulatorycascade of the nuclear receptors FXR, SHP- 1, and LRH- 1 represses bileacid biosynthesis. Molec. Cell 6: 517- 526, 2000.

GAM100 243 CYP7A1 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, 4 A c
J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid

synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000.

GAM100 243 CYP7A1 Molowa, D. T.; Chen, W. S.; Cimis, G. M.; Tan, C. P.: 4 A c
Transcriptionalregulation of the human cholesterol 7 alpha- hydroxylase
gene. Biochemistry 31:2539- 2544, 1992.

GAM100 243 CYP7A1 Nitta, M.; Ku, S.; Brown, C.; Okamoto, A. Y.; Shan, B.: CPF: anorphan 4 A c
nuclear receptor that regulates liver- specific expression ofthe human
cholesterol 7- alpha- hydroxylase gene. Proc. Nat. Acad.Sci. 96: 6660- 6665,
1999.

GAM100 243 CYP7A1 Noshiro, M.; Okuda, K.: Molecular cloning and sequence analysisof cDNA 4 A c
encoding human cholesterol 7 alpha- hydroxylase. FEBS Lett. 268:137- 140,
1990.

GAM100 243 CYP7A1 Paumgartner, G.; Sauerbruch, T.: Gallstones: pathogenesis. Lancet 338:1117- 4 A c
1121, 1991.

GAM100 243 CYP7A1 Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, 4 A c
K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation
of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers.
Science 289: 1524- 1529, 2000.

GAM100 243 CYP7A1 Wang, J.; Freeman, D. J.; Grundy, S. M.; Levine, D. M.; Guerra,R.; Cohen, J. 4 A c
C.: Linkage between cholesterol 7- alpha- hydroxylaseand high plasma low-
density lipoprotein cholesterol concentrations. J.Clin. Invest. 101: 1283-
1291, 1998.

GAM100 243 DMP1 Aplin, H. M.; Hirst, K. L.; Crosby, A. H.; Dixon, M. J.: Mappingof the human 4 A c
dentin matrix acidic phosphoprotein gene (DMP1) to thedentinogenesis
imperfecta type II critical region at chromosome 4q21. Genomics 30:347- 349,
1995.

GAM100 243 DMP1 George, A.; Sabsay, B.; Simonian, P. A.; Veis, A.: Characterizationof a 4 A c
novel dentin matrix acidic phosphoprotein: implications for inductionof
biomineralization . J. Biol. Chem. 268: 12624- 12630, 1993.

GAM100 243 DMP1 Hirst, K. L.; Simmons, D.; Feng, J.; Aplin, H.; Dixon, M. J.; MacDougall,M.: 4 A c
Elucidation of the sequence and the genomic organization of thehuman dentin
matrix acidic phosphoprotein 1 (DMP1) gene: exclusionof the locus from a
causative role in the pathogenesis of dentinogenesisimperfecta type II.
Genomics 42: 38- 45, 1997.

GAM100 243 DMP1 MacDougall, M.; DuPont, B. R.; Simmons, D.; Leach, R. J.: Assignmentof DMP1 4 A c
to human chromosome 4 band q21 by in situ hybridization. Cytogenet.Cell.
Genet. 74: 189 only, 1996.

GAM100 243 DTNB Blake, D. J.; Nawrotzki, R.; Loh, N. Y.; Gorecki, D. C.; Davies,K. E.: Beta- 4 A c
dystrobrevin, a member of the dystrophin- related proteinfamily. Proc. Nat.
Acad. Sci. 95: 241- 246, 1998.

GAM100 243 DTNB Loh, N. Y.; Ambrose, H. J.; Guay- Woodford, L. M.; DasGupta, S.;Nawrotzki, 4 A c
R. A.; Blake, D. J.; Davies, K. E.: Genomic organizationand refined mapping
of the mouse beta- dystrobrevin gene. MammalianGenome 9: 857- 862, 1998.

GAM100 243 DTNB Peters, M. F.; O'Brien, K. F.; Sadoulet- Puccio, H. M.; Kunkel,L. M.; Adams, 4 A c
M. E.; Froehner, S. C.: Beta- dystrobrevin, a new memberof the dystrophin
family: identification, cloning, and protein associations. J.Biol. Chem.
272: 50:- 31561- 31569, 1997.

GAM100 243 DYSF Anderson, L. V. B.; Davison, K.; Moss, J. A.; Young, C.; Cullen,M. J.; 4 A c
Walsh, J.; Johnson, M. A.; Bashir, R.; Britton, S.; Keers,S.; Argov, Z.;
Mahjneh, I.; Fougerousse, F.; Beckmann, J. S.; Bushby,K. M. D.: Dysferlin is
a plasma membrane protein and is expressedearly in human development. Hum.

Molec. Genet. 8: 855- 861, 1999.

GAM100 243 DYSF Bashir, R.; Britton, S.; Strachan, T.; Keers, S.; Vafiadaki, E.;Lako, M.; 4 A c
Richard, I.; Marchand, S.; Bourg, N.; Argov, Z.; Sadeh,M.; Mahjneh, I.;
Marconi, G.; Passos- Bueno, M. R.; Moreira, E. S.;Zatz, M.; Beckmann, J. S.;
Bushby, K.: A gene related to Caenorhabditiselegans spermatogenesis factor
fer- 1 is mutated in limb- girdle musculardystrophy type 2B. Nature Genet.
20: 37- 42, 1998.

GAM100 243 DYSF Bashir, R.; Strachan, T.; Keers, S.; Stephenson, A.; Mahjneh, I.;Marconi, 4 A c
G.; Nashef, L.; Bushby, K. M. D.: A gene for autosomal recessivelimb- girdle
muscular dystrophy maps to chromosome 2p. Hum. Molec.Genet. 3: 455- 457,
1994.

GAM100 243 DYSF Bittner, R. E.; Anderson, L. V. B.; Burkhardt, E.; Bashir, R.;Vafiadaki, E.; 4 A c
Ivanova, S.; Raffelsberger, T.; Maerk, I.; Hoger, H.;Jung, M.; Karbasiyan,
M.; Storch, M.; Lassmann, H.; Moss, J. A.; Davison,K.; Harrison, R.; Bushby,
K. M. D.; Reis, A.: Dysferlin deletionin SJL mice (SJL- Dysf) defines a
natural model for limb girdle musculardystrophy 2B. (Letter) Nature Genet.
23: 141- 142, 1999.

GAM100 243 DYSF Festing, M. F. W. (ed.): Inbred strains in biomedica research. NewYork: 4 A c
Oxford University Press , 1979. p. 255.

GAM100 243 DYSF Illa, I.; Serrano- Munuera, C.; Gallardo, E.; Lasa, A.; Rojas- Garcia,R.; 4 A c
Palmer, J.; Gallano, P.; Baiget, M.; Matsuda, C.; Brown, R. H.: Distal
anterior compartment myopathy: a dysferlin mutation causinga new muscular
dystrophy phenotype. Ann. Neurol. 49: 130- 134, 2001.

GAM100 243 DYSF Illarioshkin, S. N.; Ivanova- Smolenskaya, I. A.; Greenberg, C.R.; Nylen, 4 A c
E.; Sukhorukov, V. S.; Poleshchuk, V. V.; Markova, E. D.;Wrogemann, K.:
Identical dysferlin mutation in limb- girdle musculardystrophy type 2B and
distal myopathy. Neurology 55: 1931- 1933,2000.

GAM100 243 DYSF Illarioshkin, S. N.; Ivanova- Smolenskaya, I. A.; Tanaka, H.; Poleshchuk,V. 4 A c
V.; Markova, E. D.; Tsuji, S.: Refined genetic location of thechromosome 2p-
linked progressive muscular dystrophy gene. Genomics 42:345- 348, 1997.

GAM100 243 DYSF Illarioshkin, S. N.; Ivanova- Smolenskaya, I. A.; Tanaka, H.; 4 A c
Vereshchagin,N. V.; Markova, E. D.; Poleshchuk, V. V.; Lozhnikova, S. M.;
Sukhorukov,V. S.; Limborska, S. A.; Slominsky, P. A.; Bulayeva, K. B.;
Tsuji,S.: Clinical and molecular analysis of a large family with
threedistinct phenotypes of progressive muscular dystrophy. Brain 119:1895-
1909, 1996.

GAM100 243 DYSF Liu, J.; Aoki, M.; Illa, I.; Wu, C.; Fardeau, M.; Angelini, C.;Serrano, C.; 4 A c
Urtizberea, J. A.; Hentati, F.; Ben Hamida, M.; Bohlega,S.; Culper, E. J.;
Amato, A. A.; Bossie, K.; Oeltjen, J.; Bejaoui,K.; McKenna- Yasek, D.;
Hosler, B. A.; Schurr, E.; Arahata, K.; deJong, P. J.; Brown, R. H., Jr.:
Dysferlin, a novel skeletal musclegene, is mutated in Miyoshi myopathy and
limb girdle muscular dystrophy. NatureGenet. 20: 31- 36, 1998.

GAM100 243 DYSF Liu, J.; Wu, C.; Bossie, K.; Bejaoui, K.; Hosler, B. A.; Gingrich,J. C.; Ben 4 A c
Hamida, M.; Hentati, F.; Schurr, E.; de Jong, P. J.; Brown,R. H., Jr.:
Generation of 3- Mb PAC contig spanning the Miyoshi myopathy/limbgirdle
muscular dystrophy (MM/LGMD2B) locus on chromosome 2p13. Genomics 49:23- 29,
1998.

GAM100 243 DYSF Mahjneh, I.; Vannelli, G.; Bushby, K.; Marconi, G. P.: A largeinbred 4 A c
Palestinian family with two forms of muscular dystrophy. Neuromusc.Disord.
2: 277- 283, 1992.

GAM100 243 DYSF Matsuda, C.; Hayashi, Y. K.; Ogawa, M.; Aoki, M.; Murayama, K.;Nishino, I.; 4 A c
Nonaka, I.; Arahata, K.; Brown, R. H., Jr.: The sarcolemmalproteins
dysferlin and caveolin- 3 interact in skeletal muscle. Hum.Molec. Genet. 10:
1761- 1766, 2001.

GAM100 243 DYSF McNally, E. M.; Ly, C. T.; Rosenmann, H.; Rosenbaum, S. M.; Jiang,W.; 4 A c
Anderson, L. V. B.; Soffer, D.; Argov, Z.: Splicing mutationin dysferlin
produces limb- girdle muscular dystrophy with inflammation. Am.J. Med.
Genet. 91: 305- 312, 2000.

GAM100 243 DYSF Weiler, T.; Bashir, R.; Anderson, L. V. B.; Davison, K.; Moss,J. A.; 4 A c
Britton, S.; Nylen, E.; Keers, S.; Vafiadaki, E.; Greenberg,C. R.; Bushby,
K. M. D.; Wrogemann, K.: Identical mutation in patientswith limb girdle
muscular dystrophy type 2B or Miyoshi myopathy suggestsa role for modifier
gene(s). Hum. Molec. Genet. 8: 871- 877, 1999.

GAM100 243 DYSF Weiler, T.; Greenberg, C. R.; Nylen, E.; Halliday, W.; Morgan,K.; Eggertson, 4 A c
D.; Wrogemann, K.: Limb- girdle muscular dystrophyand Miyoshi myopathy in an
aboriginal Canadian kindred map to LGMD2Band segregate with the same
haplotype. Am. J. Hum. Genet. 59: 872- 878,1996.

GAM100 243 IL5 Broide, D. H.; Hoffman, H.; Sriramarao, P.: Genes that regulateeosinophilic 4 A c
inflammation. Am. J. Hum. Genet. 65: 302- 307, 1999.

GAM100 243 IL5 Campbell, H. D.; Tucker, W. Q. J.; Hort, Y.; Martinson, M. E.;Mayo, G.; 4 A c
Clutterbuck, E. J.; Sanderson, C. J.; Young, I. G.: Molecularcloning,
nucleotide sequence, and expression of the gene encodinghuman eosinophil
differentiation factor (interleukin- 5). Proc. Nat.Acad. Sci. 84: 6629-
6633, 1987.

GAM100 243 IL5 Chandrasekharappa, S. C.; Rebelsky, M. S.; Firak, T. A.; Le Beau,M. M.; 4 A c
Westbrook, C. A.: A long- range restriction map of the interleukin- 4and
interleukin- 5 linkage group on chromosome 5. Genomics 6: 94- 99,1990.

GAM100 243 IL5 Coffman, R. L.; Seymour, B. W. P.; Hudak, S.; Jackson, J.; Rennick,D.: 4 A c
Antibody to interleukin- 5 inhibits helminth- induced eosinophiliain mice.
Science 245: 308- 310, 1989.

GAM100 243 IL5 Cogan, E.; Schandene, L.; Crusiaux, A.; Cochaux, P.; Velu, T.;Goldman, M.: 4 A c
Clonal proliferation of type 2 helper T cells in a manwith the
hypereosinophilic syndrome. New Eng. J. Med. 330: 535- 538,1994.

GAM100 243 IL5 Kozak, C.: Personal Communication. Bethesda, Md. 6/9/1988. 4 A c

GAM100 243 IL5 Lacy, D. A.; Wang, Z.- E.; Symula, D. J.; McArthur, C. J.; Rubin,E. M.; 4 A c
Frazer, K. A.; Locksley, R. M.: Faithful expression of thehuman 5q31
cytokine cluster in transgenic mice. J. Immun. 164: 4569- 4574,2000.

GAM100 243 IL5 Loots, G. G.; Locksley, R. M.; Blankespoor, C. M.; Wang, Z. E.;Miller, W.; 4 A c
Rubin, E. M.; Frazer, K. A.: Identification of a coordinateregulator of
interleukins 4, 13, and 5 by cross- species sequence comparisons. Science
288:136- 140, 2000.

GAM100 243 IL5 Pereira, E.; Goldblatt, J.; Rye, P.; Sanderson, C.; Le Souef, P.: Mutation 4 A c
analysis of interleukin- 5 in an asthmatic cohort. Hum.Mutat. 11: 51- 54,
1998.

GAM100 243 IL5 Rodrigues, V., Jr.; Abel, L.; Piper, K.; Dessein, A. J.: Segregationanalysis 4 A c
indicates a major gene in the control of interleukin- 5 productionin humans
infected with Schistosoma mansoni. Am. J. Hum. Genet. 59:453- 461, 1996.

GAM100 243 IL5 Simon, H. U.; Plotz, S. G.; Dummer, R.; Blaser, K.: Abnormalclones of T 4 A c
cells producing interleukin- 5 in idiopathic eosinophilia. NewEng. J. Med
341: 1112- 1120, 1999.

GAM100 243 IL5 Sutherland, G. R.; Baker, E.; Callen, D. F.; Campbell, H. D.;Young, Y. G.; 4 A c
Sanderson, C. J.; Garson, O. M.; Lopez, A. F.; Vadas,M. A.: Interleukin- 5
is at 5q31 and is deleted in the 5q- syndrome. Blood 71:1150- 1152, 1988.

GAM100 243 IL5 Takahashi, M.; Yoshida, M. C.; Satoh, H.; Hilgers, J.; Yaoita,Y.; Honjo, T.: 4 A c
Chromosomal mapping of the mouse IL- 4 and human IL- 5genes. Genomics 4: 47-
52, 1989.

GAM100 243 IL5 Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.: Molecularcloning 4 A c
and structure of the human interleukin- 5 gene. J. Biol. Chem. 262:16580-
16584, 1987.

GAM100 243 IL5 Willman, C. L.; Sever, C. E.; Pallavicini, M. G.; Harada, H.;Tanaka, N.; 4 A c
Slovak, M. L.; Yamamoto, H.; Harada, K.; Meeker, T. C.;List, A. F.;
Taniguchi, T.: Deletion of IRF- 1, mapping to chromosome5q31.1, in human
leukemia and preleukemic myelodysplasia. Science 259:968- 971, 1993.

GAM100 243 IL5 Yokota, T.; Coffman, R. L.; Hagiwara, H.; Rennick, D. M.; Takebe,Y.; Yokota, 4 A c
K.; Gemmell, L.; Shrader, B.; Yang, G.; Meyerson, P.;Luh, J.; Hoy, P.; Pene,
J.; Briere, F.; Spits, H.; Banchereau, J.;de Vries, J.; Lee, F. D.; Arai,
N.; Arai, K.: Isolation and characterizationof lymphokine cDNA clones
encoding mouse and human IgA- enhancing factorand eosinophil colony-
stimulating factor activities: relationshipto interleukin 5. Proc. Nat.
Acad. Sci. 84: 7388- 7392, 1987.

GAM100 243 IMPG1 Felbor, U.; Gehrig, A.; Sauer, C. G.; Marquardt, A.; Kohler, M.;Schmid, M.; 4 A c
Weber, B. H. F.: Genomic organization and chromosomallocalization of the
interphotoreceptor matrix proteoglycan- 1 (IMPG1)gene: a candidate for 6q-
linked retinopathies. Cytogenet. Cell Genet. 81:12- 17, 1998.

GAM100 243 IMPG1 Gehrig, A.; Felbor, U.; Kelsell, R. E.; Hunt, D. M.; Maumenee,I. H.; Weber, 4 A c
B. H. F.: Assessment of the interphotoreceptor matrixproteoglycan- 1 (IMPG1)
gene localised to 6q13- q15 in autosomal dominantStargardt- like disease
(ADSTGD), progressive bifocal chorioretinalatrophy (PBCRA), and North
Carolina macular dystrophy (MCDR1). J.Med. Genet. 35: 641- 645, 1998.

GAM100 243 IMPG1 Kuehn, M. H.; Hageman, G. S.: Characterization of a cDNA encodingIPM 150, a 4 A c
novel human interphotoreceptor matrix chondroitin 6- sulfateproteoglycan.
(Abstract) Invest. Ophthal. Vis. Sci. 36: 510 only,1995.

GAM100 243 MADH4 Bai, R.- Y.; Koester, C.; Ouyang, T.; Hahn, S. A.; Hammerschmidt,M.; 4 A c
Peschel, C.; Duyster, J.: SMIF, a Smad4- interacting protein thatfunctions
as a co- activator in TGF- beta signalling. Nature Cell Biol. 4:181- 190,
2002.

GAM100 243 MADH4 Burger, B.; Uhlhaas, S.; Mangold, E.; Propping, P.; Friedl, W.;Jenne, D.; 4 A c
Dockter, G.; Back, W.: Novel de novo mutation of MADH4/SMAD4in a patient
with juvenile polyposis. (Letter) Am. J. Med. Genet. 110:289- 291, 2002.

GAM100 243 MADH4 Chen, C.- R.; Kang, Y.; Siegel, P. M.; Massague, J.: E2F4/5 andp107 as Smad 4 A c
cofactors linking the TGF- beta receptor to c- myc repression. Cell 110:19-
32, 2002.

GAM100 243 MADH4 Derynck, R.; Gelbart, W. M.; Harland, R. M.; Heldin, C.- H.; Kern,S. E.; 4 A c
Massague, J.; Melton, D. A.; Mlodzik, M.; Padgett, R. W.; Roberts,A. B.;
Smith, J.; Thomsen, G. H.; Vogelstein, B.; Wang, X.- F.:
Nomenclature:vertebrate mediators of TGF- beta family signals. (Letter) Cell
87:173 only, 1996.

GAM100 243 MADH4 Friedl, W.; Kruse, R.; Uhlhaas, S.; Stolte, M.; Schartmann, B.;Keller, K. 4 A c
M.; Jungck, M.; Stern, M.; Loff, S.; Back, W.; Propping,P.; Jenne, D. E.:
Frequent 4- bp deletion in exon 9 of the SMAD4/MADH4gene in familial

juvenile polyposis patients. Genes Chromosomes Cancer 25:403- 406, 1999.

GAM100 243 MADH4 Friedl, W.; Uhlhaas, S.; Schulmann, K.; Stolte, M.; Loff, S.; Back,W.; 4 A c
Mangold, E.; Stern, M.; Knaebel, H. P.; Sutter, C.; Weber, R.G.; Pistorius,
S.; Burger, B.; Propping, P.: Juvenile polyposis:massive gastric polyposis
is more common in MADH4 mutation carriersthan in BMPR1A mutation carriers.
Hum. Genet. 111: 108- 111, 2002.

GAM100 243 MADH4 Hahn, S. A.; Schutte, M.; Hoque, T. M. S.; Moskaluk, C. A.; daCosta, L. T.; 4 A c
Rozenblum, E.; Weinstein, C. L.; Fischer, A.; Yeo, C.J.; Hruban, R. H.;
Kern, S. E.: DPC4, a candidate tumor suppressorgene at human chromosome
18q21.1. Science 271: 350- 354, 1996.

GAM100 243 MADH4 Houlston, R.; Bevan, S.; Williams, A.; Young, J.; Dunlop, M.; Rozen,P.; Eng, 4 A c
C.; Markie, D.; Woodford- Richens, K.; Rodriguez- Bigas, M.A.; Leggett, B.;
Neale, K.; Phillips, R.; Sheridan, E.; Hodgson, S.;Iwama, T.; Eccles, D.;
Bodmer, W.; Tomlinson, I.: Mutations in DPC4(SMAD4) cause juvenile polyposis
syndrome, but only account for aminority of cases. Hum. Molec. Genet. 7:
1907- 1912, 1998.

GAM100 243 MADH4 Howe, J. R.; Ringold, J. C.; Summers, R. W.; Mitros, F. A.; Nishimura,D. Y.; 4 A c
Stone, E. M.: A gene for familial juvenile polyposis mapsto chromosome
18q21.1. Am. J. Hum. Genet. 62: 1129- 1136, 1998.

GAM100 243 MADH4 Howe, J. R.; Roth, S.; Ringold, J. C.; Summers, R. W.; Jarvinen,H. J.; 4 A c
Sistonen, P.; Tomlinson, I. P. M.; Houlston, R. S.; Bevan,S.; Mitros, F. A.;
Stone, E. M.; Aaltonen, L. A.: Mutations in theSMAD4/DPC4 gene in juvenile
polyposis. Science 280: 1086- 1088, 1998.

GAM100 243 MADH4 Howe, J. R.; Shellnut, J.; Wagner, B.; Ringold, J. C.; Sayed,M. G.; Ahmed, 4 A c
A. F.; Lynch, P. M.; Amos, C. I.; Sistonen, P.; Aaltonen,L. A.: Common
deletion of SMAD4 in juvenile polyposis is a mutationalhotspot. Am. J. Hum.
Genet. 70: 1357- 1362, 2002.

GAM100 243 MADH4 Inman, G. J.; Nicolas, F. J.; Hill, C. S.: Nucleocytoplasmicshuttling of 4 A c
Smads 2, 3, and 4 permits sensing of TGF- beta receptoractivity. Molec. Cell
10: 283- 294, 2002.

GAM100 243 MADH4 Kim, S. K.; Fan, Y.; Papadimitrakopoulou, V.; Clayman, G.; Hittelman,W. N.; 4 A c
Hong, W. K.; Lotan, R.; Mao, L.: DPC4, a candidate tumor suppressorgene, is
altered infrequently in head and neck squamous cell carcinoma. CancerRes.
56: 2519- 2521, 1996.

GAM100 243 MADH4 Kinzler, K. W.; Vogelstein, B.: Landscaping the cancer terrain. Science 4 A c
280:1036- 1037, 1998.

GAM100 243 MADH4 MacGrogan, D.; et al.; et al: Comparative mutational analysisof DPC4 (Smad4) 4 A c
in prostatic and colorectal carcinomas. Oncogene 15:1111- 1114, 1997.

GAM100 243 MADH4 Roth, S.; Johansson, M.; Loukola, A.; Peltomaki, P.; Jarvinen,H.; Mecklin, 4 A c
J.- P.; Aaltonen, L. A.: Mutation analysis of SMAD2,SMAD3, and SMAD4 genes
in hereditary non- polyposis colorectal cancer. J.Med. Genet. 37: 298- 300,
2000.

GAM100 243 MADH4 Schutte, M.; Hruban, R. H.; Hedrick, L.; Cho, K. R.; Nadasdy,G. M.; 4 A c
Weinstein, C. L.; Bova, G. S.; Isaacs, W. B.; Cairns, P.; Nawroz,H.;
Sidransky, D.; Casero, R. A., Jr.; Meltzer, P. S.; Hahn, S. A.;Kern, S. E.:
DPC4 gene in various tumor types. Cancer Res. 56:2527- 2530, 1996.

GAM100 243 MADH4 Shioda, T.; Lechleider, R. J.; Dunwoodie, S. L.; Li, H.; Yahata,T.; de 4 A c
Caestecker, M. P.; Fenner, M. H.; Roberts, A. B.; Isselbacher,K. J.:
Transcriptional activating activity of Smad4: roles of SMADhetero-
oligomerization and enhancement by an associating transactivator. Proc.Nat.

Acad. Sci. 95: 9785- 9790, 1998.

GAM100 243 MADH4 Sirard, C.; de la Pompa, J. L.; Elia, A.; Itie, A.; Mirtsos, C.;Cheung, A.; 4 A c
Hahn, S.; Wakeham, A.; Schwartz, L.; Kern, S. E.; Rossant,J.; Mak, T. W.:
The tumor suppressor gene Smad4/Dpc4 is requiredfor gastrulation and later
for anterior development of the mouse embryo. GenesDev. 12: 107- 119, 1998.

GAM100 243 MADH4 Tagaki, Y.; et al.; et al: Somatic alterations of the DPC4 genein human 4 A c
colorectal cancers in vivo. Gastroenterology 111: 1369- 1372,1996.

GAM100 243 MADH4 Takaku, K.; Oshima, M.; Miyoshi, H.; Matsui, M.; Seldin, M. F.;Taketo, M. 4 A c
M.: Intestinal tumorigenesis in compound mutant mice ofboth Dpc4 (Smad4) and
Apc genes. Cell 92: 645- 656, 1998.

GAM100 243 MADH4 Thiagalingam, S.; Lengauer, C.; Leach, F. S.; Schutte, M.; Hahn,S. A.; 4 A c
Overhauser, J.; Willson, J. K. V.; Markowitz, S.; Hamilton,S. R.; Kern, S.
E.; Kinzler, K. W.; Vogelstein, B.: Evaluation ofcandidate tumour suppressor
genes on chromosome 18 in colorectal cancers. NatureGenet. 13: 343- 346,
1996.

GAM100 243 MADH4 Zawel, L.; Dai, J. L.; Buckhaults, P.; Zhou, S.; Kinzler, K. W.;Vogelstein, 4 A c
B.; Kern, S. E.: Human Smad3 and Smad4 are sequence- specifictranscription
activators. Molec. Cell 1: 611- 617, 1998.

GAM100 243 MADH4 Zhou, S.; Buckhaults, P.; Zawel, L.; Bunz, F.; Riggins, G.; LeDai, J.; Kern, 4 A c
S. E.; Kinzler, K. W.; Vogelstein, B.: Targeted deletionof Smad4 shows it is
required for transforming growth factor betaand activin signaling in
colorectal cancer cells. Proc. Nat. Acad.Sci. 95: 2412- 2416, 1998.

GAM100 243 MAP2 Garner, C. C.; Tucker, R. P.; Matus, A.: Selective localizationof messenger 4 A c
RNA for cytoskeletal protein MAP2 in dendrites. Nature 336:674- 677, 1988.

GAM100 243 MAP2 Kalcheva, N.; Albala, J.; O'Guin, K.; Rubino, H.; Garner, C.; Shafit- 4 A c
Zagardo,B.: Genomic structure of human microtubule- associated protein 2
(MAP- 2)and characterization of additional MAP- 2 isoforms. Proc. Nat.
Acad.Sci. 92: 10894- 10898, 1995.

GAM100 243 MAP2 Kindler, S.; Garner, C. C.: Four repeat MAP2 isoforms in humanand rat brain. 4 A c
Molec. Brain Res. 26: 218- 224, 1994.

GAM100 243 MAP2 Marsden, K. M.; Doll, T.; Ferralli, J.; Botteri, F.; Matus, A.: Transgenic 4 A c
expression of embryonic MAP2 in adult mouse brain: implicationsfor neuronal
polarization. J. Neurosci. 16: 3265- 3273, 1996.

GAM100 243 MAP2 Neve, R. L.; Harris, P.; Kosik, K. S.; Kurnit, D. M.; Donlon, T.A.: 4 A c
Identification of cDNA clones for the human microtubule- associatedprotein
tau and chromosomal localization of the genes for tau andmicrotubule-
associated protein 2. Molec. Brain Res. 1: 271- 280,1986.

GAM100 243 NPTX1 Omeis, I. A.; Hsu, Y.- C.; Perin, M. S.: Mouse and human neuronalpentraxin 1 4 A c
(NPXT1): conservation, genomic structure, and chromosomallocalization.
Genomics 36: 543- 545, 1996.

GAM100 243 NPTX1 Schlimgen, A. K.; Helms, J. A.; Vogel, H.; Perin, M. S.: Neuronalpentraxin, 4 A c
a secreted protein with homology to acute phase proteinsof the immune
system. Neuron 14: 519- 526, 1995.

GAM100 243 NUP214 Fornerod, M.; van Duersen, J.; van Baal, S.; Reynolds, A.; Davis,D.; Murti, 4 A c
K. G.; Fransen, J.; Grosveld, G.: The human homologueof yeast CRM1 is in a
dynamic subcomplex with CAN/Nup214 and a novelnuclear pore component Nup88.
EMBO J. 16: 807- 816, 1997.

GAM100 243 NUP214 Kraemer, D.; Wozniak, R. W.; Blobel, G.; Radu, A.: The human CANprotein, a 4 A c
putative oncogene product associated with myeloid leukemogenesis,is a
nuclear pore complex protein that faces the cytoplasm. Proc.Nat. Acad. Sci.

91: 1519- 1523, 1994.

GAM100 243 NUP214 Pilz, A.; Woodward, K.; Povey, S.; Abbott, C.: Comparative mappingof 50 4 A c
human chromosome 9 loci in the laboratory mouse. Genomics 25:139- 149, 1995.

GAM100 243 NUP214 van Deursen, J.; Boer, J.; Kasper, L.; Grosveld, G.: G(2) arrestand impaired 4 A c
nucleocytoplasmic transport in mouse embryos lackingthe proto- oncogene
CAN/Nup214. EMBO J. 15: 5574- 5583, 1996.

GAM100 243 NUP214 von Lindern, M.; Poustka, A.; Lehrach, H.; Grosveld, G.: The (6;9)chromosome 4 A c
translocation, associated with a specific subtype of acutenonlymphocytic
leukemia, leads to aberrant transcription of a targetgene on 9q34. Molec.
Cell. Biol. 10: 4016- 4026, 1990.

GAM100 243 OGT Haltiwanger, R. S.; Blomberg, M. A.; Hart, G. W.: Glycosylationof nuclear 4 A c
and cytoplasmic proteins: purification and characterizationof a uridine
diphospho- N- acetylglucosamine:polypeptide beta- N-
acetylglucosaminyltransferase. J.Biol. Chem. 267: 9005- 9013, 1992.

GAM100 243 OGT Kreppel, L. K.; Blomberg, M. A.; Hart, G. W.: Dynamic glycosylationof 4 A c
nuclear and cytosolic proteins: cloning and characterization ofa unique O-
GlcNAc transferase with multiple tetratricopeptide repeats. J.Biol. Chem.
272: 9308- 9315, 1997.

GAM100 243 OGT Lubas, W. A.; Frank, D. W.; Krause, M.; Hanover, J. A.: O- linkedGlcNAc 4 A c
transferase is a conserved nucleocytoplasmic protein
containingtetratricopeptide repeats. J. Biol. Chem. 272: 9316- 9324, 1997.

GAM100 243 OGT Shafi, R.; Iyer, S. P. N.; Ellies, L. G.; O'Donnell, N.; Marek,K. W.; Chui, 4 A c
D.; Hart, G. W.; Marth, J. D.: The O- GlcNAc transferasegene resides on the
X chromosome and is essential for embyronic stemcell viability and mouse
ontogeny. Proc. Nat. Acad. Sci. 97: 5735- 5739,2000.

GAM100 243 OGT Yang, X.; Zhang, F.; Kudlow, J. E.: Recruitment of O- GlcNAc transferaseto 4 A c
promoters by corepressor mSin3A: coupling protein O- GlcNAcylationto
transcriptional repression. Cell 110: 69- 80, 2002.

GAM100 243 P2RY12 Cattaneo, M.; Lecchi, A.; Randi, A. M.; McGregor, J. L.; Mannucci,P. M.: 4 A c
Identification of a new congenital defect of platelet functioncharacterized
by severe impairment of platelet responses to adenosinediphosphate. Blood
80: 2787- 2796, 1992.

GAM100 243 P2RY12 Hollopeter, G.; Jantzen, H.- M.; Vincent, D.; Li, G.; England, 4 A c
L.;Ramakrishnan, V.; Yang, R.- B.; Nurden, P.; Nurden, A.; Julius,
D.;Conley, P. B.: Identification of the platelet ADP receptor targetedby
antithrombotic drugs. Nature 409: 202- 206, 2001.

GAM100 243 P2RY12 Nurden, P.; Savi, P.; Heilmann, E.; Bihour, C.; Herbert, J.- M.;Maffrand, 4 A c
J.- P.; Nurden, A.: An inherited bleeding disorder linkedto a defective
interaction between ADP and its receptor on platelets:its influence on
glycoprotein IIb- IIIa complex function. J. Clin.Invest. 95: 1612- 1622,
1995.

GAM100 243 PACE4 Kiefer, M. C.; Tucker, J. E.; Joh, R.; Landsberg, K. E.; Saltman,D.; Barr, 4 A c
P. J.: Identification of a second human subtilisin- likeprotease gene in the
fes/fps region of chromosome 15. DNA Cell Biol. 10:757- 769, 1991.

GAM100 243 PACE4 Mbikay, M.; Seidah, N. G.; Chretien, M.; Simpson, E. M.: 4 A c
Chromosomalassignment of the genes for proprotein convertases PC4, PC5, and
PACE4 in mouse and human. Genomics 26: 123- 129, 1995.

GAM100 243 PARN Korner, C. G.; Wahle, E.: Poly(A) tail shortening by a mammalianpoly(A)- 4 A c
specific 3- prime- exoribonuclease. J. Biol. Chem. 272: 10448- 10456,1997.

GAM100 243 PARN Korner, C. G.; Wormington, M.; Muckenthaler, M.; Schneider, S.;Dehlin, E.; 4 A c

Wahle, E.: The deadenylating nuclease (DAN) is involvedin poly(A) tail removal during the meiotic maturation of Xenopus oocytes. EMBOJ. 17: 5427-5437, 1998.

GAM100 243 PRKDC Anderson, C. W.; Lees- Miller, S. P.: The nuclear serine/threonineprotein 4 A c kinase DNA- PK. Crit. Rev. Eukaryot. Gene Expr. 2: 283- 314,1992.

GAM100 243 PRKDC Araki, R.; Fujimori, A.; Hamatani, K.; Mita, K.; Saito, T.; Mori,M.; 4 A c Fukumura, R.; Morimyo, M.; Muto, M.; Itoh, M.; Tatsumi, K.; Abe,M.: Nonsense mutation at tyr- 4046 in the DNA- dependent protein kinasecatalytic subunit of severe combined immune deficiency mice. Proc.Nat. Acad. Sci. 94: 2438-2443, 1997.

GAM100 243 PRKDC Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: 4 A c Strand- specific postreplicative processing of mammalian telomeres. Science 293:2462- 2465, 2001.

GAM100 243 PRKDC Blunt, T.; Gell, D.; Fox, M.; Taccioli, G. E.; Lehmann, A. R.;Jackson, S. 4 A c P.; Jeggo, P. A.: Identification of a nonsense mutationin the carboxyl-terminal region of DNA- dependent protein kinase catalyticsubunit in the scid mouse. Proc. Nat. Acad. Sci. 93: 10285- 10290,1996.

GAM100 243 PRKDC Connelly, M. A.; Zhang, H.; Kieleczawa, J.; Anderson, C. W.: Thepromoters 4 A c for human DNA- PK(cs) (PRKDC) and MCM4: divergently transcribedgenes located at chromosome 8 band q11. Genomics 47: 71- 83, 1998.

GAM100 243 PRKDC Daniel, R.; Katz, R. A.; Skalka, A. M.: A role for DNA- PK in retroviralDNA 4 A c integration. Science 284: 644- 647, 1999.

GAM100 243 PRKDC Danska, J. S.; Holland, D. P.; Mariathasan, S.; Williams, K. M.;Guidos, C. 4 A c J.: Biochemical and genetic defects in the DNA- dependentprotein kinase in murine scid lymphocytes. Molec. Cell. Biol. 16:5507- 5517, 1996.

GAM100 243 PRKDC Hartley, K. O.; Gell, D.; Smith, G. C. M.; Zhang, H.; Divecha,N.; Connelly, 4 A c M. A.; Admon, A.; Lees- Miller, S. P.; Anderson, C. W.;Jackson, S. P.: DNA-dependent protein kinase catalytic subunit: arelative of phosphatidylinositol 3- kinase and the ataxia telangiectasiagene product. Cell 82: 849- 856, 1995.

GAM100 243 PRKDC Hendrickson, E. A.: The SCID mouse: relevance as an animal modelsystem for 4 A c studying human disease. Am. J. Path. 143: 1511- 1522,1993.

GAM100 243 PRKDC Jimenez, G. S.; Bryntesson, F.; Torres- Arzayus, M. I.; Priestley,A.; 4 A c Beeche, M.; Saito, S.; Sakaguchi, K.; Appella, E.; Jeggo, P. A.;Taccioli, G. E.; Wahl, G. M.; Hubank, M.: DNA- dependent protein kinaseis not required for the p53- dependent response to DNA damage. Nature 400:81- 83, 1999.

GAM100 243 PRKDC Kirchgessner, C. U.; Patil, C. K.; Evans, J. W.; Cuomo, C. A.;Fried, L. M.; 4 A c Carter, T.; Oettinger, M. A.; Brown, J. M.: DNA- dependentkinase (p350) as a candidate gene for the murine SCID defect. Science 267:1178- 1183, 1995.

GAM100 243 PRKDC Komatsu, K.; Kubota, N.; Gallo, M.; Okumura, Y.; Lieber, M. R.: The scid 4 A c factor on human chromosome 8 restores V(D)J recombinationin addition to double- strand break repair. Cancer Res. 55: 1774- 1779,1995.

GAM100 243 PRKDC Kuhn, A.; Gottlieb, T. M.; Jackson, S. P.; Grummt, I.: DNA- dependentprotein 4 A c kinase: a potent inhibitor of transcription by RNA polymeraseI. Genes Dev. 9: 193- 203, 1995.

GAM100 243 PRKDC Kurimasa, A.; Nagata, Y.; Shimizu, M.; Emi, M.; Nakamura, Y.;Oshimura, M.: A 4 A c human gene that restores the DNA- repair defect inScid mice is located on 8p11.1- q11.1. Hum. Genet. 93: 21- 26, 1994.

GAM100 243 PRKDC Labhart, P.: DNA- dependent protein kinase specifically represses promoter- 4 A c directed transcription initiation by RNA polymerase I. Proc.Nat. Acad. Sci.

92: 2934- 2938, 1995.

GAM100 243 PRKDC Ladenburger, E. M.; Fackelmayer, F. O.; Hameister, H.; Knippers,R.: MCM4 and 4 A c
PRKDC, human genes encoding proteins MCM4 and DNA- PKcs,are close neighbours
located on chromosome 8q12- q13. Cytogenet. CellGenet. 77: 268- 270, 1997.

GAM100 243 PRKDC Ma, Y.; Pannicke, U.; Schwarz, K.; Lieber, M. R.: Hairpin openingand 4 A c
overhang processing by an Artemis/DNA- dependent protein kinasecomplex in
nonhomologous end joining and V(D)J recombination. Cell 108:781- 794, 2002.

GAM100 243 PRKDC Miller, R. D.; Hogg, J.; Ozaki, J. H.; Gell, D.; Jackson, S. P.;Riblet, R.: 4 A c
Gene for catalytic subunit of mouse DNA- dependent proteinkinase maps to the
scid locus. Proc. Nat. Acad. Sci. 92: 10792- 10795,1995.

GAM100 243 PRKDC Poltoratsky, V. P.; Shi, X.; York, J. D.; Lieber, M. R.; Carter,T. H.: Human 4 A c
DNA- activated protein kinase (DNA- PK) is homologousto phosphatidylinositol
kinases. J. Immun. 155: 4529- 4533, 1995.

GAM100 243 PRKDC Satoh, T.; Tsuruga, H.; Yabuta, N.; Ishidate, M., Jr.; Nojima,H.: Assignment 4 A c
of the human CDC21 (MCM4) gene to chromosome 8q11.2. Genomics 46:525- 526,
1997.

GAM100 243 PRKDC Shieh, S.- Y.; Ikeda, M.; Taya, Y.; Prives, C.: DNA damage- 4 A c
inducedphosphorylation of p53 alleviates inhibition by MDM2. Cell 91: 325-
334,1997.

GAM100 243 PRKDC Sipley, J. D.; Menninger, J. C.; Hartley, K. O.; Ward, D. C.;Jackson, S. P.; 4 A c
Anderson, C. W.: Gene for the catalytic subunit ofthe human DNA- activated
protein kinase maps to the site of the XRCC7gene on chromosome 8. Proc. Nat.
Acad. Sci. 92: 7515- 7519, 1995.

GAM100 243 PRKDC Wiler, R.; Leber, R.; Moore, B. B.; VanDyk, L. F.; Perryman, L.E.; Meek, K.: 4 A c
Equine severe combined immunodeficiency: A defect inV(D)J recombination and
DNA- dependent protein kinase activity. Proc.Nat. Acad. Sci. 92: 11485-
11489, 1995.

GAM100 243 PRKDC Woo, R. A.; McLure, K. G.; Lees- Miller, S. P.; Rancourt, D. E.;Lee, P. W.: 4 A c
DNA- dependent protein kinase acts upstream of p53 inresponse to DNA damage.
Nature 394: 700- 704, 1998.

GAM100 243 PTGS2 Erkinheimo, T.- L.; Saukkonen, K.; Narko, K.; Jalkanen, J.; Ylikorkala,O.; 4 A c
Ristimaki, A.: Expression of cyclooxygenase- 2 and prostanoidreceptors by
human myometrium. J. Clin. Endocr. Metab. 85: 3468- 3475,2000.

GAM100 243 PTGS2 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; 4 A c
Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.;
Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H
synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999.

GAM100 243 PTGS2 Hla, T.; Neilson, K.: Human cyclooxygenase- 2 cDNA. Proc. Nat.Acad. Sci. 89: 4 A c
7384- 7388, 1992.

GAM100 243 PTGS2 Jones, D. A.; Carlton, D. P.; McIntyre, T. M.; Zimmerman, G. A.;Prescott, S. 4 A c
M.: Molecular cloning of human prostaglandin endoperoxidesynthase type II
and demonstration of expression in response to cytokines. J.Biol. Chem. 268:
9049- 9054, 1993.

GAM100 243 PTGS2 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; 4 A c
Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.:
Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2
in the humanfetal and adult male reproductive tracts. J. Clin. Endocr.
Metab. 85:3436- 3441, 2000.

GAM100 243 PTGS2 Kraemer, S. A.; Meade, E. A.; DeWitt, D. L.: Prostaglandin 4 A c
endoperoxidesynthase gene structure: identification of the transcriptional

startsite and 5- prime- flanking regulatory sequences. Arch. Biochem. Biophys. 293:391- 400, 1992.

GAM100 243 PTGS2 Lassus, P.; Wolff, H.; Andersson, S.: Cyclooxygenase- 2 in humanperinatal lung. Pediat. Res. 47: 602- 605, 2000. 4 A c

GAM100 243 PTGS2 Lim, H.; Paria, B. C.; Das, S. K.; Dinchuk, J. E.; Langenbach,R.; Trzaskos, J. M.; Dey, S. K.: Multiple female reproductive failuresin cyclooxygenase 2- deficient mice. Cell 91: 197- 208, 1997. 4 A c

GAM100 243 PTGS2 Loftin, C. D.; Trivedi, D. B.; Tiano, H. F.; Clark, J. A.; Lee,C. A.; Epstein, J. A.; Morham, S. G.; Breyer, M. D.; Nguyen, M.; Hawkins,B. M.; Goulet, J. L.; Smithies, O.; Koller, B. H.; Langenbach, R.: Failure of ductus arteriosus closure and remodeling in neonatalmice deficient in cyclooxygenase- 1 and cyclooxgenase- 2. Proc. Nat.Acad. Sci. 98: 1059- 1064, 2001. 4 A c

GAM100 243 PTGS2 Macchia, L.; Di Paola, R.; Guerrese, M.- C.; Chiechi, L. M.; Tursi,A.; Caiaffa, M. F.; Haeggstrom, J. Z.: Expression of prostaglandinendoperoxide H synthase 1 and 2 in human placenta at term. Biochem.Biophys. Res. Commun. 233: 496- 501, 1997. 4 A c

GAM100 243 PTGS2 Morham, S. G.; Langenbach, R.; Loftin, C. D.; Tiano, H. F.; Vouloumanos,N.; Jennette, J. C.; Mahler, J. F.; Kluckman, K. D.; Ledford, A.;Lee, C. A.; Smithies, O.: Prostaglandin synthase 2 gene disruptioncauses severe renal pathology in the mouse. Cell 83: 473- 482, 1995. 4 A c

GAM100 243 PTGS2 Neufang, G.; Furstenberger, G.; Heidt, M.; Marks, F.; Muller- Decker,K.: Abnormal differentiation of epidermis in transgenic mice constitutivelyexpressing cyclooxygenase- 2 in skin. Proc. Nat. Acad. Sci. 98: 7629- 7634,2001. 4 A c

GAM100 243 PTGS2 O'Banion, M. K.; Sadowski, H. B.; Winn, V.; Young, D. A.: A serum- and glucocorticoid- regulated 4- kilobase mRNA encodes a cyclooxygenase- relatedprotein. J. Biol. Chem. 266: 23261- 23267, 1991. 4 A c

GAM100 243 PTGS2 O'Banion, M. K.; Winn, V. D.; Young, D. A.: cDNA cloning andfunctional activity of a glucocorticoid- regulated inflammatory cyclooxygenase. Proc.Nat. Acad. Sci. 89: 4888- 4892, 1992. 4 A c

GAM100 243 PTGS2 Oshima, M.; Dinchuk, J. E.; Kargman, S. L.; Oshima, H.; Hancock,B.; Kwong, E.; Trzaskos, J. M.; Evans, J. F.; Taketo, M. M.: Suppressionof intestinal polyposis in Apc(delta- 716) knockout mice by inhibitionof cyclooxygenase 2 (COX- 2). Cell 87: 803- 809, 1996. 4 A c

GAM100 243 PTGS2 Sales, K. J.; Katz, A. A.; Davis, M.; Hinz, S.; Soeters, R. P.;Hofmeyr, M. D.; Millar, R. P.; Jabbour, H. N.: Cyclooxygenase- 2 expressionand prostaglandin E2 synthesis are up- regulated in carcinomas of thecervix: a possible autocrine/paracrine regulation of neoplastic cellfunction via EP2/EP4 receptors. J. Clin. Endocr. Metab. 86: 2243- 2249,2001. 4 A c

GAM100 243 PTGS2 Salmenkivi, K.; Haglund, C.; Ristimaki, A.; Arola, J.; Heikkila,P.: Increased expression of cyclooxygenase- 2 in malignant pheochromocytomas. J.Clin. Endocr. Metab. 86: 5615- 5619, 2001. 4 A c

GAM100 243 PTGS2 Samad, T. A.; Moore, K. A.; Sapirstein, A.; Billet, S.; Allchorne,A.; Poole, S.; Bonventre, J. V.; Woolf, C. J.: Interleukin- 1- beta- mediatedinduction of Cox- 2 in the CNS contributes to inflammatory pain hypersensitivity. Nature 410:471- 475, 2001. 4 A c

GAM100 243 PTGS2 Swan, S. K.; Rudy, D. W.; Lasseter, K. C.; Ryan, C. F.; Buechel,K. L.; Lambrecht, L. J.; Pinto, M. B.; Dilzer, S. C.; Obrda, O.; Sundblad,K. J.; Gumbs, C. P.; Ebel, D. L.; Quan, H.; Larson, P. J.; Schwartz,J. I.; 4 A c

Musliner, T. A.; Gertz, B. J.; Brater, D. C.; Yao, S.- L.:Effect of cyclooxygenase- 2 inhibition on renal function in elderlypersons receiving a low- salt diet: a randomized controlled trial. Ann.Intern. Med. 133: 1- 9, 2000.

GAM100 243 PTGS2 Tay, A.; Squire, J. A.; Goldberg, H.; Skorecki, K.: Assignmentof the human prostaglandin- endoperoxide synthase 2 (PTGS2) gene to1q25 by fluorescence in situ hybridization. Genomics 23: 718- 719,1994. 4 A c

GAM100 243 PTGS2 Tazawa, R.; Xu, X.- M.; Wu, K. K.; Wang, L.- H.: Characterizationof the genomic structure, chromosomal location and promoter of humanprostaglandin H synthase- 2 gene. Biochem. Biophys. Res. Commun. 203:190- 199, 1994. 4 A c

GAM100 243 PTGS2 Tsujii, M.; DuBois, R. N.: Alterations in cellular adhesion andapoptosis in epithelial cells overexpressing prostaglandin endoperoxidesynthase 2. Cell 83: 493- 501, 1995. 4 A c

GAM100 243 PTGS2 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93: 705- 716, 1998. 4 A c

GAM100 243 PTGS2 Zhou, X.- L.; Lei, Z. M.; Rao, C. V.: Treatment of human endometrialgland epithelial cells with chorionic gonadotropin/luteinizing hormoneincreases the expression of the cyclooxygenase- 2 gene. J. Clin. Endocr.Metab. 84: 3364- 3377, 1999. 4 A c

GAM100 243 SELE Bevilacqua, M. P.; Stengelin, S.; Gimbrone, M. A., Jr.; Seed, B.: Endothelial leukocyte adhesion molecule 1: an inducible receptorfor neutrophils related to complement regulatory proteins and lectins. Science 243:1160- 1165, 1989. 4 A c

GAM100 243 SELE Bevilacqua, M.; Butcher, E.; Furie, B.; Furie, B.; Gallatin, M.;Gimbrone, M.; Harlan, J.; Kishimoto, K.; Lasky, L.; McEver, R.; Paulson,J.; Rosen, S.; Seed, B.; Siegelman, M.; Springer, T.; Stoolman, L.;Tedder, T.; Varki, A.; Wagner, D.; Weissman, I.; Zimmerman, G.: Selectins:a family of adhesion receptors. (Letter) Cell 67: 233 only, 1991. 4 A c

GAM100 243 SELE Collins, T.; Williams, A.; Johnston, G. I.; Kim, J.; Eddy, R.;Shows, T.; Gimbrone, M. A., Jr.; Bevilacqua, M. P.: Structure andchromosomal location of the gene for endothelial- leukocyte adhesionmolecule 1. J. Biol. Chem. 266: 2466- 2473, 1991. 4 A c

GAM100 243 SELE DeLisser, H. M.; Christofidou- Solomidou, M.; Sun, J.; Nakada, M.T.; Sullivan, K. E.: Loss of endothelial surface expression of E- selectinin a patient with recurrent infections. Blood 94: 884- 894, 1999. 4 A c

GAM100 243 SELE Wang, N.; Chintala, S. K.; Fini, M. E.; Schuman, J. S.: Activationof a tissue- specific stress response in the aqueous outflow pathwayof the eye defines the glaucoma disease phenotype. Nature Med. 7:304- 309, 2001. 4 A c

GAM100 243 SELE Watson, M. L.; Kingsmore, S. F.; Johnston, G. I.; Siegelman, M.H.; Le Beau, M. M.; Lemons, R. S.; Bora, N. S.; Howard, T. A.; Weissman,I. L.; McEver, R. P.; Seldin, M. F.: Genomic organization of theselectin family of leukocyte adhesion molecules on human and mousechromosome 1. J. Exp. Med. 172: 263- 272, 1990. 4 A c

GAM100 243 SELE Wenzel, K.; Felix, S.; Kleber, F. X.; Brachold, R.; Menke, T.;Schattke, S.; Schulte, K. L.; Glaser, C.; Rohde, K.; Baumann, G.;Speer, A.: E- selectin polymorphism and atherosclerosis: an associationstudy. Hum. Molec. Genet. 3: 1935- 1937, 1994. 4 A c

GAM100 243 SELE Zheng, F.; Chevalier, J. A.; Zhang, L. Q.; Virgil, D.; Ye, S. Q.;Kwiterovich, P. O.: An HphI polymorphism in the E- selectin gene 4 A c

isassociated with premature coronary artery disease. Clin. Genet. 59:58- 64, 2001.

GAM100 243 SIAH1 Banfi, S.; Borsani, G.; Rossi, E.; Bernard, L.; Guffanti, A.; Rubboli,F.; Marchitiello, A.; Giglio, S.; Coluccia, E.; Zollo, M.; Zuffardi,O.; Ballabio, A.: Identification and mapping of human cDNAs homologousto Drosophila mutant genes through EST database searching. NatureGenet. 13: 167- 174, 1996. 4 A c

GAM100 243 SIAH1 Hu, G.; Chung, Y.- L.; Glover, T.; Valentine, V.; Look, A T.; Fearon,E. R.: Characterization of human homologs of the Drosophila sevenin absentia (sina) gene. Genomics 46: 103- 111, 1997. 4 A c

GAM100 243 SIAH1 Liu, J.; Stevens, J.; Rote, C. A.; Yost, H. J.; Hu, Y.; Neufeld,K. L.; White, R. L.; Matsunami, N.: Siah- 1 mediates a novel beta- catenindegradation pathway linking p53 to the adenomatous polyposis coliprotein. Molec. Cell 7: 927- 936, 2001. 4 A c

GAM100 243 SIAH1 Matsuzawa, S.; Reed, J. C.: Siah- 1, SIP, and Ebi collaborate ina novel pathway for beta- catenin degradation linked to p53 responses. Molec.Cell 7: 915- 926, 2001. 4 A c

GAM100 243 SIAH1 Nemani, M.; Linares- Cruz, G.; Bruzzoni- Giovanelli, H.; Roperch,J.- P.; Tuynder, M.; Bougueleret, L.; Cherif, D.; Medhioub, M.; Pasturaud,P.; Alvaro, V.; der Sarkissan, H.; Cazes, L.; Le Paslier, D.; Le Gall,I.; Israeli, D.; Dausset, J.; Sigaux, F.; Chumakov, I.; Oren, M.;Calvo, F.; Amson, R. B.; Cohen, D.; Telerman, A.: Activation of thehuman homologue of the Drosophila SINA gene in apoptosis and tumorsuppression. Proc. Nat. Acad. Sci. 93: 9039- 9042, 1996. 4 A c

GAM100 243 TGFA Brissenden, J. E.; Derynck, R.; Francke, U.: Transforming growthfactor alpha gene (TGFA) maps to human chromosome 2 close to the breakpointof the t(2;8) variant translocation in Burkitt lymphoma. (Abstract) Cytogenet.Cell Genet. 40: 589 only, 1985. 4 A c

GAM100 243 TGFA Collin, G. B.; Marshall, J. D.; Naggert, J. K.; Nishina, P. M.: TGFA: exon- intron structure and evaluation as a candidate gene forAlstrom syndrome. (Letter) Clin. Genet. 55: 61- 62, 1999. 4 A c

GAM100 243 TGFA Ellis, D. L.; Kafka, S. P.; Chow, J. C.; Nanney, L. B.; Inman,W. H.; McCadden, M. E.; King, L. E., Jr.: Melanoma, growth factors,acanthosis nigricans, the sign of Leser- Trelat, and multiple acrochordons:a possible role for alpha- transforming growth factor in cutaneousparaneoplastic syndromes. New Eng. J. Med. 317: 1582- 1587, 1987. 4 A c

GAM100 243 TGFA Fernandez- Larrea, J.; Merlos- Suarez, A.; Urena, J. M.; Baselga,J.; Arribas, J.: A role for a PDZ protein in the early secretorypathway for the targeting of proTGF- alpha to the cell surface. Molec.Cell 3: 423- 433, 1999. 4 A c

GAM100 243 TGFA Fowler, K. J.; Mann, G. B.; Dunn, A. R.: Linkage of the murinetransforming growth factor- alpha gene with Igk, Ly- 2, and Fabp1 onchromosome 6. Genomics 16: 782- 784, 1993. 4 A c

GAM100 243 TGFA Kramer, A.; Yang, F.- C.; Snodgrass, P.; Li, X.; Scammell, T. E.;Davis, F. C.; Weitz, C. J.: Regulation of daily locomotor activityand sleep by hypothalamic EGF receptor signaling. Science 294: 2511- 2515,2001. 4 A c

GAM100 243 TGFA Tam, J. P.; Scheikh, M. A.; Solomon, D. S.; Ossowski, L.: Efficientsynthesis of human type alpha transforming growth factor: its physicaland biological characterization. Proc. Nat. Acad. Sci. 83: 8082- 8086,1986. 4 A c

GAM100 243 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. 4 A c

B.: Assignment of the gene coding for human TGF- alphato chromosome 2p13. (Abstract) Cytogenet. Cell Genet. 40: 762 only,1985.

GAM100 243 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. 4 A c
B.: The gene for human transforming growth factor alphais on the short arm of chromosome 2. Cytogenet. Cell Genet. 42:94- 98, 1986.

GAM100 243 TNFSF15 Migone, T.- S.; Zhang, J.; Luo, X.; Zhuang, L.; Chen, C.; Hu, B.;Hong, J. 4 A c
S.; Perry, J. W.; Chen, S.- F.; Zhou, J. X. H.; Cho, Y. H.;Ullrich, S.; and 14 others: TL1A is a TNF- like ligand for DR3 andTR6/DcR3 and functions as a T cell costimulator. Immunity 16: 479- 492,2002.

GAM100 243 TNFSF15 Tan, K. B.; Harrop, J.; Reddy, M.; Young, P.; Terrett, J.; Emery,J.; Moore, 4 A c
G.; Truneh, A.: Characterization of a novel TNF- like ligandand recently described TNF ligand and TNF receptor superfamily genesand their constitutive and inducible expression in hematopoietic andnon- hematopoietic cells. Gene 204: 35- 46, 1997.

GAM100 243 TNFSF15 Yue, T.- L.; Ni, J.; Romanic, A. M.; Gu, J.- L.; Keller, P.; Wang,C.; Kumar, 4 A c
S.; Yu, G.; Hart, T. K.; Wang, X.; Xia, Z.; DeWolf, W.E., Jr.; Feuerstein, G. Z.: TL1, a novel tumor necrosis factor- likecytokine, induces apoptosis in endothelial cells: involvement of activationof stress protein kinases (stress- activated protein kinase and p38mitogen- activated protein kinase) and caspase- 3- like protease. J.Biol. Chem. 274: 1479- 1486, 1999.

GAM100 243 TNFSF15 Zhai, Y.; Ni, J.; Jiang, G.- W.; Lu, J.; Xing, L.; Lincoln, C.;Carter, K. 4 A c
C.; Janat, F.; Kozak, D.; Xu, S.; Rojas, L.; Aggarwal,B. B.; Ruben, S.; Li, L.- Y.; Gentz, R.; Yu, G.- L.: VEGI, a novelcytokine of the tumor necrosis factor family, is an angiogenesis inhibitorthat suppresses the growth of colon carcinomas in vivo. FASEB J. 13:181- 189, 1999.

GAM100 243 UTY Foresta, C.; Ferlin, A.; Moro, E.: Deletion and expression analysisof AZFa 4 A c
genes on the human Y chromosome revealed a major role forDBY in male infertility. Hum. Molec. Genet. 9: 1161- 1169, 2000.

GAM100 243 UTY Greenfield, A.; Carrel, L.; Pennisi, D.; Philippe, C.; Quaderi,N.; Siggers, 4 A c
P.; Steiner, K.; Tam, P. P. L.; Monaco, A. P.; Willard,H. F.; Koopman, P.: The UTX gene escapes X inactivation in mice andhumans. Hum. Molec. Genet. 7: 737- 742, 1998.

GAM100 243 UTY Greenfield, A.; Scott, D.; Pennisi, D.; Ehrmann, I.; Ellis, P.;Cooper, L.; 4 A c
Simpson, E.; Koopman, P.: An H- YDb epitope is encodedby a novel mouse Y chromosome gene. Nature Genet. 14: 474- 478, 1996.

GAM100 243 UTY Shen, P.; Wang, F.; Underhill, P. A.; Franco, C.; Yang, W.- H.;Roxas, A.; 4 A c
Sung, R.; Lin, A. A.; Hyman, R. W.; Vollrath, D.; Davis,R. W.; Cavalli-Sforza, L. L.; Oefner, P. J.: Population genetic implicationsfrom sequence variation in four Y chromosome genes. Proc. Nat. Acad.Sci. 97: 7354- 7359, 2000.

GAM100 243 VPS26 Haft, C. R.; de la Luz Sierra, M.; Bafford, R.; Lesniak, M. A.;Barr, V. A.; 4 A c
Taylor, S. I.: Human orthologs of yeast vacuolar proteinsorting proteins Vps26, 29, and 35: assembly into multimeric complexes. Molec.Biol. Cell 11: 4105- 4116, 2000.

GAM100 243 VPS26 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 4 A c
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu, S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci. 95: 8175- 8180, 1998.

GAM103 276 ITPR3 Maranto, A. R.: Primary structure, ligand binding, and localizationof the human type 3 inositol 1,4,5- trisphosphate receptor expressedin intestinal epithelium. J. Biol. Chem. 269: 1222- 1230, 1994. 3 C c

GAM103 276 ITPR3 Ozcelik, T.; Suedhof, T. C.; Francke, U.: The genes for inositol1,4,5- triphosphate receptors 1 (ITPR1) and 3 (ITPR3) are localizedon human chromosomes 3p and 6pter- p21, respectively. (Abstract) Cytogenet.Cell Genet. 58: 1880 only, 1991. 3 C c

GAM103 276 ITPR3 Yamamoto- Hino, M.; Sugiyama, T.; Hikichi, K.; Mattei, M. G.; Hasegawa,K.; Sekine, S.; Sakurada, K.; Miyawaki, A.; Furuichi, T.; Hasegawa,M.; Mikoshiba, K.: Cloning and characterization of human type 2 andtype 3 inositol 1,4,5- triphosphate receptors. Receptors Channels 2:9- 22, 1994. 3 C c

GAM104 355 ABL2 Cazzaniga, G.; Tosi, S.; Aloisi, A.; Giudici, G.; Daniotti, M.;Pioltelli, P.; Kearney, L.; Biondi, A.: The tyrosine kinase Abl- relatedgene ARG is fused to ETV6 in an AML- M4Eo patient with a t(1;12)(q25;p13):molecular cloning of both reciprocal transcripts. Blood 94: 4370- 4373,1999. 3 B c

GAM104 355 ABL2 Iijima, Y.; Ito, T.; Oikawa, T.; Eguchi, M.; Eguchi- Ishimae, M.;Kamada, N.; Kishi, K.; Asano, S.; Sakaki, Y.; Sato, Y.: A new ETV6/TELpartner gene, ARG (ABL- related gene or ABL2), identified in an AML- M3cell line with a t(1;12)(q25;p13) translocation. Blood 95: 2126- 2131,2000. 3 B c

GAM104 355 ABL2 Kruh, G. D.; King, C. R.; Kraus, M. H.; Popescu, N. C.; Amsbaugh,S. C.; McBride, W. O.; Aaronson, S. A.: A novel human gene closelyrelated to the abl proto- oncogene. Science 234: 1545- 1548, 1986. 3 B c

GAM104 355 ABL2 Seldin, M. F.; Kruh, G. D.: Mapping of Abll within a conservedlinkage group on distal mouse chromosome 1 syntenic with human chromosome1 using an interspecific cross. Genomics 4: 221- 223, 1989. 3 B c

GAM104 355 ARNT2 Hirose, K.; Morita, M.; Ema, M.; Mimura, J.; Hamada, H.; Fujii,H.; Saijo, Y.; Gotoh, O.; Sogawa, K.; Fujii- Kuriyama, Y.: cDNA cloningand tissue-specific expression of a novel basic helix- loop- helix/PASfactor (Arnt2) with close sequence similarity to the aryl hydrocarbonreceptor nuclear translocator (Arnt). Molec. Cell. Biol. 16: 1706- 1713,1996. 3 B c

GAM104 355 ARNT2 Keith, B.; Adelman, D. M.; Simon, M. C.: Targeted mutation ofthe murine arylhydrocarbon receptor nuclear translocator 2 (Arnt2)gene reveals partial redundancy with Arnt. Proc. Nat. Acad. Sci. 98:6692- 6697, 2001. 3 B c

GAM104 355 ARNT2 Michaud, J. L.; DeRossi, C.; May, N. R.; Holdener, B. C.; Fan,C.- M.: ARNT2 acts as the dimerization partner of SIM1 for the developmentof the hypothalamus. Mech. Dev. 90: 253- 261, 2000. 3 B c

GAM104 355 ARNT2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B c

GAM104 355 BAT1 Allcock, R. J. N.; Williams, J. H.; Price, P.: The central MHCgene, BAT1, may encode a protein that down- regulates cytokine production. GenesCells 6: 487- 494, 2001. 3 B c

GAM104 355 BAT1 Nunes, M.; Peelman, L.; Vaiman, M.; Bourgeaux, N.; Chardon, P.: Characterization of six new loci within the swine major histocompatibilitycomplex class III region. Mammalian Genome 5: 616- 622, 1994. 3 B c

GAM104 355 BAT1 Peelman, L. J.; Chardon, P.; Nunes, M.; Renard, C.; Geffrotin,C.; Vaiman, M.; Van Zeveren, A.; Coppieters, W.; van de Weghe, A.;Bouquet, Y.; Choy, W. 3 B c

W.; Strominger, J. L.; Spies, T.: The BAT1gene in the MHC encodes an evolutionarily conserved putative nuclearRNA helicase of the DEAD family. Genomics 26: 210- 218, 1995.

GAM104 355 BAT1 Spies, T.; Blanck, G.; Bresnahan, M.; Sands, J.; Strominger, J.L.: A new cluster of genes within the human major histocompatibilitycomplex. Science 243: 214- 217, 1989. 3 B c

GAM104 355 BAT1 Spies, T.; Bresnahan, M.; Strominger, J. L.: Human major histocompatibilitycomplex contains a minimum of 19 genes between the complement clusterand HLA- B. Proc. Nat. Acad. Sci. 86: 8955- 8958, 1989. 3 B c

GAM104 355 C5R1 Bao, L.; Gerard, N. P.; Eddy, R. L., Jr.; Shows, T. B.; Gerard,C.: Mapping of genes for the human C5a receptor (C5AR), human FMLPreceptor (FPR), and two FMLP receptor homologue orphan receptors (FPRH1,FPRH2) to chromosome 19. Genomics 13: 437- 440, 1992. 3 B c

GAM104 355 C5R1 Collaborative Study on the Genetics of Asthma: A genome- widesearch for asthma susceptibility loci in ethnically diverse populations. NatureGenet. 15: 389- 392, 1997. 3 B c

GAM104 355 C5R1 Gavett, S. H.; O'Hearn, D. J.; Li, X.; Huang, S. K.; Finkelman,F. D.; Wills- Karp, M.: Interleukin 12 inhibits antigen- induced airwayhyperresponsiveness, inflammation, and Th2 cytokine expression inmice. J. Exp. Med. 182: 1527- 1536, 1995. 3 B c

GAM104 355 C5R1 Hopken, U. E.; Lu, D.; Gerard, N. P.; Gerard, C.: The C5a chemoattractantreceptor mediates mucosal defense to infection. Nature 383: 86- 89,1996. 3 B c

GAM104 355 C5R1 Karp, C. L.; Grupe, A.; Schadt, E.; Ewart, S. L.; Keane- Moore,M.; Cuomo, P. J.; Kohl, J.; Wahl, L.; Kuperman, D.; Germer, S.; Aud,D.; Peltz, G.; Wills-Karp, M.: Identification of complement factor5 as a susceptibility locus for experimental allergic asthma. NatureImmun. 1: 221- 226, 2000. 3 B c

GAM104 355 C5R1 Ober, C.; Cox, N. J.; Abney, M.; Di Rienzo, A.; Lander, E. S.;Changyaleket, B.; Gidley, H.; Kurtz, B.; Lee, J.; Nance, M.; Pettersson,A.; Prescott, J.; Richardson, A.; Schlenker, E.; Summerhill, E.; Willadsen,S.; Parry, R.; Collaborative Study on the Genetics of Asthma: Genome- widesearch for asthma susceptibility loci in a founder population. Hum.Molec. Genet. 7: 1393-1398, 1998. 3 B c

GAM104 355 C5R1 Wjst, M.; Fischer, G.; Immervoll, T.; Jung, M.; Saar, K.; Rueschendorf,F.; Reis, A.; Ulbrecht, M.; Gomolka, M.; Weiss, E. H.; Jaeger, L.;Nickel, R.; and 14 others: A genome- wide search for linkage toasthma. Genomics 58: 1-8, 1999. 3 B c

GAM104 355 DAZ Agulnik, A. I.; Zharkikh, A.; Boettger- Tong, H.; Bourgeron, T.;McElreavey, K.; Bishop, C. E.: Evolution of the DAZ gene family suggeststhat Y- linked DAZ plays little, or a limited, role in spermatogenesisbut underlines a recent African origin for human populations. Hum.Molec. Genet. 7: 1371-1377, 1998. 3 B c

GAM104 355 DAZ Anonymous: A missing piece on the Y. (Editorial) Nature Genet. 10:367- 368, 1995. 3 B c

GAM104 355 DAZ Cooke, H. J.; Lee, M.; Kerr, S.; Ruggiu, M.: A murine homologueof the human DAZ gene is autosomal and expressed only in male andfemale gonads. Hum. Molec. Genet. 5: 513- 516, 1996. 3 B c

GAM104 355 DAZ Foresta, C.; Bertella, A.; Moro, E.; Roverato, A.; Merico, M.;Ferlin, A.: Sertoli cell function in infertile patients with andwithout microdeletions of the azoospermia factors on the Y chromosomelong arm. J. Clin. Endocr. 3 B c

Metab. 86: 2414- 2419, 2001.

GAM104 355 DAZ Foresta, C.; Moro, E.; Garolla, A.; Onisto, M.; Ferlin, A.: Ychromosome 3 B c microdeletions in cryptorchidism and idiopathic infertility. J.Clin. Endocr. Metab. 84: 3660- 3665, 1999.

GAM104 355 DAZ Makova, K. D.; Li, W.- H.: Strong male- driven evolution of DNAsequences in 3 B c humans and apes. Nature 416: 624- 626, 2002.

GAM104 355 DAZ Menke, D. B.; Mutter, G. L.; Page, D. C.: Expression of DAZ, anazoospermia 3 B c factor candidate, in human spermatogonia. (Letter) Am.J. Hum. Genet. 60: 237- 241, 1997.

GAM104 355 DAZ Moro, E.; Ferlin, A.; Yen, P. H.; Franchi, P. G.; Palka, G.; Foresta,C.: 3 B c Male infertility caused by a de novo partial deletion of theDAZ cluster on the Y chromosome. J. Clin. Endocr. Metab. 85: 4069- 4073,2000.

GAM104 355 DAZ Najmabadi, H.; Huang, V.; Yen, P.; Subbarao, M. N.; Bhasin, D;Banaag, L.; 3 B c Naseeruddin, S.; de Kretser, D. M.; Baker, H. W. G.; McLachlan,R. I.; Loveland, K. A.; Bhasin, S.: Substantial prevalence of microdeletionsof the Y- chromosome in infertile men with idiopathic azoospermia andoligozoospermia detected using a sequence- tagged site- based mappingstrategy. J. Clin. Endocr. Metab. 81: 1347- 1352, 1996.

GAM104 355 DAZ Reijo, R.; Lee, T.- Y.; Salo, P.; Alagappan, R.; Brown, L. G.;Rosenberg, M.; 3 B c Rozen, S.; Jaffe, T.; Straus, D.; Hovatta, O.; de laChapelle, A.; Silber, S.; Page, D. C.: Diverse spermatogenic defectsin humans caused by Y chromosome deletions encompassing a novel RNA- bindingprotein gene. Nature Genet. 10: 383- 393, 1995.

GAM104 355 DAZ Reijo, R.; Seligman, J.; Dinulos, M. B.; Jaffe, T.; Brown, L.G.; Disteche, 3 B c C. M.; Page, D. C.: Mouse autosomal homolog of DAZ,a candidate male sterility gene in humans, is expressed in male germcells before and after puberty. Genomics 35: 346- 352, 1996.

GAM104 355 DAZ Saxena, R.; Brown, L. G.; Hawkins, T.; Alagappan, R. K.; Skaletsky,H.; 3 B c Reeve, M. P.; Reijo, R.; Rozen, S.; Dinulos, M. B.; Disteche,C. M.; Page, D. C.: The DAZ gene cluster on the human Y chromosomearose from an autosomal gene that was transposed, repeatedly amplifiedand pruned. Nature Genet. 14: 292- 299, 1996.

GAM104 355 DAZ Shimmin, L. C.; Chang, B.- H.; Li, W.- H.: Male- driven evolutionof DNA 3 B c sequences. Nature 362: 745- 747, 1993.

GAM104 355 DAZ Stuppia, L.; Calabrese, G.; Franchi, P. G.; Mingarelli, R.; Gatta,V.; Palka, 3 B c G.; Dallapiccola, B.: Widening of a Y- chromosome interval- 6deletion transmitted from a father to his infertile son accounts foran oligozoospermia critical region distal to the RBM1 and DAZ genes.(Letter) Am. J. Hum. Genet. 59: 1393- 1395, 1996.

GAM104 355 GRM7 Barbon, A.; Ferraboli, S.; Barlati, S.: Assignment of the humanmetabotropic 3 B c glutamate receptor gene GRM7 to chromosome 3p26.1- p25.2by radiation hybrid mapping. Cytogenet. Cell Genet. 88: 288 only,2000.

GAM104 355 GRM7 Makoff, A.; Pilling, C.; Harrington, K.; Emson, P.: Human 3 B c metabotropicglutamate receptor type 7: molecular cloning and mRNA distributionin the CNS. Molec. Brain Res. 40: 165- 170, 1996.

GAM104 355 GRM7 Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.;Mizuno, N.; 3 B c Nakanishi, S.: Molecular characterization of a new metabotropicglutamate receptor mGluR7 coupled to inhibitory cyclic AMP signaltransduction. J. Biol. Chem. 269: 1231- 1236, 1994.

GAM104 355 GRM7 Wu, S.; Wright, R. A.; Rockey, P. K.; Burgett, S. G.; Arnold, J.S.; Rosteck, 3 B c

P. R., Jr.; Johnson, B. G.; Schoepp, D. D.; Belagaje,R. M.: Group III human metabotropic glutamate receptors 4, 7 and8: molecular cloning, functional expression, and comparison of pharmacologicalproperties in RGT cells. Molec. Brain Res. 53: 88- 97, 1998.

GAM104 355 ING1 Garkavtsev, I.; Demetrick, D.; Riabowol, K.: Cellular localizationand 3 B c chromosome mapping of a novel candidate tumor suppressor gene(ING1). Cytogenet. Cell Genet. 76: 176- 178, 1997.

GAM104 355 ING1 Garkavtsev, I.; Kazarov, A.; Gudkov, A.; Riabowol, K.: Suppressionof the 3 B c novel growth inhibitor p33(ING1) promotes neoplastic transformation. NatureGenet. 14: 415- 420, 1996. Note: Erratum: Nature Genet. 23: 373 only,1999.

GAM104 355 ING1 Gunduz, M.; Ouchida, M.; Fukushima, K.; Hanafusa, H.; Etani, T.;Nishioka, 3 B c S.; Nishizaki, K.; Shimizu, K.: Genomic structure of thehuman ING1 gene and tumor- specific mutations detected in head andneck squamous cell carcinomas. Cancer Res. 60: 3143- 3146, 2000.

GAM104 355 ING1 Saito, A.; Furukawa, T.; Fukushige, S.; Koyama, S.; Hoshi, M.;Hayashi, Y.; 3 B c Horii, A.: p24/ING1- ALT1 and p47/ING1- ALT2, distinctalternative transcripts of p33/ING1. J. Hum. Genet. 45: 177- 181,2000.

GAM104 355 ING1 Zeremski, M.; Horrigan, S. K.; Grigorian, I. A.; Westbrook, C.A.; Gudkov, A. 3 B c V.: Localization of the candidate tumor suppressorgene ING1 to human chromosome 13q34. Somat. Cell Molec. Genet. 23:233- 236, 1997.

GAM104 355 JUND Sullivan, M.; Olsen, A. S.; Houslay, M. D.: Genomic organisationof the human 3 B c cyclic AMP- specific phosphodiesterase PDE4C gene andits chromosomal localisation to 19p13.1, between RAB3A and JUND. Cell.Signal. 11: 735- 742, 1999.

GAM104 355 JUND Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 B c Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993.

GAM104 355 JUND Weitzman, J. B.; Fiette, L.; Matsuo, K.; Yaniv, M.: JunD protectscells from 3 B c p53- dependent senescence and apoptosis. Molec. Cell 6:1109- 1119, 2000.

GAM104 355 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 B c protocadherin- beta one- exon gene families show high evolutionaryconservation, despite the difference in gene number. FEBS Lett. 495:120- 125, 2001.

GAM104 355 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B c Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM104 355 SFPQ Clark, J.; Lu, Y.- J.; Sidhar, S. K.; Parker, C.; Gill, S.; Smedley,D.; 3 B c Hamoudi, R.; Linehan, W. M.; Shipley, J.; Cooper, C. S.: Fusionof splicing factor genes PSF and NonO (p54- nrb) to the TFE3 gene inpapillary renal cell carcinoma. Oncogene 15: 2233- 2239, 1997.

GAM104 355 SFPQ Patton, J. G.; Porro, E. B.; Galceran, J.; Tempst, P.; Nadal- Ginard,B.: 3 B c Cloning and characterization of PSF, a novel pre- mRNA splicingfactor. Genes Dev. 7: 393- 406, 1993.

GAM105 318 COL19A1 Gerecke, D. R.; Olson, P. F.; Koch, M.; Knoll, J. H. M.; Taylor,R.; Hudson, 3 C c D. L.; Champliaud, M.- F.; Olsen, B. R.; Burgeson, R. E.: Complete primary structure of two splice variants of collagen XII,and assignment of alpha-

1(XII) collagen (COL12A1), alpha- 1(IX) collagen(COL9A1), and alpha- 1(XIX) collagen (COL19A1) to human chromosome6q12- q13. Genomics 41: 236- 242, 1997.

GAM105 318 COL19A1 Inoguchi, K.; Yoshioka, H.; Khaleduzzaman, M.; Ninomiya, Y.: ThemRNA for 3 C c alpha- 1(XIX) collagen chain, a new member of FACITs, containsa long unusual 3- prime untranslated region and displays many uniquesplicing variants. J. Biochem. 117: 137- 146, 1995.

GAM105 318 COL19A1 Khaleduzzaman, M.; Sumiyoshi, H.; Ueki, Y.; Inoguchi, K.; Ninomiya,Y.; 3 C c Yoshioka, H.: Structure of the human type XIX collagen (COL19A1)gene, which suggests it has arisen from an ancestor gene of the FACITfamily. Genomics 45: 304- 312, 1997.

GAM105 318 COL19A1 Myers, J. C.; Sun, M. J.; D'Ippolito, J. A.; Jabs, E. W.; Neilson,E. G.; 3 C c Dion, A. S.: Human cDNA clones transcribed from an unusuallyhigh molecular weight RNA encode a new collagen chain. Gene 123:211- 217, 1993.

GAM105 318 COL19A1 Yoshioka, H.; Zhang, H.; Ramirez, F.; Mattei, M.- G.; Moradi- Ameli,M.; van 3 C c der Rest, M.; Gordon, M. K.: Synteny between the loci fora novel FACIT- like collagen (D6S228E) and alpha 1(IX) collagen (COL9A1)on 6q12- q14 in humans. Genomics 13: 884- 886, 1992.

GAM105 318 EYA3 Abdelhak, S.; Kalatzis, V.; Heilig, R.; Compain, S.; Samson, D.;Vincent, C.; 3 C c Weil, D.; Cruaud, C.; Sahly, I.; Leibovici, M.; Bitner- Glindzicz,M.; Francis, M.; Lacombe, D.; Vigneron, J.; Charachon, R.; Boven,K.; Bedbeder, P.; Van Regemorter, N.; Weissenbach, J.; Petit, C.:A human homologue of the Drosophila eyes absent gene underlies branchio- oto- renal(BOR) syndrome and identifies a novel gene family. Nature Genet. 15:157- 164, 1997.

GAM105 318 EYA3 Xu, P.- X.; Cheng, J.; Epstein, J. A.; Maas, R. L.: Mouse Eya genesare 3 C c expressed during limb tendon development and encode a transcriptionalactivation function. Proc. Nat. Acad. Sci. 94: 11974- 11979, 1997.

GAM105 318 EYA3 Zimmerman, J. E.; Bui, Q. T.; Steingrimsson, E.; Nagle, D. L.;Fu, W.; Genin, 3 C c A.; Spinner, N. B.; Copeland, N. G.; Jenkins, N. A.;Bucan, M.; Bonini, N. M.: Cloning and characterization of two vertebratehomologs of the Drosophila eyes absent gene. Genome Res. 7: 128- 141,1997.

GAM105 318 SLC12A7 Boettger, T.; Hubner, C. A.; Maler, H.; Rust, M. B.; Beck, F. X.;Jentsch, T. 3 C c J.: Deafness and renal tubular acidosis in mice lackingthe K- Cl co-transporter Kcc4. Nature 416: 874- 878, 2002.

GAM105 318 SLC12A7 Mount, D. B.; Mercado, A.; Song, L.; Xu, J.; George, A. L., Jr.;Delpire, E.; 3 C c Gamba, G.: Cloning and characterization of KCC3 andKCC4, new members of the cation- chloride cotransporter gene family. J.Biol. Chem. 274: 16355- 16362, 1999.

GAM106 231 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome 1 B c assignment by polymerase chain reaction techniques: assignmentof the oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990.

GAM106 231 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator 1 B c of the hair growth cycle: evidence from targeted and spontaneousmutations. Cell 78: 1017- 1025, 1994.

GAM106 231 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 1 B c mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM106 231 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; 1 B c Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and the bcl.1 locus are contained within one megabase in bandq13 of chromosome

11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988.

GAM106 231 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8: 3487- 3495, 1988. 1 B c

GAM106 231 GJA4 Haefliger, J.- A.; Bruzzone, R.; Jenkins, N. A.; Gilbert, D. J.;Copeland, N. G.; Paul, D. L.: Four novel members of the connexinfamily of gap junction proteins: molecular cloning, expression, andchromosome mapping. J. Biol. Chem. 267: 2057- 2064, 1992. 1 B c

GAM106 231 GJA4 Reed, K. E.; Westphale, E. M.; Larson, D. M.; Wang, H.- Z.; Veenstra,R. D.; Beyer, E. C.: Molecular cloning and functional expressionof human connexin37, an endothelial cell gap junction protein. J.Clin. Invest. 91: 997- 1004, 1993. 1 B c

GAM106 231 GJA4 Van Camp, G.; Coucke, P.; Speleman, F.; Van Roy, N.; Beyer, E.C.; Oostra, B. A.; Willems, P. J.: The gene for human gap junctionprotein connexin37 (GJA4) maps to chromosome 1p35.1, in the vicinityof D1S195. Genomics 30: 402- 403, 1995. 1 B c

GAM106 231 GJA4 Willecke, K.; Jungbluth, S.; Dahl, E.; Hennemann, H.; Heynkes,R.; Grzeschik, K.- H.: Six genes of the human connexin gene familycoding for gap junctional proteins are assigned to four differenthuman chromosomes. Europ. J. Cell Biol. 53: 275- 280, 1990. 1 B c

GAM106 231 GRPR Bolton, P.; Powell, J.; Rutter, M.; Buckle, V.; Yates, J. R. W.;Ishikawa- Brush, Y.; Monaco, A. P.: Autism, mental retardation, multipleexostoses and short stature in a female with 46,X,t(X;8)(p22.13;q22.1). Psychiat.Genet. 5: 51- 55, 1995. 1 B c

GAM106 231 GRPR Ishikawa- Brush, Y.; Powell, J. F.; Bolton, P.; Miller, A. P.; Francis,F.; Willard, H. F.; Lehrach, H.; Monaco, A. P.: Autism and multipleexostoses associated with an X;8 translocation occurring within theGRPR gene and 3-prime to the SDC2 gene. Hum. Molec. Genet. 6: 1241- 1250,1997. 1 B c

GAM106 231 GRPR Maslen, G. L.; Boyd, Y.: Comparative mapping of the Grpr locuson the X chromosomes of man and mouse. Genomics 17: 106- 109, 1993. 1 B c

GAM106 231 GRPR Schantz, L. J.; Naylor, S. L.; Giladi, E.; Spindel, E. R.: Assignmentof the GRP receptor gene to the human X chromosome. (Abstract) Cytogenet.Cell Genet. 58: 2085- 2086, 1991. 1 B c

GAM106 231 GRPR Shiraishi, M.; Alitalo, T.; Sekiya, T.: The chromosomal organizationof the human endogenous retrovirus- like sequence HERV- H: clusteringof the HERV- H sequences in a 300- kb region close to the GRPR locuson the X chromosome. DNA Res. 3: 425- 429, 1996. 1 B c

GAM106 231 GRPR Shriver, S. P.; Bourdeau, H. A.; Gubish, C. T.; Tirpak, D. L.;Davis, A. L. G.; Luketich, J. D.; Siegfried, J. M.: Sex- specificexpression of gastrin-releasing peptide receptor: relationship tosmoking history and risk of lung cancer. J. Nat. Cancer Inst. 92:24- 33, 2000. 1 B c

GAM106 231 GRPR Spindel, E. R.; Giladi, E.; Brehm, P.; Goodman, R. H.; Segerson,T. P.: Cloning and functional characterization of a complementaryDNA encoding the murine fibroblast bombesin/gastrin- releasing peptidereceptor. Molec. Endocr. 4: 1956- 1963, 1990. 1 B c

GAM106 231 ITGA9 Daigo, Y.; Isomura, M.; Nishiwaki, T.; Tamari, M.; Ishikawa, S.;Kai, M.; Murata, Y.; Takeuchi, K.; Yamane, Y.; Hayashi, R.; Minami,M.; Fujino, M. A.; Hojo, Y.; Uchiyama, I.; Takagi, T.; Nakamura, Y.: Characterization of a 1200- kb genomic segment of chromosome 3p22- p21.3. DNARes. 6: 37- 44, 1999. 1 B c

GAM106 231 ITGA9 Erle, D. J.; Sheppard, D.; Breuss, J.; Ruegg, C.; Pytela, R.:Novel integrin 1 B c

alpha and beta subunit cDNAs identified in airway epithelialcells and lung leukocytes using the polymerase chain reaction. Am.J. Resp. Cell Molec. Biol. 5: 170- 177, 1991.

GAM106 231 ITGA9 Hibi, K.; Yamakawa, K.; Ueda, R.; Horio, Y.; Murata, Y.; Tamari,M.; Uchida, K.; Takahashi, T.; Nakamura, Y.; Takahashi, T.: Aberrantupregulation of a novel integrin alpha subunit gene at 3p21.3 in smallcell lung cancer. Oncogene 9: 611- 619, 1994. 1 B c

GAM106 231 ITGA9 Palmer, E. L.; Ruegg, C.; Ferrando, R.; Pytela, R.; Sheppard, D.: Sequence and tissue distribution of the integrin alpha- 9 subunit,a novel partner of beta- 1 that is widely distributed in epitheliaand muscle. J. Cell Biol. 123: 1289- 1297, 1993. 1 B c

GAM106 231 ITGA9 Yamakawa, K.; Takahashi, T.; Horio, Y.; Murata, Y.; Takahashi,E.; Hibi, K.; Yokoyama, S.; Ueda, R.; Takahashi, T.; Nakamura, Y.: Frequent homozygous deletions in lung cancer cell lines detectedby a DNA marker located at 3p21.3- p22. Oncogene 8: 327- 330, 1993. 1 B c

GAM106 231 PTGS2 Erkinheimo, T.- L.; Saukkonen, K.; Narko, K.; Jalkanen, J.; Ylikorkala,O.; Ristimaki, A.: Expression of cyclooxygenase- 2 and prostanoidreceptors by human myometrium. J. Clin. Endocr. Metab. 85: 3468- 3475,2000. 1 B c

GAM106 231 PTGS2 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.; Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999. 1 B c

GAM106 231 PTGS2 Hla, T.; Neilson, K.: Human cyclooxygenase- 2 cDNA. Proc. Nat.Acad. Sci. 89: 7384- 7388, 1992. 1 B c

GAM106 231 PTGS2 Jones, D. A.; Carlton, D. P.; McIntyre, T. M.; Zimmerman, G. A.;Prescott, S. M.: Molecular cloning of human prostaglandin endoperoxidesynthase type II and demonstration of expression in response to cytokines. J.Biol. Chem. 268: 9049- 9054, 1993. 1 B c

GAM106 231 PTGS2 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.: Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2 in the humanfetal and adult male reproductive tracts. J. Clin. Endocr. Metab. 85:3436- 3441, 2000. 1 B c

GAM106 231 PTGS2 Kraemer, S. A.; Meade, E. A.; DeWitt, D. L.: Prostaglandin endoperoxidesynthase gene structure: identification of the transcriptional startsite and 5- prime- flanking regulatory sequences. Arch. Biochem. Biophys. 293:391- 400, 1992. 1 B c

GAM106 231 PTGS2 Lassus, P.; Wolff, H.; Andersson, S.: Cyclooxygenase- 2 in humanperinatal lung. Pediat. Res. 47: 602- 605, 2000. 1 B c

GAM106 231 PTGS2 Lim, H.; Paria, B. C.; Das, S. K.; Dinchuk, J. E.; Langenbach,R.; Trzaskos, J. M.; Dey, S. K.: Multiple female reproductive failuresin cyclooxygenase 2- deficient mice. Cell 91: 197- 208, 1997. 1 B c

GAM106 231 PTGS2 Loftin, C. D.; Trivedi, D. B.; Tiano, H. F.; Clark, J. A.; Lee,C. A.; Epstein, J. A.; Morham, S. G.; Breyer, M. D.; Nguyen, M.; Hawkins,B. M.; Goulet, J. L.; Smithies, O.; Koller, B. H.; Langenbach, R.: Failure of ductus arteriosus closure and remodeling in neonatalmice deficient in cyclooxygenase- 1 and cyclooxgenase- 2. Proc. Nat.Acad. Sci. 98: 1059- 1064, 2001. 1 B c

GAM106 231 PTGS2 Macchia, L.; Di Paola, R.; Guerrese, M.- C.; Chiechi, L. M.; Tursi,A.; Caiaffa, M. F.; Haeggstrom, J. Z.: Expression of prostaglandinendoperoxide H 1 B c

synthase 1 and 2 in human placenta at term. Biochem.Biophys. Res. Commun. 233: 496- 501, 1997.

GAM106 231 PTGS2 Morham, S. G.; Langenbach, R.; Loftin, C. D.; Tiano, H. F.; Vouloumanos,N.; Jennette, J. C.; Mahler, J. F.; Kluckman, K. D.; Ledford, A.;Lee, C. A.; Smithies, O.: Prostaglandin synthase 2 gene disruptioncauses severe renal pathology in the mouse. Cell 83: 473- 482, 1995. 1 B c

GAM106 231 PTGS2 Neufang, G.; Furstenberger, G.; Heidt, M.; Marks, F.; Muller- Decker,K.: Abnormal differentiation of epidermis in transgenic mice constitutivelyexpressing cyclooxygenase- 2 in skin. Proc. Nat. Acad. Sci. 98: 7629- 7634,2001. 1 B c

GAM106 231 PTGS2 O'Banion, M. K.; Sadowski, H. B.; Winn, V.; Young, D. A.: A serum- and glucocorticoid- regulated 4- kilobase mRNA encodes a cyclooxygenase- relatedprotein. J. Biol. Chem. 266: 23261- 23267, 1991. 1 B c

GAM106 231 PTGS2 O'Banion, M. K.; Winn, V. D.; Young, D. A.: cDNA cloning andfunctional activity of a glucocorticoid- regulated inflammatory cyclooxygenase. Proc.Nat. Acad. Sci. 89: 4888- 4892, 1992. 1 B c

GAM106 231 PTGS2 Oshima, M.; Dinchuk, J. E.; Kargman, S. L.; Oshima, H.; Hancock,B.; Kwong, E.; Trzaskos, J. M.; Evans, J. F.; Taketo, M. M.: Suppressionof intestinal polyposis in Apc(delta- 716) knockout mice by inhibitionof cyclooxygenase 2 (COX- 2). Cell 87: 803- 809, 1996. 1 B c

GAM106 231 PTGS2 Sales, K. J.; Katz, A. A.; Davis, M.; Hinz, S.; Soeters, R. P.;Hofmeyr, M. D.; Millar, R. P.; Jabbour, H. N.: Cyclooxygenase- 2 expressionand prostaglandin E2 synthesis are up- regulated in carcinomas of thecervix: a possible autocrine/paracrine regulation of neoplastic cellfunction via EP2/EP4 receptors. J. Clin. Endocr. Metab. 86: 2243- 2249,2001. 1 B c

GAM106 231 PTGS2 Salmenkivi, K.; Haglund, C.; Ristimaki, A.; Arola, J.; Heikkila,P.: Increased expression of cyclooxygenase- 2 in malignant pheochromocytomas. J.Clin. Endocr. Metab. 86: 5615- 5619, 2001. 1 B c

GAM106 231 PTGS2 Samad, T. A.; Moore, K. A.; Sapirstein, A.; Billet, S.; Allchorne,A.; Poole, S.; Bonventre, J. V.; Woolf, C. J.: Interleukin- 1- beta- mediatedinduction of Cox- 2 in the CNS contributes to inflammatory pain hypersensitivity. Nature 410:471- 475, 2001. 1 B c

GAM106 231 PTGS2 Swan, S. K.; Rudy, D. W.; Lasseter, K. C.; Ryan, C. F.; Buechel,K. L.; Lambrecht, L. J.; Pinto, M. B.; Dilzer, S. C.; Obrda, O.; Sundblad,K. J.; Gumbs, C. P.; Ebel, D. L.; Quan, H.; Larson, P. J.; Schwartz,J. I.; Musliner, T. A.; Gertz, B. J.; Brater, D. C.; Yao, S.- L.:Effect of cyclooxygenase- 2 inhibition on renal function in elderlypersons receiving a low- salt diet: a randomized controlled trial. Ann.Intern. Med. 133: 1- 9, 2000. 1 B c

GAM106 231 PTGS2 Tay, A.; Squire, J. A.; Goldberg, H.; Skorecki, K.: Assignmentof the human prostaglandin- endoperoxide synthase 2 (PTGS2) gene to1q25 by fluorescence in situ hybridization. Genomics 23: 718- 719,1994. 1 B c

GAM106 231 PTGS2 Tazawa, R.; Xu, X.- M.; Wu, K. K.; Wang, L.- H.: Characterizationof the genomic structure, chromosomal location and promoter of humanprostaglandin H synthase- 2 gene. Biochem. Biophys. Res. Commun. 203:190- 199, 1994. 1 B c

GAM106 231 PTGS2 Tsujii, M.; DuBois, R. N.: Alterations in cellular adhesion andapoptosis in epithelial cells overexpressing prostaglandin endoperoxidesynthase 2. Cell 83: 493- 501, 1995. 1 B c

GAM106 231 PTGS2 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93: 1 B c

705- 716, 1998.

GAM106 231 PTGS2 Zhou, X.- L.; Lei, Z. M.; Rao, C. V.: Treatment of human endometrialgland 1 B c
epithelial cells with chorionic gonadotropin/luteinizing hormoneincreases
the expression of the cyclooxygenase- 2 gene. J. Clin. Endocr.Metab. 84:
3364- 3377, 1999.

GAM106 231 S100B Allore, R. J.; Friend, W. C.; O'Hanlon, D.; Neilson, K. M.; Baumal,R.; Dunn, 1 B c
R. J.; Marks, A.: Cloning and expression of the human S100- betagene. J.
Biol. Chem. 265: 15537- 15543, 1990.

GAM106 231 S100B Allore, R.; O'Hanlon, D.; Price, R.; Neilson, K.; Willard, H. F.;Cox, D. R.; 1 B c
Marks, A.; Dunn, R. J.: Gene encoding the beta- subunitof S100 protein is on
chromosome 21: implications for Down syndrome. Science 239:1311- 1313, 1988.

GAM106 231 S100B Duncan, A. M. V.; Higgins, J.; Dunn, R. J.; Allore, R.; Marks,A.: Refined 1 B c
sublocalization of the human gene encoding the beta subunitof the S100
protein (S100B) and confirmation of a subtle t(9;21) translocationusing in
situ hybridization. Cytogenet. Cell Genet. 50: 234- 235,1989.

GAM106 231 S100B Morii, K.; Tanaka, R.; Takahashi, Y.; Minoshima, S.; Fukuyama,R.; Shimizu, 1 B c
N.; Kuwano, R.: Structure and chromosome assignmentof human S100 alpha and
beta subunit genes. Biochem. Biophys. Res.Commun. 175: 185- 191, 1991.

GAM106 231 S100B Reeves, R. H.; Yao, J.; Crowley, M. R.; Buck, S.; Zhang, X.; Yarowsky,P.; 1 B c
Gearhart, J. D.; Hilt, D. C.: Astrocytosis and axonal proliferationin the
hippocampus of S100b transgenic mice. Proc. Nat. Acad. Sci. 91:5359- 5363,
1994.

GAM106 231 S100B Shimizu, A.; Sakai, Y.; Ohno, K.; Masaki, S.; Kuwano, R.; Takahashi,Y.; 1 B c
Miyashita, N.; Watanabe, T.: A molecular genetic linkage mapof mouse
chromosome 10, including the Myb, S100b, Pah, Sl, and Ifggenes. Biochem.
Genet. 30: 529- 535, 1992.

GAM106 231 TLL1 Clark, T. G.; Conway, S. J.; Scott, I. C.; Labosky, P. A.; Winnier,G.; 1 B c
Bundy, J.; Hogan, B. L. M.; Greenspan, D. S.: The mammalian Tolloid- like1
gene, Tll1, is necessary for normal septation and positioning ofthe heart.
Development 126: 126:- 2631- 2642, 1999.

GAM106 231 TLL1 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; 1 B c
Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.;
Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases,
including novel family member mammalian Tolloid- like2, have differential
enzymatic activities and distributions of expressionrelevant to patterning
and skeletogenesis. Dev. Biol. 213: 283- 300,1999.

GAM106 231 TLL1 Scott, I. C.; Clark, T. G.; Takahara, K.; Hoffman, G. G.; Eddy,R. L.; Haley, 1 B c
L. L.; Shows, T. B.; Greenspan, D. S.: Assignment ofTLL1 and TLL2, which
encode human BMP- 1/tolloid- related metalloproteases,to chromosomes 4q32-
q33 and 10q23- q24 and assignment of murine Tll2to chromosome 19. Cytogenet.
Cell Genet. 86: 64- 65, 1999.

GAM106 231 TLL1 Takahara, K.; Brevard, R.; Hoffman, G. G.; Suzuki, N.; Greenspan,D. S.: 1 B c
Characterization of a novel gene product (mammalian tolloid- like)with high
sequence similarity to mammalian tolloid/bone morphogeneticprotein- 1.
Genomics 34: 157- 165, 1996.

GAM107 341 DLX4 Morasso, M. I.; Yonescu, R.; Griffin, C. A.; Sargent, T. D.: Localizationof 3 C c
human DLX8 to chromosome 17q21.3- q22 by fluorescence in situ hybridization.
MammalianGenome 8: 302- 303, 1997.

GAM107 341 DLX4 Nakamura, S.; Stock, D. W.; Wydner, K. L.; Bollekens, J. A.; Takeshita,K.; 3 C c
Nagai, B. M.; Chiba, S.; Kitamura, T.; Freeland, T. M.; Zhao,Z.; Minowada,

J.; Lawrence, J. B.; Weiss, K. M.; Ruddle, F. H.: Genomicanalysis of a new mammalian distal- less gene: Dlx7. Genomics 38:314- 324, 1996.

GAM107 341 DLX4 Quinn, L. M.; Johnson, B. V.; Nicholl, J.; Sutherland, G. R.; Kalionis,B.: 3 C c Isolation and identification of homeobox genes from the humanplacenta including a novel member of the Distal- less family, DLX4. Gene 187:55- 61, 1997.

GAM109 290 ADAM10 Hattori, M.; Osterfield, M.; Flanagan, J. G.: Regulated cleavageof a 3 C c contact- mediated axon repellent. Science 289: 1360- 1365, 2000.

GAM109 290 ADAM10 Lunn, C. A.; Fan, X.; Dalie, B.; Miller, K.; Zavodny, P. J.; Narula,S. K.; 3 C c Lundell, D.: Purification of ADAM 10 from bovine spleen asa TNFalpha convertase. FEBS Lett. 400: 333- 335, 1997.

GAM109 290 ADAM10 Wolfsberg, T. G.; Primakoff, P.; Myles, D. G.; White, J. M.: ADAM,a novel 3 C c family of membrane proteins containing a disintegrin and metalloproteasedomain: multipotential functions in cell- cell and cell-matrix interactions. J.Cell Biol. 131: 275- 278, 1995.

GAM109 290 ADAM10 Yamazaki, K.; Mizui, Y.; Tanaka, I.: Radiation hybrid mappingof human ADAM10 3 C c

gene to chromosome 15. Genomics 45: 457- 459, 1997.

GAM109 290 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 C c member of a multigene family. Genomics 52: 332- 341, 1998.

GAM109 290 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 C c new member of the MTG8/ETO gene family, maps on 20q11region and is deleted in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM109 290 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 C c Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic fusion protein forms a complex with a novel member of theMTG8(ETO/CDR) family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM111 311 MGAM Naim, H. Y.; Sterchi, E. E.; Lentze, M. J.: Structure, biosynthesis,and 3 C c glycosylation of human small intestinal maltase- glucoamylase. J.Biol. Chem. 263: 19709- 19717, 1988.

GAM111 311 MGAM Nichols, B. L.; Eldering, J.; Avery, S.; Hahn, D.; Quaroni, A.;Sterchi, E.: 3 C c Human small intestinal maltase- glucoamylase cDNA cloning:homology to sucrase- isomaltase. J. Biol. Chem. 273: 3076- 3081, 1998.

GAM111 311 MGAM Schuler, G. D.; Boguski, M. S.; Stewart, E. A.; Stein, L. D.; Gyapay,G.; 3 C c Rice, K.; White, R. E.; Rodriguez- Tome, P.; Aggarwal, A.; Bajorek,E.; Bentolila, S.; Birren, B. B.; Butler, A.; Castle, A. B.; Chiannilkulchai,N.; Chu, A.; Clee, C.; Cowles, S.; Day, P. J. R.; Dibling, T.; and84 others: A gene map of the human genome. Science 274: 540- 546,1996.

GAM111 311 PPARA Aljada, A.; Ghanim, H.; Friedman, J.; Garg, R.; Mohanty, P.; Dandona,P.: 3 C c Troglitazone reduces the expression of PPAR- gamma while stimulatingthat of PPAR- alpha in mononuclear cells in obese subjects. J. Clin.Endocr. Metab. 86: 3130- 3133, 2001.

GAM111 311 PPARA Costet, P.; Legendre, C.; More, J.; Edgar, A.; Galtier, P.; Pineau,T.: 3 C c Peroxisome proliferator- activated receptor alpha- isoform deficiencyleads to progressive dyslipidemia with sexually dimorphic obesityand steatosis. J. Biol. Chem. 273: 29577- 29585, 1998.

GAM111 311 PPARA Djouadi, F.; Weinheimer, C. J.; Saffitz, J. E.; Pitchford, C.;Bastin, J.; 3 C c Gonzalez, F. J.; Kelly, D. P.: A gender- related defectin lipid metabolism and glucose homeostasis in peroxisome proliferator- activatedreceptor alpha-deficient mice. J. Clin. Invest. 102: 1083- 1091,1998.

GAM111 311 PPARA Kersten, S.; Desvergne, B.; Wahli, W.: Roles of PPARs in healthand disease. 3 C c
Nature 405: 421- 424, 2000.

GAM111 311 PPARA Kersten, S.; Seydoux, J.; Peters, J. M.; Gonzalez, F. J.; Desvergne,B.; 3 C c
Wahli, W.: Peroxisome proliferator- activated receptor alpha mediatesthe
adaptive response to fasting. J. Clin. Invest. 103: 1489- 1498,1999.

GAM111 311 PPARA Lee, S. S.- T.; Pineau, T.; Drago, J.; Lee, E. J.; Owens, J. W.;Kroetz, D. 3 C c
L.; Fernandez- Salguero, P. M.; Westphal, H.; Gonzalez,F. J.: Targeted
disruption of the alpha isoform of the peroxisomeproliferator- activated
receptor gene in mice results in abolishmentof the pleiotropic effects of
peroxisome proliferators. Molec. Cell.Biol. 15: 3012- 3022, 1995.

GAM111 311 PPARA Lee, Y.; Yu, X.; Gonzales, F.; Mangelsdorf, D. J.; Wang, M.- Y.;Richardson, 3 C c
C.; Witters, L. A.; Unger, R. H.: PPAR- alpha is necessaryfor the lipopenic
action of hyperleptinemia on white adipose and livertissue. Proc. Nat. Acad.
Sci. 99: 11848- 11853, 2002.

GAM111 311 PPARA Leone, T. C.; Weinheimer, C. J.; Kelly, D. P.: A critical rolefor the 3 C c
peroxisome proliferator- activated receptor alpha (PPAR- alpha)in the
cellular fasting response: the PPAR- alpha- null mouse as a modelof fatty
acid oxidation disorders. Proc. Nat. Acad. Sci. 96: 7473- 7478,1999.

GAM111 311 PPARA Michalik, L.; Desvergne, B.; Tan, N. S.; Basu- Modak, S.; Escher,P.; 3 C c
Rieusset, J.; Peters, J. M.; Kaya, G.; Gonzalez, F. J.; Zakany,J.; Metzger,
D.; Chambon, P.; Duboule, D.; Wahli, W.: Impaired skinwound healing in
peroxisome proliferator- activated receptor (PPAR)- alphaand PPAR- beta
mutant mice. J. Cell Biol. 154: 799- 814, 2001.

GAM111 311 PPARA Sher, T.; Yi, H.- F.; McBride, O. W.; Gonzalez, F. J.: cDNA 3 C c
cloning,chromosomal mapping, and functional characterization of the
humanperoxisome proliferator activated receptor. Biochemistry 32: 5598-
5604,1993.

GAM111 311 PPARA Xu, H. E.; Stanley, T. B.; Montana, V. G.; Lambert, M. H.; Shearer,B. G.; 3 C c
Cobb, J. E.; McKee, D. D.; Galardi, C. M.; Plunket, K. D.;Nolte, R. T.;
Parks, D. J.; Moore, J. T.; Kliewer, S. A.; Willson,T. M.; Stimmel, J. B.:
Structural basis for antagonist- mediated recruitmentof nuclear co-
repressors by PPAR- alpha. Nature 415: 813- 817, 2002.

GAM112 263 CDX2 Chawengsaksophak, K.; James, R.; Hammond, V. E.; Kontgen, F.; Beck,F.: 3 B c
Homeosis and intestinal tumours in Cdx2 mutant mice. Nature 386:84- 87,
1997.

GAM112 263 CDX2 Drummond, F.; Putt, W.; Fox, M.; Edwards, Y. H.: Cloning and 3 B c
chromosomeassignment of the human CDX2 gene. Ann. Hum. Genet. 61: 393-
400,1997.

GAM112 263 CDX2 German, M. S.; Wang, J.; Fernald, A. A.; Espinosa, R., III; LeBeau, M. M.; 3 B c
Bell, G. I.: Localization of the genes encoding twotranscription factors,
LMX1 and CDX3, regulating insulin gene expressionto human chromosomes 1 and
13. Genomics 24: 403- 404, 1994.

GAM112 263 CDX2 Woodford- Richens, K. L.; Halford, S.; Rowan, A.; Bevan, S.; Aaltonen,L. A.; 3 B c
Wasan, H.; Bicknell, D.; Bodmer, W. F.; Houlston, R. S.; Tomlinson,I. P. M.:
CDX2 mutations do not account for juvenile polyposis orPeutz- Jeghers
syndrome and occur infrequently in sporadic colorectalcancers. Brit. J.
Cancer 84: 1314- 1316, 2001.

GAM112 263 CYP7A1 Agellon, L. B.; Drover, V. A. B.; Cheema, S. K.; Gbaguidi, G. F.;Walsh, A.: 3 B c
Dietary cholesterol fails to stimulate the human cholesterol7- alpha-
hydroxylase gene (CYP7A1) in transgenic mice. J. Biol. Chem. 277:20131-

20134, 2002.

GAM112 263 CYP7A1 Angelin, B.; Einarsson, K.; Hellstrom, K.; Leijd, B.: Bile acidkinetics in relation to endogenous triglyceride metabolism in varioustypes of hyperlipoproteinemia. J. Lipid Res. 19: 1004- 1016, 1978. 3 B c

GAM112 263 CYP7A1 Angelin, B.; Hershon, K. S.; Brunzell, J. D.: Bile acid metabolismin hereditary forms of hypertriglyceridemia: evidence for an increasedsynthesis rate in monogenic familial hypertriglyceridemia. Proc.Nat. Acad. Sci. 84: 5434- 5438, 1987. 3 B c

GAM112 263 CYP7A1 Cohen, J. C.; Cali, J. J.; Jelinek, D. F.; Mehrabian, M.; Sparkes,R. S.; Lusis, A. J.; Russell, D. W.; Hobbs, H. H.: Cloning of thehuman cholesterol 7- alpha- hydroxylase gene (CYP7) and localizationto chromosome 8q11- q12. Genomics 14: 153- 161, 1992. 3 B c

GAM112 263 CYP7A1 Drover, V. A. B.; Wong, N. C. W.; Agellon, L. B.: A distinct thyroidhormone response element mediates repression of the human cholesterol7- alpha- hydroxylase (CYP7A1) gene promoter. Molec. Endocr. 16: 14- 23,2002. 3 B c

GAM112 263 CYP7A1 Goodwin, B.; Jones, S. A.; Price, R. R.; Watson, M. A.; McKee,D. D.; Moore, L. B.; Galardi, C.; Wilson, J. G.; Lewis, M. C.; Roth,M. E.; Maloney, P. R.; Willson, T. M.; Kliewer, S. A.: A regulatorycascade of the nuclear receptors FXR, SHP- 1, and LRH- 1 represses bileacid biosynthesis. Molec. Cell 6: 517- 526, 2000. 3 B c

GAM112 263 CYP7A1 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000. 3 B c

GAM112 263 CYP7A1 Molowa, D. T.; Chen, W. S.; Cimis, G. M.; Tan, C. P.: Transcriptionalregulation of the human cholesterol 7 alpha- hydroxylase gene. Biochemistry 31:2539- 2544, 1992. 3 B c

GAM112 263 CYP7A1 Nitta, M.; Ku, S.; Brown, C.; Okamoto, A. Y.; Shan, B.: CPF: anorphan nuclear receptor that regulates liver- specific expression ofthe human cholesterol 7- alpha- hydroxylase gene. Proc. Nat. Acad.Sci. 96: 6660- 6665, 1999. 3 B c

GAM112 263 CYP7A1 Noshiro, M.; Okuda, K.: Molecular cloning and sequence analysisof cDNA encoding human cholesterol 7 alpha- hydroxylase. FEBS Lett. 268:137- 140, 1990. 3 B c

GAM112 263 CYP7A1 Paumgartner, G.; Sauerbruch, T.: Gallstones: pathogenesis. Lancet 338:1117- 1121, 1991. 3 B c

GAM112 263 CYP7A1 Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers. Science 289: 1524- 1529, 2000. 3 B c

GAM112 263 CYP7A1 Wang, J.; Freeman, D. J.; Grundy, S. M.; Levine, D. M.; Guerra,R.; Cohen, J. C.: Linkage between cholesterol 7- alpha- hydroxylaseand high plasma low- density lipoprotein cholesterol concentrations. J.Clin. Invest. 101: 1283- 1291, 1998. 3 B c

GAM112 263 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2 in the allergic response. Nature 412: 186- 190,2001. 3 B c

GAM112 263 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998. 3 B c

GAM112 263 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; 3 B c
Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab-
family adapter proteins act downstream of cytokine and growthfactor
receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999.

GAM112 263 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH 3 B c
mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell
Genet. 94: 39- 42, 2001.

GAM112 263 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology 3 B c
domain- containing adapter protein, acts to uncouple signalingfrom ERK
kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999.

GAM112 263 PLAG1 Astrom, A.- K.; Voz, M. L.; Kas, K.; Roijer, E.; Wedell, B.; Mandahl,N.; Van 3 B c
de Ven, W.; Mark, J.; Stenman, G.: Conserved mechanism ofPLAG1 activation in
salivary gland tumors with and without chromosome8q12 abnormalities:
identification of SII as a new fusion partnergene. Cancer Res. 59: 918- 923,
1999.

GAM112 263 PLAG1 Kas, K.; Roijer, E.; Voz, M.; Meyen, E.; Stenman, G.; Van de Ven,W. J. M.: A 3 B c
2- Mb YAC contig and physical map covering the chromosome8q12 breakpoint
cluster region in pleomorphic adenomas of the salivaryglands. Genomics 43:
349- 358, 1997.

GAM112 263 PLAG1 Kas, K.; Voz, M. L.; Roijer, E.; Astrom, A.- K.; Meyen, E.; Stenman,G.; Van 3 B c
de Ven, W. J. M.: Promoter swapping between the genes fora novel zinc finger
protein and beta- catenin in pleiomorphic adenomaswith t(3;8)(p21;q12)
translocations. Nature Genet. 15: 170- 174,1997.

GAM114 288 ATP10C Cattanach, B. M.; Barr, J. A.; Beechey, C. V.; Martin, J.; Noebels,J.; 3 C c
Jones, J.: A candidate model for Angelman syndrome in the mouse.
MammalianGenome 8: 472- 478, 1997.

GAM114 288 ATP10C Dhar, M.; Webb, L. S.; Smith, L.; Hauser, L.; Johnson, D.; West,D. B.: A 3 C c
novel ATPase on mouse chromosome 7 is a candidate gene forincreased body
fat. Physiol. Genomics 4: 93- 100, 2000.

GAM114 288 ATP10C Gillessen- Kaesbach, G.; Demuth, S.; Thiele, H.; Theile, U.; Lich,C.; 3 C c
Horsthemke, B.: A previously unrecognised phenotype characterisedby obesity,
muscular hypotonia, and ability to speak in patients withAngelman syndrome
caused by an imprinting defect. Europ. J. Hum.Genet. 7: 638- 644, 1999.

GAM114 288 ATP10C Halleck, M. S.; Lawler, J. F., Jr.; Blackshaw, S.; Gao, L.; Nagarajan,P.; 3 C c
Hacker, C.; Pyle, S.; Newman, J. T.; Nakanishi, Y.; Ando, H.;Weinstock, D.;
Williamson, P.; Schlegel, R. A.: Differential expressionof putative
transbilayer amphipath transporters. Physiol. Genomics 1:139- 150, 1999.

GAM114 288 ATP10C Herzing, L. B. K.; Kim, S.- J.; Cook, E. H., Jr.; Ledbetter, D.H.: The human 3 C c
aminophospholipid- transporting ATPase gene ATP10C mapsadjacent to UBE3A and
exhibits similar imprinted expression. Am.J. Hum. Genet. 68: 1501- 1505,
2001.

GAM114 288 ATP10C Meguro, M.; Kashiwagi, A.; Mitsuya, K.; Nakao, M.; Kondo, I.; Saitoh,S.; 3 C c
Oshimura, M.: A novel maternally expressed gene, ATP10C, encodesa putative
aminophospholipid translocase associated with Angelmansyndrome. Nature
Genet. 28: 19- 20, 2001.

GAM114 288 ATP10C Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 C c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM116 301 ADK Boison, D.; Scheurer, L.; Zumsteg, V.; Rulicke, T.; Litynski, P.;Fowler, B.; 3 A c

Brandner, S.; Mohler, H.: Neonatal hepatic steatosisby disruption of the adenosine kinase gene. Proc. Nat. Acad. Sci. 99:6985- 6990, 2002.

GAM116 301 ADK Chan, T.- S.; Cregan, R. P.; Reardon, M. P.: Adenosine kinase asa new selective marker in somatic cell genetics: isolation of adenosinekinase-deficient mouse cell lines and human- mouse hybrid cell linescontaining adenosine kinase. Somat. Cell Genet. 4: 1- 12, 1978. 3 A c

GAM116 301 ADK Francke, U.; Thompson, L.: Regional mapping, by exclusion, ofadenosine kinase (ADK) on human chromosome 10 using the gene dosageapproach. (Abstract) Cytogenet. Cell Genet. 25: 156, 1979. 3 A c

GAM116 301 ADK Klobutcher, L. A.; Nichols, E. A.; Kucherlapati, R. S.; Ruddle,F. H.: Assignment of the gene for human adenosine kinase to chromosome10 using a somatic cell hybrid clone panel. Cytogenet. Cell Genet. 16:171- 174, 1976. 3 A c

GAM116 301 ADK McNally, T.; Helfrich, R. J.; Cowart, M.; Dorwin, S. A.; Meuth,J. L.; Idler, K. B.; Klute, K. A.; Simmer, R. L.; Kowaluk, E. A.;Halbert, D. N.: Cloning and expression of the adenosine kinase genefrom rat and human tissues. Biochem. Biophys. Res. Commun. 231:645- 650, 1997. 3 A c

GAM116 301 ADK Snyder, F. F.; Lin, C. C.; Rudd, N. L.; Shearer, J. E.; Heikkila,E. M.; Hoo, J. J.: A de novo case of trisomy 10p: gene dosage studiesof hexokinase, inorganic pyrophosphatase and adenosine kinase. Hum.Genet. 67: 187- 189, 1984. 3 A c

GAM116 301 ADK Spychala, J.; Datta, N. S.; Takabayashi, K.; Datta, M.; Fox, I.;Gribbin, T.; Mitchell, B.: Cloning of human adenosine kinase cDNA:sequenced similarity to microbial ribokinases and fructokinases, Proc.Nat. Acad. Sci. 93: 1232-1237, 1996. 3 A c

GAM116 301 ARNT2 Hirose, K.; Morita, M.; Ema, M.; Mimura, J.; Hamada, H.; Fujii,H.; Saijo, Y.; Gotoh, O.; Sogawa, K.; Fujii- Kuriyama, Y.: cDNA cloningand tissue-specific expression of a novel basic helix- loop- helix/PASfactor (Arnt2) with close sequence similarity to the aryl hydrocarbonreceptor nuclear translocator (Arnt). Molec. Cell. Biol. 16: 1706- 1713,1996. 3 A c

GAM116 301 ARNT2 Keith, B.; Adelman, D. M.; Simon, M. C.: Targeted mutation ofthe murine arylhydrocarbon receptor nuclear translocator 2 (Arnt2)gene reveals partial redundancy with Arnt. Proc. Nat. Acad. Sci. 98:6692- 6697, 2001. 3 A c

GAM116 301 ARNT2 Michaud, J. L.; DeRossi, C.; May, N. R.; Holdener, B. C.; Fan,C.- M.: ARNT2 acts as the dimerization partner of SIM1 for the developmentof the hypothalamus. Mech. Dev. 90: 253- 261, 2000. 3 A c

GAM116 301 ARNT2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 A c

GAM116 301 ATRN Duke- Cohan, J. S.; Gu, J.; McLaughlin, D. F.; Xu, Y.; Freeman,G. J.; Schlossman, S. F.: Attractin (DPPT- L), a member of the CUBfamily of cell adhesion and guidance proteins, is secreted by activatedhuman T lymphocytes and modulates immune cell interactions. Proc.Nat. Acad. Sci. 95: 11336-11341, 1998. 3 A c

GAM116 301 ATRN Gunn, T. M.; Miller, K. A.; He, L.; Hyman, R. W.; Davis, R. W.;Azarani, A.; Schlessman, S. F.; Duke- Cohan, J. S.; Barsh, G. S.:The mouse mahogany locus encodes a transmembrane form of human attractin. Nature 398:152- 156, 1999. 3 A c

GAM116 301 ATRN He, L.; Gunn, T. M.; Bouley, D. M.; Lu, X.- Y.; Watson, S. J.; Schlossman,S. F.; Duke- Cohan, J. S.; Barsh, G. S.: A biochemical function forattractin in 3 A c

agouti- induced pigmentation and obesity. Nature Genet. 27:40- 47, 2001.

GAM116 301 ATRN Nagle, D. L.; McGrail, S. H.; Vitale, J.; Woolf, E. A.; Dussault,B. J., Jr.; 3 A c
DiRocco, L.; Holmgren, L.; Montagno, J.; Bork, P.; Huszar,D.; Fairchild-
Huntress, V.; Ge, P.; Keilty, J.; Ebelling, C.; Baldini,L.; Gilchrist, J.;
Burr, P.; Carlson, G. A.; Moore, K. J.: The mahoganyprotein is a receptor
involved in suppression of obesity. Nature 398:148- 151, 1999.

GAM116 301 ATRN Tang, W.; Gunn, T. M.; McLaughlin, D. F.; Barsh, G. S.; Schlossman,S. F.; 3 A c
Duke- Cohan, J. S.: Secreted and membrane attractin resultfrom alternative
splicing of the human ATRN gene. Proc. Nat. Acad.Sci. 97: 6025- 6030, 2000.

GAM116 301 BCL6 Akasaka, T.; Miura, I.; Takahashi, N.; Akasaka, H.; Yonetani, N.;Ohno, H.; 3 A c
Fukuhara, S.; Okuma, M.: A recurring translocation, t(3;6)(q27;p21),in non-
Hodgkin's lymphoma results in replacement of the 5- prime regulatoryregion
of BCL6 with a novel H4 histone gene. Cancer Res. 57: 7- 12,1997.

GAM116 301 BCL6 Baron, B. W.; Nucifora, G.; McCabe, N.; Espinosa, R., III; Le Beau,M. M.; 3 A c
McKeithan, T. W.: Identification of the gene associated withthe recurring
chromosomal translocations t(3;14)(q27;q32) and t(3;22)(q27;q11)in B- cell
lymphomas. Proc. Nat. Acad. Sci. 90: 5262- 5266, 1993.

GAM116 301 BCL6 Capello, D.; Carbone, A.; Pastore, C.; Gloghini, A.; Saglio, G.;Gaidano, G.: 3 A c
Point mutations of the BCL- 6 gene in Burkitt's syndrome. Brit.J. Haemat.
99: 168- 170, 1997.

GAM116 301 BCL6 Cattoretti, G.; Chang, C.- C.; Cechova, K.; Zhang, J.; Ye, B. H.;Falini, B.; 3 A c
Louie, D. C.; Offit, K.; Chaganti, R. S. K.; Dalla- Favera,R.: BCL- 6
protein is expressed in germinal- center B cells. Blood 86:45- 53, 1995.

GAM116 301 BCL6 Cesarman, E.; Chadburn, A.; Liu, Y.- F.; Migliazza, A.; Dalla- Favera,R.; 3 A c
Knowles, D. M.: BCL- 6 gene mutations in posttransplantation
lymphoproliferativedisorders predict response to therapy and clinical
outcome. Blood 92:2294- 2302, 1998.

GAM116 301 BCL6 Chaganti, S. R.; Chen, W.; Parsa, N.; Offit, K.; Louie, D. C.;Dalla- Favera, 3 A c
R.; Chaganti, R. S. K.: Involvement of BCL6 in chromosomalaberrations
affecting band 3q27 in B- cell non- Hodgkin lymphoma. GenesChromosomes
Cancer 23: 323- 327, 1998.

GAM116 301 BCL6 Chaganti, S. R.; Rao, P. H.; Chen, W.; Dyomin, V.; Jhanwar, S.C.; Parsa, N. 3 A c
Z.; Dalla- Favera, R.; Chaganti, R. S. K.: Deregulationof BCL6 in non-
Hodgkin lymphoma by insertion of IGH sequences in complextranslocations
involving band 3q27. Genes Chromosomes Cancer 23:328- 336, 1998.

GAM116 301 BCL6 Chang, C.- C.; Ye, B. H.; Chaganti, R. S. K.; Dalla- Favera, R.:BCL- 6, a 3 A c
POZ/zinc- finger protein, is a sequence- specific transcriptionalrepressor.
Proc. Nat. Acad. Sci. 93: 6947- 6952, 1996.

GAM116 301 BCL6 Dhordain, P.; Albagli, O.; Honore, N.; Guidez, F.; Lantoine, D.;Schmid, M.; 3 A c
De The, H.; Zelent, A.; Koken, M. H. M.: Colocalizationand heteromerization
between the two human oncogene POZ/zinc fingerproteins, LAZ3 (BCL6) and
PLZF. Oncogene 19: 6240- 6250, 2000.

GAM116 301 BCL6 Gaidano, G.; Capello, D.; Gloghini, A.; Fassone, L.; Vivenza,D.; Ariatti, 3 A c
C.; Migliazza, A.; Saglio, G.; Carbone, A.: Frequentmutation of bcl- 6
proto- oncogene in high grade, but not low grade,MALT lymphomas of the
gastrointestinal tract. Haematologica 84:582- 588, 1999.

GAM116 301 BCL6 Galiegue- Zouitina, S.; Quief, S.; Hildebrand, M.- P.; Denis, 3 A c
C.;Detourmignies, L.; Lai, J.- L.; Kerckaert, J.- P.: Nonrandom fusionof L-
plastin (LCP1) and LAZ3 (BCL6) genes by t(3;13)(q27;q14)
chromosometranslocation in two cases of B- cell non- Hodgkin lymphoma.

GenesChromosomes Cancer 26: 97- 105, 1999.

GAM116 301 BCL6 Hamblin, T. J.; Davis, Z.; Gardiner, A.; Oscier, D. G.; Stevenson,F. K.: 3 A c
Unmutated Ig V(H) genes are associated with a more aggressiveform of chronic
lymphocytic leukemia. Blood 94: 1848- 1854, 1999.

GAM116 301 BCL6 Hosokawa, Y.; Maeda, Y.; Ichinohasama, R.; Miura, I.; Taniwaki,M.; Seto, M.: 3 A c
The Ikaros gene, a central regulator of lymphoid differentiation,fuses to
the BCL6 gene as a result of t(3;7)(q27;p12) translocationin a patient with
diffuse large B- cell lymphoma. Blood 95: 2719- 2721,2000.

GAM116 301 BCL6 Ichii, H.; Sakamoto, A.; Hatano, M.; Okada, S.; Toyama, H.; Taki,S.; Arima, 3 A c
M.; Kuroda, Y.; Tokuhisa, T.: Role of Bcl- 6 in the generationand
maintenance of memory CD8+ T cells. Nature Immun. 3: 558- 563,2002.

GAM116 301 BCL6 Ichinohasama, R.; Miura, I.; Funato, T.; Sato, I.; Suzuki, C.;Saito, Y.; 3 A c
Decoteau, J. F.; Myers, J. B.; Kadin, M. E.; Sawai, T.;Ooya, K.: A recurrent
nonrandom translocation (3;7)(q27;p12) associatedwith BCL- 6 gene
rearrangement in B- cell diffuse large cell lymphoma. CancerGenet.
Cytogenet. 104: 19- 27, 1998.

GAM116 301 BCL6 Kerckaert, J.- P.; Deweindt, C.; Tilly, H.; Quief, S.; Lecocq,G.; Bastard, 3 A c
C.: LAZ3, a novel zinc- finger encoding gene, is disruptedby recurring
chromosome 3q27 translocations in human lymphomas. NatureGenet. 5: 66- 70,
1993.

GAM116 301 BCL6 Liao, X.; Gilbert, D. J.; Dent, A.; Staudt, L. M.; Jenkins, N.A.; Copeland, 3 A c
N. G.: Mapping of the mouse Bcl6 gene to chromosome16. Mammalian Genome 7:
621- 622, 1996.

GAM116 301 BCL6 Migliazza, A.; Martinotti, S.; Chen, W.; Fusco, C.; Ye, B. H.;Knowles, D. 3 A c
M.; Offit, K.; Changanti, R. S. K.; Dalla- Favera, R.:Frequent somatic
hypermutation of the 5- prime noncoding region ofthe BCL6 gene in B- cell
lymphoma. Proc. Nat. Acad. Sci. 92: 12520- 12524,1995.

GAM116 301 BCL6 Miki, T.; Kawamata, N.; Arai, A.; Ohashi, K.; Nakamura, Y.; Kato,A.; 3 A c
Hirosawa, S.; Aoki, N.: Molecular cloning of the breakpoint for3q27
translocation in B- cell lymphomas and leukemias. Blood 83:217- 222, 1994.

GAM116 301 BCL6 Miki, T.; Kawamata, N.; Hirosawa, S.; Aoki, N.: Gene involvedin the 3q27 3 A c
translocation associated with B- cell lymphoma, BCL5, encodesa Kruppel- like
zinc- finger protein. Blood 83: 26- 32, 1994.

GAM116 301 BCL6 Sahota, S. S.; Davis, Z.; Hamblin, T. J.; Stevenson, F. K.: Somaticmutation 3 A c
of bcl- 6 genes can occur in the absence of V- H mutationsin chronic
lymphocytic leukemia. Blood 95: 3534- 3540, 2000.

GAM116 301 BCL6 Shaffer, A. L.; Yu, X.; He, Y.; Boldrick, J.; Chan, E. P.; Staudt,L. M.: 3 A c
BCL- 6 represses genes that function in lymphocyte
differentiation,inflammation, and cell cycle control. Immunity 13: 199- 212,
2000.

GAM116 301 BCL6 Shen, H. M.; Peters, A.; Baron, B.; Zhu, X.; Storb, U.: Mutationof BCL- 6 3 A c
gene in normal B cells by the process of somatic hypermutationof Ig genes.
Science 280: 1750- 1752, 1998.

GAM116 301 BCL6 Ueda, C.; Akasaka, T.; Kurata, M.; Maesako, Y.; Nishikori, M.;Ichinohasama, 3 A c
R.; Imada, K.; Uchiyama, T.; Ohno, H.: The gene forinterleukin- 21 receptor
is the partner of BCL6 in t(13;16)(q27;p11),which is recurrently observed in
diffuse large B- cell lymphoma. Oncogene 21:368- 376, 2002.

GAM116 301 BCL6 Ye, B. H.; Cattoretti, G.; Shen, Q.; Zhang, J.; Hawe, N.; de Waard,R.; 3 A c
Leung, C.; Nouri- Shirazi, M.; Orazi, A.; Chaganti, R. S. K.; Rothman,P.;
Stall, A. M.; Pandolfi, P.- P.; Dalla- Favera, R.: The BCL- 6 proto-

oncogenecontrols germinal- centre formation and Th2- type inflammation. NatureGenet. 16: 161- 170, 1997.

GAM116 301 BCL6 Ye, B. H.; Lista, F.; Lo Coco, F.; Knowles, D. M.; Offit, K.;Chaganti, R. S. 3 A c
K.; Dalla- Favera, R.: Alterations of a zinc finger- encodinggene, BCL- 6,
in diffuse large- cell lymphoma. Science 262: 747- 750,1993.

GAM116 301 BCL6 Ye, B. H.; Rao, P. H.; Chaganti, R. S. K.; Dalla- Favera, R.:Cloning of bcl- 3 A c
6, the locus involved in chromosome translocationsaffecting band 3q27 in B-
cell lymphoma. Cancer Res. 53: 2732- 2735,1993.

GAM116 301 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 A c
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM116 301 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 A c
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM116 301 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 A c
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM116 301 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 A c
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM116 301 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 A c
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell
death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM116 301 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 A c
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM116 301 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 A c
Caspase- 8 is required for cell death induced by expanded
polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM116 301 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 A c
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM116 301 CCND1 Arnold, A.; Kim, H. G.; Gaz, R. D.; Eddy, R. L.; Fukushima, Y.;Byers, M. G.; 3 A c
Shows, T. B.; Kronenberg, H. M.: Molecular cloningand chromosomal mapping of
DNA rearranged with the parathyroid hormonegene in a parathyroid adenoma. J.
Clin. Invest. 83: 2034- 2040, 1989.

GAM116 301 CCND1 Bergsagel, P. L.; Chesi, M.; Nardini, E.; Brents, L. A.; Kirby,S. L.; Kuehl, 3 A c
W. M.: Promiscuous translocations into immunoglobulinheavy chain switch
regions in multiple myeloma. Proc. Nat. Acad.Sci. 93: 13931- 13936, 1996.

GAM116 301 CCND1 Betticher, D. C.; Thatcher, N.; Altermatt, H. J.; Hoban, P.; Ryder,W. D. J.; 3 A c
Heighway, J.: Alternate splicing produces a novel cyclinD1 transcript.

Oncogene 11: 1005- 1011, 1995.

GAM116 301 CCND1 Chesi, M.; Bergsagel, P. L.; Brents, L. A.; Smith, C. M.; Gerhard,D. S.; 3 A c
Kuehl, W. M.: Dysregulation of cyclin D1 by translocationinto an IgH gamma
switch region in two multiple myeloma cell lines. Blood 88:674- 681, 1996.

GAM116 301 CCND1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 A c
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple
myeloma is associated with increased expression and activatingmutations of
fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM116 301 CCND1 Gailani, M. R.; Petty, E. M.; Horsthemke, B.; Arnold, A.; Marx,S. J.; Bale, 3 A c
A. E.: Physical mapping of chromosome 11q12- 13 by pulsedfield gel
electrophoresis (PFGE). (Abstract) Cytogenet. Cell Genet. 58:1959, 1991.

GAM116 301 CCND1 Geng, Y.; Whoriskey, W.; Park, M. Y.; Bronson, R. T.; Medema, R.H.; Li, T.; 3 A c
Weinberg, R. A.; Sicinski, P.: Rescue of cyclin D1 deficiencyby knockin
cyclin E. Cell 97: 767- 777, 1999.

GAM116 301 CCND1 Geng, Y.; Yu, Q.; Sicinska, E.; Das, M.; Bronson, R. T.; Sicinski,P.: 3 A c
Deletion of the p27(Kip1) gene restores normal development incyclin D1-
deficient mice. Proc. Nat. Acad. Sci. 98: 194- 199, 2001.

GAM116 301 CCND1 Hayette, S.; Gadoux, M.; Martel, S.; Bertrand, S.; Tigaud, I.;Magaud, J.- 3 A c
P.; Rimokh, R.: FLRG (follistatin- related gene), a newtarget of chromosomal
rearrangement in malignant blood disorders. Oncogene 16:2949- 2954, 1998.

GAM116 301 CCND1 Hinds, P. W.; Dowdy, S. F.; Eaton, E. N.; Arnold, A.; Weinberg,R. A.: 3 A c
Function of a human cyclin gene as an oncogene. Proc. Nat.Acad. Sci. 91:
709- 713, 1994.

GAM116 301 CCND1 Inaba, T.; Matsushime, H.; Valentine, M.; Roussel, M. F.; Sherr,C. J.; Look, 3 A c
A. T.: Genomic organization, chromosomal localization,and independent
expression of human cyclin D genes. Genomics 13:565- 574, 1992.

GAM116 301 CCND1 Kim, H. A.; Pomeroy, S. L.; Whoriskey, W.; Pawlitzky, I.; Benowitz,L. I.; 3 A c
Sicinski, P.; Stiles, C. D.; Roberts, T. M.: A developmentallyregulated
switch directs regenerative growth of Schwann cells throughcyclin D1. Neuron
26: 405- 416, 2000.

GAM116 301 CCND1 Komatsu, H.; Iida, S.; Yamamoto, K.; Mikuni, C.; Nitta, M.; Takahashi,T.; 3 A c
Ueda, R.; Seto, M.: A variant chromosome translocation at 11q13identifying
PRAD1/cyclin D1 as the BCL- 1 gene . Blood 84: 1226- 1231,1994.

GAM116 301 CCND1 Kong, S.; Amos, C. I.; Luthra, R.; Lynch, P. M.; Levin, B.; Frazier,M. L.: 3 A c
Effects of cyclin D1 polymorphism on age of onset of hereditarynonpolyposis
colorectal cancer. Cancer Res. 60: 249- 252, 2000.

GAM116 301 CCND1 Kong, S.; Wei, Q.; Amos, C. I.; Lynch, P. M.; Zong, J.; Frazier,M. L.: 3 A c
Cyclin D1 polymorphism and increased risk of colorectal cancerat young age.
J. Nat. Cancer Inst. 93: 1106- 1108, 2001.

GAM116 301 CCND1 Ma, C.; Papermaster, D.; Cepko, C. L.: A unique pattern of 3 A c
photoreceptordegeneration in cyclin D1 mutant mice. Proc. Nat. Acad. Sci.
95:9938- 9943, 1998.

GAM116 301 CCND1 Motokura, T.; Bloom, T.; Kim, H. G.; Juppner, H.; Ruderman, J.V.; 3 A c
Kronenberg, H. M.; Arnold, A.: A novel cyclin encoded by a bcl1-
linkedcandidate oncogene. Nature 350: 512- 515, 1991.

GAM116 301 CCND1 Muller, H.; Lukas, J.; Schneider, A.; Warthoe, P.; Bartek, J.;Eilers, M.; 3 A c
Strauss, M.: Cyclin D1 expression is regulated by theretinoblastoma protein.
Proc. Nat. Acad. Sci. 91: 2945- 2949, 1994.

GAM116 301 CCND1 Richard, C. W., III; Withers, D. A.; Meeker, T. C.; Maurer, S.;Evans, G. A.; 3 A c
Myers, R. M.; Cox, D. R.: A radiation hybrid map ofthe proximal long arm of

human chromosome 11 containing the multipleendocrine neoplasia type I (MEN-
1) and bcl- 1 disease loci. Am. J.Hum. Genet. 49: 1189- 1196, 1991.

GAM116 301 CCND1 Rimokh, R.; Berger, F.; Bastard, C.; Klein, B.; French, M.; Archimbaud,E.; 3 A c
Rouault, J. P.; Santa Lucia, B.; Duret, L.; Vuillaume, M.; etal.:
Rearrangement of CCND1 (BCL1/PRAD1) 3- prime untranslated regionin mantle-
cell lymphomas and t(11q13)- associated leukemias. Blood 83:3689- 3696,
1994.

GAM116 301 CCND1 Rimokh, R.; Berger, F.; Delsol, G.; Charrin, C.; Bertheas, M.F.; Ffrench, 3 A c
M.; Garoscio, M.; Felman, P.; Coiffier, C.; Bryon, P.A.: Rearrangement and
overexpression of the BCL- 1/PRAD- 1 gene inintermediate lymphocytic
lymphomas and in t(11q13)- bearing leukemias. Blood 81:3063- 3067, 1993.

GAM116 301 CCND1 Rosenberg, C. L.; Kim, H. G.; Shows, T. B.; Kronenberg, H. M.;Arnold, A.: 3 A c
Rearrangement and overexpression of D11S287E, a candidateoncogene on
chromosome 11q13 in benign parathyroid tumors. Oncogene 6:449- 453, 1991.

GAM116 301 CCND1 Rosenberg, C. L.; Wong, E.; Petty, E. M.; Bale, A. E.; Tsujimoto,Y.; Harris, 3 A c
N. L.; Arnold, A.: PRAD1, a candidate BCL1 oncogene:mapping and expression
in centrocytic lymphoma. Proc. Nat. Acad.Sci. 88: 9638- 9642, 1991.

GAM116 301 CCND1 Sicinski, P.; Donaher, J. L.; Parker, S. B.; Li, T.; Fazeli, A.;Gardner, H.; 3 A c
Haslam, S. Z.; Bronson, R. T.; Elledge, S. J.; Weinberg,R. A.: Cyclin D1
provides a link between development and oncogenesisin the retina and breast.
Cell 82: 621- 630, 1995.

GAM116 301 CCND1 Szepetowski, P.; Perucca- Lostanlen, D.; Gaudray, P.: Mappinggenes according 3 A c
to their amplification status in tumor cells: contributionto the map of
11q13. Genomics 16: 745- 750, 1993.

GAM116 301 CCND1 Szepetowski, P.; Simon, M.- P.; Grosgeorge, J.; Huebner, K.; Bastard,C.; 3 A c
Evans, G. A.; Tsujimoto, Y.; Birnbaum, D.; Theillet, C.; Gaudray,P.:
Localization of 11q13 loci with respect to regional chromosomalbreakpoints.
Genomics 12: 738- 744, 1992.

GAM116 301 CCND1 Tsujimoto, Y.; Jaffe, E.; Cossman, J.; Gorham, J.; Nowell, P.C.; Croce, C. 3 A c
M.: Clustering of breakpoints on chromosome 11 in humanB- cell neoplasms
with the t(11;14) chromosome translocation. Nature 315:340- 343, 1985.

GAM116 301 CCND1 Tsujimoto, Y.; Yunis, J.; Onorato- Showe, L.; Erikson, J.; Nowell,P. C.; 3 A c
Croce, C. M.: Molecular cloning of the chromosomal breakpointof B- cell
lymphomas and leukemias with the t(11;14) chromosome translocation. Science
224:1403- 1406, 1984.

GAM116 301 CCND1 Wang, T. C.; Cardiff, R. D.; Zukerberg, L.; Lees, E.; Arnold,A.; Schmidt, E. 3 A c
V.: Mammary hyperplasia and carcinoma in MMTV- cyclinD1 transgenic mice.
Nature 369: 669- 671, 1994.

GAM116 301 CCND1 Xiong, Y.; Connelly, T.; Futcher, B.; Beach, D.: Human D- typecyclin. Cell 3 A c
65: 691- 699, 1991.

GAM116 301 CCND1 Yu, Q.; Geng, Y.; Sicinski, P.: Specific protection against breastcancers by 3 A c
cyclin D1 ablation. Nature 411: 1017- 1021, 2001.

GAM116 301 CCND1 Zatyka, M.; da Silva, N. F.; Clifford, S. C.; Morris, M. R.; Wiesener,M. S.; 3 A c
Eckardt, K.- U.; Houlston, R. S.; Richards, F. M.; Latif, F.;Maher, E. R.:
Identification of cyclin D1 and other novel targetsfor the von Hippel-
Lindau tumor suppressor gene by expression arrayanalysis and investigation
of cyclin D1 genotype as a modifier invon Hippel- Lindau disease. Cancer
Res. 62: 3803- 3811, 2002.

GAM116 301 CDR2 Fathallah- Shaykh, H.; Wolf, S.; Wong, E.; Posner, J. B.: Cloningof a 3 A c
leucine- zipper protein recognized by the sera of patients withantibody-

associated paraneoplastic cerebellar degeneration. Proc.Nat. Acad. Sci. 88: 3451- 3454, 1991.

GAM116 301 CDR2 Fletcher, C. F.; Okano, H. J.; Gilbert, D. J.; Yang, Y.; Yang,C.; Copeland, 3 A c
N. G.; Jenkins, N. A.; Darnell, R. B.: Mouse chromosomallocations of nine genes encoding homologs of human paraneoplasticneurologic disorder antigens. Genomics 45: 313- 319, 1997.

GAM116 301 CDR2 Furneaux, H. M.; Rosenblum, M. K.; Dalmau, J.; Wong, E.; Woodruff,P.; Graus, 3 A c
F.; Posner, J. B.: Selective expression of Purkinje- cellantigens in tumor tissue from patients with paraneoplastic cerebellardegeneration. New Eng. J. Med. 322: 1844- 1851, 1990.

GAM116 301 CDR2 Furneaux, H. M.; Wong, E.; Posner, J. B.: Isolation of cDNA clonesencoding 3 A c
the major Yo paraneoplastic antigen. (Abstract) Neurology 40(suppl. 1): 166 only, 1990.

GAM116 301 CDR2 Gress, T.; Baldini, A.; Rocchi, M.; Furneaux, H.; Posner, J. B.;Siniscalco, 3 A c
M.: In situ mapping of the gene coding for a leucinezipper DNA binding protein (CDR 2) to the region between two rarefragile sites of autosome 16 (16p12- p13.1). (Abstract) Cytogenet.Cell Genet. 58: 1999- 2000, 1991.

GAM116 301 CDR2 Gress, T.; Baldini, A.; Rocchi, M.; Furneaux, H.; Posner, J. B.;Siniscalco, 3 A c
M.: In situ mapping of the gene coding for a leucinezipper DNA binding protein (CDR62) to 16p12- 16p13.1. Genomics 13:1340- 1342, 1992.

GAM116 301 CENTD1 Miura, K.; Jacques, K. M.; Stauffer, S.; Kubosaki, A.; Zhu, K.;Hirsch, D. 3 A c
S.; Resau, J.; Zheng, Y.; Randazzo, P. A.: ARAP1: a pointof convergence for Arf and Rho signaling. Molec. Cell 9: 109- 119,2002.

GAM116 301 CENTD1 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 A c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM116 301 CHD3 Ge, Q.; Nilasena, D. S.; O'Brien, C. A.; Frank, M. B.; Targoff,I. N.: 3 A c
Molecular analysis of a major antigenic region of the 240- kDprotein of Mi- 2 autoantigen. J. Clin. Invest. 96: 1730- 1737, 1995.

GAM116 301 CHD3 Seelig, H. P.; Renz, M.; Targoff, I. N.; Ge, Q.; Frank, M. B.:Two forms of 3 A c
the major antigenic protein of the dermatomyositis- specificMi- 2 autoantigen. (Letter) Arthritis Rheum. 39: 1769- 1771, 1996.

GAM116 301 CHD3 Woodage, T.; Basrai, M. A.; Baxevanis, A. D.; Hieter, P.; Collins,F. S.: 3 A c
Characterization of the CHD family of proteins. Proc. Nat.Acad. Sci. 94: 11472- 11477, 1997.

GAM116 301 CYP1B1 Bejjani, B. A.; Lewis, R. A.; Tomey, K. F.; Anderson, K. L.; Dueker,D. K.; 3 A c
Jabak, M.; Astle, W. F.; Otterud, B.; Leppert, M.; Lupski,J. R.: Mutations in CYP1B1, the gene for cytochrome P4501B1, arethe predominant cause of primary congenital glaucoma in Saudi Arabia. Am.J. Hum. Genet. 62: 325- 333, 1998.

GAM116 301 CYP1B1 Bejjani, B. A.; Stockton, D. W.; Lewis, R. A.; Tomey, K. F.; Dueker,D. K.; 3 A c
Jabak, M.; Astle, W. F.; Lupski, J. R.: Multiple CYP1B1 mutationsand incomplete penetrance in an inbred population segregating primarycongenital glaucoma suggest frequent de novo events and a dominantmodifier locus. Hum. Molec. Genet. 9: 367- 374, 2000.

GAM116 301 CYP1B1 Hanna, I. H.; Dawling, S.; Roodi, N.; Guengerich, F. P.; Parl,F. F.: 3 A c
Cytochrome P450 1B1 (CYP1B1) pharmacogenetics: associationof polymorphisms with functional differences in estrogen hydroxylationactivity. Cancer Res. 60: 3440- 3444, 2000.

GAM116 301 CYP1B1 Plasilova, M.; Stoilov, I.; Sarfarazi, M.; Kadasi, L.; Ferakova,E.; Ferak, V.: Identification of a single ancestral CYP1B1 mutationin Slovak Gypsies (Roms) affected with primary congenital glaucoma. J.Med. Genet. 36: 290-294, 1999. 3 A c

GAM116 301 CYP1B1 Schwartzman, M. L.; Balazy, M.; Masferrer, J.; Abraham, N. G.;McGiff, J. C.; Murphy, R. C.: 12(R)- hydroxyicosatetraenoic acid:a cytochrome P450-dependent arachidonate metabolite that inhibitsNa+,K+- ATPase in the cornea. Proc. Nat. Acad. Sci. 84: 8125- 8129,1987. 3 A c

GAM116 301 CYP1B1 Stoilov, I.; Akarsu, A. N.; Alozie, I.; Child, A.; Barsoum- Homsy,M.; Turacli, M. E.; Or, M.; Lewis, R. A.; Ozdemir, N.; Brice, G.;Aktan, S. G.; Chevrette, L.; Coca- Prados, M.; Sarfarazi, M.: Sequenceanalysis and homology modeling suggest that primary congenital glaucomaon 2p21 results from mutations disrupting either the hinge regionor the conserved core structures of cytochrome P4501B1. Am. J. Hum.Genet. 62: 573- 584, 1998. 3 A c

GAM116 301 CYP1B1 Stoilov, I.; Akarsu, A. N.; Sarfarazi, M.: Identification of threedifferent truncating mutations in cytochrome P4501B1 (CYP1B1) as theprincipal cause of primary congenital glaucoma (buphthalmos) in familieslinked to the GLC3A locus on chromosome 2p21. Hum. Molec. Genet. 6:641- 647, 1997. 3 A c

GAM116 301 CYP1B1 Sutter, T. R.; Tang, Y. M.; Hayes, C. L.; Wo, Y.- Y. P.; Jabs, E.W.; Li, X.; Yin, H.; Cody, C. W.; Greenlee, W. F.: Complete cDNAsequence of a human dioxin- inducible mRNA identifies a new gene subfamilyof cytochrome P450 that maps to chromosome 2. J. Biol. Chem. 269:13092- 13099, 1994. 3 A c

GAM116 301 CYP1B1 Tang, Y. M.; Wo, Y.- Y. P.; Stewart, J.; Hawkins, A. L.; Griffin,C. A.; Sutter, T. R.; Greenlee, W. F.: Isolation and characterizationof the human cytochrome P450 CYP1B1 gene. J. Biol. Chem. 271: 28324- 28330,1996. 3 A c

GAM116 301 CYP1B1 Vincent, A.; Billingsley, G.; Priston, M.; Williams- Lyn, D.; Sutherland,J.; Glaser, T.; Oliver, E.; Walter, M. A.; Heathcote, G.; Levin, A.;Heon, E.: Phenotypic heterogeneity of CYP1B1: mutations in a patientwith Peters' anomaly. J. Med. Genet. 38: 324- 326, 2001. 3 A c

GAM116 301 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, D. J.; Muir, W. J.: Schizophrenia and affective disorders- - cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001. 3 A b

GAM116 301 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 355:771- 772, 2000. 3 A b

GAM116 301 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 3 A b

GAM116 301 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 3 A b

GAM116 301 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000. 3 A b

GAM116 301 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced 3 A b

autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM116 301 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 A c
Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system
for platelet activation. Nature 394: 690- 694, 1998.

GAM116 301 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 A c
M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin.
Nature 404: 609- 613, 2000.

GAM116 301 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 A c
Role of thrombin signalling in platelets in haemostasis andthrombosis.
Nature 413: 74- 78, 2001.

GAM116 301 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; 3 A c
Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand
characterization of human protease- activated receptor 4. Proc.Nat. Acad.
Sci. 95: 6642- 6646, 1998.

GAM116 301 FBXO7 Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; 3 A c
Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol.
9: 1177- 1179, 1999.

GAM116 301 FBXO7 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 A c
and expression analysis of new members of the mammalianF- box protein
family. Genomics 67: 40- 47, 2000.

GAM116 301 FBXO7 Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A 3 A c
family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999.

GAM116 301 FOXM1 Korver, W.; Roose, J.; Heinen, K.; Weghuis, D. O.; de Bruijn, D.;Geurts van 3 A c
Kessel, A.; Clevers, H.: The human TRIDENT/HFH- 11/FKHL16gene: structure,
localization, and promoter characterization. Genomics 46:435- 442, 1997.

GAM116 301 FOXM1 Ly, D. H.; Lockhart, D. J.; Lerner, R. A.; Schultz, P. G.: 3 A c
Mitoticmisregulation and human aging. Science 287: 2486- 2492, 2000.

GAM116 301 FOXM1 Wang, X.; Quail, E.; Hung, N.- J.; Tan, Y.; Ye, H.; Costa, R. H.: Increased 3 A c
levels of forkhead box M1B transcription factor in transgenicmouse
hepatocytes prevent age- related proliferation defects in regeneratingliver.
Proc. Nat. Acad. Sci. 98: 11468- 11473, 2001.

GAM116 301 FOXM1 Westendorf, J. M.; Rao, P. N.; Gerace, L.: Cloning of cDNAs forM- phase 3 A c
phosphoproteins recognized by the MPM2 monoclonal antibodyand determination
of the phosphorylated epitope. Proc. Nat. Acad.Sci. 91: 714- 718, 1994.

GAM116 301 FOXM1 Yao, K.- M.; Sha, M.; Lu, Z.; Wong, G. G.: Molecular analysis ofa novel 3 A c
winged helix protein, WIN: expression pattern, DNA bindingproperty, and
alternative splicing within the DNA binding domain. J.Biol. Chem. 272:
19827- 19836, 1997.

GAM116 301 FOXM1 Ye, H.; Kelly, T. F.; Samadani, U.; Lim, L.; Rubio, S.; Overdier,D. G.; 3 A c
Roebuck, K. A.; Costa, R. H.: Hepatic nuclear factor 3/forkhead homolog 11
is expressed in proliferating epithelial and mesenchymalcells of embryonic
and adult tissues. Molec. Cell. Biol. 17: 1626- 1641,1997.

GAM116 301 HTR4 Blondel, O.; Vandecasteele, G.; Gastineau, M.; Leclerc, S.; Dahmoune,Y.; 3 A c
Langlois, M.; Fischmeister, R.: Molecular and functional characterizationof
a 5- HT(4) receptor cloned from human atrium. FEBS Lett. 412:465- 474, 1997.

GAM116 301 HTR4 Claeysen, S.; Faye, P.; Sebben, M.; Lemaire, S.; Bockaert, J.;Dumuis, A.; 3 A c
Taviaux, S.: Assignment of 5- hydroxytryptamine receptor(HTR4) to human
chromosome 5 bands q31- to- q33 by in situ hybridization. Cytogenet.Cell
Genet. 78: 133- 134, 1997.

GAM116 301 HTR4 Dumuis, A.; Bouhelal, R.; Sebben, M.; Cory, R.; Bockaert, J.:A nonclassical 3 A c

5- hydroxytryptamine receptor positively coupled withadenylate cyclase in the central nervous system. Molec. Pharm. 34:880- 887, 1988.

GAM116 301 HTR4 Eglen, R. M.; Wong, E. H. F.; Dumuis, A.; Bockaert, J.: Central5- HT4 3 A c receptors. Trends Pharm. Sci. 16: 391- 398, 1995.

GAM116 301 IL6R Kluck, P. M. C.; Wiegant, J.; Jansen, R. P. M.; Bolk, M. W. J.;Raap, A. K.; 3 A b Willemze, R.; Landegent, J. E.: The human interleukin- 6receptor alpha-chain gene is localized on chromosome 1 band q21. Hum.Genet. 90: 542- 544, 1993.

GAM116 301 IL6R Szpirer, J.; Szpirer, C.; Riviere, M.; Houart, C.; Baumann, M.;Fey, G. H.; 3 A b Poli, V.; Cortese, R.; Islam, M. Q.; Levan, G.: The interleukin- 6-dependentDNA- binding protein gene (transcription factor 5: TCF5) maps to humanchromosome 20 and rat chromosome 3, the IL6 receptor locus (IL6R)to human chromosome 1 and rat chromosome 2, and the rat IL6 gene torat chromosome 4. Genomics 10: 539- 546, 1991.

GAM116 301 IL6R Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.;Seed, B.; 3 A b Taniguchi, T.; Hirano, T.; Kishimoto, T.: Cloning and expressionof the human interleukin- 6 (BSF- 2/IFN- beta- 2) receptor. Science 241:825- 828, 1988.

GAM116 301 INSR 't Hart, L. M.; Stolk, R. P.; Dekker, J. M.; Nijpels, G.; Grobbee,D. E.; 3 A c Heine, R. J.; Maassen, J. A.: Prevalence of variants in candidategenes for type 2 diabetes mellitus in the Netherlands: the Rotterdamstudy and the Hoorn study. J. Clin. Endocr. Metab. 84: 1002- 1006,1999.

GAM116 301 INSR 't Hart, L. M.; Stolk, R. P.; Heine, R. J.; Grobbee, D. E.; vander Does, F. 3 A c E. E.; Maassen, J. A.: Association of the insulin- receptorvariant met- 985 with hyperglycemia and non- insulin- dependent diabetesmellitus in the Netherlands: a population- based study. Am. J. Hum.Genet. 59: 1119- 1125, 1996.

GAM116 301 INSR Accili, D.; Drago, J.; Lee, E. J.; Johnson, M. D.; Cool, M. H.;Salvatore, 3 A c P.; Asico, L. D.; Jose, P. A.; Taylor, S. I.; Westphal,H.: Early neonatal death in mice homozygous for a null allele ofthe insulin receptor gene. Nature Genet. 12: 106- 109, 1996.

GAM116 301 INSR Accili, D.; Frapier, C.; Mosthaf, L.; McKeon, C.; Elbein, S. C.;Permutt, M. 3 A c A.; Ramos, E.; Lander, E.; Ullrich, A.; Taylor, S. I.: A mutation in the insulin receptor gene that impairs transport ofthe receptor to the plasma membrane and causes insulin- resistant diabetes. EMBOJ. 8: 2509- 2517, 1989.

GAM116 301 INSR Al- Gazali, L. I.; Khalil, M.; Devadas, K.: A syndrome of insulinresistance 3 A c resembling leprechaunism in five sibs of consanguineousparents. J. Med. Genet. 30: 470- 475, 1993.

GAM116 301 INSR Bar, R. S.; Muggeo, M.; Roth, J.; Kahn, C. R.; Havrankova, J.;Imperato- 3 A c McGinley, J.: Insulin resistance, acanthosis nigricans,and normal insulin receptors in a young woman: evidence for a postreceptordefect. J. Clin. Endocr. Metab. 47: 620- 625, 1978.

GAM116 301 INSR Barbetti, F.; Gejman, P. V.; Taylor, S. I.; Raben, N.; Cama, A.;Bonora, E.; 3 A c Pizzo, P.; Moghetti, P.; Muggeo, M.; Roth, J.: Detectionof mutations in insulin receptor gene by denaturing gradient gel electrophoresis. Diabetes 41:408- 415, 1992.

GAM116 301 INSR Barnes, N. D.; Palumbo, P. J.; Hayles, A. B.; Folgar, H.: Insulinresistance, 3 A c skin changes, and virilization: a recessively inheritedsyndrome possibly due to pineal gland dysfunction. Diabetologia 10:285- 289, 1974.

GAM116 301 INSR Belke, D. D.; Betuing, S.; Tuttle, M. J.; Graveleau, C.; Young,M. E.; Pham, 3 A c M.; Zhang, D.; Cooksey, R. C.; McClain, D. A.; Litwin,S. E.; Taegtmeyer, H.;

Severson, D.; Kahn, C. R.; Abel, E. D.: Insulinsignaling coordinately regulates cardiac size, metabolism, and contractileprotein isoform expression. J. Clin. Invest. 109: 629- 639, 2002.

GAM116 301 INSR Benecke, H.; Flier, J. S.; Moller, D. E.: Alternatively splicedvariants of the insulin receptor protein: expression in normal anddiabetic human tissues. J. Clin. Invest. 89: 2066- 2070, 1992. 3 A c

GAM116 301 INSR Bruning, J. C.; Gautam, D.; Burks, D. J.; Gillette, J.; Schubert,M.; Orban, P. C.; Klein, R.; Krone, W.; Muller- Wieland, D.; Kahn,C. R.: Role of brain insulin receptor in control of body weight andreproduction. Science 289: 2122- 2125, 2000. 3 A c

GAM116 301 INSR Bruning, J. C.; Michael, M. D.; Winnay, J. N.; Hayashi, T.; Horsch,D.; Accili, D.; Goodyear, L. J.; Kahn, C. R.: A muscle- specific insulinreceptor knockout exhibits features of the metabolic syndrome of NIDDMwithout altering glucose tolerance. Molec. Cell 2: 559- 569, 1998. 3 A c

GAM116 301 INSR Cama, A.; de la Luz Sierra, M.; Ottini, L.; Kadowaki, T.; Gorden,P.; Imperato- McGinley, J.; Taylor, S. I.: A mutation in the tyrosinekinase domain of the insulin receptor associated with insulin resistancein an obese woman. J. Clin. Endocr. Metab. 73: 894- 901, 1991. 3 A c

GAM116 301 INSR Cama, A.; de la Luz Sierra, M.; Quon, M. J.; Ottini, L.; Gorden,P.; Taylor, S. I.: Substitution of glutamic acid for alanine 1135in the putative 'catalytic loop' of the tyrosine kinase domain ofthe human insulin receptor: a mutation that impairs proteolytic processinginto subunits and inhibits receptor tyrosine kinase activity. J.Biol. Chem. 268: 8060- 8069, 1993. 3 A c

GAM116 301 INSR Cama, A.; Quon, M. J.; de la Luz Sierra, M.; Taylor, S. I.: Substitutionof isoleucine for methionine at position 1153 in the beta- subunitof the human insulin receptor. J. Biol. Chem. 267: 8383- 8389, 1992. 3 A c

GAM116 301 INSR Caro, J. F.; Raju, S. M.; Sinha, M. K.; Goldfine, I. D.; Dohm,G. L.: Heterogeneity of human liver, muscle, and adipose tissue insulinreceptor. Biochem. Biophys. Res. Commun. 151: 123- 129, 1988. 3 A c

GAM116 301 INSR Christiansen, K.; Tranum- Jensen, J.; Carlsen, J.; Vinten, J.:A model for the quaternary structure of human placental insulin receptordeduced from electron microscopy. Proc. Nat. Acad. Sci. 88: 249- 252,1991. 3 A c

GAM116 301 INSR Cocozza, S.; Porcellini, A.; Riccardi, G.; Monticelli, A.; Condorelli,G.; Ferrara, A.; Pianese, L.; Miele, C.; Capaldo, B.; Beguinot, F.;Varrone, S.: NIDDM associated with mutation in tyrosine kinase domainof insulin receptor gene. Diabetes 41: 521- 526, 1992. 3 A c

GAM116 301 INSR Dey, B. R.; Furlanetto, R. W.; Nissley, S. P.: Cloning of humanp55- gamma, a regulatory subunit of phosphatidylinositol 3- kinase,by a yeast two- hybrid library screen with the insulin- like growthfactor- I receptor. Gene 209: 175- 183, 1998. 3 A c

GAM116 301 INSR Due, C.; Simonsen, M.; Olsson, L.: The major histocompatibilitycomplex class I heavy chain as a structural subunit of the human cellmembrane insulin receptor: implications for the range of biologicalfunctions of histocompatibility antigens. Proc. Nat. Acad. Sci. 83:6007- 6011, 1986. 3 A c

GAM116 301 INSR Ebina, Y.; Ellis, L.; Jarnagin, K.; Edery, M.; Graf, L.; Clauser,E.; Ou, J.- H.; Masiarz, F.; Kan, Y. W.; Goldfine, I. D.; Roth, R.A.; Rutter, W. J.: The human insulin receptor cDNA: the structuralbasis for hormone activated transmembrane signalling. Cell 40: 747- 758,1985. 3 A c

GAM116 301 INSR Elbein, S. C.; Corsetti, L.; Ullrich, A.; Permutt, M. A.: Multiplerestriction fragment length polymorphisms at the insulin 3 A c

receptorlocus: a highly informative marker for linkage analysis. Proc. Nat.Acad. Sci. 83: 5223- 5227, 1986.

GAM116 301 INSR Elbein, S. C.; Sorensen, L. K.; Schumacher, M. C.: Methioninefor valine substitution in exon 17 of the insulin receptor gene ina pedigree with familial NIDDM. Diabetes 42: 429- 434, 1993. 3 A c

GAM116 301 INSR Ferrannini, E.; Muggeo, M.; Navalesi, R.; Pilo, A.: Impairedinsulin degradation in a patient with insulin resistance and acanthosisnigricans. Am. J. Med. 73: 148- 154, 1982. 3 A c

GAM116 301 INSR Grigorescu, F.; Flier, J. S.; Kahn, C. R.: Characterization ofbinding and phosphorylation defects of erythrocyte insulin receptorsin the type A syndrome of insulin resistance. Diabetes 35: 127- 138,1986. 3 A c

GAM116 301 INSR Grigorescu, F.; Flier, J. S.; Kahn, C. R.: Defect in insulinreceptor phosphorylation in erythrocytes and fibroblasts associatedwith severe insulin resistance. J. Biol. Chem. 259: 15003- 15006,1984. 3 A c

GAM116 301 INSR Grunberger, G.; Zick, Y.; Gordon, G.: Defect in phosphorylationof insulin receptors in cells from an insulin- resistant patient withnormal insulin binding. Science 223: 932- 934, 1984. 3 A c

GAM116 301 INSR Hone, J.; Accili, D.; Al- Gazali, L. I.; Lestringant, G.; Orban,T.; Taylor, S. I.: Homozygosity for a new mutation (ile119- to- met)in the insulin receptor gene in five sibs with familial insulin resistance. J.Med. Genet. 31: 715- 716, 1994. 3 A c

GAM116 301 INSR Kadowaki, T.; Bevins, C. L.; Cama, A.; Ojamaa, K.; Marcus- Samuels,B.; Kadowaki, H.; Beitz, L.; McKeon, C.; Taylor, S. I.: Two mutantalleles of the insulin receptor gene in a patient with extreme insulinresistance. Science 240: 787- 790, 1988. 3 A c

GAM116 301 INSR Kadowaki, T.; Kadowaki, H.; Accili, D.; Taylor, S. I.: Substitutionof lysine for asparagine at position 15 in the alpha- subunit of thehuman insulin receptor: a mutation that impairs transport of receptorsto the cell surface and decreases the affinity of insulin binding. J.Biol. Chem. 265: 19143- 19150, 1990. 3 A c

GAM116 301 INSR Kadowaki, T.; Kadowaki, H.; Accili, D.; Yazaki, Y.; Taylor, S.I.: Substitution of arginine for histidine at position 209 in thealpha- subunit of the human insulin receptor: a mutation that impairsreceptor dimerization and transport of receptors to the cell surface. J.Biol. Chem. 266: 21224- 21231, 1991. 3 A c

GAM116 301 INSR Kadowaki, T.; Kadowaki, H.; Rechler, M. M.; Serrano- Rios, M.;Roth, J.; Gorden, P.; Taylor, S. I.: Five mutant alleles of the insulinreceptor gene in patients with genetic forms of insulin resistance. J.Clin. Invest. 86: 254- 264, 1990. 3 A c

GAM116 301 INSR Kadowaki, T.; Kadowaki, H.; Taylor, S. I.: A nonsense mutationcausing decreased levels of insulin receptor mRNA: detection by asimplified technique for direct sequencing of genomic DNA amplifiedby the polymerase chain reaction. Proc. Nat. Acad. Sci. 87: 658- 662,1990. 3 A c

GAM116 301 INSR Kahn, C. R.; Flier, J. S.; Bar, R. S.; Archer, J. A.; Gorden,P.; Martin, M. M.; Roth, J.: The syndromes of insulin resistanceand acanthosis nigricans: insulin receptor disorders in man. NewEng. J. Med. 294: 739- 745, 1976. 3 A c

GAM116 301 INSR Kahn, C. R.; Goldstein, B. J.: Molecular defects in insulin action. Science 245:13 only, 1989. 3 A c

GAM116 301 INSR Kahn, C. R.; White, M. F.: The insulin receptor and the molecularmechanism of insulin action. J. Clin. Invest. 82: 1151- 1156, 1988. 3 A c

GAM116 301 INSR Kakehi, T.; Hisatomi, A.; Kuzuya, H.; Yoshimasa, Y.; Okamoto,M.; Yamada, K.; 3 A c
Nishimura, H.; Kosaki, A.; Nawata, H.; Umeda, F.;Ibayashi, H.; Imura, H.:
Defective processing of insulin- receptorprecursor in cultured lymphocytes
from a patient with extreme insulinresistance. J. Clin. Invest. 81: 2020-
2022, 1988.

GAM116 301 INSR Kittur, D.; Shimizu, Y.; DeMars, R.; Edidin, M.: Insulin bindingto human B 3 A c
lymphoblasts is a function of HLA haplotype. Proc. Nat.Acad. Sci. 84: 1351-
1355, 1987.

GAM116 301 INSR Klinkhamer, M. P.; Groen, N. A.; van der Zon, G. C. M.; Lindhout,D.; 3 A c
Sandkuyl, L. A.; Krans, H. M. J.; Moller, W.; Maassen, J. A.:A leucine- to-
proline mutation in the insulin receptor in a familywith insulin resistance.
EMBO J. 8: 2503- 2507, 1989.

GAM116 301 INSR Krook, A.; Brueton, L.; O'Rahilly, S.: Homozygous nonsense mutationin the 3 A c
insulin receptor gene in infant with leprechaunism. Lancet 342:277- 278,
1993.

GAM116 301 INSR Kulkarni, R. N.; Bruning, J. C.; Winnay, J. N.; Postic, C.; Magnuson,M. A.; 3 A c
Kahn, C. R.: Tissue- specific knockout of the insulin receptorin pancreatic
beta cells creates an insulin secretory defect similarto that in type 2
diabetes. Cell 96: 329- 339, 1999.

GAM116 301 INSR Kusari, J.; Takata, Y.; Hatada, E.; Freidenberg, G.; Kolterman,O.; Olefsky, 3 A c
J. M.: Insulin resistance and diabetes due to differentmutations in the
tyrosine kinase domain of both insulin receptor genealleles. J. Biol. Chem.
266: 5260- 5267, 1991.

GAM116 301 INSR Lander, E. S.; Botstein, D.: Homozygosity mapping: a way to maphuman 3 A c
recessive traits with the DNA of inbred children. Science 236:1567- 1570,
1987.

GAM116 301 INSR Le Marchand- Brustel, Y.; Gremeaux, T.; Ballotti, R.; van Obberghen,E.: 3 A c
Insulin receptor tyrosine kinase is defective in skeletal muscleof insulin-
resistant obese mice. Nature 315: 676- 679, 1985.

GAM116 301 INSR Leibiger, B.; Leibiger, I. B.; Moede, T.; Kemper, S.; Kulkarni,R. N.; Kahn, 3 A c
C. R.; de Vargas, L. M.; Berggren, P.- O.: Selectiveinsulin signaling
through A and B insulin receptors regulates transcriptionof insulin and
glucokinase genes in pancreatic beta cells. Molec.Cell 7: 559- 570, 2001.

GAM116 301 INSR Leme, C. E.; Wajchenberg, B. L.; Lerario, A. C.; Goldman, J.;Borges, J. L. 3 A c
C.: Acanthosis nigricans, hirsutism, insulin resistanceand insulin receptor
defect. Clin. Endocr. 17: 43- 49, 1982.

GAM116 301 INSR Longo, N.; Langley, S. D.; Griffin, L. D.; Elsas, L. J., II:Reduced mRNA and 3 A c
a nonsense mutation in the insulin- receptor geneproduce heritable severe
insulin resistance. Am. J. Hum. Genet. 50:998- 1007, 1992.

GAM116 301 INSR Longo, N.; Langley, S. D.; Griffin, L. D.; Elsas, L. J.: Activationof 3 A c
glucose transport by a natural mutation in the human insulin receptor.
Proc.Nat. Acad. Sci. 90: 60- 64, 1993.

GAM116 301 INSR Maassen, J. A.; Klinkhamer, M. P.; Odink, R. J. H.; Sips, H.;van der Zon, G. 3 A c
C. M.; Wieringa, T.; Krans, H. M. J.; Moller, W.:Improper expression of
insulin receptors on fibroblasts from a leprechaunpatient. Europ. J.
Biochem. 172: 725- 729, 1988.

GAM116 301 INSR Mariani, S.; Pedone, A.; Meschi, F.; Di Natale, B.; Caputo, R.;Broggi, U.; 3 A c
Chiumello, G.: Insulin resistance in a child with acanthosisnigricans type
A. Acta Paediat. Scand. 71: 667- 670, 1982.

GAM116 301 INSR Michael, M. D.; Kulkarni, R. N.; Postic, C.; Previs, S. F.; Shulman,G. I.; 3 A c

Magnuson, M. A.; Kahn, C. R.: Loss of insulin signaling inhepatocytes leads to severe insulin resistance and progressive hepaticdysfunction. Molec. Cell 6: 87- 97, 2000.

GAM116 301 INSR Moller, D. E.; Cohen, O.; Yamaguchi, Y.; Assiz, R.; Grigorescu,F.; Eberle, A.; Morrow, L. A.; Moses, A. C.; Flier, J. S.: Prevalenceof mutations in the insulin receptor gene in subjects with featuresof the type A syndrome of insulin resistance. Diabetes 43: 247- 255,1994. 3 A c

GAM116 301 INSR Moller, D. E.; Flier, J. S.: Detection of an alteration in theinsulin-receptor gene in a patient with insulin resistance, acanthosisnigricans, and the polycystic ovary syndrome (type A insulin resistance). NewEng. J. Med. 319: 1526- 1529, 1988. 3 A c

GAM116 301 INSR Moller, D. E.; Flier, J. S.: Insulin resistance- - mechanisms,syndromes, and implications. New Eng. J. Med. 325: 938- 948, 1991. 3 A c

GAM116 301 INSR Moller, D. E.; Yokota, A.; Ginsberg- Fellner, F.; Flier, J. S.: Functional properties of a naturally occurring trp(1200)- to- ser(1200)mutation of the insulin receptor. Molec. Endocr. 4: 1183- 1191, 1990. 3 A c

GAM116 301 INSR Moller, D. E.; Yokota, A.; Pazianos, A.; Flier, J. S.: A missensemutation in one allele of the tyrosine kinase domain of the insulinreceptor gene is associated with dominantly inherited insulin resistance.(Abstract) Clin. Res. 38: 435A only, 1990. 3 A c

GAM116 301 INSR Moller, D. E.; Yokota, A.; White, M. F.; Pazianos, A. G.; Flier,J. S.: A naturally occurring mutation of insulin receptor alanine1134 impairs tyrosine kinase function and is associated with dominantlyinherited insulin resistance. J. Biol. Chem. 265: 14979- 14985, 1990. 3 A c

GAM116 301 INSR Moncada, V. Y.; Hedo, J. A.; Serrano- Rios, M.; Taylor, S. I.:Insulin-receptor biosynthesis in cultured lymphocytes from an insulin-resistantpatient (Rabson- Mendenhall syndrome): evidence for defect before insertionof receptor into plasma membrane. Diabetes 35: 802- 807, 1986. 3 A c

GAM116 301 INSR Norton, K. I.; Glicklich, M.; Kupchik, G.; Gray, C. E.; Ludman,M.: Leprechaunism: a case report with radiographic features. Dysmorph.Clin. Genet. 4: 57- 62, 1990. 3 A c

GAM116 301 INSR Odawara, M.; Kadowaki, T.; Yamamoto, R.; Shibasaki, Y.; Tobe,K.; Accili, D.; Bevins, C.; Mikami, Y.; Matsuura, N.; Akanuma, Y.;Takaku, F.; Taylor, S. I.; Kasuga, M.: Human diabetes associatedwith a mutation in the tyrosine kinase domain of the insulin receptor. Science 245:66- 68, 1989. 3 A c

GAM116 301 INSR Ojamaa, K.; Hedo, J. A.; Roberts, C. T., Jr.; Moncada, V. Y.;Gorden, P.; Ullrich, A.; Taylor, S. I.: Defects in human insulinreceptor gene expression. Molec. Endocr. 2: 242- 247, 1988. 3 A c

GAM116 301 INSR Prince, M. J.; Smith, F. E.; Peters, E. J.; Stuart, C. A.: Functionalcharacteristics of decreased insulin receptors on fibroblasts obtainedfrom a subject with severe insulin resistance and acanthosis nigricans. Diabetes 35:148- 154, 1986. 3 A c

GAM116 301 INSR Quin, J. D.; Fisher, B. M.; Paterson, K. R.; Inoue, A.; Beastall,G. H.; MacCuish, A. C.: Acute response to recombinant insulin- likegrowth factor- I in a patient with Mendenhall's syndrome. New Eng.J. Med. 323: 1425- 1426, 1991. 3 A c

GAM116 301 INSR Quon, M. J.; Guerre- Millo, M.; Zarnowski, M. J.; Butte, A. J.;Em, M.; Cushman, S. W.; Taylor, S. I.: Tyrosine kinase- deficientmutant human insulin receptors (met1153- to- ile) overexpressed in transfectedrat adipose cells fail to mediate translocation of epitope- taggedGLUT4. Proc. Nat. 3 A c

Acad. Sci. 91: 5587- 5591, 1994.

GAM116 301 INSR Rabson, S. M.; Mendenhall, E. N.: Familial hypertrophy of pinealbody, 3 A c
hyperplasia of adrenal cortex and diabetes mellitus. Am. J.Clin. Path. 26:
283- 290, 1956.

GAM116 301 INSR Rajala, R. V. S.; Anderson, R. E.: Interaction of the insulinreceptor beta- 3 A c
subunit with phosphatidylinositol 3- kinase in bovineROS. Invest. Ophthal.
Vis. Sci. 42: 3110- 3117, 2001.

GAM116 301 INSR Roth, R. A.; Cassell, D. J.: Insulin receptor: evidence thatit is a protein 3 A c
kinase. Science 219: 299- 301, 1983.

GAM116 301 INSR Rubin, C. S.: Personal Communication. Bronx, N. Y. 12/8/1984. 3 A c

GAM116 301 INSR Rudiger, H. W.; Ahrens, P.; Dreyer, M.; Frorath, B.; Loffel, C.;Schmidt- 3 A c
Preuss, U.: Impaired insulin- induced RNA synthesis secondaryto a
genetically defective insulin receptor. Hum. Genet. 69: 76- 78,1985.

GAM116 301 INSR Rudiger, H. W.; Dreyer, M.; Kuhnau, J.; Bartelheimer, H.: Familialinsulin- 3 A c
resistant diabetes secondary to an affinity defect of theinsulin receptor.
Hum. Genet. 64: 407- 411, 1983.

GAM116 301 INSR Salmeen, A.; Andersen, J. N.; Myers, M. P.; Tonks, N. K.; Barford,D.: 3 A c
Molecular basis for the dephosphorylation of the activation segmentof the
insulin receptor by protein tyrosine phosphatase 1B. Molec.Cell 6: 1401-
1412, 2000.

GAM116 301 INSR Scarlett, J. A.; Kolterman, O. G.; Moore, P.; Saekow, M.; Insel,J.; Griffin, 3 A c
J.; Mako, M.; Rubenstein, A. H.; Olefsky, J. M.: Insulinresistance and
diabetes due to a genetic defect in insulin receptors. J.Clin. Endocr.
Metab. 55: 123- 132, 1982.

GAM116 301 INSR Schwenk, W. F.; Rizza, R. A.; Mandarino, L. J.; Gerich, J. E.;Hayles, A. B.; 3 A c
Haymond, M. W.: Familial insulin resistance and acanthosisnigricans:
presence of a postbinding defect. Diabetes 35: 33- 37,1986.

GAM116 301 INSR Seino, S.; Seino, M.; Nishi, S.; Bell, G. I.: Structure of thehuman insulin 3 A c
receptor gene and characterization of its promoter. Proc.Nat. Acad. Sci. 86:
114- 118, 1989.

GAM116 301 INSR Shaw, D. J.; Meredith, A. L.; Brook, J. D.; Sarfarazi, M.; Harley,H. G.; 3 A c
Huson, S. M.; Bell, G. I.; Harper, P. S.: Linkage relationshipsof the
insulin receptor gene with the complement component 3, LDLreceptor,
apolipoprotein C2 and myotonic dystrophy loci on chromosome19. Hum. Genet.
74: 267- 269, 1986.

GAM116 301 INSR Shimada, F.; Suzuki, Y.; Taira, M.; Hashimoto, N.; Nozaki, O.;Makino, H.; 3 A c
Yoshida, S.: Abnormal messenger ribonucleic acid (mRNA)transcribed from a
mutant insulin receptor gene in a patient withtype A insulin resistance.
Diabetologia 35: 639- 644, 1992.

GAM116 301 INSR Shimada, F.; Taira, M.; Suzuki, Y.; Hashimoto, N.; Nozaki, O.;Taira, M.; 3 A c
Tatibana, M.; Ebina, Y.; Tawata, M.; Onaya, T.; Makino,H.; Yoshida, S.:
Insulin- resistant diabetes associated with partialdeletion of insulin-
receptor gene. Lancet 335: 1179- 1181, 1990.

GAM116 301 INSR Taira, M.; Taira, M.; Hashimoto, N.; Shimada, F.; Suzuki, Y.;Kanatsuka, A.; 3 A c
Nakamura, F.; Ebina, Y.; Tatibana, M.; Makino, H.;Yoshida, S.: Human
diabetes associated with a deletion of the tyrosinekinase domain of the
insulin receptor. Science 245: 63- 66, 1989.

GAM116 301 INSR Takahashi, Y.; Kadowaki, H.; Ando, A.; Quin, J. D.; MacCuish,A. C.; Yazaki, 3 A c
Y.; Akanuma, Y.; Kadowaki, T.: Two aberrant splicingscaused by mutations in
the insulin receptor gene in cultured lymphocytesfrom a patient with Rabson-

Mendenhall's syndrome. J. Clin. Invest. 101:588- 594, 1998.

GAM116 301 INSR Taylor, S. I.; Cama, A.; Accili, D.; Barbetti, F.; Imano, E.;Kadowaki, H.; 3 A c
Kadowaki, T.: Genetic basis of endocrine disease 1:molecular genetics of
insulin resistant diabetes mellitus. J. Clin.Endocr. Metab. 73: 1158- 1163,
1991.

GAM116 301 INSR Taylor, S. I.; Marcus- Samuels, B.; Ryan- Young, J.; Leventhal,S.; Elders, 3 A c
M. J.: Genetics of the insulin receptor defect in a patientwith extreme
insulin resistance. J. Clin. Endocr. Metab. 62: 1130- 1135,1986.

GAM116 301 INSR Taylor, S. I.; Underhill, L. H.; Hedo, J. A.; Roth, J.; SerranoRios, M.; 3 A c
Blizzard, R. M.: Decreased insulin binding to culturedcells from a patient
with the Rabson- Mendenhall syndrome: dichotomybetween studies with cultured
lymphocytes and cultured fibroblasts. J.Clin. Endocr. Metab. 56: 856- 861,
1983.

GAM116 301 INSR Tevaarwerk, G. J. M.; Strickland, K. P.; Lin, C. H.; Hudson, A.J.: Studies 3 A c
on insulin resistance and insulin receptor binding inmyotonia dystrophica.
J. Clin. Endocr. Metab. 49: 216- 222, 1979.

GAM116 301 INSR Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 A c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM116 301 INSR Ullrich, A.; Bell, J. R.; Chen, E. Y.; Herrera, R.; Petruzzelli,L. M.; Dull, 3 A c
T. J.; Gray, A.; Coussens, L.; Liao, Y.- C.; Tsubokawa,M.; Mason, A.;
Seeburg, P. H.; Grunfeld, C.; Rosen, O. M.; Ramachandran,J.: Human insulin
receptor and its relationship to the tyrosine kinasefamily of oncogenes.
Nature 313: 756- 761, 1985.

GAM116 301 INSR van der Vorm, E. R.; Kuipers, A.; Kielkopf- Renner, S.; Krans,H. M. J.; 3 A c
Moller, W.; Maassen, J. A.: A mutation in the insulin receptorthat impairs
proreceptor processing but not insulin binding. J. Biol.Chem. 269: 14297-
14302, 1994.

GAM116 301 INSR van der Vorm, E. R.; van der Zon, G. C. M.; Moller, W.; Krans,H. M. J.; 3 A c
Lindhout, D.; Maassen, J. A.: An arg for gly substitutionat position 31 in
the insulin receptor, linked to insulin resistance,inhibits receptor
processing and transport. J. Biol. Chem. 267:66- 71, 1992.

GAM116 301 INSR Ward, G. M.; Harrison, L. C.: Structure of the human erythrocyteinsulin 3 A c
receptor. Diabetes 35: 101- 105, 1986.

GAM116 301 INSR Wertheimer, E.; Lu, S.- P.; Backeljauw, P. F.; Davenport, M. L.;Taylor, S. 3 A c
I.: Homozygous deletion of the human insulin receptorgene results in
leprechaunism. Nature Genet. 5: 71- 73, 1993.

GAM116 301 INSR Williams, D. L.; Look, A. T.; Melvin, S. L.; Roberson, P. K.;Dahl, G.; 3 A c
Flake, T.; Stass, S.: New chromosomal translocations correlatewith specific
immunophenotypes of childhood acute lymphoblastic leukemia. Cell 36:101-
109, 1984.

GAM116 301 INSR Williams, J. F.; McClain, D. A.; Dull, T. J.; Ullrich, A.; Olefsky,J. M.: 3 A c
Characterization of an insulin receptor mutant lacking thesubunit processing
site. J. Biol. Chem. 265: 8463- 8469, 1990.

GAM116 301 INSR Yamamoto- Honda, R.; Koshio, O.; Tobe, K.; Shibasaki, Y.; Momomura,K.; 3 A c
Odawara, M.; Kadowaki, T.; Takaku, F.; Akanuma, Y.; Kasuga, M.:
Phosphorylation state and biological function of a mutant humaninsulin
receptor val(996). J. Biol. Chem. 265: 14777- 14783, 1990.

GAM116 301 INSR Yang- Feng, T. L.; Francke, U.; Ullrich, A.: Gene for human insulinreceptor: 3 A c
localization to site on chromosome 19 involved in pre- B- cellleukemia.
Science 228: 728- 731, 1985.

GAM116 301 INSR Yoshimasa, Y.; Seino, S.; Whittaker, J.; Kakehi, T.; Kosaki, A.;Kuzuya, H.; 3 A c
Imura, H.; Bell, G. I.; Steiner, D. F.: Insulin- resistantdiabetes due to a
point mutation that prevents insulin proreceptorprocessing. Science 240:
784- 787, 1988.

GAM116 301 KCNJ10 Doupnik, C. A.; Davidson, N.; Lester, H. A.: The inward rectifierpotassium 3 A c
channel family. Curr. Opin. Neurobiol. 5: 268- 277, 1995.

GAM116 301 KCNJ10 Tada, Y.; Horio, Y.; Takumi, T.; Terayama, M.; Tsuji, L.; Copeland,N. G.; 3 A c
Jenkins, N. A.; Kurachi, Y.: Assignment of the glial inwardlyrectifying
potassium channel K(AB)- 2/Kir4.1 (Kcnj10) gene to the distalregion of mouse
chromosome 1. Genomics 45: 629- 630, 1997.

GAM116 301 KCNJ10 Takumi, T.; Ishii, T.; Horio, Y.; Morishige, K.- I.; Takahashi,N.; Yamada, 3 A c
M.; Yamashita, T.; Kiyama, H.; Sohmiya, K.; Nakanishi,S.; Kurachi, Y.: A
novel ATP- dependent inward rectifier potassiumchannel expressed
predominantly in glial cells. J. Biol. Chem. 270:16339- 16436, 1995.

GAM116 301 KCNMA1 Pallanck, L.; Ganetzky, B.: Cloning and characterization of humanand mouse 3 A c
homologs of the Drosophila calcium- activated potassium channelgene,
slowpoke. Hum. Molec. Genet. 3: 1239- 1243, 1994.

GAM116 301 KCNMA1 Ramanathan, K.; Michael, T. H.; Jiang, G.- J.; Hiel, H.; Fuchs,P. A.: A 3 A c
molecular mechanism for electrical tuning of cochlear haircells. Science
283: 215- 217, 1999.

GAM116 301 KCNMA1 Silberberg, S. D.; Magleby, K. L.: Beating the odds with big K. Science 3 A c
285:1859- 1860, 1999.

GAM116 301 KCNMA1 Valverde, M. A.; Rojas, P.; Amigo, J.; Cosmelli, D.; Orio, P.;Bahamonde, M. 3 A c
I.; Mann, G. E.; Vergara, C.; Latorre, R.: Acute activationof maxi- K
channels (hSlo) by estradiol binding to the beta subunit. Science 285:1929-
1931, 1999.

GAM116 301 LLGL1 Campbell, H. D.; Fountain, S.; Young, I. G.; Claudianos, C.; Hoheisel,J. D.; 3 A c
Chen, K.- S.; Lupski, J. R.: Genomic structure, evolution,and expression of
human FLII, a gelsolin and leucine- rich- repeat familymember: overlap with
LLGL. Genomics 42: 46- 54, 1997.

GAM116 301 LLGL1 Koyama, K.; Fukushima, Y.; Inazawa, J.; Tomotsune, D.; Takahashi,N.; 3 A c
Nakamura, Y.: The human homologue of the murine Llglh gene (LLGL)maps within
the Smith- Magenis syndrome region in 17p11.2. Cytogenet.Cell Genet. 72: 78-
82, 1996.

GAM116 301 LLGL1 Ohshiro, T.; Yagami, T.; Zhang, C.; Matsuzaki, F.: Role of corticaltumour- 3 A c
suppressor proteins in asymmetric division of Drosophila neuroblast. Nature
408:593- 596, 2000.

GAM116 301 LLGL1 Peng, C.- Y.; Manning, L.; Albertson, R.; Doe, C. Q.: The tumour- 3 A c
suppressorgenes lgl and dlg regulate basal protein targeting in Drosophila
neuroblasts. Nature 408:596- 600, 2000.

GAM116 301 LLGL1 Strand, D.; Unger, S.; Corvi, R.; Hartenstein, K.; Schenkel, H.;Kalmes, A.; 3 A c
Merdes, G.; Neumann, B.; Krieg- Schneider, F.; Coy, J.F.; Poustka, A.;
Schwab, M.; Mechler B. M.: A human homologue ofthe Drosophila tumour
suppressor gene l(2)gl maps to 17p11.2- 12 andcodes for a cytoskeletal
protein that associates with nonmuscle myosinII heavy chain. Oncogene 11:
291- 301, 1995.

GAM116 301 MAP3K7 Dempsey, C. E.; Sakurai, H.; Sugita, T.; Guesdon, F.: Alternativesplicing 3 A c

and gene structure of the transforming growth factor beta- activatedkinase 1. Biochim. Biophys. Acta 1517: 46- 52, 2000.

GAM116 301 MAP3K7 Kondo, M.; Osada, H.; Uchida, K.; Yanagisawa, K.; Masuda, A.; Takagi,K.; Takahashi, T.; Takahashi, T.: Molecular cloning of human TAK1and its mutational analysis in human lung cancer. Int. J. Cancer 75:559- 563, 1998. 3 A c

GAM116 301 MAP3K7 Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.: TGF- beta-activatedkinase 1 stimulates NF- kappa- B activation by an NF- kappa- B-inducingkinase- independent mechanism. Biochem. Biophys. Res. Commun. 243:545- 549, 1998. 3 A c

GAM116 301 MAP3K7 Wang, C.; Deng, L.; Hong, M.; Akkaraju, G. R.; Inoue, J.; Chen,Z. J.: TAK1 is a ubiquitin- dependent kinase of MKK and IKK. Nature 412:346- 351, 2001. 3 A c

GAM116 301 MAP3K7 Yamaguchi, K.; Shirakabe, K.; Shibuya, H.; Irie, K.; Oishi, I.;Ueno, N.; Taniguchi, T.; Nishida, E.; Matsumoto, K.: Identificationof a member of the MAPKKK family as a potential mediator of TGF- betasignal transduction. Science 270: 2008- 2011, 1995. 3 A c

GAM116 301 MCL1 Bae, J.; Leo, C. P.; Hsu, S. Y.; Hsueh, A. J. W.: MCL- 1S, a splicingvariant of the antiapoptotic BCL- 2 family member MCL- 1, encodes aproapoptotic protein possessing only the BH3 domain. J. Biol. Chem. 275:25255- 25261, 2000. 3 A c

GAM116 301 MCL1 Craig, R. W.; Jabs, E. W.; Zhou, P.; Kozopas, K. M.; Hawkins, A.L.; Rochelle, J. M.; Seldin, M. F.; Griffin, C. A.: Human and mousechromosomal mapping of the myeloid cell leukemia- 1 gene: MCL1 mapsto human chromosome 1q21, a region that is frequently altered in preneoplasticand neoplastic disease. Genomics 23: 457- 463, 1994. 3 A c

GAM116 301 MCL1 Kozopas, K. M.; Yang, T.; Buchan, H. L.; Zhou, P.; Craig, R. W.: MCL1, a gene expressed in programmed myeloid cell differentiation,has sequence similarity to BCL2. Proc. Nat. Acad. Sci. 90: 3516- 3520,1993. 3 A c

GAM116 301 MCL1 Rinkenberger, J. L.; Horning, S.; Klocke, B.; Roth, K.; Korsmeyer,S. J.: Mcl- 1 deficiency results in peri- implantation embryonic lethality. GenesDev. 14: 23- 27, 2000. 3 A c

GAM116 301 MDFI Chen, C. M.; Kraut, N.; Groudine, M.; Weintraub, H.: I- mf, a novelmyogenic repressor, interacts with members of the MyoD family. Cell 86:731- 741, 1996. 3 A c

GAM116 301 MDFI Kraut, N.: The gene encoding I- mf (Mdfi) maps to human chromosome6p21 and mouse chromosome 17. Mammalian Genome 8: 618- 619, 1997. 3 A c

GAM116 301 MDFI Kraut, N.; Snider, L.; Chen, C.- M. A.; Tapscott, S. J.; Groudine,M.: Requirement of the mouse I- mfa gene for placental developmentand skeletal patterning. EMBO J. 17: 6276- 6288, 1998. 3 A c

GAM116 301 MTMR4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 A c

GAM116 301 MTMR4 Laporte, J.; Blondeau, F.; Buj- Bello, A.; Tentler, D.; Kretz, C.;Dahl, N.; Mandel, J.- L.: Characterization of the myotubularin dualspecificity phosphatase gene family from yeast to human. Hum. Molec.Genet. 7: 1703- 1712, 1998. 3 A c

GAM116 301 MTMR4 Zhao, R.; Qi, Y.; Chen, J.; Zhao, Z. J.: FYVE- DSP2, a FYVE domain-containingdual specificity protein phosphatase that dephosphorylates phosphotidylinositol(sic) 3- phosphate. Exp. Cell Res. 265: 329- 338, 2001. 3 A c

GAM116 301 NGFR Bentley, K. L.; Ferguson- Smith, A. C.; Miki, T.; Kidd, K. K.; Ruddle,F. H.: 3 A c

Physical linkage of Hox 2.1 and nerve growth factor receptor.(Abstract) Cytogenet. Cell Genet. 51: 961 only, 1989.

GAM116 301 NGFR Bibel, M.; Barde, Y.- A.: Neurotrophins: key regulators of cellfate and cell shape in the vertebrate nervous system. Genes Dev. 14:2919- 2937, 2000. 3 A c

GAM116 301 NGFR Bothwell, M.: p75(NTR): a receptor after all. Science 272: 506- 507,1996. 3 A c

GAM116 301 NGFR Carter, B. D.; Kaltschmidt, C.; Kaltschmidt, B.; Offenhauser, N.;Bohm-Matthaei, R.; Baeuerle, P. A.; Barde, Y.- A.: Selective activationof NF-kappa- B by nerve growth factor through the neurotrophin receptorp75. Science 272: 542- 545, 1996. 3 A c

GAM116 301 NGFR Carter, B. D.; Lewin, G. R.: Neurotrophins live or let die: doesp75(NTR) decide? Neuron 18: 187- 190, 1997. 3 A c

GAM116 301 NGFR Chao, M. V.; Bothwell, M. A.; Ross, A. H.; Koprowski, H.; Lanahan,A. A.; Buck, C. R.; Sehgal, A.: Gene transfer and molecular cloningof the human NGF receptor. Science 232: 518- 521, 1986. 3 A c

GAM116 301 NGFR Dobrowsky, R. T.; Werner, M. H.; Castellino, A. M.; Chao, M. V.;Hannun, Y. A.: Activation of the sphingomyelin cycle through thelow- affinity neurotrophin receptor. Science 265: 1596- 1599, 1994. 3 A c

GAM116 301 NGFR Grob, P. M.; Ross, A. H.; Koprowski, H.; Bothwell, M.: Characterizationof the human melanoma nerve growth factor receptor. J. Biol. Chem. 260:8044-8049, 1985. 3 A c

GAM116 301 NGFR Harada, T.; Harada, C.; Nakayama, N.; Okuyama, S.; Yoshida, K.;Kohsaka, S.; Matsuda, H.; Wada, K.: Modification of glial- neuronalcell interactions prevents photoreceptor apoptosis during light- inducedretinal degeneration. Neuron 26: 533- 541, 2000. 3 A c

GAM116 301 NGFR Hempstead, B. L.; Martin- Zanca, D.; Kaplan, D. R.; Parada, L.F.; Chao, M. V.: High- affinity NGF binding requires coexpressionof the trk proto-oncogene and the low- affinity NGF receptor. Nature 350:678- 683, 1991. 3 A c

GAM116 301 NGFR Huebner, K.; Isobe, M.; Chao, M.; Bothwell, M.; Ross, A. H.; Finan,J.; Hoxie, J. A.; Sehgal, A.; Buck, C. R.; Lanahan, A.; Nowell, P.C.; Koprowski, H.; Croce, C. M.: The nerve growth factor receptorgene is at human chromosome region 17q12- 17q22, distal to the chromosome17 breakpoint in acute leukemias. Proc. Nat. Acad. Sci. 83: 1403- 1407,1986. 3 A c

GAM116 301 NGFR Ip, N. Y.; Stitt, T. N.; Tapley, P.; Klein, R.; Glass, D. J.;Fandl, J.; Greene, L. A.; Barbacid, M.; Yancopoulos, G. D.: Similaritiesand differences in the way neurotrophins interact with the Trk receptorsin neuronal and nonneuronal cells. Neuron 10: 137- 149, 1993. 3 A c

GAM116 301 NGFR Johnson, D.; Lanahan, A.; Buck, C. R.; Sehgal, A.; Morgan, C.;Mercer, E.; Bothwell, M.; Chao, M.: Expression and structure of thehuman NGF receptor. Cell 47: 545- 554, 1986. 3 A c

GAM116 301 NGFR Lee, K. F.; Li, E.; Huber, J.; Landis, S. C.; Sharpe, A. H.; Chao,M. V.; Jaenisch, R.: Targeted mutation of the gene encoding the lowaffinity NGF receptor p75 leads to deficits in the peripheral sensorynervous system. Cell 69: 737- 749, 1992. 3 A c

GAM116 301 NGFR Mischel, P. S.; Smith, S. G.; Vining, E. R.; Valletta, J. S.;Mobley, W. C.; Reichardt, L. F.: The extracellular domain of p75(NTR)is necessary to inhibit neurotrophin- 3 signaling through TrkA. J.Biol. Chem. 276: 11294-11301, 2001. 3 A c

GAM116 301 NGFR Rettig, W. J.; Thomson, T. M.; Spengler, B. A.; Biedler, J. L.;Old, L. J.: Assignment of human nerve growth factor receptor geneto chromosome 17 and regulation of receptor expression in somaticcell hybrids. Somat. Cell Molec. 3 A c

Genet. 12: 441- 447, 1986.

GAM116 301 NGFR Tuffereau, C.; Benejean, J.; Blondel, D.; Kieffer, B.; Flamand,A.: Low- 3 A c
affinity nerve- growth factor receptor (p75NTR) can serveas a receptor for
rabies virus. EMBO J. 17: 7250- 7259, 1998.

GAM116 301 NGFR Welcher, A. A.; Bitler, C. M.; Radeke, M. J.; Shooter, E. M.:Nerve growth 3 A c
factor binding domain of the nerve growth factor receptor. Proc.Nat. Acad.
Sci. 88: 159- 163, 1991.

GAM116 301 OSM Miles, S. A.; Martinez- Maza, O.; Rezai, A.; Magpantay, L.; Kishimoto,T.; 3 A c
Nakamura, S.; Radka, S. F.; Linsley, P. S.: Oncostatin M as apotent mitogen
for AIDS- Kaposi's sarcoma- derived cells. Science 255:1432- 1434, 1992.

GAM116 301 OSM Modur, V.; Feldhaus, M. J.; Weyrich, A. S.; Jicha, D. L.; Prescott,S. M.; 3 A c
Zimmerman, G. A.; McIntyre, T. M.: Oncostatin M is a
proinflammatorymediator: in vivo effects correlate with endothelial cell
expressionof inflammatory cytokines and adhesion molecules. J. Clin. Invest.
100:158- 168, 1997.

GAM116 301 OSM Nair, B. C.; DeVico, A. L.; Nakamura, S.; Copeland, T. D.; Chen,Y.; Patel, 3 A c
A.; O'Neil, T.; Oroszlan, S.; Gallo, R. C.; Sarngadharan,M. G.:
Identification of a major growth factor for AIDS- Kaposi'ssarcoma cells as
oncostatin M. Science 255: 1430- 1432, 1992.

GAM116 301 OSM Rose, T. M.; Bruce, A. G.: Oncostatin M is a member of a cytokinefamily that 3 A c
includes leukemia- inhibitory factor, granulocyte colony- stimulatingfactor,
and interleukin 6. Proc. Nat. Acad. Sci. 88: 8641- 8645,1991.

GAM116 301 OSM Rose, T. M.; Lagrou, M. J.; Fransson, I.; Werelius, B.; Delattre,O.; Thomas, 3 A c
G.; de Jong, P. J.; Todaro, G. J.; Dumanski, J. P.: Thegenes for oncostatin
M (OSM) and leukemia inhibitory factor (LIF)are tightly linked on human
chromosome 22. Genomics 17: 136- 140,1993.

GAM116 301 OSM Schwaller, J.; Parganas, E.; Wang, D.; Cain, D.; Aster, J. C.;Williams, I. 3 A c
R.; Lee, C.- K.; Gerthner, R.; Kitamura, T.; Frantsve,J.; Anastasiadou, E.;
Loh, M. L.; Levy, D. E.; Ihle, J. N.; Gilliland,D. G.: Stat5 is essential
for the myelo- and lymphoproliferativedisease induced by TEL/JAK2. Molec.
Cell 6: 693- 704, 2000.

GAM116 301 OSM Zarling, J. M.; Shoyab, M.; Marquardt, H.; Hanson, M. B.; Lioubin,M. N.; 3 A c
Todaro, G. J.: Oncostatin M: a growth regulator produced bydifferentiated
histiocytic lymphoma cells. Proc. Nat. Acad. Sci. 83:9739- 9743, 1986.

GAM116 301 PDE4B Huston, E.; Lumb, S.; Russell, A.; Catterall, C.; Ross, A. H.;Steele, M. R.; 3 A c
Bolger, G. B.; Perry, M. J.; Owens, R. J.; Houslay,M. D.: Molecular cloning
and transient expression in COS7 cells ofa novel human PDE4B cAMP- specific
phosphodiesterase, HSPDE4B3. Biochem.J. 328: 549- 558, 1997.

GAM116 301 PDE4B Livi, G. P.; Kmetz, P.; McHale, M. M.; Cieslinski, L. B.; Sathe,G. M.; 3 A c
Taylor, D. P.; Davis, R. L.; Torphy, T. J.; Balcarek, J. M.: Cloning and
expression of cDNA for a human low- K(m), rolipram- sensitivecyclic AMP
phosphodiesterase. Molec. Cell. Biol. 10: 2678- 2686,1990.

GAM116 301 PDE4B Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 3 A c
Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases
inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM116 301 PDE4B Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins,M.; 3 A c
Jarnagin, K.; Shelton, E. R.: The cDNA of a human lymphocytecyclic- AMP
phosphodiesterase (PDE IV) reveals a multigene family. Gene 129:239- 247,
1993.

GAM116 301 PDE4B Szpirer, C.; Szpirer, J.; Riviere, M.; Swinnen, J.; Vicini, E.;Conti, M.: 3 A c

Chromosomal localization of the human and rat genes (PDE4Dand PDE4B) encoding the cAMP- specific phosphodiesterases 3 and 4. Cytogenet.Cell Genet. 69: 11- 14, 1995.

GAM116 301 PDE4B Xu, R. X.; Hassell, A. M.; Vanderwall, D.; Lambert, M. H.; Holmes,W. D.; 3 A c Luther, M. A.; Rocque, W. J.; Milburn, M. V.; Zhao, Y.; Ke,H.; Nolte, R. T.: Atomic structure of PDE4: insights into phosphodiesterasemechanism and specificity. Science 288: 1822- 1825, 2000.

GAM116 301 PIGF Inoue, N.; Kinoshita, T.; Orii, T.; Takeda, J.: Cloning of a humangene, PIG- 3 A c F, a component of glycosyl- phosphatidylinositol anchor biosynthesis,by a novel expression cloning strategy. J. Biol. Chem. 268: 6882- 6885,1993.

GAM116 301 PIGF Ohishi, K.; Inoue, N.; Endo, Y.; Fujita, T.; Takeda, J.; Kinoshita,T.: 3 A c Structure and chromosomal localization of the GPI- anchor synthesisgene PIGF and its pseudogene psi- PIGF. Genomics 29: 804- 807, 1995.

GAM116 301 PIGF Ohishi, K.; Kurimoto, Y.; Inoue, N.; Endo, Y.; Takeda, J.; Kinoshita,T.: 3 A c Cloning and characterization of the murine GPI anchor synthesisgene Pigf, a homologue of the human PIGF gene. Genomics 34: 340- 346,1996.

GAM116 301 PIGF Ware, R. E.; Howard, T. A.; Kamitani, T.; Chang, H.- M.; Yeh, E.T. H.; 3 A c Seldin, M. F.: Chromosomal assignment of genes involved inglycosylphosphatidylinositol anchor biosynthesis: implications forthe pathogenesis of paroxysmal nocturnal hemoglobinuria. Blood 83:3753- 3757, 1994.

GAM116 301 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 A c Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.: Genomicorganization, comparative analysis, and genetic polymorphisms of thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733, 2001.

GAM116 301 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 A c Chen, S. G.: Expression and structural characterizationof the recombinant human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM116 301 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 A c Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.; Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)- deficient mice is associated with upregulation of thenovel PrP- like protein doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM116 301 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 A c T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin the prion- like protein gene (Prnd) and their implications inhuman prion diseases, Alzheimer's disease and other neurological disorders. Hum.Genet. 109: 319- 325, 2001.

GAM116 301 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 A c P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N- glycosylated, glycosylphosphatidylinositol- anchored protein:expression in testis and ectopic production in the brains of Prnp(0/0)mice predisposed to Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM116 301 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 A c 915, 1999.

GAM116 301 PTPRF Ahmad, F.; Goldstein, B. J.: Functional association between theinsulin 3 A c receptor and the transmembrane protein- tyrosine phosphataseLAR in intact cells. J. Biol. Chem. 272: 448- 457, 1997.

GAM116 301 PTPRF Disteche, C. M.; Adler, D. A.; Tedder, T. F.; Saito, H.: Mappingof the genes 3 A c

for LYAM1, a new lymphocyte adhesion molecule, and forLAR, a new receptor-linked protein tyrosine phosphatase, to humanchromosome 1 (Abstract) Cytogenet. Cell Genet. 51: 990 only, 1989.

GAM116 301 PTPRF Harder, K. W.; Saw, J.; Miki, N.; Jirik, F.: Coexisting amplificationsof the 3 A c chromosome 1p32 genes (PTPRF and MYCL1) encoding protein tyrosinephosphatase LAR and L- myc in a small cell lung cancer line. Genomics 27:552- 553, 1995.

GAM116 301 PTPRF Jirik, F. R.; Harder, K. W.; Melhado, I. G.; Anderson, L. L.; Duncan,A. M. 3 A c V.: The gene for leukocyte antigen- related tyrosine phosphatase(LAR) is localized to human chromosome 1p32, a region frequently deletedin tumors of neuroectodermal origin. Cytogenet. Cell Genet. 61:266- 268, 1992.

GAM116 301 PTPRF Nam, H.- J.; Poy, F.; Krueger, N. X.; Saito, H.; Frederick, C. A.: Crystal 3 A c structure of the tandem phosphatase domains of RPTP LAR. Cell 97:449- 457, 1999.

GAM116 301 PTPRF O'Grady, P.; Krueger, N. X.; Streuli, M.; Saito, H.: Genomic organizationof 3 A c the human LAR protein tyrosine phosphatase gene and alternativesplicing in the extracellular fibronectin type- III domains. J. Biol.Chem. 269: 25193- 25199, 1994.

GAM116 301 PTPRF Schaapveld, R. Q. J.; van den Maagdenberg, A. M. J. M.; Schepens,J. T. G.; 3 A c Olde Weghuis, D.; Geurts van Kessel, A.; Wieringa, B.; Hendriks,W. J. A. J.: The mouse gene Ptprf encoding the leukocyte common antigen- relatedmolecule LAR: cloning, characterization, and chromosomal localization. Genomics 27:124- 130, 1995.

GAM116 301 PTPRF Schaapveld, R. Q.; Schepens, J. T.; Robinson, G. W.; Attema, J.;Oerlemans, 3 A c F. T.; Fransen, J. A.; Streuli, M.; Wieringa, B.; Hennighausen,L.; Hendriks, W. J.: Impaired mammary gland development and functionin mice lacking LAR receptor- like tyrosine phosphatase activity. Dev.Biol. 188: 134- 146, 1997.

GAM116 301 PTPRF Tsujikawa, K.; Kawakami, N.; Uchino, Y.; Ichijo, T.; Furukawa,T.; Saito, H.; 3 A c Yamamoto, H.: Distinct functions of the two proteintyrosine phosphatase domains of LAR (leukocyte common antigen- related)on tyrosine dephosphorylation of insulin receptor. Molec. Endocr. 15:271- 280, 2001.

GAM116 301 RPS24 Brown, S. J.; Jewell, A.; Maki, C. G.; Roufa, D. J.: A cDNA encodinghuman 3 A c ribosomal protein S24. Gene 91: 293- 296, 1990.

GAM116 301 RPS24 Jones, A.- M.; Marzella, R.; Rocchi, M.; Hewitt, J. E.: Mappingof the human 3 A c ribosomal small subunit protein gene RPS24 to the chromosome10q22- q23 boundary. Genomics 39: 121- 122, 1997.

GAM116 301 RPS24 Kenmochi, N.; Kawaguchi, T.; Rozen, S.; Davis, E.; Goodman, N.;Hudson, T. 3 A c J.; Tanaka, T.; Page, D. C.: A map of 75 human ribosomalprotein genes. Genome Res. 8: 509- 523, 1998.

GAM116 301 RPS24 Xu, W.- B.; Roufa, D. J.: The gene encoding human ribosomal proteinS24 and 3 A c tissue- specific expression of differentially spliced mRNAs. Gene 169:257- 262, 1996.

GAM116 301 SCN8A Burgess, D. L.; Kohrman, D. C.; Galt, J.; Plummer, N. W.; Jones,J. M.; 3 A c Spear, B.; Meisler, M. H.: Mutation of a new sodium channelgene, Scn8a, in the mouse mutant 'motor endplate disease'. NatureGenet. 10: 461- 465, 1995.

GAM116 301 SCN8A DeRepentigny, Y.; Cote, P. D.; Pool, M.; Bernier, G.; Girard, S.;Vidal, S. 3 A c M.; Kothary, R.: Pathological and genetic analysis of thedegenerating muscle (dmu) mouse: a new allele of Scn8a. Hum. Molec.Genet. 10: 1819- 1827, 2001.

GAM116 301 SCN8A Kohrman, D. C.; Harris, J. B.; Meisler, M. H.: Mutation detectionin the med 3 A c and med(J) alleles of the sodium channel Scn8a: unusualsplicing due to a minor class AT- AC intron. J. Biol. Chem. 271:17576- 17581, 1996.

GAM116 301 SCN8A Kohrman, D. C.; Plummer, N. W.; Schuster, T.; Jones, J. M.; Jang,W.; 3 A c
Burgess, D. L.; Galt, J.; Spear, B. T.; Meisler, M. H.: Insertionalmutation
of the motor endplate disease (med) locus on mouse chromosome15. Genomics
26: 171- 177, 1995.

GAM116 301 SCN8A Kohrman, D. C.; Smith, M. R.; Goldin, A. L.; Harris, J.; Meisler,M. H.: A 3 A c
missense mutation in the sodium channel Scn8a is responsiblefor cerebellar
ataxia in the mouse mutant jolting. J. Neurosci. 16:5993- 5999, 1996.

GAM116 301 SCN8A Meisler, M. H.; Sprunger, L. K.; Plummer, N. W.; Escayg, A.; Jones,J. M.: 3 A c
Ion channel mutations in mouse models of inherited neurologicaldisease. Ann.
Med. 29: 569- 574, 1997.

GAM116 301 SCN8A Plummer, N. W.; Galt, J.; Jones, J. M.; Burgess, D. L.; Sprunger,L. K.; 3 A c
Kohrman, D. C.; Meisler, M. H.: Exon organization, codingsequence, physical
mapping, and polymorphic intragenic markers forthe human neuronal sodium
channel gene SCN8A. Genomics 54: 287- 296,1998.

GAM116 301 SCN8A Plummer, N. W.; McBurney, M. W.; Meisler, M. H.: Alternative splicingof the 3 A c
sodium channel SCN8A predicts a truncated two- domain proteinin fetal brain
and non- neuronal cells. J. Biol. Chem. 272: 24008- 24015,1997.

GAM116 301 SCN8A Reid, E.; Escayg, A.; Dearlove, A. M.; Lee, D. D.; Meisler, M.H.; 3 A c
Rubinsztein, D. C.: The spastic paraplegia SPG10 locus: narrowingof critical
region and exclusion of sodium channel gene SCN8A as acandidate. J. Med.
Genet. 38: 65- 67, 2001.

GAM116 301 SCN8A Sprunger, L. K.; Escayg, A.; Tallaksen- Greene, S.; Albin, R. L.;Meisler, M. 3 A c
H.: Dystonia associated with mutation of the neuronalsodium channel Scn8a
and identification of the modifier locus Scnm1on mouse chromosome 3. Hum.
Molec. Genet. 8: 471- 479, 1999.

GAM116 301 SFRP1 Baylin, S. B.; Herman, J. G.: DNA hypermethylation in 3 A c
tumorigenesis:epigenetics joins genetics. Trends Genet. 16: 168- 174, 2000.

GAM116 301 SFRP1 Cameron, E. E.; Bachman, K. E.; Myohanen, S.; Herman, J. G.; Baylin,S. B.: 3 A c
Synergy of demethylation and histone deacetylase inhibitionin the re-
expression of genes silenced in cancer. Nature Genet. 21:103- 107, 1999.

GAM116 301 SFRP1 Finch, P. W.; He, X.; Kelley, M. J.; Uren, A.; Schaudies, R. P.;Popescu, N. 3 A c
C.; Rudikoff, S.; Aaronson, S. A.; Varmus, H. E.; Rubin,J. S.: Purification
and molecular cloning of a secreted, frizzled- relatedantagonist of Wnt
action. Proc. Nat. Acad. Sci. 94: 6770- 6775, 1997.

GAM116 301 SFRP1 Fukuhara, K.; Kariya, M.; Kita, M.; Shime, H.; Kanamori, T.; Kosaka,C.; 3 A c
Orii, A.; Fujita, J.; Fujii, S.: Secreted frizzled related protein1 is
overexpressed in uterine leiomyomas, associated with a high
estrogenicenvironment and unrelated to proliferative activity. J. Clin.
Endocr.Metab. 87: 1729- 1736, 2002.

GAM116 301 SFRP1 Melkonyan, H. S.; Chang, W. C.; Shapiro, J. P.; Mahadevappa, M.;Fitzpatrick, 3 A c
P. A.; Kiefer, M. C.; Tomei, L. D.; Umansky, S. R.:SARPs: a family of
secreted apoptosis- related proteins. Proc. Nat.Acad. Sci. 94: 13636- 13641,
1997.

GAM116 301 SFRP1 Suzuki, H.; Gabrielson, E.; Chen, W.; Anbazhagan, R.; van Engeland,M.; 3 A c
Weijenberg, M. P.; Herman, J. G.; Baylin, S. B.: A genomic screenfor genes
upregulated by demethylation and histone deacetylase inhibitionin human
colorectal cancer. Nature Genet. 31: 141- 149, 2002.

GAM116 301 SLC22A12 Enomoto, A.; Kimura, H.; Chairoungdua, A.; Shigeta, Y.; Jutabha,P.; Cha, S. 3 A c
H.; Hosoyamada, M.; Takeda, M.; Sekine, T.; Igarashi,T.; Matsuo, H.;
Kikuchi, Y.; Oda, T.; Ichida, K.; Hosoya, T.; Shimokata,K.; Niwa, T.; Kanai,

Y.; Endou, H.: Molecular identification of arenal urate- anion exchanger that regulates blood urate levels. Nature 417:447- 452, 2002.

GAM116 301 SLC9A3R1 Bonilha, V. L.; Rodriguez- Boulan, E.: Polarity and developmentalregulation 3 A c of two PDZ proteins in the retinal pigment epithelium. Invest.Ophthal. Vis. Sci. 42: 3274- 3282, 2001.

GAM116 301 SLC9A3R1 Murthy, A.; Gonzalez- Agosti, C.; Cordero, E.; Pinney, D.; Candia,C.; 3 A c Solomon, F.; Gusella, J.; Ramesh, V.: NHE- RF, a regulatory cofactorfor Na(+)- H(+) exchange, is a common interactor for merlin and ERM(MERM) proteins. J. Biol. Chem. 273: 1273- 1276, 1998.

GAM116 301 SLC9A3R1 Reczek, D.; Berryman, M.; Bretscher, A.: Identification of EBP50:a PDZ- 3 A c containing phosphoprotein that associates with members of theezrin- radixin- moesin family. J. Cell Biol. 139: 169- 179, 1997.

GAM116 301 SLC9A3R1 Shenolikar, S.; Voltz, J. W.; Minkoff, C. M.; Wade, J. B.; Weinman,E. J.: 3 A c Targeted disruption of the mouse NHERF- 1 gene promotes internalizationof proximal tubule sodium- phosphate cotransporter type IIa and renalphosphate wasting. Proc. Nat. Acad. Sci. 99: 11470- 11475, 2002.

GAM116 301 ST14 Friedrich, R.; Fuentes- Prior, P.; Ong, E.; Coombs, G.; Hunter,M.; Oehler, 3 A c R.; Pierson, D.; Gonzalez, R.; Huber, R.; Bode, W.; Madison,E. L.: Catalytic domain structures of MT- SP1/matriptase, a matrix- degrading transmembrane serine proteinase. J. Biol. Chem. 277: 2160- 2168,2002.

GAM116 301 ST14 Lin, C.- Y.; Anders, J.; Johnson, M.; Sang, Q. A.; Dickson, R. B.: Molecular 3 A c cloning of cDNA for matriptase, a matrix- degrading serineprotease with trypsin- like activity. J. Biol. Chem. 274: 18231- 18236,1999.

GAM116 301 ST14 Lin, C.- Y.; Wang, J.- K.; Torri, J.; Dou, L.; Sang, Q. A.; Dickson,R. B.: 3 A c Characterization of a novel, membrane- bound, 80- kDa matrix- degradingprotease from human breast cancer cells: monoclonal antibody production,isolation, and localization. J. Biol. Chem. 272: 9147- 9152, 1997.

GAM116 301 ST14 Oberst, M.; Anders, J.; Xie, B.; Singh, B.; Ossandon, M.; Johnson,M.; 3 A c Dickson, R. B.; Lin, C.- Y.: Matriptase and HAI- 1 are expressedby normal and malignant epithelial cells in vitro and in vivo. Am.J. Path. 158: 1301- 1311, 2001.

GAM116 301 ST14 Takeuchi, T.; Shuman, M. A.; Craik, C. S.: Reverse biochemistry:use of 3 A c macromolecular protease inhibitors to dissect complex biologicalprocesses and identify a membrane- type serine protease in epithelialcancer and normal tissue. Proc. Nat. Acad. Sci. 96: 11054- 11061,1999.

GAM116 301 ST14 Zhang, Y.; Cai, X.; Schlegelberger, B.; Zheng, S.: Assignmentof human 3 A c putative tumor suppressor genes ST13 (alias SNC6) and ST14(alias SNC19) to human chromosome bands 22q13 and 11q24- q25 by insitu hybridization. Cytogenet. Cell Genet. 83: 56- 57, 1998.

GAM116 301 TEM1 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. 3 A c W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in mice and humans. Cancer Res. 61: 6649- 6655, 2001.

GAM116 301 TEM1 Christian, S.; Ahorn, H.; Koehler, A.; Eisenhaber, F.; Rodi, H.- P.;Garin- 3 A c Chesa, P.; Park, J. E.; Rettig, W. J.; Lenter, M. C.: Molecularcloning and characterization of endosialin, a C- type lectin- like cellsurface receptor of tumor endothelium. J. Biol. Chem. 276: 7408- 7414,2001.

GAM116 301 TEM1 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; 3 A c Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.; Kinzler, K. W.: Genes expressed in human tumor endothelium. Science

289:1197- 1202, 2000.

GAM116 301 THY1 Ades, E. W.; Zwerner, R. K.; Acton, R. T.; Balch, C. M.: Isolationand 3 A c
partial characterisation of the human homologue of Thy- 1. J.Exp. Med. 151:
400- 406, 1980.

GAM116 301 THY1 Bonewald, L.; Ades, E. W.; Tung, E.; Marchalonis, J. J.; Wang,A. C.: 3 A c
Biochemical characterization of human Thy- 1. J. Immunogenet. 11:283- 296,
1984.

GAM116 301 THY1 Gatti, R. A.; Lathrop, G. M.; Salser, W.; Silver, J.; Lalouel,J. M.; White, 3 A c
R.: Location of Thy- 1 with respect to a primary linkagemap of chromosome
11q. (Abstract) Cytogenet. Cell Genet. 46: 618only, 1987.

GAM116 301 THY1 Gatti, R. A.; Shaked, R.; Wei, S.; Koyama, M.; Salser, W.; Silver,J.: DNA 3 A c
polymorphism in the human Thy- 1 gene. Hum. Immun. 22:145- 150, 1988.

GAM116 301 THY1 Greenspan, R. J.; O'Brien, M. C.: Genetic evidence for the roleof Thy- 1 in 3 A c
neurite outgrowth in the mouse. J. Neurogenet. 5: 25- 36,1989.

GAM116 301 THY1 Grzeschik, K.- H.; Kazazian, H. H.: Report of the committee onthe genetic 3 A c
constitution of chromosomes 10, 11, and 12. Cytogenet.Cell Genet. 40: 179-
205, 1985.

GAM116 301 THY1 Hood, L.; Kronenberg, M.; Hunkapiller, T.: T cell antigen receptorsand the 3 A c
immunoglobulin supergene family. Cell 40: 225- 229, 1985.

GAM116 301 THY1 Letarte- Muirhead, M.; Barclay, A. N.; Williams, A. F.: Purificationof the 3 A c
Thy- 1 molecule, a major cell surface glycoprotein of rat
thymocytes.Biochem. J. 151: 685- 697, 1975.

GAM116 301 THY1 Mansour, M. H.; Negm, H. I.; Cooper, E. L.: Thy- 1 evolution. Dev.Comp. 3 A c
Immun. 11: 3- 15, 1987.

GAM116 301 THY1 McKenzie, J. L.; Fabre, J. W.: Human Thy- 1: unusual localizationand 3 A c
possible functional significance in lymphoid tissues. J. Immun. 126:843-
850, 1981.

GAM116 301 THY1 Morris, R.: Thy- 1 in developing nervous tissue. Dev. Neurosci. 7:133- 160, 3 A c
1985.

GAM116 301 THY1 Raff, M. C.: Surface antigenic markers for distinguishing T andB lymphocytes 3 A c
in mice. Transplant. Rev. 6: 52- 80, 1971.

GAM116 301 THY1 Rettig, W. J.; Dracopoli, N. C.; Chesa, P. G.; Spengler, B. A.;Beresford, H. 3 A c
R.; Davies, P.; Biedler, J. L.; Old, L. J.: Role ofhuman chromosome 11 in
determining surface antigenic phenotype ofnormal and malignant cells:
somatic cell genetic analysis of eightantigens, including putative human
Thy- 1. J. Exp. Med. 162: 1603- 1619,1985.

GAM116 301 THY1 Rettig, W. J.; Dracopoli, N. C.; Silver, J.; Old, L. J.: HumanTHY- 1: 3 A c
regional mapping on chromosome 11 and comparison with otherchromosome 11-
encoded cell surface glycoproteins. (Abstract) Cytogenet.Cell Genet. 40:
731 only, 1985.

GAM116 301 THY1 Rettig, W. J.; Dracopoli, N. C.; Spengler, B. A.; Biedler, J.L.; Old, L. J.: 3 A c
Somatic cell genetic analysis of human cell surfaceantigens, including
putative human Thy- 1: eight distinct antigenicsystems controlled by
chromosome 11. (Abstract) Cytogenet. CellGenet. 40: 732 only, 1985.

GAM116 301 THY1 Seki, T.; Spurr, N.; Obata, F.; Goyert, S.; Goodfellow, P.; Silver,J.: The 3 A c
human Thy- 1 gene: structure and chromosomal location. Proc.Nat. Acad. Sci.
82: 6657- 6661, 1985.

GAM116 301 THY1 Tse, A. G. D.; Barclay, A. N.; Watts, A.; Williams, A. F.: 3 A c
Aglycophospholipid tail at the carboxyl terminus of the Thy- 1
glycoproteinof neurons and thymocytes. Science 230: 1003- 1008, 1985.

GAM116 301 THY1 Tunnacliffe, A.; McGuire, R. S.: A physical linkage group inhuman chromosome band 11q23 covering a region implicated in leukocyteneoplasia. Genomics 8: 447- 453, 1990. 3 A c

GAM116 301 THY1 van den Elsen, P.; Bruns, G.; Gerhard, D. S.; Pravtcheva, D.;Jones, C.; Housman, D.; Ruddle, F. A.; Orkin, S.; Terhorst, C.: Assignmentof the gene coding for the T3- delta subunit of the T3- - T- cell receptorcomplex to the long arm of human chromosome 11 and to mouse chromosome9. Proc. Nat. Acad. Sci. 82: 2920- 2924, 1985. 3 A c

GAM116 301 THY1 van Rijs, J.; Giguere, V.; Hurst, J.; van Agthoven, T.; Geurtsvan Kessel, A.; Goyert, S.; Grosveld, F.: Chromosomal localizationof the human Thy- 1 gene. Proc. Nat. Acad. Sci. 82: 5832- 5835, 1985. 3 A c

GAM116 301 THY1 Williams, A. F.; Gagnon, J.: Neuronal cell Thy- 1 glycoprotein:homology with immunoglobulin. Science 216: 696- 703, 1982. 3 A c

GAM116 301 TRAF1 Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VanArsdale, T.;Ware, C.; Kieff, E.: The Epstein- Barr virus transforming proteinLMP1 engages signaling proteins for the tumor necrosis factor receptorfamily. Cell 80: 389- 399, 1995. 3 A c

GAM116 301 TRAF1 Rothe, M.; Wong, S. C.; Henzel, W. J.; Goeddel, D. V.: A novelfamily of putative signal transducers associated with the cytoplasmicdomain of the 75 kDa tumor necrosis factor receptor. Cell 78: 681- 692,1994. 3 A c

GAM116 301 TRAF1 Siemienski, K.; Peters, N.; Scheurich, P.; Wajant, H.: Organizationof the human tumour necrosis factor receptor- associated factor 1 (TRAF1)gene and mapping to chromosome 9q33- 34. Gene 195: 35- 39, 1997. 3 A c

GAM116 301 TRAF1 Tsitsikov, E. N.; Laouini, D.; Dunn, I. F.; Sannikova, T. Y.; Davidson,L.; Alt, F. W.; Geha, R. S.: TRAF1 is a negative regulator of TNFsignaling: enhanced TNF signaling in TRAF1- deficient mice. Immunity 15:647- 657, 2001. 3 A c

GAM116 301 WNT5A Clark, C. C.; Cohen, I.; Eichstetter, I.; Cannizzaro, L. A.; McPherson,J. D.; Wasmuth, J. J.; Iozzo, R. V.: Molecular cloning of the humanproto-oncogene Wnt- 5A and mapping of the gene (WNT5A) to chromosome3p14- p21. Genomics 18: 249- 260, 1993. 3 A c

GAM116 301 WNT5A Gavin, B. J.; McMahon, J. A.; McMahon, A. P.: Expression of multiplenovel Wnt- 1/int- 1- related genes during fetal and adult mouse development. GenesDev. 4: 2319- 2332, 1990. 3 A c

GAM116 301 WNT5A He, X.; Saint- Jeannet, J.- P.; Wang, Y.; Nathans, J.; Dawid, I.;Varmus, H.: A member of the frizzled protein family mediating axisinduction by Wnt- 5A. Science 275: 1652- 1654, 1997. 3 A c

GAM116 301 XT3 Nash, S. R.; Giros, B.; Kingsmore, S. F.; Kim, K. M.; El- Mestikawy,S.; Dong, Q.; Fumagalli, F.; Seldin, M. F.; Caron, M. G.: Cloning,gene structure and genomic localization of an orphan transporter frommouse kidney with six alternatively- spliced isoforms. Receptors Channels 6:113- 128, 1998. 3 A c

GAM116 301 XT3 Scott, A. F.: Personal Communication. Baltimore, Md. 2/5/2001. 3 A c

GAM117 216 MAPRE3 Nakagawa, H.; Koyama, K.; Murata, Y.; Morito, M.; Akiyama, T.;Nakamura, Y.: EB3, a novel member of the EB1 family preferentiallyexpressed in the central nervous system, binds to a CNS- specific APChomologue. Oncogene 19: 210-216, 2000. 3 C c

GAM117 216 MAPRE3 Su, L.- K.; Qi, Y.: Characterization of human MAPRE genes and theirproteins. Genomics 71: 143- 149, 2001. 3 C c

GAM120 285 FPGS Freemantle, S. J.; Taylor, S. M.; Krystal, G.; Moran, R. G.: Upstreamorganization of and multiple transcripts from the human folylpoly-gamma- glutamatesynthetase gene. J. Biol. Chem. 270: 9579- 9584, 1995. 3 C c

GAM120 285 FPGS Garrow, T. A.; Admon, A.; Shane, B.: Expression cloning of a humancDNA 3 C c
encoding folylpoly(gamma- glutamate) synthetase and determinationof its
primary structure. Proc. Nat. Acad. Sci. 89: 9151- 9155, 1992.

GAM120 285 FPGS Jones, C.; Kao, F. T.: Assignment of the human gene complementingthe 3 C c
auxotrophic marker GAT- minus to chromosome 9. (Abstract) Cytogenet.Cell
Genet. 25: 168, 1979.

GAM120 285 FPGS Jones, C.; Kao, F.- T.: Regional mapping of the folylpolyglutamatesynthetase 3 C c
gene (FPGS) to 9cen- q34. (Abstract) Cytogenet. Cell Genet. 37:499- 500,
1984.

GAM120 285 FPGS Jones, C.; Kao, F.- T.; Taylor, R. T.: Chromosomal assignment ofthe gene for 3 C c
folylpolyglutamate synthetase to human chromosome 9. Cytogenet.Cell Genet.
28: 181- 194, 1980.

GAM120 285 FPGS Kao, F. T.; Puck, T. T.: Genetics of somatic mammalian cells.VII. Induction 3 C c
and isolation of nutritional mutants in Chinese hamstercells. Proc. Nat.
Acad. Sci. 60: 1275- 1281, 1968.

GAM120 285 FPGS Sussman, D. J.; Milman, G.; Shane, B.: Characterization of 3 C c
humanfolylpolyglutamate synthetase expressed in Chinese hamster ovary cells.
Somat.Cell Molec. Genet. 12: 531- 540, 1986.

GAM120 285 FPGS Taylor, R. T.; Hanna, M. L.: Folate- dependent enzymes in culturedChinese 3 C c
hamster cells: folylpolyglutamate synthetase and its absencein mutants
auxotrophic for glycine, adenosine and thymidine. Arch.Biochem. Biophys.
181: 331- 344, 1977.

GAM120 285 FPGS Taylor, S. M.; Freemantle, S. J.; Moran, R. G.: Structural organizationof 3 C c
the human folylpoly- gamma- glutamate synthetase gene: evidence fora single
genomic locus. Cancer Res. 55: 6030- 6034, 1995.

GAM120 285 NTRK2 Bibel, M.; Barde, Y.- A.: Neurotrophins: key regulators of cellfate and cell 3 C c
shape in the vertebrate nervous system. Genes Dev. 14:2919- 2937, 2000.

GAM120 285 NTRK2 Bothwell, M.: p75(NTR): a receptor after all. Science 272: 506- 507,1996. 3 C c

GAM120 285 NTRK2 Carter, B. D.; Lewin, G. R.: Neurotrophins live or let die: doesp75(NTR) 3 C c
decide? Neuron 18: 187- 190, 1997.

GAM120 285 NTRK2 Ip, N. Y.; Stitt, T. N.; Tapley, P.; Klein, R.; Glass, D. J.; Fandl,J.; 3 C c
Greene, L. A.; Barbacid, M.; Yancopoulos, G. D.: Similaritiesand differences
in the way neurotrophins interact with the Trk receptorsin neuronal and
nonneuronal cells. Neuron 10: 137- 149, 1993.

GAM120 285 NTRK2 Nakagawara, A.; Liu, X.- G.; Ikegaki, N.; White, P. S.; Yamashiro,D. J.; 3 C c
Nycum, L. M.; Biegel, J. A.; Brodeur, G. M.: Cloning and
chromosomallocalization of the human TRK- B tyrosine kinase receptor gene
(NTRK2). Genomics 25:538- 546, 1995.

GAM120 285 NTRK2 Rico, B.; Xu, B.; Reichardt, L. F.: TrkB receptor signaling isrequired for 3 C c
establishment of GABAergic synapses in the cerebellum. NatureNeurosci. 5:
225- 233, 2002.

GAM120 285 NTRK2 Slaugenhaupt, S. A.; Blumenfeld, A.; Liebert, C. B.; Mull, J.;Lucente, D. 3 C c
E.; Monahan, M.; Breakefield, X. O.; Maayan, C.; Parada,L.; Axelrod, F. B.;
Gusella, J. F.: The human gene for neurotrophictyrosine kinase receptor type
2 (NTRK2) is located on chromosome 9but is not the familial dysautonomia
gene. Genomics 25: 730- 732,1995.

GAM120 285 NTRK2 Soppet, D.; Escandon, E.; Maragos, J.; Middlemas, D. S.; Reid,S. W.; Blair, 3 C c
J.; Burton, L. E.; Stanton, B. R.; Kaplan, D. R.; Hunter,T.; Nikolics, K.;
Parada, L. F.: The neurotrophic factors brain- derivedneurotrophic factor
and neurotrophin- 3 are ligands for the trkB tyrosinekinase receptor. Cell

65: 895- 903, 1991.

GAM120 285 NTRK2 Squinto, S. P.; Stitt, S. N.; Aldrich, T. H.; Davis, S.; Bianco,S. M.; Radziejewski, C.; Glass, D. J.; Masiakowski, P.; Furth, M.E.; Valenzuela, D. M.; DiStefano, P. S.; Yancopoulos, G. D.: trkBencodes a functional receptor for brain- derived neurotrophic factorand neurotrophin- 3 but not nerve growth factor. Cell 65: 885- 893,1991. 3 C c

GAM120 285 NTRK2 Valent, A.; Danglot, G.; Bernheim, A.: Mapping of the tyrosinekinase receptors trkA (NTRK1), trkB (NTRK2) and trkC (NTRK3) to humanchromosomes 1q22, 9q22 and 15q25 by fluorescence in situ hybridization. Europ.J. Hum. Genet. 5: 102- 104, 1997. 3 C c

GAM121 309 ADAM11 Emi, M.; Katagiri, T.; Harada, Y.; Saito, H.; Inazawa, J.; Ito,I.; Kasumi, F.; Nakamura, Y.: A novel metalloprotease/disintegrin- likegene at 17q21.3 is somatically rearranged in two primary breast cancers. NatureGenet. 5: 151- 157, 1993. 3 C c

GAM121 309 ADAM11 Katagiri, T.; Harada, Y.; Emi, M.; Nakamura, Y.: Human metalloprotease/disintegrin- like(MDC) gene: exon- intron organization and alternative splicing. Cytogenet.Cell Genet. 68: 39- 44, 1995. 3 C c

GAM121 309 ADAM11 Sagane, K.; Ohya, Y.; Hasegawa, Y.; Tanaka, I.: Metalloproteinase- like,disintegrin- like, cysteine- rich proteins MDC2 and MDC3: novel humancellular disintegrins highly expressed in the brain. Biochem. J. 334:93- 98, 1998. 3 C c

GAM121 309 ANXA6 Davies, A. A.; Moss, S. E.; Crompton, M. R.; Jones, T. A.; Spurr,N. K.; Sheer, D.; Kozak, C.; Crumpton, M. J.: The gene coding forthe p68 calcium-binding protein is localized to bands q32- q34 of humanchromosome 5, and to mouse chromosome 11. Hum. Genet. 82: 234- 238,1989. 3 C b

GAM121 309 ANXA6 Smith, P. D.; Davies, A.; Crumpton, M. J.; Moss, S. E.: Structureof the human annexin VI gene. Proc. Nat. Acad. Sci. 91: 2713- 2717,1994. 3 C b

GAM121 309 ANXA6 Sudhof, T. C.; Slaughter, C. A.; Leznicki, I.; Barjon, P.; Reynolds,G. A.: Human 67- kDa calelectrin contains a duplication of four repeatsfound in 35-kDa lipocortins. Proc. Nat. Acad. Sci. 85: 664- 668,1988. 3 C b

GAM121 309 ANXA6 Warrington, J. A.; Bengtsson, U.: High- resolution physical mappingof human 5q31- q33 using three methods: radiation hybrid mapping, interphasefluorescence in situ hybridization, and pulsed- field gel electrophoresis. Genomics 24:395- 398, 1994. 3 C b

GAM121 309 CST6 Sotiropoulou, G.; Anisowicz, A.; Sager, R.: Identification, cloning,and characterization of cystatin M, a novel cysteine proteinase inhibitor,down-regulated in breast cancer. J. Biol. Chem. 272: 903- 910, 1997. 3 C c

GAM121 309 CST6 Stenman, G.; Astrom, A.- K.; Roijer, E.; Sotiropoulou, G.; Zhang,M.; Sager, R.: Assignment of a novel cysteine proteinase inhibitor(CST6) to 11q13 by fluorescence in situ hybridization. Cytogenet.Cell Genet. 76: 45- 46, 1997. 3 C c

GAM121 309 HMX1 Stadler, H. S.; Padanilam, B. J.; Buetow, K.; Murray, J. C.; Solursh,M.: Identification and genetic mapping of a homeobox gene to the4p16.1 region of human chromosome 4. Proc. Nat. Acad. Sci. 89: 11579- 11583,1992. 3 C c

GAM121 309 HMX1 Wang, W.; Yoshiura, K.; Murray, J.; Lufkin, T.: Assignment ofthe murine Hmx1 homeobox gene to the proximal region of mouse chromosome5. Mammalian Genome 8: 869- 876, 1997. 3 C c

GAM124 323 DTX1 Artavanis- Tsakonas, S.; Matsuono, K.; Fortini, M.: Notch signaling. Science 268:225- 232, 1995. 3 C c

GAM124 323 DTX1 Boguski, M. S.; Lowe, T. M. J.; Tolstochev, C. M.: dbEST:databasefor 'expressed sequence tags.' (Letter) Nature Genet. 4: 332- 333,1993. 3 C c

GAM124 323 DTX1 Izon, D. J.; Aster, J. C.; He, Y.; Weng, A.; Karnell, F. G.; Patriub,V.; Xu, 3 C c
L.; Bakkour, S.; Rodriguez, C.; Allman, D.; Pear, W. S.:Deltex1 redirects
lymphoid progenitors to the B cell lineage by antagonizingNotch1. Immunity
16: 231- 243, 2002.

GAM124 323 DTX1 Lee, L.; Dowhanick- Morrissette, J.; Katz, A.; Jukofsky, L.; Krantz,I. D.: 3 C c
Chromosomal localization, genomic characterization, and mappingto the Noonan
syndrome critical region of the human Deltex (DTX1)gene. Hum. Genet. 107:
577- 581, 2000.

GAM124 323 DTX1 Matsuno, K.; Eastman, D.; Mitsiades, T.; Quinn, A. M.; Carcanciu,M. L.; 3 C c
Ordentlich, P.; Kadesch, T.; Artavanis- Tsakonas, S.: Humandeltex is a
conserved regulator of Notch signalling. Nature Genet. 19:74- 78, 1998.

GAM124 323 DTX1 Sestan, N.; Artavanis- Tsakonas, S.; Rakic, P.: Contact- dependentinhibition 3 C c
of cortical neurite growth mediated by Notch signaling. Science 286:741-
746, 1999.

GAM124 323 SREBF1 DeBose- Boyd, R. A.; Brown, M. S.; Li, W.- P.; Nohturfft, A.; Goldstein,J. 3 C c
L.; Espenshade, P. J.: Transport- dependent proteolysis of SREBP:relocation
of Site- 1 protease from Golgi to ER obviates the need forSREBP transport to
Golgi. Cell 99: 703- 712, 1999.

GAM124 323 SREBF1 Hua, X.; Wu, J.; Goldstein, J. L.; Brown, M. S.; Hobbs, H. H.:Structure of 3 C c
the human gene encoding sterol regulatory element bindingprotein- 1 (SREBF1)
and localization of SREBF1 and SREBF2 to chromosomes17p11.2 and 22q13.
Genomics 25: 667- 673, 1995.

GAM124 323 SREBF1 Lloyd, D. J.; Trembath, R. C.; Shackleton, S.: A novel interactionbetween 3 C c
lamin A and SREBP1: implications for partial lipodystrophyand other
laminopathies. Hum. Molec. Genet. 11: 769- 777, 2002.

GAM124 323 SREBF1 Osborne, T. F.: CREating a SCAP- less liver keeps SREBPs pinnedin the ER 3 C c
membrane and prevents increased lipid synthesis in responseto low
cholesterol and high insulin. Genes Dev. 15: 1873- 1878, 2001.

GAM124 323 SREBF1 Shimano, H.; Shimomura, I.; Hammer, R. E.; Herz, J.; Goldstein,J. L.; Brown, 3 C c
M. S.; Horton, J. D.: Elevated levels of SREBP- 2 andcholesterol synthesis
in livers of mice homozygous for a targeteddisruption of the SREBP- 1 gene.
J. Clin. Invest. 100: 2115- 2124,1997.

GAM124 323 SREBF1 Shimomura, I.; Hammer, R. E.; Richardson, J. A.; Ikemoto, S.; Bashmakov,Y.; 3 C c
Goldstein, J. L.; Brown, M. S.: Insulin resistance and diabetesmellitus in
transgenic mice expressing nuclear SREBP- 1c in adiposetissue: model for
congenital generalized lipodystrophy. Genes Dev. 12:3182- 3194, 1998.

GAM124 323 SREBF1 Shimomura, I.; Matsuda, M.; Hammer, R. E.; Bashmakov, Y.; Brown,M. S.; 3 C c
Goldstein, J. L.: Decreased IRS- 2 and increased SREBP- 1c leadto mixed
insulin resistance and sensitivity in livers of lipodystrophicand ob/ob
mice. Molec. Cell 6: 77- 86, 2000.

GAM124 323 SREBF1 Tobe, K.; Suzuki, R.; Aoyama, M.; Yamauchi, T.; Kamon, J.; Kubota,N.; 3 C c
Terauchi, Y.; Matsui, J.; Akanuma, Y.; Kimura, S.; Tanaka, J.;Abe, M.;
Ohsumi, J.; Nagai, R.; Kadowaki, T.: Increased expressionof the sterol
regulatory element- binding protein- 1 gene in insulinreceptor substrate- 2
- /- mouse liver. J. Biol. Chem. 276: 38337- 38340,2001.

GAM124 323 SREBF1 Wang, X.; Sato, R.; Brown, M. S.; Hua, X.; Goldstein, J. L.: SREBP- 1,a 3 C c
membrane- bound transcription factor released by sterol-
regulatedproteolysis. Cell 77: 53- 62, 1994.

GAM124 323 SREBF1 Yokoyama, C.; Wang, X.; Briggs, M. R.; Admon, A.; Wu, J.; Hua,X.; Goldstein, 3 C c
J. L.; Brown, M. S.: SREBP- 1, a basic- helix- loop- helix- leucinezipper

protein that controls transcription of the low density lipoproteinreceptor gene. Cell 75: 187- 197, 1993.

GAM127 321 VAPA Nishimura, Y.; Hayashi, M.; Inada, H.; Tanaka, T.: Molecular cloningand characterization of mammalian homologues of vesicle- associatedmembrane protein- associated (VAMP- associated) proteins. Biochem.Biophys. Res. Commun. 254: 21- 26, 1999. 3 C a

GAM127 321 VAPA Weir, M. L.; Klip, A.; Trimble, W. S.: Identification of a humanhomologue of the vesicle- associated membrane protein (VAMP)- associatedprotein of 33 kDa (VAP- 33): a broadly expressed protein that bindsto VAMP. Biochem. J. 333: 247- 251, 1998. 3 C a

GAM128 316 ADAMTS8 Georgiadis, K. E.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS8,a novel metalloprotease of the ADAM- TS family located on mouse chromosome9 and human chromosome 11. Genomics 62: 312- 315, 1999. 3 C c

GAM128 316 ADAMTS8 Vazquez, F.; Hastings, G.; Ortega, M.- A.; Lane, T. F.; Oikemus,S.; Lombardo, M.; Iruela- Arispe, M. L.: METH- 1, a human orthologof ADAMTS- 1, and METH- 2 are members of a new family of proteins withangio- inhibitory activity. J. Biol. Chem. 274: 23349- 23357, 1999. 3 C c

GAM129 213 ADAM19 Hirohata, S.; Seldin, M. F.; Apte, S. S.: Chromosomal assignmentof two ADAM genes, TACE (ADAM17) and MLTNB (ADAM19), to human chromosomes2 and 5, respectively, and of Mltnb to mouse chromosome 11. Genomics 54:178- 179, 1998. 3 C c

GAM129 213 ADAM19 Inoue, D.; Reid, M.; Lum, L.; Kratzschmar, J.; Weskamp, G.; Myung,Y. M.; Baron, R.; Blobel, C. P.: Cloning and initial characterizationof mouse meltrin beta and analysis of the expression of four metalloprotease-disintegrinsin bone cells. J. Biol. Chem. 273: 4180- 4187, 1998. 3 C c

GAM129 213 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 C c

GAM129 213 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 C c

GAM129 213 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 C c

GAM129 213 BACE Cai, H.; Wang, Y.; McCarthy, D.; Wen, H.; Borchelt, D. R.; Price,D. L.; Wong, P. C.: BACE1 is the major beta- secretase for generationof A- beta peptides by neurons. Nature Neurosci. 4: 233- 234, 2001. 3 C c

GAM129 213 BACE De Strooper, B.; Konig, G.: A firm base for drug development. Nature 402:471- 472, 1999. 3 C c

GAM129 213 BACE Fan, W.; Bennett, B. D.; Babu- Khan, S.; Luo, Y.; Louis, J.- C.;McCaleb, M.; Citron, M.; Vassar, R.; Richards, W. G.: Response toSaunders et al. (1999). Science 286: 1255a, 1999. Note: ElectronicPublication. 3 C c

GAM129 213 BACE Haniu, M.; Denis, P.; Young, Y.; Mendiaz, E. A.; Fuller, J.; Hui,J. O.; Bennett, B. D.; Kahn, S.; Ross, S.; Burgess, T.; Katta, V.;Rogers, G.; Vassar, R.; Citron, M.: Characterization of Alzheimer'sbeta- secretase protein BACE: a pepsin family member with unusual properties. J.Biol. Chem. 275: 21099- 21106, 2000. 3 C c

GAM129 213 BACE Hong, L.; Koelsch, G.; Lin, X.; Wu, S.; Terzyan, S.; Ghosh, A.K.; Zhang, X. C.; Tang, J.: Structure of the protease domain of memapsin2 (beta- 3 C c

secretase) complexed with inhibitor. Science 290: 150- 153,2000.

GAM129 213 BACE Hussain, I.; Powell, D.; Howlett, D. R.; Tew, D. G.; Meek, T. D.;Chapman, C.; Gloger, I. S.; Murphy, K. E.; Southan, C. D.; Ryan, D.M.; Smith, T. S.; Simmons, D. L.; Walsh, F. S.; Dingwall, C.; Christie,G.: Identification of a novel aspartic protease (asp2) as beta- secretase Molec.Cell Neurosci. 14: 419- 427, 1999. 3 C c

GAM129 213 BACE Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643- 648, 2001. 3 C c

GAM129 213 BACE Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.- H.; Goldstein, L. S.: Axonal transport of amyloid precursor protein is mediated by directbinding to the kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000. 3 C c

GAM129 213 BACE Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis,P.; Fan, W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.;Yan, Q.; Richards, W. G.; Citron, M.; Vassar, R.: Mice deficientin BACE1, the Alzheimer's beta- secretase, have normal phenotype andabolished beta- amyloid generation. Nature Neurosci. 4: 231- 232,2001. 3 C c

GAM129 213 BACE Nicolaou, M.; Song, Y.- Q.; Sato, C. A.; Orlacchio, A.; Kawarai,T.; Medeiros, H.; Liang, Y.; Sorbi, S.; Richard, E.; Rogaev, E. I.;Moliaka, Y.; Bruni, A. C.; Jorge, R.; Percy, M.; Duara, R.; Farrer,L. A.; St George- Hyslop, P.; Rogaeva, E. A.: Mutations in the openreading frame of the beta- site APP cleaving enzyme (BACE) locus arenot a common cause of Alzheimer's disease. Neurogenetics 3: 203- 206,2001. 3 C c

GAM129 213 BACE Roberds, S. L.; Anderson, J.; Basi, G.; Bienkowski, M. J.; Branstetter,D. G.; Chen, K. S.; Freedman, S. B.; Frigon, N. L.; Games, D.; Hu,K.; Johnson- Wood, K.; Kappenman, K. E.; and 20 others: BACE knockoutmice are healthy despite lacking the primary beta- secretase activityin brain: implications for Alzheimer's disease therapeutics. Hum.Molec. Genet. 10: 1317- 1324, 2001. 3 C c

GAM129 213 BACE Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a BACE homolog, BACE2, reside in the obligate Down syndromeregion of chromosome 21. Science 286: 1255a, 1999. Note: ElectronicPublication. 3 C c

GAM129 213 BACE Sinha, S.; Anderson, J. P.; Barbour, R.; Basi, G. S.; Caccavello,R.; Davis, D.; Doan, M.; Dovey, H. F.; Frigon, N.; Hong, J.; Jacobson- Croak,K.; Jewett, N.; and 15 others: Purification and cloning of amyloidprecursor protein beta- secretase from human brain. Nature 402: 537- 540,1999. 3 C c

GAM129 213 BACE Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz,E. A.; Dents, P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff,R.; Luo, Y.; Fisher, S.; and 12 others: Beta- secretase cleavageof Alzheimer's amyloid precursor protein by the transmembrane asparticprotease BACE. Science 286: 735- 741, 1999. 3 C c

GAM129 213 BACE Yan, R.; Bienkowski, M. J.; Shuck, M. E.; Miao, H.; Tory, M. C.;Pauley, A. M.; Brashler, J. R.; Stratman, N. C.; Mathews, W. R.; Buhl,A. E.; Carter, D. B.; Tomasselli, A. G.; Parodi, L. A.; Heinrikson,R. L.; Gurney, M. E.: Membrane- anchored aspartyl protease with Alzheimer'sdisease beta- secretase activity. Nature 402: 533- 536, 1999. 3 C c

GAM129 213 CD44 Ala- Kapee, M.; Forsberg, U. H.; Jalkanen, S.; Schroder, J.: Mappingof gene for human lymphocyte homing receptor to the short arm of chromosome11. (Abstract) Cytogenet. Cell Genet. 51: 948- 949, 1989. 3 C c

GAM129 213 CD44 Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C. B.; Seed,B.: CD44 is 3 C c
the principal cell surface receptor for hyaluronate. Cell 61:1303- 1313,
1990.

GAM129 213 CD44 Cianfriglia, M.; Viora, M.; Tombesi, M.; Merendino, N.; Esposito,G.; 3 C c
Samoggia, P.; Forsberg, U. H.; Schroder, J.: The gene encodingfor MC56
determinant (drug- sensitivity marker) is located on the shortarm of human
chromosome 11. Int. J. Cancer 52: 585- 587, 1992.

GAM129 213 CD44 Cywes, C.; Wessels, M. R.: Group A Streptococcus tissue invasionby CD44- 3 C c
mediated cell signalling. Nature 414: 648- 652, 2001.

GAM129 213 CD44 Forsberg, U. H.; Ala- Kapee, M. M.; Jalkanen, S.; Andersson, L.C.; Schroder, 3 C c
J.: The gene for human lymphocyte homing receptor islocated on chromosome
11. Europ. J. Immun. 19: 409- 412, 1989.

GAM129 213 CD44 Forsberg, U. H.; Jalkanen, S.; Schroder, J.: Assignment of thehuman 3 C c
lymphocyte homing receptor gene to the short arm of chromosome11.
Immunogenetics 29: 405- 407, 1989.

GAM129 213 CD44 Francke, U.; Foellmer, B. E.; Haynes, B. F.: Chromosome mappingof human cell 3 C c
surface molecules: monoclonal anti- human lymphocyteantibodies 4F2, A3D8,
and A1G3 define antigens controlled by differentregions of chromosome 11.
Somat. Cell Genet. 9: 333- 344, 1983.

GAM129 213 CD44 Haynes, B. F.: Personal Communication. Durham, N. C. 2/28/1986. 3 C c

GAM129 213 CD44 Krainer, A. R.; Mayeda, A.; Kozak, D.; Binns, G.: Functional expressionof 3 C c
cloned human splicing factor SF2: homology to RNA- binding proteins,U1 70K,
and Drosophila splicing regulators. Cell 66: 383- 394, 1991.

GAM129 213 CD44 Matsumura, Y.; Tarin, D.: Significance of CD44 gene productsfor cancer 3 C c
diagnosis and disease evaluation. Lancet 340: 1053- 1058,1992.

GAM129 213 CD44 Mayer, B.; Jauch, K. W.; Gunthert, U.; Figdor, C. G.; Schildberg,F. W.; 3 C c
Funke, I.; Johnson, J. P.: De- novo expression of CD44 andsurvival in
gastric cancer. Lancet 342: 1019- 1022, 1993.

GAM129 213 CD44 Omary, M. B.; Trowbridge, I. S.; Letarte, M.; Kagnoff, M. F.;Isacke, C. M.: 3 C c
Structural heterogeneity of human Pgp- 1 and its relationshipwith p85.
Immunogenetics 27: 460- 464, 1988.

GAM129 213 CD44 Schlossman, S. F.; Boumsell, L.; Gilks, W.; Harlan, J. M.; Kishimoto,T.; 3 C c
Morimoto, C.; Ritz, J.; Shaw, S.; Silverstein, R. L.; Springer,T. A.;
Tedder, T. F.; Todd, R. F.: CD antigens 1993. Immun. Today 15:98- 99, 1994.

GAM129 213 CD44 Schmits, R.; Filmus, J.; Gerwin, N.; Senaldi, G.; Kiefer, F.;Kundig, T.; 3 C c
Wakeham, A.; Shahinian, A.; Catzavelos, C.; Rak, J.; Furlonger,C.; Zakarian,
A.; Simard, J. J.; Ohashi, P. S.; Paige, C. J.; Gutierrez- Romas,J. C.; Mak,
T. W.: CD44 regulates hematopoietic progenitor distribution,granuloma
formation, and tumorigenicity. Blood 90: 2217- 2233, 1997.

GAM129 213 CD44 Screaton, G. R.; Bell, M. V.; Jackson, D. G.; Cornelis, F. B.;Gerth, U.; 3 C c
Bell, J. I.: Genomic structure of DNA encoding the lymphocytehoming receptor
CD44 reveals at least 12 alternatively spliced exons. Proc.Nat. Acad. Sci.
89: 12160- 12164, 1992.

GAM129 213 CD44 Seldin, M. F.: Personal Communication. Durham, N. C. 9/19/1990. 3 C c

GAM129 213 CD44 Sherman, L.; Wainwright, D.; Ponta, H.; Herrlich, P.: A splicevariant of 3 C c
CD44 expressed in the apical ectodermal ridge presentsfibroblast growth
factors to limb mesenchyme and is required for limboutgrowth. Genes Dev. 12:
1058- 1071, 1998.

GAM129 213 CD44 Stefanova, I.; Hilgert, I.; Bazil, V.; Kristofova, H.; Horejsi,V.: Human 3 C c
leucocyte surface glycoprotein CDw44 and lymphocyte homingreceptor are

identical molecules. Immunogenetics 29: 402- 404, 1989.

GAM129 213 CD44 Teder, P.; Vandivier, R. W.; Jiang, D.; Liang, J.; Cohn, L.; Pure,E.; Henson, P. M.; Noble, P. W.: Resolution of lung inflammationby CD44. Science 296: 155- 158, 2002. 3 C c

GAM129 213 CD44 Telen, M. J.: Personal Communication. Durham, N. C. 12/30/1992. 3 C c

GAM129 213 CD44 Telen, M. J.; Eisenbarth, G. S.; Haynes, B. F.: Human erythrocyteantigens: regulation of expression of a novel erythrocyte surfaceantigen by the inhibitor Lutheran In(Lu) gene. J. Clin. Invest. 71:1878- 1886, 1983. 3 C c

GAM129 213 CD44 Telen, M. J.; Palker, T. J.; Haynes, B. F.: Human erythrocyteantigens: II. The In(Lu) gene regulates expression of an antigen onan 80- kilodalton protein of human erythrocytes. Blood 64: 599- 606,1984. 3 C c

GAM129 213 CD44 Weber, G. F.; Ashkar, S.; Glimcher, M. J.; Cantor, H.: Receptor-ligandinteraction between CD44 and osteopontin (Eta- 1). Science 271: 509-512,1996. 3 C c

GAM129 213 DNTT Chang, L. M. S.; Bollum, F. J.: Molecular biology of terminaltransferase. CRC Crit. Rev. Biochem. 21: 27- 52, 1986. 3 C c

GAM129 213 DNTT Epplen, J. T.; Chluba, J.; Hardt, C.; Hinkkanen, A.; Steimle, V.;Stockinger, H.: Mammalian T- lymphocyte antigen receptor genes: geneticand nongenetic potential to generate variability. Hum. Genet. 75:300- 310, 1987. 3 C c

GAM129 213 DNTT Isobe, M.; Huebner, K.; Erikson, J.; Peterson, R. C.; Bollum, F.J.; Chang, L. M. S.; Croce, C. M.: Chromosome localization of thegene for human terminal deoxynucleotidyltransferase to region 10q23- q25. Proc.Nat. Acad. Sci. 82: 5836- 5840, 1985. 3 C c

GAM129 213 DNTT Landau, N. R.; St. John, T. P.; Weissman, I. L.; Wolf, S. C.; Silverstone,A. E.; Baltimore, D.: Cloning of terminal transferase cDNA by antibodyscreening. Proc. Nat. Acad. Sci. 81: 5836- 5840, 1984. 3 C c

GAM129 213 DNTT Riley, L. K.; Morrow, J. K.; Danton, M. J.; Coleman, M. S.: Humanterminal deoxyribonucleotidyltransferase: molecular cloning and structuralanalysis of the gene and 5- prime flanking region. Proc. Nat. Acad.Sci. 85: 2489- 2493, 1988. 3 C c

GAM129 213 DNTT Thai, T.- H.; Purugganan, M. M.; Roth, D. B.; Kearney, J. F.: Distinctand opposite diversifying activities of terminal transferase splicevariants. Nature Immun. 3: 457- 462, 2002. 3 C c

GAM129 213 DNTT Yang- Feng, T. L.; Landau, N. R.; Baltimore, D.; Francke, U.: Theterminal deoxynucleotidyltransferase gene is located on human chromosome10 (10q23-q24) and on mouse chromosome 19. Cytogenet. Cell Genet. 43:121- 126, 1986. 3 C c

GAM129 213 DOCK1 Hasegawa, H.; Kiyokawa, E.; Tanaka, S.; Nagashima, K.; Gotoh, N.;Shibuya, M.; Kurata, T.; Matsuda, M.: DOCK180, a major CRK- bindingprotein, alters cell morphology upon translocation to the membrane. Molec.Cell Biol. 16: 1770- 176, 1996. 3 C c

GAM129 213 DOCK1 Savill, J.: Phagocytic docking without shocking. Nature 442- 443,1998. 3 C c

GAM129 213 DOCK1 Takai, S.; Hasegawa, H.; Kiyokawa, E.; Yamada, K.; Kurata, T.;Matsuda, M.: Chromosomal mapping of the gene encoding DOCK180, amajor Crk- binding protein, to 10q26.13- q26.3 by fluorescence in situhybridization. Genomics 35: 403- 404, 1996. 3 C c

GAM129 213 DOCK1 Wu, Y.- C.; Horvitz, H. R.: C. elegans phagocytosis and cell-migrationprotein CED- 5 is similar to human DOCK180. Nature 392: 501-504,1998. 3 C c

GAM129 213 FUS1 Kondo, M.; Ji, L.; Kamibayashi, C.; Tomizawa, Y.; Randle, D.; Sekido,Y.; Yokota, J.; Kashuba, V.; Zabarovsky, E.; Kuzmin, I.; Lerman, M.;Roth, J.; 3 C c

Minna, J. D.: Overexpression of candidate tumor suppressorgene FUS1 isolated from the 3p21.3 homozygous deletion region leadsto G1 arrest and growth inhibition of lung cancer cells. Oncogene 20:6258- 6262, 2001.

GAM129 213 FUS1 Lerman, M. I.; Minna, J. D.: The 630- kb lung cancer homozygousdeletion 3 C c region on human chromosome 3p21.3: identification and evaluationof the resident candidate tumor suppressor genes. Cancer Res. 60:6116- 6133, 2000.

GAM129 213 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, 3 C c J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2 in the allergic response. Nature 412: 186- 190,2001.

GAM129 213 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 C c Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM129 213 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; 3 C c Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab- family adapter proteins act downstream of cytokine and growthfactor receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999.

GAM129 213 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH 3 C c mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell Genet. 94: 39- 42, 2001.

GAM129 213 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology 3 C c domain- containing adapter protein, acts to uncouple signalingfrom ERK kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999.

GAM129 213 GRLF1 LeClerc, S.; Palaniswami, R.; Xie, B.; Govdan, M. V.: Molecularcloning and 3 C c characterization of a factor that binds the human glucocorticoidreceptor gene and represses its expression. J. Biol. Chem. 266:17333- 17340, 1991.

GAM129 213 GRLF1 Tikoo, A.; Czekay, S.; Viars, C.; White, S.; Heath, J. K.; Arden,K.; Maruta, 3 C c H.: p190- A, a human tumor suppressor gene, maps to thechromosomal region 19q13.3 that is reportedly deleted in some gliomas. Gene 257:23- 31, 2000.

GAM129 213 ITGAM Arnaout, M. A.; Gupta, S. K.; Pierce, M. W.; Tenen, D. G.: Aminoacid 3 C c sequence of the alpha subunit of human leukocyte adhesion receptorMo1 (complement receptor type 3). J. Cell Biol. 106: 2153- 2158,1988.

GAM129 213 ITGAM Arnaout, M. A.; Remold- O'Donnell, E.; Pierce, M. W.; Harris, P.;Tenen, D. 3 C c G.: Molecular cloning of the alpha- subunit of human andguinea pig leukocyte adhesion glycoprotein Mo1: chromosomal localizationand homology to the alpha- subunits of integrins. Proc. Nat. Acad.Sci. 85: 2776- 2780, 1988.

GAM129 213 ITGAM Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; 3 C c Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P. G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome 16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991.

GAM129 213 ITGAM Corbi, A. L.; Kishimoto, T. K.; Miller, L. J.; Springer, T. A.: The human 3 C c leukocyte adhesion glycoprotein Mac- 1 (complement receptortype 3, CD11b) alpha subunit: cloning, primary structure, and relationto the integrins, von Willebrand factor and factor B. J. Biol. Chem. 263:12403- 12411, 1988.

GAM129 213 ITGAM Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. 3 C c C.: Chromosomal location of the genes encoding the leukocyteadhesion receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988.

GAM129 213 ITGAM Pierce, M. W.; Remold- O'Donnell, E.; Todd, R. F., III; Arnaout,M. A.: N- 3 C c terminal sequence of human leukocyte glycoprotein Mo1: conservationacross

species and homology to platelet IIb/IIIa. Biochim. Biophys.Acta 874: 368-371, 1986.

GAM129 213 ITGAM Simon, D. I.; Chen, Z.; Seifert, P.; Edelman, E. R.; Ballantyne,C. M.; Rogers, C.: Decreased neointimal formation in Mac- 1 - /- micereveals a role for inflammation in vascular repair after angioplasty. J.Clin. Invest. 105: 293- 300, 2000. 3 C c

GAM129 213 ITGAM Springer, T. A.; Teplow, D. B.; Dreyer, W. J.: Sequence homologyof the LFA- 1 and Mac- 1 leukocyte adhesion glycoproteins and unexpectedrelation to leukocyte interferon. Nature 314: 540- 542, 1985. 3 C c

GAM129 213 MAN1A1 Bause, E.; Bieberich, E.; Rolfs, A.; Volker, C.; Schmidt, B.:Molecular cloning and primary structure of Man(9)- mannosidase fromhuman kidney. Eur. J. Biochem. 217: 535- 540, 1993. 3 C c

GAM129 213 MAN1A1 Tremblay, L. O; Campbell Dyke, N.; Herscovics, A.: Molecular cloning,chromosomal mapping and tissue- specific expression of a novel humanalpha- 1,2- mannosidase gene involved in N- glycan maturation. Glycobiology 8:585- 595, 1998. 3 C c

GAM129 213 PRX Boerkoel, C. F.; Takashima, H.; Stankiewicz, P.; Garcia, C. A.;Leber, S. M.; Rhee- Morris, L.; Lupski, J. R.: Periaxin mutationscause recessive Dejerine-Sottas neuropathy. Am. J. Hum. Genet. 68:325- 333, 2001. Note: Erratum: Am. J. Hum. Genet. 68: 557 only, 2001. 3 C c

GAM129 213 PRX Cohn, R. D.; Campbell, K. P.: Molecular basis of muscular dystrophies. MuscleNerve 23: 1456- 1471, 2000. 3 C c

GAM129 213 PRX Delague, V.; Bareil, C.; Tuffery, S.; Bouvagnet, P.; Chouery, E.;Koussa, S.; Maisonobe, T.; Loiselet, J.; Megarbane, A.; Claustres,M.: Mapping of a new locus for autosomal recessive demyelinatingCharcot- Marie- Tooth disease to 19q13.1- 13.3 in a large consanguineousLebanese family: exclusion of MAG as a candidate gene. Am. J. Hum.Genet. 67: 236- 243, 2000. 3 C c

GAM129 213 PRX Gillespie, C. S.; Lee, M.; Fantes, J. F.; Brophy, P. J.: The geneencoding the Schwann cell protein periaxin localizes on mouse chromosome7 (Prx). Genomics 41: 297- 298, 1997. 3 C c

GAM129 213 PRX Gillespie, C. S.; Sherman, D. L.; Fleetwood- Walker, S. M.; Cottrell,D. F.; Tait, S.; Garry, E. M.; Wallace, V. C. J.; Ure, J.; Griffiths,I. R.; Smith, A. Brophy, P. J.: Peripheral demyelination and neuropathicpain behavior in periaxin- deficient mice. Neuron 26: 523- 531, 2000. 3 C c

GAM129 213 PRX Guilbot, A.; Williams, A.; Ravise, N.; Verny, C.; Brice, A.; Sherman,D. L.; Brophy, P. J.; LeGuern, E.; Delague, V.; Bareil, C.; Megarbane,A.; Claustres, M.: A mutation in periaxin is responsible for CMT4F,an autosomal recessive form of Charcot- Marie- Tooth disease. Hum.Molec. Genet. 10: 415-421, 2001. 3 C c

GAM129 213 PRX Schuler, G. D.: Sequence mapping by electronic PCR. Genome Res. 7:541- 550, 1997. 3 C c

GAM129 213 PRX Takashima, H.; Boerkoel, C. F.; De Jonghe, P.; Ceuterick, C.; Martin,J.- J.; Voit, T.; Schroder, J.- M.; Williams, A.; Brophy, P. J.; Timmerman,V.; Lupski, J. R.: Periaxin mutations cause a broad spectrum of demyelinatingneuropathies. Ann. Neurol. 51: 709- 715, 2002. 3 C c

GAM129 213 RAB30 Chen, D.; Guo, J.; Miki, T.; Tachibana, M.; Gahl, W. A.: Molecularcloning of two novel rab genes from human melanocytes. Gene 174:129- 134, 1996. 3 C c

GAM129 213 RAB30 Scott, A. F.: Personal Communication. Baltimore, Md. 2/26/2001. 3 C c

GAM129 213 RBMY1A1 Chai, N. N.; Salido, E. C.; Yen, P. H.: Multiple functional copiesof the RBM gene family, a spermatogenesis candidate on the human Ychromosome. Genomics 3 C c

45: 355- 361, 1997.

GAM129 213 RBMY1A1 Delbridge, M. L.; Harry, J. L.; Toder, R.; Waugh O'Neill, R. J.;Ma, K.; 3 C c
Chandley, A. C.; Marshall Graves, J. A.: A human candidatespermatogenesis
gene, RBM1, is conserved and amplified on the marsupialY chromosome. Nature
Genet. 15: 131- 136, 1997.

GAM129 213 RBMY1A1 Delbridge, M. L.; Lingenfelter, P. A.; Disteche, C. M.; MarshallGraves, J. 3 C c
A.: The candidate spermatogenesis gene RBMY has a homologueon the human X
chromosome. (Letter) Nature Genet. 22: 223- 224, 1999.

GAM129 213 RBMY1A1 Ma, K.; Inglis, J. D.; Sharkey, A.; Bickmore, W. A.; Hill, R. E.;Prosser, E. 3 C c
J.; Speed, R. M.; Thomson, E. J.; Jobling, M.; Taylor,K.; Wolfe, J.; Cooke,
H. J.; Hargreave, T. B.; Chandley, A. C.: AY chromosome gene family with
RNA- binding protein homology: candidatesfor the azoospermia factor AZF
controlling human spermatogenesis. Cell 75:1287- 1295, 1993.

GAM129 213 RBMY1A1 Mazeyrat, S.; Saut, N.; Mattei, M.- G.; Mitchell, M. J.: RBMY evolvedon the 3 C c
Y chromosome from a ubiquitously transcribed X- Y identicalgene. (Letter)
Nature Genet. 22: 224- 226, 1999.

GAM129 213 RBMY1A1 Venables, J. P.; Elliott, D. J.; Makarova, O. V.; Makarov, E. M.;Cooke, 3 C c
H.J.; Eperon, I. C.: RBMY, a probable human spermatogenesisfactor, and other
hnRNP G proteins interact with Tra2- beta and affectsplicing. Hum. Molec.
Genet. 9: 685- 694, 2000.

GAM129 213 RERE Amler, L. C.; Bauer, A.; Corvi, R.; Dihlmann, S.; Praml, C.; Cavenee,W. K.; 3 C c
Schwab, M.; Hampton, G. M.: Identification and characterizationof novel
genes located at the t(1;15)(p36.2;q24) translocation breakpointin the
neuroblastoma cell line NGP. Genomics 64: 195- 202, 2000.

GAM129 213 RERE Yanagisawa, H.; Bundo, M.; Miyashita, T.; Okamura- Oho, Y.; Tadokoro,K.; 3 C c
Tokunaga, K.; Yamada, M.: Protein binding of a DRPLA family througharginine-
glutamic acid dipeptide repeats is enhanced by extended polyglutamine.
Hum.Molec. Genet. 9: 1433- 1442, 2000.

GAM129 213 RGS19IP1 Bunn, R. C.; Jensen, M. A.; Reed, B. C.: Protein interactionswith the 3 C c
glucose transporter binding protein GLUT1CBP that providea link between
GLUT1 and the cytoskeleton. Molec. Biol. Cell 10:819- 832, 1999.

GAM129 213 RGS19IP1 De Vries, L.; Lou, X.; Zhao, G.; Zheng, B.; Farquhar, M. G.: GIPC,a PDZ 3 C c
domain containing protein, interacts specifically with the Cterminus of RGS-
GAIP. Proc. Nat. Acad. Sci. 95: 12340- 12345, 1998.

GAM129 213 RGS19IP1 Von Kap- Herr, C.; Kandala, G.; Mann, S. S.; Hart, T. C.; Pettenati,M. J.; 3 C c
Setaluri, V.: Assignment of PDZ domain- containing proteinGIPC gene
(C19orf3) to human chromosome band 19p13.1 by in situ hybridizationand
radiation hybrid mapping. Cytogenet. Cell Genet. 89: 234- 235,2000.

GAM129 213 RNTRE Lanzetti, L.; Rybin, V.; Malabarba, M. G.; Christoforidis, S.;Scita, G.; 3 C c
Zerial, M.; Di Fiore, P. P.: The Eps8 protein coordinatesEGF receptor
signalling through Rac and trafficking through Rab5. Nature 408:374- 377,
2000.

GAM129 213 RNTRE Matoskova, B.; Wong, W. T.; Nomura, N.; Robbins, K. C.; Di Fiore,P. P.: RN- 3 C c
tre specifically binds to the SH3 domain of eps8 with highaffinity and
confers growth advantage to NIH3T3 upon carboxy- terminaltruncation.
Oncogene 12: 2679- 2688, 1996.

GAM129 213 RNTRE Matoskova, B.; Wong, W. T.; Seki, N.; Nagase, T.; Nomura, N.; Robbins,K. C.; 3 C c
Di Fiore, P. P.: RN- tre identifies a family of tre- relatedproteins
displaying a novel potential protein binding domain. Oncogene 12:2563- 2571,
1996.

GAM129 213 RNTRE Nomura, N.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Kawarabayasi,Y.; Sato, S.; 3 C c
Nagase, T.; Seki, N.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. I. The codingsequences of 40 new
genes (KIAA0001- KIAA0040) deduced by analysisof randomly samples cDNA
clones from human immature myeloid cell lineKG- 1. DNA Res. 1: 27- 35, 1994.

GAM129 213 SLC12A4 Gillen, C. M.; Brill, S.; Payne, J. A.; Forbush, B., III: Molecularcloning 3 C c
and functional expression of the K- Cl cotransporter from rabbit,rat, and
human: a new member of the cation- chloride cotransporterfamily. J. Biol.
Chem. 271: 16237- 16244, 1996.

GAM129 213 SLC12A4 Larsen, F.; Solheim, J.; Kristensen, T.; Kolsto, A. B.; Prydz,H.: A tight 3 C c
cluster of five unrelated human genes on chromosome 16q22.1. Hum.Molec.
Genet. 2: 1589- 1595, 1993.

GAM129 213 SLC12A4 Pellegrino, C. M.; Rybicki, A. C.; Musto, S.; Nagel, R. L.; Schwartz,R. S.: 3 C c
Molecular identification and expression of erythroid K:Clcotransporter in
human and mouse erythroleukemic cells. Blood CellsMolec. Dis. 24: 31- 40,
1998.

GAM129 213 SRD5A1 Andersson, S.; Russell, D. W.: Structural and biochemical propertiesof 3 C c
cloned and expressed human and rat steroid 5- alpha- reductases. Proc.Nat.
Acad. Sci. 87: 3640- 3644, 1990.

GAM129 213 SRD5A1 Ellis, J. A.; Stebbing, M.; Harrap, S. B.: Genetic analysis ofmale pattern 3 C c
baldness and the 5- alpha- reductase genes. J. Invest.Derm. 110: 849- 853,
1998.

GAM129 213 SRD5A1 Harris, G.; Azzolina, B.; Baginsky, W.; Cimis, G.; Rasmusson, G.H.; Tolman, 3 C c
R. L.; Raetz, C. R. H.; Ellsworth, K.: Identificationand selective
inhibition of an isozyme of steroid 5- alpha- reductasein human scalp. Proc.
Nat. Acad. Sci. 89: 10787- 10791, 1992.

GAM129 213 SRD5A1 Hsieh, C.- L.; Milatovich, A.; Russell, D.; Francke, U.: Chromosomalmapping 3 C c
of human steroid 5 alpha- reductase gene (SRD5A1) and pseudogene(SRD5AP1) in
human and mouse. (Abstract) Cytogenet. Cell Genet. 58:1897 only, 1991.

GAM129 213 SRD5A1 Jakimiuk, A. J.; Weitsman, S. R.; Magoffin, D. A.: 5- alpha- 3 C c
reductaseactivity in women with polycystic ovary syndrome. J. Clin.
Endocr.Metab. 84: 2414- 2418, 1999.

GAM129 213 SRD5A1 Jenkins, E. P.; Andersson, S.; Imperato- McGinley, J.; Wilson, J.D.; 3 C c
Russell, D. W.: Genetic and pharmacological evidence for morethan one human
steroid 5- alpha- reductase. J. Clin. Invest. 89: 293- 300,1992.

GAM129 213 SRD5A1 Jenkins, E. P.; Hsieh, C.- L.; Milatovich, A.; Normington, K.; Berman,D. M.; 3 C c
Francke, U.; Russell, D. W.: Characterization and chromosomalmapping of a
human steroid 5- alpha- reductase gene and pseudogene andmapping of the
mouse homologue. Genomics 11: 1102- 1112, 1991.

GAM129 213 SRD5A1 Thigpen, A. E.; Silver, R. I.; Guileyardo, J. M.; Casey, M. L.;McConnell, J. 3 C c
D.; Russell, D. W.: Tissue distribution and ontogenyof steroid 5- alpha-
reductase isozyme expression. J. Clin. Invest. 92:903- 910, 1993.

GAM129 213 SUPT6H Chiang, P.- W.; Wang, S.; Smithivas, P.; Song, W.- J.; Ramamoorthy,S.; 3 C b
Hillman, J.; Puett, S.; Van Keuren, M. L.; Crombez, E.; Kumar,A.; Glover, T.
W.; Miller, D. E.; Tsai, C.- H.; Blackburn, C. C.; Chen,X.- N.; Sun, Z.;
Cheng, J.- F.; Korenberg, J. R.; Kurnit, D. M.: Identificationand analysis
of the human and murine putative chromatin structureregulator SUPT6H and
Supt6h. Genomics 34: 328- 333, 1996.

GAM129 213 SUPT6H Segre, J. A.; Nemhauser, J. L.; Taylor, B. A.; Nadeau, J. H.; Lander,E. S.: 3 C b
Positional cloning of the nude locus: genetic, physical andtranscription

maps of the region and mutations in the mouse and rat. Genomics 28:549- 559, 1995.

GAM129 213 TEAD2 Jacquemin, P.; Depetris, D.; Mattei, M.- G.; Martial, J. A.; Davidson,I.: 3 C c
Localization of human transcription factor TEF- 4 and TEF- 5 (TEAD2,TEAD3) genes to chromosomes 19q13.3 and 6p21.2 using fluorescencein situ hybridization and radiation hybrid analysis. Genomics 55:127- 129, 1999.

GAM129 213 TEAD2 Jacquemin, P.; Hwang, J.- J.; Martial, J. A.; Dolle, P.; Davidson,I.: A 3 C c
novel family of developmentally regulated mammalian transcriptionfactors containing the TEA/ATTS DNA binding domain. J. Biol. Chem. 271:21775- 21785, 1996.

GAM130 331 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- 3 B c
glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989.

GAM130 331 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion 3 B c
data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989.

GAM130 331 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma 3 B c
alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.

GAM130 331 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human 3 B c
plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.

GAM130 331 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: 3 B c
Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988.

GAM130 331 AP1M1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation 3 B c
of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002.

GAM130 331 AP1M1 Nakayama, Y.; Goebl, M.; O'Brine Greco, B.; Lemmon, S.; PingchangChow, E.; 3 B c
Kirchhausen, T.: The medium chains of the mammalian clathrin-associatedproteins have a homolog in yeast. Europ. J. Biochem. 202: 569-574,1991.

GAM130 331 AP1M1 Peyrard, M.: Personal Communication. Stockholm, Sweden 1/7/1999. 3 B c

GAM130 331 AP1M1 Peyrard, M.; Parveneh, S.; Lagercrantz, S.; Ekman, M.; Fransson,I.; Sahlen, 3 B c
S.; Dumanski, J. P.: Cloning, expression pattern, andchromosomal assignment to 16q23 of the human gamma- adaptin gene (ADTG). Genomics 50:275- 280, 1998.

GAM130 331 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. 3 B b
C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002.

GAM130 331 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; 3 B b
Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM130 331 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- 3 B b
interacting protein, recognizes the basolateral sortingsignal of amyloid precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998.

GAM130 331 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; 3 B b
Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the
beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990.

GAM130 331 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: 3 B b
Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11
near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec.
Genet. 16: 401- 405, 1990.

GAM130 331 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K- 3 B b
ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics
6:697- 699, 1990.

GAM130 331 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: 3 B b
Identification of a putative isoform of the Na,K- ATPase beta
subunit:primary structure and tissue- specific expression. J. Biol. Chem.
164:4613- 4618, 1989.

GAM130 331 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: 3 B b
Identification of a cDNA clone specific for the neural adhesionmolecule
AMOG. J. Neurosci. Res. 22: 113- 119, 1989.

GAM130 331 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 B b
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM130 331 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 B b
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM130 331 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 B c
member of a multigene family. Genomics 52: 332- 341, 1998.

GAM130 331 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 B c
new member of the MTG8/ETO gene family, maps on 20q11region and is deleted
in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM130 331 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 B c
Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic
fusion protein forms a complex with a novel member of theMTG8(ETO/CDR)
family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM130 331 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. 3 B c
J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis
machinery through a novel motif, the F- box. Cell 86:263- 274, 1996.

GAM130 331 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; 3 B c
Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene
(CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics
24:27- 33, 1994.

GAM130 331 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F 3 B c
maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6:
149- 150, 1995.

GAM130 331 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 3 B b
membrane- associated C- type lectin that exhibits CD4- independentbinding of
human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad.
Sci. 89: 8356- 8360, 1992.

GAM130 331 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 3 B b
for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR.
Science 294: 2163- 2166, 2001.

GAM130 331 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 3 B b

Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S. L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-infection of T cells. Cell 100: 587- 597,2000.

GAM130 331 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 3 B b
F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000.

GAM130 331 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related 3 B b
gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000.

GAM130 331 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 B b
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.: Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM130 331 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 3 B b
37, 2001.

GAM130 331 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: 3 B b
Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001.

GAM130 331 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification 3 B b
of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001.

GAM130 331 DDX11 Amann, J.; Kidd, V. J.; Lahti, J. M.: Characterization of putativehuman 3 B c
homologues of the yeast chromosome transmission fidelity gene,CHL1. J. Biol. Chem. 272: 3823- 3832, 1997.

GAM130 331 DDX11 Amann, J.; Valentine, M.; Kidd, V. J.; Lahti, J. M.: Localizationof Chl1- 3 B c
related helicase genes to human chromosome regions 12p11 and12p13: similarity between parts of these genes and conserved humantelomeric-associated DNA. Genomics 32: 260- 265, 1996.

GAM130 331 DDX11 Frank, S.; Werner, S.: The human homologue of the yeast CHL1 geneis a novel 3 B c
keratinocyte growth factor- regulated gene. J. Biol. Chem. 271:24337- 24340, 1996.

GAM130 331 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; 3 B b
Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000.

GAM130 331 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 3 B b
40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461-8466, 1998.

GAM130 331 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that 3 B b
functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997.

GAM130 331 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, 3 B b
S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998.

GAM130 331 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. 3 B c
W.: Chromosomal localization and racial distributionof the polymorphic human

dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352, 1988.

GAM130 331 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies three RFLPs. Nucleic Acids Res. 15: 5501 only,1987. 3 B c

GAM130 331 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: Chromosomal localization and racial distribution of the polymorphichDHFR-psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985. 3 B c

GAM130 331 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; Nienhuis, A. W.: Chromosomal organization of the human dihydrofolatereductase genes: dispersion, selective amplification and a novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984. 3 B c

GAM130 331 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in dihydrofolatereductase that confer resistance to methotrexate: potential for clinicalapplication. Hum. Mutat. 11: 259- 263, 1998. 3 B c

GAM130 331 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: Intronless human dihydrofolate reductase genes are derivedfrom processed RNA molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982. 3 B c

GAM130 331 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association with variation in protein structure. Science 220: 1125- 1129,1983. 3 B c

GAM130 331 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 757 and 807- 812, 1975. 3 B c

GAM130 331 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5. Molec. Cell. Biol. 4: 2010- 2016, 1984. 3 B c

GAM130 331 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater-Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med. 310: 789- 790, 1984. 3 B c

GAM130 331 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986. 3 B c

GAM130 331 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: Human dihydrofolate reductase gene is located in chromosome 5and is unlinked to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984. 3 B c

GAM130 331 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human dihydrofolate reductase gene to band q23 of chromosome 5and of related pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85, 1985. 3 B c

GAM130 331 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; Attardi, G.: Chromosomal location of the normal human DHFRgene and of its amplified copies in methotrexate resistant cell variants.(Abstract) Cytogenet. Cell Genet. 37: 534 only, 1984. 3 B c

GAM130 331 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 10/7/1983. 3 B c

GAM130 331 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: Amplification of the human dihydrofolate reductase gene viadouble minutes is initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000. 3 B c

GAM130 331 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing 3 B c

megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976.

GAM130 331 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)- 3 B c
formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967.

GAM130 331 IL19 Blumberg, H.; Conklin, D.; Xu, W.; Grossmann, A.; Brender, T.;Carollo, S.; 3 B c
Eagan, M.; Foster, D.; Haldeman, B. A.; Hammond, A.;Haugen, H.; Jelinek, L.;
and 14 others: Interleukin 20: discovery,receptor identification, and role
in epidermal function. Cell 104:9- 19, 2001.

GAM130 331 IL19 Gallagher, G.; Dickensheets, H.; Eskdale, J.; Izotova, L. S.; 3 B c
Mirochnitchenko,O. V.; Peat, J. D.; Vazquez, N.; Pestka, S.; Donnelly, R.
P.; Kotenko,S. V.: Cloning, expression and initial characterisation of
interleukin- 19(IL- 19), a novel homologue of human interleukin- 10 (IL-
10). GenesImmunity 1: 442- 450, 2000.

GAM130 331 IL1RAPL2 Jin, H.; Gardner, R. J.; Viswesvaraiah, R.; Muntoni, F.; Roberts,R. G.: Two 3 B c
novel members of the interleukin- 1 receptor gene family,one deleted in
Xp22.1- Xp21.3 mental retardation. Europ. J. Hum. Genet. 8:87- 94, 2000.

GAM130 331 IL1RAPL2 Sana, T. R.; Debets, R.; Timans, J. C.; Bazan, J. F.; Kastelein,R. A.: 3 B c
Computational identification, cloning, and characterizationof IL1R9, a novel
interleukin- 1 receptor- like gene encoded over anunusually large interval
of human chromosome Xq22.2- q22.3. Genomics 69:252- 262, 2000.

GAM130 331 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand 3 B c
characterization of human Lnk, an adaptor protein with pleckstrinhomology
and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164:
5199- 5206, 2000.

GAM130 331 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; 3 B c
Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor
protein Lnk: definition of a conserved family of signal- modulatingproteins.
Immunity 13: 599- 609, 2000.

GAM130 331 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 B c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM130 331 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 B c
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22
suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci.
98: 10374- 10379, 2001.

GAM130 331 MEF2A Breitbart, R. E.; Liang, C.; Smoot, L. B.; Laheru, D. A.; Mahdavi,V.; Nadal- 3 B c
Ginard, B.: A fourth human MEF2 transcription factor, hMEF2D,is an early
marker of the myogenic lineage. Development 118: 1095- 1106,1993.

GAM130 331 MEF2A Hobson, G. M.; Krahe, R.; Garcia, E.; Siciliano, M. J.; Funanage,V. L.: 3 B c
Regional chromosomal assignments for four members of the MADSdomain
transcription enhancer factor 2 (MEF2) gene family to humanchromosomes
15q26, 19p12, 5q14, and 1q12- q23. Genomics 29: 704- 711,1995.

GAM130 331 MEF2A Mao, Z.; Bonni, A.; Xia, F.; Nadal- Vicans, M.; Greenberg, M. E.: Neuronal 3 B c
activity- dependent cell survival mediated by transcriptionfactor MEF2.
Science 286: 785- 790, 1999.

GAM130 331 MEF2A Martin, J. F.; Miano, J. M.; Hustad, C. M.; Copeland, N. G.; Jenkins,N. A.; 3 B c
Olson, E. N.: A Mef2 gene that generates a muscle- specificisoform via
alternative mRNA splicing. Molec. Cell. Biol. 14: 1647- 1656,1994.

GAM130 331 MEF2A Molkentin, J. D.; Black, B. L.; Martin, J. F.; Olson, E. N.: 3 B c
Cooperativeactivation of muscle gene expression by MEF2 and myogenic bHLH

proteins. Cell 83:1125- 1136, 1995.

GAM130 331 MEF2A Naya, F. J.; Black, B. L.; Wu, H.; Bassel- Duby, R.; Richardson,J. A.; Hill, 3 B c
J. A.; Olson, E. N.: Mitochondrial deficiency and cardiacsudden death in
mice lacking the MEF2A transcription factor. NatureMed. 15Oct, 2002. Note:
Advance Electronic Publication.

GAM130 331 MEF2A Pollock, R.; Treisman, R.: Human SRF- related proteins: DNA- 3 B c
bindingproperties and potential regulatory targets. Genes Dev. 5: 2327-
2341,1991.

GAM130 331 MEF2A Suzuki, E.; Lowry, J.; Sonoda, G.; Testa, J. R.; Walsh, K.: Structuresand 3 B c
chromosome locations of the human MEF2A gene and a pseudogeneMEF2AP.
Cytogenet. Cell Genet. 73: 244- 249, 1996.

GAM130 331 MEF2A Yu, Y.- T.; Breitbart, R. E.; Smoot, L. B.; Lee, Y.; Mahdavi, V.;Nadal- 3 B c
Ginard, B.: Human myocyte- specific enhancer factor 2 comprisesa group of
tissue- restricted MADS box transcription factors. GenesDev. 6: 1783- 1798,
1992.

GAM130 331 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to 3 B c
two putative mammalian circadian regulators, mper1 andmper2, to light. Cell
91: 1055- 1064, 1997.

GAM130 331 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM130 331 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; 3 B c
Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and
mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531-
2534, 1999.

GAM130 331 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of 3 B c
clock operative in the mammalian forebrain. Science 293:506- 509, 2001.

GAM130 331 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; 3 B c
Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.;
Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock.
Science 288: 1013- 1019, 2000.

GAM130 331 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; 3 B c
Reppert, S. M.: Two period homologs: circadian expression andphotic
regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997.

GAM130 331 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; 3 B c
Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial
advanced sleep phase syndrome. Science 291: 1040- 1043,2001.

GAM130 331 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; 3 B c
Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the
mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694,
2001.

GAM130 331 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; 3 B c
Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the
mammalian circadian clock. Nature 400: 169- 173,1999.

GAM130 331 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; 3 B c
Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx
activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C.
Genomics 47: 323- 324, 1998.

GAM130 331 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, 3 B c
S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to
human chromosome 21q22.3. Genomics 41: 193- 200,1997.

GAM130 331 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; 3 B b
Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor
integrity, and rhodopsin dephosphorylation in mice lackingboth protein
phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21:
8605- 8614, 2001.

GAM130 331 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; 3 B b
Nathans, J.: Identification and characterization of a conservedfamily of
protein serine/threonine phosphatases homologous to Drosophilaretinal
degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997.

GAM130 331 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 3 B c
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene
PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal
instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM130 331 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 3 B c
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY)
to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet.
76: 49- 52, 1997.

GAM130 331 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 3 B c
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated
protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of
all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM130 331 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 B b
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.:
Genomicorganization, comparative analysis, and genetic polymorphisms of
thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733,
2001.

GAM130 331 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 B b
Chen, S. G.: Expression and structural characterizationof the recombinant
human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM130 331 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 B b
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.;
Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-
deficient mice is associated with upregulation of thenovel PrP- like protein
doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM130 331 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 B b
T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin
the prion- like protein gene (Prnd) and their implications inhuman prion
diseases, Alzheimer's disease and other neurological disorders. Hum.Genet.
109: 319- 325, 2001.

GAM130 331 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 B b
P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-
glycosylated, glycosylphosphatidylinositol- anchored protein:expression in
testis and ectopic production in the brains of Prnp(0/0)mice predisposed to
Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM130 331 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 B b
915, 1999.

GAM130 331 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 3 B c

Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime-untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001.

GAM130 331 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 3 B c
Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM130 331 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 3 B c
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996.

GAM130 331 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 3 B c
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM130 331 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 3 B c
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996.

GAM130 331 PTGS1 Catella- Lawson, F.; Reilly, M. P.; Kapoor, S. C.; Cucchiara, A.J.; DeMarco, 3 B c
S.; Tournier, B.; Vyas, S. N.; FitzGerald, G. A.: Cyclooxygenaseinhibitors and the antiplatelet effects of aspirin. New Eng. J. Med. 345:1809- 1817, 2001.

GAM130 331 PTGS1 Dube, J.- N.; Drouin, J.; Aminian, M.; Plant, M. H.; Laneuville,O.: 3 B c
Characterization of a partial prostaglandin endoperoxide H synthase-1deficiency in a patient with a bleeding disorder. Brit. J. Haemat. 113:878-885, 2001.

GAM130 331 PTGS1 Funk, C. D.; Funk, L. B.; Kennedy, M. E.; Pong, A. S.; Fitzgerald,G. A.: 3 B c
Human platelet/erythroleukemia cell prostaglandin G/H synthase:cDNA cloning, expression, and gene chromosomal assignment. FASEBJ. 5: 2304- 2312, 1991.

GAM130 331 PTGS1 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; 3 B c
Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.; Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999.

GAM130 331 PTGS1 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; 3 B c
Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.: Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2 in the humanfetal and adult male reproductive tracts. J. Clin. Endocr. Metab. 85:3436- 3441, 2000.

GAM130 331 PTGS1 Langenbach, R.; Morham, S. G.; Tiano, H. F.; Loftin, C. D.; Ghanayem,B. I.; 3 B c
Chulada, P. C.; Mahler, J. F.; Lee, C. A.; Goulding, E. H.;Kluckman, K. D.; Kim, H. S.; Smithies, O.: Prostaglandin synthase1 gene disruption in mice reduces arachidonic acid- induced inflammationand indomethacin- induced gastric ulceration. Cell 83: 483- 492, 1995.

GAM130 331 PTGS1 Malkowski, M. G.; Ginell, S. L.; Smith, W. L.; Garavito, R. M.: The 3 B c
productive conformation of arachidonic acid bound to prostaglandinsynthase. Science 289: 1933- 1937, 2000.

GAM130 331 PTGS1 Pareti, F. I.; Manucci, P. M.; D'Angelo, A.; Smith, J. B.; Sautebin,L.; 3 B c
Galli, G.: Congenital deficiency of thromboxane and prostacyclin. Lancet I:898- 900, 1980.

GAM130 331 PTGS1 Picot, D.; Loll, P. J.; Garavito, R. M.: The x- ray crystal structureof the 3 B c

membrane protein prostaglandin H- 2 synthase- 1. Nature 367:243- 249, 1994.

GAM130 331 PTGS1 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93: 705- 716, 1998. 3 B c

GAM130 331 PTGS1 Vane, J. R.; Mitchell, J. A.; Appleton, I.; Tomlinson, A.; Bishop-Bailey,D.; Croxtall, J.; Willoughby, D. A.: Inducible isoforms of cyclooxygenaseand nitric- oxide synthase in inflammation. Proc. Nat. Acad. Sci. 91:2046- 2050, 1994. 3 B c

GAM130 331 PTGS1 Yokoyama, C.; Tanabe, T.: Cloning of human gene encoding prostaglandinendoperoxide synthase and primary structure of the enzyme. Biochem.Biophys. Res. Commun. 165: 888- 894, 1989. 3 B c

GAM130 331 PTPRK Fuchs, M.; Muller, T.; Lerch, M. M.; Ullrich, A.: Associationof human protein- tyrosine phosphatase kappa with members of the armadillofamily. J. Biol. Chem. 271: 16712- 16719, 1996. 3 B c

GAM130 331 PTPRK Yang, Y.; Gil, M. C.; Choi, E. Y.; Park, S. H.; Pyun, K. H.; Ha,H.: Molecular cloning and chromosomal localization of a human genehomologous to the murine R- PTP- kappa, a receptor- type protein tyrosinephosphatase. Gene 186: 77- 82, 1997. 3 B c

GAM130 331 PTPRK Zhang, Y.; Siebert, R.; Matthiesen, P.; Yang, Y.; Ha, H.; Schlegelberger,B.: Cytogenetical assignment and physical mapping of the human R- PTP- kappagene (PTPRK) to the putative tumor suppressor gene region 6q22.2- q22.3 Genomics 51:309- 311, 1998. 3 B c

GAM130 331 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999. 3 B b

GAM130 331 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000. 3 B b

GAM130 331 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 B b

GAM130 331 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X-linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 B b

GAM130 331 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 B b

GAM130 331 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999. 3 B b

GAM130 331 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001. 3 B b

GAM130 331 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 3 B b
Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset
of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J.
Med. Genet. 38: 409- 411, 2001.

GAM130 331 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 3 B b
A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five-
base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia
tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85:
3343- 3347, 2000.

GAM130 331 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 3 B b
for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a
non- canonical splice site. Gene 273: 285- 293, 2001.

GAM130 331 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, 3 B b
H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked
spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002.

GAM130 331 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; 3 B b
Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A
recurrent RNA- splicing mutation in the SEDL gene causes X-
linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398-
1407,2001.

GAM130 331 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked 3 B b
recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic
evolution in a 6- generation kindred and review ofthe literature. Medicine
78: 9- 25, 1999.

GAM130 331 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, 3 B c
C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe
transactivation domain induces bony abnormalities and cooperateswith LMO1 to
generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419,
1997.

GAM130 331 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; 3 B c
Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J
recombinase activity. Science 250: 1426- 1429, 1990.

GAM130 331 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; 3 B c
Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor
SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992.

GAM130 331 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, 3 B c
G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common
occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990.

GAM130 331 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and 3 B c
characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995.

GAM130 331 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; 3 B c
Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic
axial development and left- right specification. Nature 399:691- 694, 1999.

GAM130 331 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human 3 B c
intestine:biology and function. Gastroenterology 113: 332- 340, 1997.

GAM130 331 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; 3 B c
Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning
of a mammalian proton- coupled oligopeptide transporter. Nature 368:563-
566, 1994.

GAM130 331 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, 3 B c

T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995.

GAM130 331 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998. 3 B c

GAM130 331 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 3 B c

GAM130 331 SMARCD1 Ring, H. Z.; Vameghi- Meyers, V.; Wang, W.; Crabtree, G. R.; Francke,U.: Five SWI/SNF- related, matrix- associated, actin- dependent regulatorof chromatin (SMARC) genes are dispersed in the human genome. Genomics 51:140- 143, 1998. 3 B c

GAM130 331 SMARCD1 Wang, W.; Xue, Y.; Zhou, S.; Kuo, A.; Cairns, B. R.; Crabtree,G. R.: Diversity and specialization of mammalian SWI/SNF complexes. GenesDev. 10: 2117- 2130, 1996. 3 B c

GAM130 331 SPN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM- dependent movement of CD43 defines a novelprotein complex distal to the immunological synapse. Immunity 15:739- 750, 2001. 3 B c

GAM130 331 SPN Baecher, C. M.; Dorfman, K. S.; Mattei, M.- G.; Frelinger, J. G.: cDNA cloning and localization of the mouse leukosialin gene (Ly48)to chromosome 7. Immunogenetics 31: 307- 314, 1990. 3 B c

GAM130 331 SPN Bazil, V.; Strominger, J. L.: CD43, the major sialoglycoproteinof human leukocytes, is proteolytically cleaved from the surface ofstimulated lymphocytes and granulocytes. Proc. Nat. Acad. Sci. 90:3792- 3796, 1993. 3 B c

GAM130 331 SPN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe immunological synapse is mediated by phosphorylation- regulatedrelocation of the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001. 3 B c

GAM130 331 SPN Pallant, A.; Eskenazi, A.; Mattei, M.- G.; Fournier, R. E. K.; Carlsson,S. R.; Fukuda, M.; Frelinger, J. G.: Characterization of cDNAs encodinghuman leukosialin and localization of the leukosialin gene to chromosome16. Proc. Nat. Acad. Sci. 86: 1328- 1332, 1989. 3 B c

GAM130 331 SPN Park, J. K.; Rosenstein, Y. J.; Remold- O'Donnell, E.; Bierer, B.E.; Rosen, F. S.; Burakoff, S. J.: Enhancement of T- cell activationby the CD43 molecule whose expression is defective in Wiskott- Aldrichsyndrome. Nature 350: 706- 709, 1991. 3 B c

GAM130 331 SPN Rosenstein, Y.; Park, J. K.; Hahn, W. C.; Rosen, F. S.; Bierer,B. E.; Burakoff, S. J.: CD43, a molecule defective in Wiskott- Aldrichsyndrome, binds ICAM- 1. Nature 354: 233- 235, 1991. 3 B c

GAM130 331 SPN Schmid, K.; Hediger, M. A.; Brossmer, R.; Collins, J. H.; Haupt,H.; Marti, T.; Offner, G. D.; Schaller, J.; Takagaki, K.; Walsh, M.T.; Schwick, H. G.; Rosen, F. S.; Remold- O'Donnell, E.: Amino acidsequence of human plasma galactoglycoprotein: identity with the extracellularregion of CD43 (sialophorin). Proc. Nat. Acad. Sci. 89: 663- 667,1992. 3 B c

GAM130 331 SPN Shelley, C. S.; Carroll, M. C.; Davis, A. E., III; Bruns, G. A.P.; Whitehead, A. S.; Finberg, R.; Remold- O'Donnell, E.; Rosen, F.S.: Human sialophorin: cDNA cloning and gene location. (Abstract) FASEBJ. 2: A1659 only, 1988. 3 B c

GAM130 331 SPN Shelley, C. S.; Remold- O'Donnell, E.; Davis, A. E., III; Bruns,G. A. P.; 3 B c
Rosen, F. S.; Carroll, M. C.; Whitehead, A. S.: Molecularcharacterization of
sialophorin (CD43), the lymphocyte surface sialoglycoproteindefective in
Wiskott- Aldrich syndrome. Proc. Nat. Acad. Sci. 86:2819- 2823, 1989.

GAM130 331 SPN Shelley, C. S.; Remold- O'Donnell, E.; Rosen, F. S.; Whitehead,A. S.: 3 B c
Structure of the human sialophorin (CD43) gene: identificationof features
atypical of genes encoding integral membrane proteins. Biochem.J. 270: 569-
576, 1990.

GAM130 331 SPN van den Berg, T. K.; Nath, D.; Ziltener, H. J.; Vestweber, D.;Fukuda, M.; 3 B c
van Die, I.; Crocker, P. R.: Cutting edge: CD43 functionsas a T cell
counterreceptor for the macrophage adhesion receptor sialoadhesin(Siglec-
1). J. Immun. 166: 3637- 3640, 2001.

GAM130 331 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 3 B b
L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and
SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human
synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM130 331 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 3 B b
J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and
SSX2, encoding proteins with homology to the Kruppel- associatedbox in human
synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM130 331 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 3 B b
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand
characterization of the mouse homolog of SYT, a gene implicatedin the
development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM130 331 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 3 B b
G.: Mapping and characterization of the mouse and humanSS18 genes, two human
SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-
319, 2001.

GAM130 331 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 B b
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene
family with several members transcribed in normaltestis and human cancer.
Int. J. Cancer 72: 965- 971, 1997.

GAM130 331 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 B b
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand
prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM130 331 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 B b
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J.
Nat. Cancer Inst. 91: 974- 975, 1999.

GAM130 331 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 B b
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX
synovial sarcoma translocation proteins and co- localizationwith the SNF
protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM130 331 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 B b
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in
synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM130 331 ST5 Klinger, H. P.: Suppression of tumorigenicity in somatic cellhybrids. I. 3 B c
Suppression and reexpression of tumorigenicity in diploidhuman x D98/AH2
hybrids and independent segregation of tumorigenicityfrom other cell
phenotypes. Cytogenet. Cell Genet. 27: 254- 266,1980.

GAM130 331 ST5 Lichy, J. H.; Modi, W. S.; Seuanez, H. N.; Howley, P. M.: Identificationof a 3 B c

human chromosome 11 gene which is differentially regulated intumorigenic and nontumorigenic somatic cell hybrids of HeLa cells. CellGrowth Differ. 3: 541- 548, 1992.

GAM130 331 ST5 Stanbridge, E. J.: Suppression of malignancy in human cells. Nature 260:17- 20, 1976. 3 B c

GAM130 331 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double-strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence insitu hybridization. Genomics 36: 527- 529, 1996. 3 B b

GAM130 331 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence homologue of staufen is an RNA- binding protein thatis associated with polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell. Biol. 19: 2212- 2219, 1999. 3 B b

GAM130 331 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19: 2220- 2230, 1999. 3 B b

GAM130 331 TAF11 Birck, C.; Poch, O.; Romier, C.; Ruff, M.; Mengus, G.; Lavigne,A.- C.; Davidson, I.; Moras, D.: Human TAFII28 and TAFII18 interactthrough a histone fold encoded by atypical evolutionary conservedmotifs also found in the SPT3 family. Cell 94: 239- 249, 1998. 3 B c

GAM130 331 TAF11 Mengus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.;Davidson, I.: Cloning and characterization of hTAFII18, hTAFII20and hTAFII28: three subunits of the human transcription factor TFIID. EMBOJ. 14: 1520- 1531, 1995. 3 B c

GAM130 331 C TNFRSF13 Claudio, E.; Brown, K.; Park, S.; Wang, H.; Siebenlist, U.: BAFF-inducedNEMO- independent processing of NF- kappa- B2 in maturing B cells. NatureImmun. 3: 958- 965, 2002. 3 B c

GAM130 331 C TNFRSF13 Mackay, F.; Woodcock, S. A.; Lawton, P.; Ambrose, C.; Baetscher,M.; Schneider, P.; Tschopp, J.; Browning, J. L.: Mice transgenicfor BAFF develop lymphocytic disorders along with autoimmune manifestations. J.Exp. Med. 190: 1697- 1710, 1999. 3 B c

GAM130 331 C TNFRSF13 Schiemann, B.; Gommerman, J. L.; Vora, K.; Cachero, T. G.; Shulga-Morskaya,S.; Dobles, M.; Frew, E.; Scott, M. L.: An essential role for BAFFin the normal development of B cells through a BCMA- independent pathway. Science 2111- 2114,2001. 3 B c

GAM130 331 C TNFRSF13 Thompson, J. S.; Bixler, S. A.; Qian, F.; Vora, K.; Scott, M. L.;Cachero, T. G.; Hession, C.; Schneider, P.; Sizing, I. D.; Mullen,C.; Strauch, K.; Zafari, M.; Benjamin, C. D.; Tschopp, J.; Browning,J. L.; Ambrose, C.: BAFF-R, a newly identified TNF receptor thatspecifically interacts with BAFF. Science 293: 2108- 2111, 2001. 3 B c

GAM130 331 C TNFRSF13 Xu, S.; Lam, K.- P.: B- cell maturation protein, which binds thetumor necrosis factor family members BAFF and APRIL, is dispensablefor humoral immune responses. Molec. Cell. Biol. 21: 4067- 4074,2001. 3 B c

GAM130 331 C TNFRSF13 Yan, M.; Wang, H.; Chan, B.; Roose- Girma, M.; Erickson, S.; Baker,T.; Tumas, D.; Grewal, I. S.; Dixit, V. M.: Activation and accumulationof B cells in TACI- deficient mice. Nature Immun. 2: 638- 643, 2001. 3 B c

GAM130 331 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: Thiopurinemethyltransferase pharmacogenetics: alternative molecular diagnosisand preliminary data from Northern Portugal. Pharmacogenetics 9:257- 261, 1999. 3 B b

GAM130 331 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 B b
McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian
populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM130 331 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 B b
Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof
thiopurine methyltransferase alleles in Caucasian and Asian populations.
Pharmacogenetics 9:37- 42, 1999.

GAM130 331 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 B b
mercaptopurine metabolism, toxic effects, and dosagerequirement in a
thiopurine methyltransferase- deficient child withacute lymphocytic
leukemia. J. Pediat. 119: 985- 989, 1991.

GAM130 331 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 B b
Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in
African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM130 331 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 B b
Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine
methyltransferase:molecular cloning and expression of T84 colon carcinoma
cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM130 331 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 B b
thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-
749, 1993.

GAM130 331 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 B b
Evans, W. E.: A single point mutation leading to loss of catalyticactivity
in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953,
1995.

GAM130 331 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 B b
variation in response to 6- mercaptopurine for childhoodacute lymphoblastic
leukaemia. Lancet 336: 225- 229, 1990.

GAM130 331 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 B b
azathioprine toxicity: relationship to thiopurine methyltransferasegenetic
polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM130 331 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 B b
Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in
thiopurine methyltransferase pharmacogenetics: evidencefor allele
specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773-
776, 1999.

GAM130 331 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human 3 B b
thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon
splice junction mutation that results in lossof activity. J. Clin. Invest.
101: 1036- 1044, 1998.

GAM130 331 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; 3 B b
Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.;
Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene
sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997.

GAM130 331 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; 3 B b
Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine
methyltransferase pharmacogenetics: human gene cloningand characterization
of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996.

GAM130 331 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: 3 B b
Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by

mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997.

GAM130 331 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; 3 B b
Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694- 702, 1996.

GAM130 331 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine 3 B b
pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980.

GAM130 331 TRPM6 Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; 3 B c
Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.; Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.: Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002.

GAM130 331 TRPM6 Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; 3 B c
Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.; Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002.

GAM130 331 TRPM6 Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, 3 B c
D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.: Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome: genetic linkage mapping and analysis of abalanced translocation breakpoint. Hum. Molec. Genet. 6: 1491- 1497,1997.

GAM130 331 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, 3 B c
psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994.

GAM130 331 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; 3 B c
Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000.

GAM130 331 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. 3 B c
D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the pain pathway. Nature 389: 816- 824, 1997.

GAM130 331 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 B c
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001.

GAM130 331 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity 3 B c
to 'hot' chili peppers. Cell 108: 421- 430, 2002.

GAM130 331 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, 3 B c
A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000.

GAM130 331 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated 3 B c
by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996.

GAM130 331 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel 3 B c
activity by protein kinase C. Nature 408: 985- 990, 2000.

GAM130 331 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand 3 B c
multiple presentations of the oral irritant zingerone: relationshipto

frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996.

GAM130 331 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994. 3 B c

GAM130 331 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand pleasantness for the capsaicin burn between chili likers and non-likers:implications for liking development. Chem. Senses 18: 471- 482, 1993. 3 B c

GAM130 331 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000. 3 B c

GAM130 331 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002. 3 B c

GAM131 313 PTMA Eschenfeldt, W. H.; Berger, S. L.: The human prothymosin alphagene is polymorphic and induced upon growth stimulation: evidenceusing a cloned cDNA. Proc. Nat. Acad. Sci. 83: 9403- 9407, 1986. 3 C c

GAM131 313 PTMA Goodall, G. J.; Dominguez, F.; Horecker, B. L.: Molecular cloningof cDNA for human prothymosin alpha. Proc. Nat. Acad. Sci. 83: 8926- 8928,1986. 3 C c

GAM131 313 PTMA Haritos, A. A.; Goodall, G. J.; Horecker, B. L.: Prothymosin alpha:isolation and properties of the major immunoreactive form of thymosinalpha- 1 in rat thymus. Proc. Nat. Acad. Sci. 81: 1008- 1011, 1984. 3 C c

GAM131 313 PTMA Manrow, R. E.; Leone, A.; Krug, M. S.; Eschenfeldt, W. H.; Berger,S. L.: The human prothymosin alpha gene family contains several processedpseudogenes lacking deleterious lesions. Genomics 13: 319- 331, 1992. 3 C c

GAM131 313 PTMA Szabo, P.; Panneerselvam, C.; Clinton, M.; Frangou- Lazaridis, M.;Weksler, D.; Whittington, E.; Macera, M. J.; Grzeschik, K.- H.; Selvakumar,A.; Horecker, B. L.: Prothymosin alpha- gene in humans: organizationof its promoter region and localization to chromosome 2. Hum. Genet. 90:629- 634, 1993. 3 C c

GAM131 313 TGFA Brissenden, J. E.; Derynck, R.; Francke, U.: Transforming growthfactor alpha gene (TGFA) maps to human chromosome 2 close to the breakpointof the t(2;8) variant translocation in Burkitt lymphoma. (Abstract) Cytogenet.Cell Genet. 40: 589 only, 1985. 3 C c

GAM131 313 TGFA Collin, G. B.; Marshall, J. D.; Naggert, J. K.; Nishina, P. M.: TGFA: exon- intron structure and evaluation as a candidate gene forAlstrom syndrome. (Letter) Clin. Genet. 55: 61- 62, 1999. 3 C c

GAM131 313 TGFA Ellis, D. L.; Kafka, S. P.; Chow, J. C.; Nanney, L. B.; Inman,W. H.; McCadden, M. E.; King, L. E., Jr.: Melanoma, growth factors,acanthosis nigricans, the sign of Leser- Trelat, and multiple acrochordons:a possible role for alpha- transforming growth factor in cutaneousparaneoplastic syndromes. New Eng. J. Med. 317: 1582- 1587, 1987. 3 C c

GAM131 313 TGFA Fernandez- Larrea, J.; Merlos- Suarez, A.; Urena, J. M.; Baselga,J.; Arribas, J.: A role for a PDZ protein in the early secretorypathway for the targeting of proTGF- alpha to the cell surface. Molec.Cell 3: 423- 433, 1999. 3 C c

GAM131 313 TGFA Fowler, K. J.; Mann, G. B.; Dunn, A. R.: Linkage of the murinetransforming 3 C c

growth factor- alpha gene with Igk, Ly- 2, and Fabp1 onchromosome 6. Genomics 16: 782- 784, 1993.

GAM131 313 TGFA Kramer, A.; Yang, F.- C.; Snodgrass, P.; Li, X.; Scammell, T. E.;Davis, F. C.; Weitz, C. J.: Regulation of daily locomotor activityand sleep by hypothalamic EGF receptor signaling. Science 294: 2511- 2515,2001. 3 C c

GAM131 313 TGFA Tam, J. P.; Scheikh, M. A.; Solomon, D. S.; Ossowski, L.: Efficientsynthesis of human type alpha transforming growth factor: its physicaland biological characterization. Proc. Nat. Acad. Sci. 83: 8082- 8086,1986. 3 C c

GAM131 313 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. B.: Assignment of the gene coding for human TGF- alphato chromosome 2p13. (Abstract) Cytogenet. Cell Genet. 40: 762 only,1985. 3 C c

GAM131 313 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. B.: The gene for human transforming growth factor alphais on the short arm of chromosome 2. Cytogenet. Cell Genet. 42:94- 98, 1986. 3 C c

GAM132 369 PAX2 Amiel, J.; Audollent, S.; Joly, D.; Dureau, P.; Salomon, R.; Tellier,A.- L.; Auge, J.; Bouissou, F.; Antignac, C.; Gubler, M.- C.; Eccles,M. R.; Munnich, A.; Vekemans, M.; Lyonnet, S.; Attie- Bitach, T.:PAX2 mutations in renal-coloboma syndrome: mutational hotspot andgermline mosaicism. Europ. J. Hum. Genet. 8: 820- 826, 2000. 3 C c

GAM132 369 PAX2 Dehbi, M.; Ghahremani, M.; Lechner, M.; Dressler, G.; Pelletier,J.: The paired- box transcription factor, PAX2, positively modulatesexpression of the Wilms' tumor suppressor gene. Oncogene 13: 447- 453,1996. 3 C c

GAM132 369 PAX2 Devriendt, K.; Matthijs, G.; Van Damme, B.; Van Caesbroeck, D.;Eccles, M.; Vanrenterghem, Y.; Fryns, J.- P.; Leys, A.: Missense mutationand hexanucleotide duplication in the PAX2 gene in two unrelated familieswith renal- coloboma syndrome (MIM 120330). Hum. Genet. 103: 149- 153,1998. 3 C c

GAM132 369 PAX2 Dressler, G. R.; Deutsch, U.; Chowdhury, K.; Nornes, H. O.; Gruss,P.: Pax2, a new murine paired- box- containing gene and its expressionin the developing excretory system. Development 109: 787- 795, 1990. 3 C c

GAM132 369 PAX2 Favor, J.; Sandulache, R.; Neuhauser- Klaus, A.; Pretsch, W.; Chatterjee,B.; Senft, E.; Wurst, W.; Blanquet, V.; Grimes, P.; Sporle, R.; Schughart,K.: The mouse Pax2(1Neu) mutation is identical to a human PAX2 mutationin a family with renal- coloboma syndrome and results in developmentaldefects of the brain, ear, eye, and kidney. Proc. Nat. Acad. Sci. 93:13870- 13875, 1996. 3 C c

GAM132 369 PAX2 Ford, B.; Rupps, R.; Lirenman, D.; Van Allen, M. I.; Farquharson,D.; Lyons, C.; Friedman, J. M.: Renal- coloboma syndrome: prenataldetection and clinical spectrum in a large family. Am. J. Med. Genet. 99:137- 141, 2001. 3 C c

GAM132 369 PAX2 Keller, S. A.; Jones, J. M.; Boyle, A.; Barrow, L. L.; Killen,P. D.; Green, D. G.; Kapousta, N. V.; Hitchcock, P. F.; Swank, R.T.; Meisler, M. H.: Kidney and retinal defects (Krd), a transgene- inducedmutation with a deletion of mouse chromosome 19 that includes thePax2 locus. Genomics 23: 309- 320, 1994. 3 C c

GAM132 369 PAX2 Narahara, K.; Baker, E.; Ito, S.; Yokoyama, Y.; Yu, S.; Hewitt,D.; Sutherland, G. R.; Eccles, M. R.; Richards, R. I.: Localisationof a 10q breakpoint within the PAX2 gene in a patient with a de novot(10;13) translocation and optic nerve coloboma- renal disease. J.Med. Genet. 34: 213- 216, 1997. 3 C c

GAM132 369 PAX2 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman homologs of the murine paired- box- containing genes. MammalianGenome 4: 78- 3 C c

82, 1993.

GAM132 369 PAX2 Porteous, S.; Torban, E.; Cho, N.- P.; Cunliffe, H.; Chua, L.;McNoe, L.; 3 C c
Ward, T.; Souza, C.; Gus, P.; Giugliani, R.; Sato, T.;Yun, K.; Favor, J.;
Sicotte, M.; Goodyer, P.; Eccles, M.: Primaryrenal hypoplasia in humans and
mice with PAX2 mutations: evidenceof increased apoptosis in fetal kidneys of
Pax2(1Neu) +/- mutant mice. Hum.Molec. Genet. 9: 1- 11, 2000.

GAM132 369 PAX2 Sanyanusin, P.; McNoe, L. A.; Sullivan, M. J.; Weaver, R. G.;Eccles, M. R.: 3 C c
Mutation of PAX2 in two siblings with renal- colobomasyndrome. Hum. Molec.
Genet. 4: 2183- 2184, 1995.

GAM132 369 PAX2 Sanyanusin, P.; Norrish, J. H.; Ward, T. A.; Nebel, A.; McNoe,L. A.; Eccles, 3 C c
M. R.: Genomic structure of the human PAX2 gene. Genomics 35:258- 261, 1996.

GAM132 369 PAX2 Sanyanusin, P.; Schimmenti, L. A.; McNoe, L. A.; Ward, T. A.;Pierpont, M. E. 3 C c
M.; Sullivan, M. J.; Dobyns, W. B.; Eccles, M. R.: Mutation of the PAX2 gene
in a family with optic nerve colobomas,renal anomalies and vesicoureteral
reflux. Nature Genet. 9: 358- 364,1995.

GAM132 369 PAX2 Schimmenti, L. A.; Cunliffe, H. E.; McNoe, L. A.; Ward, T. A.;French, M. C.; 3 C c
Shim, H. H.; Zhang, Y.- H.; Proesmans, W.; Leys, A.;Byerly, K. A.; Braddock,
S. R.; Masuno, M.; Imaizumi, K.; Devriendt,K.; Eccles, M. R.: Further
delineation of renal- coloboma syndromein patients with extreme variability
of phenotype and identical PAX2mutations. Am. J. Hum. Genet. 60: 869- 878,
1997.

GAM132 369 PAX2 Schimmenti, L. A.; Pierpont, M. E.; Carpenter, B. L. M.; Kashtan,C. E.; 3 C c
Johnson, M. R.; Dobyns, W. B.: Autosomal dominant optic nervecolobomas,
vesicoureteral reflux, and renal anomalies. Am. J. Med.Genet. 59: 204- 208,
1995.

GAM132 369 PAX2 Schimmenti, L. A.; Shim, H. H.; Wirtschafter, J. D.; Panzarino,V. A.; 3 C c
Kashtan, C. E.; Kirkpatrick, S. J.; Wargowski, D. S.; France,T. D.; Michel,
E.; Dobyns, W. B.: Homonucleotide expansion and contractionmutations of PAX2
and inclusion of Chiari 1 malformation as part ofrenal- coloboma syndrome.
Hum. Mutat. 14: 369- 376, 1999.

GAM132 369 PAX2 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: 3 C c
Chromosomal localization of seven PAX genes and cloning of anovel family
member, PAX- 9. Nature Genet. 3: 292- 298, 1993.

GAM132 369 PAX2 Tellier, A.- L.; Amiel, J.; Delezoide, A.- L.; Audollent, S.; Auge,J.; 3 C c
Esnault, D.; Encha- Razavi, F.; Munnich, A.; Lyonnet, S.; Vekemans,M.;
Attie- Bitach, T.: Expression of the PAX2 gene in human embryosand exclusion
in the CHARGE syndrome. Am. J. Med. Genet. 93: 85- 88,2000.

GAM132 369 PAX2 Tellier, A.- L.; Amiel, J.; Salomon, R.; Jolly, D.; Delezoide,A.- L.; Auge, 3 C c
J.; Gubler, M.- C.; Munnich, A.; Lyonnet, S.; Antignac,C.; Vekemans, M.;
Broyer, M.; Attie- Bitach, T.: PAX2 expression duringearly human development
and its mutations in renal hypoplasia withor without coloboma. (Abstract)
Am. J. Hum. Genet. 63 (suppl.):A7 only, 1998.

GAM132 369 PAX2 Ward, T. A.; Nebel, A.; Reeve, A. E.; Eccles, M. R.: Alternativemessenger 3 C c
RNA forms and open reading frames within an additional conservedregion of
the human PAX- 2 gene. Cell Growth Differ. 5: 1015- 1021,1994.

GAM132 369 PAX2 Weaver, R. G.; Cashwell, L. F.; Lorentz, W.; Whiteman, D.; Geisinger,K. R.; 3 C c
Ball, M.: Optic nerve coloboma associated with renal disease. Am.J. Med.
Genet. 29: 597- 605, 1988.

GAM133 211 BCL2L2 Gibson, L.; Holmgreen, S. P.; Huang, D. C. S.; Bernard, O.; Copeland,N. G.; 1 B c
Jenkins, N. A.; Sutherland, G. R.; Baker, E.; Adams, J. M.;Cory, S.: bcl- w,

a novel member of the bcl- 2 family, promotes cellsurvival. Oncogene 13: 665- 675, 1996.

GAM133 211 BCL2L2 Ross, A. J.; Waymire, K. G.; Moss, J. E.; Parlow, A. F.; Skinner,M. K.; Russell, L. D.; MacGregor, G. R.: Testicular degenerationin Bclw- deficient mice. Nature Genet. 18: 251- 256, 1998. 1 B c

GAM133 211 CD72 Kumanogoh, A.; Watanabe, C.; Lee, I.; Wang, X.; Shi, W.; Araki,H.; Hirata, H.; Iwahori, K.; Uchida, J.; Yasui, T.; Matsumoto, M.;Yoshida, K.; Yakura, H.; Pan, C.; Parnes, J. R.; Kikutani, H.: Identificationof CD72 as a lymphocyte receptor for the class IV semaphorin CD100:a novel mechanism for regulating B cell signaling. Immunity 13:621- 631, 2000. 1 B c

GAM133 211 CD72 Ravetch, J. V.; Lanier, L. L.: Immune inhibitory receptors. Science 290:84- 89, 2000. 1 B c

GAM133 211 CD72 Von Hoegen, I.; Hsieh, C.- L.; Scharting, R.; Francke, U.; Parnes,J. R.: Identity of human Lyb- 2 and CD72 and localization of the geneto chromosome 9. Europ. J. Immun. 21: 1425- 1431, 1991. 1 B c

GAM133 211 FAT2 Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara,O.: Identification of high- molecular- weight proteins with multipleEGF- like motifs by motif- trap screening. Genomics 51: 27- 34, 1998. 1 B c

GAM133 211 FAT2 Wu, Q.; Maniatis, T.: Large exons encoding multiple ectodomainsare a characteristic feature of protocadherin genes. Proc. Nat. Acad.Sci. 97: 3124- 3129, 2000. 1 B c

GAM133 211 HOXC8 Acampora, D.; D'Esposito, M.; Faiella, A.; Pannese, M.; Migliaccio,E.; Morelli, F.; Stornaiuolo, A.; Nigro, V.; Simeone, A.; Boncinelli,E.: The human HOX gene family. Nucleic Acids Res. 17: 10385- 10402,1989. 1 B c

GAM133 211 HOXC8 Cannizzaro, L. A.; Croce, C. M.; Griffin, C. A.; Simeone, A.; Boncinelli,E.; Huebner, K.: Human homeo box- containing genes located at chromosomeregions 2q31- 2q37 and 12q12- 12q13. Am. J. Hum. Genet. 41: 1- 15,1987. 1 B c

GAM133 211 HOXC8 Masuda, R.; Yuhki, N.; O'Brien, S. J.: Molecular cloning, chromosomalassignment, and nucleotide sequence of the feline homeobox HOX3A. Genomics 11:1007- 1013, 1991. 1 B c

GAM133 211 HOXC8 Rabin, M.; Ferguson- Smith, A.; Hart, C. P.; Ruddle, F. H.: Cognatehomeo- box loci mapped on homologous human and mouse chromosomes. Proc.Nat. Acad. Sci. 83: 9104- 9108, 1986. 1 B c

GAM133 211 HOXC8 Schughart, K.; Pravtcheva, D.; Newman, M. S.; Hunihan, L. W.; Jiang,Z.; Ruddle, F. H.: Isolation and regional localization of the murinehomeobox- containing gene Hox- 3.3 to mouse chromosome region 15E. Genomics 5:76- 83, 1989. 1 B c

GAM133 211 HOXC8 Simeone, A.; Pannese, M.; Acampora, D.; D'Esposito, M.; Boncinelli,E.: At least three human homeoboxes on chromosome 12 belong to thesame transcription unit. Nucleic Acids Res. 16: 5379- 5390, 1988. 1 B c

GAM133 211 HOXC8 Yueh, Y. G.; Gardner, D. P.; Kappen, C.: Evidence for regulationof cartilage differentiation by the homeobox gene Hoxc- 8. Proc. Nat.Acad. Sci. 95: 9956- 9961, 1998. 1 B c

GAM133 211 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000. 1 B c

GAM133 211 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. 1 B c

Immunity 13: 599- 609, 2000.

GAM133 211 MASP2 Stover, C. M.; Schwaeble, W. J.; Lynch, N. J.; Thiel, S.; Speicher,M. R.: 1 B c
Assignment of the gene encoding mannan- binding lectin- associatedserine protease 2 (MASP2) to human chromosome 1p36.3- p36.2 by in situhybridization and somatic cell hybrid analysis. Cytogenet. Cell Genet. 84:148- 149, 1999.

GAM133 211 MASP2 Stover, C. M.; Thiel, S.; Thelen, M.; Lynch, N. J.; Vorup- Jensen,T.; 1 B c
Jensenius, J. C.; Schwaeble, W. J.: Two constituents of the initiationcomplex of the mannan- binding lectin activation pathway of complementare encoded by a single structural gene. J. Immun. 162: 3481- 3490,1999.

GAM133 211 MASP2 Takahashi, M.; Endo, Y.; Fujita, T.; Matsushita, M.: A truncatedform of 1 B c
mannose- binding lectin- associated serine protease (MASP)- 2expressed by alternative polyadenylation is a component of the lectincomplement pathway. Int. Immun. 11: 859- 863, 1999.

GAM133 211 MASP2 Thiel, S.; Vorup- Jensen, T.; Stover, C. M.; Schwaeble, W.; Laursen,S. B.; 1 B c
Poulsen, K.; Willis, A. C.; Eggleton, P.; Hansen, S.; Holmskov,U.; Reid, K. B. M.; Jensenius, J. C.: A second serine protease associatedwith mannan- binding lectin that activates complement. Nature 386:506- 510, 1997.

GAM133 211 NTSR1 Laurent, P.; Clerc, P.; Mattei, M.- G.; Forgez, P.; Dumont, X.;Ferrara, P.; 1 B c
Caput, D.; Rostene, W.: Chromosomal localization ofmouse and human neurotensin receptor genes. Mammalian Genome 5:303- 306, 1994.

GAM133 211 NTSR1 Le, F.; Groshan, K.; Zeng, X. P.; Richelson, E.: Characterizationof the 1 B c
genomic structure, promoter region, and a tetranucleotide repeatpolymorphism of the human neurotensin receptor gene. J. Biol. Chem. 272:1315- 1322, 1997.

GAM133 211 NTSR1 Vincent, J.- P.: Neurotensin receptors: binding properties, 1 B c
transductionpathways, and structure. Cell. Molec. Neurobiol. 15: 501- 512, 1995.

GAM133 211 NTSR1 Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad,M.; Gully, 1 B c
D.; Le Fur, G.; Ferrara, P.; Caput, D.: Cloning and expressionof a complementary DNA encoding a high affinity human neurotensinreceptor. FEBS Lett. 317: 139- 142, 1993.

GAM133 211 NUMA1 Compton, D. A.; Szilak, I.; Cleveland, D. W.: Primary structureof NuMA, an 1 B c
intranuclear protein that defines a novel pathway forsegregation of proteins at mitosis. J. Cell Biol. 116: 1395- 1408,1992.

GAM133 211 NUMA1 Lydersen, B. K.; Pettijohn, D. E.: Human- specific nuclear proteinthat 1 B c
associates with the polar region of the mitotic apparatus: distributionin a human/hamster hybrid cell. Cell 22: 489- 499, 1980.

GAM133 211 NUMA1 Merdes, A.; Ramyar, K.; Vechio, J. D.; Cleveland, D. W.: A complexof NuMA 1 B c
and cytoplasmic dynein is essential for mitotic spindle assembly. Cell 87:447- 458, 1996.

GAM133 211 NUMA1 Sparks, C. A.; Bangs, P. L.; McNeil, G. P.; Lawrence, J. B.; Fey,E. G.: 1 B c
Assignment of the nuclear mitotic apparatus protein NuMA geneto human chromosome 11q13. Genomics 17: 222- 224, 1993.

GAM133 211 NUMA1 Wells, R. A.; Catzavelos, C.; Kamel- Reid, S.: Fusion of retinoicacid 1 B c
receptor alpha to NuMA, the nuclear mitotic apparatus protein,by a variant translocation in acute promyelocytic leukaemia. NatureGenet. 17: 109- 113, 1997.

GAM133 211 NUMA1 Wiese, C.; Wilde, A.; Moore, M. S.; Adam, S. A.; Merdes, A.; Zheng,Y.: Role 1 B c
of importin- beta in coupling Ran to downstream targets inmicrotubule assembly. Science 291: 653- 656, 2001.

GAM133 211 NUMA1 Yang, C. H.; Lambie, E. J.; Snyder, M.: NuMA: an unusually longcoiled- coil 1 B c
related protein in the mammalian nucleus. J. Cell Biol. 116:1303- 1317,
1992.

GAM133 211 OSR1 Daigo, Y.; Isomura, M.; Nishiwaki, T.; Tamari, M.; Ishikawa, S.;Kai, M.; 1 B c
Murata, Y.; Takeuchi, K.; Yamane, Y.; Hayashi, R.; Minami,M.; Fujino, M. A.;
Hojo, Y.; Uchiyama, I.; Takagi, T.; Nakamura, Y.: Characterization of a
1200- kb genomic segment of chromosome 3p22- p21.3. DNARes. 6: 37- 44, 1999.

GAM133 211 OSR1 Tamari, M.; Daigo, Y.; Nakamura, Y.: Isolation and characterizationof a 1 B c
novel serine threonine kinase gene on chromosome 3q22- 21.3. J.Hum. Genet.
44: 116- 120, 1999.

GAM134 339 MAP3K7IP Ge, B.; Gram, H.; Di Padova, F.; Huang, B.; New, L.; Ulevitch,R. J.; Luo, 3 C c
1 Y.; Han, J.: MAPKK- independent activation of p38- alphamediated by TAB1-
dependent autophosphorylation of p38- alpha. Science 295:1291- 1294, 2002.

GAM134 339 MAP3K7IP Shibuya, H.; Yamaguchi, K.; Shirakabe, K.; Tonegawa, A.; Gotoh,Y.; Ueno, N.; 3 C c
1 Irie, K.; Nishida, E.; Matsumoto, K.: TAB1: an activatorof the TAK1 MAPKKK
in TGF- beta signal transduction. Science 272:1179- 1182, 1996.

GAM136 279 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 C b
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian
Genome 6: 111- 113, 1995.

GAM136 279 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 C b
members are randomly located on different chromosomes. Hum.Genet. 94: 527-
529, 1994.

GAM136 279 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: 3 C b
Chromosomal mapping of human adenylyl cyclase genestype III, type V and type
VI. Hum. Genet. 94: 69- 73, 1994.

GAM136 279 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; 3 C b
Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive
dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad.
Sci. 99: 9990- 9995, 2002.

GAM136 279 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; 3 C b
Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor:
functional expression and chromosomal assignment to 7p21. J.Biochem. 116:
845- 851, 1994.

GAM136 279 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, 3 C b
C. A.: Chromosomal localization of the human AHR locusencoding the
structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66:
172- 176, 1994.

GAM136 279 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; 3 C b
Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D.
H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression
is required for premature ovarian failure causedby biohazardous
environmental chemicals. Nature Genet. 28: 355- 360,2001.

GAM136 279 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. 3 C b
W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive
correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95-
101, 1997.

GAM136 279 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, 3 C b
J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost
in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779-
782, 2000.

GAM136 279 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001. 3 C b

GAM136 279 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001. 3 C b

GAM136 279 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998. 3 C b

GAM136 279 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: Identificationand characterization of STK12/Aik2: a human gene related to auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147- 152,1998. 3 C b

GAM136 279 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism, OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001. 3 C b

GAM136 279 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand characterization of genes associated with chromosome- 6 mediatedtumor suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996. 3 C b

GAM136 279 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a novel non- lens member of the beta- gamma- crystallin superfamily,is associated with the control of tumorigenicity in human malignantmelanoma. Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997. 3 C b

GAM136 279 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA cloning, expression, subcellular localization, and chromosomalassignment of mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem. Biophys. Res. Commun. 244: 285- 292, 1998. 3 C b

GAM136 279 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof the aurora- and Ipl1- like midbody- associated protein mitotic kinasein human cancer cells. Cancer Res. 58: 4811- 4816, 1998. 3 C b

GAM136 279 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian Genome 9: 715- 720, 1998. 3 C b

GAM136 279 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human melanoma cell lines controlled by introduction of human chromosome6. Science 247: 568- 571, 1990. 3 C b

GAM136 279 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 C b

GAM136 279 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line 3 C b

KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM136 279 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- 3 C b
interacting protein, recognizes the basolateral sortingsignal of amyloid
precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998.

GAM136 279 ATP6V1A1 van Hille, B.; Richener, H.; Evans, D. B.; Green, J. R.; Bilbe,G.: 3 C b
Identification of two subunit A isoforms of the vacuolar H(+)- ATPasein
human osteoclastoma. J. Biol. Chem. 268: 7075- 7080, 1993.

GAM136 279 ATP6V1A1 van Hille, B.; Richener, H.; Green, J. R.; Bilbe, G.: The ubiquitousVA68 3 C b
isoform of subunit A of the vacuolar H(+)- ATPase is highly expressedin
human osteoclasts. Biochem. Biophys. Res. Commun. 214: 1108- 1113,1995.

GAM136 279 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- 3 C c
evaluation of 'reactive lymphoid hyperplasia of the uvea':
animmunohistochemical and molecular analysis of 10 cases. Ophthalmology
107:151- 158, 2000.

GAM136 279 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 3 C c
mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999.

GAM136 279 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. 3 C c
J.Clin. Path. 48: 395- 397, 1995.

GAM136 279 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; 3 C c
Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T.
W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of
NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001.

GAM136 279 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; 3 C c
Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not
its cellular homologue, activates NF- kappa- B transcriptionfactor and c-
Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999.

GAM136 279 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- 3 C c
Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.;
Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in
t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types
Cell 96: 35- 45, 1999.

GAM136 279 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic 3 C c
study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer
Genet. Cytogenet. 58: 35- 38, 1992.

GAM136 279 BDKRB1 Bachvarov, D. R.; Hess, J. F.; Menke, J. G.; Larrivee, J.- F.; Marceau,F.: 3 C c
Structure and genomic organization of the human B(1) receptorgene for kinins
(BDKRB1). Genomics 33: 374- 381, 1996.

GAM136 279 BDKRB1 Chai, K. X.; Ni, A.; Wang, D.; Ward, D. C.; Chao, J.; Chao, L.: Genomic DNA 3 C c
sequence, expression, and chromosomal localization ofthe human B1 bradykinin
receptor gene BDKRB1. Genomics 31: 51- 57,1996.

GAM136 279 BDKRB1 MacNeil, T.; Bierilo, K. K.; Menke, J. G.; Hess, J. F.: Cloningand 3 C c
pharmacological characterization of a rabbit bradykinin B- 1 receptor.
Biochim.Biophys. Acta 1264: 223- 228, 1995.

GAM136 279 BDKRB1 Menke, J. G.; Borkowski, J. A.; Bierilo, K. K.; MacNeil, T.; Derrick,A. W.; 3 C c
Schneck, K. A.; Ransom, R. W.; Strader, C. D.; Linemeyer, D.L.; Hess, J. F.:
Expression cloning of a human B1 bradykinin receptor. J.Biol. Chem. 269:
21583- 21586, 1994.

GAM136 279 BDKRB1 Yang, X.; Polgar, P.: Genomic structure of the human bradykininB(1) receptor 3 C c
gene and preliminary characterization of its regulatoryregions. Biochem.
Biophys. Res. Commun. 222: 718- 725, 1996.

GAM136 279 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.: Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000. 3 C c

GAM136 279 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 3 C c

GAM136 279 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 3 C c

GAM136 279 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 3 C c

GAM136 279 CNN2 Cheng, J.- F.; Boyartchuk, V.; Zhu, Y.: Isolation and mapping ofhuman chromosome 21 cDNA: progress in constructing a chromosome 21expression map. Genomics 23: 75- 84, 1994. 3 C b

GAM136 279 CNN2 Masuda, H.; Tanaka, K.; Takagi, M.; Ohgami, K.; Sakamaki, T.; Shibata,N.; Takahashi, K.: Molecular cloning and characterization of humannon- smooth muscle calponin. J. Biochem. 120: 415- 424, 1996. 3 C b

GAM136 279 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359, 1997. 3 C c

GAM136 279 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix Biol. 18: 319- 324, 1999. 3 C c

GAM136 279 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of the gene encoding human cartilage associatedprotein (CRTAP). Cytogenet. Cell Genet. 87: 191- 194, 1999. 3 C c

GAM136 279 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996. 3 C c

GAM136 279 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989. 3 C c

GAM136 279 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000. 3 C c

GAM136 279 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. L.: The contribution of genetically determined oxidationstatus to inter-individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983. 3 C c

GAM136 279 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986. 3 C c

GAM136 279 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. 3 C c

Endocr. 3: 1399- 1408, 1989.

GAM136 279 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human 3 C c
P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the
3- prime nontranslated region, and localization ofgene to chromosome 15. J.
Exp. Path. 3: 1- 17, 1987.

GAM136 279 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, 3 C c
A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show
deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996.

GAM136 279 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 C c

GAM136 279 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, 3 C c
S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter)
Nature 398: 760- 761, 1999.

GAM136 279 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of 3 C c
cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-
deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J.
Clin. Pharm. 26: 363- 372, 1988.

GAM136 279 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof 3 C c
cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-
based caffeine test. Pharmacogenetics 9: 131- 144, 1999.

GAM136 279 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; 3 C c
Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime
of the CYP1A2 gene: implications for human populationhistory and natural
selection. Am. J. Hum. Genet. 71: 528- 542, 2002.

GAM136 279 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; 3 C c
Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene
encoding DNA fragmentation factor 40 (caspase- activatednuclease), a
candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413,
2000.

GAM136 279 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 3 C c
40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and
chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461-
8466, 1998.

GAM136 279 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that 3 C c
functions downstream of caspase- 3 to trigger DNA fragmentationduring
apoptosis. Cell 89: 175- 184, 1997.

GAM136 279 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, 3 C c
S.: Molecular cloning and characterization of human caspase- activatedDNase.
Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998.

GAM136 279 EPB72 Gallagher, P. G.; Forget, B. G.: Structure, organization, andexpression of 3 C c
the band 7.2b gene, a candidate gene for hereditaryhydrocytosis. J. Biol.
Chem. 270: 26358- 26363, 1995.

GAM136 279 EPB72 Gallagher, P. G.; Romana, M.; Lieman, J. H.; Ward, D. C.: cDNAstructure, 3 C c
tissue- specific expression, and chromosomal localizationof the murine band
7.2b gene. Blood 86: 359- 365, 1995.

GAM136 279 EPB72 Gallagher, P. G.; Upender, M.; Ward, D. C.; Forget, B. G.: Thegene for human 3 C c
erythrocyte membrane protein band 7.2 (EPB72) mapsto 9q33- q34 centromeric
to the Philadelphia chromosome translocationbreakpoint region. Genomics 18:
167- 169, 1993.

GAM136 279 EPB72 Hiebl- Dirschmied, C. M.; Entler, B.; Glotzmann, C.; Maurer- Fogy,I.; 3 C c
Stratowa, C.; Prohaska, R.: Cloning and nucleotide sequence ofcDNA encoding

human erythrocyte band 7 integral membrane protein. Biochim.Biophys. Acta 1090: 123- 124, 1991.

GAM136 279 EPB72 Pilz, A.; Prohaska, R.; Peters, J.; Abbott, C.: Genetic linkageanalysis of the Ak1, Col5a1, Epb7.2, Fpgs, Grp78, Pbx3, and Notch1genes in the region of mouse chromosome 2 homologous to human chromosome9q. Genomics 21: 104- 109, 1994. 3 C c

GAM136 279 EPB72 Unfried, I.; Entler, B.; Prohaska, R.: The organization of thegene (EPB72) encoding the human erythrocyte band 7 integral membraneprotein (protein 7.2b). Genomics 30: 521- 528, 1995. 3 C c

GAM136 279 EPB72 Westberg, J. A.; Entler, B.; Prohaska, R.; Schroder, J. P.: Thegene coding for erythrocyte protein band 7.2b (EPB72) is located inband q34.1 of human chromosome 9. Cytogenet. Cell Genet. 63: 241- 243,1993. 3 C c

GAM136 279 EPB72 Zhu, Y.; Paszty, C.; Turetsky, T.; Tsai, S.; Kuypers, F. A.; Lee,G.; Cooper, P.; Gallagher, P. G.; Stevens, M. E.; Rubin, E.; Mohandas,N.; Mentzer, W. C.: Stomatocytosis is absent in 'stomatin'- deficientmurine red blood cells. Blood 93: 2404- 2410, 1999. 3 C c

GAM136 279 F2RL2 Duperat, V. G.; Jacquelin, B.; Boisseau, P.; Arveiler, B.; Nurden,A. T.: Protease- activated receptor genes are clustered on 5q13. Blood 92:25- 31, 1998. 3 C b

GAM136 279 F2RL2 Ishihara, H.; Connolly, A. J.; Zeng, D.; Kahn, M. L.; Zheng, Y.W.; Timmons, C.; Tram, T.; Coughlin, S. R.: Protease- activated receptor3 is a second thrombin receptor in humans. Nature 386: 502- 506,1997. 3 C b

GAM136 279 F2RL2 Kahn, M. L.; Zheng, Y. W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 3 C b

GAM136 279 F2RL2 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 3 C b

GAM136 279 F2RL2 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 3 C b

GAM136 279 F2RL2 Schmidt, V.; Wainer, J.; Bahou, W.: Identification and characterizationof the human proteolytically activated receptor- 3 (PAR- 3) gene withinthe PAR gene cluster by positional mapping. (Abstract) Blood (suppl.1) 90: 284a only, 1997. 3 C b

GAM136 279 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985. 3 C c

GAM136 279 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985. 3 C c

GAM136 279 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988. 3 C c

GAM136 279 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional analysis of the human tissue factor promoter and inductionby serum. Proc. Nat. Acad. Sci. 87: 2254- 2258, 1990. 3 C c

GAM136 279 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: Completesequence of the human tissue factor gene, a highly regulated cellularreceptor that initiates the coagulation protease cascade. Biochemistry 28:1755- 1762, 1989. 3 C c

GAM136 279 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; 3 C c
Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand
mapping of RFLPs for human tissue factor (HTF) to chromosome 1p.
NucleicAcids Res. 15: 9098 only, 1987.

GAM136 279 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; 3 C c
Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA
sequenceand chromosome localization of the gene. Biochemistry 26: 5234-
5238,1987.

GAM136 279 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; 3 C c
Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA
clones coding for human tissue factor: primary structureof the protein and
cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987.

GAM136 279 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of 3 C c
tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad.
Sci. 94: 6922- 6926, 1997.

GAM136 279 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: 3 C c
Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun.
155: 1203- 1209, 1995.

GAM136 279 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; 3 C c
Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4.
Hum. Genet. 89: 107- 108, 1992.

GAM136 279 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: 3 C c
Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665-
1672, 1990.

GAM136 279 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. 3 C c
L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and
their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681-
1685, 1993.

GAM136 279 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, 3 C c
F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc
alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J.
Hum. Genet. 46: 694- 698, 2001.

GAM136 279 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing 3 C c
of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J.
318: 771- 777, 1996.

GAM136 279 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand 3 C c
characterization of the promoter for the gene encoding the humanmyeloid IgA
Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000.

GAM136 279 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin 3 C c
promoter region of Fc- alpha receptor gene in patients with IgAnephropathy.
Hum. Genet. 108: 128- 133, 2001.

GAM136 279 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 C b
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM136 279 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 C b
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22
suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci.
98: 10374- 10379, 2001.

GAM136 279 LLGL1 Campbell, H. D.; Fountain, S.; Young, I. G.; Claudianos, C.; Hoheisel,J. D.; 3 C c

Chen, K.- S.; Lupski, J. R.: Genomic structure, evolution,and expression of human FLII, a gelsolin and leucine- rich- repeat familymember: overlap with LLGL. Genomics 42: 46- 54, 1997.

GAM136 279 LLGL1 Koyama, K.; Fukushima, Y.; Inazawa, J.; Tomotsune, D.; Takahashi,N.; 3 C c
Nakamura, Y.: The human homologue of the murine Llglh gene (LLGL)maps within the Smith- Magenis syndrome region in 17p11.2. Cytogenet.Cell Genet. 72: 78- 82, 1996.

GAM136 279 LLGL1 Ohshiro, T.; Yagami, T.; Zhang, C.; Matsuzaki, F.: Role of corticaltumour- 3 C c
suppressor proteins in asymmetric division of Drosophila neuroblast. Nature 408:593- 596, 2000.

GAM136 279 LLGL1 Peng, C.- Y.; Manning, L.; Albertson, R.; Doe, C. Q.: The tumour- 3 C c
suppressorgenes lgl and dlg regulate basal protein targeting in Drosophila neuroblasts. Nature 408:596- 600, 2000.

GAM136 279 LLGL1 Strand, D.; Unger, S.; Corvi, R.; Hartenstein, K.; Schenkel, H.;Kalmes, A.; 3 C c
Merdes, G.; Neumann, B.; Krieg- Schneider, F.; Coy, J.F.; Poustka, A.; Schwab, M.; Mechler B. M.: A human homologue ofthe Drosophila tumour suppressor gene l(2)gl maps to 17p11.2- 12 andcodes for a cytoskeletal protein that associates with nonmuscle myosinII heavy chain. Oncogene 11: 291- 301, 1995.

GAM136 279 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; 3 C c
Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363- 18367,1996.

GAM136 279 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof 3 C c
leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994.

GAM136 279 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; 3 C c
Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. Nature 384: 39- 43, 1996.

GAM136 279 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 3 C c
specifictranscriptional regulation of human leukotriene B4 receptor gene. J.Exp. Med. 192: 413- 420, 2000.

GAM136 279 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 3 C c
chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM136 279 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 3 C c
Leukotrienes and lipoxins: structures, biosynthesis,and biological effects. Science 237: 1171- 1176, 1987.

GAM136 279 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127- 130, 1997.

GAM136 279 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 3 C c
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature 387:620- 624, 1997.

GAM136 279 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein 3 C b
kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990.

GAM136 279 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. 3 C b
F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome

13. Genomics 19: 397- 398, 1994.

GAM136 279 ORC1L Eki, T.; Okumura, K.; Amin, A.; Ishiai, M.; Abe, M.; Nogami, M.;Taguchi, H.; 3 C b
Hurwitz, J.; Murakami, Y.; Hanaoka, F.: Mapping of thehuman homologue
(ORC1L) of the yeast origin recognition complex subunit1 gene to chromosome
band 1p32. Genomics 36: 559- 561, 1996.

GAM136 279 ORC1L Gavin, K. A.; Hidaka, M.; Stillman, B.: Conserved initiator proteinsin 3 C b
eukaryotes. Science 270: 1667- 1671, 1995.

GAM136 279 ORC1L Mendez, J.; Zou- Yang, H.; Kim, S.- Y.; Hidaka, M.; Tansey, W. P.;Stillman, 3 C b
B.: Human origin recognition complex large subunit is degradedby ubiquitin-
mediated proteolysis after initiation of DNA replication. Molec.Cell 9: 481-
491, 2002.

GAM136 279 ORC1L Ohtani, K.; DeGregori, J.; Leone, G.; Herendeen, D. R.; Kelly,T. J.; Nevins, 3 C b
J. R.: Expression of the HsOrc1 gene, a human ORC1homolog, is regulated by
cell proliferation via the E2F transcriptionfactor. Molec. Cell. Biol. 16:
6977- 6984, 1996.

GAM136 279 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 3 C c
an ethanol- responsive potential modulator of guanine nucleotide-
bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM136 279 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 C c
Cloning and characterization of the rat and human phosducin- likeprotein
genes: structure, expression and chromosomal localization. Biochim.Biophys.
Acta 1444: 346- 354, 1999.

GAM136 279 PDZK1 Custer, M.; Spindler, B.; Verrey, F.; Murer, H.; Biber, J.: Identificationof 3 C c
a new gene product (diphor- 1) regulated by dietary phosphate. Am.J.
Physiol. 273: F801- F806, 1997.

GAM136 279 PDZK1 Ikemoto, M.; Arai, H.; Feng, D.; Tanaka, K.; Aoki, J.; Dohmae,N.; Takio, K.; 3 C c
Adachi, H.; Tsujimoto, M.; Inoue, K.: Identificationof a PDZ- domain-
containing protein that interacts with the scavengerreceptor class B type I.
Proc. Nat. Acad. Sci. 97: 6538- 6543, 2000.

GAM136 279 PDZK1 Kocher, O.; Comella, N.; Gilchrist, A.; Pal, R.; Tognazzi, K.;Brown, L. F.; 3 C c
Knoll, J. H. M.: PDZK1, a novel PDZ domain- containingprotein up- regulated
in carcinomas and mapped to chromosome 1q21,interacts with cMOAT (MRP2), the
multidrug resistance- associated protein. Lab.Invest. 79: 1161- 1170, 1999.

GAM136 279 PDZK1 Kocher, O.; Comella, N.; Tognazzi, K.; Brown, L. F.: Identificationand 3 C c
partial characterization of PDZK1: a novel protein containingPDZ interaction
domains. Lab. Invest. 78: 117- 125, 1998.

GAM136 279 PDZK1 Wang, S.; Yue, H.; Derin, R. B.; Guggino, W. B.; Li, M.: Accessoryprotein 3 C c
facilitated CFTR- CFTR interaction, a molecular mechanism topotentiate the
chloride channel activity. Cell 103: 169- 179, 2000.

GAM136 279 PDZK1 White, K. E.; Biber, J.; Murer, H.; Econs, M. J.: A PDZ domain- 3 C c
containingprotein with homology to Diphor- 1 maps to human chromosome 1q21.
Ann.Hum. Genet. 62: 287- 290, 1998.

GAM136 279 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. 3 C c
W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol
3- kinase catalytic subunit that associates withp85 and is expressed
predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997.

GAM136 279 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, 3 C c
E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J.
H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in
p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002.

GAM136 279 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; 3 C c
Nakagawara, A.: Identification and chromosome assignment of ahuman gene
encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997.

GAM136 279 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; 3 C c
Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.:
p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat.
Acad. Sci. 94: 4330- 4335, 1997.

GAM136 279 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 C c
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component
of the steroid receptor complex: cloning of thecDNA and further
characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM136 279 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 C c
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem.
267: 5503- 5507, 1992.

GAM136 279 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 C c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151
only, 1997.

GAM136 279 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 C c
J.- E.: The structure and complete nucleotide sequenceof the human
cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM136 279 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 C c
Chromosomalassignment of the interferon- inducible double- stranded RNA-
dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse
chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM136 279 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human 3 C c
interferon- gamma mRNA autoregulates its translation througha pseudoknot
that activates the interferon- inducible protein kinasePKR. Cell 108: 221-
232, 2002.

GAM136 279 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; 3 C c
Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR)
encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and
differences from its mouse homolog. Genomics 36:197- 201, 1996.

GAM136 279 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: 3 C c
sequence of the human interferon- inducible RNA- dependent proteinkinase
(PKR) deduced from genomic clones. Gene 178: 191- 193, 1996.

GAM136 279 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; 3 C c
Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand
characterization of the human double- stranded RNA- activated proteinkinase
induced by interferon. Cell 62: 379- 390, 1990.

GAM136 279 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; 3 C c
Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds
preferentially to Huntington's disease (HD) transcriptsand is activated in
HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001.

GAM136 279 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. 3 C c
G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-
RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics
16:768- 770, 1993.

GAM136 279 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: 3 C c
Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein.
Science 285: 107- 110, 1999.

GAM136 279 RBM8A Conklin, D. C.; Rixon, M. W.; Kuestner, R. E.; Maurer, M. F.; Whitmore,T. 3 C c
E.; Millar, R. P.: Cloning and gene expression of a novel
humanribonucleoprotein. Biochim. Biophys. Acta 1492: 465- 469, 2000.

GAM136 279 RBM8A Kataoka, N.; Yong, J.; Kim, V. N.; Velazquez, F.; Perkinson, R.A.; Wang, F.; 3 C c
Dreyfuss, G.: Pre- mRNA splicing imprints mRNA in thenucleus with a novel
RNA- binding protein that persists in the cytoplasm. Molec.Cell 6: 673- 682,
2000.

GAM136 279 RBM8A Salicioni, A. M.; Xi. M.; Vanderveer, L. A.; Balsara, B.; Testa,J. R.; 3 C c
Dunbrack, R. L., Jr.; Godwin, A. K.: Identification and structuralanalysis
of human RBM8A and RBM8B: two highly conserved RNA- bindingmotif proteins
that interact with OVCA1, a candidate tumor suppressor. Genomics 69:54- 62,
2000.

GAM136 279 RBM8A Zhao, X.- F.; Nowak, N. J.; Shows, T. B.; Aplan, P. D.: MAGOH interactswith 3 C c
a novel RNA- binding protein. Genomics 63: 145- 148, 2000.

GAM136 279 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two 3 C c
scleroderma autoimmune antigens that copurify with human ribonucleaseP.
Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997.

GAM136 279 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: 3 C c
Autoantigenic properties of some protein subunits of catalyticallyactive
complexes of human ribonuclease P. RNA 4: 407- 417, 1998.

GAM136 279 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, 3 C b
P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.:
Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin.
Endocr. Metab. 86: 3233- 3236, 2001.

GAM136 279 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- 3 C b
linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a
common cause of early primary osteoarthritis in men. (Letter) Clin.Genet.
62: 94- 95, 2002.

GAM136 279 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. 3 C b
C.: Gene structure and expression study of the SEDL genefor
spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000.

GAM136 279 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; 3 C b
Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the
gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda.
NatureGenet. 22: 400- 404, 1999.

GAM136 279 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; 3 C b
Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.;
Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.;
Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia
tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM136 279 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 3 C b
Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset
of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J.
Med. Genet. 38: 409- 411, 2001.

GAM136 279 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 3 C b
A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five-
base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia
tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85:
3343- 3347, 2000.

GAM136 279 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 3 C b

for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001.

GAM136 279 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002. 3 C b

GAM136 279 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001. 3 C b

GAM136 279 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999. 3 C b

GAM136 279 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001. 3 C b

GAM136 279 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996. 3 C b

GAM136 279 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001. 3 C b

GAM136 279 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 C b

GAM136 279 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996. 3 C b

GAM136 279 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 3 C c

GAM136 279 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J recombinase activity. Science 250: 1426- 1429, 1990. 3 C c

GAM136 279 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 C c

GAM136 279 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990. 3 C c

GAM136 279 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995. 3 C c

GAM136 279 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; 3 C c

Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic axial development and left- right specification. Nature 399:691- 694, 1999.

GAM136 279 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.; Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998. 3 C b

GAM136 279 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea transporter in the human kidney. FEBS Lett. 386: 156- 160,1996. 3 C b

GAM136 279 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.; Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2 is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157- 2164, 2001. 3 C b

GAM136 279 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855- 862, 2000. 3 C c

GAM136 279 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein that promotes cytochrome c- dependent caspase activation byeliminating IAP inhibition. Cell 102: 33- 42, 2000. 3 C c

GAM136 279 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000. 3 C c

GAM136 279 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509- 3517, 2002. 3 C c

GAM136 279 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 C c

GAM136 279 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.: A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates caspase activity and apoptosis. Nature 410:112- 116, 2001. 3 C c

GAM136 279 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO, a mammalian protein that promotes apoptosis by bindingto and antagonizing IAP proteins. Cell 102: 43- 53, 2000. 3 C c

GAM136 279 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012, 2000. 3 C c

GAM136 279 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998. 3 C c

GAM136 279 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle- membranefusion processes. Hum. Genet. 108: 211- 215, 2001. 3 C c

GAM136 279 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells. Biochem. Biophys. Res. Commun. 231: 808- 812, 1997. 3 C c

GAM136 279 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996. 3 C c

GAM136 279 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: Identification of three new splice variants of the SNARE proteinSNAP- 23. Biochem. Biophys. Res. Commun. 285: 320- 327, 2001. 3 C c

GAM136 279 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459- 467, 1998. 3 C b

GAM136 279 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 C b

GAM136 279 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 C b

GAM136 279 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 C b

GAM136 279 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 C b

GAM136 279 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 C b

GAM136 279 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496- 1498, 2002. 3 C b

GAM136 279 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.; Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1 are associated with human left- right lateralitydefects. Nature Genet. 26: 365- 369, 2000. 3 C c

GAM136 279 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989. 3 C c

GAM136 279 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002. 3 C c

GAM136 279 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991. 3 C c

GAM136 279 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997. 3 C c

GAM136 279 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; 3 C c

Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996.

GAM136 279 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, 3 C c
G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995.

GAM136 279 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in 3 C c
vertebratedevelopment. Trends Genet. 16: 303- 309, 2000.

GAM136 279 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: 3 C c
Strand- specific postreplicative processing of mammalian telomeres. Science 293:2462- 2465, 2001.

GAM136 279 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: 3 C c
Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet. 17: 236- 239, 1997.

GAM136 279 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres 3 C c
contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17: 231- 235, 1997.

GAM136 279 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 C c
the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001.

GAM136 279 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 C c
Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999.

GAM136 279 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered 3 C c
telomere state, not telomere loss. Science 295: 2446- 2449,2002.

GAM136 279 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; 3 C c
McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization of the transcribed human telomere repeat binding factor2 gene and comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163, 1998.

GAM136 279 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman 3 C c
telomeres from end- to- end fusions. Cell 92: 401- 413, 1998.

GAM136 279 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 C c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human telomeres. Nature Genet. 25: 347- 352, 2000.

GAM136 279 TIM3 McIntire, J. J.; Umetsu, S. E.; Akbari, O.; Potter, M.; Kuchroo,V. K.; 3 C c
Barsh, G. S.; Freeman, G. J.; Umetsu, D. T.; DeKruyff, R. H.: Identification of Tapr (an airway hyperreactivity regulatory locus)and the linked Tim gene family. Nature Immun. 2: 1109- 1116, 2001.

GAM136 279 TIM3 Monney, L.; Sabatos, C.; Gaglia, J. L.; Ryu, A.; Waldner, H.; Chernova,T.; 3 C c
Manning, S.; Greenfield, E. A.; Coyle, A. J.; Sobel, R. A.; Freeman,G. J.; Kuchroo, V. K.: Th1- specific cell surface protein regulatesmacrophage activation and severity of an autoimmune disease. Nature 415:536- 541, 2002.

GAM136 279 TJP1 Mohandas, T. K.; Chen, X.- N.; Rowe, L. B.; Birkenmeier, E. H.;Fanning, A. 3 C c
S.; Anderson, J. M.; Korenberg, J. R.: Localization ofthe tight junction protein gene TJP1 to human chromosome 15q13, distalto the Prader- Willi/Angelman region, and to mouse chromosome 7. Genomics 30:594- 597, 1995.

GAM136 279 TJP1 Willott, E.; Balda, M. S.; Fanning, A. S.; Jameson, B.; Van Itallie,C.; 3 C c
Anderson, J. M.: The tight junction protein ZO- 1 is homologousto the Drosophila discs- large tumor suppressor protein of septatejunctions. Proc.

Nat. Acad. Sci. 90: 7834- 7838, 1993.

GAM136 279 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; 3 C c
Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and
13 others: Dominant and recessive deafnesscaused by mutations of a novel
gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277-
284, 2002.

GAM136 279 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; 3 C c
Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M.
H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant,
progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002.

GAM136 279 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 3 C c
B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the
crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec.
Cell 4: 563- 571, 1999.

GAM136 279 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 C c
B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel
receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420,
1997.

GAM136 279 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 C c
B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi,
A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr.
Biol. 7: 1003- 1006, 1997.

GAM136 279 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 C c
B W. S.: Rare loss- of- function mutation of a death receptorgene in head and
neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM136 279 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 C c
B decoy receptor and a death domain- containing receptorfor TRAIL. Science
277: 815- 818, 1997.

GAM136 279 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 C c
B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334,
1997.

GAM136 279 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 C c
B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces
the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM136 279 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 C c
B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard,
A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a
family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM136 279 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 C c
B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.;
Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating
receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM136 279 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 C c
B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.;
Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA
damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141-
143, 1997.

GAM136 279 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, 3 C c
psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994.

GAM136 279 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; 3 C c
Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired
nociception and pain sensation in mice lacking the capsaicinreceptor.
Science 288: 306- 313, 2000.

GAM136 279 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. 3 C c
D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the
pain pathway. Nature 389: 816- 824, 1997.

GAM136 279 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 C c
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release
the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411:
957- 962, 2001.

GAM136 279 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity 3 C c
to 'hot' chili peppers. Cell 108: 421- 430, 2002.

GAM136 279 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, 3 C c
A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related
osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor.
Cell 103: 525- 535, 2000.

GAM136 279 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated 3 C c
by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J.
Neurophysiol. 76: 1858- 1869, 1996.

GAM136 279 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel 3 C c
activity by protein kinase C. Nature 408: 985- 990, 2000.

GAM136 279 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand 3 C c
multiple presentations of the oral irritant zingerone: relationshipto
frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996.

GAM136 279 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith 3 C c
capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994.

GAM136 279 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand 3 C c
pleasantness for the capsaicin burn between chili likers and non-
likers:implications for liking development. Chem. Senses 18: 471- 482, 1993.

GAM136 279 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; 3 C c
McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.;
Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic
cystinosis gene (CTNS): complete sequencing of a200- kb segment and
discovery of a novel gene within the common cystinosis- causingdeletion.
Genome Res. 10: 165- 173, 2000.

GAM136 279 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; 3 C c
Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.;
Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.;
Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the
vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002.

GAM136 279 TUFT1 Bashir, M. M.; Abrams, W. R.; Tucker, T.; Sellinger, B.; Budarf,M.; Emanuel, 3 C c
B.; Rosenbloom, J.: Molecular cloning and characterizationof the bovine and
human tuftelin genes. Connect. Tissue Res. 39:13- 24, 1998.

GAM136 279 TUFT1 Deutsch, D.: Structure and function of enamel gene products. Anat.Rec. 224: 3 C c
189- 210, 1989.

GAM136 279 TUFT1 Deutsch, D.; Palmon, A.; Dafni, L.; Fisher, L.; Termine, J. D.;Young, M.: 3 C c
Cloning, sequencing, and characterization of tuftelin:a novel acidic enamel
protein. Connect. Tissue Res. 27: 121 only,1992.

GAM136 279 TUFT1 Deutsch, D.; Palmon, A.; Fisher, L. W.; Kolodny, N.; Termine, J.D.; Young, 3 C c

M. F.: Sequencing of bovine enamelin (tuftelin), a novelacidic enamel protein. J. Biol. Chem. 266: 16021- 16028, 1991.

GAM136 279 TUFT1 Deutsch, D.; Palmon, A.; Young, M. F.; Selig, S.; Kearns, W. G.;Fisher, L. W.: Mapping of the human tuftelin (TUFT1) gene to chromosome1 by fluorescence in situ hybridization. (Abstract) Mammalian Genome 5:461- 462, 1994. 3 C c

GAM136 279 TUFT1 MacDougall, M.; Simmons, D.; Dodds, A.; Knight, C.; Luan, X.; Zeichner-David,M.; Zhang, C.; Ryu, O. H.; Qian, Q.; Simmer, J. P.; Hu, C.- C.: Cloning,characterization, and tissue expression pattern of mouse tuftelincDNA. J. Dent. Res. 77: 1970- 1978, 1998. 3 C c

GAM136 279 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 3 C b

GAM136 279 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 C b

GAM136 279 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x-ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 3 C b

GAM136 279 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995. 3 C b

GAM136 279 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 3 C b

GAM136 279 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 C b

GAM136 279 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 C b

GAM136 279 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997. 3 C b

GAM136 279 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995. 3 C b

GAM136 279 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma. CancerRes. 39: 3119- 3128, 1979. 3 C b

GAM136 279 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a follicular lymphoma cell line carrying a t(14;18)chromosomal translocation. Int. J. Cancer 39: 785- 788, 1987. 3 C b

GAM136 279 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. A.: STS map of genes and anonymous DNA fragments on human chromosome18 using a panel of somatic cell hybrids. Genomics 15: 387- 391,1993. 3 C b

GAM136 279 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, 3 C b

M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710- 717, 1988.

GAM136 279 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human chromosome and its expression in various tissues. Science 227:1038- 1040, 1985. 3 C b

GAM136 279 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal reassignment: YACs containing both YES1 and thymidylatesynthase map to the short arm of chromosome 18. Genomics 15: 442- 445,1993. 3 C b

GAM136 279 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c- yes gene. Molec. Cell. Biol. 7: 41- 47, 1987. 3 C b

GAM136 279 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985. 3 C b

GAM138 222 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000. 3 C c

GAM138 222 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000. 3 C c

GAM138 222 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol 3- kinase catalytic subunit that associates withp85 and is expressed predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997. 3 C c

GAM138 222 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J. H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002. 3 C c

GAM138 222 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; Nakagawara, A.: Identification and chromosome assignment of ahuman gene encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997. 3 C c

GAM138 222 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.: p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat. Acad. Sci. 94: 4330- 4335, 1997. 3 C c

GAM138 222 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two scleroderma autoimmune antigens that copurify with human ribonucleaseP. Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997. 3 C c

GAM138 222 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: Autoantigenic properties of some protein subunits of catalyticallyactive complexes of human ribonuclease P. RNA 4: 407- 417, 1998. 3 C c

GAM138 222 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998. 3 C c

GAM138 222 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and 3 C c

genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998.

GAM138 222 TBXA2R Cheng, Y.; Austin, S. C.; Rocca, B.; Koller, B. H.; Coffman, T.M.; Grosser, T.; Lawson, J. A.; FitzGerald, G. A.: Role of prostacyclinin the cardiovascular response to thromboxane A2. Science 296: 539- 541,2002. 3 C c

GAM138 222 TBXA2R Duncan, A. M. V.; Anderson, L. L.; Funk, C. D.; Abramovitz, M.;Adam, M.: Chromosomal localization of the human prostanoid receptorgene family. Genomics 25: 740- 742, 1995. 3 C c

GAM138 222 TBXA2R Fuse, I.; Mito, M.; Hattori, A.; Higuchi, W.; Shibata, A.; Ushikubi,F.; Okuma, M.; Yahata, K.: Defective signal transduction inducedby thromboxane A2 in a patient with a mild bleeding disorder: impairedphospholipase C activation despite normal phospholipase A2 activation. Blood 81:994- 1000, 1993. 3 C c

GAM138 222 TBXA2R Hirata, M.; Hayashi, Y.; Ushikubi, F.; Yokota, Y.; Kageyama, R.;Nakanishi, S.; Narumiya, S.: Cloning and expression of cDNA for ahuman thromboxane A2 receptor. Nature 349: 617- 620, 1991. 3 C c

GAM138 222 TBXA2R Hirata, T.; Kakizuka, A.; Ushikubi, F.; Fuse, I.; Okuma, M.; Narumiya,S.: Arg60- to- leu mutation of the human thromboxane A2 receptor ina dominantly inherited bleeding disorder. J. Clin. Invest. 94: 1662- 1667,1994. 3 C c

GAM138 222 TBXA2R Hirata, T.; Ushikubi, F.; Kakizuka, A.; Okuma, M.; Narumiya, S.: Two thromboxane A(2) receptor isoforms in human platelets: oppositecoupling to adenylyl cyclase with different sensitivity to arg60- to- leumutation. J. Clin. Invest. 97: 949- 956, 1996. 3 C c

GAM138 222 TBXA2R Nusing, R. M.; Hirata, M.; Kakizuka, A.; Eki, T.; Ozawa, K.; Narumiya,S.: Characterization and chromosomal mapping of the human thromboxaneA2 receptor gene. J. Biol. Chem. 268: 25253- 25259, 1993. 3 C c

GAM138 222 TBXA2R Robinson, P. R.; Cohen, G. B.; Zhukovsky, E. A.; Oprian, D. D.: Constitutively active mutants of rhodopsin. Neuron 9: 719- 725,1992. 3 C c

GAM138 222 TBXA2R Schwengel, D. A.; Nouri, N.; Meyers, D. A.; Levitt, R. C.: Linkagemapping of the human thromboxane A2 receptor (TBXA2R) to chromosome19p13.3 using transcribed 3- prime untranslated DNA sequence polymorphisms. Genomics 18:212- 215, 1993. 3 C c

GAM138 222 TBXA2R Taketo, M.; Rochelle, J. M.; Sugimoto, Y.; Namba, T.; Honda, A.;Negishi, M.; Ichikawa, A.; Narumiya, S.; Seldin, M. F.: Mapping ofthe genes encoding mouse thromboxane A2 receptor and prostaglandinE receptor subtypes EP2 and EP3. Genomics 19: 585- 588, 1994. 3 C c

GAM138 222 TBXA2R Thomas, D. W.; Mannon, R. B.; Mannon, P. J.; Latour, A.; Oliver,J. A.; Hoffman, M.; Smithies, O.; Koller, B. H.; Coffman, T. M.:Coagulation defects and altered hemodynamic responses in mice lackingreceptors for thromboxane A(2). J. Clin. Invest. 102: 1994- 2001,1998. 3 C c

GAM138 222 TBXA2R Unoki, M.; Furuta, S.; Onouchi, Y.; Watanabe, O.; Doi, S.; Fujiwara,H.; Miyatake, A.; Fujita, K.; Tamari, M.; Nakamura, Y.: Associationstudies of 33 single nucleotide polymorphisms (SNPs) in 29 candidategenes for bronchial asthma: positive association a T924C polymorphismin the thromboxane A2 receptor gene. Hum. Genet. 106: 440- 446, 2000. 3 C c

GAM138 222 TBXA2R Ushikubi, F.; Nakajima, M.; Hirata, M.; Okuma, M.; Fujiwara, M.;Narumiya, S.: Purification of the thromboxane A2/prostaglandin H2receptor from human blood platelets.. J. Biol. Chem. 264: 16496- 16501,1989. 3 C c

GAM138 222 TBXA2R Ushikubi, F.; Okuma, M.; Kanaji, K.; Sugiyama, T.; Ogorochi, T.;Narumiya, S.; Uchino, H.: Hemorrhagic thrombocytopathy with platelletthromboxane A2 3 C c

abnormality: defective signal transduction with normalbinding activity. Thromb. Haemost. 57: 158- 164, 1987.

GAM138 222 TUFT1 Bashir, M. M.; Abrams, W. R.; Tucker, T.; Sellinger, B.; Budarf,M.; Emanuel, B.; Rosenbloom, J.: Molecular cloning and characterizationof the bovine and human tuftelin genes. Connect. Tissue Res. 39:13- 24, 1998. 3 C b

GAM138 222 TUFT1 Deutsch, D.: Structure and function of enamel gene products. Anat.Rec. 224: 189- 210, 1989. 3 C b

GAM138 222 TUFT1 Deutsch, D.; Palmon, A.; Dafni, L.; Fisher, L.; Termine, J. D.;Young, M.: Cloning, sequencing, and characterization of tuftelin:a novel acidic enamel protein. Connect. Tissue Res. 27: 121 only,1992. 3 C b

GAM138 222 TUFT1 Deutsch, D.; Palmon, A.; Fisher, L. W.; Kolodny, N.; Termine, J.D.; Young, M. F.: Sequencing of bovine enamelin (tuftelin), a novelacidic enamel protein. J. Biol. Chem. 266: 16021- 16028, 1991. 3 C b

GAM138 222 TUFT1 Deutsch, D.; Palmon, A.; Young, M. F.; Selig, S.; Kearns, W. G.;Fisher, L. W.: Mapping of the human tuftelin (TUFT1) gene to chromosome1 by fluorescence in situ hybridization. (Abstract) Mammalian Genome 5:461- 462, 1994. 3 C b

GAM138 222 TUFT1 MacDougall, M.; Simmons, D.; Dodds, A.; Knight, C.; Luan, X.; Zeichner-David,M.; Zhang, C.; Ryu, O. H.; Qian, Q.; Simmer, J. P.; Hu, C.- C.: Cloning,characterization, and tissue expression pattern of mouse tuftelincDNA. J. Dent. Res. 77: 1970- 1978, 1998. 3 C b

GAM138 222 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 C c

GAM138 222 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 C c

GAM138 222 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 C c

GAM138 222 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 C c

GAM138 222 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 C c

GAM139 327 ADORA2A Chen, J.- F.; Huang, Z.; Ma, J.; Zhu, J.; Moratalla, R.; Standaert,D.; Moskowitz, M. A.; Fink, J. S.; Schwarzschild, M. A.: A2A adenosinereceptor deficiency attenuates brain injury induced by transient focalischemia in mice. J. Neurosci. 19: 9192- 9200, 1999. 1 B c

GAM139 327 ADORA2A Gaudray, P.: Personal Communication. Nice, France 6/1/1994. 1 B c

GAM139 327 ADORA2A Gusella, J. F.: Personal Communication. Boston, Mass. 4/17/1994. 1 B c

GAM139 327 ADORA2A Le, F.; Townsend- Nicholson, A.; Baker, E.; Sutherland, G. R.; Schofield,P. R.: Characterization and chromosomal localization of the humanA2a adenosine receptor gene: ADORA2A. Biochem. Biophys. Res. Commun. 223:461- 467, 1996. 1 B c

GAM139 327 ADORA2A Ledent, C.; Vaugeois, J.- M.; Schiffmann, S. N.; Pedrazzini, T.;El Yacoubi, M. E.; Vanderhaeghen, J.- J.; Costentin, J.; Heath, J.K.; Vassart, G.; Parmentier, M.: Aggressiveness, hypoalgesia andhigh blood pressure in mice lacking the adenosine A2a receptor. Nature 388:674- 678, 1997. 1 B c

GAM139 327 ADORA2A Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. Note: Erratum: Genomics 23: 305 only, 1994. 1 B c

GAM139 327 ADORA2A MacCollin, M.; Peterfreund, R.; MacDonald, M.; Fink, J. S.; Gusella,J.: Mapping of a human A2a adenosine receptor (ADORA2) to chromosome22. Genomics 20: 332- 333, 1994. 1 B c

GAM139 327 ADORA2A Ohta, A.; Sitkovsky, M.: Role of G- protein- coupled adenosine receptorsin downregulation of inflammation and protection from tissue damage. Nature 916- 920,2001. 1 B c

GAM139 327 ADORA2A Szepetowski, P.; Perucca- Lostanlen, D.; Gaudray, P.: Mapping genesaccording to their amplification status in tumor cells: contributionto the map of 11q13. Genomics 16: 745- 750, 1993. 1 B c

GAM139 327 ANXA9 Morgan, R. O.; Bell, D. W.; Testa, J. R.; Fernandez, M.- P.: Humanannexin 31 genetic mapping and origin. Gene 227: 33- 38, 1999. 1 B c

GAM139 327 ANXA9 Morgan, R. O.; Fernandez, M.- P.: Expression profile and structuraldivergence of novel human annexin 31. FEBS Lett. 434: 300- 304, 1998. 1 B c

GAM139 327 ARHGDIA Leffers, H.; Nielsen, M. S.; Andersen, A. H.; Honore, B.; Madsen,P.; Vandekerckhove, J.; Celis, J. E.: Identification of two humanrho GDP dissociation inhibitor proteins whose overexpression leadsto disruption of the actin cytoskeleton. Exp. Cell Res. 209: 165- 174,1993. 1 B c

GAM139 327 ARHGDIA Wagner, T.; Tommerup, N.; Wirth, J.; Leffers, H.; Zimmer, J.; Back,E.; Weissenbach, J.; Scherer, G.: A somatic cell hybrid panel fordistal 17q: GDIA1 maps to 17q25.3. Cytogenet. Cell Genet. 76: 172- 175,1997. 1 B c

GAM139 327 ARHGEF7 Bagrodia, S.; Taylor, S. J.; Jordon, K. A.; Van Aelst, L.; Cerione,R. A.: A novel regulator of p21- activated kinases. J. Biol. Chem. 273:23633- 23636, 1998. 1 B b

GAM139 327 ARHGEF7 Manser, E.; Loo, T.- H.; Koh, C.- G.; Zhao, Z.- S.; Chen, X.- Q.; Tan,L.; Tan, I.; Leung, T.; Lim, L.: PAK kinases are directly coupledto the PIX family of nucleotide exchange factors. Molec. Cell 1:183- 192, 1998. 1 B b

GAM139 327 ARHGEF7 Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 1 B b

GAM139 327 ARHGEF7 Oh, W. K.; Yoo, J. C.; Jo, D.; Song, Y. H.; Kim, M. G.; Park, D.: Cloning of a SH3 domain- containing proline- rich protein, p85SPR,and its localization in focal adhesion. Biochem. Biophys. Res. Commun. 235:794- 798, 1997. 1 B b

GAM139 327 ASB1 Hirosawa, M.; Nagase, T.; Ishikawa, K.; Kikuno, R.; Nomura, N.;Ohara, O.: Characterization of cDNA clones selected by the GeneMarkanalysis from size- fractionated cDNA libraries from human brain. DNARes. 6: 329- 336, 1999. 1 B c

GAM139 327 ASB1 Kile, B. T.; Viney, E. M.; Willson, T. A.; Brodnicki, T. C.; Cancilla,M. R.; 1 B c
Herlihy, A. S.; Croker, B. A.; Baca, M.; Nicola, N. A.; Hilton,D. J.;
Alexander, W. S.: Cloning and characterization of the genesencoding the
ankyrin repeat and SOCS box- containing proteins Asb- 1,Asb- 2, Asb- 3, and
Asb- 4. Gene 258: 31- 41, 2000.

GAM139 327 BACE2 Acquati, F.; Accarino, M.; Nucci, C.; Fumagalli, P.; Jovine, L.;Ottolenghi, 1 B c
S.; Taramelli, R.: The gene encoding DRAP (BACE2), aglycosylated
transmembrane protein of the aspartic protease family,maps to the Down
syndrome critical region. FEBS Lett. 468: 59- 64,2000.

GAM139 327 BACE2 Bennett, B. D.; Babu- Khan, S.; Loeloff, R.; Louis, J.- C.; Curran,E.; 1 B c
Citron, M.; Vassar, R.: Expression analysis of BACE2 in brainand peripheral
tissues. J. Biol. Chem. 275: 20647- 20651, 2000.

GAM139 327 BACE2 Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a 1 B c
BACE homolog, BACE2, reside in the obligate Down syndromeregion of
chromosome 21. Science 286: 1255A only, 1999.

GAM139 327 BACE2 Solans, A.; Estivill, X.; de la Luna, S.: A new aspartyl proteaseon 21q22.3, 1 B c
BACE2, is highly similar to Alzheimer's amyloid precursorprotein beta-
secretase. Cytogenet. Cell Genet. 89: 177- 184, 2000.

GAM139 327 BACE2 Xin, H.; Stephans, J. C.; Duan, X.; Harrowe, G.; Kim, E.; Grieshammer,U.; 1 B c
Kingsley, C.; Giese, K.: Identification of a novel aspartic- likeprotease
differentially expressed in human breast cancer cell lines. Biochim.Biophys.
Acta 1501: 125- 137, 2000.

GAM139 327 BRMS1 Phillips, K. K.; Welch, D. R.; Miele, M. E.; Lee, J. H.; Wei, L.L.; 1 B c
Weissman, B. E.: Suppression of MDA- MB- 435 breast carcinoma cellmetastasis
following the introduction of human chromosome 11. CancerRes. 56: 1222-
1227, 1996.

GAM139 327 BRMS1 Seraj, M. J.; Samant, R. S.; Verderame, M. F.; Welch, D. R.: 1 B c
Functionalevidence for a novel human breast carcinoma metastasis
suppressor,BRMS1, encoded at chromosome 11q13. Cancer Res. 60: 2764- 2769,
2000.

GAM139 327 C8G Chan, P.; Simon- Chazottes, D.; Mattei, M. G.; Guenet, J. L.; Salier,J. P.: 1 B c
Comparative mapping of lipocalin genes in human and mouse:the four genes for
complement C8 gamma chain, prostaglandin- D- synthase,oncogene- 24P3, and
progestagen- associated endometrial protein mapto HSA9 and MMU2. Genomics
23: 145- 150, 1994.

GAM139 327 C8G Dewald, G.; Cichon, S.; Bryant, S. P.; Hemmer, S.; Nothen, M. M.;Spurr, N. 1 B c
K.: The human complement C8G gene, a member of the lipocalingene family:
polymorphisms and mapping to chromosome 9q34.3. Ann.Hum. Genet. 60: 281-
291, 1996.

GAM139 327 C8G Haefliger, J.- A.; Jenne, D.; Stanley, K. K.; Tschopp, J.: 1 B c
Structuralhomology of human complement component C8- gamma and plasma
proteinHC: identity of the cysteine bond pattern. Biochem. Biophys.
Res.Commun. 149: 750- 754, 1987.

GAM139 327 C8G Hunt, L. T.; Elzanowski, A.; Barker, W. C.: The homology of complementfactor 1 B c
C8 gamma chain and alpha- 1- microglobulin. Biochem. Biophys.Res. Commun.
149: 282- 288, 1987.

GAM139 327 C8G Kaufman, K. M.; Snider, J. V.; Spurr, N. K.; Schwartz, C. E.; Sodetz,J. M.: 1 B c
Chromosomal assignment of genes encoding the alpha, beta,and gamma subunits
of human complement protein C8: identificationof a close physical linkage
between the alpha and the beta loci. Genomics 5:475- 480, 1989.

GAM139 327 C8G Ng, S. C.; Rao, A. G.; Howard, O. M. Z.; Sodetz, J. M.: The eighthcomponent of human complement: evidence that it is an oligomeric serumprotein assembled from products of three different genes. Biochemistry 26:5229-5233, 1987. 1 B c

GAM139 327 CA12 Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 1 B c

GAM139 327 CA12 Sahin, U.; Tureci, O.; Schmitt, H.; Cochlovius, B.; Johannes, T.;Schmits, R.; Stenner, F.; Luo, G.; Schobert, I.; Pfreundschuh, M.: Human neoplasms elicit multiple specific immune responses in theautologous host. Proc. Nat. Acad. Sci. 92: 11810- 11813, 1995. 1 B c

GAM139 327 CA12 Tureci, O.; Sahin, U.; Vollmar, E.; Siemer, S.; Gottert, E.; Seitz,G.; Parkkila, A. K.; Shah, G. N.; Grubb, J. H.; Pfreundschuh, M.;Sly, W. S.: Human carbonic anhydrase XII: cDNA cloning, expression,and chromosomal localization of a carbonic anhydrase gene that isoverexpressed in some renal cell cancers. Proc. Nat. Acad. Sci. 95:7608- 7613, 1998. 1 B c

GAM139 327 CASP2 Bergeron, L.; Perez, G. I.; Macdonald, G.; Shi, L.; Sun, Y.; Jurisicova,A.; Varmuza, S.; Latham, K. E.; Flaws, J. A.; Salter, J. C. M.; Hara,H.; Moskowitz, M. A.; Li, E.; Greenberg, A.; Tilly, J. L.; Yuan, J.: Defects in regulation of apoptosis in caspase- 2- deficient mice. GenesDev. 12: 1304-1314, 1998. 1 B c

GAM139 327 CASP2 Kumar, S.; Kinoshita, M.; Noda, M.; Copeland, N. G.; Jenkins, N.A.: Induction of apoptosis by the mouse Nedd2 gene, which encodesa protein similar to the product of the Caenorhabditis elegans celldeath gene ced- 3 and the mammalian IL- 1- beta- converting enzyme. GenesDev. 8: 1613- 1626, 1994. 1 B c

GAM139 327 CASP2 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith developmentally down- regulated expression in the mouse brain. Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992. 1 B c

GAM139 327 CASP2 Kumar, S.; White, D. L.; Takai, S.; Turczynowicz, S.; Juttner,C. A.; Hughes, T. P.: Apoptosis regulatory gene NEDD2 maps to humanchromosome segment 7q34-35, a region frequently affected in haematologicalneoplasms. Hum. Genet. 95: 641- 644, 1995. 1 B c

GAM139 327 CASP2 Lassus, P.; Opitz- Araya, X.; Lazebnik, Y.: Requirement for caspase- 2in stress- induced apoptosis before mitochondrial permeabilization. Science 297:1352- 1354, 2002. 1 B c

GAM139 327 CASP2 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes, CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem. Biophys. Res. Commun. 225: 983- 989, 1996. 1 B c

GAM139 327 CBFA2T1 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a member of a multigene family. Genomics 52: 332- 341, 1998. 1 B c

GAM139 327 CBFA2T1 Erickson, P.; Gao, J.; Chang, K.- S.; Look, T.; Whisenant, E.; Raimondo,S.; Lasher, R.; Trujillo, J.; Rowley, J. D.; Drabkin, H. A.: Identificationof breakpoints in t(8;21) acute myelogenous leukemia and isolationof a fusion transcript, AML1/ETO, with similarity to Drosophila segmentationgene, runt. Blood 80: 1825- 1831, 1992. 1 B c

GAM139 327 CBFA2T1 Linggi, B.; Muller- Tidow, C.; van de Locht, L.; Hu, M.; Nip, J.;Serve, H.; Berdel, W. E.; van der Reijden, B.; Quelle, D. E.; Rowley,J. D.; Cleveland, 1 B c

J.; Jansen, J. H.; Pandolfi, P. P.; Hiebert, S.W.: The t(8;21) fusion protein, AML1- ETO, specifically repressesthe transcription of the p14(ARF) tumor suppressor in acute myeloidleukemia. Nature Med. 8: 743- 750, 2002.

GAM139 327 CBFA2T1 Minucci, S.; Maccarana, M.; Cioce, M.; De Luca, P.; Gelmetti, V.;Segalla, S.; Di Croce, L.; Giavara, S.; Matteucci, C.; Gobbi, A.;Bianchini, A.; Colombo, E.; Schiavoni, I.; Badaracco, G.; Hu, X.;Lazar, M. A.; Landsberger, N.; Nervi, C.; Pelicci, P. G.: Oligomerizationof RAR and AML1 transcription factors as a novel mechanism of oncogenicactivation. Molec. Cell 5: 811- 820, 2000. 1 B c

GAM139 327 CBFA2T1 Miyamoto, T.; Weissman, I. L.; Akashi, K.: AML1/ETO- expressingnonleukemic stem cells in acute myelogenous leukemia with 8;21 chromosomaltranslocation. Proc. Nat. Acad. Sci. 97: 7521- 7526, 2000. 1 B c

GAM139 327 CBFA2T1 Miyoshi, H.; Kozu, T.; Shimizu, K.; Enomoto, K.; Maseki, N.; Kaneko,Y.; Kamada, N.; Ohki, M.: The t(8;21) translocation in acute myeloidleukemia results in production of an AML1- MTG8 fusion transcript. EMBOJ. 12: 2715- 2721, 1993. 1 B c

GAM139 327 CBFA2T1 Miyoshi, H.; Shimizu, K.; Kozu, T.; Maseki, N.; Kaneko, Y.; Ohki,M.: t(8;21) breakpoints on chromosome 21 in acute myeloid leukemiaare clustered within a limited region of a single gene, AML1. Proc.Nat. Acad. Sci. 88: 10431- 10434, 1991. 1 B c

GAM139 327 CBFA2T1 Niwa- Kawakita, M.; Miyoshi, H.; Gotoh, O.; Matsushima, Y.; Nishimura,M.; Shisa, H.; Ohki, M.: Cloning and gene mapping of the mouse homologueof the CBFA2T1 gene associated with human acute myeloid leukemia. Genomics 29:755- 759, 1995. 1 B c

GAM139 327 CBFA2T1 Nucifora, G.; Rowley, J. D.: The AML1 and ETO genes in acute myeloidleukemia with a t(8;21). Leukemia Lymphoma 14: 353- 362, 1994. 1 B c

GAM139 327 CBFA2T1 Schoch, C.; Kohlmann, A.; Schnittger, S.; Brors, B.; Dugas, M.;Mergenthaler, S.; Kern, W.; Hiddemann, S.; Eils, R.; Haferlach, T.: Acute myeloid leukemias with reciprocal rearrangements can be distinguishedby specific gene expression profiles. Proc. Nat. Acad. Sci. 99:10008- 10013, 2002. 1 B c

GAM139 327 CBFA2T1 Wolford, J. K.; Bogardus, C.; Prochazka, M.: Polymorphism inthe 3- prime untranslated region of MTG8 is associated with obesityin Pima Indian males. Biochem. Biophys. Res. Commun. 246: 624- 626,1998. 1 B c

GAM139 327 CBFA2T1 Wolford, J. K.; Prochazka, M.: Structure and expression of thehuman MTG8/ETO gene. Gene 212: 103- 109, 1998. 1 B c

GAM139 327 CBFA2T1 Yergeau, D. A.; Hetherington, C. J.; Wang, Q.; Zhang, P.; Sharpe,A. H.; Binder, M.; Marin- Padilla, M.; Tenen, D. G.; Speck, N. A.;Zhang, D.- E.: Embryonic lethality and impairment of haematopoiesisin mice heterozygous for an AML1- ETO fusion gene. Nature Genet. 15:303- 306, 1997. 1 B c

GAM139 327 CBR1 Avramopoulos, D.; Cox, T.; Forrest, G. L.; Chakravarti, A.; Antonarakis,S. E.: Linkage mapping of the carbonyl reductase (CBR) gene on humanchromosome 21 using a DNA polymorphism in the 3- prime untranslatedregion. Genomics 13: 447- 448, 1992. 1 B b

GAM139 327 CBR1 Forrest, G. L.; Akman, S.; Krutzik, S.; Paxton, R. J.; Sparkes,R. S.; Doroshow, J.; Felsted, R. L.; Glover, C. J.; Mohandas, T.;Bachur, N. R.: Induction of a human carbonyl reductase gene locatedon chromosome 21. Biochim. Biophys. Acta 1048: 149- 155, 1990. 1 B b

GAM139 327 CBR1 Lemieux, N.; Malfoy, B.; Forrest, G. L.: Human carbonyl reductase(CBR) 1 B b
localized to band 21q22.1 by high- resolution fluorescence insitu
hybridization displays gene dosage effects in trisomy 21 cells. Genomics
15:169- 172, 1993.

GAM139 327 CBR1 Watanabe, K.; Sugawara, C.; Ono, A.; Fukuzumi, Y.; Itakura, S.;Yamazaki, M.; 1 B b
Tashiro, H.; Osoegawa, K.; Soeda, E.; Nomura, T.: Mappingof a novel human
carbonyl reductase, CBR3, and ribosomal pseudogenesto human chromosome
21q22.2. Genomics 52: 95- 100, 1998.

GAM139 327 CBR1 Wei, J.; Dlouhy, S. R.; Hara, A.; Ghetti, B.; Hodes, M. E.: Cloninga cDNA 1 B b
for carbonyl reductase (Cbr) from mouse cerebellum: murinegenes that express
Cbr map to chromosomes 16 and 11. Genomics 34:147- 148, 1996.

GAM139 327 CBR1 Wermuth, B.; Bohren, K. M.; Heinemann, G.; von Wartburg, J.- P.;Gabbay, K. 1 B b
H.: Human carbonyl reductase: nucleotide sequence analysisof a cDNA and
amino acid sequence of the encoded protein. J. Biol.Chem. 263: 16185- 16188,
1988.

GAM139 327 CD1B Beckman, E. M.; Porcelli, S. A.; Morita, C. T.; Behar, S. M.; Furlong,S. T.; 1 B c
Brenner, M. B.: Recognition of a lipid antigen by CD1- restrictedalpha-
beta(+) T cells. Nature 372: 691- 694, 1994.

GAM139 327 CD1B Park, S.- H.; Bendelac, A.: CD1- restricted T- cell responses andmicrobial 1 B c
infection. Nature 406: 788- 792, 2000.

GAM139 327 CD1B Sieling, P. A.; Chatterjee, D.; Porcelli, S. A.; Prigozy, T. I.;Mazzaccaro, 1 B c
R. J.; Soriano, T.; Bloom, B. R.; Brenner, M. B.; Kronenberg,M.; Brennan, P.
J.; Modlin, R. L.: CD1- restricted T cell recognitionof microbial lipoglycan
antigens. Science 269: 227- 230, 1995.

GAM139 327 CD1B Sieling, P. A.; Jullien, D.; Dahlem, M.; Tedder, T. F.; Rea, T.H.; Modlin, 1 B c
R. L.; Porcelli, S. A.: CD1 expression by dendritic cellsin human leprosy
lesions: correlation with effective host immunity. J.Immun. 162: 1851- 1858,
1999.

GAM139 327 CD79A Ha, H.; Kubagawa, H.; Burrows, P. D.: Molecular cloning and 1 B c
expressionpattern of a human gene homologous to the murine mb- 1 gene. J.
Immun. 148:1526- 1531, 1992.

GAM139 327 CD79A Hashimoto, S.; Mohrenweiser, H. W.; Gregersen, P. K.; Chiorazzi,N.: 1 B c
Chromosomal localization, genomic structure, and allelic polymorphismof the
human CD79a (Ig- alpha/mb- 1) gene. Immunogenetics 40: 287- 295,1994.

GAM139 327 CD79A Reth, M.: Antigen receptors on B lymphocytes. Annu. Rev. Immun. 10:97- 121, 1 B c
1992.

GAM139 327 CD80 Freeman, G. J.; Disteche, C. M.; Gribben, J. G.; Adler, D. A.;Freedman, A. 1 B c
S.; Dougery, J.; Nadler, L. M.: The gene for B7, a costimulatorysignal for
T- cell activation, maps to chromosomal region 3q13.3- 3q21. Blood 79:489-
494, 1992.

GAM139 327 CD80 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, 1 B c
M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B
cells. Europ. J. Immun. 15: 103- 106, 1985.

GAM139 327 CD80 Reeves, R. H.; Patch, D.; Sharpe, A. H.; Borriello, F.; Freeman,G. J.; 1 B c
Edelhoff, S.; Disteche, C.: The costimulatory genes Cd80 andCd86 are linked
on mouse chromosome 16 and human chromosome 3. MammalianGenome 8: 581- 582,
1997.

GAM139 327 CD80 Selvakumar, A.; Mohanraj, B. K.; Eddy, R. L.; Shows, T. B.; White,P. C.; 1 B c
Dupont, B.: Genomic organization and chromosomal locationof the human gene
encoding the B- lymphocyte activation antigen B7. Immunogenetics 36:175-

181, 1992.

GAM139 327 CD80 Stamper, C. C.; Zhang, Y.; Tobin, J. F.; Erbe, D. V.; Ikemizu,S.; Davis, S. 1 B c
J.; Stahl, M. L.; Seehra, J.; Somers, W. S.; Mosyak,L.: Crystal structure of
the B7- 1/CTLA- 4 complex that inhibits humanimmune responses. Nature 410:
608- 611, 2001. Note: Erratum: Nature411: 617 only, 2001.

GAM139 327 CDKN1A Al- Awqati, Q.; Preisig, P. A.: Size does matter: will knockoutof 1 B c
p21(WAF1/CIP1) save the kidney by limiting compensatory renal
growth?(Commentary) Proc. Nat. Acad. Sci. 96: 10551- 10553, 1999.

GAM139 327 CDKN1A Amack, J. D.; Mahadevan, M. S.: The myotonic dystrophy expandedCUG repeat 1 B c
tract is necessary but not sufficient to disrupt C2C12myoblast
differentiation. Hum. Molec. Genet. 10: 1879- 1887, 2001.

GAM139 327 CDKN1A Bunz, F.; Dutriaux, A.; Lengauer, C.; Waldman, T.; Zhou, S.; Brown,J. P.; 1 B c
Sedivy, J. M.; Kinzler, K. W.; Vogelstein, B.: Requirementfor p53 and p21 to
sustain G2 arrest after DNA damage. Science 282:1497- 1501, 1998.

GAM139 327 CDKN1A Chedid, M.; Michieli, P.; Lengel, C.; Huppi, K.; Givol, D.: Asingle 1 B c
nucleotide substitution at codon 31 (ser/arg) defines a polymorphismin a
highly conserved region of the p53- inducible gene WAF1/CIP1. Oncogene
9:3021- 3024, 1994.

GAM139 327 CDKN1A Cheng, T.; Rodrigues, N.; Shen, H.; Yang, Y.; Dombkowski, D.; Sykes,M.; 1 B c
Scadden, D. T.: Hematopoietic stem cell quiescence maintainedby
p21(cip1/waf1). Science 287: 1804- 1808, 2000.

GAM139 327 CDKN1A Demetrick, D. J.; Matsumoto, S.; Hannon, G. J.; Okamoto, K.; Xiong,Y.; 1 B c
Zhang, H.; Beach, D. H.: Chromosomal mapping of the genes forthe human cell
cycle proteins cyclin C (CCNC), cyclin E (CCNE), p21(CDKN1) and KAP (CDKN3).
Cytogenet. Cell Genet. 69: 190- 192, 1995.

GAM139 327 CDKN1A El- Deiry, W. S.; Tokino, T.; Velculescu, V. E.; Levy, D. B.; Parsons,R.; 1 B c
Trent, J. M.; Lin, D.; Mercer, E.; Kinzler, K. W.; Vogelstein,B.: WAF1, a
potential mediator of p53 tumor suppression. Cell 75:817- 825, 1993.

GAM139 327 CDKN1A Harper, J. W.; Adami, G. R.; Wei, N.; Keyomarsi, K.; Elledge, S.J.: The p21 1 B c
Cdk- interacting protein Cip1 is a potent inhibitor ofG1 cyclin- dependent
kinases. Cell 75: 805- 816, 1993.

GAM139 327 CDKN1A Huppi, K.; Siwarski, D.; Dosik, J.; Michieli, P.; Chedid, M.; Reed,S.; Mock, 1 B c
B.; Givol, D.; Mushinski, J. F.: Molecular cloning, sequencing,chromosomal
localization and expression of mouse p21 (Waf1). Oncogene 9:3017- 3020,
1994.

GAM139 327 CDKN1A Levkau, B.; Koyama, H.; Raines, E. W.; Clurman, B. E.; Herren,B.; Orth, K.; 1 B c
Roberts, J. M.; Ross, R.: Cleavage of p21(Cip1/Waf1)and p27(Kip1) mediates
apoptosis in endothelial cells through activationof Cdk2: role of a caspase
cascade. Molec. Cell 1: 553- 563, 1998.

GAM139 327 CDKN1A Megyesi, J.; Price, P. M.; Tamayo, E.; Safirstein, R. L.: Thelack of a 1 B c
functional p21(WAF1/CIP1) gene ameliorates progression tochronic renal
failure. Proc. Nat. Acad. Sci. 96: 10830- 10835, 1999.

GAM139 327 CDKN1A Mousses, S.; Ozcelik, H.; Lee, P. D.; Malkin, D.; Bull, S. B.;Andrulis, I. 1 B c
L.: Two variants of the CIP1/WAF1 gene occur togetherand are associated with
human cancer. Hum. Molec. Genet. 4: 1089- 1092,1995.

GAM139 327 CDKN1A Raj, K.; Ogston, P.; Beard, P.: Virus- mediated killing of cellsthat lack 1 B c
p53 activity. Nature 412: 914- 917, 2001. Note: Addendum:Nature 416: 202
only, 2002.

GAM139 327 CDKN1A Salvador, J. M.; Hollander, M. C.; Nguyen, A. T.; Kopp, J. B.;Barisoni, L.; 1 B c

Moore, J. K.; Ashwell, J. D.; Fornace, A. J., Jr.:Mice lacking the p53-
effector gene Gadd45a develop a lupus- like syndrome. Immunity 16:499- 508,
2002.

GAM139 327 CDKN1A Sjalander, A.; Birgander, R.; Rannug, A.; Alexandrie, A.- K.; Tornling,G.; 1 B c
Beckman, G.: Association between the p21 codon 31A1 (arg) alleleand lung
cancer. Hum. Hered. 46: 221- 225, 1996.

GAM139 327 CDKN1A Wang, Y. A.; Elson, A.; Leder, P.: Loss of p21 increases sensitivityto 1 B c
ionizing radiation and delays the onset of lymphoma in atm- deficientmice.
Proc. Nat. Acad. Sci. 94: 14590- 14595, 1997.

GAM139 327 CDKN1A Yu, D.; Jing, T.; Liu, B.; Yao, J.; Tan, M.; McDonnell, T. J.;Hung, M.- C.: 1 B c
Overexpression of ErbB2 blocks Taxol- induced apoptosisby upregulation of
p21Cip1, which inhibits p34Cdc2 kinase. Molec.Cell 2: 581- 591, 1998.

GAM139 327 CDKN1A Zakut, R.; Givol, D.: The tumor suppression function of p21(Waf)is contained 1 B c
in its N- terminal half ('half- WAF'). Oncogene 11: 393- 395,1995.

GAM139 327 CNN1 Maguchi, M.; Nishida, W.; Kohara, K.; Kuwano, A.; Kondo, I.; Hiwada,K.: 1 B c
Molecular cloning and gene mapping of human basic and acidiccalponins.
Biochem. Biophys. Res. Commun. 217: 238- 244, 1995.

GAM139 327 CNN1 Miano, J. M.; Krahe, R.; Garcia, E.; Elliott, J. M.; Olson, E.N.: 1 B c
Expression, genomic structure and high resolution mapping to19p13.2 of the
human smooth muscle cell calponin gene. Gene 197:215- 224, 1997.

GAM139 327 CNN1 Miano, J. M.; Thomas, S.; Disteche, C. M.: Expression and chromosomalmapping 1 B c
of the mouse smooth muscle calponin gene. Mammalian Genome 12:187- 191,
2001.

GAM139 327 CNN1 Strasser, P.; Gimona, M.; Moessler, H.; Herzog, M.; Small, J. V.: Mammalian 1 B c
calponin: identification and expression of genetic variants. FEBSLett. 330:
13- 18, 1993.

GAM139 327 CSK Armstrong, E.; Cannizzaro, L.; Bergman, M.; Huebner, K.; Alitalo,K.: The c- 1 B c
src tyrosine kinase (CSK) gene, a potential antioncogene,localizes to human
chromosome region 15q23- q25. Cytogenet. Cell Genet. 60:119- 120, 1992.

GAM139 327 CSK Cloutier, J.- F.; Veillette, A.: Association of inhibitory tyrosineprotein 1 B c
kinase p50(csk) with protein tyrosine phosphatase PEP in Tcells and other
hemopoietic cells. EMBO J. 15: 4909- 4918, 1996.

GAM139 327 CSK Partanen, J.; Armstrong, E.; Bergman, M.; Makela, T. P.; Hirvonen,H.; 1 B c
Huebner, K.; Alitalo, K.: Cyl encodes a putative cytoplasmictyrosine kinase
lacking the conserved tyrosine autophosphorylationsite (Y416- src). Oncogene
6: 2013- 2018, 1991.

GAM139 327 DDX9 Abdelhaleem, M. M.; Hameed, S.; Klassen, D.; Greenberg, A. H.:Leukophysin: 1 B c
an RNA helicase A- related molecule identified in cytotoxicT cell granules
and vesicles. J. Immun. 156: 2026- 2035, 1996.

GAM139 327 DDX9 Lee, C. G.; Hurwitz, J.: A new RNA helicase isolated from HeLacells that 1 B c
catalytically translocates in the 3- prime to 5- prime direction. J.Biol.
Chem. 267: 4398- 4407, 1992.

GAM139 327 DDX9 Lee, C.- G.; Eki, T.; Okumura, K.; da Costa Soares, V.; Hurwitz,J.: 1 B c
Molecular analysis of the cDNA and genomic DNA encoding mouseRNA helicase A.
Genomics 47: 365- 371, 1998.

GAM139 327 DDX9 Lee, C.- G.; Hurwitz, J.: Human RNA helicase A is homologous tothe maleless 1 B c
protein of Drosophila. J. Biol. Chem. 268: 16822- 16830,1993.

GAM139 327 DDX9 Zhang, S.; Grosse, F.: Domain structure of human nuclear DNA helicaseII (RNA 1 B c
helicase A). J. Biol. Chem. 272: 11487- 11494, 1997.

GAM139 327 DDX9 Zhang, S.; Maacke, H.; Grosse, F.: Molecular cloning of the geneencoding 1 B c

nuclear DNA helicase II: a bovine homologue of human RNAhelicase A and Drosophila Mle protein. J. Biol. Chem. 270: 16422- 16427,1995.

GAM139 327 DGCR2 Augusseau, S.; Jouk, S.; Jalbert, P.; Prieur, M.: DiGeorge syndromeand 22q11 rearrangements. (Letter) Hum. Genet. 74: 206 only, 1986. 1 B c

GAM139 327 DGCR2 Bartsch, O.; Wagner, A.; Hinkel, G. K.; Lichtner, P.; Murken, J.;Schuffenhauer, S.: No evidence for chromosomal microdeletions atthe second DiGeorge syndrome locus on 10p near D10S585. (Letter) Am.J. Med. Genet. 83: 425- 426, 1999. 1 B c

GAM139 327 DGCR2 Daw, S. C. M.; Taylor, C.; Kraman, M.; Call, K.; Mao, J.; Schuffenhauer,S.; Meitinger, T.; Lipson, T.; Goodship, J.; Scambler, P.: A commonregion of 10p deleted in DiGeorge and velocardiofacial syndromes. NatureGenet. 13: 458- 461, 1996. 1 B c

GAM139 327 DGCR2 Demczuk, S.; Aledo, R.; Zucman, J.; Delattre, O.; Desmaze, C.;Dauphinot, L.; Jalbert, P.; Rouleau, G. A.; Thomas, G.; Aurias, A.: Cloning of a balanced translocation breakpoint in the DiGeorge syndromecritical region and isolation of a novel potential adhesion receptorgene in its vicinity. Hum. Molec. Genet. 4: 551- 558, 1995. 1 B c

GAM139 327 DGCR2 Hasegawa, T.; Hasegawa, Y.; Aso, T.; Koto, S.; Nagai, T.; Tsuchiya,Y.; Kim, K. C.; Ohashi, H.; Wakui, K.; Fukushima, Y.: HDR syndrome(hypoparathyroidism, sensorineural deafness, renal dysplasia) associatedwith del(10)(p13). Am. J. Med. Genet. 73: 416- 418, 1997. 1 B c

GAM139 327 DGCR2 Lichtner, P.; Konig, R.; Hasegawa, T.; Van Esch, H.; Meitinger,T.; Schuffenhauer, S.: An HDR (hypoparathyroidism, deafness, renaldysplasia) syndrome locus maps distal to the DiGeorge syndrome regionon 10p13/14. J. Med. Genet. 37: 33- 37, 2000. 1 B c

GAM139 327 DGCR2 Schuffenhauer, S.; Lichtner, P.; Peykar- Derakhshandeh, P.; Murken,J.; Haas, O. A.; Back, E.; Wolff, G.; Zabel, B.; Barisic, I.; Rauch,A.; Borochowitz, Z.; Dallapiccola, B.; Ross, M.; Meitinger, T.: Deletionmapping on chromosome 10p and definition of a critical region forthe second DiGeorge syndrome locus (DGS2). Europ. J. Hum. Genet. 6:213- 225, 1998. 1 B c

GAM139 327 DGCR2 Van Esch, H.; Groenen, P.; Daw, S.; Poffyn, A.; Holvoet, M.; Scambler,P.; Fryns, J.- P.; Van de Ven, W.; Devriendt, K.: Partial DiGeorgesyndrome in two patients with a 10p rearrangement. Clin. Genet. 55:269- 276, 1999. 1 B c

GAM139 327 DGCR2 Wadey, R.; Daw, S.; Taylor, C.; Atif, U.; Kamath, S.; Halford,S.; O'Donnell, H.; Wilson, D.; Goodship, J.; Burn, J.; Scambler, P.: Isolation of a gene encoding an integral membrane protein from thevicinity of a balanced translocation breakpoint associated with DiGeorgesyndrome. Hum. Molec. Genet. 4: 1027- 1033, 1995. 1 B c

GAM139 327 DOCK1 Hasegawa, H.; Kiyokawa, E.; Tanaka, S.; Nagashima, K.; Gotoh, N.;Shibuya, M.; Kurata, T.; Matsuda, M.: DOCK180, a major CRK- bindingprotein, alters cell morphology upon translocation to the membrane. Molec.Cell Biol. 16: 1770- 176, 1996. 1 B c

GAM139 327 DOCK1 Savill, J.: Phagocytic docking without shocking. Nature 442- 443,1998. 1 B c

GAM139 327 DOCK1 Takai, S.; Hasegawa, H.; Kiyokawa, E.; Yamada, K.; Kurata, T.;Matsuda, M.: Chromosomal mapping of the gene encoding DOCK180, amajor Crk- binding protein, to 10q26.13- q26.3 by fluorescence in situhybridization. Genomics 35: 403- 404, 1996. 1 B c

GAM139 327 DOCK1 Wu, Y.- C.; Horvitz, H. R.: C. elegans phagocytosis and cell- migrationprotein CED- 5 is similar to human DOCK180. Nature 392: 501- 504,1998. 1 B c

GAM139 327 EDN2 Arinami, T.; Ishikawa, M.; Inoue, A.; Yanagisawa, M.; Masaki, T.;Yoshida, M. 1 B c
C.; Hamaguchi, H.: Chromosomal assignments of the humanendothelin family
genes: the endothelin- 1 gene (EDN1) to 6p23- p24,the endothelin- 2 gene
(EDN2) to 1p34, and the endothelin- 3 gene (EDN3)to 20q13.2- q13.3. Am. J.
Hum. Genet. 48: 990- 996, 1991.

GAM139 327 EDN2 Bloch, K. D.; Hong, C. C.; Eddy, R. L.; Shows, T. B.; Quertermous,T.: cDNA 1 B c
cloning and chromosomal assignment of the endothelin 2 gene:vasoactive
intestinal contractor peptide is rat endothelin 2. Genomics 10:236- 242,
1991.

GAM139 327 EDN2 Deng, A. Y.; Dene, H.; Pravenec, M.; Rapp, J. P.: Genetic mappingof two new 1 B c
blood pressure quantitative trait loci in the rat by genotypingendothelin
system genes. J. Clin. Invest. 93: 2701- 2709, 1994.

GAM139 327 EDN2 Ohkubo, S.; Ogi, K.; Hosoya, M.; Matsumoto, H.; Suzuki, N.; Kimura,C.; Onda, 1 B c
H.; Fujino, M.: Specific expression of human endothelin- 2(ET- 2) gene in a
renal adenocarcinoma cell line: molecular cloningof cDNA encoding the
precursor of ET- 2 and its characterization. FEBSLett. 274: 136- 140, 1990.

GAM139 327 EGR3 Morris, M. E.; Viswanathan, N.; Kuhlman, S.; Davis, F. C.; Weitz,C. J.: A 1 B c
screen for genes induced in the suprachiasmatic nucleusby light. Science
279: 1544- 1547, 1998.

GAM139 327 EGR3 Patwardhan, S.; Gashler, A.; Siegel, M. G.; Chang, L. C.; Joseph,L. J.; 1 B c
Shows, T. B.; Le Beau, M. M.; Sukhatme, V. P.: EGR3, a novelmember of the
Egr family of genes encoding immediate- early transcriptionfactors. Oncogene
6: 917- 928, 1991.

GAM139 327 EGR3 Tourtellotte, W. G.; Milbrandt, J.: Sensory ataxia and musclespindle 1 B c
agenesis in mice lacking the transcription factor Egr3. NatureGenet. 20: 87-
91, 1998.

GAM139 327 EPHA1 Eph Nomenclature Committee: Unified nomenclature for the Ephfamily receptors 1 B c
and their ligands, the ephrins. Cell 90: 403- 404,1997.

GAM139 327 EPHA1 Hattori, M.; Osterfield, M.; Flanagan, J. G.: Regulated cleavageof a 1 B c
contact- mediated axon repellent. Science 289: 1360- 1365, 2000.

GAM139 327 EPHA1 Maru, Y.; Hirai, H.; Yoshida, M. C.; Takaku, F.: Evolution, expression,and 1 B c
chromosomal location of a novel receptor tyrosine kinase gene,eph. Molec.
Cell. Biol. 8: 3770- 3776, 1988.

GAM139 327 EPHA1 Yoshida, M. C.; Maru, H.; Hirai, H.; Takau, F.: Chromosomal locationof a 1 B c
novel receptor tyrosine kinase gene, EPH, on chromosome 7. (Abstract)
Cytogenet.Cell Genet. 51: 1113 only, 1989.

GAM139 327 FZD4 Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.;Hirai, M.; 1 B c
Katoh, M.: Molecular cloning and characterization of humanfrizzled- 4 on
chromosome 11q14- q21. Biochem. Biophys. Res. Commun. 264:955- 961, 1999.

GAM139 327 FZD4 Robitaille, J.; MacDonald, M. L. E.; Kaykas, A.; Sheldahl, L. C.;Zeisler, 1 B c
J.; Dube, M.- P.; Zhang, L.- H.; Singaraja, R. R.; Guernsey,D. L.; Zhang,
B.; Siebert, L. F.; Hoskin- Mott, A.; Trese, M. T.; Pimstone,S. N.; Shastry,
B. S.; Moon, R. T.; Hayden, M. R.; Goldberg, Y. P.;Samuels, M. E.: Mutant
frizzled- 4 disrupts retinal angiogenesis infamilial exudative
vitreoretinopathy. Nature Genet. 32: 326- 330,2002.

GAM139 327 GAS7 Ju, Y.- T.; Chang, A. C. Y.; She, B.- R.; Tsaur, M.- L.; Hwang, H.- M.;Chao, 1 B c
C. C.- K.; Cohen, S. N.; Lin- Chao, S.: Gas7: a gene expressedpreferentially
in growth- arrested fibroblasts and terminally differentiatedPurkinje
neurons affects neurite formation. Proc. Nat. Acad. Sci. 95:11423- 11428,
1998.

GAM139 327 GAS7 Kurtz, A.; Zimmer, A.: Interspecies fluorescence in situ 1 B c
hybridizationfurther defines synteny homology between mouse chromosome 11
and humanchromosome 17. Mammalian Genome 6: 379- 380, 1995.

GAM139 327 GAS7 Megonigal, M. D.; Cheung, N.- K. V.; Rappaport, E. F.; Nowell, P.C.; Wilson, 1 B c
R. B.; Jones, D. H.; Addya, K.; Leonard, D. G. B.; Kushner,B. H.; Williams,
T. M.; Lange, B. J.; Felix, C. A.: Detection ofleukemia- associated MLL-
GAS7 translocation early during chemotherapywith DNA topoisomerase II
inhibitors. Proc. Nat. Acad. Sci. 97:2814- 2819, 2000.

GAM139 327 GCNT1 Bierhuizen, M. F. A.; Mattei, M.- G.; Fukuda, M.: Expression ofthe 1 B c
developmental I antigen by a cloned human cDNA encoding a memberof a beta-
1,6- N- acetylglucosaminyltransferase gene family. GenesDev. 7: 468- 478,
1993.

GAM139 327 GCNT1 Pilz, A.; Woodward, K.; Povey, S.; Abbott, C.: Comparative mappingof 50 1 B c
human chromosome 9 loci in the laboratory mouse. Genomics 25:139- 149, 1995.

GAM139 327 GCNT1 Yeh, J.- C.; Ong, E.; Fukuda, M.: Molecular cloning and expressionof a novel 1 B c
beta- 1,6- N- acetylglucosaminyltransferase that forms core2, core 4, and I
branches. J. Biol. Chem. 274: 3215- 3221, 1999.

GAM139 327 GDI2 Bachner, D.; Sedlacek, Z.; Korn, B.; Hameister, H.; Poustka, A.: Expression 1 B c
patterns of two human genes coding for different rabGDP- dissociation
inhibitors (GDIs), extremely conserved proteins involvedin cellular
transport. Hum. Molec. Genet. 4: 701- 708, 1995.

GAM139 327 GDI2 Sedlacek, Z.; Konecki, D. S.; Korn, B.; Klauck, S. M.; Poustka,A.: 1 B c
Evolutionary conservation and genomic organization of XAP- 4,an Xq28 located
gene coding for a human rab GDP- dissociation inhibitor(GDI). Mammalian
Genome 5: 633- 639, 1995.

GAM139 327 GDI2 Sedlacek, Z.; Munstermann, E.; Mincheva, A.; Lichter, P.; Poustka,A.: The 1 B c
human rab GDI beta gene with long retroposon- rich intronsmaps to 10p15 and
its pseudogene to 7p11- p13. Mammalian Genome 9:78- 80, 1998.

GAM139 327 GDI2 Shisheva, A.; Sudhof, T. C.; Czech, M. P.: Cloning, characterization,and 1 B c
expression of a novel GDP dissociation inhibitor isoform fromskeletal
muscle. Molec. Cell. Biol. 14: 3459- 3468, 1994.

GAM139 327 GOSR1 Bui, T. D.; Levy, E. R.; Subramaniam, V. N.; Lowe, S. L.; Hong,W.: cDNA 1 B c
characterization and chromosomal mapping of human GolgiSNARE GS27 and GS28
to chromosome 17. Genomics 57: 285- 288, 1999.

GAM139 327 GOSR1 Lowe, S. L.; Peter, F.; Subramaniam, V. N.; Wong, S. H.; Hong,W.: A SNARE 1 B c
involved in protein transport through the Golgi apparatus. Nature 389:881-
884, 1997.

GAM139 327 GOSR1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 1 B c
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM139 327 GOSR1 Nagahama, M.; Orci, L.; Ravazzola, M.; Amherdt, M.; Lacomis, L.;Tempst, P.; 1 B c
Rothman, J. E.; Sollner, T. H.: A v- SNARE implicatedin intra- Golgi
transport. J. Cell Biol. 133: 507- 516, 1996.

GAM139 327 GOSR1 Subramaniam, V. N.; Peter, F.; Philp, R.; Wong, S. H.; Hong, W.: GS28, a 28- 1 B c
kilodalton Golgi SNARE that participates in ER- Golgitransport. Science 272:
1161- 1163, 1996.

GAM139 327 GPLD1 LeBoeuf, R. C.; Caldwell, M.; Guo, Y.; Metz, C.; Davitz, M. A.;Olson, L. K.; 1 B c

Deeg, M. A.: Mouse glycosylphosphatidylinositol- specificphospholipase D (Gpld1) characterization. Mammalian Genome 9: 710- 714,1998.

GAM139 327 GPLD1 Scallon, B. J.; Fung, W.- J. C.; Tsang, T. C.; Li, S.; Kado- Fong,H.; Huang, 1 B c
K.- S.; Kochan, J. P.: Primary structure and functionalactivity of a phosphatidylinositol- glycan- specific phospholipase D. Science 252:446-448, 1991.

GAM139 327 GPLD1 Schofield, J. N.; Rademacher, T. W.: Structure and expressionof the human 1 B c
glycosylphosphatidylinositol phospholipase D1 (GPLD1)gene. Biochim. Biophys. Acta 1494: 189- 194, 2000.

GAM139 327 GPLD1 Tsang, T. C.; Fung, W.- J.; Levine, J.; Metz, C. N.; Davitz, M.A.; Burns, D. 1 B c
K.; Huang, K.- S.; Kochan, J. P.: Isolation and expressionof two human glycosylphosphatidylinositol phospholipase D (GPI- PLD)cDNAs. (Abstract) FASEB J. (supp.) 6: A1922 only, 1992.

GAM139 327 GPR35 Horikawa, Y.; Oda, N.; Cox, N. J.; Li, X.; Orho- Melander, M.; Hara,M.; 1 B c
Hinokio, Y.; Lindner, T. H.; Mashima, H.; Schwarz, P. E. H.; delBosque-Plata, L.; Horikawa, Y.; and 14 others: Genetic variationin the gene encoding calpain- 10 is associated with type 2 diabetesmellitus. Nature Genet. 26: 163- 175, 2000.

GAM139 327 GPR35 O'Dowd, B. F.; Nguyen, T.; Marchese, A.; Cheng, R.; Lynch, K. R.;Heng, H. H. 1 B c
Q.; Kolakowski, L. F., Jr.; George, S. R.: Discoveryof three novel G-protein- coupled receptor genes. Genomics 310- 313,1998.

GAM139 327 HMGA1 Agalioti, T.; Lomvardas, S.; Parekh, B.; Yie, J.; Maniatas, T.;Thanos, D.: 1 B c
Ordered recruitment of chromatin modifying and generaltranscription factors to the IFN- beta promoter. Cell 103: 667- 678,2000.

GAM139 327 HMGA1 Friedmann, M.; Holth, L. T.; Zoghbi, H. Y.; Reeves, R.: 1 B c
Organization,inducible- expression and chromosome localization of the human HMG- I(Y)nonhistone protein gene. Nucleic Acids Res. 21: 4259- 4267, 1993.

GAM139 327 HMGA1 Munshi, N.; Agalioti, T.; Lomvardas, S.; Merika, M.; Chen, G.;Thanos, D.: 1 B c
Coordination of a transcriptional switch by HMGI(Y) acetylation. Science 293:1133- 1136, 2001.

GAM139 327 HMGA1 Thanos, D.; Maniatis, T.: Virus induction of human IFN- beta geneexpression 1 B c
requires the assembly of an enhanceosome. Cell 83: 1091- 1100,1995.

GAM139 327 HMGA1 Wood, L. J.; Mukherjee, M.; Dolde, C. E.; Xu, Y.; Maher, J. F.;Bunton, T. 1 B c
E.; Williams, J. B.; Resar, L. M. S.: HMG- I/Y, a new c- Myctarget gene and potential oncogene. Molec. Cell Biol. 20: 5490- 5502,2000.

GAM139 327 IGSF4 Biederer, T.; Sara, Y.; Mozhayeva, M.; Atasoy, D.; Liu, X.; Kavalali,E. T.; 1 B c
Sudhof, T. C.: SynCAM, a synaptic adhesion molecule that drivessynapse assembly. Science 297: 1525- 1531, 2002.

GAM139 327 IGSF4 Gomyo, H.; Arai, Y.; Tanigami, A.; Murakami, Y.; Hattori, M.; Hosoda,F.; 1 B c
Arai, K.; Aikawa, Y.; Tsuda, H.; Hirohashi, S.; Asakawa, S.; Shimizu,N.; Soeda, E.; Sakaki, Y.; Ohki, M.: A 2- Mb sequence- ready contigmap and a novel immunoglobulin superfamily gene IGSF4 in the LOH regionof chromosome 11q23.2. Genomics 62: 139- 146, 1999.

GAM139 327 IGSF4 Kuramochi, M.; Fukuhara, H.; Nobukuni, T.; Kanbe, T.; Maruyama,T.; Ghosh, H. 1 B c
P.; Pletcher, M.; Isomura, M.; Onizuka, M.; Kitamura,T.; Sekiya, T.; Reeves, R. H.; Murakami, Y.: TSLC1 is a tumor- suppressorgene in human non- small-cell lung cancer. Nature Genet. 27: 427- 430,2001.

GAM139 327 IGSF4 Murakami, Y.; Nobukuni, T.; Tamura, K.; Maruyama, T.; Sekiya, T.;Arai, Y.; 1 B c
Gomyou, H.; Tanigami, A.; Ohki, M.; Cabin, D.; Frischmeyer,P.; Hunt, P.; Reeves, R. H.: Localization of tumor suppressor activityimportant in

nonsmall cell lung carcinoma on chromosome 11q. Proc.Nat. Acad. Sci. 95: 8153- 8158, 1998.

GAM139 327 IGSF4 Satoh, H.; Lamb, P. W.; Dong, J.- T.; Everitt, J.; Boreiko, C.;Oshimura, M.; 1 B c
Barrett, J. C.: Suppression of tumorigenicity of A549lung adenocarcinoma cells by human chromosomes 3 and 11 introducedvia microcell- mediated chromosome transfer. Molec. Carcinogen. 7:157- 164, 1993.

GAM139 327 KCNMB1 Brenner, R.; Perez, G. J.; Bonev, A. D.; Eckman, D. M.; Kosek,J. C.; Wiler, 1 B c
S. W.; Patterson, A. J.; Nelson, M. T.; Aldrich, R.W.: Vasoregulation by the beta- 1 subunit of the calcium- activatedpotassium channel. Nature 407: 870- 876, 2000.

GAM139 327 KCNMB1 Jiang, Z.; Wallner, M.; Meera, P.; Toro, L.: Human and rodentMaxiK channel 1 B c
beta- subunit genes: cloning and characterization. Genomics 55:57- 67, 1999.

GAM139 327 KCNMB1 Knaus, H.- G.; Folander, K.; Garcia- Calvo, M.; Garcia, M. L.; 1 B c
Kaczorowski,G. J.; Smith, M.; Swanson, R.: Primary sequence and immunologicalcharacterization of beta- subunit of high conductance Ca(2+)- activatedK+ channel from smooth muscle. J. Biol. Chem. 269: 17274- 17278,1994.

GAM139 327 KCNMB1 Meera, P.; Wallner, M.; Jiang, Z.; Toro, L.: A calcium switchfor the 1 B c
functional coupling between alpha (hslo) and beta subunits(K(V), Ca- beta) of maxi K channels. FEBS Lett. 382: 84- 88, 1996.

GAM139 327 KCNMB1 Tseng- Crank, J.; Godinot, N.; Johansen, T. E.; Ahring, P. K.; Strobaek,D.; 1 B c
Mertz, R.; Foster, C. D.; Olesen, S.- P.; Reinhart, P. H.: Cloning,expression, and distribution of a Ca(2+)- activated K+ channel beta- subunitfrom human brain. Proc. Nat. Acad. Sci. 93: 9200- 9205, 1996.

GAM139 327 KCNMB1 Xie, J.; Black, D. L.: A CaMK IV responsive RNA element 1 B c
mediatesdepolarization- induced alternative splicing of ion channels. Nature 410:936- 439, 2001.

GAM139 327 KCNN2 Desai, R.; Peretz, A.; Idelson, H.; Lazarovici, P.; Attali, B.: Ca(2+)- 1 B c
activated K(+) channels in human leukemic Jurkat T cells:molecular cloning, biochemical and functional characterization. J.Biol. Chem. 275: 39954- 39963, 2000.

GAM139 327 KCNN2 Schumacher, M. A.; Rivard, A. F.; Bachinger, H. P.; Adelman, J.P.: Structure 1 B c
of the gating domain of a Ca(2+)- activated K+ channelcomplexed with Ca(2+)/calmodulin. Nature 410: 1120- 1124, 2001.

GAM139 327 KIF1B Gong, T.- W. L.; Burmeister, M.; Lomax, M. I.: The novel gene D4Mil1emaps to 1 B c
mouse chromosome 4 and human chromosome 1p36. Mammalian Genome 7:790- 791, 1996.

GAM139 327 KIF1B Nangaku, M.; Sato- Yoshitake, R.; Okada, Y.; Noda, Y.; Takemura,R.; 1 B c
Yamazaki, H.; Hirokawa, N.: KIF1B, a novel microtubule plus end- directedmonomeric motor protein for transport of mitochondria. Cell 79:1209- 1220, 1994.

GAM139 327 KIF1B Saito, M.; Hayashi, Y.; Suzuki, T.; Tanaka, H.; Hozumi, I.; Tsuji,S.: 1 B c
Linkage mapping of the gene for Charcot- Marie- Tooth disease type2 to chromosome 1p (CMT2A) and the clinical features of CMT2A. Neurology 49:1630- 1635, 1997.

GAM139 327 KIF1B Yang, H. W.; Chen, Y. Z.; Takita, J.; Soeda, E.; Piao, H. Y.; Hayashi,Y.: 1 B c
Genomic structure and mutational analysis of the human KIF1Bgene which is homozygously deleted in neuroblastoma at chromosome1p36.2. Oncogene 20: 5075- 5083, 2001.

GAM139 327 KIF1B Zhao, C.; Takita, J.; Tanaka, Y.; Setou, M.; Nakagawa, T.; Takeda,S.; Yang, 1 B c

H. W.; Terada, S.; Nakata, T.; Takei, Y.; Saito, M.; Tsuji,S.; Hayashi, Y.; Hirokawa, N.: Charcot- Marie- Tooth disease type 2Acaused by mutation in a microtubule motor KIF1B- beta. Cell 105:587- 597, 2001.

GAM139 327 LDB1 Semina, E. V.; Altherr, M. R.; Murray, J. C.: Cloning and 1 B c
chromosomallocalization of two novel human genes encoding LIM- domain
bindingfactors CLIM1 and CLIM2/LDB1/NL1. Mammalian Genome 9: 921- 924, 1998.

GAM139 327 LDB1 Yamashita, T.; Agulnick, A. D.; Copeland, N. G.; Gilbert, D. J.;Jenkins, N. 1 B c
A.; Westphal, H.: Genomic structure and chromosomal localizationof the mouse
LIM domain- binding protein 1 gene, Ldb1. Genomics 48:87- 92, 1998.

GAM139 327 MAPRE3 Nakagawa, H.; Koyama, K.; Murata, Y.; Morito, M.; Akiyama, T.;Nakamura, Y.: 1 B c
EB3, a novel member of the EB1 family preferentiallyexpressed in the central
nervous system, binds to a CNS- specific APChomologue. Oncogene 19: 210-
216, 2000.

GAM139 327 MAPRE3 Su, L.- K.; Qi, Y.: Characterization of human MAPRE genes and theirproteins. 1 B c
Genomics 71: 143- 149, 2001.

GAM139 327 MBD1 Boyes, J.; Bird, A.: DNA methylation inhibits transcription indirectlyvia a 1 B c
methyl- CpG binding protein. Cell 64: 1123- 1134, 1991.

GAM139 327 MBD1 Cross, S. H.; Meehan, R. R.; Nan, X.; Bird, A.: A component ofthe 1 B c
transcriptional repressor MeCP1 shares a motif with DNA methyltransferaseand
HRX proteins. Nature Genet. 16: 256- 259, 1997.

GAM139 327 MBD1 Hendrich, B.; Abbott, C.; McQueen, H.; Chambers, D.; Cross, S.;Bird, A.: 1 B c
Genomic structure and chromosomal mapping of the murineand human Mbd1, Mbd2,
Mbd3, and Mbd4 genes. Mammalian Genome 10:906- 912, 1999.

GAM139 327 MBD1 Levine, A.; Cantoni, G. L.; Razin, A.: Inhibition of promoteractivity by 1 B c
methylation: possible involvement of protein mediators. Proc.Nat. Acad. Sci.
88: 6515- 6518, 1991.

GAM139 327 MBD1 Nan, X.; Meehan, R. R.; Bird, A.: Dissection of the methyl- CpGbinding 1 B c
domain from the chromosomal protein MeCP2. Nucleic AcidsRes. 21: 4886- 4892,
1993.

GAM139 327 MBD1 Ohki, I.; Shimotake, N.; Fujita, N.; Jee, J.- G.; Ikegami, T.; Nakao,M.; 1 B c
Shirakawa, M.: Solution structure of the methyl- CpG binding domainof human
MBD1 in complex with methylated DNA. Cell 105: 487- 497,2001.

GAM139 327 MME Barker, P. E.; Shipp, M. A.; D'Adamio, L.; Masteller, E. L.; Reinherz,E. L.: 1 B c
The common acute lymphoblastic leukemia antigen gene mapsto chromosomal
region 3(q21- q27). J. Immun. 142: 283- 287, 1989.

GAM139 327 MME D'Adamio, L.; Shipp, M. A.; Masteller, E. L.; Reinherz, E. L.:Organization 1 B c
of the gene encoding common acute lymphoblastic leukemiaantigen (neutral
endopeptidase 24.11): multiple miniexons and separate5- prime untranslated
regions. Proc. Nat. Acad. Sci. 86: 7103- 7107,1989.

GAM139 327 MME Debiec, H.; Guigonis, V.; Mougenot, B.; Decobert, F.; Haymann,J.- P.; 1 B c
Bensman, A.; Deschenes, G.; Ronco, P. M.: Antenatal
membranousglomerulonephritis due to anti- neutral endopeptidase antibodies.
NewEng. J. Med. 346: 2053- 2060, 2002.

GAM139 327 MME Iwata, N.; Tsubuki, S.; Takaki, Y.; Shirotani, K.; Lu, B.; Gerard,N. P.; 1 B c
Gerard, C.; Hama, E.; Lee, H.- J.; Saido, T. C.: Metabolicregulation of
brain A- beta by neprilysin. Science 292: 1550- 1552,2001.

GAM139 327 MME Letarte, M.; Vera, S.; Tran, R.; Addis, J. B. L.; Onizuka, R. 1 B c
J.;Quackenbush, E. J.; Jongeneel, C. V.; McInnes, R. R.: Common
acutelymphocytic leukemia antigen is identical to neutral endopeptidase.
J.Exp. Med. 168: 1247- 1253, 1988.

GAM139 327 MME Shipp, M. A.; Vijayaraghavan, J.; Schmidt, E. V.; Masteller, E.L.; D'Adamio, L.; Hersh, L. B.; Reinherz, E. L.: Common acute lymphoblasticleukemia antigen (CALLA) is active neutral endopeptidase 24.11 ('enkephalinase'):direct evidence by cDNA transfection analysis. Proc. Nat. Acad. Sci. 86:297- 301, 1989. 1 B c

GAM139 327 MME Tran- Paterson, R.; Willard, H. F.; Letarte, M.: The common acutelymphoblastic leukemia antigen (neutral endopeptidase- - 3.4.24.11)gene is located on human chromosome 3. Cancer Genet. Cytogenet. 42:129- 134, 1989. 1 B c

GAM139 327 MYD88 Adachi, O.; Kawai, T.; Takeda, K.; Matsumoto, M.; Tsutsui, H.;Sakagami, M.; Nakanishi, K.; Akira, S.: Targeted disruption of theMyD88 gene results in loss of IL- 1- and IL- 18- mediated function. Immunity 143- 150,1998. 1 B c

GAM139 327 MYD88 Bonnert, T. P.; Garka, K. E.; Parnet, P.; Sonoda, G.; Testa, J.R.; Sims, J. E.: The cloning and characterization of human MyD88:a member of an IL- 1 receptor related family. FEBS Lett. 402: 81- 84,1997. 1 B c

GAM139 327 MYD88 Hardiman, G.; Jenkins, N. A.; Copeland, N. G.; Gilbert, D. J.;Garcia, D. K.; Naylor, S. L.; Kastelein, R. A.; Bazan, J. F.: Geneticstructure and chromosomal mapping of MyD88. Genomics 45: 332- 339,1997. 1 B c

GAM139 327 MYD88 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001. 1 B c

GAM139 327 MYD88 Jankovic, D.; Kullberg, M. C.; Hieny, S.; Caspar, P.; Collazo,C. M.; Sher, A.: In the absence of IL- 12, CD4+ T cell responses tointracellular pathogens fail to default to a Th2 pattern and are hostprotective in an IL- 10- /- setting. Immunity 16: 429- 439, 2002. 1 B c

GAM139 327 MYD88 Kawai, T.; Adachi, O.; Ogawa, T.; Takeda, K.; Akira, S.: Unresponsivenessof MyD88- deficient mice to endotoxin. Immunity 11: 115- 122, 1999. 1 B c

GAM139 327 MYD88 Lord, K. A.; Hoffman- Liebermann, B.; Liebermann, D. A.: Complexityof the immediate early response of myeloid cells to terminal differentiationand growth arrest includes ICAM- 1, Jun- B and histone variants. Oncogene 5:387- 396, 1990. 1 B c

GAM139 327 MYD88 Medzhitov, R.; Preston- Hurlburt, P.; Kopp, E.; Stadien, A.; Chen,C.; Ghosh, S.; Janeway, C. A., Jr.: MyD88 is an adaptor protein inthe hToll/Il- 1 receptor family signaling pathways. Molec. Cell 2:253- 258, 1998. 1 B c

GAM139 327 MYD88 Muzio, M.; Ni, J.; Feng, P.; Dixit, V. M.: IRAK (Pelle) familymember IRAK- 2 and MyD88 as proximal mediators of IL- 1 signaling. Science 278:1612- 1615, 1997. 1 B c

GAM139 327 MYD88 Takeuchi, O.; Hoshino, K.; Akira, S.: Cutting edge: TLR2- deficientand MyD88- deficient mice are highly susceptible to Staphylococcusaureus infection. J. Immun. 165: 5392- 5396, 2000. 1 B c

GAM139 327 NESH Matsuda, S.; Iriyama, C.; Yokozaki, S.; Ichigotani, Y.; Shirafuji,N.; Yamaki, K.; Hayakawa, T.; Hamaguchi, M.: Cloning and sequencingof a novel human gene that encodes a putative target protein of Nesh- SH3. J.Hum. Genet. 46: 483- 486, 2001. 1 B c

GAM139 327 NESH Miyazaki, K.; Matsuda, S.; Ichigotani, Y.; Takenouchi, Y.; Hayashi,K.; Fukuda, Y.; Nimura, Y.; Hamaguchi, M.: Isolation and characterizationof a novel human gene (NESH) which encodes a putative signaling moleculesimilar to e3B1 protein. Biochim. Biophys. Acta 1493: 237- 241, 2000. 1 B c

GAM139 327 NPEPPS Bauer, W. O.; Nanda, I.; Beck, G.; Schmid, M.; Jakob, F.: Humanpuromycin- 1 B c

sensitive aminopeptidase: cloning of 3- prime UTR, evidencefor a polymorphism at aa 140 and refined chromosomal localizationto 17q21. Cytogenet. Cell Genet. 92: 221- 224, 2001.

GAM139 327 NPEPPS Huber, G.; Thompson, A.; Gruninger, F.; Mechler, H.; Hochstrasser,R.; Hauri, 1 B c
H.- P.; Malherbe, P.: cDNA cloning and molecular characterizationof human brain metalloprotease MP100: a beta- secretase candidate? J.Neurochem. 72: 1215- 1223, 1999.

GAM139 327 NPEPPS Osada, T.; Sakaki, Y.; Takeuchi, T.: Puromycin- sensitive aminopeptidasegene 1 B c
(Psa) maps to mouse chromosome 11. Genomics 56: 361- 362, 1999.

GAM139 327 NPEPPS Schonlein, C.; Loffler, J.; Huber, G.: Purification and characterizationof a 1 B c
novel metalloprotease from human brain with the ability to cleavesubstrates derived from the N- terminus of beta- amyloid protein. Biochem.Biophys. Res. Commun. 201: 45- 53, 1994.

GAM139 327 NPEPPS Thompson, M. W.; Tobler, A.; Fontana, A.; Hersh, L. B.: Cloningand analysis 1 B c
of the gene for the human puromycin- sensitive aminopeptidase. Biochem.Biophys. Res. Commun. 258: 234- 240, 1999.

GAM139 327 NPEPPS Tobler, A. R.; Constam, D. B.; Schmitt- Graff, A.; Malipiero, U.;Schlapbach, 1 B c
R.; Fontana, A.: Cloning of the human puromycin- sensitiveaminopeptidase and evidence for expression in neurons. J. Neurochem. 68:889- 897, 1997.

GAM139 327 OPRD1 Befort, K.; Mattei, M.- G.; Roeckel, N.; Kieffer, B.: 1 B c
Chromosomallocalization of the delta opioid receptor gene to human 1p34.3- p36.1and mouse 4D bands by in situ hybridization. Genomics 20: 143- 145,1994.

GAM139 327 OPRD1 Bzdega, T.; Chin, H.; Kim, H.; Jung, H. H.; Kozak, C. A.; Klee,W. A.: 1 B c
Regional expression and chromosomal localization of the deltaopiate receptor gene. Proc. Nat. Acad. Sci. 90: 9305- 9309, 1993.

GAM139 327 OPRD1 Evans, C. J.; Keith, D. E.; Morrison, H.; Magendzo, K.; Edwards,R. H.: 1 B c
Cloning of a delta opioid receptor by functional expression. Science 258:1952- 1955, 1992.

GAM139 327 OPRD1 Filliol, D.; Ghozland, S.; Chluba, J.; Martin, M.; Matthes, H.W. D.; 1 B c
Simonin, F.; Befort, K.; Gaveriaux- Ruff, C.; Dierich, A.; LeMeur,M.; Valverde, O.; Maldonado, R.; Kieffer, B. L.: Mice deficient fordelta- and mu- opioid receptors exhibit opposing alterations of emotionalresponses. Nature Genet. 25: 195- 200, 2000.

GAM139 327 OPRD1 Jordan, B. A.; Devi, L. A.: G- protein- coupled receptor 1 B c
heterodimerizationmodulates receptor function. Nature 399: 697- 700, 1999.

GAM139 327 OPRD1 Kaufman, D. L.; Xia, Y.- R.; Keith, D. E., Jr.; Newman, D.; Evans,C. J.; 1 B c
Lusis, A. J.: Localization of the delta- opioid receptor geneto mouse chromosome 4 by linkage analysis. Genomics 19: 405- 406,1994.

GAM139 327 OPRD1 Mayer, P.; Tischmeyer, H.; Jayasinghe, M.; Bonnekoh, B.; Gollnick,H.; 1 B c
Teschemacher, H.; Hollt, V.: A delta- opoid receptor lacking thethird cytoplasmic loop is generated by atypical mRNA processing inhuman malignomas. FEBS Lett. 480: 156- 160, 2000.

GAM139 327 OPRD1 Whistler, J. L.; Enquist, J.; Marley, A.; Fong, J.; Gladher, F.;Tsuruda, P.; 1 B c
Murray, S. R.; von Zastrow, M.: Modulation of postendocyticsorting of G protein- coupled receptors. Science 297: 615- 620, 2002.

GAM139 327 OPRD1 Xu, K.; Liu, X.; Nagarajan, S.; Gu, X.- Y.; Goldman, D.: Relationshipof the 1 B c
delta- opioid receptor gene to heroin abuse in a large Chinesecase/control sample. Am. J. Med. Genet. 11: 45- 50, 2002.

GAM139 327 PIK4CB Meyers, R.; Cantley, L. C.: Cloning and characterization of awortmannin- 1 B c

sensitive human phosphatidylinositol 4- kinase. J. Biol.Chem. 272: 4384-4390, 1997.

GAM139 327 PIK4CB Nakanishi, S.; Catt, K. J.; Balla, T.: A wortmannin- 1 B c
sensitivephosphatidylinositol 4- kinase that regulates hormone- sensitive poolsof inositolphospholipids. Proc. Nat. Acad. Sci. 92: 5317- 5321, 1995.

GAM139 327 PIK4CB Saito, T.; Seki, N.; Ishii, H.; Ohira, M.; Hayashi, A.; Kozuma,S.; Hori, T.: 1 B c
Complementary DNA cloning and chromosomal mapping ofa novel phosphatidylinositol kinase gene. DNA Res. 4: 301- 305, 1997.

GAM139 327 PIK4CB Suzuki, K.; Hirano, H.; Okutomi, K.; Suzuki, M.; Kuga, Y.; Fujiwara,T.; 1 B c
Kanemoto, N.; Isono, K.; Horie, M.: Identification and characterizationof a novel human phosphatidylinositol 4- kinase. DNA Res. 4: 273- 280,1997.

GAM139 327 SMARCD1 Ring, H. Z.; Vameghi- Meyers, V.; Wang, W.; Crabtree, G. R.; Francke,U.: 1 B c
Five SWI/SNF- related, matrix- associated, actin- dependent regulatorof chromatin (SMARC) genes are dispersed in the human genome. Genomics 51:140-143, 1998.

GAM139 327 SMARCD1 Wang, W.; Xue, Y.; Zhou, S.; Kuo, A.; Cairns, B. R.; Crabtree,G. R.: 1 B c
Diversity and specialization of mammalian SWI/SNF complexes. GenesDev. 10: 2117- 2130, 1996.

GAM139 327 SNCG Ji, H.; Liu, Y. E.; Jia, T.; Wang, M.; Liu, J.; Xiao, G.; Joseph,B. K.; 1 B c
Rosen, C.; Shi, Y. E.: Identification of a breast cancer- specificgene, BCSG1, by direct differential cDNA sequencing. Cancer Res. 57:759- 764, 1997.

GAM139 327 SNCG Lavedan, C.; Buchholtz, S.; Auburger, G.; Albin, R. L.; Athanassiadou,A.; 1 B c
Blancato, J.; Burguera, J. A.; Ferrell, R. E.; Kostic, V.; Leroy,E.; Leube, B.; Mota- Vieira, L.; and 9 others: Absence of mutationin the beta- and gamma- synuclein genes in familial autosomal dominantParkinson's disease. DNA Research 5: 401- 402, 1998.

GAM139 327 SNCG Lavedan, C.; Leroy, E.; Dehejia, A.; Buchholtz, S.; Dutra, A.;Nussbaum, R. 1 B c
L.; Polymeropoulos, M. H.: Identification, localizationand characterization of the human gamma- synuclein gene. Hum. Genet. 103:106- 112, 1998.

GAM139 327 SNCG Ninkina, N. N.; Alimova- Kost, M. V.; Paterson, J. W. E.; Delaney,L.; Cohen, 1 B c
B. B.; Imreh, S.; Gnuchev, N. V.; Davies, A. M.; Buchman,V. L.: Organization, expression and polymorphism of the human persyngene. Hum. Molec. Genet. 7: 1417- 1424, 1998.

GAM139 327 SNCG Spillantini, M. G.; Crowther, R. A.; Jakes, R.; Hasegawa, M.; Goedert,M.: 1 B c
alpha- synuclein in filamentous inclusions of Lewy bodies fromParkinson's disease and dementia with Lewy bodies. Proc. Nat. Acad.Sci. 95: 6469- 6473, 1998.

GAM139 327 STIM1 Parker, N. J.; Begley, C. G.; Smith, P. J.; Fox, R. M.: Molecularcloning of 1 B c
a novel human gene (D11S4896E) at chromosomal region 11p15.5. Genomics 37:253- 256, 1996.

GAM139 327 STIM1 Sabbioni, S.; Veronese, A.; Trubia, M.; Taramelli, R.; Barbanti- Brodano,G.; 1 B c
Croce, C. M.; Negrini, M.: Exon structure and promoter identificationof STIM1 (alias GOK), a human gene causing growth arrest of the humantumor cell lines G401 and RD. Cytogenet. Cell. Genet. 86: 214- 218,1999.

GAM139 327 TBX1 Chieffo, C.; Garvey, N.; Gong, W.; Roe, B.; Zhang, G.; Silver,L.; Emanuel, 1 B c
B. S.; Budarf, M. L.: Isolation and characterizationof a gene from the DiGeorge chromosomal region homologous to the mouseTbx1 gene. Genomics 43: 267- 277, 1997.

GAM139 327 TBX1 Funke, B.; Epstein, J. A.; Kochilas, L. K.; Lu, M. M.; Pandita,R. K.; Liao, 1 B c

J.; Bauerndistel, R.; Schuler, T.; Schorle, H.; Brown,M. C.; Adams, J.; Morrow, B. E.: Mice overexpressing genes from the22q11 region deleted in velo- cardio- facial syndrome/DiGeorge syndromehave middle and inner ear defects. Hum. Molec. Genet. 10: 2549- 2556,2001.

GAM139 327 TBX1 Jerome, L. A.; Papaioannou, V. E.: DiGeorge syndrome phenotypein mice mutant 1 B c
for the T- box gene, Tbx1. Nature Genet. 27: 286- 291,2001.

GAM139 327 TBX1 Lindsay, E. A.; Botta, A.; Jurecic, V.; Carattini- Rivera, S.; Cheah,Y.- C.; 1 B c
Rosenblatt, H. M.; Bradley, A.; Baldini, A.: Congenital heartdisease in mice deficient for the DiGeorge syndrome region. Nature 401:379- 383, 1999.

GAM139 327 TBX1 Lindsay, E. A.; Vitelli, F.; Su, H.; Morishima, M.; Huynh, T.;Pramparo, T.; 1 B c
Jurecic, V.; Ogunrinu, G.; Sutherland, H. F.; Scambler,P. J.; Bradley, A.; Baldini, A.: Tbx1 haploinsufficiency in the DiGeorgesyndrome region causes aortic arch defects in mice. Nature 410:97- 101, 2001.

GAM139 327 TBX1 Merscher, S.; Funke, B.; Epstein, J. A.; Heyer, J.; Puech, A.;Lu, M. M.; 1 B c
Xavier, R. J.; Demay, M. B.; Russell, R. G.; Factor, S.;Tokooya, K.; St. Jore, B.; and 12 others: TBX1 is responsible forcardiovascular defects in velo- cardio- facial/DiGeorge syndrome. Cell 104:619- 629, 2001.

GAM139 327 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, 1 B c
H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor-associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF-kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997.

GAM139 327 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, 1 B c
H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661-14664, 1996.

GAM139 327 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; 1 B c
Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999.

GAM139 327 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. 1 B c
F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997.

GAM139 327 TRPS1 Hatamura, I.; Kanauchi, Y.; Takahara, M.; Fujiwara, M.; Muragaki,Y.; 1 B c
Ooshima, A.; Ogino, T.: A nonsense mutation in TRPS1 in a Japanesefamily with tricho- rhino- phalangeal syndrome type I. (Letter) Clin.Genet. 59: 366- 367, 2001.

GAM139 327 TRPS1 Hilton, M. J.; Sawyer, J. M.; Gutierrez, L.; Hogart, A.; Kung,T. C.; Wells, 1 B c
D. E.: Analysis of novel and recurrent mutations responsiblefor the tricho-rhino- phalangeal syndromes. J. Hum. Genet. 47: 103- 106,2002.

GAM139 327 TRPS1 Hou, J.; Parrish, J.; Ludecke, H.- J.; Sapru, M.; Wang, Y.; Chen,W.; Hill, 1 B c
A.; Siegel- Bartelt, J.; Northrup, H.; Elder, F. F. B.; Chinault,C.; Horsthemke, B.; Wagner, M. J.; Wells, D. E.: A 4- megabase YACcontig that spans the Langer- Giedion syndrome region on human chromosome8q24.1: use in refining the location of the trichorhinophalangealsyndrome and multiple exostoses genes (TRPS1 and EXT1). Genomics 29:87- 97, 1995.

GAM139 327 TRPS1 Kobayashi, H.; Hino, M.; Shimodahira, M.; Iwakura, T.; Ishihara,T.; Ikekubo, 1 B c
K.; Ogawa, Y.; Nakao, K.; Kurahachi, H.: Missense mutationof TRPS1 in a family of tricho- rhino- phalangeal syndrome type III. Am.J. Med. Genet.

107: 26- 29, 2002.

GAM139 327 TRPS1 Ludecke, H.- J.; Schaper, J.; Meinecke, P.; Momeni, P.; Gross, S.;von Holtum, D.; Hirche, H.; Abramowicz, M. J.; Albrecht, B.; Apacik,C.; Christen, H.- J.; Claussen, U.; and 28 others: Genotypic andphenotypic spectrum in tricho- rhino- phalangeal syndrome types I andIII. Am. J. Hum. Genet. 68: 81- 91, 2001. 1 B c

GAM139 327 TRPS1 Ludecke, H.- J.; Wagner, M. J.; Nardmann, J.; La Pillo, B.; Parrish,J. E.; Willems, P. J.; Haan, E. A.; Frydman, M.; Hamers, G. J. H.;Wells, D. E.; Horsthemke, B.: Molecular dissection of a contiguousgene syndrome: localization of the genes involved in the Langer- Giedionsyndrome. Hum. Molec. Genet. 4: 31- 36, 1995. 1 B c

GAM139 327 TRPS1 Momeni, P.; Glockner, G.; Schmidt, O.; von Holtum, D.; Albrecht,B.; Gillessen- Kaesbach, G.; Hennekam, R.; Meinecke, P.; Zabel, B.;Rosenthal, A.; Horsthemke, B.; Ludecke, H.- J.: Mutations in a newgene, encoding a zinc- finger protein, cause tricho- rhino- phalangealsyndrome type I. Nature Genet. 24: 71- 74, 2000. 1 B c

GAM139 327 WNT5B Gavin, B. J.; McMahon, J. A.; McMahon, A. P.: Expression of multiplenovel Wnt- 1/int- 1- related genes during fetal and adult mouse development. GenesDev. 4: 2319- 2332, 1990. 1 B c

GAM139 327 WNT5B Saitoh, T.; Katoh, M.: Molecular cloning and characterizationof human WNT5B on chromosome 12p13.3 region. Int. J. Oncol. 19:347- 351, 2001. 1 B c

GAM140 295 BRF1 Mital, R.; Kobayashi, R.; Hernandez, N.: RNA polymerase III transcriptionfrom the human U6 and adenovirus type 2 VAI promoters has differentrequirements for human BRF, a subunit of human TFIIIB. Molec. Cell.Biol. 16: 7031- 7042, 1996. 3 C c

GAM140 295 BRF1 Wang, Z.; Roeder, R. G.: Structure and function of a human transcriptionfactor TFIIIB subunit that is evolutionarily conserved and containsboth TFIIB- and high- mobility- group protein 2- related domains. Proc.Nat. Acad. Sci. 92: 7026- 7030, 1995. 3 C c

GAM140 295 DNASE1L1 Parrish, J. E.; Ciccodicola, A.; Wehnert, M.; Cox, G. F.; Chen,E.; Nelson, D. L.: A muscle- specific DNase I- like gene in human Xq28. Hum.Molec. Genet. 4: 1557- 1564, 1995. 3 C c

GAM140 295 DNASE1L1 Pergolizzi, R.; Appierto, V.; Bosetti, A.; DeBellis, G. L.; Rovida,E.; Biunno, I.: Cloning of a gene encoding a DNase I- like endonucleasein the human Xq28 region. Gene 168: 267- 270, 1996. 3 C c

GAM142 219 IL13RA1 Aman, M. J.; Tayebi, N.; Obiri, N. I.; Puri, R. K.; Modi, W. S.;Leonard, W. J.: cDNA cloning and characterization of the human interleukin13 receptor alpha chain. J. Biol. Chem. 271: 29265- 29270, 1996. 3 A c

GAM142 219 IL13RA1 Guo, J.; Apiou , F.; Mellerin, M.- P.; Lebeau, B.; Jacques, Y.;Minvielle, S.: Chromosome mapping and expression of the human interleukin- 13receptor. Genomics 42: 141- 5, 1997. 3 A c

GAM142 219 IL13RA1 Heinzmann, H.; Mao, X.- Q.; Akaiwa, M.; Kreomer, R. T.; Gao, P.- S.;Ohshima, K.; Umeshita, R.; Abe, Y.; Braun, S.; Yamashita, T.; Roberts,M. H.; Sugimoto, R.; and 20 others: Genetic variants of IL- 13 signallingand human asthma and atopy. Hum. Molec. Genet. 9: 549- 559, 2000. 3 A c

GAM142 219 IL13RA1 Hilton, D. J.; Zhang, J.- G.; Metcalf, D.; Alexander, W. S.; Nicola,N. A.; Willson, T. A.: Cloning and characterization of a bindingsubunit of the interleukin 13 receptor that is also a component ofthe interleukin 4 receptor. Proc. Nat. Acad. Sci. 93: 497- 501, 1996. 3 A c

GAM142 219 IL13RA1 Zurawski, S. M.; Vega, F., Jr.; Huyghe, B.; Zurawski, G.: Receptorsfor 3 A c

interleukin- 13 and interleukin- 4 are complex and share a novelcomponent that functions in signal transduction. EMBO J. 12: 2663- 2670,1993.

GAM142 219 PDGFRA Disteche, C. M.; Plowman, G. D.; Gronwald, R. G. K.; Kelly, J.;Bowen- Pope, 3 A c
D.; Adler, D. A.; Murray, J. C.: Mapping of the amphiregulinand the platelet- growth factor receptor alpha genes to the proximallong arm of chromosome 4. (Abstract) Cytogenet. Cell Genet. 51:990, 1989.

GAM142 219 PDGFRA Gronwald, R. G. K.; Adler, D. A.; Kelly, J. D.; Disteche, C. M.;Bowen- Pope, 3 A c
D. F.: The human PDGF receptor alpha- subunit gene mapsto chromosome 4 in close proximity to c- kit. Hum. Genet. 85: 383- 385,1990.

GAM142 219 PDGFRA Helwig, U.; Imai, K.; Schmahl, W.; Thomas, B. E.; Varnum, D. S.;Nadeau, J. 3 A c
H.; Balling, R.: Interaction between undulated and Patchleads to an extreme form of spina bifida in double- mutant mice. NatureGenet. 11: 60- 63, 1995.

GAM142 219 PDGFRA Hol, F. A.; Geurds, M. P. A.; Chatkupt, S.; Shugart, Y. Y.; Balling,R.; 3 A c
Schrander- Stumpel, C. T. R. M.; Johnson, W. G.; Hamel, B. C. J.;Mariman, E. C. M.: PAX genes and human neural tube defects: an aminoacid substitution in PAX1 in a patient with spina bifida. J. Med.Genet. 8: 655- 660, 1996.

GAM142 219 PDGFRA Hsieh, C.- L.; Navankasattusas, S.; Escobedo, J. A.; Williams, L.T.; 3 A c
Francke, U.: Chromosomal localization of the gene for AA- typeplatelet- derived growth factor receptor (PDGFRA) in humans and mice. Cytogenet.Cell Genet. 56: 160- 163, 1991.

GAM142 219 PDGFRA Ikuno, Y.; Kazlauskas, A.: TGF- beta- 1- dependent contraction offibroblasts 3 A c
is mediated by th PDGF- alpha receptor. Invest. Ophthal.Vis. Sci. 43: 41- 46, 2002.

GAM142 219 PDGFRA Joosten, P. H. L. J.; Hol, F. A.; van Beersum, S. E. C.; Peters,H.; Hamel, 3 A c
B. C. J.; Afink, G. B.; van Zoelen, E. J. J.; Mariman,E. C. M.: Altered regulation of platelet- derived growth factor receptor- alphagene- transcription in vitro by spina bifida- associated mutant Pax1proteins. Proc. Nat. Acad. Sci. 95: 14459- 14463, 1998.

GAM142 219 PDGFRA Joosten, P. H. L. J.; Toepoel, M.; Mariman, E. C. M.; Van Zoelen,E. J. J.: 3 A c
Promoter haplotype combinations of the platelet- derivedgrowth factor alpha- receptor gene predispose to human neural tubedefects. Nature Genet. 27: 215- 217, 2001.

GAM142 219 PDGFRA Kawagishi, J.; Kumabe, T.; Yoshimoto, T.; Yamamoto, T.: 3 A c
Structure,organization, and transcription units of the human alpha- platelet- derivedgrowth factor receptor gene, PDGFRA. Genomics 30: 224- 232, 1995.

GAM142 219 PDGFRA Klinghoffer, R. A.; Mueting- Nelsen, P. F.; Faerman, A.; Shani,M.; Soriano, 3 A c
P.: The two PDGF receptors maintain conserved signalingin vivo despite divergent embryological functions. Molec. Cell 7:343- 354, 2001.

GAM142 219 PDGFRA Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle,W.; Kraus, M.; 3 A c
Pierce, J.; Aaronson, S.: Isolation of a novel receptorcDNA establishes the existence of two PDGF receptor genes. Science 243:800- 804, 1989.

GAM142 219 PDGFRA Phillips, S. A.; Barr, V. A.; Haft, D. H.; Taylor, S. I.; Haft,C. R.: 3 A c
Identification and characterization of SNX15, a novel sortingnexin involved in protein trafficking. J. Biol. Chem. 276: 5074- 5084,2001.

GAM142 219 PDGFRA Roberts, W. M.; Look, A. T.; Ruossel, M. F.; Sherr, C. J.: Tandemlinkage of 3 A c
human CSF- 1 receptor (c- fms) and PDGF receptor genes. Cell 55:655- 661, 1988.

GAM142 219 PDGFRA Smith, E. A.; Seldin, M. F.; Martinez, L.; Watson, M. L.; GhoshChoudhury, 3 A c
G.; Lalley, P. A.; Pierce, J.; Aaronson, S.; Barker, J.;Naylor, S. L.;

Sakaguchi, A. Y.: Mouse platelet- derived growth factorreceptor alpha gene is deleted in W- 19H and patch mutations on chromosome5. Proc. Nat. Acad. Sci. 88: 4811- 4815, 1991.

GAM142 219 PDGFRA Stenman, G.; Eriksson, A.; Claesson- Welsh, L.: Human PDGFA receptorgene 3 A c maps to the same region on chromosome 4 as the KIT oncogene. GenesChromosomes Cancer 1: 155- 158, 1989.

GAM142 219 PDGFRA Stephenson, D. A.; Mercola, M.; Anderson, E.; Wang, C.; Stiles,C. D.; Bowen- Pope, D. F.; Chapman, V. M.: Platelet- derived growthfactor receptor alpha-subunit gene (Pdgfra) is deleted in the mousepatch (Ph) mutation. Proc. Nat. Acad. Sci. 88: 6- 10, 1991. 3 A c

GAM142 219 PDGFRA Xie, J.; Aszterbaum, M.; Zhang, X.; Bonifas, J. M.; Zachary, C.;Epstein, E.; McCormick, F.: A role of PDGFR- alpha in basal cell carcinomaproliferation. Proc. Nat. Acad. Sci. 98: 9255- 9259, 2001. 3 A c

GAM143 325 MUC3B Fox, M. F.; Lahbib, F.; Pratt, W.; Attwood, J.; Gum, J.; Kim, Y.;Swallow, D. M.: Regional localization of the intestinal mucin geneMUC3 to chromosome 7q22. Ann. Hum. Genet. 56: 281- 287, 1992. 3 C c

GAM143 325 MUC3B Kyo, K.; Muto, T.; Nagawa, H.; Lathrop, G. M.; Nakamura, Y.: Associationsof distinct variants of the intestinal mucin gene MUC3A with ulcerativecolitis and Crohn's disease. J. Hum. Genet. 46: 5- 20, 2001. 3 C c

GAM143 325 MUC3B Pratt, W. S.; Crawley, S.; Hicks, J.; Ho, J.; Nash, M.; Kim, Y.S.; Gum, J. R.; Swallow, D. M.: Multiple transcripts of MUC3: evidencefor two genes, MUC3A and MUC3B. Biochem. Biophys. Res. Commun. 275:916- 923, 2000. 3 C c

GAM143 325 PFKFB4 Manzano, A.; Perez, J. X.; Nadal, M.; Estivill, X.; Lange, A.;Bartrons, R.: Cloning, expression and chromosomal localization ofa human testis 6-phosphofructo- 2- kinase/fructose- 2,6- bisphosphatasegene. Gene 229: 83-89, 1999. 3 C c

GAM143 325 PFKFB4 Sakai, A.; Kato, M.; Fukasawa, M.; Ishiguro, M.; Furuya, E.; Sakakibara,R.: Cloning of cDNA encoding for a novel isozyme of fructose 6- phosphate,2-kinase/fructose2,6- bisphosphatase from human placenta. J. Biochem. 119: 506- 511,1996. 3 C c

GAM144 361 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998. 1 A c

GAM144 361 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 1 A c

GAM144 361 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527-529, 1994. 1 A c

GAM144 361 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal brain type I adenylyl cyclase. Genomics 16: 473- 478,1993. 1 A c

GAM144 361 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita-Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.: Altered sensory processing in the somatosensory cortex of the mutantmouse barrelless. Science 271: 1864- 1867, 1996. 1 A c

GAM144 361 ALDH3B2 Hsu, L. C.; Chang, W.- C.: Sequencing and expression of the humanALDH8 1 A c

encoding a new member of the aldehyde dehydrogenase family. Gene 174:319-322, 1996.

GAM144 361 ALDH3B2 Hsu, L. C.; Chang, W.- C.; Lin, S. W.; Yoshida, A.: Cloning 1 A c
andcharacterization of genes encoding four additional human aldehydededehydrogenase isozymes. Adv. Exp. Med. Biol. 372: 159- 168, 1995.

GAM144 361 ALDH3B2 Hsu, L. C.; Chang, W.- C.; Yoshida, A.: Human aldehyde dehydrogenasegenes, 1 A c
ALDH7 and ALDH8: genomic organization and gene structure comparison. Gene 189:89- 94, 1997.

GAM144 361 BCAT2 Bassett, D. E., Jr.; Boguski, M. S.; Spencer, F.; Reeves, R.; Kim,S.; 1 A c
Weaver, T.; Hieter, P.: Genome cross- referencing and XREFdb:implications for the identification and analysis of genes mutatedin human disease. Nature Genet. 15: 339- 344, 1997.

GAM144 361 BCAT2 Ben- Yosef, T.; Eden, A.; Benvenisty, N.: Characterization of murineBCAT 1 A c
genes: Bcat1, a c- Myc target, and its homolog, Bcat2. MammalianGenome 9: 595- 597, 1998.

GAM144 361 BCAT2 Eden, A.; Simchen, G.; Benvenisty, N.: Two yeast homologs of ECA39,a target 1 A c
for c- Myc regulation, code for cytosolic and mitochondrialbranched- chain amino acid aminotransferases. J. Biol. Chem. 271:20242- 20245, 1996.

GAM144 361 BCAT2 Naylor, S. L.; Shows, T. B.: Branched- chain aminotransferase deficiencyin 1 A c
Chinese hamster cells complemented by two independent genes onhuman chromosomes 12 and 19. Somat. Cell Genet. 6: 641- 652, 1980.

GAM144 361 BCAT2 Naylor, S. L.; Shows, T. B.: Branched- chain aminotransferase genes(BCT- 1 1 A c
and BCT- 2) assigned to human chromosomes 12 and 19 using alpha- ketoacid selection media. (Abstract) Cytogenet. Cell Genet. 25: 191- 192,1979.

GAM144 361 CD86 Celestin, J.; Rotschke, O.; Falk, K.; Ramesh, N.; Jabara, H.; Strominger,J.; 1 A c
Geha, R. S.: IL- 3 induces B7.2 (CD86) expression and costimulatoryactivity in human eosinophils. J. Immun. 167: 6097- 6104, 2001.

GAM144 361 CD86 Freeman, G. J.; Gribben, J. G.; Boussiotis, V. A.; Ng, J. W.; Restivo,V. A.; 1 A c
Lombard, L. A.; Gray, G. S.; Nadler, L. M. Cloning of B7- 2:a CTLA- 4 counter- receptor that costimulates human T cell proliferation. Science 262:909- 911, 1993.

GAM144 361 CD86 Jeannin, P.; Magistrelli, G.; Aubry, J.- P.; Caron, G.; Gauchat,J.- F.; 1 A c
Renno, T.; Herbault, N.; Goetsch, L.; Blaecke, A.; Dietrich,P.- Y.; Bonnefoy, J.- Y.; Delneste, Y.: Soluble CD86 is a costimulatorymolecule for human T lymphocytes. Immunity 13: 303- 312, 2000.

GAM144 361 CD86 Jellis, C. L.; Wang, S. S.; Rennert, P.; Borriello, F.; Sharpe,A. H.; Green, 1 A c
N. R.; Gray, G. S.: Genomic organization of the genecoding for the costimulatory human B- lymphocyte antigen B7- 2 (CD86). Immunogenetics 42:85- 89, 1995.

GAM144 361 CD86 Reeves, R. H.; Patch, D.; Sharpe, A. H.; Borriello, F.; Freeman,G. J.; 1 A c
Edelhoff, S.; Disteche, C.: The costimulatory genes Cd80 andCd86 are linked on mouse chromosome 16 and human chromosome 3. MammalianGenome 8: 581- 582, 1997.

GAM144 361 CD86 Schwartz, J.- C. D.; Zhang, X.; Fedorov, A. A.; Nathenson, S. G.;Almo, S. 1 A c
C.: Structural basis for co- stimulation by the human CTLA- 4/B7- 2complex. Nature 410: 604- 608, 2001.

GAM144 361 CDH5 Bussemakers, M. J. G.; van Bokhoven, A.; Voller, M.; Smit, F. P.;Schalken, 1 A c
J. A.: The genes for the calcium- dependent cell adhesionmolecules P- and E- cadherin are tandemly arranged in the human genome. Biochem.Biophys. Res.

Commun. 203: 1291- 1294, 1994.

GAM144 361 CDH5 Carmeliet, P.; Lampugnani, M.- G.; Moons, L.; Breviario, F.; Compernolle,V.; 1 A c
Bono, F.; Balconi, G.; Spagnuolo, R.; Oosthuyse, B.; Dewerchin,M.; Zanetti,
A.; Angellilo, A.; and 11 others: Targeted deficiencyof cytosolic truncation
of the VE- cadherin gene in mice impairs VEGF- mediatedendothelial survival
and angiogenesis. Cell 98: 147- 157, 1999.

GAM144 361 CDH5 Huber, P.; Dalmon, J.; Engiles, J.; Breviario, F.; Gory, S.; Siracusa,L. D.; 1 A c
Buchberg, A. M.; Dejana, E.: Genomic structure and chromosomalmapping of the
mouse VE- cadherin gene (Cdh5). Genomics 32: 21- 28,1996.

GAM144 361 CDH5 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 1 A c
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting
cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM144 361 CDH5 Salomon, D.; Ayalon, O.; Patel- King, R.; Hynes, R. O.; Geiger,B.: 1 A c
Extrajunctional distribution of N- cadherin in cultured humanendothelial
cells. J. Cell Sci. 102: 7- 17, 1992.

GAM144 361 COL19A1 Gerecke, D. R.; Olson, P. F.; Koch, M.; Knoll, J. H. M.; Taylor,R.; Hudson, 1 A c
D. L.; Champliaud, M.- F.; Olsen, B. R.; Burgeson, R. E.: Complete primary
structure of two splice variants of collagen XII,and assignment of alpha-
1(XII) collagen (COL12A1), alpha- 1(IX) collagen(COL9A1), and alpha- 1(XIX)
collagen (COL19A1) to human chromosome6q12- q13. Genomics 41: 236- 242,
1997.

GAM144 361 COL19A1 Inoguchi, K.; Yoshioka, H.; Khaleduzzaman, M.; Ninomiya, Y.: ThemRNA for 1 A c
alpha- 1(XIX) collagen chain, a new member of FACITs, containsa long unusual
3- prime untranslated region and displays many uniquesplicing variants. J.
Biochem. 117: 137- 146, 1995.

GAM144 361 COL19A1 Khaleduzzaman, M.; Sumiyoshi, H.; Ueki, Y.; Inoguchi, K.; Ninomiya,Y.; 1 A c
Yoshioka, H.: Structure of the human type XIX collagen (COL19A1)gene, which
suggests it has arisen from an ancestor gene of the FACITfamily. Genomics
45: 304- 312, 1997.

GAM144 361 COL19A1 Myers, J. C.; Sun, M. J.; D'Ippolito, J. A.; Jabs, E. W.; Neilson,E. G.; 1 A c
Dion, A. S.: Human cDNA clones transcribed from an unusuallyhigh molecular
weight RNA encode a new collagen chain. Gene 123:211- 217, 1993.

GAM144 361 COL19A1 Yoshioka, H.; Zhang, H.; Ramirez, F.; Mattei, M.- G.; Moradi- Ameli,M.; van 1 A c
der Rest, M.; Gordon, M. K.: Synteny between the loci fora novel FACIT- like
collagen (D6S228E) and alpha 1(IX) collagen (COL9A1)on 6q12- q14 in humans.
Genomics 13: 884- 886, 1992.

GAM144 361 DCC Boman, B. M.; Wildrick, D. M.; Alfaro, S. R.: Chromosome 18 alleleloss at 1 A c
the D18S6 locus in human colorectal carcinomas. Biochem.Biophys. Res.
Commun. 155: 463- 469, 1988.

GAM144 361 DCC Chan, S. S.- Y.; Zheng, H.; Su, M.- W.; Wilk, R.; Killeen, M. T.;Hedgecock, 1 A c
E. M.; Culotti, J. G.: UNC- 40, a C. elegans homolog ofthe DCC (deleted in
colorectal cancer), is required in motile cellsresponding to UNC- 6 netrin
cues. Cell 87: 187- 195, 1996.

GAM144 361 DCC Cho, K. R.; Oliner, J. D.; Simons, J. W.; Hedrick, L.; Fearon,E. R.; 1 A c
Preisinger, A. C.; Hedge, P.; Silverman, G. A.; Vogelstein,B.: The DCC gene:
structural analysis and mutations in colorectalcarcinomas. Genomics 19: 525-
531, 1994.

GAM144 361 DCC Fazeli, A.; Dickinson, S. L.; Hermiston, M. L.; Tighe, R. V.; Steen,R. G.; 1 A c
Small, C. G.; Stoeckli, E. T.; Keino- Masu, K.; Masu, M.; Rayburn,H.;
Simons, J.; Bronson, R. T.; Gordon, J. I.; Tessier- Lavigne, M.;Weinberg, R.

A.: Phenotype of mice lacking functional Deleted incolorectal cancer (Dcc) gene. Nature 386: 796- 804, 1997.

GAM144 361 DCC Fearon, E. R.; Cho, K. R.; Nigro, J. M.; Kern, S. E.; Simons, J.W.; Ruppert, 1 A c
J. M.; Hamilton, S. R.; Preisinger, A. C.; Thomas, G.;Kinzler, K. W.;
Vogelstein, B.: Identification of a chromosome 18qgene that is altered in
colorectal cancers. Science 247: 49- 56,1990.

GAM144 361 DCC Forcet, C.; Stein, E.; Pays, L.; Corset, V.; Llambi, F.; Tessier- 1 A c
Lavigne,M.; Mehlen, P.: Netrin- 1- mediated axon outgrowth requires
deletedin colorectal cancer- dependent MAPK activation. Nature 417: 443-
447,2002.

GAM144 361 DCC Galko, M. J.; Tessier- Lavigne, M.: Function of an axonal 1 A c
chemoattractantmodulated by metalloprotease activity. Science 289: 1365-
1367, 2000.

GAM144 361 DCC Gotley, D. C.; Reeder, J. A.; Fawcett, J.; Walsh, M. D.; Bates,P.; Simmons, 1 A c
D. L.; Antalis, T. M.: The deleted in colon cancer (DCC)gene is consistently
expressed in colorectal cancers and metastases. Oncogene 13:787- 795, 1996.

GAM144 361 DCC Hohne, M. W.; Halatsch, M.- E.; Kahl, G. F.; Weinel, R. J.: Frequentloss of 1 A c
expression of the potential tumor suppressor gene DCC in ductalpancreatic
adenocarcinoma. Cancer Res. 52: 2616- 2619, 1992.

GAM144 361 DCC Jen, J.; Kim, H.; Piantadosi, S.; Liu, Z.- F.; Levitt, R. C.; Sistonen,P.; 1 A c
Kinzler, K. W.; Vogelstein, B.; Hamilton, S. R.: Allelic lossof chromosome
18q and prognosis in colorectal cancer. New Eng. J.Med. 331: 213- 221, 1994.

GAM144 361 DCC Justice, M. J.; Gilbert, D. J.; Kinzler, K. W.; Vogelstein, B.;Buchberg, A. 1 A c
M.; Ceci, J. D.; Matsuda, Y.; Chapman, V. M.; Patriotis,C.; Makris, A.;
Tsichlis, P. N.; Jenkins, N. A.; Copeland, N. G.:A molecular genetic linkage
map of mouse chromosome 18 reveals extensivelinkage conservation with human
chromosomes 5 and 18. Genomics 13:1281- 1288, 1992.

GAM144 361 DCC Keino- Masu, K.; Masu, M.; Hinck, L.; Leonardo, E. D.; Chan, S.S.- Y.; 1 A c
Culotti, J. G.; Tessier- Lavigne, M.: Deleted in colorectalcancer (DCC)
encodes a netrin receptor. Cell 87: 175- 185, 1996.

GAM144 361 DCC Keynes, R.; Cook, G. M. W.: Axon guidance molecules. Cell 83:161- 169, 1995. 1 A c

GAM144 361 DCC Kolodziej, P. A.; Timpe, L. C.; Mitchell, K. J.; Fried, S. R.;Goodman, C. 1 A c
S.; Jan, L. Y.; Jan, Y. N.: Frazzled encodes a Drosophilamember of the DCC
immunoglobulin subfamily and is required for CNSand motor axon guidance.
Cell 87: 197- 204, 1996.

GAM144 361 DCC Lynch, H. T.; Schuelke, G. S.; Kimberling, W. J.; Albano, W. A.;Lynch, J. 1 A c
F.; Biscone, K. A.; Lipkin, M. L.; Deschner, E. E.; Mikol,Y. B.; Sandberg,
A. A.; Elston, R. C.; Bailey- Wilson, J. E.; Danes,B. S.: Hereditary
nonpolyposis colorectal cancer (Lynch syndromesI and II). II. Biomarker
studies. Cancer 56: 939- 951, 1985.

GAM144 361 DCC Maesawa, C.; Tamura, G.; Ogasawara, S.; Suzuki, Y.; Sakata, K.;Sugimura, J.; 1 A c
Nishizuka, S.; Sato, N.; Ishida, K.; Saito, K.; Satodate,R.: Loss of
heterozygosity at the DCC gene locus is not crucial forthe acquisition of
metastatic potential in oesophageal squamous cellcarcinoma. Europ. J.
Cancer. 32A: 896- 898, 1996.

GAM144 361 DCC Mehlen, P.; Rabizadeh, S.; Snipas, S. J.; Assa- Munt, N.; Salvesen,G. S.; 1 A c
Bredesen, D. E.: The DCC gene produce induces apoptosis bya mechanism
requiring receptor proteolysis. Nature 395: 801- 804,1998.

GAM144 361 DCC Miyake, S.; Nagai, K.; Yoshino, K.; Oto, M.; Endo, M.; Yuasa,Y.: Point 1 A c
mutations and allelic deletion of tumor suppressor geneDCC in human

esophageal squamous cell carcinomas and their relationto metastasis. Cancer Res. 54: 3007- 3010, 1994.

GAM144 361 DCC Nigro, J. M.; Cho, K. R.; Fearon, E. R.; Kern, S. E.; Ruppert,J. M.; Oliner, J. D.; Kinzler, K. W.; Vogelstein, B.: Scrambled exons. Cell 64:607- 613, 1991. 1 A c

GAM144 361 DCC Shibata, D.; Reale, M. A.; Lavin, P.; Silverman, M.; Fearon, E.R.; Steele, G., Jr.; Jessup, J. M.; Loda, M.; Summerhayes, I. C.:The DCC protein and prognosis in colorectal cancer. New Eng. J. Med. 335:1727- 1732, 1996. 1 A c

GAM144 361 DCC Stein, E.; Tessier- Lavigne, M.: Hierarchical organization ofguidance receptors: silencing of netrin attraction by Slit througha Robo/DCC receptor complex. Science 291: 1928- 1938, 2001. 1 A c

GAM144 361 DCC Stein, E.; Zou, Y.; Poo, M.; Tessier- Lavigne, M.: Binding ofDCC by netrin- 1 to mediate axon guidance independent of adenosineA2B receptor activation. Science 291: 1976- 1982, 2001. 1 A c

GAM144 361 DCC Tanaka, K.; Oshimura, M.; Kikuchi, R.; Seki, M.; Hayashi, T.;Miyaki, M.: Suppression of tumorigenicity in human colon carcinomacells by introduction of normal chromosome 5 or 18. Nature 349:340- 342, 1991. 1 A c

GAM144 361 DCC Thiagalingam, S.; Lengauer, C.; Leach, F. S.; Schutte, M.; Hahn,S. A.; Overhauser, J.; Willson, J. K. V.; Markowitz, S.; Hamilton,S. R.; Kern, S. E.; Kinzler, K. W.; Vogelstein, B.: Evaluation ofcandidate tumour suppressor genes on chromosome 18 in colorectal cancers. NatureGenet. 13: 343- 346, 1996. 1 A c

GAM144 361 DCC Uchino, S.; Tsuda, H.; Noguchi, M.; Yokota, J.; Terada, M.; Saito,T.; Kobayashi, M.; Sugimura, T.; Hirohashi, S.: Frequent loss ofheterozygosity at the DCC locus in gastric cancer. Cancer Res. 52:3099- 3102, 1992. 1 A c

GAM144 361 DCC Vogelstein, B.: Personal Communication. Baltimore, Md. 11/30/1995. 1 A c

GAM144 361 DCC Vogelstein, B.; Fearon, E. R.; Hamilton, S. R.; Kern, S. E.; Preisinger,A. C.; Leppert, M.; Nakamura, Y.; White, R.; Smits, A. M. M.; Bos,J. L.: Genetic alterations during colorectal- tumor development. NewEng. J. Med. 319: 525- 532, 1988. 1 A c

GAM144 361 DCC Zetter, B. R.: Adhesion molecules in tumor metastasis. Semin.Cancer Biol. 4: 219- 229, 1993. 1 A c

GAM144 361 DNMT3L Aapola, U.; Shibuya, K.; Scott, H. S.; Ollila, J.; Vihinen, M.;Heino, M.; Shintani, A.; Kawasaki, K.; Minoshima, S.; Krohn, K.; Antonarakis,S. E.; Shimizu, N.; Kudoh, J.; Peterson, P.: Isolation and initialcharacterization of a novel zinc finger gene, DNMT3L, on 21q22.3,related to the cysteine- 5- methyltransferase 3 gene family. Genomics 65:293- 298, 2000. 1 A c

GAM144 361 DNMT3L Bourc'his, D.; Xu, G.- L.; Lin, C.- S.; Bollman, B.; Bestor, T. H.: Dnmt3L and the establishment of maternal genomic imprints. Science 294:2536- 2539, 2001. 1 A c

GAM144 361 EIF4EBP2 Pause, A.; Belsham, G. J.; Gingras, A.- C.; Donze, O.; Lin, T.- A.;Lawrence, J. C., Jr.; Sonenberg, N.: Insulin- dependent stimulationof protein synthesis by phosphorylation of a regulator of 5- prime- capfunction. Nature 371: 762- 767, 1994. 1 A c

GAM144 361 EIF4EBP2 Tsukiyama- Kohara, K.; Vidal, S. M.; Gingras, A.- C.; Glover, T.W.; Hanash, S. M.; Heng, H.; Sonenberg, N.: Tissue distribution,genomic structure, and chromosome mapping of mouse and human eukaryoticinitiation factor 4E- binding proteins 1 and 2. Genomics 38: 353- 363,1996. 1 A c

GAM144 361 EYA4 Borsani, G.; DeGrandi, A.; Ballabio, A.; Bulfone, A.; Bernard,L.; Banfi, S.; Gattuso, C.; Mariani, M.; Dixon, M.; Donnai, D.; Metcalfe,K.; Winter, R.; 1 A c

Robertson, M.; Axton, R.; Brown, A.; van Heyningen,V.; Hanson, I.: EYA4, a novel vertebrate gene related to Drosophilaeyes absent. Hum. Molec. Genet. 8: 11- 23, 1999.

GAM144 361 EYA4 Wayne, S.; Robertson, N. G.; DeClau, F.; Chen, N.; Verhoeven, K.;Prasad, S.; 1 A c
Tranebjarg, L.; Morton, C. C.; Ryan, A. F.; Van Camp,G.; Smith, R. J. H.: Mutations in the transcriptional activator EYA4cause late- onset deafness at the DFNA10 locus. Hum. Molec. Genet. 10:195- 200, 2001.

GAM144 361 FACL2 Cantu, E. S.; Sprinkle, T. J.; Ghosh, B.; Singh, I.: The humanpalmitoyl- CoA 1 A c
ligase (FACL2) gene maps to the chromosome 4q34- q35region by fluorescence in situ hybridization (FISH) and somatic cellhybrid panels. Genomics 28: 600- 602, 1995.

GAM144 361 FACL2 Minoshima, S.; Fukuyama, R.; Yamamoto, T.; Shimizu, N.: Mappingof human 1 A c
long- chain acyl- CoA synthetase to chromosome 4. (Abstract) Cytogenet.Cell Genet. 58: 1888 only, 1991.

GAM144 361 FGF23 ADHR Consortium: Autosomal dominant hypophosphataemic ricketsis associated 1 A c
with mutations in FGF23. Nature Genet. 26: 345- 348,2000.

GAM144 361 FGF23 Bowe, A. E.; Finnegan, R.; Jan de Beur, S. M.; Cho, J.; Levine,M. A.; Kumar, 1 A c
R.; Schiavi, S. C.: FGF- 23 inhibits renal tubular phosphatetransport and is a PHEX substrate. Biochem. Biophys. Res. Commun. 284:977- 981, 2001.

GAM144 361 FGF23 Shimada, T.; Mizutani, S.; Muto, T.; Yoneya, T.; Hino, R.; Takeda,S.; 1 A c
Takeuchi, Y.; Fujita, T.; Fukumoto, S.; Yamashita, T.: Cloningand characterization of FGF23 as a causative factor of tumor-inducedosteomalacia. Proc. Nat. Acad. Sci. 98: 6500- 6505, 2001.

GAM144 361 FGF23 Strewler, G. J.: FGF23, hypophosphatemia, and rickets: has 1 A c
phosphorylationbeen found? (Commentary) Proc. Nat. Acad. Sci. 98: 5945- 5946, 2001.

GAM144 361 FGF23 White, K. E.; Jonsson, K. B.; Carn, G.; Hampson, G.; Spector, T.D.; 1 A c
Mannstadt, M.; Lorenz- Depiereux, B.; Miyauchi, A.; Yang, I. M.;Ljunggren, O.; Meitinger, T.; Strom, T. M.; Juppner, H.; Econs, M.J.: The autosomal dominant hypophosphatemic rickets (ADHR) gene isa secreted polypeptide overexpressed by tumors that cause phosphatewasting. J. Clin. Endocr. Metab. 86: 497- 500, 2001.

GAM144 361 FGF23 Yamashita, T.; Yoshioka, M.; Itoh, N.: Identification of a novelfibroblast 1 A c
growth factor, FGF- 23, preferentially expressed in theventrolateral thalamic nucleus of the brain. Biochem. Biophys. Res.Commun. 277: 494- 498, 2000.

GAM144 361 FUT7 Bengtson, P.; Larson, C.; Lundblad, A.; Larson, G.; Pahlsson, P.: 1 A c
Identification of a missense mutation (G329A; arg110- to- gln) inthe human FUT7 gene. J. Biol. Chem. 276: 31575- 31582, 2001.

GAM144 361 FUT7 Mahdavi, J.; Sonden, B.; Hurtig, M.; Olfat, F. O.; Forsberg, L.;Roche, N.; 1 A c
Angstrom, J.; Larsson, T.; Teneberg, S.; Karlsson, K.- A.;Altraja, S.; Wadstrom, T.; and 11 others: Helicobacter pylori SabAadhesin in persistent infection and chronic inflammation. Science 297:573- 578, 2002.

GAM144 361 FUT7 Natsuka, S.; Gersten, K. M.; Zenita, K.; Kannagi, R.; Lowe, J.B.: Molecular 1 A c
cloning of a cDNA encoding a novel human leukocytealpha- 1,3-fucosyltransferase capable of synthesizing the sialyl Lewisx determinant. J. Biol. Chem. 269: 16789- 16794, 1994.

GAM144 361 FUT7 Sasaki, K.; Kurata, K.; Funayama, K.; Nagata, M.; Watanabe, E.;Ohta, S.; 1 A c
Hannai, N.; Nishi, T.: Expression cloning of a novel alpha- 1,3-

fucosyltransferasethat is involved in biosynthesis of the sialyl Lewis x carbohydratedeterminants in leukocytes. J. Biol. Chem. 269: 14730- 14737, 1994.

GAM144 361 IHPK2 Morrison, B. H.; Bauer, J. A.; Hu, J.; Grane, R. W.; Ozdemir, A.M.; Chawla- 1 A c
Sarkar, M.; Gong, B.; Almasan, A.; Kalvakolanu, D. V.;Lindner, D. J.:
Inositol hexakisphosphate kinase 2 sensitizes ovariancarcinoma cells to
multiple cancer therapeutics. Oncogene 21: 1882- 1889,2002.

GAM144 361 IHPK2 Saiardi, A.; Erdjument- Bromage, H.; Snowman, A. M.; Tempst, P.;Snyder, S. 1 A c
H.: Synthesis of diphosphoinositol pentakisphosphate bya newly identified
family of higher inositol polyphosphate kinases. Curr.Biol. 9: 1323- 1326,
1999.

GAM144 361 IHPK2 Saiardi, A.; Nagata, E.; Luo, H. R.; Snowman, A. M.; Snyder, S.H.: 1 A c
Identification and characterization of a novel inositol
hexakisphosphatekinase. J. Biol. Chem. 276: 39179- 39185, 2001.

GAM144 361 ITPKB Erneux, C.; Roeckel, N.; Takazawa, K.; Mailleux, P.; Vassart, G.;Mattei, M. 1 A c
G.: Localization of the genes for human inositol 1,4,5- trisphosphate3-
kinase A (ITPKA) and B (ITPKB) to chromosome regions 15q14- q21 and1q41-
q43, respectively, by in situ hybridization. Genomics 14:546- 547, 1992.

GAM144 361 ITPKB Takazawa, K.; Perret, J.; Dumont, J. E.; Erneux, C.: Molecularcloning and 1 A c
expression of a new putative inositol 1,4,5- trisphosphate3- kinase
isoenzyme. Biochem. J. 278: 883- 886, 1991.

GAM144 361 KCNMB4 Behrens, R.; Nolting, A.; Reimann, F.; Schwarz, M.; Waldschutz,R.; Pongs, 1 A c
O.: hKCNMB3 and hKCNMB4, cloning and characterizationof two members of the
large- conductance calcium- activated potassiumchannel beta subunit family.
FEBS Lett. 474: 99- 106, 2000.

GAM144 361 KCNMB4 Brenner, R.; Jegla, T. J.; Wickenden, A.; Liu, Y.; Aldrich, R.W.: Cloning 1 A c
and functional characterization of novel large conductancecalcium- activated
potassium channel beta subunits, hKCNMB3 and hKCNMB4. J.Biol. Chem. 275:
6453- 6461, 2000.

GAM144 361 LDB2 Agulnick, A. D.; Taira, M.; Breen, J. J.; Tanaka, T.; Dawid, I.B.; Westphal, 1 A c
H.: Interactions of the LIM- domain- binding factor Ldb1with LIM homeodomain
proteins. Nature 384: 270- 272, 1996.

GAM144 361 LDB2 Bach, I.; Carriere, C.; Ostendorff, H. P.; Andersen, B.; Rosenfield,M. G.: A 1 A c
family of LIM domain- associated cofactors confer transcriptionalsynergism
between LIM and Otx homeodomain proteins. Genes Dev. 11:1370- 1380, 1997.

GAM144 361 LDB2 Jurata, L. W.; Gill, G. N.: Functional analysis of the nuclearLIM domain 1 A c
interactor NL1. Molec. Cell. Biol. 17: 5688- 5698, 1997.

GAM144 361 LDB2 Jurata, L. W.; Kenny, D. A.; Gill, G. N.: Nuclear LIM interactor,a rhombotin 1 A c
and LIM homeodomain interacting protein, is expressedearly in neuronal
development. Proc. Nat. Acad. Sci. 93: 11693- 11698,1996.

GAM144 361 LDB2 Semina, E. V.; Altherr, M. R.; Murray, J. C.: Cloning and 1 A c
chromosomallocalization of two novel human genes encoding LIM- domain
bindingfactors CLIM1 and CLIM2/LDB1/NL1. Mammalian Genome 9: 921- 924, 1998.

GAM144 361 LDB2 Yamashita, T.; Agulnick, A. D.; Copeland, N. G.; Gilbert, D. J.;Jenkins, N. 1 A c
A.; Westphal, H.: Genomic structure and chromosomal localizationof the mouse
LIM domain- binding protein 1 gene, Ldb1. Genomics 48:87- 92, 1998.

GAM144 361 LOXL1 Goy, A.; Gilles, F.; Remache, Y.; Zelenetz, A. D.: Physical linkageof the 1 A c
lysyl oxidase- like (LOXL1) gene to the PML gene on human chromosome15q22.
Cytogenet. Cell Genet. 88: 22- 24, 2000.

GAM144 361 LOXL1 Kenyon, K.; Modi, W. S.; Contente, S.; Friedman, R. M.: A novelhuman cDNA 1 A c

with a predicted protein similar to lysyl oxidase mapsto chromosome 15q24-
q25. J. Biol. Chem. 268: 18435- 18437, 1993.

GAM144 361 LOXL1 Kim, Y.; Boyd, C. D.; Csiszar, K.: A new gene with sequence andstructural 1 A c
similarity to the gene encoding human lysyl oxidase. J.Biol. Chem. 270:
7176- 7182, 1995.

GAM144 361 LOXL1 Wydner, K. S.; Kim, Y.; Csiszar, K.; Boyd, C. D.; Passmore, H.C.: An intron 1 A c
capture strategy used to identify and map a lysyl oxidase- likegene on
chromosome 9 in the mouse. Genomics 40: 342- 345, 1997.

GAM144 361 NFE2L1 Chan, J. Y.; Cheung, M.- C.; Moi, P.; Chan, K.; Kan, Y. W.: 1 A c
Chromosomallocalization of the human NF- E2 family of bZIP transcription
factorsby fluorescence in situ hybridization. Hum. Genet. 95: 265- 269,1995.

GAM144 361 NFE2L1 Chan, J. Y.; Han, X.- L.; Kan, Y. W.: Cloning of Nrf1, an NF- E2- 1 A c
relatedtranscription factor, by genetic selection in yeast. Proc. Nat.
Acad.Sci. 90: 11371- 11375, 1993.

GAM144 361 NFE2L1 Chan, J. Y.; Kwong, M.; Lu, R.; Chang, J.; Wang, B.; Yen, T. S.B.; Kan, Y. 1 A c
W.: Targeted disruption of the ubiquitous CNC- bZIP transcriptionfactor,
Nrf- 1, results in anemia and embryonic lethality in mice. EMBOJ. 17: 1779-
1787, 1998.

GAM144 361 NFE2L1 Luna, L.; Johnsen, O.; Skartlien, A. H.; Pedeutour, F.; Turc- Carel,C.; 1 A c
Prydz, H.; Kolsto, A.- B.: Molecular cloning of a putative novelhuman bZIP
transcription factor on chromosome 17q22. Genomics 22:553- 562, 1994.

GAM144 361 NFE2L1 Luna, L.; Johnsen, O.; Skartlien, A.; Pedeutour, F.; Turc- Carel,C.; Prydz, 1 A c
H.; Kolsto, A.- B.: Molecular cloning of a putative novelhuman bZIP
transcription factor on chromosome 17q22. Genomics 22:553- 562, 1994.

GAM144 361 NFE2L1 McKie, J.; Johnstone, K.; Mattei, M.- G.; Scambler, P.: Cloningand mapping 1 A c
of murine Nfe2l1. Genomics 25: 716- 719, 1995.

GAM144 361 NFE2L1 McKie, J.; Scambler, P. J.: The Nfe2l1 gene maps to distal mousechromosome 1 A c
11. Mammalian Genome 7: 89- 90, 1996.

GAM144 361 NTSR1 Laurent, P.; Clerc, P.; Mattei, M.- G.; Forgez, P.; Dumont, X.;Ferrara, P.; 1 A c
Caput, D.; Rostene, W.: Chromosomal localization ofmouse and human
neurotensin receptor genes. Mammalian Genome 5:303- 306, 1994.

GAM144 361 NTSR1 Le, F.; Groshan, K.; Zeng, X. P.; Richelson, E.: Characterizationof the 1 A c
genomic structure, promoter region, and a tetranucleotide repeatpolymorphism
of the human neurotensin receptor gene. J. Biol. Chem. 272:1315- 1322, 1997.

GAM144 361 NTSR1 Vincent, J.- P.: Neurotensin receptors: binding properties, 1 A c
transductionpathways, and structure. Cell. Molec. Neurobiol. 15: 501- 512,
1995.

GAM144 361 NTSR1 Vita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Dumont, X.; Kaghad,M.; Gully, 1 A c
D.; Le Fur, G.; Ferrara, P.; Caput, D.: Cloning and expressionof a
complementary DNA encoding a high affinity human neurotensinreceptor. FEBS
Lett. 317: 139- 142, 1993.

GAM144 361 OXTR Inoue, T.; Kimura, T.; Azuma, C.; Inazawa, J.; Takemura, M.; Kikuchi,T.; 1 A c
Kubota, Y.; Ogita, K.; Saji, F.: Structural organization of thehuman
oxytocin receptor gene. J. Biol. Chem. 269: 32451- 32456, 1994.

GAM144 361 OXTR Kimura, T.; Tanizawa, O.; Mori, K.; Brownstein, M. J.; Okayama,H.: Structure 1 A c
and expression of a human oxytocin receptor. Nature 356:526- 529, 1992.

GAM144 361 OXTR Simmons, C. F., Jr.; Clancy, T. E.; Quan, R.; Knoll, J. H. M.:The oxytocin 1 A c
receptor gene (OXTR) localizes to human chromosome 3p25by fluorescence in
situ hybridization and PCR analysis of somaticcell hybrids. Genomics 26:
623- 625, 1995.

GAM144 361 OXTR Yang, M.; Wang, W.; Zhong, M.; Philippi, A.; Lichtarge, O.; Sanborn,B. M.: 1 A c
Lysine 270 in the third intracellular domain of the oxytocinreceptor is an important determinant for G- alpha- q coupling specificity. Molec.Endocr. 16: 814- 823, 2002.

GAM144 361 PCTP Cohen, D. E.; Green, R. M.; Wu, M. K.; Beier, D. R.: Cloning,tissue- 1 A c
specific expression, gene structure and chromosomal localizationof human phosphatidylcholine transfer protein. Biochim. Biophys.Acta 1447: 265- 270, 1999.

GAM144 361 PCTP van Helvoort, A.; de Brouwer, A.; Ottenhoff, R.; Brouwers, J. F.H. M.; 1 A c
Wijnholds, J.; Beijnen, J. H.; Rijneveld, A.; van der Valk,M. A.; Majoor, D.; Voorhout, W.; Wirtz, K. W. A.; Elferink, R. P.J. O.; Borst, P.: Mice without phosphatidylcholine transfer proteinhave no defects in the secretion of phosphatidylcholine into bileor into lung airspaces. Proc. Nat. Acad. Sci. 96: 11501- 11506, 1999.

GAM144 361 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 1 A c
Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 2002.

GAM144 361 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 1 A c
cell coactivator of octamer- binding transcription factors. Nature 373:360- 362, 1995.

GAM144 361 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 1 A c
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell- specific coactivator of octamer- binding transcription factors1 and 2, to 11q23.1 by somatic cell hybridization and in situ hybridization. Genomics 33:143- 145, 1996.

GAM144 361 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 1 A c
of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995.

GAM144 361 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 1 A c
Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM144 361 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 1 A c
Immun. 9: 373- 398, 1991.

GAM144 361 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 1 A c
specificcoactivator that stimulates immunoglobulin promoter activity throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM144 361 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 1 A c
Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B, BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853- 864, 2000.

GAM144 361 RORB Andre, E.; Conquet, F.; Steinmayr, M.; Stratton, S. C.; Porciatti,V.; 1 A c
Becker- Andre, M.: Disruption of retinoid- related orphan receptorbeta changes circadian behavior, causes retinal degeneration and leadsto vacillans phenotype in mice. EMBO J. 17: 3867- 3877, 1998.

GAM144 361 RORB Carlberg, C.; Hooft van Huijsduijnen, R.; Staple, J. K.; DeLamarter,J. F.; 1 A c
Becker- Andre, M.: RZRs, a new family of retinoid- related orphanreceptors that function as both monomers and homodimers. Molec. Endocr. 8:757- 770, 1994.

GAM144 361 RORB Evans, R. M.: The steroid and thyroid hormone receptor superfamily. Science 1 A c

240:889- 895, 1988.

GAM144 361 RORB Paravicini, G.; Steinmayr, M.; Andre, E.; Becker- Andre, M.: Themetastasis 1 A c
suppressor candidate nucleotide diphosphate kinase NM23specifically
interacts with members of the ROR/RZR nuclear orphanreceptor subfamily.
Biochem. Biophys. Res. Commun. 227: 82- 87, 1996.

GAM144 361 RORB Sirlin, J. L.: Vacillans, a neurological mutant in the house mouselinked 1 A c
with brown. J. Genet. 54: 42- 48, 1956.

GAM144 361 RORB Ueda, H. R.; Chen, W.; Adachi, A.; Wakamatsu, H.; Hayashi, S.;Takasugi, T.; 1 A c
Nagano, M.; Nakahama, K.; Suzuki, Y.; Sugano, S.; Iino,M.; Shigeyoshi, Y.;
Hashimoto, S.: A transcription factor responseelement for gene expression
during circadian night. Nature 418:534- 539, 2002.

GAM144 361 RPS15 Inoue, C.; Shiga, K.; Takasawa, S.; Kitagawa, M.; Yamamoto, H.;Okamoto, H.: 1 A c
Evolutionary conservation of the insulinoma gene rigand its possible
function. Proc. Nat. Acad. Sci. 84: 6659- 6662,1987.

GAM144 361 RPS15 Kenmochi, N.; Kawaguchi, T.; Rozen, S.; Davis, E.; Goodman, N.;Hudson, T. 1 A c
J.; Tanaka, T.; Page, D. C.: A map of 75 human ribosomalprotein genes.
Genome Res. 8: 509- 523, 1998.

GAM144 361 RPS15 Kitagawa, M.; Takasawa, S.; Kikuchi, N.; Itoh, T.; Teraoka, H.;Yamamoto, H.; 1 A c
Okamoto, H.: Rig encodes ribosomal protein S15: theprimary structure of
mammalian ribosomal protein S15. FEBS Lett. 283:210- 214, 1991.

GAM144 361 RPS15 Shiga, K.; Yamamoto, H.; Okamoto, H.: Isolation and characterizationof the 1 A c
human homologue of rig and its pseudogenes: the functionalgene has features
characteristic of housekeeping genes. Proc. Nat.Acad. Sci. 87: 3594- 3598,
1990.

GAM144 361 SCD Cohen, P.; Miyazaki, M.; Socci, N. D.; Hagge- Greenberg, A. Liedtke,W.; 1 A c
Soukas, A. A.; Sharma, R.; Hudgins, L. C.; Ntambi, J. M.; Friedman,J. M.:
Role for stearoyl- CoA desaturase- 1 in leptin- mediated weightloss. Science
297: 240- 243, 2002.

GAM144 361 SCD Li, J.; Ding, S.- F.; Habib, N. A.; Fermor, B. F.; Wood, C. B.;Gilmour, R. 1 A c
S.: Partial characterization of a cDNA for human stearoyl- CoAdesaturase and
changes in its mRNA expression in some normal and malignanttissues. Int. J.
Cancer 57: 348- 352, 1994.

GAM144 361 SCD Ntambi, J. M.; Miyazaki, M.; Stoehr, J. P.; Lan, H.; Kendziorski,C. M.; 1 A c
Yandell, B. S.; Song, Y.; Cohen, P.; Friedman, J. M.; Attie,A. D.: Loss of
stearoyl- CoA desaturase- 1 function protects mice againstadiposity. Proc.
Nat. Acad. Sci. 99: 11482- 11486, 2002.

GAM144 361 SCD Thiede, M. A.; Ozols, J.; Strittmatter, P.: Construction and sequenceof cDNA 1 A c
for rat liver stearyl coenzyme A desaturase. J. Biol. Chem. 261:13230-
13235, 1986.

GAM144 361 SCD Zhang, L.; Ge, L.; Parimoo, S.; Stenn, K.; Prouty, S. M.: Humanstearoyl- CoA 1 A c
desaturase: alternative transcripts generated from asingle gene by usage of
tandem polyadenylation sites. Biochem. J. 340:255- 264, 1999.

GAM144 361 SCD Zheng, Y.; Eilertsen, K. J.; Ge, L.; Zhang, L.; Sundberg, J. P.;Prouty, S. 1 A c
M.; Stenn, K. S.; Parimoo, S.: Scd1 is expressed in sebaceousglands and is
disrupted in the asebia mouse. (Letter) Nature Genet. 23:268- 270, 1999.

GAM144 361 SIT Hubener, C.; Mincheva, A.; Lichter, P.; Schraven, B.; Bruyns, E.: Complete 1 A c
sequence, genomic organization, and chromosomal localizationof the human
gene encoding the SHP2- interacting transmembrane adaptorprotein (SIT).
Immunogenetics 53: 337- 341, 2001.

GAM144 361 SIT Marie- Cardine, A.; Kirchgessner, H.; Bruyns, E.; Shevchenko, A.;Mann, M.; 1 A c

Autschbach, F.; Ratnofsky, S.; Meuer, S.; Schraven, B.:SHP2- interacting transmembrane adaptor protein (SIT), a novel disulfide- linkeddimer regulating human T cell activation. J. Exp. Med. 189: 1181- 1194,1999.

GAM144 361 SLC12A7 Boettger, T.; Hubner, C. A.; Maler, H.; Rust, M. B.; Beck, F. X.;Jentsch, T. 1 A c
J.: Deafness and renal tubular acidosis in mice lackingthe K- Cl co-transporter Kcc4. Nature 416: 874- 878, 2002.

GAM144 361 SLC12A7 Mount, D. B.; Mercado, A.; Song, L.; Xu, J.; George, A. L., Jr.;Delpire, E.; 1 A c
Gamba, G.: Cloning and characterization of KCC3 andKCC4, new members of the cation- chloride cotransporter gene family. J.Biol. Chem. 274: 16355- 16362, 1999.

GAM144 361 SLC7A5 Gaugitsch, H. W.; Prieschl, E. E.; Kalthoff, F.; Huber, N. E.;Baumruker, T.: 1 A c
A novel transiently expressed, integral membrane proteinlinked to cell activation: molecular cloning via the rapid degradationsignal AUUUA. J. Biol. Chem 267: 11267- 11273, 1992.

GAM144 361 SLC7A5 Kanai, Y.; Segawa, H.; Miyamoto, K.; Uchino, H.; Takeda, H.; Endou,H.: 1 A c
Expression cloning and characterization of a transporter forlarge neutral amino acids activated by the heavy chain of 4F2 antigen(CD98). J. Biol. Chem. 273: 23629- 23632, 1998.

GAM144 361 SLC7A5 Maglott, D. R.; Durkin, A. S.; Lane, S. A.; Callen, D. F.; Feldblyum,T. V.; 1 A c
Nierman, W. C.: The gene for membrane protein E16 (D16S469E)maps to human chromosome 16q24.3 and is expressed in human brain,thymus, and retina. Genomics 23: 303- 304, 1994.

GAM144 361 SLC7A5 Mastroberardino, L.; Spindler, B.; Pfeiffer, R.; Skelly, P. J.;Loffing, J.; 1 A c
Shoemaker, C. B.; Verrey, F.: Amino- acid transport byheterodimers of 4F2hc/CD98 and members of a permease family. Nature 395:288- 291, 1998.

GAM144 361 SMT3H1 Lapenta, V.; Chiurazzi, P.; van der Spek, P.; Pizzuti, A.; Hanaoka,F.; 1 A c
Brahe, C.: SMT3A, a human homologue of the S. cerevisiae SMT3gene, maps to chromosome 21qter and defines a novel gene family. Genomics 40:362- 366, 1997.

GAM144 361 SMT3H1 Meluh, P. B.; Koshland, D.: Evidence that the MIF2 gene of 1 A c
Saccharomycescerevisiae encodes a centromere protein with homology to the mammaliancentromere protein CENP- C. Molec. Biol. Cell 6: 793- 807, 1995.

GAM144 361 SMT3H1 Meluh, P. B.; Koshland, D.: Suppressors of MIF2, a putative 1 A c
centromereprotein gene in Saccharomyces cerevisiae. (Abstract) Molec. Biol.Cell 6 (supp.): 360a only, 1995.

GAM144 361 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; 1 A c
De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8: 165- 167, 1990.

GAM144 361 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 1 A c
homeoprotein family are expressed in human liver. NucleicAcids Res. 19: 3553- 3559, 1991.

GAM144 361 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't 1 A c
Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.; Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene are associated with familial hypoplastic glomerulocystickidney disease. Am. J. Hum. Genet. 68: 219- 224, 2001.

GAM144 361 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; 1 A c
Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.; Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated

with a frameshift mutation in the transcription factorhepatocyte nuclear factor- 1- beta. Kidney Int. 57: 898- 907, 2000.

GAM144 361 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara, T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997. 1 A c

GAM144 361 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic glomerulocystic kidney disease: a definite entity withdominant inheritance. Am. J. Med. Genet. 34: 569- 573, 1989. 1 A c

GAM144 361 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand genital malformation associated with a partial deletion of thepseudo- POU domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001- 2008, 1999. 1 A c

GAM144 361 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, S.: A low renal threshold for glucose in diabetic patientswith a mutation in the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med. 15: 816- 820, 1998. 1 A c

GAM144 361 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in the hepatocyte nuclear factor- 1- beta gene associated with diabetesand renal dysfunction. Diabetes 47: 1354- 1355, 1998. 1 A c

GAM144 361 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18: 263- 268, 1982. 1 A c

GAM144 361 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott-Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G. U.: The mutated human gene encoding hepatocyte nuclear factor1- beta inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad. Sci. 97: 4695- 4700, 2000. 1 A c

GAM144 361 TM4SF6 Maeda, K.; Matsuhashi, S.; Hori, K.; Xin, Z.; Mukai, T.; Tabuchi,K.; Egashira, M.; Niikawa, N.: Cloning and characterization of anovel human gene, TM4SF6, encoding a protein belonging to the transmembrane4 superfamily, and mapped to Xq22. Genomics 52: 240- 242, 1998. 1 A c

GAM144 361 TM4SF6 Todd, S. C.; Doctor, V. S.; Levy, S.: Sequences and expressionof six new members of the tetraspanin/TM4SF family. Biochim. Biophys.Acta 1399: 101- 104, 1998. 1 A c

GAM144 361 TRIM14 Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 1 A c

GAM144 361 TRIM14 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci, S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell compartments. EMBO J. 20: 2140- 2151, 2001. 1 A c

GAM144 361 UMPK Cook, P. J. L.; Hamerton, J. L.: Report of the committee on thegenetic constitution of chromosome 1. Cytogenet. Cell Genet. 25:9- 20, 1979. 1 A c

GAM144 361 UMPK Gallango, M. L.; Muller, A.; Suinaga, R.: Biochemical characterizationof a red cell UMP kinase variant found in the Warao Indians of Venezuela. Biochem.Genet. 16: 1085- 1093, 1978. 1 A c

GAM144 361 UMPK Gallango, M. L.; Suinaga, R.: Uridine monophosphate kinase polymorphismin two Venezuelan populations. Am. J. Hum. Genet. 30: 215- 218, 1978. 1 A c

GAM144 361 UMPK Giblett, E. R.; Anderson, J. E.; Chen, S.- H.; Teng, Y.- S.; Cohen,F.: Uridine monophosphate kinase: a new genetic polymorphism withpossible clinical implications. Am. J. Hum. Genet. 26: 627- 635,1974. 1 A c

GAM144 361 UMPK Giblett, E. R.; Anderson, J. E.; Lewis, M.; Kaita, H.: A new polymorphicenzyme, uridine monophosphate kinase: gene frequencies and a linkageanalysis. Birth Defects Orig. Art. Ser. 11(3): 159- 161, 1975. Note:Alternate: Cytogenet. Cell Genet. 14: 329- 331, 1975. 1 A c

GAM144 361 UMPK Goss, S. J.; Harris, H.: Gene transfer by means of cell fusion.II. The mapping of 8 loci on human chromosome 1 by statistical analysisof gene assortment in somatic cell hybrids. J. Cell Sci. 25: 39- 57,1977. 1 A c

GAM144 361 UMPK Medrano, L.; Green, H.: A uridine kinase deficient mutant of 3T3and a selective method for cells containing the enzyme. Cell 1:23- 26, 1974. 1 A c

GAM144 361 UMPK Petersen, G. M.; Silimperi, D. R.; Scott, E. M.; Hall, D. B.; Rotter,J. I.; Ward, J. I.: Uridine monophosphate kinase 3: a genetic markerfor susceptibility to Haemophilus influenzae type B disease. Lancet II:417- 418, 1985. 1 A c

GAM144 361 UMPK Ranzani, G.; Bertolotti, E.; Santachiara- Benerecetti, A. S.: Thepolymorphism of the red cell uridine monophosphate kinase in two samplesof the Italian population. Hum. Hered. 27: 332- 335, 1977. 1 A c

GAM144 361 UMPK Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 1 A c

GAM144 361 UMPK Ruddle, F. H.; Creagan, R. P.: Parasexual approaches to the geneticsof man. Ann. Rev. Genet. 9: 407- 486, 1975. 1 A c

GAM144 361 UMPK Satlin, A.; Kucherlapati, R. S.; Ruddle, F. H.: Assignment ofthe gene for human uridine monophosphate kinase to chromosome 1 usingsomatic cell hybrid clone panels. Cytogenet. Cell Genet. 15: 146- 152,1975. 1 A c

GAM144 361 USP14 Deshpande, K. L.; Seubert, P. H.; Tillman, D. M.; Farkas, W. R.;Katze, J. R.: Cloning and characterization of cDNA encoding the rabbittRNA- guanine transglycosylase 60- kilodalton subunit. Arch. Biochem.Biophys. 326: 1- 7, 1996. 1 A c

GAM144 361 USP14 Wilson, S. M.; Bhattacharyya, B.; Rachel, R. A.; Coppola, V.; Tessarollo,L.; Householder, D. B.; Fletcher, C. F.; Miller, R. J.; Copeland,N. G.; Jenkins, N. A.: Synaptic defects in ataxia mice result froma mutation in Usp14, encoding a ubiquitin- specific protease. NatureGenet. 7Oct, 2002. Note: Advance Electronic Publication. 1 A c

GAM144 361 WFDC1 Larsen, M.; Ressler, S. J.; Gerdes, M. J.; Lu, B.; Byron, M.; Lawrence,J. B.; Rowley, D. R.: The WFDC1 gene encoding ps20 localizes to 16q24,a region of LOH in multiple cancers. Mammalian Genome 11: 767- 773,2000. 1 A c

GAM144 361 WFDC1 Larsen, M.; Ressler, S. J.; Lu, B.; Gerdes, M. J.; McBride, L.;Dang, T. D.; Rowley, D. R.: Molecular cloning and expression of ps20growth inhibitor: a novel WAP- type 'four- disulfide core' domain proteinexpressed in smooth muscle. J. Biol. Chem. 273: 4574- 4584, 1998. 1 A c

GAM144 361 WFDC1 Rowley, D. R.: Characterization of a fetal urogenital sinus mesenchymalcell line U4F: secretion of a negative growth factor regulatory activity. InVitro Cell. Dev. Biol. 28A: 29- 38, 1992. 1 A c

GAM144 361 WFDC1 Rowley, D. R.; Dang, T. D.; Larsen, M.; Gerdes, M. J.; McBride,L.; Lu, B.: Purification of a novel protein (ps20) from urogenitalsinus mesenchymal cells with growth inhibitory properties in vitro. J.Biol. Chem. 270: 22058- 1 A c

22065, 1995.

GAM144 361 WFDC1 Rowley, D. R.; Tindall, D. J.: Responses of NBT- II bladder carcinomacells 1 A c
to conditioned medium from normal fetal urogenital sinus. CancerRes. 47:
2955- 2960, 1987.

GAM144 361 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 1 A c
family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with
XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000.

GAM144 361 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of 1 A c
DNA double- strand breaks by homologous recombination. Nature 401:397- 399,
1999.

GAM144 361 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- 1 A c
ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286,
1987.

GAM144 361 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the 1 A c
XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis.
Genomics 26: 619- 622, 1995.

GAM144 361 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, 1 A c
T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and
filament structure formation activities of thehuman Xrcc2- Rad51D complex.
J. Biol. Chem. 277: 14315- 14320, 2002.

GAM144 361 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in 1 A c
two distinct protein complexes of Rad51 paralogs in humancells. Nucleic
Acids Res. 30: 1009- 1015, 2002.

GAM144 361 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; 1 A c
McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand
purification of two distinct complexes containing the five RAD51paralogs.
Genes Dev. 15: 3296- 3307, 2001.

GAM144 361 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; 1 A c
Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional
candidate. Genomics 41: 84- 92, 1997.

GAM144 361 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: 1 A c
Localization to chromosome 7q36.1 of the human XRCC2 gene,determining
sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995.

GAM145 335 GPRK7 Chen, C.- K.; Zhang, K.; Church- Kopish, J.; Huang, W.; Zhang, H.;Chen, Y.- 3 C c
J.; Frederick, J. M.; Baehr, W.: Characterization of humanGRK7 as a
potential cone opsin kinase. Molec. Vision 7: 305- 313,2001.

GAM145 335 GPRK7 Haribabu, B.; Snyderman, R.: Identification of additional membersof human G- 3 C c
protein- coupled receptor kinase multigene family. Proc.Nat. Acad. Sci. 90:
9398- 9402, 1993.

GAM145 335 GPRK7 Slentz- Kesler, K.; Moore, J. T.; Lombard, M.; Zhang, J.; Hollingsworth,R.; 3 C c
Weiner, M. P.: Identification of the human Mnk2 gene (MKNK2)through protein
interaction with estrogen receptor beta. Genomics 69:63- 71, 2000.

GAM145 335 GPRK7 Waskiewicz, A. J.; Flynn, A.; Proud, C. G.; Cooper, J. A.: Mitogen- 3 C c
activatedprotein kinases activate the serine/threonine kinases Mnk1 and
Mnk2. EMBOJ. 16: 1909- 1920, 1997.

GAM145 335 GPRK7 Weiss, E. R.; Ducceschi, M. H.; Horner, T. J.; Li, A.; Craft, C.M.; Osawa, 3 C c
S.: Species- specific differences in expression of G- protein-
coupledreceptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor
cells:implications for cone cell phototransduction. J. Neurosci. 21: 9175-
9184,2001.

GAM145 335 RAB31 Chen, D.; Guo, J.; Miki, T.; Tachibana, M.; Gahl, W. A.: Molecularcloning of two novel rab genes from human melanocytes. Gene 174:129- 134, 1996. 3 C c

GAM145 335 RAB31 Scott, A. F.: Personal Communication. Baltimore, Md. 2/26/2001. 3 C c

GAM145 335 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 C c

GAM145 335 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 C c

GAM145 335 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 C c

GAM145 335 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 C c

GAM145 335 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 C c

GAM146 370 ASIC4 Grunder, S.; Geisler, H.- S.; Rainer, S.; Fink, J. K.: Acid- sensingion channel (ASIC) 4 gene: physical mapping, genomic organisation,and evaluation as a candidate for paroxysmal dystonia. Europ. J.Hum. Genet. 9: 672- 676, 2001. 3 C b

GAM146 370 ASIC4 Grunder, S.; Geissler, H.- S.; Bassler, E.- L.; Ruppersberg, J. P.: A new member of acid- sensing ion channels from pituitary gland. Neuroreport 11:1607- 1611, 2000. 3 C b

GAM146 370 BACE Cai, H.; Wang, Y.; McCarthy, D.; Wen, H.; Borchelt, D. R.; Price,D. L.; Wong, P. C.: BACE1 is the major beta- secretase for generationof A- beta peptides by neurons. Nature Neurosci. 4: 233- 234, 2001. 3 C c

GAM146 370 BACE De Strooper, B.; Konig, G.: A firm base for drug development. Nature 402:471- 472, 1999. 3 C c

GAM146 370 BACE Fan, W.; Bennett, B. D.; Babu- Khan, S.; Luo, Y.; Louis, J.- C.;McCaleb, M.; Citron, M.; Vassar, R.; Richards, W. G.: Response toSaunders et al. (1999). Science 286: 1255a, 1999. Note: ElectronicPublication. 3 C c

GAM146 370 BACE Haniu, M.; Denis, P.; Young, Y.; Mendiaz, E. A.; Fuller, J.; Hui,J. O.; Bennett, B. D.; Kahn, S.; Ross, S.; Burgess, T.; Katta, V.;Rogers, G.; Vassar, R.; Citron, M.: Characterization of Alzheimer'sbeta- secretase protein BACE: a pepsin family member with unusual properties. J.Biol. Chem. 275: 21099- 21106, 2000. 3 C c

GAM146 370 BACE Hong, L.; Koelsch, G.; Lin, X.; Wu, S.; Terzyan, S.; Ghosh, A.K.; Zhang, X. C.; Tang, J.: Structure of the protease domain of memapsin2 (beta-secretase) complexed with inhibitor. Science 290: 150- 153,2000. 3 C c

GAM146 370 BACE Hussain, I.; Powell, D.; Howlett, D. R.; Tew, D. G.; Meek, T. D.;Chapman, C.; Gloger, I. S.; Murphy, K. E.; Southan, C. D.; Ryan, D.M.; Smith, T. S.; Simmons, D. L.; Walsh, F. S.; Dingwall, C.; Christie,G.: Identification of a novel aspartic protease (asp2) as beta- secretase Molec.Cell Neurosci. 14: 419- 427, 1999. 3 C c

GAM146 370 BACE Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643- 648, 2001. 3 C c

GAM146 370 BACE Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.- H.; Goldstein, L. S.: Axonal transport of amyloid precursor protein is mediated by directbinding to the kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000. 3 C c

GAM146 370 BACE Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis,P.; Fan, W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.;Yan, Q.; Richards, W. G.; Citron, M.; Vassar, R.: Mice deficientin BACE1, the Alzheimer's beta- secretase, have normal phenotype andabolished beta- amyloid generation. Nature Neurosci. 4: 231- 232,2001. 3 C c

GAM146 370 BACE Nicolaou, M.; Song, Y.- Q.; Sato, C. A.; Orlacchio, A.; Kawarai,T.; Medeiros, H.; Liang, Y.; Sorbi, S.; Richard, E.; Rogaev, E. I.;Moliaka, Y.; Bruni, A. C.; Jorge, R.; Percy, M.; Duara, R.; Farrer,L. A.; St George- Hyslop, P.; Rogaeva, E. A.: Mutations in the openreading frame of the beta- site APP cleaving enzyme (BACE) locus arenot a common cause of Alzheimer's disease. Neurogenetics 3: 203- 206,2001. 3 C c

GAM146 370 BACE Roberds, S. L.; Anderson, J.; Basi, G.; Bienkowski, M. J.; Branstetter,D. G.; Chen, K. S.; Freedman, S. B.; Frigon, N. L.; Games, D.; Hu,K.; Johnson- Wood, K.; Kappenman, K. E.; and 20 others: BACE knockoutmice are healthy despite lacking the primary beta- secretase activityin brain: implications for Alzheimer's disease therapeutics. Hum.Molec. Genet. 10: 1317- 1324, 2001. 3 C c

GAM146 370 BACE Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a BACE homolog, BACE2, reside in the obligate Down syndromeregion of chromosome 21. Science 286: 1255a, 1999. Note: ElectronicPublication. 3 C c

GAM146 370 BACE Sinha, S.; Anderson, J. P.; Barbour, R.; Basi, G. S.; Caccavello,R.; Davis, D.; Doan, M.; Dovey, H. F.; Frigon, N.; Hong, J.; Jacobson- Croak,K.; Jewett, N.; and 15 others: Purification and cloning of amyloidprecursor protein beta- secretase from human brain. Nature 402: 537- 540,1999. 3 C c

GAM146 370 BACE Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz,E. A.; Dents, P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff,R.; Luo, Y.; Fisher, S.; and 12 others: Beta- secretase cleavageof Alzheimer's amyloid precursor protein by the transmembrane asparticprotease BACE. Science 286: 735- 741, 1999. 3 C c

GAM146 370 BACE Yan, R.; Bienkowski, M. J.; Shuck, M. E.; Miao, H.; Tory, M. C.;Pauley, A. M.; Brashler, J. R.; Stratman, N. C.; Mathews, W. R.; Buhl,A. E.; Carter, D. B.; Tomasselli, A. G.; Parodi, L. A.; Heinrikson,R. L.; Gurney, M. E.: Membrane- anchored aspartyl protease with Alzheimer'sdisease beta- secretase activity. Nature 402: 533- 536, 1999. 3 C c

GAM146 370 BDP1 Kelter, A.- R.; Herchenbach, J.; Wirth, B.: The transcription factor- likenuclear regulator (TFNR) contains a novel 55- amino- acid motif repeatednine times and maps closely to SMN1. Genomics 70: 315- 326, 2000. 3 C c

GAM146 370 BDP1 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 C c

TFIIB activities direct RNA polymerase III transcription fromTATA-containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM146 370 BSN Gundelfinger, E.: Personal Communication. Madgeburg, FRG. 1/8/1999. 3 C c

GAM146 370 BSN Hashida, H.; Goto, J.; Zhao, N.; Takahashi, N.; Hirai, M.; Kanazawa,I.; Sakaki, Y.: Cloning and mapping of ZNF231, a novel brain- specificgene encoding neuronal double zinc finger protein whose expressionis enhanced in a neurodegenerative disorder, multiple system atrophy(MSA). Genomics 54: 50-58, 1998. 3 C c

GAM146 370 BSN Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VIII. 78 new cDNAclones from brain which code for large proteins in vitro. DNA Res. 4:307- 313, 1997. 3 C c

GAM146 370 BSN tom Dieck, S.; Sanmarti- Vila, L.; Langnaese, K.; Richter, K.; Kindler,S.; Soyke, A.; Wex, H.; Smalla, K.- H.; Kampf, U.; Franzer, J.- T.;Stumm, M.; Garner, C. C.; Gundelfinger, E. D.: Bassoon, a novel zinc-fingerCAG/glutamine- repeat protein selectively localized at the active zoneof presynaptic nerve terminals. J. Cell Biol. 142: 499- 509, 1998. 3 C c

GAM146 370 BSN Winter, c.; tom Dieck, S.; Boeckers, T. M.; Bockmann, J.; Kampf,U.; Sanmarti- Vila, L.; Langnaese, K.; Altrock, W.; Stumm, M.; Soyke,A.; Wieacker, P.; Garner, C. C.; Gundelfinger, E. D.: The presynapticcytomatrix protein Bassoon: sequence and chromosomal localizationof the human BSN gene. Genomics 57: 389- 397, 1999. 3 C c

GAM146 370 CSF1R Benz- Lemoine, E.; Brizard, A.; Huret, J.- L.; Babin, P.; Guilhot,F.; Couet, D.; Tanzer, J.: Malignant histiocytosis: a specific t(2;5)(p23;q35)translocation? Review of the literature. Blood 72: 1045-1047, 1988. 3 C c

GAM146 370 CSF1R Boultwood, J.; Rack, K.; Kelly, S.; Madden, J.; Sakaguchi, A. Y.;Wang, L.- M.; Oscier, D. G.; Buckle, V. J.; Wainscoat, J. S.: Lossof both CSF1R (FMS) alleles in patients with myelodysplasia and achromosome 5 deletion. Proc. Nat. Acad. Sci. 88: 6176- 6180, 1991. 3 C c

GAM146 370 CSF1R De Qi Xu; Guilhot, S.; Galibert, F.: Restriction fragment lengthpolymorphism of the human c- fms gene. Proc. Nat. Acad. Sci. 82:2862- 2865, 1985. 3 C c

GAM146 370 CSF1R Eccles, M. R.: Genes encoding the platelet- derived growth factor(PDGF) receptor and colony- stimulating factor 1 (CSF- 1) receptor arephysically associated in mice as in humans. Gene 108: 285- 288, 1991. 3 C c

GAM146 370 CSF1R Gisselbrecht, S.; Fichelson, S.; Sola, B.; Bordereaux, D.; Hampe,A.; Andre, C.; Galibert, F.; Tambourin, P. E.: Frequent c- fms activationby proviral insertion in mouse myeloblastic leukaemias. Nature 329:259- 261, 1987. 3 C c

GAM146 370 CSF1R Groffen, J.; Heisterkamp, N.; Spurr, N. K.; Dana, S. L.; Wasmuth,J. J.; Stephenson, J. R.: Regional assignment of the human c- fmsoncogene to band q34 of chromosome 5. (Abstract) Cytogenet. CellGenet. 37: 484 only, 1984. 3 C c

GAM146 370 CSF1R Hampe, A.; Gobet, M.; Sherr, C. J.; Galibert, F.: Nucleotide sequenceof the feline retroviral oncogene v- fms shows unexpected homologywith oncogenes encoding tyrosine- specific protein kinases. Proc.Nat. Acad. Sci. 81: 85-89, 1984. 3 C c

GAM146 370 CSF1R Hampe, A.; Shamoon, B.- M.; Gobet, M.; Sherr, C. J.; Galibert, F.: Nucleotide sequence and structural organization of the human FMSproto-oncogene. Oncogene Res. 4: 9- 17, 1989. 3 C c

GAM146 370 CSF1R How, G.- F.; Venkatesh, B.; Brenner, S.: Conserved linkage betweenthe puffer fish (Fugu rubripes) and human genes for platelet- derivedgrowth factor 3 C c

receptor and macrophage colony- stimulating factor receptor. GenomeRes. 6: 1185- 1191, 1996.

GAM146 370 CSF1R Kondo, M.; Scherer, D. C.; Miyamoto, T.; King, A. G.; Akashi,K.; Sugamura, 3 C c
K.; Weissman, I. L.: Cell- fate conversion of lymphoid- committedprogenitors by instructive actions of cytokines. Nature 407: 383- 386,2000.

GAM146 370 CSF1R Le Beau, M. M.; Westbrook, C. A.; Diaz, M. O.; Larson, R. A.;Rowley, J. D.; 3 C c
Gasson, J. C.; Golde, D. W.; Sherr, C. J.: Evidencefor the involvement of GM- CSF and FMS in the deletion (5q) in myeloiddisorders. Science 231: 984- 987, 1986.

GAM146 370 CSF1R Morgan, R.; Hecht, B. K.; Sandberg, A. A.; Hecht, F.; Smith, S.D.: 3 C c
Chromosome 5q35 breakpoint in malignant histiocytosis. (Letter) NewEng. J. Med. 314: 1322 only, 1986.

GAM146 370 CSF1R Ridge, S. A.; Worwood, M.; Oscier, D.; Jacobs, A.; Padua, R. A.: FMS 3 C c
mutations in myelodysplastic, leukemic, and normal subjects. Proc.Nat. Acad. Sci. 87: 1377- 1380, 1990.

GAM146 370 CSF1R Roberts, W. M.; Look, A. T.; Roussel, M. F.; Sherr, C. J.: Tandemlinkage of 3 C c
human CSF- 1 receptor (c- fms) and PDGF receptor genes. Cell 55:655- 661, 1988.

GAM146 370 CSF1R Sapi, E.; Flick, M. B.; Kacinski, B. M.: The first intron ofhuman c- fms 3 C c
proto- oncogene contains a processed pseudogene (RPL7P)for ribosomal protein L7. Genomics 22: 641- 645, 1994.

GAM146 370 CSF1R Verbeek, J. S.; Roebroek, A. J. M.; van den Ouweland, A. M. W.;Bloemers, H. 3 C c
P. J.; Van de Ven, W. J. M.: Human c- fms proto- oncogene:comparative analysis with an abnormal allele. Molec. Cell. Biol. 5:422- 426, 1985.

GAM146 370 CSF1R Verbeek, J. S.; van Heerikhuizen, H.; de Pauw, B. E.; Haanen,C.; Bloemers, 3 C c
H. P. J.; Van de Ven, W. J. M.: A hereditary abnormalc- fms proto- oncogene in a patient with acute lymphocytic leukaemiaand congenital hypothyroidism. Brit. J. Haemat. 61: 135- 138, 1985.

GAM146 370 CSF1R Yarden, Y.; Ullrich, A.: Growth factor receptor tyrosine kinases. Ann.Rev. 3 C c
Biochem. 57: 443- 478, 1988.

GAM146 370 FBXW1B Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; 3 C c
Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol. 9: 1177- 1179, 1999.

GAM146 370 FBXW1B Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM146 370 FBXW1B Koike, J.; Sagara, N.; Kirikoshi, H.; Takagi, A.; Miwa, T.; Hirai,M.; Katoh, 3 C c
M.: Molecular cloning and genomic structure of the beta- TRCP2gene on chromosome 5q35.1. Biochem. Biophys. Res. Commun. 269: 103- 109,2000.

GAM146 370 FBXW1B Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A 3 C c
family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999.

GAM146 370 FMO2 Dolphin, C. T.; Beckett, D. J.; Janmohamed, A.; Cullingford, T.E.; Smith, R. 3 C c
L.; Shephard, E. A.; Phillips, I. R.: The flavin- containingmonooxygenase 2 gene (FMO2) of humans, but not of other primates,encodes a truncated, nonfunctional protein. J. Biol. Chem. 273:30599- 30607, 1998.

GAM146 370 FMO2 McCombie, R. R.; Dolphin, C. T.; Povey, S.; Phillips, I. R.; Shephard,E. A.: 3 C c
Localization of human flavin- containing monooxygenase genesFMO2 and FMO5 to chromosome 1q. Genomics 34: 426- 429, 1996.

GAM146 370 FMO2 Williams, D. E.; Kelly, J.; Dutchuk, M.: Flavin- containing monooxygenasein 3 C c

pulmonary microsomes of primates. In: Ingelman- Sundberg, M.; Gustafsson,J.-A.; Orrenius, S. (eds.): Drug Metabolizing Enzymes: Genetics,Regulation and Toxicology: Proceedings of the 8th International Symposiumon Microsomes and Drug Oxidations. Stockholm: Karolinska Institutet1990. P. 173.

GAM146 370 HDAC6 Grozinger, C. M.; Hassig, C. A.; Schreiber, S. L.: Three proteinsdefine a class of human histone deacetylases related to yeast Hda1p. Proc.Nat. Acad. Sci. 96: 4868- 4873, 1999. 3 C c

GAM146 370 HDAC6 Hubbert, C.; Guardiola, A.; Shao, R.; Kawaguchi, Y.; Ito, A.; Nixon,A.; Yoshida, M.; Wang, X.- F.; Yao, T.- P.: HDAC6 is a microtubule-associateddeacetylase. Nature 417: 455- 458, 2002. 3 C c

GAM146 370 HDAC6 Mahlknecht, U.; Schnittger, S.; Landgraf, F.; Schoch, C.; Ottmann,O. G.; Hiddemann, W.; Hoelzer, D.: Assignment of the human histonedeacetylase 6 gene (HDAC6) to X chromosome p11.23 by in situ hybridization. Cytogenet.Cell Genet. 93: 135- 136, 2001. 3 C c

GAM146 370 HDAC6 Nagase, T.; Isikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5: 355- 364, 1998. 3 C c

GAM146 370 IGFBP1 Alitalo, T.; Koistinen, R.; Aalto- Setala, K.; Kontula, K.; Julkunen,M.; Janne, O.; de la Chapelle, A.: Gene for the human insulin- likegrowth factor- binding protein/placental protein 12: mapping to 7p12- p13and demonstration of a BglII RFLP. (Abstract) Cytogenet. Cell Genet. 51:950 only, 1989. 3 C c

GAM146 370 IGFBP1 Alitalo, T.; Kontula, K.; Koistinen, R.; Aalto- Setala, K.; Julkunen,M.; Janne, O. A.; Seppala, M.; de la Chapelle, A.: The gene encodinghuman low-molecular weight insulin- like growth- factor binding protein(IGF- BP25): regional localization to 7p12- p13 and description of aDNA polymorphism. Hum. Genet. 83: 335- 338, 1989. 3 C c

GAM146 370 IGFBP1 Ballard, F. J.; Baxter, R. C.; Binoux, M.; Clemmons, D. R.; Drop,S. L. S.; Hall, K.; Hintz, R. L.; Rechler, M. M.; Rutanen, E. M.;Schwander, J. C.: Report on the nomenclature of the IGF binding proteins. J.Clin. Endocr. Metab. 70: 817- 818, 1990. 3 C c

GAM146 370 IGFBP1 Brewer, M. T.; Stetler, G. L.; Squires, C. H.; Thompson, R. C.;Busby, W. H.; Clemmons, D. R.: Cloning, characterization, and expressionof a human insulin- like growth factor binding protein. Biochem. Biophys.Res. Commun. 152: 1289- 1297, 1988. 3 C c

GAM146 370 IGFBP1 Brinkman, A.; Groffen, C. A. H.; Kortleve, D. J.; Drop, S. L. S.: Organization of the gene encoding the insulin- like growth factorbinding protein IBP- 1. Biochem. Biophys. Res. Commun. 157: 898- 907,1988. 3 C c

GAM146 370 IGFBP1 Brinkman, A.; Groffen, C.; Kortleve, D. J.; Geurts van Kessel,A.; Drop, S. L. S.: Isolation and characterization of a cDNA encodingthe low molecular weight insulin- like growth factor binding protein(IBP- 1). EMBO J. 7: 2417-2423, 1988. 3 C c

GAM146 370 IGFBP1 Ekstrand, J.; Ehrenborg, E.; Stern, I.; Stellan, B.; Zech, L.;Luthman, H.: The gene for insulin- like growth factor binding protein- 1is localized to human chromosomal region 7p14- p12. Genomics 6: 413- 418,1990. 3 C c

GAM146 370 IGFBP1 Popovici, R. M.; Lu, M.; Bhatia, S.; Faessen, G. H.; Giaccia, A.J.; Giudice, L. C.: Hypoxia regulates insulin- like growth factor- bindingprotein 1 in human fetal hepatocytes in primary culture: suggestivemolecular mechanisms 3 C c

for in utero fetal growth restriction causedby uteroplacental insufficiency. J. Clin. Endocr. Metab. 86: 2653- 2659,2001.

GAM146 370 PLAG1 Astrom, A.- K.; Voz, M. L.; Kas, K.; Roijer, E.; Wedell, B.; Mandahl,N.; Van 3 C c
de Ven, W.; Mark, J.; Stenman, G.: Conserved mechanism ofPLAG1 activation in salivary gland tumors with and without chromosome8q12 abnormalities: identification of SII as a new fusion partnergene. Cancer Res. 59: 918- 923, 1999.

GAM146 370 PLAG1 Kas, K.; Roijer, E.; Voz, M.; Meyen, E.; Stenman, G.; Van de Ven,W. J. M.: A 3 C c
2- Mb YAC contig and physical map covering the chromosome8q12 breakpoint cluster region in pleomorphic adenomas of the salivaryglands. Genomics 43: 349- 358, 1997.

GAM146 370 PLAG1 Kas, K.; Voz, M. L.; Roijer, E.; Astrom, A.- K.; Meyen, E.; Stenman,G.; Van 3 C c
de Ven, W. J. M.: Promoter swapping between the genes fora novel zinc finger protein and beta- catenin in pleiomorphic adenomaswith t(3;8)(p21;q12) translocations. Nature Genet. 15: 170- 174,1997.

GAM146 370 RGS3 Chatterjee, T. K.; Eapen, A.; Kanis, A. B.; Fisher, R. A.: 3 C c
Genomicorganization, 5- prime- flanking region, and chromosomal localizationof the human RGS3 gene. Genomics 45: 429- 433, 1997.

GAM146 370 RGS3 Druey, K. M.; Blumer, K. J.; Kang, V. H.; Kehrl, J. H.: Inhibitionof G- 3 C c
protein- mediated MAP kinase activation by a new mammalian genefamily. Nature 379: 742- 746, 1996.

GAM146 370 RGS3 Lu, Q.; Sun, E. E.; Klein, R. S.; Flanagan, J. G.: Ephrin- B 3 C c
reversesignaling is mediated by a novel PDZ- RGS protein and selectively inhibitsG protein- coupled chemoattraction. Cell 105: 69- 79, 2001.

GAM146 370 RXRA Almasan, A.; Mangelsdorf, D. J.; Ong, E. S.; Wahl, G. M.; Evans,R. M.: 3 C c
Chromosomal localization of the human retinoid X receptors. Genomics 20:397- 403, 1994.

GAM146 370 RXRA Claudel, T.; Leibowitz, M. D.; Fievet, C.; Tailleux, A.; Wagner,B.; Repa, J. 3 C c
J.; Torpier, G.; Lobaccaro, J.- M.; Paterniti, J. R.;Mangelsdorf, D. J.; Heyman, R. A.; Auwerx, J.: Reduction of atherosclerosisin apolipoprotein E knockout mice by activation of the retinoid Xreceptor. Proc. Nat. Acad. Sci. 98: 2610- 2615, 2001.

GAM146 370 RXRA de Urquiza, A. M.; Liu, S.; Sjoberg, M.; Zetterstrom, R. H.; Griffiths,W.; 3 C c
Sjovall, J.; Perlmann, T.: Docosahexaenoic acid, a ligand forthe retinoid X receptor in mouse brain. Science 290: 2140- 2144,2000.

GAM146 370 RXRA Dyson, E.; Sucov, H. M.; Kubalak, S. W.; Schmid- Schonbein, G. W.;DeLano, F. 3 C c
A.; Evans, R. M.; Ross, J., Jr.; Chien, K. R.: Atrial- likephenotype is associated with embryonic ventricular failure in retinoidX receptor alpha - /- mice. Proc. Nat. Acad. Sci. 92: 7386- 7390,1995.

GAM146 370 RXRA Gampe, R. T., Jr.; Montana, V. G.; Lambert, M. H.; Miller, A. B.;Bledsoe, R. 3 C c
K.; Milburn, M. V.; Kliewer, S. A.; Willson, T. M.; Xu,H. E.: Asymmetry in the PPAR- gamma/RXR- alpha crystal structure revealsthe molecular basis of heterodimerization among nuclear receptors. Molec.Cell 5: 545- 555, 2000.

GAM146 370 RXRA Germain, P.; Iyer, J.; Zechel, C.; Gronemeyer, H.: Co- regulatorrecruitment 3 C c
and the mechanism of retinoic acid receptor synergy. Nature 415:187- 192, 2002.

GAM146 370 RXRA Gruber, P. J.; Kubalak, S. W.; Pexieder, T.; Sucov, H. M.; Evans,R. M.; 3 C c
Chien, K. R.: RXR- alpha deficiency confers genetic susceptibilityfor aortic sac, conotruncal, atrioventricular cushion, and ventricularmuscle defects in mice. J. Clin. Invest. 98: 1332- 1343, 1996.

GAM146 370 RXRA Heyman, R. A.; Mangelsdorf, D. J.; Dyck, J. A.; Stein, R. B.; Eichele,G.; 3 C c
Evans, R. M.; Thaller, C.: 9- cis retinoic acid is a high affinityligand for
the retinoid X receptor. Cell 68: 397- 406, 1992.

GAM146 370 RXRA Hoopes, C. W.; Taketo, M.; Ozato, K.; Liu, Q.; Howard, T. A.; Linney,E.; 3 C c
Seldin, M. F.: Mapping the mouse Rxr loci encoding nuclear retinoidX
receptors Rxr- alpha, Rxr- beta, and Rxr- gamma. Genomics 14: 611- 617,1992.

GAM146 370 RXRA Jones, K. A.; Fitzgibbon, J.; Woodward, K. J.; Goudie, D.; Ferguson- 3 C c
Smith,M. A.; Povey, S.; Wolfe, J.; Solomon, E.: Localization of the
retinoidX receptor alpha gene (RXRA) to chromosome 9q34. Ann. Hum. Genet.
57:195- 201, 1993.

GAM146 370 RXRA Li, M.; Indra, A. K.; Warot, X.; Brocard, J.; Messaddeq, N.; Kato,S.; 3 C c
Metzger, D.; Chambon, P.: Skin abnormalities generated by
temporallycontrolled RXR- alpha mutations in mouse epidermis. Nature 407:
633- 636,2000.

GAM146 370 RXRA Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, 3 C c
J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid
synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000.

GAM146 370 RXRA Mangelsdorf, D. J.; Ong, E. S.; Dyck, J. A.; Evans, R. M.: Nuclearreceptor 3 C c
that identifies a novel retinoic acid response pathway. Nature 345:224- 229,
1990.

GAM146 370 RXRA Mangelsdorf, D. J.; Umesono, K.; Kliewer, S. A.; Borgmeyer, U.;Ong, E. S.; 3 C c
Evans, R. M.: A direct repeat in the cellular retinol- bindingprotein type
II gene confers differential regulation by RXR and RAR. Cell 66:555- 561,
1991.

GAM146 370 RXRA McNamara, P.; Seo, S.; Rudic, R. D.; Sehgal, A.; Chakravarti,D.; FitzGerald, 3 C c
G. A.: Regulation of CLOCK and MOP4 by nuclear hormonereceptors in the
vasculature: a humoral mechanism to reset a peripheralclock. Cell 105: 877-
889, 2001.

GAM146 370 RXRA Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, 3 C c
K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation
of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers.
Science 289: 1524- 1529, 2000.

GAM146 370 RXRA Tontonoz, P.; Hu, E.; Spiegelman, B. M.: Stimulation of adipogenesisin 3 C c
fibroblasts by PPAR- gamma- 2, a lipid- activated transcription factor. Cell
79:1147- 1156, 1994.

GAM146 370 RXRA Wan, Y.- J. Y.; An, D.; Cai, Y.; Repa, J. J.; Chen, T. H.- P.; Flores,M.; 3 C c
Postic, C.; Magnuson, M. A.; Chen, J.; Chien, K. R.; French, S.;Mangelsdorf,
D. J.; Sucov, H. M.: Hepatocyte- specific mutation establishesretinoid X
receptor alpha as a heterodimeric integrator of multiplephysiological
processes in the liver. Molec. Cell. Biol. 20: 4436- 4444,2000.

GAM146 370 RXRA Willy, P. J.; Umesono, K.; Ong, E. S.; Evans, R. M.; Heyman, R.A.; 3 C c
Mangelsdorf, D. J.: LXR, a nuclear receptor that defines a distinctretinoid
response pathway. Genes Dev. 9: 1033- 1045, 1995.

GAM146 370 RXRA Zhong, S.; Delva, L.; Rachez, C.; Cenciarelli, C.; Gandini, D.;Zhang, H.; 3 C c
Kalantry, S.; Freedman, L. P.; Pandolfi, P. P.: A RA- dependent,tumour-
growth suppressive transcription complex is the target of thePML- RAR- alpha
and T18 oncoproteins. Nature Genet. 23: 287- 295, 1999.

GAM146 370 RXRA Zhou, M. D.; Sucov, H. M.; Evans, R. M.; Chien, K. R.: Retinoid- 3 C c
dependentpathways suppress myocardial cell hypertrophy. Proc. Nat. Acad.
Sci. 92:7391- 7395, 1995.

GAM146 370 SLC39A4 Kury, S.; Dreno, B.; Bezieau, S.; Giraudet, S.; Kharfi, M.; Kamoun,R.; Moisan, J.- P.: Identification of SLC39A4, a gene involved inacrodermatitis enteropathica. Nature Genet. 31: 239- 240, 2002. 3 C c

GAM146 370 SLC39A4 Rogers, E. E.; Eide, D. J.; Guerinot, M. L.: Altered selectivityin an Arabidopsis metal transporter. Proc. Nat. Acad. Sci. 97: 12356- 12360,2000. 3 C c

GAM146 370 SLC39A4 Wang, K.; Pugh, E. W.; Griffen, S.; Doheny, K. F.; Mostafa, W.Z.; al-Aboosi, M. M.; el- Shanti, H.; Gitschier, J.: Homozygositymapping places the acrodermatitis enteropathica gene on chromosomalregion 8q24.3. Am. J. Hum. Genet. 68: 1055- 1060, 2001. 3 C c

GAM146 370 SLC39A4 Wang, K.; Zhou, B.; Kuo, Y.- M.; Zemansky, J.; Gitschier, J.: Anovel member of a zinc transporter family is defective in acrodermatitisenteropathica. Am. J. Hum. Genet. 71: 66- 73, 2002. 3 C c

GAM146 370 SMCX Agulnik, A. I.; Mitchell, M. J.; Lerner, J. L.; Woods, D. R.; Bishop,C. E.: A mouse Y chromosome gene encoded by a region essential forspermatogenesis and expression of male- specific minor histocompatibilityantigens. Hum. Molec. Genet. 3: 873- 878, 1994. 3 C c

GAM146 370 SMCX Agulnik, A. I.; Mitchell, M. J.; Mattei, M.- G.; Borsani, G.; Avner,P. A.; Lerner, J. L.; Bishop, C. E.: A novel X gene with a widelytranscribed Y-linked homologue escapes X- inactivation in mouse andhuman. Hum. Molec. Genet. 3: 879- 884, 1994. 3 C c

GAM146 370 SMCX Brown, C. J.; Miller, A. P.; Carrel, L.; Rupert, J. L.; Davies,K. E.; Willard, H. F.: The DXS423E gene in Xp11.21 escapes X chromosomeinactivation. Hum. Molec. Genet. 4: 251- 255, 1995. 3 C c

GAM146 370 SMCX Lingenfelter, P. A.; Adler, D. A.; Poslinski, D.; Thomas, S.; Elliott,R. W.; Chapman, V. M.; Disteche, C. M.: Escape from X inactivationof Smcx is preceded by silencing during mouse development. NatureGenet. 18: 212- 213, 1998. 3 C c

GAM146 370 SMCX Wu, J.; Ellison, J.; Salido, E.; Yen, P.; Mohandas, T.; Shapiro,L. J.: Isolation and characterization of XE169, a novel human genethat escapes X-inactivation. Hum. Molec. Genet. 3: 153- 160, 1994. 3 C c

GAM146 370 SMCX Wu, J.; Salido, E. C.; Yen, P. H.; Mohandas, T. K.; Heng, H. H.Q.; Tsui, L.- C.; Park, J.; Chapman, V. M.; Shapiro, L. J.: The murineXe169 gene escapes X- inactivation like its human homologue. NatureGenet. 7: 491- 496, 1994. 3 C c

GAM146 370 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 C c

GAM146 370 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 C c

GAM146 370 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 C c

GAM146 370 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn 3 C c

syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998.

GAM146 370 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 C c

GAM148 280 ADORA1 Allegrucci, C.; Liguori, L.; Mezzasoma, I.; Minelli, A.: A1 adenosinereceptor in human spermatozoa: its role in the fertilization process. Molec.Genet. Metab. 71: 381- 386, 2000. 3 B c

GAM148 280 ADORA1 Berne, R. M.: Cardiac nucleotides in hypoxia: possible role inregulation of coronary blood flow. Am. J. Physiol. 204: 317- 322,1963. 3 B c

GAM148 280 ADORA1 Drury, A. N.; Szent- Gyorgyi, A.: The physiological activity ofadenine compounds with especial reference to their action upon themammalian heart. J. Physiol. 68: 213- 237, 1929. 3 B c

GAM148 280 ADORA1 Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. 3 B c

GAM148 280 ADORA1 Stiles, G. L.: Adenosine receptors. J. Biol. Chem. 267: 6451- 6454,1992. 3 B c

GAM148 280 ADORA1 Sun, D.; Samuelson, L. C.; Yang, T.; Huang, Y.; Paliege, A.; Saunders,T.; Briggs, J.; Schnermann, J.: Mediation of tubuloglomerular feedbackby adenosine: evidence from mice lacking adenosine 1 receptors. Proc.Nat. Acad. Sci. 98: 9983- 9988, 2001. 3 B c

GAM148 280 ADORA1 Townsend- Nicholson, A.; Baker, E.; Schofield, P. R.; Sutherland,G. R.: Localization of the adenosine A1 receptor subtype gene (ADORA1)to chromosome 1q32.1. Genomics 26: 423- 425, 1995. 3 B c

GAM148 280 AOC3 Bono, P.; Salmi, M.; Smith, D. J.; Leppanen, I.; Horelli- Kuitunen,N.; Palotie, A.; Jalkanen, S.: Isolation, structural characterization,and chromosomal mapping of the mouse vascular adhesion protein- 1 geneand promoter. J. Immun. 161: 2953- 2960, 1998. 3 B c

GAM148 280 AOC3 Morris, N. J.; Ducret, A.; Aebersold, R.; Ross, S. A.; Keller,S. R.; Lienhard, G. E.: Membrane amine oxidase cloning and identificationas a major protein in the adipocyte plasma membrane. J. Biol. Chem. 272:9388- 9392, 1997. 3 B c

GAM148 280 AOC3 Smith, D. J.; Salmi, M.; Bono, P.; Hellman, J.; Leu, T.; Jalkanen,S.: Cloning of vascular adhesion protein 1 reveals a novel multifunctionaladhesion molecule. J. Exp. Med. 188: 17- 27, 1998. 3 B c

GAM148 280 AOC3 Zhang, X.; McIntire, W. S.: Cloning and sequencing of a copper- containing,topa quinone- containing monoamine oxidase from human placenta. Gene 179:279- 286, 1996. 3 B c

GAM148 280 APBA1 Blanco, G.; Irving, N. G.; Brown, S. D. M.; Miller, C. C. J.; McLoughlin,D. M.: Mapping of the human and murine X11- like genes (APBA2 andApba2), the murine Fe65 gene (Apbb1), and the human Fe65- like gene(APBB2): genes encoding phosphotyrosine- binding domain proteins thatinteract with the Alzheimer's disease amyloid precursor protein. MammalianGenome 9: 473- 475, 1998. 3 B c

GAM148 280 APBA1 Butz, S.; Okamoto, M.; Sudhof, T. C.: A tripartite protein complexwith the potential to couple synaptic vesicle exocytosis to cell adhesionin brain. Cell 94: 773- 782, 1998. 3 B c

GAM148 280 APBA1 Chen, W.- J.; Goldstein, J. L.; Brown, M. S.: NPXY, a sequenceoften found in 3 B c

cytoplasmic tails, is required for coated pit- mediatedinternalization of the low density lipoprotein receptor. J. Biol.Chem. 265: 3116- 3123, 1990.

GAM148 280 APBA1 Duclos, F.; Boschert, U.; Sirugo, G.; Mandel, J.- L.; Hen, R.; Koenig,M.: 3 B c
Gene in the region of the Friedreich ataxia locus encodes a putativetransmembrane protein expressed in the nervous system. Proc. Nat.Acad. Sci. 90: 109- 113, 1993.

GAM148 280 APBA1 Duclos, F.; Koenig, M.: Comparison of primary structure of a neuron- 3 B c
specificprotein, X11, between human and mouse. Mammalian Genome 6: 57- 58,1995.

GAM148 280 APBA1 Fujita, R.; Hanauer, A.; Vincent, A.; Mandel, J.- L.; Koenig, M.: Physical 3 B c
mapping of two loci (D9S5 and D9S15) tightly linked toFriedreich ataxia locus (FRDA) and identification of nearby CpG islandsby pulse- field gel electrophoresis. Genomics 10: 915- 920, 1991.

GAM148 280 APBA1 Okamoto, M.; Sudhof, T. C.: Mints, Munc18- interacting proteinsin synaptic 3 B c
vesicle exocytosis. J. Biol. Chem. 272: 31459- 31464,1997.

GAM148 280 APBA1 Rodius, F.; Duclos, F.; Wrogemann, K.; Le Paslier, D.; Ougen, P.;Billault, 3 B c
A.; Belal, S.; Musenger, C.; Brice, A.; Durr, A.; Mignard,C.; Sirugo, G.; Weissenbach, J.; Cohen, D.; Hentati, F.; Ben Hamida,M.; Mandel, J.- L.; Koenig, M.: Recombinations in individuals homozygousby descent localize the Friedreich ataxia locus in a cloned 450- kbinterval. Am. J. Hum. Genet. 54: 1050- 1059, 1994.

GAM148 280 APBA1 Setou, M.; Nakagawa, T.; Seog, D.- H.; Hirokawa, N.: Kinesin 3 B c
superfamilymotor protein KIF17 and mLin- 10 in NMDA receptor- containing vesicletransport. Science 288: 1796- 1802, 2000.

GAM148 280 APBA1 van der Geer, P.; Pawson, T.: The PTB domain: a new protein moduleimplicated 3 B c
in signal transduction. Trends Biochem. Sci. 20: 277- 280,1995.

GAM148 280 CDH16 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene 3 B c
cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999.

GAM148 280 CDH16 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; 3 B c
Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck, P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with a protein related to the cadherin superfamily. Science 264:430- 433, 1994.

GAM148 280 CDH16 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 3 B c
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM148 280 CDH16 Thomson, R. B.; Igarashi, P.; Biemesderfer, D.; Kim, R.; Abu- Alfa,A.; 3 B c
Soleimani, M.; Aronson, P. S.: Isolation and cDNA cloning ofKsp- cadherin, a novel kidney- specific member of the cadherin multigenefamily. J. Biol. Chem. 270: 17594- 17601, 1995.

GAM148 280 CDH16 Thomson, R. B.; Ward, D. C.; Quaggin, S. E.; Igarashi, P.; Muckler,Z. E.; 3 B c
Aronson, P. S.: cDNA cloning and chromosomal localizationof the human and mouse isoforms of Ksp- cadherin. Genomics 51: 445- 451,1998.

GAM148 280 CNTF Barbin, G.; Manthorpe, M.; Varon, S.: Purification of the chickeye ciliary 3 B c
neuronotrophic factor. J. Neurochem. 43: 1468- 1478,1984.

GAM148 280 CNTF DeChiara, T. M.; Vejsada, R.; Poueymirou, W. T.; Acheson, A.; Suri,C.; 3 B c
Conover, J. C. Friedman, B.; McClain, J.; Pan, L.; Stahl, N.;Ip, N. Y.; Kato, A.; Yancopoulos, G. D.: Mice lacking the CNTF receptor,unlike mice lacking CNTF, exhibit profound motor neuron deficits atbirth. Cell 83: 313- 322, 1995.

GAM148 280 CNTF Emerich, D. F.; Winn, S. R.; Hantraye, P. M.; Peschanski, M.; Chen,E.- Y.; 3 B c
Chu, Y.; McDermott, P.; Baetge, E. E.; Kordower, J. H.: Protectiveeffect of
encapsulated cells producing neurotrophic factor CNTF ina monkey model of
Huntington's disease. Nature 386: 395- 399, 1997.

GAM148 280 CNTF Gelernter, J.; Van Dyck, C.; van Kammen, D. P.; Malison, R.; Price,L. H.; 3 B c
Cubells, J. F.; Berman, R.; Charney, D. S.; Heninger, G.:Ciliary
neurotrophic factor null allele frequencies in schizophrenia,affective
disorders, and Alzheimer's disease. Am. J. Med. Genet. 74:497- 500, 1997.

GAM148 280 CNTF Giess, R.; Holtmann, B.; Braga, M.; Grimm, T.; Muller- Myhsok, B.;Toyka, K. 3 B c
V.; Sendtner, M.: Early onset of severe familial amyotrophiclateral
sclerosis with a SOD- 1 mutation: potential impact of CNTFas a candidate
modifier gene. Am. J. Hum. Genet. 70: 1277- 1286,2002.

GAM148 280 CNTF Giess, R.; Maurer, M.; Linker, R.; Gold, R.; Warmuth- Metz, M.;Toyka, K. V.; 3 B c
Sendtner, M.; Rieckmann, P.: Association of a nullmutation in the CNTF gene
with early onset of multiple sclerosis. Arch.Neurol. 59: 407- 409, 2002.

GAM148 280 CNTF Giovannini, M.; Romo, A. J.; Evans, G. A.: Chromosomal localizationof the 3 B c
human ciliary neurotrophic factor gene (CNTF) to 11q12 by fluorescencein
situ hybridization. Cytogenet. Cell Genet. 63: 62- 63, 1993.

GAM148 280 CNTF Gloaguen, I.; Costa, P.; Demartis, A.; Lazzaro, D.; Di Marco, A.;Graziani, 3 B c
R.; Paonessa, G.; Chen, F.; Rosenblum, C. I.; Van der Ploeg,L. H. T.;
Cortese, R.; Ciliberto, G.; Laufer, R.: Ciliary neurotrophicfactor corrects
obesity and diabetes associated with leptin deficiencyand resistance. Proc.
Nat. Acad. Sci. 94: 6456- 6461, 1997.

GAM148 280 CNTF Kaupmann, K.; Sendtner, M.; Stockli, K. A.; Jockusch, H.: Thegene for 3 B c
ciliary neurotrophic factor (CNTF) maps to murine chromosome19 and its
expression is not affected in the hereditary motoneurondisease 'Wobbler' of
the mouse. Europ. J. Neurosci. 3: 1182- 1186,1991.

GAM148 280 CNTF Lam, A.; Fuller, F.; Miller, J.; Kloss, J.; Manthorpe, M.; Varon,S.; 3 B c
Cordell, B.: Sequence and structural organization of the humangene encoding
ciliary neurotrophic factor. Gene 102: 271- 276, 1991.

GAM148 280 CNTF Lambert, P. D.; Anderson, K. D.; Sleeman, M. W.; Wong, V.; Tan,J.; 3 B c
Hijarunguru, A.; Corcoran, T. L.; Murray, J. D.; Thabet, K. E.;Yancopoulos,
G. D.; Wiegand, S. J.: Ciliary neurotrophic factor activatesleptin- like
pathways and reduces body fat, without cachexia or reboundweight gain, even
in leptin- resistant obesity. Proc. Nat. Acad. Sci. 98:4652- 4657, 2001.

GAM148 280 CNTF Lev, A. A.; Rosen, D. R.; Kos, C.; Clifford, E.; Landes, G.; Hauser,S. L.; 3 B c
Brown, R. H., Jr.: Human ciliary neurotrophic factor: localizationto the
proximal region of the long arm of chromosome 11 and associationwith CA/GT
dinucleotide repeat. Genomics 16: 539- 541, 1993.

GAM148 280 CNTF Lichter, P.; Tang, C. C.- J.; Call, K.; Hermanson, G.; Evans, G.A.; Housman, 3 B c
D.; Ward, D. C.: High- resolution mapping of human chromosome11 by in situ
hybridization with cosmid clones. Science 247: 64- 69,1990.

GAM148 280 CNTF Masu, Y.; Wolf, E.; Holtmann, B.; Sendtner, M.; Brem, G.; Thoenen,H.: 3 B c
Disruption of the CNTF gene results in motor neuron degeneration. Nature
365:27- 32, 1993.

GAM148 280 CNTF Sendtner, M.; Schmalbruch, H.; Stockli, K. A.; Carroll, P.; Kreutzberg,G. 3 B c
W.; Thoenen, H.: Ciliary neurotrophic factor prevents degenerationof motor
neurons in mouse mutant progressive motor neuronopathy. Nature 358:502- 504,
1992.

GAM148 280 CNTF Takahashi, R.; Yokoji, H.; Misawa, H.; Hayashi, M.; Hu, J.; Deguchi,T.: A 3 B c

null mutation in the human CNTF gene is not causally relatedto neurological diseases. Nature Genet. 7: 79- 84, 1994.

GAM148 280 CNTF Yokoji, H.; Ariyama, T.; Takahashi, R.; Inazawa, J.; Misawa, H.;Deguchi, T.: 3 B c cDNA cloning and chromosomal localization of the humanciliary neurotrophic factor gene. Neurosci. Lett. 185: 175- 178,1995.

GAM148 280 CNTN3 Connelly, M. A.; Grady, R. C.; Mushinski, J. F.; Marcu, K. B.:PANG, a gene 3 B c encoding a neuronal glycoprotein, is ectopically activatedby intracisternal A- type particle long terminal repeats in murineplasmacytomas. Proc. Nat. Acad. Sci. 91: 1337- 1341, 1994.

GAM148 280 CNTN3 Mock, B. A.; Connelly, M. A.; McBride, O. W.; Kozak, C. A.; Marcu,K. B.: 3 B c Plasmacytoma- associated neuronal glycoprotein, Pang, mapsto mouse chromosome 6 and human chromosome 3. Genomics 34: 226- 228,1996.

GAM148 280 DCK Chottiner, E. G.; Shewach, D. S.; Datta, N. S.; Ashcraft, E.; Gribbin,D.; 3 B c Ginsburg, D.; Fox, I. H.; Mitchell, B. S.: Cloning and expressionof human deoxycytidine kinase cDNA. Proc. Nat. Acad. Sci. 88: 1531- 1535,1991.

GAM148 280 DCK Huang, S.- H.; Tomich, J. M.; Wu, H.; Jong, A.; Holcenberg, J.:Human 3 B c deoxycytidine kinase: sequence of cDNA clones and analysis ofexpression in cell lines with and without enzyme activity. J. Biol.Chem. 264: 14762- 14768, 1989. Note: Correction: J. Biol. Chem. 266:5353 only, 1991.

GAM148 280 DCK Johansson, M.; Brismar, S.; Karlsson, A.: Human deoxycytidinekinase is 3 B c located in the cell nucleus. Proc. Nat. Acad. Sci. 94:11941- 11945, 1997.

GAM148 280 DCK Song, J. J.; Walker, S.; Chen, E.; Johnson, E. E., II; Spychala,J.; Gribbin, 3 B c T.; Mitchell, B. S.: Genomic structure and chromosomallocalization of the human deoxycytidine kinase gene. Proc. Nat. Acad.Sci. 90: 431- 434, 1993.

GAM148 280 DCK Stegmann, A. P. A.; Honders, M. W.; Bolk, M. W. J.; Wessels, J.;Willemze, 3 B c R.; Landegent, J. E.: Assignment of the human deoxycytidinekinase (DCK) gene to chromosome 4 band q13.3- q21.1. Genomics 17:528- 529, 1993.

GAM148 280 DRD1 Albrecht, F. E.; Drago, J.; Felder, R. A.; Printz, M. P.; Eisner,G. M.; 3 B c Robillard, J. E.; Sibley, D. R.; Westphal, H. J.; Jose, P.A.: Role of the D-1A dopamine receptor in the pathogenesis of genetichypertension. J. Clin. Invest. 97: 2283- 2288, 1996.

GAM148 280 DRD1 Bermak, J. C.; Li, M.; Bullock, C.; Zhou, Q.- Y.: Regulation oftransport of 3 B c the dopamine D1 receptor by a new membrane- associatedER protein. Nature Cell Biol. 3: 492- 498, 2001.

GAM148 280 DRD1 Boultwood, J.; Lewis, M. S.; Wainscoat, J. S.: Physical linkageof 3 B c glucocorticoid receptor (GRL) and dopamine D1 receptor (DRD1) onthe long arm of chromosome 5.(Abstract) Cytogenet. Cell Genet. 58:1894 only, 1991.

GAM148 280 DRD1 Castner, S. A.; Williams, G. V.; Goldman- Rakic, P. S.: Reversalof 3 B c antipsychotic- induced working memory deficits by short- term dopamineD1 receptor stimulation. Science 287: 2020- 2022, 2000.

GAM148 280 DRD1 Dearry, A.; Gingrich, J. A.; Falardeau, P.; Fremeau, R. T., Jr.;Bates, M. 3 B c D.; Caron, M. G.: Molecular cloning and expression of thegene for a human D(1) dopamine receptor. Nature 347: 72- 76, 1990.

GAM148 280 DRD1 Grandy, D. K.; Zhou, Q.- Y.; Allen, L.; Litt, R.; Magenis, R. E.;Civelli, 3 B c O.; Litt, M.: A human D(1) dopamine receptor gene is locatedon chromosome 5 at q35.1 and identifies an EcoRI RFLP. Am. J. Hum.Genet. 47: 828- 834, 1990.

GAM148 280 DRD1 Krushkal, J.; Xiong, M.; Ferrell, R.; Sing, C. F.; Turner, S. T.;Boerwinkle, 3 B c E.: Linkage and association of adrenergic and dopaminereceptor genes in the distal portion of the long arm of chromosome5 with systolic blood pressure variation. Hum. Molec. Genet. 7:1379- 1383, 1998.

GAM148 280 DRD1 Mayerhofer, A.; Hemmings, H. C., Jr.; Snyder, G. L.; Greengard,P.; Boddien, 3 B c
S.; Berg, U.; Brucker, C.: Functional dopamine- 1 receptorsand DARPP- 32 are
expressed in human ovary and granulosa luteal cellsin vitro. J. Clin.
Endocr. Metab. 84: 257- 264, 1999.

GAM148 280 DRD1 Sunahara, R. K.; Niznik, H. B.; Weiner, D. M.; Stormann, T. M.;Brann, M. R.; 3 B c
Kennedy, J. L.; Gelernter, J. E.; Rozmahel, R.; Yang,Y.; Israel, Y.; Seeman,
P.; O'Dowd, B. F.: Human dopamine D1 receptorencoded by an intronless gene
on chromosome 5. Nature 347: 80- 83,1990.

GAM148 280 DRD1 Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; 3 B c
Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and
genome organization of mammalian G- protein- coupled receptors. Genomics
18:175- 184, 1993.

GAM148 280 DRD1 Xu, M.; Moratalla, R.; Gold, L. H.; Hiroi, N.; Koob, G. F.; Graybiel,A. M.; 3 B c
Tonegawa, S.: Dopamine D1 receptor mutant mice are deficientin striatal
expression of dynorphin and in dopamine- mediated behavioralresponses. Cell
79: 729- 742, 1994.

GAM148 280 DRD1 Zhou, Q.- Y.; Grandy, D. K.; Thambi, L.; Kushner, J. A.; Van Tol,H. H. M.; 3 B c
Cone, R.; Pribnow, D.; Salon, J.; Bunzow, J. R.; Civelli,O.: Cloning and
expression of human and rat D(1) dopamine receptors. Nature 347:76- 80,
1990.

GAM148 280 DRD2 Balk, J.- H.; Picetti, R.; Salardi, A.; Thirlet, G.; Dierich, A.;Depaulls, 3 B c
A.; Le Meur, M.; Borrelli, E.: Parkinsonian- like locomotorimpairment in
mice lacking dopamine D2 receptors. Nature 377: 424- 428,1995.

GAM148 280 DRD2 Basu, S.; Nagy, J. A.; Pal, S.; Vasile, E.; Eckelhoefer, I. A.;Bliss, V. S.; 3 B c
Manseau, E. J.; Dasgupta, P. S.; Dvorak, H. F.; Mukhopadhyay,D.: The
neurotransmitter dopamine inhibits angiogenesis induced byvascular
permeability factor/vascular endothelial growth factor. NatureMed. 7: 569-
574, 2001.

GAM148 280 DRD2 Blum, K.; Noble, E. P.; Sheridan, P. J.; Montgomery, A.; Ritchie,T.; 3 B c
Jagadeeswaran, P.; Nogami, H.; Briggs, A. H.; Cohn, J. B.:
Allelicassociation of human dopamine D(2) receptor gene in alcoholism.
J.A.M.A. 263:2055- 2060, 1990.

GAM148 280 DRD2 Bolos, A. M.; Dean, M.; Lucas- Derse, S.; Ramsburg, M.; Brown, G.L.; 3 B c
Goldman, D.: Population and pedigree studies reveal a lack ofassociation
between the dopamine D(2) receptor gene and alcoholism. J.A.M.A. 264:3156-
3160, 1990.

GAM148 280 DRD2 Bunzow, J. R.; Van Tol, H. H.; Grandy, D. K.; Albert, P.; Salon,J.; 3 B c
Christie, M.; Machida, C. A.; Neve, K. A.; Civelli, O.: Cloningand
expression of a rat D2 dopamine receptor cDNA. Nature 336: 783- 787,1988.

GAM148 280 DRD2 Castner, S. A.; Williams, G. V.; Goldman- Rakic, P. S.: Reversalof 3 B c
antipsychotic- induced working memory deficits by short- term dopamineD1
receptor stimulation. Science 287: 2020- 2022, 2000.

GAM148 280 DRD2 Dal Toso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D. B.;Bach, A.; 3 B c
Shivers, B. D.; Seeburg, P. H.: The dopamine D(2) receptor:two molecular
forms generated by alternative splicing. EMBO J. 8:4025- 4034, 1989.

GAM148 280 DRD2 Devor, E. J.; Grandy, D. K.; Civelli, O.; Litt, M.; Burgess, A.K.; Isenberg, 3 B c
K. E.; van de Wetering, B. J. M.; Oostra, B.: Geneticlinkage is excluded for
the D2- dopamine receptor lambda- HD2G1 andflanking loci on chromosome
11q22- q23 in Tourette syndrome. Hum.Hered. 40: 105- 108, 1990.

GAM148 280 DRD2 Eubanks, J. H.; Djabali, M.; Selleri, L.; Grandy, D. K.; Civelli,O.; 3 B c

McElligott, D. L.; Evans, G. A.: Structure and linkage of theD2 dopamine receptor and neural cell adhesion molecule genes on humanchromosome 11q23. Genomics 14: 1010- 1018, 1992.

GAM148 280 DRD2 Gejman, P. V.; Ram, A.; Gelernter, J.; Friedman, E.; Cao, Q.;Pickar, D.; 3 B c Blum, K.; Noble, E. P.; Kranzler, H. R.; O'Malley, S.;Hamer, D. H.; Whitsitt, F.; Rao, P.; DeLisi, L. E.; Virkkunen, M.;Linnoila, M.; Goldman, D.; Gershon, E. S.: No structural mutationin the dopamine D2 receptor gene in alcoholism or schizophrenia: analysisusing denaturing gradient gel electrophoresis. J.A.M.A. 271: 204- 208,1994.

GAM148 280 DRD2 Gelernter, J.; Grandy, D. K.; Bunzow, J.; Pakstis, A. J.; Civelli,O.; 3 B c Retief, A. E.; Litt, M.; Kidd, K. K.: D(2) dopamine receptorlocus (probe hD2G1) maps close to D11S29 (probe L7) and is also linkedto PBGD (probe PBGD0.0) and D11S84 (probe p- 2- 7- ID6) on 11q. (Abstract) Cytogenet.Cell Genet. 51: 1002 only, 1989.

GAM148 280 DRD2 Gelernter, J.; Pakstis, A. J.; Grandy, D.; Litt, M.; Retief, A.E.; Kennedy, 3 B c J. L.; Hing- Loh, A.; Schoolfield, G.; Civelli, O.; Kidd,K. K.: Linkage map of eight human chromosome 11q markers, includingDRD2, spanning 60 cM. Cytogenet. Cell Genet. 60: 26- 28, 1992.

GAM148 280 DRD2 Gelernter, J.; Pakstis, A. J.; Pauls, D. L.; Kurlan, R.; Gancher,S. T.; 3 B c Civelli, O.; Grandy, D.; Kidd, K. K.: Gilles de la Tourettesyndrome is not linked to D2- dopamine receptor. Arch. Gen. Psychiat. 47:1073- 1077, 1990.

GAM148 280 DRD2 Giros, B.; Sokoloff, P.; Martres, M.- P.; Riou, J.- F.; Emorine,L. J.; 3 B c Schwartz, J.- C.: Alternative splicing directs the expressionof two D(2) dopamine receptor isoforms. Nature 342: 923- 926, 1989.

GAM148 280 DRD2 Grandy, D. K.; Litt, M.; Allen, L.; Bunzow, J. R.; Marchionni,M.; Makam, H.; 3 B c Reed, L.; Magenis, R. E.; Civelli, O.: The human dopamineD(2) receptor gene is located on chromosome 11 at q22- q23 and identifiesa TaqI RFLP. Am. J. Hum. Genet. 45: 778- 785, 1989.

GAM148 280 DRD2 Grandy, D. K.; Marchionni, M. A.; Makam, H.; Stofko, R. E.; Alfano,M.; 3 B c Frothingham, L.; Fischer, J. B.; Burke- Howie, K. J.; Bunzow, J.R.; Server, A. C.; Civelli, O.: Cloning of the cDNA and gene fora human D2 dopamine receptor. Proc. Nat. Acad. Sci. 86: 9762- 9766,1989.

GAM148 280 DRD2 Klein, C.; Brin, M. F.; Kramer, P.; Sena- Esteves, M.; de Leon,D.; Doheny, 3 B c D.; Bressman, S.; Fahn, S.; Breakefield, X. O.; Ozelius,L. J.: Association of a missense change in the D2 dopamine receptorwith myoclonus dystonia. Proc. Nat. Acad. Sci. 96: 5173- 5176, 1999.

GAM148 280 DRD2 Maldonado, R.; Salardi, A.; Valverde, O.; Samad, T. A.; Roques,B. P.; 3 B c Borrelli, E.: Absence of opiate rewarding effects in micelacking dopamine D2 receptors. Nature 388: 586- 589, 1997.

GAM148 280 DRD2 Milligan, G.: Receptors as kissing cousins. Science 288: 65- 67,2000. 3 B c

GAM148 280 DRD2 Monsma, F. J., Jr.; McVittie, L. D.; Gerfen, C. R.; Mahan, L.C.; Sibley, D. 3 B c R.: Multiple D(2) dopamine receptors produced by alternativeRNA splicing. Nature 342: 926- 929, 1989.

GAM148 280 DRD2 Oliveri, R. L.; Annesi, G.; Zappia, M.; Civitelli, D.; Montesanti,R.; 3 B c Branca, D.; Nicoletti, G.; Spadafora, P.; Pasqua, A. A.; Cittadella,R.; Andreoli, V.; Gambardella, A.; Aguglia, U.; Quattrone, A.: DopamineD2 receptor gene polymorphism and the risk of levodopa- induced dyskinesiasin PD. Neurology 53: 1425- 1430, 1999.

GAM148 280 DRD2 Rocheville, M.; Lange, D. C.; Kumar, U.; Patel, S. C.; Patel,R. C.; Patel, 3 B c Y. C.: Receptors for dopamine and somatostatin: formationof hetero-

oligomers with enhanced functional activity. Science 288:154- 157, 2000.

GAM148 280 DRD2 Smith, M.; Wasmuth, J.; McPherson, J. D.; Wagner, C.; Grandy,D.; Civelli, O.; Potkin, S.; Litt, M.: Cosegregation of an 11q22.3- 9p22translocation with affective disorder: proximity of the dopamine D2receptor gene relative to the translocation breakpoint. (Abstract) Am.J. Hum. Genet. 45 (suppl.): A220 only, 1989. 3 B c

GAM148 280 DRD2 St Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990. 3 B c

GAM148 280 DRD2 Suarez, B. K.; Parsian, A.; Hampe, C. L.; Todd, R. D.; Reich,T.; Cloninger, C. R.: Linkage disequilibria at the D2 dopamine receptorlocus (DRD2) in alcoholics and controls. Genomics 19: 12- 20, 1994. 3 B c

GAM148 280 DRD2 Usiello, A.; Baik, J.- H.; Rouge- Pont, F.; Picetti, R.; Dierich,A.; LeMeur, M.; Piazza, P. V.; Borrelli, E.: Distinct functions ofthe two isoforms of dopamine D2 receptors. Nature 408: 199- 203,2000. 3 B c

GAM148 280 DRD2 Wang, J.; Liu, Z.- L.; Chen, B.: Association study of dopamineD2, D3 receptor gene polymorphisms with motor fluctuations in PD. Neurology 56:1757- 1759, 2001. 3 B c

GAM148 280 EGLN2 Bruick, R. K.; McKnight, S. L.: A conserved family of prolyl- 4- hydroxylasesthat modify HIF. Science 294: 1337- 1340, 2001. 3 B c

GAM148 280 EGLN2 Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell 107:43- 54, 2001. 3 B c

GAM148 280 EGR2 Boerkoel, C. F.; Takashima, H.; Bacino, C. A.; Daentl, D.; Lupski,J. R.: EGR2 mutation R359W causes a spectrum of Dejerine- Sottas neuropathy. Neurogenetics 3:153- 157, 2001. 3 B c

GAM148 280 EGR2 Chavrier, P.; Janssen- Timmen, U.; Mattei, M.- G.; Zerial, M.; Bravo,R.; Charnay, P.: Structure, chromosome location, and expression ofthe mouse zinc finger gene Krox- 20: multiple gene products and coregulationwith the proto- oncogene c- fos. Molec. Cell. Biol. 9: 787- 797, 1989. 3 B c

GAM148 280 EGR2 Joseph, L. J.; Le Beau, M. M.; Jamieson, G. A., Jr.; Acharya, S.;Shows, T. B.; Rowley, J. D.; Sukhatme, V. P.: Molecular cloning,sequencing, and mapping of EGR2, a human early growth response geneencoding a protein with 'zinc- binding finger' structure. Proc. Nat.Acad. Sci. 85: 7164- 7168, 1988. 3 B c

GAM148 280 EGR2 Nagarajan, R.; Svaren, J.; Le, N.; Araki, T.; Watson, M.; Milbrandt,J.: EGR2 mutations in inherited neuropathies dominant- negativelyinhibit myelin gene expression. Neuron 30: 355- 368, 2001. 3 B c

GAM148 280 EGR2 Nucleic Acids Res. 16: 11855 only, 1988. 3 B c

GAM148 280 EGR2 Timmerman, V.; De Jonghe, P.; Ceuterick, C.; De Vriendt, E.; Lofgren,A.; Nelis, E.; Warner, L. E.; Lupski, J. R.; Martin, J.- J.; Van Broeckhoven,C.: Novel missense mutation in the early growth response 2 gene associatedwith Dejerine- Sottas syndrome phenotype. Neurology 52: 1827- 1832,1999. 3 B c

GAM148 280 EGR2 Warner, L. E.; Mancias, P.; Butler, I. J.; McDonald, C. M.; Keppen,L.; Koob, K. G.; Lupski, J. R.: Mutations in the early growth response2 (EGR2) gene are associated with hereditary myelinopathies. NatureGenet. 18: 382- 384, 1998. 3 B c

GAM148 280 EGR2 Warner, L. E.; Mancias, P.; Butler, I.; Lupski, J. R.: Mutationin the early 3 B c

growth response 2 (EGR2) transcription factor associatedwith recessive congenital hypomyelinating neuropathy (CHN). (Abstract) Am.J. Hum. Genet. 61 (suppl.): A350 only, 1997.

GAM148 280 EGR2 Warner, L. E.; Svaren, J.; Milbrandt, J.; Lupski, J. R.: 3 B c
Functionalconsequences of mutations in the early growth response 2 gene (EGR2)correlate with severity of human myelinopathies. Hum. Molec. Genet. 8:1245- 1251, 1999.

GAM148 280 EGR2 Wu, J.; Joseph, L.; Sukhatme, V. P.; Kidd, K. K.: A HindIII 3 B c
polymorphismidentified by the human early growth response gene 2 (EGR2) on chromosome

GAM148 280 EYA2 Abdelhak, S.; Kalatzis, V.; Heilig, R.; Compain, S.; Samson, D.;Vincent, C.; 3 B c
Weil, D.; Cruaud, C.; Sahly, I.; Leibovici, M.; Bitner- Glindzicz,M.;
Francis, M.; Lacombe, D.; Vigneron, J.; Charachon, R.; Boven,K.; Bedbeder,
P.; Van Regemorter, N.; Weissenbach, J.; Petit, C.:A human homologue of the Drosophila eyes absent gene underlies branchio- oto- renal(BOR) syndrome and identifies a novel gene family. Nature Genet. 15:157- 164, 1997.

GAM148 280 EYA2 Banfi, S.; Borsani, G.; Rossi, E.; Bernard, L.; Guffanti, A.; Rubboli,F.; 3 B c
Marchitiello, A.; Giglio, S.; Coluccia, E.; Zollo, M.; Zuffardi,O.;
Ballabio, A.: Identification and mapping of human cDNAs homologousto Drosophila mutant genes through EST database searching. NatureGenet. 13: 167- 174, 1996.

GAM148 280 EYA2 Duncan, M. K.; Kos, L.; Jenkins, N. A.; Gilbert, D. J.; Copeland,N. G.; 3 B c
Tomarev, S. I.: Eyes absent: a gene family found in severalmetazoan phyla. Mammalian Genome 8: 479- 485, 1997. Note: Erratum:Mammalian Genome 8: 877 only, 1997.

GAM148 280 EYA2 Xu, P.- X.; Cheng, J.; Epstein, J. A.; Maas, R. L.: Mouse Eya genesare 3 B c
expressed during limb tendon development and encode a transcriptionalactivation function. Proc. Nat. Acad. Sci. 94: 11974- 11979, 1997.

GAM148 280 EYA2 Zimmerman, J. E.; Bui, Q. T.; Steingrimsson, E.; Nagle, D. L.;Fu, W.; Genin, 3 B c
A.; Spinner, N. B.; Copeland, N. G.; Jenkins, N. A.;Bucan, M.; Bonini, N.
M.: Cloning and characterization of two vertebratehomologs of the Drosophila eyes absent gene. Genome Res. 7: 128- 141,1997.

GAM148 280 HOXA7 Acampora, D.; D'Esposito, M.; Faiella, A.; Pannese, M.; Migliaccio,E.; 3 B c
Morelli, F.; Stornaiuolo, A.; Nigro, V.; Simeone, A.; Boncinelli,E.: The human HOX gene family. Nucleic Acids Res. 17: 10385- 10402,1989.

GAM148 280 HOXA7 Balling, R.; Mutter, G.; Gruss, P.; Kessel, M.: Craniofacial 3 B c
abnormalitiesinduced by ectopic expression of the homeobox gene Hox- 1.1 in transgenicmice. Cell 58: 337- 347, 1989.

GAM148 280 HOXA7 Bucan, M.; Yang- Feng, T.; Colberg- Poley, A. M.; Wolgemuth, D. J.;Guenet, 3 B c
J.- L.; Francke, U.; Lehrach, H.: Genetic and cytogeneticlocalisation of the homeo box containing genes on mouse chromosome6 and human chromosome 7. EMBO J. 5: 2899- 2905, 1986.

GAM148 280 HOXA7 Ferguson- Smith, A. C.; Fienberg, A.; Ruddle, F. H.: Isolation,chromosomal 3 B c
localization, and nucleotide sequence of the human HOX1.4 homeobox. Genomics 5: 250- 258, 1989.

GAM148 280 HOXA7 Gaunt, S. J.; Singh, P. B.: Homeogene expression patterns andchromosomal 3 B c
imprinting. Trends Genet. 6: 208- 212, 1990.

GAM148 280 HOXA7 Gehring, W. J.: The homeo box: a key to the understanding of development? 3 B c
Cell 40:3- 5, 1985.

GAM148 280 HOXA7 Joyner, A. L.; Lebo, R. V.; Kan, Y. W.; Tjian, R.; Cox, D. R.;Martin, G. R.: 3 B c Comparative chromosome mapping of a conserved homoeobox region in mouse and human. Nature 314: 173- 175, 1985.

GAM148 280 HOXA7 McGinnis, W.; Garber, R. L.; Wirz, J.; Kuroiwa, A.; Gehring, W.J.: A 3 B c homologous protein- coding sequence in Drosophila homeotic genesand its conservation in other metazoans. Cell 37: 403- 408, 1984.

GAM148 280 HOXA7 McGinnis, W.; Levine, M. S.; Hafen, E.; Kuroiwa, A.; Gehring, W.J.: A 3 B c conserved DNA sequence in homoeotic genes of the DrosophilaAntennapedia and bithorax complexes. Nature 308: 428- 433, 1984.

GAM148 280 HOXA7 Ohno, S.: Evolution by Gene Duplication. Heidelberg: Springer(pub.) 1970. 3 B c

GAM148 280 HOXA7 Rabin, M.; Ferguson- Smith, A.; Hart, C. P.; Ruddle, F. H.: Cognatehomeo- 3 B c box loci mapped on homologous human and mouse chromosomes. Proc.Nat. Acad. Sci. 83: 9104- 9108, 1986.

GAM148 280 HOXA7 Rabin, M.; Hart, C. P.; Ferguson- Smith, A.; McGinnis, W.; Levine,M.; 3 B c Ruddle, F. H.: Two homoeo box loci mapped in evolutionarily relatedmouse and human chromosomes. Nature 314: 175- 178, 1985.

GAM148 280 HOXA7 Rieger, R.; Michaelis, A.; Green, M. M.: Glossary of Geneticsand 3 B c Cytogenetics. New York: Springer- Verlag (pub.) 1976. Pp.281 only.

GAM148 280 HOXA7 Schughart, K.; Kappen, C.; Ruddle, F. H.: Duplication of largegenomic 3 B c regions during the evolution of vertebrate homeobox genes. Proc.Nat. Acad. Sci. 86: 7067- 7071, 1989.

GAM148 280 HOXA7 Scott, M. P.: Vertebrate homeobox gene nomenclature. (Letter) Cell 71:551- 3 B c 553, 1992.

GAM148 280 ITGAL Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; 3 B c Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P. G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome 16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991.

GAM148 280 ITGAL Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. 3 B c C.: Chromosomal location of the genes encoding the leukocyteadhesion receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988.

GAM148 280 ITGAL Fischer, A.; Durandy, A.; Sterkers, G.; Griscelli, C.: Role ofthe LFA- 1 3 B c molecule in cellular interactions required for antibodyproduction in humans. J. Immun. 136: 3198- 3203, 1986.

GAM148 280 ITGAL Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cell retentionin 3 B c the splenic marginal zone. Science 297: 409- 412, 2002.

GAM148 280 ITGAL Marlin, S. D.; Morton, C. C.; Anderson, D. C.; Springer, T. A.: LFA- 1 3 B c immunodeficiency disease: definition of the genetic defectand chromosomal mapping of alpha and beta subunits of the lymphocytefunction- associated antigen 1 (LFA- 1) by complementation in hybridcells. J. Exp. Med. 164: 855- 867, 1986.

GAM148 280 ITGAL Pischel, K. D.; Marlin, S. D.; Springer, T. A.; Woods, V. L., Jr.;Bluestein, 3 B c H. G.: Polymorphism of lymphocyte function- associatedantigen- 1 demonstrated by a lupus patient's alloantiserum. J. Clin.Invest. 79: 1607- 1614, 1987.

GAM148 280 ITGAL Sanchez- Madrid, F.; Nagy, J.; Robbins, E.; Simon, P.; Springer,T. A.: A 3 B c human leukocyte differentiation antigen family with distinctalpha subunits and a common beta subunit: the lymphocyte function- associatedantigen (LFA- 1), the C3bi complement receptor (OKM1/Mac- 1), and thep150,95 molecule. J. Exp. Med. 158: 1785- 1803, 1983.

GAM148 280 KIF5A Hamlin, P. J.; Jones, P. F.; Leek, J. P.; Bransfield, K.; Lench,N. J.; Aldersley, M. A.; Howdle, P. D.; Markham, A. F.; Robinson,P. A.: Assignment of GALGT encoding beta- 1,4N- acetylgalactosaminyl- transferase(GalNAc- T) and KIF5A encoding neuronal kinesin (D12S1889) to humanchromosome band 12q13 by assignment to ICI YAC 26EG10 and in situhybridization. Cytogenet. Cell Genet. 82: 267- 268, 1998. 3 B c

GAM148 280 KIF5A Niclas, J.; Navone, F.; Hom- Booher, N.; Vale, R. D.: Cloning andlocalization of a conventional kinesin motor expressed exclusivelyin neurons. Neuron 12: 1059- 1072, 1994. 3 B c

GAM148 280 MBTPS1 Brown, M. S.; Goldstein, J. L.: The SREBP pathway: regulationof cholesterol metabolism by proteolysis of a membrane- bound transcriptionfactor. Cell 89: 331- 340, 1997. 3 B c

GAM148 280 MBTPS1 DeBose- Boyd, R. A.; Brown, M. S.; Li, W.- P.; Nohturfft, A.; Goldstein,J. L.; Espenshade, P. J.: Transport- dependent proteolysis of SREBP:relocation of Site- 1 protease from Golgi to ER obviates the need forSREBP transport to Golgi. Cell 99: 703- 712, 1999. 3 B c

GAM148 280 MBTPS1 Duncan, E. A.; Brown, M. S.; Goldstein, J. L.; Sakai, J.: Cleavagesite for sterol- regulated protease localized to a leu- ser bond inthe lumenal loop of sterol regulatory element- binding protein- 2. J.Biol. Chem. 272: 12778- 12785, 1997. 3 B c

GAM148 280 MBTPS1 Nagase, T.; Miyajima, N.; Tanaka, A.; Sazuka, T.; Seki, N.; Sato,S.; Tabata, S.; Ishikawa, K.; Kawarabayasi, Y.; Kotani, H.; Nomura,N.: Prediction of the coding sequences of unidentified human genes.III. The coding sequences of 40 new genes (KIAA0081- KIAA0120) deducedby analysis of cDNA clones from human cell line KG- 1. DNA Res. 2:37- 43, 1995. 3 B c

GAM148 280 MBTPS1 Nakajima, T.; Iwaki, K.; Kodama, T.; Inazawa, J.; Emi, M.: Genomicstructure and chromosomal mapping of the human site- 1 protease (S1P)gene. J. Hum. Genet. 45: 212- 217, 2000. 3 B c

GAM148 280 MBTPS1 Sakai, J.; Duncan, E. A.; Rawson, R. B.; Hua, X.; Brown, M. S.;Goldstein, J. L.: Sterol- regulated release of SREBP- 2 from cell membranesrequires two sequential cleavages, one within a transmembrane segment. Cell 85:1037- 1046, 1996. 3 B c

GAM148 280 MBTPS1 Sakai, J.; Rawson, R. B.; Espenshade, P. J.; Cheng, D.; Seegmiller,A. C.; Goldstein, J. L.; Brown, M. S.: Molecular identification ofthe sterol- regulated luminal protease that cleaves SREBPs and controlslipid composition of animal cells. Molec. Cell 2: 505- 514, 1998. 3 B c

GAM148 280 MBTPS1 Ye, J.; Rawson, R. B.; Komuro, R.; Chen, X.; Dave, U. P.; Prywes,R.; Brown, M. S.; Goldstein, J. L.: ER stress induces cleavage ofmembrane- bound ATF6 by the same proteases that process SREBPs. Molec.Cell 6: 1355- 1364, 2000. 3 B c

GAM148 280 MTMR3 Laporte, J.; Blondeau, F.; Buj- Bello, A.; Tentler, D.; Kretz, C.;Dahl, N.; Mandel, J.- L.: Characterization of the myotubularin dualspecificity phosphatase gene family from yeast to human. Hum. Molec.Genet. 7: 1703- 1712, 1998. 3 B c

GAM148 280 MTMR3 Laporte, J.; Hu, L. J.; Kretz, C.; Mandel, J.- L.; Kioschis, P.;Coy, J. F.; Klauck, S. M.; Poustka, A.; Dahl, N.: A gene mutatedin X- linked myotubular myopathy defines a new putative tyrosine phosphatasefamily conserved in yeast. Nature Genet. 13: 175- 182, 1996. 3 B c

GAM148 280 MTMR3 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new 3 B c

cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM148 280 MTMR3 Zhao, R.; Qi, Y.; Chen, J.; Zhao, Z. J.: FYVE- DSP2, a FYVE domain- containingdual specificity protein phosphatase that dephosphorylates phosphotidylinositol(sic) 3- phosphate. Exp. Cell Res. 265: 329- 338, 2001. 3 B c

GAM148 280 MYD88 Adachi, O.; Kawai, T.; Takeda, K.; Matsumoto, M.; Tsutsui, H.;Sakagami, M.; Nakanishi, K.; Akira, S.: Targeted disruption of theMyD88 gene results in loss of IL- 1- and IL- 18- mediated function. Immunity 143- 150,1998. 3 B c

GAM148 280 MYD88 Bonnert, T. P.; Garka, K. E.; Parnet, P.; Sonoda, G.; Testa, J.R.; Sims, J. E.: The cloning and characterization of human MyD88:a member of an IL- 1 receptor related family. FEBS Lett. 402: 81- 84,1997. 3 B c

GAM148 280 MYD88 Hardiman, G.; Jenkins, N. A.; Copeland, N. G.; Gilbert, D. J.;Garcia, D. K.; Naylor, S. L.; Kastelein, R. A.; Bazan, J. F.: Geneticstructure and chromosomal mapping of MyD88. Genomics 45: 332- 339,1997. 3 B c

GAM148 280 MYD88 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001. 3 B c

GAM148 280 MYD88 Jankovic, D.; Kullberg, M. C.; Hieny, S.; Caspar, P.; Collazo,C. M.; Sher, A.: In the absence of IL- 12, CD4+ T cell responses tointracellular pathogens fail to default to a Th2 pattern and are hostprotective in an IL- 10- /- setting. Immunity 16: 429- 439, 2002. 3 B c

GAM148 280 MYD88 Kawai, T.; Adachi, O.; Ogawa, T.; Takeda, K.; Akira, S.: Unresponsivenessof MyD88- deficient mice to endotoxin. Immunity 11: 115- 122, 1999. 3 B c

GAM148 280 MYD88 Lord, K. A.; Hoffman- Liebermann, B.; Liebermann, D. A.: Complexityof the immediate early response of myeloid cells to terminal differentiationand growth arrest includes ICAM- 1, Jun- B and histone variants. Oncogene 5:387- 396, 1990. 3 B c

GAM148 280 MYD88 Medzhitov, R.; Preston- Hurlburt, P.; Kopp, E.; Stadien, A.; Chen,C.; Ghosh, S.; Janeway, C. A., Jr.: MyD88 is an adaptor protein inthe hToll/Il- 1 receptor family signaling pathways. Molec. Cell 2:253- 258, 1998. 3 B c

GAM148 280 MYD88 Muzio, M.; Ni, J.; Feng, P.; Dixit, V. M.: IRAK (Pelle) familymember IRAK- 2 and MyD88 as proximal mediators of IL- 1 signaling. Science 278:1612- 1615, 1997. 3 B c

GAM148 280 MYD88 Takeuchi, O.; Hoshino, K.; Akira, S.: Cutting edge: TLR2- deficientand MyD88- deficient mice are highly susceptible to Staphylococcusaureus infection. J. Immun. 165: 5392- 5396, 2000. 3 B c

GAM148 280 NRCAM Dry, K.; Kenwrick, S.; Rosenthal, A.; Platzer, M.: The completesequence of the human locus for NgCAM- related cell adhesion moleculereveals a novel alternative exon in chick and man and conserved genomicorganization for the L1 subfamily. Gene 273: 115- 122, 2001. 3 B c

GAM148 280 NRCAM Grumet, M.; Mauro, V.; Burgoon, M. P.; Edelman, G. M.; Cunningham,B. A.: Structure of a new nervous system glycoprotein, Nr- CAM, andits relationship to subgroups of neural cell adhesion molecules. J.Cell. Biol. 113: 1399- 1412, 1991. 3 B c

GAM148 280 NRCAM Kayyem, J. F.; Roman, J. M.; de la Rosa, E. J.; Schwarz, U.; Dreyer,W. J.: Bravo/Nr- CAM is closely related to the cell adhesion moleculesL1 and Ng- CAM and has a similar heterodimer structure. J. Cell. Biol. 118:1259- 1270, 1992. 3 B c

GAM148 280 NRCAM Lane, R. P.; Chen, X.- N.; Yamakawa, K.; Vielmetter, J.; Korenberg,J. R.; 3 B c

Dreyer, W. J.: Characterization of a highly conserved humanhomolog to the chicken neural cell surface protein Bravo/Nr- CAM thatmaps to chromosome band 7q31. Genomics 35: 456- 465, 1996.

GAM148 280 NRCAM Wang, B.; Williams, H.; Du, J.- S.; Terrett, J.; Kenwrick, S.:Alternative splicing of human NrCAM in neural and nonneural tissues. Molec.Cell. Neurosci. 10: 287- 295, 1998. 3 B c

GAM148 280 NUP50 Lindsay, M. E.; Plafker, K.; Smith, A. E.; Clurman, B. E.; Macara,I. G.: Npap60/Nup50 is a tri- stable switch that stimulates importin- alpha:beta- mediatednuclear protein import. Cell 110: 349- 360, 2002. 3 B c

GAM148 280 NUP50 Trichet, V.; Shkolny, D.; Dunham, I.; Beare, D.; McDermid, H. E.: Mapping and complex expression pattern of the human NPAP60L nucleoporingene. Cytogenet. Cell Genet. 85: 221- 226, 1999. 3 B c

GAM148 280 OTP Acampora, D.; Postiglione, M. P.; Avantaggiato, V.; Di Bonito,M.; Vaccarino, F. M.; Michaud, J.; Simeone, A.: Progressive impairmentof developing neuroendocrine cell lineages in the hypothalamus ofmice lacking the Orthopedia gene. Genes Dev. 13: 2787- 2800, 1999. 3 B c

GAM148 280 OTP Lin, X.; State, M. W.; Vaccarino, F. M.; Greally, J.; Hass, M.;Leckman, J. F.: Identification, chromosomal assignment, and expressionanalysis of the human homeodomain- containing gene Orthopedia (OTP). Genomics 60:96- 104, 1999. 3 B c

GAM148 280 PCOLCE Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani- Sait, S.; Shows, T. B.; Greenspan, D. S.: Type I procollagenCOOH- terminal proteinase enhancer protein: identification, primarystructure, and chromosomal localization of the cognate human gene(PCOLCE). J. Biol. Chem. 269: 26280- 26285, 1994. 3 B c

GAM148 280 PCOLCE Takahara, K.; Osborne, L.; Elliott, R. W.; Tsui, L.- C.; Scherer,S. W.; Greenspan, D. S.: Fine mapping of the human and mouse genesfor the type I procollagen COOH- terminal proteinase enhancer protein. Genomics 31:253- 256, 1996. 3 B c

GAM148 280 PLCD1 Cheng, H. F.; Jiang, M. J.; Chen, C. L.; Liu, S. M.; Wong, L. P.;Lomasney, J. W.; King, K.: Cloning and identification of amino acidresidues of human phospholipase C delta 1 essential for catalysis. J.Biol. Chem. 270: 5495- 5505, 1995. 3 B c

GAM148 280 PLCD1 Ishikawa, S.; Takahashi, T.; Ogawa, M.; Nakamura, Y.: Genomicstructure of the human PLCD1 (phospholipase C delta 1) locus on 3p22- p21.3. Cytogenet.Cell Genet. 78: 58- 60, 1997. 3 B c

GAM148 280 PLCD1 Lyu, M. S.; Park, D. J.; Rhee, S. G.; Kozak, C. A.: Genetic mappingof the human and mouse phospholipase C genes. Mammalian Genome 7:501- 504, 1996. 3 B c

GAM148 280 PLCD1 Shimohama, S.; Kamiya, S.; Fujii, M.; Ogawa, T.; Kanamori, M.;Kawamata, J.; Imura, T.; Taniguchi, T.; Yagisawa, H.: Mutation inthe pleckstrin homology domain of the human phospholipase C- delta- 1gene is associated with loss of function. Biochem. Biophys. Res.Commun. 245: 722- 728, 1998. 3 B c

GAM148 280 PPP1R11 Amadou, C.; Ribouchon, M. T.; Mattei, M. G.; Jenkins, N. A.; Gilbert,D. J.; Copeland, N. G.; Avoustin, P.; Pontarotti, P.: Localizationof new genes and markers to the distal part of the human major histocompatibilitycomplex (MHC) region and comparison with the mouse: new insights intothe evolution of mammalian genomes. Genomics 26: 9- 20, 1995. 3 B c

GAM148 280 PPP1R11 El Kahloun, A.; Chauvel, B.; Mauvieux, V.; Dorval, I.; Jouanolle,A.- M.; Gicquel, I.; Le Gall, J.- Y.; David, V.: Localization of sevennew genes around the HLA- A locus. Hum. Molec. Genet. 2: 55- 60, 1993. 3 B c

GAM148 280 PPP1R11 Giffon, T.; Lepourcelet, M.; Pichon, L.; Jezequel, P.; Bouric,P.; Carn, G.; 3 B c
Pontarotti, P.; Le Gall, J.- Y.; David, V.: Cloningof a human homologue of
the mouse Tctex- 5 gene within the MHC classI region. Immunogenetics 44:
331- 339, 1996.

GAM148 280 PPP1R11 Lepourcelet, M.; Andrieux, N.; Giffon, T.; Pichon, L.; Hampe, A.;Galibert, 3 B c
F.; Mosser, J.: Systematic sequencing of the human HLA- A/HLA- Fregion:
establishment of a cosmid contig and identification of a newgene cluster
within 37 kb of sequence. Genomics 37: 316- 326, 1996.

GAM148 280 PPP1R11 Zhang, J.; Zhang, L.; Zhao, S.; Lee, E. Y. C.: Identificationand 3 B c
characterization of the human HCG V gene product as a novel inhibitorof
protein phosphatase- 1. Biochemistry 37: 16728- 16734, 1998.

GAM148 280 PPP2R4 McCright, B.; Rivers, A. M.; Audlin, S.; Virshup, D. M.: The B56family of 3 B c
protein phosphatase 2A (PP2A) regulatory subunits encodesdifferentiation-
induced phosphoproteins that target PP2A to both nucleusand cytoplasm. J.
Biol. Chem. 271: 22081- 22089, 1996.

GAM148 280 PPP2R4 Van Hoof, C.; Aly, M. S.; Garcia, A.; Cayla, X.; Cassiman, J. J.;Merlevede, 3 B c
W.; Goris, J.: Structure and chromosomal localizationof the human gene of
the phosphotyrosyl phosphatase activator (PTPA)of protein phosphatase 2A.
Genomics 28: 261- 272, 1995.

GAM148 280 PTGFRN Charrin, S.; Le Naour, F.; Oualid, M.; Billard, M.; Faure, G.,Hanash, S. M.; 3 B c
Boucheix, C.; Rubinstein, E.: The major CD9 and CD81molecular partner:
identification and characterization of the complexes. J.Biol. Chem. 276:
14329- 14337, 2001.

GAM148 280 PTGFRN Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of 3 B c
the coding sequences of unidentified human genes. XVI.The complete sequences
of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA
Res. 7: 65- 73, 2000.

GAM148 280 PTGFRN Orlicky, D. J.; Berry, R.; Sikela, J. M.: Human chromosome 1 localizationof 3 B c
the gene for a prostaglandin F- 2- alpha receptor negative
regulatoryprotein. Hum. Genet. 97: 655- 658, 1996.

GAM148 280 PTGFRN Stipp, C. S.; Orlicky, D.; Hemler, M. E.: FPRP, a major, 3 B c
highlystoichiometric, highly specific CD81- and CD9- associated protein.
J.Biol. Chem. 276: 4853- 4862, 2001.

GAM148 280 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 3 B c
Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly,
F.: Characterization of new mutations in the codingsequence and 5- prime-
untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum.
Genet. 108: 148- 155, 2001.

GAM148 280 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 3 B c
Molecular cloning and expression of human prostacyclin synthase.
Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM148 280 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 3 B c
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.;
Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences,
gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42,
1996.

GAM148 280 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 3 B c
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM148 280 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 3 B c
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase

(PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996.

GAM148 280 SLC21A2 Kanai, N.; Lu, R.; Satriano, J. A.; Bao, Y.; Wolkoff, A. W.; Schuster,V. L.: 3 B c
Identification and characterization of a prostaglandin transporter. Science 268:866- 869, 1995.

GAM148 280 SLC21A2 Lu, R.; Kanai, N.; Bao, Y.; Schuster, V. L.: Cloning, in vitroexpression, 3 B c
and tissue distribution of a human prostaglandin transportercDNA (hPGT). J. Clin. Invest. 98: 1142- 1149, 1996.

GAM148 280 SLC21A2 Lu, R.; Schuster, V. L.: Molecular cloning of the gene for thehuman 3 B c
prostaglandin transporter hPGT: gene organization, promoteractivity, and chromosomal localization. Biochem. Biophys. Res. Commun. 246:805- 812, 1998.

GAM148 280 TLL1 Clark, T. G.; Conway, S. J.; Scott, I. C.; Labosky, P. A.; Winnier,G.; 3 B c
Bundy, J.; Hogan, B. L. M.; Greenspan, D. S.: The mammalian Tolloid- like1 gene, Tll1, is necessary for normal septation and positioning ofthe heart. Development 126: 126:- 2631- 2642, 1999.

GAM148 280 TLL1 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; 3 B c
Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.; Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases, including novel family member mammalian Tolloid- like2, have differential enzymatic activities and distributions of expressionrelevant to patterning and skeletogenesis. Dev. Biol. 213: 283- 300,1999.

GAM148 280 TLL1 Scott, I. C.; Clark, T. G.; Takahara, K.; Hoffman, G. G.; Eddy,R. L.; Haley, 3 B c
L. L.; Shows, T. B.; Greenspan, D. S.: Assignment ofTLL1 and TLL2, which encode human BMP- 1/tolloid- related metalloproteases,to chromosomes 4q32- q33 and 10q23- q24 and assignment of murine Tll2to chromosome 19. Cytogenet. Cell Genet. 86: 64- 65, 1999.

GAM148 280 TLL1 Takahara, K.; Brevard, R.; Hoffman, G. G.; Suzuki, N.; Greenspan,D. S.: 3 B c
Characterization of a novel gene product (mammalian tolloid- like)with high sequence similarity to mammalian tolloid/bone morphogeneticprotein- 1. Genomics 34: 157- 165, 1996.

GAM148 280 TNFRSF14 Carfi, A.; Willis, S. H.; Whitbeck, J. C.; Krummenacher, C.; Cohen,G. H.; 3 B c
Eisenberg, R. J.; Wiley, D. C.: Herpes simplex virus glycoproteinD bound to the human receptor HveA. Molec. Cell 8: 169- 179, 2001.

GAM148 280 TNFRSF14 Hsu, H.; Solovyev, I.; Colombero, A.; Elliott, R.; Kelley, M.;Boyle, W. J.: 3 B c
ATAR, a novel tumor necrosis factor receptor familymember, signals through TRAF2 and TRAF5. J. Biol. Chem. 272: 13471- 13474,1997.

GAM148 280 TNFRSF14 Kwon, B. S.; Tan, K. B.; Ni, J.; Oh, K.- O.; Lee, Z. H.; Kim, K.K.; Kim, Y.- 3 B c
J.; Wang, S.; Gentz, R.; Yu, G.- L.; Harrop, J.; Lyn, S.D.; Silverman, C.; Porter, T. G.; Truneh, A.; Young, P. R.: A newlyidentified member of the tumor necrosis factor receptor superfamilywith a wide tissue distribution and involvement in lymphocyte activation. J.Biol. Chem. 272: 14272- 14276, 1997.

GAM148 280 TNFRSF14 Marsters, S. A.; Ayres, T. M.; Skubatch, M.; Gray, C. L.; Rothe,M.; 3 B c
Ashkenazi, A.: Herpesvirus entry mediator, a member of the tumornecrosis factor receptor (TNFR) family, interacts with members ofthe TNFR- associated factor family and activates the transcriptionfactors NF- kappa- B and AP- 1. J. Biol. Chem. 272: 14029- 14032, 1997.

GAM148 280 TNFRSF14 Montgomery, R. I.; Warner, M. S.; Lum, B. J.; Spear, P. G.: Herpessimplex 3 B c
virus- 1 entry into cells mediated by a novel member of theTNF/NGF receptor family. Cell 87: 427- 436, 1996.

GAM148 280 TNFRSF14 Morel, Y.; Schiano de Colella, J.- M.; Harrop, J.; Deen, K. C.;Holmes, S. D.; Wattam, T. A.; Khandekar, S. S.; Truneh, A.; Sweet,R. W.; Gastaut, J.- A.; Olive, D.; Costello, R. T.: Reciprocal expressionof the TNF family receptor herpes virus entry mediator and its ligandLIGHT on activated T cells: LIGHT down- regulates its own receptor. J.Immun. 165: 4397- 4404, 2000. 3 B c

GAM148 280 TRADD Hsu, H.; Xiong, J.; Goeddel, D. V.: The TNF receptor 1- associatedprotein TRADD signals cell death and NF- kappa- B activation. Cell 81:495- 504, 1995. 3 B b

GAM148 280 TRADD Pan, M.- G.; Xiong, J.; Copeland, N. G.; Gilbert, D. J.; Jenkins,N. A.; Goeddel, D. V.: Sequence, genomic organization, and chromosomelocalization of the mouse TRADD gene. J. Inflamm. 46: 168- 175, 1996. 3 B b

GAM148 280 TRADD Park, Y. C.; Ye, H.; Hsia, C.; Segal, D.; Rich, R. L.; Liou, H.- C.;Myszka, D. G.; Wu, H.: A novel mechanism of TRAF signaling revealedby structural and functional analyses of the TRADD- TRAF2 interaction. Cell 101:777- 787, 2000. 3 B b

GAM148 280 TRADD Scheuerpflug, C. G.; Lichter, P.; Debatin, K.- M.; Mincheva, A.: Assignment of TRADD to human chromosome band 16q22 by in situ hybridization. Cytogenet.Cell Genet. 92: 347- 348, 2001. 3 B b

GAM148 280 TRAP240 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC complexes indicates novel pathways for the functionof nuclear receptors and diverse mammalian activators. Molec. Cell 3:361- 370, 1999. 3 B c

GAM148 280 TRAP240 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998. 3 B c

GAM148 280 TSN Aoki, K.; Inazawa, J.; Takahashi, T.; Nakahara, K.; Kasai, M.:Genomic structure and chromosomal localization of the gene encodingtranslin, a recombination hotspot binding protein. Genomics 43:237- 241, 1997. 3 B c

GAM148 280 TSN Aoki, K.; Nakahara, K.; Ikegawa, C.; Seto, M.; Takahashi, T.; Minowada,J.; Strominger, J. L.; Maziarz, R. T.; Kasai, M.: Nuclear proteinsbinding to a novel target sequence within the recombination hotspotregions of Bcl- 2 and the immunoglobulin D(H) gene family. Oncogene 9:1109- 1115, 1994. 3 B c

GAM148 280 TSN Aoki, K.; Suzuki, K.; Sugano, T.; Tasaka, T.; Nakahara, K.; Kuge,O.; Omori, A.; Kasai, M.: A novel gene, 'Translin,' encodes a recombinationhotspot binding protein associated with chromosomal translocations. NatureGenet. 10: 167- 174, 1995. 3 B c

GAM148 280 TSN Badge, R. M.; Yardley, J.; Jeffreys, A. J.; Armour, J. A. L.:Crossover breakpoint mapping identifies a subtelomeric hotspot formale meiotic recombination. Hum. Molec. Genet. 9: 1239- 1244, 2000. 3 B c

GAM148 280 TSN Hosaka, T.; Kanoe, H.; Nakayama, T.; Murakami, H.; Yamamoto, H.;Nakamata, T.; Tsuboyama, T.; Oka, M.; Kasai, M.; Sasaki, M. S.; Nakamura,T.; Toguchida, J.: Translin binds to the sequences adjacent to thebreakpoints of the TLS and CHOP genes in liposarcomas with translocationt(12;16). Oncogene 19: 5821- 5825, 2000. 3 B c

GAM148 280 TSN Kasai, M.; Aoki, K.; Matsuo, Y.; Minowada, J.; Maziarz, R. T.;Strominger, J. L.: Recombination hotspot associated factors specificallyrecognize novel target sequences at the site of interchromosomal rearrangementsin T- ALL patients with t(8;14)(q24;q11)and (t(1;14)(p32;q11). Int.Immun. 6: 1017- 3 B c

1025, 1994.

GAM148 280 UGT2B4 Burchell, B.; Nebert, D. W.; Nelson, D. R.; Bock, K. W.; Iyanagi,T.; Jansen, P. L. M.; Lancet, T.; Mulder, G. J.; Chowdhury, J. R.;Siest, G.; Tephly, T. R.; Mackenzie, P. I.: The UDP- glucuronosyltransferasegene superfamily: suggested nomenclature based on evolutionary divergence. DNACell Biol. 10: 487- 494, 1991. 3 B c

GAM148 280 UGT2B4 Jackson, M. R.; McCarthy, L. R.; Harding, D.; Wilson, S.; Coughtrie,M. W. H.; Burchell, B.: Cloning of a human liver microsomal UDP-glucuronosyltransferasecDNA. Biochem. J. 242: 581- 588, 1987. 3 B c

GAM148 280 UGT2B4 Jin, C.- J.; Miners, J. O.; Lillywhite, K. J.; Mackenzie, P. I.: cDNA cloning and expression of two new members of the human liverUDP-glucuronosyltransferase 2B subfamily. Biochem. Biophys. Res.Commun. 194: 496- 503, 1993. 3 B c

GAM148 280 UGT2B4 Krasnewich, D.; Kozak, C. A.; Nebert, D. W.; Mackenzie, P. I.:Localization of UDP glucuronosyltransferase gene(s) on mouse chromosome 3 B c

GAM148 280 UGT2B4 Monaghan, G.; Povey, S.; Burchell, B.; Boxer, M.: Localizationof a bile acid UDP- glucuronosyltransferase gene (UGT2B) to chromosome4 using the polymerase chain reaction. Genomics 13: 908- 909, 1992. 3 B c

GAM148 280 UGT2B4 Riedy, M.; Wang, J. Y.; Miller, A. P.; Buckler, A.; Hall, J.; Guida,M.: Genomic organization of the UGT2b gene cluster on human chromosome4q13. Pharmacogenetics 10: 251- 260, 2000. 3 B c

GAM148 280 UGT2B4 Somat. Cell Molec. Genet. 13: 179- 182, 1987.5. Monaghan, G.; Clarke, D. J.; Povey, S.; See, C. G.; Boxer, M.;Burchell, B.: Isolation of a human YAC contig encompassing a clusterof UGT2 genes and its regional localization to chromosome 4q13. Genomics 23:496- 499, 1994. 3 B c

GAM148 280 XPNPEP2 Prueitt, R. L.; Ross, J. L.; Zinn, A. R.: Physical mapping ofnine Xq translocation breakpoints and identification of XPNPEP2 asa premature ovarian failure candidate gene. Cytogenet. Cell Genet. 89:44- 50, 2000. 3 B c

GAM148 280 XPNPEP2 Sprinkle, T. J.; Stone, A. A.; Venema, R. C.; Denslow, N. D.; Caldwell,C.; Ryan, J. W.: Assignment of the membrane- bound human aminopeptidaseP gene (XPNPEP2) to chromosome Xq25. Genomics 50: 114- 116, 1998. 3 B c

GAM148 280 XPNPEP2 Venema, R. C.; Ju, H.; Zou, R.; Venema, V. J.; Ryan, J. W.: Cloningand tissue distribution of human membrane- bound aminopeptidase P. Biochim.Biophys. Acta 1354: 45- 48, 1997. 3 B c

GAM152 378 ANXA7 Burns, A. L.; Magendzo, K.; Shirvan, A.; Srivastava, M.; Rojas,E.; Alijani, M. R.; Pollard, H. B.: Calcium channel activity of purifiedhuman synexin and structure of the human synexin gene. Proc. Nat.Acad. Sci. 86: 3798- 3802, 1989. 3 C c

GAM152 378 ANXA7 Caohuy, H.; Srivastava, M.; Pollard, H. B.: Membrane fusion proteinsynexin (annexin VII) as a Ca(2+)/GTP sensor in exocytotic secretion. Proc.Nat. Acad. Sci. 93: 10797- 10802, 1996. 3 C c

GAM152 378 ANXA7 Herr, C.; Smyth, N.; Ullrich, S.; Yun, F.; Sasse, P.; Hescheler,J.; Fleischmann, B.; Lasek, K.; Brixius, K.; Schwinger, R. H. G.;Fassler, R.; Schroder, R.; Noegel, A. A.: Loss of annexin A7 leadsto alterations in frequency- induced shortening of isolated murinecardiomyocytes. Molec. Cell. Biol. 21: 4119- 4128, 2001. 3 C c

GAM152 378 ANXA7 Magendzo, K.; Shirvan, A.; Cultraro, C.; Srivastava, M.; Pollard,H. B.; Burns, A. L.: Alternative splicing of human synexin mRNA inbrain, cardiac, and skeletal muscle alters the unique N- terminal domain. J.Biol. Chem. 266: 3228- 3232, 1991. 3 C c

GAM152 378 ANXA7 Shirvan, A.; Srivastava, M.; Wang, M. G.; Cultraro, C.; Magendzo,K.; McBride, O. W.; Pollard, H. B.; Burns, A. L.: Divergent structureof the human synexin (annexin VII) gene and assignment to chromosome10. Biochemistry 33: 6888- 6901, 1994. 3 C c

GAM152 378 ANXA7 Srivastava, M.; Atwater, I.; Glasman, M.; Leighton, X.; Goping,G.; Caohuy, H.; Miller, G.; Pichel, J.; Westphal, H.; Mears, D.; Rojas,E.; Pollard, H. B.: Defects in inositol 1,4,5- trisphosphate receptorexpression, Ca(2+) signaling, and insulin secretion in the anx7(+/-)knockout mouse. Proc. Nat. Acad. Sci. 96: 13783- 13788, 1999. 3 C c

GAM152 378 ANXA7 Srivastava, M.; Bubendorf, L.; Srikantan, V.; Fossom, L.; Nolan,L.; Glasman, M.; Leighton, X.; Fehrle, W.; Pittaluga, S.; Raffeld,M.; Koivisto, P.; Willi, N.; Gasser, T. C.; Kononen, J.; Sauter, G.;Kallioniemi, O. P.; Srivastava, S.; Pollard, H. B.: ANX7, a candidatetumor suppressor gene for prostate cancer. Proc. Nat. Acad. Sci. 98:4575- 4580, 2001. 3 C c

GAM152 378 ANXA7 Zhang- Keck, Z.- Y.; Srivastava, M.; Kozak, C. A.; Caohuy, H.; Shirvan,A.; Burns, A. L.; Pollard, H. B.: Genomic organization and chromosomallocalization of the mouse synexin gene. Biochem. J. 301: 835- 845,1994. 3 C c

GAM152 378 NLGN1 Ichtchenko, K.; Hata, Y.; Nguyen, T.; Ullrich, B.; Missler, M.;Moomaw, C.; Sudhof, T. C.: Neuroligin 1: a splice site- specific ligandfor beta- neurexins. Cell 81: 435- 443, 1995. 3 C c

GAM152 378 NLGN1 Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirosawa, M.; Miyajima, N.;Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of unidentified human genes. XIV. The complete sequencesof 100 new cDNA clones from brain which code for large proteins invitro. DNA Res. 6: 197- 205, 1999. 3 C c

GAM152 378 NLGN1 Scheiffele, P.; Fan, J.; Choih, J.; Fetter, R.; Serafini, T.:Neuroligin expressed in nonneuronal cells triggers presynaptic developmentin contacting axons. Cell 101: 657- 669, 2000. 3 C c

GAM153 244 DDIT3 Aman, P.; Ron, D.; Mandahl, N.; Fioretos, T.; Heim, S.; Arheden,K.; Willen, H.; Rydholm, A.; Mitelman, F.: Rearrangement of the transcriptionfactor gene CHOP in myxoid liposarcomas with t(12;16)(q13;p11). GenesChromosomes Cancer 5: 278- 285, 1992. 3 C c

GAM153 244 DDIT3 Crozat, A.; Aman, P.; Mandahl, N.; Ron, D.: Fusion of CHOP toa novel RNA- binding protein in human myxoid liposarcoma. Nature 363:640- 644, 1993. 3 C c

GAM153 244 DDIT3 Mrozek, K.; Karakousis, C. P.; Bloomfield, C. D.: Chromosome 12breakpoints are cytogenetically different in benign and malignantlipogenic tumors: localization of breakpoints in lipoma to 12q15 andin myxoid liposarcoma to 12q13.3. Cancer Res. 53: 1670- 1675, 1993. 3 C c

GAM153 244 DDIT3 Panagopoulos, I.; Aman, P.; Mertens, F.; Mandahl, N.; Rydholm,A.; Bauer, H. F. C.; Mitelman, F.: Genomic PCR detects tumor cellsin peripheral blood from patients with myxoid liposarcoma. GenesChromosomes Cancer 17: 102- 107, 1996. 3 C c

GAM153 244 DDIT3 Park, J. S.; Luethy, J. D.; Wang, M. G.; Fargnoli, J.; Fornace,A. J., Jr.; McBride, O. W.; Holbrook, N. J.: Isolation, characterizationand chromosomal localization of the human GADD153 gene. Gene 116:259- 267, 1992. 3 C c

GAM153 244 DDIT3 Rabbitts, T. H.; Forster, A.; Larson, R.; Nathan, P.: Fusion ofthe dominant negative transcription regulator CHOP with a novel geneFUS by translocation t(12;16) in malignant liposarcoma. Nature Genet. 4:175- 180, 1993. 3 C c

GAM153 244 DDIT3 Ron, D.; Habener, J. F.: CHOP, a novel developmentally regulatednuclear 3 C c

protein that dimerizes with transcription factors C/EBP andLAP and functions as a dominant- negative inhibitor of gene transcription. GenesDev. 6: 439-453, 1992.

GAM155 207 PTGS1 Catella- Lawson, F.; Reilly, M. P.; Kapoor, S. C.; Cucchiara, A.J.; DeMarco, S.; Tournier, B.; Vyas, S. N.; FitzGerald, G. A.: Cyclooxygenaseinhibitors and the antiplatelet effects of aspirin. New Eng. J. Med. 345:1809- 1817, 2001. 3 C c

GAM155 207 PTGS1 Dube, J.- N.; Drouin, J.; Aminian, M.; Plant, M. H.; Laneuville,O.: Characterization of a partial prostaglandin endoperoxide H synthase-1deficiency in a patient with a bleeding disorder. Brit. J. Haemat. 113:878-885, 2001. 3 C c

GAM155 207 PTGS1 Funk, C. D.; Funk, L. B.; Kennedy, M. E.; Pong, A. S.; Fitzgerald,G. A.: Human platelet/erythroleukemia cell prostaglandin G/H synthase:cDNA cloning, expression, and gene chromosomal assignment. FASEBJ. 5: 2304- 2312, 1991. 3 C c

GAM155 207 PTGS1 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.; Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999. 3 C c

GAM155 207 PTGS1 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.: Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2 in the humanfetal and adult male reproductive tracts. J. Clin. Endocr. Metab. 85:3436- 3441, 2000. 3 C c

GAM155 207 PTGS1 Langenbach, R.; Morham, S. G.; Tiano, H. F.; Loftin, C. D.; Ghanayem,B. I.; Chulada, P. C.; Mahler, J. F.; Lee, C. A.; Goulding, E. H.;Kluckman, K. D.; Kim, H. S.; Smithies, O.: Prostaglandin synthase1 gene disruption in mice reduces arachidonic acid- induced inflammationand indomethacin- induced gastric ulceration. Cell 83: 483- 492, 1995. 3 C c

GAM155 207 PTGS1 Malkowski, M. G.; Ginell, S. L.; Smith, W. L.; Garavito, R. M.: The productive conformation of arachidonic acid bound to prostaglandinsynthase. Science 289: 1933- 1937, 2000. 3 C c

GAM155 207 PTGS1 Pareti, F. I.; Manucci, P. M.; D'Angelo, A.; Smith, J. B.; Sautebin,L.; Galli, G.: Congenital deficiency of thromboxane and prostacyclin. Lancet I:898- 900, 1980. 3 C c

GAM155 207 PTGS1 Picot, D.; Loll, P. J.; Garavito, R. M.: The x- ray crystal structureof the membrane protein prostaglandin H- 2 synthase- 1. Nature 367:243- 249, 1994. 3 C c

GAM155 207 PTGS1 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93: 705- 716, 1998. 3 C c

GAM155 207 PTGS1 Vane, J. R.; Mitchell, J. A.; Appleton, I.; Tomlinson, A.; Bishop-Bailey,D.; Croxtall, J.; Willoughby, D. A.: Inducible isoforms of cyclooxygenaseand nitric- oxide synthase in inflammation. Proc. Nat. Acad. Sci. 91:2046- 2050, 1994. 3 C c

GAM155 207 PTGS1 Yokoyama, C.; Tanabe, T.: Cloning of human gene encoding prostaglandinendoperoxide synthase and primary structure of the enzyme. Biochem.Biophys. Res. Commun. 165: 888- 894, 1989. 3 C c

GAM156 262 CLTCL1 Holmes, S. E.; Riazi, M. A.; Gong, W.; McDermid, H. E.; Sellinger,B. T.; Hua, A.; Chen, F.; Wang, Z.; Zhang, G.; Roe, B.; Gonzalez,I.; McDonald-McGinn, D. M.; Zackai, E.; Emanuel, B. S.; Budarf, M.L.: Disruption of the clathrin heavy chain- like gene (CLTCL) associatedwith features of DGS/VCFS: 3 C c

a balanced (21;22)(p12;q11) translocation. Hum.Molec. Genet. 6: 357- 367, 1997.

GAM156 262 CLTCL1 Kedra, D.; Peyrard, M.; Fransson, I.; Collins, J. E.; Dunham, I.;Roe, B. A.; 3 C c
Dumanski, J. P.: Characterization of a second human clathrinheavy chain polypeptide gene (CLH- 22) from chromosome 22q11. Hum.Molec. Genet. 5: 625- 631, 1996.

GAM156 262 CLTCL1 Long, K. R.; Trofatter, J. A.; Ramesh, V.; McCormick, M. K.; Buckler,A. J.: 3 C c
Cloning and characterization of a novel human clathrin heavychain gene (CLTCL). Genomics 35: 466- 472, 1996.

GAM156 262 CLTCL1 Puech, A.; Saint- Jore, B.; Funke, B.; Gilbert, D. J.; Sirotkin,H.; 3 C c
Copeland, N. G.; Jenkins, N. A.; Kucherlapati, R.; Morrow, B.;Skoultchi, A. I.: Comparative mapping of the human 22q11 chromosomalregion and the orthologous region in mice reveals complex changesin gene organization. Proc. Nat. Acad. Sci. 94: 14608- 14613, 1997.

GAM156 262 CLTCL1 Sirotkin, H.; Morrow, B.; DasGupta, R.; Goldberg, R.; Patanjali,S. R.; Shi, 3 C c
G.; Cannizzaro, L.; Shprintzen, R.; Weissman, S. M.; Kucherlapati,R.: Isolation of a new clathrin heavy chain gene with muscle- specificexpression from the region commonly deleted in velo- cardio- facialsyndrome. Hum. Molec. Genet. 5: 617- 624, 1996.

GAM156 262 DAAM2 Habas, R.; Kato, Y.; He, X.: Wnt/Frizzled activation of Rho 3 C c
regulatesvertebrate gastrulation and requires a novel Formin homology proteinDaam1. Cell 107: 843- 854, 2001.

GAM156 262 DAAM2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM158 383 STX1A Bennett, M. K.; Calakos, N.; Scheller, R. H.: Syntaxin: a synapticprotein 3 C c
implicated in docking of synaptic vesicles at presynapticactive zones. Science 257: 255- 259, 1992.

GAM158 383 STX1A Bennett, M. K.; Garcia- Arraras, J. E.; Elferink, L. A.; Peterson,K.; 3 C c
Fleming, A. M.; Hazuka, C. D.; Scheller, R. H.: The syntaxinfamily of vesicular transport receptors. Cell 74: 863- 873, 1993.

GAM158 383 STX1A Fernandez, I.; Ubach, J.; Dulubova, I.; Zhang, X.; Sudof, T. C.;Rizo, J.: 3 C c
Three- dimensional structure of an evolutionarily conservedN- terminal domain of syntaxin 1A. Cell 94: 841- 849, 1998.

GAM158 383 STX1A Fisher, R. J.; Pevsner, J.; Burgoyne, R. D.: Control of fusionpore dynamics 3 C c
during exocytosis by Munc18. Science 291: 875- 878,2001.

GAM158 383 STX1A Hu, K.; Carroll, J.; Fedorovich, S.; Rickman, C.; Sukhodub, A.;Davietov, B.: 3 C c
Vesicular restriction of synaptobrevin suggests a rolefor calcium in membrane fusion. Nature 415: 646- 650, 2002.

GAM158 383 STX1A Martin- Martin, B.; Nabokina, S. M.; Lazo, P. A.; Mollinedo, F.: Co- 3 C c
expression of several human syntaxin genes in neutrophils anddifferentiating HL- 60 cells: various isoforms and detection of syntaxin1. J. Leuko. Biol. 65: 397- 406, 1999.

GAM158 383 STX1A McNew, J. A.; Parlati, F.; Fukuda, R.; Johnston, R. J.; Paz, K.;Paumet, F.; 3 C c
Sollner, T. H.; Rothman, J. E.: Compartmental specificityof cellular membrane fusion encoded in SNARE proteins. Nature 407:153- 159, 2000.

GAM158 383 STX1A Nakayama, T.; Fujiwara, T.; Miyazawa, A.; Asakawa, S.; Shimizu,N.; Shimizu, 3 C c
Y.; Mikoshiba, K.; Akagawa, K.: Mapping of the humanHPC- 1/syntaxin 1A gene

(STX1A) to chromosome 7 band q11.2. Genomics 42:173- 176, 1997.

GAM158 383 STX1A Naren, A. P.; Di, A.; Cormet- Boyaka, E.; Boyaka, P. N.; McGhee,J. R.; Zhou, W.; Akagawa, K.; Fujiwara, T.; Thome, U.; Engelhardt,J. F.; Nelson, D. J.; Kirk, K. L.: Syntaxin 1A is expressed in airwayepithelial cells, where it modulates CFTR C1- currents. J. Clin.Invest. 105: 377- 386, 2000. 3 C c

GAM158 383 STX1A Richmond, J. E.; Weimer, R. M.; Jorgensen, E. M.: An open formof syntaxin bypasses the requirement for UNC- 13 in vesicle priming. Nature 412:338- 341, 2001. 3 C c

GAM158 383 STX1A Weber, T.; Zemelman, B. V.; McNew, J. A.; Westermann, B.; Gmachi,M.; Parlati, F.; Sollner, T. H.; Rothman, J. E.: SNAREpins: minimalmachinery for membrane fusion. Cell 92: 759- 772, 1998. 3 C c

GAM158 383 STX1A Zhang, R.; Maksymowych, A. B.; Simpson, L. L.: Cloning and sequenceanalysis of a cDNA encoding human syntaxin 1A, a polypeptide essentialfor exocytosis. Gene 159: 293- 294, 1995. 3 C c

GAM161 304 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- evaluation of 'reactive lymphoid hyperplasia of the uvea': animmunohistochemical and molecular analysis of 10 cases. Ophthalmology 107:151- 158, 2000. 3 C c

GAM161 304 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999. 3 C c

GAM161 304 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. J.Clin. Path. 48: 395- 397, 1995. 3 C c

GAM161 304 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T. W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001. 3 C c

GAM161 304 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not its cellular homologue, activates NF- kappa- B transcriptionfactor and c- Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999. 3 C c

GAM161 304 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.; Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types Cell 96: 35- 45, 1999. 3 C c

GAM161 304 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer Genet. Cytogenet. 58: 35- 38, 1992. 3 C c

GAM161 304 CDH17 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999. 3 C c

GAM161 304 CDH17 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck, P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with a protein related to the cadherin superfamily. Science 264:430- 433, 1994. 3 C c

GAM161 304 CDH17 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, D. F.: Localization of human cadherin genes to chromosomeregions exhibiting cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998. 3 C c

GAM161 304 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 3 C c

155: 1203- 1209, 1995.

GAM161 304 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 3 C c

GAM161 304 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665- 1672, 1990. 3 C c

GAM161 304 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681- 1685, 1993. 3 C c

GAM161 304 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 3 C c

GAM161 304 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 3 C c

GAM161 304 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 3 C c

GAM161 304 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001. 3 C c

GAM161 304 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999. 3 C c

GAM161 304 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 C c

GAM161 304 HTR1E Levy, F. O.; Gudermann, T.; Birnbaumer, M.; Kaumann, A. J.; Birnbaumer,L.: Molecular cloning of a human gene (S31) encoding a novel serotoninreceptor mediating inhibition of adenylyl cyclase. FEBS Lett. 296:201- 206, 1992. 3 C c

GAM161 304 HTR1E Levy, F. O.; Holtgreve- Grez, H.; Tasken, K.; Solberg, R.; Ried,T.; Gudermann, T.: Assignment of the gene encoding the 5- HT- 1E serotoninreceptor (S31) (locus HTR1E) to human chromosome 6q14- q15. Genomics 22:637- 640, 1994. 3 C c

GAM161 304 HTR1E McAllister, G.; Charlesworth, A.; Snodin, C.; Beer, M. S.; Noble,A. J.; Middlemiss, D. N.; Iversen, L. L.; Whiting, P.: Molecularcloning of a serotonin receptor from human brain (5HT1E): a fifth5HT1- like subtype. Proc. Nat. Acad. Sci. 89: 5517- 5521, 1992. 3 C c

GAM161 304 IFNAR2 Croze, E.; Russell- Harde, D.; Wagner, T. C.; Pu, H.; Pfeffer, L.M.; Perez, H. D.: The human type I interferon receptor: identificationof the interferon beta- specific receptor- associated phosphoprotein. J.Biol. Chem. 271: 33165- 33168, 1996. 3 C c

GAM161 304 IFNAR2 Croze, E.; Usacheva, A.; Asarnow, D.; Minshall, R.D.; Perez, H.D.;Colamonici, O.: Receptor for activated C- kinase (RACK- 1), a WD motif-containingprotein, specifically associates with the human type I IFN 3 C c

receptor. J.Immun. 165: 5127- 5132, 2000.

GAM161 304 IFNAR2 Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.;Pitha, P.; 3 C c
Colamonici, O. R.: Cloning and expression of a long formof the beta subunit
of the interferon alpha/beta receptor that isrequired for signaling. J.
Biol. Chem. 270: 21606- 21611, 1995.

GAM161 304 IFNAR2 Lutfalla, G.; Holland, S. J.; Cinato, E.; Monneron, D.; Reboul,J.; Rogers, 3 C c
N. C.; Smith, J. M.; Stark, G. R.; Gardiner, K.; Mogensen,K. E.; Kerr, I.
M.; Uze, G.: Mutant U5A cells are complemented byan interferon- alpha/beta
receptor subunit generated by alternativeprocessing of a new member of a
cytokine receptor gene cluster. EMBOJ. 14: 5100- 5108, 1995.

GAM161 304 IFNAR2 Novick, D.; Cohen, B.; Rubinstein, M.: The human interferon 3 C c
alpha/betareceptor: characterization and molecular cloning. Cell 77: 391-
400,1994.

GAM161 304 IFNAR2 Platanias, L. C.; Uddin, S.; Domanski, P.; Colamonici, O. R.:Differences in 3 C c
interferon alpha and beta signaling: interferon betaselectively induces the
interaction of the alpha and beta(L) subunitsof the type I interferon
receptor. J. Biol. Chem. 271: 23630- 23633,1996.

GAM161 304 IFNAR2 Raz, R.; Cheung, K.; Ling, L.; Levy, D. E.: Three distinct locion human 3 C c
chromosome 21 contribute to interferon- alpha/beta responsiveness.
Somat.Cell Molec. Genet. 21: 139- 145, 1995.

GAM161 304 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 C c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator.
J. Biol. Chem. 275: 5308- 5317, 2000.

GAM161 304 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 C c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation
of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer
Res. 56: 3446- 3450, 1996.

GAM161 304 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 C c
bindingprotein, an LXXLL motif- containing protein, functions as a
generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM161 304 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 C c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-
H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor,
ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for
ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol.
Chem. 274: 34283- 34293, 1999.

GAM161 304 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 C c
that integrate nuclear receptor signaling through CREB- bindingprotein.
Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM161 304 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 C c
coding sequences of unidentified human genes. V. The codingsequences of 40
new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM161 304 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 C c
J. K.: Isolation and characterization of peroxisomeproliferator- activated
receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.
Biol. Chem. 275: 13510- 13516, 2000.

GAM161 304 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 3 C c
an ethanol- responsive potential modulator of guanine nucleotide-
bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM161 304 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 C c
Cloning and characterization of the rat and human phosducin- likeprotein
genes: structure, expression and chromosomal localization. Biochim.Biophys.
Acta 1444: 346- 354, 1999.

GAM161 304 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 C c
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component
of the steroid receptor complex: cloning of thecDNA and further
characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM161 304 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 C c
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem.
267: 5503- 5507, 1992.

GAM161 304 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 C c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151
only, 1997.

GAM161 304 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 C c
J.- E.: The structure and complete nucleotide sequenceof the human
cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM161 304 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 C b
Chromosomalassignment of the interferon- inducible double- stranded RNA-
dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse
chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM161 304 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human 3 C b
interferon- gamma mRNA autoregulates its translation througha pseudoknot
that activates the interferon- inducible protein kinasePKR. Cell 108: 221-
232, 2002.

GAM161 304 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; 3 C b
Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR)
encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and
differences from its mouse homolog. Genomics 36:197- 201, 1996.

GAM161 304 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: 3 C b
sequence of the human interferon- inducible RNA- dependent proteinkinase
(PKR) deduced from genomic clones. Gene 178: 191- 193, 1996.

GAM161 304 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; 3 C b
Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand
characterization of the human double- stranded RNA- activated proteinkinase
induced by interferon. Cell 62: 379- 390, 1990.

GAM161 304 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; 3 C b
Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds
preferentially to Huntington's disease (HD) transcriptsand is activated in
HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001.

GAM161 304 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. 3 C b
G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-
RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics
16:768- 770, 1993.

GAM161 304 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: 3 C b
Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein.
Science 285: 107- 110, 1999.

GAM161 304 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; 3 C c
Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in
RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993.

GAM161 304 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 3 C c
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA
amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM161 304 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. 3 C c
Med. 339: 1775- 1777, 1998.

GAM161 304 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand 3 C c
molecular genetics. Blood Rev. 8: 199- 212, 1994.

GAM161 304 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; 3 C c
Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood
group polymorphism as determined by Southern analysis. Blood 78:2747- 2752,
1991.

GAM161 304 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and 3 C c
its association with universal edema of the fetus, icterusgravis neonatorum
and anemia of the newborn. J. Pediat. 1: 269- 309,1932.

GAM161 304 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies 3 C c
in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989.

GAM161 304 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with 3 C c
sickle cell disease. Transfusion 37: 357- 361, 1997.

GAM161 304 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 C c

GAM161 304 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the 3 C c
human RH locus: a family study of the red- cell Evans phenotypereveals a
transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59:
825- 833, 1996.

GAM161 304 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular 3 C c
definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J.
Hum. Genet. 58: 133- 142, 1996.

GAM161 304 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of 3 C c
Rh blood group genes: association between restrictionfragment length
polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994.

GAM161 304 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine 3 C c
years and some observations on the biochemistry and geneticsof the system.
Transfusion Med. Rev. 3: 1- 12, 1989.

GAM161 304 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh 3 C c
genes revealed by analysis of unrelated donors with therare D- - phenotype.
Am. J. Hum. Genet. 59: 1066- 1073, 1996.

GAM161 304 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, 3 C c
J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by
alternative splicing. Blood 80: 1074- 1078, 1992.

GAM161 304 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; 3 C c
Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the
human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929,
1992.

GAM161 304 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; 3 C c
Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE
genotyping for correct blood group determination inchronically transfused
patients. Transfusion 39: 852- 855, 1999.

GAM161 304 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its 3 C c
possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A.
116:825- 827, 1941.

GAM161 304 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; 3 C c

Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal plasma. New Eng. J. Med. 339: 1734- 1738, 1998.

GAM161 304 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; 3 C c
Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome 1. Am. J. Med. Genet. 104: 250- 256, 2001.

GAM161 304 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, 3 C c
E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J. Clin. Invest. 100: 373- 379, 1997.

GAM161 304 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 C c
153:771- 772, 1944.

GAM161 304 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 C c
ed.): 1975.

GAM161 304 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 3 C c
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII) category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM161 304 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 3 C c
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral transduction of K562 cells establishes the molecular basisof Rh blood group antigens. Blood 87: 2968- 2973, 1996.

GAM161 304 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 3 C c
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang. 58: 50- 55, 1990.

GAM161 304 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 3 C c
Blood 95: 3662- 3668, 2000.

GAM161 304 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 3 C c
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393, 1999.

GAM161 304 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 3 C c
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311, 2002.

GAM161 304 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 C c

GAM161 304 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from 3 C c
lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998.

GAM161 304 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; 3 C c
Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle-membranefusion processes. Hum. Genet. 108: 211- 215, 2001.

GAM161 304 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- 3 C c
membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells. Biochem. Biophys. Res. Commun. 231: 808- 812, 1997.

GAM161 304 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel 3 C c
syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996.

GAM161 304 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: 3 C c
Identification of three new splice variants of the SNARE proteinSNAP- 23. Biochem. Biophys. Res. Commun. 285: 320- 327, 2001.

GAM161 304 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459-467, 1998. 3 C c

GAM161 304 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 C c

GAM161 304 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 C c

GAM161 304 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 C c

GAM161 304 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 C c

GAM161 304 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 C c

GAM161 304 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496-1498, 2002. 3 C c

GAM161 304 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8: 165- 167, 1990. 3 C c

GAM161 304 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 homeoprotein family are expressed in human liver. NucleicAcids Res. 19: 3553- 3559, 1991. 3 C c

GAM161 304 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.; Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene are associated with familial hypoplastic glomerulocystickidney disease. Am. J. Hum. Genet. 68: 219- 224, 2001. 3 C c

GAM161 304 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.; Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated with a frameshift mutation in the transcription factorhepatocyte nuclear factor- 1- beta. Kidney Int. 57: 898- 907, 2000. 3 C c

GAM161 304 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara, T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997. 3 C c

GAM161 304 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic glomerulocystic kidney disease: a definite entity withdominant inheritance. Am. J. Med. Genet. 34: 569- 573, 1989. 3 C c

GAM161 304 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand 3 C c

genital malformation associated with a partial deletion of thepseudo- POU domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001-2008, 1999.

GAM161 304 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, S.: A low renal threshold for glucose in diabetic patientswith a mutation in the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med. 15: 816- 820, 1998. 3 C c

GAM161 304 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in the hepatocyte nuclear factor- 1- beta gene associated with diabetesand renal dysfunction. Diabetes 47: 1354- 1355, 1998. 3 C c

GAM161 304 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18: 263- 268, 1982. 3 C c

GAM161 304 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott-Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G. U.: The mutated human gene encoding hepatocyte nuclear factor1- beta inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad. Sci. 97: 4695- 4700, 2000. 3 C c

GAM161 304 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.; Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1 are associated with human left- right lateralitydefects. Nature Genet. 26: 365- 369, 2000. 3 C c

GAM161 304 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989. 3 C c

GAM161 304 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002. 3 C c

GAM161 304 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991. 3 C c

GAM161 304 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997. 3 C c

GAM161 304 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996. 3 C c

GAM161 304 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995. 3 C c

GAM161 304 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in vertebratedevelopment. Trends Genet. 16: 303- 309, 2000. 3 C c

GAM161 304 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor-associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF-kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997. 3 C c

GAM161 304 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, 3 C c
H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal
transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661-
14664, 1996.

GAM161 304 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; 3 C c
Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.;
Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted
disruption of Traf5 gene causes defectsin CD40- and CD27- mediated
lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999.

GAM161 304 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. 3 C c
F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.:
Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and
assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997.

GAM161 304 TRPM6 Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; 3 C c
Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.;
Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.:
Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a
new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002.

GAM161 304 TRPM6 Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; 3 C c
Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.;
Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with
secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002.

GAM161 304 TRPM6 Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, 3 C c
D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.:
Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome:
genetic linkage mapping and analysis of abalanced translocation breakpoint.
Hum. Molec. Genet. 6: 1491- 1497,1997.

GAM161 304 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. 3 C c
F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.;
Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and
high resolution restriction map of the2 megabase region containing the
Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM161 304 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 C c
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple
myeloma is associated with increased expression and activatingmutations of
fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM161 304 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, 3 C c
R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel
chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the
fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997.

GAM161 304 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van 3 C c
Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a
90 kb SET domain- containing gene, expressed in earlydevelopment and
homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn
syndrome critical region and is fused to IgH int(4;14) multiple myeloma.
Hum. Molec. Genet. 7: 1071- 1082, 1998.

GAM161 304 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; 3 C c
Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.;
Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly
defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet.

6: 317- 324, 1997.

GAM163 249 EDG6 Graler, M. H.; Bernhardt, G.; Lipp, M.: EDG6, a novel G- protein- 3 C c
coupledreceptor related to receptors for bioactive lysophospholipids,
isspecifically expressed in lymphoid tissue. Genomics 53: 164- 169,1998.

GAM163 249 EDG6 Jedlicka, A. E.; Taylor, E. W.; Meyers, D. A.; Liu, Z.; Levitt,R. C.: 3 C c
Localization of the highly polymorphic locus D19S120 to 19p13.3by linkage.
Cytogenet. Cell. Genet. 65: 140 only, 1994.

GAM163 249 OLIG2 Lu, Q. R.; Park, J. K.; Noll, E.; Chan, J. A.; Alberta, J.; Yuk,D.; 3 C c
Alzamora, M. G.; Louis, D. N.; Stiles, C. D.; Rowitch, D. H.;Black, P. M.:
Oligodendrocyte lineage genes (OLIG) as molecular markersfor human glial
brain tumors. Proc. Nat. Acad. Sci. 98: 10851- 10856,2001.

GAM163 249 OLIG2 Lu, Q. R.; Sun, T.; Zhu, Z.; Ma, N.; Garcia, M.; Stiles, C. D.;Rowitch, D. 3 C c
H.: Common developmental requirement for Olig functionindicates a motor
neuron/oligodendrocyte connection. Cell 109: 75- 86,2002.

GAM163 249 OLIG2 Lu, Q. R.; Yuk, D.; Alberta, J. A.; Zhu, Z.; Pawlitzky, I.; Chan,J.; 3 C c
McMahon, A. P.; Stiles, C. D.; Rowitch, D. H.: Sonic hedgehog-
regulatedoligodendrocyte lineage genes encoding bHLH proteins in the
mammaliancentral nervous system. Neuron 25: 317- 329, 2000.

GAM163 249 OLIG2 Raff, M. C.; Miller, R. H.; Noble, M.: A glial progenitor cellthat develops 3 C c
in vitro into an astrocyte or an oligodendrocyte dependingon culture medium.
Nature 303: 390- 396, 1983.

GAM163 249 OLIG2 Zhou, Q.; Anderson, D. J.: The bHLH transcription factors OLIG2and OLIG1 3 C c
couple neuronal and glial subtype specification. Cell 109:61- 73, 2002.

GAM163 249 OLIG2 Zhou, Q.; Wang, S.; Anderson, D. J.: Identification of a novelfamily of 3 C c
oligodendrocyte lineage- specific basic helix- loop- helixtranscription
factors. Neuron 25: 331- 343, 2000.

GAM165 270 ARHC Cannizzaro, L. A.; Madaule, P.; Hecht, F.; Axel, R.; Croce, C.M.; Huebner, 3 C c
K.: Chromosome localization of human ARH genes, a ras- relatedgene family.
Genomics 6: 197- 203, 1990.

GAM165 270 ARHC Chardin, P.; Madaule, P.; Tavitian, A.: Coding sequence of humanrho cDNAs 3 C c
clone 6 and clone 9. Nucleic Acid Res. 16: 2717 only,1988.

GAM165 270 ARHC Clark, E. A.; Golub, T. R.; Lander, E. S.; Hynes, R. O.: Genomicanalysis of 3 C c
metastasis reveals an essential role for RhoC. Nature 406:532- 535, 2000.

GAM165 270 ARHC Fagan, K. P.; Oliveira, L.; Pittler, S. J.: Sequence of rho smallGTP- 3 C c
binding protein cDNAs from human retina and identification ofnovel 5- prime
end cloning artifacts. Exp. Eye Res. 59: 235- 237,1994.

GAM165 270 ARHC Madaule, P.; Axel, R.: A novel ras- related gene family. Cell 41:31- 40, 3 C c
1985.

GAM165 270 ARHC Maekawa, M.; Ishizaki, T.; Boku, S.; Watanabe, N.; Fujita, A.;Iwamatsu, A.; 3 C c
Obinata, T.; Ohashi, K.; Mizuno, K.; Narumiya, S.:Signaling from Rho to the
actin cytoskeleton through protein kinasesROCK and LIM- kinase. Science 285:
895- 898, 1999.

GAM165 270 ARHC Morris, S. W.; Valentine, M. B.; Kirstein, M. N.; Huebner, K.:Reassignment 3 C c
of the human ARH9 RAS- related gene to chromosome 1p13- p21. Genomics
15:677- 679, 1993.

GAM165 270 TBL1X Bassi, M. T.; Ramesar, R. S.; Caciotti, B.; Winship, I. M.; DeGrandi, A.; 3 C c
Riboni, M.; Townes, P. L.; Beighton, P.; Ballabio, A.;Borsani, G.: X- linked
late- onset sensorineural deafness caused bya deletion involving OA1 and a
novel gene containing WD- 40 repeats. Am.J. Hum. Genet. 64: 1604- 1616,
1999.

GAM165 270 TBL1X Converse, P. J.: Personal Communication. Baltimore, Md. 8/24/2001. 3 C c

GAM165 270 TBL1X Disteche, C. M.; Dinulos, M. B.; Bassi, M. T.; Elliott, R. W.;Rugarli, E. I.: Mapping of the murine Tbl1 gene reveals a new rearrangementbetween mouse and human X chromosomes. Mammalian Genome 9: 1062- 1064,1998. 3 C c

GAM165 270 TBL1X Dong, X.; Tsuda, L.; Zavitz, K. H.; Lin, M.; Li, S.; Carthew, R.W.; Zipursky, S. L.: ebi regulates epidermal growth factor receptorsignaling pathways in Drosophila. Genes Dev. 13: 954- 965, 1999. 3 C c

GAM165 270 TBL1X Emes, R. D.; Ponting, C. P.: A new sequence motif linking lissencephaly,Treacher Collins and oral- facial- digital type 1 syndromes, microtubuledynamics and cell migration. Hum. Molec. Genet. 10: 2813- 2820, 2001. 3 C c

GAM165 270 TBL1X Matsuzawa, S.; Reed, J. C.: Siah- 1, SIP, and Ebi collaborate ina novel pathway for beta- catenin degradation linked to p53 responses. Molec.Cell 7: 915- 926, 2001. 3 C c

GAM165 270 TBL1X Zhang, J.; Kalkum, M.; Chait, B. T.; Roeder, R. G.: The N- CoR- HDAC3nuclear receptor corepressor complex inhibits the JNK pathway throughthe integral subunit GPS2. Molec. Cell 9: 611- 623, 2002. 3 C c

GAM168 217 PIR51 Kovalenko, O. V.; Golub, E. I.; Bray- Ward, P.; Ward, D. C.; Radding,C. M.: A novel nucleic acid- binding protein that interacts with humanRad51 recombinase. Nucleic Acids Res. 25: 4946- 4953, 1997. 3 C c

GAM168 217 PIR51 Mizuta, R.; LaSalle, J. M.; Cheng, H.- L.; Shinohara, A.; Ogawa,H.; Copeland, N.; Jenkins, N. A.; Lalande, M.; Alt, F. W.: RAB22and RAB163/mouse BRCA2: proteins that specifically interact with theRAD51 protein. Proc. Nat. Acad. Sci. 94: 6927- 6932, 1997. 3 C c

GAM168 217 PSG4 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999. 3 C a

GAM168 217 PSG4 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by fluorescence in situ hybridization. Genomics 12:773- 779, 1992. 3 C a

GAM168 217 PSG4 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.; Georgescu,A.; Carrano, A.; Hammarstrom, S.: Gene organization of the pregnancy-specificglycoprotein region on human chromosome 19: assembly and analysisof a 700- kb cosmid contig spanning the region. Genomics 23: 659- 668,1994. 3 C a

GAM168 217 PSG4 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19: fine structure of the 11 PSG genes and identificationof 6 new genes forming a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics 23: 669- 684, 1994. 3 C a

GAM168 217 PSG4 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.; Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly linked on the long arm of chromosome 19 and arecoordinately expressed. Biochem. Biophys. Res. Commun. 167: 848- 859,1990. 3 C a

GAM168 217 PSG4 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades-Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan, K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772, 3 C a

1992.

GAM168 217 PSG4 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 C a
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM168 217 PSG4 Tynan, K.; Olsen, A.; Trask, B.; de Jong, P.; Thompson, J.; Zimmermann,W.; 3 C a
Carrano, A.; Mohrenweiser, H.: Assembly and analysis of cosmidcontigs in the
CEA- gene family region of human chromosome 19. NucleicAcids Res. 20: 1629-
1636, 1992.

GAM168 217 PSG7 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, 3 C b
F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.;
Lucka, L.; and 13 others: Redefined nomenclaturefor members of the
carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999.

GAM168 217 PSG7 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. 3 C b
W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances
among members of the carcinoembryonic antigen (CEA) genefamily determined by
fluorescence in situ hybridization. Genomics 12:773- 779, 1992.

GAM168 217 PSG7 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.; Georgescu,A.; 3 C b
Carrano, A.; Hammarstrom, S.: Gene organization of the pregnancy-
specificglycoprotein region on human chromosome 19: assembly and analysisof
a 700- kb cosmid contig spanning the region. Genomics 23: 659- 668,1994.

GAM168 217 PSG7 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The 3 C b
pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19:
fine structure of the 11 PSG genes and identificationof 6 new genes forming
a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics
23: 669- 684, 1994.

GAM168 217 PSG7 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, 3 C b
H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.;
Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly
linked on the long arm of chromosome 19 and arecoordinately expressed.
Biochem. Biophys. Res. Commun. 167: 848- 859,1990.

GAM168 217 PSG7 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades- 3 C b
Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan,
K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the
carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772,
1992.

GAM168 217 PSG7 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 C b
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM168 217 PSG7 Tynan, K.; Olsen, A.; Trask, B.; de Jong, P.; Thompson, J.; Zimmermann,W.; 3 C b
Carrano, A.; Mohrenweiser, H.: Assembly and analysis of cosmidcontigs in the
CEA- gene family region of human chromosome 19. NucleicAcids Res. 20: 1629-
1636, 1992.

GAM169 365 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; 3 C c
Malherbe, P.: Cloning and functional expression of human kynurenine3-
monooxygenase. FEBS Lett. 410: 407- 412, 1997.

GAM169 365 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; 3 C c

Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001.

GAM169 365 NPR1 Ferrari, P.; Weidmann, P.; Ferrier, C.; Dietler, R.; Hollmann,R.; Piso, R. 3 C c
J.; Wey, J.; Shaw, S.: Dysregulation of atrial natriureticfactor in hypertension- prone man. J. Clin. Endocr. Metab. 71: 944- 951,1990.

GAM169 365 NPR1 Kishimoto, I.; Rossi, K.; Garbers, D. L.: A genetic model providesevidence 3 C c
that the receptor for atrial natriuretic peptide (guanylylcyclase- A) inhibits cardiac ventricular myocyte hypertrophy. Proc.Nat. Acad. Sci. 98: 2703- 2706, 2001.

GAM169 365 NPR1 Lowe, D. G.; Klisak, I.; Sparkes, R. S.; Mohandas, T.; Goeddel,D. V.: 3 C c
Chromosomal distribution of three members of the human natriureticpeptide receptor/guanylyl cyclase gene family. Genomics 8: 304- 312,1990.

GAM169 365 NPR1 Oliver, P. M.; Fox, J. E.; Kim, R.; Rockman, H. A.; Kim, H.- S.;Reddick, R. 3 C c
L.; Pandey, K. N.; Milgram, S. L.; Smithies, O.; Maeda,N.: Hypertension, cardiac hypertrophy, and sudden death in mice lackingnatriuretic peptide receptor A. Proc. Nat. Acad. Sci. 94: 14730- 14735,1997.

GAM169 365 NPR1 Oliver, P. M.; John, S. W. M.; Purdy, K. E.; Kim, R.; Maeda, N.;Goy, M. F.; 3 C c
Smithies, O.: Natriuretic peptide receptor 1 expressioninfluences blood pressures of mice in a dose- dependent manner. Proc.Nat. Acad. Sci. 95: 2547- 2551, 1998.

GAM169 365 PPARGC1 Agarwal, A. K.; Garg, A.: A novel heterozygous mutation in 3 C c
peroxisomeproliferator- activated receptor- gamma gene in a patient with familialpartial lipodystrophy. J. Clin. Endocr. Metab. 87: 408- 411, 2002.

GAM169 365 PPARGC1 Esterbauer, H.; Oberkofler, H.; Krempler, F.; Patsch, W.: Humanperoxisome 3 C c
proliferator activated receptor gamma coactivator 1 (PPARGC1)gene: cDNA sequence, genomic organization, chromosomal localization,and tissue expression. Genomics 62: 98- 102, 1999.

GAM169 365 PPARGC1 Herzig, S.; Long, F.; Jhala, U. S.; Hedrick, S.; Quinn, R.; Bauer,A.; 3 C c
Rudolph, D.; Schutz, G.; Yoon, C.; Puigserver, P.; Spiegelman,B.; Montminy, M.: CREB regulates hepatic gluconeogenesis throughthe coactivator PGC- 1. Nature 413: 179- 183, 2001.

GAM169 365 PPARGC1 Larrouy, D.; Vidal, H.; Andreelli, F.; Laville, M.; Langin, D.: Cloning and 3 C c
mRNA tissue distribution of human PPAR- gamma coactivator- 1. Int.J. Obesity 23: 1327- 1332, 1999.

GAM169 365 PPARGC1 Lin, J.; Wu, H.; Tarr, P. T.; Zhang, C.- Y.; Wu, Z.; Boss, O.; Michael,L. 3 C c
F.; Puigserver, P.; Isotani, E.; Olson, E. N.; Lowell, B. B.; Bassel-Duby,R.; Spiegelman, B. M.: Transcriptional co- activator PGC- 1- alpha drivesthe formation of slow- twitch muscle fibres. Nature 418: 797- 801,2002.

GAM169 365 PPARGC1 Monsalve, M.; Wu, Z.; Adelmant, G.; Puigserver, P.; Fan, M.; Spiegelman,B. 3 C c
M.: Direct coupling of transcription and mRNA processing throughthe thermogenic coactivator PGC- 1. Molec. Cell 6: 307- 316, 2000.

GAM169 365 PPARGC1 Puigserver, P.; Adelmant, G.; Wu, Z.; Fan, M.; Xu, J.; O'Malley,B.; 3 C c
Spiegelman, B. M.: Activation of PPAR- gamma coactivator- 1 throughtranscription factor docking. Science 286: 1368- 1371, 1999.

GAM169 365 PPARGC1 Puigserver, P.; Rhee, J.; Lin, J.; Wu, Z.; Yoon, J. C.; Zhang,C.- Y.; 3 C c
Krauss, S.; Mootha, V. K.; Lowell, B. B.; Spiegelman, B. M.: Cytokine stimulation of energy expenditure through p38 MAP kinaseactivation of PPAR-

gamma coactivator- 1. Molec. Cell 8: 971- 982,2001.

GAM169 365 PPARGC1 Puigserver, P.; Wu, Z.; Park, C. W.; Graves, R.; Wright, M.; Spiegelman,B. 3 C c
M.: A cold- inducible coactivator of nuclear receptors linked toadaptive
thermogenesis. Cell 92: 829- 839, 1998.

GAM169 365 PPARGC1 Waite, L. L.; Person, E. C.; Zhou, Y.; Lim, K.- H.; Scanlan, T.S.; Taylor, 3 C c
R. N.: Placental peroxisome proliferator- activated receptor- gammais up-
regulated by pregnancy serum. J. Clin. Endocr. Metab. 85:3808- 3814, 2000.

GAM169 365 PPARGC1 Wu, Z.; Puigserver, P.; Andersson, U.; Zhang, C.; Adelmant, G.;Mootha, V.; 3 C c
Troy, A.; Cinti, S.; Lowell, B.; Scarpulla, R. C.; Spiegelman,B. M.:
Mechanisms controlling mitochondrial biogenesis and respirationthrough the
thermogenic coactivator PGC- 1. Cell 98: 115- 124, 1999.

GAM169 365 PPARGC1 Yoon, J. C.; Puigserver, P.; Chen, G.; Donovan, J.; Wu, Z.; Rhee,J.; 3 C c
Adelmant, G.; Stafford, J.; Kahn, C. R.; Granner, D. K.; Newgard,C. B.;
Spiegelman, B. M.: Control of hepatic gluconeogenesis throughthe
transcriptional coactivator PGC- 1. Nature 413: 131- 138, 2001.

GAM169 365 RGS19IP1 Bunn, R. C.; Jensen, M. A.; Reed, B. C.: Protein interactionswith the 3 C c
glucose transporter binding protein GLUT1CBP that providea link between
GLUT1 and the cytoskeleton. Molec. Biol. Cell 10:819- 832, 1999.

GAM169 365 RGS19IP1 De Vries, L.; Lou, X.; Zhao, G.; Zheng, B.; Farquhar, M. G.: GIPC,a PDZ 3 C c
domain containing protein, interacts specifically with the Cterminus of RGS-
GAIP. Proc. Nat. Acad. Sci. 95: 12340- 12345, 1998.

GAM169 365 RGS19IP1 Von Kap- Herr, C.; Kandala, G.; Mann, S. S.; Hart, T. C.; Pettenati,M. J.; 3 C c
Setaluri, V.: Assignment of PDZ domain- containing proteinGIPC gene
(C19orf3) to human chromosome band 19p13.1 by in situ hybridizationand
radiation hybrid mapping. Cytogenet. Cell Genet. 89: 234- 235,2000.

GAM169 365 SLA Angrist, M.; Wells, D. E.; Chakravarti, A.; Pandey, A.: 3 C c
Chromosomallocalization of the mouse Src- like adapter protein (Slap) gene
andits putative human homolog SLA. Genomics 30: 623- 625, 1995.

GAM169 365 SLA Holland, S. J.; Liao, X. C.; Mendenhall, M. K.; Zhou, X.; Pardo,J.; Chu, P.; 3 C c
Spencer, C.; Fu, A.; Sheng, N.; Yu, P.; Pali, E.; Nagin,A.; and 14 others:
Functional cloning of Src- like adapter protein- 2(SLAP- 2), a novel
inhibitor of antigen receptor signaling. J. Exp.Med. 194: 1263- 1276, 2001.

GAM169 365 SLA Kratchmarova, I.; Sosinowski, T.; Weiss, A.; Witter, K.; Vincenz,C.; Pandey, 3 C c
A.: Characterization of promoter region and genomic structureof the murine
and human genes encoding Src like adapter protein. Gene 262:267- 273, 2001.

GAM169 365 SLA Meijerink, P. H. S.; Yanakiev, P.; Zorn, I.; Grierson, A. J.; Bikker,H.; 3 C c
Dye, D.; Kalaydjieva, L.; Baas, F.: The gene for the human Src- likeadaptor
protein (hSLAP) is located within the 64- kb intron of thethyroglobulin
gene. Europ. J. Biochem. 254: 297- 303, 1998.

GAM169 365 SLA Pandey, A.; Lindberg, R. A.; Dixit, V. M.: Receptor orphans finda family. 3 C c
Curr. Biol. 5: 986- 989, 1995.

GAM169 365 SLA Sosinowski, T.; Pandey, A.; Dixit, V. M.; Weiss, A.: Src- likeadaptor 3 C c
protein (SLAP) is a negative regulator of T cell receptorsignaling. J. Exp.
Med. 191: 463- 474, 2000.

GAM169 365 UBE2L3 Ardley, H. C.; Moynihan, T. P.; Thompson, J.; Leek, J. P.; Markham,A. F.; 3 C c
Robinson, P. A.: Rapid isolation of genomic clones for individualmembers of
human multigene families: identification and localisationof UBE2L4, a novel
member of a ubiquitin conjugating enzyme dispersedgene family. Cytogenet.
Cell Genet. 79: 188- 192, 1997.

GAM169 365 UBE2L3 Moynihan, T. P.; Ardley, H. C.; Leek, J. P.; Thompson, J.; Brindle,N. S.; 3 C c

Markham, A. F.; Robinson, P. A.: Characterization of a humanubiquitin-conjugating enzyme gene UBE2L3. Mammalian Genome 7: 520- 525,1996.

GAM169 365 UBE2L3 Moynihan, T. P.; Cole, C. G.; Dunham, I.; O'Neil, L.; Markham,A. F.; 3 C c
Robinson, P. A.: Fine- mapping, genomic organization, and transcriptanalysis of the human ubiquitin- conjugating enzyme gene UBE2L3. Genomics 51:124-127, 1998.

GAM169 365 UBE2L3 Nuber, U.; Schwarz, S.; Kaiser, P.; Schneider, R.; Scheffner, M.: Cloning of 3 C c
human ubiquitin- conjugating enzymes UbcH6 and UbcH7 (E2- F1)and characterization of their interaction with E6- AP and RSP5. J.Biol. Chem. 271: 2795- 2800, 1996.

GAM169 365 UBE2L3 Shimura, H.; Schlossmacher, M. G.; Hattori, N.; Frosch, M. P.;Trockenbacher, 3 C c
A.; Schneider, R.; Mizuno, Y.; Kosik, K. S.; Selkoe,D. J.: Ubiquitination of a new form of alpha- synuclein by parkinfrom human brain: implications for Parkinson's disease. Science 293:263- 269, 2001.

GAM170 283 P2RY6 Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.: Molecular cloningand 3 C c
functional analysis of a novel P2 nucleotide receptor. J. Biol.Chem. 270: 26152- 26158, 1995.

GAM170 283 P2RY6 Communi, D.; Parmentier, M.; Boeynaems, J.- M.: Cloning, 3 C c
functionalexpression and tissue distribution of the human P2Y6 receptor. Biochem.Biophys. Res. Commun. 222: 303- 308, 1996.

GAM170 283 P2RY6 Maier, R.; Glatz, A.; Mosbacher, J.; Bilbe, G.: Cloning of P2Y6cDNAs and 3 C c
identification of a pseudogene: comparison of P2Y receptorsubtype expression in bone and brain tissues. Biochem. Biophys. Res.Commun. 237: 297- 302, 1997.

GAM170 283 P2RY6 Pidlaoan, L. V.; Jin, J.; Sandhu, A. K.; Athwal, R. S.; Kunapuli,S. P.: 3 C c
Colocalization of P2Y2 and P2Y6 receptor genes at human chromosome11q13.3-14.1. Somat. Cell Molec. Genet. 23: 291- 296, 1997.

GAM170 283 P2RY6 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997.

GAM171 392 DDX6 Akao, Y.; Matsuda, Y.: Identification and chromosome mapping ofthe mouse 3 C c
homologue of the human gene (DDX6) that encodes a putativeRNA helicase of the DEAD box protein family. Cytogenet. Cell Genet. 75:38- 44, 1996.

GAM171 392 DDX6 Akao, Y.; Seto, M.; Takahashi, T.; Kubonishi, I.; Miyoshi, I.;Nakazawa, S.; 3 C c
Tsujimoti, Y.; Croce, C. M.; Ueda, R.: Molecular cloningof the chromosomal breakpoint of a B- cell lymphoma with the t(11;14)(q23;q32)chromosome translocation. Cancer Res. 51: 1574- 1576, 1991.

GAM171 392 DDX6 Akao, Y.; Seto, M.; Yamamoto, K.; Iida, S.; Nakazawa, S.; Inazawa,J.; Abe, 3 C c
T.; Takahashi, T.; Ueda, R.: The RCK gene associated witht(11;14) translocation is distinct from the MLL/ALL- 1 gene with t(4;11)and t(11;19) translocations. Cancer Res. 52: 6083- 6087, 1992.

GAM171 392 DDX6 Akao, Y.; Tsujimoto, Y.; Finan, J.; Nowell, P. C.; Croce, C. M.: Molecular 3 C c
characterization of a t(11;14)(q23;q32) chromosome translocationin a B- cell lymphoma. Cancer Res. 50: 4856- 4859, 1990.

GAM171 392 DDX6 Lu, D.; Yunis, J. J.: Cloning, expression and localization ofan RNA helicase 3 C c
gene from a human lymphoid cell line with chromosomalbreakpoint 11q23.3. Nucleic Acids Res. 20: 1967- 1972, 1992.

GAM171 392 DDX6 Seto, M.; Yamamoto, K.; Takahashi, T.; Ueda, R.: Cloning and expressionof a 3 C c
murine cDNA homologous to the human RCK/P54, a lymphoma- linkedchromosomal

translocation junction gene on 11q23. Gene 166: 293- 296,1995.

GAM171 392 DDX6 Tunnacliffe, A.; Perry, H.; Radice, P.; Budarf, M. L.; Emanuel,B. S.: A panel of sequence tagged sites for chromosome band 11q23. Genomics 17:744-747, 1993. 3 C c

GAM171 392 GCKR Farrelly, D.; Brown, K. S.; Tieman, A.; Ren, J.; Lira, S. A.; Hagan,D.; Gregg, R.; Mookhtiar, K. A.; Hariharan, N.: Mice mutant for glucokinaseregulatory protein exhibit decreased liver glucokinase: a sequestrationmechanism in metabolic regulation. Proc. Nat. Acad. Sci. 96: 14511- 14516,1999. 3 C c

GAM171 392 GCKR Hayward, B. E.; Fantes, J. A.; Warner, J. P.; Intody, S.; Leek,J. P.; Markham, A. F.; Bonthron, D. T.: Co- localization of the ketohexokinaseand glucokinase regulator genes to a 500- kb region of chromosome 2p23. MammalianGenome 7: 454- 458, 1996. 3 C c

GAM171 392 GCKR Vaxillaire, M.; Vionnet, N.; Vigouroux, C.; Sun, F.; Espinosa,R., III; LeBeau, M. M.; Stoffel, M.; Lehto, M.; Beckmann, J. S.; Detheux,M.; Passa, P.; Cohen, D.; Van Schaftingen, E.; Velho, G.; Bell, G.I.; Froguel, P.: Search for a third susceptibility gene for maturity- onsetdiabetes of the young: studies with eleven candidate genes. Diabetes 43:389- 395, 1994. 3 C c

GAM171 392 GCKR Warner, J. P.; Leek, J. P.; Intody, S.; Markham, A. F.; Bonthron,D. T.: Human glucokinase regulatory protein (GCKR): cDNA and genomiccloning, complete primary structure, and chromosomal localization. MammalianGenome 6: 532- 536, 1995. 3 C c

GAM174 252 AKAP13 Carr, D. W.; Hausken, Z. E.; Fraser, I. D.; Stofko- Hahn, R. E.;Scott, J. D: Association of the type II cAMP- dependent protein kinasewith a human thyroid RII- anchoring protein: cloning and characterizationof the RII-binding domain. J. Biol. Chem. 267: 13376- 13382, 1992. 3 C c

GAM174 252 AKAP13 Carr, D. W.; Stofko- Hahn, R. E.; Fraser, I. D.; Bishop, S. M.;Acott, T. S.; Brennan, R. G.; Scott, J. D.: Interaction of the regulatorysubunit (RII) of cAMP- dependent protein kinase with RII- anchoringproteins occurs through an amphipathic helix binding motif. J. Biol.Chem. 266: 14188- 14192, 1991. 3 C c

GAM174 252 AKAP13 Rubino, D.; Driggers, P.; Arbit, D.; Kemp, L.; Miller, B.; Coso,O.; Pagliai, K.; Gray, K.; Gutkind, S.; Segars, J.: Characterizationof Brx, a novel Dbl family member that modulates estrogen receptoraction. Oncogene 16: 2513-2526, 1998. 3 C c

GAM174 252 AKAP13 Sterpetti, P.; Hack, A. A.; Bashar, M. P.; Park, B.; Cheng, S.- D.;Knoll, J. H. M.; Urano, T.; Feig, L. A.; Toksoz, D.: Activation ofthe Lbc Rho exchange factor proto- oncogene by truncation of an extendedC terminus that regulates transformation and targeting. Molec. Cell.Biol. 19: 1334- 1345, 1999. 3 C c

GAM174 252 AKAP13 Toksoz, D.; Williams, D. A.: Novel human oncogene lbc detectedby transfection with distinct homology regions to signal transductionproducts. Oncogene 9: 621- 628, 1994. 3 C c

GAM174 252 INHBB Brown, C. W.; Houston- Hawkins, D. E.; Woodruff, T. K.; Matzuk,M. M.: Insertion of Inhbb into the Inhba locus rescues the Inhba- nullphenotype and reveals new activin functions. Nature Genet. 25: 453- 457,2000. 3 C c

GAM174 252 INHBB Lafuse, W. P.; Zwilling, B. S.: Localization of the inhibin beta- Bgene on mouse chromosome 1. Mammalian Genome 4: 399- 400, 1993. 3 C c

GAM174 252 INHBB Matzuk, M. M.; Kumar, T. R.; Vassalli, A.; Bickenbach, J. R.; Roop,D. R.; Jaenisch, R.; Bradley, A.: Functional analysis of activinsduring mammalian development. Nature 374: 354- 356, 1995. 3 C c

GAM174 252 INHBB Mellor, S. L.; Cranfield, M.; Ries, R.; Pedersen, J.; Cancilla,B.; de 3 C c

Kretser, D.; Groome, N. P.; Mason, A. J.; Risbridger, G. P.: Localization of activin beta(A)- , beta(B)- , and beta(C)- subunitsin human prostate and evidence for formation of new activin heterodimersof beta(C)- subunit. J. Clin. Endocr. Metab. 85: 4851- 4858, 2000.

GAM174 252 INHBB Salmenkivi, K.; Arola, J.; Voutilainen, R.; Ilvesmaki, V.; Haglund,C.; Kahri, A. I.; Heikkila, P.; Liu, J.: Inhibin/activin beta- B-subunitexpression in pheochromocytomas favors benign diagnosis. J. Clin.Endocr. Metab. 86: 2231- 2235, 2001. 3 C c

GAM174 252 INHBB Schrewe, H.; Gendron- Maguire, M.; Harbison, M. L.; Gridley, T.: Mice homozygous for a null mutation of activin beta B are viableand fertile. Mech. Dev. 47: 43- 51, 1994. 3 C c

GAM175 265 ADAR Bass, B. L.; Weintraub, H.: An unwinding activity that covalentlymodifies its double- stranded RNA substrate. Cell 55: 1089- 1098,1988. 4 B c

GAM175 265 ADAR Kim, U.; Wang, Y.; Sanford, T.; Zeng, Y.; Nishikura, K.: Molecularcloning of cDNA for double- stranded RNA adenosine deaminase, a candidateenzyme for nuclear RNA editing. Proc. Nat. Acad. Sci. 91: 11457- 11461,1994. 4 B c

GAM175 265 ADAR O'Connell, M. A.; Krause, S.; Higuchi, M.; Hsuan, J. J.; Totty,N. F.; Jenny, A.; Keller, W.: Cloning of cDNAs encoding mammaliandouble- stranded RNA-specific adenosine deaminase. Molec. Cell. Biol. 15:1389- 1397, 1995. 4 B c

GAM175 265 ADAR Patterson, J. B.; Samuel, C. E.: Expression and regulation byinterferon of a double- stranded- RNA- specific adenosine deaminase fromhuman cells: evidence for two forms of the deaminase. Molec. Cell.Biol. 15: 5376- 5388, 1995. 4 B c

GAM175 265 ADAR Wang, Q.; Khillan, J.; Gadue, P.; Nishikura, K.: Requirement ofthe RNA editing deaminase ADAR1 gene for embryonic erythropoiesis. Science 290:1765-1768, 2000. 4 B c

GAM175 265 ADAR Wang, Y.; Zeng, Y.; Murray, J. M.; Nishikura, K.: Genomic organizationand chromosomal location of the human dsRNA adenosine deaminase gene:the enzyme for glutamate- activated ion channel RNA editing. J. Molec.Biol. 254: 184-195, 1995. 4 B c

GAM175 265 ADAR Weier, H.- U. G.; George, C. X.; Greulich, K. M.; Samuel, C. E.: The interferon- inducible, double- stranded RNA- specific adenosinedeaminase gene (DSRAD) maps to human chromosome 1q21.1- 21.2. Genomics 30:372- 375, 1995. 4 B c

GAM175 265 ADAR Weier, H.- U. G.; George, C. X.; Lersch, R. A.; Breitweser, S.;Cheng, J.-F.; Samuel, C. E.: Assignment of the RNA- specific adenosinedeaminase gene (Adar) to mouse chromosome 3F2 by in situ hybridization. Cytogenet.Cell Genet. 89: 214- 215, 2000. 4 B c

GAM175 265 ANXA8 Chambers, J. A.; Gardner, E.; Hauptmann, R.; Ponder, B. A.; Mulligan,L. M.: TaqI polymorphisms at the annexin VIII locus (ANX8). Hum.Molec. Genet. 1: 550 only, 1992. 4 B c

GAM175 265 ANXA8 Chang, K.- S.; Wang, G.; Freireich, E. J.; Daly, M.; Naylor, S.L.; Trujillo, J. M.; Stass, S. A.: Specific expression of the annexinVIII gene in acute promyelocytic leukemia. Blood 79: 1802- 1810,1992. 4 B c

GAM175 265 ANXA8 Fernandez, M. P.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N.A.; Morgan, R. O.: The genetic origin of mouse annexin VIII. MammalianGenome 9: 8- 14, 1998. 4 B c

GAM175 265 ANXA8 Hauptmann, R.; Maurer- Fogy, I.; Krystek, E.; Bodo, G.; Andree,H.; Reutelingsperger, C. P. M.: Vascular anticoagulant beta, a novelhuman Ca(2+)/phospholipid binding protein that inhibits coagulationand 4 B c

phospholipase A- 2 activity: its molecular cloning, expressionand comparison with VAC- alpha. Europ. J. Biochem. 185: 63- 71, 1989.

GAM175 265 ANXA8 Sarkar, A.; Yang, P.; Fan, Y.- H.; Mu, Z. M.; Hauptmann, R.; Adolf,G. R.; Stass, S. A.; Chang, K.- S.: Regulation of the expression ofannexin VIII in acute promyelocytic leukemia. Blood 84: 279- 286,1994. 4 B c

GAM175 265 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 (CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998. 4 B c

GAM175 265 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999. 4 B c

GAM175 265 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000. 4 B c

GAM175 265 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001. 4 B c

GAM175 265 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999. 4 B c

GAM175 265 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002. 4 B c

GAM175 265 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001. 4 B c

GAM175 265 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998. 4 B c

GAM175 265 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998. 4 B c

GAM175 265 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec- dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 4 B c

GAM175 265 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: Apolipoprotein L gene family: tissue- specific expression,splicing, promoter regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001. 4 B c

GAM175 265 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya- Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a new human high density lipoprotein apolipoproteinexpressed by the pancreas: identification, cloning, characterization,and plasma distribution of apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997. 4 B c

GAM175 265 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.; Bahn, S.: Gene expression analysis in schizophrenia:reproducible up- 4 B c

regulation of several members of the apolipoproteinL family located in a high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat. Acad. Sci. 99: 4680- 4685, 2002.

GAM175 265 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The apolipoprotein L gene cluster has emerged recently in evolutionand is expressed in human vascular tissue. Genomics 79: 539- 546,2002. 4 B c

GAM175 265 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman apolipoprotein L gene cluster: identification, classification,and sites of distribution. Genomics 74: 71- 78, 2001. 4 B c

GAM175 265 ARNT2 Hirose, K.; Morita, M.; Ema, M.; Mimura, J.; Hamada, H.; Fujii,H.; Saijo, Y.; Gotoh, O.; Sogawa, K.; Fujii- Kuriyama, Y.: cDNA cloningand tissue-specific expression of a novel basic helix- loop- helix/PASfactor (Arnt2) with close sequence similarity to the aryl hydrocarbonreceptor nuclear translocator (Arnt). Molec. Cell. Biol. 16: 1706- 1713,1996. 4 B c

GAM175 265 ARNT2 Keith, B.; Adelman, D. M.; Simon, M. C.: Targeted mutation ofthe murine arylhydrocarbon receptor nuclear translocator 2 (Arnt2)gene reveals partial redundancy with Arnt. Proc. Nat. Acad. Sci. 98:6692- 6697, 2001. 4 B c

GAM175 265 ARNT2 Michaud, J. L.; DeRossi, C.; May, N. R.; Holdener, B. C.; Fan,C.- M.: ARNT2 acts as the dimerization partner of SIM1 for the developmentof the hypothalamus. Mech. Dev. 90: 253- 261, 2000. 4 B c

GAM175 265 ARNT2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 4 B c

GAM175 265 CCR2 Boring, L.; Gosling, J.; Cleary, M.; Charo, I. F.: Decreased lesionformation in CCR2 - /- mice reveals a role for chemokines in the initiationof atherosclerosis. Nature 394: 894- 897, 1998. 4 B c

GAM175 265 CCR2 Charo, I. F.; Myers, S. J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S. R.: Molecular cloning and functional expressionof two monocyte chemoattractant protein 1 receptors reveals alternativesplicing of the carboxyl- terminal tails. Proc. Nat. Acad. Sci. 91:2752- 2756, 1994. 4 B c

GAM175 265 CCR2 Choe, H.; Farzan, M.; Sun, Y.; Sullivan, N.; Rollins, B.; Ponath,P. D.; Wu, L.; Mackay, C. R.; LaRosa, G.; Newman, W.; Gerard, N.;Gerard, C.; Sodroski, J.: The beta- chemokine receptors CCR3 and CCR5facilitate infection by primary HIV- 1 isolates. Cell 85: 1135- 1148,1996. 4 B c

GAM175 265 CCR2 Combadiere, C.; Ahuja, S. K.; Murphy, P. M.: Cloning, chromosomallocalization, and RNA expression of a human beta chemokine receptor- likegene. DNA Cell Biol. 14: 673- 680, 1995. 4 B c

GAM175 265 CCR2 Combadiere, C.; Ahuja, S. K.; Van Damme, J.; Tiffany, H. L.; Gao,J.- L.; Murphy, P. M.: Monocyte chemoattractant protein- 3 is a functionalligand for CC chemokine receptors 1 and 2B. J. Biol. Chem. 270:29671- 29675, 1995. 4 B c

GAM175 265 CCR2 Daugherty, B. L.; Springer, M. S.: The beta- chemokine receptorgenes CCR1 (CMKBR1), CCR2 (CMKBR2), and CCR3 (CMKBR3) cluster within285 kb on human chromosome 3p21. Genomics 41: 294- 295, 1997. 4 B c

GAM175 265 CCR2 Doranz, B. J.; Rucker, J.; Yi, Y.; Smyth, R. J.; Samson, M.; Peiper,S. C.; Parmentier, M.; Collman, R. G.; Doms, R. W.: A dual- tropicprimary HIV- 1 isolate that uses fusin and the beta- chemokine receptorsCKR- 5, CKR- 3, and CKR- 2b as fusion cofactors. Cell 85: 1149- 1158,1996. 4 B c

GAM175 265 CCR2 Mummidi, S.; Ahuja, S. S.; Gonzalez, E.; Anderson, S. A.; Santiago,E. N.; 4 B c

Stephan, K. T.; Craig, F. E.; O'Connell, P.; Tryon, V.; Clark,R. A.; Dolan, M. J.; Ahuja, S. K.: Genealogy of the CCR5 locus andchemokine system gene variants associated with altered rates of HIV- 1disease progression. Nature Med. 4: 786- 793, 1998.

GAM175 265 CCR2 Peters, W.; Dupuis, M.; Charo, I. F.: A mechanism for the impairedIFN- gamma 4 B c production in C- C chemokine receptor 2 (CCR2) knockout mice:role of CCR2 in linking the innate and adaptive immune responses. J.Immun. 165: 7072- 7077, 2000.

GAM175 265 CCR2 Peters, W.; Scott, H. M.; Chambers, H. F.; Flynn J. L.; Charo,I. F.; Ernst, 4 B c J. D.: Chemokine receptor 2 serves an early and essentialrole in resistance to Mycobacterium tuberculosis. Proc. Nat. Acad.Sci. 98: 7958- 7963, 2001.

GAM175 265 CCR2 Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier,M.: Molecular 4 B c cloning and functional expression of a new human CC- chemokinereceptor gene. Biochemistry 35: 3362- 3367, 1996.

GAM175 265 CCR2 Samson, M.; Soularue, P.; Vassart, G.; Parmentier, M.: The genesencoding the 4 B c human CC- chemokine receptors CC- CKR1 to CC- CKR5 (CMKBR1- CMKBR5)are clustered in the p21.3- p24 region of chromosome 3. Genomics 36:522- 526, 1996.

GAM175 265 CCR2 Sanders, S. K.; Crean, S. M.; Boxer, P. A.; Kellner, D.; LaRosa,G. J.; Hunt, 4 B c S. W., III.: Functional differences between monocytechemotactic protein- 1 receptor A and monocyte chemotactic protein- 1receptor B expressed in a Jurkat T cell. J. Immun. 165: 4877- 4883,2000.

GAM175 265 CCR2 Smith, M. W.; Dean, M.; Carrington, M.; Winkler, C.; Huttley,G. A.; Lomb, D. 4 B c A.; Goedert, J. J.; O'Brien, T. R.; Jacobson, L. P.;Kaslow, R.; Buchbinder, S.; Vittinghoff, E.; Vlahov, D.; Hoots, K.;Hilgartner, M. W.; Hemophilia Growth and Development Study (HGDS);Multicenter AIDS Cohort Study (MACS); Multicenter Hemophilia CohortStudy (MHCS); San Francisco City Cohort (SFCC); ALIVE Study;O'Brien, S. J.: Contrasting genetic influence of CCR2 and CCR5 variantson HIV- 1 infection and disease progression. Science 277: 959- 965,1997.

GAM175 265 CCR2 Wong, L.- M.; Myers, S. J.; Tsou, C.- L.; Gosling, J.; Arai, H.;Charo, I. 4 B c F.: Organization and differential expression of the humanmonocyte chemoattractant protein 1 receptor gene: evidence for therole of the carboxyl- terminal tail in receptor trafficking. J. Biol.Chem. 272: 1038- 1045, 1997.

GAM175 265 CHST5 Akama, T. O.; Nishida, K.; Nakayama, J.; Watanabe, H.; Ozaki, K.;Nakamura, 4 B c T.; Dota, A.; Kawasaki, S.; Inoue, Y.; Maeda, N.; Yamamoto,S.; Fujiwara, T.; Thonar, E. J.- M. A.; Shimomura, Y.; Kinoshita, S.;Tanigami, A.; Fukuda, M. N.: Macular corneal dystrophy type I andtype II are caused by distinct mutations in a new sulphotransferasegene. Nature Genet. 26: 237- 241, 2000.

GAM175 265 CHST5 Lee, J. K.; Bhakta, S.; Rosen, S. D.; Hemmerich, S.: Cloning 4 B c andcharacterization of a mammalian N- acetylglucosamine- 6- sulfotransferasethat is highly restricted to intestinal tissue. Biochem. Biophys.Res. Commun. 263: 543- 549, 1999.

GAM175 265 CTNNA2 Claverie, J.- M.; Hardelin, J.- P.; Legouis, R.; Levilliers, J.;Bougueleret, 4 B c L.; Mattei, M.- G.; Petit, C.: Characterization and chromosomalassignment of a human cDNA encoding a protein related to the murine102- kDa cadherin- associated protein (alpha- catenin). Genomics 15:13- 20, 1993.

GAM175 265 CTNNA2 Cook, S. A.; Bronson, R. T.; Donahue, L. R.; Ben- Arie, N.; Davisson,M. T.: 4 B c Cerebellar deficient folia (cdf): a new mutation on mousechromosome 6.

Mammalian Genome 8: 108- 112, 1997.

GAM175 265 CTNNA2 Gimona, M.; Small, J. V.; Moeremans, M.; Van Damme, J.; Puype,M.; Vandekerckhove, J.: Porcine vinculin and metavinculin differby a 68- residue insert located close to the carboxy- terminal partof the molecule. EMBO J. 7: 2329- 2334, 1988. 4 B c

GAM175 265 CTNNA2 Herrenknecht, K.; Ozawa, M.; Eckerskorn, C.; Lottspeich, F.; Lenter,M.; Kemler, R.: The uvomorulin- anchorage protein alpha- catenin isa vinculin homologue. Proc. Nat. Acad. Sci. 88: 9156- 9160, 1991. 4 B c

GAM175 265 CTNNA2 Park, C.; Falls, W.; Finger, J. H.; Longo- Guess, C. M.; Ackerman,S. L.: Deletion in Catna2, encoding alpha- N- catenin, causes cerebellarand hippocampal lamination defects and impaired startle modulation. NatureGenet. 31: 279- 284, 2002. 4 B c

GAM175 265 DCLRE1C Ma, Y.; Pannicke, U.; Schwarz, K.; Lieber, M. R.: Hairpin openingand overhang processing by an Artemis/DNA- dependent protein kinasecomplex in nonhomologous end joining and V(D)J recombination. Cell 108:781- 794, 2002. 4 B c

GAM175 265 DCLRE1C Moshous, D.; Callebaut, I.; de Chasseval, R.; Corneo, B.; Cavazzana-Calvo,M.; Le Deist, F.; Tezcan, I.; Sanal, O.; Bertrand, Y.; Philippe, N.;Fischer, A.; de Villartay, J.- P.: Artemis, a novel DNA double-strandbreak repair/V(D)J recombination protein, is mutated in human severecombined immune deficiency. Cell 105: 177- 186, 2001. 4 B c

GAM175 265 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila-relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997. 4 B c

GAM175 265 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998. 4 B c

GAM175 265 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994. 4 B c

GAM175 265 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997. 4 B c

GAM175 265 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993. 4 B c

GAM175 265 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997. 4 B c

GAM175 265 FPGS Freemantle, S. J.; Taylor, S. M.; Krystal, G.; Moran, R. G.: Upstreamorganization of and multiple transcripts from the human folylpoly-gamma- glutamatesynthetase gene. J. Biol. Chem. 270: 9579- 9584, 1995. 4 B c

GAM175 265 FPGS Garrow, T. A.; Admon, A.; Shane, B.: Expression cloning of a humancDNA encoding folylpoly(gamma- glutamate) synthetase and determinationof its primary structure. Proc. Nat. Acad. Sci. 89: 9151- 9155, 1992. 4 B c

GAM175 265 FPGS Jones, C.; Kao, F. T.: Assignment of the human gene complementingthe auxotrophic marker GAT- minus to chromosome 9. (Abstract) Cytogenet.Cell Genet. 25: 168, 1979. 4 B c

GAM175 265 FPGS Jones, C.; Kao, F.- T.: Regional mapping of the folylpolyglutamatesynthetase gene (FPGS) to 9cen- q34. (Abstract) Cytogenet. Cell Genet. 37:499- 500, 1984. 4 B c

GAM175 265 FPGS Jones, C.; Kao, F.- T.; Taylor, R. T.: Chromosomal assignment ofthe gene for folylpolyglutamate synthetase to human chromosome 9. Cytogenet.Cell Genet. 28: 181- 194, 1980. 4 B c

GAM175 265 FPGS Kao, F. T.; Puck, T. T.: Genetics of somatic mammalian cells.VII. Induction and isolation of nutritional mutants in Chinese hamstercells. Proc. Nat. Acad. Sci. 60: 1275- 1281, 1968. 4 B c

GAM175 265 FPGS Sussman, D. J.; Milman, G.; Shane, B.: Characterization of humanfolylpolyglutamate synthetase expressed in Chinese hamster ovary cells. Somat.Cell Molec. Genet. 12: 531- 540, 1986. 4 B c

GAM175 265 FPGS Taylor, R. T.; Hanna, M. L.: Folate- dependent enzymes in culturedChinese hamster cells: folylpolyglutamate synthetase and its absencein mutants auxotrophic for glycine, adenosine and thymidine. Arch.Biochem. Biophys. 181: 331- 344, 1977. 4 B c

GAM175 265 FPGS Taylor, S. M.; Freemantle, S. J.; Moran, R. G.: Structural organizationof the human folylpoly- gamma- glutamate synthetase gene: evidence fora single genomic locus. Cancer Res. 55: 6030- 6034, 1995. 4 B c

GAM175 265 GPR44 Hirai, H.; Tanaka, K.; Takano, S.; Ichimasa, M.; Nakamura, M.;Nagata, K.: Cutting edge: agonistic effect of indomethacin on a prostaglandinD2 receptor, CRTH2. J. Immun. 168: 981- 985, 2002. 4 B c

GAM175 265 GPR44 Hirai, H.; Tanaka, K.; Yoshie, O.; Ogawa, K.; Kenmotsu, K.; Takamori,Y.; Ichimasa, M.; Sugamura, K.; Nakamura, M.; Takano, S.; Nagata,K.: Prostaglandin D2 selectively induces chemotaxis in T helper type2 cells, eosinophils, and basophils via seven- transmembrane receptorCRTH2. J. Exp. Med. 193: 255- 261, 2001. 4 B c

GAM175 265 GPR44 Marchese, A.; Sawzdargo, M.; Nguyen, T.; Cheng, R.; Heng, H. H.Q.; Nowak, T.; Im, D- S.; Lynch, K. R.; George, S. R.; O'Dowd, B. F.: Discovery of three novel orphan G- protein- coupled receptors. Genomics 56:12- 21, 1999. 4 B c

GAM175 265 GPR44 Nagata, K.; Tanaka, K.; Ogawa, K.; Kemmotsu, K.; Imai, Yoshie,O.; Abe, H.; Tada, K.; Nakamura, M.; Sugamura, K.; Takano, S.: Selectiveexpression of a novel surface molecule by human Th2 cells in vivo. J.Immun. 162: 1278- 1286, 1999. 4 B c

GAM175 265 KL Arking, D. E.; Krebsova, A.; Macek, M., Sr.; Macek, M., Jr.; Arking,A.; Mian, I. S.; Fried, L.; Hamosh, A.; Dey, S.; McIntosh, I.; Dietz,H. C.: Association of human aging with a functional variant of klotho. Proc.Nat. Acad. Sci. 99: 856- 861, 2002. 4 B c

GAM175 265 KL Koh, N.; Fujimori, T.; Nishiguchi, S.; Tamori, A.; Shiomi, S.;Nakatani, T.; Sugimura, K.; Kishimoto, T.; Kinoshita, S.; Kuroki,T.; Nabeshima, Y.: Severely reduced production of Klotho in humanchronic renal failure kidney. Biochem. Biophys. Res. Commun. 280:1015- 1020, 2001. 4 B c

GAM175 265 KL Kuro- o, M.; Matsumura, Y.; Aizawa, H.; Kawaguchi, H.; Suga, T.;Utsugi, T.; Ohyama, Y.; Kurabayashi, M.; Kaname, T.; Kume, E.; Iwasaki,H.; Iida, A.; Shiraki- Iida, T.; Nishikawa, S.; Nagai, R.; Nabeshima,Y.: Mutation of the mouse klotho gene leads to a syndrome resemblingageing. Nature 390: 45- 51, 1997. 4 B c

GAM175 265 KL Matsumura, Y.; Aizawa, H.; Shiraki- Iida, T.; Nagai, R.; Kuro- o,M.; Nabeshima, Y.: Identification of the human klotho gene and itstwo transcripts encoding membrane and secreted klotho protein. Biochem.Biophys. 4 B c

Res. Commun. 242: 626- 630, 1998.

GAM175 265 KL Mori, K.; Yahata, K.; Mukoyama, M.; Suganami, T.; Makino, H.; Nagae,T.; Masuzaki, H.; Ogawa, Y.; Sugawara, A.; Nabeshima, Y.; Nakao, K.: Disruption of klotho gene causes an abnormal energy homeostasisin mice. Biochem. Biophys. Res. Commun. 278: 665- 670, 2000. 4 B c

GAM175 265 KL Saito, Y.; Nakamura, T.; Ohyama, Y; Suzuki, T.; Iida, A.; Shiraki- Iida,T.; Kuro- o, M.; Nabeshima, Y.; Kurabayashi, M.; Nagai, R.: In vivoklotho gene delivery protects against endothelial dysfunction in multiplerisk factor syndrome. Biochem. Biophys. Res. Commun. 276: 767- 772,2000. 4 B c

GAM175 265 LAMA4 Haaparanta, T.; Uitto, J.; Ruoslahti, E.; Engvall, E.: Molecularcloning of the cDNA encoding human laminin A chain. Matrix 11: 151- 160,1991. 4 B c

GAM175 265 LAMA4 Iivanainen, A.; Sainio, K.; Sariola, H.; Tryggvason, K.: Primarystructure and expression of a novel human laminin alpha- 4 chain. FEBSLett. 365: 183- 188, 1995. 4 B c

GAM175 265 LAMA4 Richards, A. J.; Al- Imara, L.; Carter, N. P.; Lloyd, J. C.; Leversha,M. A.; Pope, F. M.: Localization of the gene (LAMA4) to chromosome6q21 and isolation of a partial cDNA encoding a variant laminin Achain. Genomics 22: 237- 239, 1994. 4 B c

GAM175 265 LAMA4 Richards, A. J.; Al- Imara, L.; Carter, N. P.; Lloyd, J. C.; Pope,F. M.: A laminin A variant gene (LAMA3) is present on chromosome6q21 (Abstract) J. Med. Genet. 31: 164, 1994. 4 B c

GAM175 265 LAMC1 Burgeson, R. E.; Chiquet, M.; Deutzmann, R.; Ekblom, P.; Engel,J.; Kleinman, H.; Martin, G. R.; Meneguzzi, G.; Paulsson, M.; Sanes,J.; Timpl, R.; Tryggvason, K.; Yamada, Y.; Yurchenco, P. D.: A newnomenclature for the laminins. Matrix Biol. 14: 209- 211, 1994. 4 B c

GAM175 265 LAMC1 Gedde- Dahl, T., Jr.; Dupuy, B. M.; Jonassen, R.; Winberg, J.- O.;Anton- Lamprecht, I.; Olaisen, B.: Junctional epidermolysis bullosainversa (locus EBR2A) assigned to 1q31 by linkage and associationof LAMC1. Hum. Molec. Genet. 3: 1387- 1391, 1994. 4 B c

GAM175 265 LAMC1 Kallunki, T.; Ikonen, J.; Chow, L. T.; Kallunki, P.; Tryggvason,K.: Structure of the human laminin B2 chain gene reveals extensivedivergence from the laminin B1 chain gene. J. Biol. Chem. 266: 221- 228,1991. 4 B c

GAM175 265 LAMC1 Kallunki, T.; Pikkarainen, T.; Tryggvason, K.; Savolainen, E.- R.: A Pst I polymorphism in the human laminin B2 chain gene on 1q25- q31. NucleicAcids Res. 17: 4423 only, 1989. 4 B c

GAM175 265 LAMC1 Mattei, M.- G.; Weil, D.; Passage, E.; Van Cong, N.; Pribula- Conway,D.; Timpl, R.; Chu, M.- L.: Human gene for laminin B2 chain (LAMB2)maps to the long arm of chromosome 1. (Abstract) Cytogenet. CellGenet. 46: 659 only, 1987. 4 B c

GAM175 265 LAMC1 Mattei, M.- G.; Weil, D.; Pribula- Conway, D.; Bernard, M. P.; Passage,E.; Van Cong, N.; Timpl, R.; Chu, M.- L.: cDNA cloning, expressionand mapping of human laminin B2 gene to chromosome 1q31. Hum. Genet. 79:235- 241, 1988. 4 B c

GAM175 265 LAMC1 Miner, J. H.; Patton, B. L.; Lentz, S. I.; Gilbert, D. J.; Jenkins,N. A.; Copeland, N. G.; Sanes, J. R.: The laminin alpha chains: expression,developmental transitions, and chromosomal locations of alpha1- 5,identification of heterodimeric laminins 8- 11, and cloning of a novelalpha3 isoform. J. Cell Biol. 137: 685- 701, 1997. 4 B c

GAM175 265 LAMC1 Nishimura, D.; Buetow, K. H.; Yamada, Y.; Murray, J. C.: RFLPsand linkage relationships of the human laminin B2 gene. Genomics 3:393- 395, 1988. 4 B c

GAM175 265 LAMC1 Pikkarainen, T.; Kallunki, T.; Tryggvason, K.: Human laminin B2chain: 4 B c

comparison of the complete amino acid sequence with the B1chain reveals variability in sequence homology between different structuraldomains. J. Biol. Chem. 263: 6751- 6758, 1988.

GAM175 265 LAMC1 Sasaki, M.; Yamada, Y.: The laminin B2 chain has a multidomainstructure 4 B c homologous to the B1 chain. J. Biol. Chem. 262: 17111- 17117,1987.

GAM175 265 LAMC1 Smyth, N.; Vatansever, H. S.; Murray, P.; Meyer, M.; Frie, C.;Paulsson, M.; 4 B c Edgar, D.: Absence of basement membranes after targetingthe LAMC1 gene results in embryonic lethality due to failure of endodermdifferentiation. J. Cell Biol. 144: 151- 160, 1999.

GAM175 265 LCP2 Clements, J. L.; Lee, J. R.; Gross, B.; Yang, B.; Olson, J. D.;Sandra, A.; 4 B c Watson, S. P.; Lentz, S. R.; Koretzky, G. A.: Fetal hemorrhageand platelet dysfunction in SLP- 76- deficient mice. J. Clin. Invest. 103:19- 25, 1999.

GAM175 265 LCP2 Jackman, J. K.; Motto, D. G.; Sun, Q.; Tanemoto, M.; Turck, C.W.; Peltz, G. 4 B c A.; Koretzky, G. A.; Findell, P. R.: Molecular cloningof SLP- 76, a 76- kDa tyrosine phosphoprotein associated with Grb2 inT cells. J. Biol. Chem. 270: 7029- 7032, 1995.

GAM175 265 LCP2 Motto, D. G.; Ross, S. E.; Wu, J.; Hendricks- Taylor, L. R.; Koretzky,G. A.: 4 B c Implication of the GRB2- associated phosphoprotein SLP- 76 inT cell receptor- mediated interleukin 2 production. J. Exp. Med. 183:1937- 1943, 1996.

GAM175 265 LCP2 Pivniouk, V.; Tsitsikov, E.; Swinton, P.; Rathbun, G.; Alt, F.W.; Geha, R. 4 B c S.: Impaired viability and profound block in thymocytedevelopment in mice lacking the adaptor protein SLP- 76. Cell 94:229- 238, 1998.

GAM175 265 LCP2 Sunden, S. L. F.; Carr, L. L.; Clements, J. L.; Motto, D. G.; Koretzky,G. 4 B c A.: Polymorphism in and localization of the gene LCP2 (SLP- 76)to chromosome 5q33.1- qter. Genomics 35: 269- 270, 1996.

GAM175 265 MRPS12 Johnson, D. F.; Hamon, M.; Fischel- Ghodsian, N.: Characterizationof the 4 B c human mitochondrial ribosomal S12 gene. Genomics 52: 363- 368,1998.

GAM175 265 MRPS12 Shah, Z. H.; Migliosi, V.; Miller, S. C. M.; Wang, A.; Friedman,T. B.; 4 B c Jacobs, H. T.: Chromosomal locations of three human nucleargenes (RPSM12, TUFM, and AFG3L1) specifying putative components ofthe mitochondrial gene expression apparatus. Genomics 48: 384- 388,1998.

GAM175 265 MXI1 Albarosa, R.; DiDonato, S.; Finocchiaro, G.: Redefinition of thecoding 4 B c sequence of the MXI1 gene and identification of a polymorphicrepeat in the 3- prime non- coding region that allows the detectionof loss of heterozygosity of chromosome 10q25 in glioblastomas. Hum.Genet. 95: 709- 711, 1995.

GAM175 265 MXI1 Eagle, L. R.; Yin, X.; Brothman, A. R.; Williams, B. J.; Atkin,N. B.; 4 B c Prochownik, E. V.: Mutation of the MXI1 gene in prostate cancer. NatureGenet. 9: 249- 255, 1995.

GAM175 265 MXI1 Edelhoff, S.; Ayer, D. E.; Zervos, A. S.; Steingrimsson, E.; Jenkins,N. A.; 4 B c Copeland, N. G.; Eisenman, R. N.; Brent, R.; Disteche, C. M.: Mapping of two genes encoding members of a distinct subfamily ofMAX interacting proteins: MAD to human chromosome 2 and mouse chromosome6, and MXI1 to chromosome 10 and mouse chromosome 19. Oncogene 9:665- 668, 1994.

GAM175 265 MXI1 Li, X.- J.; Wang, D.- Y.; Zhu, Y.; Guo, R.- J.; Wang, X.- D.; Lubomir,K.; 4 B c Mukai, K.; Sasaki, H.; Yoshida, H.; Oka, T.; Machinami, R.; Shinmura,K.; Tanaka, M.; Sugimura, H.: Mxi1 mutations in human neurofibrosarcomas. Jpn.J. Cancer Res. 90: 740- 746, 1999.

GAM175 265 MXI1 Prochownik, E. V.; Grove, L. E.; Deubler, D.; Zhu, X. L.; Stephenson,R. A.; 4 B c

Rohr, L. R.; Yin, X.; Brothman, A. R.: Commonly occurringloss and mutation of the MXI1 gene in prostate cancer. Genes ChromosomesCancer 22: 295- 304, 1998.

GAM175 265 MXI1 Schreiber- Agus, N.; Meng, Y.; Hoang, T.; Hou, H., Jr.; Chen, K.;Greenberg, R.; Cordon- Cardo, C.; Lee, H.- W.; DePinho, R. A.: Roleof Mxi1 in ageing organ systems and the regulation of normal and neoplasticgrowth. Nature 393: 483- 487, 1998. 4 B c

GAM175 265 MXI1 Shapiro, D. N.; Valentine, V.; Eagle, L.; Yin, X.; Morris, S. W.;Prochownik, E. V.: Assignment of the human MAD and MXI1 genes tochromosomes 2p12- p13 and 10q24- q25. Genomics 23: 282- 285, 1994. 4 B c

GAM175 265 MXI1 Steingrimsson, E.; Sawadogo, M.; Gilbert, D. J.; Zervos, A. S.;Brent, R.; Blanar, M. A.; Fisher, D. E.; Copeland, N. G.; Jenkins,N. A.: Murine chromosomal location of five bHLH- Zip transcriptionfactor genes. Genomics 28: 179- 183, 1995. 4 B c

GAM175 265 MXI1 Wechsler, D. S.; Hawkins, A. L.; Li, X.; Jabs, E. W.; Griffin,C. A.; Dang, C. V.: Localization of the human Mxi1 transcriptionfactor gene (MXI1) to chromosome 10q24- q25. Genomics 21: 669- 672,1994. 4 B c

GAM175 265 MXI1 Wechsler, D. S.; Shelly, C. A.; Dang, C. V.: Genomic organizationof human MXI1, a putative tumor suppressor gene. Genomics 32: 466- 470,1996. 4 B c

GAM175 265 MXI1 Zervos, A. S.; Gyuris, J.; Brent, R.: Mxi1, a protein that specificallyinteracts with Max to bind Myc- Max recognition sites. Cell 72: 223- 232,1993. Note: Erratum: Cell 79: 389 only, 1994. 4 B c

GAM175 265 NDRG1 Kalaydjieva, L.; Gresham, D.; Gooding, R.; Heather, L.; Baas, F.;de Jonge, R.; Blechschmidt, K.; Angelicheva, D.; Chandler, D.; Worsley,P.; Rosenthal, A.; King, R. H. M.; Thomas, P. K.: N- myc downstream- regulatedgene 1 is mutated in hereditary motor and sensory neuropathy- Lom. Am.J. Hum. Genet. 67: 47- 58, 2000. 4 B c

GAM175 265 NDRG1 Kalaydjieva, L.; Hallmayer, J.; Chandler, D.; Savov, A.; Nikolova,A.; Angelicheva, D.; King, R. H. H.; Ishpekova, B.; Honeyman, K.;Calafell, F.; Shmarov, A.; Petrova, J.; Turnev, I.; Hristova, A.;Moskov, M.; Stancheva, S.; Petkova, I.; Bittles, A. H.; Georgieva,V.; Middleton, L.; Thomas, P. K.: Gene mapping in Gypsies identifiesa novel demyelinating neuropathy on chromosome 8q24. Nature Genet. 14:214- 217, 1996. 4 B c

GAM175 265 NDRG1 Kokame, K.; Kato, H.; Miyata, T.: Homocysteine- respondent genesin vascular endothelial cells identified by differential display analysis:GRP78/BiP and novel genes. J. Biol. Chem. 271: 29659- 29665, 1996. 4 B c

GAM175 265 NDRG1 Park, H,; Adams, M. A.; Lachat, P.; Bosman, F.; Pang, S. C.; Graham,C. H.: Hypoxia induces the expression of a 43- kDa protein (PROXY- 1)in normal and malignant cells. Biochem. Biophys. Res. Commun. 276:321- 328, 2000. 4 B c

GAM175 265 NDRG1 Shimono, A.; Okuda, T.; Kondoh, H.: N- myc- dependent repressionof Ndr1, a gene identified by direct subtraction of whole mouse embryocDNAs between wild type and N- myc mutant. Mech. Dev. 83: 39- 52,1999. 4 B c

GAM175 265 NDRG1 van Belzen, N.; Dinjens, W. N. M.; Diesveld, M. P. G.; Groen, N.A.; van der Made, A. C. J.; Nozawa, Y.; Vliestra, R.; Trapman, J.;Bosman, F. T.: A novel gene which is up- regulated during colon epithelialcell differentiation and down- regulated in colorectal neoplasms. Lab.Invest. 77: 85- 92, 1997. 4 B c

GAM175 265 NDRG1 Zhou, D.; Salnikow, K.; Costa, M.: Cap43, a novel gene specificallyinduced by Ni2+ compounds. Cancer Res. 58: 2182- 2189, 1998. 4 B c

GAM175 265 PMX1 Grueneberg, D. A.; Natesan, S.; Alexandre, C.; Gilman, M. Z.:Human and Drosophila homeodomain proteins that enhance the DNA- bindingactivity of 4 B c

serum response factor. Science 257: 1089- 1095, 1992.

GAM175 265 PMX1 Kern, M. J.; Argao, E. A.; Birkenmeier, E. H.; Rowe, L. B.; Potter,S. S.: 4 B c
Genomic organization and chromosome localization of the murinehomeobox gene
Pmx. Genomics 19: 334- 340, 1994.

GAM175 265 PMX1 Nakamura, T.; Yamazaki, Y.; Hatano, Y.; Miura, I.: NUP98 is fusedto PMX1 4 B c
homeobox gene in human acute myelogenous leukemia with
chromosometranslocation t(1;11)(q23;p15). Blood 94: 741- 747, 1999.

GAM175 265 PMX1 Norris, R. A.; Scott, K. K.; Moore, C. S.; Stetten, G.; Brown,C. R.; Jabs, 4 B c
E. W.; Wulfsberg, E. A.; Yu, J.; Kern, M. J.: HumanPRRX1 and PRRX2 genes:
cloning, expression, genomic localization,and exclusion as disease genes for
Nager syndrome. Mammalian Genome 11:1000- 1005, 2000.

GAM175 265 PMX1 Riazuddin, S.; Castelein, C. M.; Ahmed, Z. M.; Lalwani, A. K.;Mastroianni, 4 B c
M. A.; Naz, S.; Smith, T. N.; Liburd, N. A.; Friedman,T. B.; Griffith, A.
J.; Riazuddin, S.; Wilcox, E. R.: Dominant modifierDFNM1 suppresses
recessive deafness DFNB26. Nature Genet. 26: 431- 434,2000.

GAM175 265 PPARBP Drane, P.; Barel, M.; Balbo, M.; Frade, R.: Identification ofRB18A, a 205 4 B c
kDa new p53 regulatory protein which shares antigenicand functional
properties with p53. Oncogene 15: 3013- 3024, 1997.

GAM175 265 PPARBP Frade, R.; Balbo, M.; Barel, M.: RB18A, whose gene is localizedon chromosome 4 B c
17q12- q21.1, regulates in vivo p53 transactivating activity. CancerRes. 60:
6585- 6589, 2000.

GAM175 265 PPARBP Ge, K.; Guermah, M.; Yuan, C.- X.; Ito, M.; Wallberg, A. E.; Spiegelman,B. 4 B c
M.; Roeder, R. G.: Transcription coactivator TRAP220 is requiredfor PPAR-
gamma- 2- stimulated adipogenesis. Nature 417: 563- 567, 2002.

GAM175 265 PPARBP Ito, M.; Yuan, C.- X.; Okano, H. J.; Darnell, R. B.; Roeder, R.G.: 4 B c
Involvement of the TRAP220 component of the TRAP/SMCC coactivatorcomplex in
embryonic development and thyroid hormone action. Molec.Cell 5: 683- 693,
2000.

GAM175 265 PPARBP Lee, J. W.; Choi, H.- S.; Gyuris, J.; Brent, R.; Moore, D. D.:Two classes of 4 B c
proteins dependent on either the presence or absenceof thyroid hormone for
interaction with the thyroid hormone receptor. Molec.Endocr. 9: 243- 254,
1995.

GAM175 265 PPARBP Yuan, C.- X.; Ito, M.; Fondell, J. D.; Fu, Z.- Y.; Roeder, R. G.: The 4 B c
TRAP220 component of a thyroid hormone receptor- associated protein(TRAP)
coactivator complex interacts directly with nuclear receptorsin a ligand-
dependent fashion. Proc. Nat. Acad. Sci. 95: 7939- 7944,1998. Note: Erratum:
Proc. Nat. Acad. Sci. 95: 14584 only, 1998.

GAM175 265 PPARBP Zhu, Y.; Qi, C.; Jain, S.; Le Beau, M. M.; Espinosa, R., III; Atkins,G. B.; 4 B c
Lazar, M. A.; Yeldandi, A. V.; Rao, M. S.; Reddy, J. K.: Amplificationand
overexpression of peroxisome proliferator- activated receptor bindingprotein
(PBP/PPARBP) gene in breast cancer. Proc. Nat. Acad. Sci. 96:10848- 10853,
1999.

GAM175 265 PPARBP Zhu, Y.; Qi, C.; Jain, S.; Rao, M. S.; Reddy, J. K.: Isolationand 4 B c
characterization of PBP, a protein that interacts with
peroxisomeproliferator- activated receptor. J. Biol. Chem. 272: 25500-
25506,1997.

GAM175 265 RPS6KA2 Goustin, A. S.: Personal Communication. Detroit, Mich. 8/17/1998. 4 B c

GAM175 265 RPS6KA2 Moller, D. E.; Xia, C. H.; Tang, W.; Zhu, A. X.; Jakubowski, M.: Human rsk 4 B c
isoforms: cloning and characterization of tissue- specificexpression. Am. J.

Physiol. 266: C351- C359, 1994.

GAM175 265 RPS6KA2 Zhao, Y.; Bjorbaek, C.; Weremowicz, S.; Morton, C. C.; Moller,D. E.: RSK3 4 B c
encodes a novel pp90rsk isoform with a unique N- terminalsequence: growth
factor- stimulated kinase function and nuclear translocation. Molec.Cell.
Biol. 15: 4353- 4363, 1995.

GAM175 265 SCD Cohen, P.; Miyazaki, M.; Socci, N. D.; Hagge- Greenberg, A. Liedtke,W.; 4 B c
Soukas, A. A.; Sharma, R.; Hudgins, L. C.; Ntambi, J. M.; Friedman,J. M.:
Role for stearoyl- CoA desaturase- 1 in leptin- mediated weightloss. Science
297: 240- 243, 2002.

GAM175 265 SCD Li, J.; Ding, S.- F.; Habib, N. A.; Fermor, B. F.; Wood, C. B.;Gilmour, R. 4 B c
S.: Partial characterization of a cDNA for human stearoyl- CoAdesaturase and
changes in its mRNA expression in some normal and malignanttissues. Int. J.
Cancer 57: 348- 352, 1994.

GAM175 265 SCD Ntambi, J. M.; Miyazaki, M.; Stoehr, J. P.; Lan, H.; Kendziorski,C. M.; 4 B c
Yandell, B. S.; Song, Y.; Cohen, P.; Friedman, J. M.; Attie,A. D.: Loss of
stearoyl- CoA desaturase- 1 function protects mice againstadiposity. Proc.
Nat. Acad. Sci. 99: 11482- 11486, 2002.

GAM175 265 SCD Thiede, M. A.; Ozols, J.; Strittmatter, P.: Construction and sequenceof cDNA 4 B c
for rat liver stearyl coenzyme A desaturase. J. Biol. Chem. 261:13230-
13235, 1986.

GAM175 265 SCD Zhang, L.; Ge, L.; Parimoo, S.; Stenn, K.; Prouty, S. M.: Humanstearoyl- CoA 4 B c
desaturase: alternative transcripts generated from asingle gene by usage of
tandem polyadenylation sites. Biochem. J. 340:255- 264, 1999.

GAM175 265 SCD Zheng, Y.; Eilertsen, K. J.; Ge, L.; Zhang, L.; Sundberg, J. P.;Prouty, S. 4 B c
M.; Stenn, K. S.; Parimoo, S.: Scd1 is expressed in sebaceousglands and is
disrupted in the asebia mouse. (Letter) Nature Genet. 23:268- 270, 1999.

GAM175 265 SLC1A4 Arriza, J. L.; Kavanaugh, M. P.; Fairman, W. A.; Wu, Y.- N.; Murdoch,G. H.; 4 B c
North, R. A.; Amara, S. G.: Cloning and expression of a humanneutral amino
acid transporter with structural similarity to the glutamatetransporter gene
family. J. Biol. Chem. 268: 15329- 15332, 1993.

GAM175 265 SLC1A4 Hofmann, K.; Duker, M.; Fink, T.; Lichter, P.; Stoffel, W.: Humanneutral 4 B c
amino acid transporter ASCT1: structure of the gene (SLC1A4)and localization
to chromosome 2p13- p15. Genomics 24: 20- 26, 1994.

GAM175 265 SLC1A4 Shafqat, S.; Tamarappoo, B. K.; Kilberg, M. S.; Puranam, R. S.;McNamara, J. 4 B c
O.; Guadano- Ferraz, A.; Fremeau, R. T., Jr.: Cloningand expression of a
novel Na(+)- dependent neutral amino acid transporterstructurally related to
mammalian Na(+)/glutamate cotransporters. J.Biol. Chem. 268: 15351- 15355,
1993.

GAM175 265 SLC1A4 Zerangue, N.; Kavanaugh, M. P.: ASCT- 1 is a neutral amino acidexchanger 4 B c
with chloride channel activity. J. Biol. Chem. 271: 27991- 27994,1996.

GAM175 265 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses 4 B c
and phylogenetic characterization of the ZIP family of metalion transport
proteins. J. Membr. Biol. 166: 1- 7, 1998.

GAM175 265 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; 4 B c
Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof
human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping
within the epidermal differentiation complex. Genomics 62:272- 280, 1999.

GAM175 265 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC 4 B c
fragmentation map of 1q21. Genomics 49: 200- 208, 1998.

GAM175 265 THY1 Ades, E. W.; Zwerner, R. K.; Acton, R. T.; Balch, C. M.: Isolationand 4 B c

partial characterisation of the human homologue of Thy- 1. J.Exp. Med. 151: 400- 406, 1980.

GAM175 265 THY1 Bonewald, L.; Ades, E. W.; Tung, E.; Marchalonis, J. J.; Wang,A. C.: 4 B c
Biochemical characterization of human Thy- 1. J. Immunogenet. 11:283- 296, 1984.

GAM175 265 THY1 Gatti, R. A.; Lathrop, G. M.; Salser, W.; Silver, J.; Lalouel,J. M.; White, 4 B c
R.: Location of Thy- 1 with respect to a primary linkagemap of chromosome 11q. (Abstract) Cytogenet. Cell Genet. 46: 618only, 1987.

GAM175 265 THY1 Gatti, R. A.; Shaked, R.; Wei, S.; Koyama, M.; Salser, W.; Silver,J.: DNA 4 B c
polymorphism in the human Thy- 1 gene. Hum. Immun. 22:145- 150, 1988.

GAM175 265 THY1 Greenspan, R. J.; O'Brien, M. C.: Genetic evidence for the roleof Thy- 1 in 4 B c
neurite outgrowth in the mouse. J. Neurogenet. 5: 25- 36,1989.

GAM175 265 THY1 Grzeschik, K.- H.; Kazazian, H. H.: Report of the committee onthe genetic 4 B c
constitution of chromosomes 10, 11, and 12. Cytogenet.Cell Genet. 40: 179- 205, 1985.

GAM175 265 THY1 Hood, L.; Kronenberg, M.; Hunkapiller, T.: T cell antigen receptorsand the 4 B c
immunoglobulin supergene family. Cell 40: 225- 229, 1985.

GAM175 265 THY1 Letarte- Muirhead, M.; Barclay, A. N.; Williams, A. F.: Purificationof the 4 B c
Thy- 1 molecule, a major cell surface glycoprotein of rat thymocytes.Biochem. J. 151: 685- 697, 1975.

GAM175 265 THY1 Mansour, M. H.; Negm, H. I.; Cooper, E. L.: Thy- 1 evolution. Dev.Comp. 4 B c
Immun. 11: 3- 15, 1987.

GAM175 265 THY1 McKenzie, J. L.; Fabre, J. W.: Human Thy- 1: unusual localizationand 4 B c
possible functional significance in lymphoid tissues. J. Immun. 126:843- 850, 1981.

GAM175 265 THY1 Morris, R.: Thy- 1 in developing nervous tissue. Dev. Neurosci. 7:133- 160, 4 B c
1985.

GAM175 265 THY1 Raff, M. C.: Surface antigenic markers for distinguishing T andB lymphocytes 4 B c
in mice. Transplant. Rev. 6: 52- 80, 1971.

GAM175 265 THY1 Rettig, W. J.; Dracopoli, N. C.; Chesa, P. G.; Spengler, B. A.;Beresford, H. 4 B c
R.; Davies, P.; Biedler, J. L.; Old, L. J.: Role ofhuman chromosome 11 in determining surface antigenic phenotype ofnormal and malignant cells: somatic cell genetic analysis of eightantigens, including putative human Thy- 1. J. Exp. Med. 162: 1603- 1619,1985.

GAM175 265 THY1 Rettig, W. J.; Dracopoli, N. C.; Silver, J.; Old, L. J.: HumanTHY- 1: 4 B c
regional mapping on chromosome 11 and comparison with otherchromosome 11- encoded cell surface glycoproteins. (Abstract) Cytogenet.Cell Genet. 40: 731 only, 1985.

GAM175 265 THY1 Rettig, W. J.; Dracopoli, N. C.; Spengler, B. A.; Biedler, J.L.; Old, L. J.: 4 B c
Somatic cell genetic analysis of human cell surfaceantigens, including putative human Thy- 1: eight distinct antigenicsystems controlled by chromosome 11. (Abstract) Cytogenet. CellGenet. 40: 732 only, 1985.

GAM175 265 THY1 Seki, T.; Spurr, N.; Obata, F.; Goyert, S.; Goodfellow, P.; Silver,J.: The 4 B c
human Thy- 1 gene: structure and chromosomal location. Proc.Nat. Acad. Sci. 82: 6657- 6661, 1985.

GAM175 265 THY1 Tse, A. G. D.; Barclay, A. N.; Watts, A.; Williams, A. F.: 4 B c
Aglycophospholipid tail at the carboxyl terminus of the Thy- 1 glycoproteinof neurons and thymocytes. Science 230: 1003- 1008, 1985.

GAM175 265 THY1 Tunnacliffe, A.; McGuire, R. S.: A physical linkage group inhuman chromosome 4 B c
band 11q23 covering a region implicated in leukocyteneoplasia. Genomics 8:

447- 453, 1990.

GAM175 265 THY1 van den Elsen, P.; Bruns, G.; Gerhard, D. S.; Pravtcheva, D.;Jones, C.; 4 B c
Housman, D.; Ruddle, F. A.; Orkin, S.; Terhorst, C.: Assignmentof the gene
coding for the T3- delta subunit of the T3- - T- cell receptorcomplex to the
long arm of human chromosome 11 and to mouse chromosome9. Proc. Nat. Acad.
Sci. 82: 2920- 2924, 1985.

GAM175 265 THY1 van Rijs, J.; Giguere, V.; Hurst, J.; van Agthoven, T.; Geurtsvan Kessel, 4 B c
A.; Goyert, S.; Grosveld, F.: Chromosomal localizationof the human Thy- 1
gene. Proc. Nat. Acad. Sci. 82: 5832- 5835, 1985.

GAM175 265 THY1 Williams, A. F.; Gagnon, J.: Neuronal cell Thy- 1 glycoprotein:homology with 4 B c
immunoglobulin. Science 216: 696- 703, 1982.

GAM176 345 MYBL1 Barletta, C.; Druck, T.; LaForgia, S.; Calabretta, B.; Drabkin,H.; 3 C c
Patterson, D.; Croce, C. M.; Huebner, K.: Chromosome locationsof the MYB
related genes, AMYB and BMYB. Cancer Res. 51: 3821- 3824,1991.

GAM176 345 MYBL1 Nomura, N.; Takahashi, M.; Matsui, M.; Ishii, S.; Date, T.; Sasamoto,S.; 3 C c
Ishizaki, R.: Isolation of human cDNA clones of MYB- related genes,A- MYB
and B- MYB. Nucleic Acids Res. 16: 11075- 11089, 1988.

GAM176 345 MYBL1 Takahashi, T.; Nakagoshi, H.; Sarai, A.; Nomura, N.; Yamamoto,T.; Ishii, S.: 3 C c
Human A- myb gene encodes a transcriptional activatorcontaining the negative
regulatory domains. FEBS Lett. 358: 89- 96,1995.

GAM178 223 DGCR2 Augusseau, S.; Jouk, S.; Jalbert, P.; Prieur, M.: DiGeorge syndromeand 22q11 3 C c
rearrangements. (Letter) Hum. Genet. 74: 206 only, 1986.

GAM178 223 DGCR2 Bartsch, O.; Wagner, A.; Hinkel, G. K.; Lichtner, P.; Murken, 3 C c
J.;Schuffenhauer, S.: No evidence for chromosomal microdeletions atthe
second DiGeorge syndrome locus on 10p near D10S585. (Letter) Am.J. Med.
Genet. 83: 425- 426, 1999.

GAM178 223 DGCR2 Daw, S. C. M.; Taylor, C.; Kraman, M.; Call, K.; Mao, J.; Schuffenhauer,S.; 3 C c
Meitinger, T.; Lipson, T.; Goodship, J.; Scambler, P.: A commonregion of 10p
deleted in DiGeorge and velocardiofacial syndromes. NatureGenet. 13: 458-
461, 1996.

GAM178 223 DGCR2 Demczuk, S.; Aledo, R.; Zucman, J.; Delattre, O.; Desmaze, C.;Dauphinot, L.; 3 C c
Jalbert, P.; Rouleau, G. A.; Thomas, G.; Aurias, A.: Cloning of a balanced
translocation breakpoint in the DiGeorge syndromecritical region and
isolation of a novel potential adhesion receptorgene in its vicinity. Hum.
Molec. Genet. 4: 551- 558, 1995.

GAM178 223 DGCR2 Hasegawa, T.; Hasegawa, Y.; Aso, T.; Koto, S.; Nagai, T.; Tsuchiya,Y.; Kim, 3 C c
K. C.; Ohashi, H.; Wakui, K.; Fukushima, Y.: HDR
syndrome(hypoparathyroidism, sensorineural deafness, renal dysplasia)
associatedwith del(10)(p13). Am. J. Med. Genet. 73: 416- 418, 1997.

GAM178 223 DGCR2 Lichtner, P.; Konig, R.; Hasegawa, T.; Van Esch, H.; Meitinger,T.; 3 C c
Schuffenhauer, S.: An HDR (hypoparathyroidism, deafness, renaldysplasia)
syndrome locus maps distal to the DiGeorge syndrome regionon 10p13/14. J.
Med. Genet. 37: 33- 37, 2000.

GAM178 223 DGCR2 Schuffenhauer, S.; Lichtner, P.; Peykar- Derakhshandeh, P.; Murken,J.; Haas, 3 C c
O. A.; Back, E.; Wolff, G.; Zabel, B.; Barisic, I.; Rauch,A.; Borochowitz,
Z.; Dallapiccola, B.; Ross, M.; Meitinger, T.: Deletionmapping on chromosome
10p and definition of a critical region forthe second DiGeorge syndrome
locus (DGS2). Europ. J. Hum. Genet. 6:213- 225, 1998.

GAM178 223 DGCR2 Van Esch, H.; Groenen, P.; Daw, S.; Poffyn, A.; Holvoet, M.; Scambler,P.; 3 C c
Fryns, J.- P.; Van de Ven, W.; Devriendt, K.: Partial DiGeorgesyndrome in

two patients with a 10p rearrangement. Clin. Genet. 55:269- 276, 1999.

GAM178 223 DGCR2 Wadey, R.; Daw, S.; Taylor, C.; Atif, U.; Kamath, S.; Halford,S.; O'Donnell, H.; Wilson, D.; Goodship, J.; Burn, J.; Scambler, P.: Isolation of a gene encoding an integral membrane protein from thevicinity of a balanced translocation breakpoint associated with DiGeorgesyndrome. Hum. Molec. Genet. 4: 1027- 1033, 1995. 3 C c

GAM178 223 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.: Neurodevelopmental delay, motor abnormalities and cognitive deficitsin transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001. 3 C c

GAM178 223 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262- 265, 1997. 3 C c

GAM178 223 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A potassium channel mutation in weaver mice implicates membraneexcitability in granule cell differentiation. Nature Genet. 11:126- 129, 1995. 3 C c

GAM178 223 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk gene from 'the Down syndrome critical region' of chromosome 21. Biochem.Biophys. Res. Commun. 225: 92- 99, 1996. 3 C c

GAM178 223 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.; Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in transgenic mice implicates minibrain in learningdefects associated with Down syndrome. Nature Genet. 16: 28- 36,1997. 3 C c

GAM178 223 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to chromosome 16, localizes to the nucleus, and can form multimers. Biochem.Biophys. Res. Commun. 231: 640- 644, 1997. 3 C c

GAM178 223 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.; Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the Drosophila minibrain gene: human homologue maps to 21q22.2in the Down syndrome 'critical region.' Genomics 38: 331- 339, 1996. 3 C c

GAM178 223 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein kinase family involved in postembryonic neurogenesisin Drosophila. Neuron 14: 287- 301, 1995. 3 C c

GAM178 223 OGT Haltiwanger, R. S.; Blomberg, M. A.; Hart, G. W.: Glycosylationof nuclear and cytoplasmic proteins: purification and characterizationof a uridine diphospho- N- acetylglucosamine:polypeptide beta- N- acetylglucosaminyltransferase. J.Biol. Chem. 267: 9005- 9013, 1992. 3 C c

GAM178 223 OGT Kreppel, L. K.; Blomberg, M. A.; Hart, G. W.: Dynamic glycosylationof nuclear and cytosolic proteins: cloning and characterization ofa unique O- GlcNAc transferase with multiple tetratricopeptide repeats. J.Biol. Chem. 272: 9308- 9315, 1997. 3 C c

GAM178 223 OGT Lubas, W. A.; Frank, D. W.; Krause, M.; Hanover, J. A.: O- linkedGlcNAc transferase is a conserved nucleocytoplasmic protein containingtetratricopeptide repeats. J. Biol. Chem. 272: 9316- 9324, 1997. 3 C c

GAM178 223 OGT Shafi, R.; Iyer, S. P. N.; Ellies, L. G.; O'Donnell, N.; Marek,K. W.; Chui, 3 C c

D.; Hart, G. W.; Marth, J. D.: The O- GlcNAc transferasegene resides on the X chromosome and is essential for embyronic stemcell viability and mouse ontogeny. Proc. Nat. Acad. Sci. 97: 5735- 5739,2000.

GAM178 223 OGT Yang, X.; Zhang, F.; Kudlow, J. E.: Recruitment of O- GlcNAc transferaseto 3 C c promoters by corepressor mSin3A: coupling protein O- GlcNAcylationto transcriptional repression. Cell 110: 69- 80, 2002.

GAM179 300 ABR Heisterkamp, N.; Kaartinen, V.; van Soest, S.; Bokoch, G. M.; Groffen,J.: 3 B c Human ABR encodes a protein with GAP- rac activity and homologyto the DBL nucleotide exchange factor domain. J. Biol. Chem. 268:16903- 16906, 1993.

GAM179 300 ABR Heisterkamp, N.; Morris, C.; Groffen, J.: ABR, an active BCR- relatedgene. 3 B c Nucleic Acids Res. 17: 8821- 8831, 1989.

GAM179 300 ABR McDonald, J. D.; Daneshvar, L.; Willert, J. R.; Matsumura, K.;Waldman, F.; 3 B c Cogen, P. H.: Physical mapping of chromosome 17p13.3in the region of a putative tumor suppressor gene important in medulloblastoma. Genomics 23:229- 232, 1994.

GAM179 300 ATP11B Halleck, M. S.; Lawler, J. F., Jr.; Blackshaw, S.; Gao, L.; Nagarajan,P.; 3 B c Hacker, C.; Pyle, S.; Newman, J. T.; Nakanishi, Y.; Ando, H.;Weinstock, D.; Williamson, P.; Schlegel, R. A.: Differential expressionof putative transbilayer amphipath transporters. Physiol. Genomics 1:139- 150, 1999.

GAM179 300 ATP11B Mansharamani, M.; Hewetson, A.; Chilton, B. S.: Cloning and 3 B c characterizationof an atypical type IV P- type ATPase that binds to the RING motifof RUSH transcription factors. J. Biol. Chem. 276: 3641- 3649, 2001.

GAM179 300 ATP11B Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 B c Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999.

GAM179 300 BPI Gray, P. W.; Corcorran, A. E.; Eddy, R. L., Jr.; Byers, M. G.;Shows, T. B.: 3 B c The genes for the lipopolysaccharide binding protein(LBP) and the bactericidal permeability increasing protein (BPI) areencoded in the same region of human chromosome 20. Genomics 15:188- 190, 1993.

GAM179 300 BPI Gray, P. W.; Flaggs, G.; Leong, S. R.; Gumina, R. J.; Weiss, J.;Ooi, C. E.; 3 B c Elsbach, P.: Cloning of the cDNA of a human neutrophilbactericidal protein: structural and functional correlations. J.Biol. Chem. 264: 9505- 9509, 1989.

GAM179 300 BPI Hubacek, J. A.; Buchler, C.; Aslanidis, C.; Schmitz, G.: The 3 B c genomicorganization of the genes for human lipopolysaccharide binding protein(LBP) and bactericidal permeability increasing protein (BPI) is highlyconserved. Biochem. Biophys. Res. Commun. 236: 427- 430, 1997.

GAM179 300 BPI Schumann, R. R.; Leong, S. R.; Flaggs, G. W.; Gray, P. W.; Wright,S. D.; 3 B c Mathison, J. C.; Tobias, P. S.; Ulevitch, R. J.: Structureand function of lipopolysaccharide binding protein. Science 249:1429- 1431, 1990.

GAM179 300 CCNT2 Nguyen, V. T.; Kiss, T.; Michels, A. A.; Bensaude, O.: 7SK smallnuclear RNA 3 B c binds to and inhibits the activity of CDK9/cyclin T complexes. Nature 414:322- 325, 2001.

GAM179 300 CCNT2 Peng, J.; Zhu, Y.; Milton, J. T.; Price, D. H.: Identificationof multiple 3 B c cyclin subunits of human P- TEFb. Genes Dev. 12: 755- 762,1998.

GAM179 300 CCNT2 Yang, Z.; Zhu, Q.; Luo, K.; Zhou, Q.: The 7SK small nuclear RNAinhibits the 3 B c CDK9/cyclin T1 kinase to control transcription. Nature 414:317- 322, 2001.

GAM179 300 DNTT Chang, L. M. S.; Bollum, F. J.: Molecular biology of terminaltransferase. 3 B c CRC Crit. Rev. Biochem. 21: 27- 52, 1986.

GAM179 300 DNTT Epplen, J. T.; Chluba, J.; Hardt, C.; Hinkkanen, A.; Steimle, V.;Stockinger, 3 B c
H.: Mammalian T- lymphocyte antigen receptor genes: geneticand nongenetic
potential to generate variability. Hum. Genet. 75:300- 310, 1987.

GAM179 300 DNTT Isobe, M.; Huebner, K.; Erikson, J.; Peterson, R. C.; Bollum, F.J.; Chang, 3 B c
L. M. S.; Croce, C. M.: Chromosome localization of thegene for human
terminal deoxynucleotidyltransferase to region 10q23- q25. Proc.Nat. Acad.
Sci. 82: 5836- 5840, 1985.

GAM179 300 DNTT Landau, N. R.; St. John, T. P.; Weissman, I. L.; Wolf, S. C.; Silverstone,A. 3 B c
E.; Baltimore, D.: Cloning of terminal transferase cDNA by
antibodyscreening. Proc. Nat. Acad. Sci. 81: 5836- 5840, 1984.

GAM179 300 DNTT Riley, L. K.; Morrow, J. K.; Danton, M. J.; Coleman, M. S.: Humanterminal 3 B c
deoxyribonucleotidyltransferase: molecular cloning and structuralanalysis of
the gene and 5- prime flanking region. Proc. Nat. Acad.Sci. 85: 2489- 2493,
1988.

GAM179 300 DNTT Thai, T.- H.; Purugganan, M. M.; Roth, D. B.; Kearney, J. F.: Distinctand 3 B c
opposite diversifying activities of terminal transferase splicevariants.
Nature Immun. 3: 457- 462, 2002.

GAM179 300 DNTT Yang- Feng, T. L.; Landau, N. R.; Baltimore, D.; Francke, U.: Theterminal 3 B c
deoxynucleotidyltransferase gene is located on human chromosome10 (10q23-
q24) and on mouse chromosome 19. Cytogenet. Cell Genet. 43:121- 126, 1986.

GAM179 300 DSCR1 Fuentes, J. J.; Genesca, L.; Kingsbury, T. J.; Cunningham, K. W.;Perez- 3 B c
Riba, M.; Estivill, X.; de la Luna, S.: DSCR1, overexpressedin Down
syndrome, is an inhibitor of calcineurin- mediated signalingpathways. Hum.
Molec. Genet. 9: 1681- 1690, 2000.

GAM179 300 DSCR1 Fuentes, J. J.; Pritchard, M. A.; Estivill, X.: Genomic 3 B c
organization,alternative splicing, and expression patterns of the DSCR1
(Down syndromecandidate region 1) gene. Genomics 44: 358- 361, 1997.

GAM179 300 DSCR1 Fuentes, J.- J.; Pritchard, M. A.; Planas, A. M.; Bosch, A.; Ferrer,I.; 3 B c
Estivill, X.: A new human gene from the Down syndrome criticalregion encodes
a proline- rich protein highly expressed in fetal brainand heart. Hum.
Molec. Genet. 4: 1935- 1944, 1995.

GAM179 300 DSCR1 Kingsbury, T. J.; Cunningham, K. W.: A conserved family of 3 B c
calcineurinregulators. Genes Dev. 14: 1595- 1604, 2000.

GAM179 300 DSCR1 Rothermel, B.; Vega, R. B.; Yang, J.; Wu, H.; Bassel- Duby, R.;Williams, R. 3 B c
S.: A protein encoded within the Down syndrome criticalregion is enriched in
striated muscles and inhibits calcineurin signaling. J.Biol. Chem. 275:
8719- 8725, 2000.

GAM179 300 DSCR1 Strippoli, P.; Petrini, M.; Lenzi, L.; Carinci, P.; Zannotti, M.: The murine 3 B c
DSCR1- like (Down syndrome candidate region 1) gene family:conserved synteny
with the human orthologous genes. Gene 257: 223- 232,2000.

GAM179 300 DSCR1 Yang, J.; Rothermel, B.; Vega, R. B.; Frey, N.; McKinsey, T. A.;Olson, E. 3 B c
N.; Bassel- Duby, R.; Williams, R. S.: Independent signalscontrol expression
of the calcineurin inhibitory proteins MCIP1 andMCIP2 in striated muscles.
Circ. Res. 87: 61e- 68e, 2000.

GAM179 300 FBLN1 Argraves, W. S.; Dickerson, K.; Burgess, W. H.; Ruoslahti, E.:Fibulin, a 3 B c
novel protein that interacts with the fibronectin receptor- betasubunit
cytoplasmic domain. Cell 58: 623- 629, 1989.

GAM179 300 FBLN1 Korenberg, J. R.; Chen, X.- N.; Tran, H.; Argraves, W. S.: Localizationof 3 B c
the human gene for fibulin- 1 (FBLN1) to chromosome band 22q13.3.Cytogenet.
Cell Genet. 68: 192- 193, 1995.

GAM179 300 FBLN1 Mattei, M.- G.; Pan, T.- C.; Zhang, R.- Z.; Timpl, R.; Chu, M.- L.: The fibulin- 1 gene (FBLN1) is located on human chromosome 22 andon mouse chromosome 15. Genomics 22: 437- 438, 1994. 3 B c

GAM179 300 GPR48 Hsu, S. Y.; Liang, S.- G.; Hsueh, A. J. W.: Characterization oftwo LGR genes homologous to gonadotropin and thyrotropin receptorswith extracellular leucine- rich repeats and a G protein- coupled, seven- transmembraneregion. Molec. Endocr. 12: 1830- 1845, 1998. 3 B c

GAM179 300 GPR48 Loh, E. D.; Broussard, S. R.; Kolakowski, L. F.: Molecular characterizationof a novel glycoprotein hormone G- protein- coupled receptor. Biochem.Biophys. Res. Commun. 282: 757- 764, 2001. 3 B c

GAM179 300 GPR48 Loh, E. D.; Broussard, S. R.; Liu, Q.; Copeland, N. G.; Gilbert,D. J.; Jenkins, N. A.; Kolakowski, L. F., Jr. Chromosomal localizationof GPR48, a novel glycoprotein hormone receptor like GPCR, in humanand mouse with radiation hybrid and interspecific backcross mapping. Cytogenet.Cell Genet. 89: 2- 5, 2000. 3 B c

GAM179 300 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, sequence, expression, and processing of the interleukin 16precursor. Proc. Nat. Acad. Sci. 94: 5273- 5277, 1997. 3 B c

GAM179 300 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 381: 30 only, 1996. 3 B c

GAM179 300 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics 49:704- 706, 1999. 3 B c

GAM179 300 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte chemoattractant factor: association of biologic functionwith CD4 expression. Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994. 3 B c

GAM179 300 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128: 2569- 2574, 1982. 3 B c

GAM179 300 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311- 314, 1993. 3 B c

GAM179 300 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M. E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945- 1954, 1995. 3 B c

GAM179 300 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure and function between human and murine IL- 16. J. Immun. 160:5945- 5954, 1998. 3 B c

GAM179 300 IL1B Auron, P. E.; Webb, A. C.; Rosenwasser, L. J.; Mucci, S. F.; Rich,A.; Wolff, S. M.; Dinarello, C. A.: Nucleotide sequence of humanmonocyte interleukin 1 precursor cDNA. Proc. Nat. Acad. Sci. 81:7907- 7911, 1984. 3 B c

GAM179 300 IL1B Baek, S. H.; Ohgi, K. A.; Rose, D. W.; Koo, E. H.; Glass, C. K.;Rosenfeld, M. G.: Exchange of N- CoR corepressor and Tip60 coactivatorcomplexes links gene expression by NF- kappa- B and beta- amyloid precursorprotein. Cell 110: 55- 67, 2002. 3 B c

GAM179 300 IL1B Cameron, P.; Limjuco, G.; Rodkey, J.; Bennett, C.; Schmidt, J.A.: Amino acid sequence analysis of human interleukin 1 (IL- 1): evidencefor biochemically 3 B c

distinct forms of IL- 1. J. Exp. Med. 162: 790- 801,1985.

GAM179 300 IL1B D'Eustachio, P.; Jadidi, S.; Fuhlbrigge, R. C.; Gray, P. W.; Chaplin,D. D.: 3 B c
Interleukin- 1 alpha and beta genes: linkage on chromosome2 in the mouse.
Immunogenetics 26: 339- 343, 1987.

GAM179 300 IL1B Dinarello, C. A.: An update on human interleukin- 1: from molecularbiology 3 B c
to clinical relevance. J. Clin. Immun. 5: 287- 297, 1985.

GAM179 300 IL1B El- Omar, E. M.; Carrington, M.; Chow, W.- H.; McColl, K. E. L.;Bream, J. 3 B c
H.; Young, H. A.; Herrera, J.; Lissowska, J.; Yuan, C.- C.;Rothman, N.;
Lanyon, G.; Martin, M.; Fraumeni, J. F., Jr.; Rabkin,C. S.: Interleukin- 1
polymorphisms associated with increased riskof gastric cancer. Nature 404:
398- 402, 2000. Note: Erratum: Nature412: 99 only, 2001.

GAM179 300 IL1B Furutani, Y.; Notake, M.; Yamayoshi, M.; Yamagishi, J.; Nomura,H.; Ohue, M.; 3 B c
Furuta, R.; Fukui, T.; Yamada, M.; Nakamura, S.: Cloningand characterization
of the cDNAs for human and rabbit interleukin- 1precursor. Nucleic Acids
Res. 13: 5869- 5882, 1985.

GAM179 300 IL1B Hamajima, N.; Matsuo, K.; Saito, T.; Tajima, K.; Okuma, K.; Yamao,K.; 3 B c
Tominaga, S.: Interleukin 1 polymorphisms, lifestyle factors,and
helicobacter pylori infection. Jpn. J. Cancer Res. 92: 383- 389,2001.

GAM179 300 IL1B Langdahl, B. L.; Lokke, E.; Carstens, M.; Stenkjaer, L. L.; Eriksen,E. F.: 3 B c
Osteoporotic fractures are associated with an 86- base pairrepeat
polymorphism in the interleukin- 1- receptor antagonist genebut not with
polymorphisms in the interleukin- 1 beta gene. J. BoneMiner. Res. 15: 402-
414, 2000.

GAM179 300 IL1B Le Beau, M. M.; Rowley, J. D.: Personal Communication. Chicago,Ill. 3 B c
6/18/1986.

GAM179 300 IL1B Mangiarini, L.; Sathasivam, K.; Seller, M.; Cozens, B.; Harper,A.; 3 B c
Hetherington, C.; Lawton, M.; Trottier, Y.; Lehrach, H.; Davies,S. W.;
Bates, G. P.: Exon 1 of the HD gene with an expanded CAG repeatis sufficient
to cause a progressive neurological phenotype in transgenicmice. Cell 87:
493- 506, 1996.

GAM179 300 IL1B March, C. J.; Mosley, B.; Larsen, A.; Cerretti, D. P.; Braedt,G.; Price, V.; 3 B c
Gillis, S.; Henney, C. S.; Kronheim, S. R.; Grabstein,K.; Conlon, P. J.;
Hopp, T. P.; Cosman, D.: Cloning, sequence andexpression of two distinct
human interleukin- 1 complementary DNAs. Nature 315:641- 647, 1985.

GAM179 300 IL1B Nicklin, M. J. H.; Weith, A.; Duff, G. W.: A physical map ofthe region 3 B c
encompassing the human interleukin- 1- alpha, interleukin- 1- beta,and
interleukin- 1 receptor antagonist genes. Genomics 19: 382- 384,1994.

GAM179 300 IL1B Ona, V. O.; Li, M.; Vonsattel, J. P. G.; Andrews, L. J.; Khan,S. Q.; Chung, 3 B c
W. M.; Frey, A. S.; Menon, A. S.; Li, X.- J.; Stieg,P. E.; Yuan, J.; Penney,
J. B.; Young, A. B.; Cha, J.- H. J.; Friedlander,R. M.: Inhibition of
caspase- 1 slows disease progression in a mousemodel of Huntington's
disease. Nature 399: 263- 267, 1999.

GAM179 300 IL1B Patterson, D.; Jones, C.; Hart, I.; Bleskan, J.; Berger, R.; Geyer,D.; 3 B c
Eisenberg, S. P.; Smith, M. F., Jr.; Arend, W. P.: The humaninterleukin- 1
receptor antagonist (IL1RN) gene is located in the chromosome2q14 region.
Genomics 15: 173- 176, 1993.

GAM179 300 IL1B Samad, T. A.; Moore, K. A.; Sapirstein, A.; Billet, S.; Allchorne,A.; Poole, 3 B c
S.; Bonventre, J. V.; Woolf, C. J.: Interleukin- 1- beta- mediatedinduction
of Cox- 2 in the CNS contributes to inflammatory pain hypersensitivity.
Nature 410:471- 475, 2001.

GAM179 300 IL1B Vidal- Vanaclocha, F.; Fantuzzi, G.; Mendoza, L.; Fuentes, A. M.;Anasagasti, 3 B c
M. J.; Martin, J.; Carrascal, T.; Walsh, P.; Reznikov,L. L.; Kim, S.- H.;
Novick, D.; Rubinstein, M.; Dinarello, C. A.:IL- 18 regulates IL- 1- beta-
dependent hepatic melanoma metastasis viavascular cell adhesion molecule- 1.
Proc. Nat. Acad. Sci. 97: 734- 739,2000.

GAM179 300 IL1B Webb, A. C.; Collins, K. L.; Auron, P. E.; Eddy, R. L.; Nakai,H.; Byers, M. 3 B c
G.; Haley, L. L.; Henry, W. M.; Shows, T. B.: Interleukin- 1gene (IL1)
assigned to long arm of human chromosome 2. LymphokineRes. 5: 77- 85, 1986.

GAM179 300 IL1B Webb, A. C.; Collins, K. L.; Auron, P. E.; Eddy, R. L.; Nakai,H.; Byers, M.; 3 B c
Shows, T. B.: The gene for interleukin- 1 (IL1) ison human chromosome 2.
(Abstract) Cytogenet. Cell Genet. 40: 774only, 1985.

GAM179 300 IL1B Webb, A.; Collins, K.; Auron, P.; Eddy, R.; Nakai, H.; Byers,M.; Shows, T. 3 B c
B.: Genetics of acute phase response: a gene for interleukin- 1is on
chromosome 2. (Abstract) Am. J. Hum. Genet. 37: A142 only,1985.

GAM179 300 IQGAP1 Fukata, M.; Watanabe, T.; Noritake, J.; Nakagawa, M.; Yamaga, M.;Kuroda, S.; 3 B c
Matsuura, Y.; Iwamatsu, A.; Perez, F.; Kaibuchi, K.:Rac1 and Cdc42 capture
microtubules through IQGAP1 and CLIP- 170. Cell 109:873- 885, 2002.

GAM179 300 IQGAP1 Hart, M. J.; Callow, M. G.; Souza, B.; Polakis, P.: IQGAP1, acalmodulin- 3 B c
binding protein with a rasGAP- related domain, is a potentialeffector for
cdc42Hs. EMBO J. 15: 2997- 3005, 1996.

GAM179 300 IQGAP1 Sugimoto, N.; Imoto, I.; Fukuda, Y.; Kurihara, N.; Kuroda, S.;Tanigami, A.; 3 B c
Kaibuchi, K.; Kamiyama, R.; Inazawa, J.: IQGAP1, anegative regulator of
cell- cell adhesion, is upregulated by gene amplificationat 15q26 in gastric
cancer cell lines HSC39 and 40A. J. Hum. Genet. 46:21- 25, 2001.

GAM179 300 IQGAP1 Weissbach, L.; Settleman, J.; Kalady, M. F.; Snijders, A. J.; Murthy,A. E.; 3 B c
Yan, Y.- X.; Bernards, A.: Identification of a human RasGAP- relatedprotein
containing calmodulin- binding motifs. J. Biol. Chem. 269:20517- 20521,
1994.

GAM179 300 MAPK4 Garcia, J. I.; Zalba, G.; Detera- Wadleigh, S. D.; de Miguel, C.: Isolation 3 B c
of a cDNA encoding the rat MAP- kinase homolog of humanp63mapk. Mammalian
Genome 7: 810- 814, 1996.

GAM179 300 MAPK4 Gonzalez, F. A.; Raden, D. L.; Rigby, M. R.; Davis, R. J.: 3 B c
Heterogeneousexpression of four MAP kinase isoforms in human tissues. FEBS
Lett. 304:170- 178, 1992.

GAM179 300 MAPK4 Li, L.; Wysk, M.; Gonzalez, F. A.; Davis, R. J.: Genomic lociof human 3 B c
mitogen- activated protein kinases. Oncogene 9: 647- 649,1994.

GAM179 300 MAPK4 Zhu, A. X.; Zhao, Y.; Moller, D. E.; Flier, J. S.: Cloning 3 B c
andcharacterization of p97(MAPK), a novel human homolog of rat ERK- 3.
Molec.Cell. Biol. 14: 8202- 8211, 1994.

GAM179 300 MCP Bora, N. S.; Lublin, D. M.; Kumar, B. V.; Hockett, R. D.; Holers,V. M.; 3 B c
Atkinson, J. P.: Structural gene for human membrane cofactorprotein (MCP) of
complement maps to within 100 kb of the 3- prime endof the C3b/C4b receptor
gene. J. Exp. Med. 169: 597- 602, 1989.

GAM179 300 MCP Cui, W.; Hourcade, D.; Post, T.; Greenlund, A. C.; Atkinson, J.P.; Kumar, 3 B c
V.: Characterization of the promoter region of the membranecofactor protein
(CD46) gene of the human complement system and comparisonto a membrane
cofactor protein- like genetic element. J. Immun. 151:4137- 4146, 1993.

GAM179 300 MCP Dorig, R. E.; Marcil, A.; Chopra, A.; Richardson, C. D.: The humanCD46 3 B c
molecule is a receptor for measles virus (Edmonston strain). Cell 75:295-
305, 1993.

GAM179 300 MCP Kallstrom, H.; Gill, D. B.; Albiger, B.; Liszewski, M. K.; Atkinson,J. P.; 3 B c
Jonsson, A.- B.: Attachment of Neisseria gonorrhoeae to thecellular pilus
receptor CD46: identification of domains importantfor bacterial adherence.
Cell. Microbiol. 3: 133- 143, 2001.

GAM179 300 MCP Lublin, D. M.; Liszewski, M. K.; Post, T. W.; Arce, M. A.; LeBeau,M. M.; 3 B c
Rebentisch, M. B.; Lemons, R. S.; Seya, T.; Atkinson, J. P.: Molecular
cloning and chromosomal localization of human complementmembrane cofactor
protein (MCP): evidence for inclusion in the multigenefamily of complement-
regulatory proteins. J. Exp. Med. 168: 181- 194,1988.

GAM179 300 MCP Marie, J. C.; Astier, A. L.; Rivailler, P.; Rabourdin- Combe, C.;Wild, T. 3 B c
F.; Horvat, B.: Linking innate and acquired immunity: divergentrole of CD46
cytoplasmic domains in T cell- induced inflammation. NatureImmun. 3: 659-
666, 2002.

GAM179 300 MCP Post, T. W.; Liszewski, M. K.; Adams, E. M.; Tedja, I.; Miller,E. A.; 3 B c
Atkinson, J. P.: Membrane cofactor protein of the complementsystem:
alternative splicing of serine/threonine/proline- rich exonsand cytoplasmic
tails produces multiple isoforms that correlate withprotein phenotype. J.
Exp. Med. 174: 93- 102, 1991.

GAM179 300 MCP Purcell, D. F. J.; Johnstone, R. W.; McKenzie, I. F. C.: Identificationof 3 B c
four different CD46 (MCP) molecules with anti- peptide antibodies.
Biochem.Biophys. Res. Commun. 180: 1091- 1097, 1991.

GAM179 300 MCP Santoro, F.; Kennedy, P. E.; Locatelli, G.; Malnati, M. S.; Berger,E. A.; 3 B c
Lusso, P.: CD46 is a cellular receptor for human herpesvirus6. Cell 99: 817-
827, 1999.

GAM179 300 MCP Tatsuo, H.; Ono, N.; Tanaka, K.; Yanagi, Y.: SLAM (CDw150) isa cellular 3 B c
receptor for measles virus. Nature 406: 893- 897, 2000.

GAM179 300 MS4A4A Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M.: Identificationof a new 3 B c
multigene four- transmembrane family (MS4A) related to CD20,HTm4 and beta
subunit of the high- affinity IgE receptor. Gene 264:87- 93, 2001.

GAM179 300 MS4A4A Liang, Y.; Tedder, T. F.: Identification of a CD20- , Fc- epsilon- RI- beta- 3 B c
relatedgene family: sixteen new MS4A family members expressed in human
andmouse. Genomics 72: 119- 127, 2001.

GAM179 300 MYO1E Bement, W. M.; Wirth, J. A.; Mooseker, M. S.: Cloning and mRNAexpression of 3 B c
human unconventional myosin- IC: a homologue of amoeboidmyosins- I with a
single IQ motif and an SH3 domain. J. Molec. Biol. 243:356- 363, 1994.

GAM179 300 MYO1E Hasson, T.; Skowron, J. F.; Gilbert, D. J.; Avraham, K. B.; Perry,W. L.; 3 B c
Bement, W. M.; Anderson, B. L.; Sherr, E. H.; Chen, Z.- Y.;Greene, L. A.;
Ward, D. C.; Corey, D. P.; Mooseker, M. S.; Copeland,N. G.; Jenkins, N. A.:
Mapping of unconventional myosins in mouseand human. Genomics 36: 431- 439,
1996.

GAM179 300 NCOA1 Carapeti, M.; Aguiar, R. C. T.; Chase, A.; Goldman, J. M.; Cross,N. C. P.: 3 B c
Assignment of the steroid receptor coactivator- 1 (SRC- 1)gene to human
chromosome band 2p23. Genomics 52: 242- 244, 1998.

GAM179 300 NCOA1 Hayashi, Y.; Ohmori, S.; Ito, T.; Seo, H.: A splicing variantof steroid 3 B c
receptor coactivator- 1 (SRC- 1E): the major isoform of SRC- 1to mediate
thyroid hormone action. Biochem. Biophys. Res. Commun. 236:83- 87, 1997.

GAM179 300 NCOA1 Jenster, G.; Spencer, T. E.; Burcin, M. M.; Tsai, S. Y.; Tsai,M.- J.; 3 B c
O'Malley, B. W.: Steroid receptor induction of gene transcription:a two-
step model. Proc. Nat. Acad. Sci. 94: 7879- 7884, 1997.

GAM179 300 NCOA1 Liu, Z.; Wong, J.; Tsai, S. Y.; Tsai, M. J.; O'Malley, B. W.:Steroid 3 B c

receptor coactivator- 1 (SRC- 1) enhances ligand- dependent andreceptor-dependent cell- free transcription of chromatin. Proc. Nat.Acad. Sci. 96: 9485- 9490, 1999.

GAM179 300 NCOA1 Onate, S. A.; Tsai, S. Y.; Tsai, M.- J.; O'Malley, B. W.: Sequenceand 3 B c
characterization of a coactivator for the steroid hormone receptorsuperfamily. Science 270: 1354- 1357, 1995.

GAM179 300 NCOA1 Takeshita, A.; Yen, P. M.; Misiti, S.; Cardona, G. R.; Liu, Y.;Chin, W. W.: 3 B c
Molecular cloning and properties of a full- length putativethyroid hormone receptor coactivator. Endocrinology 137: 3594- 3597,1996.

GAM179 300 PIP5K1B Campuzano, V.; Montermini, L.; Molto, M. D.; Pianese, L.; Cossee,M.; 3 B c
Cavalcanti, F.; Monros, E.; Rodius, F.; Duclos, F.; Monticelli,A.; Zara, F.; Canizares, J.; Koutnikova, H.; Bidichandani, S. I.;Gellera, C.; Brice, A.; Trouillas, P.; De Michele, G.; Filla, A.;De Frutos, R.; Palau, F.; Patel, P. I.; Di Donato, S.; Mandel, J.- L.; Cocozza, S.; Koenig, M.; Pandolfo, M.: Friedreich's ataxia:autosomal recessive disease caused by an intronic GAA triplet repeatexpansion. Science 271: 1423- 1427, 1996.

GAM179 300 PIP5K1B Carvajal, J. J.; Pook, M. A.; dos Santos, M.; Doudney, K.; Hillermann,R.; 3 B c
Minogue, S.; Williamson, R.; Hsuan, J. J.; Chamberlain, S.: TheFriedreich's ataxia gene encodes a novel phosphatidylinositol- 4- phosphate5- kinase. Nature Genet. 14: 157- 162, 1996.

GAM179 300 PIP5K1B Carvajal, J. J.; Pook, M. A.; Doudney, K.; Hillermann, R.; Wilkes,D.; Al- 3 B c
Mahdawi, S.; Williamson, R.; Chamberlain, S.: Friedreich'sataxia: a defect in signal transduction? Hum. Molec. Genet. 4: 1411- 1419,1995.

GAM179 300 PIP5K1B Pook, M. A.; Carvajal, J. J; Doudney, K.; Hillermann, R.; Chamberlain,S.: 3 B c
Exon- intron structure of a 2.7- kb transcript of the STM7 genewith phosphatidylinositol- 4- phosphate 5- kinase activity. Genomics 42:170- 172, 1997.

GAM179 300 PPT2 Gupta, P.; Soyombo, A. A.; Atashband, A.; Wisniewski, K. E.; Shelton,J. M.; 3 B c
Richardson, J. A.; Hammer, R. E.; Hofmann, S. L.: Disruptionof PPT1 or PPT2 causes neuronal ceroid lipofuscinosis in knockoutmice. Proc. Nat. Acad. Sci. 98: 13566- 13571, 2001.

GAM179 300 PPT2 Soyombo, A. A.; Hofmann, S. L.: Molecular cloning and expressionof 3 B c
palmitoyl- protein thioesterase 2 (PPT2), a homolog of lysosomalpalmitoyl-protein thioesterase with a distinct substrate specificity. J.Biol. Chem. 272: 27456- 27463, 1997.

GAM179 300 PRB3 Azen, E. A.; Denniston, C.: Polymorphism of Ps (parotid size variant)and 3 B c
detection of a protein (PmS) related to the Pm (parotid middleband) system with genetic linkage of Ps and Pm to G1, Db, and Pr geneticdeterminants. Biochem. Genet. 18: 483- 501, 1980.

GAM179 300 PRB3 Azen, E. A.; Hurley, C. K.; Denniston, C.: Genetic polymorphismof the major 3 B c
parotid salivary glycoprotein (G1) with linkage to genesfor Pr, Db and Pa. (Abstract) Am. J. Hum. Genet. 30: 21A only, 1978.

GAM179 300 PRB3 Azen, E. A.; Minaguchi, K.; Latreille, P.; Kim, H.- S.: Allelesat the PRB3 3 B c
locus coding for a disulfide- bonded human salivary proline-richglycoprotein (G1 8) and a null in an Ashkenazi Jew. Am. J. Hum. Genet. 47:686- 697, 1990.

GAM179 300 PRB3 Ikemoto, S.; Minaguchi, K.; Tomita, K.; Suzuki, K.: A variantprotein in 3 B c
human parotid saliva by SDS polyacrylamide gel electrophoresisand its inheritance. Ann. Hum. Genet. 43: 11- 14, 1979.

GAM179 300 PRB3 Kim, H.- S.; Maeda, N.: Structures of two HaeIII- type genes inthe human 3 B c

salivary proline- rich protein multigene family. J. Biol.Chem. 261: 6712-
6718, 1986.

GAM179 300 PRB3 Maeda, N.: Inheritance of the human salivary proline- rich proteins:a 3 B c
reinterpretation in terms of six loci forming two subfamilies.
Biochem.Genet. 23: 455- 464, 1985.

GAM179 300 PRB3 Maeda, N.; Kim, H.- S.; Azen, E. A.; Smithies, O.: DifferentialRNA splicing 3 B c
and post- translational cleavages in the human salivaryproline- rich protein
gene system. J. Biol. Chem. 260: 11123- 11130,1985.

GAM179 300 RAB5C Albertsen, H. M.; Smith, S. A.; Mazoyer, S.; Fujimoto, E.; Stevens,J.; 3 B c
Williams, B.; Rodriguez, P.; Cropp, C. S.; Slijepcevic, P.; Carlson,M.;
Robertson, M.; Bradley, P.; and 9 others: A physical map andcandidate genes
in the BRCA1 region on chromosome 17q12- 21. NatureGenet. 7: 472- 479, 1994.

GAM179 300 RAB5C Han, H.- J.; Sudo, K.; Inazawa, J.; Nakamura, Y.: Isolation andmapping of a 3 B c
human gene (RABL) encoding a small GTP- binding proteinhomologous to the
Ras- related RAB gene. Cytogenet. Cell Genet. 73:137- 139, 1996.

GAM179 300 RAD9 Lieberman, H. B.; Hopkins, K. M.; Nass, M.; Demetrick, D.; Davey,S.: A human 3 B c
homolog of the Schizosaccharomyces pombe rad9+ checkpointcontrol gene. Proc.
Nat. Acad. Sci. 93: 13890- 13895, 1996.

GAM179 300 RAD9 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe 3 B c
Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol.
Chem. 274: 567- 570, 1999.

GAM179 300 RBBP2 Baens, M.; Aerssens, J.; Van Zand, K.; Van den Berghe, H.; Marynen,P.: 3 B c
Isolation and regional assignment of human chromosome 12p cDNAs. Genomics
29:44- 52, 1995.

GAM179 300 RBBP2 Mao, S.; Neale, G. A. M.; Goorha, R. M.: T- cell oncogene rhombotin- 3 B c
2interacts with retinoblastoma- binding protein 2. Oncogene 14: 1531-
1539,1997.

GAM179 300 REGL Gharib, B.; Fox, M. F.; Bartoli, C.; Giorgi, D.; Sansonetti, A.;Swallow, D. 3 B c
M.; Dagorn, J. C.; Berge- Lefranc, J. L.: Human
regenerationprotein/lithostathine genes map to chromosome 2p12. Ann. Hum.
Genet. 57:9- 16, 1993.

GAM179 300 REGL Miyashita, H.; Nakagawara, K.; Mori, M.; Narushima, Y.; Noguchi,N.; 3 B c
Moriizumi, S.; Takasawa, S.; Yonekura, H.; Takeuchi, T.; Okamoto,H.: Human
REG family genes are tandemly ordered in a 95- kilobaseregion of chromosome
2p12. FEBS Lett. 377: 429- 433, 1995.

GAM179 300 REGL Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki,Y.; Miyashita, 3 B c
H.; Yonekura, H.; Okamoto, H.: Isolation, structuraldetermination and
expression of a novel reg gene, human regI- beta. Biochim.Biophys. Acta
1217: 199- 202, 1994.

GAM179 300 SIAT1 Grundmann, U.; Nerlich, C.; Rein, T.; Zettlmeissl, G.: CompletecDNA sequence 3 B c
encoding human beta- galactoside alpha- 2,6- sialyltransferase. NucleicAcids
Res. 18: 667 only, 1990.

GAM179 300 SIAT1 Wang, X.; Vertino, A.; Eddy, R. L.; Byers, M. G.; Jani- Sait, S.N.; Shows, 3 B c
T. B.; Lau, J. T. Y.: Chromosome mapping and organizationof the human beta-
galactoside alpha- 2,6- sialyltransferase gene: differentialand cell- type
specific usage of upstream exon sequences in B- lymphoblastoidcells. J.
Biol. Chem. 268: 4355- 4361, 1993.

GAM179 300 SLC12A7 Boettger, T.; Hubner, C. A.; Maler, H.; Rust, M. B.; Beck, F. X.;Jentsch, T. 3 B c
J.: Deafness and renal tubular acidosis in mice lackingthe K- Cl co-
transporter Kcc4. Nature 416: 874- 878, 2002.

GAM179 300 SLC12A7 Mount, D. B.; Mercado, A.; Song, L.; Xu, J.; George, A. L., Jr.;Delpire, E.; 3 B c
Gamba, G.: Cloning and characterization of KCC3 andKCC4, new members of the
cation- chloride cotransporter gene family. J.Biol. Chem. 274: 16355- 16362,
1999.

GAM179 300 SMCX Agulnik, A. I.; Mitchell, M. J.; Lerner, J. L.; Woods, D. R.; Bishop,C. E.: 3 B c
A mouse Y chromosome gene encoded by a region essential forspermatogenesis
and expression of male- specific minor histocompatibilityantigens. Hum.
Molec. Genet. 3: 873- 878, 1994.

GAM179 300 SMCX Agulnik, A. I.; Mitchell, M. J.; Mattei, M.- G.; Borsani, G.; Avner,P. A.; 3 B c
Lerner, J. L.; Bishop, C. E.: A novel X gene with a widelytranscribed Y-
linked homologue escapes X- inactivation in mouse andhuman. Hum. Molec.
Genet. 3: 879- 884, 1994.

GAM179 300 SMCX Brown, C. J.; Miller, A. P.; Carrel, L.; Rupert, J. L.; Davies,K. E.; 3 B c
Willard, H. F.: The DXS423E gene in Xp11.21 escapes X
chromosomeinactivation. Hum. Molec. Genet. 4: 251- 255, 1995.

GAM179 300 SMCX Lingenfelter, P. A.; Adler, D. A.; Poslinski, D.; Thomas, S.; Elliott,R. W.; 3 B c
Chapman, V. M.; Disteche, C. M.: Escape from X inactivationof Smcx is
preceded by silencing during mouse development. NatureGenet. 18: 212- 213,
1998.

GAM179 300 SMCX Wu, J.; Ellison, J.; Salido, E.; Yen, P.; Mohandas, T.; Shapiro,L. J.: 3 B c
Isolation and characterization of XE169, a novel human genethat escapes X-
inactivation. Hum. Molec. Genet. 3: 153- 160, 1994.

GAM179 300 SMCX Wu, J.; Salido, E. C.; Yen, P. H.; Mohandas, T. K.; Heng, H. H.Q.; Tsui, L.- 3 B c
C.; Park, J.; Chapman, V. M.; Shapiro, L. J.: The murineXe169 gene escapes
X- inactivation like its human homologue. NatureGenet. 7: 491- 496, 1994.

GAM179 300 TNR Arrigo, G.; Gherzi, R.; Bonaglia, M. C.; Leprini, A.; Zuffardi,O.; Zardi, 3 B c
L.: Assignment of the tenascin- R gene (Tnr) to mouse chromosome4 band E2 by
fluorescence in situ hybridization; refinement of thehuman TNR location to
chromosome 1q24. Cytogenet. Cell Genet. 78:145- 146, 1997.

GAM179 300 TNR Carnemolla, B.; Leprini, A.; Borsi, L.; Querze, G.; Urbini, S.;Zardi, L.: 3 B c
Human tenascin- R: complete primary structure, pre- mRNAalternative splicing
and gene localization on chromosome 1q23- q24. J.Biol. Chem. 271: 8157-
8160, 1996.

GAM179 300 TNR Erickson, H. P.: A tenascin knockout with a phenotype. NatureGenet. 17: 5- 3 B c
7, 1997.

GAM179 300 TNR Erickson, H. P.: Tenascin- C, tenascin- R and tenascin- X: a familyof 3 B c
talented proteins in search of functions. Curr. Opin. Cell Biol. 5:869- 876,
1993.

GAM179 300 TNR Leprini, A.; Gherzi, R.; Siri, A.; Querze, G.; Viti, F.; Zardi,L.: The human 3 B c
tenascin- R gene. J. Biol. Chem. 271: 31251- 31254,1996.

GAM179 300 TNR Williams, H.; Schachner, M.; Wang, B.; Kenwrick, S.: Radiationhybrid mapping 3 B c
of the genes for tenascin- R (TNR), phosducin (PDC),Laminin C1 (LAMC1), and
TAX in 1q25- q32. Genomics 46: 165- 166, 1997.

GAM180 214 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 1 B c
Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.:
Identification of Bach2 as a B- cell- specific partner for smallMaf proteins
that negatively regulate the immunoglobulin heavy chaingene 3- prime
enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM180 214 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 1 B c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-

basic leucine zipper transcription factors that interact withMafK and regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-6095, 1996.

GAM180 214 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.; Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene 19: 3739- 3749, 2000. 1 B c

GAM180 214 BVES Andree, B.; Hillemann, T.; Kessler- Ieckson, G.; Schmitt- John, T.;Jockusch, H.; Arnold, H.- H.; Brand, T.: Isolation and characterizationof the novel Popeye gene family expressed in skeletal muscle and heart. Dev.Biol. 223: 371- 382, 2000. 1 B c

GAM180 214 BVES Reese, D. E.; Bader, D. M.: Cloning and expression of hbves, anovel and highly conserved mRNA expressed in the developing and adultheart and skeletal muscle in the human. Mammalian Genome 10: 913- 915,1999. 1 B c

GAM180 214 BVES Reese, D. E.; Zavaljevski, M.; Streiff, N. L.; Bader, D.: Bves:a novel gene expressed during coronary blood vessel development. Dev.Biol. 209: 159- 171, 1999. 1 B c

GAM180 214 CALM1 Berchtold, M. W.; Egli, R.; Rhyner, J. A.; Hameister, H.; Strehler,E. E.: Localization of the human bona fide calmodulin genes CALM1,CALM2, and CALM3 to chromosomes 14q24- q31, 2p21.1- p21.3, and 19q13.2- q13.3. Genomics 16:461- 465, 1993. 1 B c

GAM180 214 CALM1 Chin, D.; Winkler, K. E.; Means, A. R.: Characterization of substratephosphorylation and use of calmodulin mutants to address implicationsfrom the enzyme crystal structure of calmodulin- dependent proteinkinase I. J. Biol. Chem. 272: 31235- 31240, 1997. 1 B c

GAM180 214 CALM1 Drum, C. L.; Yan, S.- Z.; Bard, J.; Shen, Y.- Q.; Lu, D.; Soelaiman,S.; Grabarek, Z.; Bohm, A.; Tang, W.- J.: Structural basis for theactivation of anthrax adenylyl cyclase exotoxin by calmodulin. Nature 415:396- 402, 2002. 1 B c

GAM180 214 CALM1 Koller, M.; Schnyder, B.; Strehler, E. E.: Structural organizationof the human CaMIII calmodulin gene. Biochim. Biophys. Acta 1087:180- 189, 1990. 1 B c

GAM180 214 CALM1 Kretsinger, R. H.; Rudnick, S. E.; Weissman, L. J.: Crystal structureof calmodulin. J. Inorganic Biochem. 28: 289- 302, 1986. 1 B c

GAM180 214 CALM1 McPherson, J. D.; Hickie, R. A.; Wasmuth, J. J.; Meyskens, F. L.;Perham, R. N.; Strehler, E. E.; Graham, M. T.: Chromosomal localizationof multiple genes encoding calmodulin. (Abstract) Cytogenet. CellGenet. 58: 1951 only, 1991. 1 B c

GAM180 214 CALM1 Pegues, J. C.; Friedberg, F.: Multiple mRNAs encoding human calmodulin. Biochem.Biophys. Res. Commun. 172: 1145- 1149, 1990. 1 B c

GAM180 214 CALM1 Rhyner, J. A.; Ottiger, M.; Wicki, R.; Greenwood, T. M.; Strehler,E. E.: Structure of the human CALM1 calmodulin gene and identificationof two CALM1-related pseudogenes CALM1P1 and CALM1P2. Europ. J. Biochem. 225:71- 82, 1994. 1 B c

GAM180 214 CALM1 Scambler, P. J.; McPherson, M. A.; Bates, G.; Bradbury, N. A.;Dormer, R. L.; Williamson, R.: Biochemical and genetic exclusionof calmodulin as the site of the basic defect in cystic fibrosis. Hum.Genet. 76: 278- 282, 1987. 1 B c

GAM180 214 CALM1 Schumacher, M. A.; Rivard, A. F.; Bachinger, H. P.; Adelman, J.P.: Structure of the gating domain of a Ca(2+)- activated K+ channelcomplexed with Ca(2+)/calmodulin. Nature 410: 1120- 1124, 2001. 1 B c

GAM180 214 CALM1 Sen Gupta, B.; Detera- Wadleigh, S. D.; McBride, O. W.; Friedberg,F.: A 1 B c

calmodulin pseudogene on human chromosome 17. Nucleic AcidsRes. 17: 2868 only, 1989.

GAM180 214 CALM1 Sen Gupta, B.; Friedberg, F.; Detera- Wadleigh, S. D.: Molecularanalysis of human and rat calmodulin complementary DNA clones: evidencefor additional active genes in these species. J. Biol. Chem. 262:16663- 16670, 1987. 1 B c

GAM180 214 CALU Yabe, D.; Nakamura, T.; Kanazawa, N.; Tashiro, K.; Honjo, T.:Calumenin, a Ca(2+)- binding protein retained in the endoplasmic reticulumwith a novel carboxyl- terminal sequence, HDEF. J. Biol. Chem. 272:18232- 18239, 1997. 1 B c

GAM180 214 CALU Yabe, D.; Taniwaki, M.; Nakamura, T.; Kanazawa, N.; Tashiro, K.;Honjo, T.: Human calumenin gene (CALU): cDNA isolation and chromosomalmapping to 7q32. Genomics 49: 331- 333, 1998. 1 B c

GAM180 214 CD22 Brinkman- Van der Linden, E. C. M.; Sjoberg, E. R.; Juneja, L. R.;Crocker, P. R.; Varki, N.; Varki, A.: Loss of N- glycolylneuraminicacid in human evolution: implications for sialic acid recognitionby siglecs. J. Biol. Chem. 275: 8633- 8640, 2000. 1 B c

GAM180 214 CD22 O'Keefe, T. L.; Williams, G. T.; Davies, S. L.; Neuberger, M. S.: Hyperresponsive B cells in CD22- deficient mice. Science 274: 798- 801,1996. 1 B c

GAM180 214 CD22 Ravetch, J. V.; Lanier, L. L.: Immune inhibitory receptors. Science 290:84- 89, 2000. 1 B c

GAM180 214 CD22 Wilson, G. L.; Fox, C. H.; Fauchi, A. S.; Kehrl, J. H.: cDNA cloningof the B cell membrane protein CD22: a mediator of B- B cell interactions. J.Exp. Med. 173: 137- 146, 1991. 1 B c

GAM180 214 CD22 Wilson, G. L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.;Kehrl, J. H.: Genomic structure and chromosomal mapping of the humanCD22 gene. J. Immun. 150: 5013- 5024, 1993. 1 B c

GAM180 214 CHST5 Akama, T. O.; Nishida, K.; Nakayama, J.; Watanabe, H.; Ozaki, K.;Nakamura, T.; Dota, A.; Kawasaki, S.; Inoue, Y.; Maeda, N.; Yamamoto,S.; Fujiwara, T.; Thonar, E. J.- M. A.; Shimomura, Y.; Kinoshita, S.;Tanigami, A.; Fukuda, M. N.: Macular corneal dystrophy type I andtype II are caused by distinct mutations in a new sulphotransferasegene. Nature Genet. 26: 237- 241, 2000. 1 B c

GAM180 214 CHST5 Lee, J. K.; Bhakta, S.; Rosen, S. D.; Hemmerich, S.: Cloning andcharacterization of a mammalian N- acetylglucosamine- 6- sulfotransferasethat is highly restricted to intestinal tissue. Biochem. Biophys.Res. Commun. 263: 543- 549, 1999. 1 B c

GAM180 214 DRD2 Balk, J.- H.; Picetti, R.; Salardi, A.; Thirlet, G.; Dierich, A.;Depaulls, A.; Le Meur, M.; Borrelli, E.: Parkinsonian- like locomotorimpairment in mice lacking dopamine D2 receptors. Nature 377: 424- 428,1995. 1 B c

GAM180 214 DRD2 Basu, S.; Nagy, J. A.; Pal, S.; Vasile, E.; Eckelhoefer, I. A.;Bliss, V. S.; Manseau, E. J.; Dasgupta, P. S.; Dvorak, H. F.; Mukhopadhyay,D.: The neurotransmitter dopamine inhibits angiogenesis induced byvascular permeability factor/vascular endothelial growth factor. NatureMed. 7: 569- 574, 2001. 1 B c

GAM180 214 DRD2 Blum, K.; Noble, E. P.; Sheridan, P. J.; Montgomery, A.; Ritchie,T.; Jagadeeswaran, P.; Nogami, H.; Briggs, A. H.; Cohn, J. B.: Allelicassociation of human dopamine D(2) receptor gene in alcoholism. J.A.M.A. 263:2055- 2060, 1990. 1 B c

GAM180 214 DRD2 Bolos, A. M.; Dean, M.; Lucas- Derse, S.; Ramsburg, M.; Brown, G.L.; Goldman, D.: Population and pedigree studies reveal a lack ofassociation between the dopamine D(2) receptor gene and alcoholism. J.A.M.A. 264:3156- 3160, 1990. 1 B c

GAM180 214 DRD2 Bunzow, J. R.; Van Tol, H. H.; Grandy, D. K.; Albert, P.; Salon,J.; Christie, M.; Machida, C. A.; Neve, K. A.; Civelli, O.: Cloningand expression of a rat D2 dopamine receptor cDNA. Nature 336: 783- 787,1988. 1 B c

GAM180 214 DRD2 Castner, S. A.; Williams, G. V.; Goldman- Rakic, P. S.: Reversalof antipsychotic- induced working memory deficits by short- term dopamineD1 receptor stimulation. Science 287: 2020- 2022, 2000. 1 B c

GAM180 214 DRD2 Dal Toso, R.; Sommer, B.; Ewert, M.; Herb, A.; Pritchett, D. B.;Bach, A.; Shivers, B. D.; Seeburg, P. H.: The dopamine D(2) receptor:two molecular forms generated by alternative splicing. EMBO J. 8:4025- 4034, 1989. 1 B c

GAM180 214 DRD2 Devor, E. J.; Grandy, D. K.; Civelli, O.; Litt, M.; Burgess, A.K.; Isenberg, K. E.; van de Wetering, B. J. M.; Oostra, B.: Geneticlinkage is excluded for the D2- dopamine receptor lambda- HD2G1 andflanking loci on chromosome 11q22- q23 in Tourette syndrome. Hum.Hered. 40: 105- 108, 1990. 1 B c

GAM180 214 DRD2 Eubanks, J. H.; Djabali, M.; Selleri, L.; Grandy, D. K.; Civelli,O.; McElligott, D. L.; Evans, G. A.: Structure and linkage of theD2 dopamine receptor and neural cell adhesion molecule genes on humanchromosome 11q23. Genomics 14: 1010- 1018, 1992. 1 B c

GAM180 214 DRD2 Gejman, P. V.; Ram, A.; Gelernter, J.; Friedman, E.; Cao, Q.;Pickar, D.; Blum, K.; Noble, E. P.; Kranzler, H. R.; O'Malley, S.;Hamer, D. H.; Whitsitt, F.; Rao, P.; DeLisi, L. E.; Virkkunen, M.;Linnoila, M.; Goldman, D.; Gershon, E. S.: No structural mutationin the dopamine D2 receptor gene in alcoholism or schizophrenia: analysisusing denaturing gradient gel electrophoresis. J.A.M.A. 271: 204- 208,1994. 1 B c

GAM180 214 DRD2 Gelernter, J.; Grandy, D. K.; Bunzow, J.; Pakstis, A. J.; Civelli,O.; Retief, A. E.; Litt, M.; Kidd, K. K.: D(2) dopamine receptorlocus (probe hD2G1) maps close to D11S29 (probe L7) and is also linkedto PBGD (probe PBGD0.0) and D11S84 (probe p- 2- 7- ID6) on 11q. (Abstract) Cytogenet.Cell Genet. 51: 1002 only, 1989. 1 B c

GAM180 214 DRD2 Gelernter, J.; Pakstis, A. J.; Grandy, D.; Litt, M.; Retief, A.E.; Kennedy, J. L.; Hing- Loh, A.; Schoolfield, G.; Civelli, O.; Kidd,K. K.: Linkage map of eight human chromosome 11q markers, includingDRD2, spanning 60 cM. Cytogenet. Cell Genet. 60: 26- 28, 1992. 1 B c

GAM180 214 DRD2 Gelernter, J.; Pakstis, A. J.; Pauls, D. L.; Kurlan, R.; Gancher,S. T.; Civelli, O.; Grandy, D.; Kidd, K. K.: Gilles de la Tourettesyndrome is not linked to D2- dopamine receptor. Arch. Gen. Psychiat. 47:1073- 1077, 1990. 1 B c

GAM180 214 DRD2 Giros, B.; Sokoloff, P.; Martres, M.- P.; Riou, J.- F.; Emorine,L. J.; Schwartz, J.- C.: Alternative splicing directs the expressionof two D(2) dopamine receptor isoforms. Nature 342: 923- 926, 1989. 1 B c

GAM180 214 DRD2 Grandy, D. K.; Litt, M.; Allen, L.; Bunzow, J. R.; Marchionni,M.; Makam, H.; Reed, L.; Magenis, R. E.; Civelli, O.: The human dopamineD(2) receptor gene is located on chromosome 11 at q22- q23 and identifiesa TaqI RFLP. Am. J. Hum. Genet. 45: 778- 785, 1989. 1 B c

GAM180 214 DRD2 Grandy, D. K.; Marchionni, M. A.; Makam, H.; Stofko, R. E.; Alfano,M.; Frothingham, L.; Fischer, J. B.; Burke- Howie, K. J.; Bunzow, J.R.; Server, A. C.; Civelli, O.: Cloning of the cDNA and gene fora human D2 dopamine receptor. Proc. Nat. Acad. Sci. 86: 9762- 9766,1989. 1 B c

GAM180 214 DRD2 Klein, C.; Brin, M. F.; Kramer, P.; Sena- Esteves, M.; de Leon,D.; Doheny, D.; Bressman, S.; Fahn, S.; Breakefield, X. O.; Ozelius,L. J.: Association of a missense change in the D2 dopamine receptorwith myoclonus dystonia. Proc. Nat. Acad. Sci. 96: 5173- 5176, 1999. 1 B c

GAM180 214 DRD2 Maldonado, R.; Salardi, A.; Valverde, O.; Samad, T. A.; Roques,B. P.; 1 B c
Borrelli, E.: Absence of opiate rewarding effects in micelacking dopamine D2
receptors. Nature 388: 586- 589, 1997.

GAM180 214 DRD2 Milligan, G.: Receptors as kissing cousins. Science 288: 65- 67,2000. 1 B c

GAM180 214 DRD2 Monsma, F. J., Jr.; McVittie, L. D.; Gerfen, C. R.; Mahan, L.C.; Sibley, D. 1 B c
R.: Multiple D(2) dopamine receptors produced by alternativeRNA splicing.
Nature 342: 926- 929, 1989.

GAM180 214 DRD2 Oliveri, R. L.; Annesi, G.; Zappia, M.; Civitelli, D.; Montesanti,R.; 1 B c
Branca, D.; Nicoletti, G.; Spadafora, P.; Pasqua, A. A.; Cittadella,R.;
Andreoli, V.; Gambardella, A.; Aguglia, U.; Quattrone, A.: DopamineD2
receptor gene polymorphism and the risk of levodopa- induced dyskinesiasin
PD. Neurology 53: 1425- 1430, 1999.

GAM180 214 DRD2 Rocheville, M.; Lange, D. C.; Kumar, U.; Patel, S. C.; Patel,R. C.; Patel, 1 B c
Y. C.: Receptors for dopamine and somatostatin: formationof hetero-
oligomers with enhanced functional activity. Science 288:154- 157, 2000.

GAM180 214 DRD2 Smith, M.; Wasmuth, J.; McPherson, J. D.; Wagner, C.; Grandy,D.; Civelli, 1 B c
O.; Potkin, S.; Litt, M.: Cosegregation of an 11q22.3- 9p22translocation
with affective disorder: proximity of the dopamine D2receptor gene relative
to the translocation breakpoint. (Abstract) Am.J. Hum. Genet. 45 (suppl.):
A220 only, 1989.

GAM180 214 DRD2 St Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, 1 B c
G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced
autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM180 214 DRD2 Suarez, B. K.; Parsian, A.; Hampe, C. L.; Todd, R. D.; Reich,T.; Cloninger, 1 B c
C. R.: Linkage disequilibria at the D2 dopamine receptorlocus (DRD2) in
alcoholics and controls. Genomics 19: 12- 20, 1994.

GAM180 214 DRD2 Usiello, A.; Baik, J.- H.; Rouge- Pont, F.; Picetti, R.; Dierich,A.; LeMeur, 1 B c
M.; Piazza, P. V.; Borrelli, E.: Distinct functions ofthe two isoforms of
dopamine D2 receptors. Nature 408: 199- 203,2000.

GAM180 214 DRD2 Wang, J.; Liu, Z.- L.; Chen, B.: Association study of dopamineD2, D3 1 B c
receptor gene polymorphisms with motor fluctuations in PD. Neurology
56:1757- 1759, 2001.

GAM180 214 DUSP2 Martell, K. J.; Kwak, S.; Hakes, D. J.; Dixon, J. E.; Trent, J.M.: 1 B c
Chromosomal localization of four human VH1- like protein-
tyrosinephosphatases. Genomics 22: 462- 464, 1994.

GAM180 214 DUSP2 Rohan, P. J.; Davis, P.; Moskaluk, C. A.; Kearns, M.; Krutzsch,H.; 1 B c
Siebenlist, U.; Kelly, K.: PAC- 1: a mitogen- induced nuclear
proteintyrosine phosphatase. Science 259: 1763- 1766, 1993.

GAM180 214 DUSP2 Ward, Y.; Gupta, S.; Jensen, P.; Wartmann, M.; Davis, R. J.; Kelly,K.: 1 B c
Control of MAP kinase activation by the mitogen- induced
threonine/tyrosinephosphatase PAC1. Nature 367: 651- 654, 1994.

GAM180 214 DUSP2 Yi, H.; Morton, C. C.; Weremowicz, S.; McBride, O. W.; Kelly, K.: Genomic 1 B c
organization and chromosomal localization of the DUSP2 gene,encoding a MAP
kinase phosphatase, to human 2p11.2- q11. Genomics 28:92- 96, 1995.

GAM180 214 EFNA3 Cerretti, D. P.; Lyman, S. D.; Kozlosky, C. J.; Copeland, N. G.;Gilbert, D. 1 B c
J.; Jenkins, N. A.; Valentine, V.; Kirstein, M. N.; Shapiro,D. N.; Morris,
S. W.: The genes encoding the Eph- related receptortyrosine kinase ligands
LERK- 1 (EPLG1, Epl1), LERK- 3 (EPLG3, Epl3),and LERK- 4 (EPLG4, Epl4) are
clustered on human chromosome 1 and mousechromosome 3. Genomics 33: 277-
282, 1996.

GAM180 214 EFNA3 Cerretti, D. P.; Nelson, N.: Characterization of the genes formouse LERK- 3/Ephrin- A3 (Epl3), mouse LERK- 4/Ephrin- A4 (Epl4), andhuman LERK- 6/Ephrin- A2 (EPLG6): conservation of intron/exon structure. Genomics 47:131- 135, 1998. 1 B c

GAM180 214 FUT3 Gedde- Dahl, T., Jr.; Olaisen, B.; Teisberg, P.; Wilhelmy, M. C.;Mevag, B.; Helland, R.: The locus for apolipoprotein E (apoE) isclose to the Lutheran (Lu) blood group locus on chromosome 19. Hum.Genet. 67: 178- 182, 1984. 1 B c

GAM180 214 FUT3 Grollman, E. F.; Kobata, A.; Ginsburg, V.: An enzymatic basisfor Lewis blood types in man. J. Clin. Invest. 48: 1489- 1494, 1969. 1 B c

GAM180 214 FUT3 Grubb, R.: Zur Genetik des Lewis- Systems. Naturwissenschaften 21:560- 561, 1953. 1 B c

GAM180 214 FUT3 Koda, Y.; Kimura, H.; Mekada, E.: Analysis of Lewis fucosyltransferasegenes from the human gastric mucosa of Lewis- positive and - negativeindividuals. Blood 82: 2915- 2919, 1993. 1 B c

GAM180 214 FUT3 Koprowski, H.; Blaszczyk, M.; Steplewski, Z.; Brockhaus, M.; Magnani,J.; Ginsburg, V.: Lewis blood- type may affect the incidence of gastrointestinalcancer. Lancet I: 1332- 1333, 1982. 1 B c

GAM180 214 FUT3 Nishihara, S.; Narimatsu, H.; Iwasaki, H.; Yazawa, S.; Akamatsu,S.; Ando, T.; Seno, T.; Narimatsu, I.: Molecular genetic analysisof the human Lewis histo- blood group system. J. Biol. Chem. 269:29271- 29278, 1994. 1 B c

GAM180 214 FUT3 Orntoft, T. F.; Vestergaard, E. M.; Holmes, E.; Jakobsen, J. S.;Grunnet, N.; Mortensen, M.; Johnson, P.; Bross, P.; Gregersen, N.;Skorstengaard, K.; Jensen, U. B.; Bolund, L.; Wolf, H.: Influenceof Lewis alpha- 1- 3/4- L- fucosyltransferase (FUT3) gene mutations onenzyme activity, erythrocyte phenotyping, and circulating tumor markersialyl- Lewis a levels. J. Biol. Chem. 271: 32260- 32268, 1996. 1 B c

GAM180 214 FUT3 Pang, H.; Liu, Y.; Koda, Y.; Soejima, M.; Jia, J.; Schlaphoff,T.; du Toit, E. D.; Kimura, H.: Five novel missense mutations ofthe Lewis gene (FUT3) in African (Xhosa) and Caucasian populationsin South Africa. Hum. Genet. 102: 675- 680, 1998. 1 B c

GAM180 214 FUT3 Reguigne- Arnould, I.; Couillin, P.; Mollicone, R.; Faure, S.; Fletcher,A.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Relative positions of twoclusters of human alpha- L- fucosyltransferases in 19q (FUT1- FUT2) and19p (FUT6- FUT3- FUT5) within the microsatellite genetic map of chromosome19. Cytogenet. Cell Genet. 71: 158- 162, 1995. 1 B c

GAM180 214 FUT3 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 1 B c

GAM180 214 FUT3 Sheinfeld, J.; Schaeffer, A. J.; Cordon- Cardo, C.; Rogatko, A.;Fair, W. R.: Association of the Lewis blood- group phenotype withrecurrent urinary tract infections in women. New Eng. J. Med. 320:773- 777, 1989. 1 B c

GAM180 214 FUT3 Weitkamp, L. R.; Johnston, E.; Guttormsen, S. A.: Probable geneticlinkage between the loci for the Lewis blood group and complementC3. Cytogenet. Cell Genet. 13: 183- 184, 1974. 1 B c

GAM180 214 FUT3 Yazawa, S.; Oh- Kawara, H.; Nakajima, T.; Hosomi, O.; Akamatsu,S.; Kishi, K.: Histo- blood group Lewis genotyping from human hairsand blood. Jpn. J. Hum. Genet. 41: 177- 188, 1996. 1 B c

GAM180 214 FUT5 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3 and 11q21. Genomics 26: 142- 146, 1995. 1 B c

GAM180 214 FUT5 Weston, B. W.; Nair, R. P.; Larsen, R. D.; Lowe, J. B.: Isolationof a novel 1 B c
human alpha(1,3)fucosyltransferase gene and molecular comparisonto the human
Lewis blood group alpha(1,3/1,4)fucosyltransferase gene:syntenic,
homologous, nonallelic genes encoding enzymes with distinctacceptor
substrate specificities. J. Biol. Chem. 267: 4152- 4160,1992.

GAM180 214 FUT5 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of 1 B c
a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple
homologous sequences that determine expressionof the Lewis x, sialyl Lewis
x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584,
1992.

GAM180 214 FUT6 Brinkman- Van der Linden, E. C. M.; Mollicone, R.; Oriol, R.; Larson,G.; Van 1 B c
den Eijnden, D. H.; Van Dijk, W.: A missense mutation inthe FUT6 gene
results in total absence of alpha- 3- fucosylation ofhuman alpha- 1- acid
glycoprotein. J. Biol. Chem. 271: 14492- 14495,1996.

GAM180 214 FUT6 Cameron, H. S.; Szczepaniak, D.; Weston, B. W.: Expression ofhuman 1 B c
chromosome 19p alpha- (1,3)- fucosyltransferase genes in normaltissues:
alternative splicing, polyadenylation, and isoforms. J.Biol. Chem. 270:
20112- 20122, 1995.

GAM180 214 FUT6 Koszdin, K. L.; Bowen, B. R.: The cloning and expression of ahuman alpha- 1 B c
1,3 fucosyltransferase capable of forming the E- selectinligand. Biochem.
Biophys. Res. Commun. 187: 152- 157, 1992.

GAM180 214 FUT6 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. 1 B c
C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps
of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3
and 11q21. Genomics 26: 142- 146, 1995.

GAM180 214 FUT6 Mollicone, R.; Reguigne, I.; Fletcher, A.; Aziz, A.; Rustam, M.;Weston, B. 1 B c
W.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Molecular basisfor plasma
alpha(1,3)- fucosyltransferase gene deficiency (FUT6). J.Biol. Chem. 269:
12662- 12671, 1994.

GAM180 214 FUT6 Pang, H.; Koda, Y.; Soejima, M.; Schlaphoff, T.; Du Toit, E. D.;Kimura, H.: 1 B c
Allelic diversity of the human plasma alpha(1,3)fucosyltransferasegene
(FUT6). Ann. Hum. Genet. 63: 277- 284, 1999.

GAM180 214 FUT6 Schnyder- Candrian, S.; Borsig, L.; Moser, R.; Berger, E. G.: Localizationof 1 B c
alpha- 1,3- fucosyltransferase VI in Weibel- Palade bodies of
humanendothelial cells. Proc. Nat. Acad. Sci. 97: 8369- 8374, 2000.

GAM180 214 FUT6 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of 1 B c
a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple
homologous sequences that determine expressionof the Lewis x, sialyl Lewis
x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584,
1992.

GAM180 214 GLUL Clancy, K. P.; Berger, R.; Cox, M.; Bleskan, J.; Walton, K. A.;Hart, I.; 1 B c
Patterson, D.: Localization of the L- glutamine synthetasegene to chromosome
1q23. Genomics 38: 418- 420, 1996.

GAM180 214 GLUL Gibbs, C. S.; Campbell, K. E.; Wilson, R. H.: Sequence of a humanglutamine 1 B c
synthetase cDNA. Nucleic Acids Res. 15: 6293 only, 1987.

GAM180 214 GLUL Gunnersen, D.; Haley, B.: Detection of glutamine synthetase inthe 1 B c
cerebrospinal fluid of Alzheimer diseased patients: a potentialdiagnostic
biochemical marker. Proc. Nat. Acad. Sci. 89: 11949- 11953,1992.

GAM180 214 GLUL Helou, K.; Das, A. T.; Lamers, W. H.; Hoovers, J. M. N.; Szpirer,C.; 1 B c
Szpirer, J.; Klinga- Levan, K.; Levan, G.: FISH mapping of threeammonia

metabolism genes (Glul, Cps1, Glud1) in rat, and the chromosomallocalization of GLUL in human and Cps1 in mouse. Mammalian Genome 8:362- 364, 1997.

GAM180 214 GLUL Pesole, G.; Bozzetti, M. P.; Lanave, C.; Preparata, G.; Saccone,C.: 1 B c
Glutamine synthetase gene evolution: a good molecular clock. Proc.Nat. Acad. Sci. 88: 522- 526, 1991.

GAM180 214 GLUL Wang, Y.; Kudoh, J.; Kubota, R.; Asakawa, S.; Minoshima, S.; Shimizu,N.: 1 B c
Chromosomal mapping of a family of human glutamine synthetasegenes: functional gene (GLUL) on 1q25, pseudogene (GLULP) on 9p13,and three related genes (GLULL1, GLULL2, GLULL3) on 5q33, 11p15, and11q24. Genomics 37: 195- 199, 1996.

GAM180 214 HAS3 Spicer, A. P.; Olson, J. S.; McDonald, J. A.: Molecular cloningand 1 B c
characterization of a cDNA encoding the third putative mammalianhyaluronan synthase. J. Biol. Chem. 272: 8957- 8961, 1997.

GAM180 214 HAS3 Spicer, A. P.; Seldin, M. F.; Olsen, A. S.; Brown, N.; Wells, D.E.; Doggett, 1 B c
N. A.; Itano, N.; Kimata, K.; Inazawa, J.; McDonald,J. A.: Chromosomal localization of the human and mouse hyaluronansynthase genes. Genomics 41: 493- 497, 1997.

GAM180 214 HIP1 Chopra, V. S.; Metzler, M.; Rasper, D. M.; Engqvist- Goldstein,A. E. Y.; 1 B c
Singaraja, R.; Gan, L.; Fichter, K. M.; McCutcheon, K.;Drubin, D.; Nicholson, D. W.; Hayden, M. R.: HIP12 is a non- proapoptoticmember of a gene family including HIP1, an interacting protein withhuntingtin. Mammalian Genome 11: 1006- 1015, 2000.

GAM180 214 HIP1 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 1 B c
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager, V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM180 214 HIP1 Hackam, A. S.; Yassa, A. S.; Singaraja, R.; Metzler, M.; Gutekunst,C.- A.; 1 B c
Gan, L.; Warby, S.; Wellington, C. L.; Vaillancourt, J.; Chen,N.; Gervais, F. G.; Raymond, L.; Nicholson, D. W.; Hayden, M. R.:Huntingtin interacting protein 1 induces apoptosis via a novel caspase- dependentdeath effector domain. J. Biol. Chem. 275: 41299- 41308, 2000.

GAM180 214 HIP1 Himmelbauer, H.; Wedemeyer, N.; Haaf, T.; Wanker, E. E.; Schalkwyk,L. C.; 1 B c
Lehrach, H.: IRS- PCR- based genetic mapping of the huntingtininteracting protein gene (HIP1) on mouse chromosome 5. MammalianGenome 9: 26- 31, 1998.

GAM180 214 HIP1 Kalchman, M. A.; Koide, H. B.; McCutcheon, K.; Graham, R. K.; Nichol,K.; 1 B c
Nishiyama, K.; Kazemi- Esfarjani, P.; Lynn, F. C.; Wellington,C.; Metzler, M.; Goldberg, Y. P.; Kanazawa, I.; Gietz, R. D.; Hayden,M. R.: HIP1, a human homologue of S. cerevisiae Slap2, interactswith membrane- associated huntingtin in the brain. Nature Genet. 16:44- 53, 1997.

GAM180 214 HIP1 Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof 1 B c
Huntingtin interacting protein 1 to platelet- derived growth factor- betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998.

GAM180 214 HIP1 Waelter, S.; Scherzinger, E.; Hasenbank, R.; Nordhoff, E.; Lurz,R.; Goehler, 1 B c
H.; Gauss, C.; Sathasivam, K.; Bates, G. P.; Lehrach,H.; Wanker, E. E.: The huntingtin interacting protein HIP1 is a clathrinand alpha- adaptin- binding protein involved in receptor- mediated endocytosis. Hum.Molec. Genet. 10: 1807- 1817, 2001.

GAM180 214 HIP1 Wanker, E. E.; Rovira, C.; Scherzinger, E.; Hasenbank, R.; Walter,S.; Tait, 1 B c

D.; Colicelli, J.; Lehrach, H.: HIP- I: a huntingtin interactingprotein isolated by the yeast two- hybrid system. Hum. Molec. Genet. 6:487- 495, 1997.

GAM180 214 HIP1 Wedemeyer, N.; Peoples, R.; Himmelbauer, H.; Lehrach, H.; Francke,U.; Wanker, E. E.: Localization of the human HIP1 gene close to theelastin (ELN) locus on 7q11.23. Genomics 46: 313- 315, 1997. 1 B c

GAM180 214 KPNB1 Ayala- Madrigal, M. L.; Doerr, S.; Ramirez- Duenas, M. L.; Hansmann,I.: Assignment of KPNA4 and KPNB1 encoding karyopherin alpha 4 andbeta 1 to human chromosome bands 11q22 and 17q21 respectively, byin situ hybridization. Cytogenet. Cell Genet. 89: 258- 259, 2000. 1 B c

GAM180 214 KPNB1 Bayliss, R.; Littlewood, T.; Stewart, M.: Structural basis forthe interaction between FxFG nucleoporin repeats and importin- betain nuclear trafficking. Cell 102: 99- 108, 2000. 1 B c

GAM180 214 KPNB1 Chi, N. C.; Adam, E. J. H.; Adam, S. A.: Sequence and characterizationof cytoplasmic nuclear protein import factor p97. J. Cell Biol. 130:265- 274, 1995. 1 B c

GAM180 214 KPNB1 Gorlich, D.; Kostka, S.; Kraft, R.; Dingwall, C.; Laskey, R. A.;Hartmann, E.; Prehn, S.: Two different subunits of importin cooperateto recognize nuclear localization signals and bind them to the nuclearenvelope. Curr. Biol. 5: 383- 392, 1995. 1 B c

GAM180 214 KPNB1 Kutay, U.; Izaurralde, E.; Bischoff, F. R.; Mattaj, I. W.; Gorlich,D.: Dominant- negative mutants of importin- beta block multiple pathwaysof import and export through the nuclear pore complex. EMBO J. 16:1153- 1163, 1997. 1 B c

GAM180 214 KPNB1 Matsuda, Y.; Hamatani, K.; Itoh, M.; Takahashi, E.; Araki, R.;Abe, M.: Localization of the importin- beta gene to mouse chromosome11D and rat chromosome 10q32.1. Genomics 36: 213- 215, 1996. 1 B c

GAM180 214 KPNB1 Wiese, C.; Wilde, A.; Moore, M. S.; Adam, S. A.; Merdes, A.; Zheng,Y.: Role of importin- beta in coupling Ran to downstream targets inmicrotubule assembly. Science 291: 653- 656, 2001. 1 B c

GAM180 214 MS4A6A Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M.: Identificationof a new multigene four- transmembrane family (MS4A) related to CD20,HTm4 and beta subunit of the high- affinity IgE receptor. Gene 264:87- 93, 2001. 1 B c

GAM180 214 MS4A6A Liang, Y.; Tedder, T. F.: Identification of a CD20- , Fc- epsilon- RI- beta- relatedgene family: sixteen new MS4A family members expressed in human andmouse. Genomics 72: 119- 127, 2001. 1 B c

GAM180 214 NFIB Geurts, J. M. W.; Schoenmakers, E. F. P. M.; Roijer, E.; Astrom,A.- K.; Stenman, G.; van de Ven, W. J. M.: Identification of NFIBas recurrent translocation partner gene of HMGIC in pleomorphic adenomas. Oncogene 16:865- 872, 1998. 1 B c

GAM180 214 NFIB Qian, F.; Kruse, U.; Lichter, P.; Sippel, A. E.: Chromosomal localizationof the four genes (NFIA, B, C, and X) for the human transcriptionfactor nuclear factor I by FISH. Genomics 28: 66- 73, 1995. 1 B c

GAM180 214 NOS1 Barouch, L. A.; Harrison, R. W.; Skaf, M. W.; Rosas, G. O.; Cappola,T. P.; Kobeissi, Z. A.; Hobai, I. A.; Lemmon, C. A.; Burnett, A. L.;O'Rourke, B.; Rodriguez, E. R.; Huang, P. L.; Lima, J. A. C.; Berkowitz,D. E.; Hare, J. M.: Nitric oxide regulates the heart by spatial confinementof nitric oxide synthase isoforms. Nature 416: 337- 340, 2002. 1 B c

GAM180 214 NOS1 Bredt, D. S.; Hwang, P. M.; Glatt, C. E.; Lowenstein, C.; Reed,R. R.; Snyder, S. H.: Cloned and expressed nitric oxide synthasestructurally 1 B c

resembles cytochrome P- 450 reductase. Nature 351: 714- 718,1991.

GAM180 214 NOS1 Brenman, J. E.; Chao, D. S.; Xia, H.; Aldape, K.; Bredt, D. S.: Nitric oxide synthase complexed with dystrophin and absent fromskeletal muscle sarcolemma in Duchenne muscular dystrophy. Cell 82:743- 752, 1995. 1 B c

GAM180 214 NOS1 Burnett, A. L.; Lowenstein, C. J.; Bredt, D. S.; Chang, T. S. K.;Snyder, S. H.: Nitric oxide: a physiologic mediator of penile erection. Science 257:401- 403, 1992. 1 B c

GAM180 214 NOS1 Day, B. J.; Patel, M.; Calavetta, L.; Chang, L.- Y.; Stamler, J.S.: A mechanism of paraquat toxicity involving nitric oxide synthase. Proc.Nat. Acad. Sci. 96: 12760- 12765, 1999. 1 B c

GAM180 214 NOS1 Deans, Z.; Dawson, S. J.; Xie, J.; Young, A. P.; Wallace, D.; Latchman,D. S.: Differential regulation of the two neuronal nitric- oxide synthasegene promoters by the Oct- 2 transcription factor. J. Biol. Chem. 271:32153- 32158, 1996. 1 B c

GAM180 214 NOS1 Gu, Z.; Kaul, M.; Yan, B.; Kridel, S. J.; Cui, J.; Strongin, A.;Smith, J. W.; Liddington, R. C.; Lipton, S. A.: S- nitrosylation ofmatrix metalloproteinases: signaling pathway to neuronal cell death. Science 297: 1186- 1190, 2002. 1 B c

GAM180 214 NOS1 Kharazia, V. N.; Schmidt, H. H. H. W.; Weinberg, R. J.: Type Initric oxide synthase fully accounts for NADPH- diaphorase in rat striatum,but not cortex. Neuroscience 62: 983- 987, 1994. 1 B c

GAM180 214 NOS1 Kishimoto, J.; Spurr, N.; Liao, M.; Lizhi, L.; Emson, P.; Xu, W.: Localization of brain nitric oxide synthase (NOS) to human chromosome12. Genomics 14: 802- 804, 1992. 1 B c

GAM180 214 NOS1 Kuo, R. C.; Baxter, G. T.; Thompson, S. H.; Stricker, S. A.; Patton,C.; Bonaventura, J.; Epel, D.: NO is necessary and sufficient foregg activation at fertilization. Nature 406: 633- 636, 2000. 1 B c

GAM180 214 NOS1 Lee, C. G. L.; Gregg, A. R.; O'Brien, W. E.: Localization ofthe neuronal form of nitric oxide synthase to mouse chromosome 5. MammalianGenome 6: 56- 57, 1995. 1 B c

GAM180 214 NOS1 Lowenstein, C. J.; Glatt, C. S.; Bredt, D. S.; Snyder, S. H.:Cloned and expressed macrophage nitric oxide synthase contrasts withthe brain enzyme. Proc. Nat. Acad. Sci. 89: 6711- 6715, 1992. 1 B c

GAM180 214 NOS1 Magee, T.; Fuentes, A. M.; Garban, H.; Rajavashisth, T.; Marquez,D.; Rodriguez, J. A.; Rajfer, J.; Gonzalez- Cadavid, N. F.: Cloningof a novel neuronal nitric oxide synthase expressed in penis and lowerurinary tract. Biochem. Biophys. Res. Commun. 226: 145- 151, 1996. 1 B c

GAM180 214 NOS1 Marsden, P. A.; Heng, H. H. Q.; Scherer, S. W.; Stewart, R. J.;Hall, A. V.; Shi, X.- M.; Tsui, L.- C.; Schappert, K. T.: Structureand chromosomal localization of the human constitutive endothelialnitric oxide synthase gene. J. Biol. Chem. 268: 17478- 17488, 1993. 1 B c

GAM180 214 NOS1 Nelson, R. J.; Demas, G. E.; Huang, P. L.; Fishman, M. C.; Dawson,V. L.; Dawson, T. M.; Snyder, S. H.: Behavioural abnormalities inmale mice lacking neuronal nitric oxide synthase. Nature 378: 383- 386,1995. 1 B c

GAM180 214 NOS1 Sander, M.; Chavoshan, B.; Harris, S. A.; Iannaccone, S. T.; Stull,J. T.; Thomas, G. D.; Victor, R. G.: Functional muscle ischemia inneuronal nitric oxide synthase- deficient skeletal muscle of childrenwith Duchenne muscular dystrophy. Proc. Nat. Acad. Sci. 97: 13818- 13823,2000. 1 B c

GAM180 214 NOS1 Thomas, G. D.; Sander, M.; Lau, K. S.; Huang, P. L.; Stull, J.T.; Victor, R. G.: Impaired metabolic modulation of alpha- adrenergicvasoconstriction in 1 B c

dystrophin- deficient skeletal muscle. Proc. Nat.Acad. Sci. 95: 15090-
15095, 1998.

GAM180 214 NOS1 Xie, J.; Roddy, P.; Rife, T. K.; Murad, F.; Young, A. P.: Twoclosely linked 1 B c
but separable promoters for human neuronal nitric oxidesynthase gene
transcription. Proc. Nat. Acad. Sci. 92: 1242- 1246,1995.

GAM180 214 NOS1 Xu, W.; Gorman, P.; Sheer, D.; Bates, G.; Kishimoto, J.; Lizhi,L.; Emson, 1 B c
P.: Regional localization of the gene coding for humanbrain nitric oxide
synthase (NOS1) to 12q24.2- 24.31 by fluorescentin situ hybridization.
Cytogenet. Cell Genet. 64: 62- 63, 1993.

GAM180 214 NPR3 He, X.; Chow, D.; Martick, M. M.; Garcia, K. C.: Allosteric activationof a 1 B c
spring- loaded natriuretic peptide receptor dimer by hormone. Science
293:1657- 1662, 2001.

GAM180 214 NPR3 Jaubert, J.; Jaubert, F.; Martin, N.; Washburn, L. L.; Lee, B.K.; Eicher, E. 1 B c
M.; Guenet, J.- L.: Three new allelic mouse mutationsthat cause skeletal
overgrowth involve the natriuretic peptide receptorC gene (Npr3). Proc. Nat.
Acad. Sci. 96: 10278- 10283, 1999.

GAM180 214 NPR3 Lopez, M. J.; Wong, S. K.- F.; Kishimoto, I.; Dubois, S.; Mach,V.; Friesen, 1 B c
J.; Garbers, D. L.; Beuve, A.: Salt- resistant hypertensionin mice lacking
the guanylyl cyclase- A receptor for atrial natriureticpeptide. Nature 378:
65- 68, 1995.

GAM180 214 NPR3 Lowe, D. G.; Camerato, T. R.; Goeddel, D. V.: cDNA sequence ofthe human 1 B c
atrial natriuretic peptide clearance receptor. NucleicAcids Res. 18: 3412
only, 1990.

GAM180 214 NPR3 Lowe, D. G.; Klisak, I.; Sparkes, R. S.; Mohandas, T.; Goeddel,D. V.: 1 B c
Chromosomal distribution of three members of the human natriureticpeptide
receptor/guanylyl cyclase gene family. Genomics 8: 304- 312,1990.

GAM180 214 NPR3 Porter, J. G.; Arfsten, A.; Fuller, F.; Miller, J. A.; Gregory,L. C.; 1 B c
Lewicki, J. A.: Isolation and functional expression of thehuman atrial
natriuretic peptide clearance receptor cDNA. Biochem.Biophys. Res. Commun.
171: 796- 803, 1990.

GAM180 214 NPR3 Suda, M.; Ogawa, Y.; Tanaka, K.; Tamura, N.; Yasoda, A.; Takigawa,T.; 1 B c
Uehira, M.; Nishimoto, H.; Itoh, H.; Saito, Y.; Shiota, K.; Nakao,K.:
Skeletal overgrowth in transgenic mice that overexpress brainnatriuretic
peptide. Proc. Nat. Acad. Sci. 95: 2337- 2342, 1998.

GAM180 214 OSR1 Daigo, Y.; Isomura, M.; Nishiwaki, T.; Tamari, M.; Ishikawa, S.;Kai, M.; 1 B c
Murata, Y.; Takeuchi, K.; Yamane, Y.; Hayashi, R.; Minami,M.; Fujino, M. A.;
Hojo, Y.; Uchiyama, I.; Takagi, T.; Nakamura, Y.: Characterization of a
1200- kb genomic segment of chromosome 3p22- p21.3. DNARes. 6: 37- 44, 1999.

GAM180 214 OSR1 Tamari, M.; Daigo, Y.; Nakamura, Y.: Isolation and characterizationof a 1 B c
novel serine threonine kinase gene on chromosome 3q22- 21.3. J.Hum. Genet.
44: 116- 120, 1999.

GAM180 214 PRX Boerkoel, C. F.; Takashima, H.; Stankiewicz, P.; Garcia, C. A.;Leber, S. M.; 1 B c
Rhee- Morris, L.; Lupski, J. R.: Periaxin mutationscause recessive Dejerine-
Sottas neuropathy. Am. J. Hum. Genet. 68:325- 333, 2001. Note: Erratum: Am.
J. Hum. Genet. 68: 557 only, 2001.

GAM180 214 PRX Cohn, R. D.; Campbell, K. P.: Molecular basis of muscular dystrophies. 1 B c
MuscleNerve 23: 1456- 1471, 2000.

GAM180 214 PRX Delague, V.; Bareil, C.; Tuffery, S.; Bouvagnet, P.; Chouery, E.;Koussa, S.; 1 B c
Maisonobe, T.; Loiselet, J.; Megarbane, A.; Claustres,M.: Mapping of a new
locus for autosomal recessive demyelinatingCharcot- Marie- Tooth disease to

19q13.1- 13.3 in a large consanguineousLebanese family: exclusion of MAG as a candidate gene. Am. J. Hum.Genet. 67: 236- 243, 2000.

GAM180 214 PRX Gillespie, C. S.; Lee, M.; Fantes, J. F.; Brophy, P. J.: The geneencoding the Schwann cell protein periaxin localizes on mouse chromosome7 (Prx). Genomics 41: 297- 298, 1997. 1 B c

GAM180 214 PRX Gillespie, C. S.; Sherman, D. L.; Fleetwood- Walker, S. M.; Cottrell,D. F.; Tait, S.; Garry, E. M.; Wallace, V. C. J.; Ure, J.; Griffiths,I. R.; Smith, A. Brophy, P. J.: Peripheral demyelination and neuropathicpain behavior in periaxin- deficient mice. Neuron 26: 523- 531, 2000. 1 B c

GAM180 214 PRX Guilbot, A.; Williams, A.; Ravise, N.; Verny, C.; Brice, A.; Sherman,D. L.; Brophy, P. J.; LeGuern, E.; Delague, V.; Bareil, C.; Megarbane,A.; Claustres, M.: A mutation in periaxin is responsible for CMT4F,an autosomal recessive form of Charcot- Marie- Tooth disease. Hum.Molec. Genet. 10: 415- 421, 2001. 1 B c

GAM180 214 PRX Schuler, G. D.: Sequence mapping by electronic PCR. Genome Res. 7:541- 550, 1997. 1 B c

GAM180 214 PRX Takashima, H.; Boerkoel, C. F.; De Jonghe, P.; Ceuterick, C.; Martin,J.- J.; Voit, T.; Schroder, J.- M.; Williams, A.; Brophy, P. J.; Timmerman,V.; Lupski, J. R.: Periaxin mutations cause a broad spectrum of demyelinatingneuropathies. Ann. Neurol. 51: 709- 715, 2002. 1 B c

GAM180 214 RAI14 Kutty, R. K.; Kutty, G.; Samuel, W.; Duncan, T.; Bridges, C. C.;El-Sherbeeny, A.; Nagineni, C. N.; Smith, S. B.; Wiggert, B.: Molecularcharacterization and developmental expression of NORPEG, a novel geneinduced by retinoic acid. J. Biol. Chem. 276: 2831- 2840, 2001. 1 B c

GAM180 214 RAI14 Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of the coding sequences of unidentified human genes. XVI.The complete sequences of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 65- 73, 2000. 1 B c

GAM180 214 RDS Aita, N.; Ishii, K.; Akamatsu, Y.; Ogasawara, Y.; Tanabe, S.:Cloning and expression of human liver rhodanese cDNA. Biochem. Biophys.Res. Commun. 231: 56- 60, 1997. 1 B c

GAM180 214 RDS Ali, R. R.; Sarra, G.- M.; Stephens, C.; de Alwis, M.; Bainbridge,J. W. B.; Munro, P. M.; Fauser, S.; Reichell, M. B.; Kinnon, C.; Hunt,D. M.; Bhattacharya, S. S.; Thrasher, A. J.: Restoration of photoreceptorultrastructure and function in retinal degeneration slow mice by genetherapy. Nature Genet. 25: 306- 310, 2000. 1 B c

GAM180 214 RDS Bascom, R. A.; Connell, G.; Garcia- Heras, J.; Collins, L.; Ledbetter,D.; Molday, R. S.; Kalnins, V.; McInnes, R. R.: Molecular and ultrastructuralcharacterization of the products of the human retinopathy candidategenes ROM1 and RDS. (Abstract) Am. J. Hum. Genet. 47 (suppl.): A101only, 1990. 1 B c

GAM180 214 RDS Brecher, R.; Bird, A. C.: Adult vitelliform macular dystrophy. Eye 4:210- 215, 1990. 1 B c

GAM180 214 RDS Cagianut, B.; Rhyner, K.; Furrer, W.; Schnebli, H. P.: Thiosulphate-sulphurtransferase (rhodanese) deficiency in Leber's hereditary optic atrophy.(Letter) Lancet II: 981- 982, 1981. 1 B c

GAM180 214 RDS Connell, G.; Bascom, R.; Molday, L.; Reid, D.; McInnes, R. R.;Molday, R. S.: Photoreceptor peripherin is the normal product ofthe gene responsible for retinal degeneration in the rds mouse. Proc.Nat. Acad. Sci. 88: 723- 726, 1991. 1 B c

GAM180 214 RDS Demant, P.; Ivanyi, D.; van Nie, R.: The map position of the rdsgene on the 17th chromosome of the mouse. Tissue Antigens 13: 53- 55,1979. 1 B c

GAM180 214 RDS Deutman, A. F.; van Blommestein, J. D. A.; Henkes, H. E.; Waardenburg,P. J.; Solleveld- van Driest, E.: Butterfly- shaped pigment dystrophyof the fovea. Arch. Ophthal. 83: 558- 569, 1970. 1 B c

GAM180 214 RDS Dryja, T. P.; Grondin, V. J.; Ringens, P.; Cotran, P.; Berson,E. L.; Travis, G.: Isolation of human retinal cDNA fragments homologousto the murine rds gene transcript. (Abstract) Invest. Ophthal. Vis.Sci. 30 (suppl.): 43 only, 1989. 1 B c

GAM180 214 RDS Farrar, G. J.; Jordan, S. A.; Kenna, P.; Humphries, M. M.; Kumar- Singh,R.; McWilliam, P.; Allamand, V.; Sharp, E.; Humphries, P.: Autosomaldominant retinitis pigmentosa: localization of a disease gene (RP6)to the short arm of chromosome 6. Genomics 11: 870- 874, 1991. 1 B c

GAM180 214 RDS Farrar, G. J.; Kenna, P.; Jordan, S. A.; Kumar- Singh, R.; Humphries,M. M.; Sharp, E. M.; Sheils, D. M.; Humphries, P.: A three- base- pairdeletion in the peripherin- RDS gene in one form of retinitis pigmentosa. Nature 354:478- 480, 1991. 1 B c

GAM180 214 RDS Feist, R. M.; White, M. F., Jr.; Skalka, H.; Stone, E. M.: Choroidalneovascularization in a patient with adult foveomacular dystrophyand a mutation in the retinal degeneration slow gene (pro210- to-arg). Am.J. Ophthal. 118: 259- 260, 1994. 1 B c

GAM180 214 RDS Felbor, U.; Schilling, H.; Weber, B. H. F.: Adult vitelliformmacular dystrophy is frequently associated with mutations in the peripherin/RDSgene. Hum. Mutat. 10: 301- 309, 1997. 1 B c

GAM180 214 RDS Gass, J. D. M.: A clinicopathologic study of a peculiar foveomaculardystrophy. Trans. Am. Ophthal. Soc. 72: 139- 155, 1974. 1 B c

GAM180 214 RDS Jackson, K. E.; Mitchell, E. B.; Stone, E. M.; Ferrell, R. E.;Gorin, M. B.: The identification of an exon- 2 peripherin mutationin a family with heterogeneous manifestations of a butterfly patternmacular dystrophy. (Abstract) Am. J. Hum. Genet. 53 (suppl.): 1177only, 1993. 1 B c

GAM180 214 RDS Jordan, S. A.; Farrar, G. J.; Kumar- Singh, R.; Kenna, P.; Humphries,M. M.; Allamand, V.; Sharp, E. M.; Humphries, P.: Autosomal dominantretinitis pigmentosa (adRP; RP6): cosegregation of RP6 and the peripherin- RDSlocus in a late- onset family of Irish origin. Am. J. Hum. Genet. 50:634- 639, 1992. 1 B c

GAM180 214 RDS Kajiwara, K.; Berson, E. L.; Dryja, T. P.: Digenic retinitispigmentosa due to mutations at the unlinked peripherin/RDS and ROM1loci. Science 264: 1604-1608, 1994. 1 B c

GAM180 214 RDS Kajiwara, K.; Hahn, L. B.; Mukai, S.; Travis, G. H.; Berson, E.L.; Dryja, T. P.: Mutations in the human retinal degeneration slowgene in autosomal dominant retinitis pigmentosa. Nature 354: 480- 483,1991. 1 B c

GAM180 214 RDS Kajiwara, K.; Sandberg, M. A.; Berson, E. L.; Dryja, T. P.: Anull mutation in the human peripherin/RDS gene in a family with autosomaldominant retinitis punctata albescens. Nature Genet. 3: 208- 212,1993. 1 B c

GAM180 214 RDS Kajiwara, K.; Sandberg, M. A.; Berson, E. L.; Dryja, T. P.: Anull mutation in the human RDS/peripherin gene in a family with autosomaldominant retinitis punctata albescens. (Abstract) Am. J. Hum. Genet. 51(suppl.): A6 only, 1992. 1 B c

GAM180 214 RDS Kedzierski, W.; Nusinowitz, S.; Birch, D.; Clarke, G.; McInnes,R. R.; Bok, D.; Travis, G. H.: Deficiency of rds/peripherin causesphotoreceptor death in mouse models of digenic and dominant retinitispigmentosa. Proc. Nat. Acad. 1 B c

Sci. 98: 7718- 7723, 2001.

GAM180 214 RDS Keen, T. J.; Inglehearn, C. F.: Mutations and polymorphisms inthe human peripherin- RDS gene and their involvement in inherited retinaldegeneration. Hum. Mutat. 8: 297- 303, 1996. 1 B c

GAM180 214 RDS Kikawa, E.; Nakazawa, M.; Chida, Y.; Shiono, T.; Tamai, M.: Anovel mutation (asn244- to- lys) in the peripherin/RDS gene causingautosomal dominant retinitis pigmentosa associated with bull's- eyemaculopathy detected by nonradioisotopic SSCP. Genomics 20: 137- 139,1994. 1 B c

GAM180 214 RDS Kim, R. Y.; Dollfus, H.; Keen, T. J.; Fitzke, F. W.; Arden, G.B.; Bhattacharya, S. S.; Bird, A. C.: Autosomal dominant patterndystrophy of the retina associated with a 4- base pair insertion atcodon 140 in the peripherin/RDS gene. Arch. Ophthal. 113: 451- 455,1995. 1 B c

GAM180 214 RDS Kohl, S.; Christ- Adler, M.; Apfelstedt- Sylla, E.; Kellner, U.;Eckstein, A.; Zrenner, E.; Wissinger, B.: RDS/peripherin gene mutationsare frequent causes of central retinal dystrophies. J. Med. Genet. 34:620- 626, 1997. 1 B c

GAM180 214 RDS Ma, J.; Norton, J. C.; Allen, A. C.; Burns, J. B.; Hasel, K. W.;Burns, J. L.; Sutcliffe, J. G.; Travis, G. H.: Retinal degenerationslow (rds) in mouse results from simple insertion of a t haplotype- specificelement into protein- coding exon II. Genomics 28: 212- 219, 1995. 1 B c

GAM180 214 RDS Nadeau, J. H.: Modifier genes in mice and humans. Nature Rev. 2:165- 174, 2001. 1 B c

GAM180 214 RDS Nichols, B. E.; Drack, A. V.; Vandenburgh, K.; Kimura, A. E.;Sheffield, V. C.; Stone, E. M.: A 2 base pair deletion in the RDSgene associated with butterfly- shaped pigment dystrophy of the fovea. Hum.Molec. Genet. 2: 601- 603, 1993. 1 B c

GAM180 214 RDS Nichols, B. E.; Sheffield, V. C.; Vandenburgh, K.; Drack, A. V.;Kimura, A. E.; Stone, E. M.: Butterfly- shaped pigment dystrophy ofthe fovea caused by a point mutation in codon 167 of the RDS gene. NatureGenet. 3: 202- 207, 1993. 1 B c

GAM180 214 RDS Nikoskelainen, E.: New aspects of the genetic, etiologic, andclinical puzzle of Leber's disease. Neurology 34: 1482- 1484, 1984. 1 B c

GAM180 214 RDS Payne, A. M.; Downes, S. M.; Bessant, D. A. R.; Bird, A. C.; Bhattacharya,S. S.: Founder effect, seen in the British population, of the 172peripherin/RDS mutation- - and further refinement of genetic positioningof the peripherin/RDS gene. (Letter) Am. J. Hum. Genet. 192- 195,1998. 1 B c

GAM180 214 RDS Pendleton, J. W.; Violette, S. M.; Hunihan, L. W.; Greene, L.A.; Ruddle, F. H.: The peripherin gene maps to mouse chromosome 15. Genomics 9:369- 372, 1991. 1 B c

GAM180 214 RDS Reig, C.; Serra, A.; Gean, E.; Vidal, M.; Arumi, J.; De la Calzada,M. D.; Antich, J.; Carballo, M.: A point mutation in the RDS- peripheringene in a Spanish family with central areolar choroidal dystrophy. Ophthal.Genet. 16: 35- 44, 1995. 1 B c

GAM180 214 RDS Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: World Distribution. New York: Oxford Univ. Press (pub.) 1988. 1 B c

GAM180 214 RDS Sarra, G.- M.; Stephens, C.; de Alwis, M.; Bainbridge, J. W. B.;Smith, A. J.; Thrasher, A. J.; Ali, R. R.: Gene replacement therapyin the retinal degeneration slow (rds) mouse: the effect on retinaldegeneration following partial transduction of the retina. Hum. Molec.Genet. 10: 2353- 2361, 2001. 1 B c

GAM180 214 RDS Scott, E. M.; Wright, R. C.: Genetic polymorphism of rhodanesefrom human erythrocytes. Am. J. Hum. Genet. 32: 112- 114, 1980. 1 B c

GAM180 214 RDS Travis, G. H.; Brennan, M. B.; Danielson, P. E.; Kozak, C. A.;Sutcliffe, J. G.: Identification of a photoreceptor- specific mRNAencoded by the gene responsible for retinal degeneration slow (rds). Nature 338:70- 73, 1989. 1 B c

GAM180 214 RDS Travis, G. H.; Christerson, L.; Danielson, P. E.; Klisak, I.;Sparkes, R. S.; Hahn, L. B.; Dryja, T. P.; Sutcliffe, J. G.: Thehuman retinal degeneration slow (RDS) gene: chromosome assignmentand structure of the mRNA. Genomics 10: 733- 739, 1991. 1 B c

GAM180 214 RDS Travis, G. H.; Hepler, J. E.: A medley of retinal dystrophies. NatureGenet. 3: 191- 192, 1993. 1 B c

GAM180 214 RDS Travis, G. H.; Sutcliffe, J. G.; Bok, D.: The retinal degenerationslow (rds) gene product is a photoreceptor disc membrane- associatedglycoprotein. Neuron 6: 61- 70, 1991. 1 B c

GAM180 214 RDS van Nie, R.; Ivanyi, D.; Demant, P.: A new H- 2- linked mutation,rds, causing retinal degeneration in the mouse. Tissue Antigens 12:106- 108, 1978. 1 B c

GAM180 214 RDS Vine, A. K.; Schatz, H.: Adult- onset foveomacular pigment epithelialdystrophy. Am. J. Ophthal. 89: 680- 691, 1980. 1 B c

GAM180 214 RDS Weleber, R. G.; Carr, R. E.; Murphey, W. H.; Sheffield, V. C.;Stone, E. M.: Phenotypic variation including retinitis pigmentosa,pattern dystrophy, and fundus flavimaculatus in a single family witha deletion of codon 153 or 154 of the peripherin/RDS gene. Arch.Ophthal. 111: 1531- 1542, 1993. 1 B c

GAM180 214 RDS Wells, J.; Wroblewski, J.; Keen, J.; Inglehearn, C.; Jubb, C.;Eckstein, A.; Jay, M.; Arden, G.; Bhattacharya, S.; Fitzke, F.; Bird,A.: Mutations in the human retinal degeneration slow (RDS) gene cancause either retinitis pigmentosa or macular dystrophy. Nature Genet. 3:213- 218, 1993. 1 B c

GAM180 214 RDS Weng, L.; Heinrikson, R. L.; Westley, J.: Active site cysteinyland arginyl residues of rhodanese. J. Biol. Chem. 253: 8109- 8119,1978. 1 B c

GAM180 214 RDS Whitehouse, D. B.; Pilz, A. J.; Porta, G.; Hopkinson, D. A.: Rhodaneseisozymes in human tissues. Ann. Hum. Genet. 52: 1- 10, 1988. 1 B c

GAM180 214 RDS Whitehouse, D. B.; Poole, C. J. M.; Kind, P. R. N.; Hopkinson,D. A.: Rhodanese isozymes in three subjects with Leber's optic neuropathy. J.Med. Genet. 26: 113- 115, 1989. 1 B c

GAM180 214 RDS Wroblewski, J. J.; Wells, J. A., III; Eckstein, A.; Fitzke, F.;Jubb, C.; Keen, J.; Inglehearn, C.; Bhattacharya, S.; Arden, G. B.;Jay, M.; Bird, A. C.: Macular dystrophy associated with mutationsat codon 172 in the human retinal degeneration slow gene. Ophthalmology 101:12- 22, 1994. 1 B c

GAM180 214 RERE Amler, L. C.; Bauer, A.; Corvi, R.; Dihlmann, S.; Praml, C.; Cavenee,W. K.; Schwab, M.; Hampton, G. M.: Identification and characterizationof novel genes located at the t(1;15)(p36.2;q24) translocation breakpointin the neuroblastoma cell line NGP. Genomics 64: 195- 202, 2000. 1 B c

GAM180 214 RERE Yanagisawa, H.; Bundo, M.; Miyashita, T.; Okamura- Oho, Y.; Tadokoro,K.; Tokunaga, K.; Yamada, M.: Protein binding of a DRPLA family througharginine-glutamic acid dipeptide repeats is enhanced by extended polyglutamine. Hum.Molec. Genet. 9: 1433- 1442, 2000. 1 B c

GAM180 214 SDPR Burgener, R.; Wolf, M.; Ganz, T.; Baggiolini, M.: Purificationand characterization of a major phosphatidylserine- binding phosphoproteinfrom human platelets. Biochem. J. 269: 729- 734, 1990. 1 B c

GAM180 214 SDPR Gustincich, S.; Schneider, C.: Serum deprivation response geneis induced by serum starvation but not by contact inhibition. CellGrowth Diff. 4: 753- 760, 1993. 1 B c

GAM180 214 SDPR Gustincich, S.; Vatta, P.; Goruppi, S.; Wolf, M.; Saccone, S.;Della Valle, G.; Baggiolini, M.; Schneider, C.: The human serum deprivationresponse gene (SDPR) maps to 2q32- q33 and codes for a phosphatidylserine- bindingprotein. Genomics 57: 120- 129, 1999. 1 B c

GAM180 214 SLC5A2 Kanai, Y.; Lee, W.- S.; You, G.; Brown, D.; Hediger, M. A.: Thehuman kidney low affinity Na(+)/glucose cotransporter SGLT2: delineationof the major renal reabsorptive mechanism for D- glucose. J. Clin.Invest. 93: 397- 404, 1994. 1 B c

GAM180 214 SLC5A2 Wells, R. G.; Mohandas, T. K.; Hediger, M. A.: Localization ofthe Na+/glucose cotransporter gene SGLT2 to human chromosome 16 closeto the centromere. Genomics 17: 787- 789, 1993. 1 B c

GAM180 214 SLC5A2 Wells, R. G.; Pajor, A. M.; Kanai, Y.; Turk, E.; Wright, E. M.;Hediger, M. A.: Cloning of a human kidney cDNA with similarity tothe sodium- glucose cotransporter. Am. J. Physiol. 263: F459- F465,1992. 1 B c

GAM180 214 SMPX Lee, C. C.; Yazdani, A.; Wehnert, M.; Zhao, Z. Y.; Lindsay, E.A.; Bailey, J.; Coolbaugh, M. I.; Couch, L.; Xiong, M.; Chinault,A. C.; Baldini, A.; Caskey, C. T.: Isolation of chromosome- specificgenes by reciprocal probing of arrayed cDNA and cosmid libraries. Hum.Molec. Genet. 4: 1373- 1380, 1995. 1 B b

GAM180 214 SMPX Patzak, D.; Zhuchenko, O.; Lee, C.- C.; Wehnert, M.: Identification,mapping, and genomic structure of a novel X- chromosomal human gene(SMPX) encoding a small muscular protein. Hum. Genet. 105: 506- 512,1999. 1 B b

GAM180 214 TCF4 Breschel, T. S.; McInnis, M. G.; Margolis, R. L.; Sirugo, G.; Corneliussen,B.; Simpson, S. G.; McMahon, F. J.; MacKinnon, D. F.; Xu, J. F.; Pleasant,N.; Huo, Y.; Ashworth, R. G.; Grundstrom, C.; Grundstrom, T.; Kidd,K. K.; DePaulo, J. R.; Ross, C. A.: A novel, heritable, expandingCTG repeat in an intron of the SEF2- 1 gene on chromosome 18q21.1. Hum.Molec. Genet. 6: 1855- 1863, 1997. 1 B c

GAM180 214 TCF4 Castrop, J.; van Norren, K.; Clevers, H.: A gene family of HMG- boxtranscription factors with homology to TCF- 1. Nucleic Acids Res. 20:611 only, 1992. 1 B c

GAM180 214 TCF4 Corneliussen, B.; Thornell, A.; Hallberg, B.; Grundstrom, T.:Helix- loop- helix transcriptional activators bind to a sequence inglucocorticoid response elements of retrovirus enhancers. J. Virol. 65:6084- 6093, 1991. 1 B c

GAM180 214 TCF4 Duval, A.; Busson- Leconiat, M.; Berger, R.; Hamelin, R.: Assignmentof the TCF- 4 (TCF7L2) to human chromosome band 10q25.3. Cytogenet.Cell Genet. 88: 264- 265, 2000. 1 B c

GAM180 214 TCF4 Duval, A.; Gayet, J.; Zhou, X.- P.; Iacopetta, B.; Thomas, G.; Hamelin,R.: Frequent frameshift mutations of the TCF- 4 gene in colorectalcancers with microsatellite instability. Cancer Res. 59: 4213- 4215,1999. 1 B c

GAM180 214 TCF4 Duval, A.; Rolland, S.; Tubacher, E.; Bui, H.; Thomas, G.; Hamelin,R.: The human T- cell transcription factor- 4 gene: structure, extensivecharacterization of alternative splicings, and mutational analysisin colorectal cancer cell lines. Cancer Res. 60: 3872- 3879, 2000. 1 B c

GAM180 214 TCF4 Henthorn, P.; Kiledjian, M.; Kadesch, T.: Two distinct transcriptionfactors that bind the immunoglobulin enhancer mu- E5/kappa- E2 motif. Science 247:467- 470, 1990. 1 B c

GAM180 214 TCF4 Henthorn, P.; McCarrick- Walmsley, R.; Kadesch, T.: Sequence ofthe cDNA encoding ITF- 2, a positive- acting transcription factor. NucleicAcids Res. 18: 678, 1990. 1 B c

GAM180 214 TCF4 Korinek, V.; Barker, N.; Moerer, P.; van Donselaar, E.; Huls, G.;Peters, P. 1 B c

J.; Clevers, H.: Depletion of epithelial stem- cell compartmentsin the small intestine of mice lacking Tcf- 4. Nature Genet. 19:379- 383, 1998.

GAM180 214 TCF4 Korinek, V.; Barker, N.; Morin, P. J.; van Wichen, D.; de Weger,R.; Kinzler, 1 B c
K. W.; Vogelstein, B.; Clevers, H.: Constitutive transcriptionalactivation by a beta- catenin- Tcf complex in APC- /- colon carcinoma. Science 275:1784- 1787, 1997.

GAM180 214 TCF4 Morin, P. J.; Sparks, A. B.; Korinek, V.; Barker, N.; Clevers,H.; 1 B c
Vogelstein, B.; Kinzler, K. W.: Activation of beta- catenin- Tcfsignaling in colon cancer by mutations in beta- catenin or APC. Science 275:1787- 1790, 1997.

GAM180 214 TCF4 Pscherer, A.; Dorflinger, U.; Kirfel, J.; Gawlas, K.; Ruschoff,J.; Buettner, 1 B c
R.; Schule, R.: The helix- loop- helix transcriptionfactor SEF- 2 regulates the activity of a novel initiator element inthe promoter of the human somatostatin receptor II gene. EMBO J. 15:6680- 6690, 1996.

GAM180 214 TCF4 Rodova, M.; Islam, M. R.; Maser, R. L.; Calvet, J. P.: The polycystickidney 1 B c
disease- 1 promoter is a target of the beta- catenin/T- cell factorpathway. J. Biol. Chem. 277: 29577- 29583, 2002.

GAM180 214 XT3 Nash, S. R.; Giros, B.; Kingsmore, S. F.; Kim, K. M.; El- Mestikawy,S.; 1 B c
Dong, Q.; Fumagalli, F.; Seldin, M. F.; Caron, M. G.: Cloning,gene structure and genomic localization of an orphan transporter frommouse kidney with six alternatively- spliced isoforms. Receptors Channels 6:113- 128, 1998.

GAM180 214 XT3 Scott, A. F.: Personal Communication. Baltimore, Md. 2/5/2001. 1 B c

GAM182 307 LDB3 Faulkner, G.; Pallavicini, A.; Formentin, E.; Comelli, A.; Ievolella,C.; 3 C c
Trevisan, S.; Bortoletto, G.; Scannapieco, P.; Salamon, M.; Mouly,V.; Valle, G.; Lanfranchi, G.: ZASP: a new Z- band alternatively splicedPDZ- motif protein. J. Cell Biol. 146: 465- 475, 1999.

GAM182 307 LDB3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM182 307 LDB3 Zhou, Q.; Ruiz- Lozano, P.; Martone, M. E.; Chen, J.: Cypher, astriated 3 C c
muscle- restricted PDZ and LIM domain- containing protein,binds to alpha-actinin- 2 and protein kinase C. J. Biol. Chem. 274:19807- 19813, 1999.

GAM182 307 TGFA Brissenden, J. E.; Derynck, R.; Francke, U.: Transforming growthfactor alpha 3 C c
gene (TGFA) maps to human chromosome 2 close to the breakpointof the t(2;8) variant translocation in Burkitt lymphoma. (Abstract) Cytogenet.Cell Genet. 40: 589 only, 1985.

GAM182 307 TGFA Collin, G. B.; Marshall, J. D.; Naggert, J. K.; Nishina, P. M.: TGFA: exon- 3 C c
intron structure and evaluation as a candidate gene forAlstrom syndrome. (Letter) Clin. Genet. 55: 61- 62, 1999.

GAM182 307 TGFA Ellis, D. L.; Kafka, S. P.; Chow, J. C.; Nanney, L. B.; Inman,W. H.; 3 C c
McCadden, M. E.; King, L. E., Jr.: Melanoma, growth factors,acanthosis nigricans, the sign of Leser- Trelat, and multiple acrochordons:a possible role for alpha- transforming growth factor in cutaneousparaneoplastic syndromes. New Eng. J. Med. 317: 1582- 1587, 1987.

GAM182 307 TGFA Fernandez- Larrea, J.; Merlos- Suarez, A.; Urena, J. M.; Baselga,J.; 3 C c
Arribas, J.: A role for a PDZ protein in the early secretorypathway for the targeting of proTGF- alpha to the cell surface. Molec.Cell 3: 423- 433, 1999.

GAM182 307 TGFA Fowler, K. J.; Mann, G. B.; Dunn, A. R.: Linkage of the murinetransforming 3 C c

growth factor- alpha gene with Igk, Ly- 2, and Fabp1 onchromosome 6. Genomics 16: 782- 784, 1993.

GAM182 307 TGFA Kramer, A.; Yang, F.- C.; Snodgrass, P.; Li, X.; Scammell, T. E.;Davis, F. C.; Weitz, C. J.: Regulation of daily locomotor activityand sleep by hypothalamic EGF receptor signaling. Science 294: 2511- 2515,2001. 3 C c

GAM182 307 TGFA Tam, J. P.; Scheikh, M. A.; Solomon, D. S.; Ossowski, L.: Efficientsynthesis of human type alpha transforming growth factor: its physicaland biological characterization. Proc. Nat. Acad. Sci. 83: 8082- 8086,1986. 3 C c

GAM182 307 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. B.: Assignment of the gene coding for human TGF- alphato chromosome 2p13. (Abstract) Cytogenet. Cell Genet. 40: 762 only,1985. 3 C c

GAM182 307 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. B.: The gene for human transforming growth factor alphais on the short arm of chromosome 2. Cytogenet. Cell Genet. 42:94- 98, 1986. 3 C c

GAM183 240 PTGS2 Erkinheimo, T.- L.; Saukkonen, K.; Narko, K.; Jalkanen, J.; Ylikorkala,O.; Ristimaki, A.: Expression of cyclooxygenase- 2 and prostanoidreceptors by human myometrium. J. Clin. Endocr. Metab. 85: 3468- 3475,2000. 3 C c

GAM183 240 PTGS2 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.; Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999. 3 C c

GAM183 240 PTGS2 Hla, T.; Neilson, K.: Human cyclooxygenase- 2 cDNA. Proc. Nat.Acad. Sci. 89: 7384- 7388, 1992. 3 C c

GAM183 240 PTGS2 Jones, D. A.; Carlton, D. P.; McIntyre, T. M.; Zimmerman, G. A.;Prescott, S. M.: Molecular cloning of human prostaglandin endoperoxidesynthase type II and demonstration of expression in response to cytokines. J.Biol. Chem. 268: 9049- 9054, 1993. 3 C c

GAM183 240 PTGS2 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.: Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2 in the humanfetal and adult male reproductive tracts. J. Clin. Endocr. Metab. 85:3436- 3441, 2000. 3 C c

GAM183 240 PTGS2 Kraemer, S. A.; Meade, E. A.; DeWitt, D. L.: Prostaglandin endoperoxidesynthase gene structure: identification of the transcriptional startsite and 5- prime- flanking regulatory sequences. Arch. Biochem. Biophys. 293:391- 400, 1992. 3 C c

GAM183 240 PTGS2 Lassus, P.; Wolff, H.; Andersson, S.: Cyclooxygenase- 2 in humanperinatal lung. Pediat. Res. 47: 602- 605, 2000. 3 C c

GAM183 240 PTGS2 Lim, H.; Paria, B. C.; Das, S. K.; Dinchuk, J. E.; Langenbach,R.; Trzaskos, J. M.; Dey, S. K.: Multiple female reproductive failuresin cyclooxygenase 2- deficient mice. Cell 91: 197- 208, 1997. 3 C c

GAM183 240 PTGS2 Loftin, C. D.; Trivedi, D. B.; Tiano, H. F.; Clark, J. A.; Lee,C. A.; Epstein, J. A.; Morham, S. G.; Breyer, M. D.; Nguyen, M.; Hawkins,B. M.; Goulet, J. L.; Smithies, O.; Koller, B. H.; Langenbach, R.: Failure of ductus arteriosus closure and remodeling in neonatalmice deficient in cyclooxygenase- 1 and cyclooxgenase- 2. Proc. Nat.Acad. Sci. 98: 1059- 1064, 2001. 3 C c

GAM183 240 PTGS2 Macchia, L.; Di Paola, R.; Guerrese, M.- C.; Chiechi, L. M.; Tursi,A.; Caiaffa, M. F.; Haeggstrom, J. Z.: Expression of prostaglandinendoperoxide H synthase 1 and 2 in human placenta at term. Biochem.Biophys. Res. Commun. 3 C c

233: 496- 501, 1997.

GAM183 240 PTGS2 Morham, S. G.; Langenbach, R.; Loftin, C. D.; Tiano, H. F.; Vouloumanos,N.; 3 C c
Jennette, J. C.; Mahler, J. F.; Kluckman, K. D.; Ledford, A.;Lee, C. A.;
Smithies, O.: Prostaglandin synthase 2 gene disruptioncauses severe renal
pathology in the mouse. Cell 83: 473- 482, 1995.

GAM183 240 PTGS2 Neufang, G.; Furstenberger, G.; Heidt, M.; Marks, F.; Muller- Decker,K.: 3 C c
Abnormal differentiation of epidermis in transgenic mice
constitutivelyexpressing cyclooxygenase- 2 in skin. Proc. Nat. Acad. Sci.
98: 7629- 7634,2001.

GAM183 240 PTGS2 O'Banion, M. K.; Sadowski, H. B.; Winn, V.; Young, D. A.: A serum- and 3 C c
glucocorticoid- regulated 4- kilobase mRNA encodes a cyclooxygenase-
relatedprotein. J. Biol. Chem. 266: 23261- 23267, 1991.

GAM183 240 PTGS2 O'Banion, M. K.; Winn, V. D.; Young, D. A.: cDNA cloning andfunctional 3 C c
activity of a glucocorticoid- regulated inflammatory cyclooxygenase.
Proc.Nat. Acad. Sci. 89: 4888- 4892, 1992.

GAM183 240 PTGS2 Oshima, M.; Dinchuk, J. E.; Kargman, S. L.; Oshima, H.; Hancock,B.; Kwong, 3 C c
E.; Trzaskos, J. M.; Evans, J. F.; Taketo, M. M.: Suppressionof intestinal
polyposis in Apc(delta- 716) knockout mice by inhibitionof cyclooxygenase 2
(COX- 2). Cell 87: 803- 809, 1996.

GAM183 240 PTGS2 Sales, K. J.; Katz, A. A.; Davis, M.; Hinz, S.; Soeters, R. P.;Hofmeyr, M. 3 C c
D.; Millar, R. P.; Jabbour, H. N.: Cyclooxygenase- 2 expressionand
prostaglandin E2 synthesis are up- regulated in carcinomas of thecervix: a
possible autocrine/paracrine regulation of neoplastic cellfunction via
EP2/EP4 receptors. J. Clin. Endocr. Metab. 86: 2243- 2249,2001.

GAM183 240 PTGS2 Salmenkivi, K.; Haglund, C.; Ristimaki, A.; Arola, J.; Heikkila,P.: 3 C c
Increased expression of cyclooxygenase- 2 in malignant pheochromocytomas.
J.Clin. Endocr. Metab. 86: 5615- 5619, 2001.

GAM183 240 PTGS2 Samad, T. A.; Moore, K. A.; Sapirstein, A.; Billet, S.; Allchorne,A.; Poole, 3 C c
S.; Bonventre, J. V.; Woolf, C. J.: Interleukin- 1- beta- mediatedinduction
of Cox- 2 in the CNS contributes to inflammatory pain hypersensitivity.
Nature 410:471- 475, 2001.

GAM183 240 PTGS2 Swan, S. K.; Rudy, D. W.; Lasseter, K. C.; Ryan, C. F.; Buechel,K. L.; 3 C c
Lambrecht, L. J.; Pinto, M. B.; Dilzer, S. C.; Obrda, O.; Sundblad,K. J.;
Gumbs, C. P.; Ebel, D. L.; Quan, H.; Larson, P. J.; Schwartz,J. I.;
Musliner, T. A.; Gertz, B. J.; Brater, D. C.; Yao, S.- L.:Effect of
cyclooxygenase- 2 inhibition on renal function in elderlypersons receiving a
low- salt diet: a randomized controlled trial. Ann.Intern. Med. 133: 1- 9,
2000.

GAM183 240 PTGS2 Tay, A.; Squire, J. A.; Goldberg, H.; Skorecki, K.: Assignmentof the human 3 C c
prostaglandin- endoperoxide synthase 2 (PTGS2) gene to1q25 by fluorescence
in situ hybridization. Genomics 23: 718- 719,1994.

GAM183 240 PTGS2 Tazawa, R.; Xu, X.- M.; Wu, K. K.; Wang, L.- H.: Characterizationof the 3 C c
genomic structure, chromosomal location and promoter of humanprostaglandin H
synthase- 2 gene. Biochem. Biophys. Res. Commun. 203:190- 199, 1994.

GAM183 240 PTGS2 Tsujii, M.; DuBois, R. N.: Alterations in cellular adhesion andapoptosis in 3 C c
epithelial cells overexpressing prostaglandin endoperoxidesynthase 2. Cell
83: 493- 501, 1995.

GAM183 240 PTGS2 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: 3 C c
Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93:
705- 716, 1998.

GAM183 240 PTGS2 Zhou, X.- L.; Lei, Z. M.; Rao, C. V.: Treatment of human endometrialgland 3 C c
epithelial cells with chorionic gonadotropin/luteinizing hormoneincreases
the expression of the cyclooxygenase- 2 gene. J. Clin. Endocr.Metab. 84:
3364- 3377, 1999.

GAM185 372 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, 3 C c
J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2
in the allergic response. Nature 412: 186- 190,2001.

GAM185 372 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 C c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM185 372 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; 3 C c
Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab-
family adapter proteins act downstream of cytokine and growthfactor
receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999.

GAM185 372 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH 3 C c
mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell
Genet. 94: 39- 42, 2001.

GAM185 372 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology 3 C c
domain- containing adapter protein, acts to uncouple signalingfrom ERK
kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999.

GAM185 372 GADD45B De Smaele, E.; Zazzeroni, F.; Papa, S.; Nguyen, D. U.; Jin, R.;Jones, J.; 3 C c
Cong, R.; Franzoso, G.: Induction of gadd45- beta by NF- kappa-
Bdownregulates pro- apoptotic JNK signaling. Nature 414: 308- 313,2001.

GAM185 372 GADD45B Takekawa, M.; Saito, H.: A family of stress- inducible GADD45- likeproteins 3 C c
mediate activation of the stress- responsive MTK1/MEKK4 MAPKKK. Cell 95:521-
530, 1998.

GAM186 353 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland 3 C c
biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855-
862, 2000.

GAM186 353 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein 3 C c
that promotes cytochrome c- dependent caspase activation byeliminating IAP
inhibition. Cell 102: 33- 42, 2000.

GAM186 353 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; 3 C c
Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of
Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000.

GAM186 353 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; 3 C c
Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and
characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509-
3517, 2002.

GAM186 353 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 C c

GAM186 353 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; 3 C c
Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.:
A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates
caspase activity and apoptosis. Nature 410:112- 116, 2001.

GAM186 353 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, 3 C c
G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO,
a mammalian protein that promotes apoptosis by bindingto and antagonizing
IAP proteins. Cell 102: 43- 53, 2000.

GAM186 353 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: 3 C c

Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012, 2000.

GAM187 294 EIF4EBP2 Pause, A.; Belsham, G. J.; Gingras, A.- C.; Donze, O.; Lin, T.- A.;Lawrence, 3 C c
J. C., Jr.; Sonenberg, N.: Insulin- dependent stimulationof protein synthesis by phosphorylation of a regulator of 5- prime- capfunction. Nature 371: 762- 767, 1994.

GAM187 294 EIF4EBP2 Tsukiyama- Kohara, K.; Vidal, S. M.; Gingras, A.- C.; Glover, T.W.; Hanash, 3 C c
S. M.; Heng, H.; Sonenberg, N.: Tissue distribution,genomic structure, and chromosome mapping of mouse and human eukaryoticinitiation factor 4E-binding proteins 1 and 2. Genomics 38: 353- 363,1996.

GAM187 294 PTGFRN Charrin, S.; Le Naour, F.; Oualid, M.; Billard, M.; Faure, G.,Hanash, S. M.; 3 C c
Boucheix, C.; Rubinstein, E.: The major CD9 and CD81molecular partner: identification and characterization of the complexes. J.Biol. Chem. 276: 14329- 14337, 2001.

GAM187 294 PTGFRN Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of 3 C c
the coding sequences of unidentified human genes. XVI.The complete sequences of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 65- 73, 2000.

GAM187 294 PTGFRN Orlicky, D. J.; Berry, R.; Sikela, J. M.: Human chromosome 1 localizationof 3 C c
the gene for a prostaglandin F- 2- alpha receptor negative regulatoryprotein. Hum. Genet. 97: 655- 658, 1996.

GAM187 294 PTGFRN Stipp, C. S.; Orlicky, D.; Hemler, M. E.: FPRP, a major, 3 C c
highlystoichiometric, highly specific CD81- and CD9- associated protein. J.Biol. Chem. 276: 4853- 4862, 2001.

GAM189 246 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- 3 B b
glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989.

GAM189 246 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion 3 B b
data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989.

GAM189 246 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma 3 B b
alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.

GAM189 246 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human 3 B b
plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.

GAM189 246 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: 3 B b
Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988.

GAM189 246 ABCC11 Bera, T. K.; Lee, S.; Salvatore, G.; Lee, B.; Pastan, I.: MRP8,a new member 3 B c
of ABC transporter superfamily, identified by EST databasemining and gene prediction program, is highly expressed in breastcancer. Molec. Med. 7: 509-516, 2001.

GAM189 246 ABCC11 Tammur, J.; Prades, C.; Arnould, I.; Rzhetsky, A.; Hutchinson,A.; Adachi, 3 B c
M.; Schuetz, J. D.; Swoboda, K. J.; Ptacek, L. J.; Rosier,M.; Dean, M.; Allikmets, R.: Two new genes from the human ATP- bindingcassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicatedon chromosome 16q12. Gene 273: 89- 96, 2001.

GAM189 246 ABCC11 Yabuuchi, H.; Shimizu, H.; Takayanagi, S.; Ishikawa, T.: Multiplesplicing 3 B c

variants of two new human ATP- binding cassette transporters,ABCC11 and ABCC12. Biochem. Biophys. Res. Commun. 288: 933- 939,2001.

GAM189 246 ABCD3 Gartner, J.; Kearns, W.; Pearson, P.; Valle, D.: Characterizationand 3 B c
localization of the human 70- kD peroxisomal membrane protein (PMP70)gene. (Abstract) Am. J. Hum. Genet. 51 (suppl.): A168, 1992.

GAM189 246 ABCD3 Gartner, J.; Kearns, W.; Rosenberg, C.; Pearson, P.; Copeland,N. G.; 3 B c
Gilbert, D. J.; Jenkins, N. A.; Valle, D.: Localization ofthe 70- kDa peroxisomal membrane protein to human 1p21- p22 and mouse

GAM189 246 ABCD3 Gartner, J.; Obie, C.; Watkins, P.; Valle, D.: Restoration ofperoxisome 3 B c
biogenesis in a peroxisome- deficient mammalian cell lineby expression of either the 35 kDa or the 70 kDa peroxisomal membraneproteins. J. Inherit. Metab. Dis. 17: 327- 329, 1994.

GAM189 246 ABCD3 Genomics 15: 412- 414, 1993.3. Gartner, J.; Moser, H.; Valle, D.: Mutations 3 B c
in the 70K peroxisomalmembrane protein gene in Zellweger syndrome. Nature Genet. 1: 16- 23,1992.

GAM189 246 ABCD3 Moser, A. B.; Rasmussen, M.; Naidu, S.; Watkins, P. A.; McGuinness,M.; 3 B c
Hajra, A. K.; Chen, G.; Raymond, G.; Liu, A.; Gordon, D.; Garnaas,K.; Walton, D. S.; Skjedal, O. H.; Guggenheim, M. A.; Jackson, L.G.; Elias, E. R.; Moser, H. W.: Phenotype of patients with peroxisomaldisorders subdivided into sixteen complementation groups. J. Pediat. 127:13- 22, 1995.

GAM189 246 ABCD3 Paton, B. C.; Heron, S. E.; Nelson, P. V.; Morris, C. P.; Poulos,A.: Absence 3 B c
of mutations raises doubts about the role of the 70- kDperoxisomal membrane protein in Zellweger syndrome. (Letter) Am.J. Hum. Genet. 60: 1535- 1539, 1997.

GAM189 246 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- 3 B b
TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.

GAM189 246 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 B b
Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM189 246 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM 3 B b
protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999.

GAM189 246 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; 3 B b
Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664- 1666, 1999.

GAM189 246 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 B b
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995.

GAM189 246 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 B b
members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994.

GAM189 246 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: 3 B b
Chromosomal mapping of human adenylyl cyclase genestype III, type V and type VI. Hum. Genet. 94: 69- 73, 1994.

GAM189 246 ADORA2A Chen, J.- F.; Huang, Z.; Ma, J.; Zhu, J.; Moratalla, R.; Standaert,D.; 3 B c
Moskowitz, M. A.; Fink, J. S.; Schwarzschild, M. A.: A2A adenosinereceptor

deficiency attenuates brain injury induced by transient focalischemia in mice. J. Neurosci. 19: 9192- 9200, 1999.

GAM189 246 ADORA2A Gaudray, P.: Personal Communication. Nice, France 6/1/1994. 3 B c

GAM189 246 ADORA2A Gusella, J. F.: Personal Communication. Boston, Mass. 4/17/1994. 3 B c

GAM189 246 ADORA2A Le, F.; Townsend- Nicholson, A.; Baker, E.; Sutherland, G. R.; Schofield,P. R.: Characterization and chromosomal localization of the humanA2a adenosine receptor gene: ADORA2A. Biochem. Biophys. Res. Commun. 223:461- 467, 1996. 3 B c

GAM189 246 ADORA2A Ledent, C.; Vaugeois, J.- M.; Schiffmann, S. N.; Pedrazzini, T.;El Yacoubi, M. E.; Vanderhaeghen, J.- J.; Costentin, J.; Heath, J.K.; Vassart, G.; Parmentier, M.: Aggressiveness, hypoalgesia andhigh blood pressure in mice lacking the adenosine A2a receptor. Nature 388:674- 678, 1997. 3 B c

GAM189 246 ADORA2A Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. Note: Erratum: Genomics 23: 305 only, 1994. 3 B c

GAM189 246 ADORA2A MacCollin, M.; Peterfreund, R.; MacDonald, M.; Fink, J. S.; Gusella,J.: Mapping of a human A2a adenosine receptor (ADORA2) to chromosome22. Genomics 20: 332- 333, 1994. 3 B c

GAM189 246 ADORA2A Ohta, A.; Sitkovsky, M.: Role of G- protein- coupled adenosine receptorsin downregulation of inflammation and protection from tissue damage. Nature 916- 920,2001. 3 B c

GAM189 246 ADORA2A Szepetowski, P.; Perucca- Lostanlen, D.; Gaudray, P.: Mapping genesaccording to their amplification status in tumor cells: contributionto the map of 11q13. Genomics 16: 745- 750, 1993. 3 B c

GAM189 246 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002. 3 B c

GAM189 246 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor: functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994. 3 B c

GAM189 246 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994. 3 B c

GAM189 246 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 3 B c

GAM189 246 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95- 101, 1997. 3 B c

GAM189 246 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779- 782, 2000. 3 B c

GAM189 246 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001. 3 B c

GAM189 246 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001. 3 B c

GAM189 246 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998. 3 B c

GAM189 246 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: Identificationand characterization of STK12/Aik2: a human gene related to auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147- 152,1998. 3 B c

GAM189 246 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism, OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001. 3 B c

GAM189 246 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand characterization of genes associated with chromosome- 6 mediatedtumor suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996. 3 B c

GAM189 246 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a novel non- lens member of the beta- gamma- crystallin superfamily,is associated with the control of tumorigenicity in human malignantmelanoma. Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997. 3 B c

GAM189 246 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA cloning, expression, subcellular localization, and chromosomalassignment of mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem. Biophys. Res. Commun. 244: 285- 292, 1998. 3 B c

GAM189 246 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof the aurora- and Ipl1- like midbody- associated protein mitotic kinasein human cancer cells. Cancer Res. 58: 4811- 4816, 1998. 3 B c

GAM189 246 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian Genome 9: 715- 720, 1998. 3 B c

GAM189 246 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human melanoma cell lines controlled by introduction of human chromosome6. Science 247: 568- 571, 1990. 3 B c

GAM189 246 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89: 3962- 3966,1992. 3 B c

GAM189 246 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat. Acad. Sci. 96: 4378- 4383, 1999. 3 B c

GAM189 246 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; 3 B c

Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988.

GAM189 246 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: 3 B c Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990.

GAM189 246 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 3 B b (CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998.

GAM189 246 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of 3 B b Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999.

GAM189 246 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: 3 B b Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000.

GAM189 246 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 3 B b deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001.

GAM189 246 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic 3 B b protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999.

GAM189 246 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, 3 B b P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002.

GAM189 246 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- 3 B b Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001.

GAM189 246 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: 3 B b Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998.

GAM189 246 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; 3 B b Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998.

GAM189 246 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human 3 B b protein homologous to C. elegans CED- 4, participates in cytochromec- dependent activation of caspase- 3. Cell 90: 405- 413, 1997.

GAM189 246 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: 3 B c Apolipoprotein L gene family: tissue- specific expression,splicing, promoter regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001.

GAM189 246 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya- 3 B c Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a new human high density lipoprotein apolipoproteinexpressed by the pancreas: identification, cloning, characterization,and plasma distribution of apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997.

GAM189 246 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. 3 B c L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.; Bahn, S.: Gene expression analysis in schizophrenia:reproducible up-

regulation of several members of the apolipoproteinL family located in a high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat. Acad. Sci. 99: 4680- 4685, 2002.

GAM189 246 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The apolipoprotein L gene cluster has emerged recently in evolutionand is expressed in human vascular tissue. Genomics 79: 539- 546,2002. 3 B c

GAM189 246 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman apolipoprotein L gene cluster: identification, classification,and sites of distribution. Genomics 74: 71- 78, 2001. 3 B c

GAM189 246 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 B b

GAM189 246 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 3 B b

GAM189 246 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- interacting protein, recognizes the basolateral sortingsignal of amyloid precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998. 3 B b

GAM189 246 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 B c

GAM189 246 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 B c

GAM189 246 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 B c

GAM189 246 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and Drosophila. Genomics 26: 101- 106, 1995. 3 B c

GAM189 246 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer protein delta- COP, encoded by the archain gene, is conservedacross diverse eukaryotes. Mammalian Genome 7: 784- 786, 1996. 3 B c

GAM189 246 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990. 3 B b

GAM189 246 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11 near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec. Genet. 16: 401- 405, 1990. 3 B b

GAM189 246 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K- ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics 6:697- 699, 1990. 3 B b

GAM189 246 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: Identification of a putative isoform of the Na,K- ATPase beta subunit:primary structure and tissue- specific expression. J. Biol. Chem. 3 B b

164:4613- 4618, 1989.

GAM189 246 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: 3 B b
Identification of a cDNA clone specific for the neural adhesionmolecule
AMOG. J. Neurosci. Res. 22: 113- 119, 1989.

GAM189 246 BACE2 Acquati, F.; Accarino, M.; Nucci, C.; Fumagalli, P.; Jovine, L.;Ottolenghi, 3 B c
S.; Taramelli, R.: The gene encoding DRAP (BACE2), aglycosylated
transmembrane protein of the aspartic protease family,maps to the Down
syndrome critical region. FEBS Lett. 468: 59- 64,2000.

GAM189 246 BACE2 Bennett, B. D.; Babu- Khan, S.; Loeloff, R.; Louis, J.- C.; Curran,E.; 3 B c
Citron, M.; Vassar, R.: Expression analysis of BACE2 in brainand peripheral
tissues. J. Biol. Chem. 275: 20647- 20651, 2000.

GAM189 246 BACE2 Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a 3 B c
BACE homolog, BACE2, reside in the obligate Down syndromeregion of
chromosome 21. Science 286: 1255A only, 1999.

GAM189 246 BACE2 Solans, A.; Estivill, X.; de la Luna, S.: A new aspartyl proteaseon 21q22.3, 3 B c
BACE2, is highly similar to Alzheimer's amyloid precursorprotein beta-
secretase. Cytogenet. Cell Genet. 89: 177- 184, 2000.

GAM189 246 BACE2 Xin, H.; Stephans, J. C.; Duan, X.; Harrowe, G.; Kim, E.; Grieshammer,U.; 3 B c
Kingsley, C.; Giese, K.: Identification of a novel aspartic- likeprotease
differentially expressed in human breast cancer cell lines. Biochim.Biophys.
Acta 1501: 125- 137, 2000.

GAM189 246 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- 3 B b
evaluation of 'reactive lymphoid hyperplasia of the uvea':
animmunohistochemical and molecular analysis of 10 cases. Ophthalmology
107:151- 158, 2000.

GAM189 246 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 3 B b
mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999.

GAM189 246 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. 3 B b
J.Clin. Path. 48: 395- 397, 1995.

GAM189 246 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; 3 B b
Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T.
W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of
NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001.

GAM189 246 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; 3 B b
Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not
its cellular homologue, activates NF- kappa- B transcriptionfactor and c-
Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999.

GAM189 246 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- 3 B b
Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.;
Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in
t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types
Cell 96: 35- 45, 1999.

GAM189 246 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic 3 B b
study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer
Genet. Cytogenet. 58: 35- 38, 1992.

GAM189 246 BDP1 Kelter, A.- R.; Herchenbach, J.; Wirth, B.: The transcription factor- 3 B b
likenuclear regulator (TFNR) contains a novel 55- amino- acid motif
repeatednine times and maps closely to SMN1. Genomics 70: 315- 326, 2000.

GAM189 246 BDP1 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 B b
TFIIB activities direct RNA polymerase III transcription fromTATA-

containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM189 246 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 B b
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM189 246 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 B b
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM189 246 CASP2 Bergeron, L.; Perez, G. I.; Macdonald, G.; Shi, L.; Sun, Y.; Jurisicova,A.; 3 B c
Varmuza, S.; Latham, K. E.; Flaws, J. A.; Salter, J. C. M.; Hara,H.;
Moskowitz, M. A.; Li, E.; Greenberg, A.; Tilly, J. L.; Yuan, J.: Defects in
regulation of apoptosis in caspase- 2- deficient mice. GenesDev. 12: 1304-
1314, 1998.

GAM189 246 CASP2 Kumar, S.; Kinoshita, M.; Noda, M.; Copeland, N. G.; Jenkins, N.A.: 3 B c
Induction of apoptosis by the mouse Nedd2 gene, which encodesa protein
similar to the product of the Caenorhabditis elegans celldeath gene ced- 3
and the mammalian IL- 1- beta- converting enzyme. GenesDev. 8: 1613- 1626,
1994.

GAM189 246 CASP2 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 3 B c
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM189 246 CASP2 Kumar, S.; White, D. L.; Takai, S.; Turczynowicz, S.; Juttner,C. A.; Hughes, 3 B c
T. P.: Apoptosis regulatory gene NEDD2 maps to humanchromosome segment 7q34-
35, a region frequently affected in haematologicalneoplasms. Hum. Genet. 95:
641- 644, 1995.

GAM189 246 CASP2 Lassus, P.; Opitz- Araya, X.; Lazebnik, Y.: Requirement for caspase- 2in 3 B c
stress- induced apoptosis before mitochondrial permeabilization. Science
297:1352- 1354, 2002.

GAM189 246 CASP2 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; 3 B c
Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes,
CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem.
Biophys. Res. Commun. 225: 983- 989, 1996.

GAM189 246 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 B b
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM189 246 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 B b
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM189 246 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 B b
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM189 246 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 B b
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM189 246 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 B b
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell

death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM189 246 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 B b
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM189 246 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 B b
Caspase- 8 is required for cell death induced by expanded
polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM189 246 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 B b
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM189 246 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 B c
member of a multigene family. Genomics 52: 332- 341, 1998.

GAM189 246 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 B c
new member of the MTG8/ETO gene family, maps on 20q11region and is deleted
in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM189 246 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 B c
Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic
fusion protein forms a complex with a novel member of theMTG8(ETO/CDR)
family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM189 246 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. 3 B c
J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis
machinery through a novel motif, the F- box. Cell 86:263- 274, 1996.

GAM189 246 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; 3 B c
Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene
(CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics
24:27- 33, 1994.

GAM189 246 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F 3 B c
maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6:
149- 150, 1995.

GAM189 246 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 3 B b
membrane- associated C- type lectin that exhibits CD4- independentbinding of
human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad.
Sci. 89: 8356- 8360, 1992.

GAM189 246 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 3 B b
for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR.
Science 294: 2163- 2166, 2001.

GAM189 246 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 3 B b
Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S.
L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-
SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-
infection of T cells. Cell 100: 587- 597,2000.

GAM189 246 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 3 B b
F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a
novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune
responses. Cell 100: 575- 585, 2000.

GAM189 246 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related 3 B b

gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000.

GAM189 246 CDC6 Saha, P.; Chen, J.; Thome, K. C.; Lawlis, S. J.; Hou, Z.- H.; Hendricks,M.; 3 B b
Parvin, J. D.; Dutta, A.: Human CDC6/Cdc18 associates with Orc1and cyclin-
cdk and is selectively eliminated from the nucleus at theonset of S phase.
Molec. Cell. Biol. 18: 2758- 2767, 1998.

GAM189 246 CDC6 Williams, R. S.; Shohet, R. V.; Stillman, B.: A human proteinrelated to 3 B b
yeast Cdc6p. Proc. Nat. Acad. Sci. 94: 142- 147, 1997.

GAM189 246 CDC6 Yan, Z.; DeGregori, J.; Shohet, R.; Leone, G.; Stillman, B.; Nevins,J. R.; 3 B b
Williams, R. S.: Cdc6 is regulated by E2F and is essentialfor DNA
replication in mammalian cells. Proc. Nat. Acad. Sci. 95:3603- 3608, 1998.

GAM189 246 CDC6 Yan, Z.; Fedorov, S. A.; Mumby, M. C.; Williams, R. S.: PR48,a novel 3 B b
regulatory subunit of protein phosphatase 2A, interacts withCdc6 and
modulates DNA replication in human cells. Molec. Cell. Biol. 20:1021- 1029,
2000.

GAM189 246 CDH17 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene 3 B c
cluster to a region of chromosome 5 subject to frequent allelicloss in
carcinoma. Genomics 57: 160- 163, 1999.

GAM189 246 CDH17 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; 3 B c
Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck,
P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with
a protein related to the cadherin superfamily. Science 264:430- 433, 1994.

GAM189 246 CDH17 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 3 B c
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting
cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM189 246 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, 3 B b
G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.;
Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.;
Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for
Muckle- Wells syndrome and familial cold urticaria:a novel mutation
underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002.

GAM189 246 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, 3 B b
E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile
neurological cutaneous and articular syndromeis caused by mutations in
CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes.
Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM189 246 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. 3 B b
D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes
familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature
Genet. 29: 301- 305, 2001.

GAM189 246 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 B b
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM189 246 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 B c
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.:
Identification of a novel, dendritic cell- associated molecule,dectin- 1, by
subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM189 246 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 3 B c

GAM189 246 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 3 B c

GAM189 246 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 3 B c

GAM189 246 CLNS1A Anguita, J.; Chalfant, M. L.; Civan, M. M.; Coca- Prados, M.: Molecularcloning of the human volume- sensitive chloride conductance regulatoryprotein, pI(Cln), from ocular ciliary epithelium. Biochem. Biophys.Res. Commun. 208: 89- 95, 1995. 3 B c

GAM189 246 CLNS1A Buyse, G.; De Greef, C.; Raeymaekers, L.; Droogmans, G.; Nilius,B.; Eggermont, J.: The ubiquitously expressed pI(Cln) protein formshomomeric complexes in vitro. Biochem. Biophys. Res. Commun. 218:822- 827, 1996. 3 B c

GAM189 246 CLNS1A Nagl, U. O.; Erdel, M.; Schmarda, A.; Seri, M.; Pinggera, G. M.;Gschwentner, M.; Duba, C.; Galietta, L. J. V.; Deetjen, P.; Utermann,G.; Paulmichl, M.: Chromosomal localization of the genes (CLNS1Aand CLNS1B) coding for the swelling- dependent chloride channel I(Cln). Genomics 38:438- 441, 1996. 3 B c

GAM189 246 CLNS1A Schwartz, R. S.; Rybicki, A. C.; Nagel, R. L.: Molecular cloningand expression of a chloride channel- associated protein pI(Cln) inhuman young red blood cells: association with actin. Biochem. J. 327:609- 616, 1997. 3 B c

GAM189 246 CNN2 Cheng, J.- F.; Boyartchuk, V.; Zhu, Y.: Isolation and mapping ofhuman chromosome 21 cDNA: progress in constructing a chromosome 21expression map. Genomics 23: 75- 84, 1994. 3 B b

GAM189 246 CNN2 Masuda, H.; Tanaka, K.; Takagi, M.; Ohgami, K.; Sakamaki, T.; Shibata,N.; Takahashi, K.: Molecular cloning and characterization of humannon- smooth muscle calponin. J. Biochem. 120: 415- 424, 1996. 3 B b

GAM189 246 CNP Bernier, L.; Colman, D. R.; D'Eustachio, P.: Chromosomal locationsof genes encoding 2- prime,3- prime cyclic nucleotide 3- prime- phosphodiesteraseand glial fibrillary acidic protein in the mouse. J. Neurosci. Res. 20:497- 504, 1988. 3 B c

GAM189 246 CNP Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J.: 2- prime,3- prime- cyclicnucleotide 3- prime- phosphodiesterase: a membrane- bound, microtubule- associatedprotein and membrane anchor for tubulin. Proc. Nat. Acad. Sci. 99:1807- 1812, 2002. 3 B c

GAM189 246 CNP Douglas, A. J.; Fox, M. F.; Abbott, C. M.; Hinks, L. J.; Sharpe,G.; Povey, S.; Thompson, R. J.: Structure and chromosomal localizationof the human 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasegene. Ann. Hum. Genet. 56: 243- 254, 1992. 3 B c

GAM189 246 CNP Douglas, A. J.; Fox, M. F.; Hinks, L. J.; Povey, S.; Thompson,R. J.: Localization of the myelin specific enzyme 2- prime,3- prime- cyclicnucleotide- 3- prime- phosphohydrolase to 17q21. (Abstract) Cytogenet.Cell Genet. 58: 2004 only, 1991. 3 B c

GAM189 246 CNP Kurihara, T.; Monoh, K.; Sakimura, K.; Takahashi, Y.: Alternativesplicing of mouse brain 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasemRNA. Biochem. Biophys. Res. Commun. 170: 1074- 1081, 1990. 3 B c

GAM189 246 CNP Monoh, K.; Kurihara, T.; Takahashi, Y.; Ichikawa, T.; Kumanishi,T.; Hayashi, S.; Minoshima, S.; Shimizu, N.: Structure, expressionand chromosomal localization of the gene encoding human 2- prime,3- prime- cyclic- 3 B c

nucleotide3- prime- phosphodiesterase. Gene 129: 297- 301, 1993.

GAM189 246 CNP Sprinkle, T. J.; Kouri, R. E.; Fain, P. D.; Stoming, T. A.; Whitney,J. B., 3 B c
III: Chromosomal mapping of the human CNP gene using a meioticcrossover DNA
panel, PCR, and allele- specific probes. Genomics 16:542- 545, 1993.

GAM189 246 CNP Sprinkle, T. J.; Lanclos, K. D.; Lapp, D. F.: Assignment of thehuman 2- 3 B c
prime,3- prime- cyclic nucleotide 3- prime- phosphohydrolase geneto
chromosome 17. Genomics 13: 877- 880, 1992.

GAM189 246 CNP Vogel, U. S.; Thompson, R. J.: Molecular structure, localization,and 3 B c
possible functions of the myelin- associated enzyme 2- prime,3- prime-
cyclicnucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667-
1677,1988.

GAM189 246 CRSP6 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, 3 B c
Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC
complexes indicates novel pathways for the functionof nuclear receptors and
diverse mammalian activators. Molec. Cell 3:361- 370, 1999.

GAM189 246 CRSP6 Jiang, Y.- W.; Veschambre, P.; Erdjument- Bromage, H.; Tempst, P.;Conaway, 3 B c
J. W.; Conaway, R. C.; Kornberg, R. D.: Mammalian mediatorof transcriptional
regulation and its possible role as an end- pointof signal transduction
pathways. Proc. Nat. Acad. Sci. 95: 8538- 8543,1998.

GAM189 246 CRSP6 Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R.: The transcriptionalcofactor 3 B c
complex CRSP is required for activity of the enhancer- bindingprotein Sp1.
Nature 397: 446- 450, 1999.

GAM189 246 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, 3 B b
A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel
developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359,
1997.

GAM189 246 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; 3 B b
Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome
mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix
Biol. 18: 319- 324, 1999.

GAM189 246 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; 3 B b
Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome
mapping of the gene encoding human cartilage associatedprotein (CRTAP).
Cytogenet. Cell Genet. 87: 191- 194, 1999.

GAM189 246 CSNK2A2 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation 3 B c
of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297:
1700- 1703, 2002.

GAM189 246 CSNK2A2 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; 3 B c
Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine
392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292,
2001.

GAM189 246 CSNK2A2 Lozeman, F. J.; Litchfield, D. W.; Piening, C.; Takio, K.; Walsh,K. A.; 3 B c
Krebs, E. G.: Isolation and characterization of human cDNAclones encoding
the alpha and the alpha- prime subunits of casein kinaseII. Biochemistry 29:
8436- 8447, 1990.

GAM189 246 CSNK2A2 Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C.: Globozoospermiain 3 B c
mice lacking the casein kinase II alpha- prime catalytic subunit.
NatureGenet. 23: 118- 121, 1999.

GAM189 246 CSNK2A2 Yang- Feng, T. L.; Naiman, T.; Kopatz, I.; Eli, D.; Dafni, N.; Canaani,D.: 3 B c
Assignment of the human casein kinase II alpha- prime subunitgene (CSNK2A1)

to chromosome 16p13.2- p13.3. Genomics 19: 173 only,1994.

GAM189 246 CSNK2A2 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping of the human casein kinase II catalytic subunit genes: twoloci carrying the homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125- 7129, 1991. 3 B c

GAM189 246 CTF1 Bordet, T.; Lesbordes, J.- C.; Rouhani, S.; Castelnau- Ptakhine,L.; Schmalbruch, H.; Haase, G.; Kahn, A.: Protective effects of cardiotrophin- 1adenoviral gene transfer on neuromuscular degeneration in transgenicALS mice. Hum. Molec. Genet. 10: 1925- 1933, 2001. 3 B b

GAM189 246 CTF1 Pennica, D.; Arce, V.; Swanson, T. A.; Vejsada, R.; Pollock, R.A.; Armanini, M.; Dudley, K.; Phillips, H. S..; Rosenthal, A.; Kato,A. C.; Henderson, C. E.: Cardiotrophin- 1, a cytokine present in embryonicmuscle, supports long- term survival of spinal motoneurons. Neuron 17:63- 74, 1996. 3 B b

GAM189 246 CTF1 Pennica, D.; King, K. L.; Shaw, K. J.; Luis, E.; Rullamas, J.;Luoh, S.- M.; Darbonne, W. C.; Knutzon, D. S.; Yen, R.; Chien, K. R.;Baker, J. B.; Wood, W. I.: Expression cloning of cardiotrophin 1,a cytokine that induces cardiac myocyte hypertrophy. Proc. Nat. Acad.Sci. 92: 1142- 1146, 1995. 3 B b

GAM189 246 CTF1 Pennica, D.; Swanson, T. A.; Shaw, K. J.; Kuang, W.- J.; Gray, C.L.; Beatty, B. G.; Wood, W. I.: Human cardiotrophin- 1: protein andgene structure, biological and binding activities, and chromosomallocalization. Cytokine 8: 183- 189, 1996. 3 B b

GAM189 246 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H, L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245, 1997. 3 B b

GAM189 246 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S controls the trafficking and maturation of MHC class IImolecules in dendritic cells. J. Cell Biol. 147: 775- 790, 1999. 3 B b

GAM189 246 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. J.; Chapman, H. A.: Structure and chromosomal assignmentof the human cathepsin K gene. Genomics 41: 258- 262, 1997. 3 B b

GAM189 246 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.; Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell selection and maturation by cathepsin S. Immunity 15:909- 919, 2001. 3 B b

GAM189 246 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: Molecular cloning and expression of human alveolar macrophagecathepsin S, an elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992. 3 B b

GAM189 246 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization, gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536, 1994. 3 B b

GAM189 246 CXCL16 Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G.: A transmembrane CXC chemokine is a ligand for HIV- coreceptor Bonzo. NatureImmun. 1: 298- 304, 2000. 3 B c

GAM189 246 CXCL16 Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.;Kita, T.; Yonehara, S.: Molecular cloning of a novel scavenger receptorfor oxidized low density lipoprotein, SR- PSOX, on macrophages. J.Biol. Chem. 275: 40663- 40666, 2000. 3 B c

GAM189 246 CXCL16 Wilbanks, A.; Zondlo, S. C.; Murphy, K.; Mak, S.; Soler, D.; Langdon,P.; 3 B c
Andrew, D. P.; Wu, L.; Briskin, M.: Expression cloning of
theSTRL33/BONZO/TYMSTR ligand reveals elements of CC, CXC, CX3C chemokines.
J.Immun. 166: 5145- 5154, 2001.

GAM189 246 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; 3 B b
Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism:
studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996.

GAM189 246 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human 3 B b
cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily
responsible for the hepatic 3- demethylation of caffeineand N- oxidation of
carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989.

GAM189 246 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, 3 B b
M.; Petersen, N. E.: Association between CYP1A2 polymorphismand
susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000.

GAM189 246 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. 3 B b
L.: The contribution of genetically determined oxidationstatus to inter-
individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16:
157- 166, 1983.

GAM189 246 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, 3 B b
T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450
involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986.

GAM189 246 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, 3 B b
S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat
orthologous gene, and differences in liver1A2 mRNA expression. Molec.
Endocr. 3: 1399- 1408, 1989.

GAM189 246 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human 3 B b
P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the
3- prime nontranslated region, and localization ofgene to chromosome 15. J.
Exp. Path. 3: 1- 17, 1987.

GAM189 246 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, 3 B b
A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show
deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996.

GAM189 246 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 B b

GAM189 246 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, 3 B b
S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter)
Nature 398: 760- 761, 1999.

GAM189 246 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of 3 B b
cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-
deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J.
Clin. Pharm. 26: 363- 372, 1988.

GAM189 246 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof 3 B b
cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-
based caffeine test. Pharmacogenetics 9: 131- 144, 1999.

GAM189 246 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; 3 B b
Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime
of the CYP1A2 gene: implications for human populationhistory and natural
selection. Am. J. Hum. Genet. 71: 528- 542, 2002.

GAM189 246 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, 3 B b
J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal
localization and evidence for alternative splicing. NucleicAcids Res. 16:

5783- 5795, 1988.

GAM189 246 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 B b

GAM189 246 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 3 B b

GAM189 246 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene: molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230, 1998. 3 B b

GAM189 246 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii-Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in humanpolymorphonuclear leukocytes: cDNA cloning and expression of leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993. 3 B b

GAM189 246 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 B b

GAM189 246 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 B b

GAM189 246 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4-alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 B b

GAM189 246 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000. 3 B b

GAM189 246 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461-8466, 1998. 3 B b

GAM189 246 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997. 3 B b

GAM189 246 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998. 3 B b

GAM189 246 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. W.: Chromosomal localization and racial distributionof the polymorphic human dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352, 1988. 3 B b

GAM189 246 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies three RFLPs. Nucleic Acids Res. 15: 5501 only,1987. 3 B b

GAM189 246 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: Chromosomal localization and racial distribution of the polymorphichDHFR- 3 B b

psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985.

GAM189 246 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; 3 B b
Nienhuis, A. W.: Chromosomal organization of the human
dihydrofolatereductase genes: dispersion, selective amplification and a
novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984.

GAM189 246 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in 3 B b
dihydrofolatereductase that confer resistance to methotrexate: potential for
clinicalapplication. Hum. Mutat. 11: 259- 263, 1998.

GAM189 246 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: 3 B b
Intronless human dihydrofolate reductase genes are derivedfrom processed RNA
molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982.

GAM189 246 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association 3 B b
with variation in protein structure. Science 220: 1125- 1129,1983.

GAM189 246 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 3 B b
757 and 807- 812, 1975.

GAM189 246 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the 3 B b
human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5.
Molec. Cell. Biol. 4: 2010- 2016, 1984.

GAM189 246 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater- 3 B b
Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed
ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med.
310: 789- 790, 1984.

GAM189 246 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment 3 B b
of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus
musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986.

GAM189 246 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: 3 B b
Human dihydrofolate reductase gene is located in chromosome 5and is unlinked
to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984.

GAM189 246 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human 3 B b
dihydrofolate reductase gene to band q23 of chromosome 5and of related
pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85,
1985.

GAM189 246 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; 3 B b
Attardi, G.: Chromosomal location of the normal human DHFRgene and of its
amplified copies in methotrexate resistant cell variants.(Abstract)
Cytogenet. Cell Genet. 37: 534 only, 1984.

GAM189 246 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 3 B b
10/7/1983.

GAM189 246 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: 3 B b
Amplification of the human dihydrofolate reductase gene viadouble minutes is
initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000.

GAM189 246 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. 3 B b
A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing
megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976.

GAM189 246 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)- 3 B b
formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967.

GAM189 246 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila- 3 B c
relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997.

GAM189 246 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; 3 B c
Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo,

D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998.

GAM189 246 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis 3 B c in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994.

GAM189 246 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, 3 B c M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997.

GAM189 246 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. 3 B c H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993.

GAM189 246 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; 3 B c Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997.

GAM189 246 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, 3 B c D. J.; Muir, W. J.: Schizophrenia and affective disorders- - cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001.

GAM189 246 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 3 B c 355:771- 772, 2000.

GAM189 246 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; 3 B c Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001.

GAM189 246 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; 3 B c Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970.

GAM189 246 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. 3 B c S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000.

GAM189 246 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, 3 B c G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM189 246 DNAH11 Arnold, G. L.; Bixler, D.; Girod, D.: Probable autosomal 3 B c recessiveinheritance of polysplenia, situs inversus and cardiac defects inan Amish family. Am. J. Med. Genet. 16: 35- 42, 1983.

GAM189 246 DNAH11 Brueckner, M.; D'Eustachio, P.; Horwich, A. L.: Linkage mappingof a mouse 3 B c gene, iv, that controls left- right asymmetry of the heartand viscera. Proc. Nat. Acad. Sci. 86: 5035- 5038, 1989.

GAM189 246 DNAH11 Chapelin, C.; Duriez, N.; Magnino, F.; Goossens, M.; Escudier,E.; Amselem, 3 B c S.: Isolation of several human axonemal dynein heavychain genes: genomic structure of the catalytic site, phylogeneticanalysis and chromosomal assignment. FEBS Lett. 412: 325- 330, 1997.

GAM189 246 DNAH11 Hanzlik, A. J.; Binder, M.; Layton, W. M.; Rowe, L.; Layton, M.;Taylor, B. 3 B c

A.; Osemlak, M. M.; Richards, J. E.; Kurnit, D. M.; Stewart,G. D.: The murine situs inversus viscerum (iv) gene responsiblefor visceral asymmetry is linked tightly to the Igh- C cluster on chromosome12. Genomics 7: 389-393, 1990.

GAM189 246 DNAH11 McGrath, J.; Horwich, A. L.; Brueckner, M.: Duplication/deficiencymapping of 3 B c situs inversus viscerum (iv), a gene that determines left- rightasymmetry in the mouse. Genomics 14: 643- 648, 1992.

GAM189 246 DNAH11 Nonaka, S.; Shiratori, H.; Saijoh, Y.; Hamada, H.: Determinationof left- 3 B c right patterning of the mouse embryo by artificial nodal flow. Nature 418:96- 99, 2002.

GAM189 246 DNAH11 Okada, Y.; et al.; et al: Abnormal nodal flow precedes situs inversusin iv 3 B c and inv mice. Molec. Cell 4: 459- 468, 1999.

GAM189 246 DNAH11 Supp, D. M.; Witte, D. P.; Potter, S. S.; Brueckner, M.: Mutationof an 3 B c axonemal dynein affects left- right asymmetry in inversus viscerummice. Nature 389: 963- 966, 1997.

GAM189 246 DNAH11 Supp, D.; et al.; et al: Targeted deletion of the ATP bindingdomain of left- 3 B c right dynein confirms its role in specifying developmentof left- right asymmetries. Development 126: 5495- 5504, 1999.

GAM189 246 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, 3 B c T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995.

GAM189 246 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, 3 B c H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin. J. Biol. Chem. 269: 26295- 26302, 1994.

GAM189 246 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The 3 B c desmocollins of human foreskin epidermis: identification and chromosomalassignment of a third gene and expression patterns of the three isoforms. J.Invest. Derm. 105: 314- 321, 1995.

GAM189 246 EBAF Burdine, R. D.; Schier, A. F.: Conserved and divergent mechanismsin left- 3 B c right axis formation. Genes Dev. 14: 763- 776, 2000.

GAM189 246 EBAF Kosaki, K.; Bassi, M. T.; Kosaki, R.; Lewin, M.; Belmont, J.; Schauer,G.; 3 B c Casey, B.: Characterization and mutation analysis of human LEFTYA and LEFTY B, homologues of murine genes implicated in left- rightaxis development. Am. J. Hum. Genet. 64: 712- 721, 1999.

GAM189 246 EBAF Kothapalli, R.; Buyuksal, I.; Wu, S.- Q.; Chegini, N.; Tabibzadeh,S.: 3 B c Detection of ebaf, a novel human gene of the transforming growthfactor beta superfamily: association of gene expression with endometrialbleeding. J. Clin. Invest. 99: 2342- 2350, 1997.

GAM189 246 EBAF Meno, C.; Itoh, Y.; Saijoh, Y.; Matsuda, Y.; Tashiro, K.; Kuhara,S.; Hamada, 3 B c H.: Two closely- related left- right asymmetrically expressedgenes, lefty- 1 and lefty- 2: their distinct expression domains, chromosomallinkage and direct neuralizing activity in Xenopus embryos. GenesCells 2: 513- 524, 1997.

GAM189 246 EBAF Meno, C.; Saijoh, Y.; Fujii, H.; Ikeda, M.; Yokoyama, T.; Yokoyama,M.; 3 B c Toyoda, Y.; Hamada, H.: Left- right asymmetric expression of theTGF- beta-family member lefty in mouse embryos. Nature 381: 151- 155,1996.

GAM189 246 EBAF Meno, C.; Shimono, A.; Saijoh, Y.; Yashiro, K.; Mochida, K.; Ohishi,S.; 3 B c Noji, S.; Kondoh, H.; Hamada, H.: Lefty- 1 is required for left-rightdetermination as a regulator of lefty- 2 and nodal. Cell 94: 287-

297,1998.

GAM189 246 EBAF Tabibzadeh, S.; Mason, J. M.; Shea, W.; Cai, Y.; Murray, M. J.;Lessey, B.: 3 B c
Dysregulated expression of ebaf, a novel molecular defectin the endometria
of patients with infertility. J. Clin. Endocr.Metab. 85: 2526- 2536, 2000.

GAM189 246 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- 3 B c
elongationfactor 2 kinase (calmodulin- dependent protein kinase III)
antibodiesin patients with systemic lupus erythematosus. Biochem.
Biophys.Res. Commun. 293: 1073- 1076, 2002.

GAM189 246 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 3 B c
Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C.
R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein
kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat.
Acad. Sci. 94: 4884- 4889, 1997.

GAM189 246 EHD1 Di Fiore, P. P.; Pelicci, P. G.; Sorkin, A.: EH: a novel protein- 3 B c
proteininteraction domain potentially involved in intracellular sorting.
TrendsBiochem. Sci. 22: 411- 413, 1997.

GAM189 246 EHD1 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 3 B c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.;
Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.;
Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the
2.8- Mb region containing the multiple endocrineneoplasia type 1 locus.
Genome Res. 7: 725- 735, 1997.

GAM189 246 EHD1 Haider, N. B.; Searby, C.; Galperin, E.; Mintz, L.; Horowitz, M.;Stone, E. 3 B c
M.; Sheffield, V. C.: Evaluation and molecular characterizationof EHD1, a
candidate gene for Bardet- Biedl syndrome 1 (BBS1). Gene 240:227- 232, 1999.

GAM189 246 EHD1 Mintz, L.; Galperin, E.; Pasmanik- Chor, M.; Tulzinsky, S.; Bromberg,Y.; 3 B c
Kozak, C. A.; Joyner, A.; Fein, A.; Horowitz, M.: EHD1- - an EH- domain-
containingprotein with a specific expression pattern. Genomics 59: 66-
76,1999.

GAM189 246 EHD1 Rotem- Yehudar, R.; Galperin, E.; Horowitz, M.: Association ofinsulin- like 3 B c
growth factor 1 receptor with EHD1 and SNAP29. J. Biol.Chem. 276: 33054-
33060, 2001.

GAM189 246 EIF2S3 Ehrmann, I. E.; Ellis, P. S.; Mazeyrat, S.; Duthie, S.; Brockdorff,N.; 3 B c
Mattei, M. G.; Gavin, M. A.; Affara, N. A.; Brown, G. M.; Simpson,E.;
Mitchell, M. J.; Scott, D. M.: Characterization of genes encodingtranslation
initiation factor eIF- 2- gamma in mouse and human: sexchromosome
localization, escape from X- inactivation and evolution. Hum.Molec. Genet.
7: 1725- 1737, 1998.

GAM189 246 EIF2S3 Gasper, N. J.; Kinzy, T. G.; Scherer, B. J.; Humbelin, M.; Hershey,J. W. B.; 3 B c
Merrick, W. C.: Translation initiation factor eIF- 2: cloningand expression
of the human cDNA encoding the gamma- subunit. J. Biol.Chem. 269: 3415-
3422, 1994.

GAM189 246 EPHA8 Chan, J.; Watt, V. M.: Eek and erk, new members of the eph subclassof 3 B c
receptor protein- tyrosine kinases. Oncogene 6: 1057- 1061, 1991.

GAM189 246 EPHA8 Park, S.; Frisen, J.; Barbacid, M.: Aberrant axonal projectionsin mice 3 B c
lacking EphA8 (Eek) tyrosine protein kinase receptors. EMBOJ. 16: 3106-
3114, 1997.

GAM189 246 EZH1 Abel, K. J.; Brody, L. C.; Valdes, J. M.; Erdos, M. R.; McKinley,D. R.; 3 B c
Castilla, L. H.; Merajver, S. D.; Couch, F. J.; Friedman, L.S.; Ostermeyer,
E. A.; Lynch, E. D.; King, M.- C.; Welcsh, P. L.; Osborne- Lawrence,S.;

Spillman, M.; Bowcock, A. M.; Collins, F. S.; Weber, B. L.: Characterizationof EZH1, a human homolog of Drosophila enhancer of zeste near BRCA1. Genomics 37:161- 171, 1996.

GAM189 246 EZH1 Cardoso, C.; Mignon, C.; Hetet, G.; Grandchamps, B.; Fontes, M.;Colleaux, L.: The human EZH2 gene: genomic organisation and revisedmapping in 7q35 within the critical region for malignant myeloid disorders. Europ.J. Hum. Genet. 8: 174- 180, 2000. 3 B c

GAM189 246 EZH1 Cardoso, C.; Timsit, S.; Villard, L.; Khrestchatisky, M.; Fontes,M.; Colleaux, L.: Specific interaction between the XNP/ATR- X geneproduct and the SET domain of the human EZH2 protein. Hum. Molec.Genet. 7: 679- 684, 1998. 3 B c

GAM189 246 EZH1 Chen, H.; Rossier, C.; Antonarakis, S. E.: Cloning of a humanhomolog of the Drosophila enhancer of zeste gene (EZH2) that mapsto chromosome 21q22.2. Genomics 38: 30- 37, 1996. 3 B c

GAM189 246 EZH1 Dohner, K.; Brown, J.; Hehmann, U.; Hetzel, C.; Stewart, J.; Lowther,G.; Scholl, C.; Frohling, S.; Cuneo, A.; Tsui, L. C.; Lichter, P.;Scherer, S. W.; Dohner, H.: Molecular cytogenetic characterizationof a critical region in bands 7q35- q36 commonly deleted in malignantmyeloid disorders. Blood 92: 4031- 4035, 1998. 3 B c

GAM189 246 EZH1 Laible, G.; Haynes, A. R.; Lebersorger, A.; O'Carroll, D.; Mattei,M.- G.; Denny, P.; Brown, S. D. M.; Jenuwein, T.: The murine polycomb- groupgenes Ezh1 and Ezh2 map close to Hox gene clusters on mouse chromosomes11 and 6. Mammalian Genome 10: 311- 314, 1999. 3 B c

GAM189 246 EZH1 Varambally, S.; Dhanasekaran, S. M.; Zhou, M.; Barrette, T. R.;Kumar- Sinha, C.; Sanda, M. G.; Ghosh, D.; Pienta, K. J.; Sewalt, R.G. A. B.; Otte, A. P.; Rubin, M. A.; Chinnaiyan, A. M.: The polycombgroup protein EZH2 is involved in progression of prostate cancer. Nature 419:624- 629, 2002. 3 B c

GAM189 246 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 3 B b

GAM189 246 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 3 B b

GAM189 246 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 3 B b

GAM189 246 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998. 3 B b

GAM189 246 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985. 3 B c

GAM189 246 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985. 3 B c

GAM189 246 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988. 3 B c

GAM189 246 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional analysis of the human tissue factor promoter and inductionby serum. Proc. 3 B c

Nat. Acad. Sci. 87: 2254- 2258, 1990.

GAM189 246 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: 3 B c
Completesequence of the human tissue factor gene, a highly regulated
cellularreceptor that initiates the coagulation protease cascade.
Biochemistry 28:1755- 1762, 1989.

GAM189 246 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; 3 B c
Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand
mapping of RFLPs for human tissue factor (HTF) to chromosome 1p.
NucleicAcids Res. 15: 9098 only, 1987.

GAM189 246 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; 3 B c
Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA
sequenceand chromosome localization of the gene. Biochemistry 26: 5234-
5238,1987.

GAM189 246 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; 3 B c
Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA
clones coding for human tissue factor: primary structureof the protein and
cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987.

GAM189 246 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of 3 B c
tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad.
Sci. 94: 6922- 6926, 1997.

GAM189 246 FABP2 Baier, L. J.; Sacchettini, J. C.; Knowler, W. C.; Eads, J.; Paolisso,G.; 3 B c
Tataranni, P. A.; Mochizuki, H.; Bennett, P. H.; Bogardus, C.;Prochazka, M.:
An amino acid substitution in the human intestinalfatty acid binding protein
is associated with increased fatty acidbinding, increased fat oxidation, and
insulin resistance. J. Clin.Invest. 95: 1281- 1287, 1995.

GAM189 246 FABP2 Carlsson, M.; Orho- Melander, M.; Hedenbro, J.; Almgren, P.; Groop,L. C.: 3 B c
The T54 allele of the intestinal fatty acid- binding protein2 is associated
with a parental history of stroke. J. Clin. Endocr.Metab. 85: 2801- 2804,
2000.

GAM189 246 FABP2 Georgopoulos, A.; Aras, O.; Tsai, M. Y.: Codon- 54 polymorphismof the fatty 3 B c
acid- binding protein 2 gene is associated with elevationof fasting and
postprandial triglyceride in type 2 diabetes. J. Clin.Endocr. Metab. 85:
3155- 3160, 2000.

GAM189 246 FABP2 Hegele, R. A.; Harris, S. B.; Hanley, A. J. G.; Sadikian, S.; Connelly,P. 3 B c
W.; Zinman, B.: Genetic variation of intestinal fatty acid- bindingprotein
associated with variation in body mass in aboriginal Canadians. J.Clin.
Endocr. Metab. 81: 4334- 4337, 1996.

GAM189 246 FABP2 Polymeropoulos, M. H.; Rath, D. S.; Xiao, H.; Merril, C. R.: 3 B c
Trinucleotiderepeat polymorphism at the human intestinal fatty acid binding
proteingene (FABP2). Nucleic Acids Res. 18: 7198 only, 1991.

GAM189 246 FABP2 Prochazka, M.; Lillioja, S.; Tait, J. F.; Knowler, W. C.; Mott,D. M.; 3 B c
Spraul, M.; Bennett, P. H.; Bogardus, C.: Linkage of chromosomalmarkers on
4q with a putative gene determining maximal insulin actionin Pima Indians.
Diabetes 42: 514- 519, 1993.

GAM189 246 FABP2 Sipilainen, R.; Uusitupa, M.; Heikkinen, S.; Rissanen, A.; Laakso,M.: 3 B c
Variants in the human intestinal fatty acid binding protein 2gene in obese
subjects. J. Clin. Endocr. Metab. 82: 2629- 2632, 1997.

GAM189 246 FABP2 Sparkes, R. S.; Mohandas, T.; Heinzmann, C.; Gordon, J. I.; Klisak,I.; 3 B c
Zollman, S.; Sweetser, D. A.; Ragunathan, L.; Winokur, S.; Lusis,A. J.:
Human fatty acid binding protein assignments intestinal to4q28- 4q31 and

liver to 2p11. (Abstract) Cytogenet. Cell Genet. 46:697 only, 1987.

GAM189 246 FABP2 Sweetser, D. A.; Birkenmeier, E. H.; Klisak, I. J.; Zollman, S.;Sparkes, R. S.; Mohandas, T.; Lusis, A. J.; Gordon, J. I.: The humanand rodent intestinal fatty acid binding protein genes: a comparativeanalysis of their structure, expression, and linkage relationships. J.Biol. Chem. 262: 16060-16071, 1987. 3 B c

GAM189 246 FABP2 Weber, J. L.; Kwitek, A. E.; May, P. E.; Polymeropoulos, M.:Dinucleotide repeat polymorphism at the D12S43 locus. Nucleic AcidsRes. 18: 4637 only, 1990. 3 B c

GAM189 246 FABP2 Weber, J. L.; May, P. E.: Abundant class of human DNA polymorphismswhich can be typed using the polymerase chain reaction. Am. J. Hum.Genet. 44: 388-396, 1989. 3 B c

GAM189 246 FANCE Buchwald, M.: Complementation groups: one or more per gene? NatureGenet. 11: 228- 230, 1995. 3 B c

GAM189 246 FANCE de Winter, J. P.; Leveille, F.; van Berkel, C. G. M.; Rooimans,M. A.; van der Weel, L.; Steltenpool, J.; Demuth, I.; Morgan, N. V.;Alon, N.; Bosnoyan-Collins, L.; Lightfoot, J.; Leegwater, P. A.; Waisfisz,Q.; Komatsu, K.; Arwert, F.; Pronk, J. C.; Mathew, C. G.; Digweed,M.; Buchwald, M.; Joenje, H.: Isolation of a cDNA representing theFanconi anemia complementation group E gene. Am. J. Hum. Genet. 67:1306- 1308, 2000. Note: Erratum: Am. J. Hum. Genet. 67: 1365 only,2000. 3 B c

GAM189 246 FANCE Joenje, H.: Fanconi anaemia complementation groups in Germanyand The Netherlands. Hum. Genet. 97: 280- 282, 1996. 3 B c

GAM189 246 FANCE Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G.M.; Rooimans, M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J.J. P.; Buchwald, M.; Arwert, F.: Classification of Fanconi anemiapatients by complementation analysis: evidence for a fifth geneticsubtype. Blood 86: 2156- 2160, 1995. 3 B c

GAM189 246 FANCE Joenje, H.; Oostra, A. B.; Wijker, M.; di Summa, F. M.; van Berkel,C. G. M.; Rooimans, M. A.; Ebell, W.; van Weel, M.; Pronk, J. C.;Buchwald, M.; Arwert, F.: Evidence for at least eight Fanconi anemiagenes. Am. J. Hum. Genet. 61: 940- 944, 1997. 3 B c

GAM189 246 FANCE Pace, P.; Johnson, M.; Tan, W. M.; Mosedale, G.; Sng, C.; Hoatlin,M.; de Winter, J.; Joenje, H.; Gergely, F.; Patel, K. J.: FANCE:the link between Fanconi anaemia complex assembly and activity. EMBOJ. 21: 3414- 3423, 2002. 3 B c

GAM189 246 FANCE Waisfisz, Q.; Saar, K.; Morgan, N. V.; Altay, C.; Leegwater, P.A.; de Winter, J. P.; Komatsu, K.; Evans, G. R.; Wegner, R.- D.; Reis,A.; Joenje, H.; Arwert, F.; Mathew, C. G.; Pronk, J. C.; Digweed,M.: The Fanconi anemia group E gene, FANCE, maps to chromosome 6p. Am.J. Hum. Genet. 64: 1400-1405, 1999. 3 B c

GAM189 246 FANCE Wegner, R.- D.; Henrichs, I.; Joenje, H.; Schroeder- Kurth, T.:Fanconi anemia complementation group E: clinical and cytogenetic dataof the first patient. Clin. Genet. 50: 479- 482, 1996. 3 B c

GAM189 246 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995. 3 B c

GAM189 246 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 3 B c

GAM189 246 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: 3 B c
Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665-
1672, 1990.

GAM189 246 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. 3 B c
L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and
their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681-
1685, 1993.

GAM189 246 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, 3 B c
F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc
alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J.
Hum. Genet. 46: 694- 698, 2001.

GAM189 246 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing 3 B c
of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J.
318: 771- 777, 1996.

GAM189 246 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand 3 B c
characterization of the promoter for the gene encoding the humanmyeloid IgA
Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000.

GAM189 246 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin 3 B c
promoter region of Fc- alpha receptor gene in patients with IgAnephropathy.
Hum. Genet. 108: 128- 133, 2001.

GAM189 246 FCGR2A Grundy, H. O.; Peltz, G.; Barsh, G.; Moore, K.; Golbus, M. S.;Lebo, R. V.: 3 B c
Immunoglobulin G Fc receptor II and Fc receptor IIIgenes map to chromosome 1
by spot- blot chromosome analysis. (Abstract) Am.J. Hum. Genet. 43: A145,
1988.

GAM189 246 FCGR2A Grundy, H. O.; Peltz, G.; Moore, K. W.; Golbus, M. S.; Jackson,L. G.; Lebo, 3 B c
R. V.: The polymorphic Fc- gamma receptor II gene mapsto human chromosome
1q. Immunogenetics 29: 331- 339, 1989.

GAM189 246 FCGR2A Hibbs, M. L.; Bonadonna, L.; Scott, B. M.; McKenzie, I. F. C.;Hogarth, P. 3 B c
M.: Molecular cloning of a human immunoglobulin G Fcreceptor. Proc. Nat.
Acad. Sci. 85: 2240- 2244, 1988.

GAM189 246 FCGR2A Hibbs, M. L.; Hogarth, P. M.; McKenzie, I. F. C.: The mouse Ly- 17locus 3 B c
identifies a polymorphism of the Fc receptor. Immunogenetics 22:335- 348,
1985.

GAM189 246 FCGR2A Lebo, R. V.; Lynch, E. D.; Wiegant, J.; Moore, K.; Trounstine,M.; van der 3 B c
Ploeg, M.: Multicolor fluorescence in situ hybridizationand pulsed field
electrophoresis dissect CMT1B gene region. Hum.Genet. 88: 13- 20, 1991.

GAM189 246 FCGR2A Moser, K. L.; Neas, B. R.; Salmon, J. E.; Yu, H.; Gray- McGuire,C.; Asundi, 3 B c
N.; Bruner, G. R.; Fox, J.; Kelly, J.; Henshall, S.; Bacino,D.; Dietz, M.;
Hogue, R.; Koelsch, G.; Nightingale, L.; Shaver, T.;Abdou, N. I.; Albert, D.
A.; Carson, C.; Petri, M.; Treadwell, E.L.; James, J. A.; Harley, J. B.:
Genome scan of human systemic lupuserythematosus: evidence for linkage on
chromosome 1q in African- Americanpedigrees. Proc. Nat. Acad. Sci. 95:
14869- 14874, 1998.

GAM189 246 FCGR2A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on 3 B c
mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human
DNA. Hum. Molec. Genet. 1: 613- 620,1992.

GAM189 246 FCGR2A Peltz, G. A.; Grundy, H. O.; Lebo, R. V.; Yssel, H.; Barsh, G.S.; Moore, K. 3 B c
W.: Human Fc- gamma- RIII: cloning, expression, and identificationof the
chromosomal locus of two Fc receptors for IgG. Proc. Nat.Acad. Sci. 86:
1013- 1017, 1989.

GAM189 246 FCGR2A Qiu, W. Q.; de Bruin, D.; Brownstein, B. H.; Pearse, R.; Ravetch,J. V.: 3 B c
Organization of the human and mouse low- affinity Fc- gamma- Rgenes:
duplication and recombination. Science 248: 732- 735, 1990.

GAM189 246 FCGR2A Salmon, J. E.; Millard, S.; Schachter, L. A.; Arnett, F. C.; Ginzler,E. M.; 3 B c
Gourley, M. F.; Ramsey- Goldman, R.; Peterson, M. G. E.; Kimberly,R. P.: Fc-
gamma- RIIA alleles are heritable risk factors for lupusnephritis in African
Americans. J. Clin. Invest. 97: 1348- 1354,1996.

GAM189 246 FCGR2A Sammartino, L.; Webber, L. M.; Hogarth, P. M.; McKenzie, I. F.C.; Garson, O. 3 B c
M.: Assignment of the gene coding for human FcRII(CD32) to bands q23q24 on
chromosome 1. Immunogenetics 28: 380- 381,1988.

GAM189 246 FCGR2A Stein, M.- P.; Edberg, J. C.; Kimberly, R. P.; Mangan, E. K.; Bharadwaj,D.; 3 B c
Mold, C.; Du Clos, T. W.: C- reactive protein binding to Fc- gamma- RIIaon
human monocytes and neutrophils is allele- specific. J. Clin. Invest.
105:369- 376, 2000.

GAM189 246 FCGR2A Unkeless, J. C.: Function and heterogeneity of human Fc receptorsfor 3 B c
immunoglobulin G. J. Clin. Invest. 83: 355- 361, 1989.

GAM189 246 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 B b
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM189 246 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 B b
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22
suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci.
98: 10374- 10379, 2001.

GAM189 246 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome 3 B b
assignment by polymerase chain reaction techniques: assignmentof the
oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990.

GAM189 246 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator 3 B b
of the hair growth cycle: evidence from targeted and spontaneousmutations.
Cell 78: 1017- 1025, 1994.

GAM189 246 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 3 B b
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM189 246 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; 3 B b
Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and
the bcl.1 locus are contained within one megabase in bandq13 of chromosome
11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988.

GAM189 246 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes 3 B b
a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8:
3487- 3495, 1988.

GAM189 246 FHL2 Chan, K. K.; Tsui, S. K. W.; Lee, S. M. Y.; Luk, S. C. W.; Liew,C. C.; Fung, 3 B b
K. P.; Waye, M. M. Y.; Lee, C. Y.: Molecular cloningand characterization of
FHL2, a novel LIM domain protein preferentiallyexpressed in human heart.
Gene 210: 345- 350, 1998.

GAM189 246 FHL2 Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.- 3 B b
G.;Schafer, B. W.: Subtractive cloning and characterization of DRAL,a novel
LIM- domain protein down- regulated in rhabdomyosarcoma. DNACell Biol. 16:
433- 442, 1997.

GAM189 246 FHL2 Morgan, M. J.; Madgwick, A. J. A.: Slim defines a novel familyof LIM- 3 B b
proteins expressed in skeletal muscle. Biochem. Biophys. Res.Commun. 225:
632- 638, 1996.

GAM189 246 FHL2 Tanahashi, H.; Tabira, T.: Alzheimer's disease- associated presenilin2 interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9:2281-2289, 2000. 3 B b

GAM189 246 FOXO1A Anderson, M. J.; Shelton, G. D.; Cavenee, W. K.; Arden, K. C.:Embryonic expression of the tumor- associated PAX3- FKHR fusion proteininterferes with the developmental functions of Pax3. Proc. Nat. Acad.Sci. 98: 1589- 1594, 2001. 3 B c

GAM189 246 FOXO1A Anderson, M. J.; Viars, C. S.; Czekay, S.; Cavenee, W. K.; Arden,K. C.: Cloning and characterization of three human forkhead genesthat comprise an FKHR- like gene subfamily. Genomics 47: 187- 199,1998. 3 B c

GAM189 246 FOXO1A Barr, F. G.; Galili, N.; Holick, J.; Biegel, J. A.; Rovera, G.;Emanuel, B. S.: Rearrangement of the PAX3 paired box gene in thepaediatric solid tumor alveolar rhabdomyosarcoma. Nature Genet. 3:113- 117, 1993. 3 B c

GAM189 246 FOXO1A Davis, R. J.; Barr, F. G.: Fusion genes resulting from alternativechromosomal translocations are overexpressed by gene- specific mechanismsin alveolar rhabdomyosarcoma. Proc. Nat. Acad. Sci. 94: 8047-8051,1997. 3 B c

GAM189 246 FOXO1A Fredericks, W. J.; Galili, N.; Mukhopadhyay, S.; Rovera, G.; Bennicelli,J.; Barr, F. G.; Rauscher, F. J., III: The PAX3- FKHR fusion proteincreated by the t(2;13) translocation in alveolar rhabdomyosarcomasis a more potent transcriptional activator than PAX3. Molec. Cell.Biol. 15: 1522- 1535, 1995. 3 B c

GAM189 246 FOXO1A Galili, N.; Davis, R. J.; Fredericks, W. J.; Mukhopadhyay, S.;Rauscher, F. J., III; Emanuel, B. S.; Rovera, G.; Barr, F. G.: Fusionof a fork head domain gene to PAX3 in the solid tumour alveolar rhabdomyosarcoma. NatureGenet. 5: 230- 235, 1993. 3 B c

GAM189 246 FOXO1A Khan, J.; Bittner, M. L.; Saal, L. H.; Teichmann, U.; Azorsa, D.O.; Gooden, G. C.; Pavan, W. J.; Trent, J. M.; Meltzer, P. S.: cDNAmicroarrays detect activation of a myogenic transcription programby the PAX3- FKHR fusion oncogene. Proc. Nat. Acad. Sci. 96: 13264- 13269,1999. 3 B c

GAM189 246 FOXO1A Medema, R. H.; Kops, G. J. P. L.; Bos, J. L.; Burgering, B. M.T.: AFX- like forkhead transcription factors mediate cell- cycle regulationby Ras and PKB through p27(kip1). Nature 404: 782- 787, 2000. 3 B c

GAM189 246 FOXO1A Nakae, J.; Biggs, W. H., III; Kitamura, T.; Cavenee, W. K.; Wright,C. V. E.; Arden, K. C.; Accili, D.: Regulation of insulin actionand pancreatic beta-cell function by mutated alleles of the gene encodingforkhead transcription factor Foxo1. Nature Genet. 32: 245- 253,2002. 3 B c

GAM189 246 FOXO1A Scheidler, S.; Fredericks, W. J.; Rauscher, F. J., III; Barr,F. G.; Vogt, P. K.: The hybrid PAX3- FKHR fusion protein of alveolarrhabdomyosarcoma transforms fibroblasts in culture. Proc. Nat. Acad.Sci. 93: 9805- 9809, 1996. 3 B c

GAM189 246 FOXO1A Sublett, J. E.; Jeon, I- S.; Shapiro, D. N.: The alveolar rhabdomyosarcomaPAX3/FKHR fusion protein is a transcriptional activator. Oncogene 11:545- 552, 1995. 3 B c

GAM189 246 FOXO1A Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes Cancer 5: 299- 310, 1992. 3 B c

GAM189 246 FSHPRH1 Aittomaki, K.; Lucena, J. L. D.; Pakarinen, P.; Sistonen, P.; Tapanainen,J.; Gromoll, J.; Kaskikari, R.; Sankila, E.- M.; Lehvaslaiho, H.; Engel,A. R.; Nieschlag, E.; Huhtaniemi, I.; de la Chapelle, A.: Mutationin the follicle-stimulating hormone receptor gene causes hereditaryhypergonadotropic ovarian 3 B c

failure. Cell 82: 959- 968, 1995.

GAM189 246 FSHPRH1 Roberts, R. G.; Kendall, E.; Vetrie, D.; Bobrow, M.: Sequenceand chromosomal 3 B c
location of a human homologue of LRPR1, an FSH primaryresponse gene. Genomics 37: 122- 124, 1996.

GAM189 246 FSHPRH1 Slegtenhorst- Eegdeman, K. E.; Post, M.; Baarends, W. M.; Themmen,A. P. N.; 3 B c
Grootegoed, J. A.: Regulation of gene expression in Sertolicells by follicle- stimulating hormone (FSH): cloning and characterizationof LRPR1, a primary response gene encoding a leucine- rich protein. Molec.Cell. Endocr. 108: 115- 124, 1995.

GAM189 246 FZD4 Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.;Hirai, M.; 3 B c
Katoh, M.: Molecular cloning and characterization of humanfrizzled- 4 on chromosome 11q14- q21. Biochem. Biophys. Res. Commun. 264:955- 961, 1999.

GAM189 246 FZD4 Robitaille, J.; MacDonald, M. L. E.; Kaykas, A.; Sheldahl, L. C.;Zeisler, 3 B c
J.; Dube, M.- P.; Zhang, L.- H.; Singaraja, R. R.; Guernsey,D. L.; Zhang, B.; Siebert, L. F.; Hoskin- Mott, A.; Trese, M. T.; Pimstone,S. N.; Shastry, B. S.; Moon, R. T.; Hayden, M. R.; Goldberg, Y. P.;Samuels, M. E.: Mutant frizzled- 4 disrupts retinal angiogenesis infamilial exudative vitreoretinopathy. Nature Genet. 32: 326- 330,2002.

GAM189 246 G2A Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y.: 3 B c
Lysophosphatidylcholine as a ligand for the immunoregulatory receptorG2A. Science 293: 702- 705, 2001.

GAM189 246 G2A Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.;Harvill, E. 3 B c
T.; Jensen, E. R.; Miller, J. F.; Witte, O. N.: Micelacking the orphan G protein- coupled receptor G2A develop a late- onsetautoimmune syndrome. Immunity 14: 561- 571, 2001.

GAM189 246 G2A Weng, Z.; Fluckiger, A.- C.; Nisitani, S.; Wahl, M. I.; Le, L. Q.;Hunter, C. 3 B c
A.; Fernal, A. A.; le Beau, M. M.; Witte, O. N.: A DNAdamage and stress inducible G protein- coupled receptor blocks cellsin G2/M. Proc. Nat. Acad. Sci. 95: 12334- 12339, 1998.

GAM189 246 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; 3 B c
Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N- acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001.

GAM189 246 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme 3 B c
catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2- epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313- 24318,1997.

GAM189 246 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 B c

GAM189 246 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; 3 B c
Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997.

GAM189 246 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; 3 B c
Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase

gene (GNE). J. Hum. Genet. 47: 77- 79, 2002.

GAM189 246 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999. 3 B c

GAM189 246 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993. 3 B c

GAM189 246 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001. 3 B c

GAM189 246 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981. 3 B c

GAM189 246 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002. 3 B c

GAM189 246 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N- acetylglucosamine 2- epimerase gene define the disease sialuriaand the allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999. 3 B c

GAM189 246 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N-acetylneuraminic acid biosynthesis of rat liver: molecularcloning and functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N-acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997. 3 B c

GAM189 246 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989. 3 B c

GAM189 246 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987. 3 B c

GAM189 246 GPR4 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation of three novel human genes encoding G protein- coupledreceptors. DNA Cell Biol. 14: 25- 35, 1995. 3 B c

GAM189 246 GPR4 Mahadevan, M. S.; Baird, S.; Bailly, J. E.; Shutler, G. G.; Sabourin,L. A.; Tsilfidis, C.; Neville, C. E.; Narang, M.; Korneluk, R. G.: Isolation of a novel G protein- coupled receptor (GPR4) localizedto chromosome 19q13.3. Genomics 30: 84- 88, 1995. 3 B c

GAM189 246 GPR4 Ye, R. D.; Prossnitz, E. R.; Zou, A.; Cochrane, C. G.: Characterizationof a human cDNA that encodes a functional receptor for platelet activatingfactor. Biochem. Biophys. Res. Commun. 180: 105- 111, 1991. 3 B c

GAM189 246 GPR4 Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina,K. L.; Kabarowski, J. H. S.; Witte, O. N.; Xu, Y.: Sphingosylphosphorylcholineand lysophosphatidylcholine are ligands for the G protein- coupledreceptor GPR4. J. Biol. Chem. 276: 41325- 41335, 2001. 3 B c

GAM189 246 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a novel secretin- like human G- protein- coupledreceptor gene. Genomics 55: 296- 305, 1999. 3 B b

GAM189 246 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected 3 B b

with mRNA differential display using human melanoma celllines with different metastatic potential. FEBS Lett. 446: 292- 298,1999.

GAM189 246 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; 3 B b
Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann, S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in three cases of myelodysplastic syndrome/acutemyeloid leukemia with a deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000.

GAM189 246 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain- 3 B b
containingGTPase- activating protein for Rho and Cdc42 associates with focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996.

GAM189 246 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 B b
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM189 246 GRINL1A Roginski, R. S.; Mohan Raj, B. K.; Finkernagel, S. W.; Sciorra,L. J.: 3 B b
Assignment of an ionotropic glutamate receptor- like gene (GRINL1A)to human chromosome 15q22.1 by in situ hybridization. Cytogenet.Cell Genet. 93: 143- 144, 2001.

GAM189 246 GRINL1A Wydner, K. S.; Mohan Raj, B. K.; Sciorra, L. J.; Roginski, R. S.: The mouse 3 B b
orthologue of the human ionotropic glutamate receptor- likegene (GRINL1A) maps to mouse chromosome 9. Cytogenet. Cell Genet. 95:240- 241, 2001.

GAM189 246 GSTM1 Board, P. G.: Biochemical genetics of glutathione- S- transferasein man. Am. 3 B c
J. Hum. Genet. 33: 36- 43, 1981.

GAM189 246 GSTM1 Board, P.; Coggan, M.; Johnston, P.; Ross, V.; Suzuki, T.; Webb,G.: Genetic 3 B c
heterogeneity of the human glutathione transferases:a complex of gene families. Pharm. Therap. 48: 357- 369, 1990.

GAM189 246 GSTM1 Chen, C.- L.; Liu, Q.; Relling, M. V.: Simultaneous characterizationof 3 B c
glutathione S- transferase M1 and T1 polymorphisms by polymerasechain reaction in American whites and blacks. Pharmacogenetics 6:187- 191, 1996.

GAM189 246 GSTM1 DeJong, J. L.; Chang, C.- M.; Whang- Peng, J.; Knutsen, T.; Tu, C.- P.D.: 3 B c
The human liver glutathione S- transferase gene superfamily: expressionand chromosome mapping of an H(b) subunit cDNA. Nucleic Acids Res. 16:8541- 8554, 1988.

GAM189 246 GSTM1 DeJong, J. L.; Mohandas, T.; Tu, C.- P. D.: The human H(b) (mu)class 3 B c
glutathione S- transferases are encoded by a dispersed gene family. Biochem.Biophys. Res. Commun. 180: 15- 22, 1991.

GAM189 246 GSTM1 Godschalk, R. W. L.; Dallinga, J. W.; Wikman, H.; Risch, A.; Kleinjans,J. C. 3 B c
S.; Bartsch, H.; Van Schooten, F.- J.: Modulation of DNA andprotein adducts in smokers by genetic polymorphisms in GSTM1, GSTT1,NAT1 and NAT2. Pharmacogenetics 11: 389- 398, 2001.

GAM189 246 GSTM1 Harada, S.; Abei, M.; Tanaka, N.; Agarwal, D. P.; Goedde, H. W.: Liver 3 B c
glutathione S- transferase polymorphism in Japanese and itspharmacogenetic importance. Hum. Genet. 75: 322- 325, 1987.

GAM189 246 GSTM1 Islam, M. Q.; Platz, A.; Szpirer, J.; Szpirer, C.; Levan, G.; Mannervik,B.: 3 B c
Chromosomal localization of human glutathione transferase genesof classes alpha, mu and pi. Hum. Genet. 82: 338- 342, 1989.

GAM189 246 GSTM1 Lee, K. A.; Kim, S. H.; Woo, H. Y.; Hong, Y. J.; Cho, H. C.: 3 B c
Increasedfrequencies of glutathione S- transferase (GSTM1 and GSTT1) gene deletionsin Korean patients with acquired aplastic anemia. Blood 98: 3483-

3485,2001.

GAM189 246 GSTM1 Mannervik, B.: The isozymes of glutathione transferase. Adv.Enzym. Relat. 3 B c
Areas Molec. Biol. 57: 357- 417, 1985.

GAM189 246 GSTM1 Mannervik, B.; Awasthi, Y. C.; Board, P. G.; Hayes, J. D.; Dillio, C.; 3 B c
Ketterer, B.; Listowsky, I.; Morgenstern, R.; Muramatsu,M.; Pearson, W. R.;
Pickett, C. B.; Sato, K.; Widersten, M.; Wolf,R. C.: Nomenclature for human
glutathione transferases. (Letter) Biochem.J. 282: 305- 306, 1992.

GAM189 246 GSTM1 McLellan, R. A.; Oscarson, M.; Alexandrie, A.- K.; Seidegard, J.;Evans, D. 3 B c
A. P.; Rannug, A.; Ingelman- Sundberg, M.: Characterizationof a human
glutathione S- transferase mu cluster containing a duplicatedGSTM1 gene that
causes ultrarapid enzyme activity. Molec. Pharm. 52:958- 965, 1997.

GAM189 246 GSTM1 Pearson, W. R.; Vorachek, W. R.; Xu, S.; Berger, R.; Hart, I.;Vannais, D.; 3 B c
Patterson, D.: Identification of class- mu glutathionetransferase genes
GSTM1- GSTM5 on human chromosome 1p13. Am. J. Hum.Genet. 53: 220- 233, 1993.

GAM189 246 GSTM1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 B c
New York: Oxford Univ. Press (pub.) 1988.

GAM189 246 GSTM1 Scott, E. M.; Wright, R. C.: Variability of glutathione S- transferaseof 3 B c
human erythrocytes. Am. J. Hum. Genet. 32: 115- 117, 1980.

GAM189 246 GSTM1 Seidegard, J.; Pero, R. W.; Markowitz, M. M.; Roush, G.; Miller,D. G.; 3 B c
Beattie, E. J.: Isoenzyme(s) of glutathione transferase (classmu) as a
marker for the susceptibility to lung cancer: a follow upstudy.
Carcinogenesis 11: 33- 36, 1990.

GAM189 246 GSTM1 Seidegard, J.; Pero, R. W.; Miller, D. G.; Beattie, E. J.: Aglutathione 3 B c
transferase in human leukocytes as a marker for the susceptibilityto lung
cancer. Carcinogenesis 7: 751- 753, 1986.

GAM189 246 GSTM1 Seidegard, J.; Vorachek, W. R.; Pero, R. W.; Pearson, W. R.:Hereditary 3 B c
differences in the expression of the human glutathionetransferase active on
trans- stilbene oxide are due to a gene deletion. Proc.Nat. Acad. Sci. 85:
7293- 7297, 1988.

GAM189 246 GSTM1 Strange, R. C.; Davis, B. A.; Faulder, C. G.; Cotton, W.; Bain,A. D.; 3 B c
Hopkinson, D. A.; Hume, R.: The human glutathione S-
transferases:developmental aspects of the GST1, GST2, and GST3 loci.
Biochem.Genet. 23: 1011- 1028, 1985.

GAM189 246 GSTM1 Strange, R. C.; Faulder, C. G.; Davis, B. A.; Hume, R.; Brown,J. A. H.; 3 B c
Cotton, W.; Hopkinson, D. A.: The human glutathione S- transferases:studies
on the tissue distribution and genetic variation of the GST1,GST2 and GST3
isozymes. Ann. Hum. Genet. 48: 11- 20, 1984.

GAM189 246 GSTM1 Strange, R. C.; Matharoo, B.; Faulder, G. C.; Jones, P.; Cotton,W.; Elder, 3 B c
J. B.; Deakin, M.: The human glutathione S- transferases:a case- control
study of the incidence of the GST1 0 phenotype in patientswith
adenocarcinoma. Carcinogenesis 12: 25- 28, 1991.

GAM189 246 GSTM1 van Poppel, G.; de Vogel, N.; van Bladeren, P. J.; Kok, F. J.: Increased 3 B c
cytogenetic damage in smokers deficient in glutathioneS- transferase isozyme
mu. Carcinogenesis 13: 303- 305, 1992.

GAM189 246 GSTM1 Xu, S.; Wang, Y.; Roe, B.; Pearson, W. R.: Characterization ofthe human 3 B c
class mu glutathione S- transferase gene cluster and theGSTM1 deletion. J.
Biol. Chem. 273: 3517- 3527, 1998.

GAM189 246 GSTM1 Zhong, S.; Wolf, C. R.; Spurr, N. K.: Chromosomal assignmentand linkage 3 B c
analysis of the human glutathione S- transferase mu- gene(GSTM1) using
intron specific polymerase chain reaction. Hum. Genet. 90:435- 439, 1992.

GAM189 246 GSTM1 Zhong, S.; Wyllie, A. H.; Barnes, D.; Wolf, C. R.; Spurr, N. K.: 3 B c
Relationship between the GSTM1 genetic polymorphism and susceptibilityto
bladder, breast and colon cancer. Carcinogenesis 14: 1821- 1824,1993.

GAM189 246 GSTM4 Comstock, K. E.; Johnson, K. J.; Rifenbery, D.; Henner, W. D.:Isolation and 3 B c
analysis of the gene and cDNA for a human mu class glutathioneS-
transferase, GSTM4. J. Biol. Chem. 268: 16958- 16965, 1993.

GAM189 246 GSTM4 Ross, V. L.; Board, P. G.: Molecular cloning and heterologousexpression of 3 B c
an alternatively spliced human mu class glutathioneS- transferase
transcript. Biochem. J. 294: 373- 380, 1993.

GAM189 246 GSTM4 Ross, V. L.; Board, P. G.; Webb, G. C.: Chromosomal mapping ofthe human mu 3 B c
class glutathione S- transferases to 1p13. Genomics 18:87- 91, 1993.

GAM189 246 GSTM4 Taylor, J. B.; Oliver, J.; Sherrington, R.; Pemble, S. E.: Structureof human 3 B c
glutathione S- transferase class mu genes. Biochem. J. 274:587- 593, 1991.

GAM189 246 GYG Barbetti, F.; Rocchi, M.; Bossolasco, M.; Cordera, R.; Sbraccia,P.; Finelli, 3 B b
P.; Consalez, G. G.: The human skeletal muscle glycogeningene: cDNA, tissue
expression, and chromosomal localization. Biochem.Biophys. Res. Commun. 220:
72- 77, 1996.

GAM189 246 GYG Lomako, J.; Mazuruk, K.; Lomako, W. M.; Alonso, M. D.; Whelan,W. J.; 3 B b
Rodriguez, I. R.: The human intron- containing gene for glycogeninmaps to
chromosome 3, band q24. Genomics 33: 519- 522, 1996.

GAM189 246 GYG Mu, J.; Skurat, A. V.; Roach, P. J.: Glycogenin- 2, a novel self- 3 B b
glucosylatingprotein involved in liver glycogen biosynthesis. J. Biol. Chem.
272:27589- 27597, 1997.

GAM189 246 GYG Viskupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; DePaoli- Roach, A.A.; Roach, P. 3 B b
J.: Rabbit skeletal muscle glycogenin. Molecular cloningand production of
fully functional protein in Escherichia coli. J.Biol. Chem. 267: 25759-
25763, 1992.

GAM189 246 HEPH Anderson, G. J.; Murphy, T. L.; Cowley, L.; Evans, B. A.; Halliday,J. W.; 3 B c
McLaren, G. D.: Mapping the gene for sex- linked anemia: aninherited defect
of intestinal iron absorption in the mouse. Genomics 48:34- 39, 1998.

GAM189 246 HEPH Bannerman, R. M.: Genetic defects of iron transport. Fed. Proc. 35:2281- 3 B c
2285, 1976.

GAM189 246 HEPH Edwards, J. A.; Hoke, J. E.; Mattioli, M.; Reichlin, M.: 3 B c
Ferritindistribution and synthesis in sex- linked anemia. J. Lab. Clin. Med.
90:68- 76, 1977.

GAM189 246 HEPH Falconer, D. S.; Isaacson, J. H.: The genetics of sex- linked anaemiain the 3 B c
mouse. Genet. Res. 3: 248- 250, 1962.

GAM189 246 HEPH Grewal, M. S.: A sex- linked anaemia in the mouse. Genet. Res. 3:238- 247, 3 B c
1962.

GAM189 246 HEPH Lee, G. R.; Nacht, S.; Lukens, J. N.; Cartwright, G. E.: Ironmetabolism in 3 B c
copper- deficient swine. J. Clin. Invest. 47: 2058- 2069,1968.

GAM189 246 HEPH Vulpe, C. D.; Kuo, Y.- M.; Murphy, T. L.; Cowley, L.; Askwith, C.;Libina, 3 B c
N.; Gitschier, J.; Anderson, G. J.: Hephaestin, a ceruloplasminhomologue
implicated in intestinal iron transport, is defective inthe sla mouse.
Nature Genet. 21: 195- 199, 1999.

GAM189 246 HTR1D Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S. J.; Duncan,A. M. V.; 3 B c
Rozmahel, R.; Yang, Y.; Mengod, G.; Palacios, J. M.; O'Dowd,B. F.:
Characterization of the human 5- hydroxytryptamine(1B) receptor. J.Biol.
Chem. 267: 5735- 5738, 1992.

GAM189 246 HTR1D Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 B c
M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor,
and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991.

GAM189 246 HTR1D Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T.A.; Hartig, P. 3 B c
R.: Human serotonin 1D receptor is encoded by a subfamilyof two distinct
genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat.Acad. Sci. 89: 3630-
3634, 1992.

GAM189 246 HTR1D Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; 3 B c
Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and
genome organization of mammalian G- protein- coupled receptors. Genomics
18:175- 184, 1993.

GAM189 246 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human 3 B c
homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of
homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster.
Genomics 54: 424- 436, 1998.

GAM189 246 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol- 3 B c
Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay.
Genomics 54: 278- 286, 1998.

GAM189 246 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved 3 B c
fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated
in response to DNA damage. EMBO J. 17: 2055- 2066,1998.

GAM189 246 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe 3 B c
Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol.
Chem. 274: 567- 570, 1999.

GAM189 246 ICAM1 Ballantyne, C. M.; Kozak, C. A.; O'Brien, W. E.; Beaudet, A. L.: Assignment 3 B c
of the gene for intercellular adhesion molecule- 1 (Icam- 1)to proximal
mouse chromosome 9. Genomics 9: 547- 550, 1991.

GAM189 246 ICAM1 Bella, J.; Kolatkar, P. R.; Marlor, C. W.; Greve, J. M.; Rossmann,M. G.: The 3 B c
structure of the two amino- terminal domains of human ICAM- 1suggests how it
functions as a rhinovirus receptor and as an LFA- 1integrin ligand. Proc.
Nat. Acad. Sci. 95: 4140- 4145, 1998.

GAM189 246 ICAM1 Bellamy, R.; Kwiatkowski, D.; and Hill, A. V. S.: Absence of anassociation 3 B c
between intercellular adhesion molecule 1, complementreceptor 1 and
interleukin 1 receptor antagonist gene polymorphismsand severe malaria in a
West African population. Trans. R. Soc. Trop.Med. Hyg. 92: 312- 316, 1998.

GAM189 246 ICAM1 Craig, A.; Fernandez- Reyes, D.; Mesri, M.; McDowall, A.; Altieri,D. C.; 3 B c
Hogg, N.; Newbold, C.: A functional analysis of a naturalvariant of
intercellular adhesion molecule- 1 (ICAM- 1- Kilifi). Hum.Molec. Genet. 9:
525- 530, 2000.

GAM189 246 ICAM1 Fernandez- Reyes, D.; Craig, A. G.; Kyes, S. A.; Peshu, N.; Snow,R. W.; 3 B c
Berendt, A. R.; Marsh, K.; Newbold, C. I.: A high frequencyAfrican coding
polymorphism in the N- terminal domain of ICAM- 1 predisposingto cerebral
malaria in Kenya. Hum. Molec. Genet. 6: 1357- 1360, 1997.

GAM189 246 ICAM1 Greve, J. M.; Davis, G.; Meyer, A. M.; Forte, C. P.; Yost, S. C.;Marlor, C. 3 B c
W.; Kamarck, M. E.; McClelland, A.: The major human rhinovirusreceptor is
ICAM- 1. Cell 56: 839- 847, 1989.

GAM189 246 ICAM1 Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. 3 B c
Phys. 111: 272- 277, 1999.

GAM189 246 ICAM1 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, 3 B c
M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B

cells. Europ. J. Immun. 15: 103- 106, 1985.

GAM189 246 ICAM1 Le Beau, M. M.; Ryan, D., Jr.; Pericak- Vance, M. A.: Report ofthe committee 3 B c
on the genetic constitution of chromosomes 18 and 19. Cytogenet.Cell Genet.
51: 338- 357, 1989.

GAM189 246 ICAM1 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in 3 B c
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM189 246 ICAM1 Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot- 3 B c
Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow
cytometricanalysis of conjunctival epithelium in ocular rosacea and
keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000.

GAM189 246 ICAM1 Prieto, J.; Takei, F.; Gendelman, R.; Christenson, B.; Biberfeld,P.; 3 B c
Patarroyo, M.: MALA- 2, mouse homologue of human adhesion moleculeICAM- 1
(CD54). Europ. J. Immun. 19: 1551- 1557, 1989.

GAM189 246 ICAM1 Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal 3 B c
mouse chromosome 9 linkage map that further defines linkagegroups homologous
with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685,
1991.

GAM189 246 ICAM1 Simmons, D.; Makgoba, M. W.; Seed, B.: ICAM, an adhesion ligandof LFA- 1, is 3 B c
homologous to the neural cell adhesion molecule NCAM. Nature 331:624- 627,
1988.

GAM189 246 ICAM1 Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H.K.; Smith, C. 3 B c
W.; Bradley, A.; Beaudet, A. L.: Inflammatory and immuneresponses are
impaired in mice deficient in intercellular adhesionmolecule 1. Proc. Nat.
Acad. Sci. 90: 8529- 8533, 1993.

GAM189 246 ICAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 B c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM189 246 ICAM1 Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; 3 B c
Takeuchi, T.: Regulation of human leukocyte antigenexpression in human
conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999.

GAM189 246 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 B c
M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like
growth factor- I and cognitive function inhealthy older men. J. Clin.
Endocr. Metab. 84: 471- 475, 1999.

GAM189 246 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- 3 B c
like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993.

GAM189 246 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and 3 B c
absence of association with stature among African Pygmies. Hum.Genet. 85:
349- 354, 1990.

GAM189 246 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for 3 B c
insulin- like growth factors I and II and for epidermalgrowth factor in man.
(Abstract) Am. J. Hum. Genet. 36: 133S only,1984.

GAM189 246 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of 3 B c
genes for insulin- like growth factors I and II and epidermalgrowth factor.
Nature 310: 781- 784, 1984.

GAM189 246 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, 3 B c
A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of
recombinant human insulin- like growth factor I(IGF- I) therapy on the

growth hormone- IGF system of a patient witha partial IGF- I gene deletion. J. Clin. Endocr. Metab. 84: 1611- 1616,1999.

GAM189 246 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of the growth hormone receptor in children with idiopathicshort stature. New Eng. J. Med. 333: 1093- 1098, 1995. 3 B c

GAM189 246 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; Froesch, E. R.: Small stature and insulin- like growth factors:prolonged treatment of mini- poodles with recombinant human insulin- likegrowth factor I. Acta Endocr. 121: 456- 464, 1989. 3 B c

GAM189 246 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating concentrations of insulin- like growth factor- I and riskof breast cancer. Lancet 351: 1393- 1396, 1998. 3 B c

GAM189 246 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding protein- 3, and prostate- specific antigen as predictorsof clinical prostate cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000. 3 B c

GAM189 246 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith, D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival signaling in retinal endothelial cells: direct correlationwith clinical retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001. 3 B c

GAM189 246 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer prevention. Lancet 351: 1373- 1375, 1998. 3 B c

GAM189 246 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J. S.: The human gene encoding insulin- like growthfactor I is located on chromosome 12. Hum. Genet. 69: 157- 160, 1985. 3 B c

GAM189 246 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990. 3 B c

GAM189 246 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986. 3 B c

GAM189 246 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF- 1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996. 3 B c

GAM189 246 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat. Acad. Sci. 80: 2216- 2220, 1983. 3 B c

GAM189 246 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand implications for cell type- specific growth. Nature 364: 208- 213,1993. 3 B c

GAM189 246 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: Mice carrying null mutations of the genes encoding insulin- likegrowth factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993. 3 B c

GAM189 246 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like 3 B c

growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83: 9343- 9347, 1986.

GAM189 246 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human genes for insulin- like growth factors I and II and epidermalgrowth factor are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively. Cytogenet.Cell Genet. 41: 245- 249, 1986. 3 B c

GAM189 246 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2 (IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985. 3 B c

GAM189 246 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. D.: Growth characteristics and response to growth hormonetherapy in patients with hypochondroplasia: genetic linkage of theinsulin- like growth factor I gene at chromosome 12q23 to the diseasein a subgroup of these patients. Clin. Endocr. 34: 265- 274, 1991. 3 B c

GAM189 246 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999. 3 B c

GAM189 246 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene expression sustains hypertrophy and regeneration insenescent skeletal muscle. Nature Genet. 27: 195- 200, 2001. 3 B c

GAM189 246 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like growth factor 1 regulates the location, stability,and transcriptional activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000. 3 B c

GAM189 246 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993. 3 B c

GAM189 246 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the protein which binds insulin- like growth factor in human serum. Europ.J. Biochem. 172: 421- 425, 1988. 3 B c

GAM189 246 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith, R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the insulin- like growth factor I receptor and its ligandin relation to type 2 diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000. 3 B c

GAM189 246 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986. 3 B c

GAM189 246 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I) reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991. 3 B c

GAM189 246 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999. 3 B c

GAM189 246 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980. 3 B c

GAM189 246 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 3 B c

1991.

GAM189 246 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984. 3 B c

GAM189 246 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984. 3 B c

GAM189 246 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984. 3 B c

GAM189 246 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-857,1992. 3 B c

GAM189 246 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002. 3 B c

GAM189 246 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980. 3 B c

GAM189 246 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999. 3 B c

GAM189 246 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy on body composition and insulin resistance in IGF- Igene deletion. J. Clin. Endocr. Metab. 85: 1407- 1411, 2000. 3 B c

GAM189 246 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: Intrauterine growth retardation and postnatal growth failureassociated with deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335: 1363- 1367, 1996. 3 B c

GAM189 246 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub-regional localization of human genes for insulin- like growthfactors I (IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell Genet. 40: 782 only, 1985. 3 B c

GAM189 246 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like growth factors and bone mineral density in African Americanand white girls. J. Pediat. 137: 826- 832, 2000. 3 B c

GAM189 246 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997. 3 B c

GAM189 246 IGLL1 Kudo, A.; Melchers, F.: A second gene, Vpre- B in the lambda 5locus of the mouse, which appears to be selectively expressed in pre- Blymphocytes. EMBO J. 6: 2267- 2272, 1987. 3 B c

GAM189 246 IGLL1 Mattei, M.- G.; Fumoux, F.; Roeckel, N.; Fougereau, M.; Schiff,C.: The human pre- B- specific lambda- like cluster is located in the22q11.2- 22q12.3 3 B c

region, distal to the IgC- lambda locus. Genomics 9:544- 546, 1991.

GAM189 246 IGLL1 Minegishi, Y.; Coustan- Smith, E.; Wang, Y.- H.; Cooper, M. D.; Campana,D.; 3 B c
Conley, M. E.: Mutations in the human lambda- 5/14.1 gene resultin B cell
deficiency and agammaglobulinemia. J. Exp. Med. 187: 71- 77,1998.

GAM189 246 IGLL1 Pillai, S.; Baltimore, D.: The omega and iota surrogate immunoglobulinlight 3 B c
chains. Curr. Top. Microbiol. Immun. 137: 136- 139, 1988.

GAM189 246 IGLL1 Sakaguchi, N.; Melchers, F.: Lambda 5, a new light- chain- relatedlocus 3 B c
selectively expressed in pre- B lymphocytes. Nature 324: 579- 582,1986.

GAM189 246 IGLL1 Schiff, C.; Milili, M.; Fougereau, M.: Isolation of early 3 B c
immunoglobulinlambda- like gene transcripts in human fetal liver. Europ. J.
Immun. 19:1873- 1878, 1989.

GAM189 246 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 B b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM189 246 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 B b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM189 246 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 B b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814-
819, 1992.

GAM189 246 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 B b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang,
Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell-
derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87:
7512- 7516, 1990.

GAM189 246 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 3 B b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract)
Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM189 246 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, 3 B b
sequence, expression, and processing of the interleukin 16precursor. Proc.
Nat. Acad. Sci. 94: 5273- 5277, 1997.

GAM189 246 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 3 B b
381: 30 only, 1996.

GAM189 246 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 3 B b
16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics
49:704- 706, 1999.

GAM189 246 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. 3 B b
C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte
chemoattractant factor: association of biologic functionwith CD4 expression.
Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994.

GAM189 246 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human 3 B b
lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128:
2569- 2574, 1982.

GAM189 246 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS 3 B b
human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311-
314, 1993.

GAM189 246 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; 3 B b
Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M.
E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945-
1954, 1995.

GAM189 246 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; 3 B b
Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure

and function between human and murine IL- 16. J. Immun. 160:5945- 5954, 1998.

GAM189 246 IL21R Asao, H.; Okuyama, C.; Kumaki, S.; Ishii, N.; Tsuchiya, S.; Foster,D.; Sugamura, K.: Cutting edge: the common gamma- chain is an indispensablesubunit of the IL- 21 receptor complex. J. Immun. 167: 1- 5, 2001. 3 B c

GAM189 246 IL21R Kasaian, M. T.; Whitters, M. J.; Carter, L. L.; Lowe, L. D.; Jussif,J. M.; Deng, B.; Johnson, K. A.; Witek, J. S.; Senices, M.; Konz,R. F.; Wurster, A. L.; Donaldson, D. D.; Collins, M.; Young, D. A.;Grusby, M. J.: IL- 21 limits NK cell responses and promotes antigen- specificT cell activation: a mediator of the transition from innate to adaptiveimmunity. Immunity 16: 559- 569, 2002. 3 B c

GAM189 246 IL21R Ozaki, K.; Kikly, K.; Michalovich, D.; Young, P. R.; Leonard, W.J.: Cloning of a type I cytokine receptor most related to the IL- 2receptor beta chain. Proc. Nat. Acad. Sci. 97: 11439- 11444, 2000. 3 B c

GAM189 246 IL21R Parrish- Novak, J.; Dillon, S. R.; Nelson, A.; Hammond, A.; Sprecher,C.; Gross, J. A.; Johnston, J.; Madden, K.; Xu, W.; West, J.; Schrader,S.; Burkhead, S.; and 26 others: Interleukin 21 and its receptorare involved in NK cell expansion and regulation of lymphocyte function. Nature 408:57- 63, 2000. 3 B c

GAM189 246 IL21R Ueda, C.; Akasaka, T.; Kurata, M.; Maesako, Y.; Nishikori, M.;Ichinohasama, R.; Imada, K.; Uchiyama, T.; Ohno, H.: The gene forinterleukin- 21 receptor is the partner of BCL6 in t(13;16)(q27;p11),which is recurrently observed in diffuse large B- cell lymphoma. Oncogene 21:368- 376, 2002. 3 B c

GAM189 246 IL5RA Geijsen, N.; Uings, I. J.; Pals, C.; Armstrong, J.; McKinnon, M.;Raaijmakers, J. A. M.; Lammers, J.- W. J.; Koenderman, L.; Coffer,P. J.: Cytokine- specific transcriptional regulation through an IL- 5R- alphainteracting protein. Science 293: 1136- 1138, 2001. 3 B c

GAM189 246 IL5RA Gough, N. M.; Rakar, S.: Localization of the IL- 5 receptor geneto the distal half of murine chromosome 6 using recombinant inbredstrains of mice. Genomics 12: 855- 856, 1992. 3 B c

GAM189 246 IL5RA Isobe, M.; Kumura, Y.; Murata, Y.; Takaki, S.; Tominaga, A.; Takatsu,K.; Ogita, Z.: Localization of the gene encoding the alpha subunitof human interleukin- 5 receptor (IL5RA) to chromosome region 3p24- 3p26. Genomics 14:755- 758, 1992. 3 B c

GAM189 246 IL5RA Jacob, C. O.; Mykytyn, K.; Varcony, T.; Drabkin, H. A.: Mappingof the interleukin 5 receptor gene to human chromosome 3p25- p26 andto mouse chromosome 6 close to the Raf- 1 locus with polymorphic tandemrepeat sequences. Mammalian Genome 4: 435- 439, 1993. 3 B c

GAM189 246 IL5RA Sun, Z.; Yergeau, D. A.; Tuypens, T.; Tavernier, J.; Paul, C. C.;Baumann, M. A.: Tenen, D. G.; Ackerman, S. J.: Identification andcharacterization of a functional promoter region in the human eosinophilIL- 5 receptor alpha subunit gene. J. Biol. Chem. 270: 1462- 1471,1995. 3 B c

GAM189 246 IL5RA Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden,J.; Fiers, W.; Plaetinck, G.: A human high affinity interleukin- 5receptor (IL5R) is composed of an IL5- specific alpha chain and a betachain shared with the receptor for GM- CSF. Cell 66: 1175- 1184, 1991. 3 B c

GAM189 246 IL5RA Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.;Devos, R.: Molecular basis of the membrane- anchored and two solubleisoforms of the human interleukin 5 receptor alpha subunit. Proc.Nat. Acad. Sci. 89: 7041- 3 B c

7045, 1992.

GAM189 246 IL5RA Zhang, J.; Kuvelkar, R.; Cheewatrakoolpong, B.; Williams, S.; Egan,R. W.; 3 B c
Billah, M. M.: Evidence for multiple promoters of the humanIL- 5 receptor
alpha subunit gene: a novel 6- base pair element determinescell- specific
promoter function. J. Immun. 15: 5412- 5421, 1997.

GAM189 246 JRK Morita, R.; Miyazaki, E.; Fong, C. G.; Chen, X.- N.; Korenberg,J. R.; 3 B b
Delgado- Escueta, A. V.; Yamakawa, K.: JH8, a gene highly homologousto the
mouse jerky gene, maps to the region for childhood absenceepilepsy on 8q24.
Biochem. Biophys. Res. Commun. 248: 307- 314, 1998.

GAM189 246 JRK Toth, M.; Grimsby, J.; Buzsaki, G.; Donovan, G. P.: Epilepticseizures caused 3 B b
by inactivation of a novel gene, jerky, related tocentromere binding
protein- B in transgenic mice. Nature Genet. 11:71- 75, 1995. Note: Erratum:
Nature Genet. 12: 110 only, 1996.

GAM189 246 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel 3 B
b
genes. Trends Pharm. Sci. 14: 434, 1993.

GAM189 246 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; 3 B b
Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe
pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011-
1017, 1996.

GAM189 246 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; 3 B b
Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an
inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166-
1170, 1995.

GAM189 246 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: 3 B b
Targeted overactivity of beta cell KATP channels induces profoundneonatal
diabetes. Cell 100: 645- 654, 2000.

GAM189 246 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: 3 B b
Homozygositymapping, to chromosome 11p, of the gene for familial persistent
hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421,
1995.

GAM189 246 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward 3 B b
rectifier Kir6.2 also leads to familial persistent
hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812,
1996.

GAM189 246 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, 3 B b
T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium
channels in hypoxia- induced generalized seizure. Science 292:1543- 1546,
2001.

GAM189 246 KLRD1 Braud, V. M.; Allan, D. S. J.; O'Callaghan, C. A.; Soderstrom,K.; D'Andrea, 3 B c
A.; Ogg, G. S.; Lazetic, S.; Young, N. T.; Bell, J.I.; Phillips, J. H.;
Lanier, L. L.; McMichael, A. J.: HLA- E bindsto natural killer cell
receptors CD94/NKG2A, B and C. Nature 391:795- 799, 1998.

GAM189 246 KLRD1 Chang, C.; Rodriguez, A.; Carretero, M.; Lopez- Botet, M.; Phillips,J. H.; 3 B c
Lanier, L. L.: Molecular characterization of human CD94: atype II membrane
glycoprotein related to the C- type lectin superfamily. Europ.J. Immun. 25:
2433- 2437, 1995.

GAM189 246 KLRD1 Lazetic, S.; Chang, C.; Houchins, J. P.; Lanier, L. L.; Phillips,J. H.: 3 B c
Human natural killer cell receptors involved in MHC classI recognition are
disulfide- linked heterodimers of CD94 and NKG2 subunits. J.Immun. 157:

4741- 4745, 1996.

GAM189 246 KLRD1 Plougastel, B.; Trowsdale, J.: Sequence analysis of a 62- kb regionoverlapping the human KLRC cluster of genes. Genomics 49: 193-199,1998. 3 B c

GAM189 246 KLRD1 Rodriguez, A.; Carretero, M.; Glienke, J.; Bellon, T.; Ramirez,A.; Lehrach, H.; Francis, F.; Lopez- Botet, M.: Structure of the humanCD94 C- type lectin gene. Immunogenetics 47: 305- 309, 1998. 3 B c

GAM189 246 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; Malherbe, P.: Cloning and functional expression of human kynurenine3-monooxygenase. FEBS Lett. 410: 407- 412, 1997. 3 B b

GAM189 246 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001. 3 B b

GAM189 246 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000. 3 B c

GAM189 246 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000. 3 B c

GAM189 246 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363-18367,1996. 3 B b

GAM189 246 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994. 3 B b

GAM189 246 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. Nature 384: 39- 43, 1996. 3 B b

GAM189 246 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell-specifictranscriptional regulation of human leukotriene B4 receptor gene. J.Exp. Med. 192: 413- 420, 2000. 3 B b

GAM189 246 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative chemoattractant receptor. Genomics 37: 187- 194, 1996. 3 B b

GAM189 246 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: Leukotrienes and lipoxins: structures, biosynthesis,and biological effects. Science 237: 1171- 1176, 1987. 3 B b

GAM189 246 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997. 3 B b

GAM189 246 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein-coupled receptor for leukotriene B4 that mediates chemotaxis. Nature 387:620- 624, 1997. 3 B b

GAM189 246 LYZ Camara, V. M.; Harding, J. W.; Prieur, D. J.: Inherited lysozymedeficiency 3 B b

in rabbits: the absence of a primary isozyme of lysozymeas the cause of the condition. Lab. Invest. 63: 544- 550, 1990.

GAM189 246 LYZ Canet, D.; Sunde, M.; Last, A. M.; Miranker, A.; Spencer, A.; Robinson,C. V.; Dobson, C. M.: Mechanistic studies of the folding of humanlysozyme and the origin of amyloidogenic behavior in its disease- relatedvariants. Biochemistry 38: 6419- 6427, 1999. 3 B b

GAM189 246 LYZ Dayhoff, M. O.: Atlas of Protein Sequence and Structure. Lactalbuminand Lysozyme. Washington: National Biomedical Research Foundation(pub.) 5: 1972. Pp. D133- D140. 3 B b

GAM189 246 LYZ Fleming, A.: On a remarkable bacteriolytic element found in tissuesand secretions. Proc. Roy. Soc. Ser. B. 93: 306- 317, 1922. 3 B b

GAM189 246 LYZ Fleming, A.; Allison, V. D.: Observations on a bacteriolytic substance('lysozyme') found in secretions and tissues. Brit. J. Exp. Path. 3:252- 260, 1922. 3 B b

GAM189 246 LYZ Greenwald, R. A.; Cantor, J. O.; Prieur, D. J.; Young, D. M.:Composition of cartilage from lysozyme- deficient rabbits. Biochim.Biophys. Acta 385: 435- 437, 1975. 3 B b

GAM189 246 LYZ Neufeld, E. L.: Personal Communication. Bethesda, Maryland 1972. 3 B b

GAM189 246 LYZ Pepys, M. B.; Hawkins, P. N.; Booth, D. R.; Vigushin, D. M.; Tennent,G. A.; Soutar, A. K.; Totty, N.; Nguyen, O.; Blake, C. C. F.; Terry,C. J.; Feest, T. G.; Zalin, A. M.; Hsuan, J. J.: Human lysozyme genemutations cause hereditary systemic amyloidosis. Nature 362: 553- 557,1993. 3 B b

GAM189 246 LYZ Peters, C. W. B.; Kruse, U.; Pollwein, R.; Grzeschik, K.- H.; Sippel,A. E.: The human lysozyme gene: sequence organization and chromosomallocalization. (Abstract) Cytogenet. Cell Genet. 51: 1059 only, 1989. 3 B b

GAM189 246 LYZ Prieur, D. J.: Personal Communication. Pullman, Washington 5/13/1975. 3 B b

GAM189 246 LYZ Prieur, D. J.; Olson, H. M.; Young, D. M.: Lysozyme deficiency- - aninherited disorder of rabbits. Am. J. Path. 77: 283- 296, 1974. 3 B b

GAM189 246 LYZ Spitznagel, J. K.; Cooper, M. R.; McCall, A. E.; DeChatelet, L.R.; Welsh, I. R.: Selective deficiency of granules associated withlysozyme and lactoferrin in human polymorphs (PMN) with reduced microbicidalcapacity. (Abstract) J. Clin. Invest. 51: 93A only, 1972. 3 B b

GAM189 246 LYZ Taniyama, Y.; Kuroki, R.; Omura, F.; Seko, C.; Kikuchi, M.: Evidencefor intramolecular disulfide bond shuffling in the folding of mutanthuman lysozyme. J. Biol. Chem. 266: 6456- 6461, 1991. 3 B b

GAM189 246 LYZ Yoshimura, K.; Toibana, A.; Nakahama, K.: Human lysozyme: sequencingof a cDNA, and expression and secretion by Saccharomyces cerevisiae. Biochem.Biophys. Res. Commun. 150: 794- 801, 1988. 3 B b

GAM189 246 LYZ Zalin, A. M.; Jones, S.; Fitch, N. J. S.; Ramsden, D. B.: Familialnephropathic non- neuropathic amyloidosis: clinical features, immunohistochemistryand chemistry. Quart. J. Med. 81: 945- 956, 1991. 3 B b

GAM189 246 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999. 3 B c

GAM189 246 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 B c

GAM189 246 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein 3 B b

kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990.

GAM189 246 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. 3 B b
F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994.

GAM189 246 MDM2 Boyd, M. T.; Vlatkovic, N.; Haines, D. S.: A novel cellular protein(MTBP) 3 B c
binds to MDM2 and induces a G1 arrest that is suppressed byMDM2. J. Biol. Chem. 275: 31883- 31890, 2000.

GAM189 246 MDM2 Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S.A.; Albitar, 3 B c
M.: The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82:2617- 2623, 1993.

GAM189 246 MDM2 Bureau, J. F.; Bihl, F.; Brahic, M.; Le Paslier, D.: The genecoding for 3 B c
interferon- gamma is linked to the D12S335 and D12S313 microsatellitesand to the MDM2 gene. Genomics 28: 109- 112, 1995.

GAM189 246 MDM2 Buschmann, T.; Fuchs, S. Y.; Lee, C.- G.; Pan, Z.- Q.; Ronai, Z.: SUMO- 1 3 B c
modification of Mdm2 prevents its self- ubiquitination andincreases Mdm2 ability to ubiquitinate p53. Cell 101: 753- 762, 2000.Note: Erratum: Cell 107: 549 only, 2001.

GAM189 246 MDM2 de Oca Luna, R. M.; Tabor, A. D.; Eberspaecher, H.; Hulboy, D.L.; Worth, L. 3 B c
L.; Colman, M. S.; Finlay, C. A.; Lozano, G.: The organizationand expression of the mdm2 gene. Genomics 33: 352- 357, 1996.

GAM189 246 MDM2 Fakharzadeh, S.; Trusko, S. P.; George, D. L.: Tumorigenic 3 B c
potentialassociated with enhanced expression of a gene that is amplified ina mouse tumor cell line. EMBO J. 10: 1565- 1569, 1991.

GAM189 246 MDM2 Freedman, D. A.; Epstein, C. B.; Roth, J. C.; Levine, A. J.: Agenetic 3 B c
approach to mapping the p53 binding site in the MDM2 protein. Molec.Med. 3: 248- 259, 1997.

GAM189 246 MDM2 Fuchs, S. Y.; Adler, V.; Buschmann, T.; Yin, Z.; Wu, X.; Jones,S. N.; Ronai, 3 B c
Z.: JNK targets p53 ubiquitination and degradationin nonstressed cells. Genes Dev. 12: 2658- 2663, 1998.

GAM189 246 MDM2 Mayo, L. D.; Donner, D. B.: A phosphatidylinositol 3- kinase/Aktpathway 3 B c
promotes translocation of Mdm2 from the cytoplasm to the nucleus. Proc.Nat. Acad. Sci. 98: 11598- 11603, 2001.

GAM189 246 MDM2 Mitchell, E. L. D.; White, G. R. M.; Santibanez- Koref, M. F.;Varley, J. M.; 3 B c
Heighway, J.: Mapping of gene loci in the q13- q15region of chromosome 12. Chromosome Res. 3: 261- 262, 1995.

GAM189 246 MDM2 Momand, J.; Zambetti, G. P.; Olson, D. C.; George, D. L.; Levine,A. J.: The 3 B c
mdm- 2 oncogene product forms a complex with the p53 proteinand inhibits p53- mediated transactivation. Cell 69: 1237- 1245, 1992.

GAM189 246 MDM2 Oliner, J. D.; Kinzler, K. W.; Meltzer, P. S.; George, D. L.;Vogelstein, B.: 3 B c
Amplification of a gene encoding a p53- associatedprotein in human sarcomas. Nature 358: 80- 83, 1992.

GAM189 246 MDM2 Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.;Sasazuki, T.; 3 B c
McMahon, M.; Oren, M.; McCormick, F.: Opposing effectsof Ras on p53: transcriptional activation of mdm2 and induction ofp19(ARF). Cell 103: 321- 330, 2000.

GAM189 246 MDM2 Shenoy, S. K.; McDonald, P. H.; Kohout, T. A.; Lefkowitz, R. J.: Regulation 3 B c
of receptor fate by ubiquitination of activated beta- 2- adrenergicreceptor and beta- arrestin. Science 294: 1307- 1313, 2001.

GAM189 246 MDM2 Shieh, S.- Y.; Ikeda, M.; Taya, Y.; Prives, C.: DNA damage- 3 B c

inducedphosphorylation of p53 alleviates inhibition by MDM2. Cell 91: 325-334,1997.

GAM189 246 MDM2 Testa, J. R.; Bellacosa, A.: AKT plays a central role in tumorigenesis. 3 B c
Proc.Nat. Acad. Sci. 98: 10983- 10985, 2001.

GAM189 246 MDM2 Xiao, Z.- X.; Chen, J.; Levine, A. J.; Modjtahedi, N.; Xing, J.;Sellers, W. 3 B c
R.; Livingston, D. M.: Interaction between the retinoblastomaprotein and the oncoprotein MDM2. Nature 375: 694- 698, 1995.

GAM189 246 MDM2 Zhang, Y.; Xiong, Y.: A p53 amino- terminal nuclear export signalinhibited 3 B c
by DNA damage- induced phosphorylation. Science 292: 1910- 1915,2001.

GAM189 246 MDM4 Parant, J.; Chavez- Reyes, A.; Little, N. A.; Yan, W.; Reinke, V.;Jochemsen, 3 B c
A. G.; Lozano, G.: Rescue of embryonic lethality in Mdm4- nullmice by loss of Trp53 suggests a nonoverlapping pathway with MDM2to regulate p53. Nature Genet. 29: 92- 95, 2001.

GAM189 246 MDM4 Shvarts, A.; Bazuine, M.; Dekker, P.; Ramos, Y. F. M.; Steegenga,W. T.; 3 B c
Merckx, G.; van Ham, R. C. A.; van der Houven van Oordt, W.;van der Eb, A. J.; Jochemsen, A. G.: Isolation and identificationof the human homolog of a new p53- binding protein, Mdmx. Genomics 43:34- 42, 1997.

GAM189 246 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 B c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator. J. Biol. Chem. 275: 5308- 5317, 2000.

GAM189 246 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 B c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer Res. 56: 3446- 3450, 1996.

GAM189 246 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 B c
bindingprotein, an LXXLL motif- containing protein, functions as a generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM189 246 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 B c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.- H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor, ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol. Chem. 274: 34283- 34293, 1999.

GAM189 246 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 B c
that integrate nuclear receptor signaling through CREB- bindingprotein. Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM189 246 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 B c
coding sequences of unidentified human genes. V. The codingsequences of 40 new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM189 246 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 B c
J. K.: Isolation and characterization of peroxisomeproliferator- activated receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J. Biol. Chem. 275: 13510- 13516, 2000.

GAM189 246 NONO Brown, C. J.; Carrel, L.; Willard, H. F.: Expression of genesfrom the human 3 B b
active and inactive X chromosomes. Am. J. Hum. Genet. 60:1333- 1343, 1997.

GAM189 246 NONO Dong, B.; Horowitz, D. S.; Kobayashi, R.; Krainer, A. R.: Purificationand 3 B b
cDNA cloning of HeLa cell p54(nrb), a nuclear protein with twoRNA recognition motifs and extensive homology to human splicing factorPSF and Drosophila NONA/BJ6. Nucleic Acids Res. 21: 4085- 4092, 1993.

GAM189 246 NONO Nelson, D. L.; Ballabio, A.; Cremers, F.; Monaco, A. P.; Schlessinger,D.: 3 B b
Report of the sixth international workshop on X chromosome mapping1995.
Cytogenet. Cell Genet. 71: 308- 342, 1995.

GAM189 246 NONO Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller,U.: AFX1 and 3 B b
p54(nrb): fine mapping, genomic structure, and exclusionas candidate genes
of X- linked dystonia parkinsonism. Hum. Genet. 100:569- 572, 1997.

GAM189 246 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of 3 B c
NAD(P)H:quinonereductase by dietary antioxidants: possible role in
protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77:
5216- 5220,1980.

GAM189 246 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. 3 B c
A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.;
Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of
the long arm of human chromosome 16. Genomics 10:308- 312, 1991.

GAM189 246 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof 3 B c
the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983.

GAM189 246 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman 3 B c
diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum.
Genet. 53: 189- 193, 1980.

GAM189 246 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- 3 B c
inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and
localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578,
1988.

GAM189 246 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, 3 B c
M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic
variation in the prevalence of a common NAD(P)Hquinone oxidoreductase
polymorphism and its implications for anti- cancerchemotherapy. Brit. J.
Cancer 76: 852- 854, 1997.

GAM189 246 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further 3 B c
evidence for the regional localization of human APRT and DIA4on chromosome
16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984.

GAM189 246 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe 3 B c
increased susceptibility of individuals with a polymorphism
inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat.
Acad. Sci. 96: 8150- 8155, 1999.

GAM189 246 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA- 3 B c
4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980.

GAM189 246 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. 3 B c
P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1)
gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382-
7389, 1998.

GAM189 246 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; 3 B c
Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.;
Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.;
Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological
malignancy, is associated with the NQO1 609C- T mutationand rapid fractional
excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997.

GAM189 246 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 B c
New York: Oxford Univ. Press (pub.) 1988.

GAM189 246 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to 3 B c

cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999.

GAM189 246 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, 3 B c
P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene
expression in human colon carcinoma cells: characterization ofa mutation
which modulates DT- diaphorase activity and mitomycin sensitivity.
CancerRes. 52: 797- 802, 1992.

GAM189 246 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; 3 B c
Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H:
quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997.

GAM189 246 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, 3 B c
S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and
long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese
workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998.

GAM189 246 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the 3 B c
loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes.
Leukemia Res. 22: 105- 113, 1998.

GAM189 246 NR2E1 Jackson, A.; Panayiotidis, P.; Foroni, L.: The human homologueof the 3 B c
Drosophila tailless gene (TLX): characterization and mappingto a region of
common deletion in human lymphoid leukemia on chromosome6q21. Genomics 50:
34- 43, 1998.

GAM189 246 NR2E1 Monaghan, A. P.; Bock, D.; Gass, P.; Schwager, A.; Wolfer, D. P.;Lipp, H.- 3 B c
P.; Schutz, G.: Defective limbic system in mice lackingthe tailless gene.
Nature 390: 515- 517, 1997.

GAM189 246 NR2E1 Yu, R. T.; McKeown, M.; Evans, R. M.; Umesono, K.: Relationshipbetween 3 B c
Drosophila gap gene tailless and a vertebrate nuclear receptorTlx. Nature
370: 375- 379, 1994.

GAM189 246 NUMA1 Compton, D. A.; Szilak, I.; Cleveland, D. W.: Primary structureof NuMA, an 3 B c
intranuclear protein that defines a novel pathway forsegregation of proteins
at mitosis. J. Cell Biol. 116: 1395- 1408,1992.

GAM189 246 NUMA1 Lydersen, B. K.; Pettijohn, D. E.: Human- specific nuclear proteinthat 3 B c
associates with the polar region of the mitotic apparatus: distributionin a
human/hamster hybrid cell. Cell 22: 489- 499, 1980.

GAM189 246 NUMA1 Merdes, A.; Ramyar, K.; Vechio, J. D.; Cleveland, D. W.: A complexof NuMA 3 B c
and cytoplasmic dynein is essential for mitotic spindle assembly. Cell
87:447- 458, 1996.

GAM189 246 NUMA1 Sparks, C. A.; Bangs, P. L.; McNeil, G. P.; Lawrence, J. B.; Fey,E. G.: 3 B c
Assignment of the nuclear mitotic apparatus protein NuMA geneto human
chromosome 11q13. Genomics 17: 222- 224, 1993.

GAM189 246 NUMA1 Wells, R. A.; Catzavelos, C.; Kamel- Reid, S.: Fusion of retinoicacid 3 B c
receptor alpha to NuMA, the nuclear mitotic apparatus protein,by a variant
translocation in acute promyelocytic leukaemia. NatureGenet. 17: 109- 113,
1997.

GAM189 246 NUMA1 Wiese, C.; Wilde, A.; Moore, M. S.; Adam, S. A.; Merdes, A.; Zheng,Y.: Role 3 B c
of importin- beta in coupling Ran to downstream targets inmicrotubule
assembly. Science 291: 653- 656, 2001.

GAM189 246 NUMA1 Yang, C. H.; Lambie, E. J.; Snyder, M.: NuMA: an unusually longcoiled- coil 3 B c
related protein in the mammalian nucleus. J. Cell Biol. 116:1303- 1317,
1992.

GAM189 246 ORC1L Eki, T.; Okumura, K.; Amin, A.; Ishiai, M.; Abe, M.; Nogami, M.;Taguchi, H.; 3 B b
Hurwitz, J.; Murakami, Y.; Hanaoka, F.: Mapping of thehuman homologue

(ORC1L) of the yeast origin recognition complex subunit1 gene to chromosome band 1p32. Genomics 36: 559- 561, 1996.

GAM189 246 ORC1L Gavin, K. A.; Hidaka, M.; Stillman, B.: Conserved initiator proteinsin 3 B b eukaryotes. Science 270: 1667- 1671, 1995.

GAM189 246 ORC1L Mendez, J.; Zou- Yang, H.; Kim, S.- Y.; Hidaka, M.; Tansey, W. P.;Stillman, 3 B b B.: Human origin recognition complex large subunit is degradedby ubiquitin-mediated proteolysis after initiation of DNA replication. Molec.Cell 9: 481-491, 2002.

GAM189 246 ORC1L Ohtani, K.; DeGregori, J.; Leone, G.; Herendeen, D. R.; Kelly,T. J.; Nevins, 3 B b J. R.: Expression of the HsOrc1 gene, a human ORC1homolog, is regulated by cell proliferation via the E2F transcriptionfactor. Molec. Cell. Biol. 16: 6977- 6984, 1996.

GAM189 246 P2RY1 Ayyanathan, K.; Naylor, S. L.; Kunapuli, S. P.: Structural 3 B c characterizationand fine chromosomal mapping of the human P2Y(1) purinergic receptorgene (P2RY1). Somat. Cell Molec. Genet. 22: 419- 424, 1996.

GAM189 246 P2RY1 Ayyanathan, K.; Webbs, T. E.; Sandhu, A. K.; Athwal, R. S.; Barnard,E. A.; 3 B c Kunapuli, S. P.: Cloning and chromosomal localization of thehuman P2Y1 purinoceptor. Biochem. Biophys. Res. Commun. 218: 783- 788,1996.

GAM189 246 P2RY1 Leon, C.; Hechler, B.; Freund, M.; Eckly, A.; Vial, C.; Ohlmann,P.; Dierich, 3 B c A.; LeMeur, M.; Cazenave, J.- P.; Gachet, C.: Defectiveplatelet aggregation and increased resistance to thrombosis in purinergicP2Y1 receptor- null mice. J. Clin. Invest. 104: 1731- 1737, 1999.

GAM189 246 P2RY1 Leon, C.; Hechler, B.; Vial, C.; Leray, C.; Cazenave, J.- P.; Gachet,C.: The 3 B c P2Y(1) receptor is an ADP receptor antagonized by ATP andexpressed in platelets and megakaryoblastic cells. FEBS Letts. 403:26- 30, 1997.

GAM189 246 P2RY1 Leon, C.; Vial, C.; Cazenave, J.- P.; Gachet, C.: Cloning and sequencingof a 3 B c human cDNA encoding endothelial P2Y1 purinoceptor. Gene 171:295- 297, 1996.

GAM189 246 P2RY1 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 B c Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997.

GAM189 246 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack 3 B b of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991.

GAM189 246 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; 3 B b Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine nucleotide synthesis on human chromosome 4 are closelylinked and divergently transcribed. J. Biol. Chem. 269: 5313- 5321,1994.

GAM189 246 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of 3 B b three human multifunctional de novo purine biosyntheticgenes by functional complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920, 1990.

GAM189 246 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B b Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM189 246 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene

clusters. Genome Res. 11: 389- 404, 2001.

GAM189 246 PCDHB16 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel 3 B c
cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913,
1997.

GAM189 246 PCDHB16 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of 3 B c
the coding sequences of unidentified human genes. XVIII.The complete
sequences of 100 new cDNA clones from brain which codefor large proteins in
vitro. DNA Res. 7: 273- 281, 2000.

GAM189 246 PCDHB16 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM189 246 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 B b
protocadherin- beta one- exon gene families show high
evolutionaryconservation, despite the difference in gene number. FEBS Lett.
495:120- 125, 2001.

GAM189 246 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM189 246 PDZK1 Custer, M.; Spindler, B.; Verrey, F.; Murer, H.; Biber, J.: Identificationof 3 B b
a new gene product (diphor- 1) regulated by dietary phosphate. Am.J.
Physiol. 273: F801- F806, 1997.

GAM189 246 PDZK1 Ikemoto, M.; Arai, H.; Feng, D.; Tanaka, K.; Aoki, J.; Dohmae,N.; Takio, K.; 3 B b
Adachi, H.; Tsujimoto, M.; Inoue, K.: Identificationof a PDZ- domain-
containing protein that interacts with the scavengerreceptor class B type I.
Proc. Nat. Acad. Sci. 97: 6538- 6543, 2000.

GAM189 246 PDZK1 Kocher, O.; Comella, N.; Gilchrist, A.; Pal, R.; Tognazzi, K.;Brown, L. F.; 3 B b
Knoll, J. H. M.: PDZK1, a novel PDZ domain- containingprotein up- regulated
in carcinomas and mapped to chromosome 1q21,interacts with cMOAT (MRP2), the
multidrug resistance- associated protein. Lab.Invest. 79: 1161- 1170, 1999.

GAM189 246 PDZK1 Kocher, O.; Comella, N.; Tognazzi, K.; Brown, L. F.: Identificationand 3 B b
partial characterization of PDZK1: a novel protein containingPDZ interaction
domains. Lab. Invest. 78: 117- 125, 1998.

GAM189 246 PDZK1 Wang, S.; Yue, H.; Derin, R. B.; Guggino, W. B.; Li, M.: Accessoryprotein 3 B b
facilitated CFTR- CFTR interaction, a molecular mechanism topotentiate the
chloride channel activity. Cell 103: 169- 179, 2000.

GAM189 246 PDZK1 White, K. E.; Biber, J.; Murer, H.; Econs, M. J.: A PDZ domain- 3 B b
containingprotein with homology to Diphor- 1 maps to human chromosome 1q21.
Ann.Hum. Genet. 62: 287- 290, 1998.

GAM189 246 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to 3 B b
two putative mammalian circadian regulators, mper1 andmper2, to light. Cell
91: 1055- 1064, 1997.

GAM189 246 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B b
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM189 246 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; 3 B b
Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and

mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531-2534, 1999.

GAM189 246 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of clock operative in the mammalian forebrain. Science 293:506- 509, 2001. 3 B b

GAM189 246 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.; Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock. Science 288: 1013- 1019, 2000. 3 B b

GAM189 246 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; Reppert, S. M.: Two period homologs: circadian expression andphotic regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997. 3 B b

GAM189 246 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial advanced sleep phase syndrome. Science 291: 1040- 1043,2001. 3 B b

GAM189 246 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694, 2001. 3 B b

GAM189 246 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the mammalian circadian clock. Nature 400: 169- 173,1999. 3 B b

GAM189 246 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol 3- kinase catalytic subunit that associates withp85 and is expressed predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997. 3 B b

GAM189 246 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J. H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002. 3 B b

GAM189 246 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; Nakagawara, A.: Identification and chromosome assignment of ahuman gene encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997. 3 B b

GAM189 246 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.: p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat. Acad. Sci. 94: 4330- 4335, 1997. 3 B b

GAM189 246 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C. Genomics 47: 323- 324, 1998. 3 B b

GAM189 246 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to human chromosome 21q22.3. Genomics 41: 193- 200,1997. 3 B b

GAM189 246 PON1 Adkins, S.; Gan, K. N.; Mody, M.; La Du, B. N.: Molecular basisfor the polymorphic forms of human serum paraoxonase/arylesterase:glutamine or arginine at position 191, for the respective A and Ballozymes. Am. J. Hum. Genet. 52: 598- 608, 1993. 3 B b

GAM189 246 PON1 Antikainen, M.; Murtomaki, S.; Syvanne, M.; Pahlman, R.; Tahvanainen,E.; Jauhiainen, M.; Frick, M. H.; Ehnholm, C.: The gln- arg191 polymorphismof the human paraoxonase gene (HUMPONA) is not associated with therisk of 3 B b

coronary artery disease in Finns. J. Clin. Invest. 98: 883- 885,1996.

GAM189 246 PON1 Augustinsson, K.- B.; Henricson, B.: A genetically controlled esterasein rat 3 B b
plasma. Biochim. Biophys. Acta 124: 323- 331, 1966.

GAM189 246 PON1 Barbieri, M.; Bonafe, M.; Marfella, R.; Ragno, E.; Giugliano, D.;Franceschi, 3 B b
C.; Paolisso, G.: LL- paraoxonase genotype is associatedwith a more severe
degree of homeostasis model assessment IR in healthysubjects. J. Clin.
Endocr. Metab. 87: 222- 225, 2002.

GAM189 246 PON1 Brophy, V. H.; Jampsa, R. L.; Clendenning, J. B.; McKinstry, L.A.; Jarvik, 3 B b
G. P.; Furlong, C. E.: Effects of 5- prime regulatory- regionpolymorphisms
on paraoxonase- gene (PON1) expression. Am. J. Hum.Genet. 68: 1428- 1436,
2001.

GAM189 246 PON1 Cherry, N.; Mackness, M.; Durrington, P.; Povey, A.; Dippnall,M.; Smith, T.; 3 B b
Mackness, B.: Paraoxonase (PON1) polymorphisms infarmers attributing ill
health to sheep dip. Lancet 359: 763- 764,2002.

GAM189 246 PON1 Clendenning, J. B.; Humbert, R.; Green, E. D.; Wood, C.; Traver,D.; Furlong, 3 B b
C. E.: Structural organization of the human PON1 gene. Genomics 35:586- 589,
1996.

GAM189 246 PON1 Coates, P. M.; Mestriner, M. A.; Hopkinson, D. A.: A 3 B b
preliminaryinterpretation of the esterase isozymes of human tissues. Ann.
Hum.Genet. 39: 1- 20, 1975.

GAM189 246 PON1 Davies, H. G.; Richter, R. J.; Keifer, M.; Broomfield, C. A.; Sowalla,J.; 3 B b
Furlong, C. E.: The effect of the human serum paraoxonase polymorphismis
reversed with diazoxon, soman and sarin. Nature Genet. 14: 334- 336,1996.

GAM189 246 PON1 Deakin, S.; Leviev, I.; Nicaud, V.; Meynet, M.- C. B.; Tiret, L.;James, R. 3 B b
W.: Paraoxonase- 1 L55M polymorphism is associated withan abnormal oral
glucose tolerance test and differentiates high riskcoronary disease
families. J. Clin. Endocr. Metab. 87: 1268- 1273,2002.

GAM189 246 PON1 Eckerson, H. W.; Romson, J.; Wyte, C.; La Du, B. N.: The humanserum 3 B b
paraoxonase polymorphism: identification of phenotypes by theirresponse to
salts. Am. J. Hum. Genet. 35: 214- 227, 1983.

GAM189 246 PON1 Eckerson, H. W.; Wyte, C. M.; La Du, B. N.: The human serum 3 B b
paraoxonase/arylesterasepolymorphism. Am. J. Hum. Genet. 35: 1126- 1136,
1983.

GAM189 246 PON1 Eiberg, H.; Mohr, J.: Linkage relations of the paraoxonase polymorphismwith 3 B b
43 marker systems. (Abstract) Cytogenet. Cell Genet. 25: 150,1979.

GAM189 246 PON1 Eiberg, H.; Mohr, J.; Schmiegelow, K.; Nielsen, L. S.; Williamson,R.: 3 B b
Linkage relationships of paraoxonase (PON) with other markers:indication of
PON- cystic fibrosis synteny. Clin. Genet. 28: 265- 271,1985.

GAM189 246 PON1 Furlong, C. E.; Richter, R. J.; Chapline, C.; Crabb, J. W.: Purificationof 3 B b
rabbit and human serum paraoxonase. Biochemistry 30: 10133- 10140,1991.

GAM189 246 PON1 Furlong, C. E.; Richter, R. J.; Seidel, S. L.; Motulsky, A. G.: Role of 3 B b
genetic polymorphism of human plasma paraoxonase/arylesterasein hydrolysis
of the insecticide metabolites chlorpyrifos oxon andparaoxon. Am. J. Hum.
Genet. 43: 230- 238, 1988.

GAM189 246 PON1 Garin, M.- C. B.; James, R. W.; Dussoix, P.; Blanche, H.; Passa,P.; Froguel, 3 B b
P.; Ruiz, J.: Paraoxonase polymorphism met- leu54 isassociated with modified
serum concentrations of the enzyme: a possiblelink between the paraoxonase
gene and increased risk of cardiovasculardisease in diabetes. J. Clin.
Invest. 99: 62- 66, 1997.

GAM189 246 PON1 Geldmacher- von Mallinckrodt, M.: Polymorphism of human serumparaoxonase. 3 B b

Hum. Genet. 45 (suppl. 1): 65- 68, 1978.

GAM189 246 PON1 Geldmacher- von Mallinckrodt, M.; Lindorft, H. H.; Petenyi, M.;Flugel, M.; 3 B b
Fischer, T.; Hiller, T.: Genetisch determinierter Polymorphismusde
menschlichen Serum- Paroxonase (E.C.3.1.1.2). Humangenetik 17:331- 335,
1973.

GAM189 246 PON1 Hassett, C.; Richter, R. J.; Humbert, R.; Chapline, C.; Crabb,J. W.; 3 B b
Omiecinski, C. J.; Furlong, C. E.: Characterization of cDNAclones encoding
rabbit and human serum paraoxonase: the mature proteinretains its signal
sequence. Biochemistry 30: 10141- 10149, 1991.

GAM189 246 PON1 Humbert, R.; Adler, D. A.; Disteche, C. M.; Hassett, C.; Omiecinski,C. J.; 3 B b
Furlong, C. E.: The molecular basis of the human serum paraoxonaseactivity
polymorphism. Nature Genet. 3: 73- 76, 1993.

GAM189 246 PON1 Ito, T.; Yasue, H.; Yoshimura, M.; Nakamura, S.; Nakayama, M.;Shimasaki, Y.; 3 B b
Harada, E.; Mizuno, Y.; Kawano, H.; Ogawa, H.: Paraoxonasegene gln192- to-
arg (Q192R) polymorphism is associated with coronaryartery spasm. Hum.
Genet. 110: 89- 94, 2002.

GAM189 246 PON1 Kao, Y.- L.; Donaghue, K.; Chan, A.; Knight, J.; Silink, M.: Avariant of 3 B b
paraoxonase (PON1) gene is associated with diabetic retinopathyin IDDM. J.
Clin. Endocr. Metab. 83: 2589- 2592, 1998.

GAM189 246 PON1 La Du, B. N.: The human serum paraoxonase/arylesterase 3 B b
polymorphism.(Editorial) Am. J. Hum. Genet. 43: 227- 229, 1988.

GAM189 246 PON1 Li, W.- F.; Furlong, C. E.; Costa, L. G.: Paraoxonase protectsagainst 3 B b
chlorpyrifos toxicity in mice. Toxic. Lett. 76: 219- 226,1995.

GAM189 246 PON1 Li, W.- F.; Matthews, C.; Disteche, C. M.; Costa, L. G.; Furlong,C. E.: 3 B b
Paraoxonase (Pon1) gene in mice: sequencing, chromosomal localizationand
developmental expression. Pharmacogenetics 7: 137- 144, 1997.

GAM189 246 PON1 Mackness, B.; Mackness, M. I.; Arrol, S.; Turkie, W.; Durrington,P. N.: 3 B b
Effect of the human serum paraoxonase 55 and 192 genetic polymorphismson the
protection by high density lipoprotein against low densitylipoprotein
oxidative modification. FEBS Lett. 423: 57- 60, 1998.

GAM189 246 PON1 Mochizuki, H.; Scherer, S. W.; Xi, T.; Nickle, D. C.; Majer, M.;Huizenga, J. 3 B b
J.; Tsui, L.- C.; Prochazka, M.: Human PON2 gene at 7q21.3:cloning, multiple
mRNA forms, and missense polymorphisms in the codingsequence. Gene 213: 149-
157, 1998.

GAM189 246 PON1 Mueller, R. F.; Hornung, S.; Furlong, C. E.; Anderson, J.; Giblett,E. R.; 3 B b
Motulsky, A. G.: Plasma paraoxonase polymorphism: a new enzymeassay,
population, family, biochemical, and linkage studies. Am.J. Hum. Genet. 35:
393- 408, 1983.

GAM189 246 PON1 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. 3 B b
J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly
oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J.
Clin. Invest. 99: 2005- 2019, 1997.

GAM189 246 PON1 Neel, J. V.; Tanis, R. J.; Migliazza, E. C.; Spielman, R. S.;Salzano, F. M.; 3 B b
Oliver, W. J.; Morrow, M.; Bachofer, S.: Geneticstudies of the Macushi and
Wapishana Indians. I. Rare genetic variantsand a 'private polymorphism' of
esterase A. Hum. Genet. 36: 81- 108,1977.

GAM189 246 PON1 Nielsen, A.; Eiberg, H.; Mohr, J.: Number of loci responsiblefor the 3 B b
inheritance of high and low activity of paraoxonase. Clin.Genet. 29: 216-
221, 1986.

GAM189 246 PON1 Odawara, M.; Tachi, Y.; Yamashita, K.: Paraoxonase polymorphismGln192- Arg 3 B b

is associated with coronary heart disease in Japanese noninsulin-dependentdiabetes mellitus. J. Clin. Endocr. Metab. 82: 2257- 2260, 1997.

GAM189 246 PON1 Ortigoza- Ferado, J.; Richter, R. J.; Hornung, S. K.; Motulsky,A. G.; Furlong, C. E.: Paraoxon hydrolysis in human serum mediatedby a genetically variable arylesterase and albumin. Am. J. Hum. Genet. 36:295- 305, 1984. 3 B b

GAM189 246 PON1 Paolisso, G.; Manzella, D.; Tagliamonte, M. R.; Barbieri, M.;Marfella, R.; Zito, G.; Bonafe, M.; Giugliano, D.; Franceschi, C.;Varricchio, M.: The BB-paraoxonase genotype is associated with impairedbrachial reactivity after acute hypertriglyceridemia in healthy subjects. J.Clin. Endocr. Metab. 86: 1078- 1082, 2001. 3 B b

GAM189 246 PON1 Playfer, J. R.; Eze, L. C.; Bullen, M. F.; Evans, D. A. P.: Geneticpolymorphism and interethnic variability of plasma paroxonase activity. J.Med. Genet. 13: 337- 342, 1976. 3 B b

GAM189 246 PON1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 B b

GAM189 246 PON1 Schmiegelow, K.; Eiberg, H.; Tsui, L.- C.; Buchwald, M.; Phelan,P. D.; Williamson, R.; Warwick, W.; Niebuhr, E.; Mohr, J.; Schwartz,M.; Koch, C.: Linkage between the loci for cystic fibrosis and paraoxonase. Clin.Genet. 29: 374- 377, 1986. 3 B b

GAM189 246 PON1 Serrato, M.; Marian, A. J.: A variant of human paraoxonase/arylesterase(HUMPONA) gene is a risk factor for coronary artery disease. J. Clin.Invest. 96: 3005- 3008, 1995. 3 B b

GAM189 246 PON1 Shih, D. M.; Gu, L.; Xia, Y.- R.; Navab, M.; Li, W.- F.; Hama, S.;Castellani, L. W.; Furlong, C. E.; Costa, L. G.; Fogelman, A. M.;Lusis, A. J.: Mice lacking serum paraoxonase are susceptible to organophosphatetoxicity and atherosclerosis. Nature 394: 284- 287, 1998. 3 B b

GAM189 246 PON1 Simpson, N. E.: Serum arylesterase levels of activity in twinsand their parents. Am. J. Hum. Genet. 23: 375- 382, 1971. 3 B b

GAM189 246 PON1 Sorenson, R. C.; Primo- Parmo, S. L.; Camper, S.; La Du, B. N.: The genetic mapping and gene structure of mouse paraoxonase/arylesterase. Genomics 30:431- 438, 1995. 3 B b

GAM189 246 PON1 Tashian, R. E.: Genetic variation and evolution of the carboxylicesterases and carbonic anhydrases of primate erythrocytes. Am. J.Hum. Genet. 17: 257-272, 1965. 3 B b

GAM189 246 PON1 Tashian, R. E.; Shaw, M. W.: Inheritance of an erythrocyte acetylesterasevariant of man. Am. J. Hum. Genet. 14: 295- 300, 1962. 3 B b

GAM189 246 PON1 Tsui, L.- C.; Buchwald, M.; Barker, D.; Braman, J. C.; Knowlton,R.; Schumm, J. W.; Eiberg, H.; Mohr, J.; Kennedy, D.; Plavsic, N.;Zsiga, M.; Markiewicz, D.; Akots, G.; Brown, V.; Helms, C.; Gravius,T.; Parker, C.; Rediker, K.; Donis- Keller, H.: Cystic fibrosis locusdefined by a genetically linked polymorphic DNA marker. Science 230:1054- 1057, 1985. 3 B b

GAM189 246 PON1 Watson, C. E.; Draganov, D. I.; Billecke, S. S.; Bisgaier, C.L.; La Du, B. N.: Rabbits possess a serum paraoxonase polymorphismsimilar to the human Q192R. Pharmacogenetics 11: 123- 134, 2001. 3 B b

GAM189 246 PON1 Yamasaki, Y.; Sakamoto, K.; Watada, H.; Kajimoto, Y.; Hori, M.: The arg- 192 isoform of paraoxonase with low sarin- hydrolyzing activityis dominant in the Japanese. Hum. Genet. 101: 67- 68, 1997. 3 B b

GAM189 246 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 3 B b

2002.

GAM189 246 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 3 B b
cell coactivator of octamer- binding transcription factors. Nature 373:360-
362, 1995.

GAM189 246 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 3 B b
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-
specific coactivator of octamer- binding transcription factors1 and 2, to
11q23.1 by somatic cell hybridization and in situ hybridization. Genomics
33:143- 145, 1996.

GAM189 246 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 3 B b
of action of the B- cell- specific transcriptional activatorOCA- B. Molec.
Cell. Biol. 15: 4115- 4124, 1995.

GAM189 246 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 3 B b
Matthias, P.: B cell development and immunoglobulin gene transcriptionin the
absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM189 246 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 3 B b
Immun. 9: 373- 398, 1991.

GAM189 246 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 3 B b
specificcoactivator that stimulates immunoglobulin promoter activity
throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM189 246 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 3 B b
Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B,
BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-
864, 2000.

GAM189 246 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; 3 B b
Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor
integrity, and rhodopsin dephosphorylation in mice lackingboth protein
phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21:
8605- 8614, 2001.

GAM189 246 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; 3 B b
Nathans, J.: Identification and characterization of a conservedfamily of
protein serine/threonine phosphatases homologous to Drosophilaretinal
degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997.

GAM189 246 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 B c
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component
of the steroid receptor complex: cloning of thecDNA and further
characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM189 246 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 B c
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem.
267: 5503- 5507, 1992.

GAM189 246 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 B c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151
only, 1997.

GAM189 246 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 B c
J.- E.: The structure and complete nucleotide sequenceof the human
cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM189 246 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 B b
Chromosomalassignment of the interferon- inducible double- stranded RNA-
dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse
chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM189 246 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human interferon- gamma mRNA autoregulates its translation througha pseudoknot that activates the interferon- inducible protein kinasePKR. Cell 108: 221-232, 2002. 3 B b

GAM189 246 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR) encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and differences from its mouse homolog. Genomics 36:197- 201, 1996. 3 B b

GAM189 246 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: sequence of the human interferon- inducible RNA- dependent proteinkinase (PKR) deduced from genomic clones. Gene 178: 191- 193, 1996. 3 B b

GAM189 246 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand characterization of the human double- stranded RNA- activated proteinkinase induced by interferon. Cell 62: 379- 390, 1990. 3 B b

GAM189 246 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds preferentially to Huntington's disease (HD) transcriptsand is activated in HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001. 3 B b

GAM189 246 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics 16:768- 770, 1993. 3 B b

GAM189 246 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein. Science 285: 107- 110, 1999. 3 B b

GAM189 246 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.: Genomicorganization, comparative analysis, and genetic polymorphisms of thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733, 2001. 3 B b

GAM189 246 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; Chen, S. G.: Expression and structural characterizationof the recombinant human doppel protein. Biochemistry 39: 13575- 13583,2000. 3 B b

GAM189 246 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.; Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-deficient mice is associated with upregulation of thenovel PrP- like protein doppel. J. Molec. Biol. 292: 797- 817, 1999. 3 B b

GAM189 246 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin the prion- like protein gene (Prnd) and their implications inhuman prion diseases, Alzheimer's disease and other neurological disorders. Hum.Genet. 109: 319- 325, 2001. 3 B b

GAM189 246 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-glycosylated, glycosylphosphatidylinositol- anchored protein:expression in testis and ectopic production in the brains of Prnp(0/0)mice predisposed to Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000. 3 B b

GAM189 246 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 B b

915, 1999.

GAM189 246 PRPF31 Al- Maghtheh, M.; Vithana, E.; Tarttelin, E.; Jay, M.; Evans, K.;Moore, T.; 3 B c
Bhattacharya, S.; Inglehearn, C. F.: Evidence for a majorretinitis
pigmentosa locus on 19q13.4 (RP11), and association witha unique bimodal
expressivity phenotype. Am. J. Hum. Genet. 59:864- 871, 1996.

GAM189 246 PRPF31 Vithana, E. N.; Abu- Safieh, L.; Allen, M. J.; Carey, A.; Papaioannou,M.; 3 B c
Chakarova, C.; Al- Maghtheh, M.; Ebenezer, N. D.; Willis, C.; Moore,A. T.;
Bird, A. C.; Hunt, D. M.; Bhattacharya, S. S.: A human homologof yeast pre-
mRNA splicing gene, PRP31, underlies autosomal dominantretinitis pigmentosa
on chromosome 19q13.4 (RP11). Molec. Cell 8:375- 381, 2001.

GAM189 246 PRPF31 Weidenhammer, E. M.; Singh, M.; Ruiz- Noriega, M.; Woolford, J.L., Jr.: The 3 B c
PRP31 gene encodes a novel protein required for pre- mRNAsplicing in
Saccharomyces cerevisiae. Nucleic Acids Res. 24: 1164- 1170,1996.

GAM189 246 PSMD9 Thomas, M. K.; Yao, K.- M.; Tenser, M. S.; Wong, G. G.; Habener,J. F.: 3 B c
Bridge- 1, a novel PDZ- domain coactivator of E2A- mediated regulationof
insulin gene transcription. Molec. Cell. Biol. 19: 8492- 8504,1999.

GAM189 246 PSMD9 Watanabe, T. K.; Saito, A.; Suzuki, M.; Fujiwara, T.; Takahashi,E.; 3 B c
Slaughter, C. A.; DeMartino, G. N.; Hendil, K. B.; Chung, C. H.;Tanahashi,
N.; Tanaka, K.: cDNA cloning and characterization of ahuman proteasomal
modulator subunit, p27 (PSMD9). Genomics 50: 241- 250,1998.

GAM189 246 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 3 B b
Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly,
F.: Characterization of new mutations in the codingsequence and 5- prime-
untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum.
Genet. 108: 148- 155, 2001.

GAM189 246 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 3 B b
Molecular cloning and expression of human prostacyclin synthase.
Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM189 246 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 3 B b
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.;
Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences,
gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42,
1996.

GAM189 246 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 3 B b
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM189 246 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 3 B b
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase
(PTGIS): genomic organization, chromosomal localization,and promoter
activity. Genomics 36: 296- 304, 1996.

GAM189 246 PTK2 Andre, E.; Becker- Andre, M.: Expression of an N- terminally truncatedform 3 B b
of human focal adhesion kinase in brain. Biochem. Biophys. Res.Commun. 190:
140- 147, 1993.

GAM189 246 PTK2 Fiedorek, F. T., Jr.; Kay, E. S.: Mapping of the focal adhesionkinase (Fadk) 3 B b
gene to mouse chromosome 15 and human chromosome 8. MammalianGenome 6: 123-
126, 1995.

GAM189 246 PTK2 Polte, T. R.; Hanks, S. K.: Interaction between focal adhesionkinase and 3 B b
Crk- associated tyrosine kinase substrate p130- Cas. Proc.Nat. Acad. Sci.
92: 10678- 10682, 1995.

GAM189 246 PTK2 Schaller, M. D.; Borgman, C.; Cobb, B. S.; Vines, R. R.; Reynolds,A. B.; 3 B b
Parsons, J. T.: pp125(FAK), a structurally distinctive protein-

tyrosinekinase associated with focal adhesions. Proc. Nat. Acad. Sci. 89:5192- 5196, 1992.

GAM189 246 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999. 3 B b

GAM189 246 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000. 3 B b

GAM189 246 RAB4A Barbosa, M. D. F. S.; Johnson, S. A.; Achey, K.; Gutierrez, M.;Wakeland, E. K.; Zerial, M.; Kingsmore, S. F.: The Rab protein family:genetic mapping of six Rab genes in the mouse. Genomics 30: 439- 444,1995. 3 B c

GAM189 246 RAB4A Rousseau- Merck, M.- F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350-354, 1991. 3 B c

GAM189 246 RAB4A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes encode a family of GTP- binding proteins related to yeastYPT1 and SEC4 products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989. 3 B c

GAM189 246 RBL2 Baldi, A.; Boccia, V.; Claudio, P. P.; De Luca, A.; Giordano, A.: Genomic structure of the human retinoblastoma- related Rb2/p130 gene. Proc.Nat. Acad. Sci. 93: 4629- 4632, 1996. 3 B c

GAM189 246 RBL2 Mayol, X.; Grana, X.; Baldi, A.; Sang, N.; Hu, Q.; Giordano, A.: Cloning of a new member of the retinoblastoma gene family (pRb2)which binds to the E1A transforming domain. Oncogene 8: 2561- 2566,1993. 3 B c

GAM189 246 RBL2 Yeung, R. S.; Bell, D. W.; Testa, J. R.; Mayol, X.; Baldi, A.;Grana, X.; Klinga- Levan, K.; Knudson, A. G.; Giordano, A.: The retinoblastoma-relatedgene, RB2, maps to human chromosome 16q12 and rat chromosome 19. Oncogene 8:3465- 3468, 1993. 3 B c

GAM189 246 RGS3 Chatterjee, T. K.; Eapen, A.; Kanis, A. B.; Fisher, R. A.: Genomicorganization, 5- prime- flanking region, and chromosomal localizationof the human RGS3 gene. Genomics 45: 429- 433, 1997. 3 B c

GAM189 246 RGS3 Druey, K. M.; Blumer, K. J.; Kang, V. H.; Kehrl, J. H.: Inhibitionof G-protein- mediated MAP kinase activation by a new mammalian genefamily. Nature 379: 742- 746, 1996. 3 B c

GAM189 246 RGS3 Lu, Q.; Sun, E. E.; Klein, R. S.; Flanagan, J. G.: Ephrin- B reversesignaling is mediated by a novel PDZ- RGS protein and selectively inhibitsG protein- coupled chemoattraction. Cell 105: 69- 79, 2001. 3 B c

GAM189 246 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993. 3 B b

GAM189 246 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA amplification. New Eng. J. Med. 329: 607- 610, 1993. 3 B b

GAM189 246 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. Med. 339: 1775- 1777, 1998. 3 B b

GAM189 246 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand molecular genetics. Blood Rev. 8: 199- 212, 1994. 3 B b

GAM189 246 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood 3 B b

group polymorphism as determined by Southern analysis. Blood 78:2747- 2752, 1991.

GAM189 246 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and its association with universal edema of the fetus, icterusgravis neonatorum and anemia of the newborn. J. Pediat. 1: 269- 309,1932. 3 B b

GAM189 246 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989. 3 B b

GAM189 246 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with sickle cell disease. Transfusion 37: 357- 361, 1997. 3 B b

GAM189 246 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 B b

GAM189 246 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the human RH locus: a family study of the red- cell Evans phenotypereveals a transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59: 825- 833, 1996. 3 B b

GAM189 246 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J. Hum. Genet. 58: 133- 142, 1996. 3 B b

GAM189 246 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of Rh blood group genes: association between restrictionfragment length polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994. 3 B b

GAM189 246 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine years and some observations on the biochemistry and geneticsof the system. Transfusion Med. Rev. 3: 1- 12, 1989. 3 B b

GAM189 246 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh genes revealed by analysis of unrelated donors with therare D- - phenotype. Am. J. Hum. Genet. 59: 1066- 1073, 1996. 3 B b

GAM189 246 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by alternative splicing. Blood 80: 1074- 1078, 1992. 3 B b

GAM189 246 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929, 1992. 3 B b

GAM189 246 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE genotyping for correct blood group determination inchronically transfused patients. Transfusion 39: 852- 855, 1999. 3 B b

GAM189 246 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A. 116:825- 827, 1941. 3 B b

GAM189 246 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal plasma. New Eng. J. Med. 339: 1734- 1738, 1998. 3 B b

GAM189 246 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome 1. Am. J. Med. Genet. 104: 250- 256, 2001. 3 B b

GAM189 246 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J. 3 B b

Clin. Invest. 100: 373- 379, 1997.

GAM189 246 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 B b
153:771- 772, 1944.

GAM189 246 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 B b
ed.): 1975.

GAM189 246 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 3 B b
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII)
category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM189 246 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 3 B b
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral
transduction of K562 cells establishes the molecular basisof Rh blood group
antigens. Blood 87: 2968- 2973, 1996.

GAM189 246 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 3 B b
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang.
58: 50- 55, 1990.

GAM189 246 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 3 B b
Blood 95: 3662- 3668, 2000.

GAM189 246 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 3 B b
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393,
1999.

GAM189 246 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 3 B b
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311,
2002.

GAM189 246 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 B b

GAM189 246 RPH3AL Kotake, K.; Ozaki, N.; Mizuta, M.; Sekiya, S.; Inagaki, N.; Seino,S.: Noc2, 3 B b
a putative zinc finger protein involved in exocytosis inendocrine cells. J.
Biol. Chem. 272: 29407- 29410, 1997.

GAM189 246 RPH3AL Smith, J. S.; Tachibana, I.; Allen, C.; Chiappa, S. A.; Lee, H.K.; McIver, 3 B b
B.; Jenkins, R. B.; Raffel, C.: Cloning of a human ortholog(RPH3AL) of
(RNO)Rph3al from a candidate 17p13.3 medulloblastoma tumorsuppressor locus.
Genomics 59: 97- 101, 1999.

GAM189 246 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two 3 B b
scleroderma autoimmune antigens that copurify with human ribonucleaseP.
Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997.

GAM189 246 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: 3 B b
Autoantigenic properties of some protein subunits of catalyticallyactive
complexes of human ribonuclease P. RNA 4: 407- 417, 1998.

GAM189 246 SAS Jankowski, S. A.; De Jong, P.; Meltzer, P. S.: Genomic structureof SAS, a 3 B b
member of the transmembrane 4 superfamily amplified in humansarcomas.
Genomics 25: 501- 506, 1995.

GAM189 246 SAS Meltzer, P. S.; Jankowski, S. A.; Dal Cin, P.; Sandberg, A. A.;Paz, I. B.; 3 B b
Coccia, M. A.; Smith, S. H.: Identification and cloningof a novel amplified
DNA sequence in human malignant fibrous histiocytomaderived from a region of
chromosome 12 frequently rearranged in softtissue tumors. (Abstract)
Cytogenet. Cell Genet. 58: 1979 only,1991.

GAM189 246 SCD Cohen, P.; Miyazaki, M.; Socci, N. D.; Hagge- Greenberg, A. Liedtke,W.; 3 B c
Soukas, A. A.; Sharma, R.; Hudgins, L. C.; Ntambi, J. M.; Friedman,J. M.:
Role for stearoyl- CoA desaturase- 1 in leptin- mediated weightloss. Science
297: 240- 243, 2002.

GAM189 246 SCD Li, J.; Ding, S.- F.; Habib, N. A.; Fermor, B. F.; Wood, C. B.;Gilmour, R. 3 B c

S.: Partial characterization of a cDNA for human stearoyl- CoAdesaturase and changes in its mRNA expression in some normal and malignanttissues. Int. J. Cancer 57: 348- 352, 1994.

GAM189 246 SCD Ntambi, J. M.; Miyazaki, M.; Stoehr, J. P.; Lan, H.; Kendziorski,C. M.; Yandell, B. S.; Song, Y.; Cohen, P.; Friedman, J. M.; Attie,A. D.: Loss of stearoyl- CoA desaturase- 1 function protects mice againstadiposity. Proc. Nat. Acad. Sci. 99: 11482- 11486, 2002. 3 B c

GAM189 246 SCD Thiede, M. A.; Ozols, J.; Strittmatter, P.: Construction and sequenceof cDNA for rat liver stearyl coenzyme A desaturase. J. Biol. Chem. 261:13230- 13235, 1986. 3 B c

GAM189 246 SCD Zhang, L.; Ge, L.; Parimoo, S.; Stenn, K.; Prouty, S. M.: Humanstearoyl- CoA desaturase: alternative transcripts generated from asingle gene by usage of tandem polyadenylation sites. Biochem. J. 340:255- 264, 1999. 3 B c

GAM189 246 SCD Zheng, Y.; Eilertsen, K. J.; Ge, L.; Zhang, L.; Sundberg, J. P.;Prouty, S. M.; Stenn, K. S.; Parimoo, S.: Scd1 is expressed in sebaceousglands and is disrupted in the asebia mouse. (Letter) Nature Genet. 23:268- 270, 1999. 3 B c

GAM189 246 SCN2B Bolino, A.; Seri, M.; Caroli, F.; Eubanks, J.; Srinivasan, J.;Mandich, P.; Schenone, A.; Quattrone, A.; Romeo, G.; Catterall, W.A.; Devoto, M.: Exclusion of the SCN2B gene as candidate for CMT4B. Europ.J. Hum. Genet. 6: 629- 634, 1998. 3 B c

GAM189 246 SCN2B Eubanks, J.; Srinivasan, J.; Dinulos, M. B.; Disteche, C. M.; Catterall,W. A.: Structure and chromosomal localization of the beta2 subunitof the human brain sodium channel. Neuroreport 8: 2775- 2779, 1997. 3 B c

GAM189 246 SCN2B Imai, K.; Kingsley, D. M.: Mouse chromosome 9. Mammalian Genome 5:S139- S153, 1994. 3 B c

GAM189 246 SCN2B Isom, L. L.; Ragsdale, D. S.; De Jongh, K. S.; Westenbroek, R.E.; Reber, B. F. X.; Scheuer, T.; Catterall, W. A.: Structure andfunction of the beta- 2 subunit of brain sodium channels, a transmembraneglycoprotein with a CAM motif. Cell 83: 433- 442, 1995. 3 B c

GAM189 246 SCN2B Jones, J. M.; Meisler, M. H.; Isom, L. L.: Scn2b, a voltage- gatedsodium channel beta- 2 gene on mouse chromosome 9. Genomics 34: 258- 259,1996. 3 B c

GAM189 246 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 B b

GAM189 246 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 B b

GAM189 246 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 B b

GAM189 246 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999. 3 B b

GAM189 246 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; 3 B b

Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM189 246 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001. 3 B b

GAM189 246 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five- base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000. 3 B b

GAM189 246 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001. 3 B b

GAM189 246 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002. 3 B b

GAM189 246 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001. 3 B b

GAM189 246 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999. 3 B b

GAM189 246 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001. 3 B b

GAM189 246 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996. 3 B b

GAM189 246 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001. 3 B b

GAM189 246 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 B b

GAM189 246 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996. 3 B b

GAM189 246 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 3 B c

GAM189 246 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping 3 B c

of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000.

GAM189 246 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; 3 B c
D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.;
Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification
of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and
basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000.

GAM189 246 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, 3 B b
C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe
transactivation domain induces bony abnormalities and cooperateswith LMO1 to
generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419,
1997.

GAM189 246 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; 3 B b
Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J
recombinase activity. Science 250: 1426- 1429, 1990.

GAM189 246 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; 3 B b
Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor
SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992.

GAM189 246 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, 3 B b
G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common
occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990.

GAM189 246 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and 3 B b
characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995.

GAM189 246 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; 3 B b
Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic
axial development and left- right specification. Nature 399:691- 694, 1999.

GAM189 246 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; 3 B c
Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.;
Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive
disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998.

GAM189 246 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, 3 B c
P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea
transporter in the human kidney. FEBS Lett. 386: 156- 160,1996.

GAM189 246 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; 3 B c
Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.;
Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2
is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157-
2164, 2001.

GAM189 246 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human 3 B b
intestine:biology and function. Gastroenterology 113: 332- 340, 1997.

GAM189 246 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; 3 B b
Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning
of a mammalian proton- coupled oligopeptide transporter. Nature 368:563-
566, 1994.

GAM189 246 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, 3 B b
T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal
H(+)/peptide cotransporter: cloning, functional expression,and chromosomal
localization. J. Biol. Chem. 270: 6456- 6463, 1995.

GAM189 246 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA 3 B b
cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a
revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998.

GAM189 246 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 3 B b

GAM189 246 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses and phylogenetic characterization of the ZIP family of metalion transport proteins. J. Membr. Biol. 166: 1- 7, 1998. 3 B b

GAM189 246 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping within the epidermal differentiation complex. Genomics 62:272- 280, 1999. 3 B b

GAM189 246 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC fragmentation map of 1q21. Genomics 49: 200- 208, 1998. 3 B b

GAM189 246 SLC6A3 Byerley, W.; Hoff, M.; Holik, J.; Caron, M. G.; Giros, B.: VNTRpolymorphism for the human dopamine transporter gene (DAT1). Hum.Molec. Genet. 2: 335, 1993. 3 B c

GAM189 246 SLC6A3 Cook, E. H., Jr.; Stein, M. A.; Krasowski, M. D.; Cox, N. J.; Olkon,D. M.; Kieffer, J. E.; Leventhal, B. L.: Association of attention- deficitdisorder and the dopamine transporter gene. Am. J. Hum. Genet. 56:993- 998, 1995. 3 B c

GAM189 246 SLC6A3 Doucette- Stamm, L.; Blakely, D. J.; Tian, J.; Mockus, S.; Mao,J.: Population genetic study of the human dopamine transporter gene(DAT1). Genet. Epidemiol. 12: 303- 308, 1995. 3 B c

GAM189 246 SLC6A3 Gainetdinov, R. R.; Wetsel, W. C.; Jones, S. R.; Levin, E. D.;Jaber, M.; Caron, M. G.: Role of serotonin in the paradoxical calmingeffect of psychostimulants on hyperactivity. Science 283: 397- 401,1999. 3 B c

GAM189 246 SLC6A3 Gelernter, J.; Vandenbergh, D.; Kruger, S. D.; Pauls, D. L.; Kurlan,R.; Pakstis, A. J.; Kidd, K. K.; Uhl, G.: The dopamine transporterprotein gene (SLC6A3): primary linkage mapping and linkage studiesin Tourette syndrome. Genomics 30: 459- 463, 1995. 3 B c

GAM189 246 SLC6A3 Gill, M.; Daly, G.; Heron, S.; Hawi, Z.; Fitgerald, M.: Confirmationof association between attention deficit hyperactivity disorder anda dopamine transporter polymorphism. Molec. Psychiat. 2: 311- 313,1997. 3 B c

GAM189 246 SLC6A3 Giros, B.; El Mestikawy, S.; Godinot, N.; Zheng, K.; Han, H.; Yang- Feng,T.; Caron, M. G.: Cloning, pharmacological characterization, andchromosome assignment of the human dopamine transporter. Molec. Pharm. 42:383- 390, 1992. 3 B c

GAM189 246 SLC6A3 Giros, B.; Jaber, M.; Jones, S. R.; Wightman, R. M.; Caron, M.G.: Hyperlocomotion and indifference to cocaine and amphetamine inmice lacking the dopamine receptor. Nature 370: 606- 612, 1996. 3 B c

GAM189 246 SLC6A3 Goldman, D.: Dopamine transporter, alcoholism and other diseases. NatureMed. 1: 624- 625, 1995. 3 B c

GAM189 246 SLC6A3 Kurlan, R.; Behr, J.; Medved, L.; Shoulson, I.; Pauls, D.; Kidd,J. R.; Kidd, K. K.: Familial Tourette's syndrome: report of a largepedigree and potential for linkage analysis. Neurology 36: 772- 776,1986. 3 B c

GAM189 246 SLC6A3 Lerman, C.; Caporaso, N. E.; Audrain, J.; Main, D.; Bowman, E.D.; Lockshin, B.; Boyd, N. R.; Shields, P. G.: Evidence suggestingthe role of specific genetic factors in cigarette smoking. HealthPsych. 18: 14- 20, 1999. 3 B c

GAM189 246 SLC6A3 Lossie, A. C.; Vandenbergh, D. J.; Uhl, G. R.; Camper, S. A.:Localization of the dopamine transporter gene, Dat1, on mouse chromosome 3 B c

GAM189 246 SLC6A3 Mammalian Genome 5: 117- 118, 1994.13. Sabol, S. Z.; Nelson, M. L.; Fisher, 3 B c

C.; Gunzerath, L.; Brody,C. L.; Hu, S.; Sirota, L. A.; Marcus, S. E.; Greenberg, B. D.; Lucas,F. R., IV; Benjamin, J.; Murphy, D. L.; Hamer, D. H.: A genetic associationfor cigarette smoking behavior. Health Psych. 18: 7- 13, 1999.

GAM189 246 SLC6A3 Tiihonen, J.; Kuikka, J.; Bergstrom, K.; Hakola, P.; Karhu, J.;Ryynanen, O.- 3 B c
P.; Fohr, J.: Altered striatal dopamine re- uptake sitedensities in habitually violent and non- violent alcoholics. NatureMed. 1: 654- 657, 1995.

GAM189 246 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Hawkins, A. L.; Griffin, C.A.; Li, X.; 3 B c
Jabs, E. W.; Uhl, G. R.: Human dopamine transporter gene(DAT1) maps to chromosome 5p15.3 and displays a VNTR. Genomics 14:1104- 1106, 1992.

GAM189 246 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Uhl, G. R.: A human dopaminetransporter 3 B c
cDNA predicts reduced glycosylation, displays a novelrepetitive element and provides racially- dimorphic TaqI RFLPs. Molec.Brain Res. 15: 161- 166, 1992.

GAM189 246 SLC6A3 Waldman, I. D.; Rowe, D. C.; Abramowitz, A.; Kozel, S. T.; Mohr,J. H.; 3 B c
Sherman, S. L.; Cleveland, H. H.; Sanders, M. L.; Gard, J.M. C.; Stever, C.: Association and linkage of the dopamine transportergene and attention- deficit hyperactivity disorder in children: heterogeneityowing to diagnostic subtype and severity. Am. J. Hum. Genet. 63:1767- 1776, 1998.

GAM189 246 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland 3 B b
biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855- 862, 2000.

GAM189 246 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein 3 B b
that promotes cytochrome c- dependent caspase activation byeliminating IAP inhibition. Cell 102: 33- 42, 2000.

GAM189 246 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; 3 B b
Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000.

GAM189 246 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; 3 B b
Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509- 3517, 2002.

GAM189 246 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 B b

GAM189 246 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; 3 B b
Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.: A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates caspase activity and apoptosis. Nature 410:112- 116, 2001.

GAM189 246 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, 3 B b
G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO, a mammalian protein that promotes apoptosis by bindingto and antagonizing IAP proteins. Cell 102: 43- 53, 2000.

GAM189 246 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: 3 B b
Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012, 2000.

GAM189 246 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from 3 B c
lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998.

GAM189 246 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; 3 B c
Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic

organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle-membranefusion processes. Hum. Genet. 108: 211- 215, 2001.

GAM189 246 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- 3 B c
membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells.
Biochem. Biophys. Res. Commun. 231: 808- 812, 1997.

GAM189 246 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel 3 B c
syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in
non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996.

GAM189 246 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: 3 B c
Identification of three new splice variants of the SNARE proteinSNAP- 23.
Biochem. Biophys. Res. Commun. 285: 320- 327, 2001.

GAM189 246 SPN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, 3 B b
J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM-
dependent movement of CD43 defines a novelprotein complex distal to the
immunological synapse. Immunity 15:739- 750, 2001.

GAM189 246 SPN Baecher, C. M.; Dorfman, K. S.; Mattei, M.- G.; Frelinger, J. G.: cDNA 3 B b
cloning and localization of the mouse leukosialin gene (Ly48)to chromosome
7. Immunogenetics 31: 307- 314, 1990.

GAM189 246 SPN Bazil, V.; Strominger, J. L.: CD43, the major sialoglycoproteinof human 3 B b
leukocytes, is proteolytically cleaved from the surface ofstimulated
lymphocytes and granulocytes. Proc. Nat. Acad. Sci. 90:3792- 3796, 1993.

GAM189 246 SPN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe 3 B b
immunological synapse is mediated by phosphorylation- regulatedrelocation of
the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001.

GAM189 246 SPN Pallant, A.; Eskenazi, A.; Mattei, M.- G.; Fournier, R. E. K.; Carlsson,S. 3 B b
R.; Fukuda, M.; Frelinger, J. G.: Characterization of cDNAs encodinghuman
leukosialin and localization of the leukosialin gene to chromosome16. Proc.
Nat. Acad. Sci. 86: 1328- 1332, 1989.

GAM189 246 SPN Park, J. K.; Rosenstein, Y. J.; Remold- O'Donnell, E.; Bierer, B.E.; Rosen, 3 B b
F. S.; Burakoff, S. J.: Enhancement of T- cell activationby the CD43
molecule whose expression is defective in Wiskott- Aldrichsyndrome. Nature
350: 706- 709, 1991.

GAM189 246 SPN Rosenstein, Y.; Park, J. K.; Hahn, W. C.; Rosen, F. S.; Bierer,B. E.; 3 B b
Burakoff, S. J.: CD43, a molecule defective in Wiskott- Aldrichsyndrome,
binds ICAM- 1. Nature 354: 233- 235, 1991.

GAM189 246 SPN Schmid, K.; Hediger, M. A.; Brossmer, R.; Collins, J. H.; Haupt,H.; Marti, 3 B b
T.; Offner, G. D.; Schaller, J.; Takagaki, K.; Walsh, M.T.; Schwick, H. G.;
Rosen, F. S.; Remold- O'Donnell, E.: Amino acidsequence of human plasma
galactoglycoprotein: identity with the extracellularregion of CD43
(sialophorin). Proc. Nat. Acad. Sci. 89: 663- 667,1992.

GAM189 246 SPN Shelley, C. S.; Carroll, M. C.; Davis, A. E., III; Bruns, G. A.P.; 3 B b
Whitehead, A. S.; Finberg, R.; Remold- O'Donnell, E.; Rosen, F.S.: Human
sialophorin: cDNA cloning and gene location. (Abstract) FASEBJ. 2: A1659
only, 1988.

GAM189 246 SPN Shelley, C. S.; Remold- O'Donnell, E.; Davis, A. E., III; Bruns,G. A. P.; 3 B b
Rosen, F. S.; Carroll, M. C.; Whitehead, A. S.: Molecularcharacterization of
sialophorin (CD43), the lymphocyte surface sialoglycoproteindefective in
Wiskott- Aldrich syndrome. Proc. Nat. Acad. Sci. 86:2819- 2823, 1989.

GAM189 246 SPN Shelley, C. S.; Remold- O'Donnell, E.; Rosen, F. S.; Whitehead,A. S.: 3 B b

Structure of the human sialophorin (CD43) gene: identificationof features atypical of genes encoding integral membrane proteins. Biochem.J. 270: 569-576, 1990.

GAM189 246 SPN van den Berg, T. K.; Nath, D.; Ziltener, H. J.; Vestweber, D.;Fukuda, M.; 3 B b van Die, I.; Crocker, P. R.: Cutting edge: CD43 functionsas a T cell counterreceptor for the macrophage adhesion receptor sialoadhesin(Siglec-1). J. Immun. 166: 3637- 3640, 2001.

GAM189 246 SRRM2 Blencowe, B. J.; Bauren, G.; Eldridge, A. G.; Issner, R.; Nickerson,J. A.; 3 B c Rosonina, E.; Sharp, P. A.: The SRm160/300 splicing coactivatorsubunits. RNA 6: 111- 120, 2000.

GAM189 246 SRRM2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B c Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM189 246 SRRM2 Sawada, Y.; Miura, Y.; Umeki, K.; Tamaoki, T.; Fujinaga, K.; Ohtaki,S.: 3 B c Cloning and characterization of a novel RNA- binding protein SRL300with RS domains. Biochim. Biophys. Acta 1492: 191- 195, 2000.

GAM189 246 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 3 B b L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM189 246 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 3 B b J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM189 246 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 3 B b Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand characterization of the mouse homolog of SYT, a gene implicatedin the development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM189 246 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 3 B b G.: Mapping and characterization of the mouse and humanSS18 genes, two human SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-319, 2001.

GAM189 246 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 B b Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene family with several members transcribed in normaltestis and human cancer. Int. J. Cancer 72: 965- 971, 1997.

GAM189 246 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 B b Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM189 246 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 B b Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J. Nat. Cancer Inst. 91: 974- 975, 1999.

GAM189 246 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 B b Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX synovial sarcoma translocation proteins and co- localizationwith the SNF protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM189 246 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 B b Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in

synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM189 246 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- 3 B b
strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence
insitu hybridization. Genomics 36: 527- 529, 1996.

GAM189 246 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence 3 B b
homologue of staufen is an RNA- binding protein thatis associated with
polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell.
Biol. 19: 2212- 2219, 1999.

GAM189 246 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: 3 B b
Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein
which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19:
2220- 2230, 1999.

GAM189 246 STE Aksoy, I. A.; Wood, T. C.; Weinshilboum, R.: Human liver 3 B b
estrogensulfotransferase: identification by cDNA cloning and expression.
Biochem.Biophys. Res. Commun. 200: 1621- 1629, 1994.

GAM189 246 STE Bernier, F.; Leblanc, G.; Labrie, F.; Luu- The, V.: Structure ofhuman 3 B b
estrogen and aryl sulfotransferase gene: two mRNA species issuedfrom a
single gene. J. Biol. Chem. 269: 28200- 28205, 1994.

GAM189 246 STE Her, C.; Aksoy, I. A.; Kimura, S.; Brandriff, B. F.; Wasmuth, J.J.; 3 B b
Weinshilboum, R. M.: Human estrogen sulfotransferase gene (STE):cloning,
structure, and chromosomal localization. Genomics 29: 16- 23,1995.

GAM189 246 STE Weinshilboum, R. M.; Otterness, D. M.; Aksoy, I. A.; Wood, T. C.;Her, C.; 3 B b
Raftogianis, R. B.: Sulfotransferase molecular biology:cDNAs and genes.
FASEB J. 11: 3- 14, 1997.

GAM189 246 STE Weinshilboum, R.: Personal Communication. Rochester, Minn. 10/9/1995. 3 B b

GAM189 246 TAL1 Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, 3 B c
C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe
transactivation domain induces bony abnormalities and cooperateswith LMO1 to
generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419,
1997.

GAM189 246 TAL1 Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; 3 B c
Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor
SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992.

GAM189 246 TAL1 Begley, C. G.; Aplan, P. D.; Davey, M. P.; Nakahara, K.; Tchorz,K.; 3 B c
Kurtzberg, J.; Hershfield, M. S.; Haynes, B. F.; Cohen, D. I.;Waldmann, T.
A.; Kirsch, I. R.: Chromosomal translocation in a humanleukemic stem- cell
line disrupts the T- cell antigen receptor delta- chaindiversity region and
results in a previously unreported fusion transcript. Proc.Nat. Acad. Sci.
86: 2031- 2035, 1989.

GAM189 246 TAL1 Begley, C. G.; Visvader, J.; Green, A. R.; Aplan, P. D.; Metcalf,D.; Kirsch, 3 B c
I. R.; Gough, N. M.: Molecular cloning and chromosomallocalization of the
murine homolog of the human helix- loop- helix geneSCL. Proc. Nat. Acad.
Sci. 88: 869- 873, 1991.

GAM189 246 TAL1 Finger, L. R.; Kagan, J.; Christopher, G.; Kurtzberg, J.; Hershfield,M. S.; 3 B c
Nowell, P. C.; Croce, C. M.: Involvement of the TCL5 geneon human chromosome
1 in T- cell leukemia and melanoma. Proc. Nat.Acad. Sci. 86: 5039- 5043,
1989.

GAM189 246 TAL1 Gottgens, B.; Barton, L. M.; Chapman, M. A.; Sinclair, A. M.; Knudsen,B.; 3 B c
Grafham, D.; Gilbert, J. G. R.; Rogers, J.; Bentley, D. R.; Green,A. R.:
Transcriptional regulation of the stem cell leukemia gene(SCL)- -

comparative analysis of five vertebrate SCL loci. Genome Res. 12:749- 759, 2002.

GAM189 246 TAL1 Gottgens, B.; Gilbert, J. G.; Barton, L. M.; Grafham, D.; Rogers,J.; Bentley, D. R.; Green, A. R.: Long- range comparison of humanand mouse SCL loci: localized regions of sensitivity to restrictionendonucleases correspond precisely with peaks of conserved noncodingsequences. Genome Res. 11: 87- 97, 2001. 3 B c

GAM189 246 TAL1 Kocher, O.; Cheresh, P.; Lee, S. W.: Identification and partialcharacterization of a novel membrane- associated protein (MAP17) up-regulatedin human carcinomas and modulating cell replication and tumor growth. Am.J. Path. 149: 493- 500, 1996. 3 B c

GAM189 246 TAL1 Kozak, M.: An analysis of 5- prime- noncoding sequences from 699vertebrate messenger RNAs. Nucleic Acids Res. 15: 8125- 8148, 1987. 3 B c

GAM189 246 TAL1 Kurtzberg, J.; Bigner, S. H.; Hershfield, M. S.: Establishmentof the DU.528 human lymphohemopoietic stem cell line. J. Exp. Med. 162:1561- 1578, 1985. 3 B c

GAM189 246 TAL1 Robb, L.; Lyons, I.; Li, R.; Hartley, L.; Kontgen, F.; Harvey,R. P.; Metcalf, D.; Begley, C. G.: Absence of yolk sac hematopoiesisfrom mice with a targeted disruption of the scl gene. Proc. Nat.Acad. Sci. 92: 7075- 7079, 1995. 3 B c

GAM189 246 TAL1 Shivdasani, R. A.; Mayer, E. L.; Orkin, S. H.: Absence of bloodformation in mice lacking the T- cell leukaemia oncoprotein tal- 1/SCL. Nature 373:432-434, 1995. 3 B c

GAM189 246 TAL1 Sinclair, A. M.; Bench, A. J.; Bloor, A. J. C.; Li, J.; Gottgens,B.; Stanley, M. L.; Miller, J.; Piltz, S.; Hunter, S.; Nacheva, E.P.; Sanchez, M.- J.; Green, A. R.: Rescue of the lethal scl- /- phenotypeby the human SCL locus. Blood 99: 3931- 3938, 2002. 3 B c

GAM189 246 TAL1 Williams, M.; Lyu, M. S.; Yang, Y. L.; Lin, E. P.; Dunbrack, R.;Birren, B.; Cunningham, J.; Hunter, K.: Ier5, a novel member of theslow- kinetics immediate- early genes. Genomics 44: 327- 334, 1999. 3 B c

GAM189 246 TAL1 Xia, Y.; Brown, L.; Yang, C. Y.- C.; Tsou Tsan, J.; Siciliano,M. J.; Espinosa, R., III; Le Beau, M. M.; Baer, R. J.: TAL2, a helix- loop-helixgene activated by the (7;9)(q34;q32) translocation in human T-cellleukemia. Proc. Nat. Acad. Sci. 88: 11416- 11420, 1991. 3 B c

GAM189 246 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459-467, 1998. 3 B b

GAM189 246 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 B b

GAM189 246 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 B b

GAM189 246 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 B b

GAM189 246 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 B b

GAM189 246 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; 3 B b

Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002.

GAM189 246 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; 3 B b
Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496- 1498, 2002.

GAM189 246 TAT Barton, D. E.; Yang- Feng, T. L.; Francke, U.: The human 3 B c
tyrosineaminotransferase gene mapped to the long arm of chromosome 16 (region16q22- q24) by somatic cell hybrid analysis and in situ hybridization. Hum.Genet. 72: 221- 224, 1986.

GAM189 246 TAT Beinfang, D. C.; Kuwabara, T.; Pueschel, S. M.: The Richner- 3 B c
Hanhartsyndrome: report of a case with associated tyrosinemia. Arch. Ophthal. 94:1133- 1137, 1976.

GAM189 246 TAT Bohnert, A.; Anton- Lamprecht, I.: Richner- Hanhart's 3 B c
syndrome:ultrastructural abnormalities of epidermal keratinization indicatinga causal relationship to high intracellular tyrosine levels. J. Invest.Derm. 79: 68- 74, 1982.

GAM189 246 TAT Buist, N.: Phenylketonuria and related problems.In: Nyhan, W.L.: Amino Acid 3 B c
Metabolism and Genetic Variation. New York: McGraw- Hill(pub.) 1967. Pp. 117 only.

GAM189 246 TAT Chitayat, D.; Balbul, A.; Hani, V.; Mamer, O. A.; Clow, C.; Scriver,C. R.: 3 B c
Hereditary tyrosinaemia type II in a consanguineous AshkenaziJewish family: intrafamilial variation in phenotype; absence of parentalphenotype effects on the fetus. J. Inherit. Metab. Dis. 15: 198- 203,1992.

GAM189 246 TAT Crovato, F.; Desirello, G.; Gatti, R.; Babbini, N.; Rebora, A.: Richner- 3 B c
Hanhart syndrome spares a plantar autograft. Arch. Derm. 121:539- 540, 1985.

GAM189 246 TAT Fellman, J. H.; Vanbellinghen, P. J.; Jones, R. T.; Koler, R. D.: Soluble 3 B c
and mitochondrial forms of tyrosine aminotransferase: relationshipto human tyrosinemia. Biochemistry 8: 615- 622, 1969.

GAM189 246 TAT Garibaldi, L. R.; Siliato, F.; De Martini, I.; Scarsi, M. R.; Romano,C.: 3 B c
Oculocutaneous tyrosinosis: report of two cases in the same family. Helv.Paediat. Acta 32: 173- 180, 1977.

GAM189 246 TAT Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald,P. S.; 3 B c
Baden, H. P.: Tyrosinemia with plantar and palmar keratosisand keratitis. J. Pediat. 83: 798- 805, 1973.

GAM189 246 TAT Hanhart, E.: Neue Sonderformen von Keratosis palmo- plantaris,u.a. eine 3 B c
regelmaessig- dominante mit systematisierten Lipomen, ferner2 einfach- rezessive mit Schwachsinn und z.T. mit Hornhautveraenderungendes Auges (Ektodermatosyndrom). Dermatologica 94: 286- 308, 1947.

GAM189 246 TAT Hunziker, N.: Richner- Hanhart syndrome and tyrosinemia type II. 3 B c
Dermatologica 160:180- 189, 1980.

GAM189 246 TAT Kennaway, N. G.; Buist, N. R. M.: Metabolic studies in a patientwith hepatic 3 B c
cytosol tyrosine aminotransferase deficiency. Pediat.Res. 5: 287- 297, 1971.

GAM189 246 TAT Muller, G.; Scherer, G.; Zentgraf, H.; Ruppert, S.; Herrmann,B.; Lehrach, 3 B c
H.; Schutz, G.: Isolation, characterization and chromosomalmapping of the mouse tyrosine aminotransferase gene. J. Molec. Biol. 184:367- 373, 1985.

GAM189 246 TAT Natt, E.; Kao, F.- T.; Rettenmeier, R.; Scherer, G.: Assignmentof the human 3 B c
tyrosine aminotransferase gene to chromosome 16. Hum.Genet. 72: 225- 228, 1986.

GAM189 246 TAT Natt, E.; Kida, K.; Odievre, M.; Di Rocco, M.; Scherer, G.: Pointmutations 3 B c
in the tyrosine aminotransferase gene in tyrosinemia typeII. Proc. Nat.
Acad. Sci. 89: 9297- 9301, 1992.

GAM189 246 TAT Natt, E.; Westphal, E.- M.; Toth- Fejel, S. E.; Magenis, R. E.;Buist, N. R. 3 B c
M.; Rettenmeier, R.; Scherer, G.: Inherited and de novodeletion of the
tyrosine aminotransferase gene locus at 16q22.1- q22.3in a patient with
tyrosinemia type II. Hum. Genet. 77: 352- 358,1987.

GAM189 246 TAT Pelet, B.; Antener, I.; Faggioni, R.; Spahr, A.; Gautier, E.:Tyrosinemia 3 B c
without liver or renal damage with plantar and palmarkeratosis and keratitis
(hypertyrosinemia type II). Helv. Paediat.Acta 34: 177- 183, 1979.

GAM189 246 TAT Rehak, A.; Selim, M. M.; Yadav, G.: Richner- Hanhart syndrome(tyrosinaemia- 3 B c
II) (report of four cases without ocular involvement). Brit.J. Derm. 104:
469- 475, 1981.

GAM189 246 TAT Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.: Isolationand 3 B c
characterization of the human tyrosine aminotransferase gene. NucleicAcids
Res. 18: 3853- 3861, 1990.

GAM189 246 TAT Richner, H.: Hornhautaffektion bei Keratoma palmare et plantarehereditarium. 3 B c
Klin. Mbl. Augenheilk. 100: 580- 588, 1938.

GAM189 246 TAT Schmid, W.; Muller, G.; Schutz, G.; Gluecksohn- Waelsch, S.: Deletionsnear 3 B c
the albino locus on chromosome 7 of the mouse affect the levelof tyrosine
aminotransferase mRNA. Proc. Nat. Acad. Sci. 82: 2866- 2869,1985.

GAM189 246 TAT Tallab, T.M.: Richner- Hanhart syndrome: importance of early diagnosisand 3 B c
early intervention. J. Am. Acad. Dermatol. 35: 857- 859, 1996.

GAM189 246 TAT Ventura, G.; Biasini, G.; Petrozzi, M.: Cheratomia palmoplantaredissipatum 3 B c
associato a lesioni corneali in due fratelli. Boll. Oculist. 44:497- 510,
1965.

GAM189 246 TAT Waardenburg, P. J.; Franceschetti, A.; Klein, D.: Genetics andOphthalmology. 3 B c
Springfield, Ill.: Charles C Thomas (pub.) 1:1961. Pp. 515- 517.

GAM189 246 TAT Westphal, E.- M.; Natt, E.; Grimm, T.; Odievre, M.; Scherer, G.: The human 3 B c
tyrosine aminotransferase gene: characterization of restrictionfragment
length polymorphisms and haplotype analysis in a family withtyrosinemia type
II. Hum. Genet. 79: 260- 264, 1988.

GAM189 246 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; 3 B c
De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription
factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8:
165- 167, 1990.

GAM189 246 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 3 B c
homeoprotein family are expressed in human liver. NucleicAcids Res. 19:
3553- 3559, 1991.

GAM189 246 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't 3 B c
Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.;
Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene
are associated with familial hypoplastic glomerulocystickidney disease. Am.
J. Hum. Genet. 68: 219- 224, 2001.

GAM189 246 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; 3 B c
Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.;
Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated
with a frameshift mutation in the transcription factorhepatocyte nuclear
factor- 1- beta. Kidney Int. 57: 898- 907, 2000.

GAM189 246 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. 3 B c

N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara, T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997.

GAM189 246 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic 3 B c glomerulocystic kidney disease: a definite entity withdominant inheritance. Am. J. Med. Genet. 34: 569- 573, 1989.

GAM189 246 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; 3 B c Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand genital malformation associated with a partial deletion of thepseudo- POU domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001- 2008, 1999.

GAM189 246 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, 3 B c S.: A low renal threshold for glucose in diabetic patientswith a mutation in the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med. 15: 816- 820, 1998.

GAM189 246 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; 3 B c Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in the hepatocyte nuclear factor- 1- beta gene associated with diabetesand renal dysfunction. Diabetes 47: 1354- 1355, 1998.

GAM189 246 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: 3 B c Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18: 263- 268, 1982.

GAM189 246 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott- 3 B c Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G. U.: The mutated human gene encoding hepatocyte nuclear factor1- beta inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad. Sci. 97: 4695- 4700, 2000.

GAM189 246 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; 3 B c Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.; Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1 are associated with human left- right lateralitydefects. Nature Genet. 26: 365- 369, 2000.

GAM189 246 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: 3 B c Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989.

GAM189 246 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, 3 B c A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002.

GAM189 246 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; 3 B c Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991.

GAM189 246 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. 3 B c A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997.

GAM189 246 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; 3 B c Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996.

GAM189 246 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, 3 B c

G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995.

GAM189 246 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in vertebratedevelopment. Trends Genet. 16: 303- 309, 2000. 3 B c

GAM189 246 TERF1 Broccoli, D.; Chong, L.; Oelmann, S.; Fernald, A. A.; Marziliano,N.; van Steensel, B.; Kipling, D.; Le Beau, M. M.; de Lange, T.:Comparison of the human and mouse genes encoding the telomeric protein,TRF1: chromosomal localization, expression and conserved protein domains. Hum.Molec. Genet. 6: 69- 76, 1997. 3 B b

GAM189 246 TERF1 Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.;Hanish, J.; Tempst, P.; de Lange, T.: A human telomeric protein. Science 270:1663- 1667, 1995. 3 B b

GAM189 246 TERF1 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001. 3 B b

GAM189 246 TERF1 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999. 3 B b

GAM189 246 TERF1 Kim, S.; Kaminker, P.; Campisi, J.: TIN2, a new regulator of telomerelength in human cells. Nature Genet. 23: 405- 412, 1999. 3 B b

GAM189 246 TERF1 Marcand, S.; Gilson, E.; Shore, D.: A protein- counting mechanismfor telomere length regulation in yeast. Science 275: 986- 990, 1997. 3 B b

GAM189 246 TERF1 Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M.: TRF1 is a critical trans- acting factor required for de novo telomereformation in human cells. Hum. Molec. Genet. 9: 2639- 2650, 2000. 3 B b

GAM189 246 TERF1 Young, A. C.; Chavez, M.; Giambernardi, T. A.; Mattern, V.; McGill,J. R.; Harris, J. M.; Sarosdy, M. F.; Patel, P.; Sakaguchi, A. Y.: Organization and expression of human telomere repeat binding factorgenes. Somat. Cell Molec. Genet. 23: 275- 286, 1997. 3 B b

GAM189 246 TERF1 Zakian, V. A.: Telomeres: beginning to understand the end. Science 270:1601- 1607, 1995. 3 B b

GAM189 246 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: Strand- specific postreplicative processing of mammalian telomeres. Science 293:2462- 2465, 2001. 3 B c

GAM189 246 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet. 17: 236- 239, 1997. 3 B c

GAM189 246 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17: 231- 235, 1997. 3 B c

GAM189 246 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001. 3 B c

GAM189 246 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999. 3 B c

GAM189 246 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered telomere state, not telomere loss. Science 295: 2446- 2449,2002. 3 B c

GAM189 246 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization 3 B c

of the transcribed human telomere repeat binding factor2 gene and comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163, 1998.

GAM189 246 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman 3 B c
telomeres from end- to- end fusions. Cell 92: 401- 413, 1998.

GAM189 246 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 B c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human telomeres. Nature Genet. 25: 347- 352, 2000.

GAM189 246 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, 3 B c
M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020- 4027, 1998.

GAM189 246 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. 3 B c
R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001.

GAM189 246 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; 3 B c
Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress different Toll- like receptors and respond to different microbialantigens. J. Exp. Med. 194: 863- 869, 2001.

GAM189 246 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; 3 B c
Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.; Mantovani, A.: Differential expression and regulation of Toll- likereceptors (TLR) in human leukocytes: selective expression of TLR3in dendritic cells. J. Immun. 164: 5998- 6004, 2000.

GAM189 246 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A 3 B c
family of human receptors structurally related to DrosophilaToll. Proc. Nat. Acad. Sci. 95: 588- 593, 1998.

GAM189 246 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; 3 B b
Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and 13 others: Dominant and recessive deafnesscaused by mutations of a novel gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277- 284, 2002.

GAM189 246 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; 3 B b
Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M. H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant, progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002.

GAM189 246 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 3 B b
B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999.

GAM189 246 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 B b
B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997.

GAM189 246 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 B b
B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr.

Biol. 7: 1003- 1006, 1997.

GAM189 246 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 B b
B W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM189 246 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 B b
B decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997.

GAM189 246 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 B b
B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997.

GAM189 246 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 B b
B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM189 246 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 B b
B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM189 246 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 B b
B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM189 246 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 B b
B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.

GAM189 246 TNFRSF9 Alderson, M. R.; Smith, C. A.; Tough, T. W.; Davis- Smith, T.; Armitage,R. 3 B c
J.; Falk, B.; Roux, E.; Baker, E.; Sutherland, G. R.; Din, W. S.;Goodwin, R. G.: Molecular and biological characterization of human4- 1BB and its ligand. Europ. J. Immun. 24: 2219- 2227, 1994.

GAM189 246 TNFRSF9 Kwon, B. S.; Weissman, S. M.: cDNA sequences of two inducibleT- cell genes. 3 B c
Proc. Nat. Acad. Sci. 86: 1963- 1967, 1989.

GAM189 246 TNFRSF9 Loo, D. T.; Chalupny, N. J.; Bajorath, J.; Shuford, W. W.; Mittler,R. S.; 3 B c
Aruffo, A.: Analysis of 4- 1BBL and laminin binding to murine4- 1BB, a member of the tumor necrosis factor receptor superfamily,and comparison with human 4- 1BB. J. Biol. Chem. 272: 6448- 6456,1997.

GAM189 246 TNFRSF9 Schwarz, H.; Arden, K.; Lotz, M.: CD137, a member of the tumornecrosis 3 B c
factor receptor family, is located on chromosome 1p36, ina cluster of related genes, and colocalizes with several malignancies. Biochem.Biophys. Res. Commun. 235: 699- 703, 1997.

GAM189 246 TNFRSF9 Schwarz, H.; Blanco, F. J.; von Kempis, J.; Valbracht, J.; Lotz,M.: lLA, a 3 B c
member of the human nerve growth factor/tumor necrosisfactor receptor family, regulates T- lymphocyte proliferation and survival. Blood 87:2839- 2845, 1996.

GAM189 246 TNFRSF9 Schwarz, H.; Tuckwell, J.; Lotz, M.: A receptor induced by 3 B c
lymphocyteactivation (ILA): a new member of the human nerve- growth- factor/tumor- necrosis- factorreceptor family. Gene 134: 295- 298, 1993.

GAM189 246 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 B b
Thiopurinemethyltransferase pharmacogenetics: alternative molecular diagnosisand preliminary data from Northern Portugal. Pharmacogenetics

9:257- 261, 1999.

GAM189 246 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 B b
McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian
populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM189 246 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 B b
Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof
thiopurine methyltransferase alleles in Caucasian and Asian populations.
Pharmacogenetics 9:37- 42, 1999.

GAM189 246 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 B b
mercaptopurine metabolism, toxic effects, and dosagerequirement in a
thiopurine methyltransferase- deficient child withacute lymphocytic
leukemia. J. Pediat. 119: 985- 989, 1991.

GAM189 246 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 B b
Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in
African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM189 246 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 B b
Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine
methyltransferase:molecular cloning and expression of T84 colon carcinoma
cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM189 246 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 B b
thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-
749, 1993.

GAM189 246 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 B b
Evans, W. E.: A single point mutation leading to loss of catalyticactivity
in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953,
1995.

GAM189 246 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 B b
variation in response to 6- mercaptopurine for childhoodacute lymphoblastic
leukaemia. Lancet 336: 225- 229, 1990.

GAM189 246 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 B b
azathioprine toxicity: relationship to thiopurine methyltransferasegenetic
polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM189 246 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 B b
Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in
thiopurine methyltransferase pharmacogenetics: evidencefor allele
specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773-
776, 1999.

GAM189 246 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human 3 B b
thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon
splice junction mutation that results in lossof activity. J. Clin. Invest.
101: 1036- 1044, 1998.

GAM189 246 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; 3 B b
Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.;
Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene
sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997.

GAM189 246 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; 3 B b
Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine
methyltransferase pharmacogenetics: human gene cloningand characterization
of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996.

GAM189 246 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: 3 B b

Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997.

GAM189 246 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; 3 B b
Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694- 702, 1996.

GAM189 246 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine 3 B b
pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980.

GAM189 246 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, 3 B c
H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor- associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF- kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997.

GAM189 246 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, 3 B c
H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661- 14664, 1996.

GAM189 246 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; 3 B c
Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999.

GAM189 246 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. 3 B c
F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997.

GAM189 246 TRPM6 Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; 3 B b
Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.; Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.: Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002.

GAM189 246 TRPM6 Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; 3 B b
Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.; Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002.

GAM189 246 TRPM6 Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, 3 B b
D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.: Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome: genetic linkage mapping and analysis of abalanced translocation breakpoint. Hum. Molec. Genet. 6: 1491- 1497,1997.

GAM189 246 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, 3 B b
psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994.

GAM189 246 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; 3 B b
Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000.

GAM189 246 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. 3 B b
D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the

pain pathway. Nature 389: 816- 824, 1997.

GAM189 246 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 3 B b

GAM189 246 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity to 'hot' chili peppers. Cell 108: 421- 430, 2002. 3 B b

GAM189 246 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000. 3 B b

GAM189 246 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996. 3 B b

GAM189 246 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel activity by protein kinase C. Nature 408: 985- 990, 2000. 3 B b

GAM189 246 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand multiple presentations of the oral irritant zingerone: relationshipto frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996. 3 B b

GAM189 246 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994. 3 B b

GAM189 246 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand pleasantness for the capsaicin burn between chili likers and non- likers:implications for liking development. Chem. Senses 18: 471- 482, 1993. 3 B b

GAM189 246 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000. 3 B b

GAM189 246 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002. 3 B b

GAM189 246 UGDH Bontemps, Y.; Maquart, F.- X.; , Wegrowski, Y.: Human UDP- glucosedehydrogenase gene: complete cloning and transcription start mapping. Biochem.Biophys. Res. Commun. 275: 981- 985, 2000. 3 B b

GAM189 246 UGDH Hempel, J.; Perozich, J.; Romovacek, H.; Hinich, A.; Kuo, I.; Feingold,D. S.: UDP- glucose dehydrogenase from bovine liver: primary structureand relationship to other dehydrogenases. Protein Sci. 3: 1074- 1080,1994. 3 B b

GAM189 246 UGDH Marcu, O.; Stathakis, D. G.; Marsh, J. L.: Assignment of the UGDHlocus encoding UDP- glucose dehydrogenase to human chromosome band4p15.1 by radiation hybrid mapping. Cytogenet. Cell Genet. 86: 244- 245,1999. 3 B b

GAM189 246 UGDH Spicer, A. P.; Kaback, L. A.; Smith, T. J.; Seldin, M. F.: Molecularcloning and characterization of the human and mouse UDP- glucose dehydrogenasegenes. J. Biol. Chem. 273: 25117- 25124, 1998. 3 B b

GAM189 246 UGDH Walsh, E. C.; Stainier, D. Y. R.: UDP- glucose dehydrogenase requiredfor cardiac valve formation in zebrafish. Science 293: 1670- 1674,2001. 3 B b

GAM189 246 UGT1A4 Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.;Yeatman, M. 3 B c

T.; Owens, I. S.: A novel complex locus UGT1 encodeshuman bilirubin, phenol, and other UDP- glucuronosyltransferase isozymeswith identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261,1992.

GAM189 246 UGT1A4 Ritter, J. K.; Crawford, J. M.; Owens, I. S.: Cloning of two humanliver 3 B c bilirubin UDP- glucuronosyltransferase cDNAs with expressionin COS- 1 cells. J. Biol. Chem. 266: 1043- 1047, 1991.

GAM189 246 UGT1A4 Tukey, R. H.; Strassburg, C. P.: Human UDP- 3 B c glucuronosyltransferases:metabolism, expression, and disease. Annu. Rev. Pharm. Toxicol. 40:581- 616, 2000.

GAM189 246 UGT1A8 Huang, Y.- H.; Galijatovic, A.; Nguyen, N.; Geske, D.; Beaton, D.;Green, J.; 3 B c Green, M.; Peters, W. H.; Tukey, R. H.: Identificationand functional characterization of UDP- glucuronosyltransferases UGT1A8*1,UGT1A8*2 and UGT1A8*3. Pharmacogenetics 12: 287- 297, 2002.

GAM189 246 UGT1A8 Mojarrabi, B.; Mackenzie, P. I.: Characterization of two UDP 3 B c glucuronosyltransferasesthat are predominantly expressed in human colon. Biochem. Biophys.Res. Commun. 247: 704- 709, 1998.

GAM189 246 UGT1A8 Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.;Yeatman, M. 3 B c T.; Owens, I. S.: A novel complex locus UGT1 encodeshuman bilirubin, phenol, and other UDP- glucuronosyltransferase isozymeswith identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261,1992.

GAM189 246 UGT1A8 Strassburg, C. P.; Manns, M. P.; Tukey, R. H.: Expression of theUDP- 3 B c glucuronosyltransferase 1A locus in human colon: identificationand characterization of the novel extrahepatic UGT1A8. J. Biol. Chem. 273:8719- 8726, 1998.

GAM189 246 UGT1A9 Findlay, K. A. B.; Kaptein, E.; Visser, T. J.; Burchell, B.: 3 B c Characterizationof the uridine diphosphate- glucuronosyltransferase- catalyzing thyroidhormone glucuronidation in man. J. Clin. Endocr. Metab. 85: 2879- 2883,2000.

GAM189 246 UGT1A9 Harding, D.; Jeremiah, S. J.; Povey, S.; Burchell, B.: Chromosomalmapping of 3 B c a human phenol UDP- glucuronosyltransferase, GNT1. Ann.Hum. Genet. 54: 17- 21, 1990.

GAM189 246 UGT1A9 Harding, D.; Jeremiah, S. J.; Povey, S.; Burchell, B.: PhenolUDP- 3 B c glucuronosyltransferase is coded by a gene on human chromosome2. (Abstract) Cytogenet. Cell Genet. 51: 1011, 1989.

GAM189 246 UGT1A9 Wooster, R.; Sutherland, L.; Ebner, T.; Clarke, D.; Da Cruz e Silva,O.; 3 B c Burchell, B.: Cloning and stable expression of a new member ofthe human liver phenol/bilirubin:UDP- glucuronosyltransferase cDNAfamily. Biochem. J. 278: 465- 469, 1991.

GAM189 246 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. 3 B c M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001.

GAM189 246 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; 3 B c Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979.

GAM189 246 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; 3 B c Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997.

GAM189 246 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; 3 B c
Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.;
Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age
related penetrance but no increased overall mortality. J.Med. Genet. 38:
508- 514, 2001.

GAM189 246 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; 3 B c
Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau
syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab.
85: 4568- 4574, 2000.

GAM189 246 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine 3 B c
l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et
l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938.

GAM189 246 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. 3 B c
G.: Two distinct phenotypes caused by two differentmissense mutations in the
same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999.

GAM189 246 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, 3 B c
F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL)
disease with pheochromocytoma in the Black Forest region ofGermany: evidence
for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM189 246 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 3 B c
Arch.Neurol. 28: 67- 68, 1973.

GAM189 246 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 3 B c
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM189 246 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 3 B c
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM189 246 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 3 B c
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM189 246 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 3 B c
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell,
J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.;
Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the
von Hippel- Lindau disease tumorsuppressor gene: correlations with
phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM189 246 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 B c
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification
of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM189 246 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 B c
disease. J.A.M.A. 178: 280- 282, 1961.

GAM189 246 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 B c
peculiar vascular new growth, probably primarily retinal,affecting both
eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM189 246 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 B c
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N.
A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of
the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of
allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM189 246 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 B c
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E.
R.: Identification of intragenic mutations in thevon Hippel- Lindau disease
tumour suppressor gene and correlation withdisease phenotype. Hum. Molec.

Genet. 3: 1303- 1308, 1994.

GAM189 246 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928. 3 B c

GAM189 246 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non-expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994. 3 B c

GAM189 246 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988. 3 B c

GAM189 246 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459-6463, 1995. 3 B c

GAM189 246 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995. 3 B c

GAM189 246 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001. 3 B c

GAM189 246 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995. 3 B c

GAM189 246 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell107: 43- 54, 2001. 3 B c

GAM189 246 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 B c

GAM189 246 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 3 B c

GAM189 246 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin TRiC. Molec. Cell 1051- 1061, 1999. 3 B c

GAM189 246 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof von Hippel- Lindau disease. Radiology 133: 289- 295, 1979. 3 B c

GAM189 246 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331, 1979. 3 B c

GAM189 246 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel-Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001. 3 B c

GAM189 246 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with 3 B c

hydrocephalus as a complication of cerebellar hemangioblastoma:identification of pro157leu mutation in the VHL gene. J. Hum. Genet. 45:47- 51, 2000.

GAM189 246 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C Thomas (pub.) 1946. 3 B c

GAM189 246 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989. 3 B c

GAM189 246 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg. Path. 18: 1254- 1260, 1994. 3 B c

GAM189 246 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.; Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999. 3 B c

GAM189 246 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 B c

GAM189 246 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 B c

GAM189 246 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 B c

GAM189 246 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 B c

GAM189 246 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991. 3 B c

GAM189 246 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992. 3 B c

GAM189 246 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997. 3 B c

GAM189 246 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984. 3 B c

GAM189 246 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968. 3 B c

GAM189 246 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 B c

GAM189 246 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986. 3 B c

GAM189 246 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid 3 B c
tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour,
phaeochromocytoma and the von Hippel- Lindau complex:two distinctive
neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987.

GAM189 246 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: 3 B c
Familial pheochromocytoma associated with a novel mutation inthe von Hippel-
Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996.

GAM189 246 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; 3 B c
Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam:
North Holland (pub.) 14: 1972. Pp. 241- 259.

GAM189 246 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors 3 B c
in livers with targeted inactivation of the von Hippel- Lindautumor
suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001.

GAM189 246 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 3 B c
retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022-
1034, 1971.

GAM189 246 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 3 B c
hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8:
601- 606,1967.

GAM189 246 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, 3 B c
D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing
of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas.
Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994.

GAM189 246 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; 3 B c
McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.;
Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von
Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma
only. J. Med. Genet. 37: 939- 943,2000.

GAM189 246 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 3 B c
Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips,
C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in
families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet.
106: 425- 431, 2000.

GAM189 246 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 B c
von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve
the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM189 246 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; 3 B c
Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.:
Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by
pVHL. Nature 417: 975- 978, 2002.

GAM189 246 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; 3 B c
Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease-
- a combination of adrenal pheochromocytoma and ipsilateralrenal cell
carcinoma: a case report. Surgery 105: 436- 441, 1989.

GAM189 246 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - 3 B c
clinicaland pathological manifestations in 9 families with 50 affected
members. Arch.Intern. Med. 136: 769- 777, 1976.

GAM189 246 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, 3 B c
P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch,
K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M.

M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel-Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990.

GAM189 246 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982. 3 B c

GAM189 246 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel-Lindaudisease. Brain 109: 1297- 1310, 1986. 3 B c

GAM189 246 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995. 3 B c

GAM189 246 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996. 3 B c

GAM189 246 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 3 B c

GAM189 246 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL-mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001. 3 B c

GAM189 246 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 3 B c

GAM189 246 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-regulated prolyl hydroxylation. Science 292: 468- 472, 2001. 3 B c

GAM189 246 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 B c

GAM189 246 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 3 B c

GAM189 246 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 B c

GAM189 246 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 B c

GAM189 246 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 B c

GAM189 246 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 B c

GAM189 246 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 B c

GAM189 246 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 B c

GAM189 246 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573- 581, 1995. 3 B c

GAM189 246 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 B c

GAM189 246 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 B c

GAM189 246 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel- Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 B c

GAM189 246 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 B c

GAM189 246 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 B c

GAM189 246 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel- Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 B c

GAM189 246 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 B c

GAM189 246 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 B c

GAM189 246 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317- 1320, 1993. 3 B c

GAM189 246 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 B c

GAM189 246 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 B c

GAM189 246 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 B c

GAM189 246 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 B c

GAM189 246 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of 3 B c

chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002.

GAM189 246 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 B c

GAM189 246 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 3 B c

GAM189 246 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 B c

GAM189 246 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 B c

GAM189 246 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 B c

GAM189 246 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 B c

GAM189 246 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 B c

GAM189 246 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 B c

GAM189 246 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 B c

GAM189 246 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 B c

GAM189 246 WNT5A Clark, C. C.; Cohen, I.; Eichstetter, I.; Cannizzaro, L. A.; McPherson,J. D.; Wasmuth, J. J.; Iozzo, R. V.: Molecular cloning of the humanproto-oncogene Wnt- 5A and mapping of the gene (WNT5A) to chromosome3p14- p21. Genomics 18: 249- 260, 1993. 3 B c

GAM189 246 WNT5A Gavin, B. J.; McMahon, J. A.; McMahon, A. P.: Expression of multiplenovel 3 B c
Wnt- 1/int- 1- related genes during fetal and adult mouse development.
GenesDev. 4: 2319- 2332, 1990.

GAM189 246 WNT5A He, X.; Saint- Jeannet, J.- P.; Wang, Y.; Nathans, J.; Dawid, I.;Varmus, H.: 3 B c
A member of the frizzled protein family mediating axisinduction by Wnt- 5A.
Science 275: 1652- 1654, 1997.

GAM189 246 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 3 B c
family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with
XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000.

GAM189 246 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of 3 B c
DNA double- strand breaks by homologous recombination. Nature 401:397- 399,
1999.

GAM189 246 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- 3 B c
ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286,
1987.

GAM189 246 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the 3 B c
XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis.
Genomics 26: 619- 622, 1995.

GAM189 246 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, 3 B c
T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and
filament structure formation activities of thehuman Xrcc2- Rad51D complex.
J. Biol. Chem. 277: 14315- 14320, 2002.

GAM189 246 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in 3 B c
two distinct protein complexes of Rad51 paralogs in humancells. Nucleic
Acids Res. 30: 1009- 1015, 2002.

GAM189 246 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; 3 B c
McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand
purification of two distinct complexes containing the five RAD51paralogs.
Genes Dev. 15: 3296- 3307, 2001.

GAM189 246 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; 3 B c
Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional
candidate. Genomics 41: 84- 92, 1997.

GAM189 246 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: 3 B c
Localization to chromosome 7q36.1 of the human XRCC2 gene,determining
sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995.

GAM189 246 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: 3 B b
Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma.
CancerRes. 39: 3119- 3128, 1979.

GAM189 246 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; 3 B b
Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a
follicular lymphoma cell line carrying a t(14;18)chromosomal translocation.
Int. J. Cancer 39: 785- 788, 1987.

GAM189 246 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. 3 B b
A.: STS map of genes and anonymous DNA fragments on human chromosome18 using
a panel of somatic cell hybrids. Genomics 15: 387- 391,1993.

GAM189 246 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, 3 B b
M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and
chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710-
717, 1988.

GAM189 246 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, 3 B b

M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human chromosome and its expression in various tissues. Science 227:1038- 1040, 1985.

GAM189 246 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal reassignment: YACs containing both YES1 and thymidylatesynthase map to the short arm of chromosome 18. Genomics 15: 442- 445,1993. 3 B b

GAM189 246 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c-yes gene. Molec. Cell. Biol. 7: 41- 47, 1987. 3 B b

GAM189 246 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985. 3 B b

GAM190 289 ABCC3 Belinsky, M. G.; Bain, L. J.; Balsara, B. B.; Testa, J. R.; Kruh,G. D.: Characterization of MOAT- C and MOAT- D, new members of theMRP/cMOAT subfamily of transporter proteins. J. Nat. Cancer Inst. 90:1735- 1741, 1998. 3 A c

GAM190 289 ABCC3 Fromm, M. F.; Leake, B.; Roden, D. M.; Wilkinson, G. R.; Kim, R.B.: Human MRP3 transporter: identification of the 5- prime flankingregion, genomic organization and alternative splice variants. Biochim.Biophys. Acta 1415: 369- 374, 1999. 3 A c

GAM190 289 ABCC3 Kiuchi, Y.; Suzuki, H.; Hirohashi, T.; Tyson, C. A.; Sugiyama,Y.: cDNA cloning and inducible expression of human multidrug resistanceassociated protein 3 (MRP3). FEBS Lett. 433: 149- 152, 1998. 3 A c

GAM190 289 ABCC3 Konig, J.; Rost, D.; Cui, Y.; Keppler, D.: Characterization ofthe human multidrug resistance protein isoform MRP3 localized to thebasolateral hepatocyte membrane. Hepatology 29: 1156- 1163, 1999. 3 A c

GAM190 289 ABCC3 Kool, M.; van der Linden, M.; de Haas, M.; Scheffer, G. L.; deVree, J. M. L.; Smith, A. J.; Jansen, G.; Peters, G. J.; Ponne, N.;Scheper, R. J.; Oude Elferink, R. P. J.; Baas, F.; Borst, P.: MRP3,an organic anion transporter able to transport anti- cancer drugs. Proc.Nat. Acad. Sci. 96: 6914- 6919, 1999. 3 A c

GAM190 289 ABCC3 Ortiz, D. F.; Li, S.; Iyer, R.; Zhang, X.; Novikoff, P.; Arias,I. M.: MRP3, a new ATP- binding cassette protein localized to thecanalicular domain of the hepatocyte. Am. J. Physiol. 276: G1493- G1500,1999. 3 A c

GAM190 289 ABCC3 Uchiumi, T.; Hinoshita, E.; Haga, S.; Nakamura, T.; Tanaka, T.;Toh, S.; Furukawa, M.; Kawabe, T.; Wada, M.; Kagotani, K.; Okumura,K.; Kohno, K.; Akiyama, S.; Kuwano, M.: Isolation of a novel humancanalicular multispecific organic anion transporter, cMOAT2/MRP3,and its expression in cisplatin-resistant cancer cells with decreasedATP- dependent drug transport. Biochem. Biophys. Res. Commun. 252:103- 110, 1998. 3 A c

GAM190 289 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998. 3 A c

GAM190 289 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 3 A c

GAM190 289 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527-529, 1994. 3 A c

GAM190 289 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; 3 A c

Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal brain type I adenylyl cyclase. Genomics 16: 473- 478,1993.

GAM190 289 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.: Altered sensory processing in the somatosensory cortex of the mutantmouse barrelless. Science 271: 1864- 1867, 1996. 3 A c

GAM190 289 ANKTM1 Jaquemar, D.; Schenker, T.; Trueb, B.: An ankyrin- like proteinwith transmembrane domains is specifically lost after oncogenic transformationof human fibroblasts. J. Biol. Chem. 274: 7325- 7333, 1999. 3 A c

GAM190 289 ANKTM1 Schenker, T.; Trueb, B.: Down- regulated proteins of mesenchymaltumor cells. Exp. Cell Res. 239: 161- 168, 1998. 3 A c

GAM190 289 ARHGAP6 Prakash, S. K.; Paylor, R.; Jenna, S.; Lamarche- Vane, N.; Armstrong,D. L.; Xu, B.; Mancini, M. A.; Zoghbi, H. Y.: Functional analysisof ARHGAP6, a novel GTPase- activating protein for RhoA. Hum. Molec.Genet. 9: 477- 488, 2000. 3 A c

GAM190 289 ARHGAP6 Schaefer, L.; Prakash, S.; Zoghbi, H. Y.: Cloning and characterizationof a novel rho- type GTPase- activating protein gene (ARHGAP6) fromthe critical region for microphthalmia with linear skin defects. Genomics 46:268- 277, 1997. 3 A c

GAM190 289 ARHGEF7 Bagrodia, S.; Taylor, S. J.; Jordon, K. A.; Van Aelst, L.; Cerione,R. A.: A novel regulator of p21- activated kinases. J. Biol. Chem. 273:23633- 23636, 1998. 3 A c

GAM190 289 ARHGEF7 Manser, E.; Loo, T.- H.; Koh, C.- G.; Zhao, Z.- S.; Chen, X.- Q.; Tan,L.; Tan, I.; Leung, T.; Lim, L.: PAK kinases are directly coupledto the PIX family of nucleotide exchange factors. Molec. Cell 1:183- 192, 1998. 3 A c

GAM190 289 ARHGEF7 Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 3 A c

GAM190 289 ARHGEF7 Oh, W. K.; Yoo, J. C.; Jo, D.; Song, Y. H.; Kim, M. G.; Park, D.: Cloning of a SH3 domain- containing proline- rich protein, p85SPR,and its localization in focal adhesion. Biochem. Biophys. Res. Commun. 235:794- 798, 1997. 3 A c

GAM190 289 ATP11B Halleck, M. S.; Lawler, J. F., Jr.; Blackshaw, S.; Gao, L.; Nagarajan,P.; Hacker, C.; Pyle, S.; Newman, J. T.; Nakanishi, Y.; Ando, H.;Weinstock, D.; Williamson, P.; Schlegel, R. A.: Differential expressionof putative transbilayer amphipath transporters. Physiol. Genomics 1:139- 150, 1999. 3 A c

GAM190 289 ATP11B Mansharamani, M.; Hewetson, A.; Chilton, B. S.: Cloning and characterizationof an atypical type IV P- type ATPase that binds to the RING motifof RUSH transcription factors. J. Biol. Chem. 276: 3641- 3649, 2001. 3 A c

GAM190 289 ATP11B Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999. 3 A c

GAM190 289 CARKL Phornphutkul, C.; Anikster, Y.; Huizing, M.; Braun, P.; Brodie,C.; Chou, J. Y.; Gahl, W. A.: The promoter of a lysosomal membranetransporter gene, CTNS, binds Sp- 1, shares sequences with the promoterof an adjacent gene, CARKL, and causes cystinosis if mutated in acritical region. Am. J. Hum. Genet. 69: 712- 721, 2001. 3 A c

GAM190 289 CARKL Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; 3 A c

McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000.

GAM190 289 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis machinery through a novel motif, the F- box. Cell 86:263- 274, 1996. 3 A c

GAM190 289 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene (CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics 24:27- 33, 1994. 3 A c

GAM190 289 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6: 149- 150, 1995. 3 A c

GAM190 289 CCR2 Boring, L.; Gosling, J.; Cleary, M.; Charo, I. F.: Decreased lesionformation in CCR2 - /- mice reveals a role for chemokines in the initiationof atherosclerosis. Nature 394: 894- 897, 1998. 3 A c

GAM190 289 CCR2 Charo, I. F.; Myers, S. J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S. R.: Molecular cloning and functional expressionof two monocyte chemoattractant protein 1 receptors reveals alternativesplicing of the carboxyl- terminal tails. Proc. Nat. Acad. Sci. 91:2752- 2756, 1994. 3 A c

GAM190 289 CCR2 Choe, H.; Farzan, M.; Sun, Y.; Sullivan, N.; Rollins, B.; Ponath,P. D.; Wu, L.; Mackay, C. R.; LaRosa, G.; Newman, W.; Gerard, N.;Gerard, C.; Sodroski, J.: The beta- chemokine receptors CCR3 and CCR5facilitate infection by primary HIV- 1 isolates. Cell 85: 1135- 1148,1996. 3 A c

GAM190 289 CCR2 Combadiere, C.; Ahuja, S. K.; Murphy, P. M.: Cloning, chromosomallocalization, and RNA expression of a human beta chemokine receptor- likegene. DNA Cell Biol. 14: 673- 680, 1995. 3 A c

GAM190 289 CCR2 Combadiere, C.; Ahuja, S. K.; Van Damme, J.; Tiffany, H. L.; Gao,J.- L.; Murphy, P. M.: Monocyte chemoattractant protein- 3 is a functionalligand for CC chemokine receptors 1 and 2B. J. Biol. Chem. 270:29671- 29675, 1995. 3 A c

GAM190 289 CCR2 Daugherty, B. L.; Springer, M. S.: The beta- chemokine receptorgenes CCR1 (CMKBR1), CCR2 (CMKBR2), and CCR3 (CMKBR3) cluster within285 kb on human chromosome 3p21. Genomics 41: 294- 295, 1997. 3 A c

GAM190 289 CCR2 Doranz, B. J.; Rucker, J.; Yi, Y.; Smyth, R. J.; Samson, M.; Peiper,S. C.; Parmentier, M.; Collman, R. G.; Doms, R. W.: A dual- tropicprimary HIV- 1 isolate that uses fusin and the beta- chemokine receptorsCKR- 5, CKR- 3, and CKR- 2b as fusion cofactors. Cell 85: 1149- 1158,1996. 3 A c

GAM190 289 CCR2 Mummidi, S.; Ahuja, S. S.; Gonzalez, E.; Anderson, S. A.; Santiago,E. N.; Stephan, K. T.; Craig, F. E.; O'Connell, P.; Tryon, V.; Clark,R. A.; Dolan, M. J.; Ahuja, S. K.: Genealogy of the CCR5 locus andchemokine system gene variants associated with altered rates of HIV- 1disease progression. Nature Med. 4: 786- 793, 1998. 3 A c

GAM190 289 CCR2 Peters, W.; Dupuis, M.; Charo, I. F.: A mechanism for the impairedIFN- gamma production in C- C chemokine receptor 2 (CCR2) knockout mice:role of CCR2 in linking the innate and adaptive immune responses. J.Immun. 165: 7072- 7077, 2000. 3 A c

GAM190 289 CCR2 Peters, W.; Scott, H. M.; Chambers, H. F.; Flynn J. L.; Charo,I. F.; Ernst, J. D.: Chemokine receptor 2 serves an early and essentialrole in resistance 3 A c

to Mycobacterium tuberculosis. Proc. Nat. Acad.Sci. 98: 7958- 7963, 2001.

GAM190 289 CCR2 Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier,M.: Molecular 3 A c cloning and functional expression of a new human CC- chemokinereceptor gene. Biochemistry 35: 3362- 3367, 1996.

GAM190 289 CCR2 Samson, M.; Soularue, P.; Vassart, G.; Parmentier, M.: The genesencoding the 3 A c human CC- chemokine receptors CC- CKR1 to CC- CKR5 (CMKBR1- CMKBR5)are clustered in the p21.3- p24 region of chromosome 3. Genomics 36:522- 526, 1996.

GAM190 289 CCR2 Sanders, S. K.; Crean, S. M.; Boxer, P. A.; Kellner, D.; LaRosa,G. J.; Hunt, 3 A c S. W., III.: Functional differences between monocytechemotactic protein- 1 receptor A and monocyte chemotactic protein- 1receptor B expressed in a Jurkat T cell. J. Immun. 165: 4877- 4883,2000.

GAM190 289 CCR2 Smith, M. W.; Dean, M.; Carrington, M.; Winkler, C.; Huttley,G. A.; Lomb, D. 3 A c A.; Goedert, J. J.; O'Brien, T. R.; Jacobson, L. P.;Kaslow, R.; Buchbinder, S.; Vittinghoff, E.; Vlahov, D.; Hoots, K.;Hilgartner, M. W.; Hemophilia Growth and Development Study (HGDS);Multicenter AIDS Cohort Study (MACS); Multicenter Hemophilia CohortStudy (MHCS); San Francisco City Cohort (SFCC); ALIVE Study;O'Brien, S. J.: Contrasting genetic influence of CCR2 and CCR5 variantson HIV- 1 infection and disease progression. Science 277: 959- 965,1997.

GAM190 289 CCR2 Wong, L.- M.; Myers, S. J.; Tsou, C.- L.; Gosling, J.; Arai, H.;Charo, I. 3 A c F.: Organization and differential expression of the humanmonocyte chemoattractant protein 1 receptor gene: evidence for therole of the carboxyl- terminal tail in receptor trafficking. J. Biol.Chem. 272: 1038- 1045, 1997.

GAM190 289 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 3 A c membrane- associated C- type lectin that exhibits CD4- independentbinding of human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad. Sci. 89: 8356- 8360, 1992.

GAM190 289 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 3 A c for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR. Science 294: 2163- 2166, 2001.

GAM190 289 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 3 A c Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S. L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC- SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans- infection of T cells. Cell 100: 587- 597,2000.

GAM190 289 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 3 A c F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000.

GAM190 289 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related 3 A c gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000.

GAM190 289 CD4 Ansari- Lari, M. A.; Muzny, D. M.; Lu, J.; Lu, F.; Lilley, C. E.;Spanos, S.; 3 A c Malley, T.; Gibbs, R. A.: A gene- rich cluster betweenthe CD4 and triosephosphate isomerase genes at human chromosome 12p13. GenomeRes. 6: 314- 326, 1996.

GAM190 289 CD4 Bach, M. A.; Phan- Dinh- Tuy, F.; Bach, J. F.; Wallach, D.; Biddison,W. E.; 3 A c Sharrow, S. O.; Goldstein, G.; Kung, P. C.: Unusual phenotypesof human

inducer T cells as measured by OKT4 and related monoclonalantibodies. J. Immun. 127: 980- 982, 1981.

GAM190 289 CD4 Browning, J.; Horner, J. W.; Pettoello- Mantovani, M.; Raker, C.;Yurasov, 3 A c S.; DePinho, R. A.; Goldstein, H.: Mice transgenic for humanCD4 and CCR5 are susceptible to HIV infection. Proc. Nat. Acad. Sci. 94:14637- 14641, 1997.

GAM190 289 CD4 Buttini, M.; Westland, C. E.; Masliah, E.; Yafeh, A. M.; Wyss- Coray,T.; 3 A c Mucke, L.: Novel role of human CD4 molecule identified in neurodegeneration. NatureMed. 4: 441- 446, 1998.

GAM190 289 CD4 Committee on Human Leukocyte Differentiation Antigens, IUIS WHONomenclature 3 A c

Subcommittee: Proposed nomenclature for human leukocytedifferentiation antigens. Bull. WHO 5: 809- 811, 1984. Note: Alternate:Immunology Today 5: 280 only, 1984.

GAM190 289 CD4 Fukuda, T.; Matsunaga, M.; Kurata, A.; Mine, M.; Ikari, N.; Katamine,S.; 3 A c Kanazawa, H.; Eguchi, K.; Nagataki, S.: Hereditary deficiencyof OKT4- positive cells: studies for mode of inheritance and lymphocytefunctions. Immunology 53: 643- 649, 1984.

GAM190 289 CD4 Fuller, T. C.; Trevithick, J. E.; Fuller, A. A.; Colvin, R. B.;Cosimi, A. 3 A c B.; Kung, P. C.: Antigenic polymorphism of the T4 differentiationantigen expressed on human T helper/inducer lymphocytes. Hum. Immun. 9:89- 102, 1984.

GAM190 289 CD4 Gill, J. C.; Maples, J.; Nikaein, A.; Kirchner, P.; Lockhart, D.;Snyder, A. 3 A c J.; Montgomery, R. R.; Casper, J. T.: Inherited absenceof OKT4 lymphocyte antigen in a chronically transfused patient withhomozygous sickle cell disease. J. Pediat. 107: 251- 253, 1985.

GAM190 289 CD4 Grakoui, A.; Bromley, S. K.; Sumen, C.; Davis, M. M.; Shaw, A.S.; Allen, P. 3 A c M.; Dustin, M. L.: The immunological synapse: a molecularmachine controlling T cell activation. Science 285: 221- 227, 1999.

GAM190 289 CD4 Irvine, D. J.; Purbhoo, M. A.; Krogsgaard, M.; Davis, M. M.:Direct 3 A c observation of ligand recognition by T cells. Nature 419:845- 849, 2002.

GAM190 289 CD4 Isobe, M.; Huebner, K.; Maddon, P. J.; Littman, D. R.; Axel, R.;Croce, C. 3 A c M.: The gene encoding the T- cell surface protein T4 islocated on human chromosome 12. Proc. Nat. Acad. Sci. 83: 4399- 4402,1986.

GAM190 289 CD4 Karol, R. A.; Eng, J.; Dennison, D. K.; Faris, E.; Marcus, D.M.: Hereditary 3 A c abnormalities of the OKT4 human lymphocyte epitopein two families. J. Clin. Immun. 4: 71- 74, 1984.

GAM190 289 CD4 Kozbor, D.; Finan, J.; Nowell, P. C.; Croce, C. M.: The geneencoding the T4 3 A c antigen maps to human chromosome 12. J. Immun. 136:1141- 1143, 1986.

GAM190 289 CD4 Krummel, M. F.; Sjaastad, M. D.; Wulfing, C.; Davis, M. M.: 3 A c Differentialclustering of CD4 and CD3- zeta during T cell recognition. Science 289:1349- 1352, 2000.

GAM190 289 CD4 Littman, D. R.: The structure of the CD4 and CD8 genes. Annu.Rev. Immun. 5: 3 A c 561- 584, 1987.

GAM190 289 CD4 Maddon, P. J.; Molineaux, S. M.; Maddon, D. E.; Zimmerman, K.A.; Godfrey, 3 A c M.; Alt, F. W.; Chess, L.; Axel, R.: Structure and expressionof the human and mouse T4 genes. Proc. Nat. Acad. Sci. 84: 9155- 9159,1987.

GAM190 289 CD4 Piguet, V.; Gu, F.; Foti, M.; Demaurex, N.; Gruenberg, J.; Carpentier,J.- 3 A c L.; Trono, D.: Nef- induced CD4 degradation: a diacidic- based motifin Nef functions as a lysosomal targeting signal through the bindingof beta- COP in endosomes. Cell 97: 63- 73, 1999.

GAM190 289 CD4 Sato, M.; Hayashi, Y.; Yoshida, H.; Yanagawa, T.; Yura, Y.: Afamily with 3 A c
hereditary lack of T4+ inducer/helper T cell subsets inperipheral blood
lymphocytes. J. Immun. 132: 1071- 1073, 1984.

GAM190 289 CD4 Sawada, S.; Scarborough, J. D.; Killeen, N.; Littman, D. R.:A lineage- 3 A c
specific transcriptional silencer regulates CD4 gene expressionduring T
lymphocyte development. Cell 77: 917- 929, 1994.

GAM190 289 CD4 Siu, G.; Wurster, A. L.; Duncan, D. D.; Soliman, T. M.; Hedrick,S. M.: A 3 A c
transcriptional silencer controls the developmental expressionof the CD4
gene. EMBO J. 13: 3570- 3579, 1994.

GAM190 289 CD4 Stohl, W.; Crow, M. K.; Kunkel, H. G.: Systemic lupus erythematosuswith 3 A c
deficiency of the T4 epitope on T helper/inducer cells. NewEng. J. Med. 312:
1671- 1678, 1985.

GAM190 289 CD4 Stohl, W.; Kunkel, H. G.: Heterogeneity in expression of theT4 epitope in 3 A c
black individuals. Scand. J. Immun. 20: 273- 278, 1984.

GAM190 289 CD4 Tishkoff, S. A.; Dietzsch, E.; Speed, W.; Pakstis, A. J.; Kidd,J. R.; 3 A c
Cheung, K.; Bonne- Tamir, B.; Santachiara- Benerecetti, A. S.;Moral, P.;
Krings, M.; Paabo, S.; Watson, E.; Risch, N.; Jenkins,T.; Kidd, K. K.:
Global patterns of linkage disequilibrium at theCD4 locus and modern human
origins. Science 271: 1380- 1387, 1996.

GAM190 289 CD4 van Dongen, J. J. M.; Wolvers- Tettero, I. L. M.; Versnel, M. A.;Westerveld, 3 A c
A.; Geurts van Kessel, A. H. M.: Assignment of the genescoding for the T-
cell antigens CD7 (Tp41), CD5 (T1) and CD4 (T4) tohuman chromosome 17, 11,
12 respectively. (Abstract) Cytogenet. CellGenet. 40: 767, 1985.

GAM190 289 CD4 Zou, Y.- R.; Sunshine, M.- J.; Taniuchi, I.; Hatam, F.; Killeen,N.; Littman, 3 A c
D. R.: Epigenetic silencing of CD4 in T cells committedto the cytotoxic
lineage. Nature Genet. 332- 336, 2001.

GAM190 289 CENTD2 Miura, K.; Jacques, K. M.; Stauffer, S.; Kubosaki, A.; Zhu, K.;Hirsch, D. 3 A c
S.; Resau, J.; Zheng, Y.; Randazzo, P. A.: ARAP1: a pointof convergence for
Arf and Rho signaling. Molec. Cell 9: 109- 119,2002.

GAM190 289 CENTD2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; 3 A c
Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of
unidentified human genes. XI. The complete sequencesof 100 new cDNA clones
from brain which code for large proteins invitro. DNA Res. 5: 277- 286,
1998.

GAM190 289 CLCN6 Brandt, S.; Jentsch, T. J.: ClC- 6 and ClC- 7 are two novel broadlyexpressed 3 A c
members of the CLC chloride channel family. FEBS Lett. 377:15- 20, 1995.

GAM190 289 CLCN6 Eggermont, J.; Buyse, G.; Voets, T.; Tytgat, J.; De Smedt, H.;Droogmans, G.: 3 A c
Alternative splicing of ClC- 6 (a member of the ClCchloride- channel family)
transcripts generates three truncated isoformsone of which, ClC- 6c, is
kidney- specific. Biochem. J. 325: 269- 276,1997.

GAM190 289 CLCN6 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 A c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. II. The codingsequences of 40 new
genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell
line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM190 289 CPA1 Catasus, L.; Villegas, V.; Pascual, R.; Aviles, F. X.; Wicker- Planquart,C.; 3 A c
Puigserver, A.: cDNA cloning and sequence analysis of human
pancreaticprocarboxypeptidase A1. Biochem. J. 287: 299- 303, 1992.

GAM190 289 CPA1 Honey, N. K.; Sakaguchi, A. Y.; Lalley, P. A.; Quinto, C.; Rutter,W. J.; 3 A c
Naylor, S. L.: Assignment of the gene for carboxypeptidaseA to human

chromosome 7q22- qter and to mouse chromosome 6. Hum. Genet. 72:27- 31, 1986.

GAM190 289 CPA1 Honey, N. K.; Sakaguchi, A. Y.; Quinto, C.; MacDonald, R. J.; Rutter,W. J.; 3 A c Naylor, S. L.: Assignment of the human genes for elastaseto chromosome 12, and for trypsin and carboxypeptidase A to chromosome7 (Abstract) Cytogenet. Cell Genet. 37: 492, 1984.

GAM190 289 CPA1 Stewart, E. A.; Craik, C. S.; Hake, L.; Bowcock, A. M.: 3 A c Humancarboxypeptidase A identifies a BglII RFLP and maps to 7q31- qter. Am.J. Hum. Genet. 46: 795- 800, 1990.

GAM190 289 CPA1 Velculescu, V. E.; Zhang, L.; Vogelstein, B.; Kinzler, K. W.:Serial analysis 3 A c of gene expression. Science 270: 484- 487, 1995.

GAM190 289 CPA1 Velculescu, V. E.; Zhang, L.; Zhou, W.; Vogelstein, J.; Basrai,M. A.; 3 A c Bassett, D. E., Jr.; Hieter, P.; Vogelstein, B.; Kinzler, K.W.: Characterization of the yeast transcriptome. Cell 88: 1- 20,1997.

GAM190 289 CPNE3 Caudell, E. G.; Caudell, J. J.; Tang, C.- H.; Yu, T.- K.; Frederick,M. J.; 3 A c Grimm, E. A.: Characterization of human copine III as a phosphoproteinwith associated kinase activity. Biochemistry 39: 13034- 13043, 2000.

GAM190 289 CPNE3 Creutz, C. E.; Tomsig, J. L.; Snyder, S. L.; Gautier, M.- C.; Skouri,F.; 3 A c Beisson, J.; Cohen, J.: The copines, a novel class of C2 domain-containing,calcium- dependent, phospholipid- binding proteins conserved from Parameciumto humans. J. Biol. Chem. 273: 1393- 1402, 1998.

GAM190 289 CPNE3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 A c Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM190 289 DGCR2 Augusseau, S.; Jouk, S.; Jalbert, P.; Prieur, M.: DiGeorge syndromeand 22q11 3 A c rearrangements. (Letter) Hum. Genet. 74: 206 only, 1986.

GAM190 289 DGCR2 Bartsch, O.; Wagner, A.; Hinkel, G. K.; Lichtner, P.; Murken, 3 A c J.;Schuffenhauer, S.: No evidence for chromosomal microdeletions atthe second DiGeorge syndrome locus on 10p near D10S585. (Letter) Am.J. Med. Genet. 83: 425- 426, 1999.

GAM190 289 DGCR2 Daw, S. C. M.; Taylor, C.; Kraman, M.; Call, K.; Mao, J.; Schuffenhauer,S.; 3 A c Meitinger, T.; Lipson, T.; Goodship, J.; Scambler, P.: A commonregion of 10p deleted in DiGeorge and velocardiofacial syndromes. NatureGenet. 13: 458- 461, 1996.

GAM190 289 DGCR2 Demczuk, S.; Aledo, R.; Zucman, J.; Delattre, O.; Desmaze, C.;Dauphinot, L.; 3 A c Jalbert, P.; Rouleau, G. A.; Thomas, G.; Aurias, A.: Cloning of a balanced translocation breakpoint in the DiGeorge syndromecritical region and isolation of a novel potential adhesion receptorgene in its vicinity. Hum. Molec. Genet. 4: 551- 558, 1995.

GAM190 289 DGCR2 Hasegawa, T.; Hasegawa, Y.; Aso, T.; Koto, S.; Nagai, T.; Tsuchiya,Y.; Kim, 3 A c K. C.; Ohashi, H.; Wakui, K.; Fukushima, Y.: HDR syndrome(hypoparathyroidism, sensorineural deafness, renal dysplasia) associatedwith del(10)(p13). Am. J. Med. Genet. 73: 416- 418, 1997.

GAM190 289 DGCR2 Lichtner, P.; Konig, R.; Hasegawa, T.; Van Esch, H.; Meitinger,T.; 3 A c Schuffenhauer, S.: An HDR (hypoparathyroidism, deafness, renaldysplasia) syndrome locus maps distal to the DiGeorge syndrome regionon 10p13/14. J. Med. Genet. 37: 33- 37, 2000.

GAM190 289 DGCR2 Schuffenhauer, S.; Lichtner, P.; Peykar- Derakhshandeh, P.; Murken,J.; Haas, 3 A c O. A.; Back, E.; Wolff, G.; Zabel, B.; Barisic, I.; Rauch,A.; Borochowitz,

Z.; Dallapiccola, B.; Ross, M.; Meitinger, T.: Deletionmapping on chromosome 10p and definition of a critical region forthe second DiGeorge syndrome locus (DGS2). Europ. J. Hum. Genet. 6:213- 225, 1998.

GAM190 289 DGCR2 Van Esch, H.; Groenen, P.; Daw, S.; Poffyn, A.; Holvoet, M.; Scambler,P.; Fryns, J.- P.; Van de Ven, W.; Devriendt, K.: Partial DiGeorgesyndrome in two patients with a 10p rearrangement. Clin. Genet. 55:269- 276, 1999. 3 A c

GAM190 289 DGCR2 Wadey, R.; Daw, S.; Taylor, C.; Atif, U.; Kamath, S.; Halford,S.; O'Donnell, H.; Wilson, D.; Goodship, J.; Burn, J.; Scambler, P.: Isolation of a gene encoding an integral membrane protein from thevicinity of a balanced translocation breakpoint associated with DiGeorgesyndrome. Hum. Molec. Genet. 4: 1027- 1033, 1995. 3 A c

GAM190 289 EXTL2 Saito, T.; Seki, N.; Yamauchi, M.; Tsuji, S.; Hayashi, A.; Kozuma,S.; Hori, T.: Structure, chromosomal location, and expression profileof EXTR1 and EXTR2, new members of the multiple exostoses gene family. Biochem.Biophys. Res. Commun. 243: 61- 66, 1998. 3 A c

GAM190 289 EXTL2 Wuyts, W.; Van Hul, W.: Characterization and genomic localizationof the mouse Extl2 gene. Cytogenet. Cell Genet. 89: 185- 188, 2000. 3 A c

GAM190 289 EXTL2 Wuyts, W.; Van Hul, W.; Hendrickx, J.; Speleman, F.; Wauters, J.;De Boulle, K.; Van Roy, N.; Van Agtmael, T.; Bossuyt, P.; Willems,P. J.: Identification and characterization of a novel member of theEXT gene family, EXTL2. Europ. J. Hum. Genet. 5: 382- 389, 1997. 3 A c

GAM190 289 FOXO1A Anderson, M. J.; Shelton, G. D.; Cavenee, W. K.; Arden, K. C.:Embryonic expression of the tumor- associated PAX3- FKHR fusion proteininterferes with the developmental functions of Pax3. Proc. Nat. Acad.Sci. 98: 1589- 1594, 2001. 3 A c

GAM190 289 FOXO1A Anderson, M. J.; Viars, C. S.; Czekay, S.; Cavenee, W. K.; Arden,K. C.: Cloning and characterization of three human forkhead genesthat comprise an FKHR- like gene subfamily. Genomics 47: 187- 199,1998. 3 A c

GAM190 289 FOXO1A Barr, F. G.; Galili, N.; Holick, J.; Biegel, J. A.; Rovera, G.;Emanuel, B. S.: Rearrangement of the PAX3 paired box gene in thepaediatric solid tumor alveolar rhabdomyosarcoma. Nature Genet. 3:113- 117, 1993. 3 A c

GAM190 289 FOXO1A Davis, R. J.; Barr, F. G.: Fusion genes resulting from alternativechromosomal translocations are overexpressed by gene- specific mechanismsin alveolar rhabdomyosarcoma. Proc. Nat. Acad. Sci. 94: 8047- 8051,1997. 3 A c

GAM190 289 FOXO1A Fredericks, W. J.; Galili, N.; Mukhopadhyay, S.; Rovera, G.; Bennicelli,J.; Barr, F. G.; Rauscher, F. J., III: The PAX3- FKHR fusion proteincreated by the t(2;13) translocation in alveolar rhabdomyosarcomasis a more potent transcriptional activator than PAX3. Molec. Cell.Biol. 15: 1522- 1535, 1995. 3 A c

GAM190 289 FOXO1A Galili, N.; Davis, R. J.; Fredericks, W. J.; Mukhopadhyay, S.;Rauscher, F. J., III; Emanuel, B. S.; Rovera, G.; Barr, F. G.: Fusionof a fork head domain gene to PAX3 in the solid tumour alveolar rhabdomyosarcoma. NatureGenet. 5: 230- 235, 1993. 3 A c

GAM190 289 FOXO1A Khan, J.; Bittner, M. L.; Saal, L. H.; Teichmann, U.; Azorsa, D.O.; Gooden, G. C.; Pavan, W. J.; Trent, J. M.; Meltzer, P. S.: cDNAmicroarrays detect activation of a myogenic transcription programby the PAX3- FKHR fusion oncogene. Proc. Nat. Acad. Sci. 96: 13264- 13269,1999. 3 A c

GAM190 289 FOXO1A Medema, R. H.; Kops, G. J. P. L.; Bos, J. L.; Burgering, B. M.T.: AFX- like forkhead transcription factors mediate cell- cycle regulationby Ras and PKB through p27(kip1). Nature 404: 782- 787, 2000. 3 A c

GAM190 289 FOXO1A Nakae, J.; Biggs, W. H., III; Kitamura, T.; Cavenee, W. K.; Wright,C. V. E.; 3 A c
Arden, K. C.; Accili, D.: Regulation of insulin actionand pancreatic beta-
cell function by mutated alleles of the gene encodingforkhead transcription
factor Foxo1. Nature Genet. 32: 245- 253,2002.

GAM190 289 FOXO1A Scheidler, S.; Fredericks, W. J.; Rauscher, F. J., III; Barr,F. G.; Vogt, P. 3 A c
K.: The hybrid PAX3- FKHR fusion protein of alveolarrhabdomyosarcoma
transforms fibroblasts in culture. Proc. Nat. Acad.Sci. 93: 9805- 9809,
1996.

GAM190 289 FOXO1A Sublett, J. E.; Jeon, I- S.; Shapiro, D. N.: The alveolar 3 A c
rhabdomyosarcomaPAX3/FKHR fusion protein is a transcriptional activator.
Oncogene 11:545- 552, 1995.

GAM190 289 FOXO1A Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: 3 A c
Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes
Cancer 5: 299- 310, 1992.

GAM190 289 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, 3 A c
J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a
novel secretin- like human G- protein- coupledreceptor gene. Genomics 55:
296- 305, 1999.

GAM190 289 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; 3 A c
van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected
with mRNA differential display using human melanoma celllines with different
metastatic potential. FEBS Lett. 446: 292- 298,1999.

GAM190 289 HDAC6 Grozinger, C. M.; Hassig, C. A.; Schreiber, S. L.: Three proteinsdefine a 3 A c
class of human histone deacetylases related to yeast Hda1p. Proc.Nat. Acad.
Sci. 96: 4868- 4873, 1999.

GAM190 289 HDAC6 Hubbert, C.; Guardiola, A.; Shao, R.; Kawaguchi, Y.; Ito, A.; Nixon,A.; 3 A c
Yoshida, M.; Wang, X.- F.; Yao, T.- P.: HDAC6 is a microtubule-
associateddeacetylase. Nature 417: 455- 458, 2002.

GAM190 289 HDAC6 Mahlknecht, U.; Schnittger, S.; Landgraf, F.; Schoch, C.; Ottmann,O. G.; 3 A c
Hiddemann, W.; Hoelzer, D.: Assignment of the human histonedeacetylase 6
gene (HDAC6) to X chromosome p11.23 by in situ hybridization. Cytogenet.Cell
Genet. 93: 135- 136, 2001.

GAM190 289 HDAC6 Nagase, T.; Isikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XII. The completesequences of 100 new
cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5:
355- 364, 1998.

GAM190 289 IAPP Christmanson, L.; Rorsman, F.; Stenman, G.; Westermark, P.; Betsholtz,C.: 3 A c
The human islet amyloid polypeptide (IAPP) gene: organization,chromosomal
localization and functional identification of a promoterregion. FEBS Lett.
267: 160- 166, 1990.

GAM190 289 IAPP Cockburn, D. C.; Holt, S. M.; Roberts, A. N.; Cooper, G. J. S.;Reid, K. B. 3 A c
M.; Boyd, Y.: Localization of the amylin locus to chromosome12. (Abstract)
Cytogenet. Cell Genet. 51: 977, 1989.

GAM190 289 IAPP Cooper, G. J. S.; Leighton, B.; Dimitriadis, G. D.; Parry- Billings,M.; 3 A c
Kowalchuk, J. M.; Howland, K.; Rothbard, J. B.; Willis, A. C.;Reid, K. B.
M.: Amylin found in amyloid deposits in human type 2diabetes mellitus may be
a hormone that regulates glycogen metabolismin skeletal muscle. Proc. Nat.
Acad. Sci. 85: 7763- 7766, 1988.

GAM190 289 IAPP Cooper, G. J.; Willis, A. C.; Clark, A.; Turner, R. C.; Sim, R.B.; Reid, K. 3 A c

B.: Purification and characterization of a peptide fromamyloid- rich pancreases of type 2 diabetic patients. Proc. Nat. Acad.Sci. 84: 8628- 8632, 1987.

GAM190 289 IAPP Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Sanke, T.; Steiner, D. F.; Shows, T. B.; Bell, G. I.: Localizationof the human islet amyloid polypeptide gene (IAP) to chromosome 12p12.3.(Abstract) Cytogenet. Cell Genet. 51: 997, 1989. 3 A c

GAM190 289 IAPP Harvey, A. M.: Medical students on the march: Brown, MacCallumand Opie. Johns Hopkins Med. J. 134: 330- 345, 1974. 3 A c

GAM190 289 IAPP Hoovers, J. M. N.; Redeker, E.; Speleman, F.; Hoppener, J. W. M.;Bhola, S.; Bliek, J.; van Roy, N.; Leschot, N. J.; Westerveld, A.;Mannens, M.: High-resolution chromosomal localization of the humancalcitonin/CGRP/IAPP gene family members. Genomics 15: 525- 529,1993. 3 A c

GAM190 289 IAPP Hoppener, J. W. M.; Oosterwijk, C.; van Hulst, K. L.; Verbeek,J. S.; Capel, P. J. A.; de Koning, E. J. P.; Clark, A.; Jansz, H.S.; Lips, C. J. M.: Molecular physiology of the islet amyloid polypeptide(IAPP)/amylin gene in man, rat, and transgenic mice. J. Cell. Biochem. 55S:39- 53, 1994. 3 A c

GAM190 289 IAPP Jaikaran, E. T. A. S.; Clark, A.: Islet amyloid and type 2 diabetes:from molecular misfolding to islet pathophysiology. Biochim. Biophys.Acta 1537: 179- 203, 2001. 3 A c

GAM190 289 IAPP Janson, J.; Soeller, W. C.; Roche, P. C.; Nelson, R. T.; Torchia,A. J.; Kreutter, D. K.; Butler, P. C.: Spontaneous diabetes mellitusin transgenic mice expressing human islet amyloid polypeptide. Proc.Nat. Acad. Sci. 93: 7283- 7288, 1996. 3 A c

GAM190 289 IAPP Johnson, K. H.; O'Brien, T. D.; Betsholtz, C.; Westermark, P.: Islet amyloid, islet- amyloid polypeptide, and diabetes mellitus. NewEng. J. Med. 321: 513- 518, 1989. 3 A c

GAM190 289 IAPP Lorenzo, A.; Razzaboni, B.; Weir, G. C.; Yankner, B. A.: Pancreaticislet cell toxicity of amylin associated with type- 2 diabetes mellitus. Nature 368:756- 760, 1994. 3 A c

GAM190 289 IAPP Mosselman, S.; Hoppener, J. W. M.; Lips, C. J. M.; Jansz, H. S.: The complete islet amyloid polypeptide precursor is encoded by twoexons. FEBS Lett. 247: 154- 158, 1989. 3 A c

GAM190 289 IAPP Mosselman, S.; Hoppener, J. W. M.; Zandberg, J.; van Mansfeld,A. D. M.; Geurts van Kessel, A. H. M.; Lips, C. J. M.; Jansz, H. S.: Islet amyloid polypeptide: identification and chromosomal localizationof the human gene. FEBS Lett. 239: 227- 232, 1988. 3 A c

GAM190 289 IAPP Nishi, M.; Sanke, T.; Seino, S.; Eddy, R. L.; Fan, Y.- S.; Byers,M. G.; Shows, T. B.; Bell, G. I.; Steiner, D. F.: Human islet amyloidpolypeptide gene: complete nucleotide sequence, chromosomal localization,and evolutionary history. Molec. Endocr. 3: 1775- 1781, 1989. 3 A c

GAM190 289 IAPP Opie, E. L.: On the relation of the chronic interstitial pancreatitisto the islands of Langerhans and to diabetes mellitus. J. Exp. Med. 5:397- 428, 1900. 3 A c

GAM190 289 IAPP Roberts, A. N.; Leighton, B.; Todd, J. A.; Cockburn, D.; Schofield,P. N.; Sutton, R.; Holt, S.; Boyd, Y.; Day, A. J.; Foot, E. A.; Willis,A. C.; Reid, K. B. M.; Cooper, G. J. S.: Molecular and functionalcharacterization of amylin, a peptide associated with type 2 diabetesmellitus. Proc. Nat. Acad. Sci. 86: 9662- 9666, 1989. 3 A c

GAM190 289 IAPP Sanke, T.; Bell, G. I.; Sample, C.; Rubenstein, A. H.; Steiner,D. F.: An 3 A c

islet amyloid peptide is derived from an 89- amino acidprecursor by proteolytic processing. J. Biol. Chem. 263: 17243- 17246,1988.

GAM190 289 IAPP Verchere, C. B.; D'Alessio, D. A.; Palmiter, R. D.; Weir, G. C.;Bonner- 3 A c
Weir, S.; Baskin, D. G.; Kahn, S. E.: Islet amyloid formationassociated with hyperglycemia in transgenic mice with pancreatic betacell expression of human islet amyloid polypeptide. Proc. Nat. Acad.Sci. 93: 3492- 3496, 1996.

GAM190 289 IAPP Westermark, P.; Engstrom, U.; Johnson, K. H.; Westermark, G. T.;Betsholtz, 3 A c
C.: Islet amyloid polypeptide: pinpointing amino acidresidues linked to amyloid fibril formation. Proc. Nat. Acad. Sci. 87:5036- 5040, 1990.

GAM190 289 IL10RA Ho, A. S. Y.; Liu, Y.; Khan, T. A.; Hsu, D.- H.; Bazan, J. F.; Moore,K. W.: 3 A c
A receptor for interleukin 10 is related to interferon receptors. Proc.Nat. Acad. Sci. 90: 11267- 11271, 1993.

GAM190 289 IL10RA Liu, Y.; Wei, S. H.- Y.; Ho, A. S.- Y.; de Waal Malefyt, R.; Moore,K. W.: 3 A c
Expression cloning and characterization of a human Il- 10 receptor. J.Immun. 152: 1821- 1829, 1994.

GAM190 289 IL10RA Tan, J. C.; Indelicato, S. R.; Narula, S. K.; Zavodny, P. J.; Chou,C.- C.: 3 A c
Characterization of interleukin- 10 receptors on human andmouse cells. J. Biol. Chem. 268: 21053- 21059, 1993.

GAM190 289 IL10RA Taniyama, T.; Takai, S.; Miyazaki, E.; Fukumura, R.; Sato, J.;Kobayashi, Y.; 3 A c
Hirakawa, T.; Moore, K. W.; Yamada, K.: The humaninterleukin- 10 receptor gene maps to chromosome 11q23.3. Hum. Genet. 95:99- 101, 1995.

GAM190 289 IL18R1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 3 A c
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp) on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM190 289 IL18R1 Parnet, P.; Garka, K. E.; Bonnert, T. P.; Dower, S. K.; Sims, J.E.: IL- 1Rrp 3 A c
is a novel receptor- like molecule similar to the typeI interleukin- 1 receptor and its homologues T1/ST2 and IL- 1R AcP. J.Biol. Chem. 271: 3967- 3970, 1996.

GAM190 289 IL18R1 Torigoe, K.; Ushio, S.; Okura, T.; Kobayashi, S.; Taniai, M.; Kunikata,T.; 3 A c
Murakami, T.; Sanou, O.; Kojima, H.; Fujii, M.; Ohta, T.; Ikeda,M.; Ikegami, H.; Kurimoto, M.: Purification and characterizationof the human interleukin- 18 receptor. J. Biol. Chem. 272: 25737- 25742,1997.

GAM190 289 INSRR Kurachi, H.; Jobo, K.; Ohta, M.; Kawasaki, T.; Itoh, N.: A newmember of the 3 A c
insulin receptor family, insulin receptor- related receptor,is expressed preferentially in the kidney. Biochem. Biophys. Res.Commun. 187: 934- 939, 1992.

GAM190 289 INSRR Shier, P.; Watt, V. M.: Primary structure of a putative receptorfor a ligand 3 A c
of the insulin family. J. Biol. Chem. 264: 14605- 14608,1989.

GAM190 289 INSRR Shier, P.; Willard, H. F.; Watt, V. M.: Localization of the insulinreceptor- 3 A c
related receptor gene to human chromosome 1. Cytogenet.Cell Genet. 54: 80- 81, 1990.

GAM190 289 INSRR Whitmore, T. E.; Maurer, M. F.; Day, H. L.; Jelmberg, A. C.; Dasovich,M. M.; 3 A c
Sundborg, L. M.; Burkhead, S. K.; Heipel, M. D.; Madden, K.L.; Kramer, J. M.; Kuijper, J. L.; Xu, W. F.; Jaspers, S. R.; Holly,R. D.; Lok, S.: The assignment of the human insulin receptor- relatedreceptor gene (INSRR) to chromosome 1q21- q23 by the use of radiationhybrid mapping. Cytogenet. Cell Genet. 87: 93- 94, 1999.

GAM190 289 IRS2 Bohni, R.; Riesgo- Escovar, J.; Oldham, S.; Brogiolo, W.; Stocker,H.; 3 A c
Andruss, B. F.; Beckingham, K.; Hafen, E.: Autonomous controlof cell and organ size by CHICO, a Drosophila homolog of vertebrateIRS1- 4. Cell 97:

865- 875, 1999.

GAM190 289 IRS2 Burks, D. J.; Font de Mora, J.; Schubert, M.; Withers, D. J.; Myers,M. G.; 3 A c
Towery, H. H.; Altamuro, S. L.; Flint, C. L.; White, M. F.: IRS- 2 pathways
integrate female reproduction and energy homeostasis. Nature 407:377- 382,
2000.

GAM190 289 IRS2 Fritsche, A.; Madaus, A.; Renn, W.; Tschritter, O.; Teigeler, A.;Weisser, 3 A c
M.; Maerker, E.; Machicao, F.; Haring, H.; Stumvoll, M.:The prevalent
Gly1057Asp polymorphism in the insulin receptor substrate- 2gene is not
associated with impaired insulin secretion. J. Clin.Endocr. Metab. 86: 4822-
4825, 2001.

GAM190 289 IRS2 Kubota, N.; Tobe, K.; Terauchi, Y.; Eto, K.; Yamauchi, T.; Suzuki,R.; 3 A c
Tsubamoto, Y.; Komeda, K.; Nakano, R.; Miki, H.; Satoh, S.; Sekihara,H.;
Sciacchitano, S.; Lesniak, M.; Aizawa, S.; Nagai, R.; Kimura,S.; Akanuma,
Y.; Taylor, S. I.; Kadowaki, T.: Disruption of insulinreceptor substrate 2
causes type 2 diabetes because of liver insulinresistance and lack of
compensatory beta- cell hyperplasia. Diabetes 49::- 1880- 1889, 2000.

GAM190 289 IRS2 Mammarella, S.; Romano, F.; Di Valerio, A.; Creati, B.; Esposito,D. L.; 3 A c
Palmirotta, R.; Capani, F.; Vitullo, P.; Volpe, G.; Battista,P.; Della
Loggia, F.; Mariani- Costantini, R.; Cama, A.: Interactionbetween the G1057D
variant of IRS- 2 and overweight in the pathogenesisof type 2 diabetes. Hum.
Molec. Genet. 9: 2517- 2521, 2000.

GAM190 289 IRS2 Ogihara, T.; Isobe, T.; Ichimura, T.; Taoka, M.; Funaki, M.; Sakoda,H.; 3 A c
Onishi, Y.; Inukai, K.; Anai, M.; Fukushima, Y.; Kikuchi, M.;Yazaki, Y.;
Oka, Y.; Asano, T.: 14- 3- 3 protein binds to insulin receptorsubstrate- 1,
one of the binding sites of which is in the phosphotyrosinebinding domain.
J. Biol. Chem. 272: 25267- 25274, 1997.

GAM190 289 IRS2 Shimomura, I.; Matsuda, M.; Hammer, R. E.; Bashmakov, Y.; Brown,M. S.; 3 A c
Goldstein, J. L.: Decreased IRS- 2 and increased SREBP- 1c leadto mixed
insulin resistance and sensitivity in livers of lipodystrophicand ob/ob
mice. Molec. Cell 6: 77- 86, 2000.

GAM190 289 IRS2 Sun, X. J.; Wang, L.- M.; Zhang, Y.; Yenush, L.; Myers, M. G., Jr.;Glasheen, 3 A c
E.; Lane, W. S.; Pierce, J. H.; White, M. F.: Role of IRS- 2in insulin and
cytokine signalling. Nature 377: 173- 177, 1995.

GAM190 289 IRS2 Tobe, K.; Suzuki, R.; Aoyama, M.; Yamauchi, T.; Kamon, J.; Kubota,N.; 3 A c
Terauchi, Y.; Matsui, J.; Akanuma, Y.; Kimura, S.; Tanaka, J.;Abe, M.;
Ohsumi, J.; Nagai, R.; Kadowaki, T.: Increased expressionof the sterol
regulatory element- binding protein- 1 gene in insulinreceptor substrate- 2
- /- mouse liver. J. Biol. Chem. 276: 38337- 38340,2001.

GAM190 289 IRS2 Withers, D. J.; Burks, D. J.; Towery, H. H.; Altamuro, S. L.;Flint, C. L.; 3 A c
White, M. F.: Irs- 2 coordinates Igf- 1 receptor- mediatedbeta- cell
development and peripheral insulin signalling. Nature Genet. 23:32- 40,
1999.

GAM190 289 IRS2 Withers, D. J.; Gutierrez, J. S.; Towery, H.; Burks, D. J.; Ren,J.- M.; 3 A c
Previs, S.; Zhang, Y.; Bernal, D.; Pons, S.; Shulman, G. I.;Bonner- Weir,
S.; White, M. F.: Disruption of IRS- 2 causes type 2diabetes in mice. Nature
391: 900- 902, 1998.

GAM190 289 ITIH1 Bost, F.; Bourguignon, J.; Martin, J.- P.; Sesboue, R.; Thiberville,L.; 3 A c
Diarra- Mehrpour, M.: Isolation and characterization of the humaninter-
alpha- trypsin inhibitor heavy- chain H1 gene. Europ. J. Biochem. 218:283-
291, 1993.

GAM190 289 ITIH1 Diarra- Mehrpour, M.; Bourguignon, J.; Bost, F.; Sesboue, R.; Muschio,F.; 3 A c
Sarafan, N.; Martin, J.- P.: Human inter- alpha- trypsin inhibitor:full-
length cDNA sequence of the heavy chain H1. Biochim. Biophys.Acta 1132: 114-
118, 1992.

GAM190 289 ITIH1 Diarra- Mehrpour, M.; Bourguignon, J.; Sarafan, N.; Bost, F.; Sesboue,R.; 3 A c
Muschio- Bonnet, F.; Martin, J.- P.: Tandem orientation of theinter- alpha-
trypsin inhibitor heavy chain H1 and H3 genes. Biochim.Biophys. Acta 1219:
551- 554, 1994.

GAM190 289 ITIH1 Diarra- Mehrpour, M.; Bourguignon, J.; Sesboue, R.; Mattei, M.- G.;Passage, 3 A c
E.; Salier, J.- P.; Martin, J.- P.: Human plasma inter- alpha-
trypsininhibitor is encoded by four genes on three chromosomes. Europ.
J.Biochem. 179: 147- 154, 1989.

GAM190 289 ITIH1 Diarra- Mehrpour, M.; Sarafan, N.; Bourguignon, J.; Bonnet, F.;Bost, F.; 3 A c
Martin, J.- P.: Human inter- alpha- trypsin inhibitor heavychain H3 gene:
genomic organization, promoter analysis, and gene linkage. J.Biol. Chem.
273: 26809- 26819, 1998.

GAM190 289 ITIH1 Ding, M.; Umetsu, K.; Yuasa, I.; Sato, M.; Harada, A.; Suzuki,T.: Molecular 3 A c
basis of inter- alpha- trypsin inhibitor heavy chainH1 (ITIH1) polymorphism.
Hum. Genet. 95: 435- 436, 1995.

GAM190 289 ITIH1 Leveillard, T.; Salier, J. P.; Sesboue, R.; Bourguignon, J.; Diarra- 3 A c
Mehrpour,M.; Martin, J. P.: Sst I RFLP in the human inter- alpha- trypsin
inhibitorheavy chain gene ITIH1. Nucleic Acids Res. 16: 11852 only, 1988.

GAM190 289 ITIH1 Salier, J. P.; Diarra- Mehrpour, M.; Sesboue, R.; Bourguignon, J.;Benarous, 3 A c
R.; Ohkubo, I.; Kurachi, S.; Kurachi, K.; Martin, J. P.: Isolation and
characterization of cDNAs encoding the heavy chainof human inter- alpha-
trypsin inhibitor (IATI): unambiguous evidencefor multipolypeptide chain
structure of IATI. Proc. Nat. Acad. Sci. 84:8272- 8276, 1987.

GAM190 289 ITIH1 Vogt, U.; Cleve, H.: A 'new' genetic polymorphism of a human serumprotein: 3 A c
inter- alpha- trypsin- inhibitor. Hum. Genet. 84: 151- 154,1990.

GAM190 289 ITIH1 Vogt, U.; Sesboue, R.; Bourguignon, J.; Diarra- Mehrpour, M.; Martin,J.- P.; 3 A c
Cleve, H.: The polymorphism of the plasma inter- alpha- trypsininhibitor
(ITI) and its relationship to the heavy chain H1 subunitgene (ITIH1) at
3p211- 212. Hum. Genet. 94: 39- 44, 1994.

GAM190 289 MBD4 Bellacosa, A.; Cicchillitti, L.; Schepis, F.; Riccio, A.; Yeung,A. T.; 3 A c
Matsumoto, Y.; Golemis, E. A.; Genuardi, M.; Neri, G.: MED1,a novel human
methyl- CpG- binding endonuclease, interacts with DNAmismatch repair protein
MLH1. Proc. Nat. Acad. Sci. 96: 3969- 3974,1999.

GAM190 289 MBD4 Boland, C. R.; Thibodeau, S. N.; Hamilton, S. R.; Sidransky, D.;Eshleman, J. 3 A c
R.; Burt, R. W.; Meltzer, S. J.; Rodriguez- Bigas, M.A.; Fodde, R.; Ranzani,
G. N.; Srivastava, S.: A National CancerInstitute workshop on microsatellite
instability for cancer detectionand familial predisposition: development of
international criteriafor the determination of microsatellite instability in
colorectalcancer. Cancer Res. 58: 5248- 5257, 1998.

GAM190 289 MBD4 Hendrich, B.; Abbott, C.; McQueen, H.; Chambers, D.; Cross, S.;Bird, A.: 3 A c
Genomic structure and chromosomal mapping of the murineand human Mbd1, Mbd2,
Mbd3, and Mbd4 genes. Mammalian Genome 10:906- 912, 1999.

GAM190 289 MBD4 Hendrich, B.; Bird, A.: Identification and characterization ofa family of 3 A c
mammalian methyl- CpG binding proteins. Molec. Cell. Biol. 18:6538- 6547,
1998.

GAM190 289 MBD4 Hendrich, B.; Hardeland, U.; Ng, H.- H.; Jiricny, J.; Bird, A.:The thymine 3 A c

glycosylase MBD4 can bind to the product of deaminationat methylated CpG sites. Nature 401: 301- 304, 1999.

GAM190 289 MBD4 Millar, C. B.; Guy, J.; Sansom, O. J.; Selfridge, J.; MacDougall,E.; Hendrich, B.; Keightley, P. D.; Bishop, S. M.; Clarke, A. R.;Bird, A.: Enhanced CpG mutability and tumorigenesis in MBD4- deficientmice. Science 297: 403- 405, 2002. 3 A c

GAM190 289 MBD4 Riccio, A.; Aaltonen, L. A.; Godwin, A. K.; Loukola, A.; Percesepe,A.; Salovaara, R.; Masciullo, V.; Genuardi M.; Paravatou- Petsotas,M.; Bassi, D. E.; Ruggeri, B. A.; Klein- Szanto, A. J. P.; Testa, J.R.; Neri, G.; Bellacosa, A.: The DNA repair gene MBD4 (MED1) is mutatedin human carcinomas with microsatellite instability. (Letter) NatureGenet. 23: 266- 268, 1999. 3 A c

GAM190 289 MT1G Foster, R.; Jahroudi, N.; Varshney, U.; Gedamu, L.: Structureand expression of the human metallothionein- IG gene: differentialpromoter activity of two linked metallothionein- I genes in responseto heavy metals. J. Biol. Chem. 263: 11528- 11535, 1988. 3 A c

GAM190 289 MT1G Karin, M.; Eddy, R. L.; Henry, W. M.; Haley, L. L.; Byers, M. G.;Shows, T. B.: Human metallothionein genes are clustered on chromosome16. Proc. Nat. Acad. Sci. 81: 5494- 5498, 1984. 3 A c

GAM190 289 MT1G West, A. K.; Stallings, R.; Hildebrand, C. E.; Chiu, R.; Karin,M.; Richards, R. I.: Human metallothionein genes: structure of thefunctional locus at 16q13. Genomics 8: 513- 518, 1990. 3 A c

GAM190 289 MT1L Karin, M.; Eddy, R. L.; Henry, W. M.; Haley, L. L.; Byers, M. G.;Shows, T. B.: Human metallothionein genes are clustered on chromosome16. Proc. Nat. Acad. Sci. 81: 5494- 5498, 1984. 3 A c

GAM190 289 MT1L West, A. K.; Stallings, R.; Hildebrand, C. E.; Chiu, R.; Karin,M.; Richards, R. I.: Human metallothionein genes: structure of thefunctional locus at 16q13. Genomics 8: 513- 518, 1990. 3 A c

GAM190 289 NLGN1 Ichtchenko, K.; Hata, Y.; Nguyen, T.; Ullrich, B.; Missler, M.;Moomaw, C.; Sudhof, T. C.: Neuroligin 1: a splice site- specific ligandfor beta- neurexins. Cell 81: 435- 443, 1995. 3 A c

GAM190 289 NLGN1 Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirosawa, M.; Miyajima, N.;Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of unidentified human genes. XIV. The complete sequencesof 100 new cDNA clones from brain which code for large proteins invitro. DNA Res. 6: 197- 205, 1999. 3 A c

GAM190 289 NLGN1 Scheiffele, P.; Fan, J.; Choih, J.; Fetter, R.; Serafini, T.:Neuroligin expressed in nonneuronal cells triggers presynaptic developmentin contacting axons. Cell 101: 657- 669, 2000. 3 A c

GAM190 289 NOTCH1 Artavanis- Tsakonas, S.; Matsuono, K.; Fortini, M.: Notch signaling. Science 268:225- 232, 1995. 3 A c

GAM190 289 NOTCH1 Axelrod, J. D.; Matsuno, K.; Artavanis- Tsakonas, S.; Perrimon,N.: Interaction between Wingless and Notch signaling pathways mediatedby Dishevelled. Science 271: 1826- 1832, 1996. 3 A c

GAM190 289 NOTCH1 Brou, C.; Logeat, F.; Gupta, N.; Bessia, C.; LeBail, O.; Doedens,J. R.; Cumano, A.; Roux, P.; Black, R. A.; Israel, A.: A novel proteolyticcleavage involved in Notch signaling: the role of the disintegrin- metalloproteaseTACE. Molec. Cell 5: 207- 216, 2000. 3 A c

GAM190 289 NOTCH1 Bruckner, K.; Perez, L.; Clausen, H.; Cohen, S.: Glycosyltransferaseactivity of Fringe modulates Notch- Delta interactions. Nature 406:411- 415, 2000. 3 A c

GAM190 289 NOTCH1 Chan, Y.- M.; Jan, Y. N.: Roles for proteolysis and traffickingin Notch 3 A c

maturation and signal transduction. Cell 94: 423- 426, 1998.

GAM190 289 NOTCH1 Conlon, R. A.; Reaume, A. G.; Rossant, J.: Notch1 is requiredfor the 3 A c
coordinate segmentation of somites. Development 121: 1533- 1545,1995.

GAM190 289 NOTCH1 De Strooper, B.; Annaert, W.; Cupers, P.; Saftig, P.; Craessaerts,K.; Mumm, 3 A c
J. S.; Schroeter, E. H.; Schrijvers, V.; Wolfe, M. S.; Ray,W. J.; Goate, A.;
Kopan, R.: A presenilin- 1- dependent gamma- secretase- likeprotease
mediates release of Notch intracellular domain. Nature 398:518- 522, 1999.

GAM190 289 NOTCH1 Ellisen, L. W.; Bird, J.; West, D. C.; Soreng, A. L.; Reynolds,T. C.; Smith, 3 A c
S. D.; Sklar, J.: TAN- 1, the human homolog of the DrosophilaNotch gene, is
broken by chromosomal translocations in T lymphoblasticneoplasms. Cell 66:
649- 661, 1991.

GAM190 289 NOTCH1 Franco del Amo, F.; Gendron- Maguire, M.; Swiatek, P. J.; Jenkins,N. A.; 3 A c
Copeland, N. G.; Gridley, T.: Cloning, analysis, and chromosomallocalization
of Notch- 1, a mouse homolog of Drosophila Notch. Genomics 15:259- 264,
1993.

GAM190 289 NOTCH1 Hadland, B. K.; Manley, N. R.; Su, D.; Longmore, G. D.; Moore,C. L.; Wolfe, 3 A c
M. S.; Schroeter, E. H.; Kopan, R.: Gamma- secretaseinhibitors repress
thymocyte development. Proc. Nat. Acad. Sci. 98:7487- 7491, 2001.

GAM190 289 NOTCH1 Hardy, J.; Israel, A.: In search of gamma- secretase. Nature 398:466- 467, 3 A c
1999.

GAM190 289 NOTCH1 Huppert, S. S.; Le, A.; Schroeter, E. H.; Mumm, J. S.; Saxena,M. T.; Milner, 3 A c
L. A.; Kopan, R.: Embryonic lethality in mice homozygousfor a processing-
deficient allele of Notch1. Nature 405: 966- 970,2000.

GAM190 289 NOTCH1 Jarriault, S.; Brou, C.; Logeat, F.; Schroeter, E. H.; Kopan,R.; Israel, A.: 3 A c
Signalling downstream of activated mammalian Notch. Nature 377:355- 358,
1995.

GAM190 289 NOTCH1 Jiang, Y.- J.; Aerne, B. L.; Smithers, L.; Haddon, C.; Ish- Horowitz,D.; 3 A c
Lewis, J.: Notch signalling and the synchronization of the
somitesegmentation clock. Nature 408: 475- 479, 2000.

GAM190 289 NOTCH1 Krebs, L. T.; Xue, Y.; Norton, C. R.; Shutter, J. R.; Maguire,M.; Sundberg, 3 A c
J. P.; Gallahan, D.; Closson, V.; Kitajewski, J.; Callahan,R.; Smith, G. H.;
Stark, K. L.; Gridley, T.: Notch signaling is essentialfor vascular
morphogenesis in mice. Genes Dev. 14: 1343- 1352, 2000.

GAM190 289 NOTCH1 Larsson, C.; Lardelli, M.; White, I.; Lendahl, U.: The humanNOTCH1, 2, and 3 3 A c
genes are located at chromosome positions 9q34, 1p13- p11,and 19p13.2- p13.1
in regions of neoplasia- associated translocation. Genomics 24:253- 258,
1994.

GAM190 289 NOTCH1 Logeat, F.; Bessia, C.; Brou, C.; LeBail, O.; Jarriault, S.; Seidah,N. G.; 3 A c
Israel, A.: The Notch1 receptor is cleaved constitutivelyby a furin- like
convertase. Proc. Nat. Acad. Sci. 95: 8108- 8112,1998.

GAM190 289 NOTCH1 Milner, L. A.; Kopan, R.; Martin, D. I. K.; Bernstein, I. D.:A human 3 A c
homologue of the Drosophila developmental gene, Notch, isexpressed in CD34+
hematopoietic precursors. Blood 83: 2057- 2062,1994.

GAM190 289 NOTCH1 Moloney, D. J.; Panin, V. M.; Johnston, S. H.; Chen, J.; Shao,L.; Wilson, 3 A c
R.; Wang, Y.; Stanley, P.; Irvine, K. D.; Haltiwanger,R. S.; Vogt, T. F.:
Fringe is a glycosyltransferase that modifiesNotch. Nature 406: 369- 375,
2000.

GAM190 289 NOTCH1 Mumm, J. S.; Schroeter, E. H.; Saxena, M. T.; Griesemer, A.; Tian,X.; Pan, 3 A c
D. J.; Ray, W. J.; Kopan, R.: A ligand- induced extracellularcleavage
regulates gamma- secretase- like proteolytic activation ofNotch1. Molec.

Cell 5: 197- 206, 2000.

GAM190 289 NOTCH1 Pilz, A.; Prohaska, R.; Peters, J.; Abbott, C.: Genetic linkageanalysis of 3 A c
the Ak1, Col5a1, Epb7.2, Fpgs, Grp78, Pbx3, and Notch1genes in the region of
mouse chromosome 2 homologous to human chromosome9q. Genomics 21: 104- 109,
1994.

GAM190 289 NOTCH1 Schroeter, E. H.; Kisslinger, J. A.; Kopan, R.: Notch- 1 signallingrequires 3 A c
ligand- induced proteolytic release of intracellular domain. Nature 393:382-
386, 1998.

GAM190 289 NOTCH1 Sestan, N.; Artavanis- Tsakonas, S.; Rakic, P.: Contact- dependentinhibition 3 A c
of cortical neurite growth mediated by Notch signaling. Science 286:741-
746, 1999.

GAM190 289 NOTCH1 Struhl, G.; Greenwald, I.: Presenilin is required for activityand nuclear 3 A c
access of Notch in Drosophila. Nature 398: 522- 525,1999.

GAM190 289 NOTCH1 Swiatek, P. J.; Lindsell, C. E.; del Amo, F. F.; Weinmaster, G.;Gridley, T.: 3 A c
Notch1 is essential for postimplantation developmentin mice. Genes Dev. 8:
707- 719, 1994.

GAM190 289 NOTCH1 Takahashi, Y.; Koizumi, K.; Takagi, A.; Kitajima, S.; Inoue, T.;Koseki, H.; 3 A c
Saga, Y.: Mesp2 initiates somite segmentation throughthe Notch signalling
pathway. Nature Genet. 25: 390- 396, 2000.

GAM190 289 NOTCH1 Tanigaki, K.; Nogaki, F.; Takahashi, J.; Tashiro, K.; Kurooka,H.; Honjo, T.: 3 A c
Notch1 and Notch3 instructively restrict bFGF- responsivemultipotent neural
progenitor cells to an astroglial fate. Neuron 29:45- 55, 2001.

GAM190 289 NOTCH1 Wang, J.; Shelly, L.; Miele, L.; Boykins, R.; Norcross, M. A.;Guan, E.: 3 A c
Human Notch- 1 inhibits NF- kappa- B activity in the nucleusthrough a direct
interaction involving a novel domain. J. Immun. 167:289- 295, 2001.

GAM190 289 NOTCH1 Weijzen, S.; Rizzo, P.; Braid, M.; Vaishnav, R.; Jonkheer, S.M.; Zlobin, A.; 3 A c
Osborne, B. A.; Gottipati, S.; Aster, J. C.; Hahn,W. C.; Rudolf, M.;
Siziopikou, K.; Kast, W. M.; Miele, L.: Activationof Notch- 1 signaling
maintains the neoplastic phenotype in human Ras- transformedcells. Nature
Med. 8: 979- 986, 2002.

GAM190 289 NOTCH1 Ye, Y.; Lukinova, N.; Fortini, M. E.: Neurogenic phenotypes andaltered Notch 3 A c
processing in Drosophila presenilin mutants. Nature 398:525- 529, 1999.

GAM190 289 NOTCH1 Yu, H.; Saura, C. A.; Choi, S.- Y.; Sun, L. D.; Yang, X.; Handler,M.; 3 A c
Kawarabayashi, T.; Younkin, L.; Fedeles, B.; Wilson, M. A.; Younkin,S.;
Kandel, E. R.; Kirkwood, A.; Shen, J.: APP processing and synapticplasticity
in presenilin- 1 conditional knockout mice. Neuron 31:713- 726, 2001.

GAM190 289 NOX1 Banfi, B.; Maturana, A.; Jaconi, S.; Arnaudeau, S.; Laforge, T.;Sinha, S.; 3 A c
Ligeti, E.; Demaurex, N.; Krause, K.- H.: A mammalian H+channel generated
through alternative splicing of the NADPH oxidasehomolog NOH- 1. Science
287: 138- 141, 2000.

GAM190 289 NOX1 Kikuchi, H.; Hikage, M.; Miyashita, H.; Fukumoto, M.: NADPH oxidasesubunit, 3 A c
gp9l- phox homologue, preferentially expressed in human colonepithelial
cells. Gene 254: 237- 243, 2000.

GAM190 289 NOX1 Starace, D. M; Stefani, E.; Bezanilla, F.: Voltage- dependent 3 A c
protontransport by the voltage sensor of the Shaker K+ channel. Neuron
19:1319- 1327, 1997.

GAM190 289 NOX1 Suh, Y.- A.; Arnold, R. S.; Lassegue, B.; Shi, J.; Xu, X.; Sorescu,D.; 3 A c
Chung, A. B.; Griendling, K. K.; Lambeth, J. D.: Cell transformationby the
superoxide- generating oxidase Mox1. Nature 401: 79- 82, 1999.

GAM190 289 NPTX2 Abernethy, T. J.; Avery, O. T.: The occurrence during acute infectionsof a 3 A c

protein not normally present in the blood. I. Distribution ofthe reactive protein in patients' sera and the effect of calcium onthe flocculation reaction with C polysaccharide of pneumococcus. J.Exp. Med. 73: 173- 182, 1941.

GAM190 289 NPTX2 Hsu, Y.- C.; Perin, M. S.: Human neuronal pentraxin II (NPTX2):conservation, 3 A c
genomic structure, and chromosomal localization. Genomics 28:220- 227, 1995.

GAM190 289 NPTX2 Schlimgen, A. K.; Helms, J. A.; Vogel, H.; Perin, M. S.: Neuronalpentraxin, 3 A c
a secreted protein with homology to acute phase proteinsof the immune system. Neuron 14: 519- 526, 1995.

GAM190 289 NPTX2 Tillett, W. S.; Francis, T., Jr.: Serological reactions in pneumoniawith a 3 A c
nonprotein somatic fraction of pneumococcus. J. Exp. Med. 52:561- 585, 1930.

GAM190 289 NRG1 Cannella, B.; Hoban, C. J.; Gao, Y.- L.; Garcia- Arenas, R.; Lawson,D.; 3 A c
Marchionni, M.; Gwynne, D.; Raine, C. S.: The neuregulin, glialgrowth factor 2, diminishes autoimmune demyelination and enhancesremyelination in a chronic relapsing model for multiple sclerosis. Proc.Nat. Acad. Sci. 95: 10100- 10105, 1998.

GAM190 289 NRG1 Falls, D. L.; Rosen, K. M.; Corfas, G.; Lane, W. S.; Fischbach,G. D.: ARIA, 3 A c
a protein that stimulates acetylcholine receptor synthesis,is a member of the Neu ligand family. Cell 72: 801- 815, 1993.

GAM190 289 NRG1 Fernandez, P.- A.; Tang, D. G.; Cheng, L.; Prochiantz, A.; Mudge,A. W.; 3 A c
Raff, M. C.: Evidence that axon- derived neuregulin promotesoligodendrocyte survival in the developing rat optic nerve. Neuron 28:81- 90, 2000.

GAM190 289 NRG1 Holmes, W. E.; Sliwkowski, M. X.; Akita, R. W.; Henzel, W. J.;Lee, J.; Park, 3 A c
J. W.; Yansura, D.; Abadi, N.; Raab, H.; Lewis, G.D.; Shepard, H. M.; Kuang, W.- J.; Wood, W. I.; Goeddel, D. V.; Vandlen,R. L.: Identification of heregulin, a specific activator of p185(erbB2). Science 256:1205- 1210, 1992.

GAM190 289 NRG1 Huang, Y. Z.; Won, S.; Ali, D. W.; Wang, Q.; Tanowitz, M.; Du,Q. S.; Pelkey, 3 A c
K. A.; Yang, D. J.; Xiong, W. C.; Salter, M. W.; Mei,L.: Regulation of neuregulin signaling by PSD- 95 interacting withErbB4 at CNS synapses. Neuron 26: 443- 455, 2000.

GAM190 289 NRG1 Lee, J.; Wood, W. I.: Assignment of heregulin (HGL) to human chromosome8p22- 3 A c
p11 by PCR analysis of somatic cell hybrid DNA. Genomics 16:790- 791, 1993.

GAM190 289 NRG1 Martinou, J.- C.; Falls, D. L.; Fischbach, G. D.; Merlie, J. P.: 3 A c
Acetylcholine receptor- inducing activity stimulates expression ofthe epsilon- subunit gene of the muscle acetylcholine receptor. Proc.Nat. Acad. Sci. 88: 7669- 7673, 1991.

GAM190 289 NRG1 Ni, C.- Y.; Murphy, M. P.; Golde, T. E.; Carpenter, G.: Gamma- 3 A c
secretasecleavage and nuclear localization of ErbB- 4 receptor tyrosine kinase. Science 294:2179- 2181, 2001.

GAM190 289 NRG1 Orr- Urtreger, A.; Trakhtenbrot, L.; Ben- Levy, R.; Wen, D.; Rechavi,G.; 3 A c
Lonai, P.; Yarden, Y.: Neural expression and chromosomal mappingof NEU differentiation factor to 8p12- p21. Proc. Nat. Acad. Sci. 90:1867- 1871, 1993.

GAM190 289 NRG1 Thomas, W.; Rubenstein, M.; Goto, M.; Drayna, D.: A genetic analysisof the 3 A c
Werner syndrome region on human chromosome 8p. Genomics 16:685- 690, 1993.

GAM190 289 NRG1 Wolpowitz, D.; Mason, T. B. A.; Dietrich, P.; Mendelsohn, M.;Talmage, D. A.; 3 A c
Role, L. W.: Cysteine- rich domain isoforms of theneuregulin- 1 gene are required for maintenance of peripheral synapses. Neuron 25:79- 91, 2000.

GAM190 289 NRXN3 Missler, M.; Sudhof, T. C.: Neurexins: three genes and 1001 products. 3 A c
TrendsGenet. 14: 20- 26, 1998.

GAM190 289 NRXN3 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; 3 A c
Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of
unidentified human genes. XI. The complete sequencesof 100 new cDNA clones
from brain which code for large proteins invitro. DNA Res. 5: 277- 286,
1998.

GAM190 289 NRXN3 Rowen, L.; Young, J.; Birditt, B.; Kaur, A.; Madan, A.; Philipps,D. L.; Qin, 3 A c
S.; Minx, P.; Wilson, R. K.; Hood, L.; Graveley, B. R.: Analysis of the
human neurexin genes: alternative splicing and thegeneration of protein
diversity. Genomics 79: 587- 597, 2002.

GAM190 289 NRXN3 Tabuchi, K.; Sudhof, T. C.: Structure and evolution of neurexingenes: 3 A c
insight into the mechanism of alternative splicing. Genomics 79:849- 859,
2002.

GAM190 289 NRXN3 Ushkaryov, Y. A.; Petrenko, A. G.; Geppert, M.; Sudhof, T. C.:Neurexins: 3 A c
synaptic cell surface proteins related to the alpha- latrotoxinreceptor and
laminin. Science 257: 50- 56, 1992.

GAM190 289 OLR1 Sawamura, T.; Kume, N.; Aoyama, T.; Moriwaki, H.; Hoshikawa, H.;Aiba, Y.; 3 A c
Tanaka, T.; Miwa, S.; Katsura, Y.; Kita, T.; Masaki, T.: An endothelial
receptor for oxidized low- density lipoprotein. Nature 386:73- 77, 1997.

GAM190 289 OLR1 Yamanaka, S.; Zhang, X.- Y.; Miura, K.; Kim, S.; Iwao, H.: Thehuman gene 3 A c
encoding the lectin- type oxidized LDL receptor (OLR1) isa novel member of
the natural killer gene complex with a unique expressionprofile. Genomics
54: 191- 199, 1998.

GAM190 289 PPIA Braaten, D.; Wellington, S.; Warburton, D.; Luban, J.: Assignmentof 3 A c
cyclophilin A (PPIA) to human chromosome band 7p13 by in situ hybridization.
Cytogenet.Cell Genet. 74: 262 only, 1996.

GAM190 289 PPIA Liu, J.; Albers, M. W.; Chen, C.- M.; Schreiber, S. L.; Walsh, C.T.: 3 A c
Cloning, expression, and purification of human cyclophilin inEscherichia
coli and assessment of the catalytic role of cysteinesby site- directed
mutagenesis. Proc. Nat. Acad. Sci. 87: 2304- 2308,1990.

GAM190 289 PPIA Luban, J.; Bossolt, K. L.; Franke, E. K.; Kalpana, G. V.; Goff,S. P.: Human 3 A c
immunodeficiency virus type 1 gag protein binds to cyclophilinsA and B. Cell
73: 1067- 1078, 1993.

GAM190 289 PPIA Takahashi, N.; Hayano, T.; Suzuki, M.: Peptidyl- prolyl cis- transisomerase 3 A c
is the cyclosporin A- binding protein cyclophilin. Nature 337:473- 475,
1989.

GAM190 289 PPIA Willenbrink, W.; Halaschek, J.; Schuffenhauer, S.; Kunz, J.; 3 A c
Steinkasserer,A.: Cyclophilin A, the major intracellular receptor for the
immunosuppressantcyclosporin A, maps to chromosome 7p11.2- p13: four
pseudogenes mapto chromosomes 3, 10, 14, and 18. Genomics 28: 101- 104,
1995.

GAM190 289 PSMD5 Deveraux, Q.; Jensen, C.; Rechsteiner, M.: Molecular cloning andexpression 3 A c
of a 26 S protease subunit enriched in dileucine repeats. J.Biol. Chem. 270:
23726- 23729, 1995.

GAM190 289 PSMD5 Deveraux, Q.; Ustrell, V.; Pickart, C.; Rechsteiner, M.: A 26S protease 3 A c
subunit that binds ubiquitin conjugates. J. Biol. Chem. 269:7059- 7061,
1994.

GAM190 289 PSMD5 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 A c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding

sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM190 289 PTGS1 Catella- Lawson, F.; Reilly, M. P.; Kapoor, S. C.; Cucchiara, A.J.; DeMarco, 3 A c
S.; Tournier, B.; Vyas, S. N.; FitzGerald, G. A.: Cyclooxygenaseinhibitors
and the antiplatelet effects of aspirin. New Eng. J. Med. 345:1809- 1817,
2001.

GAM190 289 PTGS1 Dube, J.- N.; Drouin, J.; Aminian, M.; Plant, M. H.; Laneuville,O.: 3 A c
Characterization of a partial prostaglandin endoperoxide H synthase-
1deficiency in a patient with a bleeding disorder. Brit. J. Haemat. 113:878-
885, 2001.

GAM190 289 PTGS1 Funk, C. D.; Funk, L. B.; Kennedy, M. E.; Pong, A. S.; Fitzgerald,G. A.: 3 A c
Human platelet/erythroleukemia cell prostaglandin G/H synthase:cDNA cloning,
expression, and gene chromosomal assignment. FASEBJ. 5: 2304- 2312, 1991.

GAM190 289 PTGS1 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; 3 A c
Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.;
Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H
synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999.

GAM190 289 PTGS1 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; 3 A c
Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.:
Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2
in the humanfetal and adult male reproductive tracts. J. Clin. Endocr.
Metab. 85:3436- 3441, 2000.

GAM190 289 PTGS1 Langenbach, R.; Morham, S. G.; Tiano, H. F.; Loftin, C. D.; Ghanayem,B. I.; 3 A c
Chulada, P. C.; Mahler, J. F.; Lee, C. A.; Goulding, E. H.;Kluckman, K. D.;
Kim, H. S.; Smithies, O.: Prostaglandin synthase1 gene disruption in mice
reduces arachidonic acid- induced inflammationand indomethacin- induced
gastric ulceration. Cell 83: 483- 492, 1995.

GAM190 289 PTGS1 Malkowski, M. G.; Ginell, S. L.; Smith, W. L.; Garavito, R. M.: The 3 A c
productive conformation of arachidonic acid bound to prostaglandinsynthase.
Science 289: 1933- 1937, 2000.

GAM190 289 PTGS1 Pareti, F. I.; Manucci, P. M.; D'Angelo, A.; Smith, J. B.; Sautebin,L.; 3 A c
Galli, G.: Congenital deficiency of thromboxane and prostacyclin. Lancet
I:898- 900, 1980.

GAM190 289 PTGS1 Picot, D.; Loll, P. J.; Garavito, R. M.: The x- ray crystal structureof the 3 A c
membrane protein prostaglandin H- 2 synthase- 1. Nature 367:243- 249, 1994.

GAM190 289 PTGS1 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: 3 A c
Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93:
705- 716, 1998.

GAM190 289 PTGS1 Vane, J. R.; Mitchell, J. A.; Appleton, I.; Tomlinson, A.; Bishop- 3 A c
Bailey,D.; Croxtall, J.; Willoughby, D. A.: Inducible isoforms of
cyclooxygenaseand nitric- oxide synthase in inflammation. Proc. Nat. Acad.
Sci. 91:2046- 2050, 1994.

GAM190 289 PTGS1 Yokoyama, C.; Tanabe, T.: Cloning of human gene encoding 3 A c
prostaglandinendoperoxide synthase and primary structure of the enzyme.
Biochem.Biophys. Res. Commun. 165: 888- 894, 1989.

GAM190 289 RERE Amler, L. C.; Bauer, A.; Corvi, R.; Dihlmann, S.; Praml, C.; Cavenee,W. K.; 3 A c
Schwab, M.; Hampton, G. M.: Identification and characterizationof novel
genes located at the t(1;15)(p36.2;q24) translocation breakpointin the
neuroblastoma cell line NGP. Genomics 64: 195- 202, 2000.

GAM190 289 RERE Yanagisawa, H.; Bundo, M.; Miyashita, T.; Okamura- Oho, Y.; Tadokoro,K.; 3 A c
Tokunaga, K.; Yamada, M.: Protein binding of a DRPLA family througharginine-
glutamic acid dipeptide repeats is enhanced by extended polyglutamine.
Hum.Molec. Genet. 9: 1433- 1442, 2000.

GAM190 289 SLC9A1 Denker, S. P.; Huang, D. C.; Orlowski, J.; Furthmayr, H.; Barber,D. L.: 3 A c
Direct binding of the Na- H exchanger NHE1 to ERM proteinsregulates the
cortical cytoskeleton and cell shape independently ofH(+) translocation.
Molec. Cell 6: 1425- 1436, 2000.

GAM190 289 SLC9A1 Dudley, C. R. K.; Giuffra, L. A.; Tippett, P.; Kidd, K. K.; Reeders,S. T.: 3 A c
The Na+/H+ antiporter: a 'melt' polymorphism allows regionalmapping to the
short arm of chromosome 1. Hum. Genet. 86: 79- 83,1990.

GAM190 289 SLC9A1 Franchi, A.; Perucca- Lostanlen, D.; Pouyssegur, J.: Functionalexpression of 3 A c
a human Na+/H+ antiporter gene transfected into antiporter- deficientmouse L
cells. Proc. Nat. Acad. Sci. 83: 9388- 9392, 1986.

GAM190 289 SLC9A1 Lifton, R. P.; Sardet, C.; Pouyssegur, J.; Lalouel, J.- M.: Cloningof the 3 A c
human genomic amiloride- sensitive Na+/H+ antiporter gene, identificationof
genetic polymorphisms, and localization on the genetic map of chromosome1p.
Genomics 7: 131- 135, 1990.

GAM190 289 SLC9A1 Mattei, M.- G.; Galloni, M.; Sardet, C.; Franchi, A.; Counillon,L.; Passage, 3 A c
E.; Pouyssegur, J.: Localization of the antiporter gene(APNH) and
chromosomal homology between human 1p, mouse 4 and Chinesehamster 2q.
(Abstract) Cytogenet. Cell Genet. 51: 1041, 1989.

GAM190 289 SLC9A1 Mattei, M.- G.; Sardet, C.; Franchi, A.; Pouyssegur, J.: Chromosomalmapping 3 A c
of the amiloride- sensitive Na+/H+ antiporter gene. (Abstract)
Cytogenet.Cell Genet. 46: 658- 659, 1987.

GAM190 289 SLC9A1 Mattei, M.- G.; Sardet, C.; Franchi, A.; Pouyssegur, J.: The humanamiloride- 3 A c
sensitive Na+/H+ antiporter: localization to chromosome1 by in situ
hybridization. Cytogenet. Cell Genet. 48: 6- 8, 1988.

GAM190 289 SLC9A1 Mendoza, S. A.: The Na+/H+ antiport is a mediator of cell proliferation. 3 A c
ActaPaediat. Scand. 76: 545- 547, 1987.

GAM190 289 SLC9A1 Morahan, G.; Rakar, S.: Localization of the mouse Na+/H+ exchangergene on 3 A c
distal chromosome 4. Genomics 15: 231- 232, 1993.

GAM190 289 SLC9A1 Sardet, C.; Franchi, A.; Pouyssegur, J.: Molecular cloning, 3 A c
primarystructure, and expression of the human growth factor- activatable
Na(+)/H(+)antiporter. Cell 56: 271- 280, 1989.

GAM190 289 SUV39H2 O'Carroll, D.; Scherthan, H.; Peters, A. H. F. M.; Opravil, S.;Haynes, A. 3 A c
R.; Laible, G.; Rea, S.; Schmid, M.; Lebersorger, A.; Jerratsch,M.; Sattler,
L.; Mattei, M. G.; Denny, P.; Brown, S. D. M.; Schweizer,D.; Jenuwein, T.:
Isolation and characterization of Suv39h2, a secondhistone H3
methyltransferase gene that displays testis- specific expression.
Molec.Cell. Biol. 20: 9423- 9433, 2000.

GAM190 289 SUV39H2 Peters, A. H. F. M.; O'Carroll, D.; Scherthan, H.; Mechtler, K.;Sauer, S.; 3 A c
Schofer, C.; Weipoltshammer, K.; Pagani, M.; Lachner, M.;Kohlmaier, A.;
Opravil, S.; Doyle, M.; Sibilia, M.; Jenuwein, T.:Loss of the Suv39h histone
methyltransferases impairs mammalian heterochromatinand genome stability.
Cell 107: 323- 337, 2001.

GAM190 289 TRO Fukuda, M. N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami, M.; Aoki,D.; 3 A c
Nozawa, S.: Trophinin and tastin, a novel cell adhesion moleculecomplex with
potential involvement in embryo implantation. GenesDev. 9: 1199- 1210, 1995.

GAM190 289 TRO Pack, S. D.; Tanigami, A.; Ledbetter, D. H.; Sato, T.; Fukuda,M. N.: 3 A c

Assignment of trophoblast/endometrial epithelium cell adhesionmolecule trophinin gene TRO to human chromosome bands Xp11.22- p11.21by in situ hybridization. Cytogenet. Cell Genet. 79: 123- 124, 1997.

GAM190 289 TRO Suzuki, N.; Nakayama, J.; Shih, I. M.; Aoki, D.; Nozawa, S.; Fukuda,M. N.: 3 A c
Expression of trophinin, tastin, and bystin by trophoblastand endometrial cells in human placenta. Biol. Reprod. 60: 621- 627,1999.

GAM190 289 UBQLN2 Kaye, F. J.; Modi, S.; Ivanovska, I.; Koonin, E. V.; Thress, K.;Kubo, A.; 3 A c
Kornbluth, S.; Rose, M. D.: A family of ubiquitin- likeproteins binds the ATPase domain of Hsp70- like Stch. FEBS Lett. 467:348- 352, 2000.

GAM190 289 UBQLN2 Kaye, F. J.; Shows, T. B.: Assignment of ubiquilin 2 (UBQLN2)to human 3 A c
chromosome xp11.23- p11.1 by GeneBridge radiation hybrids. Cytogenet.Cell Genet. 89: 116- 117, 2000.

GAM190 289 UBQLN2 Kleijnen, M. F.; Shih, A. H.; Zhou, P.; Kumar, S.; Soccio, R. E.;Kedersha, 3 A c
N. L.; Gill, G.; Howley, P. M.: The hPLIC proteins mayprovide a link between the ubiquitination machinery and the proteasome. Molec.Cell 6: 409- 419, 2000.

GAM190 289 UNC5C Ackerman, S. L.; Knowles, B. B.: Cloning and mapping of the UNC5Cgene to 3 A c
human chromosome 4q21- q23. Genomics 52: 205- 208, 1998.

GAM190 289 UNC5C Ackerman, S. L.; Kozak, L. P.; Przyborski, S. A.; Rund, L. A.;Boyer, B. B.; 3 A c
Knowles, B. B.: The mouse rostral cerebellar malformationgene encodes an UNC- 5- like protein. Nature 386: 838- 842, 1997.

GAM190 289 UNC5C Lane, P. W.; Bronson, R. T.; Spencer, C. A.: Rostral cerebellarmalformation, 3 A c
(rcm): a new recessive mutation on chromosome 3 of themouse. J. Hered. 83: 315- 318, 1992.

GAM190 289 UNC5C Leonardo, E. D.; Hinck, L.; Masu, M.; Keino- Masu, K.; Ackerman,S. L.; 3 A c
Tessier- Lavigne, M.: Vertebrate homologues of C. elegans UNC- 5are candidate netrin receptors. Nature 386: 833- 838, 1997.

GAM190 289 UNC5C Przyborski, S. A.; Knowles, B. B.; Ackerman, S. L.: Embryonicphenotype of 3 A c
Unc5h3 mutant mice suggests chemorepulsion during theformation of the rostral cerebellar boundary. Development 125: 41- 50,1998.

GAM190 289 ZNF179 Kimura, T.; Arakawa, Y.; Inoue, S.; Fukushima, Y.; Kondo, I.; Koyama,K.; 3 A c
Hosoi, T.; Orimo, A.; Muramatsu, M.; Nakamura, Y.; Abe, T.; Inazawa,J.: The brain finger protein gene (ZNF179), a member of the RINGfinger family, maps within the Smith- Magenis syndrome region at 17p11.2. Am.J. Med. Genet. 69: 320- 324, 1997.

GAM190 289 ZNF179 Matsuda, Y.; Inue, S.; Seki, N.; Hosoi, T.; Orimo, A.; Muramatsu,M.; Hori, 3 A c
T.: Chromosome mapping of human (ZNF179), mouse, and ratgenes for brain finger protein (bfp), a member of the RING fingerfamily. Genomics 33: 325- 327, 1996.

GAM192 393 AKAP2 Dong, F.; Feldmesser, M.; Casadevall, A.; Rubin, C. S.: 3 C c
Molecularcharacterization of a cDNA that encodes six isoforms of a novel murineA kinase anchor protein. J. Biol. Chem. 273: 6533- 6541, 1998.

GAM192 393 AKAP2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999.

GAM193 268 CPD McGwire, G. B.; Tan, F.; Michel, B.; Rehli, M.; Skidgel, R. A.: 4 A c
Identification of a membrane- bound carboxypeptidase as the mammalianhomolog of duck gp180, a hepatitis B virus- binding protein. LifeSci. 60: 715- 724,

1997.

GAM193 268 CPD Riley, D. A.; Tan, F.; Miletich, D. J.; Skidgel, R. A.: 4 A c
Chromosomallocalization of the genes for human carboxypeptidase D (CPD) and theactive 50- kilodalton subunit of human carboxypeptidase N (CPN1). Genomics 50:105- 108, 1998.

GAM193 268 CPD Tan, F.; Rehli, M.; Krause, S. W.; Skidgel, R. A.: Sequence ofhuman 4 A c
carboxypeptidase D reveals it to be a member of the regulatorycarboxypeptidase family with three tandem active site domains. Biochem.J. 327: 81- 87, 1997.

GAM193 268 ETV5 Monte, D.; Baert, J. L.; Defossez, P. A.; de Launoit, Y.; Stehelin,D.: 4 A c
Molecular cloning and characterization of human ERM, a new memberof the Ets family closely related to mouse PEA3 and ER81 transcriptionfactors. Oncogene 9: 1397- 1406, 1994.

GAM193 268 ETV5 Monte, D.; Coutte, L.; Dewitte, F.; Defossez, P.- A.; Le Coniat,M.; 4 A c
Stehelin, D.; Berger, R.; de Launoit, Y.: Genomic organizationof the human ERM (ETV5) gene, a PEA3 group member of ETS transcriptionfactors. Genomics 35: 236- 240, 1996.

GAM193 268 ETV5 Protopopova, M. V.; Vorobieva, N. V.; Protopopov, A. I.; Gizatullin,R. Z.; 4 A c
Kashuba, V. I.; Klein, G.; Zabarovsky, E. R.; Graphodatsky,A. S.: Assignment of the ERM gene (ETV5) coding for the ets- relatedprotein to human chromosome band 3q28 by in situ hybridization. Cytogenet.Cell Genet. 74: 220 only, 1996.

GAM193 268 GAS41 Fischer, U.; Heckel, D.; Michel, A.; Janka, M.; Hulsebos, T.; Meese,E.: 4 A c
Cloning of a novel transcription factor- like gene amplified inhuman glioma including astrocytoma grade I. Hum. Molec. Genet. 6:1817- 1822, 1997.

GAM193 268 GAS41 Gracia, E.; Fischer, U.; Elkahloun, A.; Trent, J. M.; Meese, E.;Meltzer, P. 4 A c
S.: Isolation of genes amplified in human cancers bymicrodissection mediated cDNA capture. Hum. Molec. Genet. 5: 595- 600,1996.

GAM193 268 GTF2H2 Carter, T. A.; Bonnemann, C. G.; Wang, C. H.; Obici, S.; Parano,E.; De 4 A c
Fatima Bonaldo, M.; Ross, B. M.; Penchaszadeh, G. K.; Mackenzie,A.; Bento Soares, M.; Kunkel, L. M.; Gilliam, T. C.: A multicopytranscription- repair gene, BTF2p44, maps to the SMA region and demonstratesSMA associated deletions. Hum. Molec. Genet. 6: 229- 236, 1997.

GAM193 268 GTF2H2 Humbert, S.; van Vuuren, H.; Lutz, Y.; Hoeijmakers, J. H.; Egly,J. M.; 4 A c
Moncollin, V.: p44 and p34 subunits of the BTF2/TFIIH transcriptionfactor have homologies with SSL1, a yeast protein involved in DNArepair. EMBO J. 13: 2393- 2398, 1994.

GAM193 268 GTF2H2 van der Steege, G.; Draaijers, T. G.; Grootscholten, P. M.; Osinga,J.; 4 A c
Anzevino, R.; Velona, I.; Den Dunnen, J. T.; Scheffer, H.; Brahe,C.; van Ommen, G. J.; Buys, H. C. M.: A provisional transcript mzpof the spinal muscular atrophy (SMA) critical region. Europ. J. Hum.Genet. 3: 87- 95, 1995.

GAM193 268 GYG2 Mu, J.; Roach, P. J.: Characterization of human glycogenin- 2,a self- 4 A c
glucosylating initiator of liver glycogen metabolism. J. Biol.Chem. 273: 34850- 34856, 1998.

GAM193 268 GYG2 Mu, J.; Skurat, A. V.; Roach, P. J.: Glycogenin- 2, a novel self- 4 A c
glucosylatingprotein involved in liver glycogen biosynthesis. J. Biol. Chem. 272:27589- 27597, 1997.

GAM193 268 ITGAV Bader, B. L.; Rayburn, H.; Crowley, D.; Hynes, R. O.: 4 A c
Extensivevasculogenesis, angiogenesis, and organogenesis precede lethalityin

mice lacking all alpha- V integrins. Cell 95: 507- 519, 1998.

GAM193 268 ITGAV Fernandez- Ruiz, E.; de Villena, F. P.- M.; Rodriguez de Cordoba,S.; Sanchez- Madrid, F.: Regional localization of the human vitronectinreceptor alpha- subunit gene (VNRA) to chromosome 2q31- q32. Cytogenet.Cell Genet. 62: 26- 28, 1993. 4 A c

GAM193 268 ITGAV Fitzgerald, L. A.; Poncz, M.; Steiner, B.; Rall, S. C., Jr.; Bennett,J. S.; Phillips, D. R.: Comparison of cDNA- derived protein sequencesof the human fibronectin and vitronectin receptor alpha- subunits andplatelet glycoprotein IIb. Biochemistry 26: 8158- 8165, 1987. 4 A c

GAM193 268 ITGAV Sims, M. A.; Field, S. D.; Barnes, M. R.; Shaikh, N.; Ellington,K.; Murphy, K. E.; Spurr, N.; Campbell, D. A.: Cloning and characterisationof ITGAV, the genomic sequence for human cell adhesion protein (vitronectin)receptor alpha subunit, CD51. Cytogenet. Cell Genet. 89: 268- 271,2000. 4 A c

GAM193 268 ITGAV Sosnoski, D.; Emanuel, B. S.; Hawkins, A. L.; van Tuinen, P.; Ledbetter,D. H.; Nussbaum, R. L.; Kaos, F.- T.; Schwartz, E.; Phillips, D.; Bennett,J. S.; Fitzgerald, L. A.; Poncz, M.: Chromosomal localization ofthe genes for the vitronectin and fibronectin receptors alpha- subunitsand for platelet glycoproteins IIb and IIIa. J. Clin. Invest. 81:1993- 1998, 1988. 4 A c

GAM193 268 ITGAV Spurr, N. K.; Rooke, L.: Confirmation of the assignment of thevitronectin (VNRA) and fibronectin (FNRA) receptor alpha- subunits. Ann.Hum. Genet. 55: 217- 223, 1991. 4 A c

GAM193 268 ITGAV Suzuki, S.; Argraves, W. S.; Pytela, R.; Arai, H.; Krusius, T.;Pierschbacher, M. D.; Ruoslahti, E.: cDNA and amino acid sequencesof the cell adhesion protein receptor recognizing vitronectin reveala transmembrane domain and homologies with other adhesion proteinreceptors. Proc. Nat. Acad. Sci. 83: 8614- 8618, 1986. 4 A c

GAM193 268 ITGAV Xiong, J.- P.; Stehle, T.; Diefenbach, B.; Zhang, R.; Dunker, R.;Scott, D. L.; Joachimiak, A.; Goodman, S. L.; Arnaout, M. A.: Crystalstructure of the extracellular segment of integrin alpha- V- beta- 3. Science 294:339- 345, 2001. 4 A c

GAM193 268 ITGAV Xiong, J.- P.; Stehle, T.; Zhang, R.; Joachimiak, A.; Frech, M.;Goodman, S. L.; Arnaout, M. A.: Crystal structure of the extracellularsegment of integrin alpha- V- beta- 3 in complex with an Arg- Gly- Aspligand. Science 296: 151- 155, 2002. 4 A c

GAM193 268 KIT Barker, P. E.; Besmer, P.; Ruddle, F. H.: Human c- kit oncogeneon human chromosome 4. (Abstract) Am. J. Hum. Genet. 37: A143, 1985. 4 A c

GAM193 268 KIT Beghini, A.; Larizza, L.; Cairoli, R.; Morra, E.: c- kit activatingmutations and mast cell proliferation in human leukemia. (Letter) Blood 92:701- 702, 1998. 4 A c

GAM193 268 KIT Beghini, A.; Tibiletti, M.; Roversi, G.; Chiaravalli, A.; Serio,G.; Capella, C.; Larizza, L.: Germline mutation in the juxtamembranedomain of the KIT gene in a family with gastrointestinal stromal tumorsand urticaria pigmentosa. Cancer 92: 657- 662, 2001. 4 A c

GAM193 268 KIT Blume- Jensen, P.; Jiang, G.; Hyman, R.; Lee, K.- F.; O'Gorman, S.;Hunter, T.: Kit/stem cell factor receptor- induced activation of phosphatidylinositol3- prime- kinase is essential for male fertility. Nature Genet. 24:157- 162, 2000. 4 A c

GAM193 268 KIT Bolognia, J. L.; Pawelek, J. M.: Biology of hypopigmentation. J.Am. Acad. Derm. 19: 217- 255, 1988. 4 A c

GAM193 268 KIT Brannan, C. I.; Lyman, S. D.; Williams, D. E.; Eisenman, J.; Anderson,D. M.; 4 A c

Cosman, D.; Bedell, M. A.; Jenkins, N. A.; Copeland, N. G.: Steel- Dickie mutation encodes a c- kit ligand lacking transmembraneand cytoplasmic domains. Proc. Nat. Acad. Sci. 88: 4671- 4674, 1991.

GAM193 268 KIT Chabot, B.; Stephenson, D. A.; Chapman, V. M.; Besmer, P.; Bernstein,A.: The 4 A c proto- oncogene c- kit encoding a transmembrane tyrosine kinasereceptor maps to the mouse W locus. Nature 335: 88- 89, 1988.

GAM193 268 KIT d'Auriol, L.; Mattei, M.- G.; Andre, C.; Galibert, F.: Localizationof the 4 A c human c- kit protooncogene on the q11- q12 region of chromosome4. Hum. Genet. 78: 374- 376, 1988.

GAM193 268 KIT De Miguel, M. P.; Cheng, L.; Holland, E. C.; Federspiel, M. J.;Donovan, P. 4 A c J.: Dissection of the c- Kit signaling pathway in mouseprimordial germ cells by retroviral- mediated gene transfer. Proc.Nat. Acad. Sci. 99: 10458- 10463, 2002.

GAM193 268 KIT Dubreuil, P.; Forrester, L.; Rottapel, R.; Reedijk, M.; Fujita,J.; 4 A c Bernstein, A.: The c- fms gene complements the mitogenic defectin mast cells derived from mutant W mice but not mi (microphthalmia)mice. Proc. Nat. Acad. Sci. 88: 2341- 2345, 1991.

GAM193 268 KIT el- Omar, M.; Davies, J.; Gupta, S.; Ross, H.; Thompson, R.: 4 A c Leiomyosarcomain leiomyomatosis of the small intestine. Postgrad. Med. J. 70:661- 664, 1994.

GAM193 268 KIT Fleischman, R. A.: Human piebald trait resulting from a dominantnegative 4 A c mutant allele of the c- kit membrane receptor gene. J. Clin.Invest. 89: 1713- 1717, 1992.

GAM193 268 KIT Fleischman, R. A.; Saltman, D. L.; Stastny, V.; Zneimer, S.:Deletion of the 4 A c c- kit protooncogene in the human developmental defectpiebald trait. Proc. Nat. Acad. Sci. 88: 10885- 10889, 1991.

GAM193 268 KIT Fritsche- Polanz, R.; Jordan, J.- H.; Feix, A.; Sperr, W. R.; Sunder- 4 A c Plassmann,G.; Valent, P.; Fodinger, M.: Mutation analysis of C- KIT in patientswith myelodysplastic syndromes without mastocytosis and cases of systemicmastocytosis. Brit. J. Haemat. 113: 357- 364, 2001.

GAM193 268 KIT Furitsu, T.; Tsujimura, T.; Tono, T.; Ikeda, H.; Kitayama, H.;Koshimizu, U.; 4 A c Sugahara, H.; Butterfield, J. H.; Ashman, L. K.; Kanayama,Y.; Matsuzawa, Y.; Kitamura, Y.; Kanakura, Y.: Identification ofmutations in the coding sequence of the proto- oncogene c- kit in ahuman mast cell leukemia cell line causing ligand- independent activationof c- kit product. J. Clin. Invest. 92: 1736- 1744, 1993.

GAM193 268 KIT Geissler, E. N.; Ryan, M. A.; Housman, D. E.: The dominant- whitespotting 4 A c (W) locus of the mouse encodes the c- kit proto- oncogene. Cell 55:185- 192, 1988.

GAM193 268 KIT Giebel, L. B.; Spritz, R. A.: Mutation of the KIT (mast/stemcell growth 4 A c factor receptor) protooncogene in human piebaldism. Proc.Nat. Acad. Sci. 88: 8696- 8699, 1991.

GAM193 268 KIT Hirota, S.; Isozaki, K.; Moriyama, Y.; Hashimoto, K.; Nishida,T.; Ishiguro, 4 A c S.; Kawano, K.; Hanada, M.; Kurata, A.; Takeda, M.;Tunio, G. M.; Matsuzawa, Y.; Kanakura, Y.; Shinomura, Y.; Kitamura,Y.: Gain- of- function mutations of c- kit in human gastrointestinalstromal tumors. Science 279: 577- 580, 1998.

GAM193 268 KIT Huizinga, J. D.; Thuneberg, L.; Kluppel, M.; Malysz, J.; Mikkelsen,H. B.; 4 A c Bernstein, A.: W/kit gene required for interstitial cellsof Cajal and for intestinal pacemaker activity. Nature 373: 347- 349,1995.

GAM193 268 KIT Ingram, D. A.; Yang, F.- C.; Travers, J. B.; Wenning, M. J.; Hiatt,K.; New, S.; Hood, A.; Shannon, K.; Williams, D. A.; Clapp, D. W.: Genetic and biochemical evidence that haploinsufficiency of theNf1 tumor suppressor gene modulates melanocyte and mast cell fatesin vivo. J. Exp. Med. 191: 181- 187, 2000. 4 A c

GAM193 268 KIT Isozaki, K.; Terris, B.; Belghiti, J.; Schiffmann, S.; Hirota,S.; Vanderwinden, J.- M.: Germline- activating mutation in the kinasedomain of KIT gene in familial gastrointestinal stromal tumors. Am.J. Path. 157: 1581- 1585, 2000. 4 A c

GAM193 268 KIT Joensuu, H.; Roberts, P. J.; Sarlomo- Rikala, M.; Andersson, L.C.; Tervahartiala, P.; Tuveson, D.; Silberman, S. L.; Capdeville,R.; Dimitrijevic, S.; Druker, B.; Demetri, G. D.: Effect of the tyrosinekinase inhibitor STI571 in a patient with a metastatic gastrointestinalstromal tumor. New Eng. J. Med. 344: 1052- 1056, 2001. 4 A c

GAM193 268 KIT Johansson Moller, M.; Chaudhary, R.; Hellmen, E.; Hoyheim, B.;Chowdhary, B.; Andersson, L.: Pigs with the dominant white coat colorphenotype carry a duplication of the KIT gene encoding the mast/stemcell growth factor receptor. Mammalian Genome 7: 822- 830, 1996. 4 A c

GAM193 268 KIT Lasota, J.; Jasinski, M.; Sarlomo- Rikala, M.; Miettinen, M.:Mutations in exon 11 of c- kit occur preferentially in malignant versusbenign gastrointestinal stromal tumors and do not occur in leiomyomasor leiomyosarcomas. Am. J. Path. 154: 53- 60, 1999. 4 A c

GAM193 268 KIT Longley, B. J., Jr.; Metcalfe, D. D.; Tharp, M.; Wang, X.; Tyrrell,L.; Lu, S.- Z.; Heitjan, D.; Ma, Y.: Activating and dominant inactivatingc- KIT catalytic domain mutations in distinct clinical forms of humanmastocytosis. Proc. Nat. Acad. Sci. 96: 1609- 1614, 1999. 4 A c

GAM193 268 KIT Longley, B. J.; Tyrrell, L.; Lu, S.- Z.; Ma, Y.- S.; Langley, K.;Ding, T.; Duffy, T.; Jacobs, P.; Tang, L. H.; Modlin, I.: Somaticc- KIT activating mutation in urticaria pigmentosa and aggressive mastocytosis:establishment of clonality in a human mast cell neoplasm. NatureGenet. 12: 312- 314, 1996. 4 A c

GAM193 268 KIT Marklund, S.; Kijas, J.; Rodriguez- Martinez, H.; Ronnstrand, L.;Funa, K.; Moller, M.; Lange, D.; Edfors- Lilja, I.; Andersson, L.:Molecular basis for the dominant white phenotype in the domestic pig. GenomeRes. 8: 826- 833, 1998. 4 A c

GAM193 268 KIT Marshall, J. B.; Diaz- Arias, A. A.; Bochna, G. S.; Vogele, K.A.: Achalasia due to diffuse esophageal leiomyomatosis and inheritedas an autosomal dominant disorder. Gastroenterology 98: 1358- 1365,1990. 4 A c

GAM193 268 KIT Mattei, M. G.; d'Auriol, L.; Andre, C.; Passage, E.; Mattei, J.F.; Galibert, F.: Assignment of the human c- kit proto- oncogene tothe q11- q12 region of chromosome 4, using in situ hybridization. (Abstract) Cytogenet.Cell Genet. 46: 657, 1987. 4 A c

GAM193 268 KIT Nagata, H.; Worobec, A. S.; Oh, C. K.; Chowdhury, B. A.; Tannenbaum,S.; Suzuki, Y.; Metcalfe, D. D.: Identification of a point mutationin the catalytic domain of the protooncogene c- kit in peripheral bloodmononuclear cells of patients who have mastocytosis with an associatedhematologic disorder. Proc. Nat. Acad. Sci. 92: 10560- 10564, 1995. 4 A c

GAM193 268 KIT Nishida, T.; Hirota, S.; Taniguchi, M.; Hashimoto, K.; Isozaki,K.; Nakamura, H.; Kanakura, Y.; Tanaka, T.; Takabayashi, A.; Matsuda,H.; Kitamura, Y.: Familial gastrointestinal stromal tumours withgermline mutation of the KIT gene. (Letter) Nature Genet. 19: 323- 324,1998. 4 A c

GAM193 268 KIT Nocka, K.; Tan, J. C.; Chiu, E.; Chu, T. Y.; Ray, P.; Traktman,P.; Besmer, P.: Molecular bases of dominant negative and loss offunction mutations at the murine c- kit/white spotting locus: W- 37,W- v, W- 41 and W. EMBO J. 9: 1805- 1813, 1990. 4 A c

GAM193 268 KIT Nomura, K.; Hatayama, I.; Narita, T.; Kaneko, T.; Shiraishi, M.: A novel KIT gene missense mutation in a Japanese family with piebaldism.(Letter) J. Invest. Derm. 111: 337- 338, 1998. 4 A c

GAM193 268 KIT Pignon, J.- M.; Giraudier, S.; Duquesnoy, P.; Jouault, H.; Imbert,M.; Vainchenker, W.; Vernant, J.- P.; Tulliez, M.: A new c- kit mutationin a case of aggressive mast cell disease. Brit. J. Haemat. 96:374- 376, 1997. 4 A c

GAM193 268 KIT Poduslo, S. E.; Dean, M.; Kolch, U.; O'Brien, S. J.: Detectinghigh- resolution polymorphisms in human coding loci by combining PCRand single- strand conformation polymorphism (SSCP) analysis. Am.J. Hum. Genet. 49: 106- 111, 1991. 4 A c

GAM193 268 KIT Reinsch, N.; Thomsen, H.; Xu, N.; Brink, M.; Looft, C.; Kalm,E.; Brockmann, G. A.; Grupe, S.; Kuhn, C.; Schwerin, M.; Leyhe, B.;Hiendleder, S.; Erhardt, G.; Medjugorac, I.; Russ, I.; Forster, M.;Reents, R.; Averdunk, G.: A QTL for the degree of spotting in cattleshows synteny with the KIT locus on chromosome 6. J. Hered. 90:629- 634, 1999. 4 A c

GAM193 268 KIT Savage, D. G.; Antman, K. H.: Imatinib mesylate- - a new oral targetedtherapy. New Eng. J. Med. 346: 683- 693, 2002. 4 A c

GAM193 268 KIT Selmanowitz, V. J.; Rabinowitz, A. D.; Orentreich, N.; Wenk, E.: Pigmentary correction of piebaldism by autografts. I. Proceduresand clinical findings. J. Derm. Surg. Oncol. 3: 615- 622, 1977. 4 A c

GAM193 268 KIT Spritz, R. A.; Beighton, P.: Piebaldism with deafness: molecularevidence for an expanded syndrome. Am. J. Med. Genet. 75: 101- 103,1998. 4 A c

GAM193 268 KIT Spritz, R. A.; Droetto, S.; Fukushima, Y.: Deletion of the KITand PDGFRA genes in a patient with piebaldism. Am. J. Med. Genet. 44:492- 495, 1992. 4 A c

GAM193 268 KIT Spritz, R. A.; Giebel, L. B.: Mutation of the c- kit (mast/stemcell growth factor receptor) proto- oncogene in human piebaldism. (Abstract) Am.J. Hum. Genet. 49 (suppl.): 38, 1991. 4 A c

GAM193 268 KIT Spritz, R. A.; Giebel, L. B.; Holmes, S. A.: Dominant negativeand loss of function mutations of the c- kit (mast/stem cell growthfactor receptor) proto- oncogene in human piebaldism. Am. J. Hum.Genet. 50: 261- 269, 1992. 4 A c

GAM193 268 KIT Spritz, R. A.; Holmes, S. A.; Ramesar, R.; Greenberg, J.; Curtis,D.; Beighton, P.: Mutations of the KIT (mast/stem cell growth factorreceptor) proto- oncogene account for a continuous range of phenotypesin human piebaldism. Am. J. Hum. Genet. 51: 1058- 1065, 1992. 4 A c

GAM193 268 KIT Syrris, P.; Malik, N. M.; Murday, V. A.; Patton, M. A.; Carter,N. D.; Hughes, H. E.; Metcalfe, K.: Three novel mutations of theproto- oncogene KIT cause human piebaldism. (Letter) Am. J. Med. Genet. 95:79- 81, 2000. 4 A c

GAM193 268 KIT Tan, J. C.; Nocka, K.; Ray, P.; Traktman, P.; Besmer, P.: Thedominant W42 spotting phenotype results from a missense mutation inthe c- kit receptor kinase. Science 247: 209- 212, 1990. 4 A c

GAM193 268 KIT Taylor, M. L.; Dastych, J.; Sehgal, D.; Sundstrom, M.; Nilsson,G.; Akin, C.; Mage, R. G.; Metcalfe, D. D.: The Kit- activating mutationD816V enhances stem cell factor- dependent chemotaxis. Blood 98:1195- 1199, 2001. 4 A c

GAM193 268 KIT Thomsen, L.; Robinson, T. L.; Lee, J. C. F.; Farraway, L. A.;Hughes, M. J. G.; Andrews, D. W.; Huizinga, J. D.: Interstitial cellsof Cajal generate a rhythmic pacemaker current. Nature Med. 4: 848- 851,1998. 4 A c

GAM193 268 KIT Tian, Q.; Frierson, H. F., Jr.; Krystal, G. W.; Moskaluk, C. A.: Activating 4 A c
c- kit gene mutations in human germ cell tumors. Am.J. Path. 154: 1643-
1647, 1999.

GAM193 268 KIT Tsujimura, T.; Furitsu, T.; Morimoto, M.; Isozaki, K.; Nomura,S.; Matsuzawa, 4 A c
Y.; Kitamura, Y.; Kanakura, Y.: Ligand- independentactivation of c- kit
receptor tyrosine kinase in a murine mastocytomacell line P- 815 generated
by a point mutation. Blood 83: 2619- 2626,1994.

GAM193 268 KIT Vandenbark, G. R.; deCastro, C. M.; Taylor, H.; Dew- Knight, S.;Kaufman, R. 4 A c
E.: Cloning and structural analysis of the human c- kitgene. Oncogene 7:
1259- 1266, 1992.

GAM193 268 KIT Worobec, A. S.; Semere, T.; Nagata, H.; Metcalfe, D. D.: Clinicalcorrelates 4 A c
of the presence of the asp816val c- kit mutation in theperipheral blood
mononuclear cells of patients with mastocytosis. Cancer 83:2120- 2129, 1998.

GAM193 268 KIT Yarden, Y.; Kuang, W.- J.; Yang- Feng, T.; Coussens, L.; Munemitsu,S.; Dull, 4 A c
T. J.; Chen, E.; Schlessinger, J.; Francke, U.; Ullrich,A.: Human proto-
oncogene c- kit: a new cell surface receptor tyrosinekinase for an
unidentified ligand. EMBO J. 6: 3341- 3351, 1987.

GAM193 268 NPY Allen, J. M.; Bloom, S. R.: Neuropeptide Y: a putative neurotransmitter. 4 A c
Neurochem.Int. 8: 1- 8, 1986.

GAM193 268 NPY Bahary, N.; Zorich, G.; Pachter, J. E.; Leibel, R. L.; Friedman,J. M.: 4 A c
Molecular genetic linkage maps of mouse chromosomes 4 and6. Genomics 11: 33-
47, 1991.

GAM193 268 NPY Baker, E.; Hort, Y. J.; Ball, H.; Sutherland, G. R.; Shine, J.;Herzog, H.: 4 A c
Assignment of the human neuropeptide Y gene to chromosome7p15.1 by
nonisotopic in situ hybridization. Genomics 26: 163- 164,1995.

GAM193 268 NPY Carr, L. G.; Foroud, T.; Bice, P.; Gobbett, T.; Ivashina, J.; Edenberg,H.; 4 A c
Lumeng, L.; Li, T. K.: A quantitative trait locus for alcoholconsumption in
selectively bred rat lines. Alcohol Clin. Exp. Res. 22:884- 887, 1998.

GAM193 268 NPY Dockray, G. J.: Neuropeptide Y: in search of a function. Neurochem.Int. 8: 4 A c
9- 11, 1986.

GAM193 268 NPY Erickson, J. C.; Clegg, K. E.; Palmiter, R. D.: Sensitivity toleptin and 4 A c
susceptibility to seizures of mice lacking neuropeptideY. Nature 381: 415-
421, 1996.

GAM193 268 NPY Erickson, J. C.; Hollopeter, G.; Palmiter, R. D.: Attenuationof the obesity 4 A c
syndrome of ob/ob mice by the loss of neuropeptideY. Science 274: 1704-
1706, 1996.

GAM193 268 NPY Hansel, D. E.; Eipper, B. A.; Ronnett, G. V.: Neuropeptide Y functionsas a 4 A c
neuroproliferative factor. Nature 410: 940- 943, 2001.

GAM193 268 NPY Karvonen, M. K.; Koulu, M.; Pesonen, U.; Uusitupa, M. I. J.; Tammi,A.; 4 A c
Viikari, J.; Simell, O.; Ronnemaa, T.: Leucine 7 to proline 7polymorphism in
the preproneuropeptide Y is associated with birthweight and serum
triglyceride concentration in preschool- aged children. J.Clin. Endocr.
Metab. 85: 1455- 1460, 2000.

GAM193 268 NPY Karvonen, M. K.; Pesonen, U.; Koulu, M.; Niskanen, L.; Laakso,M.; Rissanen, 4 A c
A.; Dekker, J. M.; 't Hart, L. M.; Valve, R.; Uusitupa,M. I.: Association of
a leucine(7)- to- proline(7) polymorphism inthe signal peptide of
neuropeptide Y with high serum cholesterol andLDL cholesterol levels. Nature
Med. 4: 1434- 1437, 1998.

GAM193 268 NPY Kauhanen, J.; Karvonen, M. K.; Pesonen, U.; Koulu, M.; Tuomainen,T.- P.; 4 A c
Uusitupa, M. I. J.; Salonen, J. T.: Neuropeptide Y polymorphismand alcohol

consumption in middle- aged men. Am. J. Med. Genet. 93:117- 121, 2000.

GAM193 268 NPY Maccarrone, C.; Jarrott, B.: Neuropeptide Y: a putative neurotransmitter. 4 A c
Neurochem.Int. 8: 13- 22, 1986.

GAM193 268 NPY Meisler, M. H.; Spence, J. E.; Dixon, J. E.; Caldwell, R. M.;Minth, C. D.; 4 A c
Beaudet, A. L.: Exclusion of close linkage betweenthe loci for cystic
fibrosis and neuropeptide Y on human chromosome7. Cytogenet. Cell Genet. 44:
175- 176, 1987.

GAM193 268 NPY Minth, C. D.; Andrews, P. C.; Dixon, J. E.: Characterization,sequence, and 4 A c
expression of the cloned human neuropeptide Y gene. J.Biol. Chem. 261:
11974- 11979, 1986.

GAM193 268 NPY Minth, C. D.; Bloom, S. R.; Polak, J. M.; Dixon, J. E.: 4 A c
Cloning,characterization, and DNA sequence of a human cDNA encoding
neuropeptidetyrosine. Proc. Nat. Acad. Sci. 81: 4577- 4581, 1984.

GAM193 268 NPY Niskanen, L.; Karvonen, M. K.; Valve, R.; Koulu, M.; Pesonen,U.; Mercuri, 4 A c
M.; Rauramaa, R.; Toyry, J.; Laakso, M.; Uusitupa, M.I. J.: Leucine 7 to
proline 7 polymorphism in the neuropeptide Ygene is associated with enhanced
carotid atherosclerosis in elderlypatients with type 2 diabetes and control
subjects. J. Clin. Endocr.Metab. 85: 2266- 2269, 2000.

GAM193 268 NPY Takeuchi, T.; Gumucio, D. L.; Yamada, T.; Meisler, M. H.; Minth,C. D.; 4 A c
Dixon, J. E.; Eddy, R. E.; Shows, T. B.: Genes encoding
pancreaticpolypeptide and neuropeptide Y are on human chromosomes 17 and 7.
J.Clin. Invest. 77: 1038- 1041, 1986.

GAM193 268 NPY Takeuchi, T.; Gumucio, D.; Eddy, R.; Meisler, M.; Minth, C.; Dixon,J.; 4 A c
Yamada, T.; Shows, T.: Assignment of the related pancreatic polypeptide(PPY)
and neuropeptide Y (NPY) genes to regions on human chromosomes17 and 7.
(Abstract) Cytogenet. Cell Genet. 40: 759 only, 1985.

GAM193 268 NPY Terenghi, G.; Polak, J. M.; Hamid, Q.; O'Brien, E.; Denny, P.;Legon, S.; 4 A c
Dixon, J.; Minth, C. D.; Palay, S. L.; Yasargil, G.; Chan- Palay,V.:
Localization of neuropeptide Y mRNA in neurons of human cerebralcortex by
means of in situ hybridization with a complementary RNAprobe. Proc. Nat.
Acad. Sci. 84: 7315- 7318, 1987.

GAM193 268 NPY Thiele, T. E.; Marsh, D. J.; Ste. Marie, L.; Bernstein, I. L.;Palmiter, R. 4 A c
D.: Ethanol consumption and resistance are inverselyrelated to neuropeptide
Y levels. Nature 396: 366- 369, 1998.

GAM193 268 NPY Uusitupa, M. I. J.; Karvonen, M. K.; Pesonen, U.; Koulu, M.:Neuropeptide Y: 4 A c
a novel link between the neuroendocrine system andcholesterol metabolism.
Ann. Med. 30: 508- 510, 1998.

GAM193 268 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 4 A c
Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J
recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585,
2002.

GAM193 268 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 4 A c
cell coactivator of octamer- binding transcription factors. Nature 373:360-
362, 1995.

GAM193 268 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 4 A c
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-
specific coactivator of octamer- binding transcription factors1 and 2, to
11q23.1 by somatic cell hybridization and in situ hybridization. Genomics
33:143- 145, 1996.

GAM193 268 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 4 A c

of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995.

GAM193 268 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001. 4 A c

GAM193 268 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. Immun. 9: 373- 398, 1991. 4 A c

GAM193 268 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell-specificcoactivator that stimulates immunoglobulin promoter activity throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995. 4 A c

GAM193 268 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B, BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-864, 2000. 4 A c

GAM193 268 RSN Bilbe, G.; Delabie, J.; Bruggen, J.; Richener, H.; Asselbergs,F. A. M.; Cerletti, N.; Sorg, C.; Odink, K.; Tarcsay, L.; Wiesendanger,W.; DeWolf-Peeters, C.; Shipman, R.: Restin: a novel intermediatefilament- associated protein highly expressed in the Reed- Sternbergcells of Hodgkin's disease. EMBO J. 11: 2103- 2113, 1992. 4 A c

GAM193 268 RSN Delabie, J.; Shipman, R.; Bruggen, J.; De Strooper, B.; van Leuven,F.; Tarcsay, L.; Cerletti, N.; Odink, K.; Diehl, V.; Bilbe, G.; DeWolf- Peeters, C.: Expression of the novel intermediate filament- associatedprotein restin in Hodgkin's disease and anaplastic large- cell lymphoma. Blood 80:2891-2896, 1992. 4 A c

GAM193 268 RSN Fukata, M.; Watanabe, T.; Noritake, J.; Nakagawa, M.; Yamaga, M.;Kuroda, S.; Matsuura, Y.; Iwamatsu, A.; Perez, F.; Kaibuchi, K.:Rac1 and Cdc42 capture microtubules through IQGAP1 and CLIP- 170. Cell 109:873- 885, 2002. 4 A c

GAM193 268 RSN Griparic, L.; Keller, T. C. S., III: Identification and expressionof two novel CLIP- 170/restin isoforms expressed predominantly in muscle. Biochim.Biophys. Acta 1405: 35- 46, 1998. 4 A c

GAM193 268 RSN Hilliker, C.; Delabie, J.; Speleman, F.; Bilbe, G.; Bruggen, J.;Van Leuven, F.; Van Den Berghe, H.: Localization of the gene (RSN)coding for restin, a marker for Reed- Sternberg cells in Hodgkin'sdisease, to human chromosome band 12q24.3 and YAC cloning of the locus. Cytogenet.Cell Genet. 65: 172-176, 1994. 4 A c

GAM193 268 RSN Irsch, J.; Nitsch, S.; Hansmann, M.- L.; Rajewsky, K.; Tesch, H.;Diehl, V.; Jox, A.; Kuppers, R.; Radbruch, A.: Isolation of viableHodgkin and Reed-Sternberg cells from Hodgkin disease tissues. Proc.Nat. Acad. Sci. 95: 10117- 10122, 1998. 4 A c

GAM193 268 RSN Perez, F.; Diamantopoulos, G. S.; Stalder, R.; Kreis, T. E.: CLIP-170highlights growing microtubule ends in vivo. Cell 96: 517- 527, 1999. 4 A c

GAM193 268 RSN Pierre, P.; Pepperkok, R.; Kreis, T. E.: Molecular characterizationof two functional domains of CLIP- 170 in vivo. J. Cell Sci. 107:1909- 1920, 1994. 4 A c

GAM193 268 RSN Pierre, P.; Scheel, J.; Rickard, J. E.; Kreis, T. E.: CLIP- 170links endocytic vesicles to microtubules. Cell 70: 887- 900, 1992. 4 A c

GAM193 268 SEL1L Biunno, I.; Appierto, V.; Cattaneo, M.; Leone, B. E.; Balzano,G.; Socci, C.; Saccone, S.; Letizia, A.; Valle, G. D.; Sgaramella,V.: Isolation of a pancreas- specific gene located on human chromosome14q31: expression analysis in human pancreatic ductal carcinomas. Genomics 46:284- 286, 1997. 4 A c

GAM193 268 SEL1L Donoviel, D. B.; Bernstein, A.: SEL- 1L maps to human chromosome14, near the 4 A c

insulin- dependent diabetes mellitus locus 11. Genomics 56:232- 233, 1999.

GAM193 268 SEL1L Grant, B.; Greenwald, I.: Structure, function and expression ofSEL- 1, a negative regulator of LIN- 12 and GLP- 1 in C. elegans. Development 124:637- 644, 1997. 4 A c

GAM193 268 SEL1L Grant, B.; Greenwald, I.: The Caenorhabditis. elegans sel- 1 gene,a negative regulator of lin- 12 and glp- 1, encodes a predicted extracellularprotein. Genetics 143: 237- 247, 1996. 4 A c

GAM193 268 SLC12A2 Delpire, E.; Lu, J.; England, R.; Dull, C.; Thorne, T.: Deafnessand imbalance associated with inactivation of the secretory Na- K- 2Clco- transporter. Nature Genet. 22: 192- 195, 1999. 4 A c

GAM193 268 SLC12A2 Dixon, M. J.; Gazzard, J.; Chaudhry, S. S.; Sampson, N.; Schulte,B. A.; Steel, K. P.: Mutation of the Na- K- Cl co- transporter geneSlc12a2 results in deafness in mice. Hum. Molec. Genet. 8: 1579- 1584,1999. 4 A c

GAM193 268 SLC12A2 Evans, R. L.; Park, K.; Turner, R. J.; Watson, G. E.; Nguyen, H.- V.;Dennett, M. R.; Hand, A. R.; Flagella, M.; Shull, G. E.; Melvin, J.E.: Severe impairment of salivation in Na+/K+/2Cl- cotransporter(NKCC1)- deficient mice. J. Biol. Chem. 275: 26720- 26726, 2000. 4 A c

GAM193 268 SLC12A2 Payne, J. A.; Xu, J.- C.; Haas, M.; Lytle, C. Y.; Ward, D.; Forbush,B., III: Primary structure, functional expression, and chromosomallocalization of the bumetanide- sensitive Na- K- Cl cotransporter inhuman colon. J. Biol. Chem. 270: 17977- 17985, 1995. 4 A c

GAM193 268 SLC12A2 Quaggin, S. E.; Payne, J. A.; Forbush, B., III; Igarashi, P.:Localization of the renal Na- K- Cl cotransporter gene (Slc12a1) onmouse chromosome 2. Mammalian Genome 6: 557- 561, 1995. 4 A c

GAM193 268 SLC12A2 Xu, J.- C.; Lytle, C.; Zhu, T. T.; Payne, J. A.; Benz, E., Jr.;Forbush, B., III: Molecular cloning and functional expression ofthe bumetanide- sensitive Na- K- Cl cotransporter. Proc. Nat. Acad.Sci. 91: 2201- 2205, 1994. 4 A c

GAM193 268 SLC6A3 Byerley, W.; Hoff, M.; Holik, J.; Caron, M. G.; Giros, B.: VNTRpolymorphism for the human dopamine transporter gene (DAT1). Hum.Molec. Genet. 2: 335, 1993. 4 A c

GAM193 268 SLC6A3 Cook, E. H., Jr.; Stein, M. A.; Krasowski, M. D.; Cox, N. J.; Olkon,D. M.; Kieffer, J. E.; Leventhal, B. L.: Association of attention- deficitdisorder and the dopamine transporter gene. Am. J. Hum. Genet. 56:993- 998, 1995. 4 A c

GAM193 268 SLC6A3 Doucette- Stamm, L.; Blakely, D. J.; Tian, J.; Mockus, S.; Mao,J.: Population genetic study of the human dopamine transporter gene(DAT1). Genet. Epidemiol. 12: 303- 308, 1995. 4 A c

GAM193 268 SLC6A3 Gainetdinov, R. R.; Wetsel, W. C.; Jones, S. R.; Levin, E. D.;Jaber, M.; Caron, M. G.: Role of serotonin in the paradoxical calmingeffect of psychostimulants on hyperactivity. Science 283: 397- 401,1999. 4 A c

GAM193 268 SLC6A3 Gelernter, J.; Vandenbergh, D.; Kruger, S. D.; Pauls, D. L.; Kurlan,R.; Pakstis, A. J.; Kidd, K. K.; Uhl, G.: The dopamine transporterprotein gene (SLC6A3): primary linkage mapping and linkage studiesin Tourette syndrome. Genomics 30: 459- 463, 1995. 4 A c

GAM193 268 SLC6A3 Gill, M.; Daly, G.; Heron, S.; Hawi, Z.; Fitgerald, M.: Confirmationof association between attention deficit hyperactivity disorder anda dopamine transporter polymorphism. Molec. Psychiat. 2: 311- 313,1997. 4 A c

GAM193 268 SLC6A3 Giros, B.; El Mestikawy, S.; Godinot, N.; Zheng, K.; Han, H.; Yang- Feng,T.; Caron, M. G.: Cloning, pharmacological characterization, andchromosome assignment of the human dopamine transporter. Molec. Pharm. 42:383- 390, 1992. 4 A c

GAM193 268 SLC6A3 Giros, B.; Jaber, M.; Jones, S. R.; Wightman, R. M.; Caron, M.G.: 4 A c
Hyperlocomotion and indifference to cocaine and amphetamine inmice lacking
the dopamine receptor. Nature 370: 606- 612, 1996.

GAM193 268 SLC6A3 Goldman, D.: Dopamine transporter, alcoholism and other diseases. NatureMed. 4 A c
1: 624- 625, 1995.

GAM193 268 SLC6A3 Kurlan, R.; Behr, J.; Medved, L.; Shoulson, I.; Pauls, D.; Kidd,J. R.; Kidd, 4 A c
K. K.: Familial Tourette's syndrome: report of a largepedigree and potential
for linkage analysis. Neurology 36: 772- 776,1986.

GAM193 268 SLC6A3 Lerman, C.; Caporaso, N. E.; Audrain, J.; Main, D.; Bowman, E.D.; Lockshin, 4 A c
B.; Boyd, N. R.; Shields, P. G.: Evidence suggestingthe role of specific
genetic factors in cigarette smoking. HealthPsych. 18: 14- 20, 1999.

GAM193 268 SLC6A3 Lossie, A. C.; Vandenbergh, D. J.; Uhl, G. R.; Camper, S. A.:Localization of 4 A c
the dopamine transporter gene, Dat1, on mouse chromosome

GAM193 268 SLC6A3 Mammalian Genome 5: 117- 118, 1994.13. Sabol, S. Z.; Nelson, M. L.; Fisher, 4 A c
C.; Gunzerath, L.; Brody,C. L.; Hu, S.; Sirota, L. A.; Marcus, S. E.;
Greenberg, B. D.; Lucas,F. R., IV; Benjamin, J.; Murphy, D. L.; Hamer, D.
H.: A genetic associationfor cigarette smoking behavior. Health Psych. 18:
7- 13, 1999.

GAM193 268 SLC6A3 Tiihonen, J.; Kuikka, J.; Bergstrom, K.; Hakola, P.; Karhu, J.;Ryynanen, O.- 4 A c
P.; Fohr, J.: Altered striatal dopamine re- uptake sitedensities in
habitually violent and non- violent alcoholics. NatureMed. 1: 654- 657,
1995.

GAM193 268 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Hawkins, A. L.; Griffin, C.A.; Li, X.; 4 A c
Jabs, E. W.; Uhl, G. R.: Human dopamine transporter gene(DAT1) maps to
chromosome 5p15.3 and displays a VNTR. Genomics 14:1104- 1106, 1992.

GAM193 268 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Uhl, G. R.: A human dopaminetransporter 4 A c
cDNA predicts reduced glycosylation, displays a novelrepetitive element and
provides racially- dimorphic TaqI RFLPs. Molec.Brain Res. 15: 161- 166,
1992.

GAM193 268 SLC6A3 Waldman, I. D.; Rowe, D. C.; Abramowitz, A.; Kozel, S. T.; Mohr,J. H.; 4 A c
Sherman, S. L.; Cleveland, H. H.; Sanders, M. L.; Gard, J.M. C.; Stever, C.:
Association and linkage of the dopamine transportergene and attention-
deficit hyperactivity disorder in children: heterogeneityowing to diagnostic
subtype and severity. Am. J. Hum. Genet. 63:1767- 1776, 1998.

GAM195 334 DSC1 King, I. A.; Arnemann, J.; Spurr, N. K.; Buxton, R. S.: Cloningof the cDNA 3 B c
(DSC1) coding for human type 1 desmocollin and its assignmentto chromosome
18. Genomics 18: 185- 194, 1993.

GAM195 334 DSC1 Troyanovsky, S. M.; Eshkind, L. G.; Troyanovsky, R. B.; Leube,R. E.; Franke, 3 B c
W. W.: Contributions of cytoplasmic domains of desmosomalcadherins to
desmosome assembly and intermediate filament anchorage. Cell 72:561- 574,
1993.

GAM195 334 FGF2 Abraham, J. A.; Mergia, A.; Whang, J. L.; Tumolo, A.; Friedman,J.; Hjerild, 3 B c
K. A.; Gospodarowicz, D.; Fiddes, J. C.: Nucleotidesequence of a bovine
clone encoding the angiogenic protein, basicfibroblast growth factor.
Science 233: 545- 548, 1986.

GAM195 334 FGF2 Abraham, J. A.; Whang, J. L.; Tumolo, A.; Mergia, A.; Friedman,J.; 3 B c
Gospodarowicz, D.; Fiddes, J. C.: Human basic fibroblast growthfactor:
nucleotide sequence and genomic organization. EMBO J. 5:2523- 2528, 1986.

GAM195 334 FGF2 Doniach, T.: Basic FGF as an inducer of anteroposterior neuralpattern. Cell 3 B c
83: 1067- 1070, 1995.

GAM195 334 FGF2 Dono, R.; Texido, G.; Dussel, R.; Ehmke, H.; Zeller, R.: Impairedcerebral 3 B c
cortex development and blood pressure regulation in FGF2- deficientmice.
EMBO J. 17: 4213- 4225, 1998.

GAM195 334 FGF2 Eckenstein, F. P.: Fibroblast growth factors in the nervous system. 3 B c
J.Neurobiol. 25: 1467- 1480, 1994.

GAM195 334 FGF2 Fukushima, Y.; Byers, M. G.; Fiddes, J. C.; Shows, T. B.: Thehuman basic 3 B c
fibroblast growth factor gene (FGFB) is assigned to chromosome4q25.
Cytogenet. Cell Genet. 54: 159- 160, 1990.

GAM195 334 FGF2 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; 3 B c
Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast
growth factor homologous factor 2 (FHF2): gene structure,expression and
mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated
by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63,
1999.

GAM195 334 FGF2 Gritti, A.; Parati, E. A.; Cova, L.; Frolichsthal, P.; Galli, R.;Wanke, E.; 3 B c
Faravelli, L.; Morassutti, D. J.; Roisen, F.; Nickel, D.D.; Vescovi, A. L.:
Multipotential stem cells from the adult mousebrain proliferate and self-
renew in response to basic fibroblast growthfactor. J. Neurosci. 16: 1091-
1100, 1996.

GAM195 334 FGF2 Johnson, R. L.; Tabin, C. J.: Molecular models for vertebratelimb 3 B c
development. Cell 90: 979- 990, 1997.

GAM195 334 FGF2 Jung, J.; Zheng, M.; Goldfarb, M.; Zaret, K. S.: Initiation ofmammalian 3 B c
liver development from endoderm by fibroblast growth factors. Science
284:1998- 2003, 1999.

GAM195 334 FGF2 Kawaguchi, H.; Nakamura, K.; Tabata, Y.; Ikada, Y.; Aoyama, I.;Anzai, J.; 3 B c
Nakamura, T.; Hiyama, Y.; Tamura, M.: Acceleration offracture healing in
nonhuman primates by fibroblast growth factor- 2. J.Clin. Endocr. Metab. 86:
875- 880, 2001.

GAM195 334 FGF2 Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.: Cloning andexpression of 3 B c
cDNA encoding human basic fibroblast growth factor. FEBSLett. 213: 189- 194,
1987.

GAM195 334 FGF2 Lafage- Pochitaloff, M.; Galland, F.; Simonetti, J.; Prats, H.;Mattei, M.- 3 B c
G.; Birnbaum, D.: The human basic fibroblast growth factorgene is located on
the long arm of chromosome 4 at bands q26- q27. OncogeneRes. 5: 241- 244,
1990.

GAM195 334 FGF2 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; 3 B c
Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21
by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997.

GAM195 334 FGF2 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 3 B c
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM195 334 FGF2 Mergia, A.; Eddy, R.; Abraham, J. A.; Fiddes, J. C.; Shows, T.B.: The genes 3 B c
for basic and acidic fibroblast growth factors areon different human
chromosomes. Biochem. Biophys. Res. Commun. 138:644- 651, 1986.

GAM195 334 FGF2 Montero, A.; Okada, Y.; Tomita, M.; Ito, M.; Tsurukami, H.; Nakamura,T.; 3 B c
Doetschman, T.; Coffin, J. D.; Hurley, M. M.: Disruption of thefibroblast
growth factor- 2 gene results in decreased bone mass andbone formation. J.
Clin. Invest. 105: 1085- 1093, 2000.

GAM195 334 FGF2 Ortega, S.; Ittmann, M.; Tsang, S. H.; Ehrlich, M.; Basilico,C.: Neuronal 3 B c
defects and delayed wound healing in mice lacking fibroblastgrowth factor 2.
Proc. Nat. Acad. Sci. 95: 5672- 5677, 1998.

GAM195 334 FGF2 Plotnikov, A. N.; Hubbard, S. R.; Schlessinger, J.; Mohammadi,M.: Crystal 3 B c
structures of two FGF- FGFR complexes reveal the determinantsof ligand-
receptor specificity. Cell 101: 413- 424, 2000.

GAM195 334 FGF2 Plotnikov, A. N.; Schlessinger, J.; Hubbard, S. R.; Mohammadi,M.: Structural 3 B c
basis for FGF receptor dimerization and activation. Cell 98:641- 650, 1999.

GAM195 334 FGF2 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. 3 B c
C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast
growth factor (FGF) homologous factors: new membersof the FGF family
implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850-
9857, 1996.

GAM195 334 MTL5 De, S. K.; Enders, G. C.; Andrews, G. K.: High levels of 3 B c
metallothioneinmessenger RNAs in male germ cells of the adult mouse. Molec.
Endocr. 5:628- 636, 1991.

GAM195 334 MTL5 Salehi- Ashtiani, K.; Widrow, R. J.; Markert, C. L.; Goldberg, E.: Testis- 3 B c
specific expression of a metallothionein I- driven transgenecorrelates with
undermethylation of the locus in testicular DNA. Proc.Nat. Acad. Sci. 90:
8886- 8890, 1993.

GAM195 334 MTL5 Sugihara, T.; Wadhwa, R.; Kaul, S. C.; Mitsui, Y.: A novel testis- 3 B c
specificmetallothionein- like protein, tesmin, is an early marker of male
germcell differentiation. Genomics 57: 130- 136, 1999.

GAM195 334 NRCAM Dry, K.; Kenwrick, S.; Rosenthal, A.; Platzer, M.: The completesequence of 3 B c
the human locus for NgCAM- related cell adhesion moleculereveals a novel
alternative exon in chick and man and conserved genomicorganization for the
L1 subfamily. Gene 273: 115- 122, 2001.

GAM195 334 NRCAM Grumet, M.; Mauro, V.; Burgoon, M. P.; Edelman, G. M.; Cunningham,B. A.: 3 B c
Structure of a new nervous system glycoprotein, Nr- CAM, andits relationship
to subgroups of neural cell adhesion molecules. J.Cell. Biol. 113: 1399-
1412, 1991.

GAM195 334 NRCAM Kayyem, J. F.; Roman, J. M.; de la Rosa, E. J.; Schwarz, U.; Dreyer,W. J.: 3 B c
Bravo/Nr- CAM is closely related to the cell adhesion moleculesL1 and Ng-
CAM and has a similar heterodimer structure. J. Cell. Biol. 118:1259- 1270,
1992.

GAM195 334 NRCAM Lane, R. P.; Chen, X.- N.; Yamakawa, K.; Vielmetter, J.; Korenberg,J. R.; 3 B c
Dreyer, W. J.: Characterization of a highly conserved humanhomolog to the
chicken neural cell surface protein Bravo/Nr- CAM thatmaps to chromosome
band 7q31. Genomics 35: 456- 465, 1996.

GAM195 334 NRCAM Wang, B.; Williams, H.; Du, J.- S.; Terrett, J.; Kenwrick, S.:Alternative 3 B c
splicing of human NrCAM in neural and nonneural tissues. Molec.Cell.
Neurosci. 10: 287- 295, 1998.

GAM195 334 PLGL Frank, S. L.; Klisak, I.; Sparkes, R. S.; Lusis, A. J.: A genehomologous to 3 B c
plasminogen located on human chromosome 2q11- p11. Genomics 4:449- 451,
1989.

GAM195 334 PLGL Magnaghi, P.; Agazzi, A.; Semino, O.; Ferrari, M.; Barbui, T.;D'Angelo, A.; 3 B c
Taramelli, R.: A recombination event in the closelylinked plasminogen and
apolipoprotein(a) gene loci. Clin. Genet. 47:285- 289, 1995.

GAM195 334 SLC38A2 Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of 3 B c
the coding sequences of unidentified human genes. XVI.The complete sequences
of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA
Res. 7: 65- 73, 2000.

GAM195 334 SLC38A2 Sugawara, M.; Nakanishi, T.; Fei, Y.- J.; Huang, W.; Ganapathy,M. E.; 3 B c

Leibach, F. H.; Ganapathy, V.: Cloning of an amino acid transporterwith functional characteristics and tissue expression pattern identicalto that of system A. J. Biol. Chem. 275: 16473- 16477, 2000.

GAM195 334 TRIM9 Li, Y.; Chin, L.- S.; Weigel, C.; Li, L.: Spring, a novel RINGfinger protein 3 B c that regulates synaptic vesicle exocytosis. J. Biol.Chem. 276: 40824- 40833, 2001.

GAM195 334 TRIM9 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; 3 B c Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci, S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell compartments. EMBO J. 20: 2140- 2151, 2001.

GAM195 334 WASF3 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 B c Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5: 355- 364, 1998.

GAM195 334 WASF3 Suetsugu, S.; Miki, H.; Takenawa, T.: Identification of two humanWAVE/SCAR 3 B c homologues as general actin regulatory molecules which associatewith the Arp2/3 complex. Biochem. Biophys. Res. Commun. 260: 296- 302,1999.

GAM196 209 AP1M1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation 3 C c of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002.

GAM196 209 AP1M1 Nakayama, Y.; Goebl, M.; O'Brine Greco, B.; Lemmon, S.; PingchangChow, E.; 3 C c Kirchhausen, T.: The medium chains of the mammalian clathrin-associatedproteins have a homolog in yeast. Europ. J. Biochem. 202: 569-574,1991.

GAM196 209 AP1M1 Peyrard, M.: Personal Communication. Stockholm, Sweden 1/7/1999. 3 C c

GAM196 209 AP1M1 Peyrard, M.; Parveneh, S.; Lagercrantz, S.; Ekman, M.; Fransson,I.; Sahlen, 3 C c S.; Dumanski, J. P.: Cloning, expression pattern, andchromosomal assignment to 16q23 of the human gamma- adaptin gene (ADTG). Genomics 50:275- 280, 1998.

GAM196 209 AP1S1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation 3 C c of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002.

GAM196 209 AP1S1 Kirchhausen, T.; Davis, A. C.; Frucht, S.; O'Brine Greco, B.; Payne,G. S.; 3 C c Tubb, B.: AP17 and AP19, the mammalian small chains of theclathrin-associated protein complexes show homology to Yap17p, theirputative homolog in yeast. J. Biol. Chem. 266: 11153- 11157, 1991.

GAM196 209 AP1S1 Peyrard, M.; Parveneh, S.; Lagercrantz, S.; Ekman, M.; Fransson,I.; Sahlen, 3 C c S.; Dumanski, J. P.: Cloning, expression pattern, andchromosomal assignment to 16q23 of the human gamma- adaptin gene (ADTG). Genomics 50:275- 280, 1998.

GAM196 209 AP1S1 Takatsu, H.; Sakurai, M.; Shin, H.- W.; Murakami, K.; Nakayama,K.: 3 C c Identification and characterization of novel clathrin adaptor-relatedproteins. J. Biol. Chem. 273: 24693- 24700, 1998.

GAM196 209 CLCN6 Brandt, S.; Jentsch, T. J.: ClC- 6 and ClC- 7 are two novel broadlyexpressed 3 C b members of the CLC chloride channel family. FEBS Lett. 377:15- 20, 1995.

GAM196 209 CLCN6 Eggermont, J.; Buyse, G.; Voets, T.; Tytgat, J.; De Smedt, H.;Droogmans, G.: 3 C b Alternative splicing of ClC- 6 (a member of the ClCchloride- channel family) transcripts generates three truncated isoformsone of which, ClC- 6c, is kidney- specific. Biochem. J. 325: 269- 276,1997.

GAM196 209 CLCN6 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 C b
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding
sequences of unidentified human genes. II. The codingsequences of 40 new
genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell
line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM196 209 Nrap Luo, G.; Leroy, E.; Kozak, C. A.; Polymeropoulos, M. H.; Horowits,R.: 3 C c
Mapping of the gene (NRAP) encoding N- RAP in the mouse and humangenomes.
Genomics 45: 229- 232, 1997.

GAM196 209 Nrap Luo, G.; Zhang, J. Q.; Nguyen, T.- P.; Herrera, A. H.; Paterson,B.; 3 C c
Horowits, R.: Complete cDNA sequence and tissue localizationof N- RAP, a
novel nebulin- related protein of striated muscle. CellMotil. Cytoskeleton
38: 75- 90, 1997.

GAM196 209 SHB Pawson, T.; Gish, G. D.: SH2 and SH3 domains: from structure tofunction. 3 C c
Cell 71: 359- 362, 1992.

GAM196 209 SHB Welsh, M.; Mares, J.; Karlsson, T.; Lavergne, C.; Breant, B.; Claesson- 3 C c
Welsh,L.: Shb is a ubiquitously expressed Src homology 2 protein. Oncogene
9:19- 27, 1994.

GAM196 209 SHB Yulug, I. G.; Hillermann, R.; Fisher, E. M. C.: The SHB adaptorprotein maps 3 C c
to human chromosome 9. Genomics 24: 615- 617, 1994.

GAM196 209 TSLP Quentmeier, H.; Drexler, H. G.; Fleckenstein, D.; Zaborski, M.;Armstrong, 3 C c
A.; Sims, J. E.; Lyman, S. D.: Cloning of human thymicstromal lymphopoietin
(TSLP) and signaling mechanisms leading to proliferation. Leukemia 15:1286-
1292, 2001.

GAM196 209 TSLP Reche, P. A.; Soumelis, V.; Gorman, D. M.; Clifford, T.; Liu, M.;Travis, M.; 3 C c
Zurawski, S. M.; Johnston, J.; Liu, Y.- J.; Spits, H.;de Waal Malefyt, R.;
Kastelein, R. A.; Bazan, J. F.: Human thymicstromal lymphopoietin
preferentially stimulates myeloid cells. J.Immun. 167: 336- 343, 2001.

GAM196 209 TSLP Soumelis, V.; Reche, P. A.; Kanzler, H.; Yuan, W.; Edward, G.;Homey, B.; 3 C c
Gilliet, M.; Ho, S.; Antonenko, S.; Lauerma, A.; Smith,K.; Gorman, D.;
Zurawski, S.; Abrams, J.; Menon, S.; McClanahan, T.;de Waal- Malefyt, R.;
Bazan, F.; Kastelein, R. A.; Liu, Y.- J.: Humanepithelial cells trigger
dendritic cell- mediated allergic inflammationby producing TSLP. Nature
Immun. 3: 673- 680, 2002.

GAM281 278 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- 3 B b
glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to
chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989.

GAM281 278 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion 3 B b
data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract)
Cytogenet. Cell Genet. 51: 994 only, 1989.

GAM281 278 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma 3 B b
alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple
method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.

GAM281 278 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human 3 B b
plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene
family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.

GAM281 278 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: 3 B b
Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new
alleles and allele frequencies in Caucasians and in Americanblacks. Hum.
Hered. 38: 267- 272, 1988.

GAM281 278 ABCC11 Bera, T. K.; Lee, S.; Salvatore, G.; Lee, B.; Pastan, I.: MRP8,a new member 3 B c

of ABC transporter superfamily, identified by EST databasemining and gene prediction program, is highly expressed in breastcancer. Molec. Med. 7: 509-516, 2001.

GAM281 278 ABCC11 Tammur, J.; Prades, C.; Arnould, I.; Rzhetsky, A.; Hutchinson,A.; Adachi, M.; Schuetz, J. D.; Swoboda, K. J.; Ptacek, L. J.; Rosier,M.; Dean, M.; Allikmets, R.: Two new genes from the human ATP- bindingcassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicatedon chromosome 16q12. Gene 273: 89- 96, 2001. 3 B c

GAM281 278 ABCC11 Yabuuchi, H.; Shimizu, H.; Takayanagi, S.; Ishikawa, T.: Multiplesplicing variants of two new human ATP- binding cassette transporters,ABCC11 and ABCC12. Biochem. Biophys. Res. Commun. 288: 933- 939,2001. 3 B c

GAM281 278 ADAMTS3 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999. 3 B c

GAM281 278 ADAMTS3 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B c

GAM281 278 ADAMTS3 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999. 3 B c

GAM281 278 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999. 3 B b

GAM281 278 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 B b

GAM281 278 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999. 3 B b

GAM281 278 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664-1666, 1999. 3 B b

GAM281 278 ADARB1 Higuchi, M.; Maas, S.; Single, F. N.; Hartner, J.; Rozov, A.; Burnashev,N.; Feldmeyer, D.; Sprengel, R.; Seeburg, P. H.: Point mutation inan AMPA receptor gene rescues lethality in mice deficient in the RNA- editingenzyme ADAR2. Nature 406: 78- 81, 2000. 3 B c

GAM281 278 ADARB1 Lai, F.; Chen, C.- X.; Carter, K. C.; Nishikura, K.: Editing ofglutamate receptor B subunit ion channel RNAs by four alternativelyspliced DRADA2 double- stranded RNA adenosine deaminases. Molec. Cell.Biol. 17: 2413- 2424, 1997. 3 B c

GAM281 278 ADARB1 Melcher, T.; Maas, S.; Herb, A.; Sprengel, R.; Seeburg, P. H.;Higuchi, M.: A mammalian RNA editing enzyme. Nature 379: 460- 463,1996. 3 B c

GAM281 278 ADARB1 Mittaz, L.; Scott, H. S.; Rossier, C.; Seeburg, P. H.; Higuchi,M.; Antonarakis, S. E.: Cloning of a human RNA editing deaminase(ADARB1) of glutamate receptors that maps to chromosome 21q22.3. Genomics 41:210- 217, 3 B c

1997.

GAM281 278 ADARB1 O'Connell, M. A.; Gerber, A.; Keller, W.: Purification of humandouble- 3 B c
stranded RNA- specific editase 1 (hRED1) involved in editingof brain
glutamate receptor B pre- mRNA. J. Biol. Chem. 272: 473- 478,1997.

GAM281 278 ADARB1 Villard, L.; Tassone, F.; Haymowicz, M.; Welborn, R.; Gardiner,K.: Map 3 B c
location, genomic organization and expression patterns ofthe human RED1 RNA
editase. Somat. Cell Molec. Genet. 23: 135- 145,1997.

GAM281 278 ADARB1 Yang, J.- H.; Sklar, P.; Axel, R.; Maniatis, T.: Purification 3 B c
andcharacterization of a human RNA adenosine deaminase for glutamatereceptor
B pre- mRNA editing. Proc. Nat. Acad. Sci. 94: 4354- 4359,1997.

GAM281 278 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, 3 B c
S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P.
E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse
somatosensory cortex. Nature Genet. 19: 289- 291,1998.

GAM281 278 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 B c
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian
Genome 6: 111- 113, 1995.

GAM281 278 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 B c
members are randomly located on different chromosomes. Hum.Genet. 94: 527-
529, 1994.

GAM281 278 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; 3 B c
Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal
brain type I adenylyl cyclase. Genomics 16: 473- 478,1993.

GAM281 278 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- 3 B c
Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.:
Altered sensory processing in the somatosensory cortex of the mutantmouse
barrelless. Science 271: 1864- 1867, 1996.

GAM281 278 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 B c
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian
Genome 6: 111- 113, 1995.

GAM281 278 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 B c
members are randomly located on different chromosomes. Hum.Genet. 94: 527-
529, 1994.

GAM281 278 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: 3 B c
Chromosomal mapping of human adenylyl cyclase genestype III, type V and type
VI. Hum. Genet. 94: 69- 73, 1994.

GAM281 278 ADORA2A Chen, J.- F.; Huang, Z.; Ma, J.; Zhu, J.; Moratalla, R.; Standaert,D.; 3 B c
Moskowitz, M. A.; Fink, J. S.; Schwarzschild, M. A.: A2A adenosinereceptor
deficiency attenuates brain injury induced by transient focalischemia in
mice. J. Neurosci. 19: 9192- 9200, 1999.

GAM281 278 ADORA2A Gaudray, P.: Personal Communication. Nice, France 6/1/1994. 3 B c

GAM281 278 ADORA2A Gusella, J. F.: Personal Communication. Boston, Mass. 4/17/1994. 3 B c

GAM281 278 ADORA2A Le, F.; Townsend- Nicholson, A.; Baker, E.; Sutherland, G. R.; Schofield,P. 3 B c
R.: Characterization and chromosomal localization of the humanA2a adenosine
receptor gene: ADORA2A. Biochem. Biophys. Res. Commun. 223:461- 467, 1996.

GAM281 278 ADORA2A Ledent, C.; Vaugeois, J.- M.; Schiffmann, S. N.; Pedrazzini, T.;El Yacoubi, 3 B c
M. E.; Vanderhaeghen, J.- J.; Costentin, J.; Heath, J.K.; Vassart, G.;
Parmentier, M.: Aggressiveness, hypoalgesia andhigh blood pressure in mice
lacking the adenosine A2a receptor. Nature 388:674- 678, 1997.

GAM281 278 ADORA2A Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 B c

M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. Note: Erratum: Genomics 23: 305 only, 1994.

GAM281 278 ADORA2A MacCollin, M.; Peterfreund, R.; MacDonald, M.; Fink, J. S.; Gusella,J.: 3 B c Mapping of a human A2a adenosine receptor (ADORA2) to chromosome22. Genomics 20: 332- 333, 1994.

GAM281 278 ADORA2A Ohta, A.; Sitkovsky, M.: Role of G- protein- coupled adenosine receptorsin 3 B c downregulation of inflammation and protection from tissue damage. Nature 916- 920,2001.

GAM281 278 ADORA2A Szepetowski, P.; Perucca- Lostanlen, D.; Gaudray, P.: Mapping genesaccording 3 B c to their amplification status in tumor cells: contributionto the map of 11q13. Genomics 16: 745- 750, 1993.

GAM281 278 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; 3 B c Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002.

GAM281 278 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; 3 B c Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor: functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994.

GAM281 278 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, 3 B c C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994.

GAM281 278 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; 3 B c Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001.

GAM281 278 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. 3 B c W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95- 101, 1997.

GAM281 278 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, 3 B c J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779- 782, 2000.

GAM281 278 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a 3 B c novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001.

GAM281 278 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use 3 B c of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001.

GAM281 278 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; 3 B c Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998.

GAM281 278 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: 3 B c Identificationand characterization of STK12/Aik2: a human gene related to

auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147-
152,1998.

GAM281 278 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. 3 B c
T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the
mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism,
OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001.

GAM281 278 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand 3 B c
characterization of genes associated with chromosome- 6 mediatedtumor
suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996.

GAM281 278 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a 3 B c
novel non- lens member of the beta- gamma- crystallin superfamily,is
associated with the control of tumorigenicity in human malignantmelanoma.
Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997.

GAM281 278 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, 3 B c
D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA
cloning, expression, subcellular localization, and chromosomalassignment of
mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem.
Biophys. Res. Commun. 244: 285- 292, 1998.

GAM281 278 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; 3 B c
Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof
the aurora- and Ipl1- like midbody- associated protein mitotic kinasein
human cancer cells. Cancer Res. 58: 4811- 4816, 1998.

GAM281 278 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. 3 B c
S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse
ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian
Genome 9: 715- 720, 1998.

GAM281 278 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; 3 B c
Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human
melanoma cell lines controlled by introduction of human chromosome6. Science
247: 568- 571, 1990.

GAM281 278 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: 3 B b
Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89:
3962- 3966,1992.

GAM281 278 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- 3 B b
lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene
expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat.
Acad. Sci. 96: 4378- 4383, 1999.

GAM281 278 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; 3 B b
Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of
human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988.

GAM281 278 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: 3 B b
Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase
of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990.

GAM281 278 ANPEP Delmas, B.; Gelfi, J.; L'Haridon, R.; Vogel, L. K.; Sjostrom, H.;Noren, O.; 3 B c
Laude, H.: Aminopeptidase N is a major receptor for theenteropathogenic
coronavirus TGEV. Nature 357: 417- 420, 1992.

GAM281 278 ANPEP Kruse, T. A.; Bolund, L.; Grzeschik, K.- H.; Ropers, H. H.; Olsen,J.; 3 B c
Sjostrom, H.; Noren, O.: Assignment of the human aminopeptidaseN (peptidase
E) gene to chromosome 15q13- qter. FEBS Lett. 239: 305- 308,1988.

GAM281 278 ANPEP Look, A. T.; Ashmun, R. A.; Shapiro, L. H.; Peiper, S. C.: Humanmyeloid 3 B c

plasma membrane glycoprotein CD13 (gp150) is identical toaminopeptidase N. J. Clin. Invest. 83: 1299- 1307, 1989.

GAM281 278 ANPEP Look, A. T.; Peiper, S. C.; Rebentisch, M. B.; Ashmun, R. A.; Roussel,M. F.; Lemons, R. S.; Le Beau, M. M.; Rubin, C. M.; Sherr, C. J.:Molecular cloning, expression, and chromosomal localization of thegene encoding a human myeloid membrane antigen (gp150). J. Clin.Invest. 78: 914- 921, 1986. 3 B c

GAM281 278 ANPEP Watt, V. M.; Willard, H. F.: The human aminopeptidase N gene:isolation, chromosome localization, and DNA polymorphism analysis. Hum.Genet. 85: 651- 654, 1990. 3 B c

GAM281 278 ANPEP Yeager, C. L.; Ashmun, R. A.; Williams, R. K.; Cardellichio, C.B.; Shapiro, L. H.; Look, A. T.; Holmes, K. V.: Human aminopeptidaseN is a receptor for human coronavirus 229E. Nature 357: 420- 422,1992. 3 B c

GAM281 278 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 (CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998. 3 B b

GAM281 278 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999. 3 B b

GAM281 278 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000. 3 B b

GAM281 278 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001. 3 B b

GAM281 278 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999. 3 B b

GAM281 278 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002. 3 B b

GAM281 278 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001. 3 B b

GAM281 278 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998. 3 B b

GAM281 278 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998. 3 B b

GAM281 278 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 3 B b

GAM281 278 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 B b

GAM281 278 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; 3 B b
Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding
sequences of unidentified human genes. VI. The codingsequences of 80 new
genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line
KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM281 278 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- 3 B b
interacting protein, recognizes the basolateral sortingsignal of amyloid
precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998.

GAM281 278 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene 3 B b
structure of a novel water channel expressed exclusively in humankidney:
evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics
35: 543- 550, 1996.

GAM281 278 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem 3 B b
arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at
chromosome locus 12q13. Genomics 43: 387- 389, 1997.

GAM281 278 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: 3 B b
an intracellular vesicle water channel protein in renalepithelia. Proc. Nat.
Acad. Sci. 96: 5808- 5813, 1999.

GAM281 278 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, 3 B c
A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and
Drosophila. Genomics 26: 101- 106, 1995.

GAM281 278 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer 3 B c
protein delta- COP, encoded by the archain gene, is conservedacross diverse
eukaryotes. Mammalian Genome 7: 784- 786, 1996.

GAM281 278 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; 3 B b
Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the
beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990.

GAM281 278 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: 3 B b
Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11
near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec.
Genet. 16: 401- 405, 1990.

GAM281 278 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K- 3 B b
ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics
6:697- 699, 1990.

GAM281 278 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: 3 B b
Identification of a putative isoform of the Na,K- ATPase beta
subunit:primary structure and tissue- specific expression. J. Biol. Chem.
164:4613- 4618, 1989.

GAM281 278 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: 3 B b
Identification of a cDNA clone specific for the neural adhesionmolecule
AMOG. J. Neurosci. Res. 22: 113- 119, 1989.

GAM281 278 BACE Cai, H.; Wang, Y.; McCarthy, D.; Wen, H.; Borchelt, D. R.; Price,D. L.; 3 B c
Wong, P. C.: BACE1 is the major beta- secretase for generationof A- beta
peptides by neurons. Nature Neurosci. 4: 233- 234, 2001.

GAM281 278 BACE De Strooper, B.; Konig, G.: A firm base for drug development. Nature 3 B c
402:471- 472, 1999.

GAM281 278 BACE Fan, W.; Bennett, B. D.; Babu- Khan, S.; Luo, Y.; Louis, J.- C.;McCaleb, M.; 3 B c
Citron, M.; Vassar, R.; Richards, W. G.: Response toSaunders et al. (1999).
Science 286: 1255a, 1999. Note: ElectronicPublication.

GAM281 278 BACE Haniu, M.; Denis, P.; Young, Y.; Mendiaz, E. A.; Fuller, J.; Hui,J. O.; 3 B c

Bennett, B. D.; Kahn, S.; Ross, S.; Burgess, T.; Katta, V.;Rogers, G.; Vassar, R.; Citron, M.: Characterization of Alzheimer'sbeta- secretase protein BACE: a pepsin family member with unusual properties. J.Biol. Chem. 275: 21099- 21106, 2000.

GAM281 278 BACE Hong, L.; Koelsch, G.; Lin, X.; Wu, S.; Terzyan, S.; Ghosh, A.K.; Zhang, X. C.; Tang, J.: Structure of the protease domain of memapsin2 (beta-secretase) complexed with inhibitor. Science 290: 150- 153,2000. 3 B c

GAM281 278 BACE Hussain, I.; Powell, D.; Howlett, D. R.; Tew, D. G.; Meek, T. D.;Chapman, C.; Gloger, I. S.; Murphy, K. E.; Southan, C. D.; Ryan, D.M.; Smith, T. S.; Simmons, D. L.; Walsh, F. S.; Dingwall, C.; Christie,G.: Identification of a novel aspartic protease (asp2) as beta- secretase Molec.Cell Neurosci. 14: 419- 427, 1999. 3 B c

GAM281 278 BACE Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643-648, 2001. 3 B c

GAM281 278 BACE Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.- H.; Goldstein, L. S.: Axonal transport of amyloid precursor protein is mediated by directbinding to the kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000. 3 B c

GAM281 278 BACE Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis,P.; Fan, W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.;Yan, Q.; Richards, W. G.; Citron, M.; Vassar, R.: Mice deficientin BACE1, the Alzheimer's beta- secretase, have normal phenotype andabolished beta-amyloid generation. Nature Neurosci. 4: 231- 232,2001. 3 B c

GAM281 278 BACE Nicolaou, M.; Song, Y.- Q.; Sato, C. A.; Orlacchio, A.; Kawarai,T.; Medeiros, H.; Liang, Y.; Sorbi, S.; Richard, E.; Rogaev, E. I.;Moliaka, Y.; Bruni, A. C.; Jorge, R.; Percy, M.; Duara, R.; Farrer,L. A.; St George-Hyslop, P.; Rogaeva, E. A.: Mutations in the openreading frame of the beta-site APP cleaving enzyme (BACE) locus arenot a common cause of Alzheimer's disease. Neurogenetics 3: 203- 206,2001. 3 B c

GAM281 278 BACE Roberds, S. L.; Anderson, J.; Basi, G.; Bienkowski, M. J.; Branstetter,D. G.; Chen, K. S.; Freedman, S. B.; Frigon, N. L.; Games, D.; Hu,K.; Johnson-Wood, K.; Kappenman, K. E.; and 20 others: BACE knockoutmice are healthy despite lacking the primary beta- secretase activityin brain: implications for Alzheimer's disease therapeutics. Hum.Molec. Genet. 10: 1317- 1324, 2001. 3 B c

GAM281 278 BACE Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a BACE homolog, BACE2, reside in the obligate Down syndromeregion of chromosome 21. Science 286: 1255a, 1999. Note: ElectronicPublication. 3 B c

GAM281 278 BACE Sinha, S.; Anderson, J. P.; Barbour, R.; Basi, G. S.; Caccavello,R.; Davis, D.; Doan, M.; Dovey, H. F.; Frigon, N.; Hong, J.; Jacobson- Croak,K.; Jewett, N.; and 15 others: Purification and cloning of amyloidprecursor protein beta- secretase from human brain. Nature 402: 537- 540,1999. 3 B c

GAM281 278 BACE Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz,E. A.; Dents, P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff,R.; Luo, Y.; Fisher, S.; and 12 others: Beta- secretase cleavageof Alzheimer's amyloid precursor protein by the transmembrane asparticprotease BACE. Science 286: 735- 741, 1999. 3 B c

GAM281 278 BACE Yan, R.; Bienkowski, M. J.; Shuck, M. E.; Miao, H.; Tory, M. C.;Pauley, A. M.; Brashler, J. R.; Stratman, N. C.; Mathews, W. R.; Buhl,A. E.; Carter, D. 3 B c

B.; Tomasselli, A. G.; Parodi, L. A.; Heinrikson,R. L.; Gurney, M. E.: Membrane- anchored aspartyl protease with Alzheimer'sdisease beta- secretase activity. Nature 402: 533- 536, 1999.

GAM281 278 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.: Identification of Bach2 as a B- cell- specific partner for smallMaf proteins that negatively regulate the immunoglobulin heavy chaingene 3- prime enhancer. EMBO J. 17: 5734- 5743, 1998. 3 B c

GAM281 278 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB- basic leucine zipper transcription factors that interact withMafK and regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083- 6095, 1996. 3 B c

GAM281 278 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.; Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene 19: 3739- 3749, 2000. 3 B c

GAM281 278 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- evaluation of 'reactive lymphoid hyperplasia of the uvea': animmunohistochemical and molecular analysis of 10 cases. Ophthalmology 107:151- 158, 2000. 3 B b

GAM281 278 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999. 3 B b

GAM281 278 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. J.Clin. Path. 48: 395- 397, 1995. 3 B b

GAM281 278 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T. W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001. 3 B b

GAM281 278 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not its cellular homologue, activates NF- kappa- B transcriptionfactor and c- Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999. 3 B b

GAM281 278 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.; Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types Cell 96: 35- 45, 1999. 3 B b

GAM281 278 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer Genet. Cytogenet. 58: 35- 38, 1992. 3 B b

GAM281 278 BDKRB1 Bachvarov, D. R.; Hess, J. F.; Menke, J. G.; Larrivee, J.- F.; Marceau,F.: Structure and genomic organization of the human B(1) receptorgene for kinins (BDKRB1). Genomics 33: 374- 381, 1996. 3 B c

GAM281 278 BDKRB1 Chai, K. X.; Ni, A.; Wang, D.; Ward, D. C.; Chao, J.; Chao, L.: Genomic DNA sequence, expression, and chromosomal localization ofthe human B1 bradykinin receptor gene BDKRB1. Genomics 31: 51- 57,1996. 3 B c

GAM281 278 BDKRB1 MacNeil, T.; Bierilo, K. K.; Menke, J. G.; Hess, J. F.: Cloningand pharmacological characterization of a rabbit bradykinin B- 1 receptor. 3 B c

Biochim.Biophys. Acta 1264: 223- 228, 1995.

GAM281 278 BDKRB1 Menke, J. G.; Borkowski, J. A.; Bierilo, K. K.; MacNeil, T.; Derrick,A. W.; 3 B c
Schneck, K. A.; Ransom, R. W.; Strader, C. D.; Linemeyer, D.L.; Hess, J. F.:
Expression cloning of a human B1 bradykinin receptor. J.Biol. Chem. 269:
21583- 21586, 1994.

GAM281 278 BDKRB1 Yang, X.; Polgar, P.: Genomic structure of the human bradykininB(1) receptor 3 B c
gene and preliminary characterization of its regulatoryregions. Biochem.
Biophys. Res. Commun. 222: 718- 725, 1996.

GAM281 278 BDKRB2 AbdAlla, S.; Lother, H.; Quitterer, U.: AT(1)- receptor heterodimersshow 3 B c
enhanced G- protein activation and altered receptor sequestration. Nature
407:94- 98, 2000.

GAM281 278 BDKRB2 Braun, A.; Kammerer, S.; Bohme, E.; Muller, B.; Roscher, A. A.: 3 B c
Identification of polymorphic sites of the human bradykinin B(2)receptor
gene. Biochem. Biophys. Res. Commun. 211: 234- 240, 1995.

GAM281 278 BDKRB2 Erdmann, J.; Hegemann, N.; Weidemann, A.; Kallisch, H.; Hummel,M.; Hetzer, 3 B c
R.; Fleck, E.; Regitz- Zagrosek, V.: Screening the humanbradykinin B2
receptor gene in patients with cardiovascular diseases:identification of a
functional mutation in the promoter and a newcoding variant (T21M). Am. J.
Med. Genet. 80: 521- 525, 1998.

GAM281 278 BDKRB2 Hess, J. F.; Borkowski, J. A.; Young, G. S.; Strader, C. D.; Ransom,R. W.: 3 B c
Cloning and pharmacological characterization of a human bradykinin(BK- 2)
receptor. Biochem. Biophys. Res. Commun. 184: 260- 268, 1992.

GAM281 278 BDKRB2 Kammerer, S.; Braun, A.; Arnold, N.; Roscher, A. A.: The humanbradykinin 3 B c
B(2) receptor gene: full length cDNA, genomic organizationand identification
of the regulatory region. Biochem. Biophys. Res.Commun. 211: 226- 233, 1995.

GAM281 278 BDKRB2 Ma, J.; Wang, D.; Ward, D. C.; Chen, L.; Dessai, T.; Chao, J.;Chao, L.: 3 B c
Structure and chromosomal localization of the gene (BDKRB2)encoding human
bradykinin B2 receptor. Genomics 23: 362- 369, 1994.

GAM281 278 BDKRB2 Powell, S. J.; Slynn, G.; Thomas, C.; Hopkins, B.; Briggs, I.;Graham, A.: 3 B c
Human bradykinin B2 receptor: nucleotide sequence analysisand assignment to
chromosome 14. Genomics 15: 435- 438, 1993.

GAM281 278 BDKRB2 Taketo, M.; Yokoyama, S.; Rochelle, J.; Kimura, S.; Higashida,H.; Taketo, 3 B c
M.; Seldin, M. F.: Mouse B2 bradykinin receptor genemaps to distal
chromosome 12. Genomics 27: 222- 223, 1995.

GAM281 278 BDP1 Kelter, A.- R.; Herchenbach, J.; Wirth, B.: The transcription factor- 3 B b
likenuclear regulator (TFNR) contains a novel 55- amino- acid motif
repeatednine times and maps closely to SMN1. Genomics 70: 315- 326, 2000.

GAM281 278 BDP1 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 B b
TFIIB activities direct RNA polymerase III transcription fromTATA-
containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM281 278 BID Chou, J. J.; Li, H.; Salvesen, G. S.; Yuan, J.; Wagner, G.: 3 B c
Solutionstructure of BID, an intracellular amplifier of apoptotic signaling.
Cell 95:615- 624, 1999.

GAM281 278 BID Footz, T. K.; Birren, B.; Minoshima, S.; Asakawa, S.; Shimizu,N.; Ali Riazi, 3 B c
M.; McDermid, H. E.: The gene for death agonist BIDmaps to the region of
human 22q11.2 duplicated in cat eye syndromechromosomes and to mouse
chromosome 6. Genomics 51: 472- 475, 1998.

GAM281 278 BID Li, H.; Zhu, H.; Xu, C.; Yuan, J.: Cleavage of BID by caspase8 mediates the 3 B c
mitochondrial damage in the Fas pathway of apoptosis. Cell 94:491- 501,
1998.

GAM281 278 BID Luo, X.; Budihardjo, I.; Zou, H.; Slaughter, C.; Wang, X.: Bid,a Bcl2 3 B c
interacting protein, mediates cytochrome c release from mitochondriain
response to activation of cell surface death receptors. Cell 94:481- 490,
1998.

GAM281 278 BID McDonnell, J. M.; Fushman, D.; Milliman, C. L.; Korsmeyer, S. J.;Cowburn, 3 B c
D.: Solution structure of the proapoptotic molecule BID:a structural basis
for apoptotic agonists and antagonists. Cell 96:625- 634, 1999.

GAM281 278 BID Wang, K.; Yin, X.- M.; Chao, D. T.; Milliman, C. L.; Korsmeyer,S. J.: BID: a 3 B c
novel BH3 domain- only death agonist. Genes Dev. 10:2859- 2869, 1996.

GAM281 278 BID Wang, K.; Yin, X.- M.; Copeland, N. G.; Gilbert, D. J.; Jenkins,N. A.; Keck, 3 B c
C. L.; Zimonjic, D. B.; Popescu, N. C.; Korsmeyer, S.J.: BID, a proapoptotic
BCL- 2 family member, is localized to mousechromosome 6 and human chromosome
22q11. Genomics 53: 235- 238, 1998.

GAM281 278 BID Wei, M. C.; Zong, W.- X.; Cheng, E. H.- Y.; Lindsten, T.; 3 B c
Panoutsakopoulou,V.; Ross, A. J.; Roth, K. A.; MacGregor, G. R.; Thompson,
C. B.; Korsmeyer,S. J.: Proapoptotic BAX or BAK: a requisite gateway to
mitochondrialdysfunction and death. Science 292: 727- 730, 2001.

GAM281 278 BID Yin, X.- M.; Wang, K.; Gross, A.; Zhao, Y.; Zinkel, S.; Klocke,B.; Roth, K. 3 B c
A.; Korsmeyer, S. J.: Bid- deficient mice are resistantto Fas- induced
hepatocellular apoptosis. Nature 400: 886- 891, 1999.

GAM281 278 BID Zha, J.; Weiler, S.; Oh, K. J.; Wei, M. C.; Korsmeyer, S. 3 B c
J.:Posttranslational N- myristoylation of BID as a molecular switch
fortargeting mitochondria and apoptosis. Science 290: 1761- 1765, 2000.

GAM281 278 BMP6 Dickinson, M. E.; Kobrin, M. S.; Silan, C. M.; Kingsley, D. M.;Justice, M. 3 B c
J.; Miller, D. A.; Ceci, J. D.; Lock, L. F.; Lee, A.;Buchberg, A. M.;
Siracusa, L. D.; Lyons, K. M.; Derynck, R.; Hogan,B. L. M.; Copeland, N. G.;
Jenkins, N. A.: Chromosomal localizationof seven members of the murine TGF-
beta superfamily suggests closelinkage to several morphogenetic mutant loci.
Genomics 6: 505- 520,1990.

GAM281 278 BMP6 Hahn, G. V.; Cohen, R. B.; Wozney, J. M.; Levitz, C. L.; Shore,E. M.; 3 B c
Zasloff, M. A.; Kaplan, F. S.: A bone morphogenetic proteinsubfamily:
chromosomal localization of human genes for BMP5, BMP6,and BMP7. Genomics
14: 759- 762, 1992.

GAM281 278 BMP6 Lyons, K.; Graycar, J. L.; Lee, A.; Hashmi, S.; Lindquist, P. B.;Chen, E. 3 B c
Y.; Hogan, B. L. M.; Derynck, R.: Vgr- 1, a mammalian generelated to Xenopus
Vg- 1, is a member of the transforming growth factorbeta gene superfamily.
Proc. Nat. Acad. Sci. 86: 4554- 4558, 1989.

GAM281 278 BMP6 Olavesen, M. G.; Bentley, E.; Mason, R. V. F.; Stephens, R. J.;Ragoussis, 3 B c
J.: Fine mapping of 39 ESTs on human chromosome 6p23- p25. Genomics 46:303-
306, 1997.

GAM281 278 BMP6 Rickard, D. J.; Hofbauer, L. C.; Bonde, S. K.; Gori, F.; Spelsberg,T. C.; 3 B c
Riggs, B. L.: Bone morphogenetic protein- 6 production in humanosteoblastic
cell lines: selective regulation by estrogen. J. Clin.Invest. 101: 413- 422,
1998.

GAM281 278 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 B b
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM281 278 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 B b
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM281 278 CASP2 Bergeron, L.; Perez, G. I.; Macdonald, G.; Shi, L.; Sun, Y.; Jurisicova,A.; 3 B b
Varmuza, S.; Latham, K. E.; Flaws, J. A.; Salter, J. C. M.; Hara,H.;
Moskowitz, M. A.; Li, E.; Greenberg, A.; Tilly, J. L.; Yuan, J.: Defects in
regulation of apoptosis in caspase- 2- deficient mice. GenesDev. 12: 1304-
1314, 1998.

GAM281 278 CASP2 Kumar, S.; Kinoshita, M.; Noda, M.; Copeland, N. G.; Jenkins, N.A.: 3 B b
Induction of apoptosis by the mouse Nedd2 gene, which encodesa protein
similar to the product of the Caenorhabditis elegans celldeath gene ced- 3
and the mammalian IL- 1- beta- converting enzyme. GenesDev. 8: 1613- 1626,
1994.

GAM281 278 CASP2 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 3 B b
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM281 278 CASP2 Kumar, S.; White, D. L.; Takai, S.; Turczynowicz, S.; Juttner,C. A.; Hughes, 3 B b
T. P.: Apoptosis regulatory gene NEDD2 maps to humanchromosome segment 7q34-
35, a region frequently affected in haematologicalneoplasms. Hum. Genet. 95:
641- 644, 1995.

GAM281 278 CASP2 Lassus, P.; Opitz- Araya, X.; Lazebnik, Y.: Requirement for caspase- 2in 3 B b
stress- induced apoptosis before mitochondrial permeabilization. Science
297:1352- 1354, 2002.

GAM281 278 CASP2 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; 3 B b
Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes,
CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem.
Biophys. Res. Commun. 225: 983- 989, 1996.

GAM281 278 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 B b
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM281 278 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 B b
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM281 278 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 B b
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM281 278 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 B b
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM281 278 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 B b
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell
death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM281 278 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 B b
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM281 278 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 B b
Caspase- 8 is required for cell death induced by expanded

polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM281 278 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 B b
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM281 278 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 B c
member of a multigene family. Genomics 52: 332- 341, 1998.

GAM281 278 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 B c
new member of the MTG8/ETO gene family, maps on 20q11region and is deleted
in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM281 278 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 B c
Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic
fusion protein forms a complex with a novel member of theMTG8(ETO/CDR)
family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM281 278 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. 3 B c
J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis
machinery through a novel motif, the F- box. Cell 86:263- 274, 1996.

GAM281 278 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; 3 B c
Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene
(CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics
24:27- 33, 1994.

GAM281 278 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F 3 B c
maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6:
149- 150, 1995.

GAM281 278 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 3 B b
membrane- associated C- type lectin that exhibits CD4- independentbinding of
human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad.
Sci. 89: 8356- 8360, 1992.

GAM281 278 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 3 B b
for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR.
Science 294: 2163- 2166, 2001.

GAM281 278 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 3 B b
Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S.
L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-
SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-
infection of T cells. Cell 100: 587- 597,2000.

GAM281 278 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 3 B b
F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a
novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune
responses. Cell 100: 575- 585, 2000.

GAM281 278 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related 3 B b
gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942,
2000.

GAM281 278 CDC6 Saha, P.; Chen, J.; Thome, K. C.; Lawlis, S. J.; Hou, Z.- H.; Hendricks,M.; 3 B b
Parvin, J. D.; Dutta, A.: Human CDC6/Cdc18 associates with Orc1and cyclin-
cdk and is selectively eliminated from the nucleus at theonset of S phase.
Molec. Cell. Biol. 18: 2758- 2767, 1998.

GAM281 278 CDC6 Williams, R. S.; Shohet, R. V.; Stillman, B.: A human proteinrelated to 3 B b

yeast Cdc6p. Proc. Nat. Acad. Sci. 94: 142- 147, 1997.

GAM281 278 CDC6 Yan, Z.; DeGregori, J.; Shohet, R.; Leone, G.; Stillman, B.; Nevins,J. R.; 3 B b
Williams, R. S.: Cdc6 is regulated by E2F and is essentialfor DNA
replication in mammalian cells. Proc. Nat. Acad. Sci. 95:3603- 3608, 1998.

GAM281 278 CDC6 Yan, Z.; Fedorov, S. A.; Mumby, M. C.; Williams, R. S.: PR48,a novel 3 B b
regulatory subunit of protein phosphatase 2A, interacts withCdc6 and
modulates DNA replication in human cells. Molec. Cell. Biol. 20:1021- 1029,
2000.

GAM281 278 CDH17 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene 3 B b
cluster to a region of chromosome 5 subject to frequent allelicloss in
carcinoma. Genomics 57: 160- 163, 1999.

GAM281 278 CDH17 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; 3 B b
Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck,
P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with
a protein related to the cadherin superfamily. Science 264:430- 433, 1994.

GAM281 278 CDH17 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 3 B b
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting
cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM281 278 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, 3 B b
G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.;
Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.;
Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for
Muckle- Wells syndrome and familial cold urticaria:a novel mutation
underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002.

GAM281 278 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, 3 B b
E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile
neurological cutaneous and articular syndromeis caused by mutations in
CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes.
Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM281 278 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. 3 B b
D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes
familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature
Genet. 29: 301- 305, 2001.

GAM281 278 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 B b
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM281 278 CLDN14 Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.;Park, H.- 3 B c
S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.- K.; Groner,Y.; Soeda, E.;
and 52 others: The DNA sequence of human chromosome21. Nature 405: 311- 319,
2000. Note: Erratum: Nature: 407: 110 only,2000.

GAM281 278 CLDN14 Wilcox, E. R.; Burton, Q. L.; Naz, S.; Riazuddin, S.; Smith, T.N.; Ploplis, 3 B c
B.; Belyatseva, I.; Ben- Yosef, T.; Liburd, N. A.; Morell,R. J.; Kachar, B.;
Wu, D. K.; Griffith, A. J.; Riazuddin, S.; Friedman,T. B.: Mutations in the
gene encoding tight junction claudin- 14 causerecessive deafness DFNB29.
Cell 104: 165- 172, 2001.

GAM281 278 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 B b
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.:

Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM281 278 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 3 B b

GAM281 278 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 3 B b

GAM281 278 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 3 B b

GAM281 278 CNN2 Cheng, J.- F.; Boyartchuk, V.; Zhu, Y.: Isolation and mapping ofhuman chromosome 21 cDNA: progress in constructing a chromosome 21expression map. Genomics 23: 75- 84, 1994. 3 B b

GAM281 278 CNN2 Masuda, H.; Tanaka, K.; Takagi, M.; Ohgami, K.; Sakamaki, T.; Shibata,N.; Takahashi, K.: Molecular cloning and characterization of humannon- smooth muscle calponin. J. Biochem. 120: 415- 424, 1996. 3 B b

GAM281 278 CNP Bernier, L.; Colman, D. R.; D'Eustachio, P.: Chromosomal locationsof genes encoding 2- prime,3- prime cyclic nucleotide 3- prime- phosphodiesteraseand glial fibrillary acidic protein in the mouse. J. Neurosci. Res. 20:497- 504, 1988. 3 B c

GAM281 278 CNP Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J.: 2- prime,3- prime- cyclicnucleotide 3- prime- phosphodiesterase: a membrane- bound, microtubule- associatedprotein and membrane anchor for tubulin. Proc. Nat. Acad. Sci. 99:1807- 1812, 2002. 3 B c

GAM281 278 CNP Douglas, A. J.; Fox, M. F.; Abbott, C. M.; Hinks, L. J.; Sharpe,G.; Povey, S.; Thompson, R. J.: Structure and chromosomal localizationof the human 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasegene. Ann. Hum. Genet. 56: 243- 254, 1992. 3 B c

GAM281 278 CNP Douglas, A. J.; Fox, M. F.; Hinks, L. J.; Povey, S.; Thompson,R. J.: Localization of the myelin specific enzyme 2- prime,3- prime- cyclicnucleotide- 3- prime- phosphohydrolase to 17q21. (Abstract) Cytogenet.Cell Genet. 58: 2004 only, 1991. 3 B c

GAM281 278 CNP Kurihara, T.; Monoh, K.; Sakimura, K.; Takahashi, Y.: Alternativesplicing of mouse brain 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasemRNA. Biochem. Biophys. Res. Commun. 170: 1074- 1081, 1990. 3 B c

GAM281 278 CNP Monoh, K.; Kurihara, T.; Takahashi, Y.; Ichikawa, T.; Kumanishi,T.; Hayashi, S.; Minoshima, S.; Shimizu, N.: Structure, expressionand chromosomal localization of the gene encoding human 2- prime,3- prime- cyclic- nucleotide3- prime- phosphodiesterase. Gene 129: 297- 301, 1993. 3 B c

GAM281 278 CNP Sprinkle, T. J.; Kouri, R. E.; Fain, P. D.; Stoming, T. A.; Whitney,J. B., III: Chromosomal mapping of the human CNP gene using a meioticcrossover DNA panel, PCR, and allele- specific probes. Genomics 16:542- 545, 1993. 3 B c

GAM281 278 CNP Sprinkle, T. J.; Lanclos, K. D.; Lapp, D. F.: Assignment of thehuman 2- prime,3- prime- cyclic nucleotide 3- prime- phosphohydrolase geneto chromosome 17. Genomics 13: 877- 880, 1992. 3 B c

GAM281 278 CNP Vogel, U. S.; Thompson, R. J.: Molecular structure, localization,and possible functions of the myelin- associated enzyme 2- prime,3- prime- cyclicnucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667- 1677,1988. 3 B c

GAM281 278 CRSP6 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, 3 B b

Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC complexes indicates novel pathways for the functionof nuclear receptors and diverse mammalian activators. Molec. Cell 3:361- 370, 1999.

GAM281 278 CRSP6 Jiang, Y.- W.; Veschambre, P.; Erdjument- Bromage, H.; Tempst, P.;Conaway, J. W.; Conaway, R. C.; Kornberg, R. D.: Mammalian mediatorof transcriptional regulation and its possible role as an end- pointof signal transduction pathways. Proc. Nat. Acad. Sci. 95: 8538- 8543,1998. 3 B b

GAM281 278 CRSP6 Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R.: The transcriptionalcofactor complex CRSP is required for activity of the enhancer- bindingprotein Sp1. Nature 397: 446- 450, 1999. 3 B b

GAM281 278 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359, 1997. 3 B b

GAM281 278 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix Biol. 18: 319- 324, 1999. 3 B b

GAM281 278 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of the gene encoding human cartilage associatedprotein (CRTAP). Cytogenet. Cell Genet. 87: 191- 194, 1999. 3 B b

GAM281 278 CSNK2A2 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 3 B b

GAM281 278 CSNK2A2 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine 392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292, 2001. 3 B b

GAM281 278 CSNK2A2 Lozeman, F. J.; Litchfield, D. W.; Piening, C.; Takio, K.; Walsh,K. A.; Krebs, E. G.: Isolation and characterization of human cDNAclones encoding the alpha and the alpha- prime subunits of casein kinaseII. Biochemistry 29: 8436- 8447, 1990. 3 B b

GAM281 278 CSNK2A2 Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C.: Globozoospermiain mice lacking the casein kinase II alpha- prime catalytic subunit. NatureGenet. 23: 118- 121, 1999. 3 B b

GAM281 278 CSNK2A2 Yang- Feng, T. L.; Naiman, T.; Kopatz, I.; Eli, D.; Dafni, N.; Canaani,D.: Assignment of the human casein kinase II alpha- prime subunitgene (CSNK2A1) to chromosome 16p13.2- p13.3. Genomics 19: 173 only,1994. 3 B b

GAM281 278 CSNK2A2 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping of the human casein kinase II catalytic subunit genes: twoloci carrying the homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125- 7129, 1991. 3 B b

GAM281 278 CST Ishida, N.; Ito, M.; Yoshioka, S.; Sun- Wada, G.- H.; Kawakita, M.: Functional expression of human Golgi CMP- sialic acid transporterin the Golgi complex of a transporter- deficient Chinese hamster ovarycell mutant. J. Biochem. 124: 171- 178, 1998. 3 B c

GAM281 278 CST Ishida, N.; Miura, N.; Yoshioka, S.; Kawakita, M.: Molecular cloningand characterization of a novel isoform of the human UDP- galactosetransporter, and of related complementary DNAs belonging to the nucleotide- 3 B c

sugartransporter gene family. J. Biochem. 120: 1074- 1078, 1996.

GAM281 278 CTF1 Bordet, T.; Lesbordes, J.- C.; Rouhani, S.; Castelnau- Ptakhine,L.; Schmalbruch, H.; Haase, G.; Kahn, A.: Protective effects of cardiotrophin-1adenoviral gene transfer on neuromuscular degeneration in transgenicALS mice. Hum. Molec. Genet. 10: 1925- 1933, 2001. 3 B b

GAM281 278 CTF1 Pennica, D.; Arce, V.; Swanson, T. A.; Vejsada, R.; Pollock, R.A.; Armanini, M.; Dudley, K.; Phillips, H. S..; Rosenthal, A.; Kato,A. C.; Henderson, C. E.: Cardiotrophin- 1, a cytokine present in embryonicmuscle, supports long-term survival of spinal motoneurons. Neuron 17:63- 74, 1996. 3 B b

GAM281 278 CTF1 Pennica, D.; King, K. L.; Shaw, K. J.; Luis, E.; Rullamas, J.;Luoh, S.- M.; Darbonne, W. C.; Knutzon, D. S.; Yen, R.; Chien, K. R.;Baker, J. B.; Wood, W. I.: Expression cloning of cardiotrophin 1,a cytokine that induces cardiac myocyte hypertrophy. Proc. Nat. Acad.Sci. 92: 1142- 1146, 1995. 3 B b

GAM281 278 CTF1 Pennica, D.; Swanson, T. A.; Shaw, K. J.; Kuang, W.- J.; Gray, C.L.; Beatty, B. G.; Wood, W. I.: Human cardiotrophin- 1: protein andgene structure, biological and binding activities, and chromosomallocalization. Cytokine 8: 183- 189, 1996. 3 B b

GAM281 278 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H, L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245, 1997. 3 B b

GAM281 278 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S controls the trafficking and maturation of MHC class IImolecules in dendritic cells. J. Cell Biol. 147: 775- 790, 1999. 3 B b

GAM281 278 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. J.; Chapman, H. A.: Structure and chromosomal assignmentof the human cathepsin K gene. Genomics 41: 258- 262, 1997. 3 B b

GAM281 278 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.; Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell selection and maturation by cathepsin S. Immunity 15:909- 919, 2001. 3 B b

GAM281 278 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: Molecular cloning and expression of human alveolar macrophagecathepsin S, an elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992. 3 B b

GAM281 278 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization, gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536, 1994. 3 B b

GAM281 278 CXCL16 Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G.: A transmembrane CXC chemokine is a ligand for HIV- coreceptor Bonzo. NatureImmun. 1: 298- 304, 2000. 3 B c

GAM281 278 CXCL16 Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.;Kita, T.; Yonehara, S.: Molecular cloning of a novel scavenger receptorfor oxidized low density lipoprotein, SR- PSOX, on macrophages. J.Biol. Chem. 275: 40663-40666, 2000. 3 B c

GAM281 278 CXCL16 Wilbanks, A.; Zondlo, S. C.; Murphy, K.; Mak, S.; Soler, D.; Langdon,P.; Andrew, D. P.; Wu, L.; Briskin, M.: Expression cloning of theSTRL33/BONZO/TYMSTR ligand reveals elements of CC, CXC, CX3C chemokines. J.Immun. 166: 5145- 5154, 2001. 3 B c

GAM281 278 CXCL6 Modi, W. S.; Chen, Z.- Q.: Localization of the human CXC chemokinesubfamily 3 B c
on the long arm of chromosome 4 using radiation hybrids. Genomics 47:136-
139, 1998.

GAM281 278 CXCL6 O'Donovan, N.; Galvin, M.; Morgan, J. G.: Physical mapping ofthe CXC 3 B c
chemokine locus on human chromosome 4. Cytogenet. Cell Genet. 84:39- 42,
1999.

GAM281 278 CXCL6 Proost, P.; Wuyts, A.; Conings, R.; Lenaerts, J.- P.; Billiau, 3 B c
A.;Opdenakker, G.; Van Damme, J.: Human and bovine granulocyte
chemotacticprotein- 2: complete amino acid sequence and functional
characterizationas chemokines. Biochemistry 32: 10170- 10177, 1993.

GAM281 278 CXCL6 Rovai, L. E.; Herschman, H. R.; Smith, J. B.: Cloning and characterizationof 3 B c
the human granulocyte chemotactic protein- 2 gene. J. Immun. 158:5257- 5266,
1997.

GAM281 278 CXCL6 Wuyts, A.; van Osselaer, N.; Haelens, A.; Samson, I.; Herdewijn,P.; Ben- 3 B c
Baruch, A.; Oppenheim, J. J.; Proost, P.; van Damme, J.:Characterization of
synthetic human granulocyte chemotactic protein2: usage of chemokine
receptors CXCR1 and CXCR2 and in vivo inflammatoryproperties. Biochemistry
36: 2716- 2723, 1997.

GAM281 278 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; 3 B b
Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism:
studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996.

GAM281 278 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human 3 B b
cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily
responsible for the hepatic 3- demethylation of caffeineand N- oxidation of
carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989.

GAM281 278 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, 3 B b
M.; Petersen, N. E.: Association between CYP1A2 polymorphismand
susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000.

GAM281 278 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. 3 B b
L.: The contribution of genetically determined oxidationstatus to inter-
individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16:
157- 166, 1983.

GAM281 278 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, 3 B b
T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450
involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986.

GAM281 278 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, 3 B b
S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat
orthologous gene, and differences in liver1A2 mRNA expression. Molec.
Endocr. 3: 1399- 1408, 1989.

GAM281 278 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human 3 B b
P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the
3- prime nontranslated region, and localization ofgene to chromosome 15. J.
Exp. Path. 3: 1- 17, 1987.

GAM281 278 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, 3 B b
A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show
deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996.

GAM281 278 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 B b

GAM281 278 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, 3 B b
S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter)
Nature 398: 760- 761, 1999.

GAM281 278 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 3 B b

GAM281 278 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 3 B b

GAM281 278 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002. 3 B b

GAM281 278 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 3 B b

GAM281 278 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 B b

GAM281 278 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 3 B b

GAM281 278 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene: molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230, 1998. 3 B b

GAM281 278 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii-Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in humanpolymorphonuclear leukocytes: cDNA cloning and expression of leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993. 3 B b

GAM281 278 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 B b

GAM281 278 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 B b

GAM281 278 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4-alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 B b

GAM281 278 DCK Chottiner, E. G.; Shewach, D. S.; Datta, N. S.; Ashcraft, E.; Gribbin,D.; Ginsburg, D.; Fox, I. H.; Mitchell, B. S.: Cloning and expressionof human deoxycytidine kinase cDNA. Proc. Nat. Acad. Sci. 88: 1531- 1535,1991. 3 B c

GAM281 278 DCK Huang, S.- H.; Tomich, J. M.; Wu, H.; Jong, A.; Holcenberg, J.:Human deoxycytidine kinase: sequence of cDNA clones and analysis ofexpression in cell lines with and without enzyme activity. J. Biol.Chem. 264: 14762-14768, 1989. Note: Correction: J. Biol. Chem. 266:5353 only, 1991. 3 B c

GAM281 278 DCK Johansson, M.; Brismar, S.; Karlsson, A.: Human deoxycytidinekinase is located in the cell nucleus. Proc. Nat. Acad. Sci. 94:11941- 11945, 1997. 3 B c

GAM281 278 DCK Song, J. J.; Walker, S.; Chen, E.; Johnson, E. E., II; Spychala,J.; Gribbin, 3 B c

T.; Mitchell, B. S.: Genomic structure and chromosomallocalization of the human deoxycytidine kinase gene. Proc. Nat. Acad.Sci. 90: 431- 434, 1993.

GAM281 278 DCK Stegmann, A. P. A.; Honders, M. W.; Bolk, M. W. J.; Wessels, J.;Willemze, R.; Landegent, J. E.: Assignment of the human deoxycytidinekinase (DCK) gene to chromosome 4 band q13.3- q21.1. Genomics 17:528- 529, 1993. 3 B c

GAM281 278 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000. 3 B b

GAM281 278 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461- 8466, 1998. 3 B b

GAM281 278 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997. 3 B b

GAM281 278 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998. 3 B b

GAM281 278 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. W.: Chromosomal localization and racial distributionof the polymorphic human dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352, 1988. 3 B c

GAM281 278 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies three RFLPs. Nucleic Acids Res. 15: 5501 only,1987. 3 B c

GAM281 278 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: Chromosomal localization and racial distribution of the polymorphichDHFR- psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985. 3 B c

GAM281 278 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; Nienhuis, A. W.: Chromosomal organization of the human dihydrofolatereductase genes: dispersion, selective amplification and a novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984. 3 B c

GAM281 278 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in dihydrofolatereductase that confer resistance to methotrexate: potential for clinicalapplication. Hum. Mutat. 11: 259- 263, 1998. 3 B c

GAM281 278 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: Intronless human dihydrofolate reductase genes are derivedfrom processed RNA molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982. 3 B c

GAM281 278 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association with variation in protein structure. Science 220: 1125- 1129,1983. 3 B c

GAM281 278 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 757 and 807- 812, 1975. 3 B c

GAM281 278 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5. Molec. Cell. Biol. 4: 2010- 2016, 1984. 3 B c

GAM281 278 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater-Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med. 3 B c

310: 789- 790, 1984.

GAM281 278 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986. 3 B c

GAM281 278 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: Human dihydrofolate reductase gene is located in chromosome 5and is unlinked to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984. 3 B c

GAM281 278 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human dihydrofolate reductase gene to band q23 of chromosome 5and of related pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85, 1985. 3 B c

GAM281 278 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; Attardi, G.: Chromosomal location of the normal human DHFRgene and of its amplified copies in methotrexate resistant cell variants.(Abstract) Cytogenet. Cell Genet. 37: 534 only, 1984. 3 B c

GAM281 278 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 10/7/1983. 3 B c

GAM281 278 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: Amplification of the human dihydrofolate reductase gene viadouble minutes is initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000. 3 B c

GAM281 278 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976. 3 B c

GAM281 278 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)-formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967. 3 B c

GAM281 278 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila-relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997. 3 B c

GAM281 278 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998. 3 B c

GAM281 278 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994. 3 B c

GAM281 278 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997. 3 B c

GAM281 278 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993. 3 B c

GAM281 278 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997. 3 B c

GAM281 278 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, D. J.; Muir, W. J.: Schizophrenia and affective disorders- -cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. 3 B c

Genet. 69:428- 433, 2001.

GAM281 278 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 355:771- 772, 2000. 3 B c

GAM281 278 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 3 B c

GAM281 278 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 3 B c

GAM281 278 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000. 3 B c

GAM281 278 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990. 3 B c

GAM281 278 DLG2 Kim, E.; Cho, K.- O.; Rothschild, A.; Sheng, M.: Heteromultimerizationand NMDA receptor- clustering activity of Chapsyn- 110, a member ofthe PSD- 95 family of proteins. Neuron 17: 103- 113, 1996. 3 B c

GAM281 278 DLG2 Kim, E.; Niethammer, M.; Rothschild, A.; Jan, Y. N.; Sheng, M.: Clustering of Shaker- type K+ channels by interaction with a familyof membrane- associated guanylate kinases. Nature 378: 85- 88, 1995. 3 B c

GAM281 278 DLG2 Stathakis, D. G.; Lee, D.; Bryant, P. J.: Fine- scale physicalmap of the 11q21 region surrounding the human DLG2 locus, the geneencoding Chapsyn- 110. Genomics 54: 186- 188, 1998. 3 B c

GAM281 278 DNAH11 Arnold, G. L.; Bixler, D.; Girod, D.: Probable autosomal recessiveinheritance of polysplenia, situs inversus and cardiac defects inan Amish family. Am. J. Med. Genet. 16: 35- 42, 1983. 3 B c

GAM281 278 DNAH11 Brueckner, M.; D'Eustachio, P.; Horwich, A. L.: Linkage mappingof a mouse gene, iv, that controls left- right asymmetry of the heartand viscera. Proc. Nat. Acad. Sci. 86: 5035- 5038, 1989. 3 B c

GAM281 278 DNAH11 Chapelin, C.; Duriez, N.; Magnino, F.; Goossens, M.; Escudier,E.; Amselem, S.: Isolation of several human axonemal dynein heavychain genes: genomic structure of the catalytic site, phylogeneticanalysis and chromosomal assignment. FEBS Lett. 412: 325- 330, 1997. 3 B c

GAM281 278 DNAH11 Hanzlik, A. J.; Binder, M.; Layton, W. M.; Rowe, L.; Layton, M.;Taylor, B. A.; Osemlak, M. M.; Richards, J. E.; Kurnit, D. M.; Stewart,G. D.: The murine situs inversus viscerum (iv) gene responsiblefor visceral asymmetry is linked tightly to the Igh- C cluster on chromosome12. Genomics 7: 389- 393, 1990. 3 B c

GAM281 278 DNAH11 McGrath, J.; Horwich, A. L.; Brueckner, M.: Duplication/deficiencymapping of situs inversus viscerum (iv), a gene that determines left- rightasymmetry in the mouse. Genomics 14: 643- 648, 1992. 3 B c

GAM281 278 DNAH11 Nonaka, S.; Shiratori, H.; Saijoh, Y.; Hamada, H.: Determinationof left- right patterning of the mouse embryo by artificial nodal flow. Nature 418:96- 99, 2002. 3 B c

GAM281 278 DNAH11 Okada, Y.; et al.; et al: Abnormal nodal flow precedes situs inversusin iv and inv mice. Molec. Cell 4: 459- 468, 1999. 3 B c

GAM281 278 DNAH11 Supp, D. M.; Witte, D. P.; Potter, S. S.; Brueckner, M.: Mutationof an axonemal dynein affects left- right asymmetry in inversus viscerummice. Nature 389: 963- 966, 1997. 3 B c

GAM281 278 DNAH11 Supp, D.; et al.; et al: Targeted deletion of the ATP bindingdomain of left- right dynein confirms its role in specifying developmentof left- right asymmetries. Development 126: 5495- 5504, 1999. 3 B c

GAM281 278 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995. 3 B b

GAM281 278 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin. J. Biol. Chem. 269: 26295- 26302, 1994. 3 B b

GAM281 278 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The desmocollins of human foreskin epidermis: identification and chromosomalassignment of a third gene and expression patterns of the three isoforms. J.Invest. Derm. 105: 314- 321, 1995. 3 B b

GAM281 278 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.: Neurodevelopmental delay, motor abnormalities and cognitive deficitsin transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001. 3 B c

GAM281 278 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262- 265, 1997. 3 B c

GAM281 278 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A potassium channel mutation in weaver mice implicates membraneexcitability in granule cell differentiation. Nature Genet. 11:126- 129, 1995. 3 B c

GAM281 278 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk gene from 'the Down syndrome critical region' of chromosome 21. Biochem.Biophys. Res. Commun. 225: 92- 99, 1996. 3 B c

GAM281 278 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.; Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in transgenic mice implicates minibrain in learningdefects associated with Down syndrome. Nature Genet. 16: 28- 36,1997. 3 B c

GAM281 278 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to chromosome 16, localizes to the nucleus, and can form multimers. Biochem.Biophys. Res. Commun. 231: 640- 644, 1997. 3 B c

GAM281 278 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.; Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the Drosophila minibrain gene: human homologue maps to 21q22.2in the Down syndrome 'critical region.' Genomics 38: 331- 339, 1996. 3 B c

GAM281 278 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein kinase family involved in postembryonic neurogenesisin Drosophila. Neuron 14: 287- 301, 1995. 3 B c

GAM281 278 EBAF Burdine, R. D.; Schier, A. F.: Conserved and divergent mechanismsin left- 3 B c

right axis formation. Genes Dev. 14: 763- 776, 2000.

GAM281 278 EBAF Kosaki, K.; Bassi, M. T.; Kosaki, R.; Lewin, M.; Belmont, J.; Schauer,G.; 3 B c
Casey, B.: Characterization and mutation analysis of human LEFTYA and LEFTY
B, homologues of murine genes implicated in left- rightaxis development. Am.
J. Hum. Genet. 64: 712- 721, 1999.

GAM281 278 EBAF Kothapalli, R.; Buyuksal, I.; Wu, S.- Q.; Chegini, N.; Tabibzadeh,S.: 3 B c
Detection of ebaf, a novel human gene of the transforming growthfactor beta
superfamily: association of gene expression with endometrialbleeding. J.
Clin. Invest. 99: 2342- 2350, 1997.

GAM281 278 EBAF Meno, C.; Itoh, Y.; Saijoh, Y.; Matsuda, Y.; Tashiro, K.; Kuhara,S.; Hamada, 3 B c
H.: Two closely- related left- right asymmetrically expressedgenes, lefty- 1
and lefty- 2: their distinct expression domains, chromosomallinkage and
direct neuralizing activity in Xenopus embryos. GenesCells 2: 513- 524,
1997.

GAM281 278 EBAF Meno, C.; Saijoh, Y.; Fujii, H.; Ikeda, M.; Yokoyama, T.; Yokoyama,M.; 3 B c
Toyoda, Y.; Hamada, H.: Left- right asymmetric expression of theTGF- beta-
family member lefty in mouse embryos. Nature 381: 151- 155,1996.

GAM281 278 EBAF Meno, C.; Shimono, A.; Saijoh, Y.; Yashiro, K.; Mochida, K.; Ohishi,S.; 3 B c
Noji, S.; Kondoh, H.; Hamada, H.: Lefty- 1 is required for left-
rightdetermination as a regulator of lefty- 2 and nodal. Cell 94: 287-
297,1998.

GAM281 278 EBAF Tabibzadeh, S.; Mason, J. M.; Shea, W.; Cai, Y.; Murray, M. J.;Lessey, B.: 3 B c
Dysregulated expression of ebaf, a novel molecular defectin the endometria
of patients with infertility. J. Clin. Endocr.Metab. 85: 2526- 2536, 2000.

GAM281 278 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- 3 B b
elongationfactor 2 kinase (calmodulin- dependent protein kinase III)
antibodiesin patients with systemic lupus erythematosus. Biochem.
Biophys.Res. Commun. 293: 1073- 1076, 2002.

GAM281 278 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 3 B b
Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C.
R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein
kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat.
Acad. Sci. 94: 4884- 4889, 1997.

GAM281 278 EHD1 Di Fiore, P. P.; Pelicci, P. G.; Sorkin, A.: EH: a novel protein- 3 B c
proteininteraction domain potentially involved in intracellular sorting.
TrendsBiochem. Sci. 22: 411- 413, 1997.

GAM281 278 EHD1 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 3 B c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.;
Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.;
Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the
2.8- Mb region containing the multiple endocrineneoplasia type 1 locus.
Genome Res. 7: 725- 735, 1997.

GAM281 278 EHD1 Haider, N. B.; Searby, C.; Galperin, E.; Mintz, L.; Horowitz, M.;Stone, E. 3 B c
M.; Sheffield, V. C.: Evaluation and molecular characterizationof EHD1, a
candidate gene for Bardet- Biedl syndrome 1 (BBS1). Gene 240:227- 232, 1999.

GAM281 278 EHD1 Mintz, L.; Galperin, E.; Pasmanik- Chor, M.; Tulzinsky, S.; Bromberg,Y.; 3 B c
Kozak, C. A.; Joyner, A.; Fein, A.; Horowitz, M.: EHD1- - an EH- domain-
containingprotein with a specific expression pattern. Genomics 59: 66-
76,1999.

GAM281 278 EHD1 Rotem- Yehudar, R.; Galperin, E.; Horowitz, M.: Association ofinsulin- like 3 B c

growth factor 1 receptor with EHD1 and SNAP29. J. Biol.Chem. 276: 33054-33060, 2001.

GAM281 278 EIF2C1 Koesters, R.; Adams, V.; Betts, D.; Moos, R.; Schmid, M.; Siermann,A.; Hassam, S.; Weitz, S.; Lichter, P.; Heitz, P. U.; von Knebel Doeberitz,M.; Briner, J.: Human eukaryotic initiation factor EIF2C1 gene: cDNAsequence, genomic organization, localization to chromosomal bands1q34- p35, and expression. Genomics 61: 210- 218, 1999. 3 B c

GAM281 278 EIF2C1 Martinez, J.; Patkaniowska, A.; Urlaub, H.; Luhrmann, R.; Tuschi,T.: Single-stranded antisense siRNAs guide target RNA cleavage inRNAi. Cell 110: 563-574, 2002. 3 B c

GAM281 278 EIF2S3 Ehrmann, I. E.; Ellis, P. S.; Mazeyrat, S.; Duthie, S.; Brockdorff,N.; Mattei, M. G.; Gavin, M. A.; Affara, N. A.; Brown, G. M.; Simpson,E.; Mitchell, M. J.; Scott, D. M.: Characterization of genes encodingtranslation initiation factor eIF- 2- gamma in mouse and human: sexchromosome localization, escape from X- inactivation and evolution. Hum.Molec. Genet. 7: 1725- 1737, 1998. 3 B b

GAM281 278 EIF2S3 Gasper, N. J.; Kinzy, T. G.; Scherer, B. J.; Humbelin, M.; Hershey,J. W. B.; Merrick, W. C.: Translation initiation factor eIF- 2: cloningand expression of the human cDNA encoding the gamma- subunit. J. Biol.Chem. 269: 3415-3422, 1994. 3 B b

GAM281 278 F2RL2 Duperat, V. G.; Jacquelin, B.; Boisseau, P.; Arveiler, B.; Nurden,A. T.: Protease- activated receptor genes are clustered on 5q13. Blood 92:25- 31, 1998. 3 B c

GAM281 278 F2RL2 Ishihara, H.; Connolly, A. J.; Zeng, D.; Kahn, M. L.; Zheng, Y.W.; Timmons, C.; Tram, T.; Coughlin, S. R.: Protease- activated receptor3 is a second thrombin receptor in humans. Nature 386: 502- 506,1997. 3 B c

GAM281 278 F2RL2 Kahn, M. L.; Zheng, Y. W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 3 B c

GAM281 278 F2RL2 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 3 B c

GAM281 278 F2RL2 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 3 B c

GAM281 278 F2RL2 Schmidt, V.; Wainer, J.; Bahou, W.: Identification and characterizationof the human proteolytically activated receptor- 3 (PAR- 3) gene withinthe PAR gene cluster by positional mapping. (Abstract) Blood (suppl.1) 90: 284a only, 1997. 3 B c

GAM281 278 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 3 B b

GAM281 278 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 3 B b

GAM281 278 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 3 B b

GAM281 278 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand 3 B b

characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998.

GAM281 278 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985. 3 B b

GAM281 278 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985. 3 B b

GAM281 278 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988. 3 B b

GAM281 278 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional analysis of the human tissue factor promoter and inductionby serum. Proc. Nat. Acad. Sci. 87: 2254- 2258, 1990. 3 B b

GAM281 278 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: Completesequence of the human tissue factor gene, a highly regulated cellularreceptor that initiates the coagulation protease cascade. Biochemistry 28:1755- 1762, 1989. 3 B b

GAM281 278 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand mapping of RFLPs for human tissue factor (HTF) to chromosome 1p. NucleicAcids Res. 15: 9098 only, 1987. 3 B b

GAM281 278 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA sequenceand chromosome localization of the gene. Biochemistry 26: 5234- 5238,1987. 3 B b

GAM281 278 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA clones coding for human tissue factor: primary structureof the protein and cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987. 3 B b

GAM281 278 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad. Sci. 94: 6922- 6926, 1997. 3 B b

GAM281 278 FABP2 Baier, L. J.; Sacchettini, J. C.; Knowler, W. C.; Eads, J.; Paolisso,G.; Tataranni, P. A.; Mochizuki, H.; Bennett, P. H.; Bogardus, C.;Prochazka, M.: An amino acid substitution in the human intestinalfatty acid binding protein is associated with increased fatty acidbinding, increased fat oxidation, and insulin resistance. J. Clin.Invest. 95: 1281- 1287, 1995. 3 B c

GAM281 278 FABP2 Carlsson, M.; Orho- Melander, M.; Hedenbro, J.; Almgren, P.; Groop,L. C.: The T54 allele of the intestinal fatty acid- binding protein2 is associated with a parental history of stroke. J. Clin. Endocr.Metab. 85: 2801- 2804, 2000. 3 B c

GAM281 278 FABP2 Georgopoulos, A.; Aras, O.; Tsai, M. Y.: Codon- 54 polymorphismof the fatty acid- binding protein 2 gene is associated with elevationof fasting and postprandial triglyceride in type 2 diabetes. J. Clin.Endocr. Metab. 85: 3155- 3160, 2000. 3 B c

GAM281 278 FABP2 Hegele, R. A.; Harris, S. B.; Hanley, A. J. G.; Sadikian, S.; Connelly,P. W.; Zinman, B.: Genetic variation of intestinal fatty acid- bindingprotein associated with variation in body mass in aboriginal Canadians. J.Clin. Endocr. Metab. 81: 4334- 4337, 1996. 3 B c

GAM281 278 FABP2 Polymeropoulos, M. H.; Rath, D. S.; Xiao, H.; Merril, C. R.: 3 B c

Trinucleotiderepeat polymorphism at the human intestinal fatty acid binding proteingene (FABP2). Nucleic Acids Res. 18: 7198 only, 1991.

GAM281 278 FABP2 Prochazka, M.; Lillioja, S.; Tait, J. F.; Knowler, W. C.; Mott,D. M.; Spraul, M.; Bennett, P. H.; Bogardus, C.: Linkage of chromosomalmarkers on 4q with a putative gene determining maximal insulin actionin Pima Indians. Diabetes 42: 514- 519, 1993. 3 B c

GAM281 278 FABP2 Sipilainen, R.; Uusitupa, M.; Heikkinen, S.; Rissanen, A.; Laakso,M.: Variants in the human intestinal fatty acid binding protein 2gene in obese subjects. J. Clin. Endocr. Metab. 82: 2629- 2632, 1997. 3 B c

GAM281 278 FABP2 Sparkes, R. S.; Mohandas, T.; Heinzmann, C.; Gordon, J. I.; Klisak,I.; Zollman, S.; Sweetser, D. A.; Ragunathan, L.; Winokur, S.; Lusis,A. J.: Human fatty acid binding protein assignments intestinal to4q28- 4q31 and liver to 2p11. (Abstract) Cytogenet. Cell Genet. 46:697 only, 1987. 3 B c

GAM281 278 FABP2 Sweetser, D. A.; Birkenmeier, E. H.; Klisak, I. J.; Zollman, S.;Sparkes, R. S.; Mohandas, T.; Lusis, A. J.; Gordon, J. I.: The humanand rodent intestinal fatty acid binding protein genes: a comparativeanalysis of their structure, expression, and linkage relationships. J.Biol. Chem. 262: 16060- 16071, 1987. 3 B c

GAM281 278 FABP2 Weber, J. L.; Kwitek, A. E.; May, P. E.; Polymeropoulos, M.:Dinucleotide repeat polymorphism at the D12S43 locus. Nucleic AcidsRes. 18: 4637 only, 1990. 3 B c

GAM281 278 FABP2 Weber, J. L.; May, P. E.: Abundant class of human DNA polymorphismswhich can be typed using the polymerase chain reaction. Am. J. Hum.Genet. 44: 388- 396, 1989. 3 B c

GAM281 278 FANCE Buchwald, M.: Complementation groups: one or more per gene? NatureGenet. 11: 228- 230, 1995. 3 B c

GAM281 278 FANCE de Winter, J. P.; Leveille, F.; van Berkel, C. G. M.; Rooimans,M. A.; van der Weel, L.; Steltenpool, J.; Demuth, I.; Morgan, N. V.;Alon, N.; Bosnoyan-Collins, L.; Lightfoot, J.; Leegwater, P. A.; Waisfisz,Q.; Komatsu, K.; Arwert, F.; Pronk, J. C.; Mathew, C. G.; Digweed,M.; Buchwald, M.; Joenje, H.: Isolation of a cDNA representing theFanconi anemia complementation group E gene. Am. J. Hum. Genet. 67:1306- 1308, 2000. Note: Erratum: Am. J. Hum. Genet. 67: 1365 only,2000. 3 B c

GAM281 278 FANCE Joenje, H.: Fanconi anaemia complementation groups in Germanyand The Netherlands. Hum. Genet. 97: 280- 282, 1996. 3 B c

GAM281 278 FANCE Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G.M.; Rooimans, M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J.J. P.; Buchwald, M.; Arwert, F.: Classification of Fanconi anemiapatients by complementation analysis: evidence for a fifth geneticsubtype. Blood 86: 2156- 2160, 1995. 3 B c

GAM281 278 FANCE Joenje, H.; Oostra, A. B.; Wijker, M.; di Summa, F. M.; van Berkel,C. G. M.; Rooimans, M. A.; Ebell, W.; van Weel, M.; Pronk, J. C.;Buchwald, M.; Arwert, F.: Evidence for at least eight Fanconi anemiagenes. Am. J. Hum. Genet. 61: 940- 944, 1997. 3 B c

GAM281 278 FANCE Pace, P.; Johnson, M.; Tan, W. M.; Mosedale, G.; Sng, C.; Hoatlin,M.; de Winter, J.; Joenje, H.; Gergely, F.; Patel, K. J.: FANCE:the link between Fanconi anaemia complex assembly and activity. EMBOJ. 21: 3414- 3423, 2002. 3 B c

GAM281 278 FANCE Waisfisz, Q.; Saar, K.; Morgan, N. V.; Altay, C.; Leegwater, P.A.; de Winter, J. P.; Komatsu, K.; Evans, G. R.; Wegner, R.- D.; Reis,A.; Joenje, 3 B c

H.; Arwert, F.; Mathew, C. G.; Pronk, J. C.; Digweed,M.: The Fanconi anemia group E gene, FANCE, maps to chromosome 6p. Am.J. Hum. Genet. 64: 1400-1405, 1999.

GAM281 278 FANCE Wegner, R.- D.; Henrichs, I.; Joenje, H.; Schroeder- Kurth, T.:Fanconi 3 B c
anemia complementation group E: clinical and cytogenetic dataof the first patient. Clin. Genet. 50: 479- 482, 1996.

GAM281 278 FBXL7 Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; 3 B c
Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol. 9: 1177- 1179, 1999.

GAM281 278 FBXL7 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 B c
and expression analysis of new members of the mammalianF- box protein family. Genomics 67: 40- 47, 2000.

GAM281 278 FBXL7 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5: 355- 364, 1998.

GAM281 278 FBXL7 Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A 3 B c
family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999.

GAM281 278 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: 3 B b
Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995.

GAM281 278 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; 3 B b
Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992.

GAM281 278 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: 3 B b
Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665-1672, 1990.

GAM281 278 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. 3 B b
L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681-1685, 1993.

GAM281 278 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, 3 B b
F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001.

GAM281 278 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing 3 B b
of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996.

GAM281 278 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand 3 B b
characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000.

GAM281 278 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin 3 B b
promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001.

GAM281 278 FCGR2A Grundy, H. O.; Peltz, G.; Barsh, G.; Moore, K.; Golbus, M. S.;Lebo, R. V.: 3 B b
Immunoglobulin G Fc receptor II and Fc receptor IIIgenes map to chromosome 1 by spot- blot chromosome analysis. (Abstract) Am.J. Hum. Genet. 43: A145, 1988.

GAM281 278 FCGR2A Grundy, H. O.; Peltz, G.; Moore, K. W.; Golbus, M. S.; Jackson,L. G.; Lebo, 3 B b

R. V.: The polymorphic Fc- gamma receptor II gene mapsto human chromosome 1q. Immunogenetics 29: 331- 339, 1989.

GAM281 278 FCGR2A Hibbs, M. L.; Bonadonna, L.; Scott, B. M.; McKenzie, I. F. C.;Hogarth, P. M.: Molecular cloning of a human immunoglobulin G Fcreceptor. Proc. Nat. Acad. Sci. 85: 2240- 2244, 1988. 3 B b

GAM281 278 FCGR2A Hibbs, M. L.; Hogarth, P. M.; McKenzie, I. F. C.: The mouse Ly- 17locus identifies a polymorphism of the Fc receptor. Immunogenetics 22:335- 348, 1985. 3 B b

GAM281 278 FCGR2A Lebo, R. V.; Lynch, E. D.; Wiegant, J.; Moore, K.; Trounstine,M.; van der Ploeg, M.: Multicolor fluorescence in situ hybridizationand pulsed field electrophoresis dissect CMT1B gene region. Hum.Genet. 88: 13- 20, 1991. 3 B b

GAM281 278 FCGR2A Moser, K. L.; Neas, B. R.; Salmon, J. E.; Yu, H.; Gray- McGuire,C.; Asundi, N.; Bruner, G. R.; Fox, J.; Kelly, J.; Henshall, S.; Bacino,D.; Dietz, M.; Hogue, R.; Koelsch, G.; Nightingale, L.; Shaver, T.;Abdou, N. I.; Albert, D. A.; Carson, C.; Petri, M.; Treadwell, E.L.; James, J. A.; Harley, J. B.: Genome scan of human systemic lupuserythematosus: evidence for linkage on chromosome 1q in African- Americanpedigrees. Proc. Nat. Acad. Sci. 95: 14869- 14874, 1998. 3 B b

GAM281 278 FCGR2A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human DNA. Hum. Molec. Genet. 1: 613- 620,1992. 3 B b

GAM281 278 FCGR2A Peltz, G. A.; Grundy, H. O.; Lebo, R. V.; Yssel, H.; Barsh, G.S.; Moore, K. W.: Human Fc- gamma- RIII: cloning, expression, and identificationof the chromosomal locus of two Fc receptors for IgG. Proc. Nat.Acad. Sci. 86: 1013- 1017, 1989. 3 B b

GAM281 278 FCGR2A Qiu, W. Q.; de Bruin, D.; Brownstein, B. H.; Pearse, R.; Ravetch,J. V.: Organization of the human and mouse low- affinity Fc- gamma- Rgenes: duplication and recombination. Science 248: 732- 735, 1990. 3 B b

GAM281 278 FCGR2A Salmon, J. E.; Millard, S.; Schachter, L. A.; Arnett, F. C.; Ginzler,E. M.; Gourley, M. F.; Ramsey- Goldman, R.; Peterson, M. G. E.; Kimberly,R. P.: Fc- gamma- RIIA alleles are heritable risk factors for lupusnephritis in African Americans. J. Clin. Invest. 97: 1348- 1354,1996. 3 B b

GAM281 278 FCGR2A Sammartino, L.; Webber, L. M.; Hogarth, P. M.; McKenzie, I. F.C.; Garson, O. M.: Assignment of the gene coding for human FcRII(CD32) to bands q23q24 on chromosome 1. Immunogenetics 28: 380- 381,1988. 3 B b

GAM281 278 FCGR2A Stein, M.- P.; Edberg, J. C.; Kimberly, R. P.; Mangan, E. K.; Bharadwaj,D.; Mold, C.; Du Clos, T. W.: C- reactive protein binding to Fc- gamma- RIIaon human monocytes and neutrophils is allele- specific. J. Clin. Invest. 105:369- 376, 2000. 3 B b

GAM281 278 FCGR2A Unkeless, J. C.: Function and heterogeneity of human Fc receptorsfor immunoglobulin G. J. Clin. Invest. 83: 355- 361, 1989. 3 B b

GAM281 278 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999. 3 B b

GAM281 278 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 B b

GAM281 278 FGF2 Abraham, J. A.; Mergia, A.; Whang, J. L.; Tumolo, A.; Friedman,J.; Hjerild, 3 B c

K. A.; Gospodarowicz, D.; Fiddes, J. C.: Nucleotidesequence of a bovine clone encoding the angiogenic protein, basicfibroblast growth factor. Science 233: 545- 548, 1986.

GAM281 278 FGF2 Abraham, J. A.; Whang, J. L.; Tumolo, A.; Mergia, A.; Friedman,J.; Gospodarowicz, D.; Fiddes, J. C.: Human basic fibroblast growthfactor: nucleotide sequence and genomic organization. EMBO J. 5:2523- 2528, 1986. 3 B c

GAM281 278 FGF2 Doniach, T.: Basic FGF as an inducer of anteroposterior neuralpattern. Cell 83: 1067- 1070, 1995. 3 B c

GAM281 278 FGF2 Dono, R.; Texido, G.; Dussel, R.; Ehmke, H.; Zeller, R.: Impairedcerebral cortex development and blood pressure regulation in FGF2- deficientmice. EMBO J. 17: 4213- 4225, 1998. 3 B c

GAM281 278 FGF2 Eckenstein, F. P.: Fibroblast growth factors in the nervous system. J.Neurobiol. 25: 1467- 1480, 1994. 3 B c

GAM281 278 FGF2 Fukushima, Y.; Byers, M. G.; Fiddes, J. C.; Shows, T. B.: Thehuman basic fibroblast growth factor gene (FGFB) is assigned to chromosome4q25. Cytogenet. Cell Genet. 54: 159- 160, 1990. 3 B c

GAM281 278 FGF2 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast growth factor homologous factor 2 (FHF2): gene structure,expression and mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63, 1999. 3 B c

GAM281 278 FGF2 Gritti, A.; Parati, E. A.; Cova, L.; Frolichsthal, P.; Galli, R.;Wanke, E.; Faravelli, L.; Morassutti, D. J.; Roisen, F.; Nickel, D.D.; Vescovi, A. L.: Multipotential stem cells from the adult mousebrain proliferate and self-renew in response to basic fibroblast growthfactor. J. Neurosci. 16: 1091-1100, 1996. 3 B c

GAM281 278 FGF2 Johnson, R. L.; Tabin, C. J.: Molecular models for vertebratelimb development. Cell 90: 979- 990, 1997. 3 B c

GAM281 278 FGF2 Jung, J.; Zheng, M.; Goldfarb, M.; Zaret, K. S.: Initiation ofmammalian liver development from endoderm by fibroblast growth factors. Science 284:1998- 2003, 1999. 3 B c

GAM281 278 FGF2 Kawaguchi, H.; Nakamura, K.; Tabata, Y.; Ikada, Y.; Aoyama, I.;Anzai, J.; Nakamura, T.; Hiyama, Y.; Tamura, M.: Acceleration offracture healing in nonhuman primates by fibroblast growth factor- 2. J.Clin. Endocr. Metab. 86: 875- 880, 2001. 3 B c

GAM281 278 FGF2 Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.: Cloning andexpression of cDNA encoding human basic fibroblast growth factor. FEBSLett. 213: 189- 194, 1987. 3 B c

GAM281 278 FGF2 Lafage- Pochitaloff, M.; Galland, F.; Simonetti, J.; Prats, H.;Mattei, M.- G.; Birnbaum, D.: The human basic fibroblast growth factorgene is located on the long arm of chromosome 4 at bands q26- q27. OncogeneRes. 5: 241- 244, 1990. 3 B c

GAM281 278 FGF2 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21 by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997. 3 B c

GAM281 278 FGF2 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992. 3 B c

GAM281 278 FGF2 Mergia, A.; Eddy, R.; Abraham, J. A.; Fiddes, J. C.; Shows, T.B.: The genes for basic and acidic fibroblast growth factors areon different human 3 B c

chromosomes. Biochem. Biophys. Res. Commun. 138:644- 651, 1986.

GAM281 278 FGF2 Montero, A.; Okada, Y.; Tomita, M.; Ito, M.; Tsurukami, H.; Nakamura,T.; 3 B c
Doetschman, T.; Coffin, J. D.; Hurley, M. M.: Disruption of thefibroblast
growth factor- 2 gene results in decreased bone mass andbone formation. J.
Clin. Invest. 105: 1085- 1093, 2000.

GAM281 278 FGF2 Ortega, S.; Ittmann, M.; Tsang, S. H.; Ehrlich, M.; Basilico,C.: Neuronal 3 B c
defects and delayed wound healing in mice lacking fibroblastgrowth factor 2.
Proc. Nat. Acad. Sci. 95: 5672- 5677, 1998.

GAM281 278 FGF2 Plotnikov, A. N.; Hubbard, S. R.; Schlessinger, J.; Mohammadi,M.: Crystal 3 B c
structures of two FGF- FGFR complexes reveal the determinantsof ligand-
receptor specificity. Cell 101: 413- 424, 2000.

GAM281 278 FGF2 Plotnikov, A. N.; Schlessinger, J.; Hubbard, S. R.; Mohammadi,M.: Structural 3 B c
basis for FGF receptor dimerization and activation. Cell 98:641- 650, 1999.

GAM281 278 FGF2 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. 3 B c
C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast
growth factor (FGF) homologous factors: new membersof the FGF family
implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850-
9857, 1996.

GAM281 278 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome 3 B b
assignment by polymerase chain reaction techniques: assignmentof the
oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990.

GAM281 278 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator 3 B b
of the hair growth cycle: evidence from targeted and spontaneousmutations.
Cell 78: 1017- 1025, 1994.

GAM281 278 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 3 B b
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM281 278 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; 3 B b
Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and
the bcl.1 locus are contained within one megabase in bandq13 of chromosome
11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988.

GAM281 278 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes 3 B b
a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8:
3487- 3495, 1988.

GAM281 278 FHL2 Chan, K. K.; Tsui, S. K. W.; Lee, S. M. Y.; Luk, S. C. W.; Liew,C. C.; Fung, 3 B b
K. P.; Waye, M. M. Y.; Lee, C. Y.: Molecular cloningand characterization of
FHL2, a novel LIM domain protein preferentiallyexpressed in human heart.
Gene 210: 345- 350, 1998.

GAM281 278 FHL2 Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.- 3 B b
G.;Schafer, B. W.: Subtractive cloning and characterization of DRAL,a novel
LIM- domain protein down- regulated in rhabdomyosarcoma. DNACell Biol. 16:
433- 442, 1997.

GAM281 278 FHL2 Morgan, M. J.; Madgwick, A. J. A.: Slim defines a novel familyof LIM- 3 B b
proteins expressed in skeletal muscle. Biochem. Biophys. Res.Commun. 225:
632- 638, 1996.

GAM281 278 FHL2 Tanahashi, H.; Tabira, T.: Alzheimer's disease- associated presenilin2 3 B b
interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9:2281-
2289, 2000.

GAM281 278 FOXO1A Anderson, M. J.; Shelton, G. D.; Cavenee, W. K.; Arden, K. C.:Embryonic 3 B c
expression of the tumor- associated PAX3- FKHR fusion proteininterferes with
the developmental functions of Pax3. Proc. Nat. Acad.Sci. 98: 1589- 1594,

2001.

GAM281 278 FOXO1A Anderson, M. J.; Viars, C. S.; Czekay, S.; Cavenee, W. K.; Arden,K. C.: 3 B c
Cloning and characterization of three human forkhead genesthat comprise an
FKHR- like gene subfamily. Genomics 47: 187- 199,1998.

GAM281 278 FOXO1A Barr, F. G.; Galili, N.; Holick, J.; Biegel, J. A.; Rovera, G.;Emanuel, B. 3 B c
S.: Rearrangement of the PAX3 paired box gene in thepaediatric solid tumor
alveolar rhabdomyosarcoma. Nature Genet. 3:113- 117, 1993.

GAM281 278 FOXO1A Davis, R. J.; Barr, F. G.: Fusion genes resulting from 3 B c
alternativechromosomal translocations are overexpressed by gene- specific
mechanismsin alveolar rhabdomyosarcoma. Proc. Nat. Acad. Sci. 94: 8047-
8051,1997.

GAM281 278 FOXO1A Fredericks, W. J.; Galili, N.; Mukhopadhyay, S.; Rovera, G.; Bennicelli,J.; 3 B c
Barr, F. G.; Rauscher, F. J., III: The PAX3- FKHR fusion proteincreated by
the t(2;13) translocation in alveolar rhabdomyosarcomasis a more potent
transcriptional activator than PAX3. Molec. Cell.Biol. 15: 1522- 1535, 1995.

GAM281 278 FOXO1A Galili, N.; Davis, R. J.; Fredericks, W. J.; Mukhopadhyay, S.;Rauscher, F. 3 B c
J., III; Emanuel, B. S.; Rovera, G.; Barr, F. G.: Fusionof a fork head
domain gene to PAX3 in the solid tumour alveolar rhabdomyosarcoma.
NatureGenet. 5: 230- 235, 1993.

GAM281 278 FOXO1A Khan, J.; Bittner, M. L.; Saal, L. H.; Teichmann, U.; Azorsa, D.O.; Gooden, 3 B c
G. C.; Pavan, W. J.; Trent, J. M.; Meltzer, P. S.: cDNAmicroarrays detect
activation of a myogenic transcription programby the PAX3- FKHR fusion
oncogene. Proc. Nat. Acad. Sci. 96: 13264- 13269,1999.

GAM281 278 FOXO1A Medema, R. H.; Kops, G. J. P. L.; Bos, J. L.; Burgering, B. M.T.: AFX- like 3 B c
forkhead transcription factors mediate cell- cycle regulationby Ras and PKB
through p27(kip1). Nature 404: 782- 787, 2000.

GAM281 278 FOXO1A Nakae, J.; Biggs, W. H., III; Kitamura, T.; Cavenee, W. K.; Wright,C. V. E.; 3 B c
Arden, K. C.; Accili, D.: Regulation of insulin actionand pancreatic beta-
cell function by mutated alleles of the gene encodingforkhead transcription
factor Foxo1. Nature Genet. 32: 245- 253,2002.

GAM281 278 FOXO1A Scheidler, S.; Fredericks, W. J.; Rauscher, F. J., III; Barr,F. G.; Vogt, P. 3 B c
K.: The hybrid PAX3- FKHR fusion protein of alveolarrhabdomyosarcoma
transforms fibroblasts in culture. Proc. Nat. Acad.Sci. 93: 9805- 9809,
1996.

GAM281 278 FOXO1A Sublett, J. E.; Jeon, I- S.; Shapiro, D. N.: The alveolar 3 B c
rhabdomyosarcomaPAX3/FKHR fusion protein is a transcriptional activator.
Oncogene 11:545- 552, 1995.

GAM281 278 FOXO1A Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: 3 B c
Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes
Cancer 5: 299- 310, 1992.

GAM281 278 FSHPRH1 Aittomaki, K.; Lucena, J. L. D.; Pakarinen, P.; Sistonen, P.; Tapanainen,J.; 3 B b
Gromoll, J.; Kaskikari, R.; Sankila, E.- M.; Lehvaslaiho, H.; Engel,A. R.;
Nieschlag, E.; Huhtaniemi, I.; de la Chapelle, A.: Mutationin the follicle-
stimulating hormone receptor gene causes hereditaryhypergonadotropic ovarian
failure. Cell 82: 959- 968, 1995.

GAM281 278 FSHPRH1 Roberts, R. G.; Kendall, E.; Vetrie, D.; Bobrow, M.: Sequenceand chromosomal 3 B b
location of a human homologue of LRPR1, an FSH primaryresponse gene.
Genomics 37: 122- 124, 1996.

GAM281 278 FSHPRH1 Slegtenhorst- Eegdeman, K. E.; Post, M.; Baarends, W. M.; Themmen,A. P. N.; 3 B
b

Grootegoed, J. A.: Regulation of gene expression in Sertolicells by follicle- stimulating hormone (FSH): cloning and characterizationof LRPR1, a primary response gene encoding a leucine- rich protein. Molec.Cell. Endocr. 108: 115- 124, 1995.

GAM281 278 FSTL1 Shibanuma, M.; Mashimo, J.; Mita, A.; Kuroki, T.; Nose, K.: Cloningfrom a 3 B c mouse osteoblastic cell line of a set of transforming- growth- factor- beta- 1- regulated genes, one of which seems to encode a follistatin- relatedpolypeptide. Europ. J. Biochem. 217: 13- 19, 1993.

GAM281 278 FSTL1 Tanaka, M.; Ozaki, S.; Osakada, F.; Mori, K.; Okubo, M.; Nakao,K.: Cloning 3 B c of follistatin- related protein as a novel autoantigenin systemic rheumatic diseases. Int. Immun. 10: 1305- 1314, 1998.

GAM281 278 FSTL1 Zwijsen, A.; Blockx, H.; van Arnhem, W.; Willems, J.; Fransen,L.; Devos, K.; 3 B c Raymackers, J.; van de Voorde, A.; Slegers, H.: Characterizationof a rat C6 glioma- secreted follistatin- related protein (FRP): cloningand sequence of the human homologue. Europ. J. Biochem. 225: 937- 946,1994.

GAM281 278 FZD4 Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.;Hirai, M.; 3 B c Katoh, M.: Molecular cloning and characterization of humanfrizzled- 4 on chromosome 11q14- q21. Biochem. Biophys. Res. Commun. 264:955- 961, 1999.

GAM281 278 FZD4 Robitaille, J.; MacDonald, M. L. E.; Kaykas, A.; Sheldahl, L. C.;Zeisler, 3 B c J.; Dube, M.- P.; Zhang, L.- H.; Singaraja, R. R.; Guernsey,D. L.; Zhang, B.; Siebert, L. F.; Hoskin- Mott, A.; Trese, M. T.; Pimstone,S. N.; Shastry, B. S.; Moon, R. T.; Hayden, M. R.; Goldberg, Y. P.;Samuels, M. E.: Mutant frizzled- 4 disrupts retinal angiogenesis infamilial exudative vitreoretinopathy. Nature Genet. 32: 326- 330,2002.

GAM281 278 G1P3 Clauss, I. M.; Wathelet, M. G.; Szpirer, J.; Content, J.; Islam,M. Q.; 3 B b Levan, G.; Szpirer, C.; Huez, G. A.: Chromosomal localizationof two human genes inducible by interferons, double- stranded RNA,and viruses. Cytogenet. Cell Genet. 53: 166- 168, 1990.

GAM281 278 G1P3 Itzhaki, J. E.; Barnett, M. A.; MacCarthy, A. B.; Buckle, V. J.;Brown, W. R. 3 B b A.; Porter, A. C. G.: Targeted breakage of a human chromosomemediated by cloned human telomeric DNA. Nature Genet. 2: 283- 287,1992.

GAM281 278 G1P3 Itzhaki, J. E.; Porter, A. C. G.: Targeted disruption of a humaninterferon- 3 B b inducible gene detected by secretion of human growth hormone. NucleicAcids Res. 19: 3835- 3842, 1991.

GAM281 278 G1P3 Kelly, J. M.; Porter, A. C. G.; Chernajovsky, Y.; Gilbert, C. S.;Stark, G. 3 B b R.; Kerr, I. M.: Characterization of a human gene inducibleby alpha- and beta- interferons and its expression in mouse cells. EMBOJ. 5: 1601- 1606, 1986.

GAM281 278 G1P3 Porter, A. C. G.; Chernajovsky, Y.; Dale, T. C.; Gilbert, C. S.;Stark, G. 3 B b R.; Kerr, I. M.: Interferon response element of the humangene 6- 16. EMBO J. 7: 85- 92, 1988.

GAM281 278 G2A Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y.: 3 B c Lysophosphatidylcholine as a ligand for the immunoregulatory receptorG2A. Science 293: 702- 705, 2001.

GAM281 278 G2A Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.;Harvill, E. 3 B c T.; Jensen, E. R.; Miller, J. F.; Witte, O. N.: Micelacking the orphan G protein- coupled receptor G2A develop a late- onsetautoimmune syndrome. Immunity 14: 561- 571, 2001.

GAM281 278 G2A Weng, Z.; Fluckiger, A.- C.; Nisitani, S.; Wahl, M. I.; Le, L. Q.;Hunter, C. 3 B c A.; Fernal, A. A.; le Beau, M. M.; Witte, O. N.: A DNAdamage and stress

inducible G protein- coupled receptor blocks cellsin G2/M. Proc. Nat. Acad. Sci. 95: 12334- 12339, 1998.

GAM281 278 GGT1 Bulle, F.; Mattei, M. G.; Siegrist, S.; Pawlak, A.; Passage, E.;Chobert, M. N.; Laperche, Y.; Guellaen, G.: Assignment of the humangamma- glutamyl transferase gene to the long arm of chromosome 22. Hum.Genet. 76: 283- 286, 1987. 3 B c

GAM281 278 GGT1 Figlewicz, D. A.; Delattre, O.; Guellaen, G.; Krizus, A.; Thomas,G.; Zucman, J.; Rouleau, G. A.: Mapping of human gamma- glutamyl transpeptidasegenes on chromosome 22 and other human autosomes. Genomics 17: 299- 305,1993. 3 B c

GAM281 278 GGT1 Hammond, J. W.; Potter, M.; Wilcken, B.; Truscott, R.: Siblingswith gamma- glutamyltransferase deficiency. J. Inherit. Metab. Dis. 18:82- 83, 1995. 3 B c

GAM281 278 GGT1 Heisterkamp, N.; Groffen, J.: Duplication of the bcr and gamma-glutamyltranspeptidase genes. Nucleic Acids Res. 16: 8045- 8056, 1988. 3 B c

GAM281 278 GGT1 Laperche, Y.; Bulle, F.; Aissani, T.; Chobert, M. N.; Aggerbeck,M.; Hanoune, J.; Guellaen, G.: Molecular cloning and nucleotide sequenceof rat kidney gamma- glutamyl transpeptidase cDNA. Proc. Nat. Acad.Sci. 83: 937- 941, 1986. 3 B c

GAM281 278 GGT1 O'Daley, S.: An abnormal sulphydryl compound in urine. (Abstract) IrishJ. Med. Sci. 7: 578- 579, 1968. 3 B c

GAM281 278 GGT1 Pawlak, A.; Lahuna, O.; Bulle, F.; Suzuki, A.; Ferry, N.; Siegrist,S.; Chikhi, N.; Chobert, M. N.; Guellaen, G.; Laperche, Y.: Gamma-glutamyltranspeptidase: a single copy gene in the rat and a multigene familyin the human genome. J. Biol. Chem. 263: 9913- 9916, 1988. 3 B c

GAM281 278 GGT1 Pawlak, A.; Wu, S.- J.; Bulle, F.; Suzuki, A.; Chikhi, N.; Ferry,N.; Baik, J.- H.; Siegrist, S.; Guellaen, G.: Different gamma- glutamyltranspeptidase mRNAs are expressed in human liver and kidney. Biochem.Biophys. Res. Commun. 164: 912- 918, 1989. 3 B c

GAM281 278 GGT1 Rajpert- De Meyts, E.; Heisterkamp, N.; Groffen, J.: Cloning andnucleotide sequence of human gamma- glutamyl transpeptidase. Proc.Nat. Acad. Sci. 85: 8840- 8844, 1988. 3 B c

GAM281 278 GGT1 Rouleau, G. A.; Bazanowski, A.; Cohen, E. H.; Guellaen, G.; Gusella,J. F.: Gamma- glutamyl transferase locus (GGT) displays a PvuII polymorphism. NucleicAcids Res. 16: 11848 only, 1988. 3 B c

GAM281 278 GGT1 Sakamuro, D.; Yamazoe, M.; Matsuda, Y.; Kangawa, K.; Taniguchi,N.; Matsuo, H.; Yoshikawa, H.; Ogasawara, N.: The primary structureof human gamma-glutamyl transpeptidase. Gene 73: 1- 9, 1988. 3 B c

GAM281 278 GGT1 Schulman, J. D.; Goodman, S. I.; Mace, J. W.; Patrick, A. D.;Tietze, F.; Butler, E. J.: Glutathionuria: inborn error of metabolismdue to tissue deficiency of gamma- glutamyl transpeptidase. Biochem.Biophys. Res. Commun. 65: 68- 74, 1975. 3 B c

GAM281 278 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N-acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001. 3 B b

GAM281 278 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2-epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313- 3 B b

24318,1997.

GAM281 278 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 B b

GAM281 278 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997. 3 B b

GAM281 278 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase gene (GNE). J. Hum. Genet. 47: 77- 79, 2002. 3 B b

GAM281 278 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999. 3 B b

GAM281 278 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993. 3 B b

GAM281 278 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001. 3 B b

GAM281 278 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981. 3 B b

GAM281 278 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002. 3 B b

GAM281 278 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N- acetylglucosamine 2- epimerase gene define the disease sialuriaand the allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999. 3 B b

GAM281 278 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N- acetylneuraminic acid biosynthesis of rat liver: molecularcloning and functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N- acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997. 3 B b

GAM281 278 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989. 3 B b

GAM281 278 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987. 3 B b

GAM281 278 GPR4 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation of three novel human genes encoding G protein- coupledreceptors. DNA Cell Biol. 14: 25- 35, 1995. 3 B b

GAM281 278 GPR4 Mahadevan, M. S.; Baird, S.; Bailly, J. E.; Shutler, G. G.; Sabourin,L. A.; Tsilfidis, C.; Neville, C. E.; Narang, M.; Korneluk, R. G.: Isolation of a novel G protein- coupled receptor (GPR4) localizedto chromosome 19q13.3. Genomics 30: 84- 88, 1995. 3 B b

GAM281 278 GPR4 Ye, R. D.; Prossnitz, E. R.; Zou, A.; Cochrane, C. G.: Characterizationof a human cDNA that encodes a functional receptor for platelet activatingfactor. Biochem. Biophys. Res. Commun. 180: 105- 111, 1991. 3 B b

GAM281 278 GPR4 Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina,K. L.; 3 B b

Kabarowski, J. H. S.; Witte, O. N.; Xu, Y.: Sphingosylphosphorylcholineand lysophosphatidylcholine are ligands for the G protein- coupledreceptor GPR4. J. Biol. Chem. 276: 41325- 41335, 2001.

GAM281 278 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a novel secretin- like human G- protein- coupledreceptor gene. Genomics 55: 296- 305, 1999. 3 B b

GAM281 278 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected with mRNA differential display using human melanoma celllines with different metastatic potential. FEBS Lett. 446: 292- 298,1999. 3 B b

GAM281 278 GPR61 Cikos, S.; Gregor, P.; Koppel, J.: Cloning of a novel biogenicamine receptor- like G protein- coupled receptor expressed in humanbrain. Biochim. Biophys. Acta 1521: 66- 72, 2001. 3 B c

GAM281 278 GPR61 Lee, D. K.; George, S. R.; Cheng, R.; Nguyen, T.; Liu, Y.; Brown,M.; Lynch, K. R.; O'Dowd, B. F.: Identification of four novel humanG protein- coupled receptors expressed in the brain. Molec. BrainRes. 86: 13- 22, 2001. 3 B c

GAM281 278 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann, S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in three cases of myelodysplastic syndrome/acutemyeloid leukemia with a deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000. 3 B b

GAM281 278 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain-containingGTPase- activating protein for Rho and Cdc42 associates with focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996. 3 B b

GAM281 278 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 B b

GAM281 278 GRINL1A Roginski, R. S.; Mohan Raj, B. K.; Finkernagel, S. W.; Sciorra,L. J.: Assignment of an ionotropic glutamate receptor- like gene (GRINL1A)to human chromosome 15q22.1 by in situ hybridization. Cytogenet.Cell Genet. 93: 143-144, 2001. 3 B b

GAM281 278 GRINL1A Wydner, K. S.; Mohan Raj, B. K.; Sciorra, L. J.; Roginski, R. S.: The mouse orthologue of the human ionotropic glutamate receptor- likegene (GRINL1A) maps to mouse chromosome 9. Cytogenet. Cell Genet. 95:240- 241, 2001. 3 B b

GAM281 278 GSTM1 Board, P. G.: Biochemical genetics of glutathione- S- transferasein man. Am. J. Hum. Genet. 33: 36- 43, 1981. 3 B c

GAM281 278 GSTM1 Board, P.; Coggan, M.; Johnston, P.; Ross, V.; Suzuki, T.; Webb,G.: Genetic heterogeneity of the human glutathione transferases:a complex of gene families. Pharm. Therap. 48: 357- 369, 1990. 3 B c

GAM281 278 GSTM1 Chen, C.- L.; Liu, Q.; Relling, M. V.: Simultaneous characterizationof glutathione S- transferase M1 and T1 polymorphisms by polymerasechain reaction in American whites and blacks. Pharmacogenetics 6:187- 191, 1996. 3 B c

GAM281 278 GSTM1 DeJong, J. L.; Chang, C.- M.; Whang- Peng, J.; Knutsen, T.; Tu, C.- P.D.: The human liver glutathione S- transferase gene superfamily: expressionand chromosome mapping of an H(b) subunit cDNA. Nucleic Acids Res. 16:8541-8554, 1988. 3 B c

GAM281 278 GSTM1 DeJong, J. L.; Mohandas, T.; Tu, C.- P. D.: The human H(b) (mu)class 3 B c

glutathione S- transferases are encoded by a dispersed gene family. Biochem.Biophys. Res. Commun. 180: 15- 22, 1991.

GAM281 278 GSTM1 Godschalk, R. W. L.; Dallinga, J. W.; Wikman, H.; Risch, A.; Kleinjans,J. C. 3 B c S.; Bartsch, H.; Van Schooten, F.- J.: Modulation of DNA andprotein adducts in smokers by genetic polymorphisms in GSTM1, GSTT1,NAT1 and NAT2. Pharmacogenetics 11: 389- 398, 2001.

GAM281 278 GSTM1 Harada, S.; Abei, M.; Tanaka, N.; Agarwal, D. P.; Goedde, H. W.: Liver 3 B c glutathione S- transferase polymorphism in Japanese and itspharmacogenetic importance. Hum. Genet. 75: 322- 325, 1987.

GAM281 278 GSTM1 Islam, M. Q.; Platz, A.; Szpirer, J.; Szpirer, C.; Levan, G.; Mannervik,B.: 3 B c Chromosomal localization of human glutathione transferase genesof classes alpha, mu and pi. Hum. Genet. 82: 338- 342, 1989.

GAM281 278 GSTM1 Lee, K. A.; Kim, S. H.; Woo, H. Y.; Hong, Y. J.; Cho, H. C.: 3 B c Increasedfrequencies of glutathione S- transferase (GSTM1 and GSTT1) gene deletionsin Korean patients with acquired aplastic anemia. Blood 98: 3483- 3485,2001.

GAM281 278 GSTM1 Mannervik, B.: The isozymes of glutathione transferase. Adv.Enzym. Relat. 3 B c Areas Molec. Biol. 57: 357- 417, 1985.

GAM281 278 GSTM1 Mannervik, B.; Awasthi, Y. C.; Board, P. G.; Hayes, J. D.; Dillio, C.; 3 B c Ketterer, B.; Listowsky, I.; Morgenstern, R.; Muramatsu,M.; Pearson, W. R.; Pickett, C. B.; Sato, K.; Widersten, M.; Wolf,R. C.: Nomenclature for human glutathione transferases. (Letter) Biochem.J. 282: 305- 306, 1992.

GAM281 278 GSTM1 McLellan, R. A.; Oscarson, M.; Alexandrie, A.- K.; Seidegard, J.;Evans, D. 3 B c A. P.; Rannug, A.; Ingelman- Sundberg, M.: Characterizationof a human glutathione S- transferase mu cluster containing a duplicatedGSTM1 gene that causes ultrarapid enzyme activity. Molec. Pharm. 52:958- 965, 1997.

GAM281 278 GSTM1 Pearson, W. R.; Vorachek, W. R.; Xu, S.; Berger, R.; Hart, I.;Vannais, D.; 3 B c Patterson, D.: Identification of class- mu glutathionetransferase genes GSTM1- GSTM5 on human chromosome 1p13. Am. J. Hum.Genet. 53: 220- 233, 1993.

GAM281 278 GSTM1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 B c New York: Oxford Univ. Press (pub.) 1988.

GAM281 278 GSTM1 Scott, E. M.; Wright, R. C.: Variability of glutathione S- transferaseof 3 B c human erythrocytes. Am. J. Hum. Genet. 32: 115- 117, 1980.

GAM281 278 GSTM1 Seidegard, J.; Pero, R. W.; Markowitz, M. M.; Roush, G.; Miller,D. G.; 3 B c Beattie, E. J.: Isoenzyme(s) of glutathione transferase (classmu) as a marker for the susceptibility to lung cancer: a follow upstudy. Carcinogenesis 11: 33- 36, 1990.

GAM281 278 GSTM1 Seidegard, J.; Pero, R. W.; Miller, D. G.; Beattie, E. J.: Aglutathione 3 B c transferase in human leukocytes as a marker for the susceptibilityto lung cancer. Carcinogenesis 7: 751- 753, 1986.

GAM281 278 GSTM1 Seidegard, J.; Vorachek, W. R.; Pero, R. W.; Pearson, W. R.:Hereditary 3 B c differences in the expression of the human glutathionetransferase active on trans- stilbene oxide are due to a gene deletion. Proc.Nat. Acad. Sci. 85: 7293- 7297, 1988.

GAM281 278 GSTM1 Strange, R. C.; Davis, B. A.; Faulder, C. G.; Cotton, W.; Bain,A. D.; 3 B c Hopkinson, D. A.; Hume, R.: The human glutathione S- transferases:developmental aspects of the GST1, GST2, and GST3 loci. Biochem.Genet. 23: 1011- 1028, 1985.

GAM281 278 GSTM1 Strange, R. C.; Faulder, C. G.; Davis, B. A.; Hume, R.; Brown,J. A. H.; 3 B c Cotton, W.; Hopkinson, D. A.: The human glutathione S- transferases:studies

on the tissue distribution and genetic variation of the GST1,GST2 and GST3 isozymes. Ann. Hum. Genet. 48: 11- 20, 1984.

GAM281 278 GSTM1 Strange, R. C.; Matharoo, B.; Faulder, G. C.; Jones, P.; Cotton,W.; Elder, J. B.; Deakin, M.: The human glutathione S- transferases:a case- control study of the incidence of the GST1 0 phenotype in patientswith adenocarcinoma. Carcinogenesis 12: 25- 28, 1991. 3 B c

GAM281 278 GSTM1 van Poppel, G.; de Vogel, N.; van Bladeren, P. J.; Kok, F. J.: Increased cytogenetic damage in smokers deficient in glutathioneS- transferase isozyme mu. Carcinogenesis 13: 303- 305, 1992. 3 B c

GAM281 278 GSTM1 Xu, S.; Wang, Y.; Roe, B.; Pearson, W. R.: Characterization ofthe human class mu glutathione S- transferase gene cluster and theGSTM1 deletion. J. Biol. Chem. 273: 3517- 3527, 1998. 3 B c

GAM281 278 GSTM1 Zhong, S.; Wolf, C. R.; Spurr, N. K.: Chromosomal assignmentand linkage analysis of the human glutathione S- transferase mu- gene(GSTM1) using intron specific polymerase chain reaction. Hum. Genet. 90:435- 439, 1992. 3 B c

GAM281 278 GSTM1 Zhong, S.; Wyllie, A. H.; Barnes, D.; Wolf, C. R.; Spurr, N. K.: Relationship between the GSTM1 genetic polymorphism and susceptibilityto bladder, breast and colon cancer. Carcinogenesis 14: 1821- 1824,1993. 3 B c

GAM281 278 GSTM4 Comstock, K. E.; Johnson, K. J.; Rifenbery, D.; Henner, W. D.:Isolation and analysis of the gene and cDNA for a human mu class glutathioneS- transferase, GSTM4. J. Biol. Chem. 268: 16958- 16965, 1993. 3 B c

GAM281 278 GSTM4 Ross, V. L.; Board, P. G.: Molecular cloning and heterologousexpression of an alternatively spliced human mu class glutathioneS- transferase transcript. Biochem. J. 294: 373- 380, 1993. 3 B c

GAM281 278 GSTM4 Ross, V. L.; Board, P. G.; Webb, G. C.: Chromosomal mapping ofthe human mu class glutathione S- transferases to 1p13. Genomics 18:87- 91, 1993. 3 B c

GAM281 278 GSTM4 Taylor, J. B.; Oliver, J.; Sherrington, R.; Pemble, S. E.: Structureof human glutathione S- transferase class mu genes. Biochem. J. 274:587- 593, 1991. 3 B c

GAM281 278 GYG Barbetti, F.; Rocchi, M.; Bossolasco, M.; Cordera, R.; Sbraccia,P.; Finelli, P.; Consalez, G. G.: The human skeletal muscle glycogeningene: cDNA, tissue expression, and chromosomal localization. Biochem.Biophys. Res. Commun. 220: 72- 77, 1996. 3 B b

GAM281 278 GYG Lomako, J.; Mazuruk, K.; Lomako, W. M.; Alonso, M. D.; Whelan,W. J.; Rodriguez, I. R.: The human intron- containing gene for glycogeninmaps to chromosome 3, band q24. Genomics 33: 519- 522, 1996. 3 B b

GAM281 278 GYG Mu, J.; Skurat, A. V.; Roach, P. J.: Glycogenin- 2, a novel self- glucosylatingprotein involved in liver glycogen biosynthesis. J. Biol. Chem. 272:27589- 27597, 1997. 3 B b

GAM281 278 GYG Viskupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; DePaoli- Roach, A.A.; Roach, P. J.: Rabbit skeletal muscle glycogenin. Molecular cloningand production of fully functional protein in Escherichia coli. J.Biol. Chem. 267: 25759- 25763, 1992. 3 B b

GAM281 278 HCK Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J. M.; Pettenati,M. J.; Le Beau, M. M.; Diaz, M. O.; Rowley, J. D.: Identificationof a human gene (HCK) that encodes a protein- tyrosine kinase and isexpressed in hemopoietic cells. Molec. Cell. Biol. 7: 2267- 2275,1987. 3 B c

GAM281 278 HCK Ziegler, S. F.; Marth, J. D.; Lewis, D. B.; Perlmutter, R. M.:Novel protein- tyrosine kinase gene (hck) preferentially expressedin cells of hematopoietic origin. Molec. Cell. Biol. 7: 2276- 2285,1987. 3 B c

GAM281 278 HEPH Anderson, G. J.; Murphy, T. L.; Cowley, L.; Evans, B. A.; Halliday,J. W.; 3 B c
McLaren, G. D.: Mapping the gene for sex- linked anemia: aninherited defect
of intestinal iron absorption in the mouse. Genomics 48:34- 39, 1998.

GAM281 278 HEPH Bannerman, R. M.: Genetic defects of iron transport. Fed. Proc. 35:2281- 3 B c
2285, 1976.

GAM281 278 HEPH Edwards, J. A.; Hoke, J. E.; Mattioli, M.; Reichlin, M.: 3 B c
Ferritindistribution and synthesis in sex- linked anemia. J. Lab. Clin. Med.
90:68- 76, 1977.

GAM281 278 HEPH Falconer, D. S.; Isaacson, J. H.: The genetics of sex- linked anaemiain the 3 B c
mouse. Genet. Res. 3: 248- 250, 1962.

GAM281 278 HEPH Grewal, M. S.: A sex- linked anaemia in the mouse. Genet. Res. 3:238- 247, 3 B c
1962.

GAM281 278 HEPH Lee, G. R.; Nacht, S.; Lukens, J. N.; Cartwright, G. E.: Ironmetabolism in 3 B c
copper- deficient swine. J. Clin. Invest. 47: 2058- 2069,1968.

GAM281 278 HEPH Vulpe, C. D.; Kuo, Y.- M.; Murphy, T. L.; Cowley, L.; Askwith, C.;Libina, 3 B c
N.; Gitschier, J.; Anderson, G. J.: Hephaestin, a ceruloplasminhomologue
implicated in intestinal iron transport, is defective inthe sla mouse.
Nature Genet. 21: 195- 199, 1999.

GAM281 278 HTR1D Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S. J.; Duncan,A. M. V.; 3 B c
Rozmahel, R.; Yang, Y.; Mengod, G.; Palacios, J. M.; O'Dowd,B. F.:
Characterization of the human 5- hydroxytryptamine(1B) receptor. J.Biol.
Chem. 267: 5735- 5738, 1992.

GAM281 278 HTR1D Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 B c
M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor,
and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991.

GAM281 278 HTR1D Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T.A.; Hartig, P. 3 B c
R.: Human serotonin 1D receptor is encoded by a subfamilyof two distinct
genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat.Acad. Sci. 89: 3630-
3634, 1992.

GAM281 278 HTR1D Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; 3 B c
Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and
genome organization of mammalian G- protein- coupled receptors. Genomics
18:175- 184, 1993.

GAM281 278 HTR1E Levy, F. O.; Gudermann, T.; Birnbaumer, M.; Kaumann, A. J.; Birnbaumer,L.: 3 B c
Molecular cloning of a human gene (S31) encoding a novel serotoninreceptor
mediating inhibition of adenylyl cyclase. FEBS Lett. 296:201- 206, 1992.

GAM281 278 HTR1E Levy, F. O.; Holtgreve- Grez, H.; Tasken, K.; Solberg, R.; Ried,T.; 3 B c
Gudermann, T.: Assignment of the gene encoding the 5- HT- 1E
serotoninreceptor (S31) (locus HTR1E) to human chromosome 6q14- q15.
Genomics 22:637- 640, 1994.

GAM281 278 HTR1E McAllister, G.; Charlesworth, A.; Snodin, C.; Beer, M. S.; Noble,A. J.; 3 B c
Middlemiss, D. N.; Iversen, L. L.; Whiting, P.: Molecularcloning of a
serotonin receptor from human brain (5HT1E): a fifth5HT1- like subtype.
Proc. Nat. Acad. Sci. 89: 5517- 5521, 1992.

GAM281 278 HTR3B Davies, P. A.; Pistis, M.; Hanna, M. C.; Peters, J. A.; Lambert,J. J.; 3 B c
Hales, T. G.; Kirkness, E. F.: The 5- HT(3B) subunit is a majordeterminant
of serotonin- receptor function. Nature 397: 359- 363,1999.

GAM281 278 HTR3B Dubin, A. E.; Huvar, R.; D'Andrea, M. R.; Pyati, J.; Zhu, J. Y.;Joy, K. C.; 3 B c
Wilson, S. J.; Galindo, J. E.; Glass, C. A.; Luo, L.;Jackson, M. R.;
Lovenberg, T. W.; Erlander, M. G.: The pharmacologicaland functional

characteristics of the serotonin 5- HT(3A) receptorare specifically modified by a 5- HT(3B) receptor subunit. J. Biol.Chem. 274: 30799- 30810, 1999.

GAM281 278 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998. 3 B c

GAM281 278 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol-Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay. Genomics 54: 278- 286, 1998. 3 B c

GAM281 278 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated in response to DNA damage. EMBO J. 17: 2055- 2066,1998. 3 B c

GAM281 278 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999. 3 B c

GAM281 278 HYAL1 Csoka, T. B.; Frost, G. I.; Heng, H. H. Q.; Scherer, S. W.; Mohapatra,G.; Stern, R.: The hyaluronidase gene HYAL1 maps to chromosome 3p21.2- p21.3in human and 9F1- F2 in mouse, a conserved candidate tumor suppressorlocus. Genomics 48: 63- 70, 1998. 3 B c

GAM281 278 HYAL1 Frost, G. I.; Csoka, T. B.; Wong, T.; Stern, R.: Purification,cloning, and expression of human plasma hyaluronidase. Biochem. Biophys.Res. Commun. 236: 10- 15, 1997. 3 B c

GAM281 278 HYAL1 Laurent, T. C.; Fraser, J. R. E.: Hyaluronan. FASEB J. 6: 2397- 2404,1992. 3 B c

GAM281 278 HYAL1 Lerman, M. I.; Minna, J. D.: The 630- kb lung cancer homozygousdeletion region on human chromosome 3p21.3: identification and evaluationof the resident candidate tumor suppressor genes. Cancer Res. 60:6116- 6133, 2000. 3 B c

GAM281 278 HYAL1 Natowicz, M. R.; Short, M. P.; Wang, Y.; Dickersin, G. R.; Gebhardt,M. C.; Rosenthal, D. I.; Sims, K. B.; Rosenberg, A. E.: Clinicaland biochemical manifestations of hyaluronidase deficiency. New Eng.J. Med. 335: 1029- 1033, 1996. 3 B c

GAM281 278 HYAL1 Triggs- Raine, B.; Salo, T. J.; Zhang, H.; Wicklow, B. A.; Natowicz,M. R.: Mutations in HYAL1, a member of a tandemly distributed multigenefamily encoding disparate hyaluronidase activities, cause a newlydescribed lysosomal disorder, mucopolysaccharidosis IX. Proc. Nat.Acad. Sci. 96: 6296- 6300, 1999. 3 B c

GAM281 278 ICAM1 Ballantyne, C. M.; Kozak, C. A.; O'Brien, W. E.; Beaudet, A. L.: Assignment of the gene for intercellular adhesion molecule- 1 (Icam- 1)to proximal mouse chromosome 9. Genomics 9: 547- 550, 1991. 3 B b

GAM281 278 ICAM1 Bella, J.; Kolatkar, P. R.; Marlor, C. W.; Greve, J. M.; Rossmann,M. G.: The structure of the two amino- terminal domains of human ICAM- 1suggests how it functions as a rhinovirus receptor and as an LFA- 1integrin ligand. Proc. Nat. Acad. Sci. 95: 4140- 4145, 1998. 3 B b

GAM281 278 ICAM1 Bellamy, R.; Kwiatkowski, D.; and Hill, A. V. S.: Absence of anassociation between intercellular adhesion molecule 1, complementreceptor 1 and interleukin 1 receptor antagonist gene polymorphismsand severe malaria in a West African population. Trans. R. Soc. Trop.Med. Hyg. 92: 312- 316, 1998. 3 B b

GAM281 278 ICAM1 Craig, A.; Fernandez- Reyes, D.; Mesri, M.; McDowall, A.; Altieri,D. C.; Hogg, N.; Newbold, C.: A functional analysis of a naturalvariant of intercellular adhesion molecule- 1 (ICAM- 1- Kilifi). Hum.Molec. Genet. 9: 525- 530, 2000. 3 B b

GAM281 278 ICAM1 Fernandez- Reyes, D.; Craig, A. G.; Kyes, S. A.; Peshu, N.; Snow,R. W.; 3 B b
Berendt, A. R.; Marsh, K.; Newbold, C. I.: A high frequencyAfrican coding
polymorphism in the N- terminal domain of ICAM- 1 predisposingto cerebral
malaria in Kenya. Hum. Molec. Genet. 6: 1357- 1360, 1997.

GAM281 278 ICAM1 Greve, J. M.; Davis, G.; Meyer, A. M.; Forte, C. P.; Yost, S. C.;Marlor, C. 3 B b
W.; Kamarck, M. E.; McClelland, A.: The major human rhinovirusreceptor is
ICAM- 1. Cell 56: 839- 847, 1989.

GAM281 278 ICAM1 Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. 3 B b
Phys. 111: 272- 277, 1999.

GAM281 278 ICAM1 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, 3 B b
M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B
cells. Europ. J. Immun. 15: 103- 106, 1985.

GAM281 278 ICAM1 Le Beau, M. M.; Ryan, D., Jr.; Pericak- Vance, M. A.: Report ofthe committee 3 B b
on the genetic constitution of chromosomes 18 and 19. Cytogenet.Cell Genet.
51: 338- 357, 1989.

GAM281 278 ICAM1 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in 3 B b
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM281 278 ICAM1 Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot- 3 B b
Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow
cytometricanalysis of conjunctival epithelium in ocular rosacea and
keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000.

GAM281 278 ICAM1 Prieto, J.; Takei, F.; Gendelman, R.; Christenson, B.; Biberfeld,P.; 3 B b
Patarroyo, M.: MALA- 2, mouse homologue of human adhesion moleculeICAM- 1
(CD54). Europ. J. Immun. 19: 1551- 1557, 1989.

GAM281 278 ICAM1 Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal 3 B b
mouse chromosome 9 linkage map that further defines linkagegroups homologous
with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685,
1991.

GAM281 278 ICAM1 Simmons, D.; Makgoba, M. W.; Seed, B.: ICAM, an adhesion ligandof LFA- 1, is 3 B b
homologous to the neural cell adhesion molecule NCAM. Nature 331:624- 627,
1988.

GAM281 278 ICAM1 Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H.K.; Smith, C. 3 B b
W.; Bradley, A.; Beaudet, A. L.: Inflammatory and immuneresponses are
impaired in mice deficient in intercellular adhesionmolecule 1. Proc. Nat.
Acad. Sci. 90: 8529- 8533, 1993.

GAM281 278 ICAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 B b
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM281 278 ICAM1 Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; 3 B b
Takeuchi, T.: Regulation of human leukocyte antigenexpression in human
conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999.

GAM281 278 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 B b
M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like
growth factor- I and cognitive function inhealthy older men. J. Clin.
Endocr. Metab. 84: 471- 475, 1999.

GAM281 278 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- 3 B b
like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993.

GAM281 278 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and 3 B b

absence of association with stature among African Pygmies. Hum.Genet. 85: 349- 354, 1990.

GAM281 278 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for 3 B b insulin- like growth factors I and II and for epidermalgrowth factor in man. (Abstract) Am. J. Hum. Genet. 36: 133S only,1984.

GAM281 278 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of 3 B b genes for insulin- like growth factors I and II and epidermalgrowth factor. Nature 310: 781- 784, 1984.

GAM281 278 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, 3 B b A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of recombinant human insulin- like growth factor I(IGF- I) therapy on the growth hormone- IGF system of a patient witha partial IGF- I gene deletion. J. Clin. Endocr. Metab. 84: 1611- 1616,1999.

GAM281 278 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; 3 B b Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of the growth hormone receptor in children with idiopathicshort stature. New Eng. J. Med. 333: 1093- 1098, 1995.

GAM281 278 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; 3 B b Froesch, E. R.: Small stature and insulin- like growth factors:prolonged treatment of mini- poodles with recombinant human insulin- likegrowth factor I. Acta Endocr. 121: 456- 464, 1989.

GAM281 278 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. 3 B b S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating concentrations of insulin- like growth factor- I and riskof breast cancer. Lancet 351: 1393- 1396, 1998.

GAM281 278 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: 3 B b Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding protein- 3, and prostate- specific antigen as predictorsof clinical prostate cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000.

GAM281 278 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; 3 B b Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith, D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival signaling in retinal endothelial cells: direct correlationwith clinical retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001.

GAM281 278 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer 3 B b prevention. Lancet 351: 1373- 1375, 1998.

GAM281 278 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; 3 B b Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J. S.: The human gene encoding insulin- like growthfactor I is located on chromosome 12. Hum. Genet. 69: 157- 160, 1985.

GAM281 278 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, 3 B b J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990.

GAM281 278 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete 3 B b characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986.

GAM281 278 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; 3 B b Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF-

1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996.

GAM281 278 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: 3 B b
Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat.
Acad. Sci. 80: 2216- 2220, 1983.

GAM281 278 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; 3 B b
Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand
implications for cell type- specific growth. Nature 364: 208- 213,1993.

GAM281 278 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: 3 B b
Mice carrying null mutations of the genes encoding insulin- likegrowth
factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993.

GAM281 278 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like 3 B b
growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83:
9343- 9347, 1986.

GAM281 278 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human 3 B b
genes for insulin- like growth factors I and II and epidermalgrowth factor
are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively.
Cytogenet.Cell Genet. 41: 245- 249, 1986.

GAM281 278 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 3 B b
1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2
(IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985.

GAM281 278 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. 3 B b
D.: Growth characteristics and response to growth hormonetherapy in patients
with hypochondroplasia: genetic linkage of theinsulin- like growth factor I
gene at chromosome 12q23 to the diseasein a subgroup of these patients.
Clin. Endocr. 34: 265- 274, 1991.

GAM281 278 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: 3 B b
IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin
association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999.

GAM281 278 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, 3 B b
M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene
expression sustains hypertrophy and regeneration insenescent skeletal
muscle. Nature Genet. 27: 195- 200, 2001.

GAM281 278 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like 3 B b
growth factor 1 regulates the location, stability,and transcriptional
activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000.

GAM281 278 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, 3 B b
S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal
embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993.

GAM281 278 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the 3 B b
protein which binds insulin- like growth factor in human serum. Europ.J.
Biochem. 172: 421- 425, 1988.

GAM281 278 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; 3 B b
Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith,
R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the
insulin- like growth factor I receptor and its ligandin relation to type 2
diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000.

GAM281 278 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed 3 B b
in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986.

GAM281 278 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; 3 B b
Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I)

reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991.

GAM281 278 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; 3 B b
Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999.

GAM281 278 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. 3 B b
E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980.

GAM281 278 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like 3 B b
growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 1991.

GAM281 278 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- 3 B b
like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984.

GAM281 278 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: 3 B b
Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984.

GAM281 278 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of 3 B b
the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984.

GAM281 278 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; 3 B b
Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-857,1992.

GAM281 278 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; 3 B b
Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002.

GAM281 278 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand 3 B b
assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980.

GAM281 278 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish 3 B b
Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999.

GAM281 278 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. 3 B b
L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy on body composition and insulin resistance in IGF- Igene deletion. J. Clin. Endocr. Metab. 85: 1407- 1411, 2000.

GAM281 278 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 3 B b
Intrauterine growth retardation and postnatal growth failureassociated with deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335: 1363- 1367, 1996.

GAM281 278 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 3 B b
regional localization of human genes for insulin- like growthfactors I (IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell

Genet. 40: 782 only, 1985.

GAM281 278 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 3 B b
growth factors and bone mineral density in African Americanand white girls.
J. Pediat. 137: 826- 832, 2000.

GAM281 278 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 3 B b
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM281 278 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 B b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM281 278 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 B b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM281 278 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 B b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814-
819, 1992.

GAM281 278 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 B b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang,
Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell-
derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87:
7512- 7516, 1990.

GAM281 278 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 3 B b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract)
Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM281 278 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, 3 B b
sequence, expression, and processing of the interleukin 16precursor. Proc.
Nat. Acad. Sci. 94: 5273- 5277, 1997.

GAM281 278 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 3 B b
381: 30 only, 1996.

GAM281 278 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 3 B b
16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics
49:704- 706, 1999.

GAM281 278 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. 3 B b
C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte
chemoattractant factor: association of biologic functionwith CD4 expression.
Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994.

GAM281 278 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human 3 B b
lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128:
2569- 2574, 1982.

GAM281 278 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS 3 B b
human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311-
314, 1993.

GAM281 278 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; 3 B b
Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M.
E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945-
1954, 1995.

GAM281 278 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; 3 B b
Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure
and function between human and murine IL- 16. J. Immun. 160:5945- 5954,
1998.

GAM281 278 IL21R Asao, H.; Okuyama, C.; Kumaki, S.; Ishii, N.; Tsuchiya, S.; Foster,D.; 3 B b
Sugamura, K.: Cutting edge: the common gamma- chain is an
indispensablesubunit of the IL- 21 receptor complex. J. Immun. 167: 1- 5,

2001.

GAM281 278 IL21R Kasaian, M. T.; Whitters, M. J.; Carter, L. L.; Lowe, L. D.; Jussif,J. M.; 3 B b
Deng, B.; Johnson, K. A.; Witek, J. S.; Senices, M.; Konz,R. F.; Wurster, A.
L.; Donaldson, D. D.; Collins, M.; Young, D. A.;Grusby, M. J.: IL- 21 limits
NK cell responses and promotes antigen- specificT cell activation: a
mediator of the transition from innate to adaptiveimmunity. Immunity 16:
559- 569, 2002.

GAM281 278 IL21R Ozaki, K.; Kikly, K.; Michalovich, D.; Young, P. R.; Leonard, W.J.: Cloning 3 B b
of a type I cytokine receptor most related to the IL- 2receptor beta chain.
Proc. Nat. Acad. Sci. 97: 11439- 11444, 2000.

GAM281 278 IL21R Parrish- Novak, J.; Dillon, S. R.; Nelson, A.; Hammond, A.; Sprecher,C.; 3 B b
Gross, J. A.; Johnston, J.; Madden, K.; Xu, W.; West, J.; Schrader,S.;
Burkhead, S.; and 26 others: Interleukin 21 and its receptorare involved in
NK cell expansion and regulation of lymphocyte function. Nature 408:57- 63,
2000.

GAM281 278 IL21R Ueda, C.; Akasaka, T.; Kurata, M.; Maesako, Y.; Nishikori, M.;Ichinohasama, 3 B b
R.; Imada, K.; Uchiyama, T.; Ohno, H.: The gene forinterleukin- 21 receptor
is the partner of BCL6 in t(13;16)(q27;p11),which is recurrently observed in
diffuse large B- cell lymphoma. Oncogene 21:368- 376, 2002.

GAM281 278 IRTA2 Hatzivassiliou, G.; Miller, I.; Takizawa, J.; Palanisamy, N.; Rao,P. H.; 3 B c
Iida, S.; Tagawa, S.; Taniwaki, M.; Russo, J.; Neri, A.; Cattoretti,G.;
Clynes, R.; Mendelsohn, C.; Chaganti, R. S. K.; Dalla- Favera,R.: IRTA1 and
IRTA2, novel immunoglobulin superfamily receptors expressedin B cells and
involved in chromosome 1q21 abnormalities in B cellmalignancy. Immunity 14:
277- 289, 2001.

GAM281 278 IRTA2 Nakayama, Y.; Weissman, S. M.; Bothwell, A. L. M.: BXMAS1 identifiesa 3 B c
cluster of homologous genes differentially expressed in B cells.
Biochem.Biophys. Res. Commun. 285: 830- 837, 2001.

GAM281 278 ITGAM Arnaout, M. A.; Gupta, S. K.; Pierce, M. W.; Tenen, D. G.: Aminoacid 3 B c
sequence of the alpha subunit of human leukocyte adhesion receptorMo1
(complement receptor type 3). J. Cell Biol. 106: 2153- 2158,1988.

GAM281 278 ITGAM Arnaout, M. A.; Remold- O'Donnell, E.; Pierce, M. W.; Harris, P.;Tenen, D. 3 B c
G.: Molecular cloning of the alpha- subunit of human andguinea pig leukocyte
adhesion glycoprotein Mo1: chromosomal localizationand homology to the
alpha- subunits of integrins. Proc. Nat. Acad.Sci. 85: 2776- 2780, 1988.

GAM281 278 ITGAM Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; 3 B c
Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P.
G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome
16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991.

GAM281 278 ITGAM Corbi, A. L.; Kishimoto, T. K.; Miller, L. J.; Springer, T. A.: The human 3 B c
leukocyte adhesion glycoprotein Mac- 1 (complement receptortype 3, CD11b)
alpha subunit: cloning, primary structure, and relationto the integrins, von
Willebrand factor and factor B. J. Biol. Chem. 263:12403- 12411, 1988.

GAM281 278 ITGAM Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. 3 B c
C.: Chromosomal location of the genes encoding the leukocyteadhesion
receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster
involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988.

GAM281 278 ITGAM Pierce, M. W.; Remold- O'Donnell, E.; Todd, R. F., III; Arnaout,M. A.: N- 3 B c
terminal sequence of human leukocyte glycoprotein Mo1: conservationacross
species and homology to platelet IIb/IIIa. Biochim. Biophys.Acta 874: 368-

371, 1986.

GAM281 278 ITGAM Simon, D. I.; Chen, Z.; Seifert, P.; Edelman, E. R.; Ballantyne,C. M.; Rogers, C.: Decreased neointimal formation in Mac- 1 - /- micereveals a role for inflammation in vascular repair after angioplasty. J.Clin. Invest. 105: 293- 300, 2000. 3 B c

GAM281 278 ITGAM Springer, T. A.; Teplow, D. B.; Dreyer, W. J.: Sequence homologyof the LFA- 1 and Mac- 1 leukocyte adhesion glycoproteins and unexpectedrelation to leukocyte interferon. Nature 314: 540- 542, 1985. 3 B c

GAM281 278 JRK Morita, R.; Miyazaki, E.; Fong, C. G.; Chen, X.- N.; Korenberg,J. R.; Delgado- Escueta, A. V.; Yamakawa, K.: JH8, a gene highly homologousto the mouse jerky gene, maps to the region for childhood absenceepilepsy on 8q24. Biochem. Biophys. Res. Commun. 248: 307- 314, 1998. 3 B b

GAM281 278 JRK Toth, M.; Grimsby, J.; Buzsaki, G.; Donovan, G. P.: Epilepticseizures caused by inactivation of a novel gene, jerky, related tocentromere binding protein- B in transgenic mice. Nature Genet. 11:71- 75, 1995. Note: Erratum: Nature Genet. 12: 110 only, 1996. 3 B b

GAM281 278 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel genes. Trends Pharm. Sci. 14: 434, 1993. 3 B b

GAM281 278 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011- 1017, 1996. 3 B b

GAM281 278 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166- 1170, 1995. 3 B b

GAM281 278 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: Targeted overactivity of beta cell KATP channels induces profoundneonatal diabetes. Cell 100: 645- 654, 2000. 3 B b

GAM281 278 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: Homozygositymapping, to chromosome 11p, of the gene for familial persistent hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421, 1995. 3 B b

GAM281 278 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward rectifier Kir6.2 also leads to familial persistent hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812, 1996. 3 B b

GAM281 278 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium channels in hypoxia- induced generalized seizure. Science 292:1543- 1546, 2001. 3 B b

GAM281 278 KCNK3 Duprat, F.; Lesage, F.; Fink, M.; Reyes, R.; Heurteaux, C.; Lazdunski,M.: TASK, a human background K+ channel to sense external pH variationsnear physiological pH. EMBO J. 16: 5464- 5471, 1997. 3 B c

GAM281 278 KCNK3 Lesage, F.; Lazdunski, M.: Mapping of human potassium channelgenes TREK- 1 (KCNK2) and TASK (KCNK3) to chromosomes 1q41 and 2p23. Genomics 51:478- 479, 1998. 3 B c

GAM281 278 KCNK3 Manjunath, N. A.; Bray- Ward, P.; Goldstein, S. A. N.; Gallagher,P. G.: 3 B c

Assignment of the 2P domain, acid- sensitive potassium channelOAT1 gene KCNK3 to human chromosome bands 2p24.1- p23.3 and murine5B by in situ hybridization. Cytogenet. Cell Genet. 86: 242- 243,1999.

GAM281 278 KLRD1 Braud, V. M.; Allan, D. S. J.; O'Callaghan, C. A.; Soderstrom,K.; D'Andrea, A.; Ogg, G. S.; Lazetic, S.; Young, N. T.; Bell, J.I.; Phillips, J. H.; Lanier, L. L.; McMichael, A. J.: HLA- E bindsto natural killer cell receptors CD94/NKG2A, B and C. Nature 391:795- 799, 1998. 3 B b

GAM281 278 KLRD1 Chang, C.; Rodriguez, A.; Carretero, M.; Lopez- Botet, M.; Phillips,J. H.; Lanier, L. L.: Molecular characterization of human CD94: atype II membrane glycoprotein related to the C- type lectin superfamily. Europ.J. Immun. 25: 2433- 2437, 1995. 3 B b

GAM281 278 KLRD1 Lazetic, S.; Chang, C.; Houchins, J. P.; Lanier, L. L.; Phillips,J. H.: Human natural killer cell receptors involved in MHC classI recognition are disulfide- linked heterodimers of CD94 and NKG2 subunits. J.Immun. 157: 4741- 4745, 1996. 3 B b

GAM281 278 KLRD1 Plougastel, B.; Trowsdale, J.: Sequence analysis of a 62- kb regionoverlapping the human KLRC cluster of genes. Genomics 49: 193- 199,1998. 3 B b

GAM281 278 KLRD1 Rodriguez, A.; Carretero, M.; Glienke, J.; Bellon, T.; Ramirez,A.; Lehrach, H.; Francis, F.; Lopez- Botet, M.: Structure of the humanCD94 C- type lectin gene. Immunogenetics 47: 305- 309, 1998. 3 B b

GAM281 278 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; Malherbe, P.: Cloning and functional expression of human kynurenine3- monooxygenase. FEBS Lett. 410: 407- 412, 1997. 3 B b

GAM281 278 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001. 3 B b

GAM281 278 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000. 3 B c

GAM281 278 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000. 3 B c

GAM281 278 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363- 18367,1996. 3 B b

GAM281 278 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994. 3 B b

GAM281 278 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. Nature 384: 39- 43, 1996. 3 B b

GAM281 278 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- specifictranscriptional regulation of human leukotriene B4 receptor gene. 3 B b

J.Exp. Med. 192: 413- 420, 2000.

GAM281 278 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 3 B b
chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM281 278 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 3 B b
Leukotrienes and lipoxins: structures, biosynthesis,and biological effects.
Science 237: 1171- 1176, 1987.

GAM281 278 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 B b
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene
and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-
130, 1997.

GAM281 278 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 3 B b
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature
387:620- 624, 1997.

GAM281 278 LYZ Camara, V. M.; Harding, J. W.; Prieur, D. J.: Inherited lysozymedeficiency 3 B b
in rabbits: the absence of a primary isozyme of lysozymeas the cause of the
condition. Lab. Invest. 63: 544- 550, 1990.

GAM281 278 LYZ Canet, D.; Sunde, M.; Last, A. M.; Miranker, A.; Spencer, A.; Robinson,C. 3 B b
V.; Dobson, C. M.: Mechanistic studies of the folding of humanlysozyme and
the origin of amyloidogenic behavior in its disease- relatedvariants.
Biochemistry 38: 6419- 6427, 1999.

GAM281 278 LYZ Dayhoff, M. O.: Atlas of Protein Sequence and Structure. Lactalbuminand 3 B b
Lysozyme. Washington: National Biomedical Research Foundation(pub.) 5:
1972. Pp. D133- D140.

GAM281 278 LYZ Fleming, A.: On a remarkable bacteriolytic element found in tissuesand 3 B b
secretions. Proc. Roy. Soc. Ser. B. 93: 306- 317, 1922.

GAM281 278 LYZ Fleming, A.; Allison, V. D.: Observations on a bacteriolytic 3 B b
substance('lysozyme') found in secretions and tissues. Brit. J. Exp. Path.
3:252- 260, 1922.

GAM281 278 LYZ Greenwald, R. A.; Cantor, J. O.; Prieur, D. J.; Young, D. M.:Composition of 3 B b
cartilage from lysozyme- deficient rabbits. Biochim.Biophys. Acta 385: 435-
437, 1975.

GAM281 278 LYZ Neufeld, E. L.: Personal Communication. Bethesda, Maryland 1972. 3 B b

GAM281 278 LYZ Pepys, M. B.; Hawkins, P. N.; Booth, D. R.; Vigushin, D. M.; Tennent,G. A.; 3 B b
Soutar, A. K.; Totty, N.; Nguyen, O.; Blake, C. C. F.; Terry,C. J.; Feest,
T. G.; Zalin, A. M.; Hsuan, J. J.: Human lysozyme genemutations cause
hereditary systemic amyloidosis. Nature 362: 553- 557,1993.

GAM281 278 LYZ Peters, C. W. B.; Kruse, U.; Pollwein, R.; Grzeschik, K.- H.; Sippel,A. E.: 3 B b
The human lysozyme gene: sequence organization and chromosomallocalization.
(Abstract) Cytogenet. Cell Genet. 51: 1059 only, 1989.

GAM281 278 LYZ Prieur, D. J.: Personal Communication. Pullman, Washington 5/13/1975. 3 B b

GAM281 278 LYZ Prieur, D. J.; Olson, H. M.; Young, D. M.: Lysozyme deficiency- - 3 B b
aninherited disorder of rabbits. Am. J. Path. 77: 283- 296, 1974.

GAM281 278 LYZ Spitznagel, J. K.; Cooper, M. R.; McCall, A. E.; DeChatelet, L.R.; Welsh, I. 3 B b
R.: Selective deficiency of granules associated withlysozyme and lactoferrin
in human polymorphs (PMN) with reduced microbicidalcapacity. (Abstract) J.
Clin. Invest. 51: 93A only, 1972.

GAM281 278 LYZ Taniyama, Y.; Kuroki, R.; Omura, F.; Seko, C.; Kikuchi, M.: Evidencefor 3 B b
intramolecular disulfide bond shuffling in the folding of mutanthuman
lysozyme. J. Biol. Chem. 266: 6456- 6461, 1991.

GAM281 278 LYZ Yoshimura, K.; Toibana, A.; Nakahama, K.: Human lysozyme: sequencingof a 3 B b

cDNA, and expression and secretion by Saccharomyces cerevisiae. Biochem.Biophys. Res. Commun. 150: 794- 801, 1988.

GAM281 278 LYZ Zalin, A. M.; Jones, S.; Fitch, N. J. S.; Ramsden, D. B.: 3 B b
Familialnephropathic non- neuropathic amyloidosis: clinical features, immunohistochemistryand chemistry. Quart. J. Med. 81: 945- 956, 1991.

GAM281 278 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 B b
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM281 278 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 B b
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001.

GAM281 278 MADD Chow, V. T. K.; Lee, S. S.: DENN, a novel human gene differentiallyexpressed 3 B c
in normal and neoplastic cells. DNA Seq. 6: 263- 273, 1996.

GAM281 278 MADD Chow, V. T. K.; Lim, K. M.; Lim, D.: The human DENN gene: 3 B c
genomicorganization, alternative splicing, and localization to chromosome11p11.21- p11.22. Genome 41: 543- 552, 1998.

GAM281 278 MADD Schievella, A. R.; Chen, J. H.; Graham, J. R.; Lin, L.- L.: MADD,a novel 3 B c
death domain protein that interacts with the type 1 tumornecrosis factor receptor and activates mitogen- activated protein kinase. J.Biol. Chem. 272: 12069- 12075, 1997.

GAM281 278 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein 3 B b
kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990.

GAM281 278 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. 3 B b
F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994.

GAM281 278 MAP2K1 Brott, B. K.; Alessandrini, A.; Largaespada, D. A.; Copeland, N.G.; Jenkins, 3 B c
N. A.; Crews, C. M.; Erikson, R. L.: MEK2 is a kinaserelated to MEK1 and is differentially expressed in murine tissues. CellGrowth Differ. 4: 921- 929, 1993.

GAM281 278 MAP2K1 Crews, C. M.; Alessandrini, A.; Erikson, R. L.: The primary structureof MEK, 3 B c
a protein kinase that phosphorylates the ERK gene product. Science 258:478- 480, 1992.

GAM281 278 MAP2K1 Favata, M. F.; Horiuchi, K. Y.; Manos, E. J.; Daulerio, A. J.;Stradley, D. 3 B c
A.; Feeser, W. S.; Van Dyk, D. E.; Pitts, W. J.; Earl,R. A.; Hobbs, F.; Copeland, R. A.; Magolda, R. L.; Scherle, P. A.;Trzaskos, J. M.: Identification of a novel inhibitor of mitogen- activatedprotein kinase kinase. J. Biol. Chem. 273: 18623- 18632, 1998.

GAM281 278 MAP2K1 Meloche, S.; Gopalbhai, K.; Beatty, B. G.; Scherer, S. W.; Pellerin,J.: 3 B c
Chromosome mapping of the human genes encoding the MAP kinasekinase MEK1 (MAP2K1) to 15q21 and MEK2 (MAP2K2) to 7q32. Cytogenet.Cell Genet. 88: 249- 252, 2000.

GAM281 278 MAP2K1 Orth, K.; Palmer, L. E.; Bao, Z. Q.; Stewart, S.; Rudolph, A. E.;Bliska, J. 3 B c
B.; Dixon, J. E.: Inhibition of the mitogen- activatedprotein kinase kinase superfamily by a Yersinia effector. Science 285:1920- 1923, 1999.

GAM281 278 MAP2K1 Perry, R. L. S.; Parker, M. H.; Rudnicki, M. A.: Activated MEK1binds the 3 B c
nuclear MyoD transcriptional complex to repress transactivation. Molec.Cell 8: 291- 301, 2001.

GAM281 278 MAP2K1 Pleschka, S.; Wolff, T.; Ehrhardt, C.; Hobom, G.; Planz, O.; Rapp,U. R.; 3 B c
Ludwig, S.: Influenza virus propagation is impaired by inhibitionof the
Raf/MEK/ERK signalling cascade. Nature Cell Biol. 3: 301- 305,2001.

GAM281 278 MAP2K1 Rampoldi, L.; Zimbello, R.; Bortoluzzi, S.; Tiso, N.; Valle, G.;Lanfranchi, 3 B c
G.; Danieli, G. A.: Chromosomal localization of fourMAPK signaling cascade
genes: MEK1, MEK3, MEK4 and MEKK5. Cytogenet.Cell Genet. 78: 301- 303, 1997.

GAM281 278 MAP2K1 Ryan, K. M.; Ernst, M. K.; Rice, N. R.; Vousden, K. H.: Role ofNF- kappa- B 3 B c
in p53- mediated programmed cell death. Nature 404: 892- 897,2000.

GAM281 278 MAP2K1 Sebolt- Leopold, J. S.; Dudley, D. T.; Herrera, R.; Van Becelaere,K.; 3 B c
Wiland, A.; Gowan, R. C.; Tecle, H.; Barrett, S. D.; Bridges,A.;
Przybranowski, S.; Leopold, W. R.; Saltiel, A. R.: Blockade ofthe MAP kinase
pathway suppresses growth of colon tumors in vivo. NatureMed. 5: 810- 816,
1999.

GAM281 278 MAP2K1 Seger, R.; Krebs, E. G.: The MAPK signaling cascade. FASEB J. 9:726- 735, 3 B c
1995.

GAM281 278 MAP2K1 Seger, R.; Seger, D.; Lozeman, F. J.; Ahn, N. G.; Graves, L. M.;Campbell, J. 3 B c
S.; Ericsson, L.; Harrylock, M.; Jensen, A. M.; Krebs,E. G.: Human T- cell
mitogen- activated protein kinase kinases arerelated to yeast signal
transduction kinases. J. Biol. Chem. 267:25628- 25631, 1992.

GAM281 278 MAP2K1 Zheng, C. F.; Guan, K. L.: Cloning and characterization of twodistinct human 3 B c
extracellular signal- regulated kinase activator kinases,MEK1 and MEK2. J.
Biol. Chem. 268: 11435- 11439, 1993.

GAM281 278 MDM2 Boyd, M. T.; Vlatkovic, N.; Haines, D. S.: A novel cellular protein(MTBP) 3 B b
binds to MDM2 and induces a G1 arrest that is suppressed byMDM2. J. Biol.
Chem. 275: 31883- 31890, 2000.

GAM281 278 MDM2 Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S.A.; Albitar, 3 B b
M.: The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82:2617-
2623, 1993.

GAM281 278 MDM2 Bureau, J. F.; Bihl, F.; Brahic, M.; Le Paslier, D.: The genecoding for 3 B b
interferon- gamma is linked to the D12S335 and D12S313 microsatellitesand to
the MDM2 gene. Genomics 28: 109- 112, 1995.

GAM281 278 MDM2 Buschmann, T.; Fuchs, S. Y.; Lee, C.- G.; Pan, Z.- Q.; Ronai, Z.: SUMO- 1 3 B b
modification of Mdm2 prevents its self- ubiquitination andincreases Mdm2
ability to ubiquitinate p53. Cell 101: 753- 762, 2000.Note: Erratum: Cell
107: 549 only, 2001.

GAM281 278 MDM2 de Oca Luna, R. M.; Tabor, A. D.; Eberspaecher, H.; Hulboy, D.L.; Worth, L. 3 B b
L.; Colman, M. S.; Finlay, C. A.; Lozano, G.: The organizationand expression
of the mdm2 gene. Genomics 33: 352- 357, 1996.

GAM281 278 MDM2 Fakharzadeh, S.; Trusko, S. P.; George, D. L.: Tumorigenic 3 B b
potentialassociated with enhanced expression of a gene that is amplified ina
mouse tumor cell line. EMBO J. 10: 1565- 1569, 1991.

GAM281 278 MDM2 Freedman, D. A.; Epstein, C. B.; Roth, J. C.; Levine, A. J.: Agenetic 3 B b
approach to mapping the p53 binding site in the MDM2 protein. Molec.Med. 3:
248- 259, 1997.

GAM281 278 MDM2 Fuchs, S. Y.; Adler, V.; Buschmann, T.; Yin, Z.; Wu, X.; Jones,S. N.; Ronai, 3 B b
Z.: JNK targets p53 ubiquitination and degradationin nonstressed cells.
Genes Dev. 12: 2658- 2663, 1998.

GAM281 278 MDM2 Mayo, L. D.; Donner, D. B.: A phosphatidylinositol 3- kinase/Aktpathway 3 B b
promotes translocation of Mdm2 from the cytoplasm to the nucleus. Proc.Nat.
Acad. Sci. 98: 11598- 11603, 2001.

GAM281 278 MDM2 Mitchell, E. L. D.; White, G. R. M.; Santibanez- Koref, M. F.;Varley, J. M.; 3 B b
Heighway, J.: Mapping of gene loci in the q13- q15region of chromosome 12.
Chromosome Res. 3: 261- 262, 1995.

GAM281 278 MDM2 Momand, J.; Zambetti, G. P.; Olson, D. C.; George, D. L.; Levine,A. J.: The 3 B b
mdm- 2 oncogene product forms a complex with the p53 proteinand inhibits
p53- mediated transactivation. Cell 69: 1237- 1245, 1992.

GAM281 278 MDM2 Oliner, J. D.; Kinzler, K. W.; Meltzer, P. S.; George, D. L.;Vogelstein, B.: 3 B b
Amplification of a gene encoding a p53- associatedprotein in human sarcomas.
Nature 358: 80- 83, 1992.

GAM281 278 MDM2 Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.;Sasazuki, T.; 3 B b
McMahon, M.; Oren, M.; McCormick, F.: Opposing effectsof Ras on p53:
transcriptional activation of mdm2 and induction ofp19(ARF). Cell 103: 321-
330, 2000.

GAM281 278 MDM2 Shenoy, S. K.; McDonald, P. H.; Kohout, T. A.; Lefkowitz, R. J.: Regulation 3 B b
of receptor fate by ubiquitination of activated beta- 2- adrenergicreceptor
and beta- arrestin. Science 294: 1307- 1313, 2001.

GAM281 278 MDM2 Shieh, S.- Y.; Ikeda, M.; Taya, Y.; Prives, C.: DNA damage- 3 B b
inducedphosphorylation of p53 alleviates inhibition by MDM2. Cell 91: 325-
334,1997.

GAM281 278 MDM2 Testa, J. R.; Bellacosa, A.: AKT plays a central role in tumorigenesis. 3 B b
Proc.Nat. Acad. Sci. 98: 10983- 10985, 2001.

GAM281 278 MDM2 Xiao, Z.- X.; Chen, J.; Levine, A. J.; Modjtahedi, N.; Xing, J.;Sellers, W. 3 B b
R.; Livingston, D. M.: Interaction between the retinoblastomaprotein and the
oncoprotein MDM2. Nature 375: 694- 698, 1995.

GAM281 278 MDM2 Zhang, Y.; Xiong, Y.: A p53 amino- terminal nuclear export signalinhibited 3 B b
by DNA damage- induced phosphorylation. Science 292: 1910- 1915,2001.

GAM281 278 MDM4 Parant, J.; Chavez- Reyes, A.; Little, N. A.; Yan, W.; Reinke, V.;Jochemsen, 3 B c
A. G.; Lozano, G.: Rescue of embryonic lethality in Mdm4- nullmice by loss
of Trp53 suggests a nonoverlapping pathway with MDM2to regulate p53. Nature
Genet. 29: 92- 95, 2001.

GAM281 278 MDM4 Shvarts, A.; Bazuine, M.; Dekker, P.; Ramos, Y. F. M.; Steegenga,W. T.; 3 B c
Merckx, G.; van Ham, R. C. A.; van der Houven van Oordt, W.;van der Eb, A.
J.; Jochemsen, A. G.: Isolation and identificationof the human homolog of a
new p53- binding protein, Mdmx. Genomics 43:34- 42, 1997.

GAM281 278 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 B c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator.
J. Biol. Chem. 275: 5308- 5317, 2000.

GAM281 278 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 B c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation
of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer
Res. 56: 3446- 3450, 1996.

GAM281 278 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 B c
bindingprotein, an LXXLL motif- containing protein, functions as a
generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM281 278 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 B c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-
H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor,
ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for
ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol.
Chem. 274: 34283- 34293, 1999.

GAM281 278 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 B c
that integrate nuclear receptor signaling through CREB- bindingprotein.
Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM281 278 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 B c
coding sequences of unidentified human genes. V. The codingsequences of 40
new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM281 278 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 B c
J. K.: Isolation and characterization of peroxisomeproliferator- activated
receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.
Biol. Chem. 275: 13510- 13516, 2000.

GAM281 278 NONO Brown, C. J.; Carrel, L.; Willard, H. F.: Expression of genesfrom the human 3 B b
active and inactive X chromosomes. Am. J. Hum. Genet. 60:1333- 1343, 1997.

GAM281 278 NONO Dong, B.; Horowitz, D. S.; Kobayashi, R.; Krainer, A. R.: Purificationand 3 B b
cDNA cloning of HeLa cell p54(nrb), a nuclear protein with twoRNA
recognition motifs and extensive homology to human splicing factorPSF and
Drosophila NONA/BJ6. Nucleic Acids Res. 21: 4085- 4092, 1993.

GAM281 278 NONO Nelson, D. L.; Ballabio, A.; Cremers, F.; Monaco, A. P.; Schlessinger,D.: 3 B b
Report of the sixth international workshop on X chromosome mapping1995.
Cytogenet. Cell Genet. 71: 308- 342, 1995.

GAM281 278 NONO Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller,U.: AFX1 and 3 B b
p54(nrb): fine mapping, genomic structure, and exclusionas candidate genes
of X- linked dystonia parkinsonism. Hum. Genet. 100:569- 572, 1997.

GAM281 278 NOTCH2 Gao, X.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Gridley,T.: 3 B c
Assignment of the murine Notch2 and Notch3 genes to chromosomes3 and 17.
Genomics 49: 160- 161, 1998.

GAM281 278 NOTCH2 Katsanis, N.; Fitzgibbon, J.; Fisher, E. M. C.: Paralogy 3 B c
mapping:identification of a region in the human MHC triplicated onto
humanchromosomes 1 and 9 allows the prediction and isolation of novel PBXand
NOTCH loci. Genomics 35: 101- 108, 1996.

GAM281 278 NOTCH2 Larsson, C.; Lardelli, M.; White, I.; Lendahl, U.: The human NOTCH1,2, and 3 3 B c
genes are located at chromosome positions 9q34, 1p13- p11,and 19p13.2- p13.1
in regions of neoplasia- associated translocation. Genomics 24:253- 258,
1994.

GAM281 278 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of 3 B b
NAD(P)H:quinonereductase by dietary antioxidants: possible role in
protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77:
5216- 5220,1980.

GAM281 278 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. 3 B b
A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.;
Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of
the long arm of human chromosome 16. Genomics 10:308- 312, 1991.

GAM281 278 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof 3 B b
the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983.

GAM281 278 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman 3 B b
diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum.
Genet. 53: 189- 193, 1980.

GAM281 278 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- 3 B b
inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and
localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578,

1988.

GAM281 278 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic variation in the prevalence of a common NAD(P)Hquinone oxidoreductase polymorphism and its implications for anti- cancerchemotherapy. Brit. J. Cancer 76: 852- 854, 1997. 3 B b

GAM281 278 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further evidence for the regional localization of human APRT and DIA4on chromosome 16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984. 3 B b

GAM281 278 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe increased susceptibility of individuals with a polymorphism inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat. Acad. Sci. 96: 8150- 8155, 1999. 3 B b

GAM281 278 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA- 4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980. 3 B b

GAM281 278 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1) gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382- 7389, 1998. 3 B b

GAM281 278 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.; Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.; Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological malignancy, is associated with the NQO1 609C- T mutationand rapid fractional excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997. 3 B b

GAM281 278 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 B b

GAM281 278 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999. 3 B b

GAM281 278 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene expression in human colon carcinoma cells: characterization ofa mutation which modulates DT- diaphorase activity and mitomycin sensitivity. CancerRes. 52: 797- 802, 1992. 3 B b

GAM281 278 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H: quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997. 3 B b

GAM281 278 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998. 3 B b

GAM281 278 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes. Leukemia Res. 22: 105- 113, 1998. 3 B b

GAM281 278 NR2E1 Jackson, A.; Panayiotidis, P.; Foroni, L.: The human homologueof the Drosophila tailless gene (TLX): characterization and mappingto a region of common deletion in human lymphoid leukemia on chromosome6q21. Genomics 50: 34- 43, 1998. 3 B c

GAM281 278 NR2E1 Monaghan, A. P.; Bock, D.; Gass, P.; Schwager, A.; Wolfer, D. P.;Lipp, H.- P.; Schutz, G.: Defective limbic system in mice lackingthe tailless gene. 3 B c

Nature 390: 515- 517, 1997.

GAM281 278 NR2E1 Yu, R. T.; McKeown, M.; Evans, R. M.; Umesono, K.: Relationshipbetween 3 B c
Drosophila gap gene tailless and a vertebrate nuclear receptorTlx. Nature
370: 375- 379, 1994.

GAM281 278 ORC1L Eki, T.; Okumura, K.; Amin, A.; Ishiai, M.; Abe, M.; Nogami, M.;Taguchi, H.; 3 B b
Hurwitz, J.; Murakami, Y.; Hanaoka, F.: Mapping of thehuman homologue
(ORC1L) of the yeast origin recognition complex subunit1 gene to chromosome
band 1p32. Genomics 36: 559- 561, 1996.

GAM281 278 ORC1L Gavin, K. A.; Hidaka, M.; Stillman, B.: Conserved initiator proteinsin 3 B b
eukaryotes. Science 270: 1667- 1671, 1995.

GAM281 278 ORC1L Mendez, J.; Zou- Yang, H.; Kim, S.- Y.; Hidaka, M.; Tansey, W. P.;Stillman, 3 B b
B.: Human origin recognition complex large subunit is degradedby ubiquitin-
mediated proteolysis after initiation of DNA replication. Molec.Cell 9: 481-
491, 2002.

GAM281 278 ORC1L Ohtani, K.; DeGregori, J.; Leone, G.; Herendeen, D. R.; Kelly,T. J.; Nevins, 3 B b
J. R.: Expression of the HsOrc1 gene, a human ORC1homolog, is regulated by
cell proliferation via the E2F transcriptionfactor. Molec. Cell. Biol. 16:
6977- 6984, 1996.

GAM281 278 P2RX7 Buell, G. N.; Talabot, F.; Gos, A.; Lorenz, J.; Lai, E.; Morris,M. A.; 3 B c
Antonarakis, S. E.: Gene structure and chromosomal localizationof the human
P2X7 receptor. Receptors Channels 5: 347- 354, 1998.

GAM281 278 P2RX7 Gu, B. J.; Zhang, W.; Worthington, R. A.; Sluyter, R.; Dao- Ung,P.; Petrou, 3 B c
S.; Barden, J. A.; Wiley, J. S.: A glu- 496 to ala polymorphismleads to loss
of function of the human P2X(7) receptor. J. Biol.Chem. 276: 11135- 11142,
2001.

GAM281 278 P2RX7 Rassendren, F.; Buell, G. N.; Virginio, C.; Collo, G.; North, R.A.; 3 B c
Surprenant, A.: The permeabilizing ATP receptor, P2X(7). J.Biol. Chem. 272:
5482- 5486, 1997.

GAM281 278 P2RX7 Solle, M.; Labasi, J.; Perregaux, D. G.; Stam, E.; Petrushova,N.; Koller, B. 3 B c
H.; Griffiths, R. J.; Gabel, C. A.: Altered cytokineproduction in mice
lacking P2X7 receptors. J. Biol. Chem. 276: 125- 132,2001.

GAM281 278 P2RX7 Wiley, J. S.; Dao- Ung, L. P.; Gu, B. J.; Sluyter, R.; Shemon, A.N.; Li, C.; 3 B c
Taper, J.; Gallo, J.; Manoharan, A.: A loss- of- functionpolymorphic
mutation in the cytolytic P2X7 receptor gene and chroniclymphocyte
leukaemia: a molecular study. Lancet 359: 1114- 1119,2002.

GAM281 278 P2RX7 Worthington, R. A.; Smart, M. L.; Gu, B. J.; Williams, D. A.; Petrou,S.; 3 B c
Wiley, J. S.; Barden, J. A.: Point mutations confer loss of ATP-
inducedhuman P2X(7) receptor function. FEBS Lett. 512: 43- 46, 2002.

GAM281 278 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack 3 B b
of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary
cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991.

GAM281 278 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; 3 B b
Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine
nucleotide synthesis on human chromosome 4 are closelylinked and divergently
transcribed. J. Biol. Chem. 269: 5313- 5321,1994.

GAM281 278 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of 3 B b
three human multifunctional de novo purine biosyntheticgenes by functional
complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920,
1990.

GAM281 278 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B b

Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM281 278 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM281 278 PCDHB16 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel 3 B b
cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997.

GAM281 278 PCDHB16 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of 3 B b
the coding sequences of unidentified human genes. XVIII.The complete sequences of 100 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 273- 281, 2000.

GAM281 278 PCDHB16 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM281 278 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 B b
protocadherin- beta one- exon gene families show high evolutionaryconservation, despite the difference in gene number. FEBS Lett. 495:120- 125, 2001.

GAM281 278 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM281 278 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 3 B c
an ethanol- responsive potential modulator of guanine nucleotide-bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM281 278 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 B c
Cloning and characterization of the rat and human phosducin- likeprotein genes: structure, expression and chromosomal localization. Biochim.Biophys. Acta 1444: 346- 354, 1999.

GAM281 278 PDZK1 Custer, M.; Spindler, B.; Verrey, F.; Murer, H.; Biber, J.: Identificationof 3 B b
a new gene product (diphor- 1) regulated by dietary phosphate. Am.J. Physiol. 273: F801- F806, 1997.

GAM281 278 PDZK1 Ikemoto, M.; Arai, H.; Feng, D.; Tanaka, K.; Aoki, J.; Dohmae,N.; Takio, K.; 3 B b
Adachi, H.; Tsujimoto, M.; Inoue, K.: Identificationof a PDZ- domain-containing protein that interacts with the scavengerreceptor class B type I. Proc. Nat. Acad. Sci. 97: 6538- 6543, 2000.

GAM281 278 PDZK1 Kocher, O.; Comella, N.; Gilchrist, A.; Pal, R.; Tognazzi, K.;Brown, L. F.; 3 B b
Knoll, J. H. M.: PDZK1, a novel PDZ domain- containingprotein up- regulated in carcinomas and mapped to chromosome 1q21,interacts with cMOAT (MRP2), the multidrug resistance- associated protein. Lab.Invest. 79: 1161- 1170, 1999.

GAM281 278 PDZK1 Kocher, O.; Comella, N.; Tognazzi, K.; Brown, L. F.: Identificationand 3 B b
partial characterization of PDZK1: a novel protein containingPDZ interaction domains. Lab. Invest. 78: 117- 125, 1998.

GAM281 278 PDZK1 Wang, S.; Yue, H.; Derin, R. B.; Guggino, W. B.; Li, M.: Accessoryprotein 3 B b
facilitated CFTR- CFTR interaction, a molecular mechanism topotentiate the

chloride channel activity. Cell 103: 169- 179, 2000.

GAM281 278 PDZK1 White, K. E.; Biber, J.; Murer, H.; Econs, M. J.: A PDZ domain- containingprotein with homology to Diphor- 1 maps to human chromosome 1q21. Ann.Hum. Genet. 62: 287- 290, 1998. 3 B b

GAM281 278 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to two putative mammalian circadian regulators, mper1 andmper2, to light. Cell 91: 1055- 1064, 1997. 3 B b

GAM281 278 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B b

GAM281 278 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531- 2534, 1999. 3 B b

GAM281 278 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of clock operative in the mammalian forebrain. Science 293:506- 509, 2001. 3 B b

GAM281 278 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.; Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock. Science 288: 1013- 1019, 2000. 3 B b

GAM281 278 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; Reppert, S. M.: Two period homologs: circadian expression andphotic regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997. 3 B b

GAM281 278 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial advanced sleep phase syndrome. Science 291: 1040- 1043,2001. 3 B b

GAM281 278 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694, 2001. 3 B b

GAM281 278 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the mammalian circadian clock. Nature 400: 169- 173,1999. 3 B b

GAM281 278 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol 3- kinase catalytic subunit that associates withp85 and is expressed predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997. 3 B b

GAM281 278 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J. H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002. 3 B b

GAM281 278 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; Nakagawara, A.: Identification and chromosome assignment of ahuman gene encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997. 3 B b

GAM281 278 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.: p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat. Acad. Sci. 94: 4330- 4335, 1997. 3 B b

GAM281 278 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C. Genomics 47: 323- 324, 1998. 3 B b

GAM281 278 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to human chromosome 21q22.3. Genomics 41: 193- 200,1997. 3 B b

GAM281 278 PON1 Adkins, S.; Gan, K. N.; Mody, M.; La Du, B. N.: Molecular basisfor the polymorphic forms of human serum paraoxonase/arylesterase:glutamine or arginine at position 191, for the respective A and Ballozymes. Am. J. Hum. Genet. 52: 598- 608, 1993. 3 B b

GAM281 278 PON1 Antikainen, M.; Murtomaki, S.; Syvanne, M.; Pahlman, R.; Tahvanainen,E.; Jauhiainen, M.; Frick, M. H.; Ehnholm, C.: The gln- arg191 polymorphismof the human paraoxonase gene (HUMPONA) is not associated with therisk of coronary artery disease in Finns. J. Clin. Invest. 98: 883- 885,1996. 3 B b

GAM281 278 PON1 Augustinsson, K.- B.; Henricson, B.: A genetically controlled esterasein rat plasma. Biochim. Biophys. Acta 124: 323- 331, 1966. 3 B b

GAM281 278 PON1 Barbieri, M.; Bonafe, M.; Marfella, R.; Ragno, E.; Giugliano, D.;Franceschi, C.; Paolisso, G.: LL- paraoxonase genotype is associatedwith a more severe degree of homeostasis model assessment IR in healthysubjects. J. Clin. Endocr. Metab. 87: 222- 225, 2002. 3 B b

GAM281 278 PON1 Brophy, V. H.; Jampsa, R. L.; Clendenning, J. B.; McKinstry, L.A.; Jarvik, G. P.; Furlong, C. E.: Effects of 5- prime regulatory- regionpolymorphisms on paraoxonase- gene (PON1) expression. Am. J. Hum.Genet. 68: 1428- 1436, 2001. 3 B b

GAM281 278 PON1 Cherry, N.; Mackness, M.; Durrington, P.; Povey, A.; Dippnall,M.; Smith, T.; Mackness, B.: Paraoxonase (PON1) polymorphisms infarmers attributing ill health to sheep dip. Lancet 359: 763- 764,2002. 3 B b

GAM281 278 PON1 Clendenning, J. B.; Humbert, R.; Green, E. D.; Wood, C.; Traver,D.; Furlong, C. E.: Structural organization of the human PON1 gene. Genomics 35:586- 589, 1996. 3 B b

GAM281 278 PON1 Coates, P. M.; Mestriner, M. A.; Hopkinson, D. A.: A preliminaryinterpretation of the esterase isozymes of human tissues. Ann. Hum.Genet. 39: 1- 20, 1975. 3 B b

GAM281 278 PON1 Davies, H. G.; Richter, R. J.; Keifer, M.; Broomfield, C. A.; Sowalla,J.; Furlong, C. E.: The effect of the human serum paraoxonase polymorphismis reversed with diazoxon, soman and sarin. Nature Genet. 14: 334- 336,1996. 3 B b

GAM281 278 PON1 Deakin, S.; Leviev, I.; Nicaud, V.; Meynet, M.- C. B.; Tiret, L.;James, R. W.: Paraoxonase- 1 L55M polymorphism is associated withan abnormal oral glucose tolerance test and differentiates high riskcoronary disease families. J. Clin. Endocr. Metab. 87: 1268- 1273,2002. 3 B b

GAM281 278 PON1 Eckerson, H. W.; Romson, J.; Wyte, C.; La Du, B. N.: The humanserum paraoxonase polymorphism: identification of phenotypes by theirresponse to salts. Am. J. Hum. Genet. 35: 214- 227, 1983. 3 B b

GAM281 278 PON1 Eckerson, H. W.; Wyte, C. M.; La Du, B. N.: The human serum paraoxonase/arylesterasepolymorphism. Am. J. Hum. Genet. 35: 1126- 1136, 1983. 3 B b

GAM281 278 PON1 Eiberg, H.; Mohr, J.: Linkage relations of the paraoxonase polymorphismwith 43 marker systems. (Abstract) Cytogenet. Cell Genet. 25: 150,1979. 3 B b

GAM281 278 PON1 Eiberg, H.; Mohr, J.; Schmiegelow, K.; Nielsen, L. S.; Williamson,R.: 3 B b

Linkage relationships of paraoxonase (PON) with other markers:indication of PON- cystic fibrosis synteny. Clin. Genet. 28: 265- 271,1985.

GAM281 278 PON1 Furlong, C. E.; Richter, R. J.; Chapline, C.; Crabb, J. W.: Purificationof 3 B b
rabbit and human serum paraoxonase. Biochemistry 30: 10133- 10140,1991.

GAM281 278 PON1 Furlong, C. E.; Richter, R. J.; Seidel, S. L.; Motulsky, A. G.: Role of 3 B b
genetic polymorphism of human plasma paraoxonase/arylesterasein hydrolysis of the insecticide metabolites chlorpyrifos oxon andparaoxon. Am. J. Hum. Genet. 43: 230- 238, 1988.

GAM281 278 PON1 Garin, M.- C. B.; James, R. W.; Dussoix, P.; Blanche, H.; Passa,P.; Froguel, 3 B b
P.; Ruiz, J.: Paraoxonase polymorphism met- leu54 isassociated with modified serum concentrations of the enzyme: a possiblelink between the paraoxonase gene and increased risk of cardiovasculardisease in diabetes. J. Clin. Invest. 99: 62- 66, 1997.

GAM281 278 PON1 Geldmacher- von Mallinckrodt, M.: Polymorphism of human serumparaoxonase. 3 B b

Hum. Genet. 45 (suppl. 1): 65- 68, 1978.

GAM281 278 PON1 Geldmacher- von Mallinckrodt, M.; Lindorft, H. H.; Petenyi, M.;Flugel, M.; 3 B b
Fischer, T.; Hiller, T.: Genetisch determinierter Polymorphismusde menschlichen Serum- Paroxonase (E.C.3.1.1.2). Humangenetik 17:331- 335, 1973.

GAM281 278 PON1 Hassett, C.; Richter, R. J.; Humbert, R.; Chapline, C.; Crabb,J. W.; 3 B b
Omiecinski, C. J.; Furlong, C. E.: Characterization of cDNAclones encoding rabbit and human serum paraoxonase: the mature proteinretains its signal sequence. Biochemistry 30: 10141- 10149, 1991.

GAM281 278 PON1 Humbert, R.; Adler, D. A.; Disteche, C. M.; Hassett, C.; Omiecinski,C. J.; 3 B b
Furlong, C. E.: The molecular basis of the human serum paraoxonaseactivity polymorphism. Nature Genet. 3: 73- 76, 1993.

GAM281 278 PON1 Ito, T.; Yasue, H.; Yoshimura, M.; Nakamura, S.; Nakayama, M.;Shimasaki, Y.; 3 B b
Harada, E.; Mizuno, Y.; Kawano, H.; Ogawa, H.: Paraoxonasegene gln192- to-arg (Q192R) polymorphism is associated with coronaryartery spasm. Hum. Genet. 110: 89- 94, 2002.

GAM281 278 PON1 Kao, Y.- L.; Donaghue, K.; Chan, A.; Knight, J.; Silink, M.: Avariant of 3 B b
paraoxonase (PON1) gene is associated with diabetic retinopathyin IDDM. J. Clin. Endocr. Metab. 83: 2589- 2592, 1998.

GAM281 278 PON1 La Du, B. N.: The human serum paraoxonase/arylesterase 3 B b
polymorphism.(Editorial) Am. J. Hum. Genet. 43: 227- 229, 1988.

GAM281 278 PON1 Li, W.- F.; Furlong, C. E.; Costa, L. G.: Paraoxonase protectsagainst 3 B b
chlorpyrifos toxicity in mice. Toxic. Lett. 76: 219- 226,1995.

GAM281 278 PON1 Li, W.- F.; Matthews, C.; Disteche, C. M.; Costa, L. G.; Furlong,C. E.: 3 B b
Paraoxonase (Pon1) gene in mice: sequencing, chromosomal localizationand developmental expression. Pharmacogenetics 7: 137- 144, 1997.

GAM281 278 PON1 Mackness, B.; Mackness, M. I.; Arrol, S.; Turkie, W.; Durrington,P. N.: 3 B b
Effect of the human serum paraoxonase 55 and 192 genetic polymorphismson the protection by high density lipoprotein against low densitylipoprotein oxidative modification. FEBS Lett. 423: 57- 60, 1998.

GAM281 278 PON1 Mochizuki, H.; Scherer, S. W.; Xi, T.; Nickle, D. C.; Majer, M.;Huizenga, J. 3 B b
J.; Tsui, L.- C.; Prochazka, M.: Human PON2 gene at 7q21.3:cloning, multiple mRNA forms, and missense polymorphisms in the codingsequence. Gene 213: 149-157, 1998.

GAM281 278 PON1 Mueller, R. F.; Hornung, S.; Furlong, C. E.; Anderson, J.; Giblett,E. R.; 3 B b

Motulsky, A. G.: Plasma paraoxonase polymorphism: a new enzymeassay, population, family, biochemical, and linkage studies. Am.J. Hum. Genet. 35: 393- 408, 1983.

GAM281 278 PON1 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J. Clin. Invest. 99: 2005- 2019, 1997. 3 B b

GAM281 278 PON1 Neel, J. V.; Tanis, R. J.; Migliazza, E. C.; Spielman, R. S.;Salzano, F. M.; Oliver, W. J.; Morrow, M.; Bachofer, S.: Geneticstudies of the Macushi and Wapishana Indians. I. Rare genetic variantsand a 'private polymorphism' of esterase A. Hum. Genet. 36: 81- 108,1977. 3 B b

GAM281 278 PON1 Nielsen, A.; Eiberg, H.; Mohr, J.: Number of loci responsiblefor the inheritance of high and low activity of paraoxonase. Clin.Genet. 29: 216- 221, 1986. 3 B b

GAM281 278 PON1 Odawara, M.; Tachi, Y.; Yamashita, K.: Paraoxonase polymorphismGln192- Arg is associated with coronary heart disease in Japanese noninsulin- dependentdiabetes mellitus. J. Clin. Endocr. Metab. 82: 2257- 2260, 1997. 3 B b

GAM281 278 PON1 Ortigoza- Ferado, J.; Richter, R. J.; Hornung, S. K.; Motulsky,A. G.; Furlong, C. E.: Paraoxon hydrolysis in human serum mediatedby a genetically variable arylesterase and albumin. Am. J. Hum. Genet. 36:295- 305, 1984. 3 B b

GAM281 278 PON1 Paolisso, G.; Manzella, D.; Tagliamonte, M. R.; Barbieri, M.;Marfella, R.; Zito, G.; Bonafe, M.; Giugliano, D.; Franceschi, C.;Varricchio, M.: The BB- paraoxonase genotype is associated with impairedbrachial reactivity after acute hypertriglyceridemia in healthy subjects. J.Clin. Endocr. Metab. 86: 1078- 1082, 2001. 3 B b

GAM281 278 PON1 Playfer, J. R.; Eze, L. C.; Bullen, M. F.; Evans, D. A. P.: Geneticpolymorphism and interethnic variability of plasma paroxonase activity. J.Med. Genet. 13: 337- 342, 1976. 3 B b

GAM281 278 PON1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 B b

GAM281 278 PON1 Schmiegelow, K.; Eiberg, H.; Tsui, L.- C.; Buchwald, M.; Phelan,P. D.; Williamson, R.; Warwick, W.; Niebuhr, E.; Mohr, J.; Schwartz,M.; Koch, C.: Linkage between the loci for cystic fibrosis and paraoxonase. Clin.Genet. 29: 374- 377, 1986. 3 B b

GAM281 278 PON1 Serrato, M.; Marian, A. J.: A variant of human paraoxonase/arylesterase(HUMPONA) gene is a risk factor for coronary artery disease. J. Clin.Invest. 96: 3005- 3008, 1995. 3 B b

GAM281 278 PON1 Shih, D. M.; Gu, L.; Xia, Y.- R.; Navab, M.; Li, W.- F.; Hama, S.;Castellani, L. W.; Furlong, C. E.; Costa, L. G.; Fogelman, A. M.;Lusis, A. J.: Mice lacking serum paraoxonase are susceptible to organophosphatetoxicity and atherosclerosis. Nature 394: 284- 287, 1998. 3 B b

GAM281 278 PON1 Simpson, N. E.: Serum arylesterase levels of activity in twinsand their parents. Am. J. Hum. Genet. 23: 375- 382, 1971. 3 B b

GAM281 278 PON1 Sorenson, R. C.; Primo- Parmo, S. L.; Camper, S.; La Du, B. N.: The genetic mapping and gene structure of mouse paraoxonase/arylesterase. Genomics 30:431- 438, 1995. 3 B b

GAM281 278 PON1 Tashian, R. E.: Genetic variation and evolution of the carboxylicesterases and carbonic anhydrases of primate erythrocytes. Am. J.Hum. Genet. 17: 257- 272, 1965. 3 B b

GAM281 278 PON1 Tashian, R. E.; Shaw, M. W.: Inheritance of an erythrocyte 3 B b

acetylesterasevariant of man. Am. J. Hum. Genet. 14: 295- 300, 1962.

GAM281 278 PON1 Tsui, L.- C.; Buchwald, M.; Barker, D.; Braman, J. C.; Knowlton,R.; Schumm, 3 B b
J. W.; Eiberg, H.; Mohr, J.; Kennedy, D.; Plavsic, N.;Zsiga, M.; Markiewicz,
D.; Akots, G.; Brown, V.; Helms, C.; Gravius,T.; Parker, C.; Rediker, K.;
Donis- Keller, H.: Cystic fibrosis locusdefined by a genetically linked
polymorphic DNA marker. Science 230:1054- 1057, 1985.

GAM281 278 PON1 Watson, C. E.; Draganov, D. I.; Billecke, S. S.; Bisgaier, C.L.; La Du, B. 3 B b
N.: Rabbits possess a serum paraoxonase polymorphismsimilar to the human
Q192R. Pharmacogenetics 11: 123- 134, 2001.

GAM281 278 PON1 Yamasaki, Y.; Sakamoto, K.; Watada, H.; Kajimoto, Y.; Hori, M.: The arg- 192 3 B b
isoform of paraoxonase with low sarin- hydrolyzing activityis dominant in
the Japanese. Hum. Genet. 101: 67- 68, 1997.

GAM281 278 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 3 B b
Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J
recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585,
2002.

GAM281 278 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 3 B b
cell coactivator of octamer- binding transcription factors. Nature 373:360-
362, 1995.

GAM281 278 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 3 B b
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-
specific coactivator of octamer- binding transcription factors1 and 2, to
11q23.1 by somatic cell hybridization and in situ hybridization. Genomics
33:143- 145, 1996.

GAM281 278 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 3 B b
of action of the B- cell- specific transcriptional activatorOCA- B. Molec.
Cell. Biol. 15: 4115- 4124, 1995.

GAM281 278 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 3 B b
Matthias, P.: B cell development and immunoglobulin gene transcriptionin the
absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM281 278 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 3 B b
Immun. 9: 373- 398, 1991.

GAM281 278 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 3 B b
specificcoactivator that stimulates immunoglobulin promoter activity
throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM281 278 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 3 B b
Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B,
BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-
864, 2000.

GAM281 278 POU3F1 Avraham, K. B.; Cho, B. C.; Gilbert, D.; Fujii, H.; Okamoto, K.;Shimazaki, 3 B b
T.; Ito, T.; Shoji, H.; Wakamatsu, Y.; Kondoh, H.; Takahashi,N.; Muramatsu,
M.; Hamada, H.; Copeland, N. G.; Jenkins, N. A.: Murinechromosomal location
of four class III POU transcription factors. Genomics 18:131- 133, 1993.

GAM281 278 POU3F1 Bermingham, J. R., Jr.; Scherer, S. S.; O'Connell, S.; Arroyo,E.; Kalla, K. 3 B b
A.; Powell, F. L.; Rosenfeld, M. G.: Tst- 1/Oct- 6/SCIPregulates a unique
step in peripheral myelination and is requiredfor normal respiration. Genes
Dev. 10: 1751- 1762, 1996.

GAM281 278 POU3F1 Jaegle, M.; Mandemakers, W.; Broos, L.; Zwart, R.; Karis, A.; Visser,P.; 3 B b
Grosveld, F.; Meijer, D.: The POU factor Oct- 6 and Schwann
celldifferentiation. Science 273: 507- 510, 1996.

GAM281 278 POU3F1 Sumiyama, K.; Washio- Watanabe, K.; Ono, T.; Yoshida, M. C.; Hayakawa,T.; 3 B b
Ueda, S.: Human class III POU genes, POU3F1 and POU3F3, map tochromosomes
1p34.1 and 3p14.1. Mammalian Genome 9: 180- 181, 1998.

GAM281 278 POU3F1 Xia, Y.- R.; Andersen, B.; Mehrabian, M.; Diep, A. T.; Warden, C.H.; 3 B b
Mohandas, T.; McEvilly, R. J.; Rosenfeld, M. G.; Lusis, A. J.: Chromosomal
organization of mammalian POU domain factors. Genomics 18:126- 130, 1993.

GAM281 278 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; 3 B b
Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor
integrity, and rhodopsin dephosphorylation in mice lackingboth protein
phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21:
8605- 8614, 2001.

GAM281 278 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; 3 B b
Nathans, J.: Identification and characterization of a conservedfamily of
protein serine/threonine phosphatases homologous to Drosophilaretinal
degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997.

GAM281 278 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 B c
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component
of the steroid receptor complex: cloning of thecDNA and further
characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM281 278 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 B c
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem.
267: 5503- 5507, 1992.

GAM281 278 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 B c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151
only, 1997.

GAM281 278 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 B c
J.- E.: The structure and complete nucleotide sequenceof the human
cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM281 278 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 B b
Chromosomalassignment of the interferon- inducible double- stranded RNA-
dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse
chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM281 278 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human 3 B b
interferon- gamma mRNA autoregulates its translation througha pseudoknot
that activates the interferon- inducible protein kinasePKR. Cell 108: 221-
232, 2002.

GAM281 278 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; 3 B b
Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR)
encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and
differences from its mouse homolog. Genomics 36:197- 201, 1996.

GAM281 278 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: 3 B b
sequence of the human interferon- inducible RNA- dependent proteinkinase
(PKR) deduced from genomic clones. Gene 178: 191- 193, 1996.

GAM281 278 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; 3 B b
Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand
characterization of the human double- stranded RNA- activated proteinkinase
induced by interferon. Cell 62: 379- 390, 1990.

GAM281 278 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; 3 B b
Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds
preferentially to Huntington's disease (HD) transcriptsand is activated in

HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001.

GAM281 278 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. 3 B b
G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-
RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics
16:768- 770, 1993.

GAM281 278 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: 3 B b
Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein.
Science 285: 107- 110, 1999.

GAM281 278 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 3 B c
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene
PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal
instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM281 278 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 3 B c
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY)
to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet.
76: 49- 52, 1997.

GAM281 278 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 3 B c
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated
protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of
all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM281 278 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 B b
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.:
Genomicorganization, comparative analysis, and genetic polymorphisms of
thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733,
2001.

GAM281 278 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 B b
Chen, S. G.: Expression and structural characterizationof the recombinant
human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM281 278 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 B b
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.;
Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-
deficient mice is associated with upregulation of thenovel PrP- like protein
doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM281 278 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 B b
T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin
the prion- like protein gene (Prnd) and their implications inhuman prion
diseases, Alzheimer's disease and other neurological disorders. Hum.Genet.
109: 319- 325, 2001.

GAM281 278 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 B b
P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-
glycosylated, glycosylphosphatidylinositol- anchored protein:expression in
testis and ectopic production in the brains of Prnp(0/0)mice predisposed to
Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM281 278 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 B b
915, 1999.

GAM281 278 PSMD9 Thomas, M. K.; Yao, K.- M.; Tenser, M. S.; Wong, G. G.; Habener,J. F.: 3 B b
Bridge- 1, a novel PDZ- domain coactivator of E2A- mediated regulationof
insulin gene transcription. Molec. Cell. Biol. 19: 8492- 8504,1999.

GAM281 278 PSMD9 Watanabe, T. K.; Saito, A.; Suzuki, M.; Fujiwara, T.; Takahashi,E.; 3 B b
Slaughter, C. A.; DeMartino, G. N.; Hendil, K. B.; Chung, C. H.;Tanahashi,

N.; Tanaka, K.: cDNA cloning and characterization of ahuman proteasomal modulator subunit, p27 (PSMD9). Genomics 50: 241- 250,1998.

GAM281 278 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime-untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001. 3 B b

GAM281 278 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994. 3 B b

GAM281 278 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996. 3 B b

GAM281 278 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996. 3 B b

GAM281 278 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996. 3 B b

GAM281 278 PTK2 Andre, E.; Becker- Andre, M.: Expression of an N- terminally truncatedform of human focal adhesion kinase in brain. Biochem. Biophys. Res.Commun. 190: 140- 147, 1993. 3 B b

GAM281 278 PTK2 Fiedorek, F. T., Jr.; Kay, E. S.: Mapping of the focal adhesionkinase (Fadk) gene to mouse chromosome 15 and human chromosome 8. MammalianGenome 6: 123-126, 1995. 3 B b

GAM281 278 PTK2 Polte, T. R.; Hanks, S. K.: Interaction between focal adhesionkinase and Crk- associated tyrosine kinase substrate p130- Cas. Proc.Nat. Acad. Sci. 92: 10678- 10682, 1995. 3 B b

GAM281 278 PTK2 Schaller, M. D.; Borgman, C.; Cobb, B. S.; Vines, R. R.; Reynolds,A. B.; Parsons, J. T.: pp125(FAK), a structurally distinctive protein-tyrosinekinase associated with focal adhesions. Proc. Nat. Acad. Sci. 89:5192- 5196, 1992. 3 B b

GAM281 278 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999. 3 B b

GAM281 278 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000. 3 B b

GAM281 278 RAB4A Barbosa, M. D. F. S.; Johnson, S. A.; Achey, K.; Gutierrez, M.;Wakeland, E. K.; Zerial, M.; Kingsmore, S. F.: The Rab protein family:genetic mapping of six Rab genes in the mouse. Genomics 30: 439- 444,1995. 3 B c

GAM281 278 RAB4A Rousseau- Merck, M.- F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350-354, 1991. 3 B c

GAM281 278 RAB4A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes encode a family of GTP- binding proteins related to yeastYPT1 and SEC4 3 B c

products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989.

GAM281 278 REGL Gharib, B.; Fox, M. F.; Bartoli, C.; Giorgi, D.; Sansonetti, A.;Swallow, D. 3 B c
M.; Dagorn, J. C.; Berge- Lefranc, J. L.: Human
regenerationprotein/lithostathine genes map to chromosome 2p12. Ann. Hum.
Genet. 57:9- 16, 1993.

GAM281 278 REGL Miyashita, H.; Nakagawara, K.; Mori, M.; Narushima, Y.; Noguchi,N.; 3 B c
Moriizumi, S.; Takasawa, S.; Yonekura, H.; Takeuchi, T.; Okamoto,H.: Human
REG family genes are tandemly ordered in a 95- kilobaseregion of chromosome
2p12. FEBS Lett. 377: 429- 433, 1995.

GAM281 278 REGL Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki,Y.; Miyashita, 3 B c
H.; Yonekura, H.; Okamoto, H.: Isolation, structuraldetermination and
expression of a novel reg gene, human regI- beta. Biochim.Biophys. Acta
1217: 199- 202, 1994.

GAM281 278 RGS16 Buckbinder, L.; Velasco- Miguel, S.; Chen, Y.; Xu, N.; Talbott,R.; Gelbert, 3 B c
L.; Gao, J.; Seizinger, B. R.; Gutkind, J. S.; Kley,N.: The p53 tumor
suppressor targets a novel regulator of G proteinsignaling. Proc. Nat. Acad.
Sci. 94: 7868- 7872, 1997.

GAM281 278 RGS16 Chen, C.- K.; Wieland, T.; Simon, M. I.: RGS- r, a retinal specificRGS 3 B c
protein, binds an intermediate conformation of transducin andenhances
recycling. Proc. Nat. Acad. Sci. 93: 12885- 12889, 1996.

GAM281 278 RGS16 Snow, B. E.; Antonio, L.; Suggs, S.; Siderovski, D. P.: Cloningof a 3 B c
retinally abundant regulator of G- protein signaling (RGS- r/RGS16):genomic
structure and chromosomal localization of the human gene. Gene 206:247- 253,
1998.

GAM281 278 RGS16 Zheng, B.; Chen, D.; Farquhar, M. G.: MIR16, a putative 3 B c
membraneglycerophosphodiester phosphodiesterase, interacts with RGS16.
Proc.Nat. Acad. Sci. 97: 3999- 4004, 2000.

GAM281 278 RGS3 Chatterjee, T. K.; Eapen, A.; Kanis, A. B.; Fisher, R. A.: 3 B c
Genomicorganization, 5- prime- flanking region, and chromosomal
localizationof the human RGS3 gene. Genomics 45: 429- 433, 1997.

GAM281 278 RGS3 Druey, K. M.; Blumer, K. J.; Kang, V. H.; Kehrl, J. H.: Inhibitionof G- 3 B c
protein- mediated MAP kinase activation by a new mammalian genefamily.
Nature 379: 742- 746, 1996.

GAM281 278 RGS3 Lu, Q.; Sun, E. E.; Klein, R. S.; Flanagan, J. G.: Ephrin- B 3 B c
reversesignaling is mediated by a novel PDZ- RGS protein and selectively
inhibitsG protein- coupled chemoattraction. Cell 105: 69- 79, 2001.

GAM281 278 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; 3 B b
Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in
RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993.

GAM281 278 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 3 B b
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA
amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM281 278 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. 3 B b
Med. 339: 1775- 1777, 1998.

GAM281 278 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand 3 B b
molecular genetics. Blood Rev. 8: 199- 212, 1994.

GAM281 278 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; 3 B b
Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood
group polymorphism as determined by Southern analysis. Blood 78:2747- 2752,
1991.

GAM281 278 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and its association with universal edema of the fetus, icterusgravis neonatorum and anemia of the newborn. J. Pediat. 1: 269- 309,1932. 3 B b

GAM281 278 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989. 3 B b

GAM281 278 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with sickle cell disease. Transfusion 37: 357- 361, 1997. 3 B b

GAM281 278 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 B b

GAM281 278 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the human RH locus: a family study of the red- cell Evans phenotypereveals a transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59: 825- 833, 1996. 3 B b

GAM281 278 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J. Hum. Genet. 58: 133- 142, 1996. 3 B b

GAM281 278 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of Rh blood group genes: association between restrictionfragment length polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994. 3 B b

GAM281 278 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine years and some observations on the biochemistry and geneticsof the system. Transfusion Med. Rev. 3: 1- 12, 1989. 3 B b

GAM281 278 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh genes revealed by analysis of unrelated donors with therare D- - phenotype. Am. J. Hum. Genet. 59: 1066- 1073, 1996. 3 B b

GAM281 278 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by alternative splicing. Blood 80: 1074- 1078, 1992. 3 B b

GAM281 278 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929, 1992. 3 B b

GAM281 278 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE genotyping for correct blood group determination inchronically transfused patients. Transfusion 39: 852- 855, 1999. 3 B b

GAM281 278 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A. 116:825- 827, 1941. 3 B b

GAM281 278 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal plasma. New Eng. J. Med. 339: 1734- 1738, 1998. 3 B b

GAM281 278 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome 1. Am. J. Med. Genet. 104: 250- 256, 2001. 3 B b

GAM281 278 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J. Clin. Invest. 100: 373- 379, 1997. 3 B b

GAM281 278 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 B b

153:771- 772, 1944.

GAM281 278 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th ed.): 1975. 3 B b

GAM281 278 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- to- pro substitution in the RhD polypeptide is responsiblefor the D(VII) category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995. 3 B b

GAM281 278 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral transduction of K562 cells establishes the molecular basisof Rh blood group antigens. Blood 87: 2968- 2973, 1996. 3 B b

GAM281 278 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang. 58: 50- 55, 1990. 3 B b

GAM281 278 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. Blood 95: 3662- 3668, 2000. 3 B b

GAM281 278 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393, 1999. 3 B b

GAM281 278 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311, 2002. 3 B b

GAM281 278 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 B b

GAM281 278 RPH3AL Kotake, K.; Ozaki, N.; Mizuta, M.; Sekiya, S.; Inagaki, N.; Seino,S.: Noc2, a putative zinc finger protein involved in exocytosis inendocrine cells. J. Biol. Chem. 272: 29407- 29410, 1997. 3 B b

GAM281 278 RPH3AL Smith, J. S.; Tachibana, I.; Allen, C.; Chiappa, S. A.; Lee, H.K.; McIver, B.; Jenkins, R. B.; Raffel, C.: Cloning of a human ortholog(RPH3AL) of (RNO)Rph3al from a candidate 17p13.3 medulloblastoma tumorsuppressor locus. Genomics 59: 97- 101, 1999. 3 B b

GAM281 278 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two scleroderma autoimmune antigens that copurify with human ribonucleaseP. Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997. 3 B b

GAM281 278 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: Autoantigenic properties of some protein subunits of catalyticallyactive complexes of human ribonuclease P. RNA 4: 407- 417, 1998. 3 B b

GAM281 278 SAS Jankowski, S. A.; De Jong, P.; Meltzer, P. S.: Genomic structureof SAS, a member of the transmembrane 4 superfamily amplified in humansarcomas. Genomics 25: 501- 506, 1995. 3 B b

GAM281 278 SAS Meltzer, P. S.; Jankowski, S. A.; Dal Cin, P.; Sandberg, A. A.;Paz, I. B.; Coccia, M. A.; Smith, S. H.: Identification and cloningof a novel amplified DNA sequence in human malignant fibrous histiocytomaderived from a region of chromosome 12 frequently rearranged in softtissue tumors. (Abstract) Cytogenet. Cell Genet. 58: 1979 only,1991. 3 B b

GAM281 278 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 B b

GAM281 278 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 3 B b

62: 94- 95, 2002.

GAM281 278 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 B b

GAM281 278 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999. 3 B b

GAM281 278 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001. 3 B b

GAM281 278 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001. 3 B b

GAM281 278 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five- base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000. 3 B b

GAM281 278 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001. 3 B b

GAM281 278 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002. 3 B b

GAM281 278 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001. 3 B b

GAM281 278 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999. 3 B b

GAM281 278 SERPINB8 Bartuski, A. J.; Kamachi, Y.; Schick, C.; Overhauser, J.; Silverman,G. A.: Cytoplasmic antiproteinase 2 (PI8) and bomapin (PI10) mapto the serpin cluster at 18q21.3. Genomics 43: 321- 328, 1997. 3 B c

GAM281 278 SERPINB8 Huber, R.; Carrell, R. W.: Implications of the three- dimensionalstructure of alpha 1- antitrypsin for structure and function of serpins. Biochemistry 28:8951- 8966, 1989. 3 B c

GAM281 278 SERPINB8 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 B c

GAM281 278 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic 3 B b

cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001.

GAM281 278 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996. 3 B b

GAM281 278 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001. 3 B b

GAM281 278 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 B b

GAM281 278 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996. 3 B b

GAM281 278 SHFM3 Gurrieri, F.; Genuardi, M.; Chiurazzi, P.; Gillessen- Kaesbach,G.; Neri, G.: Exclusion of linkage between autosomal dominant splithand/split foot and markers from chromosome 7q: further evidence forgenetic heterogeneity. (Letter) Am. J. Hum. Genet. 55: 853- 855,1994. 3 B c

GAM281 278 SHFM3 Gurrieri, F.; Prinos, P.; Tackels, D.; Kilpatrick, M. W.; Allanson,J.; Genuardi, M.; Vuckov, A.; Nanni, L.; Sangiorgi, E.; Garofalo,G.; Nunes, M. E.; Neri, G.; Schwartz, C.; Tsipouras, P.: A splithand- split foot (SHFM3) gene is located at 10q24- q25. Am. J. Med.Genet. 62: 427- 436, 1996. 3 B c

GAM281 278 SHFM3 Ianakiev, P.; Kilpatrick, M. W.; Dealy, C.; Kosher, R.; Korenberg,J. R.; Chen, X.- N.; Tsipouras, P.: A novel human gene encoding anF- box/WD40 containing protein maps in the SHFM3 critical region on10q24. Biochem. Biophys. Res. Commun. 261: 64- 70, 1999. 3 B c

GAM281 278 SHFM3 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning and expression analysis of new members of the mammalianF- box protein family. Genomics 67: 40- 47, 2000. 3 B c

GAM281 278 SHFM3 Johnson, K. R.; Lane, P. W.; Ward- Bailey, P.; Davisson, M. T.:Mapping the mouse dactylaplasia mutation, Dac, and a gene that controlsits expression, mdac. Genomics 29: 457- 464, 1995. 3 B c

GAM281 278 SHFM3 Nunes, M. E.; Schutt, G.; Kapur, R. P.; Luthardt, F.; Kukolich,M.; Byers, P.; Evans, J. P.: A second autosomal split hand/foot locusmaps to chromosome 10q24- q25. Hum. Molec. Genet. 4: 2165- 2170, 1995. 3 B c

GAM281 278 SHFM3 Ozen, R. S.; Baysal, B. E.; Devlin, B.; Farr, J. E.; Gorry, M.;Ehrlich, G. D.; Richard, C. W., III: Fine mapping of the split- hand/split- footlocus (SHFM3) at 10q24: evidence for anticipation and segregationdistortion. Am. J. Hum. Genet. 64: 1646- 1654, 1999. 3 B c

GAM281 278 SHFM3 Palmer, S. E.; Scherer, S. W.; Kukolich, M.; Wijsman, E. M.; Tsui,L.- C.; Stephens, K.; Evans, J. P.: Evidence for locus heterogeneityin human autosomal dominant split hand/split foot malformation. Am.J. Hum. Genet. 55: 21- 26, 1994. 3 B c

GAM281 278 SHFM3 Raas- Rothschild, A.; Manouvrier, S.; Gonzales, M.; Farriaux, J.P.; Lyonnet, S.; Munnich, A.: Refined mapping of a gene for splithand- split foot malformation (SHFM3) on chromosome 10q25. J. Med.Genet. 33: 996- 1001, 1996. 3 B c

GAM281 278 SHFM3 Sidow, A.; Bulotsky, M. S.; Kerrebrock, A. W.; Birren, B. W.;Altshuler, D; Jaenisch, R.; Johnson, K. R.; Lander, E. S.: A novelmember of the F- 3 B c

box/WD40 gene family, encoding dactylin, is disruptedin the mouse dactylaplasia mutant. Nature Genet. 23: 104- 107, 1999.

GAM281 278 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 3 B c

GAM281 278 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 3 B c

GAM281 278 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 3 B c

GAM281 278 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 3 B b

GAM281 278 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J recombinase activity. Science 250: 1426- 1429, 1990. 3 B b

GAM281 278 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 B b

GAM281 278 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990. 3 B b

GAM281 278 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995. 3 B b

GAM281 278 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic axial development and left- right specification. Nature 399:691- 694, 1999. 3 B b

GAM281 278 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.; Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998. 3 B c

GAM281 278 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea transporter in the human kidney. FEBS Lett. 386: 156- 160,1996. 3 B c

GAM281 278 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.; Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2 is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157- 2164, 2001. 3 B c

GAM281 278 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human intestine:biology and function. Gastroenterology 113: 332- 340, 1997. 3 B b

GAM281 278 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563- 566, 1994. 3 B b

GAM281 278 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 3 B b

GAM281 278 SLC21A2 Kanai, N.; Lu, R.; Satriano, J. A.; Bao, Y.; Wolkoff, A. W.; Schuster,V. L.: Identification and characterization of a prostaglandin transporter. Science 268:866- 869, 1995. 3 B c

GAM281 278 SLC21A2 Lu, R.; Kanai, N.; Bao, Y.; Schuster, V. L.: Cloning, in vitroexpression, and tissue distribution of a human prostaglandin transportercDNA (hPGT). J. Clin. Invest. 98: 1142- 1149, 1996. 3 B c

GAM281 278 SLC21A2 Lu, R.; Schuster, V. L.: Molecular cloning of the gene for thehuman prostaglandin transporter hPGT: gene organization, promoteractivity, and chromosomal localization. Biochem. Biophys. Res. Commun. 246:805- 812, 1998. 3 B c

GAM281 278 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998. 3 B b

GAM281 278 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 3 B b

GAM281 278 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses and phylogenetic characterization of the ZIP family of metalion transport proteins. J. Membr. Biol. 166: 1- 7, 1998. 3 B b

GAM281 278 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping within the epidermal differentiation complex. Genomics 62:272- 280, 1999. 3 B b

GAM281 278 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC fragmentation map of 1q21. Genomics 49: 200- 208, 1998. 3 B b

GAM281 278 SLC6A3 Byerley, W.; Hoff, M.; Holik, J.; Caron, M. G.; Giros, B.: VNTRpolymorphism for the human dopamine transporter gene (DAT1). Hum.Molec. Genet. 2: 335, 1993. 3 B c

GAM281 278 SLC6A3 Cook, E. H., Jr.; Stein, M. A.; Krasowski, M. D.; Cox, N. J.; Olkon,D. M.; Kieffer, J. E.; Leventhal, B. L.: Association of attention- deficitdisorder and the dopamine transporter gene. Am. J. Hum. Genet. 56:993- 998, 1995. 3 B c

GAM281 278 SLC6A3 Doucette- Stamm, L.; Blakely, D. J.; Tian, J.; Mockus, S.; Mao,J.: Population genetic study of the human dopamine transporter gene(DAT1). Genet. Epidemiol. 12: 303- 308, 1995. 3 B c

GAM281 278 SLC6A3 Gainetdinov, R. R.; Wetsel, W. C.; Jones, S. R.; Levin, E. D.;Jaber, M.; Caron, M. G.: Role of serotonin in the paradoxical calmingeffect of psychostimulants on hyperactivity. Science 283: 397- 401,1999. 3 B c

GAM281 278 SLC6A3 Gelernter, J.; Vandenbergh, D.; Kruger, S. D.; Pauls, D. L.; Kurlan,R.; Pakstis, A. J.; Kidd, K. K.; Uhl, G.: The dopamine transporterprotein gene (SLC6A3): primary linkage mapping and linkage studiesin Tourette syndrome. Genomics 30: 459- 463, 1995. 3 B c

GAM281 278 SLC6A3 Gill, M.; Daly, G.; Heron, S.; Hawi, Z.; Fitgerald, M.: Confirmationof association between attention deficit hyperactivity disorder anda dopamine transporter polymorphism. Molec. Psychiat. 2: 311- 313,1997. 3 B c

GAM281 278 SLC6A3 Giros, B.; El Mestikawy, S.; Godinot, N.; Zheng, K.; Han, H.; Yang- Feng,T.; Caron, M. G.: Cloning, pharmacological characterization, andchromosome 3 B c

assignment of the human dopamine transporter. Molec. Pharm. 42:383- 390, 1992.

GAM281 278 SLC6A3 Giros, B.; Jaber, M.; Jones, S. R.; Wightman, R. M.; Caron, M.G.: 3 B c
Hyperlocomotion and indifference to cocaine and amphetamine inmice lacking the dopamine receptor. Nature 370: 606- 612, 1996.

GAM281 278 SLC6A3 Goldman, D.: Dopamine transporter, alcoholism and other diseases. NatureMed. 3 B c
1: 624- 625, 1995.

GAM281 278 SLC6A3 Kurlan, R.; Behr, J.; Medved, L.; Shoulson, I.; Pauls, D.; Kidd,J. R.; Kidd, 3 B c
K. K.: Familial Tourette's syndrome: report of a largepedigree and potential for linkage analysis. Neurology 36: 772- 776,1986.

GAM281 278 SLC6A3 Lerman, C.; Caporaso, N. E.; Audrain, J.; Main, D.; Bowman, E.D.; Lockshin, 3 B c
B.; Boyd, N. R.; Shields, P. G.: Evidence suggestingthe role of specific genetic factors in cigarette smoking. HealthPsych. 18: 14- 20, 1999.

GAM281 278 SLC6A3 Lossie, A. C.; Vandenbergh, D. J.; Uhl, G. R.; Camper, S. A.:Localization of 3 B c
the dopamine transporter gene, Dat1, on mouse chromosome

GAM281 278 SLC6A3 Mammalian Genome 5: 117- 118, 1994.13. Sabol, S. Z.; Nelson, M. L.; Fisher, 3 B c
C.; Gunzerath, L.; Brody,C. L.; Hu, S.; Sirota, L. A.; Marcus, S. E.; Greenberg, B. D.; Lucas,F. R., IV; Benjamin, J.; Murphy, D. L.; Hamer, D. H.: A genetic associationfor cigarette smoking behavior. Health Psych. 18: 7- 13, 1999.

GAM281 278 SLC6A3 Tiihonen, J.; Kuikka, J.; Bergstrom, K.; Hakola, P.; Karhu, J.;Ryynanen, O.- 3 B c
P.; Fohr, J.: Altered striatal dopamine re- uptake sitedensities in habitually violent and non- violent alcoholics. NatureMed. 1: 654- 657, 1995.

GAM281 278 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Hawkins, A. L.; Griffin, C.A.; Li, X.; 3 B c
Jabs, E. W.; Uhl, G. R.: Human dopamine transporter gene(DAT1) maps to chromosome 5p15.3 and displays a VNTR. Genomics 14:1104- 1106, 1992.

GAM281 278 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Uhl, G. R.: A human dopaminetransporter 3 B c
cDNA predicts reduced glycosylation, displays a novelrepetitive element and provides racially- dimorphic TaqI RFLPs. Molec.Brain Res. 15: 161- 166, 1992.

GAM281 278 SLC6A3 Waldman, I. D.; Rowe, D. C.; Abramowitz, A.; Kozel, S. T.; Mohr,J. H.; 3 B c
Sherman, S. L.; Cleveland, H. H.; Sanders, M. L.; Gard, J.M. C.; Stever, C.: Association and linkage of the dopamine transportergene and attention- deficit hyperactivity disorder in children: heterogeneityowing to diagnostic subtype and severity. Am. J. Hum. Genet. 63:1767- 1776, 1998.

GAM281 278 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland 3 B b
biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855- 862, 2000.

GAM281 278 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein 3 B b
that promotes cytochrome c- dependent caspase activation byeliminating IAP inhibition. Cell 102: 33- 42, 2000.

GAM281 278 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; 3 B b
Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000.

GAM281 278 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; 3 B b
Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509- 3517, 2002.

GAM281 278 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 B b

GAM281 278 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; 3 B b
Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.:
A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates
caspase activity and apoptosis. Nature 410:112- 116, 2001.

GAM281 278 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, 3 B b
G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO,
a mammalian protein that promotes apoptosis by bindingto and antagonizing
IAP proteins. Cell 102: 43- 53, 2000.

GAM281 278 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: 3 B b
Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012,
2000.

GAM281 278 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from 3 B c
lamellipodia- like cell surface projections regulates compoundexocytosis in
mast cells. Cell 94: 537- 548, 1998.

GAM281 278 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; 3 B c
Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic
organization,chromosomal localization, alternative splicing, and isoforms of
thehuman synaptosome- associated protein- 23 gene implicated in vesicle-
membranefusion processes. Hum. Genet. 108: 211- 215, 2001.

GAM281 278 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- 3 B c
membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells.
Biochem. Biophys. Res. Commun. 231: 808- 812, 1997.

GAM281 278 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel 3 B c
syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in
non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996.

GAM281 278 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: 3 B c
Identification of three new splice variants of the SNARE proteinSNAP- 23.
Biochem. Biophys. Res. Commun. 285: 320- 327, 2001.

GAM281 278 SPN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, 3 B b
J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM-
dependent movement of CD43 defines a novelprotein complex distal to the
immunological synapse. Immunity 15:739- 750, 2001.

GAM281 278 SPN Baecher, C. M.; Dorfman, K. S.; Mattei, M.- G.; Frelinger, J. G.: cDNA 3 B b
cloning and localization of the mouse leukosialin gene (Ly48)to chromosome
7. Immunogenetics 31: 307- 314, 1990.

GAM281 278 SPN Bazil, V.; Strominger, J. L.: CD43, the major sialoglycoproteinof human 3 B b
leukocytes, is proteolytically cleaved from the surface ofstimulated
lymphocytes and granulocytes. Proc. Nat. Acad. Sci. 90:3792- 3796, 1993.

GAM281 278 SPN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe 3 B b
immunological synapse is mediated by phosphorylation- regulatedrelocation of
the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001.

GAM281 278 SPN Pallant, A.; Eskenazi, A.; Mattei, M.- G.; Fournier, R. E. K.; Carlsson,S. 3 B b
R.; Fukuda, M.; Frelinger, J. G.: Characterization of cDNAs encodinghuman
leukosialin and localization of the leukosialin gene to chromosome16. Proc.
Nat. Acad. Sci. 86: 1328- 1332, 1989.

GAM281 278 SPN Park, J. K.; Rosenstein, Y. J.; Remold- O'Donnell, E.; Bierer, B.E.; Rosen, 3 B b
F. S.; Burakoff, S. J.: Enhancement of T- cell activationby the CD43
molecule whose expression is defective in Wiskott- Aldrichsyndrome. Nature
350: 706- 709, 1991.

GAM281 278 SPN Rosenstein, Y.; Park, J. K.; Hahn, W. C.; Rosen, F. S.; Bierer,B. E.; 3 B b

Burakoff, S. J.: CD43, a molecule defective in Wiskott- Aldrichsyndrome, binds ICAM- 1. Nature 354: 233- 235, 1991.

GAM281 278 SPN Schmid, K.; Hediger, M. A.; Brossmer, R.; Collins, J. H.; Haupt,H.; Marti, T.; Offner, G. D.; Schaller, J.; Takagaki, K.; Walsh, M.T.; Schwick, H. G.; Rosen, F. S.; Remold- O'Donnell, E.: Amino acidsequence of human plasma galactoglycoprotein: identity with the extracellularregion of CD43 (sialophorin). Proc. Nat. Acad. Sci. 89: 663- 667,1992. 3 B b

GAM281 278 SPN Shelley, C. S.; Carroll, M. C.; Davis, A. E., III; Bruns, G. A.P.; Whitehead, A. S.; Finberg, R.; Remold- O'Donnell, E.; Rosen, F.S.: Human sialophorin: cDNA cloning and gene location. (Abstract) FASEBJ. 2: A1659 only, 1988. 3 B b

GAM281 278 SPN Shelley, C. S.; Remold- O'Donnell, E.; Davis, A. E., III; Bruns,G. A. P.; Rosen, F. S.; Carroll, M. C.; Whitehead, A. S.: Molecularcharacterization of sialophorin (CD43), the lymphocyte surface sialoglycoproteindefective in Wiskott- Aldrich syndrome. Proc. Nat. Acad. Sci. 86:2819- 2823, 1989. 3 B b

GAM281 278 SPN Shelley, C. S.; Remold- O'Donnell, E.; Rosen, F. S.; Whitehead,A. S.: Structure of the human sialophorin (CD43) gene: identificationof features atypical of genes encoding integral membrane proteins. Biochem.J. 270: 569- 576, 1990. 3 B b

GAM281 278 SPN van den Berg, T. K.; Nath, D.; Ziltener, H. J.; Vestweber, D.;Fukuda, M.; van Die, I.; Crocker, P. R.: Cutting edge: CD43 functionsas a T cell counterreceptor for the macrophage adhesion receptor sialoadhesin(Siglec- 1). J. Immun. 166: 3637- 3640, 2001. 3 B b

GAM281 278 SRRM2 Blencowe, B. J.; Bauren, G.; Eldridge, A. G.; Issner, R.; Nickerson,J. A.; Rosonina, E.; Sharp, P. A.: The SRm160/300 splicing coactivatorsubunits. RNA 6: 111- 120, 2000. 3 B c

GAM281 278 SRRM2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B c

GAM281 278 SRRM2 Sawada, Y.; Miura, Y.; Umeki, K.; Tamaoki, T.; Fujinaga, K.; Ohtaki,S.: Cloning and characterization of a novel RNA- binding protein SRL300with RS domains. Biochim. Biophys. Acta 1492: 191- 195, 2000. 3 B c

GAM281 278 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994. 3 B b

GAM281 278 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995. 3 B b

GAM281 278 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand characterization of the mouse homolog of SYT, a gene implicatedin the development of human synovial sarcomas. Oncogene 13: 643- 648,1996. 3 B b

GAM281 278 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. G.: Mapping and characterization of the mouse and humanSS18 genes, two human SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310- 319, 2001. 3 B b

GAM281 278 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 B b
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene
family with several members transcribed in normaltestis and human cancer.
Int. J. Cancer 72: 965- 971, 1997.

GAM281 278 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 B b
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand
prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM281 278 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 B b
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J.
Nat. Cancer Inst. 91: 974- 975, 1999.

GAM281 278 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 B b
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX
synovial sarcoma translocation proteins and co- localizationwith the SNF
protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM281 278 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 B b
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in
synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM281 278 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- 3 B b
strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence
insitu hybridization. Genomics 36: 527- 529, 1996.

GAM281 278 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence 3 B b
homologue of staufen is an RNA- binding protein thatis associated with
polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell.
Biol. 19: 2212- 2219, 1999.

GAM281 278 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: 3 B b
Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein
which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19:
2220- 2230, 1999.

GAM281 278 STE Aksoy, I. A.; Wood, T. C.; Weinshilboum, R.: Human liver 3 B b
estrogensulfotransferase: identification by cDNA cloning and expression.
Biochem.Biophys. Res. Commun. 200: 1621- 1629, 1994.

GAM281 278 STE Bernier, F.; Leblanc, G.; Labrie, F.; Luu- The, V.: Structure ofhuman 3 B b
estrogen and aryl sulfotransferase gene: two mRNA species issuedfrom a
single gene. J. Biol. Chem. 269: 28200- 28205, 1994.

GAM281 278 STE Her, C.; Aksoy, I. A.; Kimura, S.; Brandriff, B. F.; Wasmuth, J.J.; 3 B b
Weinshilboum, R. M.: Human estrogen sulfotransferase gene (STE):cloning,
structure, and chromosomal localization. Genomics 29: 16- 23,1995.

GAM281 278 STE Weinshilboum, R. M.; Otterness, D. M.; Aksoy, I. A.; Wood, T. C.;Her, C.; 3 B b
Raftogianis, R. B.: Sulfotransferase molecular biology:cDNAs and genes.
FASEB J. 11: 3- 14, 1997.

GAM281 278 STE Weinshilboum, R.: Personal Communication. Rochester, Minn. 10/9/1995. 3 B b

GAM281 278 STK10 Kuramochi, S.; Matsuda, Y.; Okamoto, M.; Kitamura, F.; Yonekawa,H.; 3 B c
Karasuyama, H.: Molecular cloning of the human gene STK10
encodinglymphocyte- oriented kinase, and comparative chromosomal mapping
ofthe human, mouse, and rat homologues. Immunogenetics 49: 369- 375,1999.

GAM281 278 STK10 Kuramochi, S.; Moriguchi, T.; Kuida, K.; Endo, J.; Semba, K.; Nishida,E.; 3 B c
Karasuyama, H.: LOK is a novel mouse STE20- like protein kinasethat is
expressed predominantly in lymphocytes. J. Biol. Chem. 272:22679- 22684,
1997.

GAM281 278 TAF11 Birck, C.; Poch, O.; Romier, C.; Ruff, M.; Mengus, G.; Lavigne,A.- C.; 3 B c

Davidson, I.; Moras, D.: Human TAFII28 and TAFII18 interactthrough a histone fold encoded by atypical evolutionary conservedmotifs also found in the SPT3 family. Cell 94: 239- 249, 1998.

GAM281 278 TAF11 Mengus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.;Davidson, I.: Cloning and characterization of hTAFII18, hTAFII20and hTAFII28: three subunits of the human transcription factor TFIID. EMBOJ. 14: 1520- 1531, 1995. 3 B c

GAM281 278 TAL1 Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 3 B c

GAM281 278 TAL1 Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 B c

GAM281 278 TAL1 Begley, C. G.; Aplan, P. D.; Davey, M. P.; Nakahara, K.; Tchorz,K.; Kurtzberg, J.; Hershfield, M. S.; Haynes, B. F.; Cohen, D. I.;Waldmann, T. A.; Kirsch, I. R.: Chromosomal translocation in a humanleukemic stem- cell line disrupts the T- cell antigen receptor delta- chaindiversity region and results in a previously unreported fusion transcript. Proc.Nat. Acad. Sci. 86: 2031- 2035, 1989. 3 B c

GAM281 278 TAL1 Begley, C. G.; Visvader, J.; Green, A. R.; Aplan, P. D.; Metcalf,D.; Kirsch, I. R.; Gough, N. M.: Molecular cloning and chromosomallocalization of the murine homolog of the human helix- loop- helix geneSCL. Proc. Nat. Acad. Sci. 88: 869- 873, 1991. 3 B c

GAM281 278 TAL1 Finger, L. R.; Kagan, J.; Christopher, G.; Kurtzberg, J.; Hershfield,M. S.; Nowell, P. C.; Croce, C. M.: Involvement of the TCL5 geneon human chromosome 1 in T- cell leukemia and melanoma. Proc. Nat.Acad. Sci. 86: 5039- 5043, 1989. 3 B c

GAM281 278 TAL1 Gottgens, B.; Barton, L. M.; Chapman, M. A.; Sinclair, A. M.; Knudsen,B.; Grafham, D.; Gilbert, J. G. R.; Rogers, J.; Bentley, D. R.; Green,A. R.: Transcriptional regulation of the stem cell leukemia gene(SCL)- - comparative analysis of five vertebrate SCL loci. Genome Res. 12:749- 759, 2002. 3 B c

GAM281 278 TAL1 Gottgens, B.; Gilbert, J. G.; Barton, L. M.; Grafham, D.; Rogers,J.; Bentley, D. R.; Green, A. R.: Long- range comparison of humanand mouse SCL loci: localized regions of sensitivity to restrictionendonucleases correspond precisely with peaks of conserved noncodingsequences. Genome Res. 11: 87- 97, 2001. 3 B c

GAM281 278 TAL1 Kocher, O.; Cheresh, P.; Lee, S. W.: Identification and partialcharacterization of a novel membrane- associated protein (MAP17) up-regulatedin human carcinomas and modulating cell replication and tumor growth. Am.J. Path. 149: 493- 500, 1996. 3 B c

GAM281 278 TAL1 Kozak, M.: An analysis of 5- prime- noncoding sequences from 699vertebrate messenger RNAs. Nucleic Acids Res. 15: 8125- 8148, 1987. 3 B c

GAM281 278 TAL1 Kurtzberg, J.; Bigner, S. H.; Hershfield, M. S.: Establishmentof the DU.528 human lymphohemopoietic stem cell line. J. Exp. Med. 162:1561- 1578, 1985. 3 B c

GAM281 278 TAL1 Robb, L.; Lyons, I.; Li, R.; Hartley, L.; Kontgen, F.; Harvey,R. P.; Metcalf, D.; Begley, C. G.: Absence of yolk sac hematopoiesisfrom mice with a targeted disruption of the scl gene. Proc. Nat.Acad. Sci. 92: 7075- 7079, 3 B c

1995.

GAM281 278 TAL1 Shivdasani, R. A.; Mayer, E. L.; Orkin, S. H.: Absence of bloodformation in mice lacking the T- cell leukaemia oncoprotein tal- 1/SCL. Nature 373:432-434, 1995. 3 B c

GAM281 278 TAL1 Sinclair, A. M.; Bench, A. J.; Bloor, A. J. C.; Li, J.; Gottgens,B.; Stanley, M. L.; Miller, J.; Piltz, S.; Hunter, S.; Nacheva, E.P.; Sanchez, M.- J.; Green, A. R.: Rescue of the lethal scl- /- phenotypeby the human SCL locus. Blood 99: 3931- 3938, 2002. 3 B c

GAM281 278 TAL1 Williams, M.; Lyu, M. S.; Yang, Y. L.; Lin, E. P.; Dunbrack, R.;Birren, B.; Cunningham, J.; Hunter, K.: Ier5, a novel member of theslow- kinetics immediate- early genes. Genomics 44: 327- 334, 1999. 3 B c

GAM281 278 TAL1 Xia, Y.; Brown, L.; Yang, C. Y.- C.; Tsou Tsan, J.; Siciliano,M. J.; Espinosa, R., III; Le Beau, M. M.; Baer, R. J.: TAL2, a helix- loop-helixgene activated by the (7;9)(q34;q32) translocation in human T-cellleukemia. Proc. Nat. Acad. Sci. 88: 11416- 11420, 1991. 3 B c

GAM281 278 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459-467, 1998. 3 B b

GAM281 278 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 B b

GAM281 278 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 B b

GAM281 278 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 B b

GAM281 278 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 B b

GAM281 278 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 B b

GAM281 278 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496-1498, 2002. 3 B b

GAM281 278 TAT Barton, D. E.; Yang- Feng, T. L.; Francke, U.: The human tyrosineaminotransferase gene mapped to the long arm of chromosome 16 (region16q22- q24) by somatic cell hybrid analysis and in situ hybridization. Hum.Genet. 72: 221- 224, 1986. 3 B b

GAM281 278 TAT Beinfang, D. C.; Kuwabara, T.; Pueschel, S. M.: The Richner-Hanhartsyndrome: report of a case with associated tyrosinemia. Arch. Ophthal. 94:1133- 1137, 1976. 3 B b

GAM281 278 TAT Bohnert, A.; Anton- Lamprecht, I.: Richner- Hanhart's syndrome:ultrastructural abnormalities of epidermal keratinization indicatinga causal relationship to high intracellular tyrosine levels. J. Invest.Derm. 79: 68- 74, 1982. 3 B b

GAM281 278 TAT Buist, N.: Phenylketonuria and related problems.In: Nyhan, W.L.: Amino Acid 3 B b
Metabolism and Genetic Variation. New York: McGraw- Hill(pub.) 1967. Pp.
117 only.

GAM281 278 TAT Chitayat, D.; Balbul, A.; Hani, V.; Mamer, O. A.; Clow, C.; Scriver,C. R.: 3 B b
Hereditary tyrosinaemia type II in a consanguineous AshkenaziJewish family:
intrafamilial variation in phenotype; absence of parentalphenotype effects
on the fetus. J. Inherit. Metab. Dis. 15: 198- 203,1992.

GAM281 278 TAT Crovato, F.; Desirello, G.; Gatti, R.; Babbini, N.; Rebora, A.: Richner- 3 B b
Hanhart syndrome spares a plantar autograft. Arch. Derm. 121:539- 540, 1985.

GAM281 278 TAT Fellman, J. H.; Vanbellinghen, P. J.; Jones, R. T.; Koler, R. D.: Soluble 3 B b
and mitochondrial forms of tyrosine aminotransferase: relationshipto human
tyrosinemia. Biochemistry 8: 615- 622, 1969.

GAM281 278 TAT Garibaldi, L. R.; Siliato, F.; De Martini, I.; Scarsi, M. R.; Romano,C.: 3 B b
Oculocutaneous tyrosinosis: report of two cases in the same family.
Helv.Paediat. Acta 32: 173- 180, 1977.

GAM281 278 TAT Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald,P. S.; 3 B b
Baden, H. P.: Tyrosinemia with plantar and palmar keratosisand keratitis. J.
Pediat. 83: 798- 805, 1973.

GAM281 278 TAT Hanhart, E.: Neue Sonderformen von Keratosis palmo- plantaris,u.a. eine 3 B b
regelmaessig- dominante mit systematisierten Lipomen, ferner2 einfach-
rezessive mit Schwachsinn und z.T. mit Hornhautveraenderungendes Auges
(Ektodermatosyndrom). Dermatologica 94: 286- 308, 1947.

GAM281 278 TAT Hunziker, N.: Richner- Hanhart syndrome and tyrosinemia type II. 3 B b
Dermatologica 160:180- 189, 1980.

GAM281 278 TAT Kennaway, N. G.; Buist, N. R. M.: Metabolic studies in a patientwith hepatic 3 B b
cytosol tyrosine aminotransferase deficiency. Pediat.Res. 5: 287- 297, 1971.

GAM281 278 TAT Muller, G.; Scherer, G.; Zentgraf, H.; Ruppert, S.; Herrmann,B.; Lehrach, 3 B b
H.; Schutz, G.: Isolation, characterization and chromosomalmapping of the
mouse tyrosine aminotransferase gene. J. Molec. Biol. 184:367- 373, 1985.

GAM281 278 TAT Natt, E.; Kao, F.- T.; Rettenmeier, R.; Scherer, G.: Assignmentof the human 3 B b
tyrosine aminotransferase gene to chromosome 16. Hum.Genet. 72: 225- 228,
1986.

GAM281 278 TAT Natt, E.; Kida, K.; Odievre, M.; Di Rocco, M.; Scherer, G.: Pointmutations 3 B b
in the tyrosine aminotransferase gene in tyrosinemia typeII. Proc. Nat.
Acad. Sci. 89: 9297- 9301, 1992.

GAM281 278 TAT Natt, E.; Westphal, E.- M.; Toth- Fejel, S. E.; Magenis, R. E.;Buist, N. R. 3 B b
M.; Rettenmeier, R.; Scherer, G.: Inherited and de novodeletion of the
tyrosine aminotransferase gene locus at 16q22.1- q22.3in a patient with
tyrosinemia type II. Hum. Genet. 77: 352- 358,1987.

GAM281 278 TAT Pelet, B.; Antener, I.; Faggioni, R.; Spahr, A.; Gautier, E.:Tyrosinemia 3 B b
without liver or renal damage with plantar and palmarkeratosis and keratitis
(hypertyrosinemia type II). Helv. Paediat.Acta 34: 177- 183, 1979.

GAM281 278 TAT Rehak, A.; Selim, M. M.; Yadav, G.: Richner- Hanhart syndrome(tyrosinaemia- 3 B b
II) (report of four cases without ocular involvement). Brit.J. Derm. 104:
469- 475, 1981.

GAM281 278 TAT Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.: Isolationand 3 B b
characterization of the human tyrosine aminotransferase gene. NucleicAcids
Res. 18: 3853- 3861, 1990.

GAM281 278 TAT Richner, H.: Hornhautaffektion bei Keratoma palmare et plantarehereditarium. 3 B b
Klin. Mbl. Augenheilk. 100: 580- 588, 1938.

GAM281 278 TAT Schmid, W.; Muller, G.; Schutz, G.; Gluecksohn- Waelsch, S.: Deletionsnear 3 B b
the albino locus on chromosome 7 of the mouse affect the levelof tyrosine
aminotransferase mRNA. Proc. Nat. Acad. Sci. 82: 2866- 2869,1985.

GAM281 278 TAT Tallab, T.M.: Richner- Hanhart syndrome: importance of early diagnosisand 3 B b
early intervention. J. Am. Acad. Dermatol. 35: 857- 859, 1996.

GAM281 278 TAT Ventura, G.; Biasini, G.; Petrozzi, M.: Cheratomia palmoplantaredissipatum 3 B b
associato a lesioni corneali in due fratelli. Boll. Oculist. 44:497- 510,
1965.

GAM281 278 TAT Waardenburg, P. J.; Franceschetti, A.; Klein, D.: Genetics andOphthalmology. 3 B b
Springfield, Ill.: Charles C Thomas (pub.) 1:1961. Pp. 515- 517.

GAM281 278 TAT Westphal, E.- M.; Natt, E.; Grimm, T.; Odievre, M.; Scherer, G.: The human 3 B b
tyrosine aminotransferase gene: characterization of restrictionfragment
length polymorphisms and haplotype analysis in a family withtyrosinemia type
II. Hum. Genet. 79: 260- 264, 1988.

GAM281 278 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; 3 B c
De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription
factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8:
165- 167, 1990.

GAM281 278 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 3 B c
homeoprotein family are expressed in human liver. NucleicAcids Res. 19:
3553- 3559, 1991.

GAM281 278 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't 3 B c
Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.;
Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene
are associated with familial hypoplastic glomerulocystickidney disease. Am.
J. Hum. Genet. 68: 219- 224, 2001.

GAM281 278 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; 3 B c
Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.;
Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated
with a frameshift mutation in the transcription factorhepatocyte nuclear
factor- 1- beta. Kidney Int. 57: 898- 907, 2000.

GAM281 278 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. 3 B c
N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara,
T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta
gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997.

GAM281 278 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic 3 B c
glomerulocystic kidney disease: a definite entity withdominant inheritance.
Am. J. Med. Genet. 34: 569- 573, 1989.

GAM281 278 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; 3 B c
Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand
genital malformation associated with a partial deletion of thepseudo- POU
domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001-
2008, 1999.

GAM281 278 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, 3 B c
S.: A low renal threshold for glucose in diabetic patientswith a mutation in
the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med.
15: 816- 820, 1998.

GAM281 278 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; 3 B c
Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in
the hepatocyte nuclear factor- 1- beta gene associated with diabetesand

renal dysfunction. Diabetes 47: 1354- 1355, 1998.

GAM281 278 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: 3 B c
Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18:
263- 268, 1982.

GAM281 278 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott- 3 B c
Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G.
U.: The mutated human gene encoding hepatocyte nuclear factor1- beta
inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad.
Sci. 97: 4695- 4700, 2000.

GAM281 278 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; 3 B c
Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.;
Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1
are associated with human left- right lateralitydefects. Nature Genet. 26:
365- 369, 2000.

GAM281 278 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: 3 B c
Molecular characterization of a gene of the 'EGF family' expressedin
undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991,
1989.

GAM281 278 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, 3 B c
A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation
in the CFC domain of TDGF1 is associated with human forebraindefects. Hum.
Genet. 110: 422- 428, 2002.

GAM281 278 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; 3 B c
Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene
and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991.

GAM281 278 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. 3 B c
A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes.
Mammalian Genome 8: 502- 505, 1997.

GAM281 278 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; 3 B c
Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and
Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996.

GAM281 278 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, 3 B c
G.: Regional localization of the human EGF- like growthfactor CRIPTO gene
(TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995.

GAM281 278 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in 3 B c
vertebratedevelopment. Trends Genet. 16: 303- 309, 2000.

GAM281 278 TERF1 Broccoli, D.; Chong, L.; Oelmann, S.; Fernald, A. A.; Marziliano,N.; van 3 B b
Steensel, B.; Kipling, D.; Le Beau, M. M.; de Lange, T.:Comparison of the
human and mouse genes encoding the telomeric protein,TRF1: chromosomal
localization, expression and conserved protein domains. Hum.Molec. Genet. 6:
69- 76, 1997.

GAM281 278 TERF1 Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.;Hanish, 3 B b
J.; Tempst, P.; de Lange, T.: A human telomeric protein. Science 270:1663-
1667, 1995.

GAM281 278 TERF1 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 B b
the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2.
Molec. Cell 8: 351- 361, 2001.

GAM281 278 TERF1 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 B b
Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell
97: 503- 514, 1999.

GAM281 278 TERF1 Kim, S.; Kaminker, P.; Campisi, J.: TIN2, a new regulator of telomerelength 3 B b
in human cells. Nature Genet. 23: 405- 412, 1999.

GAM281 278 TERF1 Marcand, S.; Gilson, E.; Shore, D.: A protein- counting mechanismfor 3 B b
telomere length regulation in yeast. Science 275: 986- 990, 1997.

GAM281 278 TERF1 Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M.: TRF1 is a 3 B b
critical trans- acting factor required for de novo telomereformation in
human cells. Hum. Molec. Genet. 9: 2639- 2650, 2000.

GAM281 278 TERF1 Young, A. C.; Chavez, M.; Giambernardi, T. A.; Mattern, V.; McGill,J. R.; 3 B b
Harris, J. M.; Sarosdy, M. F.; Patel, P.; Sakaguchi, A. Y.: Organization and
expression of human telomere repeat binding factorgenes. Somat. Cell Molec.
Genet. 23: 275- 286, 1997.

GAM281 278 TERF1 Zakian, V. A.: Telomeres: beginning to understand the end. Science 270:1601- 3 B b
1607, 1995.

GAM281 278 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: 3 B b
Strand- specific postreplicative processing of mammalian telomeres. Science
293:2462- 2465, 2001.

GAM281 278 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: 3 B b
Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet.
17: 236- 239, 1997.

GAM281 278 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres 3 B b
contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17:
231- 235, 1997.

GAM281 278 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 B b
the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2.
Molec. Cell 8: 351- 361, 2001.

GAM281 278 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 B b
Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell
97: 503- 514, 1999.

GAM281 278 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered 3 B b
telomere state, not telomere loss. Science 295: 2446- 2449,2002.

GAM281 278 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; 3 B b
McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization
of the transcribed human telomere repeat binding factor2 gene and
comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163,
1998.

GAM281 278 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman 3 B b
telomeres from end- to- end fusions. Cell 92: 401- 413, 1998.

GAM281 278 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 B b
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human
telomeres. Nature Genet. 25: 347- 352, 2000.

GAM281 278 TK2 Johansson, M.; Karlsson, A.: Cloning of the cDNA and chromosomelocalization 3 B c
of the gene for human thymidine kinase 2. J. Biol. Chem. 272:8454- 8458,
1997.

GAM281 278 TK2 Mandel, H.; Szargel, R.; Labay, V.; Elpeleg, O.; Saada, A.; Shalata,A.; 3 B c
Anbinder, Y.; Berkowitz, D.; Hartman, C.; Barak, M.; Eriksson,S.; Cohen, N.:
The deoxyguanosine kinase gene is mutated in individualswith depleted
hepatocerebral mitochondrial DNA. Nature Genet. 29:337- 341, 2001. Note:
Erratum: Nature Genet. 29: 491 only, 2001.

GAM281 278 TK2 Saada, A.; Shaag, A.; Mandel, H.; Nevo, Y.; Eriksson, S.; Elpeleg,O.: Mutant 3 B c
mitochondrial thymidine kinase in mitochondrial DNA depletionmyopathy.

Nature Genet. 29: 342- 344, 2001.

GAM281 278 TK2 Wang, L.; Munch- Petersen, B.; Herrstrom Sjoberg, A.; Hellman, U.;Bergman, T.; Jornvall, H.; Eriksson, S.: Human thymidine kinase 2:molecular cloning and characterisation of the enzyme activity withantiviral and cytostatic nucleoside substrates. FEBS Lett. 443:170- 174, 1999. 3 B c

GAM281 278 TK2 Willecke, K.; Reuber, T.; Kucherlapati, R. S.; Ruddle, F. H.:Human mitochondrial thymidine kinase is coded for by a gene on chromosome16 of the nucleus. Somat. Cell Genet. 3: 237- 245, 1977. 3 B c

GAM281 278 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020- 4027, 1998. 3 B b

GAM281 278 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001. 3 B b

GAM281 278 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress different Toll- like receptors and respond to different microbialantigens. J. Exp. Med. 194: 863- 869, 2001. 3 B b

GAM281 278 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.; Mantovani, A.: Differential expression and regulation of Toll- likereceptors (TLR) in human leukocytes: selective expression of TLR3in dendritic cells. J. Immun. 164: 5998- 6004, 2000. 3 B b

GAM281 278 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A family of human receptors structurally related to DrosophilaToll. Proc. Nat. Acad. Sci. 95: 588- 593, 1998. 3 B b

GAM281 278 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and 13 others: Dominant and recessive deafnesscaused by mutations of a novel gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277- 284, 2002. 3 B b

GAM281 278 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M. H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant, progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002. 3 B b

GAM281 278 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999. 3 B c B

GAM281 278 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997. 3 B c B

GAM281 278 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. 3 B c B

Biol. 7: 1003- 1006, 1997.

GAM281 278 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 B c B W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM281 278 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 B c B decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997.

GAM281 278 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 B c B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997.

GAM281 278 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 B c B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM281 278 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 B c B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM281 278 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 B c B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM281 278 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 B c B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.

GAM281 278 TNFRSF18 Gurney, A. L.; Marsters, S. A.; Huang, A.; Pitti, R. M.; Mark,M.; Baldwin, 3 B c D. T.; Gray, A. M.; Dowd, P.; Brush, J.; Heldens, S.;Schow, P.; Goddard, A. D.; Wood, W. I.; Baker, K. P.; Godowski, P.J.; Ashkenazi, A.: Identification of a new member of the tumor necrosisfactor family and its receptor, a human ortholog of mouse GITR. Curr.Biol. 9: 215- 218, 1999.

GAM281 278 TNFRSF18 Kwon, B.; Yu, K.- Y.; Ni, J.; Yu, G.- L.; Jang, I.- K.; Kim, Y.- J.;Xing, 3 B c L.; Liu, D.; Wang, S.- X.; Kwon, B. S.: Identification of anovel activation- inducible protein of the tumor necrosis factor receptorsuperfamily and its ligand. J. Biol. Chem. 274: 6056- 6061, 1999.

GAM281 278 TNFRSF18 Nocentini, G.; Giunchi, L.; Ronchetti, S.; Krausz, L. T.; Bartoli,A.; 3 B c Moraca, R.; Migliorati, G.; Riccardi, C.: A new member of thetumor necrosis factor/nerve growth factor receptor family inhibitsT cell receptor- induced apoptosis. Proc. Nat. Acad. Sci. 94: 6216- 6221,1997.

GAM281 278 TNFRSF9 Alderson, M. R.; Smith, C. A.; Tough, T. W.; Davis- Smith, T.; Armitage,R. 3 B b J.; Falk, B.; Roux, E.; Baker, E.; Sutherland, G. R.; Din, W. S.;Goodwin, R. G.: Molecular and biological characterization of human4- 1BB and its ligand. Europ. J. Immun. 24: 2219- 2227, 1994.

GAM281 278 TNFRSF9 Kwon, B. S.; Weissman, S. M.: cDNA sequences of two inducibleT- cell genes. 3 B b Proc. Nat. Acad. Sci. 86: 1963- 1967, 1989.

GAM281 278 TNFRSF9 Loo, D. T.; Chalupny, N. J.; Bajorath, J.; Shuford, W. W.; Mittler,R. S.; 3 B b Aruffo, A.: Analysis of 4- 1BBL and laminin binding to murine4- 1BB, a member of the tumor necrosis factor receptor superfamily,and comparison with human 4- 1BB. J. Biol. Chem. 272: 6448- 6456,1997.

GAM281 278 TNFRSF9 Schwarz, H.; Arden, K.; Lotz, M.: CD137, a member of the tumornecrosis 3 B b

factor receptor family, is located on chromosome 1p36, ina cluster of related genes, and colocalizes with several malignancies. Biochem.Biophys. Res. Commun. 235: 699- 703, 1997.

GAM281 278 TNFRSF9 Schwarz, H.; Blanco, F. J.; von Kempis, J.; Valbracht, J.; Lotz,M.: ILA, a 3 B b member of the human nerve growth factor/tumor necrosisfactor receptor family, regulates T- lymphocyte proliferation and survival. Blood 87:2839-2845, 1996.

GAM281 278 TNFRSF9 Schwarz, H.; Tuckwell, J.; Lotz, M.: A receptor induced by 3 B b lymphocyteactivation (ILA): a new member of the human nerve- growth-factor/tumor- necrosis- factorreceptor family. Gene 134: 295- 298, 1993.

GAM281 278 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 B b Thiopurinemethyltransferase pharmacogenetics: alternative molecular diagnosisand preliminary data from Northern Portugal. Pharmacogenetics 9:257- 261, 1999.

GAM281 278 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 B b McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM281 278 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 B b Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof thiopurine methyltransferase alleles in Caucasian and Asian populations. Pharmacogenetics 9:37- 42, 1999.

GAM281 278 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 B b mercaptopurine metabolism, toxic effects, and dosagerequirement in a thiopurine methyltransferase- deficient child withacute lymphocytic leukemia. J. Pediat. 119: 985- 989, 1991.

GAM281 278 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 B b Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM281 278 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 B b Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine methyltransferase:molecular cloning and expression of T84 colon carcinoma cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM281 278 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 B b thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-749, 1993.

GAM281 278 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 B b Evans, W. E.: A single point mutation leading to loss of catalyticactivity in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953, 1995.

GAM281 278 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 B b variation in response to 6- mercaptopurine for childhoodacute lymphoblastic leukaemia. Lancet 336: 225- 229, 1990.

GAM281 278 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 B b azathioprine toxicity: relationship to thiopurine methyltransferasegenetic polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM281 278 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 B b Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in thiopurine methyltransferase pharmacogenetics: evidencefor allele specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773-776, 1999.

GAM281 278 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon splice junction mutation that results in lossof activity. J. Clin. Invest. 101: 1036- 1044, 1998. 3 B b

GAM281 278 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.; Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997. 3 B b

GAM281 278 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine methyltransferase pharmacogenetics: human gene cloningand characterization of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996. 3 B b

GAM281 278 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997. 3 B b

GAM281 278 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694- 702, 1996. 3 B b

GAM281 278 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980. 3 B b

GAM281 278 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor- associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF- kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997. 3 B c

GAM281 278 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661- 14664, 1996. 3 B c

GAM281 278 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999. 3 B c

GAM281 278 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997. 3 B c

GAM281 278 TRPM6 Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.; Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.: Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002. 3 B c

GAM281 278 TRPM6 Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.; Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002. 3 B c

GAM281 278 TRPM6 Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, 3 B c
D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.:
Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome:
genetic linkage mapping and analysis of abalanced translocation breakpoint.
Hum. Molec. Genet. 6: 1491- 1497,1997.

GAM281 278 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, 3 B b
psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994.

GAM281 278 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; 3 B b
Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired
nociception and pain sensation in mice lacking the capsaicinreceptor.
Science 288: 306- 313, 2000.

GAM281 278 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. 3 B b
D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the
pain pathway. Nature 389: 816- 824, 1997.

GAM281 278 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 B b
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release
the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411:
957- 962, 2001.

GAM281 278 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity 3 B b
to 'hot' chili peppers. Cell 108: 421- 430, 2002.

GAM281 278 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, 3 B b
A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related
osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor.
Cell 103: 525- 535, 2000.

GAM281 278 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated 3 B b
by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J.
Neurophysiol. 76: 1858- 1869, 1996.

GAM281 278 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel 3 B b
activity by protein kinase C. Nature 408: 985- 990, 2000.

GAM281 278 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand 3 B b
multiple presentations of the oral irritant zingerone: relationshipto
frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996.

GAM281 278 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith 3 B b
capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994.

GAM281 278 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand 3 B b
pleasantness for the capsaicin burn between chili likers and non-
likers:implications for liking development. Chem. Senses 18: 471- 482, 1993.

GAM281 278 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; 3 B b
McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.;
Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic
cystinosis gene (CTNS): complete sequencing of a200- kb segment and
discovery of a novel gene within the common cystinosis- causingdeletion.
Genome Res. 10: 165- 173, 2000.

GAM281 278 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; 3 B b
Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.;
Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.;
Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the
vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002.

GAM281 278 TUFT1 Bashir, M. M.; Abrams, W. R.; Tucker, T.; Sellinger, B.; Budarf,M.; Emanuel, 3 B c
B.; Rosenbloom, J.: Molecular cloning and characterizationof the bovine and

human tuftelin genes. Connect. Tissue Res. 39:13- 24, 1998.

GAM281 278 TUFT1 Deutsch, D.: Structure and function of enamel gene products. Anat.Rec. 224: 3 B c 189- 210, 1989.

GAM281 278 TUFT1 Deutsch, D.; Palmon, A.; Dafni, L.; Fisher, L.; Termine, J. D.;Young, M.: 3 B c Cloning, sequencing, and characterization of tuftelin:a novel acidic enamel protein. Connect. Tissue Res. 27: 121 only,1992.

GAM281 278 TUFT1 Deutsch, D.; Palmon, A.; Fisher, L. W.; Kolodny, N.; Termine, J.D.; Young, 3 B c M. F.: Sequencing of bovine enamelin (tuftelin), a novelacidic enamel protein. J. Biol. Chem. 266: 16021- 16028, 1991.

GAM281 278 TUFT1 Deutsch, D.; Palmon, A.; Young, M. F.; Selig, S.; Kearns, W. G.;Fisher, L. 3 B c W.: Mapping of the human tuftelin (TUFT1) gene to chromosome1 by fluorescence in situ hybridization. (Abstract) Mammalian Genome 5:461- 462, 1994.

GAM281 278 TUFT1 MacDougall, M.; Simmons, D.; Dodds, A.; Knight, C.; Luan, X.; Zeichner- 3 B c David,M.; Zhang, C.; Ryu, O. H.; Qian, Q.; Simmer, J. P.; Hu, C.- C.: Cloning,characterization, and tissue expression pattern of mouse tuftelincDNA. J. Dent. Res. 77: 1970- 1978, 1998.

GAM281 278 UGDH Bontemps, Y.; Maquart, F.- X.; , Wegrowski, Y.: Human UDP- 3 B b glucosedehydrogenase gene: complete cloning and transcription start mapping. Biochem.Biophys. Res. Commun. 275: 981- 985, 2000.

GAM281 278 UGDH Hempel, J.; Perozich, J.; Romovacek, H.; Hinich, A.; Kuo, I.; Feingold,D. 3 B b S.: UDP- glucose dehydrogenase from bovine liver: primary structureand relationship to other dehydrogenases. Protein Sci. 3: 1074- 1080,1994.

GAM281 278 UGDH Marcu, O.; Stathakis, D. G.; Marsh, J. L.: Assignment of the UGDHlocus 3 B b encoding UDP- glucose dehydrogenase to human chromosome band4p15.1 by radiation hybrid mapping. Cytogenet. Cell Genet. 86: 244- 245,1999.

GAM281 278 UGDH Spicer, A. P.; Kaback, L. A.; Smith, T. J.; Seldin, M. F.: Molecularcloning 3 B b and characterization of the human and mouse UDP- glucose dehydrogenasegenes. J. Biol. Chem. 273: 25117- 25124, 1998.

GAM281 278 UGDH Walsh, E. C.; Stainier, D. Y. R.: UDP- glucose dehydrogenase requiredfor 3 B b cardiac valve formation in zebrafish. Science 293: 1670- 1674,2001.

GAM281 278 UGT1A4 Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.;Yeatman, M. 3 B c T.; Owens, I. S.: A novel complex locus UGT1 encodeshuman bilirubin, phenol, and other UDP- glucuronosyltransferase isozymeswith identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261,1992.

GAM281 278 UGT1A4 Ritter, J. K.; Crawford, J. M.; Owens, I. S.: Cloning of two humanliver 3 B c bilirubin UDP- glucuronosyltransferase cDNAs with expressionin COS- 1 cells. J. Biol. Chem. 266: 1043- 1047, 1991.

GAM281 278 UGT1A4 Tukey, R. H.; Strassburg, C. P.: Human UDP- 3 B c glucuronosyltransferases:metabolism, expression, and disease. Annu. Rev. Pharm. Toxicol. 40:581- 616, 2000.

GAM281 278 UGT1A8 Huang, Y.- H.; Galijatovic, A.; Nguyen, N.; Geske, D.; Beaton, D.;Green, J.; 3 B c Green, M.; Peters, W. H.; Tukey, R. H.: Identificationand functional characterization of UDP- glucuronosyltransferases UGT1A8*1,UGT1A8*2 and UGT1A8*3. Pharmacogenetics 12: 287- 297, 2002.

GAM281 278 UGT1A8 Mojarrabi, B.; Mackenzie, P. I.: Characterization of two UDP 3 B c glucuronosyltransferasesthat are predominantly expressed in human colon. Biochem. Biophys.Res. Commun. 247: 704- 709, 1998.

GAM281 278 UGT1A8 Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.;Yeatman, M. 3 B c T.; Owens, I. S.: A novel complex locus UGT1 encodeshuman bilirubin, phenol,

and other UDP- glucuronosyltransferase isozymeswith identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261,1992.

GAM281 278 UGT1A8 Strassburg, C. P.; Manns, M. P.; Tukey, R. H.: Expression of theUDP- glucuronosyltransferase 1A locus in human colon: identificationand characterization of the novel extrahepatic UGT1A8. J. Biol. Chem. 273:8719-8726, 1998. 3 B c

GAM281 278 UGT1A9 Findlay, K. A. B.; Kaptein, E.; Visser, T. J.; Burchell, B.: Characterizationof the uridine diphosphate- glucuronosyltransferase-catalyzing thyroidhormone glucuronidation in man. J. Clin. Endocr. Metab. 85: 2879- 2883,2000. 3 B c

GAM281 278 UGT1A9 Harding, D.; Jeremiah, S. J.; Povey, S.; Burchell, B.: Chromosomalmapping of a human phenol UDP- glucuronosyltransferase, GNT1. Ann.Hum. Genet. 54: 17-21, 1990. 3 B c

GAM281 278 UGT1A9 Harding, D.; Jeremiah, S. J.; Povey, S.; Burchell, B.: PhenolUDP-glucuronosyltransferase is coded by a gene on human chromosome2. (Abstract) Cytogenet. Cell Genet. 51: 1011, 1989. 3 B c

GAM281 278 UGT1A9 Wooster, R.; Sutherland, L.; Ebner, T.; Clarke, D.; Da Cruz e Silva,O.; Burchell, B.: Cloning and stable expression of a new member ofthe human liver phenol/bilirubin:UDP- glucuronosyltransferase cDNAfamily. Biochem. J. 278: 465- 469, 1991. 3 B c

GAM281 278 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 B b

GAM281 278 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 B b

GAM281 278 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 B b

GAM281 278 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 B b

GAM281 278 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000. 3 B b

GAM281 278 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938. 3 B b

GAM281 278 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999. 3 B b

GAM281 278 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence 3 B b

for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM281 278 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 3 B b
Arch.Neurol. 28: 67- 68, 1973.

GAM281 278 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 3 B b
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM281 278 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 3 B b
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM281 278 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 3 B b
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM281 278 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 3 B b
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell,
J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.;
Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the
von Hippel- Lindau disease tumorsuppressor gene: correlations with
phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM281 278 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 B b
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification
of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM281 278 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 B b
disease. J.A.M.A. 178: 280- 282, 1961.

GAM281 278 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 B b
peculiar vascular new growth, probably primarily retinal,affecting both
eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM281 278 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 B b
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N.
A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of
the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of
allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM281 278 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 B b
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E.
R.: Identification of intragenic mutations in thevon Hippel- Lindau disease
tumour suppressor gene and correlation withdisease phenotype. Hum. Molec.
Genet. 3: 1303- 1308, 1994.

GAM281 278 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's 3 B b
disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928.

GAM281 278 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- 3 B b
expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin.
Genet. 45: 104- 106, 1994.

GAM281 278 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p 3 B b
involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region
of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65,
1988.

GAM281 278 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, 3 B b
S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the
VHL tumor suppressor gene product: localization, complex formation,and the
effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459-
6463, 1995.

GAM281 278 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. 3 B b
P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.:
Inhibition of transcription elongation by the VHL tumor suppressorprotein.

Science 269: 1402- 1406, 1995.

GAM281 278 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; 3 B b
Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W.
M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple
endocrine neoplasia type 2 display distinctbiochemical and clinical
phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001.

GAM281 278 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; 3 B b
Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P.
A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-
oncogene and the von Hippel- Lindau disease tumoursuppressor gene in
sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937,
1995.

GAM281 278 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, 3 B b
J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian,
Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.;
Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans
EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate
HIF by prolyl hydroxylation. Cell107: 43- 54, 2001.

GAM281 278 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 B b

GAM281 278 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of 3 B b
cancer. Science 278: 1043- 1050, 1997.

GAM281 278 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of 3 B b
the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin
TRiC. Molec. Cell 1051- 1061, 1999.

GAM281 278 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof 3 B b
von Hippel- Lindau disease. Radiology 133: 289- 295, 1979.

GAM281 278 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three 3 B b
generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331,
1979.

GAM281 278 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- 3 B b
Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001.

GAM281 278 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with 3 B b
hydrocephalus as a complication of cerebellar
hemangioblastoma:identification of pro157leu mutation in the VHL gene. J.
Hum. Genet. 45:47- 51, 2000.

GAM281 278 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C 3 B b
Thomas (pub.) 1946.

GAM281 278 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a 3 B b
patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989.

GAM281 278 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of 3 B b
middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg.
Path. 18: 1254- 1260, 1994.

GAM281 278 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; 3 B b
Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.;
Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic
renal cell carcinoma: definition of a risk factorfor VHL patients to develop
an RCC. Hum. Mutat. 13: 464- 475, 1999.

GAM281 278 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; 3 B b
De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred
with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359-

363, 1997.

GAM281 278 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; 3 B b
Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney
cancer gene suppresses growth and functionswith VHL in a common pathway.
Oncogene 21: 3507- 3516, 2002.

GAM281 278 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von 3 B b
Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988.

GAM281 278 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, 3 B b
T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary
cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995.

GAM281 278 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, 3 B b
M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.:
Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one
mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991.

GAM281 278 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; 3 B b
Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther,
M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.:
Screening for von Hippel- Lindau disease by DNA polymorphismanalysis.
J.A.M.A. 267: 1226- 1231, 1992.

GAM281 278 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; 3 B b
Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston
Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in
VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997.

GAM281 278 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: 3 B b
Segregation and linkage analyses of von Hippel Lindau diseaseamong 220
descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984.

GAM281 278 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: 3 B b
histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66:
693- 705,1968.

GAM281 278 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 B b

GAM281 278 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a 3 B b
Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986.

GAM281 278 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid 3 B b
tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour,
phaeochromocytoma and the von Hippel- Lindau complex:two distinctive
neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987.

GAM281 278 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: 3 B b
Familial pheochromocytoma associated with a novel mutation inthe von Hippel-
Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996.

GAM281 278 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; 3 B b
Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam:
North Holland (pub.) 14: 1972. Pp. 241- 259.

GAM281 278 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors 3 B b
in livers with targeted inactivation of the von Hippel- Lindautumor
suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001.

GAM281 278 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 3 B b
retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022-
1034, 1971.

GAM281 278 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 3 B b
hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8:

601- 606,1967.

GAM281 278 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas. Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994. 3 B b

GAM281 278 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.; Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma only. J. Med. Genet. 37: 939- 943,2000. 3 B b

GAM281 278 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips, C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet. 106: 425- 431, 2000. 3 B b

GAM281 278 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001. 3 B b

GAM281 278 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002. 3 B b

GAM281 278 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989. 3 B b

GAM281 278 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976. 3 B b

GAM281 278 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990. 3 B b

GAM281 278 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982. 3 B b

GAM281 278 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986. 3 B b

GAM281 278 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995. 3 B b

GAM281 278 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996. 3 B b

GAM281 278 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 3 B b

GAM281 278 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; 3 B b
Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL-
mediated destruction by proline hydroxylation: implicationsfor O(2) sensing.
Science 292: 464- 468, 2001.

GAM281 278 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; 3 B b
Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic
anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-
Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998.

GAM281 278 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; 3 B b
Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.;
Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting
of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-
regulated prolyl hydroxylation. Science 292: 468- 472, 2001.

GAM281 278 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 B b

GAM281 278 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; 3 B b
Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British
family: clinicopathological features and recommendationsfor screening and
follow- up. Quart. J. Med. 66: 233- 249, 1988.

GAM281 278 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, 3 B b
N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-
Lindau tumor suppressor gene in sporadic centralnervous system
hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994.

GAM281 278 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, 3 B b
H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during
neuronal differentiation. Cancer Res. 60: 2820- 2824,2000.

GAM281 278 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in 3 B b
Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961.

GAM281 278 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; 3 B b
Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.;
Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease:
new strategies in early detection and treatment. Am.J. Med. 97: 158- 168,
1994.

GAM281 278 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell 3 B b
carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992.

GAM281 278 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the 3 B b
VHL gene is associated exclusively with the developmentof non- papillary
renal cell carcinomas. J. Path. 179: 157- 161, 1996.

GAM281 278 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. 3 B b
J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-
581, 1995.

GAM281 278 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of 3 B b
the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science
269: 1444- 1446, 1995.

GAM281 278 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; 3 B b
Wullich, B.; Schempp, W.: Cytogenetic studies on three
pheochromocytomasderived from patients with von Hippel- Lindau syndrome.
Hum. Genet. 82:127- 130, 1989.

GAM281 278 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3 B b
3p deletion in renal cell carcinoma cells from a patientwith von Hippel-
Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987.

GAM281 278 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 B b

GAM281 278 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 B b

GAM281 278 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel- Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 B b

GAM281 278 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 B b

GAM281 278 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 B b

GAM281 278 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.;Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317- 1320, 1993. 3 B b

GAM281 278 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 B b

GAM281 278 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 B b

GAM281 278 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 B b

GAM281 278 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 B b

GAM281 278 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002. 3 B b

GAM281 278 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 B b

GAM281 278 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 3 B b

GAM281 278 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 B b

GAM281 278 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 B b

GAM281 278 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis 3 B b
of the two stage mutation model in von Hippel- Lindau disease,and in
sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med.
Genet. 27: 311- 314, 1990.

GAM281 278 WBSCR1 Osborne, L. R.; Martindale, D.; Scherer, S. W.; Shi, X.- M.; Huizenga,J.; 3 B c
Heng, H. H. Q.; Costa, T.; Pober, B.; Lew, L.; Brinkman, J.; Rommens,J.;
Koop, B.; Tsui, L.- C.: Identification of genes from a 500- kbregion at
7q11.23 that is commonly deleted in Williams syndrome patients. Genomics
36:328- 336, 1996.

GAM281 278 WBSCR1 Richter- Cook, N. J.; Dever, T. E.; Hensold, J. O.; Merrick, W.C.: 3 B c
Purification and characterization of a new eukaryotic proteintranslation
factor: eukaryotic initiation factor 4H. J. Biol. Chem. 273:7579- 7587,
1998.

GAM281 278 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. 3 B c
F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.;
Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and
high resolution restriction map of the2 megabase region containing the
Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM281 278 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 B c
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple
myeloma is associated with increased expression and activatingmutations of
fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM281 278 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, 3 B c
R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel
chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the
fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997.

GAM281 278 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van 3 B c
Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a
90 kb SET domain- containing gene, expressed in earlydevelopment and
homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn
syndrome critical region and is fused to IgH int(4;14) multiple myeloma.
Hum. Molec. Genet. 7: 1071- 1082, 1998.

GAM281 278 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; 3 B c
Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.;
Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly
defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet.
6: 317- 324, 1997.

GAM281 278 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 3 B b
family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with
XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000.

GAM281 278 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of 3 B b
DNA double- strand breaks by homologous recombination. Nature 401:397- 399,
1999.

GAM281 278 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- 3 B b
ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286,
1987.

GAM281 278 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the 3 B b
XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis.
Genomics 26: 619- 622, 1995.

GAM281 278 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, 3 B b

T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002.

GAM281 278 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 B b

GAM281 278 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 B b

GAM281 278 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997. 3 B b

GAM281 278 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995. 3 B b

GAM281 278 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma. CancerRes. 39: 3119- 3128, 1979. 3 B b

GAM281 278 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a follicular lymphoma cell line carrying a t(14;18)chromosomal translocation. Int. J. Cancer 39: 785- 788, 1987. 3 B b

GAM281 278 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. A.: STS map of genes and anonymous DNA fragments on human chromosome18 using a panel of somatic cell hybrids. Genomics 15: 387- 391,1993. 3 B b

GAM281 278 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710- 717, 1988. 3 B b

GAM281 278 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human chromosome and its expression in various tissues. Science 227:1038- 1040, 1985. 3 B b

GAM281 278 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal reassignment: YACs containing both YES1 and thymidylatesynthase map to the short arm of chromosome 18. Genomics 15: 442- 445,1993. 3 B b

GAM281 278 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c- yes gene. Molec. Cell. Biol. 7: 41- 47, 1987. 3 B b

GAM281 278 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985. 3 B b

GAM391 326 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 C c

GAM391 326 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new 3 C c

genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM391 326 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- 3 C c interacting protein, recognizes the basolateral sortingsignal of amyloid precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998.

GAM391 326 ASB1 Hirosawa, M.; Nagase, T.; Ishikawa, K.; Kikuno, R.; Nomura, N.;Ohara, O.: 3 C c Characterization of cDNA clones selected by the GeneMarkanalysis from size-fractionated cDNA libraries from human brain. DNARes. 6: 329- 336, 1999.

GAM391 326 ASB1 Kile, B. T.; Viney, E. M.; Willson, T. A.; Brodnicki, T. C.; Cancilla,M. R.; 3 C c Herlihy, A. S.; Croker, B. A.; Baca, M.; Nicola, N. A.; Hilton,D. J.; Alexander, W. S.: Cloning and characterization of the genesencoding the ankyrin repeat and SOCS box- containing proteins Asb- 1,Asb- 2, Asb- 3, and Asb- 4. Gene 258: 31- 41, 2000.

GAM391 326 CCR2 Boring, L.; Gosling, J.; Cleary, M.; Charo, I. F.: Decreased lesionformation 3 C c in CCR2 - /- mice reveals a role for chemokines in the initiationof atherosclerosis. Nature 394: 894- 897, 1998.

GAM391 326 CCR2 Charo, I. F.; Myers, S. J.; Herman, A.; Franci, C.; Connolly, A.J.; 3 C c Coughlin, S. R.: Molecular cloning and functional expressionof two monocyte chemoattractant protein 1 receptors reveals alternativesplicing of the carboxyl- terminal tails. Proc. Nat. Acad. Sci. 91:2752- 2756, 1994.

GAM391 326 CCR2 Choe, H.; Farzan, M.; Sun, Y.; Sullivan, N.; Rollins, B.; Ponath,P. D.; Wu, 3 C c L.; Mackay, C. R.; LaRosa, G.; Newman, W.; Gerard, N.;Gerard, C.; Sodroski, J.: The beta- chemokine receptors CCR3 and CCR5facilitate infection by primary HIV- 1 isolates. Cell 85: 1135- 1148,1996.

GAM391 326 CCR2 Combadiere, C.; Ahuja, S. K.; Murphy, P. M.: Cloning, 3 C c chromosomallocalization, and RNA expression of a human beta chemokine receptor- likegene. DNA Cell Biol. 14: 673- 680, 1995.

GAM391 326 CCR2 Combadiere, C.; Ahuja, S. K.; Van Damme, J.; Tiffany, H. L.; Gao,J.- L.; 3 C c Murphy, P. M.: Monocyte chemoattractant protein- 3 is a functionalligand for CC chemokine receptors 1 and 2B. J. Biol. Chem. 270:29671- 29675, 1995.

GAM391 326 CCR2 Daugherty, B. L.; Springer, M. S.: The beta- chemokine receptorgenes CCR1 3 C c (CMKBR1), CCR2 (CMKBR2), and CCR3 (CMKBR3) cluster within285 kb on human chromosome 3p21. Genomics 41: 294- 295, 1997.

GAM391 326 CCR2 Doranz, B. J.; Rucker, J.; Yi, Y.; Smyth, R. J.; Samson, M.; Peiper,S. C.; 3 C c Parmentier, M.; Collman, R. G.; Doms, R. W.: A dual- tropicprimary HIV- 1 isolate that uses fusin and the beta- chemokine receptorsCKR- 5, CKR- 3, and CKR- 2b as fusion cofactors. Cell 85: 1149- 1158,1996.

GAM391 326 CCR2 Mummidi, S.; Ahuja, S. S.; Gonzalez, E.; Anderson, S. A.; Santiago,E. N.; 3 C c Stephan, K. T.; Craig, F. E.; O'Connell, P.; Tryon, V.; Clark,R. A.; Dolan, M. J.; Ahuja, S. K.: Genealogy of the CCR5 locus andchemokine system gene variants associated with altered rates of HIV- 1disease progression. Nature Med. 4: 786- 793, 1998.

GAM391 326 CCR2 Peters, W.; Dupuis, M.; Charo, I. F.: A mechanism for the impairedIFN- gamma 3 C c production in C- C chemokine receptor 2 (CCR2) knockout mice:role of CCR2 in linking the innate and adaptive immune responses. J.Immun. 165: 7072- 7077, 2000.

GAM391 326 CCR2 Peters, W.; Scott, H. M.; Chambers, H. F.; Flynn J. L.; Charo,I. F.; Ernst, 3 C c J. D.: Chemokine receptor 2 serves an early and essentialrole in resistance to Mycobacterium tuberculosis. Proc. Nat. Acad.Sci. 98: 7958- 7963, 2001.

GAM391 326 CCR2 Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier,M.: Molecular 3 C c

cloning and functional expression of a new human CC- chemokinereceptor gene. Biochemistry 35: 3362- 3367, 1996.

GAM391 326 CCR2 Samson, M.; Soularue, P.; Vassart, G.; Parmentier, M.: The genesencoding the human CC- chemokine receptors CC- CKR1 to CC- CKR5 (CMKBR1- CMKBR5)are clustered in the p21.3- p24 region of chromosome 3. Genomics 36:522- 526, 1996. 3 C c

GAM391 326 CCR2 Sanders, S. K.; Crean, S. M.; Boxer, P. A.; Kellner, D.; LaRosa,G. J.; Hunt, S. W., III.: Functional differences between monocytechemotactic protein- 1 receptor A and monocyte chemotactic protein- 1receptor B expressed in a Jurkat T cell. J. Immun. 165: 4877- 4883,2000. 3 C c

GAM391 326 CCR2 Smith, M. W.; Dean, M.; Carrington, M.; Winkler, C.; Huttley,G. A.; Lomb, D. A.; Goedert, J. J.; O'Brien, T. R.; Jacobson, L. P.;Kaslow, R.; Buchbinder, S.; Vittinghoff, E.; Vlahov, D.; Hoots, K.;Hilgartner, M. W.; Hemophilia Growth and Development Study (HGDS);Multicenter AIDS Cohort Study (MACS); Multicenter Hemophilia CohortStudy (MHCS); San Francisco City Cohort (SFCC); ALIVE Study;O'Brien, S. J.: Contrasting genetic influence of CCR2 and CCR5 variantson HIV- 1 infection and disease progression. Science 277: 959- 965,1997. 3 C c

GAM391 326 CCR2 Wong, L.- M.; Myers, S. J.; Tsou, C.- L.; Gosling, J.; Arai, H.;Charo, I. F.: Organization and differential expression of the humanmonocyte chemoattractant protein 1 receptor gene: evidence for therole of the carboxyl- terminal tail in receptor trafficking. J. Biol.Chem. 272: 1038- 1045, 1997. 3 C c

GAM391 326 CENTD2 Miura, K.; Jacques, K. M.; Stauffer, S.; Kubosaki, A.; Zhu, K.;Hirsch, D. S.; Resau, J.; Zheng, Y.; Randazzo, P. A.: ARAP1: a pointof convergence for Arf and Rho signaling. Molec. Cell 9: 109- 119,2002. 3 C c

GAM391 326 CENTD2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of unidentified human genes. XI. The complete sequencesof 100 new cDNA clones from brain which code for large proteins invitro. DNA Res. 5: 277- 286, 1998. 3 C c

GAM391 326 CHRNB4 Elliott, K. J.; Ellis, S. B.; Berckhan, K. J.; Urrutia, A.; Chavez-Noriega,L. E.; Johnson, E. C.; Velicelebi, G.; Harpold, M. M.: Comparativestructure of human neuronal alpha(2)- alpha(7) and beta(2)- beta(4)nicotinic acetylcholine receptor subunits and functional expressionof the alpha(2), alpha(3), alpha(4), alpha(7), beta(2), and beta(4)subunits. J. Molec. Neurosci. 7: 217- 228, 1996. 3 C c

GAM391 326 CHRNB4 Groot Kormelink, P. J.; Luyten, W. H. M. L.: Cloning and sequenceof full- length cDNAs encoding the human neuronal nicotinic acetylcholinereceptor (nAChR) subunits beta- 3 and beta- 4 and expression of sevennAChR subunits in the human neuroblastoma cell line SH- SY5Y and/orIMR- 32. FEBS Lett. 400: 309- 314, 1997. 3 C c

GAM391 326 CHRNB4 Khakh, B. S.; Zhou, X.; Sydes, J.; Galligan, J. J.; Lester, H.A.: State- dependent cross- inhibition between transmitter- gated cationchannels. Nature 406: 405- 410, 2000. 3 C c

GAM391 326 CHRNB4 Raimondi, E.; Rubboli, F.; Moralli, D.; Chini, B.; Fornasari, D.;Tarroni, P.; De Carli, L.; Clementi, F.: Chromosomal localizationand physical linkage of the genes encoding the human alpha- 3, alpha- 5,and beta- 4 neuronal nicotinic receptor subunits. Genomics 12: 849- 850,1992. 3 C c

GAM391 326 CHRNB4 Tarroni, P.; Rubboli, F.; Chini, B.; Zwart, R.; Oortgiesen, M.;Sher, E.; 3 C c

Clementi, F.: Neuronal- type nicotinic receptors in humanneuroblastoma and small- cell lung carcinoma cell lines. FEBS Lett. 312:66- 70, 1992.

GAM391 326 E2F3 Cloud, J. E.; Rogers, C.; Reza, T. L.; Ziebold, U.; Stone, J. R.;Picard, M. H.; Caron, A. M.; Bronson, R. T.; Lees, J. A.: Mutantmouse models reveal the relative roles of E2F1 and E2F3 in vivo. Molec.Cell. Biol. 22: 2663- 2672, 2002. 3 C c

GAM391 326 E2F3 He, Y.; Armanious, M. K.; Thomas, M. J.; Cress, W. D.: Identificationof E2F- 3B, an alternative form of E2F- 3 lacking a conserved N- terminalregion. Oncogene 19: 3422- 3433, 2000. 3 C c

GAM391 326 E2F3 Lees, J. A.; Saito, M.; Vidal, M.; Valentine, M.; Look, T.; Harlow,E.; Dyson, N.; Helin, K.: The retinoblastoma protein binds to a familyof E2F transcription factors. Molec. Cell. Biol. 13: 7813- 7825,1993. 3 C c

GAM391 326 E2F3 Leone, G.; Sears, R.; Huang, E.; Rempel, R.; Nuckolls, F.; Park,C.- H.; Giangrande, P.; Wu, L.; Saavedra, H. I.; Field, S. J.; Thompson,M. A.; Yang, H.; Fujiwara, Y.; Greenberg, M. E.; Orkin, S.; Smith,C.; Nevins, J. R.: Myc requires distinct E2F activities to induceS phase and apoptosis. Molec. Cell 8: 105- 113, 2001. 3 C c

GAM391 326 E2F3 Wu, L.; Timmers, C.; Maiti, B.; Saavedra, H. I.; Sang, L.; Chong,G. T.; Nuckolls, F.; Giangrande, P.; Wright, F. A.; Field, S. J.;Greenberg, M. E.; Orkin, S.; Nevins, J. R.; Robinson, M. L.; Leone,G.: The E2F1- 3 transcription factors are essential for cellular proliferation. Nature 414:457- 462, 2001. 3 C c

GAM391 326 FOXM1 Korver, W.; Roose, J.; Heinen, K.; Weghuis, D. O.; de Bruijn, D.;Geurts van Kessel, A.; Clevers, H.: The human TRIDENT/HFH- 11/FKHL16gene: structure, localization, and promoter characterization. Genomics 46:435- 442, 1997. 3 C c

GAM391 326 FOXM1 Ly, D. H.; Lockhart, D. J.; Lerner, R. A.; Schultz, P. G.: Mitoticmisregulation and human aging. Science 287: 2486- 2492, 2000. 3 C c

GAM391 326 FOXM1 Wang, X.; Quail, E.; Hung, N.- J.; Tan, Y.; Ye, H.; Costa, R. H.: Increased levels of forkhead box M1B transcription factor in transgenicmouse hepatocytes prevent age- related proliferation defects in regeneratingliver. Proc. Nat. Acad. Sci. 98: 11468- 11473, 2001. 3 C c

GAM391 326 FOXM1 Westendorf, J. M.; Rao, P. N.; Gerace, L.: Cloning of cDNAs forM- phase phosphoproteins recognized by the MPM2 monoclonal antibodyand determination of the phosphorylated epitope. Proc. Nat. Acad.Sci. 91: 714- 718, 1994. 3 C c

GAM391 326 FOXM1 Yao, K.- M.; Sha, M.; Lu, Z.; Wong, G. G.: Molecular analysis ofa novel winged helix protein, WIN: expression pattern, DNA bindingproperty, and alternative splicing within the DNA binding domain. J.Biol. Chem. 272: 19827- 19836, 1997. 3 C c

GAM391 326 FOXM1 Ye, H.; Kelly, T. F.; Samadani, U.; Lim, L.; Rubio, S.; Overdier,D. G.; Roebuck, K. A.; Costa, R. H.: Hepatic nuclear factor 3/forkhead homolog 11 is expressed in proliferating epithelial and mesenchymalcells of embryonic and adult tissues. Molec. Cell. Biol. 17: 1626- 1641,1997. 3 C c

GAM391 326 JMJ Berge- Lefranc, J.- L.; Jay, P.; Massacrier, A.; Cau, P.; Mattei,M. G.; Bauer, S.; Marsollier, C.; Berta, P.; Fontes, M.: Characterizationof the human jumonji gene. Hum. Molec. Genet. 5: 1637- 1641, 1996. 3 C c

GAM391 326 JMJ Toyoda, M.; Kojima, M.; Takeuchi, T.: Jumonji is a nuclear proteinthat participates in the negative regulation of cell growth. Biochem.Biophys. Res. Commun. 274: 332- 336, 2000. 3 C c

GAM391 326 KCNA5 Albrecht, B.; Weber, K.; Pongs, O.: Characterization of a voltage- activatedK- channel gene cluster on human chromosome 12p13. Receptors 3 C c

Channels 3:213- 220, 1995.

GAM391 326 KCNA5 Curran, M. E.; Landes, G. M.; Keating, M. T.: Molecular 3 C c
cloning,characterization, and genomic localization of a human potassium
channelgene. Genomics 12: 729- 737, 1992.

GAM391 326 KCNA5 Klocke, R.; Roberds, S. L.; Tamkun, M. M.; Gronemeier, M.; Augustin,A.; 3 C c
Albrecht, B.; Pongs, O.; Jockusch, H.: Chromosomal mapping inthe mouse of
eight K(+)- channel genes representing the four Shaker- likesubfamilies
Shaker, Shab, Shaw, and Shal. Genomics 18: 568- 574,1993.

GAM391 326 KCNA5 McPherson, J. D.; Wasmuth, J. J.; Chandy, K. G.; Swanson, R.; Dethlefs,B.; 3 C c
Chandy, G.; Wymore, R.; Ghanshani, S.: Chromosomal localizationof 7
potassium channel genes. (Abstract) Cytogenet. Cell Genet. 58:1979 only,
1991.

GAM391 326 KCNA5 Philipson, L. H.; Hice, R. E.; Schaefer, K.; LaMendola, J.; Bell,G. I.; 3 C c
Neldon, D. J.; Steiner, D. F.: Sequence and functional expressionin Xenopus
oocytes of a human insulinoma and islet potassium channel. Proc.Nat. Acad.
Sci. 88: 53- 57, 1991.

GAM391 326 KCNA5 Phromchotikul, T.; Browne, D. L.; Curran, M. E.; Keating, M. T.;Litt, M.: 3 C c
Dinucleotide repeat polymorphism at the KCNA5 locus. Hum.Molec. Genet. 2:
1512 only, 1993.

GAM391 326 KCNA5 Tamkun, M. M.; Knoth, K. M.; Walbridge, J. A.; Kroemer, H.; Roden,D. M.; 3 C c
Glover, D. M.: Molecular cloning and characterization of twovoltage- gated
K+ channel cDNAs from human ventricle. FASEB J. 5:331- 337, 1991.

GAM391 326 LDB3 Faulkner, G.; Pallavicini, A.; Formentin, E.; Comelli, A.; Ievolella,C.; 3 C c
Trevisan, S.; Bortoletto, G.; Scannapieco, P.; Salamon, M.; Mouly,V.; Valle,
G.; Lanfranchi, G.: ZASP: a new Z- band alternatively splicedPDZ- motif
protein. J. Cell Biol. 146: 465- 475, 1999.

GAM391 326 LDB3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM391 326 LDB3 Zhou, Q.; Ruiz- Lozano, P.; Martone, M. E.; Chen, J.: Cypher, astriated 3 C c
muscle- restricted PDZ and LIM domain- containing protein,binds to alpha-
actinin- 2 and protein kinase C. J. Biol. Chem. 274:19807- 19813, 1999.

GAM391 326 MYLK Garcia, J. G.; Lazar, V.; Gilbert- McClain, L. I.; Gallagher, P.J.; Verin, 3 C c
A. D.: Myosin light chain kinase in endothelium: molecularcloning and
regulation. Am. J. Resp. Cell Molec. Biol. 16: 489- 494,1997.

GAM391 326 MYLK Giorgi, D.; Brand- Arpon, V.; Rouquier, S.: The functional myosinlight chain 3 C c
kinase (MYLK) gene localizes with marker D3S3552 on humanchromosome 3q21 in
a greater than 5- Mb yeast artificial chromosomeregion and is not linked to
olfactory receptor genes. Cytogenet.Cell Genet. 92: 85- 88, 2001.

GAM391 326 MYLK Lazar, V.; Garcia, J. G. N.: A single human myosin light chainkinase gene 3 C c
(MLCK; MYLK) transcribes multiple nonmuscle isoforms. Genomics 57:256- 267,
1999.

GAM391 326 MYLK Potier, M.- C.; Chelot, E.; Pekarsky, Y.; Gardiner, K.; Rossier,J.; Turnell, 3 C c
W. G.: The human myosin light chain kinase (MLCK) fromhippocampus: cloning,
sequencing, expression, and localization to3cen- q21. Genomics 29: 562- 570,
1995.

GAM391 326 MYLK Walker, L. A.; MacDonald, J. A.; Liu, X.; Nakamoto, R. K.; Haystead,T. A. 3 C c
J.; Somlyo, A. V.; Somlyo, A. P.: Site- specific phosphorylationand point
mutations of telokin modulate its Ca(2+)- desensitizing effectin smooth

muscle. J. Biol. Chem. 276: 24519- 24524, 2001.

GAM391 326 MYLK Watterson, D. M.; Schavocky, J. P.; Guo, L.; Weiss, C.; Chlenski,A.; Shirinsky, V. P.; Van Eldik, L. J.; Haiech, J.: Analysis of thekinase-related protein gene found at human chromosome 3q21 in a multi- genecluster: organization, expression, alternative splicing, and polymorphicmarker. J. Cell. Biochem. 75: 481- 491, 1999. 3 C c

GAM391 326 N33 Bova, G. S.; MacGrogan, D.; Levy, A.; Pin, S. S.; Bookstein, R.;Isaacs, W. B.: Physical mapping of chromosome 8p22 markers and theirhomozygous deletion in a metastatic prostate cancer. Genomics 35:46- 54, 1996. 3 C c

GAM391 326 N33 MacGrogan, D.; Levy, A.; Bova, G. S.; Isaacs, W. B.; Bookstein,R.: Structure and methylation- associated silencing of a gene withina homozygously deleted region of human chromosome band 8p22. Genomics 35:55- 65, 1996. 3 C c

GAM391 326 OTP Acampora, D.; Postiglione, M. P.; Avantaggiato, V.; Di Bonito,M.; Vaccarino, F. M.; Michaud, J.; Simeone, A.: Progressive impairmentof developing neuroendocrine cell lineages in the hypothalamus ofmice lacking the Orthopedia gene. Genes Dev. 13: 2787- 2800, 1999. 3 C c

GAM391 326 OTP Lin, X.; State, M. W.; Vaccarino, F. M.; Greally, J.; Hass, M.;Leckman, J. F.: Identification, chromosomal assignment, and expressionanalysis of the human homeodomain- containing gene Orthopedia (OTP). Genomics 60:96- 104, 1999. 3 C c

GAM391 326 PRSS11 Hu, S.- I.; Carozza, M.; Klein, M.; Nantermet, P.; Luk, D.; Crowl,R. M.: Human HtrA, an evolutionarily conserved serine protease identifiedas a differentially expressed gene product in osteoarthritic cartilage. J.Biol. Chem. 273: 34406- 34412, 1998. 3 C c

GAM391 326 PRSS11 Zumbrunn, J.; Trueb, B.: Localization of the gene for a serineprotease with IGF- binding domain (PRSS11) to human chromosome 10q25.3- q26.2. Genomics 45:461- 462, 1997. 3 C c

GAM391 326 PRSS11 Zumbrunn, J.; Trueb, B.: Primary structure of a putative serineprotease specific for IGF- binding proteins. FEBS Lett. 398: 187- 192,1996. 3 C c

GAM391 326 SLC20A1 Kaelbling, M.; Eddy, R.; Shows, T. B.; Copeland, N. G.; Gilbert,D. J.; Jenkins, N. A.; Klinger, H. P.; O'Hara, B.: Localization ofthe human gene allowing infection by gibbon ape leukemia virus tohuman chromosome region 2q11- q14 and to the homologous region on mousechromosome 2. J. Virol. 65: 1743- 1747, 1991. 3 C c

GAM391 326 SLC20A1 Kavanaugh, M. P.; Miller, D. G.; Zhang, W.; Law, W.; Kozak, S.L.; Kabat, D.; Miller, A. D.: Cell- surface receptors for gibbon apeleukemia virus and amphotropic murine retrovirus are inducible sodium- dependentphosphate symporters. Proc. Nat. Acad. Sci. 91: 7071- 7075, 1994. 3 C c

GAM391 326 SLC20A1 O'Hara, B.; Johann, S. V.; Klinger, H. P.; Blair, D. G.; Rubinson,H.; Dunn, K. J.; Sass, P.; Vitek, S. M.; Robins, T.: Characterizationof a human gene conferring sensitivity to infection by gibbon apeleukemia virus. Cell Growth Differ. 1: 119- 127, 1990. 3 C c

GAM391 326 SLC20A1 Palmer, G.; Manen, D.; Bonjour, J.- P.; Caverzasio, J.: Characterizationof the human Glvr- 1 phosphate transporter/retrovirus receptor geneand promoter region. Gene 226: 25- 33, 1999. 3 C c

GAM391 326 SLC20A1 Palmer, G.; Manen, D.; Bonjour, J.- P.; Caverzasio, J.: Species-specificmechanisms control the activity of the Pit1/PIT1 phosphate transportergene promoter in mouse and human. Gene 279: 49- 62, 2001. 3 C c

GAM391 326 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a 3 C c

revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998.

GAM391 326 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 3 C c

GAM391 326 SPR Blau, N.; Thony, B.; Renneberg, A.; Arnold, L. A.; Hyland, K.:Dihydropteridine reductase deficiency localized to the central nervoussystem. J. Inherit. Metab. Dis. 21: 433- 434, 1998. 3 C c

GAM391 326 SPR Blau, N.; Thony, B.; Renneberg, A.; Penzien, J. M.; Hyland, K.;Hoffmann, G.: Variant of dihydropteridine reductase deficiency withouthyperphenylalaninemia: effect of oral phenylalanine loading. J. Inherit.Metab. Dis. 22: 216- 220, 1999. 3 C c

GAM391 326 SPR Bonafe, L.; Thony, B.; Penzien, J. M.; Czarnecki, B.; Blau, N.: Mutations in the sepiapterin reductase gene cause a novel tetrahydrobiopterin-dependentmonoamine- neurotransmitter deficiency without hyperphenylalaninemia. Am.J. Hum. Genet. 69: 269- 277, 2001. 3 C c

GAM391 326 SPR Ichinose, H.; Katoh, S.; Sueoka, T.; Titani, K.; Fujita, K.; Nagatsu,T.: Cloning and sequencing of cDNA encoding human sepiapterin reductase:an enzyme involved in tetrahydrobiopterin biosynthesis. Biochem.Biophys. Res. Commun. 179: 183- 189, 1991. 3 C c

GAM391 326 SPR Murdoch, J. N.; Eddleston, J.; Stanier, P.; Copp, A. J.: Localizationof the mouse gene encoding tyrosine kinase receptor type 10 on distalchromosome 1. Mammalian Genome 8: 941- 952, 1997. 3 C c

GAM391 326 SPR Thony, B.; Heizmann, C. W.; Mattei, M.- G.: Human GTP- cyclohydrolasel gene and sepiapterin reductase gene map to region 14q21- q22 and2p14- p12, respectively, by in situ hybridization. Genomics 26: 168- 170,1995. 3 C c

GAM391 326 STAT3 Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.- J.; Wei, S.; Matsusaka,T.; Yoshida, K.; Sudo, T.; Naruto, M.; Kishimoto, T.: Molecular cloningof APRF, a novel IFN- stimulated gene factor 3 p91- related transcriptionfactor involved in the gp130- mediated signaling pathway. Cell 77:63- 71, 1994. 3 C c

GAM391 326 STAT3 Bromberg, J. F.; Wrzeszczynska, M. H.; Devgan, G.; Zhao, Y.; Pestell,R. G.; Albanese, C.; Darnell, J. E., Jr.: Stat3 as an oncogene. Cell 98:295- 303, 1999. 3 C c

GAM391 326 STAT3 Caldenhoven, E.; van Dijk, T. B.; Solari, R.; Armstrong, J.; Raaijmakers,J. A. M.; Lammers, J.- W. J.; Koenderman, L.; de Groot, R. P.: STAT3- beta,a splice variant of transcription factor STAT3, is a dominant negativeregulator of transcription. J. Biol. Chem. 271: 13221- 13227, 1996. 3 C c

GAM391 326 STAT3 Choi, J. Y.; Li, W. L.; Kouri, R. E.; Yu, J.; Kao, F. T.; Ruano,G.: Assignment of the acute phase response factor (APRF) gene to17q21 by microdissection clone sequencing and fluorescence in situhybridization of a p1 clone. Genomics 37: 264- 265, 1996. 3 C c

GAM391 326 STAT3 Chung, C. D.; Liao, J.; Liu, B.; Rao, X.; Jay, P.; Berta, P.; Shuai,K.: Specific inhibition of Stat3 signal transduction by PIAS3. Science 278:1803-1805, 1997. 3 C c

GAM391 326 STAT3 Foley, H. A.; Ofori- Acquah, S. F.; Yoshimura, A.; Critz, S.; Baliga,B. S.; Pace, B. S.: Stat- 3 beta inhibits gamma- globin gene expressionin erythroid cells. J. Biol. Chem. 277: 16211- 16219, 2002. 3 C c

GAM391 326 STAT3 Lutticken, C.; Wegenka, U. M.; Yuan, J.; Buschmann, J.; Schindler,C.; Ziemiecki, A.; Harpur, A. G.; Wilks, A. F.; Yasukawa, K.; Taga,T.; Kishimoto, T.; Barbieri, G.; Pellegrini, S.; Sendtner, M.; Heinrich,P. C.; 3 C c

Horn, F.: Association of transcription factor APRF and proteinkinase Jak1 with the interleukin- 6 signal transducer gp130. Science 263:89- 92, 1994.

GAM391 326 STAT3 Nakashima, K.; Yanagisawa, M.; Arakawa, H.; Kimura, N.; Hisatsune,T.; Kawabata, M.; Miyazono, K.; Taga, T.: Synergistic signaling infetal brain by STAT3- Smad1 complex bridged by p300. Science 284:479- 482, 1999. 3 C c

GAM391 326 STAT3 Pfeffer, L. M.; Mullersman, J. E.; Pfeffer, S. R.; Murti, A.; Shi,W.; Yang, C. H.: STAT3 as an adapter to couple phosphatidylinositol3- kinase to the IFNAR1 chain of the type I interferon receptor. Science 276:1418- 1420, 1997. 3 C c

GAM391 326 STAT3 Ram, P. T.; Horvath, C. M.; Iyengar, R.: Stat3- mediated transformationof NIH- 3T3 cells by the constitutively active Q205L G- alpha(O) protein. Science 287:142- 144, 2000. 3 C c

GAM391 326 STAT3 Simon, A. R.; Vikis, H. G.; Stewart, S.; Fanburg, B. L.; Cochran,B. H.; Guan, K.- L.: Regulation of STAT3 by direct binding to theRac1 GTPase. Science 290: 144- 147, 2000. 3 C c

GAM391 326 STAT3 Vaisse, C.; Halaas, J. L.; Horvath, C. M.; Darnell, J. E., Jr.;Stoffel, M.; Friedman, J. M.: Leptin activation of Stat3 in the hypothalamusof wildtype and ob/ob mice but not in db/db mice. Nature Genet. 14:95- 100, 1996. 3 C c

GAM391 326 STAT3 Yoo, J.- Y.; Huso, D. L.; Nathans, D.; Desiderio, S.: Specificablation of Stat3- beta distorts the pattern of Stat3- responsive geneexpression and impairs recovery from endotoxic shock. Cell 108:331- 344, 2002. 3 C c

GAM633 340 ADCY7 Hellevuo, K.; Berry, R.; Sikela, J. M.; Tabakoff, B.: Localizationof the gene for a novel human adenylyl cyclase (ADCY7) to chromosome16. Hum. Genet. 95: 197- 200, 1995. 3 C c

GAM633 340 ADCY7 Hellevuo, K.; Yoshimura, M.; Kao, M.; Hoffman, P. L.; Cooper, D.M. F.; Tabakoff, B.: A novel adenylyl cyclase sequence cloned fromthe human erythroleukemia cell line. Biochem. Biophys. Res. Commun. 192:311- 318, 1993. 3 C c

GAM895 379 ABCA1 Becq, F.; Hamon, Y.; Bajetto, A.; Gola, M.; Verrier, B.; Chimini,G.: ABC1, an ATP binding cassette transporter required for phagocytosisof apoptotic cells, generates a regulated anion flux after expressionin Xenopus laevis oocytes. J. Biol. Chem. 272: 2695- 2699, 1997. 7 A c

GAM895 379 ABCA1 Bodzioch, M.; Orso, E.; Klucken, J.; Langmann, T.; Bottcher, A.;Diederich, W.; Drobnik, W.; Barlage, S.; Buchler, C.; Porsch- Ozcurumez,M.; Kaminski, W. E.; Hahmann, H. W.; Oette, K.; Rothe, G.; Aslanidis,C.; Lackner, K. J.; Schmitz, G.: The gene encoding ATP- binding cassettetransporter 1 is mutated in Tangier disease. Nature Genet. 22: 347- 351,1999. 7 A c

GAM895 379 ABCA1 Brooks- Wilson, A.; Marcil, M.; Clee, S. M.; Zhang, L.- H.; Roomp,K.; van Dam, M.; Yu, L.; Brewer, C.; Collins, J. A.; Molhuizen, H.O. F.; Loubser, O.; Ouelette, B. F. F.; and 14 others: Mutationsin ABC1 in Tangier disease and familial high- density lipoprotein deficiency. NatureGenet. 22: 336- 345, 1999. 7 A c

GAM895 379 ABCA1 Decottignies, A.; Goffeau, A.: Complete inventory of the yeastABC proteins. Nature Genet. 15: 137- 145, 1997. 7 A c

GAM895 379 ABCA1 Goossens, M.; Brauner, R.; Czernichow, P.; Duquesnoy, P.; Rappaport,R.: Isolated growth hormone (GH) deficiency type 1A associated witha double deletion in the human GH gene cluster. J. Clin. Endocr.Metab. 62: 712- 716, 1986. 7 A c

GAM895 379 ABCA1 Guo, Z.; Inazu, A.; Yu, W.; Suzumura, T.; Okamoto, M.; Nohara,A.; Higashikata, T.; Sano, R.; Wakasugi, K.; Hayakawa, T.; Yoshida,K.; Suehiro, 7 A c

T.; Schmitz, G.; Mabuchi, H.: Double deletions and missensemutations in the first nucleotide- binding fold of the ATP- bindingcassette transporter A1 (ABCA1) gene in Japanese patients with Tangierdisease. J. Hum. Genet. 47: 325- 329, 2002.

GAM895 379 ABCA1 Hong, S. H.; Rhyne, J.; Zeller, K.; Miller, M.: Novel ABCA1 compoundvariant 7 A c associated with HDL cholesterol deficiency. Biochim. Biophys.Acta 1587: 60- 64, 2002.

GAM895 379 ABCA1 Hoop, R. C.; Russo, L. S.; Riconda, D. L.; Schwartz, L. S.; Hoffman,E. P.: 7 A c Restoration of half the normal dystrophin sequence in a double- deletionDuchenne muscular dystrophy family. Am. J. Med. Genet. 49: 323- 327,1994.

GAM895 379 ABCA1 Huang, W.; Moriyama, K.; Koga, T.; Hua, H.; Ageta, M.; Kawabata,S.; 7 A c Mawatari, K.; Imamura, T.; Eto, T.; Kawamura, M.; Teramoto, T.;Sasaki, J.: Novel mutations in ABCA1 gene in Japanese patients withTangier disease and familial high density lipoprotein deficiency withcoronary heart disease. Biochim. Biophys. Acta 1537: 71- 78, 2001.

GAM895 379 ABCA1 Ishii, J.; Nagano, M.; Kujiraoka, T.; Ishihara, M.; Egashira,T.; Takada, D.; 7 A c Tsuji, M.; Hattori, H.; Emi, M.: Clinical variantof Tangier disease in Japan: mutation of the ABCA1 gene in hypoalphalipoproteinemiawith corneal lipidosis. J. Hum. Genet. 47: 366- 369, 2002.

GAM895 379 ABCA1 Jennings, M. W.; Jones, R. W.; Wood, W. G.; Weatherall, D. J.: Analysis of 7 A c an inversion within the human beta globin gene cluster. NucleicAcids Res. 13: 2897- 2906, 1985.

GAM895 379 ABCA1 Kulozik, A. E.; Bellan- Koch, A.; Kohne, E.; Kleihauer, E.: 7 A c Adeletion/inversion rearrangement of the beta- globin gene cluster ina Turkish family with delta- beta(0)- thalassemia intermedia. Blood 79:2455- 2459, 1992.

GAM895 379 ABCA1 Langmann, T.; Klucken, J.; Reil, M.; Liebisch, G.; Luciani, M.- F.;Chimini, 7 A c G.; Kaminski, W. E.; Schmitz, G.: Molecular cloning of thehuman ATP- binding cassette transporter 1 (hABC1): evidence for sterol- dependentregulation in macrophages. Biochem. Biophys. Res. Commun. 257: 29- 33,1999.

GAM895 379 ABCA1 Lapicka- Bodzioch, K.; Bodzioch, M.; Krull, M.; Kielar, D.; Probst,M.; Kiec, 7 A c B.; Andrikovics, H.; Bottcher, A.; Hubacek, J.; Aslanidis,C.; Suttorp, N.; Schmitz, G.: Homogeneous assay based on 52 primersets to scan for mutations of the ABCA1 gene and its application ingenetic analysis of a new patient with familial high- density lipoproteindeficiency syndrome. Biochim. Biophys. Acta 1537: 42- 48, 2001.

GAM895 379 ABCA1 Lawn, R. M.; Wade, D. P.; Garvin, M. R.; Wang, X.; Schwartz, K.;Porter, J. 7 A c G.; Seilhamer, J. J.; Vaughan, A. M.; Oram, J. F.: TheTangier disease gene product ABC1 controls the cellular apolipoprotein- mediatedlipid removal pathway. J. Clin. Invest. 104: R25- R31, 1999.

GAM895 379 ABCA1 Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, 7 A c J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000.

GAM895 379 ABCA1 Luciani, M. F.; Denizot, F.; Savary, S.; Mattei, M. G.; Chimini,G.: Cloning 7 A c of two novel ABC transporters mapping on human chromosome9. Genomics 21: 150- 159, 1994.

GAM895 379 ABCA1 Marcil, M.; Boucher, B.; Krimbou, L.; Solymoss, B. C.; Davignon,J.; 7 A c Frohlich, J.; Genest, J., Jr.: Severe familial HDL deficiencyin French- Canadian kindreds: clinical, biochemical, and molecularcharacterization.

Arterioscler. Thromb. Vasc. Biol. 15: 1015- 1024,1995.

GAM895 379 ABCA1 Marcil, M.; Yu, L.; Krimbou, L.; Boucher, B.; Oram, J. F.; Cohn,J. S.; Genest, J., Jr.: Cellular cholesterol transport and effluxin fibroblasts are abnormal in subjects with familial HDL deficiency. Arterioscler.Thromb. Vasc. Biol. 19: 159- 169, 1999. 7 A c

GAM895 379 ABCA1 McNeish, J.; Aiello, R. J.; Guyot, D.; Turi, T.; Gabel, C.; Aldinger,C.; Hoppe, K. L.; Roach, M. L.; Royer, L. J.; de Wet, J.; Broccardo,C.; Chimini, G.; Francone, O. L.: High density lipoprotein deficiencyand foam cell accumulation in mice with targeted disruption of ATP- bindingcassette transporter- 1. Proc. Nat. Acad. Sci. 97: 4245- 4250, 2000. 7 A c

GAM895 379 ABCA1 Orso, E.; Broccardo, C.; Kaminski, W. E.; Bottcher, A.; Liebisch,G.; Drobnik, W.; Gotz, A.; Chambenoit, O.; Diederich, W.; Langmann,T.; Spruss, T.; Luciani, M.- F.; Rothe, G.; Lackner, K. J.; Chimini,G.; Schmitz, G.: Transport of lipids from Golgi to plasma membraneis defective in Tangier disease patients and Abc1- deficient mice. NatureGenet. 24: 192- 196, 2000. 7 A c

GAM895 379 ABCA1 Pullinger, C. R.; Hakamata, H.; Duchateau, P. N.; Eng, C.; Aouizerat,B. E.; Cho, M. H.; Fielding, C. J.; Kane, J. P.: Analysis of hABC1gene 5- prime end: additional peptide sequence, promoter region, andfour polymorphisms. Biochem. Biophys. Res. Commun. 271: 451- 455,2000. 7 A c

GAM895 379 ABCA1 Remaley, A. T.; Rust, S.; Rosier, M.; Knapper, C.; Naudin, L.;Broccardo, C.; Peterson, K. M.; Koch, C.; Arnould, I.; Prades, C.;Duverger, N.; Funke, H.; Assman, G.; Dinger, M.; Dean, M.; Chimini,G.; Santamarina- Fojo, S.; Fredrickson, D. S.; Denefle, P. Brewer,H. B., Jr.: Human ATP- binding cassette transporter 1 (ABC1): genomicorganization and identification of the genetic defect in the originalTangier disease kindred. Proc. Nat. Acad. Sci. 96: 12685- 12690,1999. 7 A c

GAM895 379 ABCA1 Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers. Science 289: 1524- 1529, 2000. 7 A c

GAM895 379 ABCA1 Rust, S.; Rosier, M.; Funke, H.; Real, J.; Amoura, Z.; Piette,J.- C.; Deleuze, J.- F.; Brewer, H. B.; Duverger, N.; Denefle, P.; Assmann,G.: Tangier disease is caused by mutations in the gene encoding ATP- bindingcassette transporter 1. Nature Genet. 22: 352- 355, 1999. 7 A c

GAM895 379 ABCA1 Santamarina- Fojo, S.; Peterson, K.; Knapper, C.; Qiu, Y.; Freeman,L.; Cheng, J.- F.; Osorio, J.; Remaley, A.; Yang, X.- P.; Haudenschild,C.; Prades, C.; Chimini, G.; Blackmon, E.; Francois, T.; Duverger,N.; Rubin, E. M.; Rosier, M.; Denefle, P.; Fredrickson, D. S.; Brewer,H. B., Jr.: Complete genomic sequence of the human ABCA1 gene: analysisof the human and mouse ATP- binding cassette A promoter. Proc. Nat.Acad. Sci. 97: 7987- 7992, 2000. Note: Erratum: Proc. Nat. Acad. Sci.99: 1098 only, 2002. 7 A c

GAM895 379 ABCA1 Szakacs, G.; Langmann, T.; Ozvegy, C.; Orso, E.; Schmitz, G.;Varadi, A.; Sarkadi, B.: Characterization of the ATPase cycle ofhuman ABCA1: implications for its function as a regulator rather thanan active transporter. Biochem. Biophys. Res. Commun. 288: 1258- 1264,2001. 7 A c

GAM895 379 ABCA1 Tanaka, A. R.; Ikeda, Y.; Abe- Dohmae, S.; Arakawa, R.; Sadanami,K.; Kidera, A.; Nakagawa, S.; Nagase, T.; Aoki, R.; Kioka, N.; Amachi,T.; Yokoyama, S.; Ueda, K.: Human ABCA1 contains a large amino terminalextracellular domain homologous to an epitope of Sjogren's syndrome. Biochem.Biophys. Res. Commun. 283: 1019- 1025, 2001. 7 A c

GAM895 379 ABCA1 Utech, M.; Hobbel, G.; Rust, S.; Reinecke, H.; Assmann, G.; Walter,M.: 7 A c
Accumulation of RhoA, RhoB, RhoG, and Rac1 in fibroblasts fromTangier
disease subjects suggests a regulatory role of Rho familyproteins in
cholesterol efflux. Biochem. Biophys. Res. Commun. 280:229- 236, 2001.

GAM895 379 ABCA1 Young, S. G.; Fielding, C. J.: The ABCs of cholesterol efflux. NatureGenet. 7 A c
22: 316- 318, 1999.

GAM895 379 ABCA1 Zhao, L.- X.; Zhou, C.- J.; Tanaka, A.; Nakata, M.; Hirabayashi,T.; Amachi, 7 A c
T.; Shioda, S.; Ueda, K.; Inagaki, N.: Cloning, characterizationand tissue
distribution of the rat ATP- binding cassette (ABC) transporterABC2/ABCA2.
Biochem J. 350: 865- 872, 2000.

GAM895 379 ABCA1 Zwarts, K. Y.; Clee, S. M.; Zwinderman, A. H.; Engert, J. C.;Singaraja, R.; 7 A c
Loubser, O.; James, E.; Roomp, K.; Hudson, T. J.; Jukema,J. W.; Kastelein,
J. J. P.; Hayden, M. R.: ABCA1 regulatory variantsinfluence coronary artery
disease independent of effects on plasmalipid levels. Clin. Genet. 61: 115-
125, 2002.

GAM895 379 BNC Teumer, J.; Tseng, H.; Green, H.: The human basonuclin gene. Gene 188:1- 7, 7 A c
1997.

GAM895 379 BNC Tseng, H.; Green, H.: Association of basonuclin with ability ofkeratinocytes 7 A c
to multiply and with absence of terminal differentiation. J.Cell Biol. 126:
495- 506, 1994.

GAM895 379 BNC Tseng, H.; Green, H.: Basonuclin: a keratinocyte protein withmultiple paired 7 A c
zinc fingers. Proc. Nat. Acad. Sci. 89: 10311- 10315,1992.

GAM895 379 CALM1 Berchtold, M. W.; Egli, R.; Rhyner, J. A.; Hameister, H.; Strehler,E. E.: 7 A c
Localization of the human bona fide calmodulin genes CALM1,CALM2, and CALM3
to chromosomes 14q24- q31, 2p21.1- p21.3, and 19q13.2- q13.3. Genomics
16:461- 465, 1993.

GAM895 379 CALM1 Chin, D.; Winkler, K. E.; Means, A. R.: Characterization of 7 A c
substratephosphorylation and use of calmodulin mutants to address
implicationsfrom the enzyme crystal structure of calmodulin- dependent
proteinkinase I. J. Biol. Chem. 272: 31235- 31240, 1997.

GAM895 379 CALM1 Drum, C. L.; Yan, S.- Z.; Bard, J.; Shen, Y.- Q.; Lu, D.; Soelaiman,S.; 7 A c
Grabarek, Z.; Bohm, A.; Tang, W.- J.: Structural basis for theactivation of
anthrax adenylyl cyclase exotoxin by calmodulin. Nature 415:396- 402, 2002.

GAM895 379 CALM1 Koller, M.; Schnyder, B.; Strehler, E. E.: Structural organizationof the 7 A c
human CaMIII calmodulin gene. Biochim. Biophys. Acta 1087:180- 189, 1990.

GAM895 379 CALM1 Kretsinger, R. H.; Rudnick, S. E.; Weissman, L. J.: Crystal structureof 7 A c
calmodulin. J. Inorganic Biochem. 28: 289- 302, 1986.

GAM895 379 CALM1 McPherson, J. D.; Hickie, R. A.; Wasmuth, J. J.; Meyskens, F. L.;Perham, R. 7 A c
N.; Strehler, E. E.; Graham, M. T.: Chromosomal localizationof multiple
genes encoding calmodulin. (Abstract) Cytogenet. CellGenet. 58: 1951 only,
1991.

GAM895 379 CALM1 Pegues, J. C.; Friedberg, F.: Multiple mRNAs encoding human calmodulin. 7 A c
Biochem.Biophys. Res. Commun. 172: 1145- 1149, 1990.

GAM895 379 CALM1 Rhyner, J. A.; Ottiger, M.; Wicki, R.; Greenwood, T. M.; Strehler,E. E.: 7 A c
Structure of the human CALM1 calmodulin gene and identificationof two CALM1-
related pseudogenes CALM1P1 and CALM1P2. Europ. J. Biochem. 225:71- 82,
1994.

GAM895 379 CALM1 Scambler, P. J.; McPherson, M. A.; Bates, G.; Bradbury, N. A.;Dormer, R. L.; 7 A c
Williamson, R.: Biochemical and genetic exclusionof calmodulin as the site
of the basic defect in cystic fibrosis. Hum.Genet. 76: 278- 282, 1987.

GAM895 379 CALM1 Schumacher, M. A.; Rivard, A. F.; Bachinger, H. P.; Adelman, J.P.: Structure 7 A c
of the gating domain of a Ca(2+)- activated K+ channelcomplexed with
Ca(2+)/calmodulin. Nature 410: 1120- 1124, 2001.

GAM895 379 CALM1 Sen Gupta, B.; Detera- Wadleigh, S. D.; McBride, O. W.; Friedberg,F.: A 7 A c
calmodulin pseudogene on human chromosome 17. Nucleic AcidsRes. 17: 2868
only, 1989.

GAM895 379 CALM1 Sen Gupta, B.; Friedberg, F.; Detera- Wadleigh, S. D.: Molecularanalysis of 7 A c
human and rat calmodulin complementary DNA clones: evidencefor additional
active genes in these species. J. Biol. Chem. 262:16663- 16670, 1987.

GAM895 379 CNTN3 Connelly, M. A.; Grady, R. C.; Mushinski, J. F.; Marcu, K. B.:PANG, a gene 7 A c
encoding a neuronal glycoprotein, is ectopically activatedby intracisternal
A- type particle long terminal repeats in murineplasmacytomas. Proc. Nat.
Acad. Sci. 91: 1337- 1341, 1994.

GAM895 379 CNTN3 Mock, B. A.; Connelly, M. A.; McBride, O. W.; Kozak, C. A.; Marcu,K. B.: 7 A c
Plasmacytoma- associated neuronal glycoprotein, Pang, mapsto mouse
chromosome 6 and human chromosome 3. Genomics 34: 226- 228,1996.

GAM895 379 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- 7 A c
elongationfactor 2 kinase (calmodulin- dependent protein kinase III)
antibodiesin patients with systemic lupus erythematosus. Biochem.
Biophys.Res. Commun. 293: 1073- 1076, 2002.

GAM895 379 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 7 A c
Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C.
R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein
kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat.
Acad. Sci. 94: 4884- 4889, 1997.

GAM895 379 FOSB Bibb, J. A.; Chen, J.; Taylor, J. R.; Svenningsson, P.; Nishi,A.; Snyder, G. 7 A c
L.; Yan, Z.; Sagawa, Z. K.; Ouimet, C. C.; Nairn, A.C.; Nestler, E. J.;
Greengard, P.: Effects of chronic exposure tococaine are regulated by the
neuronal protein Cdk5. Nature 410:376- 380, 2001.

GAM895 379 FOSB Brown, J. R.; Ye, H.; Bronson, R. T.; Dikkes, P.; Greenberg, M.E.: A defect 7 A c
in nurturing in mice lacking the immediate early genefosB. Cell 86: 297-
309, 1996.

GAM895 379 FOSB Forsdyke, D.: Personal Communication. Kingston, Ontario, Canada 6/8/1992. 7 A c

GAM895 379 FOSB Kelz, M. B.; Chen, J.; Carlezon, W. A., Jr.; Whisler, K.; Gilden,L.; 7 A c
Beckmann, A. M.; Steffen, C.; Zhang, Y.- J.; Marotti, L.; Self,D. W.;
Tkatch, T.; Baranauskas, G.; Surmeier, D. J.; Neve, R. L.;Duman, R. S.;
Picciotto, M. R.; Nestler, E. J.: Expression of thetranscription factor
delta- FosB in the brain controls sensitivityto cocaine. Nature 401: 272-
276, 1999.

GAM895 379 FOSB Lazo, P. S.; Dorfman, K.; Noguchi, T.; Mattei, M. G.; Bravo, R.: Structure 7 A c
and mapping of the fosB gene: FosB downregulates the activityof the fosB
promoter. Nucleic Acids Res. 20: 343- 350, 1992.

GAM895 379 FOSB Martin- Gallardo, A.; McCombie, W. R.; Gocayne, J. D.; FitzGerald,M. G.; 7 A c
Wallace, S.; Lee, B. M. B.; Lamerdin, J.; Trapp, S.; Kelley,J. M.; Liu, L.-
I.; Dubnick, M.; Johnston- Dow, L. A.; Kerlavage, A.R.; de Jong, P.;
Carrano, A.; Fields, C.; Venter, J. C.: AutomatedDNA sequencing and analysis
of 106 kilobases from human chromosome19q13.3. Nature Genet. 1: 34- 39,
1992.

GAM895 379 FOSB Nakabeppu, Y.; Nathans, D.: A naturally occurring truncated formof FosB that 7 A c
inhibits Fos/Jun transcriptional activity. Cell 64:751- 759, 1991.

GAM895 379 FOSB Siderovski, D. P.; Blum, S.; Forsdyke, R. E.; Forsdyke, D. R.:A set of human 7 A c
putative lymphocyte G0/G1 switch genes includes geneshomologous to rodent
cytokine and zinc finger protein- encoding genes. DNACell Biol. 9: 579- 587,
1990.

GAM895 379 KCNAB1 England, S. K.; Uebele, V. N.; Kodali, J.; Bennett, P. B.; Tamkun,M. M.: A 7 A c
novel K+ channel beta- subunit (hKv- beta- 1.3) is producedvia alternative
mRNA splicing. J. Biol. Chem. 270: 28531- 28534,1995.

GAM895 379 KCNAB1 England, S. K.; Uebele, V. N.; Shear, H.; Kodali, J.; Bennett,P. B.; Tamkun, 7 A c
M. M.: Characterization of a voltage- gated K+ channelbeta subunit expressed
in human heart. Proc. Nat. Acad. Sci. 92:6309- 6313, 1995.

GAM895 379 KCNAB1 Jones, J. M.; Bentley, E.; Meisler, M. H.; Darling, S. M.: Geneticmapping of 7 A c
the voltage- gated shaker potassium channel beta subunitKcnab1 to mouse
chromosome 3. Mammalian Genome 9: 260 only, 1998.

GAM895 379 KCNAB1 Leicher, T. Roeper, J.; Weber, K.; Wang, X.; Pongs, O.: Structuraland 7 A c
functional characterization of human potassium channel subunitbeta- 1
(KCNA1B). Neuropharmacology 35: 787- 795, 1996.

GAM895 379 KCNAB1 Leicher, T.; Bahring, R.; Isbrandt, D.; Pongs, O.: Coexpressionof the KCNA3B 7 A c
gene product with Kv1.5 leads to a novel A- type potassiumchannel. J. Biol.
Chem. 273: 35095- 35101, 1998.

GAM895 379 KCNAB1 McCormack, K.; McCormack, T.; Tanouye, M.; Rudy, B.; Stuhmer, W.: 7 A c
Alternative splicing of the human Shaker K+ channel beta- 1 geneand
functional expression of the beta- 2 gene product. FEBS Lett. 370:32- 36,
1995.

GAM895 379 KCNAB1 Schultz, D.; Litt, M.; Smith, L.; Thayer, M.; McCormack, K.: Localizationof 7 A c
two potassium channel beta subunit genes, KCNA1B and KCNA2B. Genomics
31:389- 391, 1996.

GAM895 379 MAGEA12 De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J. J.; Szikora,J.- P.; De 7 A c
Smet, C.; Brasseur, F.; van der Bruggen, P.; Lethe, B.;Lurquin, C.;
Brasseur, R.; Chomez, P.; De Backer, O.; Cavenee, W.;Boon, T.: Structure,
chromosomal localization, and expression of12 genes of the MAGE family.
Immunogenetics 40: 360- 369, 1994.

GAM895 379 MAGEA12 Rogner, U. C.; Wilke, K.; Steck, E.; Korn, B.; Poustka, A.: Themelanoma 7 A c
antigen gene (MAGE) family is clustered in the chromosomalband Xq28.
Genomics 29: 725- 731, 1995.

GAM895 379 MAGEA3 De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J. J.; Szikora,J.- P.; De 7 A c
Smet, C.; Brasseur, F.; van der Bruggen, P.; Lethe, B.;Lurquin, C.;
Brasseur, R.; Chomez, P.; De Backer, O.; Cavenee, W.;Boon, T.: Structure,
chromosomal localization, and expression of12 genes of the MAGE family.
Immunogenetics 40: 360- 369, 1994.

GAM895 379 MAGEA3 Rogner, U. C.; Wilke, K.; Steck, E.; Korn, B.; Poustka, A.: Themelanoma 7 A c
antigen gene (MAGE) family is clustered in the chromosomalband Xq28.
Genomics 29: 725- 731, 1995.

GAM895 379 MAGEA9 De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J. J.; Szikora,J.- P.; De 7 A c
Smet, C.; Brasseur, F.; van der Bruggen, P.; Lethe, B.;Lurquin, C.;
Brasseur, R.; Chomez, P.; De Backer, O.; Cavenee, W.;Boon, T.: Structure,
chromosomal localization, and expression of12 genes of the MAGE family.
Immunogenetics 40: 360- 369, 1994.

GAM895 379 MAGEA9 Rogner, U. C.; Wilke, K.; Steck, E.; Korn, B.; Poustka, A.: Themelanoma 7 A c
antigen gene (MAGE) family is clustered in the chromosomalband Xq28.
Genomics 29: 725- 731, 1995.

GAM895 379 MYO5A Copeland, N. G.; Hutchison, K. W.; Jenkins, N. A.: Excision ofthe DBA 7 A c
ecotropic provirus in dilute coat- color revertants of miceoccurs by
homologous recombination involving the viral LTRs. Cell 33:379- 387, 1983.

GAM895 379 MYO5A El- Husseini, A. E.; Vincent, S. R.: Cloning and characterizationof a novel 7 A c
RING finger protein that interacts with class V myosins. J.Biol. Chem. 274:
19771- 19777, 1999.

GAM895 379 MYO5A Engle, L. J.; Kennett, R. H.: Cloning, analysis, and chromosomallocalization 7 A c
of myoxin (MYH12): the human homologue to the mouse dilutegene. Genomics 19:
407- 416, 1994.

GAM895 379 MYO5A Espreafico, E. M.; Coling, D. E.; Tsakraklides, V.; Krogh, K.;Wolenski, J. 7 A c
S.; Kalinec, G.; Kachar, B.: Localization of myosin- Vin the centrosome.
Proc. Nat. Acad. Sci. 95: 8636- 8641, 1998.

GAM895 379 MYO5A Jenkins, N. A.; Copeland, N. G.; Taylor, B. A.; Lee, B. K.: Dilute(d) coat 7 A c
colour mutation of DNA/2J mice is associated with the siteof integration of
an ecotropic MuLV genome. Nature 293: 370- 374,1981.

GAM895 379 MYO5A Jones, J. M.; Huang, J.- D.; Mermall, V.; Hamilton, B. A.; Mooseker,M. S.; 7 A c
Escayg, A.; Copeland, N. G.; Jenkins, N. A.; Meisler, M. H.: The mouse
neurological mutant flailer expresses a novel hybrid genederived by exon
shuffling between Gnb5 and Myo5a. Hum. Molec. Genet. 9:821- 828, 2000.

GAM895 379 MYO5A Karcher, R. L.; Roland, J. T.; Zappacosta, F.; Huddleston, M. J.;Annan, R. 7 A c
S.; Carr, S. A.; Gelfand, V. I.: Cell cycle regulationof myosin- V by
calcium/calmodulin- dependent protein kinase II. Science 293:1317- 1320,
2001.

GAM895 379 MYO5A Markert, C. L.; Silvers, W. K.: The effects of genotype and cellenvironment 7 A c
on melanoblast differentiation in the house mouse. Genetics 41:429- 450,
1956.

GAM895 379 MYO5A Mehta, A. D.; Rock, R. S.; Rief, M.; Spudich, J. A.; Mooseker,M. S.; Cheney, 7 A c
R. E.: Myosin- V is a processive actin- based motor. Nature 400:590- 593,
1999.

GAM895 379 MYO5A Mercer, J. A.; Seperack, P. K.; Strobel, M. C.; Copeland, N. G.;Jenkins, N. 7 A c
A.: Novel myosin heavy chain encoded by murine dilutecoat colour locus.
Nature 349: 709- 713, 1991.

GAM895 379 MYO5A Moore, K. J.; Testa, J. R.; Francke, U.; Milatovich, A.; Copeland,N. G.; 7 A c
Jenkins, N. A.: Cloning and regional assignment of the humanmyosin heavy
chain 12 (MYH12) gene to chromosome band 15q21. Cytogenet.Cell Genet. 69:
53- 58, 1995.

GAM895 379 MYO5A Pastural, E.; Barrat, F. J.; Dufourcq- Lagelouse, R.; Certain,S.; Sanal, O.; 7 A c
Jabado, N.; Seger, R.; Griscelli, C.; Fischer, A.;de Saint Basile, G.:
Griscelli disease maps to chromosome 15q21 andis associated with mutations
in the myosin- Va gene. Nature Genet. 16:289- 292, 1997. Note: Erratum:
Nature Genet. 23: 373 only, 1999.

GAM895 379 MYO5A Rief, M.; Rock, R. S.; Mehta, A. D.; Mooseker, M. S.; Cheney,R. E.; Spudich, 7 A c
J. A.: Myosin- V stepping kinetics: a molecular modelfor processivity. Proc.
Nat. Acad. Sci. 97: 9482- 9486, 2000.

GAM895 379 MYO5A Russell, E. S.: A quantitative histological study of the pigmentfound in the 7 A c
coat- color mutants of the house mouse. IV. The natureof the effects of
genic substitution in five major allelic series. Genetics 34:146- 166, 1949.

GAM895 379 MYO5A Strobel, M. C.; Seperack, P. K.; Copeland, N. G.; Jenkins, N.A.: Molecular 7 A c
analysis of two mouse dilute locus deletion mutations:spontaneous dilute
lethal- 20J and radiation- induced dilute prenatallethal Aa2 alleles. Molec.

Cell. Biol. 10: 501- 509, 1990.

GAM895 379 MYO5A Tanaka, H.; Homma, K.; Iwane, A. H.; Katayama, E.; Ikebe, R.;Saito, J.; 7 A c
Yanagida, T.; Ikebe, M.: The motor domain determines thelarge step of
myosin- V. Nature 415: 192- 195, 2002.

GAM895 379 MYO5A Walker, M. L.; Burgess, S. A.; Sellers, J. R.; Wang, F.; Hammer,J. A., III; 7 A c
Trinick, J.; Knight, P. J.: Two- headed binding of a processivemyosin to F-
actin. Nature 405: 804- 807, 2000.

GAM895 379 MYO5A Yanagida, T.; Iwane, A. H.: A large step for myosin. Proc. Nat.Acad. Sci. 7 A c
97: 9357- 9359, 2000.

GAM895 379 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of 7 A c
NAD(P)H:quinonereductase by dietary antioxidants: possible role in
protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77:
5216- 5220,1980.

GAM895 379 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. 7 A c
A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.;
Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of
the long arm of human chromosome 16. Genomics 10:308- 312, 1991.

GAM895 379 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof 7 A c
the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983.

GAM895 379 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman 7 A c
diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum.
Genet. 53: 189- 193, 1980.

GAM895 379 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- 7 A c
inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and
localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578,
1988.

GAM895 379 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, 7 A c
M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic
variation in the prevalence of a common NAD(P)Hquinone oxidoreductase
polymorphism and its implications for anti- cancerchemotherapy. Brit. J.
Cancer 76: 852- 854, 1997.

GAM895 379 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further 7 A c
evidence for the regional localization of human APRT and DIA4on chromosome
16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984.

GAM895 379 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe 7 A c
increased susceptibility of individuals with a polymorphism
inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat.
Acad. Sci. 96: 8150- 8155, 1999.

GAM895 379 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA- 7 A c
4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980.

GAM895 379 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. 7 A c
P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1)
gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382-
7389, 1998.

GAM895 379 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; 7 A c
Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.;
Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.;
Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological
malignancy, is associated with the NQO1 609C- T mutationand rapid fractional
excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997.

GAM895 379 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 7 A c
New York: Oxford Univ. Press (pub.) 1988.

GAM895 379 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to 7 A c
cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999.

GAM895 379 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, 7 A c
P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene
expression in human colon carcinoma cells: characterization ofa mutation
which modulates DT- diaphorase activity and mitomycin sensitivity.
CancerRes. 52: 797- 802, 1992.

GAM895 379 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; 7 A c
Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H:
quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997.

GAM895 379 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, 7 A c
S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and
long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese
workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998.

GAM895 379 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the 7 A c
loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes.
Leukemia Res. 22: 105- 113, 1998.

GAM895 379 PPP3CA De Windt, L. J.; Lim, H. W.; Bueno, O. F.; Liang, Q.; Delling,U.; Braz, J. 7 A c
C.; Glascock, B. J.; Kimball, T. F.; del Monte, F.; Hajjar,R. J.; Molkentin,
J. D.: Targeted inhibition of calcineurin attenuatescardiac hypertrophy in
vivo. Proc. Nat. Acad. Sci. 98: 3322- 3327,2001.

GAM895 379 PPP3CA Fuentes, J. J.; Genesca, L.; Kingsbury, T. J.; Cunningham, K. W.;Perez- 7 A c
Riba, M.; Estivill, X.; de la Luna, S.: DSCR1, overexpressedin Down
syndrome, is an inhibitor of calcineurin- mediated signalingpathways. Hum.
Molec. Genet. 9: 1681- 1690, 2000.

GAM895 379 PPP3CA Giri, P.; Higuchi, S.; Kincaid, R. L.: Chromosomal mapping ofthe human genes 7 A c
for the calmodulin- dependent protein phosphatase (calcineurin)catalytic
subunit. Biochem. Biophys. Res. Commun. 181: 252- 258,1991.

GAM895 379 PPP3CA Guerini, D.; Klee, C. B.: Cloning of human calcineurin A: evidencefor two 7 A c
isozymes and identification of a polyproline structural domain. Proc.Nat.
Acad. Sci. 86: 9183- 9187, 1989.

GAM895 379 PPP3CA Leinwand, L. A.: Calcineurin inhibition and cardiac hypertrophy:a matter of 7 A c
balance. Proc. Nat. Acad. Sci. 98: 2947- 2949, 2001.

GAM895 379 PPP3CA Malleret, G.; Haditsch, U.; Genoux, D.; Jones, M. W.; Bliss, T.V. P.; 7 A c
Vanhoose, A. M.; Weitlauf, C.; Kandel, E. R.; Winder, D. G.;Mansuy, I. M.:
Inducible and reversible enhancement of learning,memory, and long- term
potentiation by genetic inhibition of calcineurin. Cell 104:675- 686, 2001.

GAM895 379 PPP3CA Mansuy, I. M.; Mayford, M.; Jacob, B.; Kandel, E. R.; Bach, M.E.: Restricted 7 A c
and regulated overexpression reveals calcineurin asa key component in the
transition from short- term to long- term memory. Cell 92:39- 49, 1998.

GAM895 379 PPP3CA Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: 7 A c
IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin
association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999.

GAM895 379 PPP3CA Rothermel, B. A.; McKinsey, T. A.; Vega, R. B.; Nicol, R. L.; Mammen,P.; 7 A c
Yang, J.; Antos, C. L.; Shelton, J. M.; Bassel- Duby, R.; Olson,E. N.;
Williams, R. S.: Myocyte- enriched calcineurin- interactingprotein, MCIP1,
inhibits cardiac hypertrophy in vivo. Proc. Nat.Acad. Sci. 98: 3328- 3333,
2001.

GAM895 379 PPP3CA Seitz, D. P.; Pasha, M. K.; Singh, B.; Chu, A.; Sharma, R. K.: Localization 7 A c
and characterization of calcineurin in bovine eye. Invest.Ophthal. Vis. Sci.
43: 15- 21, 2002.

GAM895 379 PPP3CA Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; 7 A c
Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a
Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999.

GAM895 379 PPP3CA Wang, M. G.; Yi, H.; Guerini, D.; Klee, C. B.; McBride, O. W.: Calcineurin A 7 A c
alpha (PPP3CA), calcineurin A beta (PPP3CB) and calcineurinB (PPP3R1) are
located on human chromosomes 4, 10q21- q22 and 2p16- p15respectively.
Cytogenet. Cell Genet. 72: 236- 241, 1996.

GAM895 379 PPP3CA Winder, D. G.; Mansuy, I. M.; Osman, M.; Moallem, T. M.; Kandel,E. R.: 7 A c
Genetic and pharmacological evidence for a novel, intermediatephase of long-
term potentiation suppressed by calcineurin. Cell 92:25- 37, 1998.

GAM895 379 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 7 A c
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene
PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal
instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM895 379 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 7 A c
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY)
to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet.
76: 49- 52, 1997.

GAM895 379 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 7 A c
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated
protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of
all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM895 379 PXF Braun, A.; Kammerer, S.; Weissenhorn, W.; Weiss, E. H.; Cleve,H.: Sequence 7 A c
of a putative human housekeeping gene (HK33) localizedon chromosome 1. Gene
146: 291- 295, 1994.

GAM895 379 PXF Gotte, K.; Girzalsky, W.; Linkert, M.; Baumgart, E.; Kammerer,S.; Kunau, W.- 7 A c
H.; Erdmann, R.: Pex19p, a farnesylated protein essentialfor peroxisome
biogenesis. Molec. Cell. Biol. 18: 616- 628, 1998.

GAM895 379 PXF James, G. L.; Goldstein, J. L.; Pathak, R. K.; Anderson, R. G.W.; Brown, M. 7 A c
S.: PxF, a prenylated protein of peroxisomes J. Biol.Chem. 269: 14182-
14190, 1994.

GAM895 379 PXF Kammerer, S.; Arnold, N.; Gutensohn, W.; Mewes, H.- W.; Kunau, W.- 7 A c
H.;Hofler, G.; Roscher, A. A.; Braun, A.: Genomic organization and
molecularcharacterization of a gene encoding HsPXF, a human peroxisomal
farnesylatedprotein. Genomics 45: 200- 210, 1997.

GAM895 379 PXF Kinoshita, N.; Ghaedi, K.; Shimozawa, N.; Wanders, R. J. A.; Matsuzono,Y.; 7 A c
Imanaka, T.; Okumoto, K.; Suzuki, Y.; Kondo, N.; Fujiki, Y.:Newly identified
Chinese hamster ovary cell mutants are defectivein biogenesis of peroxisomal
membrane vesicles (peroxisomal ghosts),representing a novel complementation
group in mammals J. Biol. Chem. 273:24122- 24130, 1998.

GAM895 379 PXF Matsuzono, Y.; Kinoshita, N.; Tamura, S.; Shimozawa, N.; Hamasaki,M.; 7 A c
Ghaedi, K.; Wanders, R. J. A.; Suzuki, Y.; Kondo, N.; Fujiki,Y.: Human
PEX19: cDNA cloning by functional complementation, mutationanalysis in a
patient with Zellweger syndrome, and potential rolein peroxisomal membrane
assembly. Proc. Nat. Acad. Sci. 96: 2116- 2121,1999.

GAM895 379 RAB5A Bucci, C.; Parton, R. G.; Mather, I. H.; Stunnenberg, H.; Simons,K.; 7 A c
Hoflack, B.; Zerial, M.: The small GTPase rab5 functions as aregulatory

factor in the early endocytic pathway. Cell 70: 715- 728,1992.

GAM895 379 RAB5A Lanzetti, L.; Rybin, V.; Malabarba, M. G.; Christoforidis, S.;Scita, G.; 7 A c
Zerial, M.; Di Fiore, P. P.: The Eps8 protein coordinatesEGF receptor
signalling through Rac and trafficking through Rab5. Nature 408:374- 377,
2000.

GAM895 379 RAB5A Rousseau- Merck, M. F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: 7 A c
Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350-
354, 1991.

GAM895 379 RAB5A Stenmark, H.; Vitale, G.; Ullrich, O.; Zerial, M.: Rabaptin- 5is a direct 7 A c
effector of the small GTPase Rab5 in endocytic membranefusion. Cell 83: 423-
432, 1995.

GAM895 379 RAB5A Xiao, G.- H.; Shoarinejad, F.; Jin, F.; Golemis, E. A.; Yeung, R.S.: The 7 A c
tuberous sclerosis 2 gene product, tuberin, functions asa Rab5 GTPase
activating protein (GAP) in modulating endocytosis. J.Biol. Chem. 272: 6097-
6100, 1997.

GAM895 379 RAB5A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes 7 A c
encode a family of GTP- binding proteins related to yeastYPT1 and SEC4
products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989.

GAM895 379 STAT1 Chen, X.; Vinkemeier, U.; Zhao, Y.; Jeruzalmi, D.; Darnell, J.E., Jr.; 7 A c
Kuriyan, J.: Crystal structure of a tyrosine phosphorylatedSTAT- 1 dimer
bound to DNA. Cell 93: 827- 839, 1998.

GAM895 379 STAT1 Copeland, N. G.; Gilbert, D. J.; Schindler, C.; Zhong, Z.; Wen,Z.; Darnell, 7 A c
J. E., Jr.; Mui, A. L.- F.; Miyajima, A.; Quelle, F. W.;Ihle, J. N.;
Jenkins, N. A.: Distribution of the mammalian Stat genefamily in mouse
chromosomes. Genomics 29: 225- 228, 1995.

GAM895 379 STAT1 Darnell, J. E., Jr.; Kerr, I. M.; Stark, G. M.: Jak- STAT pathwaysand 7 A c
transcriptional activation in response to IFNs and other
extracellularsignaling proteins. Science 264: 1415- 1421, 1994.

GAM895 379 STAT1 Dupuis, S.; Dargemont, C.; Fieschi, C.; Thomassin, N.; Rosenzweig,S.; 7 A c
Harris, J.; Holland, S. M.; Schreiber, R. D.; Casanova, J.- L.: Impairment
of mycobacterial but not viral immunity by a germlinehuman STAT1 mutation.
Science 293: 300- 303, 2001.

GAM895 379 STAT1 Durbin, J. E.; Hackenmiller, R.; Simon, M. C.; Levy, D. E.: 7 A c
Targeteddisruption of the mouse Stat1 gene results in compromised innate
immunityto viral disease. Cell 84: 443- 450, 1996.

GAM895 379 STAT1 Haddad, B.; Pabon- Pena, C. R.; Young, H.; Sun, W. H.: Assignmentof STAT1 to 7 A c
human chromosome 2q32 by FISH and radiation hybrids. Cytogenet.Cell Genet.
83: 58- 59, 1998.

GAM895 379 STAT1 Ihle, J. N.: Cytokine receptor signalling. Nature 377: 591- 594,1995. 7 A c

GAM895 379 STAT1 Ihle, J. N.: STATs: signal transducers and activators of transcription. Cell 7 A c
84:331- 334, 1996.

GAM895 379 STAT1 Ihle, J. N.; Kerr, I. M.: Jaks and Stats in signaling by the 7 A c
cytokinereceptor superfamily. Trends Genet. 11: 69- 74, 1995.

GAM895 379 STAT1 Kaplan, D. H.; Shankaran, V.; Dighe, A. S.; Stockert, E.; Aguet,M.; Old, L. 7 A c
J.; Schreiber, R. D.: Demonstration of an interferongamma- dependent tumor
surveillance system in immunocompetent mice. Proc.Nat. Acad. Sci. 95: 7556-
7561, 1998.

GAM895 379 STAT1 Meraz, M. A.; White, J. M.; Sheehan, K. C. F.; Bach, E. A.; Rodig,S. J.; 7 A c
Dighe, A. S.; Kaplan, D. H.; Riley, J. K.; Greenlund, A. C.Campbell, D.;
Carver- Moore, K.; DuBois, R. N.; Clark, R.; Aguet, M.;Schreiber, R. D.:

Targeted disruption of the Stat1 gene in mice revealsunexpected physiologic specificity in the JAK- STAT signaling pathway. Cell 84:431- 442, 1996.

GAM895 379 STAT1 Mowen, K. A.; Tang, J.; Zhu, W.; Schurter, B. T.; Shuai, K.; Herschman,H. R.; David, M.: Arginine methylation of STAT1 modulates IFN- alpha/beta-inducedtranscription. Cell 104: 731- 741, 2001. 7 A c

GAM895 379 STAT1 Ramana, C. V.; Chatterjee- Kishore, M.; Nguyen, H.; Stark, G. R.: Complex roles of Stat1 in regulating gene expression. Oncogene 19:2619- 2627, 2000. 7 A c

GAM895 379 STAT1 Schindler, C.; Fu, X.- Y.; Improta, T.; Aebersold, R.; Darnell,J. E., Jr.: Proteins of transcription factor ISGF- 3: one gene encodesthe 91- and 84- kDa ISGF- 3 proteins that are activated by interferonalpha. Proc. Nat. Acad. Sci. 89: 7836- 7839, 1992. 7 A c

GAM895 379 STAT1 Shankaran, V.; Ikeda, H.; Bruce, A. T.; White, J. M.; Swanson,P. E.; Old, L. J.; Schreiber, R. D.: IFN- gamma and lymphocytes preventprimary tumour development and shape tumour immunogenicity. Nature 410:1107- 1111, 2001. 7 A c

GAM895 379 STAT1 Yamamoto, K.; Kobayashi, H.; Arai, A.; Miura, O.; Hirosawa, S.;Miyasaka, N.: cDNA cloning, expression and chromosome mapping ofthe human STAT4 gene: both STAT4 and STAT1 genes are mapped to 2q32.2- q32.3. Cytogenet.Cell Genet. 77: 207- 210, 1997. 7 A c

GAM895 379 TPT Balci, S.; Demirtas, M.; Civelek, B.; Piskin, M.; Sensoz, O.; Akarsu,A. N.: Phenotypic variability of triphalangeal thumb- polysyndactylysyndrome linked to chromosome 7q36. Am. J. Med. Genet. 87: 399- 406,1999. 7 A c

GAM895 379 TPT Heus, H. C.; Hing, A.; van Baren, M. J.; Joosse, M.; Breedveld,G. J.; Wang, J. C.; Burgess, A.; Donnis- Keller, H.; Berglund, C.;Zguricas, J.; Scherer, S. W.; Rommens, J. M.; Oostra, B. A.; Heutink,P.: A physical and transcriptional map of the preaxial polydactylylocus on chromosome 7q36. Genomics 57: 342- 351, 1999. 7 A c

GAM895 379 TPT Heutink, P.; Zguricas, J.; van Oosterhout, L.; Breedveld, G. J.;Testers, L.; Sandkuijl, L. A.; Snijders, P. J. L. M.; Weissenbach,J.; Lindhout, D.; Hovius, S. E. R.; Oostra, B. A.: The gene for triphalangealthumb maps to the subtelomeric region of chromosome 7q. Nature Genet. 6:287- 292, 1994. 7 A c

GAM895 379 TPT Hing, A. V.; Helms, C.; Slaugh, R.; Burgess, A.; Wang, J. C.; Herman,T.; Dowton, S. B.; Donis- Keller, H.: Linkage of preaxial polydactylytype 2 to 7q36. Am. J. Med. Genet. 58: 128- 135, 1995. 7 A c

GAM895 379 TPT Kantaputra, P. N.; Chalidapong, P.: Are triphalangeal thumb-polysyndactylysyndrome (TPTPS) and tibial hemimelia- polysyndactyly-triphalangealthumb syndrome (THPTTS) identical?: A father with TPTPS and his daughterwith THPTTS in a Thai family. Am. J. Med. Genet. 93: 126- 131, 2000. 7 A c

GAM895 379 TPT Nicolai, J.- P. A.; Hamel, B. C. J.: A family with complex bilateralpolysyndactyly. J. Hand Surg. 13A: 405- 407, 1988. 7 A c

GAM895 379 TPT Seidman, C.: Personal Communication. Boston, Mass. 3/17/1994. 7 A c

GAM895 379 TPT Temtamy, S. A.: Personal Communication. Cairo, Egypt 4/25/1994. 7 A c

GAM895 379 TPT Tsukurov, O.; Boehmer, A.; Flynn, J.; Nicolai, J.- P.; Hamel, B.C. J.; Traill, S.; Zaleske, D.; Mankin, H. J.; Yeon, H.; Ho, C.; Tabin,C.; Seidman, J. G.; Seidman, C.: A complex bilateral polysyndactylydisease locus maps to chromosome 7q36. Nature Genet. 6: 282- 286,1994. 7 A c

GAM895 379 TPT Zguricas, J.; Heus, H.; Morales- Peralta, E.; Breedveld, G.; Kuyt,B.; Mumcu, E. F.; Bakker, W.; Akarsu, N.; Kay, S. P. J.; Hovius, S.E. R.; Heredero-Baute, L.; Oostra, B. A.; Heutink, P.: Clinical andgenetic studies on 12 preaxial polydactyly families and refinementof the localisation of the gene responsible to a 1.9 cM region onchromosome 7q36. J. Med. Genet. 36: 32- 40, 7 A c

1999.

GAM895 379 TPT Zguricas, J.; Snijders, P. J. L. M.; Hovius, S. E. R.; Heutink,P.; Oostra, 7 A c
B. A.; Lindhout, D.: Phenotypic analysis of triphalangealthumb and
associated hand malformations. J. Med. Genet. 31: 462- 467,1994.

GAM1032 303 ACP1 Arnaud, J.; Vavrusa, B.; Sevin, J.; Constans, J.: Human red- cellacid 6 A c
phosphatase (ACP1): a new mutant (ACP1*KUK) detected by isoelectricfocusing,
kinetics of thermostability and substrate activity. Hum.Hered. 39: 288- 293,
1989.

GAM1032 303 ACP1 Arnaud, J.; Vavrusa, B.; Wiederanders, G.; Constans, J.: Humanred- cell acid 6 A c
phosphatase (ACP1): kinetic and thermodynamic characterizationof the KUK
variant. Hum. Hered. 42: 140- 142, 1992.

GAM1032 303 ACP1 Beemer, F. A.; van der Heiden, C.; Van Hemel, J. O.; Jansen, M.: Letter to 6 A c
the editors. (Letter) Clin. Genet. 24: 151, 1983.

GAM1032 303 ACP1 Berg, K.: Close linkage between APOB and ACP1 excluded. (Abstract) 6 A c
Cytogenet.Cell Genet. 46: 580, 1987.

GAM1032 303 ACP1 Bottini, E.; Carapella, E.; Orzalesi, M.; Lucarelli, P.; Pascone,R.; Gloria- 6 A c
Bottini, F.; Coccia, M.: Is there a role of erythrocyteacid phosphatase
polymorphism in intrauterine development? (Letter) Am.J. Hum. Genet. 32:
764- 767, 1980.

GAM1032 303 ACP1 Bryson, G. L. M.; Massa, H.; Trask, B. J.; Van Etten, R. L.: Genestructure, 6 A c
sequence, and chromosomal localization of the human redcell- type low
molecular weight acid phosphotyrosyl phosphatase gene,ACP1. Genomics 30:
133- 140, 1995.

GAM1032 303 ACP1 Chautard- Freire- Maia, E. A.: Linkage relationships between 22autosomal 6 A c
markers. Ann. Hum. Genet. 38: 191- 198, 1974.

GAM1032 303 ACP1 Chu, E. H. Y.; Chang, C. C.; Sun, N. C.: Synteny of the humangenes for gal- 6 A c
1- PT, ACP- 1, MDH- 1, and gal- plus- activator and assignmentto chromosome
2. Birth Defects Orig. Art. Ser. XI(3): 103- 106, 1975.Note: Alternate:
Cytogenet. Cell Genet. 14: 273- 276, 1975...

GAM1032 303 ACP1 Dissing, J.; Johnsen, A. H.: Human red cell acid phosphatase (ACP1):the 6 A c
primary structure of the two pairs of isozymes encoded by theACP1*A and
ACP1*C alleles. Biochim. Biophys. Acta 1121: 261- 268,1992.

GAM1032 303 ACP1 Dissing, J.; Johnsen, A. H.; Sensabaugh, G. F.: Human red cellacid 6 A c
phosphatase (ACP1): the amino acid sequence of the two isozymesBf and Bs
encoded by the ACP1*B allele. J. Biol. Chem. 266: 20619- 20625,1991.

GAM1032 303 ACP1 Emanuel, B. S.; Zackai, E. H.; Van Dyke, D. C.; Swallow, D. M.;Allen, F. H.; 6 A c
Mellman, W. J.: Deletion mapping: further evidencefor the location of acid
phosphatase (ACP- 1) within 2p23. Am. J.Med. Genet. 4: 167- 172, 1979.

GAM1032 303 ACP1 Ferguson- Smith, M. A.; Newman, B. F.; Ellis, P. M.; Thomson, D.M. G.; 6 A c
Riley, I. D.: Assignment by deletion of human red cell acidphosphatase gene
locus to the short arm of chromosome 2. Nature 243:271- 273, 1973.

GAM1032 303 ACP1 Fisher, R. A.; Harris, H.: Studies on the separate isoenzymesof red cell 6 A c
acid phosphatase phenotypes A and B: chromatographic separationof the
isoenzymes. Ann. Hum. Genet. 34: 431- 438, 1971.

GAM1032 303 ACP1 Fuhrmann, W.; Lichte, K. H.: Human red cell acid phosphatasepolymorphism: a 6 A c
study on gene frequency and forensic use of the systemin cases of disputed
paternity. Humangenetik 3: 121- 126, 1966.

GAM1032 303 ACP1 Giblett, E. R.; Scott, N. M.: Red cell acid phosphatase: racialdistribution 6 A c
and report of a new phenotype. Am. J. Hum. Genet. 17:425- 432, 1965.

GAM1032 303 ACP1 Hamerton, J. L.; Mohandas, T.; McAlpine, P. J.; Douglas, G. R.: Localization 6 A c

of human gene loci using spontaneous chromosome rearrangementsin human-Chinese hamster somatic cell hybrids. Am. J. Hum. Genet. 27:595- 608, 1975.

GAM1032 303 ACP1 Herbich, J.; Fisher, R. A.; Hopkinson, D. A.: Atypical segregationof human red cell acid phosphatase phenotypes: evidence for a rare'silent' allele P(O). Ann. Hum. Genet. 34: 145- 152, 1970. 6 A c

GAM1032 303 ACP1 Herbich, J.; Meinhart, K.: The rare 'silent' allele P(O) or P(V)(P Vienna) of human red cell acid phosphatase, typed in a second family. Humangenetik 15:345- 348, 1972. 6 A c

GAM1032 303 ACP1 Hopkinson, D. A.; Spencer, N.; Harris, H.: Red cell acid phosphatasevariants: a new human polymorphism. Nature 199: 969- 971, 1963. 6 A c

GAM1032 303 ACP1 Hulten, M.; Lindsten, J.; Pen- Ming, L. M.; Fraccaro, M.; Mannini,A.; Tiepolo, L.; Robson, E. B.; Heiken, A.; Tillinger, K. G.: Possiblelocalization of the genes for the Kidd blood group on an autosomeinvolved in a reciprocal translocation. Nature 211: 1067- 1068, 1966. 6 A c

GAM1032 303 ACP1 Junien, C.; Kaplan, J.- C.; Bernheim, A.; Berger, R.: Regionalassignment of red cell acid phosphatase locus to band 2p25. Hum.Genet. 48: 17- 21, 1979. 6 A c

GAM1032 303 ACP1 Karp, G. W., Jr.; Sutton, H. E.: Some new phenotypes of humanred cell acid phosphatase. Am. J. Hum. Genet. 19: 54- 62, 1967. 6 A c

GAM1032 303 ACP1 Larson, L. M.; Bruce, A. W.; Saumur, J. H.; Wasdahl, W. A.: Furtherevidence by gene dosage for the regional assignment of erythrocyteacid phosphatase (ACP1) and malate dehydrogenase (MDH1) loci on chromosome2p. Clin. Genet. 22: 220- 225, 1982. 6 A c

GAM1032 303 ACP1 Lothe, R. A.; Gedde- Dahl, T.; Olaisen, B.; Bakker, E.; Pearson,P.: Very close linkage between D2S1 and ACP1 on chromosome 2p. Ann.Hum. Genet. 50: 361- 367, 1986. 6 A c

GAM1032 303 ACP1 Mace, M. A.; Cook, P. J. L.; Robson, E. B.: Linkage data on redcell acid phosphatase from family studies. Ann. Hum. Genet. 38:471- 477, 1975. 6 A c

GAM1032 303 ACP1 Mace, M. A.; Robson, E. B.: Linkage data on ACP- 1 and MNSs. Cytogenet.Cell Genet. 13: 123- 125, 1974. 6 A c

GAM1032 303 ACP1 Magenis, R. E.; Koler, R. D.; Lovrien, E. W.; Bigley, R. H.; Duval,M. C.; Overton, K. M.: Gene dosage: evidence for assignment of erythrocyteacid phosphatase locus to chromosome 2. Proc. Nat. Acad. Sci. 72:4526- 4530, 1975. 6 A c

GAM1032 303 ACP1 Mayr, W. R.: No close linkage between MNSs and red cell acidphosphatase. Hum. Hered. 26: 1- 3, 1976. 6 A c

GAM1032 303 ACP1 Miller, S. A.; Nelson, M. S.; Dykes, D. D.; Polesky, H. F.: Comparisonof acid phosphatase ACP1 variants by isoelectric focusing and conventionalelectrophoresis: identification of three new alleles, ACP1*N, ACP1*Pand ACP1*S. Hum. Hered. 37: 371- 375, 1987. 6 A c

GAM1032 303 ACP1 Mohrenweiser, H. W.; Novotny, J. E.: ACP- 1- GUA- 1: a low- activityvariant of human erythrocyte acid phosphatase: association with increasedglutathione reductase activity. Am. J. Hum. Genet. 34: 425- 433,1982. 6 A c

GAM1032 303 ACP1 Nezbeda, P.: Occurrence of the ACP- 1 null allele in Czechoslovakia. Hum.Genet. 46: 227- 229, 1979. 6 A c

GAM1032 303 ACP1 Palmarino, R.; Agostino, R.; Gloria, F.; Lucarelli, P.; Businco,L.; Antognoni, G.; Maggioni, G.; Workman, P. L.; Bottini, E.: Redcell acid phosphatase: another polymorphism correlated with malaria? Am.J. Phys. Anthrop. 43: 177- 186, 1975. 6 A c

GAM1032 303 ACP1 Povey, S.; Swallow, D. M.; Bobrow, M.; Craig, I.; Van Heyningen,V.: Probable 6 A c

assignment of the locus determining human red cell acidphosphatase ACP(1) to chromosome 2 using somatic cell hybrids. Ann.Hum. Genet. 38: 1- 5, 1974.

GAM1032 303 ACP1 Renwick, J. H.: Assignment and map- positioning of human lociusing chromosomal variation. Ann. Hum. Genet. 35: 79- 97, 1971. 6 A c

GAM1032 303 ACP1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 6 A c

GAM1032 303 ACP1 Sensabaugh, G. F.; Golden, V. L.: Phenotype dependence in theinhibition of red cell acid phosphatase (ACP) by folates. Am. J.Hum. Genet. 30: 553- 560, 1978. 6 A c

GAM1032 303 ACP1 Siciliano, M. J.; Bachinski, L.; Dolf, G.; Carrano, A. V.; Thompson,L. H.: Chromosomal assignments of human DNA repair genes that complementChinese hamster ovary (CHO) cell mutants. (Abstract) Cytogenet. CellGenet. 46: 691- 692, 1987. 6 A c

GAM1032 303 ACP1 Swallow, D. M.; Povey, S.; Harris, H.: Activity of the 'red cell'acid phosphatase locus in other tissues. Ann. Hum. Genet. 37: 31- 38,1973. 6 A c

GAM1032 303 ACP1 Thompson, L. H.; Carrano, A. V.; Sato, K.; Salazar, E. P.; White,B. F.; Stewart, S. A.; Minkler, J. L.; Siciliano, M. J.: Identificationof nucleotide- excision- repair genes on human chromosomes 2 and 13by functional complementation in hamster- human hybrids. Somat. CellMolec. Genet. 13: 539- 551, 1987. 6 A c

GAM1032 303 ACP1 Van Cong, N.; Moullec, J.: Linkage probable entre les groupesde phosphatase acide des globules rouges et le systeme Lewis. Ann.Genet. 14: 121- 125, 1971. 6 A c

GAM1032 303 ACP1 Wakita, Y.; Narahara, K.; Takahashi, Y.; Kikkawa, K.; Kimura,S.; Oda, M.; Kimoto, H.: Duplication of 2p25: confirmation of theassignment of soluble acid phosphatase (ACP1) locus to 2p25. Hum.Genet. 71: 259- 260, 1985. 6 A c

GAM1032 303 ACP1 Weitkamp, L. R.; Janzen, M. K.; Guttormsen, S. A.; Gershowitz,H.: Inherited pericentric inversion of chromosome number two: a linkagestudy. Ann. Hum. Genet. 33: 53- 59, 1969. 6 A c

GAM1032 303 ACP1 Weitkamp, L. R.; Lovrien, E. W.; Olaisen, B.; Fenger, K.; Gedde- Dahl,T., Jr.; Sorensen, S. A.; Conneally, P. M.; Bias, W. B.; Ott, J.:Linkage relations of the loci for the MN blood group and red cellphosphate. Birth Defects Orig. Art. Ser. 11(3): 276- 280, 1975. Note:Alternate: Cytogenet. Cell Genet. 14: 446- 450, 1975... 6 A c

GAM1032 303 ACP1 Wo, Y.- Y. P.; McCormack, A. L.; Shabanowitz, J.; Hunt, D. F.;Davis, J. P.; Mitchell, G. L.; Van Etten, R. L.: Sequencing, cloning,and expression of human red cell- type acid phosphatase, a cytoplasmicphosphotyrosyl protein phosphatase. J. Biol. Chem. 267: 10856- 10865,1992. 6 A c

GAM1032 303 ACP1 Yoshihara, C. M.; Mohrenweiser, H. W.: Characterization of ACP1(TIC- 1),an electrophoretic variant of erythrocyte acid phosphatase restrictedto the Ticuna Indians of Central Amazonas. Am. J. Hum. Genet. 32:898- 907, 1980. 6 A c

GAM1032 303 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998. 6 A c

GAM1032 303 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 6 A c

GAM1032 303 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527- 6 A c

529, 1994.

GAM1032 303 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; 6 A c
Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal
brain type I adenylyl cyclase. Genomics 16: 473- 478,1993.

GAM1032 303 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- 6 A c
Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.:
Altered sensory processing in the somatosensory cortex of the mutantmouse
barrelless. Science 271: 1864- 1867, 1996.

GAM1032 303 BPHL Puente, X. S.; Lopez- Otin, C.: Cloning and expression analysisof a novel 6 A c
human serine hydrolase with sequence similarity to prokaryoticenzymes
involved in the degradation of aromatic compounds. J. Biol.Chem. 270: 12926-
12932, 1995.

GAM1032 303 BPHL Puente, X. S.; Pendas, A. M.; Lopez- Otin, C.: Structural 6 A c
characterizationand chromosomal localization of the gene encoding human
biphenyl hydrolase- relatedprotein (BPHL). Genomics 51: 459- 462, 1998.

GAM1032 303 CASP4 Faucheu, C.; Diu, A.; Chan, A. W. E.; Blanchet, A.- M.; Miossec,C.; Herve, 6 A c
F.; Collard- Dutilleul, V.; Gu, Y.; Aldape, R. A.; Lippke,J. A.; Rocher, C.;
Su, M. S.- S.; Livingston, D. J.; Hercend, T.; Lalanne,J.- L.: A novel human
protease similar to the interleukin- 1- beta convertingenzyme induces
apoptosis in transfected cells. EMBO J. 14: 1914- 1922,1995.

GAM1032 303 CASP4 Kamens, J.; Paskind, M.; Hugunin, M.; Talanian, R. V.; Allen, H.;Banach, D.; 6 A c
Bump, N.; Hackett, M.; Johnston, C. G.; Li, P.; Mankovich,J. A.; Terranova,
M.; Ghayur, T.: Identification and characterizationof ICH- 2, a novel member
of the interleukin- 1- beta- converting enzymefamily of cysteine proteases.
J. Biol. Chem. 270: 15250- 15256, 1995.

GAM1032 303 CASP4 Munday, N. A.; Vaillancourt, J. P.; Ali, A.; Casano, F. J.; Miller,D. K.; 6 A c
Molineaux, S. M.; Yamin, T.- T.; Yu, V. L.; Nicholson, D. W.: Molecular
cloning and pro- apoptotic activity of ICE(rel)II and ICE(rel)III,members of
the ICE/CED- 3 family of cysteine proteases. J. Biol. Chem. 270:15870-
15876, 1995.

GAM1032 303 CASP4 Wang, S.; Miura, M.; Jung, Y.; Zhu, H.; Li, E.; Yuan, J.: Murinecaspase- 11, 6 A c
an ICE- interacting protease, is essential for the activationof ICE. Cell
92: 501- 509, 1998.

GAM1032 303 CD1D Balk, S. P.; Burke, S.; Polischuk, J. E.; Frantz, M. E.; Yang,L.; Porcelli, 6 A c
S.; Colgan, S. P.; Blumberg, R. S.: Beta- 2- microglobulin- independentMHC
class Ib molecule expressed by human intestinal epithelium. Science 265:259-
262, 1994.

GAM1032 303 CD1D Benlagha, K.; Kyin, T.; Beavis, A.; Teyton, L.; Bendelac, A.:A thymic 6 A c
precursor to NK T cell lineage. Science 296: 553- 555, 2002.

GAM1032 303 CD1D Bradbury, A.; Milstein, C.; Kozak, C. A.: Chromosomal localizationof Cd1d 6 A c
genes in the mouse. Somat. Cell Molec. Genet. 17: 93- 96,1991.

GAM1032 303 CD1D Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; 6 A c
Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S
controls the trafficking and maturation of MHC class IImolecules in
dendritic cells. J. Cell Biol. 147: 775- 790, 1999.

GAM1032 303 CD1D Honey, K.; Benlagha, K.; Beers, C.; Forbush, K.; Teyton, L.; Kleijmeer,M. 6 A c
J.; Rudensky, A. Y.; Bendelac, A.: Thymocyte expression of cathepsinL is
essential for NKT cell development. Nature Immun. 7Oct, 2002.Note: Advance
Electronic Publication.

GAM1032 303 CD1D Jayawardena- Wolf, J.; Benlagha, K.; Chiu, Y.- H.; Mehr, R.; Bendelac,A.: 6 A c

CD1d endosomal trafficking is independently regulated by an intrinsicCD1d-encoded tyrosine motif and by the invariant chain. Immunity 15:897- 908, 2001.

GAM1032 303 CD1D MacDonald, H. R.: T before NK. Science 296: 481- 482, 2002. 6 A c

GAM1032 303 CD1D Nieuwenhuis, E. E. S.; Matsumoto, T.; Exley, M.; Schleipman, R.A.; Glickman, J.; Bailey, D. T.; Corazza, N.; Colgan, S. P.; Onderdonk,A. B.; Blumberg, R. S.: CD1d- dependent macrophage- mediated clearanceof Pseudomonas aeruginosa from lung. Nature Med. 8: 588- 593, 2002. 6 A c

GAM1032 303 CD1D Park, S.- H.; Bendelac, A.: CD1- restricted T- cell responses andmicrobial infection. Nature 406: 788- 792, 2000. 6 A c

GAM1032 303 CD1D Pellicci, D. G.; Hammond, K. J. L.; Uldrich, A. P.; Baxter, A.G.; Smyth, M. J.; Godfrey, D. I.: A natural killer T (NKT) cell developmentalpathway involving a thymus- dependent NK1.1(-)CD4(+) CD1d- dependentprecursor stage. J. Exp. Med. 195: 835- 844, 2002. 6 A c

GAM1032 303 CD1D Prigozy, T. I.; Naidenko, O.; Qasba, P.; Elewaut, D.; Brossay,L.; Khurana, A.; Natori, T.; Koezuka, Y.; Kulkarni, A.; Kronenberg,M.: Glycolipid antigen processing for presentation by CD1d molecules. Science 291:664- 667, 2001. 6 A c

GAM1032 303 CD1D Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.; Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell selection and maturation by cathepsin S. Immunity 15:909- 919, 2001. 6 A c

GAM1032 303 CD1D Shi, F.- D.; Flodstrom, M.; Balasa, B.; Kim, S. H.; Van Gunst,K.; Strominger, J. L.; Wilson, S. B.; Sarvetnick, N.: Germ line deletionof the CD1 locus exacerbates diabetes in the NOD mouse. Proc. Nat.Acad. Sci. 98: 6777- 6782, 2001. 6 A c

GAM1032 303 CD1D Zeng, Z.- H.; Castano, A. R.; Segelke, B. W.; Stura, E. A.; Peterson,P. A.; Wilson, I. A.: Crystal structure of mouse CD1: an MHC- likefold with a large hydrophobic binding groove. Science 277: 339- 345,1997. 6 A c

GAM1032 303 CDC25B Bulavin, D. V.; Higashimoto, Y.; Popoff, I. J.; Gaarde, W. A.;Basrur, V.; Potapova, O.; Appella, E.; Fornace, A. J., Jr.: Initiationof a G2/M checkpoint after ultraviolet radiation requires p38 kinase. Nature 411:102-107, 2001. 6 A c

GAM1032 303 CDC25B Demetrick, D. J.; Beach, D. H.: Chromosome mapping of human CDC25Aand CDC25B phosphatases. Genomics 18: 144- 147, 1993. 6 A c

GAM1032 303 CDC25B Lane, S. A.; Baker, E.; Sutherland, G. R.; Tonks, I.; Hayward,N.; Ellem, K.: The human cell cycle gene CDC25B is located at 20p13. Genomics 15:693- 694, 1993. 6 A c

GAM1032 303 CDC25B Lincoln, A. J.; Wickramasinghe, D.; Stein, P.; Schultz, R. M.;Palko, M. E.; De Miguel, M. P.; Tessarollo, L.; Donovan, P. J.: Cdc25bphosphatase is required for resumption of meiosis during oocyte maturation. NatureGenet. 30: 446- 449, 2002. 6 A c

GAM1032 303 COL19A1 Gerecke, D. R.; Olson, P. F.; Koch, M.; Knoll, J. H. M.; Taylor,R.; Hudson, D. L.; Champliaud, M.- F.; Olsen, B. R.; Burgeson, R. E.: Complete primary structure of two splice variants of collagen XII,and assignment of alpha-1(XII) collagen (COL12A1), alpha- 1(IX) collagen(COL9A1), and alpha- 1(XIX) collagen (COL19A1) to human chromosome6q12- q13. Genomics 41: 236- 242, 1997. 6 A c

GAM1032 303 COL19A1 Inoguchi, K.; Yoshioka, H.; Khaleduzzaman, M.; Ninomiya, Y.: ThemRNA for alpha- 1(XIX) collagen chain, a new member of FACITs, containsa long unusual 6 A c

3- prime untranslated region and displays many uniquesplicing variants. J. Biochem. 117: 137- 146, 1995.

GAM1032 303 COL19A1 Khaleduzzaman, M.; Sumiyoshi, H.; Ueki, Y.; Inoguchi, K.; Ninomiya,Y.; Yoshioka, H.: Structure of the human type XIX collagen (COL19A1)gene, which suggests it has arisen from an ancestor gene of the FACITfamily. Genomics 45: 304- 312, 1997. 6 A c

GAM1032 303 COL19A1 Myers, J. C.; Sun, M. J.; D'Ippolito, J. A.; Jabs, E. W.; Neilson,E. G.; Dion, A. S.: Human cDNA clones transcribed from an unusuallyhigh molecular weight RNA encode a new collagen chain. Gene 123:211- 217, 1993. 6 A c

GAM1032 303 COL19A1 Yoshioka, H.; Zhang, H.; Ramirez, F.; Mattei, M.- G.; Moradi- Ameli,M.; van der Rest, M.; Gordon, M. K.: Synteny between the loci fora novel FACIT- like collagen (D6S228E) and alpha 1(IX) collagen (COL9A1)on 6q12- q14 in humans. Genomics 13: 884- 886, 1992. 6 A c

GAM1032 303 DMRT2 Muroya, K.; Okuyama, T.; Goishi, K.; Ogiso, Y.; Fukuda, S.; Kameyama,J.; Sato, H.; Suzuki, Y.; Terasaki, H.; Gomyo, H.; Wakui, K.; Fukushima,Y.; Ogata, T.: Sex- determining gene(s) on distal 9p: clinical andmolecular studies in six cases. J. Clin. Endocr. Metab. 85: 3094- 3100,2000. 6 A c

GAM1032 303 DMRT2 Raymond, C. S.; Parker, E. D.; Kettlewell, J. R.; Brown, L. G.;Page, D. C.; Kusz, K.; Jaruzelska, J.; Reinberg, Y.; Fletjer, W. L.;Bardwell, V. J.; Hirsch, B.; Zarkower, D.: A region of human chromosome9p required for testis development contains two genes related to knownsexual regulators. Hum. Molec. Genet. 8: 989- 996, 1999. 6 A c

GAM1032 303 DMRT2 Raymond, C. S.; Shamu, C. E.; Shen, M. M.; Seifert, K. J.; Hirsch,B.; Hodgkin, J.; Zarkower, D.: Evidence for evolutionary conservationof sex-determining genes. Nature 391: 691- 695, 1998. 6 A c

GAM1032 303 DNM2 Diatloff- Zito, C.; Gordon, A. J. E.; Duchaud, E.; Merlin, G.:Isolation of an ubiquitously expressed cDNA encoding human dynaminII, a member of the large GTP- binding protein family. Gene 163:301- 306, 1995. 6 A c

GAM1032 303 DNM2 Klocke, R.; Augustin, A.; Ronsiek, M.; Stief, A.; van der Putten,H.; Jockusch, H.: Dynamin genes Dnm1 and Dnm2 are located on proximalmouse chromosomes 2 and 9, respectively. Genomics 41: 290- 292, 1997. 6 A c

GAM1032 303 E2F3 Cloud, J. E.; Rogers, C.; Reza, T. L.; Ziebold, U.; Stone, J. R.;Picard, M. H.; Caron, A. M.; Bronson, R. T.; Lees, J. A.: Mutantmouse models reveal the relative roles of E2F1 and E2F3 in vivo. Molec.Cell. Biol. 22: 2663- 2672, 2002. 6 A c

GAM1032 303 E2F3 He, Y.; Armanious, M. K.; Thomas, M. J.; Cress, W. D.: Identificationof E2F- 3B, an alternative form of E2F- 3 lacking a conserved N- terminalregion. Oncogene 19: 3422- 3433, 2000. 6 A c

GAM1032 303 E2F3 Lees, J. A.; Saito, M.; Vidal, M.; Valentine, M.; Look, T.; Harlow,E.; Dyson, N.; Helin, K.: The retinoblastoma protein binds to a familyof E2F transcription factors. Molec. Cell. Biol. 13: 7813- 7825,1993. 6 A c

GAM1032 303 E2F3 Leone, G.; Sears, R.; Huang, E.; Rempel, R.; Nuckolls, F.; Park,C.- H.; Giangrande, P.; Wu, L.; Saavedra, H. I.; Field, S. J.; Thompson,M. A.; Yang, H.; Fujiwara, Y.; Greenberg, M. E.; Orkin, S.; Smith,C.; Nevins, J. R.: Myc requires distinct E2F activities to induceS phase and apoptosis. Molec. Cell 8: 105- 113, 2001. 6 A c

GAM1032 303 E2F3 Wu, L.; Timmers, C.; Maiti, B.; Saavedra, H. I.; Sang, L.; Chong,G. T.; Nuckolls, F.; Giangrande, P.; Wright, F. A.; Field, S. J.;Greenberg, M. E.; Orkin, S.; Nevins, J. R.; Robinson, M. L.; Leone,G.: The E2F1- 3 transcription factors are essential for cellular proliferation. Nature 6 A c

414:457- 462, 2001.

GAM1032 303 ESR1 Andersen, T. I.; Wooster, R.; Laake, K.; Collins, N.; Warren, W.;Skrede, M.; 6 A c
Eeles, R.; Tveit, K. M.; Johnston, S. R. D.; Dowsett,M.; Olsen, A. O.;
Moller, P.; Stratton, M. R.; Borresen- Dale, A.- L.: Screening for ESR
mutations in breast and ovarian cancer patients. Hum.Mutat. 9: 531- 536,
1997.

GAM1032 303 ESR1 Auboeuf, D.; Honig, A.; Berget, S. M.; O'Malley, B. W.: Coordinateregulation 6 A c
of transcription and splicing by steroid receptor coregulators. Science
298:416- 419, 2002.

GAM1032 303 ESR1 Balleine, R. L.; Hunt, S. M. N.; Clarke, C. L.: Coexpression ofalternatively 6 A c
spliced estrogen and progesterone receptor transcriptsin human breast
cancer. J. Clin. Endocr. Metab. 84: 1370- 1377, 1999.

GAM1032 303 ESR1 Becherini, L.; Gennari, L.; Masi, L.; Mansani, R.; Massart, F.;Morelli, A.; 6 A c
Falchetti, A.; Gonnelli, S.; Fiorelli, G.; Tanini, A.;Brandi, M. L.:
Evidence of a linkage disequilibrium between polymorphismsin the human
estrogen receptor- alpha gene and their relationship tobone mass variation
in postmenopausal Italian women. Hum. Molec.Genet. 9: 2043- 2050, 2000.

GAM1032 303 ESR1 Bord, S.; Horner, A.; Beavan, S.; Compston, J.: Estrogen receptorsalpha and 6 A c
beta are differentially expressed in developing human bone. J.Clin. Endocr.
Metab. 86: 2309- 2314, 2001.

GAM1032 303 ESR1 Castagnoli, A.; Maestri, I.; Bernardi, F.; Del Senno, L.: PvuIIRFLP inside 6 A c
the human estrogen receptor gene. Nucleic Acids Res. 15:866 only, 1987.

GAM1032 303 ESR1 Chaidarun, S. S.; Alexander, J. M.: A tumor- specific truncatedestrogen 6 A c
receptor splice variant enhances estrogen- stimulated geneexpression. Molec.
Endocr. 12: 1355- 1366, 1998.

GAM1032 303 ESR1 Chiang, C.- H.; Cheng, K. W.; Igarashi, S.; Nathwani, P. S.; Leung,P. C. K.: 6 A c
Hormonal regulation of estrogen receptor alpha and betagene expression in
human granulosa- luteal cells in vitro. J. Clin.Endocr. Metab. 85: 3828-
3839, 2000.

GAM1032 303 ESR1 Clark, G. M.; McGuire, W. L.: Steroid receptors and other prognosticfactors 6 A c
in primary breast cancer. Semin. Oncol. 15 (suppl. 1): 20- 25,1988.

GAM1032 303 ESR1 Couse, J. F.; Hewitt, S. C.; Bunch, D. O.; Sar, M.; Walker, V.R.; Davis, B. 6 A c
J.; Korach, K. S.: Postnatal sex reversal of the ovariesin mice lacking
estrogen receptors alpha and beta. Science 286:2328- 2331, 1999.

GAM1032 303 ESR1 Davis, V. L.; Chan, C.- C.; Schoen, T. J.; Couse, J. F.; Chader,G. J.; 6 A c
Korach, K. S.: An estrogen receptor repressor induces cataractformation in
transgenic mice. Proc. Nat. Acad. Sci. 99: 9427- 9432,2002.

GAM1032 303 ESR1 Esmaeli, B.; Harvey, J. T.; Hewlett, B.: Immunohistochemicalevidence for 6 A c
estrogen receptors in meibomian glands. Ophthalmology 107:180- 184, 2000.

GAM1032 303 ESR1 Fan, S.; Wang, J.- A.; Yuan, R.; Ma, Y.; Meng, Q.; Erdos, M. R.;Pestell, R. 6 A c
G.; Yuan, F.; Auborn, K. J.; Goldberg, I. D.; Rosen, E.M.: BRCA1 inhibition
of estrogen receptor signaling in transfectedcells. Science 284: 1354- 1356,
1999.

GAM1032 303 ESR1 Fuqua, S. A. W.; Chamness, G. C.; McGuire, W. L.: Estrogen receptormutations 6 A c
in breast cancer. J. Cell. Biochem. 51: 135- 139, 1993.

GAM1032 303 ESR1 Gosden, J. R.; Middleton, P. G.; Rout, D.: Localization of thehuman 6 A c
oestrogen receptor gene to chromosome 6q24- q27 by in situ hybridization.
Cytogenet.Cell Genet. 43: 218- 220, 1986.

GAM1032 303 ESR1 Green, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.- M.; Argos,P.; 6 A c
Chambon, P.: Human oestrogen receptor cDNA: sequence, expressionand homology

to v- erb- A. Nature 320: 134- 139, 1986.

GAM1032 303 ESR1 Greene, G. L.; Gilna, P.; Waterfield, M.; Baker, A.; Hort, Y.;Shine, J.: 6 A c
Sequence and expression of human estrogen receptor complementaryDNA. Science 231: 1150- 1154, 1986.

GAM1032 303 ESR1 Heine, P. A.; Taylor, J. A.; Iwamoto, G. A.; Lubahn, D. B.; Cooke,P. S.: 6 A c
Increased adipose tissue in male and female estrogen receptor- alphaknockout mice. Proc. Nat. Acad. Sci. 97: 12729- 12734, 2000.

GAM1032 303 ESR1 Herrington, D. M.; Howard, T. D.; Hawkins, G. A.; Reboussin, D.M.; Xu, J.; 6 A c
Zheng, S. L.; Brosnihan, K. B.; Meyers, D. A.; Bleecker,E. R.: Estrogen-
receptor polymorphisms and effects of estrogen replacementon high- density
lipoprotein cholesterol in women with coronary disease. NewEng. J. Med. 346:
967- 974, 2002.

GAM1032 303 ESR1 Issa, J.- P. J.; Ottaviano, Y. L.; Celano, P.; Hamilton, S. R.;Davidson, N. 6 A c
E.; Baylin, S. B.: Methylation of the oestrogen receptorCpG island links
ageing and neoplasia in human colon. Nature Genet. 7:536- 540, 1994.

GAM1032 303 ESR1 Jeltsch, J. M.; Roberts, M.; Schatz, C.; Garnier, J. M.; Brown,A. M. C.; 6 A c
Chambon, P.: Structure of the human oestrogen- responsivegene pS2. Nucleic
Acids Res. 15: 1401- 1414, 1987.

GAM1032 303 ESR1 Jones, M. E. E.; Thorburn, A. W.; Britt, K. L.; Hewitt, K. N.;Wreford, N. 6 A c
G.; Proietto, J.; Oz, O. K.; Leury, B. J.; Robertson,K. M.; Yao, S.;
Simpson, E. R.: Aromatase- deficient (ArKO) mice havea phenotype of
increased adiposity. Proc. Nat. Acad. Sci. 97: 12735- 12740,2000.

GAM1032 303 ESR1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, 6 A c
J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic
linkage map of mouse chromosome 10: localizationof eighteen molecular
markers using a single interspecific backcross. Genetics 125:855- 866, 1990.

GAM1032 303 ESR1 King, M. C.: Personal Communication. Berkeley, Calif. 5/1996. 6 A c

GAM1032 303 ESR1 Korach, K. S.: Insights from the study of animals lacking functionalestrogen 6 A c
receptor. Science 266: 1524- 1527, 1994.

GAM1032 303 ESR1 Kos, M.; Reid, G.; Denger, S.; Gannon, F.: Minireview: genomicorganization 6 A c
of the human ER- alpha gene promoter region. Molec. Endocr. 15:2057- 2063,
2001.

GAM1032 303 ESR1 Kumar, R.; Wang, R.- A.; Mazumdar, A.; Talukder, A. H.; Mandal,M.; Yang, Z.; 6 A c
Bagheri- Yarmand, R.; Sahin, A.; Hortobagyi, G.; Adam,L.; Barnes, C. J.;
Vadlamudi, R. K.: A naturally occurring MTA1 variantsequesters oestrogen
receptor- alpha in the cytoplasm. Nature 418:654- 657, 2002.

GAM1032 303 ESR1 Lawson, J. S.; Field, A. S.; Champion, S.; Tran, D.; Ishikura,H.; 6 A c
Trichopoulos, D.: Low oestrogen receptor alpha expression innormal breast
tissue underlies low breast cancer incidence in Japan.(Letter) Lancet 354:
1787- 1788, 1999.

GAM1032 303 ESR1 Lonard, D. M.; Nawaz, Z.; Smith, C. L.; O'Malley, B. W.: The26S proteasome 6 A c
is required for estrogen receptor- alpha and coactivatorturnover and for
efficient estrogen receptor- alpha transactivation. Molec.Cell 5: 939- 948,
2000.

GAM1032 303 ESR1 Lorentzon, M.; Lorentzon, R.; Backstrom, T.; Nordstrom, P.: Estrogenreceptor 6 A c
gene polymorphism, but not estradiol levels, is related tobone density in
healthy adolescent boys: a cross- sectional and longitudinalstudy. J. Clin.
Endocr. Metab. 84: 4597- 4601, 1999.

GAM1032 303 ESR1 Mader, S.; Kumar, V.; de Verneuil, H.; Chambon, P.: Three aminoacids of the 6 A c
oestrogen receptor are essential to its ability to distinguishan oestrogen

from a glucocorticoid- responsive element. Nature 338:271- 274, 1989.

GAM1032 303 ESR1 McGuire, W. L.; Chamness, G. C.; Fuqua, S. A. W.: Abnormal estrogenreceptor 6 A c
in clinical breast cancer. J. Steroid Biochem. Molec. Biol. 43:243- 247,
1992.

GAM1032 303 ESR1 McGuire, W. L.; Chamness, G. C.; Fuqua, S. A. W.: Estrogen receptorvariants 6 A c
in clinical breast cancer. Molec. Endocr. 5: 1571- 1577,1991.

GAM1032 303 ESR1 McInerney, E. M.; Ince, B. A.; Shapiro, D. J.; Katzenellenbogen,B. S.: A 6 A c
transcriptionally active estrogen receptor mutant is a noveltype of dominant
negative inhibitor of estrogen action. Molec. Endocr. 10:1519- 1526, 1996.

GAM1032 303 ESR1 Menasce, L. P.; White, G. R. M.; Harrison, C. J.; Boyle, J. M.: Localization 6 A c
of the estrogen receptor locus (ESR) to chromosome6q25.1 by FISH and a
simple post- FISH banding technique. Genomics 17:263- 265, 1993.

GAM1032 303 ESR1 Metzger, D.; White, J. H.; Chambon, P.: The human oestrogen 6 A c
receptorfunctions in yeast. Nature 334: 31- 36, 1988.

GAM1032 303 ESR1 Murphy, L. C.; Wang, M.; Coutt, A.; Dotzlaw, H.: Novel mutationsin the 6 A c
estrogen receptor messenger RNA in human breast cancers. J.Clin. Endocr.
Metab. 81: 1420- 1427, 1996.

GAM1032 303 ESR1 Pelletier, G.; El- Alfy, M.: Immunocytochemical localization ofestrogen 6 A c
receptors alpha and beta in the human reproductive organs. J.Clin. Endocr.
Metab. 85: 4835- 4840, 2000.

GAM1032 303 ESR1 Ponglikitmongkol, M.; Green, S.; Chambon, P.: Genomic organizationof the 6 A c
human oestrogen receptor gene. EMBO J. 7: 3385- 3388, 1988.

GAM1032 303 ESR1 Reese, J. C.; Katzenellenbogen, B. S.: Characterization of atemperature- 6 A c
sensitive mutation in the hormone binding domain of thehuman estrogen
receptor: studies in cell extracts and intact cellsand their implications
for hormone- dependent transcriptional activation. J.Biol. Chem. 267: 9868-
9873, 1992.

GAM1032 303 ESR1 Reese, J. C.; Katzenellenbogen, B. S.: Mutagenesis of cysteinesin the 6 A c
hormone binding domain of the human estrogen receptor: alterationsin binding
and transcriptional activation by covalently and reversiblyattaching
ligands. J. Biol. Chem. 266: 10880- 10887, 1991.

GAM1032 303 ESR1 Scott, G. K.; Kushner, P.; Vigne, J.- L.; Benz, C. C.: Truncatedforms of 6 A c
DNA- binding estrogen receptors in human breast cancer. J.Clin. Invest. 88:
700- 706, 1991.

GAM1032 303 ESR1 Shang, Y.; Brown, M.: Molecular determinants for the tissue specificityof 6 A c
SERMs. Science 295: 2465- 2468, 2002.

GAM1032 303 ESR1 Shiau, A. K.; Barstad, D.; Loria, P. M.; Cheng, L.; Kushner, P.J.; Agard, D. 6 A c
A.; Greene, G. L.: The structural basis of estrogenreceptor/coactivator
recognition and the antagonism of this interactionby tamoxifen. Cell 95:
927- 937, 1998.

GAM1032 303 ESR1 Shupnik, M. A.; Pitt, L. K.; Soh, A. Y.; Anderson, A.; Lopes,M. B.; Laws, E. 6 A c
R., Jr.: Selective expression of estrogen receptoralpha and beta isoforms in
human pituitary tumors. J. Clin. Endocr.Metab. 83: 3965- 3972, 1998.

GAM1032 303 ESR1 Simoncini, T.; Hafezi- Moghadam, A.; Brazil, D. P.; Ley, K.; Chin,W. W.; 6 A c
Liao, J. K.: Interaction of oestrogen receptor with the regulatorysubunit of
phosphatidylinositol- 3- OH kinase. Nature 407: 538- 541,2000.

GAM1032 303 ESR1 Sluyser, M.: Mutations in the estrogen receptor gene. Hum. Mutat. 6:97- 103, 6 A c
1995.

GAM1032 303 ESR1 Sluyser, M.; Mester, J.: Oncogenes homologous to steroid receptors?(Letter) 6 A c
Nature 315: 546 only, 1985.

GAM1032 303 ESR1 Smith, E. P.; Boyd, J.; Frank, G. R.; Takahashi, H.; Cohen, R.M.; Specker, 6 A c
B.; Williams, T. C.; Lubahn, D. B.; Korach, K. S.: Estrogenresistance caused
by a mutation in the estrogen- receptor gene in aman. New Eng. J. Med. 331:
1056- 1061, 1994.

GAM1032 303 ESR1 Sudhir, K.; Chou, T. M.; Chatterjee, K.; Smith, E. P.; Williams,T. C.; Kane, 6 A c
J. P.; Malloy, M. J.; Korach, K. S.; Rubanyi, G. M.:Premature coronary
artery disease associated with a disruptive mutationin the estrogen receptor
gene in a man. Circulation 96: 3774- 3777,1997.

GAM1032 303 ESR1 Takeyama, J.; Suzuki, T.; Inoue, S.; Kaneko, C.; Nagura, H.; Harada,N.; 6 A c
Sasano, H.: Expression and cellular localization of estrogenreceptors alpha
and beta in the human fetus. J. Clin. Endocr. Metab. 86:2258- 2262, 2001.

GAM1032 303 ESR1 Walter, P.; Green, S.; Greene, G.; Krust, A.; Bornert, J.- M.;Jeltsch, J.- 6 A c
M.; Staub, A.; Jensen, E.; Scrace, G.; Waterfield, M.;Chambon, P.: Cloning
of the human estrogen receptor cDNA. Proc.Nat. Acad. Sci. 82: 7889- 7893,
1985.

GAM1032 303 ESR1 Weel, A. E. A. M.; Uitterlinden, A. G.; Westendorp, I. C. D.;Burger, H.; 6 A c
Schuit, S. C. E.; Hofman, A.; Helmerhorst, T. J. M.; vanLeeuwen, J. P. T.
M.; Pols, H. A. P.: Estrogen receptor polymorphismpredicts the onset of
natural and surgical menopause. J. Clin. Endocr.Metab. 84: 3146- 3150, 1999.

GAM1032 303 ESR1 Weis, K. E.; Ekena, K.; Thomas, J. A.; Lazennec, G.; Katzenellenbogen,B. S.: 6 A c
Constitutively active human estrogen receptors containingamino acid
substitutions for tyrosine 537 in the receptor protein. Molec.Endocr. 10:
1388- 1398, 1996.

GAM1032 303 ESR1 Ye, Q.; Chung, L. W. K.; Li, S.; Zhau, H. E.: Identificationof a novel 6 A c
FAS/ER- alpha fusion transcript expressed in human cancercells. Biochim.
Biophys. Acta 1493: 373- 377, 2000.

GAM1032 303 ESR1 Zuppan, P. J.; Hall, J. M.; Ponglikitmongkol, M.; Spielman, R.;King, M. C.: 6 A c
Polymorphisms at the estrogen receptor (ESR) locus andlinkage relationships
on chromosome 6q. (Abstract) Cytogenet. CellGenet. 51: 1116 only, 1989.

GAM1032 303 ESR1 Zuppan, P.; Hall, J. M.; Lee, M. K.; Ponglikitmongkol, M.; King,M.- C.: 6 A c
Possible linkage of the estrogen receptor gene to breast cancerin a family
with late- onset disease. Am. J. Hum. Genet. 48: 1065- 1068,1991.

GAM1032 303 GNA11 Davignon, I.; Barnard, M.; Gavrilova, O.; Sweet, K.; Wilkie, T.M.: Gene 6 A c
structure of murine Gna11 and Gna15: tandemly duplicatedGq class G protein
alpha subunit genes. Genomics 31: 359- 366, 1996.

GAM1032 303 GNA11 Jiang, M.; Pandey, S.; Tran, V. T.; Fong, H. K.: Guanine nucleotide- 6 A c
bindingregulatory proteins in retinal pigment epithelial cells. Proc.
Nat.Acad. Sci. 88: 3907- 3911, 1991.

GAM1032 303 GNA11 Offermanns, S.; Zhao, L.- P.; Gohla, A.; Sarosi, I.; Simon, M. I.;Wilkie, T. 6 A c
M.: Embryonic cardiomyocyte hypoplasia and craniofacialdefects in G- alpha-
q/G- alpha- 11- mutant mice. EMBO J. 17: 4304- 4312,1998.

GAM1032 303 GNA11 Strathmann, M. P.; Simon, M. I.: G- alpha- 12 and G- alpha- 13 6 A c
subunitsdefine a fourth class of G protein alpha subunits. Proc. Nat.
Acad.Sci. 88: 5582- 5586, 1991.

GAM1032 303 GNA11 Wilkie, T. M.; Gilbert, D. J.; Olsen, A. S.; Chen, X.- N.; Amatruda,T. T.; 6 A c
Korenberg, J. R.; Trask, B. J.; de Jong, P.; Reed, R. R.; Simon,M. I.;
Jenkins, N. A.; Copeland, N. G.: Evolution of the mammalianG protein alpha
subunit multigene family. Nature Genet. 1: 85- 91,1992.

GAM1032 303 GUCY2C de Sauvage, F. J.; Camerato, T. R.; Goeddel, D. V.: Primary structureand 6 A c
functional expression of the human receptor for Escherichia coliheat- stable

enterotoxin. J. Biol. Chem. 266: 17912- 17918, 1991.

GAM1032 303 GUCY2C Mann, E. A.; Swenson, E. S.; Copeland, N. G.; Gilbert, D. J.; Jenkins,N. A.; 6 A c
Taguchi, T.; Testa, J. R.; Giannella, R. A.: Localizationof the guanylyl
cyclase C gene to mouse chromosome 6 and human chromosome12p12. Genomics 34:
265- 267, 1996.

GAM1032 303 GUCY2C Singh, S.; Singh, G.; Heim, J. M.; Gerzer, R.: Isolation and expressionif a 6 A c
guanylate cyclase- coupled heat stable enterotoxin receptor cDNAfrom a human
colonic cell line. Biochem. Biophys. Res. Commun. 179:1455- 1463, 1991.

GAM1032 303 HAS1 Hall, C. L.; Yang, B.; Yang, X.; Zhang, S.; Turley, M.; Samuel,S.; Lange, L. 6 A c
A.; Wang, C.; Curpen, G. D.; Savani, R. C.; Greenberg,A. H.; Turley, E. A.:
Overexpression of the hyaluronan receptor RHAMMis transforming and is also
required for H- ras transformation. Cell 82:19- 26, 1995.

GAM1032 303 HAS1 Itano, N.; Kimata, K.: Expression cloning and molecular characterizationof 6 A c
HAS protein, a eukaryotic hyaluronan synthase. J. Biol. Chem. 271:9875-
9878, 1996.

GAM1032 303 HAS1 Itano, N.; Kimata, K.: Molecular cloning of human hyaluronan synthase. 6 A c
Biochem.Biophys. Res. Commun. 222: 816- 820, 1996.

GAM1032 303 HAS1 Shyjan, A. M.; Heldin, P.; Bucher, E. C.; Yoshino, T.; Briskin,M. J.: 6 A c
Functional cloning of the cDNA for a human hyaluronan synthase. J.Biol.
Chem. 271: 23395- 23399, 1996.

GAM1032 303 HAS1 Spicer, A. P.; Seldin, M. F.; Olsen, A. S.; Brown, N.; Wells, D.E.; Doggett, 6 A c
N. A.; Itano, N.; Kimata, K.; Inazawa, J.; McDonald,J. A.: Chromosomal
localization of the human and mouse hyaluronansynthase genes. Genomics 41:
493- 497, 1997.

GAM1032 303 HAS1 Watanabe, K.; Yamaguchi, Y.: Molecular identification of a putativehuman 6 A c
hyaluronan synthase. J. Biol. Chem. 271: 22945- 22948, 1996.

GAM1032 303 HIVEP1 Gaynor, R. B.; Muchardt, C.; Diep, A.; Mohandas, T. K.; Sparkes,R. S.; 6 A c
Lusis, A. J.: Localization of the zinc finger DNA- bindingprotein HIV-
EP1/MBP- 1/PRDII- BF1 to human chromosome 6p22.3- p24. Genomics 9:758- 761,
1991.

GAM1032 303 HIVEP1 Olavesen, M. G.; Bentley, E.; Mason, R. V. F.; Stephens, R. J.;Ragoussis, 6 A c
J.: Fine mapping of 39 ESTs on human chromosome 6p23- p25. Genomics 46:303-
306, 1997.

GAM1032 303 IL18R1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 6 A c
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp)
on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM1032 303 IL18R1 Parnet, P.; Garka, K. E.; Bonnert, T. P.; Dower, S. K.; Sims, J.E.: IL- 1Rrp 6 A c
is a novel receptor- like molecule similar to the typel interleukin- 1
receptor and its homologues T1/ST2 and IL- 1R AcP. J.Biol. Chem. 271: 3967-
3970, 1996.

GAM1032 303 IL18R1 Torigoe, K.; Ushio, S.; Okura, T.; Kobayashi, S.; Taniai, M.; Kunikata,T.; 6 A c
Murakami, T.; Sanou, O.; Kojima, H.; Fujii, M.; Ohta, T.; Ikeda,M.; Ikegami,
H.; Kurimoto, M.: Purification and characterizationof the human interleukin-
18 receptor. J. Biol. Chem. 272: 25737- 25742,1997.

GAM1032 303 INPP5D Damen, J. E.; Liu, L.; Rosten, P.; Humphries, R. K.; Jefferson,A. B.; 6 A c
Majerus, P. W.; Krystal, G.: The 145- kDa protein induced toassociate with
Shc by multiple cytokines is an inositol tetraphosphateand
phosphatidylinositol 3,4,5- triphosphate 5- phosphatase. Proc.Nat. Acad.
Sci. 93: 1689- 1693, 1996.

GAM1032 303 INPP5D Drayer, A. L.; Pesesse, X.; De Smedt, F.; Woscholski, R.; Parker,P.; Erneux, 6 A c

C.: Cloning and expression of a human placenta inositol1,3,4,5-
tetrakisphosphate and phosphatidylinositol 3,4,5- triphosphate5-
phosphatase. Biochem. Biophys. Res. Commun. 225: 243- 249, 1996.

GAM1032 303 INPP5D Helgason, C. D.; Damen, J. E.; Rosten, P.; Grewal, R.; Sorensen,P.; Chappel, 6 A c
S. M.; Borowski, A.; Jirik, F.; Krystal, G.; Humphries,R. K.: Targeted
disruption of SHIP leads to hemopoietic perturbations,lung pathology, and a
shortened life span. Genes Dev. 12: 1610- 1620,1998.

GAM1032 303 INPP5D Huber, M.; Helgason, C. D.; Damen, J. E.; Liu, L.; Humphries, R.K.; Krystal, 6 A c
G.: The src homology 2- containing inositol phosphatase(SHIP) is the
gatekeeper of mast cell degranulation. Proc. Nat. Acad.Sci. 95: 11330-
11335, 1998.

GAM1032 303 INPP5D Kavanaugh, W. M.; Pot, D. A.; Chin, S. M.; Deuter- Reinhard, M.;Jefferson, 6 A c
A. B.; Norris, F. A.; Masiarz, F. R.; Cousens, L. S.; Majerus,P. W.;
Williams, L. T.: Multiple forms of an inositol polyphosphate5- phosphatase
form signaling complexes with Shc and Grb2. Curr. Biol. 6: 438- 445, 1996.

GAM1032 303 INPP5D Lioubin, M. N.; Algate, P. A.; Tsai, S.; Carlberg, K.; Aebersold,R.; 6 A c
Rohrschneider, L. R.: p150(Ship), a signal transduction moleculewith
inositol polyphosphate- 5- phosphatase activity. Genes Dev. 10:1084- 1095,
1996.

GAM1032 303 INPP5D Liu, Q.; Amgen EST Program; Dumont, D. J.: Molecular cloningand chromosomal 6 A
c
localization in human and mouse of the SH2- containinginositol phosphatase,
INPP5D (SHIP). Genomics 39: 109- 112, 1997.

GAM1032 303 INPP5D Liu, Q.; Shalaby, F.; Jones, J.; Bouchard, D.; Dumont, D. J.:The SH2- 6 A c
containing inositol polyphosphate 5- phosphatase, Ship, isexpressed during
hematopoiesis and spermatogenesis. Blood 91: 2753- 2759,1998.

GAM1032 303 INPP5D Takeshita, S.; Namba, N.; Zhao, J. J.; Jiang, Y.; Genant, H. K.;Silva, M. 6 A c
J.; Brodt, M. D.; Helgason, C. D.; Kalesnikoff, J.; Rauh,M. J.; Humphries,
R. K.; Krystal, G.; Teitelbaum, S. L.; Ross, F.P.: SHIP- deficient mice are
severely osteoporotic due to increasednumbers of hyper- resorptive
osteoclasts. Nature Med. 8: 943- 949,2002.

GAM1032 303 INPP5D Wang, J.- W.; Howson, J. M.; Ghansah, T.; Desponts, C.; Ninos,J. M.; May, S. 6 A c
L.; Nguyen, K. H. T.; Toyama- Sorimachi, N.; Kerr, W.G.: Influence of SHIP
on the NK repertoire and allogeneic bone marrowtransplantation. Science 295:
2094- 2097, 2002.

GAM1032 303 INPP5D Ware, M. D.; Rosten, P.; Damen, J. E.; Liu, L.; Humphries, R.K.; Krystal, 6 A c
G.: Cloning and characterization of human SHIP, the145- kD inositol 5-
phosphatase that associates with SHC after cytokinestimulation. Blood 88:
2833- 2840, 1996.

GAM1032 303 ITK Cheng, G.; Ye, Z.- S.; Baltimore, D.: Binding of Bruton's tyrosinekinase to 6 A c
Fyn, Lyn, or Hck through a Src homology 3 domain- mediatedinteraction. Proc.
Nat. Acad. Sci. 91: 8152- 8155, 1994.

GAM1032 303 ITK Gibson, S.; Leung, B.; Squire, J. A.; Hill, M.; Arima, N.; Goss,P.; Hogg, 6 A c
D.; Mills, G. B.: Identification, cloning, and characterizationof a novel
human T- cell- specific tyrosine kinase located at the hematopoietincomplex
on chromosome 5q. Blood 82: 1561- 1572, 1993.

GAM1032 303 ITK Janis, E. M.; Siliciano, J. D.; Isaac, D. D.; Griffin, C. A.; Hawkins,A. L.; 6 A c
Kozak, C. A.; Desiderio, S.: Mapping of the gene for the tyrosinekinase ltk
to a region of conserved synteny between mouse chromosome11 and human
chromosome 5q. Genomics 23: 269- 271, 1994.

GAM1032 303 ITK Schaeffer, E. M.; Debnath, J.; Yap, G.; McVicar, D.; Liao, X. C.;Littman, D. R.; Sher, A.; Varmus, H. E.; Lenardo, M. J.; Schwartzberg,P. L.: Requirement for Tec kinases Rlk and Itk in T cell receptorsignaling and immunity. Science 284: 638- 641, 1999. 6 A c

GAM1032 303 ITK Woods, M. L.; Kivens, W. J.; Adelsman, M. A.; Qiu, Y.; August,A.; Shimizu, Y.: A novel function for the Tec family tyrosine kinaseltk in activation of beta- 1 integrins by the T- cell receptor. EMBOJ. 20: 1232- 1244, 2001. 6 A c

GAM1032 303 KIR2DL1 Andre, P.; Biassoni, R.; Colonna, M.; Cosman, D.; Lanier, L. L.;Long, E. O.; Lopez- Botet, M.; Moretta, A.; Moretta, L.; Parham, P.;Trowsdale, J.; Vivier, E.; Wagtmann, N.; Wilson, M. J.: New nomenclaturefor MHC receptors. Nature Immun. 2: 661 only, 2001. 6 A c

GAM1032 303 KIR2DL1 Colonna, M.; Samaridis, J.: Cloning of immunoglobulin- superfamilymembers associated with HLA- C and HLA- B recognition by human naturalkiller cells. Science 268: 405- 408, 1995. 6 A c

GAM1032 303 KIR2DL1 Fan, Q. R.; Long, E. O.; Wiley, D. C.: Crystal structure of thehuman natural killer cell inhibitory receptor KIR2DL1- HLA- Cw4 complex. NatureImmun. 2: 452- 460, 2001. 6 A c

GAM1032 303 KIR2DL1 Lanier, L. L.: Follow the leader: NK cell receptors for classicaland nonclassical MHC class I. Cell 92: 705- 707, 1998. 6 A c

GAM1032 303 KIR2DL1 Lanier, L. L.: Natural killer cells: from no receptors to toomany. Immunity 6: 371- 378, 1997. 6 A c

GAM1032 303 KIR2DL1 Lanier, L. L.: Turning on natural killer cells. J. Exp. Med. 191:1259- 1262, 2000. 6 A c

GAM1032 303 KIR2DL1 Ljunggren, H. G.; Karre, K.: In search of the 'missing self':MHC molecules and NK cell recognition. Immun. Today 11: 237- 244,1990. 6 A c

GAM1032 303 KIR2DL1 Rajalingam, R.; Krausa, P.; Shilling, H. G.; Stein, J. B.; Balamurugan,A.; McGinnis, M. D.; Cheng, N. W.; Mehra, N. K.; Parham, P.: DistinctiveKIR and HLA diversity in a panel of north Indian Hindus. Immunogenetics 53:1009- 1019, 2002. 6 A c

GAM1032 303 KIR2DL1 Wagtmann, N.; Biassoni, R.; Cantoni, C.; Verdiani, S.; Malnati,M. S.; Vitale, M.; Bottino, C.; Moretta, L.; Moretta, A.; Long, E.O.: Molecular clones of the p58 NK cell receptor reveal immunoglobulin- relatedmolecules with diversity in both the extra- and intracellular domains. Immunity 2:439- 449, 1995. 6 A c

GAM1032 303 KIR2DL1 Wagtmann, N.; Rajagopalan, S.; Winter, C. C.; Peruzzi, M.; Long,E. O.: Killer cell inhibitory receptors specific for HLA- C and HLA- Bidentified by direct binding and by functional transfer. Immunity 3:801- 809, 1995. 6 A c

GAM1032 303 KIR2DL1 Wende, H.; Colonna, M.; Ziegler, A.; Volz, A.: Organization ofthe leukocyte receptor cluster (LRC) on human chromosome 19q13.4. MammalianGenome 10: 154- 160, 1999. 6 A c

GAM1032 303 KIR2DL2 Colonna, M.; Samaridis, J.: Cloning of immunoglobulin- superfamilymembers associated with HLA- C and HLA- B recognition by human naturalkiller cells. Science 268: 405- 408, 1995. 6 A c

GAM1032 303 KIR2DL2 Dohring, C.; Samaridis, J.; Colonna, M.: Alternatively splicedforms of human killer inhibitory receptors. Immunogenetics 44: 227- 230,1996. 6 A c

GAM1032 303 KIR2DL2 Wagtmann, N.; Biassoni, R.; Cantoni, C.; Verdiani, S.; Malnati,M. S.; Vitale, M.; Bottino, C.; Moretta, L.; Moretta, A.; Long, E.O.: Molecular clones of the p58 NK cell receptor reveal immunoglobulin- relatedmolecules with diversity in both the extra- and intracellular domains. Immunity 2:439- 449, 1995. 6 A c

GAM1032 303 MKI67 Fonatsch, C.; Duchrow, M.; Rieder, H.; Schluter, C.; Gerdes, J.: Assignment 6 A c
of the human Ki- 67 gene (MKI67) to 10q25- qter. Genomics 11:476- 477, 1991.

GAM1032 303 MKI67 Schluter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M. H. G; Key,G.; Flad, 6 A c
H.- D.; Gerdes, J.: The cell proliferation- associated antigenof antibody
Ki- 67: a very large, ubiquitous nuclear protein with numerousrepeated
elements, representing a new kind of cell cycle- maintainingproteins. J.
Cell. Biol. 123: 513- 522, 1993.

GAM1032 303 MKI67 Schonk, D. M.; Kuijpers, H. J. H.; vanDrunen, E.; vanDalen, C.H.; Geurts van 6 A c
Kessel, A. H. M.; Verheijen, R.; Ramaekers, F. C. S.: Assignment of the
gene(s) involved in the expression of the proliferation- relatedKi- 67
antigen to human chromosome 10. Hum. Genet. 83: 297- 299, 1989.

GAM1032 303 MKI67 Traut, W.; Scholzen, T.; Winking, H.; Kubbutat, M. H. G.; Gerdes,J.: 6 A c
Assignment of the murine Ki- 67 gene (Mki67) to chromosome band7F3- F5 by in
situ hybridization. Cytogenet. Cell Genet. 83: 12- 13,1998.

GAM1032 303 MPO Borregaard, N.; Cowland, J. B.: Granules of the human 6 A c
neutrophilicpolymorphonuclear leukocyte. Blood 89: 3503- 3521, 1997.

GAM1032 303 MPO Chang, K. S.; Schroeder, W.; Siciliano, M. J.; Thompson, L. H.;McCredie, K.; 6 A c
Beran, M.; Freireich, E. J.; Liang, J. C.; Trujillo,J. M.; Stass, S. A.: The
localization of the human myeloperoxidasegene is in close proximity to the
translocation breakpoint in acutepromyelocytic leukemia. Leukemia 1: 458-
462, 1987.

GAM1032 303 MPO DeLeo, F. R.; Goedken, M.; McCormick, S. J.; Nauseef, W. M.: Anovel form of 6 A c
hereditary myeloperoxidase deficiency linked to
endoplasmicreticulum/proteasome degradation. J. Clin. Invest. 101: 2900-
2909,1998.

GAM1032 303 MPO Eiserich, J. P.; Baldus, S.; Brennan, M.- L.; Ma, W.; Zhang, C.;Tousson, A.; 6 A c
Castro, L.; Lusis, A. J.; Nauseef, W. M.; White, C. R.;Freeman, B. A.:
Myeloperoxidase, a leukocyte- derived vascular NOoxidase. Science 296: 2391-
2394, 2002.

GAM1032 303 MPO Inazawa, J.; Inoue, K.; Nishigaki, H.; Tsuda, S.; Taniwaki, M.;Misawa, S.; 6 A c
Abe, T.: Assignment of the human myeloperoxidase gene(MPO) to bands q21.3-
q23 of chromosome 17. Cytogenet. Cell Genet. 50:135- 136, 1989.

GAM1032 303 MPO Johnson, K.; Gemperlein, I.; Hudson, S.; Shane, S.; Rovera, G.: Complete 6 A c
nucleotide sequence of the human myeloperoxidase gene. NucleicAcids Res. 17:
7985- 7986, 1989.

GAM1032 303 MPO Kizaki, M.; Miller, C. W.; Selsted, M. E.; Koeffler, H. P.: 6 A c
Myeloperoxidase(MPO) gene mutation in hereditary MPO deficiency. Blood 83:
1935- 1940,1994.

GAM1032 303 MPO Klebanoff, S. J.: Myeloperoxidase. Proc. Assoc. Am. Physicians 111:383- 389, 6 A c
1999.

GAM1032 303 MPO Kudoh, J.; Minoshima, S.; Hashinaka, K.; Nishio, C.; Yamada, M.;Shimizu, Y.; 6 A c
Shimizu, N.: Assignment of the myeloperoxidase (MPO)gene to human chromosome
17. (Abstract) Cytogenet. Cell Genet. 46:641- 642, 1987.

GAM1032 303 MPO Kudoh, J.; Minoshima, S.; Hashinaka, K.; Nishio, C.; Yamada, M.;Shimizu, Y.; 6 A c
Shimizu, N.: Assignment of the myeloperoxidase geneMPO to human chromosome
17 using somatic cell hybrids and flow- sortedchromosomes. Jpn. J. Hum.
Genet. 33: 315- 324, 1988.

GAM1032 303 MPO Law, D. J.; Prasad, M. A.; King, S. E.; Spranger, K. D.; Lee,Y. H.; Fox, R. 6 A c
E.; Collins, E. E.; Gebuhr, T. C.; Miller, D. E.; Petty,E. M.: Localization
of the human estrogen- responsive finger protein(EFP) gene (ZNF147) within a

YAC contig containing the myeloperoxidase(MPO) gene. Genomics 28: 361- 363, 1995.

GAM1032 303 MPO Le Beau, M. M.; Lemons, R. S.; Rosner, G. L.; Carrino, J. C.;Reid, M. S.; 6 A c Chisholm, R. L.; Diaz, M. O.; Weil, S. C.: Chromosomallocalization of the gene encoding myeloperoxidase. (Abstract) Cytogenet.Cell Genet. 46: 645, 1987.

GAM1032 303 MPO Liang, J. C.; Chang, K. S.; Schroeder, W. T.; Freireich, E. J.;Stass, S. A.; 6 A c Trujillo, J. M.: The myeloperoxidase gene is translocatedfrom chromosome 17 to 15 in a patient with acute promyelocytic leukemia. CancerGenet. Cytogenet. 30: 103- 107, 1988.

GAM1032 303 MPO Liang, J. C.; Chang, K. S.; Schroeder, W.; Siciliano, M.; Trujillo,J.; 6 A c Stass, S.: The human myeloperoxidase gene locates on chromosome17q22- 24 and is translocated in acute promyelocytic leukemia. (Abstract) Am.J. Hum. Genet. 41: A226, 1987.

GAM1032 303 MPO Miki, T.; Weil, S. C.; Rosner, G. L.; Reid, M. S.; Kidd, K. K.: An MPO cDNA 6 A c clone identifies an RFLP with PstI. Nucleic Acids Res. 16:1649, 1988.

GAM1032 303 MPO Morishita, K.; Kubota, N.; Asano, S.; Kaziro, Y.; Nagata, S.:Molecular 6 A c cloning and characterization of cDNA for human myeloperoxidase. J.Biol. Chem. 262: 3844- 3851, 1987.

GAM1032 303 MPO Murao, S.- I.; Stevens, F. J.; Ito, A.; Huberman, E.: Myeloperoxidase:a 6 A c myeloid cell nuclear antigen with DNA- binding properties. Proc.Nat. Acad. Sci. 85: 1232- 1236, 1988.

GAM1032 303 MPO Nauseef, W. M.; Brigham, S.; Cogley, M.: Hereditary 6 A c myeloperoxidasedeficiency due to a missense mutation of arginine 569 to tryptophan. J.Biol. Chem. 269: 1212- 1216, 1994.

GAM1032 303 MPO Nauseef, W. M.; Olsson, I.; Arnljots, K.: Biosynthesis and processingof 6 A c myeloperoxidase- - a marker for myeloid cell differentiation. Europ.J. Haemat. 40: 97- 110, 1988.

GAM1032 303 MPO Nauseef, W.; Cogley, M.; McCormick, S.: Effect of the R569W missensemutation 6 A c on the biosynthesis of myeloperoxidase. J. Biol. Chem. 271:9546- 9549, 1996.

GAM1032 303 MPO Reynolds, W. F.; Hiltunen, M.; Pirskanen, M.; Mannermaa, A.; Helisalmi,S.; 6 A c Lehtovirta, M.; Alafuzoff, I.; Soininen, H.: MPO and APOE epsilon-4polymorphisms interact to increase risk for AD in Finnish males. Neurology 55:1284- 1290, 2000.

GAM1032 303 MPO Robinson, T. J.; Morris, D. J.; Ledbetter, D. H.: Chromosomalassignment and 6 A c regional localization of myeloperoxidase in the mouse. Cytogenet.Cell Genet. 53: 83- 86, 1990.

GAM1032 303 MPO Romano, M.; Dri, P.; Dadalt, L.; Patriarca, P.; Baralle, F. E.: Biochemical 6 A c and molecular characterization of hereditary myeloproliferativedeficiency. Blood 90: 4126- 4134, 1997.

GAM1032 303 MPO van Tuinen, P.; Johnson, K. R.; Ledbetter, S. A.; Nussbaum, R.L.; Rovera, 6 A c G.; Ledbetter, D. H.: Localization of myeloperoxidaseto the long arm of human chromosome 17: relationship to the 15;17translocation of acute promyelocytic leukemia. Oncogene 1: 319- 322,1987.

GAM1032 303 MPO Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Farber,N. M.; 6 A c Spitznagel, J. K.; Swanson, M. S.: cDNA cloning of human myeloperoxidase:decrease in myeloperoxidase mRNA upon induction of HL- 60 cells. Proc.Nat. Acad. Sci. 84: 2057- 2061, 1987.

GAM1032 303 MPO Weil, S. C.; Rosner, G. L.; Reid, M. S.; Chisholm, R. L.; Lemons,R. S.; 6 A c Swanson, M. S.; Carrino, J. J.; Diaz, M. O.; Le Beau, M. M.: Translocation

and rearrangement of myeloperoxidase gene in acutepromyelocytic leukemia. Science 240: 790- 792, 1988.

GAM1032 303 MPO Yamada, M.; Hur, S.- J.; Hashinaka, K.; Tsuneoka, K.; Saeki, T.;Nishio, C.; 6 A c
Sakiyama, F.; Tsunasawa, S.: Isolation and characterizationof a cDNA coding for human myeloperoxidase. Arch. Biochem. Biophys. 255:147- 155, 1987.

GAM1032 303 MPO Zaki, S. R.; Austin, G. E.; Chan, W. C.; Conaty, A. L.; Trusler,S.; 6 A c
Trappier, S.; Lindsey, R. B.; Swan, D. C.: Chromosomal localizationof the human myeloperoxidase gene by in situ hybridization using oligonucleotideprobes. Genes Chromosomes Cancer 2: 266- 270, 1990.

GAM1032 303 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 6 A c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator. J. Biol. Chem. 275: 5308- 5317, 2000.

GAM1032 303 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 6 A c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer Res. 56: 3446- 3450, 1996.

GAM1032 303 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 6 A c
bindingprotein, an LXXLL motif- containing protein, functions as a generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM1032 303 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 6 A c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.- H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor, ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol. Chem. 274: 34283- 34293, 1999.

GAM1032 303 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 6 A c
that integrate nuclear receptor signaling through CREB- bindingprotein. Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM1032 303 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 6 A c
coding sequences of unidentified human genes. V. The codingsequences of 40 new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM1032 303 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 6 A c
J. K.: Isolation and characterization of peroxisomeproliferator- activated receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J. Biol. Chem. 275: 13510- 13516, 2000.

GAM1032 303 NEDD4 Harvey, K. F.; Dinudom, A.; Cook, D. I.; Kumar, S.: The Nedd4- likeprotein 6 A c
KIAA0439 is a potential regulator of the epithelial sodiumchannel. J. Biol. Chem. 276: 8597- 8601, 2001.

GAM1032 303 NEDD4 Imhof, M. O.; McDonnell, D. P.: Yeast RSP5 and its human homologhRPF1 6 A c
potentiate hormone- dependent activation of transcription byhuman progesterone and glucocorticoid receptors. Molec. Cell. Biol. 16:2594- 2605, 1996.

GAM1032 303 NEDD4 Kumar, S.; Harvey, K. F.; Kinoshita, M.; Copeland, N. G.; Noda,M.; Jenkins, 6 A c
N. A.: cDNA cloning, expression analysis, and mappingof the mouse Nedd4 gene. Genomics 40: 435- 443, 1997.

GAM1032 303 NEDD4 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 6 A c
developmentally down- regulated expression in the mouse brain. Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM1032 303 NOTCH3 Dichgans, M.; Herzog, J.; Gasser, T.: NOTCH3 mutation involvingthree 6 A c

cysteine residues in a family with typical CADASIL. Neurology 57:1714- 1717, 2001.

GAM1032 303 NOTCH3 Gao, X.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Gridley,T.: 6 A c
Assignment of the murine Notch2 and Notch3 genes to chromosomes3 and 17. Genomics 49: 160- 161, 1998.

GAM1032 303 NOTCH3 Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabriat, H.;Mouton, P.; 6 A c
Alamowitch, S.; Domenga, V.; Cecillion, M.; Marechal,E.; Maciazek, J.; Vayssiere, C.; Cruaud, C.; Cabanis, E.- A.; Ruchoux,M. M.; Weissenbach, J.; Bach, J. F.; Bousser, M. G.; Tournier- Lasserve,E.: Notch3 mutations in CADASIL, a hereditary adult- onset conditioncausing stroke and dementia. Nature 383: 707- 710, 1996.

GAM1032 303 NOTCH3 Joutel, A.; Dodick, D. D.; Parisi, J. E.; Cecillon, M.; Tournier- 6 A c
Lasserve,E.; Bousser, M. G.: De novo mutation in the Notch3 gene causing CADASIL. Ann.Neurol. 47: 388- 391, 2000.

GAM1032 303 NOTCH3 Joutel, A.; Favrole, P.; Labauge, P.; Chabriat, H.; Lescoat, C.;Andreux, F.; 6 A c
Domenga, V.; Cecillon, M.; Vahedi, K.; Ducros, A.; Cave- Riant,F.; Bousser, M. G.; Tournier- Lasserve, E.: Skin biopsy immunostainingwith a Notch3 monoclonal antibody for CADASIL diagnosis. Lancet 358:2049- 2051, 2001.

GAM1032 303 NOTCH3 Joutel, A.; Vahedi, K.; Corpechot, C.; Troesch, A.; Chabriat, H.;Vayssiere, 6 A c
C.; Cruaud, C.; Maciazek, J.; Weissenbach, J.; Bousser,M.- G.; Bach, J.- F.; Tournier- Lasserve, E.: Strong clustering andstereotyped nature of Notch3 mutations in CADASIL patients. Lancet 350:1511- 1515, 1997.

GAM1032 303 NOTCH3 Larsson, C.; Lardelli, M.; White, I.; Lendahl, U.: The human NOTCH1,2, and 3 6 A c
genes are located at chromosome positions 9q34, 1p13- p11,and 19p13.2- p13.1 in regions of neoplasia- associated translocation. Genomics 24:253- 258, 1994.

GAM1032 303 NOTCH3 Rebay, I.; Fehon, R. G.; Artavanis- Tsakonas, S.: Specific truncationsof 6 A c
Drosophila Notch define dominant activated and dominant negativeforms of the receptor. Cell 74: 319- 329, 1993.

GAM1032 303 NOTCH3 Tanigaki, K.; Nogaki, F.; Takahashi, J.; Tashiro, K.; Kurooka,H.; Honjo, T.: 6 A c
Notch1 and Notch3 instructively restrict bFGF- responsivemultipotent neural progenitor cells to an astroglial fate. Neuron 29:45- 55, 2001.

GAM1032 303 PIK3CG Barbier, M.; Attoub, S.; Calvez, R.; Laffargue, M.; Jarry, A.;Mareel, M.; 6 A c
Altruda, F.; Gespach, C.; Wu, D.; Lu, B.; Hirsch, E.;Wymann, M. P.: Weakening link to colorectal cancer? Nature 413:796 only, 2001.

GAM1032 303 PIK3CG Crackower, M. A.; Oudit, G. Y.; Kozieradzki, I.; Sarao, R.; Sun,H.; Sasaki, 6 A c
T.; Hirsch, E.; Suzuki, A.; Shioi, T.; Irie- Sasaki, J.;Sah, R.; Cheng, H.- Y. M.; and 13 others: Regulation of myocardialcontractility and cell size by distinct PI3K- PTEN signaling pathways. Cell 110:737- 749, 2002.

GAM1032 303 PIK3CG Hirsch, E.; Katanaev, V. L.; Garlanda, C.; Azzolino, O.; Pirola,L.; Silengo, 6 A c
L.; Sozzani, S.; Mantovani, A.; Altruda, F.; Wymann,M. P.: Central role for G protein- coupled phosphoinositide 3- kinasegamma in inflammation. Science 287: 1049- 1053, 2000.

GAM1032 303 PIK3CG Jiang, K.; Zhong, B.; Gilvary, D. L.; Corliss, B. C. Hong- Geller,E.; Wei, 6 A c
S; Djeu, J. Y.: Pivotal role of phosphoinositide- 3 kinasein regulation of cytotoxicity in natural killer cells. Nature Immun. 1:419- 425, 2000.

GAM1032 303 PIK3CG Kratz, C. P.; Emerling, B. M.; Bonifas, J.; Wang, W.; Green, E.D.; Le Beau, 6 A c
M. M.; Shannon, K. M.: Genomic structure of the PIK3CGgene on chromosome band 7q22 and evaluation as a candidate myeloidtumor suppressor. Blood 99: 372- 374, 2002.

GAM1032 303 PIK3CG Li, Z.; Jiang, H.; Xie, W.; Zhang, Z.; Smrcka, A. V.; Wu, D.:Roles of PLC- 6 A c
beta- 2 and - beta- 3 and PI3K- gamma in chemoattractant- mediatedsignal
transduction. Science 287: 1046- 1049, 2000.

GAM1032 303 PIK3CG Niswender, K. D.; Morton, G. J.; Stearns, W. H.; Rhodes, C. J.;Myers, M. G., 6 A c
Jr.; Schwartz, M. W.: Key enzyme in leptin- inducedanorexia. Nature 413:
794- 795, 2001.

GAM1032 303 PIK3CG Sasaki, T.; Irie- Sasaki, J.; Horie, Y.; Bachmaier, K.; Fata, J.E.; Li, M.; 6 A c
Suzuki, A.; Bouchard, D.; Ho, A.; Redston, M.; Gallinger,S.; Khokha, R.;
Mak, T. W.; Hawkins, P. T.; Stephens, L.; Scherer,S. W.; Tsao, M.;
Penninger, J. M.: Colorectal carcinomas in micelacking the catalytic subunit
of PI(3)K- gamma. Nature 406: 897- 902,2000.

GAM1032 303 PIK3CG Sasaki, T.; Irie- Sasaki, J.; Jones, R. G.; Oliveira- dos- Santos,A. J.; 6 A c
Stanford, W. L.; Bolon, B.; Wakeham, A.; Itie, A.; Bouchard,D.; Kozieradzki,
I.; Joza, N.; Mak, T. W.; Ohashi, P. S.; Suzuki,A.; Penninger, J. M.:
Function of PI3K- gamma in thymocyte development,T cell activation, and
neutrophil migration. Science 287: 1040- 1046,2000.

GAM1032 303 PIK3CG Stoyanov, B.; Volinia, S.; Hanck, T.; Rubio, I.; Loubtchenkov,M.; Malek, D.; 6 A c
Stoyanova, S.; Vanhaesebroeck, B.; Dhand, R.; Nurnberg,B.; Gierschik, P.;
Seedorf, K.; Hsuan, J. J.; Waterfield, M. D.; Wetzker,R.: Cloning and
characterization of a G protein- activated human phosphoinositide- 3kinase.
Science 269: 690- 693, 1995.

GAM1032 303 PPARGC1 Agarwal, A. K.; Garg, A.: A novel heterozygous mutation in 6 A c
peroxisomeproliferator- activated receptor- gamma gene in a patient with
familialpartial lipodystrophy. J. Clin. Endocr. Metab. 87: 408- 411, 2002.

GAM1032 303 PPARGC1 Esterbauer, H.; Oberkofler, H.; Krempler, F.; Patsch, W.: Humanperoxisome 6 A c
proliferator activated receptor gamma coactivator 1 (PPARGC1)gene: cDNA
sequence, genomic organization, chromosomal localization,and tissue
expression. Genomics 62: 98- 102, 1999.

GAM1032 303 PPARGC1 Herzig, S.; Long, F.; Jhala, U. S.; Hedrick, S.; Quinn, R.; Bauer,A.; 6 A c
Rudolph, D.; Schutz, G.; Yoon, C.; Puigserver, P.; Spiegelman,B.; Montminy,
M.: CREB regulates hepatic gluconeogenesis throughthe coactivator PGC- 1.
Nature 413: 179- 183, 2001.

GAM1032 303 PPARGC1 Larrouy, D.; Vidal, H.; Andreelli, F.; Laville, M.; Langin, D.: Cloning and 6 A c
mRNA tissue distribution of human PPAR- gamma coactivator- 1. Int.J.
Obesity 23: 1327- 1332, 1999.

GAM1032 303 PPARGC1 Lin, J.; Wu, H.; Tarr, P. T.; Zhang, C.- Y.; Wu, Z.; Boss, O.; Michael,L. 6 A c
F.; Puigserver, P.; Isotani, E.; Olson, E. N.; Lowell, B. B.; Bassel-
Duby,R.; Spiegelman, B. M.: Transcriptional co- activator PGC- 1- alpha
drivesthe formation of slow- twitch muscle fibres. Nature 418: 797-
801,2002.

GAM1032 303 PPARGC1 Monsalve, M.; Wu, Z.; Adelmant, G.; Puigserver, P.; Fan, M.; Spiegelman,B. 6 A c
M.: Direct coupling of transcription and mRNA processing throughthe
thermogenic coactivator PGC- 1. Molec. Cell 6: 307- 316, 2000.

GAM1032 303 PPARGC1 Puigserver, P.; Adelmant, G.; Wu, Z.; Fan, M.; Xu, J.; O'Malley,B.; 6 A c
Spiegelman, B. M.: Activation of PPAR- gamma coactivator- 1
throughtranscription factor docking. Science 286: 1368- 1371, 1999.

GAM1032 303 PPARGC1 Puigserver, P.; Rhee, J.; Lin, J.; Wu, Z.; Yoon, J. C.; Zhang,C.- Y.; 6 A c
Krauss, S.; Mootha, V. K.; Lowell, B. B.; Spiegelman, B. M.: Cytokine
stimulation of energy expenditure through p38 MAP kinaseactivation of PPAR-
gamma coactivator- 1. Molec. Cell 8: 971- 982,2001.

GAM1032 303 PPARGC1 Puigserver, P.; Wu, Z.; Park, C. W.; Graves, R.; Wright, M.; Spiegelman,B. M.: A cold- inducible coactivator of nuclear receptors linked toadaptive thermogenesis. Cell 92: 829- 839, 1998. 6 A c

GAM1032 303 PPARGC1 Waite, L. L.; Person, E. C.; Zhou, Y.; Lim, K.- H.; Scanlan, T.S.; Taylor, R. N.: Placental peroxisome proliferator- activated receptor- gammais up-regulated by pregnancy serum. J. Clin. Endocr. Metab. 85:3808- 3814, 2000. 6 A c

GAM1032 303 PPARGC1 Wu, Z.; Puigserver, P.; Andersson, U.; Zhang, C.; Adelmant, G.;Mootha, V.; Troy, A.; Cinti, S.; Lowell, B.; Scarpulla, R. C.; Spiegelman,B. M.: Mechanisms controlling mitochondrial biogenesis and respirationthrough the thermogenic coactivator PGC- 1. Cell 98: 115- 124, 1999. 6 A c

GAM1032 303 PPARGC1 Yoon, J. C.; Puigserver, P.; Chen, G.; Donovan, J.; Wu, Z.; Rhee,J.; Adelmant, G.; Stafford, J.; Kahn, C. R.; Granner, D. K.; Newgard,C. B.; Spiegelman, B. M.: Control of hepatic gluconeogenesis throughthe transcriptional coactivator PGC- 1. Nature 413: 131- 138, 2001. 6 A c

GAM1032 303 PTPRO Seimiya, H.; Sawabe, T.; Inazawa, J.; Tsuruo, T.: Cloning, expressionand chromosomal localization of a novel gene for protein tyrosinephosphatase (PTP- U2) induced by various differentiation- inducing agents. Oncogene 10:1731- 1738, 1995. 6 A c

GAM1032 303 PTPRO Wang, B.; Kishihara, K.; Zhang, D.; Hara, H.; Nomoto, K.: Molecularcloning and characterization of a novel human receptor protein tyrosinephosphatase gene, hPTP- J: down- regulation of gene expression by PMAand calcium ionophore in Jurkat T lymphoma cells. Biochem. Biophys.Res. Commun. 231: 77-81, 1997. 6 A c

GAM1032 303 PTPRO Wang, H; Lian, Z; Lerch, M. M.; Chen, Z; Xie, W; Ullrich, A.:Characterization of PCP- 2, a novel receptor protein tyrosine phosphataseof the MAM domain family. Oncogene 12: 2555- 2562, 1996. 6 A c

GAM1032 303 PTPRO Wiggins, R. C.; Wiggins, J. E.; Goyal, M.; Wharram, B. L.; Thomas,P. E.: Molecular cloning of cDNAs encoding human GLEPP1, a membraneprotein tyrosine phosphatase: characterization of the GLEPP1 proteindistribution in human kidney and assignment of the GLEPP1 gene tohuman chromosome 12p12- p13. Genomics 27: 174- 181, 1995. 6 A c

GAM1032 303 PXN Fernandez- Valle, C.; Tang, Y.; Ricard, J.; Rodenas- Ruano, A.; Taylor,A.; Hackler, E.; Biggerstaff, J.; Iacovelli, J.: Paxillin binds schwannominand regulates its density- dependent localization and effect on cellmorphology. Nature Genet. 31: 354- 362, 2002. 6 A c

GAM1032 303 PXN Glenney, J. R., Jr.; Zokas, L.: Novel tyrosine kinase substratesfrom Rous sarcoma virus- transformed cells are present in the membraneskeleton. J. Cell Biol. 108: 2401- 2408, 1989. 6 A c

GAM1032 303 PXN Horikoshi, N.; Cong, J.; Kley, N.; Shenk, T.: Isolation of differentiallyexpressed cDNAs from p53- dependent apoptotic cells: activation ofthe human homologue of the Drosophila peroxidasin gene. Biochem.Biophys. Res. Commun. 261: 864- 869, 1999. 6 A c

GAM1032 303 PXN Mazaki, Y.; Hashimoto, S.; Sabe, H.: Monocyte cells and cancercells express novel paxillin isoforms with different binding propertiesto focal adhesion proteins. J. Biol. Chem. 272: 7437- 7444, 1997. 6 A c

GAM1032 303 PXN Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 6 A c

GAM1032 303 PXN Salgia, R.; Li, J.- L.; Lo, S. H.; Brunkhorst, B.; Kansas, G. S.;Sobhany, E. S.; Sun, Y.; Pisick, E.; Hallek, M.; Ernst, T.; Tantravahi,R.; Chen, L. B.; Griffin, J. D.: Molecular cloning of human paxillin,a focal adhesion protein phosphorylated by P210(BCR/ABL). J. Biol.Chem. 270: 5039- 5047, 1995. 6 A c

GAM1032 303 PXN Turner, C. E.; Glenney, J. R., Jr.; Burridge, K.: Paxillin: anew vinculin- binding protein present in focal adhesions. J. CellBiol. 111: 1059- 1068, 1990. 6 A c

GAM1032 303 PXN Weiler, S. R.; Taylor, S. M.; Deans, R. J.; Kan- Mitchell, J.; Mitchell,M. S.; Trent, J. M.: Assignment of a human melanoma associated geneMG50 (D2S448) to chromosome 2p25.3 by fluorescence in situ hybridization. Genomics 22:243- 244, 1994. 6 A c

GAM1032 303 RB1 Abramson, D. H.; Ellsworth, R. M.; Zimmerman, L. E.: Monocularcancer in retinoblastoma survivors. Trans. Am. Acad. Ophthal. Otolaryng. 81:454- 457, 1976. 6 A c

GAM1032 303 RB1 Aherne, G. E. S.; Roberts, D. F.: Retinoblastoma- - a clinical surveyand its genetic implications. Clin. Genet. 8: 275- 290, 1975. 6 A c

GAM1032 303 RB1 Alonso, J.; Garcia- Miguel, P.; Abelairas, J.; Mendiola, M.; Sarret,E.; Vendrell, M. T.; Navajas, A.; Pestana, A.: Spectrum of germlineRB1 gene mutations in Spanish retinoblastoma patients: phenotypicand molecular epidemiological implications. Hum. Mutat. 17: 412- 422,2001. 6 A c

GAM1032 303 RB1 Amoaku, W. M. K.; Willshaw, H. E.; Parkes, S. E.; Shah, K. J.;Mann, J. R.: Trilateral retinoblastoma: a report of five patients. Cancer 78:858- 863, 1996. 6 A c

GAM1032 303 RB1 Bader, J. L.; Meadows, A. T.; Zimmerman, L. E.; Rorke, L. B.; Voute,P. A.; Champion, L. A. A.; Miller, R. W.: Bilateral retinoblastomawith ectopic intracranial retinoblastoma: trilateral retinoblastoma. CancerGenet. Cytogenet. 5: 203- 213, 1982. 6 A c

GAM1032 303 RB1 Balaban- Malenbaum, G.; Gilbert, F.; Nichols, W. W.; Hill, R.; Shields,J.; Meadows, A. T.: A deleted chromosome no. 13 in human retinoblastomacells: relevance to tumorigenesis. Cancer Genet. Cytogenet. 3: 243- 250,1981. 6 A c

GAM1032 303 RB1 Bandara, L. R.; Adamczewski, J. P.; Hunt, T.; La Thangue, N. B.: Cyclin A and the retinoblastoma gene product complex with a commontranscription factor. Nature 352: 249- 251, 1991. 6 A c

GAM1032 303 RB1 Benedict, W. F.; Murphree, A. L.; Banerjee, A.; Spina, C. A.; Sparkes,M. C.; Sparkes, R. S.: Patient with 13 chromosome deletion: evidencethat the retinoblastoma gene is a recessive cancer gene. Science 219:973- 975, 1983. 6 A c

GAM1032 303 RB1 Benedict, W. F.; Xu, H.- J.; Hu, S.- X.; Takahashi, R.: Role ofthe retinoblastoma gene in the initiation and progression of humancancer. J. Clin. Invest. 85: 988- 993, 1990. 6 A c

GAM1032 303 RB1 Bia, B.; Cowell, J. K.: Independent constitutional germline mutationsoccurring in the RB1 gene in cousins with bilateral retinoblastoma. Oncogene 11:977- 979, 1995. 6 A c

GAM1032 303 RB1 Blanquet, V.; Turleau, C.; de Grouchy, J.; Creau- Goldberg, N.: Physical map around the retinoblastoma gene: possible genomic imprintingsuggested by Nrul digestion. Genomics 10: 350- 355, 1991. 6 A c

GAM1032 303 RB1 Blanquet, V.; Turleau, C.; Gross- Morand, M. S.; Senamaud- Beaufort,C.; Doz, F.; Besmond, C.: Spectrum of germline mutations in the RB1gene: a study of 232 patients with hereditary and non hereditary retinoblastoma. Hum.Molec. Genet. 4: 383- 388, 1995. 6 A c

GAM1032 303 RB1 Bogenmann, E.; Lochrie, M. A.; Simon, M. I.: Cone cell- specificgenes 6 A c

expressed in retinoblastoma. Science 240: 76- 78, 1988.

GAM1032 303 RB1 Bonaiti- Pellie, C.; Briard- Guillemot, M. L.: Segregation analysisin 6 A c
hereditary retinoblastoma. Hum. Genet. 57: 411- 419, 1981.

GAM1032 303 RB1 Bonaiti- Pellie, C.; Briard- Guillemot, M. L.; Feingold, J.; Frezal,J.: 6 A c
Associated congenital malformations in retinoblastoma. Clin.Genet. 7: 37-
39, 1975.

GAM1032 303 RB1 Bookstein, R.; Lee, E. Y.- H. P.; To, H.; Young, L.- J.; Sery, T.W.; Hayes, 6 A c
R. C.; Friedmann, T.; Lee, W.- H.: Human retinoblastomasusceptibility gene:
genomic organization and analysis of heterozygousintragenic deletion
mutants. Proc. Nat. Acad. Sci. 85: 2210- 2214,1988.

GAM1032 303 RB1 Brantley, M. A.; Worley, L.; Harbour, J. W.: Altered expressionof Rb and p53 6 A c
in uveal melanomas following plaque radiotherapy. Am.J. Ophthal. 133: 242-
248, 2002.

GAM1032 303 RB1 Bremner, R.; Du, D. C.; Connolly- Wilson, M. J.; Bridge, P.; Ahmad,K. F.; 6 A c
Mostachfi, H.; Rushlow, D.; Dunn, J. M.; Gallie, B. L.: Deletionof RB exons
24 and 25 causes low- penetrance retinoblastoma. Am. J.Hum. Genet. 61: 556-
570, 1997.

GAM1032 303 RB1 Briard- Guillemot, M. L.; Bonaiti- Pellie, C.; Feingold, J.; Frezal,J.: 6 A c
Etude genetique du retinoblastome. Humangenetik 24: 271- 284,1974.

GAM1032 303 RB1 Brownstein, S.; de Chadarevian, J.- P.; Little, J. M.: 6 A c
Trilateralretinoblastoma: report of two cases. Arch. Ophthal. 102: 257-
262,1984.

GAM1032 303 RB1 Buchkovich, K.; Duffy, L. A.; Harlow, E.: The retinoblastomaprotein is 6 A c
phosphorylated during specific phases of the cell cycle. Cell 58:1097- 1105,
1989.

GAM1032 303 RB1 Bundey, S.: Recent views on genetic factors in retinoblastoma.(Abstract) J. 6 A c
Med. Genet. 17: 386- 387, 1980.

GAM1032 303 RB1 Bundey, S.; Morten, J. E. N.: An unusual pedigree with retinoblastoma.Does 6 A c
it shed light on the delayed mutation and host resistance theories?
Hum.Genet. 59: 434- 436, 1981.

GAM1032 303 RB1 Cance, W. G.; Brennan, M. F.; Dudas, M. E.; Huang, C.- M.; Cordon- Cardo,C.: 6 A c
Altered expression of the retinoblastoma gene product in humansarcomas. New
Eng. J. Med. 323: 1457- 1462, 1990.

GAM1032 303 RB1 Canning, S.; Dryja, T. P.: Short, direct repeats at the breakpointsof 6 A c
deletions of the retinoblastoma gene. Proc. Nat. Acad. Sci. 86:5044- 5048,
1989.

GAM1032 303 RB1 Carlson, E. A.; Desnick, R. J.: Mutational mosaicism and geneticcounseling 6 A c
in retinoblastoma. Am. J. Med. Genet. 4: 365- 381, 1979.

GAM1032 303 RB1 Cavenee, W. K.: The genetic basis of neoplasia: the retinoblastomaparadigm. 6 A c
Trends Genet. 2: 299- 300, 1986.

GAM1032 303 RB1 Cavenee, W. K.; Dryja, T. P.; Phillips, R. A.; Benedict, W. F.;Godbout, R.; 6 A c
Gallie, B. L.; Murphree, A. L.; Strong, L. C.; White,R. L.: Expression of
recessive alleles by chromosomal mechanismsin retinoblastoma. Nature 305:
779- 784, 1983.

GAM1032 303 RB1 Cavenee, W. K.; Hansen, M. F.; Nordenskjold, M.; Kock, E.; Maumenee,I.; 6 A c
Squire, J. A.; Phillips, R. A.; Gallie, B. L.: Genetic originof mutations
predisposing to retinoblastoma. Science 228: 501- 503,1985.

GAM1032 303 RB1 Cavenee, W. K.; Murphree, A. L.; Shull, M. M.; Benedict, W. F.;Sparkes, R. 6 A c
S.; Kock, E.; Nordenskjold, M.: Prediction of familialpredisposition to
retinoblastoma. New Eng. J. Med. 314: 1201- 1207,1986.

GAM1032 303 RB1 Chano, T.; Ikegawa, S.; Kontani, K.; Okabe, H.; Baldini, N.; Saeki,Y.: 6 A c
Identification of RB1CC1, a novel human gene that can induceRB1 in various
human cells. Oncogene 21: 1295- 1298, 2002.

GAM1032 303 RB1 Chauveinc, L.; Mosseri, V.; Quintana, E.; Desjardins, L.; Schlienger,P.; 6 A c
Doz, F.; Dutrillaux, B.: Osteosarcoma following retinoblastoma:age at onset
and latency period. Ophthalmic Genet. 22: 77- 88, 2001.

GAM1032 303 RB1 Chen, P.- L.; Scully, P.; Shew, J.- Y.; Wang, J. Y. J.; Lee, W.- H.: 6 A c
Phosphorylation of the retinoblastoma gene product is modulatedduring the
cell cycle and cellular differentiation. Cell 58: 1193- 1198,1989.

GAM1032 303 RB1 Connolly, M. J.; Payne, R. H.; Johnson, G.; Gallie, B. L.; Allderdice,P. W.; 6 A c
Marshall, W. H.; Lawton, R. D.: Familial, EsD- linked, retinoblastomawith
reduced penetrance and variable expressivity. Hum. Genet. 65:122- 124, 1983.

GAM1032 303 RB1 Cowell, J. K.; Bia, B.: A novel missense mutation in patientsfrom a 6 A c
retinoblastoma pedigree showing only mild expression of thetumor phenotype.
Oncogene 16: 3211- 3213, 1998.

GAM1032 303 RB1 Cowell, J. K.; Rutland, P.; Hungerford, J.; Jay, M.: Deletionof chromosome 6 A c
region 13q14 is transmissible and does not always predisposeto
retinoblastoma. Hum. Genet. 80: 43- 45, 1988.

GAM1032 303 RB1 Cowell, J. K.; Rutland, P.; Jay, M.; Hungerford, J.: Deletionsof the 6 A c
esterase D locus from a survey of 200 retinoblastoma patients. Hum.Genet.
72: 164- 167, 1986.

GAM1032 303 RB1 Cowell, J. K.; Smith, T.; Bia, B.: Frequent constitutional Cto T mutations 6 A c
in CGA- arginine codons in the RB1 gene produce prematurestop codons in
patients with bilateral (hereditary) retinoblastoma. Europ.J. Hum. Genet. 2:
281- 290, 1994.

GAM1032 303 RB1 Dahiya, A.; Wong, S.; Gonzalo, S.; Gavin, M.; Dean, D. C.: Linkingthe Rb and 6 A c
Polycomb pathways. Molec. Cell 8: 557- 568, 2001.

GAM1032 303 RB1 Davison, E. V.; Gibbons, B.; Aherne, G. E. S.; Roberts, D. F.: Chromosomes 6 A c
in retinoblastoma patients. Clin. Genet. 15: 505- 508,1979.

GAM1032 303 RB1 de Grouchy, J.; Turleau, C.; Cabanis, M. O.; Richardet, J. M.: 6 A c
Retinoblastome et deletion intercalaire du chromosome 13. Arch.Franc.
Pediat. 37: 531- 535, 1980.

GAM1032 303 RB1 DeCaprio, J. A.; Ludlow, J. W.; Lynch, D.; Furukawa, Y.; Griffin,J.; 6 A c
Piwnica- Worms, H.; Huang, C.- M.; Livingston, D. M.: The productof the
retinoblastoma susceptibility gene has properties of a cellcycle regulatory
element. Cell 58: 1085- 1095, 1989.

GAM1032 303 RB1 DerKinderen, D. J.; Koten, J. W.; Tan, K. E. W. P.; Beemer, F.A.; Van 6 A c
Romunde, L. K. J.; Den Otter, W.: Parental age in sporadichereditary
retinoblastoma. Am. J. Ophthal. 110: 605- 609, 1990.

GAM1032 303 RB1 Dryja, T. P.; Bruns, G. A. P.; Gallie, B.; Petersen, R.; Green,W.; Rapaport, 6 A c
J. M.; Albert, D. M.; Gerald, P. S.: Low incidenceof deletion of the
esterase D locus in retinoblastoma patients. Hum.Genet. 64: 151- 155, 1983.

GAM1032 303 RB1 Dryja, T. P.; Cavenee, W.; White, R.; Rapaport, J. M.; Petersen,R.; Albert, 6 A c
D. M.; Bruns, G. A. P.: Homozygosity of chromosome 13in retinoblastoma. New
Eng. J. Med. 310: 550- 553, 1984.

GAM1032 303 RB1 Dryja, T. P.; Friend, S.; Weinberg, R. A.: Isolation of a cDNAfragment 6 A c
derived from human retina mRNA which detects a locus within13q14 often
deleted in retinoblastomas. (Abstract) Am. J. Hum. Genet. 39:A29, 1986.

GAM1032 303 RB1 Dryja, T. P.; Mukai, S.; Petersen, R.; Rapaport, J. M.; Walton,D.; Yandell, 6 A c
D. W.: Parental origin of mutations of the retinoblastomagene. Nature 339:

556- 558, 1989.

GAM1032 303 RB1 Dryja, T. P.; Mukai, S.; Rapaport, J. M.; Yandell, D. W.: Parentalorigin of 6 A c
mutations of the retinoblastoma gene. (Abstract) Am. J.Hum. Genet. 45
(suppl.): A19, 1989.

GAM1032 303 RB1 Dryja, T. P.; Rapaport, J. M.; Joyce, J. M.; Petersen, R. A.:Molecular 6 A c
detection of deletions involving band q14 of chromosome13 in
retinoblastomas. Proc. Nat. Acad. Sci. 83: 7391- 7394, 1986.

GAM1032 303 RB1 Dryja, T. P.; Rapaport, J. M.; Weichselbaum, R.; Bruns, G. A.P.: Chromosome 6 A c
13 restriction fragment length polymorphisms. Hum.Genet. 65: 320- 324, 1984.

GAM1032 303 RB1 Dryja, T. P.; Rapaport, J.; McGee, T. L.; Nork, T. M.; Schwartz,T. L.: 6 A c
Molecular etiology of low- penetrance retinoblastoma in twopedigrees. Am. J.
Hum. Genet. 52: 1122- 1128, 1993.

GAM1032 303 RB1 Dryja, T.; Cavenee, W.; Epstein, J.; Rapaport, J.; Goorin, A.;Koufos, A.: 6 A c
Chromosome 13 homozygosity in osteogenic sarcoma withoutretinoblastoma.
(Abstract) Am. J. Hum. Genet. 36: 28S, 1984.

GAM1032 303 RB1 Duane, T. B.: Clinical Ophthalmology. Hagerstown: Harper andRow (pub.) 3: 6 A c
1980. Pp. 13 only.

GAM1032 303 RB1 Duncan, A. M. V.; Morgan, C.; Gallie, B. L.; Phillips, R. A.;Squire, J.: Re- 6 A c
evaluation of the sublocalization of esterase D andits relation to the
retinoblastoma locus by in situ hybridization. Cytogenet.Cell Genet. 44:
153- 157, 1987.

GAM1032 303 RB1 Dunn, J. M.; Phillips, R. A.; Becker, A. J.; Gallie, B. L.: Identificationof 6 A c
germline and somatic mutations affecting the retinoblastoma gene. Science
241:1797- 1800, 1988.

GAM1032 303 RB1 Dunn, J. M.; Phillips, R. A.; Zhu, X.; Becker, A.; Gallie, B.L.: Mutations 6 A c
in the RB1 gene and their effects on transcription. Molec.Cell. Biol. 9:
4596- 4604, 1989.

GAM1032 303 RB1 Efstratiadis, A.; Posakony, J. W.; Maniatis, T.; Lawn, R. M.;O'Connell, C.; 6 A c
Spritz, R. A.; DeRiel, J. K.; Forget, B. G.; Weissman,S. M.; Slightom, J.
L.; Blechl, A. E.; Smithies, O.; Baralle, F. E.;Shoulders, C. C.; Proudfoot,
N. J.: The structure and evolution ofthe human beta- globin gene family.
Cell 21: 653- 668, 1980.

GAM1032 303 RB1 Ejima, Y.; Sasaki, M. S.; Kaneko, A.; Tanooka, H.: Types, rates,origin and 6 A c
expressivity of chromosome mutations involving 13q14 inretinoblastoma
patients. Hum. Genet. 79: 118- 123, 1988.

GAM1032 303 RB1 Ejima, Y.; Sasaki, M. S.; Kaneko, A.; Tanooka, H.; Hara, Y.; Hida,T.; 6 A c
Kinoshita, Y.: Possible inactivation of part of chromosome 13due to 13qXp
translocation associated with retinoblastoma. Clin.Genet. 21: 357- 361,
1982.

GAM1032 303 RB1 Eldridge, R.; O'Meara, K.; Kitchin, D.: Superior intelligencein sighted 6 A c
retinoblastoma patients and their families. J. Med. Genet. 9:331- 335, 1972.

GAM1032 303 RB1 Falls, H. F.; Neel, J. V.: Genetics of retinoblastoma. Arch.Ophthal. 46: 6 A c
367- 389, 1951.

GAM1032 303 RB1 Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of 6 A c
cancer. Science 278: 1043- 1050, 1997.

GAM1032 303 RB1 Fitzgerald, P. H.; Stewart, J.; Suckling, R. D.: Retinoblastomamutation rate 6 A c
in New Zealand and support for the two- hit model. Hum.Genet. 64: 128- 130,
1983.

GAM1032 303 RB1 Francke, U.: Retinoblastoma and chromosome 13. Cytogenet. CellGenet. 14: 6 A c
131- 134, 1976.

GAM1032 303 RB1 Francois, J.: Hereditary malignant tumor of the eye. CongenitalAnomalies of 6 A c
The Eye. St. Louis: C. V. Mosby Co. (pub.) 1968.Pp. 205- 246.

GAM1032 303 RB1 Francois, J.: Retinoblastoma and osteogenic sarcoma. Ophthalmologica 6 A c
175:185- 191, 1977.

GAM1032 303 RB1 Francois, J.; Matton, M. T.; De Bie, S.; Tanaka, Y.; Vandenbulcke,D.: 6 A c
Genesis and genetics of retinoblastoma. Ophthalmologica 170:405- 425, 1975.

GAM1032 303 RB1 Friend, S. H.; Bernards, R.; Rogelj, S.; Weinberg, R. A.; Rapaport,J. M.; 6 A c
Albert, D. M.; Dryja, T. P.: A human DNA segment with propertiesof the gene
that predisposes to retinoblastoma and osteosarcoma. Nature 323:643- 646,
1986.

GAM1032 303 RB1 Friend, S. H.; Dryja, T. P.; Weinberg, R. A.: Oncogenes and tumor- 6 A c
suppressinggenes. New Eng. J. Med. 318: 618- 622, 1988.

GAM1032 303 RB1 Friend, S. H.; Horowitz, J. M.; Gerber, M. R.; Wang, X.- F.; Bogenmann,E.; 6 A c
Li, F. P.; Weinberg, R. A.: Deletions of a DNA sequence in
retinoblastomasand mesenchymal tumors: organization of the sequence and its
encodedprotein. Proc. Nat. Acad. Sci. 84: 9059- 9063, 1987. Note:
Correction:Proc. Nat. Acad. Sci. 85: 2234 only, 1988..

GAM1032 303 RB1 Fukushima, Y.; Kuroki, Y.; Ito, T.; Kondo, I.; Nishigaki, I.:Familial 6 A c
retinoblastoma (mother and son) with 13q14 deletion. Hum.Genet. 77: 104-
107, 1987.

GAM1032 303 RB1 Fung, Y.- K. T.; Murphree, A. L.; T'Ang, A.; Qian, J.; Hinrichs,S. H.; 6 A c
Benedict, W. F.: Structural evidence for the authenticityof the human
retinoblastoma gene. Science 236: 1657- 1661, 1987.

GAM1032 303 RB1 Gallie, B. L.: Predictive testing for retinoblastoma comes ofage. 6 A c
(Editorial) Am. J. Hum. Genet. 61: 279- 281, 1997.

GAM1032 303 RB1 Gallie, B. L.; Ellsworth, R. M.; Abramson, D. M.; Phillips, R.A.: Retinoma: 6 A c
spontaneous regression of retinoblastoma or benignmanifestation of the
mutation? Brit. J. Cancer 45: 513- 521, 1982.

GAM1032 303 RB1 Gallie, B. L.; Phillips, R. A.: Multiple manifestations of theretinoblastoma 6 A c
gene. Birth Defects Orig. Art. Ser. 18(6): 689- 701,1982.

GAM1032 303 RB1 Garcia- Cao, M.; Gonzalo, S.; Dean, D.; Blasco, M. A.: A rolefor the Rb 6 A c
family of proteins in controlling telomere length. NatureGenet. 15Oct.: ,
2002. Note: Advance Electronic Publication.

GAM1032 303 RB1 Gey, W.: Dq- , multiple Missbildungen und Retinoblastom. Humangenetik 6 A c
10:362- 365, 1970.

GAM1032 303 RB1 Gibbons, B.; Scott, D.; Hungerford, J. L.; Cheung, K. L.; Harrison,C.; 6 A c
Attard- Montalto, S.; Evans, M.; Birch, J. M.; Kingston, J. E.:
Retinoblastoma in association with the chromosome breakage
syndromesFanconi's anaemia and Bloom's syndrome: clinical and cytogenetic
findings. Clin.Genet. 47: 311- 317, 1995.

GAM1032 303 RB1 Girardet, A.; McPeek, M. S.; Leeflang, E. P.; Munier, F.; Arnheim,N.; 6 A c
Claustres, M.; Pellestor, F.: Meiotic segregation analysis ofRB1 alleles in
retinoblastoma pedigrees by use of single- sperm typing. Am.J. Hum. Genet.
66: 167- 175, 2000.

GAM1032 303 RB1 Godbout, R.; Dryja, T. P.; Squire, J.; Gallie, B. L.; Phillips,R. A.: 6 A c
Somatic inactivation of genes on chromosome 13 is a commonevent in
retinoblastoma. Nature 304: 451- 453, 1983.

GAM1032 303 RB1 Goodrich, D. W.; Wang, N. P.; Qian, Y.- W.; Lee, E. Y.- H. P.; Lee,W.- H.: 6 A c
The retinoblastoma gene product regulates progression throughthe G1 phase of
the cell cycle. Cell 67: 293- 302, 1991.

GAM1032 303 RB1 Grace, E.; Drennan, J.; Colver, D.; Gordon, R. R.: The 13q deletionsyndrome. 6 A c
J. Med. Genet. 8: 351- 357, 1971.
GAM1032 303 RB1 Green, A. R.; Wyke, J. A.: Anti- oncogenes: a subset of regulatorygenes 6 A c
involved in carcinogenesis? Lancet II: 475- 477, 1985.
GAM1032 303 RB1 Greger, V.; Kerst, S.; Messmer, E.; Hopping, W.; Passarge, E.;Horsthemke, 6 A c
B.: Application of linkage analysis to genetic counsellingin families with
hereditary retinoblastoma. J. Med. Genet. 25: 217- 221,1988.
GAM1032 303 RB1 Greger, V.; Passarge, E.; Horsthemke, B.: Somatic mosaicism ina patient with 6 A c
bilateral retinoblastoma. Am. J. Hum. Genet. 46:1187- 1193, 1990.
GAM1032 303 RB1 Hagstrom, S. A.; Dryja, T. P.: Mitotic recombination map of 13cen- 6 A c
13q14derived from an investigation of loss of heterozygosity in
retinoblastomas. Proc.Nat. Acad. Sci. 96: 2952- 2957, 1999.
GAM1032 303 RB1 Hall, J. G.: Personal Communication. Vancouver, British Columbia,Canada 6 A c
5/29/1993.
GAM1032 303 RB1 Hanahan, D.; Weinberg, R. A.: The hallmarks of cancer. Cell 100:57- 70, 6 A c
2000.
GAM1032 303 RB1 Harbour, J. W.: Molecular basis of low- penetrance retinoblastoma. 6 A c
Arch.Ophthal. 119: 1699- 1704, 2001.
GAM1032 303 RB1 Harbour, J. W.; Lai, S.- L.; Whang- Peng, J.; Gazdar, A. F.; Minna,J. D.; 6 A c
Kaye, F. J.: Abnormalities in structure and expression ofthe human
retinoblastoma gene in SCLC. Science 241: 353- 357, 1988.
GAM1032 303 RB1 Harbour, J. W.; Luo, R. X.; Dei Santi, A.; Postigo, A. A.; Dean,D. C.: Cdk 6 A c
phosphorylation triggers sequential intramolecular interactionsthat
progressively block Rb functions as cells move through G1. Cell 98:859- 869,
1999.
GAM1032 303 RB1 Hensel, C.; Hsieh, C.- L.; Lee, W.- H.; Pam- Lee, E.; Gazdar, A.;Sakaguchi, 6 A c
A. Y.; Naylor, S. L.: Allele loss and lack of expressionof the RB- 1 locus
in small cell lung cancer. (Abstract) Am. J. Hum.Genet. 43: A25, 1988.
GAM1032 303 RB1 Henson, J. W.; Schnitker, B. L.; Correa, K. M.; von Diemling,A.; Fassbender, 6 A c
F.; Xu, H.- J.; Benedict, W. F.; Yandell, D. W.; Louis,D. N.: The
retinoblastoma gene is involved in malignant progressionof astrocytomas.
Ann. Neurol. 36: 714- 721, 1994.
GAM1032 303 RB1 Higgins, M. J.; Hansen, M. F.; Cavenee, W. K.; Lalande, M.: 6 A c
Moleculardetection of chromosomal translocations that disrupt the
putativeretinoblastoma susceptibility locus. Molec. Cell. Biol. 9: 1-
5,1989.
GAM1032 303 RB1 Hoegerman, S. F.: Chromosome 13 long arm interstitial deletionmay result 6 A c
from maternal inverted insertion. Science 205: 1035- 1036,1979.
GAM1032 303 RB1 Hogg, A.; Bia, B.; Onadim, Z.; Cowell, J. K.: Molecular mechanismsof 6 A c
oncogenic mutations in tumours from patients with bilateral andunilateral
retinoblastoma. Proc. Nat. Acad. Sci. 90: 7351- 7355,1993.
GAM1032 303 RB1 Honavar, S. G.; Shields, C. L.; Shields, J. A.; Demirci, H.; Naduvilath,T. 6 A c
J.: Intraocular surgery after treatment of retinoblastoma. Arch.Ophthal.
119: 1613- 1621, 2001.
GAM1032 303 RB1 Honavar, S. G.; Singh, A. D.; Shields, C. L.; Meadows, A. T.;Demirci, H.; 6 A c
Cater, J.; Shields, J. A.: Postenucleation adjuvanttherapy in high- risk
retinoblastoma. Arch. Ophthal. 120: 923- 931,2002.
GAM1032 303 RFX5 Douhan, J., III; Hauber, I.; Eibl, M. M.; Glimcher, L. H.: Geneticevidence 6 A c
for a new type of major histocompatibility complex classII combined
immunodeficiency characterized by a dyscoordinate regulationof HLA- D alpha

and beta chains. J. Exp. Med. 183: 1063- 1069, 1996.

GAM1032 303 RFX5 Durand, B.; Sperisen, P.; Emery, P.; Barras, E.; Zufferey, M.;Mach, B.; Reith, W.: RFXAP, a novel subunit of the RFX DNA bindingcomplex is mutated in MHC class II deficiency. EMBO J. 16: 1045- 1055,1997. 6 A c

GAM1032 303 RFX5 Emery, P.; Durand, B.; Mach, B.; Reith, W.: RFX proteins, a novelfamily of DNA binding proteins conserved in the eukaryotic kingdom. NucleicAcids Res. 24: 803- 807, 1996. 6 A c

GAM1032 303 RFX5 Mach, B.; Steimle, V.; Martinez- Soria, E.; Reith, W.: Regulationof MHC class II genes: lessons from a disease. Annu. Rev. Immun. 14:301- 331, 1996. 6 A c

GAM1032 303 RFX5 Nekrep, N.; Jabrane- Ferrat, N.; Peterlin, B. M.: Mutations inthe bare lymphocyte syndrome define critical steps in the assemblyof the regulatory factor X complex. Molec. Cell Biol. 20: 4455- 4461,2000. 6 A c

GAM1032 303 RFX5 Nekrep, N.; Jabrane- Ferrat, N.; Wolf, H. M.; Eibl, M. M.; Geyer,M.; Peterlin, B. M.: Mutation in a winged- helix DNA- binding motifcauses atypical bare lymphocyte syndrome. Nature Immun. 30Sept,2002. Note: Advance Electronic Publication. 6 A c

GAM1032 303 RFX5 Peijnenburg, A.; Van Eggermond, M. C. J. A.; Van den Berg, R.;Sanal, O.; Vossen, J. M. J. J.; Van den Elsen, P. J.: Molecular analysisof an MHC class II deficiency patient reveals a novel mutation inthe RFX5 gene. Immunogenetics 49: 338- 345, 1999. 6 A c

GAM1032 303 RFX5 Scholl, T.; Mahanta, S. K.; Strominger, J. L.: Specific complexformation between the type II bare lymphocyte syndrome- associatedtransactivators CIITA and RFX5. Proc. Nat. Acad. Sci. 94: 6330- 6334,1997. 6 A c

GAM1032 303 RFX5 Steimle, V.; Durand, B.; Barras, E.; Zuffrey, M.; Hadam, M. R.;Mach, B.; Reith, W.: A novel DNA binding regulatory factor is mutatedin primary MHC class II deficiency (bare lymphocyte syndrome). GenesDev. 9: 1021- 1032, 1995. 6 A c

GAM1032 303 RFX5 Villard, J.; Reith, W.; Barras, E.; Gos, A.; Morris, M. A.; Antonarakis,S. E.; Van den Elsen, P. J.; Mach, B.: Analysis of mutations andchromosomal localisation of the gene encoding RFX5, a novel transcriptionfactor affected in major histocompatibility complex class II deficiency. Hum.Mutat. 10: 430- 435, 1997. 6 A c

GAM1032 303 RFX5 Wolf, H. M.; Hauber, I.; Gulle, H.; Thon, V.; Eggenbauer, H.;Fischer, M. B.; Fiala, S.; Eibl, M. M.: Brief report: Twin boys withmajor histocompatibility complex class II deficiency but inducibleimmune responses. New Eng. J. Med. 332: 86- 90, 1995. 6 A c

GAM1032 303 RFX5 Zhong, G.; Fan, P.; Ji, H.; Dong, F.; Huang, Y.: Identificationof a chlamydial protease- like activity factor responsible for thedegradation of host transcription factors. J. Exp. Med. 193: 935- 942,2001. 6 A c

GAM1032 303 RNF6 La Starza, R.; Wlodarska, I.; Aventin, A.; Falzetti, D.; Crescenzi,B.; Martelli, M. F.; Van den Berghe, H.; Mecucci, C.: Molecular delineationof 13q deletion boundaries in 20 patients with myeloid malignancies. Blood 91:231- 237, 1998. 6 A c

GAM1032 303 RNF6 Li, G.; Hu, N.; Goldstein, A. M.; Tang, Z.- Z.; Roth, M. J.; Wang,Q.- H.; Dawsey, S. M.; Han, X.- Y.; Ding, T.; Huang, J.; Giffen, C.;Taylor, P. R.; Emmert- Buck, M. R.: Allelic loss on chromosome bands13q11- q13 in esophageal squamous cell carcinoma. Genes ChromosomesCancer 31: 390- 397, 2001. 6 A c

GAM1032 303 RNF6 Lo, H. S.; Hu, N.; Gere, S.; Lu, N.; Su, H.; Goldstein, A. M.;Taylor, P. R.; Lee, M. P.: Identification of somatic mutations ofthe RNF6 gene in human 6 A c

esophageal squamous cell carcinoma. CancerRes. 62: 4191- 4193, 2002.

GAM1032 303 RNF6 Macdonald, D. H. C.; Lahiri, D.; Sampath, A.; Chase, A.; Sohal,J.; Cross, N. C. P.: Cloning and characterization of RNF6, a novelRING finger gene mapping to 13q12. Genomics 58: 94- 97, 1999. 6 A c

GAM1032 303 RXRA Almasan, A.; Mangelsdorf, D. J.; Ong, E. S.; Wahl, G. M.; Evans,R. M.: Chromosomal localization of the human retinoid X receptors. Genomics 20:397- 403, 1994. 6 A c

GAM1032 303 RXRA Claudel, T.; Leibowitz, M. D.; Fievet, C.; Tailleux, A.; Wagner,B.; Repa, J. J.; Torpier, G.; Lobaccaro, J.- M.; Paterniti, J. R.;Mangelsdorf, D. J.; Heyman, R. A.; Auwerx, J.: Reduction of atherosclerosisin apolipoprotein E knockout mice by activation of the retinoid Xreceptor. Proc. Nat. Acad. Sci. 98: 2610- 2615, 2001. 6 A c

GAM1032 303 RXRA de Urquiza, A. M.; Liu, S.; Sjoberg, M.; Zetterstrom, R. H.; Griffiths,W.; Sjovall, J.; Perlmann, T.: Docosahexaenoic acid, a ligand forthe retinoid X receptor in mouse brain. Science 290: 2140- 2144,2000. 6 A c

GAM1032 303 RXRA Dyson, E.; Sucov, H. M.; Kubalak, S. W.; Schmid- Schonbein, G. W.;DeLano, F. A.; Evans, R. M.; Ross, J., Jr.; Chien, K. R.: Atrial- likephenotype is associated with embryonic ventricular failure in retinoidX receptor alpha -/- mice. Proc. Nat. Acad. Sci. 92: 7386- 7390,1995. 6 A c

GAM1032 303 RXRA Gampe, R. T., Jr.; Montana, V. G.; Lambert, M. H.; Miller, A. B.;Bledsoe, R. K.; Milburn, M. V.; Kliewer, S. A.; Willson, T. M.; Xu,H. E.: Asymmetry in the PPAR- gamma/RXR- alpha crystal structure revealsthe molecular basis of heterodimerization among nuclear receptors. Molec.Cell 5: 545- 555, 2000. 6 A c

GAM1032 303 RXRA Germain, P.; Iyer, J.; Zechel, C.; Gronemeyer, H.: Co- regulatorrecruitment and the mechanism of retinoic acid receptor synergy. Nature 415:187- 192, 2002. 6 A c

GAM1032 303 RXRA Gruber, P. J.; Kubalak, S. W.; Pexieder, T.; Sucov, H. M.; Evans,R. M.; Chien, K. R.: RXR- alpha deficiency confers genetic susceptibilityfor aortic sac, conotruncal, atrioventricular cushion, and ventricularmuscle defects in mice. J. Clin. Invest. 98: 1332- 1343, 1996. 6 A c

GAM1032 303 RXRA Heyman, R. A.; Mangelsdorf, D. J.; Dyck, J. A.; Stein, R. B.; Eichele,G.; Evans, R. M.; Thaller, C.: 9- cis retinoic acid is a high affinityligand for the retinoid X receptor. Cell 68: 397- 406, 1992. 6 A c

GAM1032 303 RXRA Hoopes, C. W.; Taketo, M.; Ozato, K.; Liu, Q.; Howard, T. A.; Linney,E.; Seldin, M. F.: Mapping the mouse Rxr loci encoding nuclear retinoidX receptors Rxr- alpha, Rxr- beta, and Rxr- gamma. Genomics 14: 611- 617,1992. 6 A c

GAM1032 303 RXRA Jones, K. A.; Fitzgibbon, J.; Woodward, K. J.; Goudie, D.; Ferguson-Smith,M. A.; Povey, S.; Wolfe, J.; Solomon, E.: Localization of the retinoidX receptor alpha gene (RXRA) to chromosome 9q34. Ann. Hum. Genet. 57:195- 201, 1993. 6 A c

GAM1032 303 RXRA Li, M.; Indra, A. K.; Warot, X.; Brocard, J.; Messaddeq, N.; Kato,S.; Metzger, D.; Chambon, P.: Skin abnormalities generated by temporallycontrolled RXR- alpha mutations in mouse epidermis. Nature 407: 633- 636,2000. 6 A c

GAM1032 303 RXRA Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000. 6 A c

GAM1032 303 RXRA Mangelsdorf, D. J.; Ong, E. S.; Dyck, J. A.; Evans, R. M.: Nuclearreceptor that identifies a novel retinoic acid response pathway. Nature 345:224- 229, 1990. 6 A c

GAM1032 303 RXRA Mangelsdorf, D. J.; Umesono, K.; Kliewer, S. A.; Borgmeyer, U.;Ong, E. S.; 6 A c
Evans, R. M.: A direct repeat in the cellular retinol- bindingprotein type
II gene confers differential regulation by RXR and RAR. Cell 66:555- 561,
1991.

GAM1032 303 RXRA McNamara, P.; Seo, S.; Rudic, R. D.; Sehgal, A.; Chakravarti,D.; FitzGerald, 6 A c
G. A.: Regulation of CLOCK and MOP4 by nuclear hormonereceptors in the
vasculature: a humoral mechanism to reset a peripheralclock. Cell 105: 877-
889, 2001.

GAM1032 303 RXRA Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, 6 A c
K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation
of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers.
Science 289: 1524- 1529, 2000.

GAM1032 303 RXRA Tontonoz, P.; Hu, E.; Spiegelman, B. M.: Stimulation of adipogenesisin 6 A c
fibroblasts by PPAR- gamma- 2, a lipid- activated transcription factor. Cell
79:1147- 1156, 1994.

GAM1032 303 RXRA Wan, Y.- J. Y.; An, D.; Cai, Y.; Repa, J. J.; Chen, T. H.- P.; Flores,M.; 6 A c
Postic, C.; Magnuson, M. A.; Chen, J.; Chien, K. R.; French, S.;Mangelsdorf,
D. J.; Sucov, H. M.: Hepatocyte- specific mutation establishesretinoid X
receptor alpha as a heterodimeric integrator of multiplephysiological
processes in the liver. Molec. Cell. Biol. 20: 4436- 4444,2000.

GAM1032 303 RXRA Willy, P. J.; Umesono, K.; Ong, E. S.; Evans, R. M.; Heyman, R.A.; 6 A c
Mangelsdorf, D. J.: LXR, a nuclear receptor that defines a distinctretinoid
response pathway. Genes Dev. 9: 1033- 1045, 1995.

GAM1032 303 RXRA Zhong, S.; Delva, L.; Rachez, C.; Cenciarelli, C.; Gandini, D.;Zhang, H.; 6 A c
Kalantry, S.; Freedman, L. P.; Pandolfi, P. P.: A RA- dependent,tumour-
growth suppressive transcription complex is the target of thePML- RAR- alpha
and T18 oncoproteins. Nature Genet. 23: 287- 295, 1999.

GAM1032 303 RXRA Zhou, M. D.; Sucov, H. M.; Evans, R. M.; Chien, K. R.: Retinoid- 6 A c
dependentpathways suppress myocardial cell hypertrophy. Proc. Nat. Acad.
Sci. 92:7391- 7395, 1995.

GAM1032 303 SCN2B Bolino, A.; Seri, M.; Caroli, F.; Eubanks, J.; Srinivasan, J.;Mandich, P.; 6 A c
Schenone, A.; Quattrone, A.; Romeo, G.; Catterall, W.A.; Devoto, M.:
Exclusion of the SCN2B gene as candidate for CMT4B. Europ.J. Hum. Genet. 6:
629- 634, 1998.

GAM1032 303 SCN2B Eubanks, J.; Srinivasan, J.; Dinulos, M. B.; Disteche, C. M.; Catterall,W. 6 A c
A.: Structure and chromosomal localization of the beta2 subunitof the human
brain sodium channel. Neuroreport 8: 2775- 2779, 1997.

GAM1032 303 SCN2B Imai, K.; Kingsley, D. M.: Mouse chromosome 9. Mammalian Genome 5:S139- 6 A c
S153, 1994.

GAM1032 303 SCN2B Isom, L. L.; Ragsdale, D. S.; De Jongh, K. S.; Westenbroek, R.E.; Reber, B. 6 A c
F. X.; Scheuer, T.; Catterall, W. A.: Structure andfunction of the beta- 2
subunit of brain sodium channels, a transmembraneglycoprotein with a CAM
motif. Cell 83: 433- 442, 1995.

GAM1032 303 SCN2B Jones, J. M.; Meisler, M. H.; Isom, L. L.: Scn2b, a voltage- gatedsodium 6 A c
channel beta- 2 gene on mouse chromosome 9. Genomics 34: 258- 259,1996.

GAM1032 303 SERPINA3 Chandra, T.; Stackhouse, R.; Kidd, V. J.; Robson, K. J. H.; Woo,S. L. C.: 6 A c
Sequence homology between human alpha- 1- antichymotrypsin,alpha- 1-
antitrypsin, and antithrombin III. Biochemistry 22: 5055- 5061,1983.

GAM1032 303 SERPINA3 Eriksson, S.; Lindmark, B.; Lilia, H.: Familial alpha- 1- 6 A c

antichymotrypsindeficiency. Acta Med. Scand. 220: 447- 453, 1986.

GAM1032 303 SERPINA3 Gilfix, B. M.; Briones, L.: Absence of the A1252G mutation inalpha 1- 6 A c
antichymotrypsin in a North American population sufferingfrom dementia. J.
Cereb. Blood Flow Metab. 17: 233- 235, 1997.

GAM1032 303 SERPINA3 Haines, J. L.; Pritchard, M. L.; Saunders, A. M.; Schildkraut,J. M.; 6 A c
Growdon, J. H.; Gaskell, P. C.; Farrer, L. A.; Auerbach, S.A.; Gusella, J.
F.; Locke, P. A.; Rosi, B. L.; Yamaoka, L.; Small,G. W.; Conneally, P. M.;
Roses, A. D.; Pericak- Vance, M. A.: No geneticeffect of alpha- 1-
antichymotrypsin in Alzheimer disease. Genomics 33:53- 56, 1996.

GAM1032 303 SERPINA3 Haines, J. L.; Scott, W. K.; Pericak- Vance, M. A.: Reply to 'Geneticeffect 6 A c
of alpha- 1- antichymotrypsin on the risk of Alzheimer disease.'(Letter)
Genomics 40: 384- 385, 1997.

GAM1032 303 SERPINA3 Kamboh, M. I.; Aston, C. E.; Ferrell, R. E.; Dekosky, S. T.: Geneticeffect 6 A c
of alpha- 1- antichymotrypsin on the risk of Alzheimer disease.(Letter)
Genomics 41: 382- 385, 1997.

GAM1032 303 SERPINA3 Kamboh, M. I.; Sanghera, D. K.; Ferrell, R. E.; DeKosky, S. T.: APOE*4- 6 A c
associated Alzheimer's disease risk is modified by alpha- 1-
antichymotrypsinpolymorphism. Nature Genet. 10: 486- 488, 1995.

GAM1032 303 SERPINA3 Kelsey, G. D.; Abeliovich, D.; McMahon, C. J.; Whitehouse, D.;Corney, G.; 6 A c
Povey, S.; Hopkinson, D. A.; Wolfe, J.; Mieli- Vergani,G.; Mowat, A. P.:
Cloning of the human alpha- 1 antichymotrypsin geneand genetic analysis of
the gene in relation to alpha- 1 antitrypsindeficiency. J. Med. Genet. 25:
361- 368, 1988.

GAM1032 303 SERPINA3 Morgan, K.; Licastro, F.; Tilley, L.; Ritchie, A.; Morgan, L.;Pedrini, S.; 6 A c
Kalsheker, N.: Polymorphism in the alpha- 1- antichymotrypsin(ACT) gene
promoter: effect on expression in transfected glial andliver cell lines and
plasma ACT concentrations. Hum. Genet. 109:303- 310, 2001.

GAM1032 303 SERPINA3 Morgan, K.; Morgan, L.; Carpenter, K.; Lowe, J.; Lam, L.; Cave,S.; Xuereb, 6 A c
J.; Wischik, C.; Harrington, C.; Kalsheker, N. A.:
Microsatellitepolymorphism of the alpha- 1- antichymotrypsin gene locus
associatedwith sporadic Alzheimer's disease. Hum. Genet. 99: 27- 31, 1997.

GAM1032 303 SERPINA3 Munoz, E.; Obach, V.; Oliva, R.; Marti, M. J.; Ezquerra, M.; Pastor,P.; 6 A c
Ballesta, F.; Tolosa, E.: Alpha- 1- antichymotrypsin gene polymorphismand
susceptibility to Parkinson's disease. Neurology 52: 297- 301,1999.

GAM1032 303 SERPINA3 Poller, W.; Faber, J.- P.; Scholz, S.; Weidinger, S.; Bartholome,K.; Olek, 6 A c
K.; Eriksson, S.: Mis- sense mutation of alpha- 1- antichymotrypsingene
associated with chronic lung disease. (Letter) Lancet 339:1538, 1992.

GAM1032 303 SERPINA3 Poller, W.; Faber, J.- P.; Weidinger, S.; Tief, K.; Scholz, S.;Fischer, M.; 6 A c
Olek, K.; Kirchgesser, M.; Heidtmann, H.- H.: A leucine- to-
prolinesubstitution causes a defective alpha- 1- antichymotrypsin allele
associatedwith familial obstructive lung disease. Genomics 17: 740- 743,
1993.

GAM1032 303 SERPINA3 Rabin, M.; Watson, M.; Breg, W. R.; Kidd, V.; Woo, S. L. C.; Ruddle,F. H.: 6 A c
Human alpha- 1- antichymotrypsin and alpha- 1- antitrypsin (PI)genes map to
the same region on chromosome 14. (Abstract) Cytogenet.Cell Genet. 40: 728,
1985.

GAM1032 303 SERPINA3 Rabin, M.; Watson, M.; Kidd, V.; Woo, S. L. C.; Breg, W. R.; Ruddle,F. H.: 6 A c
Regional location of alpha- 1- antichymotrypsin and alpha- 1-
antitrypsingenes on human chromosome 14. Somat. Cell Molec. Genet. 12: 209-
214,1986.

GAM1032 303 SERPINA3 Samilchuk, E. I.; Chuchalin, A. G.: Mis- sense mutation of alpha- 1- antichymotrypsingene and chronic lung disease. (Letter) Lancet 342: 624, 1993. 6 A c

GAM1032 303 SERPINA3 Sefton, L.; Kearney, P.; Kelsey, G.; Povey, S.; Wolfe, J.: Physicallinkage of the genes PI and AACT. (Abstract) Cytogenet. Cell Genet. 51:1076, 1989. 6 A c

GAM1032 303 SERPINA3 Sefton, L.; Kelsey, G.; Kearney, P.; Povey, S.; Wolfe, J.: Aphysical map of the human PI and AACT genes. Genomics 7: 382- 388,1990. 6 A c

GAM1032 303 SERPINA3 Tachikawa, H.; Tsuda, M.; Onoe, K.; Ueno, M.; Takagi, S.; Shinohara,Y.: Alpha- 1- antichymotrypsin gene A1252G variant (ACT Isehara- 1)is associated with a lacunar type of ischemic cerebrovascular disease. J.Hum. Genet. 46: 45- 47, 2001. 6 A c

GAM1032 303 SERPINA3 Tsuda, M.; Sei, Y.; Matsumoto, M.; Kamiguchi, H.; Yamamoto, M.;Shinohara, Y.; Igarashi, T.; Yamamura, M.: Alpha- 1- antichymotrypsinvariant detected by PCR- single strand conformation polymorphism (PCR- SSCP)and direct sequencing. Hum. Genet. 90: 467- 468, 1992. 6 A c

GAM1032 303 SERPINA3 Tsuda, M.; Sei, Y.; Yamamura, M.; Yamamoto, M.; Shinohara, Y.: Detection of a new mutant alpha- 1- antichymotrypsin in patients withocclusive- cerebrovascular disease. FEBS Lett. 304: 66- 68, 1992. 6 A c

GAM1032 303 SERPINA3 Wang, X.; DeKosky, S. T.; Luedecking- Zimmer, E.; Ganguli, M.;Kamboh, M. I.: Genetic variation in alpha- 1- antichymotrypsin andits association with Alzheimer's disease. Hum. Genet. 110: 356- 365,2002. 6 A c

GAM1032 303 SERPINA3 Yamamoto, M.; Kondo, I.; Ogawa, N.; Asanuma, M.; Yamashita, Y.;Mizuno, Y.: Genetic association between susceptibility to Parkinson'sdisease and alpha- 1- antichymotrypsin polymorphism. Brain Res. 759:153- 155, 1997. 6 A c

GAM1032 303 SIAT1 Grundmann, U.; Nerlich, C.; Rein, T.; Zettlmeissl, G.: CompletecDNA sequence encoding human beta- galactoside alpha- 2,6- sialyltransferase. NucleicAcids Res. 18: 667 only, 1990. 6 A c

GAM1032 303 SIAT1 Wang, X.; Vertino, A.; Eddy, R. L.; Byers, M. G.; Jani- Sait, S.N.; Shows, T. B.; Lau, J. T. Y.: Chromosome mapping and organizationof the human beta- galactoside alpha- 2,6- sialyltransferase gene: differentialand cell- type specific usage of upstream exon sequences in B- lymphoblastoidcells. J. Biol. Chem. 268: 4355- 4361, 1993. 6 A c

GAM1032 303 SLC12A7 Boettger, T.; Hubner, C. A.; Maler, H.; Rust, M. B.; Beck, F. X.;Jentsch, T. J.: Deafness and renal tubular acidosis in mice lackingthe K- Cl co- transporter Kcc4. Nature 416: 874- 878, 2002. 6 A c

GAM1032 303 SLC12A7 Mount, D. B.; Mercado, A.; Song, L.; Xu, J.; George, A. L., Jr.;Delpire, E.; Gamba, G.: Cloning and characterization of KCC3 andKCC4, new members of the cation- chloride cotransporter gene family. J.Biol. Chem. 274: 16355- 16362, 1999. 6 A c

GAM1032 303 SUOX Garrett, R. M.; Bellissimo, D. B.; Rajagopalan, K. V.: Molecularcloning of human liver sulfite oxidase. Biochim. Biophys. Acta 1262:147- 149, 1995. 6 A c

GAM1032 303 SUOX Garrett, R. M.; Johnson, J. L.; Graf, T. N.; Feigenbaum, A.; Rajagopalan,K. V.: Human sulfite oxidase R160Q: identification of the mutationin a sulfite oxidase- deficient patient and expression and characterizationof the mutant enzyme. Proc. Nat. Acad. Sci. 95: 6394- 6398, 1998. 6 A c

GAM1032 303 SUOX Johnson, J. L.; Coyne, K. E.; Garrett, R. M.; Zabot, M.- T.; Dorche,C.; 6 A c

Kisker, C.; Rajagopalan, K. V.: Isolated sulfite oxidase deficiency:identification of 12 novel SUOX mutations in 10 patients.(Abstract) Hum.Mutat. 20: 74 only, 2002.

GAM1032 303 SUOX Kisker, C.; Schindelin, H.; Pacheco, A.; Wehbi, W. A.; Garrett,R. M.; Rajagopalan, K. V.; Enemark, J. H.; Rees, D. C.: Molecularbasis of sulfite oxidase deficiency from the structure of sulfiteoxidase. Cell 91: 973- 983, 1997. 6 A c

GAM1032 303 TK2 Johansson, M.; Karlsson, A.: Cloning of the cDNA and chromosomelocalization of the gene for human thymidine kinase 2. J. Biol. Chem. 272:8454- 8458, 1997. 6 A c

GAM1032 303 TK2 Mandel, H.; Szargel, R.; Labay, V.; Elpeleg, O.; Saada, A.; Shalata,A.; Anbinder, Y.; Berkowitz, D.; Hartman, C.; Barak, M.; Eriksson,S.; Cohen, N.: The deoxyguanosine kinase gene is mutated in individualswith depleted hepatocerebral mitochondrial DNA. Nature Genet. 29:337- 341, 2001. Note: Erratum: Nature Genet. 29: 491 only, 2001. 6 A c

GAM1032 303 TK2 Saada, A.; Shaag, A.; Mandel, H.; Nevo, Y.; Eriksson, S.; Elpeleg,O.: Mutant mitochondrial thymidine kinase in mitochondrial DNA depletionmyopathy. Nature Genet. 29: 342- 344, 2001. 6 A c

GAM1032 303 TK2 Wang, L.; Munch- Petersen, B.; Herrstrom Sjoberg, A.; Hellman, U.;Bergman, T.; Jornvall, H.; Eriksson, S.: Human thymidine kinase 2:molecular cloning and characterisation of the enzyme activity withantiviral and cytostatic nucleoside substrates. FEBS Lett. 443:170- 174, 1999. 6 A c

GAM1032 303 TK2 Willecke, K.; Reuber, T.; Kucherlapati, R. S.; Ruddle, F. H.:Human mitochondrial thymidine kinase is coded for by a gene on chromosome16 of the nucleus. Somat. Cell Genet. 3: 237- 245, 1977. 6 A c

GAM1032 303 WBP2 Chen, H. I.; Einbond, A.; Kwak, S.- J.; Linn, H.; Koepf, E.; Peterson,S.; Kelly, J. W.; Sudol, M.: Characterization of the WW domain ofhuman Yes-associated protein and its polyproline containing ligands. J.Biol. Chem. 272: 17070- 17077, 1997. 6 A c

GAM1032 303 WBP2 Chen, H. I.; Sudol, M.: The WW domain of Yes- associated proteinbinds a proline- rich ligand that differs from the consensus establishedfor Src homology 3- binding modules. Proc. Nat. Acad. Sci. 92: 7819- 7823,1995. 6 A c

GAM1338 360 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B-glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989. 3 C c

GAM1338 360 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989. 3 C c

GAM1338 360 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987. 3 C c

GAM1338 360 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986. 3 C c

GAM1338 360 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988. 3 C c

GAM1338 360 ABCC11 Bera, T. K.; Lee, S.; Salvatore, G.; Lee, B.; Pastan, I.: MRP8,a new member of ABC transporter superfamily, identified by EST databasemining and gene 3 C c

prediction program, is highly expressed in breastcancer. Molec. Med. 7: 509-516, 2001.

GAM1338 360 ABCC11 Tammur, J.; Prades, C.; Arnould, I.; Rzhetsky, A.; Hutchinson,A.; Adachi, M.; Schuetz, J. D.; Swoboda, K. J.; Ptacek, L. J.; Rosier,M.; Dean, M.; Allikmets, R.: Two new genes from the human ATP- bindingcassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicatedon chromosome 16q12. Gene 273: 89- 96, 2001. 3 C c

GAM1338 360 ABCC11 Yabuuchi, H.; Shimizu, H.; Takayanagi, S.; Ishikawa, T.: Multiplesplicing variants of two new human ATP- binding cassette transporters,ABCC11 and ABCC12. Biochem. Biophys. Res. Commun. 288: 933- 939,2001. 3 C c

GAM1338 360 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002. 3 C c

GAM1338 360 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor: functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994. 3 C c

GAM1338 360 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994. 3 C c

GAM1338 360 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 3 C c

GAM1338 360 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95-101, 1997. 3 C c

GAM1338 360 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779-782, 2000. 3 C c

GAM1338 360 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001. 3 C c

GAM1338 360 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001. 3 C c

GAM1338 360 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998. 3 C c

GAM1338 360 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: Identificationand characterization of STK12/Aik2: a human gene related to auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147-152,1998. 3 C c

GAM1338 360 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. 3 C c

T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism, OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001.

GAM1338 360 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand 3 C c
characterization of genes associated with chromosome- 6 mediatedtumor suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996.

GAM1338 360 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a 3 C c
novel non- lens member of the beta- gamma- crystallin superfamily,is associated with the control of tumorigenicity in human malignantmelanoma. Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997.

GAM1338 360 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, 3 C c
D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA cloning, expression, subcellular localization, and chromosomalassignment of mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem. Biophys. Res. Commun. 244: 285- 292, 1998.

GAM1338 360 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; 3 C c
Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof the aurora- and Ipl1- like midbody- associated protein mitotic kinasein human cancer cells. Cancer Res. 58: 4811- 4816, 1998.

GAM1338 360 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. 3 C c
S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian Genome 9: 715- 720, 1998.

GAM1338 360 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; 3 C c
Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human melanoma cell lines controlled by introduction of human chromosome6. Science 247: 568- 571, 1990.

GAM1338 360 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: 3 C c
Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89: 3962- 3966,1992.

GAM1338 360 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- 3 C c
lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat. Acad. Sci. 96: 4378- 4383, 1999.

GAM1338 360 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; 3 C c
Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988.

GAM1338 360 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: 3 C c
Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990.

GAM1338 360 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 3 C b
(CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998.

GAM1338 360 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of 3 C b
Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999.

GAM1338 360 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: 3 C b
Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000.

GAM1338 360 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 3 C b

deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001.

GAM1338 360 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999. 3 C b

GAM1338 360 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002. 3 C b

GAM1338 360 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001. 3 C b

GAM1338 360 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998. 3 C b

GAM1338 360 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998. 3 C b

GAM1338 360 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 3 C b

GAM1338 360 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 C c

GAM1338 360 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 3 C c

GAM1338 360 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- interacting protein, recognizes the basolateral sortingsignal of amyloid precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998. 3 C c

GAM1338 360 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 C b

GAM1338 360 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 C b

GAM1338 360 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 C b

GAM1338 360 AR Abel, A.; Walcott, J.; Woods, J.; Duda, J.; Merry, D. E.: Expressionof expanded repeat androgen receptor produces neurologic disease intransgenic mice. Hum. Molec. Genet. 10: 107- 116, 2001. 3 C c

GAM1338 360 AR Bailey, C. K.; Andriola, I. F. M.; Kampinga, H. H.; Merry, D. E.: Molecular 3 C c

chaperones enhance the degradation of expanded polyglutaminerepeat androgen receptor in a cellular model of spinal and bulbarmuscular atrophy. Hum. Molec. Genet. 11: 515- 523, 2002.

GAM1338 360 AR Batch, J. A.; Evans, B. A. J.; Hughes, I. A.; Patterson, M. N.: Mutations of 3 C c
the androgen receptor gene identified in perineal hypospadias. J.Med. Genet. 30: 198- 201, 1993.

GAM1338 360 AR Batch, J. A.; Williams, D. M.; Davies, H. R.; Brown, B. D.; Evans,B. A. J.; 3 C c
Hughes, I. A.; Patterson, M. N.: Androgen receptor genemutations identified by SSCP in fourteen subjects with androgen insensitivitysyndrome. Hum. Molec. Genet. 1: 497- 503, 1992.

GAM1338 360 AR Beitel, L. K.; Kazemi- Esfarjani, P.; Kaufman, M.; Lumbroso, R.;DiGeorge, A. 3 C c
M.; Killinger, D. W.; Trifiro, M. A.; Pinsky, L.: Substitutionof arginine- 839 by cysteine or histidine in the androgen receptorcauses different receptor phenotypes in cultured cells and coordinatedegrees of clinical androgen resistance. J. Clin. Invest. 94: 546- 554,1994.

GAM1338 360 AR Belsham, D. D.; Pereira, F.; Greenberg, C. R.; Liao, S.; Wrogemann,K.: 3 C c
Leu676- to- pro mutation of the androgen receptor causes completeandrogen insensitivity syndrome in a large Hutterite kindred. Hum.Mutat. 5: 28- 33, 1995.

GAM1338 360 AR Bevan, C. L.; Brown, B. B.; Davies, H. R.; Evans, B. A. J.; Hughes,I. A.; 3 C c
Patterson, M. N.: Functional analysis of six androgen receptormutations identified in patients with partial androgen insensitivitysyndrome. Hum. Molec. Genet. 5: 265- 273, 1996.

GAM1338 360 AR Biancalana, V.; Serville, F.; Pommier, J.; Julien, J.; Hanauer,A.; Mandel, 3 C c
J. L.: Moderate instability of the trinucleotide repeatin spinobulbar muscular atrophy. Hum. Molec. Genet. 1: 255- 258,1992.

GAM1338 360 AR Boehmer, A. L. M.; Brinkmann, A. O.; Niermeijer, M. F.; Bakker,L.; Halley, 3 C c
D. J. J.; Drop, S. L. S.: Germ- line and somatic mosaicismin the androgen insensitivity syndrome: implications for genetic counseling.(Letter) Am. J. Hum. Genet. 60: 1003- 1006, 1997.

GAM1338 360 AR Boehmer, A. L. M.; Brinkmann, A. O.; Nijman, R. M.; Verleun- Mooijman,M. C. 3 C c
T.; de Ruiter, P.; Niermeijer, M. F.; Drop, S. L. S.: Phenotypicvariation in a family with partial androgen insensitivity syndromeexplained by differences in 5- alpha dihydrotestosterone availability. J.Clin. Endocr. Metab. 86: 1240- 1246, 2001.

GAM1338 360 AR Bouvattier, C.; Carel, J.- C.; Lecointre, C.; David, A.; Sultan,C.; 3 C c
Bertrand, A.- M., Morel, Y.; Chaussain, J.- L.: Postnatal changesof T, LH, and FSH in 46,XY infants with mutations in the AR gene. J.Clin. Endocr. Metab. 87: 29- 32, 2002.

GAM1338 360 AR Brown, C. J.; Goss, S. J.; Lubahn, D. B.; Joseph, D. R.; Wilson,E. M.; 3 C c
French, F. S.; Willard, H. F.: Androgen receptor locus onthe human X chromosome: regional localization to Xq11- 12 and descriptionof a DNA polymorphism. Am. J. Hum. Genet. 44: 264- 269, 1989.

GAM1338 360 AR Brown, T. R.; Lubahn, D. B.; Wilson, E. M.; Joseph, D. R.; French,F. S.; 3 C c
Migeon, C. J.: Deletion of the steroid- binding domain of thehuman androgen receptor gene in one family with complete androgeninsensitivity syndrome: evidence for further genetic heterogeneityin this syndrome. Proc. Nat. Acad. Sci. 85: 8151- 8155, 1988.

GAM1338 360 AR Bruggenwirth, H. T.; Boehmer, A. L. M.; Ramnarain, S.; Verleun- Mooijman,M. 3 C c
C. T.; Satijn, D. P. E.; Trapman, J.; Grootegoed, J. A.; Brinkmann,A. O.:

Molecular analysis of the androgen- receptor gene in a familywith receptor-positive partial androgen insensitivity: an unusualtype of intronic mutation. Am. J. Hum. Genet. 61: 1067- 1077, 1997.

GAM1338 360 AR Buchanan, G.; Yang, M.; Harris, J. M.; Nahm, H. S.; Han, G.; Moore,N.; Bentel, J. M.; Matusik, R. J.; Horsfall, D. J.; Marshall, V. R.;Greenberg, N. M.; Tilley, W. D.: Mutations at the boundary of thehinge and ligand binding domain of the androgen receptor confer increasedtransactivation function. Molec. Endocr. 15: 46- 56, 2001. 3 C c

GAM1338 360 AR Butler, R.; Leigh, P. N.; McPhaul, M. J.; Gallo, J.- M.: Truncatedforms of the androgen receptor are associated with polyglutamine expansionin X-linked spinal and bulbar muscular atrophy. Hum. Molec. Genet. 7:121- 127, 1998. 3 C c

GAM1338 360 AR Calvo, R. M.; Asuncion, M.; Sancho, J.; San Millan, J. L.; Escobar-Morreale,H. F.: The role of the CAG repeat polymorphism in the androgen receptorgene and of skewed X- chromosome inactivation, in the pathogenesisof hirsutism. J. Clin. Endocr. Metab. 85: 1735- 1740, 2000. 3 C c

GAM1338 360 AR Caplen, N. J.; Taylor, J. P.; Statham, V. S.; Tanaka, F.; Fire,A.; Morgan, R. A.: Rescue of polyglutamine- mediated cytotoxicityby double- stranded RNA- mediated RNA interference. Hum. Molec. Genet. 11:175- 184, 2002. 3 C c

GAM1338 360 AR Caskey, C. T.; Pizzuti, A.; Fu, Y.- H.; Fenwick, R. G., Jr.; Nelson,D. L.: Triplet repeat mutations in human disease. Science 256:784- 789, 1992. 3 C c

GAM1338 360 AR Chang, B.; Zheng, S. L.; Hawkins, G. A.; Isaacs, S. D.; Wiley,K. E.; Turner, A.; Carpten, J. D.; Bleecker, E. R.; Walsh, P. C.;Trent, J. M.; Meyers, D. A.; Isaacs, W. B.; Xu, J.: Polymorphic GGCrepeats in the androgen receptor gene are associated with hereditaryand sporadic prostate cancer risk. Hum. Genet. 110: 122- 129, 2002. 3 C c

GAM1338 360 AR Chang, C.; Kokontis, J.; Liao, S.: Molecular cloning of humanand rat complementary DNA encoding androgen receptors. Science 240:324- 326, 1988. 3 C c

GAM1338 360 AR Choong, C. S.; Kemppainen, J. A.; Zhou, Z.- X.; Wilson, E. M.:Reduced androgen receptor gene expression with first exon CAG repeatexpansion. Molec. Endocr. 10: 1527- 1535, 1996. 3 C c

GAM1338 360 AR Choong, C. S.; Quigley, C. A.; French, F. S.; Wilson, E. M.:A novel missense mutation in the amino- terminal domain of the humanandrogen receptor gene in a family with partial androgen insensitivitysyndrome causes reduced efficiency of protein translation. J. Clin.Invest. 98: 1423- 1431, 1996. 3 C c

GAM1338 360 AR Chu, J.; Zhang, R.; Zhao, Z.; Zou, W.; Han, Y.; Qi, Q.; Zhang,H.; Wang, J.- C.; Tao, S.; Liu, X.; Luo, Z.: Male fertility is compatiblewith an Arg840Cys substitution in the AR in a large Chinese familywith divergent phenotypes of AR insensitivity syndrome. J. Clin.Endocr. Metab. 87: 347- 351, 2002. 3 C c

GAM1338 360 AR Coetzee, G. A.; Ross, R. K.: Re: Prostate cancer and the androgenreceptor. (Letter) J. Nat. Cancer Inst. 86: 872- 873, 1994. 3 C c

GAM1338 360 AR Correa- Cerro, L.; Wohr, G.; Haussler, J.; Berthon, P.; Drelon,E.; Mangin, P.; Fournier, G.; Cussenot, O.; Kraus, P.; Just, W.; Paiss,T.; Cantu, J. M.; Vogel, W.: (CAG)nCAA and GGN repeats in the humanandrogen receptor gene are not associated with prostate cancer ina French- German population. Europ. J. Hum. Genet. 7: 347- 362, 1999. 3 C c

GAM1338 360 AR Dowsing, A. T.; Yong, E. L.; Clark, M.; McLachlan, R. I.; de Kretser,D. M.; Trounson, A. O.: Linkage between male infertility and trinucleotiderepeat expansion in the androgen- receptor gene. Lancet 354: 640- 643,1999. 3 C c

GAM1338 360 AR Edwards, A.; Hammond, H. A.; Jin, L.; Caskey, C. T.; Chakraborty,R.: Genetic 3 C c

variation at five trimeric and tetrameric tandem repeatloci in four human population groups. Genomics 12: 241- 253, 1992.

GAM1338 360 AR Elo, J. P.; Kvist, L.; Leinonen, K.; Isomaa, V.; Hentuu, P.; Lukkarinen,O.; 3 C c
Vihko, P.: Mutated human androgen receptor gene detected in aprostatic cancer patient is also activated by estradiol. J. Clin.Endocr. Metab. 80: 3494- 3500, 1995.

GAM1338 360 AR Gaddipati, J. P.; McLeod, D. G.; Heidenberg, H. B.; Sesterhenn,I. A.; 3 C c
Finger, M. J.; Moul, J. W.; Srivastava, S.: Frequent detectionof codon 877 mutation in the androgen receptor gene in advanced prostatecancers. Cancer Res. 54: 2861- 2864, 1994.

GAM1338 360 AR Gehring, U.; Tomkins, G. M.: Characterization of a hormone receptordefect in 3 C c
the androgen- insensitivity mutant. Cell 3: 59- 64, 1974.

GAM1338 360 AR Gingrich, J. R.; Barrios, R. J.; Kattan, M. W.; Nahm, H. S.; Finegold,M. J.; 3 C c
Greenberg, N. M.: Androgen- independent prostate cancer progressionin the TRAMP model. Cancer Res. 57: 4687- 4691, 1997.

GAM1338 360 AR Gingrich, J. R.; Greenberg, N. M.: A transgenic mouse prostatecancer model. 3 C c
Toxicol. Path. 24: 502- 504, 1996.

GAM1338 360 AR Giovannucci, E.; Stampfer, M. J.; Krithivas, K.; Brown, M.; Brufsky,A.; 3 C c
Talcott, J.; Hennekens, C. H.; Kantoff, P. W.: The CAG repeatwithin the androgen receptor gene and its relationship to prostatecancer. Proc. Nat. Acad. Sci. 94: 3320- 3323, 1997.

GAM1338 360 AR Gottlieb, B.; Beitel, L. K.; Trifiro, M. A.: Variable expressivityand 3 C c
mutation databases: the androgen receptor gene mutations database. Hum.Mutat. 17: 382- 388, 2001.

GAM1338 360 AR Gottlieb, B.; Trifiro, M.; Lumbroso, R.; Pinsky, L.: The androgenreceptor 3 C c
gene mutations database. Nucleic Acids Res. 25: 158- 162,1997.

GAM1338 360 AR Gottlieb, B.; Trifiro, M.; Lumbroso, R.; Vasiliou, D. M.; Pinsky,L.: The 3 C c
androgen receptor gene mutations database. Nucleic AcidsRes. 24: 151- 154, 1996.

GAM1338 360 AR Griffin, J. E.: Androgen resistance- - the clinical and molecularspectrum. 3 C c
New Eng. J. Med. 326: 611- 618, 1992.

GAM1338 360 AR Grino, P. B.; Griffin, J. E.; Cushard, W. G., Jr.; Wilson, J.D.: A mutation 3 C c
of the androgen receptor associated with partial androgenresistance, familial gynecomastia, and fertility. J. Clin. Endocr.Metab. 66: 754- 761, 1988.

GAM1338 360 AR Grino, P. B.; Isidro- Gutierrez, R. F.; Griffin, J. E.; Wilson,J. D.: 3 C c
Androgen resistance associated with a qualitative abnormalityof the androgen receptor and responsive to high dose androgen therapy. J.Clin. Endocr. Metab. 68: 578- 584, 1989.

GAM1338 360 AR Hardy, D. O.; Scher, H. I.; Bogenreider, T.; Sabbatini, P.; Zhang,Z.- F.; 3 C c
Nanus, D. M.; Catterall, J. F.: Androgen receptor CAG repeatlengths in prostate cancer: correlation with age of onset. J. Clin.Endocr. Metab. 81: 4400- 4405, 1996.

GAM1338 360 AR Hellwinkel, O. J.- C.; Holterhus, P.- M.; Struve, D.; Marschke,C.; Homburg, 3 C c
N.; Hiort, O.: A unique exonic splicing mutation inthe human androgen receptor gene indicates a physiologic relevanceof regular androgen receptor transcript variants. J. Clin. Endocr.Metab. 86: 2569- 2575, 2001.

GAM1338 360 AR Hickey, T.; Chandy, A.; Norman, R. J.: The androgen receptorCAG repeat 3 C c
polymorphism and X- chromosome inactivation in AustralianCaucasian women with infertility related to polycystic ovary syndrome. J.Clin. Endocr.

Metab. 87: 161- 165, 2002.

GAM1338 360 AR Hiort, O.; Sinnecker, G. H. G.; Holterhus, P.- M.; Nitsche, E.M.; Kruse, K.: 3 C c
Inherited and de novo androgen receptor gene mutations:investigation of
single- case families. J. Pediat. 132: 939- 943,1998.

GAM1338 360 AR Holterhus, P. M.; Sinnecker, G. H. G.; Wollmann, H. A.; Struve,D.; Homburg, 3 C c
N.; Kruse, K.; Hiort, O.: Expression of two functionallydifferent androgen
receptors in a patient with androgen insensitivity. Europ.J. Pediat. 158:
702- 706, 1999.

GAM1338 360 AR Holterhus, P.- M.; Bruggenwirth, H. T.; Hiort, O.; Kleinkauf- Houcken,A.; 3 C c
Kruse, K.; Sinnecker, G. H. G.; Brinkmann, A. O.: Mosaicism dueto a somatic
mutation of the androgen receptor gene determines phenotypein androgen
insensitivity syndrome. J. Clin. Endocr. Metab. 82:3584- 3589, 1997.

GAM1338 360 AR Holterhus, P.- M.; Sinnecker, G. H. G.; Hiort, O.: Phenotypicdiversity and 3 C c
testosterone- induced normalization of mutant L712F androgenreceptor
function in a kindred with androgen insensitivity. J. Clin.Endocr. Metab.
85: 3245- 3250, 2000.

GAM1338 360 AR Holterhus, P.- M.; Wiebel, J.; Sinnecker, G. H. G.; Bruggenwirth,H. T.; 3 C c
Sippell, W. G.; Brinkmann, A. O.; Kruse, K.; Hiort, O.: Clinicaland
molecular spectrum of somatic mosaicism in androgen insensitivitysyndrome.
Pediat. Res. 46: 684- 690, 1999.

GAM1338 360 AR Hughes, I. A.; Evans, B. A. J.: Complete androgen insensitivitysyndrome 3 C c
characterized by increased concentration of a normal androgenreceptor in
genital skin fibroblasts. J. Clin. Endocr. Metab. 63:309- 315, 1986.

GAM1338 360 AR Imasaki, K.; Okabe, T.; Murakami, H.; Tanaka, Y.; Haji, M.; Takayanagi,R.; 3 C c
Nawata, H.: Androgen insensitivity syndrome due to new mutationsin the DNA-
binding domain of the androgen receptor. Molec. Cell.Endocr. 120: 15- 24,
1996.

GAM1338 360 AR Imperato- McGinley, J.; Ip, N. Y.; Gautier, T.; Neuweiler, J.;Gruenspan, H.; 3 C c
Liao, S.; Chang, C.; Balazs, I.: DNA linkage analysisand studies of the
androgen receptor gene in a large kindred withcomplete androgen
insensitivity. Am. J. Med. Genet. 36: 104- 108,1990.

GAM1338 360 AR Irvine, R. A.; Yu, M. C.; Ross, R. K.; Coetzee, G. A.: The CAGand GGC 3 C c
microsatellites of the androgen receptor gene are in linkagedisequilibrium
in men with prostate cancer. Cancer. Res. 55: 1937- 1940,1995.

GAM1338 360 AR Jakubiczka, S.; Nedel, S.; Werder, E. A.; Schleiermacher, E.;Theile, U.; 3 C c
Wolff, G.; Wieacker, P.: Mutations of the androgen receptorgene in patients
with complete androgen insensitivity. Hum. Mutat. 9:57- 61, 1997.

GAM1338 360 AR Jukier, L.; Kaufman, M.; Pinsky, L.; Peterson, R. E.: Partialandrogen 3 C c
resistance associated with secondary 5- alpha- reductase
deficiency:identification of a novel qualitative androgen receptor defect
andclinical implications. J. Clin. Endocr. Metab. 59: 679- 688, 1984.

GAM1338 360 AR Kang, H.- Y.; Yeh, S.; Fujimoto, N.; Chang, C.: Cloning and 3 C c
characterizationof human prostate coactivator ARA54, a novel protein that
associateswith the androgen receptor. J. Biol. Chem. 274: 8570- 8576, 1999.

GAM1338 360 AR Kaufman, M.; Pinsky, L.; Bowin, A.; Au, M. W. S.: Familial externalgenital 3 C c
ambiguity due to a transformation defect of androgen- receptorcomplexes that
is expressed with 5- alpha- dihydrotestosterone and thesynthetic androgen
methyltrienolone. Am. J. Med. Genet. 18: 493- 507,1984.

GAM1338 360 AR Kaufman, M.; Straisfeld, C.; Pinsky, L.: Male 3 C c
pseudohermaphroditismpresumably due to target organ unresponsiveness to

androgens: deficient5- alpha- dihydrotestosterone binding in cultured skin fibroblasts. J.Clin. Invest. 58: 345- 350, 1976.

GAM1338 360 AR Kazemi- Esfarjani, P.; Beitel, L. K.; Trifiro, M.; Kaufman, M.;Rennie, P.; 3 C c
Sheppard, P.; Matusik, R.; Pinsky, L.: Substitution ofvaline- 865 by methionine or leucine in the human androgen receptorcauses complete or partial androgen insensitivity, respectively withdistinct androgen receptor phenotypes. Molec. Endocr. 7: 37- 46,1993.

GAM1338 360 AR Keenan, B. S.; Meyer, W. J., III; Hadjian, A. J.; Jones, H. W.;Migeon, C. 3 C c
J.: Syndrome of androgen insensitivity in man: absenceof 5- alpha- dihydrotestosterone binding protein in skin fibroblasts. J.Clin. Endocr. 38: 1143- 1146, 1974.

GAM1338 360 AR Kittles, R. A.; Young, D.; Weinrich, S.; Hudson, J.; Argyropoulos,G.; Ukoli, 3 C c
F.; Adams- Campbell, L.; Dunston, G. M.: Extent of linkagedisequilibrium between the androgen receptor gene CAG and GGC repeatsin human populations: implications for prostate cancer risk. Hum.Genet. 109: 253- 261, 2001.

GAM1338 360 AR Klocker, H.; Kaspar, F.; Eberle, J.; Uberreiter, S.; Radmayr,C.; Bartsch, 3 C c
G.: Point mutation in the DNA binding domain of theandrogen receptor in two families with Reifenstein syndrome. Am.J. Med. Genet. 50: 1318- 1327, 1992.

GAM1338 360 AR Knoke, I.; Allera, A.; Wieacker, P.: Significance of the CAGrepeat length in 3 C c
the androgen receptor gene (AR) for the transactivationfunction of an M780I mutant AR. Hum. Genet. 104: 257- 261, 1999.

GAM1338 360 AR Kobayashi, Y.; Miwa, S.; Merry, D. E.; Kume, A.; Mei, L.; Doyu,M.; Sobue, 3 C c
G.: Caspase- 3 cleaves the expanded androgen receptor proteinof spinal and bulbar muscular atrophy in a polyglutamine repeat length- dependentmanner. Biochem. Biophys. Res. Commun. 252: 145- 150, 1998.

GAM1338 360 AR Koivisto, P. A.; Schleutker, J.; Helin, H.; Ehren- van Eekelen,C.; 3 C c
Kallioniemi, O.- P.; Trapman, J.: Androgen receptor gene alterationsand chromosomal gains and losses in prostate carcinomas appearingduring finasteride treatment for benign prostatic hyperplasia. Clin.Cancer Res. 5: 3578- 3582, 1999.

GAM1338 360 AR Kooy, R. F.; Reyniers, E.; Storm, K.; Vits, L.; van Velzen, D.;de Ruiter, P. 3 C c
E.; Brinkmann, A. O.; de Paepe, A.; Willems, P. J.:CAG repeat contraction in the androgen receptor gene in three brotherswith mental retardation. Am. J. Med. Genet. 85: 209- 213, 1999.

GAM1338 360 AR La Spada, A. R.; Wilson, E. M.; Lubahn, D. B.; Harding, A. E.;Fischbeck, K. 3 C c
H.: Androgen receptor gene mutations in X- linked spinaland bulbar muscular atrophy. Nature 352: 77- 79, 1991.

GAM1338 360 AR La Spada, A.; Fischbeck, K. H.: Androgen receptor gene defectin X- linked 3 C c
spinal and bulbar muscular atrophy. (Abstract) Am. J.Hum. Genet. 49 (suppl.): 20, 1991.

GAM1338 360 AR Lewis, M.; Kaita, H.; Giblett, E. R.; Anderson, J.; Philipps,S.; Steinberg, 3 C c
A. G.; McAlpine, P. J.: Multiplicity of genetic polymorphismsof blood in the Schmiedeleut Hutterites. Am. J. Med. Genet. 22:477- 485, 1985.

GAM1338 360 AR Liao, S.; Witte, D.: Autoimmune anti- androgen- receptor antibodiesin human 3 C c
serum. Proc. Nat. Acad. Sci. 82: 8345- 8348, 1985.

GAM1338 360 AR Lim, H. N.; Chen, H.; McBride, S.; Dunning, A. M.; Nixon, R. M.;Hughes, I. 3 C c
A.; Hawkins, J. R.: Longer polyglutamine tracts in theandrogen receptor are associated with moderate to severe undermasculinizedgenitalia in XY males. Hum. Molec. Genet. 9: 829- 834, 2000.

GAM1338 360 AR Lin, S.- Y.; Ohno, S.: The binding of androgen receptor to DNAand RNA. 3 C c

Biochim. Biophys. Acta 654: 181- 186, 1981.

GAM1338 360 AR Lobaccaro, J.- M.; Lumbroso, S.; Belon, C.; Galtier- Dereure, F.;Bringer, J.; Lesimple, T.; Namer, M.; Cutuli, B. F.; Pujol, H.; Sultan,C.: Androgen receptor gene mutation in male breast cancer. Hum.Molec. Genet. 2: 1799- 1802, 1993. 3 C c

GAM1338 360 AR Lubahn, D. B.; Brown, T. R.; Simental, J. A.; Higgs, H. N.; Migeon,C. J.; Wilson, E. M.; French, F. S.: Sequence of the intron/exonjunctions of the coding region of the human androgen receptor geneand identification of a point mutation in a family with complete androgeninsensitivity. Proc. Nat. Acad. Sci. 86: 9534- 9538, 1989. 3 C c

GAM1338 360 AR Lubahn, D. B.; Joseph, D. R.; Sar, M.; Tan, J.; Higgs, H. N.;Larson, R. E.; French, F. S.; Wilson, E. M.: The human androgen receptor:complementary deoxyribonucleic acid cloning, sequence analysis andgene expression in prostate. Molec. Endocr. 2: 1265- 1275, 1988. 3 C c

GAM1338 360 AR Lubahn, D. B.; Joseph, D. R.; Sullivan, P. M.; Willard, H. F.;French, F. S.; Wilson, E. M.: Cloning of human androgen receptorcomplementary DNA and localization to the X chromosome. Science 240:327- 330, 1988. 3 C c

GAM1338 360 AR Lumbroso, S.; Lobaccaro, J. M.; Georget, V.; Leger, J.; Poujol,N.; Terouanne, B.; Evain- Brion, D.; Czernichow, P.; Sultan, C.: Anovel substitution (leu707- to- arg) in exon 4 of the androgen receptorgene causes complete androgen resistance. J. Clin. Endocr. Metab. 81:1984- 1988, 1996. 3 C c

GAM1338 360 AR Lund, A.; Udd, B.; Juvonen, V.; Andersen, P. M.; Cederquist, K.;Davis, M.; Gellera, C.; Kolmel, C.; Ronnevi, L.- O.; Sperfeld, A.- D.;Sorensen, S.- A.; Tranebjaerg, L.; Van Maldergem, L.; Watanabe, M.;Weber, M.; Yeung, L.; Savontaus, M.- L.: Multiple founder effectsin spinal and bulbar muscular atrophy (SBMA, Kennedy disease) aroundthe world. Europ. J. Hum. Genet. 9: 431- 436, 2001. 3 C c

GAM1338 360 AR Macke, J. P.; Hu, N.; Hu, S.; Bailey, M.; King, V. L.; Brown,T.; Hamer, D.; Nathans, J.: Sequence variation in the androgen receptorgene is not a common determinant of male sexual orientation. Am.J. Hum. Genet. 53: 844- 852, 1993. 3 C c

GAM1338 360 AR MacLean, H. E.; Chu, S.; Warne, G. L.; Zajac, J. D.: Relatedindividuals with different androgen receptor gene deletions. J. Clin.Invest. 91: 1123- 1128, 1993. 3 C c

GAM1338 360 AR Madgar, I.; Green, L.; Kent- First, M.; Weissenberg, R.; Gershoni-Baruch,R.; Goldman, B.; Friedman, E.: Genotyping of Israeli infertile menwith idiopathic oligozoospermia. Clin. Genet. 62: 203- 207, 2002. 3 C c

GAM1338 360 AR Marcelli, M.; Tilley, W. D.; Wilson, C. M.; Griffin, J. E.; Wilson,J. D.; McPhaul, M. J.: Definition of the human androgen receptorgene structure permits the identification of mutations that causeandrogen resistance: premature termination of the receptor proteinat amino acid residue 588 causes complete androgen resistance. Molec.Endocr. 4: 1105- 1116, 1990. 3 C c

GAM1338 360 AR Marcelli, M.; Tilley, W. D.; Wilson, C. M.; Wilson, J. D.; Griffin,J. E.; McPhaul, M. J.: A single nucleotide substitution introducesa premature termination codon into the androgen receptor gene of apatient with receptor-negative androgen resistance. J. Clin. Invest. 85:1522- 1528, 1990. 3 C c

GAM1338 360 AR Marcelli, M.; Tilley, W. D.; Zoppi, S.; Griffin, J. E.; Wilson,J. D.; McPhaul, M. J.: Androgen resistance associated with a mutationof the androgen receptor at amino acid 772 (arg- to- cys) results froma combination of decreased messenger ribonucleic acid levels and impairmentof receptor 3 C c

function. J. Clin. Endocr. 73: 318- 325, 1991.

GAM1338 360 AR McCampbell, A.; Taylor, J. P.; Taye, A. A.; Robitschek, J.; Li,M.; Walcott, J.; Merry, D.; Chai, Y.; Paulson, H.; Sobue, G.; Fischbeck,K. H.: CREB-binding protein sequestration by expanded polyglutamine. Hum.Molec. Genet. 9: 2197- 2202, 2000. 3 C c

GAM1338 360 AR McGuire, W. L.; Chamness, G. C.; Fuqua, S. A. W.: Estrogen receptorvariants in clinical breast cancer. Molec. Endocr. 5: 1571- 1577,1991. 3 C c

GAM1338 360 AR McPhaul, M. J.; Griffin, J. E.: Male pseudohermaphroditism causedby mutations of the human androgen receptor. J. Clin. Endocr. Metab. 84:3435-3441, 1999. 3 C c

GAM1338 360 AR McPhaul, M. J.; Marcelli, M.; Tilley, W. D.; Griffin, J. E.; Isidro-Gutierrez,R. F.; Wilson, J. D.: Molecular basis of androgen resistance in afamily with a qualitative abnormality of the androgen receptor andresponsive to high- dose androgen therapy. J. Clin. Invest. 87: 1413-1421,1991. 3 C c

GAM1338 360 AR McPhaul, M. J.; Marcelli, M.; Zoppi, S.; Griffin, J. E.; Wilson,J. D.: Genetic basis of endocrine disease 4: the spectrum of mutationsin the androgen receptor gene that causes androgen resistance. J.Clin. Endocr. Metab. 76: 17- 23, 1993. 3 C c

GAM1338 360 AR McPhaul, M. J.; Marcelli, M.; Zoppi, S.; Wilson, C. M.; Griffin,J. E.; Wilson, J. D.: Mutations in the ligand- binding domain of theandrogen receptor gene cluster in two regions of the gene. J. Clin.Invest. 90: 2097-2101, 1992. 3 C c

GAM1338 360 AR McPhaul, M. J.; Schweikert, H.- U.; Allman, D. R.: Assessmentof androgen receptor function in genital skin fibroblasts using arecombinant adenovirus to deliver an androgen- responsive reportergene. J. Clin. Endocr. Metab. 82: 1944- 1948, 1997. 3 C c

GAM1338 360 AR Mifsud, A.; Ramirez, S.; Yong, E. L.: Androgen receptor geneCAG trinucleotide repeats in anovulatory infertility and polycysticovaries. J. Clin. Endocr. Metab. 85: 3484- 3488, 2000. 3 C c

GAM1338 360 AR Migeon, B. R.; Brown, T. R.; Axelman, J.; Migeon, C. J.: Studiesof the locus for androgen receptor: localization on the human X andevidence for homology with the Tfm locus in the mouse. Proc. Nat.Acad. Sci. 78: 6339- 6343, 1981. 3 C c

GAM1338 360 AR Mongan, N. P.; Jaaskelainen, J.; Green, K.; Schwabe, J. W.; Shimura,N.; Dattani, M.; Hughes, I. A.: Two de novo mutations in the AR genecause the complete androgen insensitivity syndrome in a pair of monozygotictwins. J. Clin. Endocr. Metab. 87: 1057- 1061, 2002. 3 C c

GAM1338 360 AR Mononen, N.; Syrjakoski, K.; Matikainen, M.; Tammela, T. L. J.;Schleutker, J.; Kallioniemi, O.- P.; Trapman, J.; Koivisto, P. A.:Two percent of Finnish prostate cancer patients have a germ- line mutationin the hormone- binding domain of the androgen receptor gene. CancerRes. 60: 6479- 6481, 2000. 3 C c

GAM1338 360 AR Murono, K.; Mendonca, B. B.; Arnhold, I. J. P.; Rigon, A. C. M.M.; Migeon, C. J.; Brown, T. R.: Human androgen insensitivity dueto point mutations encoding amino acid substitutions in the androgenreceptor steroid- binding domain. Hum. Mutat. 6: 152- 162, 1995. 3 C c

GAM1338 360 AR Nakao, R.; Haji, M.; Yanase, T.; Ogo, A.; Takayanagi, R.; Katsube,T.; Fukumaki, Y.; Nawata, H.: A single amino acid substitution (met786- to-val)in the steroid- binding domain of human androgen receptor leads tocomplete androgen insensitivity syndrome. J. Clin. Endocr. Metab. 74:1152-1157, 1992. 3 C c

GAM1338 360 AR Newmark, J. R.; Hardy, D. O.; Tonb, D. C.; Carter, B. S.; Epstein,J. I.; 3 C c
Isaacs, W. B.; Brown, T. R.; Barrack, E. R.: Androgen receptorgene mutations
in human prostate cancer. Proc. Nat. Acad. Sci. 89:6319- 6323, 1992.

GAM1338 360 AR Nguyen, D.; Steinberg, S. V.; Rouault, E.; Chagnon, S.; Gottlieb,B.; Pinsky, 3 C c
L.; Trifiro, M.; Mader, S.: A G577R mutation in the humanAR P box results in
selective decreases in DNA binding and in partialandrogen insensitivity
syndrome. Molec. Endocr. 15: 1790- 1802, 2001.

GAM1338 360 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; 3 C c
Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the
beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990.

GAM1338 360 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: 3 C c
Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11
near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec.
Genet. 16: 401- 405, 1990.

GAM1338 360 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K- 3 C c
ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics
6:697- 699, 1990.

GAM1338 360 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: 3 C c
Identification of a putative isoform of the Na,K- ATPase beta
subunit:primary structure and tissue- specific expression. J. Biol. Chem.
164:4613- 4618, 1989.

GAM1338 360 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: 3 C c
Identification of a cDNA clone specific for the neural adhesionmolecule
AMOG. J. Neurosci. Res. 22: 113- 119, 1989.

GAM1338 360 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- 3 C b
evaluation of 'reactive lymphoid hyperplasia of the uvea':
animmunohistochemical and molecular analysis of 10 cases. Ophthalmology
107:151- 158, 2000.

GAM1338 360 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 3 C b
mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999.

GAM1338 360 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. 3 C b
J.Clin. Path. 48: 395- 397, 1995.

GAM1338 360 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; 3 C b
Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T.
W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of
NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001.

GAM1338 360 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; 3 C b
Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not
its cellular homologue, activates NF- kappa- B transcriptionfactor and c-
Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999.

GAM1338 360 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- 3 C b
Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.;
Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in
t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types
Cell 96: 35- 45, 1999.

GAM1338 360 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic 3 C b
study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer
Genet. Cytogenet. 58: 35- 38, 1992.

GAM1338 360 BDKRB1 Bachvarov, D. R.; Hess, J. F.; Menke, J. G.; Larrivee, J.- F.; Marceau,F.: 3 C c
Structure and genomic organization of the human B(1) receptorgene for kinins

(BDKRB1). Genomics 33: 374- 381, 1996.

GAM1338 360 BDKRB1 Chai, K. X.; Ni, A.; Wang, D.; Ward, D. C.; Chao, J.; Chao, L.: Genomic DNA 3 C c
sequence, expression, and chromosomal localization ofthe human B1 bradykinin
receptor gene BDKRB1. Genomics 31: 51- 57,1996.

GAM1338 360 BDKRB1 MacNeil, T.; Bierilo, K. K.; Menke, J. G.; Hess, J. F.: Cloningand 3 C c
pharmacological characterization of a rabbit bradykinin B- 1 receptor.
Biochim.Biophys. Acta 1264: 223- 228, 1995.

GAM1338 360 BDKRB1 Menke, J. G.; Borkowski, J. A.; Bierilo, K. K.; MacNeil, T.; Derrick,A. W.; 3 C c
Schneck, K. A.; Ransom, R. W.; Strader, C. D.; Linemeyer, D.L.; Hess, J. F.:
Expression cloning of a human B1 bradykinin receptor. J.Biol. Chem. 269:
21583- 21586, 1994.

GAM1338 360 BDKRB1 Yang, X.; Polgar, P.: Genomic structure of the human bradykininB(1) receptor 3 C c
gene and preliminary characterization of its regulatoryregions. Biochem.
Biophys. Res. Commun. 222: 718- 725, 1996.

GAM1338 360 BDP1 Kelter, A.- R.; Herchenbach, J.; Wirth, B.: The transcription factor- 3 C b
likenuclear regulator (TFNR) contains a novel 55- amino- acid motif
repeatednine times and maps closely to SMN1. Genomics 70: 315- 326, 2000.

GAM1338 360 BDP1 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 C b
TFIIB activities direct RNA polymerase III transcription fromTATA-
containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM1338 360 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 C c
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM1338 360 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 C c
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM1338 360 CASP2 Bergeron, L.; Perez, G. I.; Macdonald, G.; Shi, L.; Sun, Y.; Jurisicova,A.; 3 C c
Varmuza, S.; Latham, K. E.; Flaws, J. A.; Salter, J. C. M.; Hara,H.;
Moskowitz, M. A.; Li, E.; Greenberg, A.; Tilly, J. L.; Yuan, J.: Defects in
regulation of apoptosis in caspase- 2- deficient mice. GenesDev. 12: 1304-
1314, 1998.

GAM1338 360 CASP2 Kumar, S.; Kinoshita, M.; Noda, M.; Copeland, N. G.; Jenkins, N.A.: 3 C c
Induction of apoptosis by the mouse Nedd2 gene, which encodesa protein
similar to the product of the Caenorhabditis elegans celldeath gene ced- 3
and the mammalian IL- 1- beta- converting enzyme. GenesDev. 8: 1613- 1626,
1994.

GAM1338 360 CASP2 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 3 C c
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM1338 360 CASP2 Kumar, S.; White, D. L.; Takai, S.; Turczynowicz, S.; Juttner,C. A.; Hughes, 3 C c
T. P.: Apoptosis regulatory gene NEDD2 maps to humanchromosome segment 7q34-
35, a region frequently affected in haematologicalneoplasms. Hum. Genet. 95:
641- 644, 1995.

GAM1338 360 CASP2 Lassus, P.; Opitz- Araya, X.; Lazebnik, Y.: Requirement for caspase- 2in 3 C c
stress- induced apoptosis before mitochondrial permeabilization. Science
297:1352- 1354, 2002.

GAM1338 360 CASP2 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; 3 C c
Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes,
CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem.
Biophys. Res. Commun. 225: 983- 989, 1996.

GAM1338 360 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 C b
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM1338 360 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 C b
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM1338 360 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 C b
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM1338 360 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 C b
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM1338 360 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 C b
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell
death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM1338 360 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 C b
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM1338 360 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 C b
Caspase- 8 is required for cell death induced by expanded
polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM1338 360 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 C b
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM1338 360 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 C c
member of a multigene family. Genomics 52: 332- 341, 1998.

GAM1338 360 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 C c
new member of the MTG8/ETO gene family, maps on 20q11region and is deleted
in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM1338 360 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 C c
Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic
fusion protein forms a complex with a novel member of theMTG8(ETO/CDR)
family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM1338 360 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. 3 C c
J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis
machinery through a novel motif, the F- box. Cell 86:263- 274, 1996.

GAM1338 360 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; 3 C c
Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene
(CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics
24:27- 33, 1994.

GAM1338 360 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F 3 C c

maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6: 149- 150, 1995.

GAM1338 360 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a membrane- associated C- type lectin that exhibits CD4- independentbinding of human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad. Sci. 89: 8356- 8360, 1992. 3 C b

GAM1338 360 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR. Science 294: 2163- 2166, 2001. 3 C b

GAM1338 360 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S. L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-infection of T cells. Cell 100: 587- 597,2000. 3 C b

GAM1338 360 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000. 3 C b

GAM1338 360 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000. 3 C b

GAM1338 360 CDC6 Saha, P.; Chen, J.; Thome, K. C.; Lawlis, S. J.; Hou, Z.- H.; Hendricks,M.; Parvin, J. D.; Dutta, A.: Human CDC6/Cdc18 associates with Orc1and cyclin-cdk and is selectively eliminated from the nucleus at theonset of S phase. Molec. Cell. Biol. 18: 2758- 2767, 1998. 3 C c

GAM1338 360 CDC6 Williams, R. S.; Shohet, R. V.; Stillman, B.: A human proteinrelated to yeast Cdc6p. Proc. Nat. Acad. Sci. 94: 142- 147, 1997. 3 C c

GAM1338 360 CDC6 Yan, Z.; DeGregori, J.; Shohet, R.; Leone, G.; Stillman, B.; Nevins,J. R.; Williams, R. S.: Cdc6 is regulated by E2F and is essentialfor DNA replication in mammalian cells. Proc. Nat. Acad. Sci. 95:3603- 3608, 1998. 3 C c

GAM1338 360 CDC6 Yan, Z.; Fedorov, S. A.; Mumby, M. C.; Williams, R. S.: PR48,a novel regulatory subunit of protein phosphatase 2A, interacts withCdc6 and modulates DNA replication in human cells. Molec. Cell. Biol. 20:1021- 1029, 2000. 3 C c

GAM1338 360 CDH17 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999. 3 C c

GAM1338 360 CDH17 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck, P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with a protein related to the cadherin superfamily. Science 264:430- 433, 1994. 3 C c

GAM1338 360 CDH17 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, D. F.: Localization of human cadherin genes to chromosomeregions exhibiting cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998. 3 C c

GAM1338 360 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.; Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.; Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for Muckle- Wells syndrome and familial cold urticaria:a novel mutation underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002. 3 C c

GAM1338 360 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, 3 C c
E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile
neurological cutaneous and articular syndromeis caused by mutations in
CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes.
Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM1338 360 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. 3 C c
D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes
familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature
Genet. 29: 301- 305, 2001.

GAM1338 360 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 C c
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM1338 360 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 C b
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.:
Identification of a novel, dendritic cell- associated molecule,dectin- 1, by
subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM1338 360 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 3 C b
37, 2001.

GAM1338 360 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: 3 C b
Cloning of human dectin- 1, a novel C- type lectin- like receptorgene
expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001.

GAM1338 360 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification 3 C b
of a human homologue of the dendritic cell- associatedC- type lectin- 1,
dectin- 1. Gene 272: 51- 60, 2001.

GAM1338 360 CNN2 Cheng, J.- F.; Boyartchuk, V.; Zhu, Y.: Isolation and mapping ofhuman 3 C b
chromosome 21 cDNA: progress in constructing a chromosome 21expression map.
Genomics 23: 75- 84, 1994.

GAM1338 360 CNN2 Masuda, H.; Tanaka, K.; Takagi, M.; Ohgami, K.; Sakamaki, T.; Shibata,N.; 3 C b
Takahashi, K.: Molecular cloning and characterization of humannon- smooth
muscle calponin. J. Biochem. 120: 415- 424, 1996.

GAM1338 360 CNP Bernier, L.; Colman, D. R.; D'Eustachio, P.: Chromosomal locationsof genes 3 C c
encoding 2- prime,3- prime cyclic nucleotide 3- prime- phosphodiesteraseand
glial fibrillary acidic protein in the mouse. J. Neurosci. Res. 20:497- 504,
1988.

GAM1338 360 CNP Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J.: 2- prime,3- prime- 3 C c
cyclicnucleotide 3- prime- phosphodiesterase: a membrane- bound,
microtubule- associatedprotein and membrane anchor for tubulin. Proc. Nat.
Acad. Sci. 99:1807- 1812, 2002.

GAM1338 360 CNP Douglas, A. J.; Fox, M. F.; Abbott, C. M.; Hinks, L. J.; Sharpe,G.; Povey, 3 C c
S.; Thompson, R. J.: Structure and chromosomal localizationof the human 2-
prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasegene. Ann. Hum.
Genet. 56: 243- 254, 1992.

GAM1338 360 CNP Douglas, A. J.; Fox, M. F.; Hinks, L. J.; Povey, S.; Thompson,R. J.: 3 C c
Localization of the myelin specific enzyme 2- prime,3- prime-
cyclicnucleotide- 3- prime- phosphohydrolase to 17q21. (Abstract)
Cytogenet.Cell Genet. 58: 2004 only, 1991.

GAM1338 360 CNP Kurihara, T.; Monoh, K.; Sakimura, K.; Takahashi, Y.: Alternativesplicing of 3 C c

mouse brain 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasemRNA. Biochem. Biophys. Res. Commun. 170: 1074- 1081, 1990.

GAM1338 360 CNP Monoh, K.; Kurihara, T.; Takahashi, Y.; Ichikawa, T.; Kumanishi,T.; Hayashi, 3 C c
S.; Minoshima, S.; Shimizu, N.: Structure, expressionand chromosomal localization of the gene encoding human 2- prime,3- prime- cyclic-nucleotide3- prime- phosphodiesterase. Gene 129: 297- 301, 1993.

GAM1338 360 CNP Sprinkle, T. J.; Kouri, R. E.; Fain, P. D.; Stoming, T. A.; Whitney,J. B., 3 C c
III: Chromosomal mapping of the human CNP gene using a meioticcrossover DNA panel, PCR, and allele- specific probes. Genomics 16:542- 545, 1993.

GAM1338 360 CNP Sprinkle, T. J.; Lanclos, K. D.; Lapp, D. F.: Assignment of thehuman 2- 3 C c
prime,3- prime- cyclic nucleotide 3- prime- phosphohydrolase geneto chromosome 17. Genomics 13: 877- 880, 1992.

GAM1338 360 CNP Vogel, U. S.; Thompson, R. J.: Molecular structure, localization,and 3 C c
possible functions of the myelin- associated enzyme 2- prime,3- prime-cyclicnucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667-1677,1988.

GAM1338 360 CRSP6 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, 3 C c
Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC complexes indicates novel pathways for the functionof nuclear receptors and diverse mammalian activators. Molec. Cell 3:361- 370, 1999.

GAM1338 360 CRSP6 Jiang, Y.- W.; Veschambre, P.; Erdjument- Bromage, H.; Tempst, P.;Conaway, 3 C c
J. W.; Conaway, R. C.; Kornberg, R. D.: Mammalian mediatorof transcriptional regulation and its possible role as an end- pointof signal transduction pathways. Proc. Nat. Acad. Sci. 95: 8538- 8543,1998.

GAM1338 360 CRSP6 Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R.: The transcriptionalcofactor 3 C c
complex CRSP is required for activity of the enhancer- bindingprotein Sp1. Nature 397: 446- 450, 1999.

GAM1338 360 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, 3 C c
A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359, 1997.

GAM1338 360 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; 3 C c
Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix Biol. 18: 319- 324, 1999.

GAM1338 360 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; 3 C c
Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of the gene encoding human cartilage associatedprotein (CRTAP). Cytogenet. Cell Genet. 87: 191- 194, 1999.

GAM1338 360 CSNK2A2 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation 3 C c
of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002.

GAM1338 360 CSNK2A2 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; 3 C c
Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine 392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292, 2001.

GAM1338 360 CSNK2A2 Lozeman, F. J.; Litchfield, D. W.; Piening, C.; Takio, K.; Walsh,K. A.; 3 C c
Krebs, E. G.: Isolation and characterization of human cDNAclones encoding the alpha and the alpha- prime subunits of casein kinaseII. Biochemistry 29: 8436- 8447, 1990.

GAM1338 360 CSNK2A2 Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C.: Globozoospermiain mice lacking the casein kinase II alpha- prime catalytic subunit. NatureGenet. 23: 118- 121, 1999. 3 C c

GAM1338 360 CSNK2A2 Yang- Feng, T. L.; Naiman, T.; Kopatz, I.; Eli, D.; Dafni, N.; Canaani,D.: Assignment of the human casein kinase II alpha- prime subunitgene (CSNK2A1) to chromosome 16p13.2- p13.3. Genomics 19: 173 only,1994. 3 C c

GAM1338 360 CSNK2A2 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping of the human casein kinase II catalytic subunit genes: twoloci carrying the homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125- 7129, 1991. 3 C c

GAM1338 360 CTF1 Bordet, T.; Lesbordes, J.- C.; Rouhani, S.; Castelnau- Ptakhine,L.; Schmalbruch, H.; Haase, G.; Kahn, A.: Protective effects of cardiotrophin- 1adenoviral gene transfer on neuromuscular degeneration in transgenicALS mice. Hum. Molec. Genet. 10: 1925- 1933, 2001. 3 C c

GAM1338 360 CTF1 Pennica, D.; Arce, V.; Swanson, T. A.; Vejsada, R.; Pollock, R.A.; Armanini, M.; Dudley, K.; Phillips, H. S..; Rosenthal, A.; Kato,A. C.; Henderson, C. E.: Cardiotrophin- 1, a cytokine present in embryonicmuscle, supports long- term survival of spinal motoneurons. Neuron 17:63- 74, 1996. 3 C c

GAM1338 360 CTF1 Pennica, D.; King, K. L.; Shaw, K. J.; Luis, E.; Rullamas, J.;Luoh, S.- M.; Darbonne, W. C.; Knutzon, D. S.; Yen, R.; Chien, K. R.;Baker, J. B.; Wood, W. I.: Expression cloning of cardiotrophin 1,a cytokine that induces cardiac myocyte hypertrophy. Proc. Nat. Acad.Sci. 92: 1142- 1146, 1995. 3 C c

GAM1338 360 CTF1 Pennica, D.; Swanson, T. A.; Shaw, K. J.; Kuang, W.- J.; Gray, C.L.; Beatty, B. G.; Wood, W. I.: Human cardiotrophin- 1: protein andgene structure, biological and binding activities, and chromosomallocalization. Cytokine 8: 183- 189, 1996. 3 C c

GAM1338 360 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H, L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245, 1997. 3 C b

GAM1338 360 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S controls the trafficking and maturation of MHC class IImolecules in dendritic cells. J. Cell Biol. 147: 775- 790, 1999. 3 C b

GAM1338 360 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. J.; Chapman, H. A.: Structure and chromosomal assignmentof the human cathepsin K gene. Genomics 41: 258- 262, 1997. 3 C b

GAM1338 360 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.; Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell selection and maturation by cathepsin S. Immunity 15:909- 919, 2001. 3 C b

GAM1338 360 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: Molecular cloning and expression of human alveolar macrophagecathepsin S, an elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992. 3 C b

GAM1338 360 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization, gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536, 1994. 3 C b

GAM1338 360 CXCL16 Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G.: A transmembrane CXC chemokine is a ligand for HIV- coreceptor Bonzo. 3 C c

NatureImmun. 1: 298- 304, 2000.

GAM1338 360 CXCL16 Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.;Kita, T.; Yonehara, S.: Molecular cloning of a novel scavenger receptorfor oxidized low density lipoprotein, SR- PSOX, on macrophages. J.Biol. Chem. 275: 40663- 40666, 2000. 3 C c

GAM1338 360 CXCL16 Wilbanks, A.; Zondlo, S. C.; Murphy, K.; Mak, S.; Soler, D.; Langdon,P.; Andrew, D. P.; Wu, L.; Briskin, M.: Expression cloning of theSTRL33/BONZO/TYMSTR ligand reveals elements of CC, CXC, CX3C chemokines. J.Immun. 166: 5145- 5154, 2001. 3 C c

GAM1338 360 CXCL6 Modi, W. S.; Chen, Z.- Q.: Localization of the human CXC chemokinesubfamily on the long arm of chromosome 4 using radiation hybrids. Genomics 47:136- 139, 1998. 3 C c

GAM1338 360 CXCL6 O'Donovan, N.; Galvin, M.; Morgan, J. G.: Physical mapping ofthe CXC chemokine locus on human chromosome 4. Cytogenet. Cell Genet. 84:39- 42, 1999. 3 C c

GAM1338 360 CXCL6 Proost, P.; Wuyts, A.; Conings, R.; Lenaerts, J.- P.; Billiau, A.;Opdenakker, G.; Van Damme, J.: Human and bovine granulocyte chemotacticprotein- 2: complete amino acid sequence and functional characterizationas chemokines. Biochemistry 32: 10170- 10177, 1993. 3 C c

GAM1338 360 CXCL6 Rovai, L. E.; Herschman, H. R.; Smith, J. B.: Cloning and characterizationof the human granulocyte chemotactic protein- 2 gene. J. Immun. 158:5257- 5266, 1997. 3 C c

GAM1338 360 CXCL6 Wuyts, A.; van Osselaer, N.; Haelens, A.; Samson, I.; Herdewijn,P.; Ben- Baruch, A.; Oppenheim, J. J.; Proost, P.; van Damme, J.:Characterization of synthetic human granulocyte chemotactic protein2: usage of chemokine receptors CXCR1 and CXCR2 and in vivo inflammatoryproperties. Biochemistry 36: 2716- 2723, 1997. 3 C c

GAM1338 360 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996. 3 C b

GAM1338 360 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989. 3 C b

GAM1338 360 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000. 3 C b

GAM1338 360 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. L.: The contribution of genetically determined oxidationstatus to inter- individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983. 3 C b

GAM1338 360 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986. 3 C b

GAM1338 360 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. Endocr. 3: 1399- 1408, 1989. 3 C b

GAM1338 360 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the 3 C b

3- prime nontranslated region, and localization ofgene to chromosome 15. J. Exp. Path. 3: 1- 17, 1987.

GAM1338 360 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996. 3 C b

GAM1338 360 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 C b

GAM1338 360 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 3 C b

GAM1338 360 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 3 C b

GAM1338 360 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 3 C b

GAM1338 360 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002. 3 C b

GAM1338 360 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 3 C b

GAM1338 360 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 C b

GAM1338 360 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 3 C b

GAM1338 360 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene: molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230, 1998. 3 C b

GAM1338 360 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii-Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in humanpolymorphonuclear leukocytes: cDNA cloning and expression of leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993. 3 C b

GAM1338 360 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 C b

GAM1338 360 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 C b

GAM1338 360 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4-alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 C b

GAM1338 360 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; 3 C b

Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000.

GAM1338 360 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461- 8466, 1998. 3 C b

GAM1338 360 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997. 3 C b

GAM1338 360 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998. 3 C b

GAM1338 360 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila- relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997. 3 C c

GAM1338 360 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998. 3 C c

GAM1338 360 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994. 3 C c

GAM1338 360 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997. 3 C c

GAM1338 360 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993. 3 C c

GAM1338 360 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997. 3 C c

GAM1338 360 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, D. J.; Muir, W. J.: Schizophrenia and affective disorders- - cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001. 3 C c

GAM1338 360 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 355:771- 772, 2000. 3 C c

GAM1338 360 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 3 C c

GAM1338 360 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 3 C c

GAM1338 360 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. 3 C c
S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood,
D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation
co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000.

GAM1338 360 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, 3 C c
G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced
autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM1338 360 DNAH11 Arnold, G. L.; Bixler, D.; Girod, D.: Probable autosomal 3 C c
recessiveinheritance of polysplenia, situs inversus and cardiac defects inan
Amish family. Am. J. Med. Genet. 16: 35- 42, 1983.

GAM1338 360 DNAH11 Brueckner, M.; D'Eustachio, P.; Horwich, A. L.: Linkage mappingof a mouse 3 C c
gene, iv, that controls left- right asymmetry of the heartand viscera. Proc.
Nat. Acad. Sci. 86: 5035- 5038, 1989.

GAM1338 360 DNAH11 Chapelin, C.; Duriez, N.; Magnino, F.; Goossens, M.; Escudier,E.; Amselem, 3 C c
S.: Isolation of several human axonemal dynein heavychain genes: genomic
structure of the catalytic site, phylogeneticanalysis and chromosomal
assignment. FEBS Lett. 412: 325- 330, 1997.

GAM1338 360 DNAH11 Hanzlik, A. J.; Binder, M.; Layton, W. M.; Rowe, L.; Layton, M.;Taylor, B. 3 C c
A.; Osemlak, M. M.; Richards, J. E.; Kurnit, D. M.; Stewart,G. D.: The
murine situs inversus viscerum (iv) gene responsiblefor visceral asymmetry
is linked tightly to the Igh- C cluster on chromosome12. Genomics 7: 389-
393, 1990.

GAM1338 360 DNAH11 McGrath, J.; Horwich, A. L.; Brueckner, M.: Duplication/deficiencymapping of 3 C c
situs inversus viscerum (iv), a gene that determines left- rightasymmetry in
the mouse. Genomics 14: 643- 648, 1992.

GAM1338 360 DNAH11 Nonaka, S.; Shiratori, H.; Saijoh, Y.; Hamada, H.: Determinationof left- 3 C c
right patterning of the mouse embryo by artificial nodal flow. Nature
418:96- 99, 2002.

GAM1338 360 DNAH11 Okada, Y.; et al.; et al: Abnormal nodal flow precedes situs inversusin iv 3 C c
and inv mice. Molec. Cell 4: 459- 468, 1999.

GAM1338 360 DNAH11 Supp, D. M.; Witte, D. P.; Potter, S. S.; Brueckner, M.: Mutationof an 3 C c
axonemal dynein affects left- right asymmetry in inversus viscerummice.
Nature 389: 963- 966, 1997.

GAM1338 360 DNAH11 Supp, D.; et al.; et al: Targeted deletion of the ATP bindingdomain of left- 3 C c
right dynein confirms its role in specifying developmentof left- right
asymmetries. Development 126: 5495- 5504, 1999.

GAM1338 360 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, 3 C c
T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and
desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995.

GAM1338 360 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, 3 C c
H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin.
J. Biol. Chem. 269: 26295- 26302, 1994.

GAM1338 360 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The 3 C c
desmocollins of human foreskin epidermis: identification and
chromosomalassignment of a third gene and expression patterns of the three
isoforms. J.Invest. Derm. 105: 314- 321, 1995.

GAM1338 360 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; 3 C c
Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.:
Neurodevelopmental delay, motor abnormalities and cognitive deficitsin

transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001.

GAM1338 360 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262- 265, 1997. 3 C c

GAM1338 360 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A potassium channel mutation in weaver mice implicates membraneexcitability in granule cell differentiation. Nature Genet. 11:126- 129, 1995. 3 C c

GAM1338 360 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk gene from 'the Down syndrome critical region' of chromosome 21. Biochem.Biophys. Res. Commun. 225: 92- 99, 1996. 3 C c

GAM1338 360 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.; Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in transgenic mice implicates minibrain in learningdefects associated with Down syndrome. Nature Genet. 16: 28- 36,1997. 3 C c

GAM1338 360 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to chromosome 16, localizes to the nucleus, and can form multimers. Biochem.Biophys. Res. Commun. 231: 640- 644, 1997. 3 C c

GAM1338 360 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.; Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the Drosophila minibrain gene: human homologue maps to 21q22.2in the Down syndrome 'critical region.' Genomics 38: 331- 339, 1996. 3 C c

GAM1338 360 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein kinase family involved in postembryonic neurogenesisin Drosophila. Neuron 14: 287- 301, 1995. 3 C c

GAM1338 360 EBAF Burdine, R. D.; Schier, A. F.: Conserved and divergent mechanismsin left- right axis formation. Genes Dev. 14: 763- 776, 2000. 3 C c

GAM1338 360 EBAF Kosaki, K.; Bassi, M. T.; Kosaki, R.; Lewin, M.; Belmont, J.; Schauer,G.; Casey, B.: Characterization and mutation analysis of human LEFTYA and LEFTY B, homologues of murine genes implicated in left- rightaxis development. Am. J. Hum. Genet. 64: 712- 721, 1999. 3 C c

GAM1338 360 EBAF Kothapalli, R.; Buyuksal, I.; Wu, S.- Q.; Chegini, N.; Tabibzadeh,S.: Detection of ebaf, a novel human gene of the transforming growthfactor beta superfamily: association of gene expression with endometrialbleeding. J. Clin. Invest. 99: 2342- 2350, 1997. 3 C c

GAM1338 360 EBAF Meno, C.; Itoh, Y.; Saijoh, Y.; Matsuda, Y.; Tashiro, K.; Kuhara,S.; Hamada, H.: Two closely- related left- right asymmetrically expressedgenes, lefty- 1 and lefty- 2: their distinct expression domains, chromosomallinkage and direct neuralizing activity in Xenopus embryos. GenesCells 2: 513- 524, 1997. 3 C c

GAM1338 360 EBAF Meno, C.; Saijoh, Y.; Fujii, H.; Ikeda, M.; Yokoyama, T.; Yokoyama,M.; Toyoda, Y.; Hamada, H.: Left- right asymmetric expression of theTGF- beta- family member lefty in mouse embryos. Nature 381: 151- 155,1996. 3 C c

GAM1338 360 EBAF Meno, C.; Shimono, A.; Saijoh, Y.; Yashiro, K.; Mochida, K.; Ohishi,S.; Noji, S.; Kondoh, H.; Hamada, H.: Lefty- 1 is required for left- rightdetermination as a regulator of lefty- 2 and nodal. Cell 94: 287- 3 C c

297,1998.

GAM1338 360 EBAF Tabibzadeh, S.; Mason, J. M.; Shea, W.; Cai, Y.; Murray, M. J.;Lessey, B.: 3 C c
Dysregulated expression of ebaf, a novel molecular defectin the endometria
of patients with infertility. J. Clin. Endocr.Metab. 85: 2526- 2536, 2000.

GAM1338 360 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- 3 C c
elongationfactor 2 kinase (calmodulin- dependent protein kinase III)
antibodiesin patients with systemic lupus erythematosus. Biochem.
Biophys.Res. Commun. 293: 1073- 1076, 2002.

GAM1338 360 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 3 C c
Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C.
R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein
kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat.
Acad. Sci. 94: 4884- 4889, 1997.

GAM1338 360 EHD1 Di Fiore, P. P.; Pelicci, P. G.; Sorkin, A.: EH: a novel protein- 3 C c
proteininteraction domain potentially involved in intracellular sorting.
TrendsBiochem. Sci. 22: 411- 413, 1997.

GAM1338 360 EHD1 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 3 C c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.;
Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.;
Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the
2.8- Mb region containing the multiple endocrineneoplasia type 1 locus.
Genome Res. 7: 725- 735, 1997.

GAM1338 360 EHD1 Haider, N. B.; Searby, C.; Galperin, E.; Mintz, L.; Horowitz, M.;Stone, E. 3 C c
M.; Sheffield, V. C.: Evaluation and molecular characterizationof EHD1, a
candidate gene for Bardet- Biedl syndrome 1 (BBS1). Gene 240:227- 232, 1999.

GAM1338 360 EHD1 Mintz, L.; Galperin, E.; Pasmanik- Chor, M.; Tulzinsky, S.; Bromberg,Y.; 3 C c
Kozak, C. A.; Joyner, A.; Fein, A.; Horowitz, M.: EHD1- - an EH- domain-
containingprotein with a specific expression pattern. Genomics 59: 66-
76,1999.

GAM1338 360 EHD1 Rotem- Yehudar, R.; Galperin, E.; Horowitz, M.: Association ofinsulin- like 3 C c
growth factor 1 receptor with EHD1 and SNAP29. J. Biol.Chem. 276: 33054-
33060, 2001.

GAM1338 360 EIF2S3 Ehrmann, I. E.; Ellis, P. S.; Mazeyrat, S.; Duthie, S.; Brockdorff,N.; 3 C c
Mattei, M. G.; Gavin, M. A.; Affara, N. A.; Brown, G. M.; Simpson,E.;
Mitchell, M. J.; Scott, D. M.: Characterization of genes encodingtranslation
initiation factor eIF- 2- gamma in mouse and human: sexchromosome
localization, escape from X- inactivation and evolution. Hum.Molec. Genet.
7: 1725- 1737, 1998.

GAM1338 360 EIF2S3 Gasper, N. J.; Kinzy, T. G.; Scherer, B. J.; Humbelin, M.; Hershey,J. W. B.; 3 C c
Merrick, W. C.: Translation initiation factor eIF- 2: cloningand expression
of the human cDNA encoding the gamma- subunit. J. Biol.Chem. 269: 3415-
3422, 1994.

GAM1338 360 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 C b
Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system
for platelet activation. Nature 394: 690- 694, 1998.

GAM1338 360 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 C b
M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin.
Nature 404: 609- 613, 2000.

GAM1338 360 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 C b
Role of thrombin signalling in platelets in haemostasis andthrombosis.

Nature 413: 74- 78, 2001.

GAM1338 360 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998. 3 C b

GAM1338 360 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985. 3 C b

GAM1338 360 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985. 3 C b

GAM1338 360 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988. 3 C b

GAM1338 360 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional analysis of the human tissue factor promoter and inductionby serum. Proc. Nat. Acad. Sci. 87: 2254- 2258, 1990. 3 C b

GAM1338 360 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: Completesequence of the human tissue factor gene, a highly regulated cellularreceptor that initiates the coagulation protease cascade. Biochemistry 28:1755- 1762, 1989. 3 C b

GAM1338 360 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand mapping of RFLPs for human tissue factor (HTF) to chromosome 1p. NucleicAcids Res. 15: 9098 only, 1987. 3 C b

GAM1338 360 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA sequenceand chromosome localization of the gene. Biochemistry 26: 5234- 5238,1987. 3 C b

GAM1338 360 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA clones coding for human tissue factor: primary structureof the protein and cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987. 3 C b

GAM1338 360 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad. Sci. 94: 6922- 6926, 1997. 3 C b

GAM1338 360 F8A Inaba, H.; Fujimaki, M.; Kazazian, H. H., Jr.; Antonarakis, S.E.: MspI polymorphic site in intron 22 of the factor VIII gene inthe Japanese population. Hum. Genet. 84: 214- 215, 1990. 3 C c

GAM1338 360 F8A Levinson, B.; Bermingham, J. R., Jr.; Metzenberg, A.; Kenwrick,S.; Chapman, V.; Gitschier, J.: Sequence of the human factor VIII- associatedgene is conserved in mouse. Genomics 13: 862- 865, 1992. 3 C c

GAM1338 360 F8A Levinson, B.; Kenwrick, S.; Lakich, D.; Hammonds, G.; Gitschier,J.: A transcribed gene in an intron of the human factor VIII gene. Genomics 7:1- 11, 1990. 3 C c

GAM1338 360 F8A Peters, M. F.; Ross, C. A.: Isolation of a 40- kDa huntingtin- associatedprotein. J. Biol. Chem. 276: 3188- 3194, 2001. 3 C c

GAM1338 360 FANCE Buchwald, M.: Complementation groups: one or more per gene? NatureGenet. 11: 228- 230, 1995. 3 C c

GAM1338 360 FANCE de Winter, J. P.; Leveille, F.; van Berkel, C. G. M.; Rooimans,M. A.; van 3 C c

der Weel, L.; Steltenpool, J.; Demuth, I.; Morgan, N. V.;Alon, N.; Bosnoyan-Collins, L.; Lightfoot, J.; Leegwater, P. A.; Waisfisz,Q.; Komatsu, K.; Arwert, F.; Pronk, J. C.; Mathew, C. G.; Digweed,M.; Buchwald, M.; Joenje, H.: Isolation of a cDNA representing theFanconi anemia complementation group E gene. Am. J. Hum. Genet. 67:1306- 1308, 2000. Note: Erratum: Am. J. Hum. Genet. 67: 1365 only,2000.

GAM1338 360 FANCE Joenje, H.: Fanconi anaemia complementation groups in Germanyand The 3 C c
Netherlands. Hum. Genet. 97: 280- 282, 1996.

GAM1338 360 FANCE Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G.M.; Rooimans, 3 C c
M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J.J. P.; Buchwald, M.; Arwert, F.: Classification of Fanconi anemiapatients by complementation analysis: evidence for a fifth geneticsubtype. Blood 86: 2156- 2160, 1995.

GAM1338 360 FANCE Joenje, H.; Oostra, A. B.; Wijker, M.; di Summa, F. M.; van Berkel,C. G. M.; 3 C c
Rooimans, M. A.; Ebell, W.; van Weel, M.; Pronk, J. C.;Buchwald, M.; Arwert, F.: Evidence for at least eight Fanconi anemiagenes. Am. J. Hum. Genet. 61: 940- 944, 1997.

GAM1338 360 FANCE Pace, P.; Johnson, M.; Tan, W. M.; Mosedale, G.; Sng, C.; Hoatlin,M.; de 3 C c
Winter, J.; Joenje, H.; Gergely, F.; Patel, K. J.: FANCE:the link between Fanconi anaemia complex assembly and activity. EMBOJ. 21: 3414- 3423, 2002.

GAM1338 360 FANCE Waisfisz, Q.; Saar, K.; Morgan, N. V.; Altay, C.; Leegwater, P.A.; de 3 C c
Winter, J. P.; Komatsu, K.; Evans, G. R.; Wegner, R.- D.; Reis,A.; Joenje, H.; Arwert, F.; Mathew, C. G.; Pronk, J. C.; Digweed,M.: The Fanconi anemia group E gene, FANCE, maps to chromosome 6p. Am.J. Hum. Genet. 64: 1400-1405, 1999.

GAM1338 360 FANCE Wegner, R.- D.; Henrichs, I.; Joenje, H.; Schroeder- Kurth, T.:Fanconi 3 C c
anemia complementation group E: clinical and cytogenetic dataof the first patient. Clin. Genet. 50: 479- 482, 1996.

GAM1338 360 FBXL7 Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; 3 C c
Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol. 9: 1177- 1179, 1999.

GAM1338 360 FBXL7 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 C c
and expression analysis of new members of the mammalianF- box protein family. Genomics 67: 40- 47, 2000.

GAM1338 360 FBXL7 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5: 355- 364, 1998.

GAM1338 360 FBXL7 Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A 3 C c
family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999.

GAM1338 360 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: 3 C c
Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995.

GAM1338 360 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; 3 C c
Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992.

GAM1338 360 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: 3 C c
Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665-1672, 1990.

GAM1338 360 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. 3 C c

L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681-1685, 1993.

GAM1338 360 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 3 C c

GAM1338 360 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 3 C c

GAM1338 360 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 3 C c

GAM1338 360 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001. 3 C c

GAM1338 360 FCGR2A Grundy, H. O.; Peltz, G.; Barsh, G.; Moore, K.; Golbus, M. S.;Lebo, R. V.: Immunoglobulin G Fc receptor II and Fc receptor IIIgenes map to chromosome 1 by spot- blot chromosome analysis. (Abstract) Am.J. Hum. Genet. 43: A145, 1988. 3 C b

GAM1338 360 FCGR2A Grundy, H. O.; Peltz, G.; Moore, K. W.; Golbus, M. S.; Jackson,L. G.; Lebo, R. V.: The polymorphic Fc- gamma receptor II gene mapsto human chromosome 1q. Immunogenetics 29: 331- 339, 1989. 3 C b

GAM1338 360 FCGR2A Hibbs, M. L.; Bonadonna, L.; Scott, B. M.; McKenzie, I. F. C.;Hogarth, P. M.: Molecular cloning of a human immunoglobulin G Fcreceptor. Proc. Nat. Acad. Sci. 85: 2240- 2244, 1988. 3 C b

GAM1338 360 FCGR2A Hibbs, M. L.; Hogarth, P. M.; McKenzie, I. F. C.: The mouse Ly- 17locus identifies a polymorphism of the Fc receptor. Immunogenetics 22:335- 348, 1985. 3 C b

GAM1338 360 FCGR2A Lebo, R. V.; Lynch, E. D.; Wiegant, J.; Moore, K.; Trounstine,M.; van der Ploeg, M.: Multicolor fluorescence in situ hybridizationand pulsed field electrophoresis dissect CMT1B gene region. Hum.Genet. 88: 13- 20, 1991. 3 C b

GAM1338 360 FCGR2A Moser, K. L.; Neas, B. R.; Salmon, J. E.; Yu, H.; Gray- McGuire,C.; Asundi, N.; Bruner, G. R.; Fox, J.; Kelly, J.; Henshall, S.; Bacino,D.; Dietz, M.; Hogue, R.; Koelsch, G.; Nightingale, L.; Shaver, T.;Abdou, N. I.; Albert, D. A.; Carson, C.; Petri, M.; Treadwell, E.L.; James, J. A.; Harley, J. B.: Genome scan of human systemic lupuserythematosus: evidence for linkage on chromosome 1q in African- Americanpedigrees. Proc. Nat. Acad. Sci. 95: 14869- 14874, 1998. 3 C b

GAM1338 360 FCGR2A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human DNA. Hum. Molec. Genet. 1: 613- 620,1992. 3 C b

GAM1338 360 FCGR2A Peltz, G. A.; Grundy, H. O.; Lebo, R. V.; Yssel, H.; Barsh, G.S.; Moore, K. W.: Human Fc- gamma- RIII: cloning, expression, and identificationof the chromosomal locus of two Fc receptors for IgG. Proc. Nat.Acad. Sci. 86: 1013- 1017, 1989. 3 C b

GAM1338 360 FCGR2A Qiu, W. Q.; de Bruin, D.; Brownstein, B. H.; Pearse, R.; Ravetch,J. V.: Organization of the human and mouse low- affinity Fc- gamma- Rgenes: duplication and recombination. Science 248: 732- 735, 1990. 3 C b

GAM1338 360 FCGR2A Salmon, J. E.; Millard, S.; Schachter, L. A.; Arnett, F. C.; Ginzler,E. M.; 3 C b

Gourley, M. F.; Ramsey- Goldman, R.; Peterson, M. G. E.; Kimberly,R. P.: Fc-gamma- RIIA alleles are heritable risk factors for lupusnephritis in African Americans. J. Clin. Invest. 97: 1348- 1354,1996.

GAM1338 360 FCGR2A Sammartino, L.; Webber, L. M.; Hogarth, P. M.; McKenzie, I. F.C.; Garson, O. M.: Assignment of the gene coding for human FcRII(CD32) to bands q23q24 on chromosome 1. Immunogenetics 28: 380- 381,1988. 3 C b

GAM1338 360 FCGR2A Stein, M.- P.; Edberg, J. C.; Kimberly, R. P.; Mangan, E. K.; Bharadwaj,D.; Mold, C.; Du Clos, T. W.: C- reactive protein binding to Fc- gamma- RIIaon human monocytes and neutrophils is allele- specific. J. Clin. Invest. 105:369- 376, 2000. 3 C b

GAM1338 360 FCGR2A Unkeless, J. C.: Function and heterogeneity of human Fc receptorsfor immunoglobulin G. J. Clin. Invest. 83: 355- 361, 1989. 3 C b

GAM1338 360 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome assignment by polymerase chain reaction techniques: assignmentof the oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990. 3 C b

GAM1338 360 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator of the hair growth cycle: evidence from targeted and spontaneousmutations. Cell 78: 1017- 1025, 1994. 3 C b

GAM1338 360 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992. 3 C b

GAM1338 360 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and the bcl.1 locus are contained within one megabase in bandq13 of chromosome 11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988. 3 C b

GAM1338 360 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8: 3487- 3495, 1988. 3 C b

GAM1338 360 FHL2 Chan, K. K.; Tsui, S. K. W.; Lee, S. M. Y.; Luk, S. C. W.; Liew,C. C.; Fung, K. P.; Waye, M. M. Y.; Lee, C. Y.: Molecular cloningand characterization of FHL2, a novel LIM domain protein preferentiallyexpressed in human heart. Gene 210: 345- 350, 1998. 3 C b

GAM1338 360 FHL2 Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.- G.;Schafer, B. W.: Subtractive cloning and characterization of DRAL,a novel LIM- domain protein down- regulated in rhabdomyosarcoma. DNACell Biol. 16: 433- 442, 1997. 3 C b

GAM1338 360 FHL2 Morgan, M. J.; Madgwick, A. J. A.: Slim defines a novel familyof LIM-proteins expressed in skeletal muscle. Biochem. Biophys. Res.Commun. 225: 632- 638, 1996. 3 C b

GAM1338 360 FHL2 Tanahashi, H.; Tabira, T.: Alzheimer's disease- associated presenilin2 interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9:2281-2289, 2000. 3 C b

GAM1338 360 FSHPRH1 Aittomaki, K.; Lucena, J. L. D.; Pakarinen, P.; Sistonen, P.; Tapanainen,J.; Gromoll, J.; Kaskikari, R.; Sankila, E.- M.; Lehvaslaiho, H.; Engel,A. R.; Nieschlag, E.; Huhtaniemi, I.; de la Chapelle, A.: Mutationin the follicle-stimulating hormone receptor gene causes hereditaryhypergonadotropic ovarian failure. Cell 82: 959- 968, 1995. 3 C c

GAM1338 360 FSHPRH1 Roberts, R. G.; Kendall, E.; Vetrie, D.; Bobrow, M.: Sequenceand chromosomal location of a human homologue of LRPR1, an FSH primaryresponse gene. Genomics 37: 122- 124, 1996. 3 C c

GAM1338 360 FSHPRH1 Slegtenhorst- Eegdeman, K. E.; Post, M.; Baarends, W. M.; Themmen,A. P. N.; 3 C c
Grootegoed, J. A.: Regulation of gene expression in Sertolicells by follicle- stimulating hormone (FSH): cloning and characterizationof LRPR1, a primary response gene encoding a leucine- rich protein. Molec.Cell. Endocr. 108: 115- 124, 1995.

GAM1338 360 FSTL1 Shibanuma, M.; Mashimo, J.; Mita, A.; Kuroki, T.; Nose, K.: Cloningfrom a 3 C c
mouse osteoblastic cell line of a set of transforming- growth- factor- beta- 1- regulated genes, one of which seems to encode a follistatin- relatedpolypeptide. Europ. J. Biochem. 217: 13- 19, 1993.

GAM1338 360 FSTL1 Tanaka, M.; Ozaki, S.; Osakada, F.; Mori, K.; Okubo, M.; Nakao,K.: Cloning 3 C c
of follistatin- related protein as a novel autoantigenin systemic rheumatic diseases. Int. Immun. 10: 1305- 1314, 1998.

GAM1338 360 FSTL1 Zwijsen, A.; Blockx, H.; van Arnhem, W.; Willems, J.; Fransen,L.; Devos, K.; 3 C c
Raymackers, J.; van de Voorde, A.; Slegers, H.: Characterizationof a rat C6 glioma- secreted follistatin- related protein (FRP): cloningand sequence of the human homologue. Europ. J. Biochem. 225: 937- 946,1994.

GAM1338 360 G1P3 Clauss, I. M.; Wathelet, M. G.; Szpirer, J.; Content, J.; Islam,M. Q.; 3 C b
Levan, G.; Szpirer, C.; Huez, G. A.: Chromosomal localizationof two human genes inducible by interferons, double- stranded RNA,and viruses. Cytogenet. Cell Genet. 53: 166- 168, 1990.

GAM1338 360 G1P3 Itzhaki, J. E.; Barnett, M. A.; MacCarthy, A. B.; Buckle, V. J.;Brown, W. R. 3 C b
A.; Porter, A. C. G.: Targeted breakage of a human chromosomemediated by cloned human telomeric DNA. Nature Genet. 2: 283- 287,1992.

GAM1338 360 G1P3 Itzhaki, J. E.; Porter, A. C. G.: Targeted disruption of a humaninterferon- 3 C b
inducible gene detected by secretion of human growth hormone. NucleicAcids Res. 19: 3835- 3842, 1991.

GAM1338 360 G1P3 Kelly, J. M.; Porter, A. C. G.; Chernajovsky, Y.; Gilbert, C. S.;Stark, G. 3 C b
R.; Kerr, I. M.: Characterization of a human gene inducibleby alpha- and beta- interferons and its expression in mouse cells. EMBOJ. 5: 1601- 1606, 1986.

GAM1338 360 G1P3 Porter, A. C. G.; Chernajovsky, Y.; Dale, T. C.; Gilbert, C. S.;Stark, G. 3 C b
R.; Kerr, I. M.: Interferon response element of the humangene 6- 16. EMBO J. 7: 85- 92, 1988.

GAM1338 360 G2A Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y.: 3 C c
Lysophosphatidylcholine as a ligand for the immunoregulatory receptorG2A. Science 293: 702- 705, 2001.

GAM1338 360 G2A Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.;Harvill, E. 3 C c
T.; Jensen, E. R.; Miller, J. F.; Witte, O. N.: Micelacking the orphan G protein- coupled receptor G2A develop a late- onsetautoimmune syndrome. Immunity 14: 561- 571, 2001.

GAM1338 360 G2A Weng, Z.; Fluckiger, A.- C.; Nisitani, S.; Wahl, M. I.; Le, L. Q.;Hunter, C. 3 C c
A.; Fernal, A. A.; le Beau, M. M.; Witte, O. N.: A DNAdamage and stress inducible G protein- coupled receptor blocks cellsin G2/M. Proc. Nat. Acad. Sci. 95: 12334- 12339, 1998.

GAM1338 360 GLP1R Dillon, J. S.; Tanizawa, Y.; Wheeler, M. B.; Leng, X.- H.; Ligon,B. B.; 3 C c
Rabin, D. U.; Yoo- Warren, H.; Permutt, M. A.; Boyd, A. E.,III: Cloning and functional expression of the human glucagon- likepeptide- 1 (GLP- 1) receptor. Endocrinology 133: 1907- 1910, 1993.

GAM1338 360 GLP1R Kershaw, E. E.; Chua, S. C., Jr.; Leibel, R. L.: Localizationof a (CA)n 3 C c

repeat in glucagon- like peptide- 1 receptor gene (Glp1r)to proximal mouse chromosome 17 and its linkage to other markers. MammalianGenome 6: 301- 303, 1995.

GAM1338 360 GLP1R Stoffel, M.; Espinosa, R., III; Le Beau, M. M.; Bell, G. I.: Humanglucagon- 3 C c
like peptide- 1 receptor gene: localization to chromosomeband 6p21 by fluorescence in situ hybridization and linkage of a highlypolymorphic simple tandem repeat DNA polymorphism to other markerson chromosome 6. Diabetes 42: 1215- 1218, 1993.

GAM1338 360 GLP1R Thorens, B.: Expression cloning of the pancreatic beta cell receptorfor the 3 C c
gluco- incretin hormone glucagon- like peptide 1. Proc. Nat.Acad. Sci. 89: 8641- 8645, 1992.

GAM1338 360 GLP1R Wildhage, I.; Trusheim, H.; Goke, B.; Lankat- Buttgereit, B.: Geneexpression 3 C c
of the human glucagon- like peptide- 1 receptor is regulatedby Sp1 and Sp3. Endocrinology 140: 624- 631, 1999.

GAM1338 360 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; 3 C c
Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N- acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001.

GAM1338 360 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme 3 C c
catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2- epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313- 24318,1997.

GAM1338 360 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 C c

GAM1338 360 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; 3 C c
Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997.

GAM1338 360 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; 3 C c
Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase gene (GNE). J. Hum. Genet. 47: 77- 79, 2002.

GAM1338 360 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, 3 C c
W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999.

GAM1338 360 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; 3 C c
Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993.

GAM1338 360 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van 3 C c
Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001.

GAM1338 360 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal 3 C c
myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981.

GAM1338 360 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; 3 C c
Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002.

GAM1338 360 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N- 3 C c
acetylglucosamine 2- epimerase gene define the disease sialuriaand the
allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999.

GAM1338 360 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; 3 C c
Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N-
acetylneuraminic acid biosynthesis of rat liver: molecularcloning and
functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N-
acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997.

GAM1338 360 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification 3 C c
of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989.

GAM1338 360 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a 3 C c
second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987.

GAM1338 360 GPR4 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; 3 C b
Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation
of three novel human genes encoding G protein- coupledreceptors. DNA Cell
Biol. 14: 25- 35, 1995.

GAM1338 360 GPR4 Mahadevan, M. S.; Baird, S.; Bailly, J. E.; Shutler, G. G.; Sabourin,L. A.; 3 C b
Tsilfidis, C.; Neville, C. E.; Narang, M.; Korneluk, R. G.: Isolation of a
novel G protein- coupled receptor (GPR4) localizedto chromosome 19q13.3.
Genomics 30: 84- 88, 1995.

GAM1338 360 GPR4 Ye, R. D.; Prossnitz, E. R.; Zou, A.; Cochrane, C. G.: Characterizationof a 3 C b
human cDNA that encodes a functional receptor for platelet activatingfactor.
Biochem. Biophys. Res. Commun. 180: 105- 111, 1991.

GAM1338 360 GPR4 Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina,K. L.; 3 C b
Kabarowski, J. H. S.; Witte, O. N.; Xu, Y.: Sphingosylphosphorylcholineand
lysophosphatidylcholine are ligands for the G protein- coupledreceptor GPR4.
J. Biol. Chem. 276: 41325- 41335, 2001.

GAM1338 360 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, 3 C c
J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a
novel secretin- like human G- protein- coupledreceptor gene. Genomics 55:
296- 305, 1999.

GAM1338 360 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; 3 C c
van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected
with mRNA differential display using human melanoma celllines with different
metastatic potential. FEBS Lett. 446: 292- 298,1999.

GAM1338 360 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; 3 C b
Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann,
S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is
fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in
three cases of myelodysplastic syndrome/acutemyeloid leukemia with a
deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000.

GAM1338 360 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain- 3 C b
containingGTPase- activating protein for Rho and Cdc42 associates with
focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996.

GAM1338 360 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C b
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM1338 360 GRINL1A Roginski, R. S.; Mohan Raj, B. K.; Finkernagel, S. W.; Sciorra,L. J.: 3 C b
Assignment of an ionotropic glutamate receptor- like gene (GRINL1A)to human

chromosome 15q22.1 by in situ hybridization. Cytogenet.Cell Genet. 93: 143-144, 2001.

GAM1338 360 GRINL1A Wydner, K. S.; Mohan Raj, B. K.; Sciorra, L. J.; Roginski, R. S.: The mouse orthologue of the human ionotropic glutamate receptor- likegene (GRINL1A) maps to mouse chromosome 9. Cytogenet. Cell Genet. 95:240- 241, 2001. 3 C b

GAM1338 360 GYG Barbetti, F.; Rocchi, M.; Bossolasco, M.; Cordera, R.; Sbraccia,P.; Finelli, P.; Consalez, G. G.: The human skeletal muscle glycogeningene: cDNA, tissue expression, and chromosomal localization. Biochem.Biophys. Res. Commun. 220: 72- 77, 1996. 3 C b

GAM1338 360 GYG Lomako, J.; Mazuruk, K.; Lomako, W. M.; Alonso, M. D.; Whelan,W. J.; Rodriguez, I. R.: The human intron- containing gene for glycogeninmaps to chromosome 3, band q24. Genomics 33: 519- 522, 1996. 3 C b

GAM1338 360 GYG Mu, J.; Skurat, A. V.; Roach, P. J.: Glycogenin- 2, a novel self-glucosylatingprotein involved in liver glycogen biosynthesis. J. Biol. Chem. 272:27589- 27597, 1997. 3 C b

GAM1338 360 GYG Viskupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; DePaoli- Roach, A.A.; Roach, P. J.: Rabbit skeletal muscle glycogenin. Molecular cloningand production of fully functional protein in Escherichia coli. J.Biol. Chem. 267: 25759-25763, 1992. 3 C b

GAM1338 360 HEPH Anderson, G. J.; Murphy, T. L.; Cowley, L.; Evans, B. A.; Halliday,J. W.; McLaren, G. D.: Mapping the gene for sex- linked anemia: aninherited defect of intestinal iron absorption in the mouse. Genomics 48:34- 39, 1998. 3 C c

GAM1338 360 HEPH Bannerman, R. M.: Genetic defects of iron transport. Fed. Proc. 35:2281-2285, 1976. 3 C c

GAM1338 360 HEPH Edwards, J. A.; Hoke, J. E.; Mattioli, M.; Reichlin, M.: Ferritindistribution and synthesis in sex- linked anemia. J. Lab. Clin. Med. 90:68- 76, 1977. 3 C c

GAM1338 360 HEPH Falconer, D. S.; Isaacson, J. H.: The genetics of sex- linked anaemiain the mouse. Genet. Res. 3: 248- 250, 1962. 3 C c

GAM1338 360 HEPH Grewal, M. S.: A sex- linked anaemia in the mouse. Genet. Res. 3:238- 247, 1962. 3 C c

GAM1338 360 HEPH Lee, G. R.; Nacht, S.; Lukens, J. N.; Cartwright, G. E.: Ironmetabolism in copper- deficient swine. J. Clin. Invest. 47: 2058- 2069,1968. 3 C c

GAM1338 360 HEPH Vulpe, C. D.; Kuo, Y.- M.; Murphy, T. L.; Cowley, L.; Askwith, C.;Libina, N.; Gitschier, J.; Anderson, G. J.: Hephaestin, a ceruloplasminhomologue implicated in intestinal iron transport, is defective inthe sla mouse. Nature Genet. 21: 195- 199, 1999. 3 C c

GAM1338 360 HTR1D Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S. J.; Duncan,A. M. V.; Rozmahel, R.; Yang, Y.; Mengod, G.; Palacios, J. M.; O'Dowd,B. F.: Characterization of the human 5- hydroxytryptamine(1B) receptor. J.Biol. Chem. 267: 5735- 5738, 1992. 3 C c

GAM1338 360 HTR1D Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. 3 C c

GAM1338 360 HTR1D Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T.A.; Hartig, P. R.: Human serotonin 1D receptor is encoded by a subfamilyof two distinct genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat.Acad. Sci. 89: 3630-3634, 1992. 3 C c

GAM1338 360 HTR1D Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and 3 C c

genome organization of mammalian G- protein- coupled receptors. Genomics 18:175- 184, 1993.

GAM1338 360 HTR1E Levy, F. O.; Gudermann, T.; Birnbaumer, M.; Kaumann, A. J.; Birnbaumer,L.: Molecular cloning of a human gene (S31) encoding a novel serotoninreceptor mediating inhibition of adenylyl cyclase. FEBS Lett. 296:201- 206, 1992. 3 C c

GAM1338 360 HTR1E Levy, F. O.; Holtgreve- Grez, H.; Tasken, K.; Solberg, R.; Ried,T.; Gudermann, T.: Assignment of the gene encoding the 5- HT- 1E serotoninreceptor (S31) (locus HTR1E) to human chromosome 6q14- q15. Genomics 22:637- 640, 1994. 3 C c

GAM1338 360 HTR1E McAllister, G.; Charlesworth, A.; Snodin, C.; Beer, M. S.; Noble,A. J.; Middlemiss, D. N.; Iversen, L. L.; Whiting, P.: Molecularcloning of a serotonin receptor from human brain (5HT1E): a fifth5HT1- like subtype. Proc. Nat. Acad. Sci. 89: 5517- 5521, 1992. 3 C c

GAM1338 360 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998. 3 C c

GAM1338 360 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol-Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay. Genomics 54: 278- 286, 1998. 3 C c

GAM1338 360 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated in response to DNA damage. EMBO J. 17: 2055- 2066,1998. 3 C c

GAM1338 360 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999. 3 C c

GAM1338 360 ICAM1 Ballantyne, C. M.; Kozak, C. A.; O'Brien, W. E.; Beaudet, A. L.: Assignment of the gene for intercellular adhesion molecule- 1 (Icam- 1)to proximal mouse chromosome 9. Genomics 9: 547- 550, 1991. 3 C c

GAM1338 360 ICAM1 Bella, J.; Kolatkar, P. R.; Marlor, C. W.; Greve, J. M.; Rossmann,M. G.: The structure of the two amino- terminal domains of human ICAM- 1suggests how it functions as a rhinovirus receptor and as an LFA- 1integrin ligand. Proc. Nat. Acad. Sci. 95: 4140- 4145, 1998. 3 C c

GAM1338 360 ICAM1 Bellamy, R.; Kwiatkowski, D.; and Hill, A. V. S.: Absence of anassociation between intercellular adhesion molecule 1, complementreceptor 1 and interleukin 1 receptor antagonist gene polymorphismsand severe malaria in a West African population. Trans. R. Soc. Trop.Med. Hyg. 92: 312- 316, 1998. 3 C c

GAM1338 360 ICAM1 Craig, A.; Fernandez- Reyes, D.; Mesri, M.; McDowall, A.; Altieri,D. C.; Hogg, N.; Newbold, C.: A functional analysis of a naturalvariant of intercellular adhesion molecule- 1 (ICAM- 1- Kilifi). Hum.Molec. Genet. 9: 525- 530, 2000. 3 C c

GAM1338 360 ICAM1 Fernandez- Reyes, D.; Craig, A. G.; Kyes, S. A.; Peshu, N.; Snow,R. W.; Berendt, A. R.; Marsh, K.; Newbold, C. I.: A high frequencyAfrican coding polymorphism in the N- terminal domain of ICAM- 1 predisposingto cerebral malaria in Kenya. Hum. Molec. Genet. 6: 1357- 1360, 1997. 3 C c

GAM1338 360 ICAM1 Greve, J. M.; Davis, G.; Meyer, A. M.; Forte, C. P.; Yost, S. C.;Marlor, C. W.; Kamarck, M. E.; McClelland, A.: The major human rhinovirusreceptor is ICAM- 1. Cell 56: 839- 847, 1989. 3 C c

GAM1338 360 ICAM1 Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. Phys. 111: 272- 277, 1999. 3 C c

GAM1338 360 ICAM1 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, 3 C c
M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B
cells. Europ. J. Immun. 15: 103- 106, 1985.

GAM1338 360 ICAM1 Le Beau, M. M.; Ryan, D., Jr.; Pericak- Vance, M. A.: Report ofthe committee 3 C c
on the genetic constitution of chromosomes 18 and 19. Cytogenet.Cell Genet.
51: 338- 357, 1989.

GAM1338 360 ICAM1 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in 3 C c
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM1338 360 ICAM1 Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot- 3 C c
Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow
cytometricanalysis of conjunctival epithelium in ocular rosacea and
keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000.

GAM1338 360 ICAM1 Prieto, J.; Takei, F.; Gendelman, R.; Christenson, B.; Biberfeld,P.; 3 C c
Patarroyo, M.: MALA- 2, mouse homologue of human adhesion moleculeICAM- 1
(CD54). Europ. J. Immun. 19: 1551- 1557, 1989.

GAM1338 360 ICAM1 Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal 3 C c
mouse chromosome 9 linkage map that further defines linkagegroups homologous
with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685,
1991.

GAM1338 360 ICAM1 Simmons, D.; Makgoba, M. W.; Seed, B.: ICAM, an adhesion ligandof LFA- 1, is 3 C c
homologous to the neural cell adhesion molecule NCAM. Nature 331:624- 627,
1988.

GAM1338 360 ICAM1 Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H.K.; Smith, C. 3 C c
W.; Bradley, A.; Beaudet, A. L.: Inflammatory and immuneresponses are
impaired in mice deficient in intercellular adhesionmolecule 1. Proc. Nat.
Acad. Sci. 90: 8529- 8533, 1993.

GAM1338 360 ICAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 C c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM1338 360 ICAM1 Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; 3 C c
Takeuchi, T.: Regulation of human leukocyte antigenexpression in human
conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999.

GAM1338 360 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 C b
M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like
growth factor- I and cognitive function inhealthy older men. J. Clin.
Endocr. Metab. 84: 471- 475, 1999.

GAM1338 360 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- 3 C b
like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993.

GAM1338 360 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and 3 C b
absence of association with stature among African Pygmies. Hum.Genet. 85:
349- 354, 1990.

GAM1338 360 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for 3 C b
insulin- like growth factors I and II and for epidermalgrowth factor in man.
(Abstract) Am. J. Hum. Genet. 36: 133S only,1984.

GAM1338 360 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of 3 C b
genes for insulin- like growth factors I and II and epidermalgrowth factor.
Nature 310: 781- 784, 1984.

GAM1338 360 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, 3 C b

A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of recombinant human insulin- like growth factor I(IGF- I) therapy on the growth hormone- IGF system of a patient witha partial IGF- I gene deletion. J. Clin. Endocr. Metab. 84: 1611- 1616,1999.

GAM1338 360 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; 3 C b
Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of the growth hormone receptor in children with idiopathicshort stature. New Eng. J. Med. 333: 1093- 1098, 1995.

GAM1338 360 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; 3 C b
Froesch, E. R.: Small stature and insulin- like growth factors:prolonged treatment of mini- poodles with recombinant human insulin- likegrowth factor I. Acta Endocr. 121: 456- 464, 1989.

GAM1338 360 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. 3 C b
S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating concentrations of insulin- like growth factor- I and riskof breast cancer. Lancet 351: 1393- 1396, 1998.

GAM1338 360 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: 3 C b
Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding protein- 3, and prostate- specific antigen as predictorsof clinical prostate cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000.

GAM1338 360 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; 3 C b
Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith, D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival signaling in retinal endothelial cells: direct correlationwith clinical retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001.

GAM1338 360 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer 3 C b
prevention. Lancet 351: 1373- 1375, 1998.

GAM1338 360 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; 3 C b
Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J. S.: The human gene encoding insulin- like growthfactor I is located on chromosome 12. Hum. Genet. 69: 157- 160, 1985.

GAM1338 360 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, 3 C b
J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990.

GAM1338 360 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete 3 C b
characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986.

GAM1338 360 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; 3 C b
Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF- 1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996.

GAM1338 360 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: 3 C b
Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat. Acad. Sci. 80: 2216- 2220, 1983.

GAM1338 360 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; 3 C b
Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand implications for cell type- specific growth. Nature 364: 208- 213,1993.

GAM1338 360 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: 3 C b
Mice carrying null mutations of the genes encoding insulin- likegrowth

factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993.

GAM1338 360 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83: 9343- 9347, 1986. 3 C b

GAM1338 360 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human genes for insulin- like growth factors I and II and epidermalgrowth factor are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively. Cytogenet.Cell Genet. 41: 245- 249, 1986. 3 C b

GAM1338 360 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2 (IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985. 3 C b

GAM1338 360 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. D.: Growth characteristics and response to growth hormonetherapy in patients with hypochondroplasia: genetic linkage of theinsulin- like growth factor I gene at chromosome 12q23 to the diseasein a subgroup of these patients. Clin. Endocr. 34: 265- 274, 1991. 3 C b

GAM1338 360 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999. 3 C b

GAM1338 360 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene expression sustains hypertrophy and regeneration insenescent skeletal muscle. Nature Genet. 27: 195- 200, 2001. 3 C b

GAM1338 360 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like growth factor 1 regulates the location, stability,and transcriptional activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000. 3 C b

GAM1338 360 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993. 3 C b

GAM1338 360 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the protein which binds insulin- like growth factor in human serum. Europ.J. Biochem. 172: 421- 425, 1988. 3 C b

GAM1338 360 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith, R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the insulin- like growth factor I receptor and its ligandin relation to type 2 diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000. 3 C b

GAM1338 360 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986. 3 C b

GAM1338 360 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I) reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991. 3 C b

GAM1338 360 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999. 3 C b

GAM1338 360 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980. 3 C b

GAM1338 360 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 1991. 3 C b

GAM1338 360 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984. 3 C b

GAM1338 360 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984. 3 C b

GAM1338 360 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984. 3 C b

GAM1338 360 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-857,1992. 3 C b

GAM1338 360 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002. 3 C b

GAM1338 360 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980. 3 C b

GAM1338 360 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999. 3 C b

GAM1338 360 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy on body composition and insulin resistance in IGF- Igene deletion. J. Clin. Endocr. Metab. 85: 1407- 1411, 2000. 3 C b

GAM1338 360 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: Intrauterine growth retardation and postnatal growth failureassociated with deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335: 1363- 1367, 1996. 3 C b

GAM1338 360 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub-regional localization of human genes for insulin- like growthfactors I (IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell Genet. 40: 782 only, 1985. 3 C b

GAM1338 360 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like growth factors and bone mineral density in African Americanand white girls. J. Pediat. 137: 826- 832, 2000. 3 C b

GAM1338 360 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997. 3 C b

GAM1338 360 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994. 3 C b

GAM1338 360 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 C b

and clinical use. Blood 89: 3897- 3908, 1997.

GAM1338 360 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 C b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814-
819, 1992.

GAM1338 360 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 C b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang,
Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell-
derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87:
7512- 7516, 1990.

GAM1338 360 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 3 C b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract)
Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM1338 360 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, 3 C b
sequence, expression, and processing of the interleukin 16precursor. Proc.
Nat. Acad. Sci. 94: 5273- 5277, 1997.

GAM1338 360 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 3 C b
381: 30 only, 1996.

GAM1338 360 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 3 C b
16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics
49:704- 706, 1999.

GAM1338 360 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. 3 C b
C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte
chemoattractant factor: association of biologic functionwith CD4 expression.
Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994.

GAM1338 360 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human 3 C b
lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128:
2569- 2574, 1982.

GAM1338 360 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS 3 C b
human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311-
314, 1993.

GAM1338 360 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; 3 C b
Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M.
E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945-
1954, 1995.

GAM1338 360 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; 3 C b
Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure
and function between human and murine IL- 16. J. Immun. 160:5945- 5954,
1998.

GAM1338 360 IL21R Asao, H.; Okuyama, C.; Kumaki, S.; Ishii, N.; Tsuchiya, S.; Foster,D.; 3 C c
Sugamura, K.: Cutting edge: the common gamma- chain is an
indispensablesubunit of the IL- 21 receptor complex. J. Immun. 167: 1- 5,
2001.

GAM1338 360 IL21R Kasaian, M. T.; Whitters, M. J.; Carter, L. L.; Lowe, L. D.; Jussif,J. M.; 3 C c
Deng, B.; Johnson, K. A.; Witek, J. S.; Senices, M.; Konz,R. F.; Wurster, A.
L.; Donaldson, D. D.; Collins, M.; Young, D. A.;Grusby, M. J.: IL- 21 limits
NK cell responses and promotes antigen- specificT cell activation: a
mediator of the transition from innate to adaptiveimmunity. Immunity 16:
559- 569, 2002.

GAM1338 360 IL21R Ozaki, K.; Kikly, K.; Michalovich, D.; Young, P. R.; Leonard, W.J.: Cloning 3 C c
of a type I cytokine receptor most related to the IL- 2receptor beta chain.

Proc. Nat. Acad. Sci. 97: 11439- 11444, 2000.

GAM1338 360 IL21R Parrish- Novak, J.; Dillon, S. R.; Nelson, A.; Hammond, A.; Sprecher,C.; 3 C c
Gross, J. A.; Johnston, J.; Madden, K.; Xu, W.; West, J.; Schrader,S.;
Burkhead, S.; and 26 others: Interleukin 21 and its receptorare involved in
NK cell expansion and regulation of lymphocyte function. Nature 408:57- 63,
2000.

GAM1338 360 IL21R Ueda, C.; Akasaka, T.; Kurata, M.; Maesako, Y.; Nishikori, M.;Ichinohasama, 3 C c
R.; Imada, K.; Uchiyama, T.; Ohno, H.: The gene forinterleukin- 21 receptor
is the partner of BCL6 in t(13;16)(q27;p11),which is recurrently observed in
diffuse large B- cell lymphoma. Oncogene 21:368- 376, 2002.

GAM1338 360 JRK Morita, R.; Miyazaki, E.; Fong, C. G.; Chen, X.- N.; Korenberg,J. R.; 3 C b
Delgado- Escueta, A. V.; Yamakawa, K.: JH8, a gene highly homologousto the
mouse jerky gene, maps to the region for childhood absenceepilepsy on 8q24.
Biochem. Biophys. Res. Commun. 248: 307- 314, 1998.

GAM1338 360 JRK Toth, M.; Grimsby, J.; Buzsaki, G.; Donovan, G. P.: Epilepticseizures caused 3 C b
by inactivation of a novel gene, jerky, related tocentromere binding
protein- B in transgenic mice. Nature Genet. 11:71- 75, 1995. Note: Erratum:
Nature Genet. 12: 110 only, 1996.

GAM1338 360 KCNE3 Abbott, G. W.; Butler, M. H.; Bendahhou, S.; Dalakas, M. C.; Ptacek,L. J.; 3 C c
Goldstein, S. A. N.: MiRP2 forms potassium channels in skeletalmuscle with
Kv3.4 and is associated with periodic paralysis. Cell 104:217- 231, 2001.

GAM1338 360 KCNE3 Abbott, G. W.; Sesti, F.; Splawski, I.; Buck, M. E.; Lehmann, M.H.; Timothy, 3 C c
K. W.; Keating, M. T.; Goldstein, S. A. N.: MiRP1 formsI(Kr) potassium
channels with HERG and is associated with cardiacarrhythmia. Cell 97: 175-
187, 1999.

GAM1338 360 KCNE3 Schroeder, B. C.; Waldegger, S.; Fehr, S.; Bleich, M.; Warth, R.;Greger, R.; 3 C c
Jentsch, T. J.: A constitutively open potassium channelformed by KCNQ1 and
KCNE3. Nature 403: 196- 199, 2000.

GAM1338 360 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel 3 C
b
genes. Trends Pharm. Sci. 14: 434, 1993.

GAM1338 360 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; 3 C b
Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe
pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011-
1017, 1996.

GAM1338 360 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; 3 C b
Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an
inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166-
1170, 1995.

GAM1338 360 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: 3 C b
Targeted overactivity of beta cell KATP channels induces profoundneonatal
diabetes. Cell 100: 645- 654, 2000.

GAM1338 360 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: 3 C b
Homozygositymapping, to chromosome 11p, of the gene for familial persistent
hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421,
1995.

GAM1338 360 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward 3 C b
rectifier Kir6.2 also leads to familial persistent
hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812,
1996.

GAM1338 360 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium channels in hypoxia- induced generalized seizure. Science 292:1543- 1546, 2001. 3 C b

GAM1338 360 KLRD1 Braud, V. M.; Allan, D. S. J.; O'Callaghan, C. A.; Soderstrom,K.; D'Andrea, A.; Ogg, G. S.; Lazetic, S.; Young, N. T.; Bell, J.I.; Phillips, J. H.; Lanier, L. L.; McMichael, A. J.: HLA- E bindsto natural killer cell receptors CD94/NKG2A, B and C. Nature 391:795- 799, 1998. 3 C c

GAM1338 360 KLRD1 Chang, C.; Rodriguez, A.; Carretero, M.; Lopez- Botet, M.; Phillips,J. H.; Lanier, L. L.: Molecular characterization of human CD94: atype II membrane glycoprotein related to the C- type lectin superfamily. Europ.J. Immun. 25: 2433- 2437, 1995. 3 C c

GAM1338 360 KLRD1 Lazetic, S.; Chang, C.; Houchins, J. P.; Lanier, L. L.; Phillips,J. H.: Human natural killer cell receptors involved in MHC classI recognition are disulfide- linked heterodimers of CD94 and NKG2 subunits. J.Immun. 157: 4741- 4745, 1996. 3 C c

GAM1338 360 KLRD1 Plougastel, B.; Trowsdale, J.: Sequence analysis of a 62- kb regionoverlapping the human KLRC cluster of genes. Genomics 49: 193- 199,1998. 3 C c

GAM1338 360 KLRD1 Rodriguez, A.; Carretero, M.; Glienke, J.; Bellon, T.; Ramirez,A.; Lehrach, H.; Francis, F.; Lopez- Botet, M.: Structure of the humanCD94 C- type lectin gene. Immunogenetics 47: 305- 309, 1998. 3 C c

GAM1338 360 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; Malherbe, P.: Cloning and functional expression of human kynurenine3- monooxygenase. FEBS Lett. 410: 407- 412, 1997. 3 C b

GAM1338 360 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001. 3 C b

GAM1338 360 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000. 3 C b

GAM1338 360 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000. 3 C b

GAM1338 360 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363- 18367,1996. 3 C c

GAM1338 360 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994. 3 C c

GAM1338 360 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. Nature 384: 39- 43, 1996. 3 C c

GAM1338 360 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 3 C c

specifictranscriptional regulation of human leukotriene B4 receptor gene. J.Exp. Med. 192: 413- 420, 2000.

GAM1338 360 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 3 C c chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM1338 360 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 3 C c Leukotrienes and lipoxins: structures, biosynthesis,and biological effects. Science 237: 1171- 1176, 1987.

GAM1338 360 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C c Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127- 130, 1997.

GAM1338 360 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 3 C c coupled receptor for leukotriene B4 that mediates chemotaxis. Nature 387:620- 624, 1997.

GAM1338 360 LYZ Camara, V. M.; Harding, J. W.; Prieur, D. J.: Inherited lysozymedeficiency 3 C b in rabbits: the absence of a primary isozyme of lysozymeas the cause of the condition. Lab. Invest. 63: 544- 550, 1990.

GAM1338 360 LYZ Canet, D.; Sunde, M.; Last, A. M.; Miranker, A.; Spencer, A.; Robinson,C. 3 C b V.; Dobson, C. M.: Mechanistic studies of the folding of humanlysozyme and the origin of amyloidogenic behavior in its disease- relatedvariants. Biochemistry 38: 6419- 6427, 1999.

GAM1338 360 LYZ Dayhoff, M. O.: Atlas of Protein Sequence and Structure. Lactalbuminand 3 C b Lysozyme. Washington: National Biomedical Research Foundation(pub.) 5: 1972. Pp. D133- D140.

GAM1338 360 LYZ Fleming, A.: On a remarkable bacteriolytic element found in tissuesand 3 C b secretions. Proc. Roy. Soc. Ser. B. 93: 306- 317, 1922.

GAM1338 360 LYZ Fleming, A.; Allison, V. D.: Observations on a bacteriolytic 3 C b substance('lysozyme') found in secretions and tissues. Brit. J. Exp. Path. 3:252- 260, 1922.

GAM1338 360 LYZ Greenwald, R. A.; Cantor, J. O.; Prieur, D. J.; Young, D. M.:Composition of 3 C b cartilage from lysozyme- deficient rabbits. Biochim.Biophys. Acta 385: 435- 437, 1975.

GAM1338 360 LYZ Neufeld, E. L.: Personal Communication. Bethesda, Maryland 1972. 3 C b

GAM1338 360 LYZ Pepys, M. B.; Hawkins, P. N.; Booth, D. R.; Vigushin, D. M.; Tennent,G. A.; 3 C b Soutar, A. K.; Totty, N.; Nguyen, O.; Blake, C. C. F.; Terry,C. J.; Feest, T. G.; Zalin, A. M.; Hsuan, J. J.: Human lysozyme genemutations cause hereditary systemic amyloidosis. Nature 362: 553- 557,1993.

GAM1338 360 LYZ Peters, C. W. B.; Kruse, U.; Pollwein, R.; Grzeschik, K.- H.; Sippel,A. E.: 3 C b The human lysozyme gene: sequence organization and chromosomallocalization. (Abstract) Cytogenet. Cell Genet. 51: 1059 only, 1989.

GAM1338 360 LYZ Prieur, D. J.: Personal Communication. Pullman, Washington 5/13/1975. 3 C b

GAM1338 360 LYZ Prieur, D. J.; Olson, H. M.; Young, D. M.: Lysozyme deficiency- - 3 C b aninherited disorder of rabbits. Am. J. Path. 77: 283- 296, 1974.

GAM1338 360 LYZ Spitznagel, J. K.; Cooper, M. R.; McCall, A. E.; DeChatelet, L.R.; Welsh, I. 3 C b R.: Selective deficiency of granules associated withlysozyme and lactoferrin in human polymorphs (PMN) with reduced microbicidalcapacity. (Abstract) J. Clin. Invest. 51: 93A only, 1972.

GAM1338 360 LYZ Taniyama, Y.; Kuroki, R.; Omura, F.; Seko, C.; Kikuchi, M.: Evidencefor 3 C b intramolecular disulfide bond shuffling in the folding of mutanthuman lysozyme. J. Biol. Chem. 266: 6456- 6461, 1991.

GAM1338 360 LYZ Yoshimura, K.; Toibana, A.; Nakahama, K.: Human lysozyme: sequencingof a cDNA, and expression and secretion by Saccharomyces cerevisiae. Biochem.Biophys. Res. Commun. 150: 794- 801, 1988. 3 C b

GAM1338 360 LYZ Zalin, A. M.; Jones, S.; Fitch, N. J. S.; Ramsden, D. B.: Familialnephropathic non- neuropathic amyloidosis: clinical features, immunohistochemistryand chemistry. Quart. J. Med. 81: 945- 956, 1991. 3 C b

GAM1338 360 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999. 3 C b

GAM1338 360 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 C b

GAM1338 360 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990. 3 C b

GAM1338 360 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994. 3 C b

GAM1338 360 MAML1 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. V. The codingsequences of 40 new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 3: 17- 24, 1996. 3 C c

GAM1338 360 MAML1 Wu, L.; Aster, J. C.; Blacklow, S. C.; Lake, R.; Artavanis- Tsakonas,S.; Griffin, J. D.: MAML1, a human homologue of Drosophila mastermind,is a transcriptional co- activator for NOTCH receptors. Nature Genet. 26:484- 489, 2000. 3 C c

GAM1338 360 MDM2 Boyd, M. T.; Vlatkovic, N.; Haines, D. S.: A novel cellular protein(MTBP) binds to MDM2 and induces a G1 arrest that is suppressed byMDM2. J. Biol. Chem. 275: 31883- 31890, 2000. 3 C b

GAM1338 360 MDM2 Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S.A.; Albitar, M.: The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82:2617- 2623, 1993. 3 C b

GAM1338 360 MDM2 Bureau, J. F.; Bihl, F.; Brahic, M.; Le Paslier, D.: The genecoding for interferon- gamma is linked to the D12S335 and D12S313 microsatellitesand to the MDM2 gene. Genomics 28: 109- 112, 1995. 3 C b

GAM1338 360 MDM2 Buschmann, T.; Fuchs, S. Y.; Lee, C.- G.; Pan, Z.- Q.; Ronai, Z.: SUMO- 1 modification of Mdm2 prevents its self- ubiquitination andincreases Mdm2 ability to ubiquitinate p53. Cell 101: 753- 762, 2000.Note: Erratum: Cell 107: 549 only, 2001. 3 C b

GAM1338 360 MDM2 de Oca Luna, R. M.; Tabor, A. D.; Eberspaecher, H.; Hulboy, D.L.; Worth, L. L.; Colman, M. S.; Finlay, C. A.; Lozano, G.: The organizationand expression of the mdm2 gene. Genomics 33: 352- 357, 1996. 3 C b

GAM1338 360 MDM2 Fakharzadeh, S.; Trusko, S. P.; George, D. L.: Tumorigenic potentialassociated with enhanced expression of a gene that is amplified ina mouse tumor cell line. EMBO J. 10: 1565- 1569, 1991. 3 C b

GAM1338 360 MDM2 Freedman, D. A.; Epstein, C. B.; Roth, J. C.; Levine, A. J.: Agenetic approach to mapping the p53 binding site in the MDM2 protein. Molec.Med. 3: 248- 259, 1997. 3 C b

GAM1338 360 MDM2 Fuchs, S. Y.; Adler, V.; Buschmann, T.; Yin, Z.; Wu, X.; Jones,S. N.; Ronai, 3 C b
Z.: JNK targets p53 ubiquitination and degradationin nonstressed cells.
Genes Dev. 12: 2658- 2663, 1998.

GAM1338 360 MDM2 Mayo, L. D.; Donner, D. B.: A phosphatidylinositol 3- kinase/Aktpathway 3 C b
promotes translocation of Mdm2 from the cytoplasm to the nucleus. Proc.Nat.
Acad. Sci. 98: 11598- 11603, 2001.

GAM1338 360 MDM2 Mitchell, E. L. D.; White, G. R. M.; Santibanez- Koref, M. F.;Varley, J. M.; 3 C b
Heighway, J.: Mapping of gene loci in the q13- q15region of chromosome 12.
Chromosome Res. 3: 261- 262, 1995.

GAM1338 360 MDM2 Momand, J.; Zambetti, G. P.; Olson, D. C.; George, D. L.; Levine,A. J.: The 3 C b
mdm- 2 oncogene product forms a complex with the p53 proteinand inhibits
p53- mediated transactivation. Cell 69: 1237- 1245, 1992.

GAM1338 360 MDM2 Oliner, J. D.; Kinzler, K. W.; Meltzer, P. S.; George, D. L.;Vogelstein, B.: 3 C b
Amplification of a gene encoding a p53- associatedprotein in human sarcomas.
Nature 358: 80- 83, 1992.

GAM1338 360 MDM2 Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.;Sasazuki, T.; 3 C b
McMahon, M.; Oren, M.; McCormick, F.: Opposing effectsof Ras on p53:
transcriptional activation of mdm2 and induction ofp19(ARF). Cell 103: 321-
330, 2000.

GAM1338 360 MDM2 Shenoy, S. K.; McDonald, P. H.; Kohout, T. A.; Lefkowitz, R. J.: Regulation 3 C b
of receptor fate by ubiquitination of activated beta- 2- adrenergicreceptor
and beta- arrestin. Science 294: 1307- 1313, 2001.

GAM1338 360 MDM2 Shieh, S.- Y.; Ikeda, M.; Taya, Y.; Prives, C.: DNA damage- 3 C b
inducedphosphorylation of p53 alleviates inhibition by MDM2. Cell 91: 325-
334,1997.

GAM1338 360 MDM2 Testa, J. R.; Bellacosa, A.: AKT plays a central role in tumorigenesis. 3 C b
Proc.Nat. Acad. Sci. 98: 10983- 10985, 2001.

GAM1338 360 MDM2 Xiao, Z.- X.; Chen, J.; Levine, A. J.; Modjtahedi, N.; Xing, J.;Sellers, W. 3 C b
R.; Livingston, D. M.: Interaction between the retinoblastomaprotein and the
oncoprotein MDM2. Nature 375: 694- 698, 1995.

GAM1338 360 MDM2 Zhang, Y.; Xiong, Y.: A p53 amino- terminal nuclear export signalinhibited 3 C b
by DNA damage- induced phosphorylation. Science 292: 1910- 1915,2001.

GAM1338 360 MDM4 Parant, J.; Chavez- Reyes, A.; Little, N. A.; Yan, W.; Reinke, V.;Jochemsen, 3 C c
A. G.; Lozano, G.: Rescue of embryonic lethality in Mdm4- nullmice by loss
of Trp53 suggests a nonoverlapping pathway with MDM2to regulate p53. Nature
Genet. 29: 92- 95, 2001.

GAM1338 360 MDM4 Shvarts, A.; Bazuine, M.; Dekker, P.; Ramos, Y. F. M.; Steegenga,W. T.; 3 C c
Merckx, G.; van Ham, R. C. A.; van der Houven van Oordt, W.;van der Eb, A.
J.; Jochemsen, A. G.: Isolation and identificationof the human homolog of a
new p53- binding protein, Mdmx. Genomics 43:34- 42, 1997.

GAM1338 360 MYO1D Hasson, T.; Skowron, J. F.; Gilbert, D. J.; Avraham, K. B.; Perry,W. L.; 3 C c
Bement, W. M.; Anderson, B. L.; Sherr, E. H.; Chen, Z.- Y.;Greene, L. A.;
Ward, D. C.; Corey, D. P.; Mooseker, M. S.; Copeland,N. G.; Jenkins, N. A.:
Mapping of unconventional myosins in mouseand human. Genomics 36: 431- 439,
1996.

GAM1338 360 MYO1D Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; 3 C c
Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of
unidentified human genes. XI. The complete sequencesof 100 new cDNA clones
from brain which code for large proteins invitro. DNA Res. 5: 277- 286,
1998.

GAM1338 360 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 C b
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator.
J. Biol. Chem. 275: 5308- 5317, 2000.

GAM1338 360 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 C b
Hybrid selection of transcribed sequences from microdissectedDNA: isolation
of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer
Res. 56: 3446- 3450, 1996.

GAM1338 360 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 C b
bindingprotein, an LXXLL motif- containing protein, functions as a
generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM1338 360 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 C b
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-
H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor,
ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for
ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol.
Chem. 274: 34283- 34293, 1999.

GAM1338 360 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 C b
that integrate nuclear receptor signaling through CREB- bindingprotein.
Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM1338 360 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 C b
coding sequences of unidentified human genes. V. The codingsequences of 40
new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM1338 360 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 C b
J. K.: Isolation and characterization of peroxisomeproliferator- activated
receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.
Biol. Chem. 275: 13510- 13516, 2000.

GAM1338 360 NOL3 Koseki, T.; Inohara, N.; Chen, S.; Nunez, G.: ARC, an inhibitorof apoptosis 3 C c
expressed in skeletal muscle and heart that interactsselectively with
caspases. Proc. Nat. Acad. Sci. 95: 5156- 5160,1998.

GAM1338 360 NOL3 Li, P.- F.; Li, J.; Muller, E.- C.; Otto, A.; Dietz, R.; von Harsdorf,R.: 3 C c
Phosphorylation by protein kinase CK2: a signaling switch forthe caspase-
inhibiting protein ARC. Molec. Cell 10: 247- 258, 2002.

GAM1338 360 NOL3 Stoss, O.; Schwaiger, F.- W.; Cooper, T. A.; Stamm, S.: Alternativesplicing 3 C c
determines the intracellular localization of the novel nuclearprotein Nop30
and its interaction with the splicing factor SRp30c. J.Biol. Chem. 274:
10951- 10962, 1999.

GAM1338 360 NONO Brown, C. J.; Carrel, L.; Willard, H. F.: Expression of genesfrom the human 3 C c
active and inactive X chromosomes. Am. J. Hum. Genet. 60:1333- 1343, 1997.

GAM1338 360 NONO Dong, B.; Horowitz, D. S.; Kobayashi, R.; Krainer, A. R.: Purificationand 3 C c
cDNA cloning of HeLa cell p54(nrb), a nuclear protein with twoRNA
recognition motifs and extensive homology to human splicing factorPSF and
Drosophila NONA/BJ6. Nucleic Acids Res. 21: 4085- 4092, 1993.

GAM1338 360 NONO Nelson, D. L.; Ballabio, A.; Cremers, F.; Monaco, A. P.; Schlessinger,D.: 3 C c
Report of the sixth international workshop on X chromosome mapping1995.
Cytogenet. Cell Genet. 71: 308- 342, 1995.

GAM1338 360 NONO Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller,U.: AFX1 and 3 C c
p54(nrb): fine mapping, genomic structure, and exclusionas candidate genes
of X- linked dystonia parkinsonism. Hum. Genet. 100:569- 572, 1997.

GAM1338 360 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of 3 C b

NAD(P)H:quinonereductase by dietary antioxidants: possible role in protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77: 5216- 5220,1980.

GAM1338 360 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.; Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of the long arm of human chromosome 16. Genomics 10:308- 312, 1991. 3 C b

GAM1338 360 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983. 3 C b

GAM1338 360 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum. Genet. 53: 189- 193, 1980. 3 C b

GAM1338 360 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin-inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578, 1988. 3 C b

GAM1338 360 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic variation in the prevalence of a common NAD(P)Hquinone oxidoreductase polymorphism and its implications for anti- cancerchemotherapy. Brit. J. Cancer 76: 852- 854, 1997. 3 C b

GAM1338 360 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further evidence for the regional localization of human APRT and DIA4on chromosome 16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984. 3 C b

GAM1338 360 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe increased susceptibility of individuals with a polymorphism inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat. Acad. Sci. 96: 8150- 8155, 1999. 3 C b

GAM1338 360 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA-4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980. 3 C b

GAM1338 360 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1) gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382-7389, 1998. 3 C b

GAM1338 360 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.; Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.; Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological malignancy, is associated with the NQO1 609C- T mutationand rapid fractional excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997. 3 C b

GAM1338 360 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 C b

GAM1338 360 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999. 3 C b

GAM1338 360 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene expression in human colon carcinoma cells: characterization ofa mutation which modulates DT- diaphorase activity and mitomycin sensitivity. CancerRes. 52: 797- 802, 1992. 3 C b

GAM1338 360 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; 3 C b

Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H: quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997.

GAM1338 360 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998. 3 C b

GAM1338 360 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes. Leukemia Res. 22: 105- 113, 1998. 3 C b

GAM1338 360 ORC1L Eki, T.; Okumura, K.; Amin, A.; Ishiai, M.; Abe, M.; Nogami, M.;Taguchi, H.; Hurwitz, J.; Murakami, Y.; Hanaoka, F.: Mapping of thehuman homologue (ORC1L) of the yeast origin recognition complex subunit1 gene to chromosome band 1p32. Genomics 36: 559- 561, 1996. 3 C b

GAM1338 360 ORC1L Gavin, K. A.; Hidaka, M.; Stillman, B.: Conserved initiator proteinsin eukaryotes. Science 270: 1667- 1671, 1995. 3 C b

GAM1338 360 ORC1L Mendez, J.; Zou- Yang, H.; Kim, S.- Y.; Hidaka, M.; Tansey, W. P.;Stillman, B.: Human origin recognition complex large subunit is degradedby ubiquitin-mediated proteolysis after initiation of DNA replication. Molec.Cell 9: 481-491, 2002. 3 C b

GAM1338 360 ORC1L Ohtani, K.; DeGregori, J.; Leone, G.; Herendeen, D. R.; Kelly,T. J.; Nevins, J. R.: Expression of the HsOrc1 gene, a human ORC1homolog, is regulated by cell proliferation via the E2F transcriptionfactor. Molec. Cell. Biol. 16: 6977- 6984, 1996. 3 C b

GAM1338 360 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991. 3 C b

GAM1338 360 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine nucleotide synthesis on human chromosome 4 are closelylinked and divergently transcribed. J. Biol. Chem. 269: 5313- 5321,1994. 3 C b

GAM1338 360 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of three human multifunctional de novo purine biosyntheticgenes by functional complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920, 1990. 3 C b

GAM1338 360 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C b

GAM1338 360 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C b

GAM1338 360 PCDHB16 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997. 3 C c

GAM1338 360 PCDHB16 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of the coding sequences of unidentified human genes. XVIII.The complete sequences of 100 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 273- 281, 2000. 3 C c

GAM1338 360 PCDHB16 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM1338 360 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 C b
protocadherin- beta one- exon gene families show high
evolutionaryconservation, despite the difference in gene number. FEBS Lett.
495:120- 125, 2001.

GAM1338 360 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM1338 360 PDZK1 Custer, M.; Spindler, B.; Verrey, F.; Murer, H.; Biber, J.: Identificationof 3 C b
a new gene product (diphor- 1) regulated by dietary phosphate. Am.J.
Physiol. 273: F801- F806, 1997.

GAM1338 360 PDZK1 Ikemoto, M.; Arai, H.; Feng, D.; Tanaka, K.; Aoki, J.; Dohmae,N.; Takio, K.; 3 C b
Adachi, H.; Tsujimoto, M.; Inoue, K.: Identificationof a PDZ- domain-
containing protein that interacts with the scavengerreceptor class B type I.
Proc. Nat. Acad. Sci. 97: 6538- 6543, 2000.

GAM1338 360 PDZK1 Kocher, O.; Comella, N.; Gilchrist, A.; Pal, R.; Tognazzi, K.;Brown, L. F.; 3 C b
Knoll, J. H. M.: PDZK1, a novel PDZ domain- containingprotein up- regulated
in carcinomas and mapped to chromosome 1q21,interacts with cMOAT (MRP2), the
multidrug resistance- associated protein. Lab.Invest. 79: 1161- 1170, 1999.

GAM1338 360 PDZK1 Kocher, O.; Comella, N.; Tognazzi, K.; Brown, L. F.: Identificationand 3 C b
partial characterization of PDZK1: a novel protein containingPDZ interaction
domains. Lab. Invest. 78: 117- 125, 1998.

GAM1338 360 PDZK1 Wang, S.; Yue, H.; Derin, R. B.; Guggino, W. B.; Li, M.: Accessoryprotein 3 C b
facilitated CFTR- CFTR interaction, a molecular mechanism topotentiate the
chloride channel activity. Cell 103: 169- 179, 2000.

GAM1338 360 PDZK1 White, K. E.; Biber, J.; Murer, H.; Econs, M. J.: A PDZ domain- 3 C b
containingprotein with homology to Diphor- 1 maps to human chromosome 1q21.
Ann.Hum. Genet. 62: 287- 290, 1998.

GAM1338 360 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to 3 C b
two putative mammalian circadian regulators, mper1 andmper2, to light. Cell
91: 1055- 1064, 1997.

GAM1338 360 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C b
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM1338 360 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; 3 C b
Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and
mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531-
2534, 1999.

GAM1338 360 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of 3 C b
clock operative in the mammalian forebrain. Science 293:506- 509, 2001.

GAM1338 360 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; 3 C b
Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.;
Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock.
Science 288: 1013- 1019, 2000.

GAM1338 360 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; 3 C b
Reppert, S. M.: Two period homologs: circadian expression andphotic
regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997.

GAM1338 360 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; 3 C b
Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial
advanced sleep phase syndrome. Science 291: 1040- 1043,2001.

GAM1338 360 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; 3 C b
Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the
mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694,
2001.

GAM1338 360 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; 3 C b
Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the
mammalian circadian clock. Nature 400: 169- 173,1999.

GAM1338 360 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. 3 C b
W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol
3- kinase catalytic subunit that associates withp85 and is expressed
predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997.

GAM1338 360 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, 3 C b
E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J.
H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in
p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002.

GAM1338 360 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; 3 C b
Nakagawara, A.: Identification and chromosome assignment of ahuman gene
encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997.

GAM1338 360 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; 3 C b
Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.:
p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat.
Acad. Sci. 94: 4330- 4335, 1997.

GAM1338 360 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; 3 C c
Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx
activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C.
Genomics 47: 323- 324, 1998.

GAM1338 360 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, 3 C c
S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to
human chromosome 21q22.3. Genomics 41: 193- 200,1997.

GAM1338 360 PON1 Adkins, S.; Gan, K. N.; Mody, M.; La Du, B. N.: Molecular basisfor the 3 C b
polymorphic forms of human serum paraoxonase/arylesterase:glutamine or
arginine at position 191, for the respective A and Ballozymes. Am. J. Hum.
Genet. 52: 598- 608, 1993.

GAM1338 360 PON1 Antikainen, M.; Murtomaki, S.; Syvanne, M.; Pahlman, R.; Tahvanainen,E.; 3 C b
Jauhiainen, M.; Frick, M. H.; Ehnholm, C.: The gln- arg191 polymorphismof
the human paraoxonase gene (HUMPONA) is not associated with therisk of
coronary artery disease in Finns. J. Clin. Invest. 98: 883- 885,1996.

GAM1338 360 PON1 Augustinsson, K.- B.; Henricson, B.: A genetically controlled esterasein rat 3 C b
plasma. Biochim. Biophys. Acta 124: 323- 331, 1966.

GAM1338 360 PON1 Barbieri, M.; Bonafe, M.; Marfella, R.; Ragno, E.; Giugliano, D.;Franceschi, 3 C b
C.; Paolisso, G.: LL- paraoxonase genotype is associatedwith a more severe
degree of homeostasis model assessment IR in healthysubjects. J. Clin.
Endocr. Metab. 87: 222- 225, 2002.

GAM1338 360 PON1 Brophy, V. H.; Jampsa, R. L.; Clendenning, J. B.; McKinstry, L.A.; Jarvik, 3 C b

G. P.; Furlong, C. E.: Effects of 5- prime regulatory- regionpolymorphisms on paraoxonase- gene (PON1) expression. Am. J. Hum.Genet. 68: 1428- 1436, 2001.

GAM1338 360 PON1 Cherry, N.; Mackness, M.; Durrington, P.; Povey, A.; Dippnall,M.; Smith, T.; 3 C b Mackness, B.: Paraoxonase (PON1) polymorphisms infarmers attributing ill health to sheep dip. Lancet 359: 763- 764,2002.

GAM1338 360 PON1 Clendenning, J. B.; Humbert, R.; Green, E. D.; Wood, C.; Traver,D.; Furlong, 3 C b C. E.: Structural organization of the human PON1 gene. Genomics 35:586- 589, 1996.

GAM1338 360 PON1 Coates, P. M.; Mestriner, M. A.; Hopkinson, D. A.: A 3 C b preliminaryinterpretation of the esterase isozymes of human tissues. Ann. Hum.Genet. 39: 1- 20, 1975.

GAM1338 360 PON1 Davies, H. G.; Richter, R. J.; Keifer, M.; Broomfield, C. A.; Sowalla,J.; 3 C b Furlong, C. E.: The effect of the human serum paraoxonase polymorphismis reversed with diazoxon, soman and sarin. Nature Genet. 14: 334- 336,1996.

GAM1338 360 PON1 Deakin, S.; Leviev, I.; Nicaud, V.; Meynet, M.- C. B.; Tiret, L.;James, R. 3 C b W.: Paraoxonase- 1 L55M polymorphism is associated withan abnormal oral glucose tolerance test and differentiates high riskcoronary disease families. J. Clin. Endocr. Metab. 87: 1268- 1273,2002.

GAM1338 360 PON1 Eckerson, H. W.; Romson, J.; Wyte, C.; La Du, B. N.: The humanserum 3 C b paraoxonase polymorphism: identification of phenotypes by theirresponse to salts. Am. J. Hum. Genet. 35: 214- 227, 1983.

GAM1338 360 PON1 Eckerson, H. W.; Wyte, C. M.; La Du, B. N.: The human serum 3 C b paraoxonase/arylesterasepolymorphism. Am. J. Hum. Genet. 35: 1126- 1136, 1983.

GAM1338 360 PON1 Eiberg, H.; Mohr, J.: Linkage relations of the paraoxonase polymorphismwith 3 C b 43 marker systems. (Abstract) Cytogenet. Cell Genet. 25: 150,1979.

GAM1338 360 PON1 Eiberg, H.; Mohr, J.; Schmiegelow, K.; Nielsen, L. S.; Williamson,R.: 3 C b Linkage relationships of paraoxonase (PON) with other markers:indication of PON- cystic fibrosis synteny. Clin. Genet. 28: 265- 271,1985.

GAM1338 360 PON1 Furlong, C. E.; Richter, R. J.; Chapline, C.; Crabb, J. W.: Purificationof 3 C b rabbit and human serum paraoxonase. Biochemistry 30: 10133- 10140,1991.

GAM1338 360 PON1 Furlong, C. E.; Richter, R. J.; Seidel, S. L.; Motulsky, A. G.: Role of 3 C b genetic polymorphism of human plasma paraoxonase/arylesterasein hydrolysis of the insecticide metabolites chlorpyrifos oxon andparaoxon. Am. J. Hum. Genet. 43: 230- 238, 1988.

GAM1338 360 PON1 Garin, M.- C. B.; James, R. W.; Dussoix, P.; Blanche, H.; Passa,P.; Froguel, 3 C b P.; Ruiz, J.: Paraoxonase polymorphism met- leu54 isassociated with modified serum concentrations of the enzyme: a possiblelink between the paraoxonase gene and increased risk of cardiovasculardisease in diabetes. J. Clin. Invest. 99: 62- 66, 1997.

GAM1338 360 PON1 Geldmacher- von Mallinckrodt, M.: Polymorphism of human serumparaoxonase. 3 C b

Hum. Genet. 45 (suppl. 1): 65- 68, 1978.

GAM1338 360 PON1 Geldmacher- von Mallinckrodt, M.; Lindorft, H. H.; Petenyi, M.;Flugel, M.; 3 C b Fischer, T.; Hiller, T.: Genetisch determinierter Polymorphismusde menschlichen Serum- Paroxonase (E.C.3.1.1.2). Humangenetik 17:331- 335, 1973.

GAM1338 360 PON1 Hassett, C.; Richter, R. J.; Humbert, R.; Chapline, C.; Crabb,J. W.; 3 C b Omiecinski, C. J.; Furlong, C. E.: Characterization of cDNAclones encoding

rabbit and human serum paraoxonase: the mature proteinretains its signal sequence. Biochemistry 30: 10141- 10149, 1991.

GAM1338 360 PON1 Humbert, R.; Adler, D. A.; Disteche, C. M.; Hassett, C.; Omiecinski,C. J.; 3 C b Furlong, C. E.: The molecular basis of the human serum paraoxonaseactivity polymorphism. Nature Genet. 3: 73- 76, 1993.

GAM1338 360 PON1 Ito, T.; Yasue, H.; Yoshimura, M.; Nakamura, S.; Nakayama, M.;Shimasaki, Y.; 3 C b Harada, E.; Mizuno, Y.; Kawano, H.; Ogawa, H.: Paraoxonasegene gln192- to-arg (Q192R) polymorphism is associated with coronaryartery spasm. Hum. Genet. 110: 89- 94, 2002.

GAM1338 360 PON1 Kao, Y.- L.; Donaghue, K.; Chan, A.; Knight, J.; Silink, M.: Avariant of 3 C b paraoxonase (PON1) gene is associated with diabetic retinopathyin IDDM. J. Clin. Endocr. Metab. 83: 2589- 2592, 1998.

GAM1338 360 PON1 La Du, B. N.: The human serum paraoxonase/arylesterase 3 C b polymorphism.(Editorial) Am. J. Hum. Genet. 43: 227- 229, 1988.

GAM1338 360 PON1 Li, W.- F.; Furlong, C. E.; Costa, L. G.: Paraoxonase protectsagainst 3 C b chlorpyrifos toxicity in mice. Toxic. Lett. 76: 219- 226,1995.

GAM1338 360 PON1 Li, W.- F.; Matthews, C.; Disteche, C. M.; Costa, L. G.; Furlong,C. E.: 3 C b Paraoxonase (Pon1) gene in mice: sequencing, chromosomal localizationand developmental expression. Pharmacogenetics 7: 137- 144, 1997.

GAM1338 360 PON1 Mackness, B.; Mackness, M. I.; Arrol, S.; Turkie, W.; Durrington,P. N.: 3 C b Effect of the human serum paraoxonase 55 and 192 genetic polymorphismson the protection by high density lipoprotein against low densitylipoprotein oxidative modification. FEBS Lett. 423: 57- 60, 1998.

GAM1338 360 PON1 Mochizuki, H.; Scherer, S. W.; Xi, T.; Nickle, D. C.; Majer, M.;Huizenga, J. 3 C b J.; Tsui, L.- C.; Prochazka, M.: Human PON2 gene at 7q21.3:cloning, multiple mRNA forms, and missense polymorphisms in the codingsequence. Gene 213: 149-157, 1998.

GAM1338 360 PON1 Mueller, R. F.; Hornung, S.; Furlong, C. E.; Anderson, J.; Giblett,E. R.; 3 C b Motulsky, A. G.: Plasma paraoxonase polymorphism: a new enzymeassay, population, family, biochemical, and linkage studies. Am.J. Hum. Genet. 35: 393- 408, 1983.

GAM1338 360 PON1 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. 3 C b J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J. Clin. Invest. 99: 2005- 2019, 1997.

GAM1338 360 PON1 Neel, J. V.; Tanis, R. J.; Migliazza, E. C.; Spielman, R. S.;Salzano, F. M.; 3 C b Oliver, W. J.; Morrow, M.; Bachofer, S.: Geneticstudies of the Macushi and Wapishana Indians. I. Rare genetic variantsand a 'private polymorphism' of esterase A. Hum. Genet. 36: 81- 108,1977.

GAM1338 360 PON1 Nielsen, A.; Eiberg, H.; Mohr, J.: Number of loci responsiblefor the 3 C b inheritance of high and low activity of paraoxonase. Clin.Genet. 29: 216-221, 1986.

GAM1338 360 PON1 Odawara, M.; Tachi, Y.; Yamashita, K.: Paraoxonase polymorphismGln192- Arg 3 C b is associated with coronary heart disease in Japanese noninsulin-dependentdiabetes mellitus. J. Clin. Endocr. Metab. 82: 2257- 2260, 1997.

GAM1338 360 PON1 Ortigoza- Ferado, J.; Richter, R. J.; Hornung, S. K.; Motulsky,A. G.; 3 C b Furlong, C. E.: Paraoxon hydrolysis in human serum mediatedby a genetically variable arylesterase and albumin. Am. J. Hum. Genet. 36:295- 305, 1984.

GAM1338 360 PON1 Paolisso, G.; Manzella, D.; Tagliamonte, M. R.; Barbieri, M.;Marfella, R.; 3 C b

Zito, G.; Bonafe, M.; Giugliano, D.; Franceschi, C.;Varricchio, M.: The BB-paraoxonase genotype is associated with impairedbrachial reactivity after acute hypertriglyceridemia in healthy subjects. J.Clin. Endocr. Metab. 86: 1078- 1082, 2001.

GAM1338 360 PON1 Playfer, J. R.; Eze, L. C.; Bullen, M. F.; Evans, D. A. P.: 3 C b
Geneticpolymorphism and interethnic variability of plasma paroxonase activity. J.Med. Genet. 13: 337- 342, 1976.

GAM1338 360 PON1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 C b
New York: Oxford Univ. Press (pub.) 1988.

GAM1338 360 PON1 Schmiegelow, K.; Eiberg, H.; Tsui, L.- C.; Buchwald, M.; Phelan,P. D.; 3 C b
Williamson, R.; Warwick, W.; Niebuhr, E.; Mohr, J.; Schwartz,M.; Koch, C.: Linkage between the loci for cystic fibrosis and paraoxonase. Clin.Genet. 29: 374- 377, 1986.

GAM1338 360 PON1 Serrato, M.; Marian, A. J.: A variant of human 3 C b
paraoxonase/arylesterase(HUMPONA) gene is a risk factor for coronary artery disease. J. Clin.Invest. 96: 3005- 3008, 1995.

GAM1338 360 PON1 Shih, D. M.; Gu, L.; Xia, Y.- R.; Navab, M.; Li, W.- F.; Hama, 3 C b
S.;Castellani, L. W.; Furlong, C. E.; Costa, L. G.; Fogelman, A. M.;Lusis, A. J.: Mice lacking serum paraoxonase are susceptible to organophosphatetoxicity and atherosclerosis. Nature 394: 284- 287, 1998.

GAM1338 360 PON1 Simpson, N. E.: Serum arylesterase levels of activity in twinsand their 3 C b
parents. Am. J. Hum. Genet. 23: 375- 382, 1971.

GAM1338 360 PON1 Sorenson, R. C.; Primo- Parmo, S. L.; Camper, S.; La Du, B. N.: The genetic 3 C b
mapping and gene structure of mouse paraoxonase/arylesterase. Genomics 30:431- 438, 1995.

GAM1338 360 PON1 Tashian, R. E.: Genetic variation and evolution of the carboxylicesterases 3 C b
and carbonic anhydrases of primate erythrocytes. Am. J.Hum. Genet. 17: 257-272, 1965.

GAM1338 360 PON1 Tashian, R. E.; Shaw, M. W.: Inheritance of an erythrocyte 3 C b
acetylesterasevariant of man. Am. J. Hum. Genet. 14: 295- 300, 1962.

GAM1338 360 PON1 Tsui, L.- C.; Buchwald, M.; Barker, D.; Braman, J. C.; Knowlton,R.; Schumm, 3 C b
J. W.; Eiberg, H.; Mohr, J.; Kennedy, D.; Plavsic, N.;Zsiga, M.; Markiewicz, D.; Akots, G.; Brown, V.; Helms, C.; Gravius,T.; Parker, C.; Rediker, K.; Donis- Keller, H.: Cystic fibrosis locusdefined by a genetically linked polymorphic DNA marker. Science 230:1054- 1057, 1985.

GAM1338 360 PON1 Watson, C. E.; Draganov, D. I.; Billecke, S. S.; Bisgaier, C.L.; La Du, B. 3 C b
N.: Rabbits possess a serum paraoxonase polymorphismsimilar to the human Q192R. Pharmacogenetics 11: 123- 134, 2001.

GAM1338 360 PON1 Yamasaki, Y.; Sakamoto, K.; Watada, H.; Kajimoto, Y.; Hori, M.: The arg- 192 3 C b
isoform of paraoxonase with low sarin- hydrolyzing activityis dominant in the Japanese. Hum. Genet. 101: 67- 68, 1997.

GAM1338 360 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 3 C c
Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 2002.

GAM1338 360 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 3 C c
cell coactivator of octamer- binding transcription factors. Nature 373:360-362, 1995.

GAM1338 360 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 3 C c
Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-

specific coactivator of octamer- binding transcription factors1 and 2, to 11q23.1 by somatic cell hybridization and in situ hybridization. Genomics 33:143- 145, 1996.

GAM1338 360 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995. 3 C c

GAM1338 360 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001. 3 C c

GAM1338 360 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. Immun. 9: 373- 398, 1991. 3 C c

GAM1338 360 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- specificcoactivator that stimulates immunoglobulin promoter activity throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995. 3 C c

GAM1338 360 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B, BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853- 864, 2000. 3 C c

GAM1338 360 POU3F1 Avraham, K. B.; Cho, B. C.; Gilbert, D.; Fujii, H.; Okamoto, K.;Shimazaki, T.; Ito, T.; Shoji, H.; Wakamatsu, Y.; Kondoh, H.; Takahashi,N.; Muramatsu, M.; Hamada, H.; Copeland, N. G.; Jenkins, N. A.: Murinechromosomal location of four class III POU transcription factors. Genomics 18:131- 133, 1993. 3 C c

GAM1338 360 POU3F1 Bermingham, J. R., Jr.; Scherer, S. S.; O'Connell, S.; Arroyo,E.; Kalla, K. A.; Powell, F. L.; Rosenfeld, M. G.: Tst- 1/Oct- 6/SCIPregulates a unique step in peripheral myelination and is requiredfor normal respiration. Genes Dev. 10: 1751- 1762, 1996. 3 C c

GAM1338 360 POU3F1 Jaegle, M.; Mandemakers, W.; Broos, L.; Zwart, R.; Karis, A.; Visser,P.; Grosveld, F.; Meijer, D.: The POU factor Oct- 6 and Schwann celldifferentiation. Science 273: 507- 510, 1996. 3 C c

GAM1338 360 POU3F1 Sumiyama, K.; Washio- Watanabe, K.; Ono, T.; Yoshida, M. C.; Hayakawa,T.; Ueda, S.: Human class III POU genes, POU3F1 and POU3F3, map tochromosomes 1p34.1 and 3p14.1. Mammalian Genome 9: 180- 181, 1998. 3 C c

GAM1338 360 POU3F1 Xia, Y.- R.; Andersen, B.; Mehrabian, M.; Diep, A. T.; Warden, C.H.; Mohandas, T.; McEvilly, R. J.; Rosenfeld, M. G.; Lusis, A. J.: Chromosomal organization of mammalian POU domain factors. Genomics 18:126- 130, 1993. 3 C c

GAM1338 360 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor integrity, and rhodopsin dephosphorylation in mice lackingboth protein phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21: 8605- 8614, 2001. 3 C c

GAM1338 360 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; Nathans, J.: Identification and characterization of a conservedfamily of protein serine/threonine phosphatases homologous to Drosophilaretinal degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997. 3 C c

GAM1338 360 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component of the steroid receptor complex: cloning of thecDNA and further characterization. J. Biol. Chem. 268: 12303- 12310,1993. 3 C c

GAM1338 360 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 C c

characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem. 267: 5503- 5507, 1992.

GAM1338 360 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 C c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151 only, 1997.

GAM1338 360 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 C c
J.- E.: The structure and complete nucleotide sequenceof the human cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM1338 360 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 C c
Chromosomalassignment of the interferon- inducible double- stranded RNA-dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM1338 360 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human 3 C c
interferon- gamma mRNA autoregulates its translation througha pseudoknot that activates the interferon- inducible protein kinasePKR. Cell 108: 221-232, 2002.

GAM1338 360 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; 3 C c
Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR) encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and differences from its mouse homolog. Genomics 36:197- 201, 1996.

GAM1338 360 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: 3 C c
sequence of the human interferon- inducible RNA- dependent proteinkinase (PKR) deduced from genomic clones. Gene 178: 191- 193, 1996.

GAM1338 360 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; 3 C c
Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand characterization of the human double- stranded RNA- activated proteinkinase induced by interferon. Cell 62: 379- 390, 1990.

GAM1338 360 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; 3 C c
Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds preferentially to Huntington's disease (HD) transcriptsand is activated in HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001.

GAM1338 360 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. 3 C c
G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics 16:768- 770, 1993.

GAM1338 360 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: 3 C c
Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein. Science 285: 107- 110, 1999.

GAM1338 360 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 C b
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.: Genomicorganization, comparative analysis, and genetic polymorphisms of thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733, 2001.

GAM1338 360 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 C b
Chen, S. G.: Expression and structural characterizationof the recombinant human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM1338 360 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 C b
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.; Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-deficient mice is associated with upregulation of thenovel PrP- like protein

doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM1338 360 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin the prion- like protein gene (Prnd) and their implications inhuman prion diseases, Alzheimer's disease and other neurological disorders. Hum.Genet. 109: 319- 325, 2001. 3 C b

GAM1338 360 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-glycosylated, glycosylphosphatidylinositol- anchored protein:expression in testis and ectopic production in the brains of Prnp(0/0)mice predisposed to Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000. 3 C b

GAM1338 360 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 915, 1999. 3 C b

GAM1338 360 PSMD9 Thomas, M. K.; Yao, K.- M.; Tenser, M. S.; Wong, G. G.; Habener,J. F.: Bridge- 1, a novel PDZ- domain coactivator of E2A- mediated regulationof insulin gene transcription. Molec. Cell. Biol. 19: 8492- 8504,1999. 3 C c

GAM1338 360 PSMD9 Watanabe, T. K.; Saito, A.; Suzuki, M.; Fujiwara, T.; Takahashi,E.; Slaughter, C. A.; DeMartino, G. N.; Hendil, K. B.; Chung, C. H.;Tanahashi, N.; Tanaka, K.: cDNA cloning and characterization of ahuman proteasomal modulator subunit, p27 (PSMD9). Genomics 50: 241- 250,1998. 3 C c

GAM1338 360 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime-untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001. 3 C b

GAM1338 360 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994. 3 C b

GAM1338 360 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996. 3 C b

GAM1338 360 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996. 3 C b

GAM1338 360 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996. 3 C b

GAM1338 360 PTK2 Andre, E.; Becker- Andre, M.: Expression of an N- terminally truncatedform of human focal adhesion kinase in brain. Biochem. Biophys. Res.Commun. 190: 140- 147, 1993. 3 C c

GAM1338 360 PTK2 Fiedorek, F. T., Jr.; Kay, E. S.: Mapping of the focal adhesionkinase (Fadk) gene to mouse chromosome 15 and human chromosome 8. MammalianGenome 6: 123-126, 1995. 3 C c

GAM1338 360 PTK2 Polte, T. R.; Hanks, S. K.: Interaction between focal adhesionkinase and Crk- associated tyrosine kinase substrate p130- Cas. Proc.Nat. Acad. Sci. 92: 10678- 10682, 1995. 3 C c

GAM1338 360 PTK2 Schaller, M. D.; Borgman, C.; Cobb, B. S.; Vines, R. R.; Reynolds,A. B.; Parsons, J. T.: pp125(FAK), a structurally distinctive protein- 3 C c

tyrosinekinase associated with focal adhesions. Proc. Nat. Acad. Sci. 89:5192- 5196, 1992.

GAM1338 360 RAB31 Chen, D.; Guo, J.; Miki, T.; Tachibana, M.; Gahl, W. A.: Molecularcloning of two novel rab genes from human melanocytes. Gene 174:129- 134, 1996. 3 C c

GAM1338 360 RAB31 Scott, A. F.: Personal Communication. Baltimore, Md. 2/26/2001. 3 C c

GAM1338 360 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999. 3 C c

GAM1338 360 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000. 3 C c

GAM1338 360 RERE Amler, L. C.; Bauer, A.; Corvi, R.; Dihlmann, S.; Praml, C.; Cavenee,W. K.; Schwab, M.; Hampton, G. M.: Identification and characterizationof novel genes located at the t(1;15)(p36.2;q24) translocation breakpointin the neuroblastoma cell line NGP. Genomics 64: 195- 202, 2000. 3 C c

GAM1338 360 RERE Yanagisawa, H.; Bundo, M.; Miyashita, T.; Okamura- Oho, Y.; Tadokoro,K.; Tokunaga, K.; Yamada, M.: Protein binding of a DRPLA family throughargininе-glutamic acid dipeptide repeats is enhanced by extended polyglutamine. Hum.Molec. Genet. 9: 1433- 1442, 2000. 3 C c

GAM1338 360 RGS3 Chatterjee, T. K.; Eapen, A.; Kanis, A. B.; Fisher, R. A.: Genomicorganization, 5- prime- flanking region, and chromosomal localizationof the human RGS3 gene. Genomics 45: 429- 433, 1997. 3 C c

GAM1338 360 RGS3 Druey, K. M.; Blumer, K. J.; Kang, V. H.; Kehrl, J. H.: Inhibitionof G-protein- mediated MAP kinase activation by a new mammalian genefamily. Nature 379: 742- 746, 1996. 3 C c

GAM1338 360 RGS3 Lu, Q.; Sun, E. E.; Klein, R. S.; Flanagan, J. G.: Ephrin- B reversesignaling is mediated by a novel PDZ- RGS protein and selectively inhibitsG protein- coupled chemoattraction. Cell 105: 69- 79, 2001. 3 C c

GAM1338 360 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993. 3 C b

GAM1338 360 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA amplification. New Eng. J. Med. 329: 607- 610, 1993. 3 C b

GAM1338 360 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. Med. 339: 1775- 1777, 1998. 3 C b

GAM1338 360 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand molecular genetics. Blood Rev. 8: 199- 212, 1994. 3 C b

GAM1338 360 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood group polymorphism as determined by Southern analysis. Blood 78:2747- 2752, 1991. 3 C b

GAM1338 360 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and its association with universal edema of the fetus, icterusgravis neonatorum and anemia of the newborn. J. Pediat. 1: 269- 309,1932. 3 C b

GAM1338 360 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989. 3 C b

GAM1338 360 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with 3 C b

sickle cell disease. Transfusion 37: 357- 361, 1997.

GAM1338 360 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 C b

GAM1338 360 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the human RH locus: a family study of the red- cell Evans phenotypereveals a transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59: 825- 833, 1996. 3 C b

GAM1338 360 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J. Hum. Genet. 58: 133- 142, 1996. 3 C b

GAM1338 360 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of Rh blood group genes: association between restrictionfragment length polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994. 3 C b

GAM1338 360 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine years and some observations on the biochemistry and geneticsof the system. Transfusion Med. Rev. 3: 1- 12, 1989. 3 C b

GAM1338 360 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh genes revealed by analysis of unrelated donors with therare D- - phenotype. Am. J. Hum. Genet. 59: 1066- 1073, 1996. 3 C b

GAM1338 360 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by alternative splicing. Blood 80: 1074- 1078, 1992. 3 C b

GAM1338 360 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929, 1992. 3 C b

GAM1338 360 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE genotyping for correct blood group determination inchronically transfused patients. Transfusion 39: 852- 855, 1999. 3 C b

GAM1338 360 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A. 116:825- 827, 1941. 3 C b

GAM1338 360 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal plasma. New Eng. J. Med. 339: 1734- 1738, 1998. 3 C b

GAM1338 360 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome 1. Am. J. Med. Genet. 104: 250- 256, 2001. 3 C b

GAM1338 360 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J. Clin. Invest. 100: 373- 379, 1997. 3 C b

GAM1338 360 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 153:771- 772, 1944. 3 C b

GAM1338 360 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th ed.): 1975. 3 C b

GAM1338 360 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- to- pro substitution in the RhD polypeptide is responsiblefor the D(VII) category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995. 3 C b

GAM1338 360 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral transduction of K562 cells establishes the molecular basisof Rh blood group antigens. Blood 87: 2968- 2973, 1996. 3 C b

GAM1338 360 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang. 58: 50- 55, 1990. 3 C b

GAM1338 360 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. Blood 95: 3662- 3668, 2000. 3 C b

GAM1338 360 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393, 1999. 3 C b

GAM1338 360 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311, 2002. 3 C b

GAM1338 360 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 C b

GAM1338 360 RPH3AL Kotake, K.; Ozaki, N.; Mizuta, M.; Sekiya, S.; Inagaki, N.; Seino,S.: Noc2, a putative zinc finger protein involved in exocytosis inendocrine cells. J. Biol. Chem. 272: 29407- 29410, 1997. 3 C b

GAM1338 360 RPH3AL Smith, J. S.; Tachibana, I.; Allen, C.; Chiappa, S. A.; Lee, H.K.; McIver, B.; Jenkins, R. B.; Raffel, C.: Cloning of a human ortholog(RPH3AL) of (RNO)Rph3al from a candidate 17p13.3 medulloblastoma tumorsuppressor locus. Genomics 59: 97- 101, 1999. 3 C b

GAM1338 360 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two scleroderma autoimmune antigens that copurify with human ribonucleaseP. Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997. 3 C b

GAM1338 360 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: Autoantigenic properties of some protein subunits of catalyticallyactive complexes of human ribonuclease P. RNA 4: 407- 417, 1998. 3 C b

GAM1338 360 SAS Jankowski, S. A.; De Jong, P.; Meltzer, P. S.: Genomic structureof SAS, a member of the transmembrane 4 superfamily amplified in humansarcomas. Genomics 25: 501- 506, 1995. 3 C c

GAM1338 360 SAS Meltzer, P. S.; Jankowski, S. A.; Dal Cin, P.; Sandberg, A. A.;Paz, I. B.; Coccia, M. A.; Smith, S. H.: Identification and cloningof a novel amplified DNA sequence in human malignant fibrous histiocytomaderived from a region of chromosome 12 frequently rearranged in softtissue tumors. (Abstract) Cytogenet. Cell Genet. 58: 1979 only,1991. 3 C c

GAM1338 360 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 C b

GAM1338 360 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 C b

GAM1338 360 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 C b

GAM1338 360 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the 3 C b

gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999.

GAM1338 360 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; 3 C b Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM1338 360 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 3 C b Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001.

GAM1338 360 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 3 C b A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five- base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000.

GAM1338 360 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 3 C b for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001.

GAM1338 360 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, 3 C b H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002.

GAM1338 360 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; 3 C b Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001.

GAM1338 360 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked 3 C b recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999.

GAM1338 360 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; 3 C b Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001.

GAM1338 360 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the 3 C b gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996.

GAM1338 360 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen 3 C b responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001.

GAM1338 360 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, 3 C b S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995.

GAM1338 360 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. 3 C b A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996.

GAM1338 360 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 3 C c

GAM1338 360 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 3 C c

GAM1338 360 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 3 C c

GAM1338 360 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human intestine:biology and function. Gastroenterology 113: 332- 340, 1997. 3 C c

GAM1338 360 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563- 566, 1994. 3 C c

GAM1338 360 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 3 C c

GAM1338 360 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998. 3 C c

GAM1338 360 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 3 C c

GAM1338 360 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses and phylogenetic characterization of the ZIP family of metalion transport proteins. J. Membr. Biol. 166: 1- 7, 1998. 3 C b

GAM1338 360 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping within the epidermal differentiation complex. Genomics 62:272- 280, 1999. 3 C b

GAM1338 360 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC fragmentation map of 1q21. Genomics 49: 200- 208, 1998. 3 C b

GAM1338 360 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855- 862, 2000. 3 C b

GAM1338 360 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein that promotes cytochrome c- dependent caspase activation byeliminating IAP inhibition. Cell 102: 33- 42, 2000. 3 C b

GAM1338 360 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000. 3 C b

GAM1338 360 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509- 3517, 2002. 3 C b

GAM1338 360 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 C b

GAM1338 360 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.: A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates caspase activity and apoptosis. Nature 410:112- 116, 2001. 3 C b

GAM1338 360 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO, a mammalian protein that promotes apoptosis by bindingto and antagonizing IAP proteins. Cell 102: 43- 53, 2000. 3 C b

GAM1338 360 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012, 2000. 3 C b

GAM1338 360 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998. 3 C c

GAM1338 360 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle- membranefusion processes. Hum. Genet. 108: 211- 215, 2001. 3 C c

GAM1338 360 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells. Biochem. Biophys. Res. Commun. 231: 808- 812, 1997. 3 C c

GAM1338 360 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996. 3 C c

GAM1338 360 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: Identification of three new splice variants of the SNARE proteinSNAP- 23. Biochem. Biophys. Res. Commun. 285: 320- 327, 2001. 3 C c

GAM1338 360 SRRM2 Blencowe, B. J.; Bauren, G.; Eldridge, A. G.; Issner, R.; Nickerson,J. A.; Rosonina, E.; Sharp, P. A.: The SRm160/300 splicing coactivatorsubunits. RNA 6: 111- 120, 2000. 3 C c

GAM1338 360 SRRM2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C c

GAM1338 360 SRRM2 Sawada, Y.; Miura, Y.; Umeki, K.; Tamaoki, T.; Fujinaga, K.; Ohtaki,S.: Cloning and characterization of a novel RNA- binding protein SRL300with RS domains. Biochim. Biophys. Acta 1492: 191- 195, 2000. 3 C c

GAM1338 360 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994. 3 C b

GAM1338 360 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995. 3 C b

GAM1338 360 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand 3 C b

characterization of the mouse homolog of SYT, a gene implicatedin the development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM1338 360 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. G.: Mapping and characterization of the mouse and humanSS18 genes, two human SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310- 319, 2001. 3 C b

GAM1338 360 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene family with several members transcribed in normaltestis and human cancer. Int. J. Cancer 72: 965- 971, 1997. 3 C b

GAM1338 360 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998. 3 C b

GAM1338 360 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J. Nat. Cancer Inst. 91: 974- 975, 1999. 3 C b

GAM1338 360 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX synovial sarcoma translocation proteins and co- localizationwith the SNF protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999. 3 C b

GAM1338 360 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in synovial sarcomas. Oncogene 21: 4181- 4190, 2002. 3 C b

GAM1338 360 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence insitu hybridization. Genomics 36: 527- 529, 1996. 3 C b

GAM1338 360 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence homologue of staufen is an RNA- binding protein thatis associated with polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell. Biol. 19: 2212- 2219, 1999. 3 C b

GAM1338 360 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19: 2220- 2230, 1999. 3 C b

GAM1338 360 STE Aksoy, I. A.; Wood, T. C.; Weinshilboum, R.: Human liver estrogensulfotransferase: identification by cDNA cloning and expression. Biochem.Biophys. Res. Commun. 200: 1621- 1629, 1994. 3 C b

GAM1338 360 STE Bernier, F.; Leblanc, G.; Labrie, F.; Luu- The, V.: Structure ofhuman estrogen and aryl sulfotransferase gene: two mRNA species issuedfrom a single gene. J. Biol. Chem. 269: 28200- 28205, 1994. 3 C b

GAM1338 360 STE Her, C.; Aksoy, I. A.; Kimura, S.; Brandriff, B. F.; Wasmuth, J.J.; Weinshilboum, R. M.: Human estrogen sulfotransferase gene (STE):cloning, structure, and chromosomal localization. Genomics 29: 16- 23,1995. 3 C b

GAM1338 360 STE Weinshilboum, R. M.; Otterness, D. M.; Aksoy, I. A.; Wood, T. C.;Her, C.; Raftogianis, R. B.: Sulfotransferase molecular biology:cDNAs and genes. FASEB J. 11: 3- 14, 1997. 3 C b

GAM1338 360 STE Weinshilboum, R.: Personal Communication. Rochester, Minn. 10/9/1995. 3 C b

GAM1338 360 TAL1 Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to 3 C c

generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997.

GAM1338 360 TAL1 Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 C c

GAM1338 360 TAL1 Begley, C. G.; Aplan, P. D.; Davey, M. P.; Nakahara, K.; Tchorz,K.; Kurtzberg, J.; Hershfield, M. S.; Haynes, B. F.; Cohen, D. I.;Waldmann, T. A.; Kirsch, I. R.: Chromosomal translocation in a humanleukemic stem- cell line disrupts the T- cell antigen receptor delta- chaindiversity region and results in a previously unreported fusion transcript. Proc.Nat. Acad. Sci. 86: 2031- 2035, 1989. 3 C c

GAM1338 360 TAL1 Begley, C. G.; Visvader, J.; Green, A. R.; Aplan, P. D.; Metcalf,D.; Kirsch, I. R.; Gough, N. M.: Molecular cloning and chromosomallocalization of the murine homolog of the human helix- loop- helix geneSCL. Proc. Nat. Acad. Sci. 88: 869- 873, 1991. 3 C c

GAM1338 360 TAL1 Finger, L. R.; Kagan, J.; Christopher, G.; Kurtzberg, J.; Hershfield,M. S.; Nowell, P. C.; Croce, C. M.: Involvement of the TCL5 geneon human chromosome 1 in T- cell leukemia and melanoma. Proc. Nat.Acad. Sci. 86: 5039- 5043, 1989. 3 C c

GAM1338 360 TAL1 Gottgens, B.; Barton, L. M.; Chapman, M. A.; Sinclair, A. M.; Knudsen,B.; Grafham, D.; Gilbert, J. G. R.; Rogers, J.; Bentley, D. R.; Green,A. R.: Transcriptional regulation of the stem cell leukemia gene(SCL)- - comparative analysis of five vertebrate SCL loci. Genome Res. 12:749- 759, 2002. 3 C c

GAM1338 360 TAL1 Gottgens, B.; Gilbert, J. G.; Barton, L. M.; Grafham, D.; Rogers,J.; Bentley, D. R.; Green, A. R.: Long- range comparison of humanand mouse SCL loci: localized regions of sensitivity to restrictionendonucleases correspond precisely with peaks of conserved noncodingsequences. Genome Res. 11: 87- 97, 2001. 3 C c

GAM1338 360 TAL1 Kocher, O.; Cheresh, P.; Lee, S. W.: Identification and partialcharacterization of a novel membrane- associated protein (MAP17) up-regulatedin human carcinomas and modulating cell replication and tumor growth. Am.J. Path. 149: 493- 500, 1996. 3 C c

GAM1338 360 TAL1 Kozak, M.: An analysis of 5- prime- noncoding sequences from 699vertebrate messenger RNAs. Nucleic Acids Res. 15: 8125- 8148, 1987. 3 C c

GAM1338 360 TAL1 Kurtzberg, J.; Bigner, S. H.; Hershfield, M. S.: Establishmentof the DU.528 human lymphohemopoietic stem cell line. J. Exp. Med. 162:1561- 1578, 1985. 3 C c

GAM1338 360 TAL1 Robb, L.; Lyons, I.; Li, R.; Hartley, L.; Kontgen, F.; Harvey,R. P.; Metcalf, D.; Begley, C. G.: Absence of yolk sac hematopoiesisfrom mice with a targeted disruption of the scl gene. Proc. Nat.Acad. Sci. 92: 7075- 7079, 1995. 3 C c

GAM1338 360 TAL1 Shivdasani, R. A.; Mayer, E. L.; Orkin, S. H.: Absence of bloodformation in mice lacking the T- cell leukaemia oncoprotein tal- 1/SCL. Nature 373:432-434, 1995. 3 C c

GAM1338 360 TAL1 Sinclair, A. M.; Bench, A. J.; Bloor, A. J. C.; Li, J.; Gottgens,B.; Stanley, M. L.; Miller, J.; Piltz, S.; Hunter, S.; Nacheva, E.P.; Sanchez, M.- J.; Green, A. R.: Rescue of the lethal scl- /- phenotypeby the human SCL locus. Blood 99: 3931- 3938, 2002. 3 C c

GAM1338 360 TAL1 Williams, M.; Lyu, M. S.; Yang, Y. L.; Lin, E. P.; Dunbrack, R.;Birren, B.; Cunningham, J.; Hunter, K.: Ier5, a novel member of theslow- kinetics 3 C c

immediate- early genes. Genomics 44: 327- 334, 1999.

GAM1338 360 TAL1 Xia, Y.; Brown, L.; Yang, C. Y.- C.; Tsou Tsan, J.; Siciliano,M. J.; Espinosa, R., III; Le Beau, M. M.; Baer, R. J.: TAL2, a helix- loop-helixgene activated by the (7;9)(q34;q32) translocation in human T-cellleukemia. Proc. Nat. Acad. Sci. 88: 11416- 11420, 1991. 3 C c

GAM1338 360 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459-467, 1998. 3 C b

GAM1338 360 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 C b

GAM1338 360 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 C b

GAM1338 360 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 C b

GAM1338 360 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 C b

GAM1338 360 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 C b

GAM1338 360 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496-1498, 2002. 3 C b

GAM1338 360 TAT Barton, D. E.; Yang- Feng, T. L.; Francke, U.: The human tyrosineaminotransferase gene mapped to the long arm of chromosome 16 (region16q22- q24) by somatic cell hybrid analysis and in situ hybridization. Hum.Genet. 72: 221- 224, 1986. 3 C c

GAM1338 360 TAT Beinfang, D. C.; Kuwabara, T.; Pueschel, S. M.: The Richner-Hanhartsyndrome: report of a case with associated tyrosinemia. Arch. Ophthal. 94:1133- 1137, 1976. 3 C c

GAM1338 360 TAT Bohnert, A.; Anton- Lamprecht, I.: Richner- Hanhart's syndrome:ultrastructural abnormalities of epidermal keratinization indicatinga causal relationship to high intracellular tyrosine levels. J. Invest.Derm. 79: 68- 74, 1982. 3 C c

GAM1338 360 TAT Buist, N.: Phenylketonuria and related problems.In: Nyhan, W.L.: Amino Acid Metabolism and Genetic Variation. New York: McGraw- Hill(pub.) 1967. Pp. 117 only. 3 C c

GAM1338 360 TAT Chitayat, D.; Balbul, A.; Hani, V.; Mamer, O. A.; Clow, C.; Scriver,C. R.: Hereditary tyrosinaemia type II in a consanguineous AshkenaziJewish family: intrafamilial variation in phenotype; absence of parentalphenotype effects on the fetus. J. Inherit. Metab. Dis. 15: 198- 203,1992. 3 C c

GAM1338 360 TAT Crovato, F.; Desirello, G.; Gatti, R.; Babbini, N.; Rebora, A.: Richner-Hanhart syndrome spares a plantar autograft. Arch. Derm. 121:539- 540, 1985. 3 C c

GAM1338 360 TAT Fellman, J. H.; Vanbellinghen, P. J.; Jones, R. T.; Koler, R. D.: Soluble 3 C c

and mitochondrial forms of tyrosine aminotransferase: relationshipto human tyrosinemia. Biochemistry 8: 615- 622, 1969.

GAM1338 360 TAT Garibaldi, L. R.; Siliato, F.; De Martini, I.; Scarsi, M. R.; Romano,C.: 3 C c
Oculocutaneous tyrosinosis: report of two cases in the same family. Helv.Paediat. Acta 32: 173- 180, 1977.

GAM1338 360 TAT Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald,P. S.; 3 C c
Baden, H. P.: Tyrosinemia with plantar and palmar keratosisand keratitis. J. Pediat. 83: 798- 805, 1973.

GAM1338 360 TAT Hanhart, E.: Neue Sonderformen von Keratosis palmo- plantaris,u.a. eine 3 C c
regelmaessig- dominante mit systematisierten Lipomen, ferner2 einfach-rezessive mit Schwachsinn und z.T. mit Hornhautveraenderungendes Auges (Ektodermatosyndrom). Dermatologica 94: 286- 308, 1947.

GAM1338 360 TAT Hunziker, N.: Richner- Hanhart syndrome and tyrosinemia type II. 3 C c
Dermatologica 160:180- 189, 1980.

GAM1338 360 TAT Kennaway, N. G.; Buist, N. R. M.: Metabolic studies in a patientwith hepatic 3 C c
cytosol tyrosine aminotransferase deficiency. Pediat.Res. 5: 287- 297, 1971.

GAM1338 360 TAT Muller, G.; Scherer, G.; Zentgraf, H.; Ruppert, S.; Herrmann,B.; Lehrach, 3 C c
H.; Schutz, G.: Isolation, characterization and chromosomalmapping of the mouse tyrosine aminotransferase gene. J. Molec. Biol. 184:367- 373, 1985.

GAM1338 360 TAT Natt, E.; Kao, F.- T.; Rettenmeier, R.; Scherer, G.: Assignmentof the human 3 C c
tyrosine aminotransferase gene to chromosome 16. Hum.Genet. 72: 225- 228, 1986.

GAM1338 360 TAT Natt, E.; Kida, K.; Odievre, M.; Di Rocco, M.; Scherer, G.: Pointmutations 3 C c
in the tyrosine aminotransferase gene in tyrosinemia typeII. Proc. Nat. Acad. Sci. 89: 9297- 9301, 1992.

GAM1338 360 TAT Natt, E.; Westphal, E.- M.; Toth- Fejel, S. E.; Magenis, R. E.;Buist, N. R. 3 C c
M.; Rettenmeier, R.; Scherer, G.: Inherited and de novodeletion of the tyrosine aminotransferase gene locus at 16q22.1- q22.3in a patient with tyrosinemia type II. Hum. Genet. 77: 352- 358,1987.

GAM1338 360 TAT Pelet, B.; Antener, I.; Faggioni, R.; Spahr, A.; Gautier, E.:Tyrosinemia 3 C c
without liver or renal damage with plantar and palmarkeratosis and keratitis (hypertyrosinemia type II). Helv. Paediat.Acta 34: 177- 183, 1979.

GAM1338 360 TAT Rehak, A.; Selim, M. M.; Yadav, G.: Richner- Hanhart syndrome(tyrosinaemia- 3 C c
II) (report of four cases without ocular involvement). Brit.J. Derm. 104: 469- 475, 1981.

GAM1338 360 TAT Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.: Isolationand 3 C c
characterization of the human tyrosine aminotransferase gene. NucleicAcids Res. 18: 3853- 3861, 1990.

GAM1338 360 TAT Richner, H.: Hornhautaffektion bei Keratoma palmare et plantarehereditarium. 3 C c
Klin. Mbl. Augenheilk. 100: 580- 588, 1938.

GAM1338 360 TAT Schmid, W.; Muller, G.; Schutz, G.; Gluecksohn- Waelsch, S.: Deletionsnear 3 C c
the albino locus on chromosome 7 of the mouse affect the levelof tyrosine aminotransferase mRNA. Proc. Nat. Acad. Sci. 82: 2866- 2869,1985.

GAM1338 360 TAT Tallab, T.M.: Richner- Hanhart syndrome: importance of early diagnosisand 3 C c
early intervention. J. Am. Acad. Dermatol. 35: 857- 859, 1996.

GAM1338 360 TAT Ventura, G.; Biasini, G.; Petrozzi, M.: Cheratomia palmoplantaredissipatum 3 C c
associato a lesioni corneali in due fratelli. Boll. Oculist. 44:497- 510, 1965.

GAM1338 360 TAT Waardenburg, P. J.; Franceschetti, A.; Klein, D.: Genetics andOphthalmology. 3 C c
Springfield, Ill.: Charles C Thomas (pub.) 1:1961. Pp. 515- 517.

GAM1338 360 TAT Westphal, E.- M.; Natt, E.; Grimm, T.; Odievre, M.; Scherer, G.: The human 3 C c
tyrosine aminotransferase gene: characterization of restrictionfragment
length polymorphisms and haplotype analysis in a family withtyrosinemia type
II. Hum. Genet. 79: 260- 264, 1988.

GAM1338 360 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; 3 C c
De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription
factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8:
165- 167, 1990.

GAM1338 360 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 3 C c
homeoprotein family are expressed in human liver. NucleicAcids Res. 19:
3553- 3559, 1991.

GAM1338 360 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't 3 C c
Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.;
Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene
are associated with familial hypoplastic glomerulocystickidney disease. Am.
J. Hum. Genet. 68: 219- 224, 2001.

GAM1338 360 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; 3 C c
Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.;
Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated
with a frameshift mutation in the transcription factorhepatocyte nuclear
factor- 1- beta. Kidney Int. 57: 898- 907, 2000.

GAM1338 360 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. 3 C c
N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara,
T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta
gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997.

GAM1338 360 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic 3 C c
glomerulocystic kidney disease: a definite entity withdominant inheritance.
Am. J. Med. Genet. 34: 569- 573, 1989.

GAM1338 360 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; 3 C c
Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand
genital malformation associated with a partial deletion of thepseudo- POU
domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001-
2008, 1999.

GAM1338 360 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, 3 C c
S.: A low renal threshold for glucose in diabetic patientswith a mutation in
the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med.
15: 816- 820, 1998.

GAM1338 360 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; 3 C c
Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in
the hepatocyte nuclear factor- 1- beta gene associated with diabetesand
renal dysfunction. Diabetes 47: 1354- 1355, 1998.

GAM1338 360 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: 3 C c
Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18:
263- 268, 1982.

GAM1338 360 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott- 3 C c
Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G.
U.: The mutated human gene encoding hepatocyte nuclear factor1- beta
inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad.
Sci. 97: 4695- 4700, 2000.

GAM1338 360 TCIRG1 Frattini, A.; Orchard, P. J.; Sobacchi, C.; Giliani, S.; Abinun,M.; 3 C c

Mattsson, J. P.; Keeling, D. J.; Andersson, A.- K.; Wallbrandt,P.; Zecca, L.; Notarangelo, L. D.; Vezzoni, P.; Villa, A.: Defectsin TCIRG1 subunit of the vacuolar proton pump are responsible fora subset of human autosomal recessive osteopetrosis. Nature Genet. 25:343- 346, 2000.

GAM1338 360 TCIRG1 Heinemann, T.; Bulwin, G. C.; Randall, J.; Schnieders, B.; Sandhoff,K.; Volk, H. D.; Milford, E.; Gullans, S. R.; Utku, N.: Genomic organizationof the gene coding for TIRC7, a novel membrane protein essential forT cell activation. Genomics 57: 398- 406, 1999. 3 C c

GAM1338 360 TCIRG1 Kornak, U.; Schulz, A.; Friedrich, W.; Uhlhaas, S.; Kremens, B.;Voit, T.; Hasan, C.; Bode, U.; Jentsch, T. J.; Kubisch, C.: Mutationsin the a3 subunit of the vacuolar H(+)- ATPase cause infantile malignantosteopetrosis. Hum. Molec. Genet. 9: 2059- 2063, 2000. 3 C c

GAM1338 360 TCIRG1 Li, Y.- P.; Chen, W.; Liang, Y.; Li, E.; Stashenko, P.: ATP6i- deficientmice exhibit severe osteopetrosis due to loss of osteoclast-mediatedextracellular acidification. Nature Genet. 23: 447- 451, 1999. 3 C c

GAM1338 360 TCIRG1 Li, Y.- P.; Chen, W.; Stashenko, P.: Molecular cloning and characterizationof a putative novel human osteoclast- specific 116- kDa vacuolar protonpump subunit. Biochem. Biophys. Res. Commun. 218: 813- 821, 1996. 3 C c

GAM1338 360 TCIRG1 Scimeca, J.- C.; Franchi, A.; Trojani, C.; Parrinello, H.; Grosgeorge,J.; Robert, C.; Jaillon, O.; Poirier, C.; Gaudray, P.; Carle, G. F.: The gene encoding the mouse homologue of the human osteoclast- specific116- kDa V-ATPase subunit bears a deletion in osteosclerotic (oc/oc)mutants. Bone 26: 207- 213, 2000. 3 C c

GAM1338 360 TCIRG1 Sobacchi, C.; Frattini, A.; Orchard, P.; Porras, O.; Tezcan, I.;Andolina, M.; Babul- Hirji, R.; Baric, I.; Canham, N.; Chitayat, D.;Dupuis- Girod, S.; Ellis, I.; and 21 others: The mutational spectrumof human malignant autosomal recessive osteopetrosis. Hum. Molec.Genet. 10: 1767- 1773, 2001. 3 C c

GAM1338 360 TCIRG1 Utku, N.; Heinemann, T.; Tullius, S. G.; Bulwin, G. C.; Beinke,S.; Blumberg, R. S.; Beato, F.; Randall, J.; Kojima, R.; Busconi,L.; Robertson, E. S.; Schulein, R.; Volk, H. D.; Milford, E. L.; Gullans,S. R.: Prevention of acute allograft rejection by antibody targetingof TIRC7, a novel T cell membrane protein. Immunity 9: 509- 518,1998. 3 C c

GAM1338 360 TERF1 Broccoli, D.; Chong, L.; Oelmann, S.; Fernald, A. A.; Marziliano,N.; van Steensel, B.; Kipling, D.; Le Beau, M. M.; de Lange, T.:Comparison of the human and mouse genes encoding the telomeric protein,TRF1: chromosomal localization, expression and conserved protein domains. Hum.Molec. Genet. 6: 69- 76, 1997. 3 C b

GAM1338 360 TERF1 Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.;Hanish, J.; Tempst, P.; de Lange, T.: A human telomeric protein. Science 270:1663-1667, 1995. 3 C b

GAM1338 360 TERF1 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001. 3 C b

GAM1338 360 TERF1 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999. 3 C b

GAM1338 360 TERF1 Kim, S.; Kaminker, P.; Campisi, J.: TIN2, a new regulator of telomerelength in human cells. Nature Genet. 23: 405- 412, 1999. 3 C b

GAM1338 360 TERF1 Marcand, S.; Gilson, E.; Shore, D.: A protein- counting mechanismfor 3 C b

telomere length regulation in yeast. Science 275: 986- 990, 1997.

GAM1338 360 TERF1 Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M.: TRF1 is a critical trans- acting factor required for de novo telomereformation in human cells. Hum. Molec. Genet. 9: 2639- 2650, 2000. 3 C b

GAM1338 360 TERF1 Young, A. C.; Chavez, M.; Giambernardi, T. A.; Mattern, V.; McGill,J. R.; Harris, J. M.; Sarosdy, M. F.; Patel, P.; Sakaguchi, A. Y.: Organization and expression of human telomere repeat binding factorgenes. Somat. Cell Molec. Genet. 23: 275- 286, 1997. 3 C b

GAM1338 360 TERF1 Zakian, V. A.: Telomeres: beginning to understand the end. Science 270:1601- 1607, 1995. 3 C b

GAM1338 360 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: Strand- specific postreplicative processing of mammalian telomeres. Science 293:2462- 2465, 2001. 3 C c

GAM1338 360 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet. 17: 236- 239, 1997. 3 C c

GAM1338 360 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17: 231- 235, 1997. 3 C c

GAM1338 360 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001. 3 C c

GAM1338 360 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999. 3 C c

GAM1338 360 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered telomere state, not telomere loss. Science 295: 2446- 2449,2002. 3 C c

GAM1338 360 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization of the transcribed human telomere repeat binding factor2 gene and comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163, 1998. 3 C c

GAM1338 360 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman telomeres from end- to- end fusions. Cell 92: 401- 413, 1998. 3 C c

GAM1338 360 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human telomeres. Nature Genet. 25: 347- 352, 2000. 3 C c

GAM1338 360 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020- 4027, 1998. 3 C c

GAM1338 360 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001. 3 C c

GAM1338 360 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress different Toll- like receptors and respond to different microbialantigens. J. Exp. Med. 194: 863- 869, 2001. 3 C c

GAM1338 360 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; 3 C c
Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.;
Mantovani, A.: Differential expression and regulation of Toll- likereceptors
(TLR) in human leukocytes: selective expression of TLR3in dendritic cells.
J. Immun. 164: 5998- 6004, 2000.

GAM1338 360 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A 3 C c
family of human receptors structurally related to DrosophilaToll. Proc. Nat.
Acad. Sci. 95: 588- 593, 1998.

GAM1338 360 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; 3 C b
Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and
13 others: Dominant and recessive deafnesscaused by mutations of a novel
gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277-
284, 2002.

GAM1338 360 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; 3 C b
Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M.
H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant,
progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002.

GAM1338 360 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 3 C c
B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the
crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec.
Cell 4: 563- 571, 1999.

GAM1338 360 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 C
c
B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel
receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420,
1997.

GAM1338 360 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 C c
B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi,
A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr.
Biol. 7: 1003- 1006, 1997.

GAM1338 360 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 C c
B W. S.: Rare loss- of- function mutation of a death receptorgene in head and
neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM1338 360 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 C c
B decoy receptor and a death domain- containing receptorfor TRAIL. Science
277: 815- 818, 1997.

GAM1338 360 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 C c
B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334,
1997.

GAM1338 360 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 C c
B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces
the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM1338 360 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 C c
B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard,
A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a
family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM1338 360 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 C c
B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.;
Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating
receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM1338 360 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 C c B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.

GAM1338 360 TNFRSF9 Alderson, M. R.; Smith, C. A.; Tough, T. W.; Davis- Smith, T.; Armitage,R. 3 C c J.; Falk, B.; Roux, E.; Baker, E.; Sutherland, G. R.; Din, W. S.;Goodwin, R. G.: Molecular and biological characterization of human4- 1BB and its ligand. Europ. J. Immun. 24: 2219- 2227, 1994.

GAM1338 360 TNFRSF9 Kwon, B. S.; Weissman, S. M.: cDNA sequences of two inducibleT- cell genes. 3 C c Proc. Nat. Acad. Sci. 86: 1963- 1967, 1989.

GAM1338 360 TNFRSF9 Loo, D. T.; Chalupny, N. J.; Bajorath, J.; Shuford, W. W.; Mittler,R. S.; 3 C c Aruffo, A.: Analysis of 4- 1BBL and laminin binding to murine4- 1BB, a member of the tumor necrosis factor receptor superfamily,and comparison with human 4- 1BB. J. Biol. Chem. 272: 6448- 6456,1997.

GAM1338 360 TNFRSF9 Schwarz, H.; Arden, K.; Lotz, M.: CD137, a member of the tumornecrosis 3 C c factor receptor family, is located on chromosome 1p36, ina cluster of related genes, and colocalizes with several malignancies. Biochem.Biophys. Res. Commun. 235: 699- 703, 1997.

GAM1338 360 TNFRSF9 Schwarz, H.; Blanco, F. J.; von Kempis, J.; Valbracht, J.; Lotz,M.: ILA, a 3 C c member of the human nerve growth factor/tumor necrosisfactor receptor family, regulates T- lymphocyte proliferation and survival. Blood 87:2839- 2845, 1996.

GAM1338 360 TNFRSF9 Schwarz, H.; Tuckwell, J.; Lotz, M.: A receptor induced by 3 C c lymphocyteactivation (ILA): a new member of the human nerve- growth- factor/tumor- necrosis- factorreceptor family. Gene 134: 295- 298, 1993.

GAM1338 360 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 C b Thiopurinemethyltransferase pharmacogenetics: alternative molecular diagnosisand preliminary data from Northern Portugal. Pharmacogenetics 9:257- 261, 1999.

GAM1338 360 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 C b McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM1338 360 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 C b Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof thiopurine methyltransferase alleles in Caucasian and Asian populations. Pharmacogenetics 9:37- 42, 1999.

GAM1338 360 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 C b mercaptopurine metabolism, toxic effects, and dosagerequirement in a thiopurine methyltransferase- deficient child withacute lymphocytic leukemia. J. Pediat. 119: 985- 989, 1991.

GAM1338 360 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 C b Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM1338 360 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 C b Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine methyltransferase:molecular cloning and expression of T84 colon carcinoma cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM1338 360 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 C b

thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-749, 1993.

GAM1338 360 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 C b
Evans, W. E.: A single point mutation leading to loss of catalyticactivity in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953, 1995.

GAM1338 360 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 C b
variation in response to 6- mercaptopurine for childhoodacute lymphoblastic leukaemia. Lancet 336: 225- 229, 1990.

GAM1338 360 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 C b
azathioprine toxicity: relationship to thiopurine methyltransferasegenetic polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM1338 360 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 C b
Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in thiopurine methyltransferase pharmacogenetics: evidencefor allele specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773-776, 1999.

GAM1338 360 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human 3 C b
thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon splice junction mutation that results in lossof activity. J. Clin. Invest. 101: 1036- 1044, 1998.

GAM1338 360 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; 3 C b
Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.; Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997.

GAM1338 360 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; 3 C b
Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine methyltransferase pharmacogenetics: human gene cloningand characterization of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996.

GAM1338 360 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: 3 C b
Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997.

GAM1338 360 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; 3 C b
Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694-702, 1996.

GAM1338 360 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine 3 C b
pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980.

GAM1338 360 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, 3 C c
H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor-associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF-kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997.

GAM1338 360 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, 3 C c
H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661-14664, 1996.

GAM1338 360 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; 3 C c

Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999.

GAM1338 360 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. 3 C c
F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997.

GAM1338 360 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, 3 C b
psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994.

GAM1338 360 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; 3 C b
Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000.

GAM1338 360 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. 3 C b
D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the pain pathway. Nature 389: 816- 824, 1997.

GAM1338 360 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 C b
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001.

GAM1338 360 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity 3 C b
to 'hot' chili peppers. Cell 108: 421- 430, 2002.

GAM1338 360 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, 3 C b
A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000.

GAM1338 360 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated 3 C b
by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996.

GAM1338 360 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel 3 C b
activity by protein kinase C. Nature 408: 985- 990, 2000.

GAM1338 360 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand 3 C b
multiple presentations of the oral irritant zingerone: relationshipto frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996.

GAM1338 360 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith 3 C b
capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994.

GAM1338 360 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand 3 C b
pleasantness for the capsaicin burn between chili likers and non- likers:implications for liking development. Chem. Senses 18: 471- 482, 1993.

GAM1338 360 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; 3 C b
McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000.

GAM1338 360 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; 3 C b
Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the

vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002.

GAM1338 360 TUFT1 Bashir, M. M.; Abrams, W. R.; Tucker, T.; Sellinger, B.; Budarf,M.; Emanuel, B.; Rosenbloom, J.: Molecular cloning and characterizationof the bovine and human tuftelin genes. Connect. Tissue Res. 39:13- 24, 1998. 3 C c

GAM1338 360 TUFT1 Deutsch, D.: Structure and function of enamel gene products. Anat.Rec. 224: 189- 210, 1989. 3 C c

GAM1338 360 TUFT1 Deutsch, D.; Palmon, A.; Dafni, L.; Fisher, L.; Termine, J. D.;Young, M.: Cloning, sequencing, and characterization of tuftelin:a novel acidic enamel protein. Connect. Tissue Res. 27: 121 only,1992. 3 C c

GAM1338 360 TUFT1 Deutsch, D.; Palmon, A.; Fisher, L. W.; Kolodny, N.; Termine, J.D.; Young, M. F.: Sequencing of bovine enamelin (tuftelin), a novelacidic enamel protein. J. Biol. Chem. 266: 16021- 16028, 1991. 3 C c

GAM1338 360 TUFT1 Deutsch, D.; Palmon, A.; Young, M. F.; Selig, S.; Kearns, W. G.;Fisher, L. W.: Mapping of the human tuftelin (TUFT1) gene to chromosome1 by fluorescence in situ hybridization. (Abstract) Mammalian Genome 5:461- 462, 1994. 3 C c

GAM1338 360 TUFT1 MacDougall, M.; Simmons, D.; Dodds, A.; Knight, C.; Luan, X.; Zeichner-David,M.; Zhang, C.; Ryu, O. H.; Qian, Q.; Simmer, J. P.; Hu, C.- C.: Cloning,characterization, and tissue expression pattern of mouse tuftelincDNA. J. Dent. Res. 77: 1970- 1978, 1998. 3 C c

GAM1338 360 UBE2L3 Ardley, H. C.; Moynihan, T. P.; Thompson, J.; Leek, J. P.; Markham,A. F.; Robinson, P. A.: Rapid isolation of genomic clones for individualmembers of human multigene families: identification and localisationof UBE2L4, a novel member of a ubiquitin conjugating enzyme dispersedgene family. Cytogenet. Cell Genet. 79: 188- 192, 1997. 3 C c

GAM1338 360 UBE2L3 Moynihan, T. P.; Ardley, H. C.; Leek, J. P.; Thompson, J.; Brindle,N. S.; Markham, A. F.; Robinson, P. A.: Characterization of a humanubiquitin-conjugating enzyme gene UBE2L3. Mammalian Genome 7: 520- 525,1996. 3 C c

GAM1338 360 UBE2L3 Moynihan, T. P.; Cole, C. G.; Dunham, I.; O'Neil, L.; Markham,A. F.; Robinson, P. A.: Fine- mapping, genomic organization, and transcriptanalysis of the human ubiquitin- conjugating enzyme gene UBE2L3. Genomics 51:124-127, 1998. 3 C c

GAM1338 360 UBE2L3 Nuber, U.; Schwarz, S.; Kaiser, P.; Schneider, R.; Scheffner, M.: Cloning of human ubiquitin- conjugating enzymes UbcH6 and UbcH7 (E2- F1)and characterization of their interaction with E6- AP and RSP5. J.Biol. Chem. 271: 2795- 2800, 1996. 3 C c

GAM1338 360 UBE2L3 Shimura, H.; Schlossmacher, M. G.; Hattori, N.; Frosch, M. P.;Trockenbacher, A.; Schneider, R.; Mizuno, Y.; Kosik, K. S.; Selkoe,D. J.: Ubiquitination of a new form of alpha- synuclein by parkinfrom human brain: implications for Parkinson's disease. Science 293:263- 269, 2001. 3 C c

GAM1338 360 UGDH Bontemps, Y.; Maquart, F.- X.; , Wegrowski, Y.: Human UDP-glucosedehydrogenase gene: complete cloning and transcription start mapping. Biochem.Biophys. Res. Commun. 275: 981- 985, 2000. 3 C b

GAM1338 360 UGDH Hempel, J.; Perozich, J.; Romovacek, H.; Hinich, A.; Kuo, I.; Feingold,D. S.: UDP- glucose dehydrogenase from bovine liver: primary structureand relationship to other dehydrogenases. Protein Sci. 3: 1074- 1080,1994. 3 C b

GAM1338 360 UGDH Marcu, O.; Stathakis, D. G.; Marsh, J. L.: Assignment of the UGDHlocus encoding UDP- glucose dehydrogenase to human chromosome band4p15.1 by radiation hybrid mapping. Cytogenet. Cell Genet. 86: 244- 245,1999. 3 C b

GAM1338 360 UGDH Spicer, A. P.; Kaback, L. A.; Smith, T. J.; Seldin, M. F.: Molecularcloning 3 C b

and characterization of the human and mouse UDP- glucose dehydrogenasegenes. J. Biol. Chem. 273: 25117- 25124, 1998.

GAM1338 360 UGDH Walsh, E. C.; Stainier, D. Y. R.: UDP- glucose dehydrogenase requiredfor cardiac valve formation in zebrafish. Science 293: 1670- 1674,2001. 3 C b

GAM1338 360 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 C b

GAM1338 360 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 C b

GAM1338 360 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 C b

GAM1338 360 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 C b

GAM1338 360 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000. 3 C b

GAM1338 360 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938. 3 C b

GAM1338 360 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999. 3 C b

GAM1338 360 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence for a founder effect. Hum. Genet. 95: 551- 556,1995. 3 C b

GAM1338 360 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. Arch.Neurol. 28: 67- 68, 1973. 3 C b

GAM1338 360 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942. 3 C b

GAM1338 360 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures of phaeochromocytoma. Lancet I: 492- 494, 1970. 3 C b

GAM1338 360 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962. 3 C b

GAM1338 360 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell, J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.; Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the von Hippel- Lindau disease tumorsuppressor gene: correlations with phenotype. Hum. Mutat. 5: 66- 75,1995. 3 C b

GAM1338 360 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 C b

Genotype- phenotype correlation in von Hippel- Lindaudisease: identification of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM1338 360 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's disease. J.A.M.A. 178: 280- 282, 1961. 3 C b

GAM1338 360 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with peculiar vascular new growth, probably primarily retinal,affecting both eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894. 3 C b

GAM1338 360 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994. 3 C b

GAM1338 360 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E. R.: Identification of intragenic mutations in thevon Hippel- Lindau disease tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994. 3 C b

GAM1338 360 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928. 3 C b

GAM1338 360 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994. 3 C b

GAM1338 360 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988. 3 C b

GAM1338 360 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459- 6463, 1995. 3 C b

GAM1338 360 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995. 3 C b

GAM1338 360 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001. 3 C b

GAM1338 360 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto- oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995. 3 C b

GAM1338 360 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans 3 C b

EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell107: 43- 54, 2001.

GAM1338 360 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 C b

GAM1338 360 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 3 C b

GAM1338 360 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin TRiC. Molec. Cell 1051- 1061, 1999. 3 C b

GAM1338 360 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof von Hippel- Lindau disease. Radiology 133: 289- 295, 1979. 3 C b

GAM1338 360 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331, 1979. 3 C b

GAM1338 360 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001. 3 C b

GAM1338 360 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with hydrocephalus as a complication of cerebellar hemangioblastoma:identification of pro157leu mutation in the VHL gene. J. Hum. Genet. 45:47- 51, 2000. 3 C b

GAM1338 360 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C Thomas (pub.) 1946. 3 C b

GAM1338 360 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989. 3 C b

GAM1338 360 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg. Path. 18: 1254- 1260, 1994. 3 C b

GAM1338 360 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.; Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999. 3 C b

GAM1338 360 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 C b

GAM1338 360 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 C b

GAM1338 360 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 C b

GAM1338 360 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 C b

GAM1338 360 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991. 3 C b

GAM1338 360 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, 3 C b

M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992.

GAM1338 360 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997. 3 C b

GAM1338 360 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984. 3 C b

GAM1338 360 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968. 3 C b

GAM1338 360 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 C b

GAM1338 360 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986. 3 C b

GAM1338 360 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour, phaeochromocytoma and the von Hippel- Lindau complex:two distinctive neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987. 3 C b

GAM1338 360 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: Familial pheochromocytoma associated with a novel mutation inthe von Hippel- Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996. 3 C b

GAM1338 360 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam: North Holland (pub.) 14: 1972. Pp. 241- 259. 3 C b

GAM1338 360 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors in livers with targeted inactivation of the von Hippel- Lindautumor suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001. 3 C b

GAM1338 360 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022- 1034, 1971. 3 C b

GAM1338 360 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8: 601- 606,1967. 3 C b

GAM1338 360 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas. Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994. 3 C b

GAM1338 360 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.; Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma only. J. Med. Genet. 37: 939- 943,2000. 3 C b

GAM1338 360 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips, C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet. 106: 425- 431, 2000. 3 C b

GAM1338 360 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 C b

von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM1338 360 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002. 3 C b

GAM1338 360 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989. 3 C b

GAM1338 360 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976. 3 C b

GAM1338 360 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990. 3 C b

GAM1338 360 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982. 3 C b

GAM1338 360 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986. 3 C b

GAM1338 360 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995. 3 C b

GAM1338 360 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996. 3 C b

GAM1338 360 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 3 C b

GAM1338 360 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL- mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001. 3 C b

GAM1338 360 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel- Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 3 C b

GAM1338 360 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)- regulated prolyl hydroxylation. Science 292: 468- 472, 2001. 3 C b

GAM1338 360 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 C b

GAM1338 360 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British 3 C b

family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988.

GAM1338 360 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 C b

GAM1338 360 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 C b

GAM1338 360 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 C b

GAM1338 360 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 C b

GAM1338 360 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 C b

GAM1338 360 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 C b

GAM1338 360 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-581, 1995. 3 C b

GAM1338 360 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 C b

GAM1338 360 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 C b

GAM1338 360 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel-Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 C b

GAM1338 360 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 C b

GAM1338 360 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 C b

GAM1338 360 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel-Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 C b

GAM1338 360 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 C b

GAM1338 360 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 C b

GAM1338 360 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of 3 C b

the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317-
1320, 1993.

GAM1338 360 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; 3 C b
Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau
tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad.
Sci. 93: 1770- 1775, 1996.

GAM1338 360 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, 3 C b
K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with
pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992.

GAM1338 360 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. 3 C b
ActaOphthal. 4: 193- 226, 1927.

GAM1338 360 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel 3 C b
mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424,
1994.

GAM1338 360 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; 3 C b
Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of
chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene
21: 1117- 1122, 2002.

GAM1338 360 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. 3 C b
J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G.
R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33:
120- 127, 1996.

GAM1338 360 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; 3 C b
Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.;
Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome
3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990.

GAM1338 360 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; 3 C b
Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau
disease locus to a small region of chromosome 3pby genetic linkage analysis.
Genomics 10: 957- 960, 1991.

GAM1338 360 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; 3 C b
Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.:
Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447,
1991.

GAM1338 360 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis 3 C b
of the two stage mutation model in von Hippel- Lindau disease,and in
sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med.
Genet. 27: 311- 314, 1990.

GAM1338 360 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. 3 C b
F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.;
Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and
high resolution restriction map of the2 megabase region containing the
Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM1338 360 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 C b
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple
myeloma is associated with increased expression and activatingmutations of
fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM1338 360 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, 3 C b
R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel
chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the

fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997.

GAM1338 360 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 C b

GAM1338 360 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 C b

GAM1338 360 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 3 C b

GAM1338 360 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 C b

GAM1338 360 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 3 C b

GAM1338 360 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995. 3 C b

GAM1338 360 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 3 C b

GAM1338 360 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 C b

GAM1338 360 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 C b

GAM1338 360 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997. 3 C b

GAM1338 360 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995. 3 C b

GAM1338 360 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma. CancerRes. 39: 3119- 3128, 1979. 3 C b

GAM1338 360 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a follicular lymphoma cell line carrying a t(14;18)chromosomal translocation. Int. J. Cancer 39: 785- 788, 1987. 3 C b

GAM1338 360 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. A.: STS map of genes and anonymous DNA fragments on human chromosome18 using 3 C b

a panel of somatic cell hybrids. Genomics 15: 387- 391,1993.

GAM1338 360 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710- 717, 1988. 3 C b

GAM1338 360 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human chromosome and its expression in various tissues. Science 227:1038- 1040, 1985. 3 C b

GAM1338 360 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal reassignment: YACs containing both YES1 and thymidylatesynthase map to the short arm of chromosome 18. Genomics 15: 442- 445,1993. 3 C b

GAM1338 360 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c- yes gene. Molec. Cell. Biol. 7: 41- 47, 1987. 3 C b

GAM1338 360 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985. 3 C b

GAM2033 305 ANGPT1 Cheung, A. H.; Stewart, R. J.; Marsden, P. A.: Endothelial Tie2/Tekligands angiopoietin- 1 (ANGPT1) and angiopoietin- 2 (ANGPT2): regionallocalization of the human genes to 8q22.3- q23 and 8p23. Genomics 48:389- 391, 1998. 3 C c

GAM2033 305 ANGPT1 Davis, S.; Aldrich, T. H.; Jones, P. F.; Acheson, A.; Compton,D. L.; Jain, V.; Ryan, T. E.; Bruno, J.; Radziejewski, C.; Maisonpierre,P. C.; Yancopoulos, G. D.: Isolation of angiopoietin- 1, a ligandfor the TIE2 receptor, by secretion- trap expression cloning. Cell 87:1161- 1169, 1996. 3 C c

GAM2033 305 ANGPT1 Folkman, J.; D'Amore, P. A.: Blood vessel formation: what is itsmolecular basis? Cell 87: 1153- 1155, 1996. 3 C c

GAM2033 305 ANGPT1 Holash, J.; Maisonpierre, P. C.; Compton, D.; Boland, P.; Alexander,C. R.; Zagzag, D.; Yancopoulos, G. D.; Wiegand, S. J.: Vessel cooption,regression, and growth in tumors mediated by angiopoietins and VEGF. Science 284:1994- 1998, 1999. 3 C c

GAM2033 305 ANGPT1 Loughna, S.; Sato, T. N.: A combinatorial role of angiopoietin- 1and orphan receptor TIE1 pathways in establishing vascular polarityduring angiogenesis. Molec. Cell 7: 233- 239, 2001. 3 C c

GAM2033 305 ANGPT1 Marziliano, N.; Crovella, S.; Audero, E.; Pecile, V.; Bussolino,F.; Amoroso, A.; Garagna, S.: Genetic mapping of the mouse homologueof the human angiopoietin- 1 gene (Agpt) to mouse chromosome 9E2 byin situ hybridization. Cytogenet. Cell Genet. 87: 199- 200, 1999. 3 C c

GAM2033 305 ANGPT1 Sato, T. N.; Tozawa, Y.; Deutsch, U.; Wolburg- Buchholz, K.; Fujiwara,Y.; Gendron- Maguire, M.; Gridley, T.; Wolburg, H.; Risau, W.; Qin,Y.: Distinct roles of the receptor tyrosine kinases Tie- 1 and Tie- 2in blood vessel formation. Nature 376: 70- 73, 1995. 3 C c

GAM2033 305 ANGPT1 Suri, C.; Jones, P. F.; Patan, S.; Bartunkova, S.; Maisonpierre,P. C.; Davis, S.; Sato, T. N.; Yancopoulos, G. D.: Requisite roleof angiopoietin- 1, a ligand for the TIE2 receptor, during embryonicangiogenesis. Cell 87: 1171- 1180, 1996. 3 C c

GAM2033 305 ANGPT1 Suri, C.; McClain, J.; Thurston, G.; McDonald, D. M.; Zhou, H.;Oldmixon, E. H.; Sato, T. N.; Yancopoulos, G. D.: Increased vascularizationin mice overexpressing angiopoietin- 1. Science 282: 468- 471, 1998. 3 C c

GAM2033 305 ANGPT1 Thurston, G.; Suri, C.; Smith, K.; McClain, J.; Sato, T. N.; Yancopoulos,G. 3 C c

D.; McDonald, D. M.: Leakage- resistant blood vessels in mice transgenicallyoverexpressing angiopoietin- 1. Science 286: 2511- 2514, 1999.

GAM2033 305 ANGPT1 Valenzuela, D. M.; Griffiths, J. A.; Rojas, J.; Aldrich, T. H.;Jones, P. F.; 3 C c Zhou, H.; McClain, J.; Copeland, N. G.; Gilbert, D.J.; Jenkins, N. A.; Huang, T.; Papadopoulos, N.; Maisonpierre, P.C.; Davis, S.; Yancopoulos, G. D.: Angiopoietins 3 and 4: diverginggene counterparts in mice and humans. Proc. Nat. Acad. Sci. 96:1904- 1909, 1999.

GAM2033 305 ANGPT1 Vikkula, M.; Boon, L. M.; Carraway, K. L., III; Calvert, J. T.;Diamonti, A. 3 C c J.; Goumnerov, B.; Pasyk, K. A.; Marchuk, D. A.; Warman,M. L.; Cantley, L. C.; Mulliken, J. B.; Olsen, B. R.: Vascular dysmorphogenesiscaused by an activating mutation in the receptor tyrosine kinase TIE2. Cell 87:1181- 1190, 1996.

GAM2033 305 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene 3 C c structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996.

GAM2033 305 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem 3 C c arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997.

GAM2033 305 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: 3 C c an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999.

GAM2033 305 CBL Baumann, C. A.; Ribon, V.; Kanzaki, M.; Thurmond, D. C.; Mora,S.; 3 C c Shigematsu, S.; Bickel, P. E.; Pessin, J. E.; Saltiel, A. R.:CAP defines a second signalling pathway required for insulin- stimulatedglucose transport. Nature 407: 202- 207, 2000.

GAM2033 305 CBL Joazeiro, C. A. P.; Wing, S. S.; Huang, H.; Leverson, J. D.; Hunter,T.; Liu, 3 C c Y.- C.: The tyrosine kinase negative regulator c- Cbl as aRING- type, E2- dependent ubiquitin- protein ligase. Science 286: 309- 312,1999.

GAM2033 305 CBL Jones, C.; Penny, L.; Mattina, T.; Yu, S.; Baker, E.; Voullaire,L.; Langdon, 3 C c W. Y.; Sutherland, G. R.; Richards, R. I.; Tunnacliffe,A.: Association of a chromosome deletion syndrome with a fragilesite within the proto- oncogene CBL2. Nature 376: 145- 149, 1995.

GAM2033 305 CBL Jones, C.; Slijepcevic, P.; Marsh, S.; Baker, E.; Langdon, W. Y.;Richards, 3 C c R. I.; Tunnacliffe, A.: Physical linkage of the fragilesite FRA11B and a Jacobsen syndrome chromosome deletion breakpointin 11q23.3. Hum. Molec. Genet. 3: 2123- 2130, 1994.

GAM2033 305 CBL Langdon, W. Y.; Hartley, J. W.; Klinken, S. P.; Ruscetti, S. K.;Morse, H. 3 C c C., III: v- cbl, an oncogene from a dual- recombinant murineretrovirus that induces early B- lineage lymphomas. Proc. Nat. Acad.Sci. 86: 1168- 1172, 1989.

GAM2033 305 CBL Mastick, C. C.; Brady, M. J.; Saltiel, A. R.: Insulin stimulatesthe tyrosine 3 C c phosphorylation of caveolin. J. Cell Biol. 129: 1523- 1531,1995.

GAM2033 305 CBL Petrelli, A.; Gilestro, G. F.; Lanzardo, S.; Comoglio, P. M.; Migone,N.; 3 C c Giordano, S.: The endophilin- CIN85- Cbl complex mediates ligand- dependentdownregulation of c- Met. Nature 416: 187- 190, 2002.

GAM2033 305 CBL Savage, P. D.; Shapiro, M.; Langdon, W. Y.; Geurts van Kessel,A. D.; 3 C c Seuanez, H. N.; Akao, Y.; Croce, C.; Morse, H. C., III; Kersey,J. H.: Relationship of the human protooncogene CBL2 on 11q23 to thet(4;11), t(11;22), and t(11;14) breakpoints. Cytogenet. Cell Genet. 56:112- 115,

1991.

GAM2033 305 CBL Soubeyran, P.; Kowanetz, K.; Szymkiewicz, I.; Langdon, W. Y.; Dikic,I.: Cbl- 3 C c
CIN85- endophilin complex mediates ligand- induced downregulationof EGF
receptors. Nature 416: 183- 187, 2002.

GAM2033 305 CBL Thien, C. B. F.; Walker, F.; Langdon, W. Y.: RING finger mutationsthat 3 C c
abolish c- Cbl- directed polyubiquitination and downregulationof the EGF
receptor are insufficient for cell transformation. Molec.Cell 7: 355- 365,
2001.

GAM2033 305 CBL Wei, S.; Rocchi, M.; Archidiacono, N.; Sacchi, N.; Romeo, G.;Gatti, R. A.: 3 C c
Physical mapping of the human chromosome 11q23 regioncontaining the ataxia-
telangiectasia locus. Cancer Genet. Cytogenet. 46:1- 8, 1990.

GAM2033 305 CBL Yoon, C. H.; Lee, J.; Jongeward, G. D.; Sternberg, P. W.: Similarityof sli- 3 C c
1, a regulator of vulval development in C. elegans, to themammalian proto-
oncogene c- cbl. Science 269: 1102- 1105, 1995.

GAM2033 305 CCKAR Boden, P.; Hall, M. D.; Hughes, J.: Cholecystokinin receptors. Cell.Molec. 3 C c
Neurobiol. 15: 545- 559, 1995.

GAM2033 305 CCKAR de Weerth, A.; Pisegna, J. R.; Huppi, K.; Wank, S. A.: Molecularcloning, 3 C c
functional expression and chromosomal localization of thehuman
cholecystokinin type A receptor. Biochem. Biophys. Res. Commun. 194:811-
818, 1993.

GAM2033 305 CCKAR Funakoshi, A.; Miyasaka, K.; Shinozaki, H.; Masuda, M.; Kawanami,T.; Takata, 3 C c
Y.; Kono, A.: An animal model of congenital defect ofgene expression of
cholecystokinin (CCK)- A receptor. Biochem. Biophys.Res. Commun. 210: 787-
796, 1995.

GAM2033 305 CCKAR Hamann, A.; Busing, B.; Munzberg, H.; de Weerth, A.; Hinney, A.;Mayer, H.; 3 C c
Siegfried, W.; Hebebrand, J.; Greten, H.: Missense variantsin the human
cholecystokinin type A receptor gene: no evidence forassociation with early-
onset obesity. Horm. Metab. Res. 31: 287- 288,1999.

GAM2033 305 CCKAR Huppi, K.; Siwarski, D.; Pisegna, J. R.; Wank, S.: Chromosomallocalization 3 C c
of the gastric and brain receptors for cholecystokinin(CCKAR and CCKBR) in
human and mouse. Genomics 25: 727- 729, 1995.

GAM2033 305 CCKAR Inoue, H.; Iannotti, C. A.; Welling, C. M.; Veile, R.; Donis- Keller,H.; 3 C c
Permutt, M. A.: Human cholecystokinin type A receptor gene:
cytogeneticlocalization, physical mapping, and identification of two
missensevariants in patients with obesity and non- insulin- dependent
diabetesmellitus (NIDDM). Genomics 42: 331- 335, 1997.

GAM2033 305 CCKAR Marchal- Victorion, S.; Vionnet, N.; Escrieut, C.; Dematos, F.;Dina, C.; 3 C c
Dufresne, M.; Vaysse, N.; Pradayrol, L.; Froguel, P.; Fourmy,D.: Genetic,
pharmacological and functional analysis of cholecystokinin- 1and
cholecystokinin- 2 receptor polymorphism in type 2 diabetes andobese
patients. Pharmacogenetics 12: 23- 30, 2002.

GAM2033 305 CCKAR Miller, L. J.; Holicky, E. L.; Ulrich, C. D.; Wieben, E. D.: 3 C c
Abnormalprocessing of the human cholecystokinin receptor gene in
associationwith gallstones and obesity. Gastroenterology 109: 1375- 1380,
1995.

GAM2033 305 CCKAR Samuelson, L. C.; Isakoff, M. S.; Lacourse, K. A.: Localizationof the murine 3 C c
cholecystokinin A and B receptor genes. Mammalian Genome 6:242- 246, 1995.

GAM2033 305 CCKAR Ulrich, C. D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.;Miller, L. J.: 3 C c
Molecular cloning and functional expression of thehuman gallbladder
cholecystokinin A receptor. Biochem. Biophys. Res.Commun. 193: 204- 211,

1993.

GAM2033 305 CDH3 Donalies, M.; Cramer, M.; Ringwald, M.; Starzinski- Powitz, A.:Expression of 3 C c
M- cadherin, a member of the cadherin multigene family,correlates with
differentiation of skeletal muscle cells. Proc. Nat.Acad. Sci. 88: 8024-
8028, 1991.

GAM2033 305 CDH3 Kaupmann, K.; Becker- Follmann, J.; Scherer, G.; Jockusch, H.; Starzinski- 3 C c
Powitz,A.: The gene for the cell adhesion molecule M- cadherin maps to
mousechromosome 8 and human chromosome 16q24.1- qter and is near the E-
cadherin(uvomorulin) locus in both species. Genomics 14: 488- 490, 1992.

GAM2033 305 CDH3 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 3 C c
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting
cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM2033 305 CDH6 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene 3 C c
cluster to a region of chromosome 5 subject to frequent allelicloss in
carcinoma. Genomics 57: 160- 163, 1999.

GAM2033 305 CDH6 Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi,S.: 3 C c
Isolation and sequence analysis of human cadherin- 6 complementaryDNA for
the full coding sequence and its expression in human carcinomacells. Cancer
Res. 55: 2206- 2211, 1995.

GAM2033 305 CDH6 Suzuki, S.; Sano, K.; Tanihara, H.: Diversity of the cadherinfamily: 3 C c
evidence for eight new cadherins in nervous tissue. CellRegul. 2: 261- 270,
1991.

GAM2033 305 CLDN14 Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.;Park, H.- 3 C c
S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.- K.; Groner,Y.; Soeda, E.;
and 52 others: The DNA sequence of human chromosome21. Nature 405: 311- 319,
2000. Note: Erratum: Nature: 407: 110 only,2000.

GAM2033 305 CLDN14 Wilcox, E. R.; Burton, Q. L.; Naz, S.; Riazuddin, S.; Smith, T.N.; Ploplis, 3 C c
B.; Belyatseva, I.; Ben- Yosef, T.; Liburd, N. A.; Morell,R. J.; Kachar, B.;
Wu, D. K.; Griffith, A. J.; Riazuddin, S.; Friedman,T. B.: Mutations in the
gene encoding tight junction claudin- 14 causerecessive deafness DFNB29.
Cell 104: 165- 172, 2001.

GAM2033 305 ERBB3 Carraway, K. L., III; Sliwkowski, M. X.; Akita, R.; Platko, J.V.; Guy, P. 3 C c
M.; Nuijens, A.; Diamonti, A. J.; Vandlen, R. L.; Cantley,L. C.; Cerione, R.
A.: The erbB3 gene product is a receptor for heregulin. J.Biol. Chem. 269:
14303- 14306, 1994.

GAM2033 305 ERBB3 Cho, H.- S.; Leahy, D. J.: Structure of the extracellular regionof HER3 3 C c
reveals an interdomain tether. Science 297: 1330- 1333, 2002.

GAM2033 305 ERBB3 Kraus, M. H.; Issing, W.; Miki, T.; Popescu, N. C.; Aaronson, S.A.: 3 C c
Isolation and characterization of ERBB3, a third member of theERBB/epidermal
growth factor receptor family: evidence for overexpressionin a subset of
human mammary tumors. Proc. Nat. Acad. Sci. 86: 9193- 9197,1989.

GAM2033 305 ERBB3 Plowman, G. D.; Whitney, G. S.; Neubauer, M. G.; Green, J. M.;McDonald, V. 3 C c
L.; Todaro, G. J.; Shoyab, M.: Molecular cloning andexpression of an
additional epidermal growth factor receptor- relatedgene. Proc. Nat. Acad.
Sci. 87: 4905- 4909, 1990.

GAM2033 305 ESRRB Giguere, V.; Yang, N.; Segui, P.; Evans, R. M.: Identificationof a new class 3 C c
of steroid hormone receptors. Nature 331: 91- 94,1988.

GAM2033 305 ESRRB Luo, J.; Sladek, R.; Bader, J. A.; Matthyssen, A.; Rossant, J.;Giguere, V.: 3 C c
Placental abnormalities in mouse embryos lacking orphannuclear receptor ERR-
beta. Nature 388: 778- 782, 1997.

GAM2033 305 ESRRB Sladek, R.; Beatty, B.; Squire, J.; Copeland, N. G.; Gilbert, D.J.; Jenkins, 3 C c
N. A.; Giguere, V.: Chromosomal mapping of the humanand murine orphan
receptors ERR- alpha (ESRRA) and ERR- beta (ESRRB)and identification of a
novel human ERR- alpha- related pseudogene. Genomics 45:320- 326, 1997.

GAM2033 305 FBXL7 Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; 3 C c
Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol.
9: 1177- 1179, 1999.

GAM2033 305 FBXL7 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 C c
and expression analysis of new members of the mammalianF- box protein
family. Genomics 67: 40- 47, 2000.

GAM2033 305 FBXL7 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XII. The completesequences of 100 new
cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5:
355- 364, 1998.

GAM2033 305 FBXL7 Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A 3 C c
family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999.

GAM2033 305 HCFC1 Faranda, S.; Frattini, A.; Vezzoni, P.: The human genes encodingrenin- 3 C c
binding protein and host cell factor are closely linked in Xq28and
transcribed in the same direction. Gene 155: 237- 239, 1995.

GAM2033 305 HCFC1 Frattini, A.; Chatterjee, A.; Faranda, S.; Sacco, M. G.; Villa,A.; Herman, 3 C c
G. E.; Vezzoni, P.: The chromosome localization and theHCF repeats of the
human host cell factor gene (HCFC1) are conservedin the mouse homologue.
Genomics 32: 277- 280, 1996.

GAM2033 305 HCFC1 Frattini, A.; Faranda, S.; Redolfi, E.; Zucchi, I.; Villa, A.;Patrosso, M. 3 C c
C.; Strina, D.; Susani, L.; Vezzoni, P.: Genomic organizationof the human
VP16 accessory protein, a housekeeping gene (HCFC1) mappingto Xq28. Genomics
23: 30- 35, 1994.

GAM2033 305 HCFC1 Wilson, A. C.; LaMarco, K.; Peterson, M. G.; Herr, W.: The VP16accessory 3 C c
protein HCF is a family of polypeptides processed from alarge precursor
protein. Cell 74: 115- 125, 1993.

GAM2033 305 HCFC1 Wilson, A. C.; Parrish, J. E.; Massa, H. F.; Nelson, D. L.; Trask,B. J.; 3 C c
Herr, W.: The gene encoding the VP16- accessory protein HCF(HCFC1) resides
in human Xq28 and is highly expressed in fetal tissuesand the adult kidney.
Genomics 25: 462- 468, 1995.

GAM2033 305 HCFC1 Zoppe, M.; Frattini, A.; Faranda, S.; Vezzoni, P.: The completesequence of 3 C c
the host cell factor 1 (HCFC1) gene and its promoter:a role for YY1
transcription factor in the regulation of its expression. Genomics 34:85-
91, 1996.

GAM2033 305 HK2 Ardehali, H.; Tiller, G. E.; Printz, R. L.; Mochizuki, H.; Prochazka,M.; 3 C c
Granner, D. K.: A novel (TA)n polymorphism in the hexokinaseII gene:
application to noninsulin- dependent diabetes mellitus inthe Pima Indians.
Hum. Genet. 97: 482- 485, 1996.

GAM2033 305 HK2 Echwald, S. M.; Bjorbaek, C.; Hansen, T.; Clausen, J. O.; Vestergaard,H.; 3 C c
Zierarth, J. R.; Printz, R. L.; Granner, D. K.; Pedersen, O.:Identification
of four amino acid substitutions in hexokinase II andstudies of
relationships to NIDDM, glucose effectiveness, and insulinsensitivity.
Diabetes 44: 347- 353, 1995.

GAM2033 305 HK2 Heikkinen, S.; Suppola, S.; Malkki, M.; Deeb, S. S.; Janne, J.;Laakso, M.: 3 C c
Mouse hexokinase II gene: structure, cDNA, promoter analysis,and expression

pattern. Mammalian Genome 11: 91- 96, 2000.

GAM2033 305 HK2 Laakso, M.; Malkki, M.; Deeb, S. S.: Amino acid substitutionsin hexokinase 3 C c
II among patients with NIDDM. Diabetes 44: 330- 334,1995.

GAM2033 305 HK2 Lehto, M.; Xiang, K.; Stoffel, M.; Espinosa, R., III; Groop, L.C.; Le Beau, 3 C c
M. M.; Bell, G. I.: Human hexokinase II: localizationof the polymorphic gene
to chromosome 2. Diabetologia 36: 1299- 1302,1993.

GAM2033 305 HK2 Mathupala, S. P.; Heese, C.; Pedersen, P. L.: Glucose catabolismin cancer 3 C c
cells: the type II hexokinase promoter contains functionallyactive response
elements for the tumor suppressor p53. J. Biol. Chem. 272:22776- 22780,
1997.

GAM2033 305 HK2 Mathupala, S. P.; Rempel, A.; Pedersen, P. L.: Glucose catabolismin cancer 3 C c
cells: isolation, sequence, and activity of the promoterfor type II
hexokinase. J. Biol. Chem. 270: 16918- 16925, 1995.

GAM2033 305 HK2 Vidal- Puig, A.; Printz, R. L.; Stratton, I. M.; Granner, D. K.;Moller, D. 3 C c
E.: Analysis of the hexokinase II gene in subjects withinsulin resistance
and NIDDM and detection of a gln142- to- his substitution. Diabetes 44:340-
346, 1995.

GAM2033 305 HOXC4 Apiou, F.; Flagiello, D.; Cillo, C.; Malfoy, B.; Poupon, M.- F.;Dutrillaux, 3 C c
B.: Fine mapping of human HOX gene clusters. Cytogenet.Cell Genet. 73: 114-
115, 1996.

GAM2033 305 HOXC6 Chariot, A.; Castronovo, V.; Le, P.; Gillet, C.; Sobel, M. E.;Gielen, J.: 3 C c
Cloning and expression of a new HOXC6 transcript encodinga repressing
protein. Biochem. J. 319: 91- 97, 1996.

GAM2033 305 HOXC6 Simeone, A.; Mavilio, F.; Acampora, D.; Giampaolo, A.; Faiella,A.; 3 C c
Zappavigna, V.; D'Esposito, M.; Pannese, M.; Russo, G.; Boncinelli,E.;
Peschle, C.: Two human homeobox genes, c1 and c8: structure analysisand
expression in embryonic development. Proc. Nat. Acad. Sci. 84:4914- 4918,
1987.

GAM2033 305 INHBA Brown, C. W.; Houston- Hawkins, D. E.; Woodruff, T. K.; Matzuk,M. M.: 3 C c
Insertion of Inhbb into the Inhba locus rescues the Inhba- nullphenotype and
reveals new activin functions. Nature Genet. 25: 453- 457,2000.

GAM2033 305 INHBA Burger, H. G.; Igarashi, M.; Baird, D.; Mason, T.; Bardin, W.;McLachlan, R.; 3 C c
Chappel, S.; Miyamoto, K.; de Jong, F.; Moudgal, A.;Demoulin, A.; Nieschlag,
E.; de Kretser, D.; Robertson, D.; Findlay,J.; Sasamoto, S.; Forage, R.;
Schwartz, N.; Fukuda, M.; Steinberger,A.; Hasegawa, Y.; Tanabe, K.; Ling,
N.; Ying, S.- Y.: Inhibin: definitionand nomenclature, including related
substances. (Letter) J. Clin.Endocr. Metab. 66: 885- 886, 1988.

GAM2033 305 INHBA Ferguson, C. A.; Tucker, A. S.; Christensen, L.; Lau, A. L.; Matzuk,M. M.; 3 C c
Sharpe, P. T.: Activin is an essential early mesenchymal signalin tooth
development that is required for patterning of the murinedentition. Genes
Dev. 12: 2636- 2649, 1998.

GAM2033 305 INHBA Lumpkin, M. D.; Moltz, J. H.; Yu, W. H.; Samson, W. K.; McCann,S. M.: 3 C c
Purification of FSH- releasing factor: its dissimilarity fromLHRH of
mammalian, avian, and piscian origin. Brain Res. Bull. 18:175- 178, 1987.

GAM2033 305 INHBA Matzuk, M. M.; Kumar, T. R.; Vassalli, A.; Bickenbach, J. R.; Roop,D. R.; 3 C c
Jaenisch, R.; Bradley, A.: Functional analysis of activinsduring mammalian
development. Nature 374: 354- 356, 1995.

GAM2033 305 INHBA Mellor, S. L.; Cranfield, M.; Ries, R.; Pedersen, J.; Cancilla,B.; de 3 C c
Kretser, D.; Groome, N. P.; Mason, A. J.; Risbridger, G. P.: Localization of
activin beta(A)- , beta(B)- , and beta(C)- subunitsin human prostate and

evidence for formation of new activin heterodimersof beta(C)- subunit. J. Clin. Endocr. Metab. 85: 4851- 4858, 2000.

GAM2033 305 INHBA Murata, M.; Eto, Y.; Shibai, H.; Sakai, M.; Muramatsu, M.: 3 C c
Erythroiddifferentiation factor is encoded by the same mRNA as that of theinhibin beta- A chain. Proc. Nat. Acad. Sci. 85: 2434- 2438, 1988.

GAM2033 305 INHBA You, L.; Kruse, F. E.: Differential effect of activin A and BMP- 7on 3 C c
myofibroblast differentiation and the role of the Smad signalingpathway. Invest. Ophthal. Vis. Sci. 43: 72- 81, 2002.

GAM2033 305 KCNA7 Bardien- Kruger, S.; Wulff, H.; Arieff, Z.; Brink, P.; Chandy, K.G.; 3 C c
Corfield, V.: Characterisation of the human voltage- gated potassiumchannel gene, KCNA7, a candidate gene for inherited cardiac disorders,and its exclusion as cause of progressive familial heart block I (PFHBI). Europ.J. Hum. Genet. 10: 36- 43, 2002.

GAM2033 305 KCNA7 Kalman, K.; Nguyen, A.; Tseng- Crank, J.; Dukes, I. D.; Chandy,G.; Hustad, 3 C c
C. M.; Copeland, N. G.; Jenkins, N. A.; Mohrenweiser,H.; Brandriff, B.; Cahalan, M.; Gutman, G. A.; Chandy, K. G.: Genomicorganization, chromosomal localization, tissue distribution, and biophysicalcharacterization of a novel mammalian Shaker- related voltage- gatedpotassium channel, Kv1.7. J. Biol. Chem. 273: 5851- 5857, 1998.

GAM2033 305 KCNA7 McPherson, J. D.; Wasmuth, J. J.; Chandy, K. G.; Swanson, R.; Dethlefs,B.; 3 C c
Chandy, G.; Wymore, R.; Ghanshani, S.: Chromosomal localizationof 7 potassium channel genes. (Abstract) Cytogenet. Cell Genet. 58:1979 only, 1991.

GAM2033 305 NDST2 Ahmed, Z. M.; Riazuddin, S.; Bernstein, S. L.; Ahmed, Z.; Khan,S.; Griffith, 3 C c
A. J.; Morell, R. J.; Friedman, T. B.; Riazuddin, S.;Wilcox, E. R.: Mutations of the protocadherin gene PCDH15 cause Ushersyndrome type 1F. Am. J. Hum. Genet. 69: 25- 34, 2001.

GAM2033 305 NDST2 Eriksson, I.; Sandback, D.; Ek, B.; Lindahl, U.; Kjellen, L.:cDNA cloning 3 C c
and sequencing of mouse mastocytoma glucosaminyl N- deacetylase/N- sulfotransferase,an enzyme involved in the biosynthesis of heparin. J. Biol. Chem. 269:10438- 10443, 1994.

GAM2033 305 NDST2 Forsberg, E.; Pejler, G.; Ringvall, M.; Lunderius, C.; Tomasini- 3 C c
Johansson,B.; Kusche- Gullberg, M.; Eriksson, I.; Ledin, J.; Hellman, L.; Kjellen,L.: Abnormal mast cells in mice deficient in a heparin- synthesizingenzyme. Nature 400: 773- 776, 1999.

GAM2033 305 NDST2 Humphries, D. E.; Lanciotti, J.; Karlinsky, J. B.: cDNA cloning,genomic 3 C c
organization and chromosomal localization of human heparanglucosaminyl N- deacetylase/N- sulphotransferase- 2. Biochem. J. 332:303- 307, 1998.

GAM2033 305 NDST2 Humphries, D. E.; Wong, G. W.; Friend, D. S.; Gurish, M. F.; Qiu,W.- T.; 3 C c
Huang, C.; Sharpe, A. H.; Stevens, R. L.: Heparin is essentialfor the storage of specific granule proteases in mast cells. Nature 400:769- 772, 1999.

GAM2033 305 NDST2 Orellana, A.; Hirschberg, C. B.; Wei, Z.; Swiedler, S. J.; Ishihara,M.: 3 C c
Molecular cloning and expression of a glycosaminoglycan N- acetylglucosaminylN- deacetylase/N- sulfotransferase from a heparin- producing cell line. J.Biol. Chem. 269: 2270- 2276, 1994.

GAM2033 305 NDST2 Zehnder, J. L.; Galli, S. J.: Mast- cell heparin demystified. Nature 3 C c
400:714- 715, 1999.

GAM2033 305 NHLH1 Begley, C. G.; Lipkowitz, S.; Gobel, V.; Mahon, K. A.; Bertness,V.; Green, 3 C c
A. R.; Gough, N. M.; Kirsch, I. R.: Molecular characterizationof NSCL, a

gene encoding a helix- loop- helix protein expressed in thedeveloping nervous system. Proc. Nat. Acad. Sci. 89: 38- 42, 1992.

GAM2033 305 NHLH1 Brown, L.; Espinosa, R., III; Le Beau, M. M.; Siciliano, M. J.;Baer, R.: 3 C c HEN1 and HEN2: a subgroup of basic helix- loop- helix genesthat are coexpressed in a human neuroblastoma. Proc. Nat. Acad. Sci. 89:8492- 8496, 1992.

GAM2033 305 NHLH1 Cogliati, T.; Good, D. J.; Haigney, M.; Delgado- Romero, P.; Eckhaus,M. A.; 3 C c Koch, W. J.; Kirsch, I. R.: Predisposition to arrhythmia andautonomic dysfunction in Nhlh1- deficient mice. Molec. Cell. Biol. 22:4977- 4983, 2002.

GAM2033 305 NHLH1 Lipkowitz, S.; Gobel, V.; Varterasian, M. L.; Nakahara, K.; Tchorz,K.; 3 C c Kirsch, I. R.: A comparative structural characterization of thehuman NSCL- 1 and NSCL- 2 genes: two basic helix- loop- helix genes expressedin the developing nervous system. J. Biol. Chem. 267: 21065- 21071,1992.

GAM2033 305 NHLH1 Mullick, A.; Groulx, N.; Trasler, D.; Gros, P.: Nhlh1, a basichelix- loop- 3 C c helix transcription factor, is very tightly linked to themouse looptail (Lp) mutation. Mammalian Genome 6: 700- 704, 1995.

GAM2033 305 P2RY6 Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.: Molecular cloningand 3 C c functional analysis of a novel P2 nucleotide receptor. J. Biol.Chem. 270: 26152- 26158, 1995.

GAM2033 305 P2RY6 Communi, D.; Parmentier, M.; Boeynaems, J.- M.: Cloning, 3 C c functionalexpression and tissue distribution of the human P2Y6 receptor. Biochem.Biophys. Res. Commun. 222: 303- 308, 1996.

GAM2033 305 P2RY6 Maier, R.; Glatz, A.; Mosbacher, J.; Bilbe, G.: Cloning of P2Y6cDNAs and 3 C c identification of a pseudogene: comparison of P2Y receptorsubtype expression in bone and brain tissues. Biochem. Biophys. Res.Commun. 237: 297- 302, 1997.

GAM2033 305 P2RY6 Pidlaoan, L. V.; Jin, J.; Sandhu, A. K.; Athwal, R. S.; Kunapuli,S. P.: 3 C c Colocalization of P2Y2 and P2Y6 receptor genes at human chromosome11q13.3-14.1. Somat. Cell Molec. Genet. 23: 291- 296, 1997.

GAM2033 305 P2RY6 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C c Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997.

GAM2033 305 PMP2 Ben Othmane, K.; Loeb, D.; Hayworth- Hodgte, R.; Hentati, F.; Rao,N.; Roses, 3 C c A. D.; Ben Hamida, M.; Pericak- Vance, M. A.; Vance, J.M.: Physical and genetic mapping of the CMT4A locus and exclusionof PMP- 2 as the defect in CMT4A. Genomics 28: 286- 290, 1995.

GAM2033 305 PMP2 Hayasaka, K.; Himoro, M.; Takada, G.; Takahashi, E.; Minoshima,S.; Shimizu, 3 C c N.: Structure and localization of the gene encodinghuman peripheral myelin protein 2 (PMP2). Genomics 18: 244- 248,1993.

GAM2033 305 PMP2 Hayasaka, K.; Nanao, K.; Tahara, M.; Sato, W.; Takada, G.; Miura,M.; 3 C c Uyemura, K.: Isolation and sequence determination of cDNA encodingP2 protein of human peripheral myelin. Biochem. Biophys. Res. Commun. 181:204- 207, 1991.

GAM2033 305 PMP2 Narayanan, V.; Ripepi, B.; Jabs, E. W.; Hawkins, A.; Griffin, C.;Tennekoon, 3 C c G.: Partial structure and mapping of the human myelinP2 protein gene. J. Neurochem. 63: 2010- 2013, 1994.

GAM2033 305 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 3 C c Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J

recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 2002.

GAM2033 305 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 3 C c cell coactivator of octamer- binding transcription factors. Nature 373:360- 362, 1995.

GAM2033 305 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 3 C c Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell- specific coactivator of octamer- binding transcription factors1 and 2, to 11q23.1 by somatic cell hybridization and in situ hybridization. Genomics 33:143- 145, 1996.

GAM2033 305 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 3 C c of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995.

GAM2033 305 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 3 C c Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM2033 305 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 3 C c Immun. 9: 373- 398, 1991.

GAM2033 305 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 3 C c specificcoactivator that stimulates immunoglobulin promoter activity throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM2033 305 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 3 C c Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B, BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853- 864, 2000.

GAM2033 305 RAB13 Leek, J. P.; Hamlin, P. J.; Wilton, J.; Lench, N. J.: Assignmentof the Rab13 3 C c gene (RAB13) to human chromosome band 12q13 by in situhybridization. Cytogenet. Cell Genet. 79: 210- 211, 1997.

GAM2033 305 RAB13 Novick, P.; Zerial, M.: The diversity of Rab proteins in vesicletransport. 3 C c Curr. Opin. Cell Biol. 9: 496- 504, 1997.

GAM2033 305 RAB13 Salminen, A.; Novick, P. J.: A ras- like protein is required fora post- 3 C c Golgi event in yeast secretion. Cell 49: 527- 538, 1987.

GAM2033 305 RAB13 Zahraoui, A.; Joberty, G.; Arpin, M.; Fontaine, J. J.; Hellio,R.; Tavitian, 3 C c A.; Louvard, D.: A small rab GTPase is distributedin cytoplasmic vesicles in nonpolarized cells but colocalizes withthe tight junction marker ZO- 1 in polarized epithelial cells. J.Cell. Biol. 124: 101- 115, 1994.

GAM2033 305 ROR1 Masiakowski, P.; Carroll, R. D.: A novel family of cell surfacereceptors 3 C c with tyrosine kinase- like domain. J. Biol. Chem. 267:26181- 26190, 1992.

GAM2033 305 ROR1 Nomi, M.; Oishi, I.; Kani, S.; Suzuki, H.; Matsuda, T.; Yoda, A.;Kitamura, 3 C c M.; Itoh, K.; Takeuchi, S.; Takeda, K.; Akira, S.; Ikeya,M.; Takada, S.; Minami, Y.: Loss of mRor1 enhances the heart andskeletal abnormalities in mRor2- deficient mice: redundant and pleiotropicfunctions of mRor1 and mRor2 receptor tyrosine kinases. Molec. Cell.Biol. 21: 8329- 8335, 2001.

GAM2033 305 ROR1 Reddy, U. R.; Phatak, S.; Allen, C.; Nycum, L. M.; Sulman, E. P.;White, P. 3 C c S.; Biegel, J. A.: Localization of the human Ror1 gene(NTRKR1) to chromosome 1p31- p32 by fluorescence in situ hybridizationand somatic cell hybrid analysis. Genomics 41: 283- 285, 1997.

GAM2033 305 ROR1 Reddy, U. R.; Phatak, S.; Pleasure, D.: Human neural tissues expressa 3 C c truncated Ror1 receptor tyrosine kinase, lacking both extracellularand transmembrane domains. Oncogene 13: 1555- 1559, 1996.

GAM2033 305 RTN2 Martin- Gallardo, A.; McCombie, W. R.; Gocayne, J. D.; FitzGerald,M. G.; 3 C c
Wallace, S.; Lee, B. M. B.; Lamerdin, J.; Trapp, S.; Kelley,J. M.; Liu, L.-
I.; Dubnick, M.; Johnston- Dow, L. A.; Kerlavage, A.R.; de Jong, P.;
Carrano, A.; Fields, C.; Venter, J. C.: AutomatedDNA sequencing and analysis
of 106 kilobases from human chromosome19q13.3. Nature Genet. 1: 34- 39,
1992.

GAM2033 305 RTN2 Roebroek, A. J. M.; Contreras, B.; Pauli, I. G. L.; Van de Ven,W. J. M.: 3 C c
cDNA cloning, genomic organization, and expression of thehuman RTN2 gene, a
member of a gene family encoding reticulons. Genomics 51:98- 106, 1998.

GAM2033 305 SFTPA2 Katyal, S. L.; Singh, G.; Locker, J.: Characterization of a secondhuman 3 C c
pulmonary surfactant- associated protein SP- A gene. Am. J. Resp.Cell Molec.
Biol. 6: 446- 452, 1992.

GAM2033 305 SFTPA2 Kolble, K.; Lu, J.; Mole, S. E.; Kaluz, S.; Reid, K. B. M.: Assignmentof the 3 C c
human pulmonary surfactant protein D gene (SFTP4) to 10q22- q23close to the
surfactant protein A gene cluster. Genomics 17: 294- 298,1993.

GAM2033 305 SFTPA2 Ramet, M.; Lofgren, J.; Albo, O.- P.; Hallman, M.: Surfactant protein- Agene 3 C c
locus associated with recurrent otitis media. J. Pediat. 138:266- 268, 2001.

GAM2033 305 TEP1 Harrington, L.; McPhail, T.; Mar, V.; Zhou, W.; Oulton, R.; Bass,M. B.; 3 C c
Arruda, I.; Robinson, M. O.: A mammalian telomerase- associatedprotein.
Science 275: 973- 976, 1997.

GAM2033 305 TEP1 Saito, T.; Matsuda, Y.; Suzuki, T.; Hayashi, A.; Yuan, X.; Saito,M.; 3 C c
Nakayama, J.; Hori, T.; Ishikawa, F.: Comparative gene mappingof the human
and mouse TEP1 genes, which encode one protein componentof telomerases.
Genomics 46: 46- 50, 1997.

GAM2033 305 TGFA Brissenden, J. E.; Derynck, R.; Francke, U.: Transforming growthfactor alpha 3 C c
gene (TGFA) maps to human chromosome 2 close to the breakpointof the t(2;8)
variant translocation in Burkitt lymphoma. (Abstract) Cytogenet.Cell Genet.
40: 589 only, 1985.

GAM2033 305 TGFA Collin, G. B.; Marshall, J. D.; Naggert, J. K.; Nishina, P. M.: TGFA: exon- 3 C c
intron structure and evaluation as a candidate gene forAlstrom syndrome.
(Letter) Clin. Genet. 55: 61- 62, 1999.

GAM2033 305 TGFA Ellis, D. L.; Kafka, S. P.; Chow, J. C.; Nanney, L. B.; Inman,W. H.; 3 C c
McCadden, M. E.; King, L. E., Jr.: Melanoma, growth factors,acanthosis
nigricans, the sign of Leser- Trelat, and multiple acrochordons:a possible
role for alpha- transforming growth factor in cutaneousparaneoplastic
syndromes. New Eng. J. Med. 317: 1582- 1587, 1987.

GAM2033 305 TGFA Fernandez- Larrea, J.; Merlos- Suarez, A.; Urena, J. M.; Baselga,J.; 3 C c
Arribas, J.: A role for a PDZ protein in the early secretorypathway for the
targeting of proTGF- alpha to the cell surface. Molec.Cell 3: 423- 433,
1999.

GAM2033 305 TGFA Fowler, K. J.; Mann, G. B.; Dunn, A. R.: Linkage of the murinetransforming 3 C c
growth factor- alpha gene with Igk, Ly- 2, and Fabp1 onchromosome 6.
Genomics 16: 782- 784, 1993.

GAM2033 305 TGFA Kramer, A.; Yang, F.- C.; Snodgrass, P.; Li, X.; Scammell, T. E.;Davis, F. 3 C c
C.; Weitz, C. J.: Regulation of daily locomotor activityand sleep by
hypothalamic EGF receptor signaling. Science 294: 2511- 2515,2001.

GAM2033 305 TGFA Tam, J. P.; Scheikh, M. A.; Solomon, D. S.; Ossowski, L.: Efficientsynthesis 3 C c
of human type alpha transforming growth factor: its physicaland biological
characterization. Proc. Nat. Acad. Sci. 83: 8082- 8086,1986.

GAM2033 305 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. 3 C c

B.: Assignment of the gene coding for human TGF- alphato chromosome 2p13. (Abstract) Cytogenet. Cell Genet. 40: 762 only,1985.

GAM2033 305 TGFA Tricoli, J. V.; Nakai, H.; Byers, M. G.; Rall, L. B.; Bell, G.I.; Shows, T. 3 C c B.: The gene for human transforming growth factor alphais on the short arm of chromosome 2. Cytogenet. Cell Genet. 42:94- 98, 1986.

GAM2033 305 TGFB3 Barton, D. E.; Foellmer, B. E.; Du, J.; Tamm, J.; Derynck, R.;Francke, U.: 3 C c Chromosomal mapping of genes for transforming growthfactors beta- 2 and beta- 3 in man and mouse: dispersion of TGF- betagene family. Oncogene Res. 3: 323- 331, 1988.

GAM2033 305 TGFB3 Dickinson, M. E.; Kobrin, M. S.; Silan, C. M.; Kingsley, D. M.;Justice, M. 3 C c J.; Miller, D. A.; Ceci, J. D.; Lock, L. F.; Lee, A.;Buchberg, A. M.; Siracusa, L. D.; Lyons, K. M.; Derynck, R.; Hogan,B. L. M.; Copeland, N. G.; Jenkins, N. A.: Chromosomal localizationof seven members of the murine TGF- beta superfamily suggests closelinkage to several morphogenetic mutant loci. Genomics 6: 505- 520,1990.

GAM2033 305 TGFB3 Graycar, J. L.; Miller, D. A.; Arrick, B. A.; Lyons, R. M.; Moses,H. L.; 3 C c Derynck, R.: Human transforming growth factor- beta- 3: recombinantexpression, purification, and biological activities in comparisonwith transforming growth factors- beta- 1 and beta- 2. Molec. Endocr. 3:1977- 1986, 1989.

GAM2033 305 TGFB3 Kaartinen, V.; Voncken, J. W.; Shuler, C.; Warburton, D.; Bu, 3 C c D.;Heisterkamp, N.; Groffen, J.: Abnormal lung development and cleftpalate in mice lacking TGF- beta- 3 indicates defects of epithelial- mesenchymalinteraction. Nature Genet. 11: 415- 421, 1995.

GAM2033 305 TGFB3 Lee, B.- S.; Nowak, R. A.: Human leiomyoma smooth muscle cellsshow increased 3 C c expression of transforming growth factor- beta- 3 (TGF- beta- 3)and altered responses to the antiproliferative effects of TGF- beta. J.Clin. Endocr. Metab. 86: 913- 920, 2001.

GAM2033 305 TGFB3 Moren, A.; Ichijo, H.; Miyazono, K.: Molecular cloning and 3 C c characterizationof the human and porcine transforming growth factor- beta type IIIreceptors. Biochem. Biophys. Res. Commun. 189: 356- 362, 1992.

GAM2033 305 TGFB3 Proetzel, G.; Pawlowski, S. A.; Wiles, M. V.; Yin, M.; Boivin,G. P.; Howles, 3 C c P. N.; Ding, J.; Ferguson, M. W. J.; Doetschman, T.: Transforming growth factor- beta- 3 is required for secondary palatefusion. Nature Genet. 11: 409- 414, 1995.

GAM2033 305 TGFB3 ten Dijke, P.; Geurts van Kessel, A. H. M.; Foulkes, J. G.; LeBeau, M. M.: 3 C c Transforming growth factor type beta- 3 maps to humanchromosome 14, region q23- q24. Oncogene 3: 721- 724, 1988.

GAM2033 305 TGFB3 ten Dijke, P.; Hansen, P.; Iwata, K. K.; Pieler, C.; Foulkes, J.G.: 3 C c Identification of another member of the transforming growth factortype beta gene family. Proc. Nat. Acad. Sci. 85: 4715- 4719, 1988.

GAM2033 305 TNFSF4 Akiba, H.; Atsuta, M.; Yagita, H.; Okumura, K.: Identificationof rat OX40 3 C c ligand by molecular cloning. Biochem. Biophys. Res. Commun. 251:131- 136, 1998.

GAM2033 305 TNFSF4 Baum, P. R.; Gayle, R. B., III; Ramsdell, F.; Srinivasan, S.; Sorensen,R. 3 C c A.; Watson, M. L.; Seldin, M. F.; Baker, E.; Sutherland, G. R.;Clifford, K. N.; Alderson, M. R.; Goodwin, R. G.; Fanslow, W. C.:Molecular characterization of murine and human OX40/OX40 ligand systems:identification of a human OX40 ligand as the HTLV- 1- regulated proteingp34. EMBO J. 13:

3992- 4001, 1994.

GAM2033 305 TNFSF4 Godfrey, W. R.; Fagnoni, F. F.; Harara, M. A.; Buck, D.; Engleman,E. G.: 3 C c
Identification of a human OX- 40 ligand, a costimulator ofCD4+ T cells with
homology to tumor necrosis factor. J. Exp. Med. 180:757- 762, 1994.

GAM2033 305 TNFSF4 Malmstrom, V.; Shipton, D.; Singh, B.; Al- Shamkhani, A.; Puklavec,M. J.; 3 C c
Barclay, A. N.; Powrie, F.: CD134L expression on dendriticcells in the
mesenteric lymph nodes drives colitis in T cell- restoredSCID mice. J.
Immun. 166: 6972- 6981, 2001.

GAM2033 305 TNFSF4 Miura, S.; Ohtani, K.; Numata, N.; Niki, M.; Ohbo, K.; Ina, Y.;Gojobori, T.; 3 C c
Tanaka, Y.; Tozawa, H.; Nakamura, M.; Sugamura, K.:Molecular cloning and
characterization of a novel glycoprotein, gp34,that is specifically induced
by the human T- cell leukemia virus typel transactivator p40- tax. Molec.
Cell. Biol. 11: 1313- 1325, 1991.

GAM2033 305 TRIM9 Li, Y.; Chin, L.- S.; Weigel, C.; Li, L.: Spring, a novel RINGfinger protein 3 C c
that regulates synaptic vesicle exocytosis. J. Biol.Chem. 276: 40824- 40833,
2001.

GAM2033 305 TRIM9 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; 3 C c
Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci,
S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell
compartments. EMBO J. 20: 2140- 2151, 2001.

GAM2033 305 TSN Aoki, K.; Inazawa, J.; Takahashi, T.; Nakahara, K.; Kasai, M.:Genomic 3 C c
structure and chromosomal localization of the gene encodingtranslin, a
recombination hotspot binding protein. Genomics 43:237- 241, 1997.

GAM2033 305 TSN Aoki, K.; Nakahara, K.; Ikegawa, C.; Seto, M.; Takahashi, T.; Minowada,J.; 3 C c
Strominger, J. L.; Maziarz, R. T.; Kasai, M.: Nuclear proteinsbinding to a
novel target sequence within the recombination hotspotregions of Bcl- 2 and
the immunoglobulin D(H) gene family. Oncogene 9:1109- 1115, 1994.

GAM2033 305 TSN Aoki, K.; Suzuki, K.; Sugano, T.; Tasaka, T.; Nakahara, K.; Kuge,O.; Omori, 3 C c
A.; Kasai, M.: A novel gene, 'Translin,' encodes a recombinationhotspot
binding protein associated with chromosomal translocations. NatureGenet. 10:
167- 174, 1995.

GAM2033 305 TSN Badge, R. M.; Yardley, J.; Jeffreys, A. J.; Armour, J. A. L.:Crossover 3 C c
breakpoint mapping identifies a subtelomeric hotspot formale meiotic
recombination. Hum. Molec. Genet. 9: 1239- 1244, 2000.

GAM2033 305 TSN Hosaka, T.; Kanoe, H.; Nakayama, T.; Murakami, H.; Yamamoto, H.;Nakamata, 3 C c
T.; Tsuboyama, T.; Oka, M.; Kasai, M.; Sasaki, M. S.; Nakamura,T.;
Toguchida, J.: Translin binds to the sequences adjacent to thebreakpoints of
the TLS and CHOP genes in liposarcomas with translocationt(12;16). Oncogene
19: 5821- 5825, 2000.

GAM2033 305 TSN Kasai, M.; Aoki, K.; Matsuo, Y.; Minowada, J.; Maziarz, R. T.;Strominger, J. 3 C c
L.: Recombination hotspot associated factors specificallyrecognize novel
target sequences at the site of interchromosomal rearrangementsin T- ALL
patients with t(8;14)(q24;q11)and (t(1;14)(p32;q11). Int.Immun. 6: 1017-
1025, 1994.

GAM2033 305 WBSCR1 Osborne, L. R.; Martindale, D.; Scherer, S. W.; Shi, X.- M.; Huizenga,J.; 3 C c
Heng, H. H. Q.; Costa, T.; Pober, B.; Lew, L.; Brinkman, J.; Rommens,J.;
Koop, B.; Tsui, L.- C.: Identification of genes from a 500- kbregion at
7q11.23 that is commonly deleted in Williams syndrome patients. Genomics
36:328- 336, 1996.

GAM2033 305 WBSCR1 Richter- Cook, N. J.; Dever, T. E.; Hensold, J. O.; Merrick, W.C.: 3 C c

Purification and characterization of a new eukaryotic proteintranslation factor: eukaryotic initiation factor 4H. J. Biol. Chem. 273:7579- 7587, 1998.

GAM2071 371 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- 3 B b
glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989.

GAM2071 371 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion 3 B b
data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989.

GAM2071 371 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma 3 B b
alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.

GAM2071 371 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human 3 B b
plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.

GAM2071 371 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: 3 B b
Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988.

GAM2071 371 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- 3 B c
TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.

GAM2071 371 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 B c
Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM2071 371 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM 3 B c
protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999.

GAM2071 371 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; 3 B c
Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664- 1666, 1999.

GAM2071 371 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 B c
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995.

GAM2071 371 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 B c
members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994.

GAM2071 371 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: 3 B c
Chromosomal mapping of human adenylyl cyclase genestype III, type V and type VI. Hum. Genet. 94: 69- 73, 1994.

GAM2071 371 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; 3 B c
Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002.

GAM2071 371 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; 3 B c
Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor:

functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994.

GAM2071 371 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994. 3 B c

GAM2071 371 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 3 B c

GAM2071 371 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95- 101, 1997. 3 B c

GAM2071 371 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779- 782, 2000. 3 B c

GAM2071 371 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001. 3 B c

GAM2071 371 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001. 3 B c

GAM2071 371 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998. 3 B c

GAM2071 371 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: Identificationand characterization of STK12/Aik2: a human gene related to auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147- 152,1998. 3 B c

GAM2071 371 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism, OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001. 3 B c

GAM2071 371 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand characterization of genes associated with chromosome- 6 mediatedtumor suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996. 3 B c

GAM2071 371 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a novel non- lens member of the beta- gamma- crystallin superfamily,is associated with the control of tumorigenicity in human malignantmelanoma. Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997. 3 B c

GAM2071 371 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA cloning, expression, subcellular localization, and chromosomalassignment of mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem. Biophys. Res. Commun. 244: 285- 292, 1998. 3 B c

GAM2071 371 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; 3 B c

Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof the aurora- and Ipl1- like midbody- associated protein mitotic kinasein human cancer cells. Cancer Res. 58: 4811- 4816, 1998.

GAM2071 371 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. 3 B c
S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian Genome 9: 715- 720, 1998.

GAM2071 371 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; 3 B c
Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human melanoma cell lines controlled by introduction of human chromosome6. Science 247: 568- 571, 1990.

GAM2071 371 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: 3 B b
Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89: 3962- 3966,1992.

GAM2071 371 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- 3 B b
lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat. Acad. Sci. 96: 4378- 4383, 1999.

GAM2071 371 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; 3 B b
Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988.

GAM2071 371 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: 3 B b
Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990.

GAM2071 371 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 3 B b
(CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998.

GAM2071 371 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of 3 B b
Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999.

GAM2071 371 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: 3 B b
Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000.

GAM2071 371 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 3 B b
deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001.

GAM2071 371 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic 3 B b
protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999.

GAM2071 371 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, 3 B b
P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002.

GAM2071 371 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- 3 B b
Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001.

GAM2071 371 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: 3 B b

Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998.

GAM2071 371 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998. 3 B b

GAM2071 371 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 3 B b

GAM2071 371 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 B b

GAM2071 371 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 B b

GAM2071 371 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 B b

GAM2071 371 ARHA Cannizzaro, L. A.; Madaule, P.; Hecht, F.; Axel, R.; Croce, C.M.; Huebner, K.: Chromosome localization of human ARH genes, a ras- relatedgene family. Genomics 6: 197- 203, 1990. 3 B c

GAM2071 371 ARHA Kiss, C.; Li, J.; Szeles, A.; Gizatullin, R. Z.; Kashuba, V. I.;Lushnikova, T.; Protopopov, A. I.; Kelve, M.; Kiss, H.; Kholodnyuk,I. D.; Imreh, S.; Klein, G.; Zabarovsky, E. R.: Assignment of theARHA and GPX1 genes to human chromosome bands 3p21.3 by in situ hybridizationand with somatic cell hybrids. Cytogenet. Cell Genet. 79: 228- 230,1997. 3 B c

GAM2071 371 ARHA Maekawa, M.; Ishizaki, T.; Boku, S.; Watanabe, N.; Fujita, A.;Iwamatsu, A.; Obinata, T.; Ohashi, K.; Mizuno, K.; Narumiya, S.:Signaling from Rho to the actin cytoskeleton through protein kinasesROCK and LIM- kinase. Science 285: 895- 898, 1999. 3 B c

GAM2071 371 ARHA Maesaki, R.; Ihara, K.; Shimizu, T.; Kuroda, S.; Kaibuchi, K.;Hakoshima, T.: The structural basis of Rho effector recognition revealedby the crystal structure of human RhoA complexed with the effectordomain of PKN/PRK1. Molec. Cell 4: 793- 803, 1999. 3 B c

GAM2071 371 ARHA Nakamura, M.; Nagano, T.; Chikama, T.; Nishida, T.: Role of thesmall GTP- binding protein Rho in epithelial cell migration in therabbit cornea. Invest. Ophthal. Vis. Sci. 42: 941- 947, 2001. 3 B c

GAM2071 371 ARHA Rao, P. V.; Deng, P.- F.; Kumar, J.; Epstein, D. L.: Modulationof aqueous humor outflow facility by the Rho kinase- specific inhibitorY- 27632. Invest. Ophthal. Vis. Sci. 42: 1029- 1037, 2001. 3 B c

GAM2071 371 BACH1 Blouin, J.- L.; Sail, G. D.; Guipponi, M.; Rossier, C.; Pappasavas,M.- P.; Antonarakis, S. E.: Isolation of the human BACH1 transcriptionregulator gene, which maps to chromosome 21q22.1. Hum. Genet. 102:282- 288, 1998. 3 B c

GAM2071 371 BACH1 Kanezaki, R.; Toki, T.; Yokoyama, M.; Yomogida, K.; Sugiyama, K.;Yamamoto, M.; Igarashi, K.; Ito, E.: Transcription factor BACH1 isrecruited to the nucleus by its novel alternative spliced isoform. J.Biol. Chem. 276: 7278- 7284, 2001. 3 B c

GAM2071 371 BACH1 Ohira, M.; Seki, N.; Nagase, T.; Ishikawa, K.; Nomura, N.; Ohara,O.: Characterization of a human homolog (BACH1) of the mouse Bach1gene encoding 3 B c

a BTB- basic leucine zipper transcription factor andits mapping to chromosome 21q22.1. Genomics 47: 300- 306, 1998.

GAM2071 371 BACH1 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 3 B c Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB- basic leucine zipper transcription factors that interact withMafK and regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083- 6095, 1996.

GAM2071 371 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- 3 B b evaluation of 'reactive lymphoid hyperplasia of the uvea': animmunohistochemical and molecular analysis of 10 cases. Ophthalmology 107:151- 158, 2000.

GAM2071 371 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 3 B b mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999.

GAM2071 371 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. 3 B b J.Clin. Path. 48: 395- 397, 1995.

GAM2071 371 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; 3 B b Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T. W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001.

GAM2071 371 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; 3 B b Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not its cellular homologue, activates NF- kappa- B transcriptionfactor and c- Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999.

GAM2071 371 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- 3 B b Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.; Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types Cell 96: 35- 45, 1999.

GAM2071 371 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic 3 B b study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer Genet. Cytogenet. 58: 35- 38, 1992.

GAM2071 371 BDKRB1 Bachvarov, D. R.; Hess, J. F.; Menke, J. G.; Larrivee, J.- F.; Marceau,F.: 3 B b Structure and genomic organization of the human B(1) receptorgene for kinins (BDKRB1). Genomics 33: 374- 381, 1996.

GAM2071 371 BDKRB1 Chai, K. X.; Ni, A.; Wang, D.; Ward, D. C.; Chao, J.; Chao, L.: Genomic DNA 3 B b sequence, expression, and chromosomal localization ofthe human B1 bradykinin receptor gene BDKRB1. Genomics 31: 51- 57,1996.

GAM2071 371 BDKRB1 MacNeil, T.; Bierilo, K. K.; Menke, J. G.; Hess, J. F.: Cloningand 3 B b pharmacological characterization of a rabbit bradykinin B- 1 receptor. Biochim.Biophys. Acta 1264: 223- 228, 1995.

GAM2071 371 BDKRB1 Menke, J. G.; Borkowski, J. A.; Bierilo, K. K.; MacNeil, T.; Derrick,A. W.; 3 B b Schneck, K. A.; Ransom, R. W.; Strader, C. D.; Linemeyer, D.L.; Hess, J. F.: Expression cloning of a human B1 bradykinin receptor. J.Biol. Chem. 269: 21583- 21586, 1994.

GAM2071 371 BDKRB1 Yang, X.; Polgar, P.: Genomic structure of the human bradykininB(1) receptor 3 B b gene and preliminary characterization of its regulatoryregions. Biochem. Biophys. Res. Commun. 222: 718- 725, 1996.

GAM2071 371 BDP1 Kelter, A.- R.; Herchenbach, J.; Wirth, B.: The transcription factor- 3 B c likenuclear regulator (TFNR) contains a novel 55- amino- acid motif repeatednine times and maps closely to SMN1. Genomics 70: 315- 326, 2000.

GAM2071 371 BDP1 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 B c
TFIIB activities direct RNA polymerase III transcription fromTATA-
containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM2071 371 BMP1 Amano, S.; Scott, I. C.; Takahara, K.; Koch, M.; Champliaud, M.- F.;Gerecke, 3 B c
D. R.; Keene, D. R.; Hudson, D. L.; Nishiyama, T.; Lee, S.;Greenspan, D. S.;
Burgeson, R. E.: Bone morphogenetic protein 1 isan extracellular processing
enzyme of the laminin 5 gamma- 2 chain. J.Biol. Chem. 275: 22728- 22735,
2000.

GAM2071 371 BMP1 Bond, J. S.; Beynon, R. J.: The astacin family of metalloendopeptidases. 3 B c
ProteinSci. 4: 1247- 1261, 1995.

GAM2071 371 BMP1 Ceci, J. D.; Kingsley, D. M.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: 3 B c
An interspecific backcross linkage map of the proximal halfof mouse
chromosome 14. Genomics 6: 673- 678, 1990.

GAM2071 371 BMP1 Kessler, E.; Takahara, K.; Biniaminov, L.; Brusel, M.; Greenspan,D.: Bone 3 B c
morphogenic protein- 1: the type I procollagen C- proteinase. Science
271:360- 362, 1996.

GAM2071 371 BMP1 Reddi, A. H.: BMP- 1: resurrection as procollagen C- proteinase. Science 3 B c
271:5- 6, 1996.

GAM2071 371 BMP1 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; 3 B c
Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.;
Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases,
including novel family member mammalian Tolloid- like2, have differential
enzymatic activities and distributions of expressionrelevant to patterning
and skeletogenesis. Dev. Biol. 213: 283- 300,1999.

GAM2071 371 BMP1 Tabas, J. A.; Zasloff, M.; Wasmuth, J. J.; Emanuel, B. S.; Altherr,M. R.; 3 B c
McPherson, J. D.; Wozney, J. M.; Kaplan, F. S.: Bone morphogeneticprotein:
chromosomal localization of human genes for BMP1, BMP2A,and BMP3. Genomics
9: 283- 289, 1991.

GAM2071 371 BMP1 Takahara, K.; Lee, S.; Wood, S.; Greenspan, D. S.: Structuralorganization 3 B c
and genetic localization of the human bone morphogeneticprotein 1/mammalian
tolloid gene. Genomics 29: 9- 15, 1995.

GAM2071 371 BMP1 Takahara, K.; Lyons, G. E.; Greenspan, D. S.: Bone morphogeneticprotein- 1 3 B c
and a mammalian tolloid homologue (mTld) are encoded byalternatively spliced
transcripts which are differentially expressedin some tissues. J. Biol.
Chem. 269: 32572- 32578, 1994.

GAM2071 371 BMP1 Wozney, J. M.; Rosen, V.; Celeste, A. J.; Mitsock, L. M.; Whitters,M. J.; 3 B c
Kriz, R. W.; Hewick, R. M.; Wang, E. A.: Novel regulatorsof bone formation:
molecular clones and activities. Science 242:1528- 1534, 1988.

GAM2071 371 BMP1 Yoshiura, K.; Tamura, T.; Hong, H.- S.; Ohta, T.; Soejima, H.;Kishino, T.; 3 B c
Jinno, Y.; Niikawa, N.: Mapping of the bone morphogeneticprotein 1 gene
(BMP1) to 8p21: removal of BMP1 from candidacy forthe bone disorder in
Langer- Giedion syndrome. Cytogenet. Cell Genet. 64:208- 209, 1993.

GAM2071 371 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 B b
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM2071 371 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 B b
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a

novel human apoptotic cysteine protease containingtwo FADD- like domains. Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM2071 371 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 B b B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager, V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM2071 371 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 B b chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM2071 371 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 B b Expanded polyglutamine in the Machado- Joseph disease proteininduces cell death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM2071 371 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 B b P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to the murine syntenic region on chromosome 1B- proximalC by in situ hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM2071 371 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 B b Caspase- 8 is required for cell death induced by expanded polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM2071 371 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 B b J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet, O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.; Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1, and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM2071 371 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 B c member of a multigene family. Genomics 52: 332- 341, 1998.

GAM2071 371 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 B c new member of the MTG8/ETO gene family, maps on 20q11region and is deleted in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM2071 371 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 B c Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic fusion protein forms a complex with a novel member of theMTG8(ETO/CDR) family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM2071 371 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. 3 B b J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis machinery through a novel motif, the F- box. Cell 86:263- 274, 1996.

GAM2071 371 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; 3 B b Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene (CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics 24:27- 33, 1994.

GAM2071 371 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F 3 B b maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6: 149- 150, 1995.

GAM2071 371 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 3 B b membrane- associated C- type lectin that exhibits CD4- independentbinding of human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad. Sci. 89: 8356- 8360, 1992.

GAM2071 371 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 3 B b for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR.

Science 294: 2163- 2166, 2001.

GAM2071 371 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S. L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-infection of T cells. Cell 100: 587- 597,2000. 3 B b

GAM2071 371 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000. 3 B b

GAM2071 371 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000. 3 B b

GAM2071 371 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.; Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.; Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for Muckle- Wells syndrome and familial cold urticaria:a novel mutation underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002. 3 B b

GAM2071 371 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile neurological cutaneous and articular syndromeis caused by mutations in CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes. Am. J. Hum. Genet. 71: 198- 203, 2002. 3 B b

GAM2071 371 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature Genet. 29: 301- 305, 2001. 3 B b

GAM2071 371 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu, S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci. 95: 8175- 8180, 1998. 3 B b

GAM2071 371 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.: Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000. 3 B b

GAM2071 371 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 3 B b

GAM2071 371 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 3 B b

GAM2071 371 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 3 B b

GAM2071 371 CLNS1A Anguita, J.; Chalfant, M. L.; Civan, M. M.; Coca- Prados, M.: Molecularcloning of the human volume- sensitive chloride conductance regulatoryprotein, pI(Cln), from ocular ciliary epithelium. Biochem. Biophys.Res. Commun. 208: 89- 95, 1995. 3 B c

GAM2071 371 CLNS1A Buyse, G.; De Greef, C.; Raeymaekers, L.; Droogmans, G.; Nilius,B.; 3 B c
Eggermont, J.: The ubiquitously expressed pI(Cln) protein formshomomeric
complexes in vitro. Biochem. Biophys. Res. Commun. 218:822- 827, 1996.

GAM2071 371 CLNS1A Nagl, U. O.; Erdel, M.; Schmarda, A.; Seri, M.; Pinggera, G. M.;Gschwentner, 3 B c
M.; Duba, C.; Galietta, L. J. V.; Deetjen, P.; Utermann,G.; Paulmichl, M.:
Chromosomal localization of the genes (CLNS1Aand CLNS1B) coding for the
swelling- dependent chloride channel I(Cln). Genomics 38:438- 441, 1996.

GAM2071 371 CLNS1A Schwartz, R. S.; Rybicki, A. C.; Nagel, R. L.: Molecular cloningand 3 B c
expression of a chloride channel- associated protein pI(Cln) inhuman young
red blood cells: association with actin. Biochem. J. 327:609- 616, 1997.

GAM2071 371 CNN2 Cheng, J.- F.; Boyartchuk, V.; Zhu, Y.: Isolation and mapping ofhuman 3 B b
chromosome 21 cDNA: progress in constructing a chromosome 21expression map.
Genomics 23: 75- 84, 1994.

GAM2071 371 CNN2 Masuda, H.; Tanaka, K.; Takagi, M.; Ohgami, K.; Sakamaki, T.; Shibata,N.; 3 B b
Takahashi, K.: Molecular cloning and characterization of humannon- smooth
muscle calponin. J. Biochem. 120: 415- 424, 1996.

GAM2071 371 CNP Bernier, L.; Colman, D. R.; D'Eustachio, P.: Chromosomal locationsof genes 3 B c
encoding 2- prime,3- prime cyclic nucleotide 3- prime- phosphodiesteraseand
glial fibrillary acidic protein in the mouse. J. Neurosci. Res. 20:497- 504,
1988.

GAM2071 371 CNP Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J.: 2- prime,3- prime- 3 B c
cyclicnucleotide 3- prime- phosphodiesterase: a membrane- bound,
microtubule- associatedprotein and membrane anchor for tubulin. Proc. Nat.
Acad. Sci. 99:1807- 1812, 2002.

GAM2071 371 CNP Douglas, A. J.; Fox, M. F.; Abbott, C. M.; Hinks, L. J.; Sharpe,G.; Povey, 3 B c
S.; Thompson, R. J.: Structure and chromosomal localizationof the human 2-
prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasegene. Ann. Hum.
Genet. 56: 243- 254, 1992.

GAM2071 371 CNP Douglas, A. J.; Fox, M. F.; Hinks, L. J.; Povey, S.; Thompson,R. J.: 3 B c
Localization of the myelin specific enzyme 2- prime,3- prime-
cyclicnucleotide- 3- prime- phosphohydrolase to 17q21. (Abstract)
Cytogenet.Cell Genet. 58: 2004 only, 1991.

GAM2071 371 CNP Kurihara, T.; Monoh, K.; Sakimura, K.; Takahashi, Y.: Alternativesplicing of 3 B c
mouse brain 2- prime,3- prime- cyclic nucleotide 3- prime-
phosphodiesterasemRNA. Biochem. Biophys. Res. Commun. 170: 1074- 1081, 1990.

GAM2071 371 CNP Monoh, K.; Kurihara, T.; Takahashi, Y.; Ichikawa, T.; Kumanishi,T.; Hayashi, 3 B c
S.; Minoshima, S.; Shimizu, N.: Structure, expressionand chromosomal
localization of the gene encoding human 2- prime,3- prime- cyclic-
nucleotide3- prime- phosphodiesterase. Gene 129: 297- 301, 1993.

GAM2071 371 CNP Sprinkle, T. J.; Kouri, R. E.; Fain, P. D.; Stoming, T. A.; Whitney,J. B., 3 B c
III: Chromosomal mapping of the human CNP gene using a meioticcrossover DNA
panel, PCR, and allele- specific probes. Genomics 16:542- 545, 1993.

GAM2071 371 CNP Sprinkle, T. J.; Lanclos, K. D.; Lapp, D. F.: Assignment of thehuman 2- 3 B c
prime,3- prime- cyclic nucleotide 3- prime- phosphohydrolase geneto
chromosome 17. Genomics 13: 877- 880, 1992.

GAM2071 371 CNP Vogel, U. S.; Thompson, R. J.: Molecular structure, localization,and 3 B c
possible functions of the myelin- associated enzyme 2- prime,3- prime-
cyclicnucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667-
1677,1988.

GAM2071 371 CRSP6 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, 3 B c

Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC complexes indicates novel pathways for the functionof nuclear receptors and diverse mammalian activators. Molec. Cell 3:361- 370, 1999.

GAM2071 371 CRSP6 Jiang, Y.- W.; Veschambre, P.; Erdjument- Bromage, H.; Tempst, P.;Conaway, J. W.; Conaway, R. C.; Kornberg, R. D.: Mammalian mediatorof transcriptional regulation and its possible role as an end- pointof signal transduction pathways. Proc. Nat. Acad. Sci. 95: 8538- 8543,1998. 3 B c

GAM2071 371 CRSP6 Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R.: The transcriptionalcofactor complex CRSP is required for activity of the enhancer- bindingprotein Sp1. Nature 397: 446- 450, 1999. 3 B c

GAM2071 371 CSNK2A2 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 3 B b

GAM2071 371 CSNK2A2 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine 392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292, 2001. 3 B b

GAM2071 371 CSNK2A2 Lozeman, F. J.; Litchfield, D. W.; Piening, C.; Takio, K.; Walsh,K. A.; Krebs, E. G.: Isolation and characterization of human cDNAclones encoding the alpha and the alpha- prime subunits of casein kinaseII. Biochemistry 29: 8436- 8447, 1990. 3 B b

GAM2071 371 CSNK2A2 Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C.: Globozoospermiain mice lacking the casein kinase II alpha- prime catalytic subunit. NatureGenet. 23: 118- 121, 1999. 3 B b

GAM2071 371 CSNK2A2 Yang- Feng, T. L.; Naiman, T.; Kopatz, I.; Eli, D.; Dafni, N.; Canaani,D.: Assignment of the human casein kinase II alpha- prime subunitgene (CSNK2A1) to chromosome 16p13.2- p13.3. Genomics 19: 173 only,1994. 3 B b

GAM2071 371 CSNK2A2 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping of the human casein kinase II catalytic subunit genes: twoloci carrying the homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125- 7129, 1991. 3 B b

GAM2071 371 CST Ishida, N.; Ito, M.; Yoshioka, S.; Sun- Wada, G.- H.; Kawakita, M.: Functional expression of human Golgi CMP- sialic acid transporterin the Golgi complex of a transporter- deficient Chinese hamster ovarycell mutant. J. Biochem. 124: 171- 178, 1998. 3 B c

GAM2071 371 CST Ishida, N.; Miura, N.; Yoshioka, S.; Kawakita, M.: Molecular cloningand characterization of a novel isoform of the human UDP- galactosetransporter, and of related complementary DNAs belonging to the nucleotide- sugartransporter gene family. J. Biochem. 120: 1074- 1078, 1996. 3 B c

GAM2071 371 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H, L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245, 1997. 3 B b

GAM2071 371 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S controls the trafficking and maturation of MHC class IImolecules in dendritic cells. J. Cell Biol. 147: 775- 790, 1999. 3 B b

GAM2071 371 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. J.; Chapman, H. A.: Structure and chromosomal assignmentof the human cathepsin K gene. Genomics 41: 258- 262, 1997. 3 B b

GAM2071 371 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.; Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell selection and maturation by cathepsin S. Immunity 15:909- 919, 2001. 3 B b

GAM2071 371 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: Molecular cloning and expression of human alveolar macrophagecathepsin S, an elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992. 3 B b

GAM2071 371 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization, gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536, 1994. 3 B b

GAM2071 371 CXCL16 Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G.: A transmembrane CXC chemokine is a ligand for HIV- coreceptor Bonzo. NatureImmun. 1: 298- 304, 2000. 3 B b

GAM2071 371 CXCL16 Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.;Kita, T.; Yonehara, S.: Molecular cloning of a novel scavenger receptorfor oxidized low density lipoprotein, SR- PSOX, on macrophages. J.Biol. Chem. 275: 40663- 40666, 2000. 3 B b

GAM2071 371 CXCL16 Wilbanks, A.; Zondlo, S. C.; Murphy, K.; Mak, S.; Soler, D.; Langdon,P.; Andrew, D. P.; Wu, L.; Briskin, M.: Expression cloning of theSTRL33/BONZO/TYMSTR ligand reveals elements of CC, CXC, CX3C chemokines. J.Immun. 166: 5145- 5154, 2001. 3 B b

GAM2071 371 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996. 3 B b

GAM2071 371 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989. 3 B b

GAM2071 371 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000. 3 B b

GAM2071 371 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. L.: The contribution of genetically determined oxidationstatus to inter- individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983. 3 B b

GAM2071 371 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986. 3 B b

GAM2071 371 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. Endocr. 3: 1399- 1408, 1989. 3 B b

GAM2071 371 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the 3- prime nontranslated region, and localization ofgene to chromosome 15. J. Exp. Path. 3: 1- 17, 1987. 3 B b

GAM2071 371 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996. 3 B b

GAM2071 371 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 B b

GAM2071 371 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 3 B b

GAM2071 371 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 3 B b

GAM2071 371 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 3 B b

GAM2071 371 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002. 3 B b

GAM2071 371 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 3 B b

GAM2071 371 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 B b

GAM2071 371 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 3 B b

GAM2071 371 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene: molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230, 1998. 3 B b

GAM2071 371 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii-Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in humanpolymorphonuclear leukocytes: cDNA cloning and expression of leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993. 3 B b

GAM2071 371 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 B c

GAM2071 371 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 B c

GAM2071 371 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4-alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 B c

GAM2071 371 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000. 3 B b

GAM2071 371 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 3 B b

40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461- 8466, 1998.

GAM2071 371 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997. 3 B b

GAM2071 371 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998. 3 B b

GAM2071 371 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila-relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997. 3 B b

GAM2071 371 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998. 3 B b

GAM2071 371 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994. 3 B b

GAM2071 371 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997. 3 B b

GAM2071 371 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993. 3 B b

GAM2071 371 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997. 3 B b

GAM2071 371 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, D. J.; Muir, W. J.: Schizophrenia and affective disorders- - cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001. 3 B b

GAM2071 371 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 355:771- 772, 2000. 3 B b

GAM2071 371 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 3 B b

GAM2071 371 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 3 B b

GAM2071 371 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000. 3 B b

GAM2071 371 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, 3 B b

G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM2071 371 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995. 3 B c

GAM2071 371 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin. J. Biol. Chem. 269: 26295- 26302, 1994. 3 B c

GAM2071 371 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The desmocollins of human foreskin epidermis: identification and chromosomalassignment of a third gene and expression patterns of the three isoforms. J.Invest. Derm. 105: 314- 321, 1995. 3 B c

GAM2071 371 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.: Neurodevelopmental delay, motor abnormalities and cognitive deficitsin transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001. 3 B c

GAM2071 371 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262- 265, 1997. 3 B c

GAM2071 371 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A potassium channel mutation in weaver mice implicates membraneexcitability in granule cell differentiation. Nature Genet. 11:126- 129, 1995. 3 B c

GAM2071 371 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk gene from 'the Down syndrome critical region' of chromosome 21. Biochem.Biophys. Res. Commun. 225: 92- 99, 1996. 3 B c

GAM2071 371 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.; Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in transgenic mice implicates minibrain in learningdefects associated with Down syndrome. Nature Genet. 16: 28- 36,1997. 3 B c

GAM2071 371 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to chromosome 16, localizes to the nucleus, and can form multimers. Biochem.Biophys. Res. Commun. 231: 640- 644, 1997. 3 B c

GAM2071 371 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.; Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the Drosophila minibrain gene: human homologue maps to 21q22.2in the Down syndrome 'critical region.' Genomics 38: 331- 339, 1996. 3 B c

GAM2071 371 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein kinase family involved in postembryonic neurogenesisin Drosophila. Neuron 14: 287- 301, 1995. 3 B c

GAM2071 371 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- elongationfactor 2 kinase (calmodulin- dependent protein kinase III) antibodiesin patients with systemic lupus erythematosus. Biochem. Biophys.Res. Commun. 293: 1073- 1076, 2002. 3 B b

GAM2071 371 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 3 B b

Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C. R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat. Acad. Sci. 94: 4884- 4889, 1997.

GAM2071 371 EIF2S3 Ehrmann, I. E.; Ellis, P. S.; Mazeyrat, S.; Duthie, S.; Brockdorff,N.; 3 B b
Mattei, M. G.; Gavin, M. A.; Affara, N. A.; Brown, G. M.; Simpson,E.; Mitchell, M. J.; Scott, D. M.: Characterization of genes encodingtranslation initiation factor eIF- 2- gamma in mouse and human: sexchromosome localization, escape from X- inactivation and evolution. Hum.Molec. Genet. 7: 1725- 1737, 1998.

GAM2071 371 EIF2S3 Gasper, N. J.; Kinzy, T. G.; Scherer, B. J.; Humbelin, M.; Hershey,J. W. B.; 3 B b
Merrick, W. C.: Translation initiation factor eIF- 2: cloningand expression of the human cDNA encoding the gamma- subunit. J. Biol.Chem. 269: 3415- 3422, 1994.

GAM2071 371 EPHB6 Matsuoka, H.; Iwata, N.; Ito, M.; Shimoyama, M.; Nagata, A.; Chihara,K.; 3 B c
Takai, S.; Matsui, T.: Expression of a kinase- defective Eph- likereceptor in the normal human brain. Biochem. Biophys. Res. Commun. 235:487- 492, 1997.

GAM2071 371 EPHB6 Tang, X. X.; Zhao, H.; Robinson, M. E.; Cohen, B.; Cnaan, A.; London,W.; 3 B c
Cohn, S. L.; Cheung, N.- K. V.; Brodeur, G. M.; Evans, A. E.; Ikegaki,N.: Implications of EPHB6, EFNB2, and EFNB3 expressions in humanneuroblastoma. Proc. Nat. Acad. Sci. 97: 10936- 10941, 2000.

GAM2071 371 F2RL2 Duperat, V. G.; Jacquelin, B.; Boisseau, P.; Arveiler, B.; Nurden,A. T.: 3 B b
Protease- activated receptor genes are clustered on 5q13. Blood 92:25- 31, 1998.

GAM2071 371 F2RL2 Ishihara, H.; Connolly, A. J.; Zeng, D.; Kahn, M. L.; Zheng, Y.W.; Timmons, 3 B b
C.; Tram, T.; Coughlin, S. R.: Protease- activated receptor3 is a second thrombin receptor in humans. Nature 386: 502- 506,1997.

GAM2071 371 F2RL2 Kahn, M. L.; Zheng, Y. W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 B b
Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998.

GAM2071 371 F2RL2 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 B b
M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000.

GAM2071 371 F2RL2 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 B b
Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001.

GAM2071 371 F2RL2 Schmidt, V.; Wainer, J.; Bahou, W.: Identification and characterizationof 3 B b
the human proteolytically activated receptor- 3 (PAR- 3) gene withinthe PAR gene cluster by positional mapping. (Abstract) Blood (suppl.1) 90: 284a only, 1997.

GAM2071 371 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 B b
Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998.

GAM2071 371 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 B b
M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000.

GAM2071 371 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 B b
Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001.

GAM2071 371 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998. 3 B b

GAM2071 371 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985. 3 B b

GAM2071 371 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985. 3 B b

GAM2071 371 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988. 3 B b

GAM2071 371 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional analysis of the human tissue factor promoter and inductionby serum. Proc. Nat. Acad. Sci. 87: 2254- 2258, 1990. 3 B b

GAM2071 371 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: Completesequence of the human tissue factor gene, a highly regulated cellularreceptor that initiates the coagulation protease cascade. Biochemistry 28:1755- 1762, 1989. 3 B b

GAM2071 371 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand mapping of RFLPs for human tissue factor (HTF) to chromosome 1p. NucleicAcids Res. 15: 9098 only, 1987. 3 B b

GAM2071 371 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA sequenceand chromosome localization of the gene. Biochemistry 26: 5234- 5238,1987. 3 B b

GAM2071 371 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA clones coding for human tissue factor: primary structureof the protein and cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987. 3 B b

GAM2071 371 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad. Sci. 94: 6922- 6926, 1997. 3 B b

GAM2071 371 FANCE Buchwald, M.: Complementation groups: one or more per gene? NatureGenet. 11: 228- 230, 1995. 3 B b

GAM2071 371 FANCE de Winter, J. P.; Leveille, F.; van Berkel, C. G. M.; Rooimans,M. A.; van der Weel, L.; Steltenpool, J.; Demuth, I.; Morgan, N. V.;Alon, N.; Bosnoyan-Collins, L.; Lightfoot, J.; Leegwater, P. A.; Waisfisz,Q.; Komatsu, K.; Arwert, F.; Pronk, J. C.; Mathew, C. G.; Digweed,M.; Buchwald, M.; Joenje, H.: Isolation of a cDNA representing theFanconi anemia complementation group E gene. Am. J. Hum. Genet. 67:1306- 1308, 2000. Note: Erratum: Am. J. Hum. Genet. 67: 1365 only,2000. 3 B b

GAM2071 371 FANCE Joenje, H.: Fanconi anaemia complementation groups in Germanyand The Netherlands. Hum. Genet. 97: 280- 282, 1996. 3 B b

GAM2071 371 FANCE Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G.M.; Rooimans, M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J.J. P.; Buchwald, M.; Arwert, F.: Classification of Fanconi anemiapatients by complementation analysis: evidence for a fifth geneticsubtype. Blood 86: 2156- 2160, 1995. 3 B b

GAM2071 371 FANCE Joenje, H.; Oostra, A. B.; Wijker, M.; di Summa, F. M.; van Berkel,C. G. M.; Rooimans, M. A.; Ebell, W.; van Weel, M.; Pronk, J. C.;Buchwald, M.; Arwert, F.: Evidence for at least eight Fanconi anemiagenes. Am. J. Hum. Genet. 61: 940- 944, 1997. 3 B b

GAM2071 371 FANCE Pace, P.; Johnson, M.; Tan, W. M.; Mosedale, G.; Sng, C.; Hoatlin,M.; de Winter, J.; Joenje, H.; Gergely, F.; Patel, K. J.: FANCE:the link between Fanconi anaemia complex assembly and activity. EMBOJ. 21: 3414- 3423, 2002. 3 B b

GAM2071 371 FANCE Waisfisz, Q.; Saar, K.; Morgan, N. V.; Altay, C.; Leegwater, P.A.; de Winter, J. P.; Komatsu, K.; Evans, G. R.; Wegner, R.- D.; Reis,A.; Joenje, H.; Arwert, F.; Mathew, C. G.; Pronk, J. C.; Digweed,M.: The Fanconi anemia group E gene, FANCE, maps to chromosome 6p. Am.J. Hum. Genet. 64: 1400- 1405, 1999. 3 B b

GAM2071 371 FANCE Wegner, R.- D.; Henrichs, I.; Joenje, H.; Schroeder- Kurth, T.:Fanconi anemia complementation group E: clinical and cytogenetic dataof the first patient. Clin. Genet. 50: 479- 482, 1996. 3 B b

GAM2071 371 FBLN1 Argraves, W. S.; Dickerson, K.; Burgess, W. H.; Ruoslahti, E.:Fibulin, a novel protein that interacts with the fibronectin receptor- betasubunit cytoplasmic domain. Cell 58: 623- 629, 1989. 3 B c

GAM2071 371 FBLN1 Korenberg, J. R.; Chen, X.- N.; Tran, H.; Argraves, W. S.: Localizationof the human gene for fibulin- 1 (FBLN1) to chromosome band 22q13.3.Cytogenet. Cell Genet. 68: 192- 193, 1995. 3 B c

GAM2071 371 FBLN1 Mattei, M.- G.; Pan, T.- C.; Zhang, R.- Z.; Timpl, R.; Chu, M.- L.: The fibulin- 1 gene (FBLN1) is located on human chromosome 22 andon mouse chromosome 15. Genomics 22: 437- 438, 1994. 3 B c

GAM2071 371 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995. 3 B b

GAM2071 371 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 3 B b

GAM2071 371 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665- 1672, 1990. 3 B b

GAM2071 371 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681- 1685, 1993. 3 B b

GAM2071 371 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 3 B b

GAM2071 371 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 3 B b

GAM2071 371 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 3 B b

GAM2071 371 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001. 3 B b

GAM2071 371 FCGR2A Grundy, H. O.; Peltz, G.; Barsh, G.; Moore, K.; Golbus, M. S.;Lebo, R. V.: 3 B b
Immunoglobulin G Fc receptor II and Fc receptor IIIgenes map to chromosome 1
by spot- blot chromosome analysis. (Abstract) Am.J. Hum. Genet. 43: A145,
1988.

GAM2071 371 FCGR2A Grundy, H. O.; Peltz, G.; Moore, K. W.; Golbus, M. S.; Jackson,L. G.; Lebo, 3 B b
R. V.: The polymorphic Fc- gamma receptor II gene mapsto human chromosome
1q. Immunogenetics 29: 331- 339, 1989.

GAM2071 371 FCGR2A Hibbs, M. L.; Bonadonna, L.; Scott, B. M.; McKenzie, I. F. C.;Hogarth, P. 3 B b
M.: Molecular cloning of a human immunoglobulin G Fcreceptor. Proc. Nat.
Acad. Sci. 85: 2240- 2244, 1988.

GAM2071 371 FCGR2A Hibbs, M. L.; Hogarth, P. M.; McKenzie, I. F. C.: The mouse Ly- 17locus 3 B b
identifies a polymorphism of the Fc receptor. Immunogenetics 22:335- 348,
1985.

GAM2071 371 FCGR2A Lebo, R. V.; Lynch, E. D.; Wiegant, J.; Moore, K.; Trounstine,M.; van der 3 B b
Ploeg, M.: Multicolor fluorescence in situ hybridizationand pulsed field
electrophoresis dissect CMT1B gene region. Hum.Genet. 88: 13- 20, 1991.

GAM2071 371 FCGR2A Moser, K. L.; Neas, B. R.; Salmon, J. E.; Yu, H.; Gray- McGuire,C.; Asundi, 3 B b
N.; Bruner, G. R.; Fox, J.; Kelly, J.; Henshall, S.; Bacino,D.; Dietz, M.;
Hogue, R.; Koelsch, G.; Nightingale, L.; Shaver, T.;Abdou, N. I.; Albert, D.
A.; Carson, C.; Petri, M.; Treadwell, E.L.; James, J. A.; Harley, J. B.:
Genome scan of human systemic lupuserythematosus: evidence for linkage on
chromosome 1q in African- Americanpedigrees. Proc. Nat. Acad. Sci. 95:
14869- 14874, 1998.

GAM2071 371 FCGR2A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on 3 B b
mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human
DNA. Hum. Molec. Genet. 1: 613- 620,1992.

GAM2071 371 FCGR2A Peltz, G. A.; Grundy, H. O.; Lebo, R. V.; Yssel, H.; Barsh, G.S.; Moore, K. 3 B b
W.: Human Fc- gamma- RIII: cloning, expression, and identificationof the
chromosomal locus of two Fc receptors for IgG. Proc. Nat.Acad. Sci. 86:
1013- 1017, 1989.

GAM2071 371 FCGR2A Qiu, W. Q.; de Bruin, D.; Brownstein, B. H.; Pearse, R.; Ravetch,J. V.: 3 B b
Organization of the human and mouse low- affinity Fc- gamma- Rgenes:
duplication and recombination. Science 248: 732- 735, 1990.

GAM2071 371 FCGR2A Salmon, J. E.; Millard, S.; Schachter, L. A.; Arnett, F. C.; Ginzler,E. M.; 3 B b
Gourley, M. F.; Ramsey- Goldman, R.; Peterson, M. G. E.; Kimberly,R. P.: Fc-
gamma- RIIA alleles are heritable risk factors for lupusnephritis in African
Americans. J. Clin. Invest. 97: 1348- 1354,1996.

GAM2071 371 FCGR2A Sammartino, L.; Webber, L. M.; Hogarth, P. M.; McKenzie, I. F.C.; Garson, O. 3 B b
M.: Assignment of the gene coding for human FcRII(CD32) to bands q23q24 on
chromosome 1. Immunogenetics 28: 380- 381,1988.

GAM2071 371 FCGR2A Stein, M.- P.; Edberg, J. C.; Kimberly, R. P.; Mangan, E. K.; Bharadwaj,D.; 3 B b
Mold, C.; Du Clos, T. W.: C- reactive protein binding to Fc- gamma- RIIaon
human monocytes and neutrophils is allele- specific. J. Clin. Invest.
105:369- 376, 2000.

GAM2071 371 FCGR2A Unkeless, J. C.: Function and heterogeneity of human Fc receptorsfor 3 B b
immunoglobulin G. J. Clin. Invest. 83: 355- 361, 1989.

GAM2071 371 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 B c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM2071 371 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 B c

GAM2071 371 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome assignment by polymerase chain reaction techniques: assignmentof the oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990. 3 B b

GAM2071 371 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator of the hair growth cycle: evidence from targeted and spontaneousmutations. Cell 78: 1017- 1025, 1994. 3 B b

GAM2071 371 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992. 3 B b

GAM2071 371 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and the bcl.1 locus are contained within one megabase in bandq13 of chromosome 11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988. 3 B b

GAM2071 371 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8: 3487- 3495, 1988. 3 B b

GAM2071 371 FHL2 Chan, K. K.; Tsui, S. K. W.; Lee, S. M. Y.; Luk, S. C. W.; Liew,C. C.; Fung, K. P.; Waye, M. M. Y.; Lee, C. Y.: Molecular cloningand characterization of FHL2, a novel LIM domain protein preferentiallyexpressed in human heart. Gene 210: 345- 350, 1998. 3 B b

GAM2071 371 FHL2 Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.- G.;Schafer, B. W.: Subtractive cloning and characterization of DRAL,a novel LIM- domain protein down- regulated in rhabdomyosarcoma. DNACell Biol. 16: 433- 442, 1997. 3 B b

GAM2071 371 FHL2 Morgan, M. J.; Madgwick, A. J. A.: Slim defines a novel familyof LIM- proteins expressed in skeletal muscle. Biochem. Biophys. Res.Commun. 225: 632- 638, 1996. 3 B b

GAM2071 371 FHL2 Tanahashi, H.; Tabira, T.: Alzheimer's disease- associated presenilin2 interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9:2281- 2289, 2000. 3 B b

GAM2071 371 FSHPRH1 Aittomaki, K.; Lucena, J. L. D.; Pakarinen, P.; Sistonen, P.; Tapanainen,J.; Gromoll, J.; Kaskikari, R.; Sankila, E.- M.; Lehvaslaiho, H.; Engel,A. R.; Nieschlag, E.; Huhtaniemi, I.; de la Chapelle, A.: Mutationin the follicle- stimulating hormone receptor gene causes hereditaryhypergonadotropic ovarian failure. Cell 82: 959- 968, 1995. 3 B b

GAM2071 371 FSHPRH1 Roberts, R. G.; Kendall, E.; Vetrie, D.; Bobrow, M.: Sequenceand chromosomal location of a human homologue of LRPR1, an FSH primaryresponse gene. Genomics 37: 122- 124, 1996. 3 B b

GAM2071 371 FSHPRH1 Slegtenhorst- Eegdeman, K. E.; Post, M.; Baarends, W. M.; Themmen,A. P. N.; Grootegoed, J. A.: Regulation of gene expression in Sertolicells by follicle- stimulating hormone (FSH): cloning and characterizationof LRPR1, a primary response gene encoding a leucine- rich protein. Molec.Cell. Endocr. 108: 115- 124, 1995. 3 B b

GAM2071 371 G1P3 Clauss, I. M.; Wathelet, M. G.; Szpirer, J.; Content, J.; Islam,M. Q.; Levan, G.; Szpirer, C.; Huez, G. A.: Chromosomal localizationof two human 3 B c

genes inducible by interferons, double- stranded RNA,and viruses. Cytogenet. Cell Genet. 53: 166- 168, 1990.

GAM2071 371 G1P3 Itzhaki, J. E.; Barnett, M. A.; MacCarthy, A. B.; Buckle, V. J.;Brown, W. R. 3 B c
A.; Porter, A. C. G.: Targeted breakage of a human chromosomemediated by cloned human telomeric DNA. Nature Genet. 2: 283- 287,1992.

GAM2071 371 G1P3 Itzhaki, J. E.; Porter, A. C. G.: Targeted disruption of a humaninterferon- 3 B c
inducible gene detected by secretion of human growth hormone. NucleicAcids Res. 19: 3835- 3842, 1991.

GAM2071 371 G1P3 Kelly, J. M.; Porter, A. C. G.; Chernajovsky, Y.; Gilbert, C. S.;Stark, G. 3 B c
R.; Kerr, I. M.: Characterization of a human gene inducibleby alpha- and beta- interferons and its expression in mouse cells. EMBOJ. 5: 1601- 1606, 1986.

GAM2071 371 G1P3 Porter, A. C. G.; Chernajovsky, Y.; Dale, T. C.; Gilbert, C. S.;Stark, G. 3 B c
R.; Kerr, I. M.: Interferon response element of the humangene 6- 16. EMBO J. 7: 85- 92, 1988.

GAM2071 371 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; 3 B c
Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N- acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001.

GAM2071 371 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme 3 B c
catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2- epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313- 24318,1997.

GAM2071 371 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 B c

GAM2071 371 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; 3 B c
Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997.

GAM2071 371 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; 3 B c
Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase gene (GNE). J. Hum. Genet. 47: 77- 79, 2002.

GAM2071 371 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, 3 B c
W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999.

GAM2071 371 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; 3 B c
Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993.

GAM2071 371 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van 3 B c
Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001.

GAM2071 371 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal 3 B c
myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981.

GAM2071 371 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; 3 B c
Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential

for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002.

GAM2071 371 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N- 3 B c
acetylglucosamine 2- epimerase gene define the disease sialuriaand the
allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999.

GAM2071 371 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; 3 B c
Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N-
acetylneuraminic acid biosynthesis of rat liver: molecularcloning and
functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N-
acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997.

GAM2071 371 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification 3 B c
of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989.

GAM2071 371 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a 3 B c
second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987.

GAM2071 371 GPR4 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; 3 B b
Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation
of three novel human genes encoding G protein- coupledreceptors. DNA Cell
Biol. 14: 25- 35, 1995.

GAM2071 371 GPR4 Mahadevan, M. S.; Baird, S.; Bailly, J. E.; Shutler, G. G.; Sabourin,L. A.; 3 B b
Tsilfidis, C.; Neville, C. E.; Narang, M.; Korneluk, R. G.: Isolation of a
novel G protein- coupled receptor (GPR4) localizedto chromosome 19q13.3.
Genomics 30: 84- 88, 1995.

GAM2071 371 GPR4 Ye, R. D.; Prossnitz, E. R.; Zou, A.; Cochrane, C. G.: Characterizationof a 3 B b
human cDNA that encodes a functional receptor for platelet activatingfactor.
Biochem. Biophys. Res. Commun. 180: 105- 111, 1991.

GAM2071 371 GPR4 Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina,K. L.; 3 B b
Kabarowski, J. H. S.; Witte, O. N.; Xu, Y.: Sphingosylphosphorylcholineand
lysophosphatidylcholine are ligands for the G protein- coupledreceptor GPR4.
J. Biol. Chem. 276: 41325- 41335, 2001.

GAM2071 371 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, 3 B b
J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a
novel secretin- like human G- protein- coupledreceptor gene. Genomics 55:
296- 305, 1999.

GAM2071 371 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; 3 B b
van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected
with mRNA differential display using human melanoma celllines with different
metastatic potential. FEBS Lett. 446: 292- 298,1999.

GAM2071 371 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; 3 B b
Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann,
S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is
fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in
three cases of myelodysplastic syndrome/acutemyeloid leukemia with a
deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000.

GAM2071 371 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain- 3 B b
containingGTPase- activating protein for Rho and Cdc42 associates with
focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996.

GAM2071 371 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 B b
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM2071 371 GRINL1A Roginski, R. S.; Mohan Raj, B. K.; Finkernagel, S. W.; Sciorra,L. J.: 3 B b

Assignment of an ionotropic glutamate receptor- like gene (GRINL1A)to human chromosome 15q22.1 by in situ hybridization. Cytogenet.Cell Genet. 93: 143-144, 2001.

GAM2071 371 GRINL1A Wydner, K. S.; Mohan Raj, B. K.; Sciorra, L. J.; Roginski, R. S.: The mouse orthologue of the human ionotropic glutamate receptor- likegene (GRINL1A) maps to mouse chromosome 9. Cytogenet. Cell Genet. 95:240- 241, 2001. 3 B b

GAM2071 371 HTR1D Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S. J.; Duncan,A. M. V.; Rozmahel, R.; Yang, Y.; Mengod, G.; Palacios, J. M.; O'Dowd,B. F.: Characterization of the human 5- hydroxytryptamine(1B) receptor. J.Biol. Chem. 267: 5735- 5738, 1992. 3 B b

GAM2071 371 HTR1D Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor, and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. 3 B b

GAM2071 371 HTR1D Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T.A.; Hartig, P. R.: Human serotonin 1D receptor is encoded by a subfamilyof two distinct genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat.Acad. Sci. 89: 3630-3634, 1992. 3 B b

GAM2071 371 HTR1D Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and genome organization of mammalian G- protein- coupled receptors. Genomics 18:175- 184, 1993. 3 B b

GAM2071 371 HTR1E Levy, F. O.; Gudermann, T.; Birnbaumer, M.; Kaumann, A. J.; Birnbaumer,L.: Molecular cloning of a human gene (S31) encoding a novel serotoninreceptor mediating inhibition of adenylyl cyclase. FEBS Lett. 296:201- 206, 1992. 3 B c

GAM2071 371 HTR1E Levy, F. O.; Holtgreve- Grez, H.; Tasken, K.; Solberg, R.; Ried,T.; Gudermann, T.: Assignment of the gene encoding the 5- HT- 1E serotoninreceptor (S31) (locus HTR1E) to human chromosome 6q14- q15. Genomics 22:637- 640, 1994. 3 B c

GAM2071 371 HTR1E McAllister, G.; Charlesworth, A.; Snodin, C.; Beer, M. S.; Noble,A. J.; Middlemiss, D. N.; Iversen, L. L.; Whiting, P.: Molecularcloning of a serotonin receptor from human brain (5HT1E): a fifth5HT1- like subtype. Proc. Nat. Acad. Sci. 89: 5517- 5521, 1992. 3 B c

GAM2071 371 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998. 3 B b

GAM2071 371 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol-Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay. Genomics 54: 278- 286, 1998. 3 B b

GAM2071 371 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated in response to DNA damage. EMBO J. 17: 2055- 2066,1998. 3 B b

GAM2071 371 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999. 3 B b

GAM2071 371 ICAM1 Ballantyne, C. M.; Kozak, C. A.; O'Brien, W. E.; Beaudet, A. L.: Assignment of the gene for intercellular adhesion molecule- 1 (Icam- 1)to proximal mouse chromosome 9. Genomics 9: 547- 550, 1991. 3 B b

GAM2071 371 ICAM1 Bella, J.; Kolatkar, P. R.; Marlor, C. W.; Greve, J. M.; Rossmann,M. G.: The structure of the two amino- terminal domains of human ICAM- 1suggests how it 3 B b

functions as a rhinovirus receptor and as an LFA- 1integrin ligand. Proc. Nat. Acad. Sci. 95: 4140- 4145, 1998.

GAM2071 371 ICAM1 Bellamy, R.; Kwiatkowski, D.; and Hill, A. V. S.: Absence of anassociation between intercellular adhesion molecule 1, complementreceptor 1 and interleukin 1 receptor antagonist gene polymorphismsand severe malaria in a West African population. Trans. R. Soc. Trop.Med. Hyg. 92: 312- 316, 1998. 3 B b

GAM2071 371 ICAM1 Craig, A.; Fernandez- Reyes, D.; Mesri, M.; McDowall, A.; Altieri,D. C.; Hogg, N.; Newbold, C.: A functional analysis of a naturalvariant of intercellular adhesion molecule- 1 (ICAM- 1- Kilifi). Hum.Molec. Genet. 9: 525- 530, 2000. 3 B b

GAM2071 371 ICAM1 Fernandez- Reyes, D.; Craig, A. G.; Kyes, S. A.; Peshu, N.; Snow,R. W.; Berendt, A. R.; Marsh, K.; Newbold, C. I.: A high frequencyAfrican coding polymorphism in the N- terminal domain of ICAM- 1 predisposingto cerebral malaria in Kenya. Hum. Molec. Genet. 6: 1357- 1360, 1997. 3 B b

GAM2071 371 ICAM1 Greve, J. M.; Davis, G.; Meyer, A. M.; Forte, C. P.; Yost, S. C.;Marlor, C. W.; Kamarck, M. E.; McClelland, A.: The major human rhinovirusreceptor is ICAM- 1. Cell 56: 839- 847, 1989. 3 B b

GAM2071 371 ICAM1 Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. Phys. 111: 272- 277, 1999. 3 B b

GAM2071 371 ICAM1 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B cells. Europ. J. Immun. 15: 103- 106, 1985. 3 B b

GAM2071 371 ICAM1 Le Beau, M. M.; Ryan, D., Jr.; Pericak- Vance, M. A.: Report ofthe committee on the genetic constitution of chromosomes 18 and 19. Cytogenet.Cell Genet. 51: 338- 357, 1989. 3 B b

GAM2071 371 ICAM1 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in the splenic marginal zone. Science 297: 409- 412, 2002. 3 B b

GAM2071 371 ICAM1 Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot-Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow cytometricanalysis of conjunctival epithelium in ocular rosacea and keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000. 3 B b

GAM2071 371 ICAM1 Prieto, J.; Takei, F.; Gendelman, R.; Christenson, B.; Biberfeld,P.; Patarroyo, M.: MALA- 2, mouse homologue of human adhesion moleculeICAM- 1 (CD54). Europ. J. Immun. 19: 1551- 1557, 1989. 3 B b

GAM2071 371 ICAM1 Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal mouse chromosome 9 linkage map that further defines linkagegroups homologous with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685, 1991. 3 B b

GAM2071 371 ICAM1 Simmons, D.; Makgoba, M. W.; Seed, B.: ICAM, an adhesion ligandof LFA- 1, is homologous to the neural cell adhesion molecule NCAM. Nature 331:624- 627, 1988. 3 B b

GAM2071 371 ICAM1 Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H.K.; Smith, C. W.; Bradley, A.; Beaudet, A. L.: Inflammatory and immuneresponses are impaired in mice deficient in intercellular adhesionmolecule 1. Proc. Nat. Acad. Sci. 90: 8529- 8533, 1993. 3 B b

GAM2071 371 ICAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993. 3 B b

GAM2071 371 ICAM1 Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; 3 B b
Takeuchi, T.: Regulation of human leukocyte antigenexpression in human
conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999.

GAM2071 371 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 B b
M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like
growth factor- I and cognitive function inhealthy older men. J. Clin.
Endocr. Metab. 84: 471- 475, 1999.

GAM2071 371 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- 3 B b
like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993.

GAM2071 371 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and 3 B b
absence of association with stature among African Pygmies. Hum.Genet. 85:
349- 354, 1990.

GAM2071 371 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for 3 B b
insulin- like growth factors I and II and for epidermalgrowth factor in man.
(Abstract) Am. J. Hum. Genet. 36: 133S only,1984.

GAM2071 371 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of 3 B b
genes for insulin- like growth factors I and II and epidermalgrowth factor.
Nature 310: 781- 784, 1984.

GAM2071 371 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, 3 B b
A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of
recombinant human insulin- like growth factor I(IGF- I) therapy on the
growth hormone- IGF system of a patient witha partial IGF- I gene deletion.
J. Clin. Endocr. Metab. 84: 1611- 1616,1999.

GAM2071 371 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; 3 B b
Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of
the growth hormone receptor in children with idiopathicshort stature. New
Eng. J. Med. 333: 1093- 1098, 1995.

GAM2071 371 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; 3 B b
Froesch, E. R.: Small stature and insulin- like growth factors:prolonged
treatment of mini- poodles with recombinant human insulin- likegrowth factor
I. Acta Endocr. 121: 456- 464, 1989.

GAM2071 371 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. 3 B b
S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating
concentrations of insulin- like growth factor- I and riskof breast cancer.
Lancet 351: 1393- 1396, 1998.

GAM2071 371 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: 3 B b
Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding
protein- 3, and prostate- specific antigen as predictorsof clinical prostate
cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000.

GAM2071 371 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; 3 B b
Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith,
D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival
signaling in retinal endothelial cells: direct correlationwith clinical
retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001.

GAM2071 371 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer 3 B b
prevention. Lancet 351: 1373- 1375, 1998.

GAM2071 371 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; 3 B b
Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J.
S.: The human gene encoding insulin- like growthfactor I is located on
chromosome 12. Hum. Genet. 69: 157- 160, 1985.

GAM2071 371 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990. 3 B b

GAM2071 371 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986. 3 B b

GAM2071 371 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF- 1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996. 3 B b

GAM2071 371 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat. Acad. Sci. 80: 2216- 2220, 1983. 3 B b

GAM2071 371 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand implications for cell type- specific growth. Nature 364: 208- 213,1993. 3 B b

GAM2071 371 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: Mice carrying null mutations of the genes encoding insulin- likegrowth factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993. 3 B b

GAM2071 371 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83: 9343- 9347, 1986. 3 B b

GAM2071 371 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human genes for insulin- like growth factors I and II and epidermalgrowth factor are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively. Cytogenet.Cell Genet. 41: 245- 249, 1986. 3 B b

GAM2071 371 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2 (IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985. 3 B b

GAM2071 371 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. D.: Growth characteristics and response to growth hormonetherapy in patients with hypochondroplasia: genetic linkage of theinsulin- like growth factor I gene at chromosome 12q23 to the diseasein a subgroup of these patients. Clin. Endocr. 34: 265- 274, 1991. 3 B b

GAM2071 371 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999. 3 B b

GAM2071 371 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene expression sustains hypertrophy and regeneration insenescent skeletal muscle. Nature Genet. 27: 195- 200, 2001. 3 B b

GAM2071 371 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like growth factor 1 regulates the location, stability,and transcriptional activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000. 3 B b

GAM2071 371 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993. 3 B b

GAM2071 371 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the protein which binds insulin- like growth factor in human serum. Europ.J. 3 B b

Biochem. 172: 421- 425, 1988.

GAM2071 371 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith, R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the insulin- like growth factor I receptor and its ligandin relation to type 2 diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000. 3 B b

GAM2071 371 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986. 3 B b

GAM2071 371 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I) reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991. 3 B b

GAM2071 371 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999. 3 B b

GAM2071 371 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980. 3 B b

GAM2071 371 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 1991. 3 B b

GAM2071 371 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984. 3 B b

GAM2071 371 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984. 3 B b

GAM2071 371 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984. 3 B b

GAM2071 371 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-857,1992. 3 B b

GAM2071 371 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002. 3 B b

GAM2071 371 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980. 3 B b

GAM2071 371 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999. 3 B b

GAM2071 371 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. 3 B b

L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy on body composition and insulin resistance in IGF- Igene deletion. J. Clin. Endocr. Metab. 85: 1407- 1411, 2000.

GAM2071 371 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 3 B b
Intrauterine growth retardation and postnatal growth failureassociated with deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335: 1363- 1367, 1996.

GAM2071 371 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 3 B b
regional localization of human genes for insulin- like growthfactors I (IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell Genet. 40: 782 only, 1985.

GAM2071 371 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 3 B b
growth factors and bone mineral density in African Americanand white girls. J. Pediat. 137: 826- 832, 2000.

GAM2071 371 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 3 B b
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM2071 371 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 B b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM2071 371 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 B b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM2071 371 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 B b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814- 819, 1992.

GAM2071 371 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 B b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang, Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell- derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87: 7512- 7516, 1990.

GAM2071 371 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 3 B b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract) Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM2071 371 IL20RA Blumberg, H.; Conklin, D.; Xu, W.; Grossmann, A.; Brender, T.;Carollo, S.; 3 B c
Eagan, M.; Foster, D.; Haldeman, B. A.; Hammond, A.;Haugen, H.; Jelinek, L.; and 14 others: Interleukin 20: discovery,receptor identification, and role in epidermal function. Cell 104:9- 19, 2001.

GAM2071 371 IL20RA Scott, A. F.: Personal Communication. Baltimore, Md. 3/13/2001. 3 B c

GAM2071 371 ITGAL Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; 3 B c
Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P. G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome 16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991.

GAM2071 371 ITGAL Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. 3 B c
C.: Chromosomal location of the genes encoding the leukocyteadhesion receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988.

GAM2071 371 ITGAL Fischer, A.; Durandy, A.; Sterkers, G.; Griscelli, C.: Role ofthe LFA- 1 3 B c
molecule in cellular interactions required for antibodyproduction in humans. J. Immun. 136: 3198- 3203, 1986.

GAM2071 371 ITGAL Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cell retentionin 3 B c
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM2071 371 ITGAL Marlin, S. D.; Morton, C. C.; Anderson, D. C.; Springer, T. A.: LFA- 1 3 B c

immunodeficiency disease: definition of the genetic defectand chromosomal mapping of alpha and beta subunits of the lymphocytefunction- associated antigen 1 (LFA- 1) by complementation in hybridcells. J. Exp. Med. 164: 855-867, 1986.

GAM2071 371 ITGAL Pischel, K. D.; Marlin, S. D.; Springer, T. A.; Woods, V. L., Jr.;Bluestein, 3 B c
H. G.: Polymorphism of lymphocyte function- associatedantigen- 1 demonstrated by a lupus patient's alloantiserum. J. Clin.Invest. 79: 1607-1614, 1987.

GAM2071 371 ITGAL Sanchez- Madrid, F.; Nagy, J.; Robbins, E.; Simon, P.; Springer,T. A.: A 3 B c
human leukocyte differentiation antigen family with distinctalpha subunits and a common beta subunit: the lymphocyte function- associatedantigen (LFA-1), the C3bi complement receptor (OKM1/Mac- 1), and thep150,95 molecule. J. Exp. Med. 158: 1785- 1803, 1983.

GAM2071 371 JRK Morita, R.; Miyazaki, E.; Fong, C. G.; Chen, X.- N.; Korenberg,J. R.; 3 B c
Delgado- Escueta, A. V.; Yamakawa, K.: JH8, a gene highly homologousto the mouse jerky gene, maps to the region for childhood absenceepilepsy on 8q24. Biochem. Biophys. Res. Commun. 248: 307- 314, 1998.

GAM2071 371 JRK Toth, M.; Grimsby, J.; Buzsaki, G.; Donovan, G. P.: Epilepticseizures caused 3 B c
by inactivation of a novel gene, jerky, related tocentromere binding protein- B in transgenic mice. Nature Genet. 11:71- 75, 1995. Note: Erratum: Nature Genet. 12: 110 only, 1996.

GAM2071 371 KCNA5 Albrecht, B.; Weber, K.; Pongs, O.: Characterization of a voltage- 3 B c
activatedK- channel gene cluster on human chromosome 12p13. Receptors Channels 3:213- 220, 1995.

GAM2071 371 KCNA5 Curran, M. E.; Landes, G. M.; Keating, M. T.: Molecular 3 B c
cloning,characterization, and genomic localization of a human potassium channelgene. Genomics 12: 729- 737, 1992.

GAM2071 371 KCNA5 Klocke, R.; Roberds, S. L.; Tamkun, M. M.; Gronemeier, M.; Augustin,A.; 3 B c
Albrecht, B.; Pongs, O.; Jockusch, H.: Chromosomal mapping inthe mouse of eight K(+)- channel genes representing the four Shaker- likesubfamilies Shaker, Shab, Shaw, and Shal. Genomics 18: 568- 574,1993.

GAM2071 371 KCNA5 McPherson, J. D.; Wasmuth, J. J.; Chandy, K. G.; Swanson, R.; Dethlefs,B.; 3 B c
Chandy, G.; Wymore, R.; Ghanshani, S.: Chromosomal localizationof 7 potassium channel genes. (Abstract) Cytogenet. Cell Genet. 58:1979 only, 1991.

GAM2071 371 KCNA5 Philipson, L. H.; Hice, R. E.; Schaefer, K.; LaMendola, J.; Bell,G. I.; 3 B c
Neldon, D. J.; Steiner, D. F.: Sequence and functional expressionin Xenopus oocytes of a human insulinoma and islet potassium channel. Proc.Nat. Acad. Sci. 88: 53- 57, 1991.

GAM2071 371 KCNA5 Phromchotikul, T.; Browne, D. L.; Curran, M. E.; Keating, M. T.;Litt, M.: 3 B c
Dinucleotide repeat polymorphism at the KCNA5 locus. Hum.Molec. Genet. 2: 1512 only, 1993.

GAM2071 371 KCNA5 Tamkun, M. M.; Knoth, K. M.; Walbridge, J. A.; Kroemer, H.; Roden,D. M.; 3 B c
Glover, D. M.: Molecular cloning and characterization of twovoltage- gated K+ channel cDNAs from human ventricle. FASEB J. 5:331- 337, 1991.

GAM2071 371 KCNE3 Abbott, G. W.; Butler, M. H.; Bendahhou, S.; Dalakas, M. C.; Ptacek,L. J.; 3 B b
Goldstein, S. A. N.: MiRP2 forms potassium channels in skeletalmuscle with Kv3.4 and is associated with periodic paralysis. Cell 104:217- 231, 2001.

GAM2071 371 KCNE3 Abbott, G. W.; Sesti, F.; Splawski, I.; Buck, M. E.; Lehmann, M.H.; Timothy, 3 B b
K. W.; Keating, M. T.; Goldstein, S. A. N.: MiRP1 formsI(Kr) potassium

channels with HERG and is associated with cardiacarrhythmia. Cell 97: 175-187, 1999.

GAM2071 371 KCNE3 Schroeder, B. C.; Waldegger, S.; Fehr, S.; Bleich, M.; Warth, R.;Greger, R.; 3 B b
Jentsch, T. J.: A constitutively open potassium channelformed by KCNQ1 and KCNE3. Nature 403: 196- 199, 2000.

GAM2071 371 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel 3 B b
genes. Trends Pharm. Sci. 14: 434, 1993.

GAM2071 371 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; 3 B b
Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011-1017, 1996.

GAM2071 371 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; 3 B b
Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166-1170, 1995.

GAM2071 371 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: 3 B b
Targeted overactivity of beta cell KATP channels induces profoundneonatal diabetes. Cell 100: 645- 654, 2000.

GAM2071 371 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: 3 B b
Homozygositymapping, to chromosome 11p, of the gene for familial persistent hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421, 1995.

GAM2071 371 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward 3 B b
rectifier Kir6.2 also leads to familial persistent hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812, 1996.

GAM2071 371 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, 3 B b
T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium channels in hypoxia- induced generalized seizure. Science 292:1543- 1546, 2001.

GAM2071 371 KLK10 Liu, X.- L.; Wazer, D. E.; Watanabe, K.; Band, V.: Identificationof a novel 3 B c
serine protease- like gene, the expression of which is down- regulatedduring breast cancer progression. Cancer Res. 56: 3371- 3379, 1996.

GAM2071 371 KLK10 Polikoff, D.; Kuo, W.- L.; Cochran, J. F.; Wernick, M.; Kowbel,D.; Myambo, 3 B c
K.; Collins, C. C.: Assignment of protease, serine- like1 (PRSSL1) to human chromosome 19q13 by in situ hybridization andradiation hybrid mapping. Cytogenet. Cell Genet. 79: 147- 148, 1997.

GAM2071 371 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; 3 B b
Malherbe, P.: Cloning and functional expression of human kynurenine3-monooxygenase. FEBS Lett. 410: 407- 412, 1997.

GAM2071 371 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; 3 B b
Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001.

GAM2071 371 LEF1 de Lau, W.; Clevers, H.: LEF1 turns over a new leaf. Nature Genet. 28:3- 5, 3 B c
2001.

GAM2071 371 LEF1 Hovanes, K.; Li, T. W. H.; Munguia, J. E.; Truong, T.; Milovanovic,T.; 3 B c
Marsh, J. L.; Holcombe, R. F.; Waterman, M. L.: Beta- catenin-

sensitiveisoforms of lymphoid enhancer factor- 1 are selectively expressed incolon cancer. Nature Genet. 28: 53- 57, 2001.

GAM2071 371 LEF1 Love, J. J.; Li, X.; Case, D. A.; Giese, K.; Grosschedl, R.; Wright,P. E.: 3 B c Structural basis for DNA bending by the architectural transcriptionfactor LEF- 1. Nature 376: 791- 795, 1995.

GAM2071 371 LEF1 Milatovich, A.; Travis, A.; Grosschedl, R.; Francke, U.: Genefor lymphoid 3 B c enhancer- binding factor 1 (LEF1) mapped to human chromosome4 (q23- q25) and mouse chromosome 3 near Egf. Genomics 11: 1040- 1048,1991.

GAM2071 371 LEF1 Milatovich, A.; Travis, A.; Grosschedl, R.; Francke, U.: LEF1,the gene for 3 B c lymphoid enhancer- binding factor 1, mapped to human chromosome4 (q23- q25) and distal mouse chromosome 3 by Southern blot analysisand fluorescence in situ hybridization. (Abstract) Cytogenet. CellGenet. 58: 1888 only, 1991.

GAM2071 371 LEF1 van Genderen, C.; Okamura, R. M.; Farinas, I.; Quo, R. G.; Parslow,T. G.; 3 B c Bruhn, L.; Grosschedl, R.: Development of several organs thatrequire inductive epithelial- mesenchymal interactions is impairedin LEF- 1- deficient mice. Genes Dev. 8: 2691- 2703, 1994.

GAM2071 371 LEF1 Waterman, M. L.; Fischer, W. H.; Jones, K. A.: A thymus- specificmember of 3 B c the HMG protein family regulates the human T cell receptorC alpha enhancer. Genes Dev. 5: 656- 669, 1991.

GAM2071 371 LEF1 Zhou, P.; Byrne, C.; Jacobs, J.; Fuchs, E.: Lymphoid enhancerfactor 1 3 B c directs hair follicle patterning and epithelial cell fate. GenesDev. 9: 700- 713, 1995.

GAM2071 371 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand 3 B b characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000.

GAM2071 371 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; 3 B b Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000.

GAM2071 371 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; 3 B b Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363- 18367,1996.

GAM2071 371 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof 3 B b leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994.

GAM2071 371 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; 3 B b Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. Nature 384: 39- 43, 1996.

GAM2071 371 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 3 B b specifictranscriptional regulation of human leukotriene B4 receptor gene. J.Exp. Med. 192: 413- 420, 2000.

GAM2071 371 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 3 B b chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM2071 371 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 3 B b Leukotrienes and lipoxins: structures, biosynthesis,and biological effects. Science 237: 1171- 1176, 1987.

GAM2071 371 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 B b

Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997.

GAM2071 371 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 3 B b
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature 387:620- 624, 1997.

GAM2071 371 LYZ Camara, V. M.; Harding, J. W.; Prieur, D. J.: Inherited lysozymedeficiency 3 B b
in rabbits: the absence of a primary isozyme of lysozymeas the cause of the condition. Lab. Invest. 63: 544- 550, 1990.

GAM2071 371 LYZ Canet, D.; Sunde, M.; Last, A. M.; Miranker, A.; Spencer, A.; Robinson,C. 3 B b
V.; Dobson, C. M.: Mechanistic studies of the folding of humanlysozyme and the origin of amyloidogenic behavior in its disease- relatedvariants. Biochemistry 38: 6419- 6427, 1999.

GAM2071 371 LYZ Dayhoff, M. O.: Atlas of Protein Sequence and Structure. Lactalbuminand 3 B b
Lysozyme. Washington: National Biomedical Research Foundation(pub.) 5: 1972. Pp. D133- D140.

GAM2071 371 LYZ Fleming, A.: On a remarkable bacteriolytic element found in tissuesand 3 B b
secretions. Proc. Roy. Soc. Ser. B. 93: 306- 317, 1922.

GAM2071 371 LYZ Fleming, A.; Allison, V. D.: Observations on a bacteriolytic 3 B b
substance('lysozyme') found in secretions and tissues. Brit. J. Exp. Path. 3:252- 260, 1922.

GAM2071 371 LYZ Greenwald, R. A.; Cantor, J. O.; Prieur, D. J.; Young, D. M.:Composition of 3 B b
cartilage from lysozyme- deficient rabbits. Biochim.Biophys. Acta 385: 435-437, 1975.

GAM2071 371 LYZ Neufeld, E. L.: Personal Communication. Bethesda, Maryland 1972. 3 B b

GAM2071 371 LYZ Pepys, M. B.; Hawkins, P. N.; Booth, D. R.; Vigushin, D. M.; Tennent,G. A.; 3 B b
Soutar, A. K.; Totty, N.; Nguyen, O.; Blake, C. C. F.; Terry,C. J.; Feest, T. G.; Zalin, A. M.; Hsuan, J. J.: Human lysozyme genemutations cause hereditary systemic amyloidosis. Nature 362: 553- 557,1993.

GAM2071 371 LYZ Peters, C. W. B.; Kruse, U.; Pollwein, R.; Grzeschik, K.- H.; Sippel,A. E.: 3 B b
The human lysozyme gene: sequence organization and chromosomallocalization. (Abstract) Cytogenet. Cell Genet. 51: 1059 only, 1989.

GAM2071 371 LYZ Prieur, D. J.: Personal Communication. Pullman, Washington 5/13/1975. 3 B b

GAM2071 371 LYZ Prieur, D. J.; Olson, H. M.; Young, D. M.: Lysozyme deficiency- - 3 B b
aninherited disorder of rabbits. Am. J. Path. 77: 283- 296, 1974.

GAM2071 371 LYZ Spitznagel, J. K.; Cooper, M. R.; McCall, A. E.; DeChatelet, L.R.; Welsh, I. 3 B b
R.: Selective deficiency of granules associated withlysozyme and lactoferrin in human polymorphs (PMN) with reduced microbicidalcapacity. (Abstract) J. Clin. Invest. 51: 93A only, 1972.

GAM2071 371 LYZ Taniyama, Y.; Kuroki, R.; Omura, F.; Seko, C.; Kikuchi, M.: Evidencefor 3 B b
intramolecular disulfide bond shuffling in the folding of mutanthuman lysozyme. J. Biol. Chem. 266: 6456- 6461, 1991.

GAM2071 371 LYZ Yoshimura, K.; Toibana, A.; Nakahama, K.: Human lysozyme: sequencingof a 3 B b
cDNA, and expression and secretion by Saccharomyces cerevisiae. Biochem.Biophys. Res. Commun. 150: 794- 801, 1988.

GAM2071 371 LYZ Zalin, A. M.; Jones, S.; Fitch, N. J. S.; Ramsden, D. B.: 3 B b
Familialnephropathic non- neuropathic amyloidosis: clinical features, immunohistochemistryand chemistry. Quart. J. Med. 81: 945- 956, 1991.

GAM2071 371 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 B b
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome

8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM2071 371 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 B b

GAM2071 371 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990. 3 B c

GAM2071 371 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994. 3 B c

GAM2071 371 MDM2 Boyd, M. T.; Vlatkovic, N.; Haines, D. S.: A novel cellular protein(MTBP) binds to MDM2 and induces a G1 arrest that is suppressed byMDM2. J. Biol. Chem. 275: 31883- 31890, 2000. 3 B b

GAM2071 371 MDM2 Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S.A.; Albitar, M.: The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82:2617- 2623, 1993. 3 B b

GAM2071 371 MDM2 Bureau, J. F.; Bihl, F.; Brahic, M.; Le Paslier, D.: The genecoding for interferon- gamma is linked to the D12S335 and D12S313 microsatellitesand to the MDM2 gene. Genomics 28: 109- 112, 1995. 3 B b

GAM2071 371 MDM2 Buschmann, T.; Fuchs, S. Y.; Lee, C.- G.; Pan, Z.- Q.; Ronai, Z.: SUMO- 1 modification of Mdm2 prevents its self- ubiquitination andincreases Mdm2 ability to ubiquitinate p53. Cell 101: 753- 762, 2000.Note: Erratum: Cell 107: 549 only, 2001. 3 B b

GAM2071 371 MDM2 de Oca Luna, R. M.; Tabor, A. D.; Eberspaecher, H.; Hulboy, D.L.; Worth, L. L.; Colman, M. S.; Finlay, C. A.; Lozano, G.: The organizationand expression of the mdm2 gene. Genomics 33: 352- 357, 1996. 3 B b

GAM2071 371 MDM2 Fakharzadeh, S.; Trusko, S. P.; George, D. L.: Tumorigenic potentialassociated with enhanced expression of a gene that is amplified ina mouse tumor cell line. EMBO J. 10: 1565- 1569, 1991. 3 B b

GAM2071 371 MDM2 Freedman, D. A.; Epstein, C. B.; Roth, J. C.; Levine, A. J.: Agenetic approach to mapping the p53 binding site in the MDM2 protein. Molec.Med. 3: 248- 259, 1997. 3 B b

GAM2071 371 MDM2 Fuchs, S. Y.; Adler, V.; Buschmann, T.; Yin, Z.; Wu, X.; Jones,S. N.; Ronai, Z.: JNK targets p53 ubiquitination and degradationin nonstressed cells. Genes Dev. 12: 2658- 2663, 1998. 3 B b

GAM2071 371 MDM2 Mayo, L. D.; Donner, D. B.: A phosphatidylinositol 3- kinase/Aktpathway promotes translocation of Mdm2 from the cytoplasm to the nucleus. Proc.Nat. Acad. Sci. 98: 11598- 11603, 2001. 3 B b

GAM2071 371 MDM2 Mitchell, E. L. D.; White, G. R. M.; Santibanez- Koref, M. F.;Varley, J. M.; Heighway, J.: Mapping of gene loci in the q13- q15region of chromosome 12. Chromosome Res. 3: 261- 262, 1995. 3 B b

GAM2071 371 MDM2 Momand, J.; Zambetti, G. P.; Olson, D. C.; George, D. L.; Levine,A. J.: The mdm- 2 oncogene product forms a complex with the p53 proteinand inhibits p53- mediated transactivation. Cell 69: 1237- 1245, 1992. 3 B b

GAM2071 371 MDM2 Oliner, J. D.; Kinzler, K. W.; Meltzer, P. S.; George, D. L.;Vogelstein, B.: Amplification of a gene encoding a p53- associatedprotein in human sarcomas. Nature 358: 80- 83, 1992. 3 B b

GAM2071 371 MDM2 Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.;Sasazuki, T.; 3 B b

McMahon, M.; Oren, M.; McCormick, F.: Opposing effectsof Ras on p53: transcriptional activation of mdm2 and induction ofp19(ARF). Cell 103: 321-330, 2000.

GAM2071 371 MDM2 Shenoy, S. K.; McDonald, P. H.; Kohout, T. A.; Lefkowitz, R. J.: Regulation 3 B b of receptor fate by ubiquitination of activated beta- 2- adrenergicreceptor and beta- arrestin. Science 294: 1307- 1313, 2001.

GAM2071 371 MDM2 Shieh, S.- Y.; Ikeda, M.; Taya, Y.; Prives, C.: DNA damage- 3 B b inducedphosphorylation of p53 alleviates inhibition by MDM2. Cell 91: 325-334,1997.

GAM2071 371 MDM2 Testa, J. R.; Bellacosa, A.: AKT plays a central role in tumorigenesis. 3 B b Proc.Nat. Acad. Sci. 98: 10983- 10985, 2001.

GAM2071 371 MDM2 Xiao, Z.- X.; Chen, J.; Levine, A. J.; Modjtahedi, N.; Xing, J.;Sellers, W. 3 B b R.; Livingston, D. M.: Interaction between the retinoblastomaprotein and the oncoprotein MDM2. Nature 375: 694- 698, 1995.

GAM2071 371 MDM2 Zhang, Y.; Xiong, Y.: A p53 amino- terminal nuclear export signalinhibited 3 B b by DNA damage- induced phosphorylation. Science 292: 1910- 1915,2001.

GAM2071 371 MDM4 Parant, J.; Chavez- Reyes, A.; Little, N. A.; Yan, W.; Reinke, V.;Jochemsen, 3 B b A. G.; Lozano, G.: Rescue of embryonic lethality in Mdm4- nullmice by loss of Trp53 suggests a nonoverlapping pathway with MDM2to regulate p53. Nature Genet. 29: 92- 95, 2001.

GAM2071 371 MDM4 Shvarts, A.; Bazuine, M.; Dekker, P.; Ramos, Y. F. M.; Steegenga,W. T.; 3 B b Merckx, G.; van Ham, R. C. A.; van der Houven van Oordt, W.;van der Eb, A. J.; Jochemsen, A. G.: Isolation and identificationof the human homolog of a new p53- binding protein, Mdmx. Genomics 43:34- 42, 1997.

GAM2071 371 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 B b Cloning and characterization of RAP250, a novel nuclear receptorcoactivator. J. Biol. Chem. 275: 5308- 5317, 2000.

GAM2071 371 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 B b Hybrid selection of transcribed sequences from microdissectedDNA: isolation of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer Res. 56: 3446- 3450, 1996.

GAM2071 371 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 B b bindingprotein, an LXXLL motif- containing protein, functions as a generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM2071 371 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 B b Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.- H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor, ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol. Chem. 274: 34283- 34293, 1999.

GAM2071 371 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 B b that integrate nuclear receptor signaling through CREB- bindingprotein. Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM2071 371 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 B b coding sequences of unidentified human genes. V. The codingsequences of 40 new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM2071 371 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 B b J. K.: Isolation and characterization of peroxisomeproliferator- activated receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.

Biol. Chem. 275: 13510- 13516, 2000.

GAM2071 371 NONO Brown, C. J.; Carrel, L.; Willard, H. F.: Expression of genesfrom the human 3 B b
active and inactive X chromosomes. Am. J. Hum. Genet. 60:1333- 1343, 1997.

GAM2071 371 NONO Dong, B.; Horowitz, D. S.; Kobayashi, R.; Krainer, A. R.: Purificationand 3 B b
cDNA cloning of HeLa cell p54(nrb), a nuclear protein with twoRNA
recognition motifs and extensive homology to human splicing factorPSF and
Drosophila NONA/BJ6. Nucleic Acids Res. 21: 4085- 4092, 1993.

GAM2071 371 NONO Nelson, D. L.; Ballabio, A.; Cremers, F.; Monaco, A. P.; Schlessinger,D.: 3 B b
Report of the sixth international workshop on X chromosome mapping1995.
Cytogenet. Cell Genet. 71: 308- 342, 1995.

GAM2071 371 NONO Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller,U.: AFX1 and 3 B b
p54(nrb): fine mapping, genomic structure, and exclusionas candidate genes
of X- linked dystonia parkinsonism. Hum. Genet. 100:569- 572, 1997.

GAM2071 371 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of 3 B b
NAD(P)H:quinonereductase by dietary antioxidants: possible role in
protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77:
5216- 5220,1980.

GAM2071 371 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. 3 B b
A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.;
Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of
the long arm of human chromosome 16. Genomics 10:308- 312, 1991.

GAM2071 371 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof 3 B b
the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983.

GAM2071 371 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman 3 B b
diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum.
Genet. 53: 189- 193, 1980.

GAM2071 371 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- 3 B b
inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and
localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578,
1988.

GAM2071 371 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, 3 B b
M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic
variation in the prevalence of a common NAD(P)Hquinone oxidoreductase
polymorphism and its implications for anti- cancerchemotherapy. Brit. J.
Cancer 76: 852- 854, 1997.

GAM2071 371 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further 3 B b
evidence for the regional localization of human APRT and DIA4on chromosome
16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984.

GAM2071 371 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe 3 B b
increased susceptibility of individuals with a polymorphism
inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat.
Acad. Sci. 96: 8150- 8155, 1999.

GAM2071 371 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA- 3 B b
4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980.

GAM2071 371 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. 3 B b
P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1)
gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382-
7389, 1998.

GAM2071 371 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; 3 B b
Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.;

Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.; Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological malignancy, is associated with the NQO1 609C- T mutationand rapid fractional excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997.

GAM2071 371 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 B b
New York: Oxford Univ. Press (pub.) 1988.

GAM2071 371 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to 3 B b
cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999.

GAM2071 371 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, 3 B b
P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene expression in human colon carcinoma cells: characterization ofa mutation which modulates DT- diaphorase activity and mitomycin sensitivity. CancerRes. 52: 797- 802, 1992.

GAM2071 371 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; 3 B b
Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H: quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997.

GAM2071 371 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, 3 B b
S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998.

GAM2071 371 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the 3 B b
loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes. Leukemia Res. 22: 105- 113, 1998.

GAM2071 371 ORC1L Eki, T.; Okumura, K.; Amin, A.; Ishiai, M.; Abe, M.; Nogami, M.;Taguchi, H.; 3 B b
Hurwitz, J.; Murakami, Y.; Hanaoka, F.: Mapping of thehuman homologue (ORC1L) of the yeast origin recognition complex subunit1 gene to chromosome band 1p32. Genomics 36: 559- 561, 1996.

GAM2071 371 ORC1L Gavin, K. A.; Hidaka, M.; Stillman, B.: Conserved initiator proteinsin 3 B b
eukaryotes. Science 270: 1667- 1671, 1995.

GAM2071 371 ORC1L Mendez, J.; Zou- Yang, H.; Kim, S.- Y.; Hidaka, M.; Tansey, W. P.;Stillman, 3 B b
B.: Human origin recognition complex large subunit is degradedby ubiquitin-mediated proteolysis after initiation of DNA replication. Molec.Cell 9: 481-491, 2002.

GAM2071 371 ORC1L Ohtani, K.; DeGregori, J.; Leone, G.; Herendeen, D. R.; Kelly,T. J.; Nevins, 3 B b
J. R.: Expression of the HsOrc1 gene, a human ORC1homolog, is regulated by cell proliferation via the E2F transcriptionfactor. Molec. Cell. Biol. 16: 6977- 6984, 1996.

GAM2071 371 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack 3 B b
of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991.

GAM2071 371 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; 3 B b
Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine nucleotide synthesis on human chromosome 4 are closelylinked and divergently transcribed. J. Biol. Chem. 269: 5313- 5321,1994.

GAM2071 371 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of 3 B b
three human multifunctional de novo purine biosyntheticgenes by functional complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920, 1990.

GAM2071 371 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 B b
Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding

sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM2071 371 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM2071 371 PCDHB16 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel 3 B b
cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997.

GAM2071 371 PCDHB16 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of 3 B b
the coding sequences of unidentified human genes. XVIII.The complete sequences of 100 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 273- 281, 2000.

GAM2071 371 PCDHB16 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM2071 371 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 B b
protocadherin- beta one- exon gene families show high evolutionaryconservation, despite the difference in gene number. FEBS Lett. 495:120- 125, 2001.

GAM2071 371 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 B b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM2071 371 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 3 B c
an ethanol- responsive potential modulator of guanine nucleotide-bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM2071 371 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 B c
Cloning and characterization of the rat and human phosducin- likeprotein genes: structure, expression and chromosomal localization. Biochim.Biophys. Acta 1444: 346- 354, 1999.

GAM2071 371 PDZK1 Custer, M.; Spindler, B.; Verrey, F.; Murer, H.; Biber, J.: Identificationof 3 B b
a new gene product (diphor- 1) regulated by dietary phosphate. Am.J. Physiol. 273: F801- F806, 1997.

GAM2071 371 PDZK1 Ikemoto, M.; Arai, H.; Feng, D.; Tanaka, K.; Aoki, J.; Dohmae,N.; Takio, K.; 3 B b
Adachi, H.; Tsujimoto, M.; Inoue, K.: Identificationof a PDZ- domain-containing protein that interacts with the scavengerreceptor class B type I. Proc. Nat. Acad. Sci. 97: 6538- 6543, 2000.

GAM2071 371 PDZK1 Kocher, O.; Comella, N.; Gilchrist, A.; Pal, R.; Tognazzi, K.;Brown, L. F.; 3 B b
Knoll, J. H. M.: PDZK1, a novel PDZ domain- containingprotein up- regulated in carcinomas and mapped to chromosome 1q21,interacts with cMOAT (MRP2), the multidrug resistance- associated protein. Lab.Invest. 79: 1161- 1170, 1999.

GAM2071 371 PDZK1 Kocher, O.; Comella, N.; Tognazzi, K.; Brown, L. F.: Identificationand 3 B b
partial characterization of PDZK1: a novel protein containingPDZ interaction domains. Lab. Invest. 78: 117- 125, 1998.

GAM2071 371 PDZK1 Wang, S.; Yue, H.; Derin, R. B.; Guggino, W. B.; Li, M.: Accessoryprotein 3 B b
facilitated CFTR- CFTR interaction, a molecular mechanism topotentiate the chloride channel activity. Cell 103: 169- 179, 2000.

GAM2071 371 PDZK1 White, K. E.; Biber, J.; Murer, H.; Econs, M. J.: A PDZ domain- containingprotein with homology to Diphor- 1 maps to human chromosome 1q21. Ann.Hum. Genet. 62: 287- 290, 1998. 3 B b

GAM2071 371 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to two putative mammalian circadian regulators, mper1 andmper2, to light. Cell 91: 1055- 1064, 1997. 3 B b

GAM2071 371 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B b

GAM2071 371 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531- 2534, 1999. 3 B b

GAM2071 371 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of clock operative in the mammalian forebrain. Science 293:506- 509, 2001. 3 B b

GAM2071 371 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.; Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock. Science 288: 1013- 1019, 2000. 3 B b

GAM2071 371 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; Reppert, S. M.: Two period homologs: circadian expression andphotic regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997. 3 B b

GAM2071 371 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial advanced sleep phase syndrome. Science 291: 1040- 1043,2001. 3 B b

GAM2071 371 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694, 2001. 3 B b

GAM2071 371 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the mammalian circadian clock. Nature 400: 169- 173,1999. 3 B b

GAM2071 371 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol 3- kinase catalytic subunit that associates withp85 and is expressed predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997. 3 B b

GAM2071 371 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J. H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002. 3 B b

GAM2071 371 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; Nakagawara, A.: Identification and chromosome assignment of ahuman gene encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997. 3 B b

GAM2071 371 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.: p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat. Acad. Sci. 94: 4330- 4335, 1997. 3 B b

GAM2071 371 PITPNB Tanaka, S.; Yamashita, S.; Hosaka, K.: Cloning and expressionof human cDNA 3 B c

encoding phosphatidylinositol transfer protein beta. Biochim.Biophys. Acta 1259: 199- 202, 1995.

GAM2071 371 PITPNB Wirtz, K. W. A.: Phospholipid transfer proteins. Annu. Rev. Biochem. 60:73- 99, 1991. 3 B c

GAM2071 371 PON1 Adkins, S.; Gan, K. N.; Mody, M.; La Du, B. N.: Molecular basisfor the polymorphic forms of human serum paraoxonase/arylesterase:glutamine or arginine at position 191, for the respective A and Ballozymes. Am. J. Hum. Genet. 52: 598- 608, 1993. 3 B b

GAM2071 371 PON1 Antikainen, M.; Murtomaki, S.; Syvanne, M.; Pahlman, R.; Tahvanainen,E.; Jauhiainen, M.; Frick, M. H.; Ehnholm, C.: The gln- arg191 polymorphismof the human paraoxonase gene (HUMPONA) is not associated with therisk of coronary artery disease in Finns. J. Clin. Invest. 98: 883- 885,1996. 3 B b

GAM2071 371 PON1 Augustinsson, K.- B.; Henricson, B.: A genetically controlled esterasein rat plasma. Biochim. Biophys. Acta 124: 323- 331, 1966. 3 B b

GAM2071 371 PON1 Barbieri, M.; Bonafe, M.; Marfella, R.; Ragno, E.; Giugliano, D.;Franceschi, C.; Paolisso, G.: LL- paraoxonase genotype is associatedwith a more severe degree of homeostasis model assessment IR in healthysubjects. J. Clin. Endocr. Metab. 87: 222- 225, 2002. 3 B b

GAM2071 371 PON1 Brophy, V. H.; Jampsa, R. L.; Clendenning, J. B.; McKinstry, L.A.; Jarvik, G. P.; Furlong, C. E.: Effects of 5- prime regulatory- regionpolymorphisms on paraoxonase- gene (PON1) expression. Am. J. Hum.Genet. 68: 1428- 1436, 2001. 3 B b

GAM2071 371 PON1 Cherry, N.; Mackness, M.; Durrington, P.; Povey, A.; Dippnall,M.; Smith, T.; Mackness, B.: Paraoxonase (PON1) polymorphisms infarmers attributing ill health to sheep dip. Lancet 359: 763- 764,2002. 3 B b

GAM2071 371 PON1 Clendenning, J. B.; Humbert, R.; Green, E. D.; Wood, C.; Traver,D.; Furlong, C. E.: Structural organization of the human PON1 gene. Genomics 35:586- 589, 1996. 3 B b

GAM2071 371 PON1 Coates, P. M.; Mestriner, M. A.; Hopkinson, D. A.: A preliminaryinterpretation of the esterase isozymes of human tissues. Ann. Hum.Genet. 39: 1- 20, 1975. 3 B b

GAM2071 371 PON1 Davies, H. G.; Richter, R. J.; Keifer, M.; Broomfield, C. A.; Sowalla,J.; Furlong, C. E.: The effect of the human serum paraoxonase polymorphismis reversed with diazoxon, soman and sarin. Nature Genet. 14: 334- 336,1996. 3 B b

GAM2071 371 PON1 Deakin, S.; Leviev, I.; Nicaud, V.; Meynet, M.- C. B.; Tiret, L.;James, R. W.: Paraoxonase- 1 L55M polymorphism is associated withan abnormal oral glucose tolerance test and differentiates high riskcoronary disease families. J. Clin. Endocr. Metab. 87: 1268- 1273,2002. 3 B b

GAM2071 371 PON1 Eckerson, H. W.; Romson, J.; Wyte, C.; La Du, B. N.: The humanserum paraoxonase polymorphism: identification of phenotypes by theirresponse to salts. Am. J. Hum. Genet. 35: 214- 227, 1983. 3 B b

GAM2071 371 PON1 Eckerson, H. W.; Wyte, C. M.; La Du, B. N.: The human serum paraoxonase/arylesterasepolymorphism. Am. J. Hum. Genet. 35: 1126- 1136, 1983. 3 B b

GAM2071 371 PON1 Eiberg, H.; Mohr, J.: Linkage relations of the paraoxonase polymorphismwith 43 marker systems. (Abstract) Cytogenet. Cell Genet. 25: 150,1979. 3 B b

GAM2071 371 PON1 Eiberg, H.; Mohr, J.; Schmiegelow, K.; Nielsen, L. S.; Williamson,R.: Linkage relationships of paraoxonase (PON) with other markers:indication of PON- cystic fibrosis synteny. Clin. Genet. 28: 265- 271,1985. 3 B b

GAM2071 371 PON1 Furlong, C. E.; Richter, R. J.; Chapline, C.; Crabb, J. W.: Purificationof 3 B b

rabbit and human serum paraoxonase. Biochemistry 30: 10133- 10140,1991.

GAM2071 371 PON1 Furlong, C. E.; Richter, R. J.; Seidel, S. L.; Motulsky, A. G.: Role of genetic polymorphism of human plasma paraoxonase/arylesterasein hydrolysis of the insecticide metabolites chlorpyrifos oxon andparaoxon. Am. J. Hum. Genet. 43: 230- 238, 1988. 3 B b

GAM2071 371 PON1 Garin, M.- C. B.; James, R. W.; Dussoix, P.; Blanche, H.; Passa,P.; Froguel, P.; Ruiz, J.: Paraoxonase polymorphism met- leu54 isassociated with modified serum concentrations of the enzyme: a possiblelink between the paraoxonase gene and increased risk of cardiovasculardisease in diabetes. J. Clin. Invest. 99: 62- 66, 1997. 3 B b

GAM2071 371 PON1 Geldmacher- von Mallinckrodt, M.: Polymorphism of human serumparaoxonase. Hum. Genet. 45 (suppl. 1): 65- 68, 1978. 3 B b

GAM2071 371 PON1 Geldmacher- von Mallinckrodt, M.; Lindorft, H. H.; Petenyi, M.;Flugel, M.; Fischer, T.; Hiller, T.: Genetisch determinierter Polymorphismusde menschlichen Serum- Paroxonase (E.C.3.1.1.2). Humangenetik 17:331- 335, 1973. 3 B b

GAM2071 371 PON1 Hassett, C.; Richter, R. J.; Humbert, R.; Chapline, C.; Crabb,J. W.; Omiecinski, C. J.; Furlong, C. E.: Characterization of cDNAclones encoding rabbit and human serum paraoxonase: the mature proteinretains its signal sequence. Biochemistry 30: 10141- 10149, 1991. 3 B b

GAM2071 371 PON1 Humbert, R.; Adler, D. A.; Disteche, C. M.; Hassett, C.; Omiecinski,C. J.; Furlong, C. E.: The molecular basis of the human serum paraoxonaseactivity polymorphism. Nature Genet. 3: 73- 76, 1993. 3 B b

GAM2071 371 PON1 Ito, T.; Yasue, H.; Yoshimura, M.; Nakamura, S.; Nakayama, M.;Shimasaki, Y.; Harada, E.; Mizuno, Y.; Kawano, H.; Ogawa, H.: Paraoxonasegene gln192- to-arg (Q192R) polymorphism is associated with coronaryartery spasm. Hum. Genet. 110: 89- 94, 2002. 3 B b

GAM2071 371 PON1 Kao, Y.- L.; Donaghue, K.; Chan, A.; Knight, J.; Silink, M.: Avariant of paraoxonase (PON1) gene is associated with diabetic retinopathyin IDDM. J. Clin. Endocr. Metab. 83: 2589- 2592, 1998. 3 B b

GAM2071 371 PON1 La Du, B. N.: The human serum paraoxonase/arylesterase polymorphism.(Editorial) Am. J. Hum. Genet. 43: 227- 229, 1988. 3 B b

GAM2071 371 PON1 Li, W.- F.; Furlong, C. E.; Costa, L. G.: Paraoxonase protectsagainst chlorpyrifos toxicity in mice. Toxic. Lett. 76: 219- 226,1995. 3 B b

GAM2071 371 PON1 Li, W.- F.; Matthews, C.; Disteche, C. M.; Costa, L. G.; Furlong,C. E.: Paraoxonase (Pon1) gene in mice: sequencing, chromosomal localizationand developmental expression. Pharmacogenetics 7: 137- 144, 1997. 3 B b

GAM2071 371 PON1 Mackness, B.; Mackness, M. I.; Arrol, S.; Turkie, W.; Durrington,P. N.: Effect of the human serum paraoxonase 55 and 192 genetic polymorphismson the protection by high density lipoprotein against low densitylipoprotein oxidative modification. FEBS Lett. 423: 57- 60, 1998. 3 B b

GAM2071 371 PON1 Mochizuki, H.; Scherer, S. W.; Xi, T.; Nickle, D. C.; Majer, M.;Huizenga, J. J.; Tsui, L.- C.; Prochazka, M.: Human PON2 gene at 7q21.3:cloning, multiple mRNA forms, and missense polymorphisms in the codingsequence. Gene 213: 149-157, 1998. 3 B b

GAM2071 371 PON1 Mueller, R. F.; Hornung, S.; Furlong, C. E.; Anderson, J.; Giblett,E. R.; Motulsky, A. G.: Plasma paraoxonase polymorphism: a new enzymeassay, population, family, biochemical, and linkage studies. Am.J. Hum. Genet. 35: 393- 408, 1983. 3 B b

GAM2071 371 PON1 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J. Clin. Invest. 99: 2005- 2019, 1997. 3 B b

GAM2071 371 PON1 Neel, J. V.; Tanis, R. J.; Migliazza, E. C.; Spielman, R. S.;Salzano, F. M.; Oliver, W. J.; Morrow, M.; Bachofer, S.: Geneticstudies of the Macushi and Wapishana Indians. I. Rare genetic variantsand a 'private polymorphism' of esterase A. Hum. Genet. 36: 81- 108,1977. 3 B b

GAM2071 371 PON1 Nielsen, A.; Eiberg, H.; Mohr, J.: Number of loci responsiblefor the inheritance of high and low activity of paraoxonase. Clin.Genet. 29: 216- 221, 1986. 3 B b

GAM2071 371 PON1 Odawara, M.; Tachi, Y.; Yamashita, K.: Paraoxonase polymorphismGln192- Arg is associated with coronary heart disease in Japanese noninsulin- dependentdiabetes mellitus. J. Clin. Endocr. Metab. 82: 2257- 2260, 1997. 3 B b

GAM2071 371 PON1 Ortigoza- Ferado, J.; Richter, R. J.; Hornung, S. K.; Motulsky,A. G.; Furlong, C. E.: Paraoxon hydrolysis in human serum mediatedby a genetically variable arylesterase and albumin. Am. J. Hum. Genet. 36:295- 305, 1984. 3 B b

GAM2071 371 PON1 Paolisso, G.; Manzella, D.; Tagliamonte, M. R.; Barbieri, M.;Marfella, R.; Zito, G.; Bonafe, M.; Giugliano, D.; Franceschi, C.;Varricchio, M.: The BB- paraoxonase genotype is associated with impairedbrachial reactivity after acute hypertriglyceridemia in healthy subjects. J.Clin. Endocr. Metab. 86: 1078- 1082, 2001. 3 B b

GAM2071 371 PON1 Playfer, J. R.; Eze, L. C.; Bullen, M. F.; Evans, D. A. P.: Geneticpolymorphism and interethnic variability of plasma paroxonase activity. J.Med. Genet. 13: 337- 342, 1976. 3 B b

GAM2071 371 PON1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 B b

GAM2071 371 PON1 Schmiegelow, K.; Eiberg, H.; Tsui, L.- C.; Buchwald, M.; Phelan,P. D.; Williamson, R.; Warwick, W.; Niebuhr, E.; Mohr, J.; Schwartz,M.; Koch, C.: Linkage between the loci for cystic fibrosis and paraoxonase. Clin.Genet. 29: 374- 377, 1986. 3 B b

GAM2071 371 PON1 Serrato, M.; Marian, A. J.: A variant of human paraoxonase/arylesterase(HUMPONA) gene is a risk factor for coronary artery disease. J. Clin.Invest. 96: 3005- 3008, 1995. 3 B b

GAM2071 371 PON1 Shih, D. M.; Gu, L.; Xia, Y.- R.; Navab, M.; Li, W.- F.; Hama, S.;Castellani, L. W.; Furlong, C. E.; Costa, L. G.; Fogelman, A. M.;Lusis, A. J.: Mice lacking serum paraoxonase are susceptible to organophosphatetoxicity and atherosclerosis. Nature 394: 284- 287, 1998. 3 B b

GAM2071 371 PON1 Simpson, N. E.: Serum arylesterase levels of activity in twinsand their parents. Am. J. Hum. Genet. 23: 375- 382, 1971. 3 B b

GAM2071 371 PON1 Sorenson, R. C.; Primo- Parmo, S. L.; Camper, S.; La Du, B. N.: The genetic mapping and gene structure of mouse paraoxonase/arylesterase. Genomics 30:431- 438, 1995. 3 B b

GAM2071 371 PON1 Tashian, R. E.: Genetic variation and evolution of the carboxylicesterases and carbonic anhydrases of primate erythrocytes. Am. J.Hum. Genet. 17: 257- 272, 1965. 3 B b

GAM2071 371 PON1 Tashian, R. E.; Shaw, M. W.: Inheritance of an erythrocyte acetylesterasevariant of man. Am. J. Hum. Genet. 14: 295- 300, 1962. 3 B b

GAM2071 371 PON1 Tsui, L.- C.; Buchwald, M.; Barker, D.; Braman, J. C.; Knowlton,R.; Schumm, 3 B b

J. W.; Eiberg, H.; Mohr, J.; Kennedy, D.; Plavsic, N.;Zsiga, M.; Markiewicz, D.; Akots, G.; Brown, V.; Helms, C.; Gravius,T.; Parker, C.; Rediker, K.; Donis- Keller, H.: Cystic fibrosis locusdefined by a genetically linked polymorphic DNA marker. Science 230:1054- 1057, 1985.

GAM2071 371 PON1 Watson, C. E.; Draganov, D. I.; Billecke, S. S.; Bisgaier, C.L.; La Du, B. 3 B b
N.: Rabbits possess a serum paraoxonase polymorphismsimilar to the human Q192R. Pharmacogenetics 11: 123- 134, 2001.

GAM2071 371 PON1 Yamasaki, Y.; Sakamoto, K.; Watada, H.; Kajimoto, Y.; Hori, M.: The arg- 192 3 B b
isoform of paraoxonase with low sarin- hydrolyzing activityis dominant in the Japanese. Hum. Genet. 101: 67- 68, 1997.

GAM2071 371 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 B b
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component of the steroid receptor complex: cloning of thecDNA and further characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM2071 371 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 B b
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem. 267: 5503- 5507, 1992.

GAM2071 371 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 B b
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151 only, 1997.

GAM2071 371 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 B b
J.- E.: The structure and complete nucleotide sequenceof the human cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM2071 371 PPP2R1B Arai, Y.; Hosoda, F.; Nakayama, K.; Ohki, M.: A yeast artificialchromosome 3 B c
contig and NotI restriction map that spans the tumor suppressorgene(s) locus, 11q.22.2- q23.3. Genomics 35: 196- 206, 1996.

GAM2071 371 PPP2R1B Hemmer, S.; Wasenius, V.- M.; Haglund, C.; Zhu, Y.; Knuutila, S.;Franssila, 3 B c
K.; Joensuu, H.: Alterations in the suppressor gene PPP2R1Bin parathyroid hyperplasias and adenomas. Cancer Genet. Cytogenet. 134:13- 17, 2002.

GAM2071 371 PPP2R1B Walter, G.; Mumby, M.: Protein serine/threonine phosphatases andcell 3 B c
transformation. Biochim. Biophys. Acta 1155: 207- 226, 1993.

GAM2071 371 PPP2R1B Wang, S. S.; Esplin, E. D.; Li, J. L.; Huang, L.; Gazdar, A.; Minna,J.; 3 B c
Evans, G. A.: Alterations of the PPP2R1B gene in human lung andcolon cancer. Science 282: 284- 287, 1998.

GAM2071 371 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 3 B c
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM2071 371 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 3 B c
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY) to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet. 76: 49- 52, 1997.

GAM2071 371 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 3 B c
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM2071 371 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 B b
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.:
Genomicorganization, comparative analysis, and genetic polymorphisms of thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733,

2001.

GAM2071 371 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 B b
Chen, S. G.: Expression and structural characterizationof the recombinant
human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM2071 371 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 B b
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.;
Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-
deficient mice is associated with upregulation of thenovel PrP- like protein
doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM2071 371 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 B b
T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin
the prion- like protein gene (Prnd) and their implications inhuman prion
diseases, Alzheimer's disease and other neurological disorders. Hum.Genet.
109: 319- 325, 2001.

GAM2071 371 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 B b
P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-
glycosylated, glycosylphosphatidylinositol- anchored protein:expression in
testis and ectopic production in the brains of Prnp(0/0)mice predisposed to
Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM2071 371 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 B b
915, 1999.

GAM2071 371 PSMD9 Thomas, M. K.; Yao, K.- M.; Tenser, M. S.; Wong, G. G.; Habener,J. F.: 3 B b
Bridge- 1, a novel PDZ- domain coactivator of E2A- mediated regulationof
insulin gene transcription. Molec. Cell. Biol. 19: 8492- 8504,1999.

GAM2071 371 PSMD9 Watanabe, T. K.; Saito, A.; Suzuki, M.; Fujiwara, T.; Takahashi,E.; 3 B b
Slaughter, C. A.; DeMartino, G. N.; Hendil, K. B.; Chung, C. H.;Tanahashi,
N.; Tanaka, K.: cDNA cloning and characterization of ahuman proteasomal
modulator subunit, p27 (PSMD9). Genomics 50: 241- 250,1998.

GAM2071 371 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 3 B c
Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly,
F.: Characterization of new mutations in the codingsequence and 5- prime-
untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum.
Genet. 108: 148- 155, 2001.

GAM2071 371 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 3 B c
Molecular cloning and expression of human prostacyclin synthase.
Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM2071 371 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 3 B c
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.;
Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences,
gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42,
1996.

GAM2071 371 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 3 B c
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM2071 371 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 3 B c
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase
(PTGIS): genomic organization, chromosomal localization,and promoter
activity. Genomics 36: 296- 304, 1996.

GAM2071 371 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; 3 B c
Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-
family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted

in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999.

GAM2071 371 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation 3 B c
of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000.

GAM2071 371 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; 3 B b
Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993.

GAM2071 371 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 3 B b
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM2071 371 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. 3 B b
Med. 339: 1775- 1777, 1998.

GAM2071 371 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand 3 B b
molecular genetics. Blood Rev. 8: 199- 212, 1994.

GAM2071 371 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; 3 B b
Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood group polymorphism as determined by Southern analysis. Blood 78:2747- 2752, 1991.

GAM2071 371 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and 3 B b
its association with universal edema of the fetus, icterusgravis neonatorum and anemia of the newborn. J. Pediat. 1: 269- 309,1932.

GAM2071 371 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies 3 B b
in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989.

GAM2071 371 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with 3 B b
sickle cell disease. Transfusion 37: 357- 361, 1997.

GAM2071 371 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 B b

GAM2071 371 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the 3 B b
human RH locus: a family study of the red- cell Evans phenotypereveals a transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59: 825- 833, 1996.

GAM2071 371 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular 3 B b
definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J. Hum. Genet. 58: 133- 142, 1996.

GAM2071 371 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of 3 B b
Rh blood group genes: association between restrictionfragment length polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994.

GAM2071 371 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine 3 B b
years and some observations on the biochemistry and geneticsof the system. Transfusion Med. Rev. 3: 1- 12, 1989.

GAM2071 371 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh 3 B b
genes revealed by analysis of unrelated donors with therare D- - phenotype. Am. J. Hum. Genet. 59: 1066- 1073, 1996.

GAM2071 371 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, 3 B b
J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by alternative splicing. Blood 80: 1074- 1078, 1992.

GAM2071 371 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; 3 B b
Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929, 1992.

GAM2071 371 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; 3 B b
Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE
genotyping for correct blood group determination inchronically transfused
patients. Transfusion 39: 852- 855, 1999.

GAM2071 371 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its 3 B b
possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A.
116:825- 827, 1941.

GAM2071 371 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; 3 B b
Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.:
Prenatal diagnosis of fetal RhD status by molecular analysisof maternal
plasma. New Eng. J. Med. 339: 1734- 1738, 1998.

GAM2071 371 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; 3 B b
Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases
of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome
1. Am. J. Med. Genet. 104: 250- 256, 2001.

GAM2071 371 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, 3 B b
E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J.
Clin. Invest. 100: 373- 379, 1997.

GAM2071 371 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 B b
153:771- 772, 1944.

GAM2071 371 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 B b
ed.): 1975.

GAM2071 371 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 3 B b
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII)
category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM2071 371 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 3 B b
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral
transduction of K562 cells establishes the molecular basisof Rh blood group
antigens. Blood 87: 2968- 2973, 1996.

GAM2071 371 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 3 B b
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang.
58: 50- 55, 1990.

GAM2071 371 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 3 B b
Blood 95: 3662- 3668, 2000.

GAM2071 371 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 3 B b
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393,
1999.

GAM2071 371 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 3 B b
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311,
2002.

GAM2071 371 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 B b

GAM2071 371 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two 3 B b
scleroderma autoimmune antigens that copurify with human ribonucleaseP.
Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997.

GAM2071 371 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: 3 B b
Autoantigenic properties of some protein subunits of catalyticallyactive
complexes of human ribonuclease P. RNA 4: 407- 417, 1998.

GAM2071 371 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, 3 B c
P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.:
Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin.

Endocr. Metab. 86: 3233- 3236, 2001.

GAM2071 371 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- 3 B c
linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a
common cause of early primary osteoarthritis in men. (Letter) Clin.Genet.
62: 94- 95, 2002.

GAM2071 371 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. 3 B c
C.: Gene structure and expression study of the SEDL genefor
spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000.

GAM2071 371 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; 3 B c
Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the
gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda.
NatureGenet. 22: 400- 404, 1999.

GAM2071 371 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; 3 B c
Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.;
Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.;
Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia
tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM2071 371 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 3 B c
Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset
of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J.
Med. Genet. 38: 409- 411, 2001.

GAM2071 371 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 3 B c
A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five-
base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia
tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85:
3343- 3347, 2000.

GAM2071 371 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 3 B c
for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a
non- canonical splice site. Gene 273: 285- 293, 2001.

GAM2071 371 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, 3 B c
H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked
spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002.

GAM2071 371 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; 3 B c
Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A
recurrent RNA- splicing mutation in the SEDL gene causes X-
linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398-
1407,2001.

GAM2071 371 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked 3 B c
recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic
evolution in a 6- generation kindred and review ofthe literature. Medicine
78: 9- 25, 1999.

GAM2071 371 SEL1L Biunno, I.; Appierto, V.; Cattaneo, M.; Leone, B. E.; Balzano,G.; Socci, C.; 3 B c
Saccone, S.; Letizia, A.; Valle, G. D.; Sgaramella,V.: Isolation of a
pancreas- specific gene located on human chromosome14q31: expression
analysis in human pancreatic ductal carcinomas. Genomics 46:284- 286, 1997.

GAM2071 371 SEL1L Donoviel, D. B.; Bernstein, A.: SEL- 1L maps to human chromosome14, near the 3 B c
insulin- dependent diabetes mellitus locus 11. Genomics 56:232- 233, 1999.

GAM2071 371 SEL1L Grant, B.; Greenwald, I.: Structure, function and expression ofSEL- 1, a 3 B c
negative regulator of LIN- 12 and GLP- 1 in C. elegans. Development 124:637-
644, 1997.

GAM2071 371 SEL1L Grant, B.; Greenwald, I.: The Caenorhabditis. elegans sel- 1 gene,a negative regulator of lin- 12 and glp- 1, encodes a predicted extracellularprotein. Genetics 143: 237- 247, 1996. 3 B c

GAM2071 371 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001. 3 B b

GAM2071 371 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996. 3 B b

GAM2071 371 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001. 3 B b

GAM2071 371 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 B b

GAM2071 371 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996. 3 B b

GAM2071 371 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 3 B b

GAM2071 371 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 3 B b

GAM2071 371 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 3 B b

GAM2071 371 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.; Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998. 3 B c

GAM2071 371 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea transporter in the human kidney. FEBS Lett. 386: 156- 160,1996. 3 B c

GAM2071 371 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.; Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2 is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157- 2164, 2001. 3 B c

GAM2071 371 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses and phylogenetic characterization of the ZIP family of metalion transport proteins. J. Membr. Biol. 166: 1- 7, 1998. 3 B b

GAM2071 371 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof 3 B b

human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping within the epidermal differentiation complex. Genomics 62:272- 280, 1999.

GAM2071 371 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC 3 B b
fragmentation map of 1q21. Genomics 49: 200- 208, 1998.

GAM2071 371 SLC4A4 Abuladze, N.; Lee, I.; Newman, D.; Hwang, J.; Boorer, K.; Pushkin,A.; Kurtz, 3 B c
I.: Molecular cloning, chromosomal localization, tissuedistribution, and functional expression of the human pancreatic sodiumbicarbonate cotransporter. J. Biol. Chem. 273: 17689- 17695, 1998.

GAM2071 371 SLC4A4 Burnham, C. E.; Amlal, H.; Wang, Z.; Shull, G. E.; Soleimani, M.: Cloning 3 B c
and functional expression of a human kidney Na+:HCO3- cotransporter. J.Biol. Chem. 272: 19111- 19114, 1997.

GAM2071 371 SLC4A4 Choi, I.; Romero, M. F.; Khandoudi, N.; Bril, A.; Boron, W. F.: Cloning and 3 B c
characterization of a human electrogenic Na(+)- HCO(3-)cotransporter isoform (hhNBC). Am. J. Physiol. 276: C576- C584, 1999.

GAM2071 371 SLC4A4 Igarashi, T.; Inatomi, J.; Sekine, T.; Cha, S. H.; Kanai, Y.; Kunimi,M.; 3 B c
Tsukamoto, K.; Satoh, H.; Shimadzu, M.; Tozawa, F.; Mori, T.;Shiobara, M.; Seki, G.; Endou, H.: Mutations in SLC4A4 cause permanentisolated proximal renal tubular acidosis with ocular abnormalities.(Letter) Nature Genet. 23: 264- 265, 1999.

GAM2071 371 SLC4A4 Romero, M. F.; Boron, W. F.: Electrogenic Na(+)/HCO(3-) 3 B c
cotransporters:cloning and physiology. Annu. Rev. Physiol. 61: 699- 723, 1999.

GAM2071 371 SLC4A4 Soleimani, M.; Burnham, C. E.: Physiologic and molecular aspectsof the 3 B c
Na(+):HCO(3-) cotransporter in health and disease processes. KidneyInt. 57: 371- 384, 2000.

GAM2071 371 SLC4A4 Usui, T.; et al.; et al. :Pflugers Arch. 438: 458- 462, 1999. 3 B c

GAM2071 371 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland 3 B b
biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855- 862, 2000.

GAM2071 371 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein 3 B b
that promotes cytochrome c- dependent caspase activation byeliminating IAP inhibition. Cell 102: 33- 42, 2000.

GAM2071 371 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; 3 B b
Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000.

GAM2071 371 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; 3 B b
Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509- 3517, 2002.

GAM2071 371 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 B b

GAM2071 371 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; 3 B b
Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.: A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates caspase activity and apoptosis. Nature 410:112- 116, 2001.

GAM2071 371 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, 3 B b
G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO, a mammalian protein that promotes apoptosis by bindingto and antagonizing IAP proteins. Cell 102: 43- 53, 2000.

GAM2071 371 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: 3 B b
Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012,

2000.

GAM2071 371 SOX8 Pfeifer, D.; Poulat, F.; Holinski- Feder, E.; Kooy, F.; Scherer,G.: The SOX8 3 B c
gene is located within 700 kb of the tip of chromosome16p and is deleted in
a patient with ATR- 16 syndrome. Genomics 63:108- 116, 2000.

GAM2071 371 SOX8 Sock, E.; Schmidt, K.; Hermanns- Borgmeyer, I.; Bosl, M. R.; Wegner,M.: 3 B c
Idiopathic weight reduction in mice deficient in the high- mobility-
grouptranscription factor Sox8. Molec. Cell. Biol. 21: 6951- 6959, 2001.

GAM2071 371 SPN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, 3 B c
J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM-
dependent movement of CD43 defines a novelprotein complex distal to the
immunological synapse. Immunity 15:739- 750, 2001.

GAM2071 371 SPN Baecher, C. M.; Dorfman, K. S.; Mattei, M.- G.; Frelinger, J. G.: cDNA 3 B c
cloning and localization of the mouse leukosialin gene (Ly48)to chromosome
7. Immunogenetics 31: 307- 314, 1990.

GAM2071 371 SPN Bazil, V.; Strominger, J. L.: CD43, the major sialoglycoproteinof human 3 B c
leukocytes, is proteolytically cleaved from the surface ofstimulated
lymphocytes and granulocytes. Proc. Nat. Acad. Sci. 90:3792- 3796, 1993.

GAM2071 371 SPN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe 3 B c
immunological synapse is mediated by phosphorylation- regulatedrelocation of
the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001.

GAM2071 371 SPN Pallant, A.; Eskenazi, A.; Mattei, M.- G.; Fournier, R. E. K.; Carlsson,S. 3 B c
R.; Fukuda, M.; Frelinger, J. G.: Characterization of cDNAs encodinghuman
leukosialin and localization of the leukosialin gene to chromosome16. Proc.
Nat. Acad. Sci. 86: 1328- 1332, 1989.

GAM2071 371 SPN Park, J. K.; Rosenstein, Y. J.; Remold- O'Donnell, E.; Bierer, B.E.; Rosen, 3 B c
F. S.; Burakoff, S. J.: Enhancement of T- cell activationby the CD43
molecule whose expression is defective in Wiskott- Aldrichsyndrome. Nature
350: 706- 709, 1991.

GAM2071 371 SPN Rosenstein, Y.; Park, J. K.; Hahn, W. C.; Rosen, F. S.; Bierer,B. E.; 3 B c
Burakoff, S. J.: CD43, a molecule defective in Wiskott- Aldrichsyndrome,
binds ICAM- 1. Nature 354: 233- 235, 1991.

GAM2071 371 SPN Schmid, K.; Hediger, M. A.; Brossmer, R.; Collins, J. H.; Haupt,H.; Marti, 3 B c
T.; Offner, G. D.; Schaller, J.; Takagaki, K.; Walsh, M.T.; Schwick, H. G.;
Rosen, F. S.; Remold- O'Donnell, E.: Amino acidsequence of human plasma
galactoglycoprotein: identity with the extracellularregion of CD43
(sialophorin). Proc. Nat. Acad. Sci. 89: 663- 667,1992.

GAM2071 371 SPN Shelley, C. S.; Carroll, M. C.; Davis, A. E., III; Bruns, G. A.P.; 3 B c
Whitehead, A. S.; Finberg, R.; Remold- O'Donnell, E.; Rosen, F.S.: Human
sialophorin: cDNA cloning and gene location. (Abstract) FASEBJ. 2: A1659
only, 1988.

GAM2071 371 SPN Shelley, C. S.; Remold- O'Donnell, E.; Davis, A. E., III; Bruns,G. A. P.; 3 B c
Rosen, F. S.; Carroll, M. C.; Whitehead, A. S.: Molecularcharacterization of
sialophorin (CD43), the lymphocyte surface sialoglycoproteindefective in
Wiskott- Aldrich syndrome. Proc. Nat. Acad. Sci. 86:2819- 2823, 1989.

GAM2071 371 SPN Shelley, C. S.; Remold- O'Donnell, E.; Rosen, F. S.; Whitehead,A. S.: 3 B c
Structure of the human sialophorin (CD43) gene: identificationof features
atypical of genes encoding integral membrane proteins. Biochem.J. 270: 569-
576, 1990.

GAM2071 371 SPN van den Berg, T. K.; Nath, D.; Ziltener, H. J.; Vestweber, D.;Fukuda, M.; 3 B c
van Die, I.; Crocker, P. R.: Cutting edge: CD43 functionsas a T cell

counterreceptor for the macrophage adhesion receptor sialoadhesin(Siglec-1). J. Immun. 166: 3637- 3640, 2001.

GAM2071 371 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 3 B b
L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM2071 371 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 3 B b
J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM2071 371 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 3 B b
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand characterization of the mouse homolog of SYT, a gene implicatedin the development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM2071 371 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 3 B b
G.: Mapping and characterization of the mouse and humanSS18 genes, two human SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-319, 2001.

GAM2071 371 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 B b
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene family with several members transcribed in normaltestis and human cancer. Int. J. Cancer 72: 965- 971, 1997.

GAM2071 371 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 B b
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM2071 371 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 B b
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J. Nat. Cancer Inst. 91: 974- 975, 1999.

GAM2071 371 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 B b
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX synovial sarcoma translocation proteins and co- localizationwith the SNF protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM2071 371 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 B b
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM2071 371 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- 3 B b
strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence insitu hybridization. Genomics 36: 527- 529, 1996.

GAM2071 371 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence 3 B b
homologue of staufen is an RNA- binding protein thatis associated with polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell. Biol. 19: 2212- 2219, 1999.

GAM2071 371 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: 3 B b
Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19: 2220- 2230, 1999.

GAM2071 371 TAF11 Birck, C.; Poch, O.; Romier, C.; Ruff, M.; Mengus, G.; Lavigne,A.- C.; 3 B c
Davidson, I.; Moras, D.: Human TAFII28 and TAFII18 interactthrough a histone fold encoded by atypical evolutionary conservedmotifs also found in the SPT3 family. Cell 94: 239- 249, 1998.

GAM2071 371 TAF11 Mengus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.;Davidson, I.: Cloning and characterization of hTAFII18, hTAFII20and hTAFII28: three subunits of the human transcription factor TFIID. EMBOJ. 14: 1520- 1531, 1995. 3 B c

GAM2071 371 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459- 467, 1998. 3 B b

GAM2071 371 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 B b

GAM2071 371 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 B b

GAM2071 371 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 B b

GAM2071 371 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 B b

GAM2071 371 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 B b

GAM2071 371 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496- 1498, 2002. 3 B b

GAM2071 371 TAT Barton, D. E.; Yang- Feng, T. L.; Francke, U.: The human tyrosineaminotransferase gene mapped to the long arm of chromosome 16 (region16q22- q24) by somatic cell hybrid analysis and in situ hybridization. Hum.Genet. 72: 221- 224, 1986. 3 B b

GAM2071 371 TAT Beinfang, D. C.; Kuwabara, T.; Pueschel, S. M.: The Richner- Hanhartsyndrome: report of a case with associated tyrosinemia. Arch. Ophthal. 94:1133- 1137, 1976. 3 B b

GAM2071 371 TAT Bohnert, A.; Anton- Lamprecht, I.: Richner- Hanhart's syndrome:ultrastructural abnormalities of epidermal keratinization indicatinga causal relationship to high intracellular tyrosine levels. J. Invest.Derm. 79: 68- 74, 1982. 3 B b

GAM2071 371 TAT Buist, N.: Phenylketonuria and related problems.In: Nyhan, W.L.: Amino Acid Metabolism and Genetic Variation. New York: McGraw- Hill(pub.) 1967. Pp. 117 only. 3 B b

GAM2071 371 TAT Chitayat, D.; Balbul, A.; Hani, V.; Mamer, O. A.; Clow, C.; Scriver,C. R.: Hereditary tyrosinaemia type II in a consanguineous AshkenaziJewish family: intrafamilial variation in phenotype; absence of parentalphenotype effects on the fetus. J. Inherit. Metab. Dis. 15: 198- 203,1992. 3 B b

GAM2071 371 TAT Crovato, F.; Desirello, G.; Gatti, R.; Babbini, N.; Rebora, A.: Richner- Hanhart syndrome spares a plantar autograft. Arch. Derm. 121:539- 540, 1985. 3 B b

GAM2071 371 TAT Fellman, J. H.; Vanbellinghen, P. J.; Jones, R. T.; Koler, R. D.: Soluble and mitochondrial forms of tyrosine aminotransferase: relationshipto human 3 B b

tyrosinemia. Biochemistry 8: 615- 622, 1969.

GAM2071 371 TAT Garibaldi, L. R.; Siliato, F.; De Martini, I.; Scarsi, M. R.; Romano,C.: 3 B b
Oculocutaneous tyrosinosis: report of two cases in the same family.
Helv.Paediat. Acta 32: 173- 180, 1977.

GAM2071 371 TAT Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald,P. S.; 3 B b
Baden, H. P.: Tyrosinemia with plantar and palmar keratosisand keratitis. J.
Pediat. 83: 798- 805, 1973.

GAM2071 371 TAT Hanhart, E.: Neue Sonderformen von Keratosis palmo- plantaris,u.a. eine 3 B b
regelmaessig- dominante mit systematisierten Lipomen, ferner2 einfach-
rezessive mit Schwachsinn und z.T. mit Hornhautveraenderungendes Auges
(Ektodermatosyndrom). Dermatologica 94: 286- 308, 1947.

GAM2071 371 TAT Hunziker, N.: Richner- Hanhart syndrome and tyrosinemia type II. 3 B b
Dermatologica 160:180- 189, 1980.

GAM2071 371 TAT Kennaway, N. G.; Buist, N. R. M.: Metabolic studies in a patientwith hepatic 3 B b
cytosol tyrosine aminotransferase deficiency. Pediat.Res. 5: 287- 297, 1971.

GAM2071 371 TAT Muller, G.; Scherer, G.; Zentgraf, H.; Ruppert, S.; Herrmann,B.; Lehrach, 3 B b
H.; Schutz, G.: Isolation, characterization and chromosomalmapping of the
mouse tyrosine aminotransferase gene. J. Molec. Biol. 184:367- 373, 1985.

GAM2071 371 TAT Natt, E.; Kao, F.- T.; Rettenmeier, R.; Scherer, G.: Assignmentof the human 3 B b
tyrosine aminotransferase gene to chromosome 16. Hum.Genet. 72: 225- 228,
1986.

GAM2071 371 TAT Natt, E.; Kida, K.; Odievre, M.; Di Rocco, M.; Scherer, G.: Pointmutations 3 B b
in the tyrosine aminotransferase gene in tyrosinemia typeII. Proc. Nat.
Acad. Sci. 89: 9297- 9301, 1992.

GAM2071 371 TAT Natt, E.; Westphal, E.- M.; Toth- Fejel, S. E.; Magenis, R. E.;Buist, N. R. 3 B b
M.; Rettenmeier, R.; Scherer, G.: Inherited and de novodeletion of the
tyrosine aminotransferase gene locus at 16q22.1- q22.3in a patient with
tyrosinemia type II. Hum. Genet. 77: 352- 358,1987.

GAM2071 371 TAT Pelet, B.; Antener, I.; Faggioni, R.; Spahr, A.; Gautier, E.:Tyrosinemia 3 B b
without liver or renal damage with plantar and palmarkeratosis and keratitis
(hypertyrosinemia type II). Helv. Paediat.Acta 34: 177- 183, 1979.

GAM2071 371 TAT Rehak, A.; Selim, M. M.; Yadav, G.: Richner- Hanhart syndrome(tyrosinaemia- 3 B b
II) (report of four cases without ocular involvement). Brit.J. Derm. 104:
469- 475, 1981.

GAM2071 371 TAT Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.: Isolationand 3 B b
characterization of the human tyrosine aminotransferase gene. NucleicAcids
Res. 18: 3853- 3861, 1990.

GAM2071 371 TAT Richner, H.: Hornhautaffektion bei Keratoma palmare et plantarehereditarium. 3 B b
Klin. Mbl. Augenheilk. 100: 580- 588, 1938.

GAM2071 371 TAT Schmid, W.; Muller, G.; Schutz, G.; Gluecksohn- Waelsch, S.: Deletionsnear 3 B b
the albino locus on chromosome 7 of the mouse affect the levelof tyrosine
aminotransferase mRNA. Proc. Nat. Acad. Sci. 82: 2866- 2869,1985.

GAM2071 371 TAT Tallab, T.M.: Richner- Hanhart syndrome: importance of early diagnosisand 3 B b
early intervention. J. Am. Acad. Dermatol. 35: 857- 859, 1996.

GAM2071 371 TAT Ventura, G.; Biasini, G.; Petrozzi, M.: Cheratomia palmoplantaredissipatum 3 B b
associato a lesioni corneali in due fratelli. Boll. Oculist. 44:497- 510,
1965.

GAM2071 371 TAT Waardenburg, P. J.; Franceschetti, A.; Klein, D.: Genetics andOphthalmology. 3 B b
Springfield, Ill.: Charles C Thomas (pub.) 1:1961. Pp. 515- 517.

GAM2071 371 TAT Westphal, E.- M.; Natt, E.; Grimm, T.; Odievre, M.; Scherer, G.: The human 3 B b

tyrosine aminotransferase gene: characterization of restrictionfragment length polymorphisms and haplotype analysis in a family withtyrosinemia type II. Hum. Genet. 79: 260- 264, 1988.

GAM2071 371 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8: 165- 167, 1990. 3 B b

GAM2071 371 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 homeoprotein family are expressed in human liver. NucleicAcids Res. 19: 3553- 3559, 1991. 3 B b

GAM2071 371 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.; Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene are associated with familial hypoplastic glomerulocystickidney disease. Am. J. Hum. Genet. 68: 219- 224, 2001. 3 B b

GAM2071 371 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.; Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated with a frameshift mutation in the transcription factorhepatocyte nuclear factor- 1- beta. Kidney Int. 57: 898- 907, 2000. 3 B b

GAM2071 371 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara, T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997. 3 B b

GAM2071 371 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic glomerulocystic kidney disease: a definite entity withdominant inheritance. Am. J. Med. Genet. 34: 569- 573, 1989. 3 B b

GAM2071 371 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand genital malformation associated with a partial deletion of thepseudo- POU domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001- 2008, 1999. 3 B b

GAM2071 371 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, S.: A low renal threshold for glucose in diabetic patientswith a mutation in the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med. 15: 816- 820, 1998. 3 B b

GAM2071 371 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in the hepatocyte nuclear factor- 1- beta gene associated with diabetesand renal dysfunction. Diabetes 47: 1354- 1355, 1998. 3 B b

GAM2071 371 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18: 263- 268, 1982. 3 B b

GAM2071 371 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott-Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G. U.: The mutated human gene encoding hepatocyte nuclear factor1- beta inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad. Sci. 97: 4695- 4700, 2000. 3 B b

GAM2071 371 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.; 3 B c

Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1 are associated with human left- right lateralitydefects. Nature Genet. 26: 365- 369, 2000.

GAM2071 371 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: 3 B c Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989.

GAM2071 371 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, 3 B c A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002.

GAM2071 371 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; 3 B c Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991.

GAM2071 371 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. 3 B c A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997.

GAM2071 371 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; 3 B c Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996.

GAM2071 371 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, 3 B c G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995.

GAM2071 371 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in 3 B c vertebratedevelopment. Trends Genet. 16: 303- 309, 2000.

GAM2071 371 TERF1 Broccoli, D.; Chong, L.; Oelmann, S.; Fernald, A. A.; Marziliano,N.; van 3 B b Steensel, B.; Kipling, D.; Le Beau, M. M.; de Lange, T.:Comparison of the human and mouse genes encoding the telomeric protein,TRF1: chromosomal localization, expression and conserved protein domains. Hum.Molec. Genet. 6: 69- 76, 1997.

GAM2071 371 TERF1 Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.;Hanish, 3 B b J.; Tempst, P.; de Lange, T.: A human telomeric protein. Science 270:1663- 1667, 1995.

GAM2071 371 TERF1 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 B b the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001.

GAM2071 371 TERF1 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 B b Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999.

GAM2071 371 TERF1 Kim, S.; Kaminker, P.; Campisi, J.: TIN2, a new regulator of telomerelength 3 B b in human cells. Nature Genet. 23: 405- 412, 1999.

GAM2071 371 TERF1 Marcand, S.; Gilson, E.; Shore, D.: A protein- counting mechanismfor 3 B b telomere length regulation in yeast. Science 275: 986- 990, 1997.

GAM2071 371 TERF1 Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M.: TRF1 is a 3 B b critical trans- acting factor required for de novo telomereformation in human cells. Hum. Molec. Genet. 9: 2639- 2650, 2000.

GAM2071 371 TERF1 Young, A. C.; Chavez, M.; Giambernardi, T. A.; Mattern, V.; McGill,J. R.; 3 B b Harris, J. M.; Sarosdy, M. F.; Patel, P.; Sakaguchi, A. Y.: Organization and expression of human telomere repeat binding factorgenes. Somat. Cell Molec. Genet. 23: 275- 286, 1997.

GAM2071 371 TERF1 Zakian, V. A.: Telomeres: beginning to understand the end. Science 270:1601- 1607, 1995. 3 B b

GAM2071 371 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: Strand- specific postreplicative processing of mammalian telomeres. Science 293:2462- 2465, 2001. 3 B b

GAM2071 371 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet. 17: 236- 239, 1997. 3 B b

GAM2071 371 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17: 231- 235, 1997. 3 B b

GAM2071 371 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001. 3 B b

GAM2071 371 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999. 3 B b

GAM2071 371 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered telomere state, not telomere loss. Science 295: 2446- 2449,2002. 3 B b

GAM2071 371 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization of the transcribed human telomere repeat binding factor2 gene and comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163, 1998. 3 B b

GAM2071 371 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman telomeres from end- to- end fusions. Cell 92: 401- 413, 1998. 3 B b

GAM2071 371 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human telomeres. Nature Genet. 25: 347- 352, 2000. 3 B b

GAM2071 371 TGFBR3 Brown, C. B.; Boyer, A. S.; Runyan, R. B.; Barnett, J. V.: Requirementof type III TGF- beta receptor for endocardial cell transformationin the heart. Science 283: 2080- 2082, 1999. 3 B c

GAM2071 371 TGFBR3 Johnson, D. W.; Qumsiyeh, M.; Benkhalifa, M.; Marchuk, D. A.:Assignment of human transforming growth factor- beta type I and typeIII receptor genes (TGFBR1 and TGFBR3) to 9q33- q34 and 1p32- p33, respectively. Genomics 28:356- 357, 1995. 3 B c

GAM2071 371 TGFBR3 Lewis, K. A.; Gray, P. C.; Blount, A. L.; MacConell, L. A.; Wiater,E.; Bilezikjian, L. M.; Vale, W.: Betaglycan binds inhibin and canmediate functional antagonism of activin signalling. Nature 404:411- 414, 2000. 3 B c

GAM2071 371 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and 13 others: Dominant and recessive deafnesscaused by mutations of a novel gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277- 284, 2002. 3 B b

GAM2071 371 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M. H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant, progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002. 3 B b

GAM2071 371 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the 3 B c B

crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999.

GAM2071 371 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 B c B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997.

GAM2071 371 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 B c B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997.

GAM2071 371 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 B c B W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM2071 371 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 B c B decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997.

GAM2071 371 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 B c B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997.

GAM2071 371 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 B c B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM2071 371 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 B c B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM2071 371 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 B c B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM2071 371 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 B c B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.

GAM2071 371 TNFRSF9 Alderson, M. R.; Smith, C. A.; Tough, T. W.; Davis- Smith, T.; Armitage,R. 3 B b J.; Falk, B.; Roux, E.; Baker, E.; Sutherland, G. R.; Din, W. S.;Goodwin, R. G.: Molecular and biological characterization of human4- 1BB and its ligand. Europ. J. Immun. 24: 2219- 2227, 1994.

GAM2071 371 TNFRSF9 Kwon, B. S.; Weissman, S. M.: cDNA sequences of two inducibleT- cell genes. 3 B b Proc. Nat. Acad. Sci. 86: 1963- 1967, 1989.

GAM2071 371 TNFRSF9 Loo, D. T.; Chalupny, N. J.; Bajorath, J.; Shuford, W. W.; Mittler,R. S.; 3 B b Aruffo, A.: Analysis of 4- 1BBL and laminin binding to murine4- 1BB, a member of the tumor necrosis factor receptor superfamily,and comparison with human 4- 1BB. J. Biol. Chem. 272: 6448- 6456,1997.

GAM2071 371 TNFRSF9 Schwarz, H.; Arden, K.; Lotz, M.: CD137, a member of the tumornecrosis 3 B b factor receptor family, is located on chromosome 1p36, ina cluster of related genes, and colocalizes with several malignancies. Biochem.Biophys.

Res. Commun. 235: 699- 703, 1997.

GAM2071 371 TNFRSF9 Schwarz, H.; Blanco, F. J.; von Kempis, J.; Valbracht, J.; Lotz,M.: ILA, a 3 B b
member of the human nerve growth factor/tumor necrosisfactor receptor
family, regulates T- lymphocyte proliferation and survival. Blood 87:2839-
2845, 1996.

GAM2071 371 TNFRSF9 Schwarz, H.; Tuckwell, J.; Lotz, M.: A receptor induced by 3 B b
lymphocyteactivation (ILA): a new member of the human nerve- growth-
factor/tumor- necrosis- factorreceptor family. Gene 134: 295- 298, 1993.

GAM2071 371 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 B c
Thiopurinemethyltransferase pharmacogenetics: alternative molecular
diagnosisand preliminary data from Northern Portugal. Pharmacogenetics
9:257- 261, 1999.

GAM2071 371 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 B c
McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian
populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM2071 371 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 B c
Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof
thiopurine methyltransferase alleles in Caucasian and Asian populations.
Pharmacogenetics 9:37- 42, 1999.

GAM2071 371 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 B c
mercaptopurine metabolism, toxic effects, and dosagerequirement in a
thiopurine methyltransferase- deficient child withacute lymphocytic
leukemia. J. Pediat. 119: 985- 989, 1991.

GAM2071 371 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 B c
Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in
African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM2071 371 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 B c
Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine
methyltransferase:molecular cloning and expression of T84 colon carcinoma
cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM2071 371 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 B c
thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-
749, 1993.

GAM2071 371 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 B c
Evans, W. E.: A single point mutation leading to loss of catalyticactivity
in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953,
1995.

GAM2071 371 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 B c
variation in response to 6- mercaptopurine for childhoodacute lymphoblastic
leukaemia. Lancet 336: 225- 229, 1990.

GAM2071 371 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 B c
azathioprine toxicity: relationship to thiopurine methyltransferasegenetic
polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM2071 371 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 B c
Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in
thiopurine methyltransferase pharmacogenetics: evidencefor allele
specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773-
776, 1999.

GAM2071 371 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human 3 B c
thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon

splice junction mutation that results in lossof activity. J. Clin. Invest. 101: 1036- 1044, 1998.

GAM2071 371 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.; Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997. 3 B c

GAM2071 371 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine methyltransferase pharmacogenetics: human gene cloningand characterization of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996. 3 B c

GAM2071 371 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997. 3 B c

GAM2071 371 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694- 702, 1996. 3 B c

GAM2071 371 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980. 3 B c

GAM2071 371 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor- associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF- kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997. 3 B b

GAM2071 371 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661- 14664, 1996. 3 B b

GAM2071 371 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999. 3 B b

GAM2071 371 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997. 3 B b

GAM2071 371 TRPM6 Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.; Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.: Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002. 3 B c

GAM2071 371 TRPM6 Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.; Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002. 3 B c

GAM2071 371 TRPM6 Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.: 3 B c

Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome: genetic linkage mapping and analysis of abalanced translocation breakpoint. Hum. Molec. Genet. 6: 1491- 1497,1997.

GAM2071 371 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994. 3 B b

GAM2071 371 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000. 3 B b

GAM2071 371 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the pain pathway. Nature 389: 816- 824, 1997. 3 B b

GAM2071 371 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 3 B b

GAM2071 371 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity to 'hot' chili peppers. Cell 108: 421- 430, 2002. 3 B b

GAM2071 371 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000. 3 B b

GAM2071 371 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996. 3 B b

GAM2071 371 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel activity by protein kinase C. Nature 408: 985- 990, 2000. 3 B b

GAM2071 371 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand multiple presentations of the oral irritant zingerone: relationshipto frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996. 3 B b

GAM2071 371 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994. 3 B b

GAM2071 371 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand pleasantness for the capsaicin burn between chili likers and non- likers:implications for liking development. Chem. Senses 18: 471- 482, 1993. 3 B b

GAM2071 371 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000. 3 B b

GAM2071 371 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002. 3 B b

GAM2071 371 TUFT1 Bashir, M. M.; Abrams, W. R.; Tucker, T.; Sellinger, B.; Budarf,M.; Emanuel, B.; Rosenbloom, J.: Molecular cloning and characterizationof the bovine and human tuftelin genes. Connect. Tissue Res. 39:13- 24, 1998. 3 B b

GAM2071 371 TUFT1 Deutsch, D.: Structure and function of enamel gene products. Anat.Rec. 224: 3 B b

189- 210, 1989.

GAM2071 371 TUFT1 Deutsch, D.; Palmon, A.; Dafni, L.; Fisher, L.; Termine, J. D.;Young, M.: Cloning, sequencing, and characterization of tuftelin:a novel acidic enamel protein. Connect. Tissue Res. 27: 121 only,1992. 3 B b

GAM2071 371 TUFT1 Deutsch, D.; Palmon, A.; Fisher, L. W.; Kolodny, N.; Termine, J.D.; Young, M. F.: Sequencing of bovine enamelin (tuftelin), a novelacidic enamel protein. J. Biol. Chem. 266: 16021- 16028, 1991. 3 B b

GAM2071 371 TUFT1 Deutsch, D.; Palmon, A.; Young, M. F.; Selig, S.; Kearns, W. G.;Fisher, L. W.: Mapping of the human tuftelin (TUFT1) gene to chromosome1 by fluorescence in situ hybridization. (Abstract) Mammalian Genome 5:461- 462, 1994. 3 B b

GAM2071 371 TUFT1 MacDougall, M.; Simmons, D.; Dodds, A.; Knight, C.; Luan, X.; Zeichner-David,M.; Zhang, C.; Ryu, O. H.; Qian, Q.; Simmer, J. P.; Hu, C.- C.: Cloning,characterization, and tissue expression pattern of mouse tuftelincDNA. J. Dent. Res. 77: 1970- 1978, 1998. 3 B b

GAM2071 371 UGDH Bontemps, Y.; Maquart, F.- X.; , Wegrowski, Y.: Human UDP-glucosedehydrogenase gene: complete cloning and transcription start mapping. Biochem.Biophys. Res. Commun. 275: 981- 985, 2000. 3 B b

GAM2071 371 UGDH Hempel, J.; Perozich, J.; Romovacek, H.; Hinich, A.; Kuo, I.; Feingold,D. S.: UDP- glucose dehydrogenase from bovine liver: primary structureand relationship to other dehydrogenases. Protein Sci. 3: 1074- 1080,1994. 3 B b

GAM2071 371 UGDH Marcu, O.; Stathakis, D. G.; Marsh, J. L.: Assignment of the UGDHlocus encoding UDP- glucose dehydrogenase to human chromosome band4p15.1 by radiation hybrid mapping. Cytogenet. Cell Genet. 86: 244- 245,1999. 3 B b

GAM2071 371 UGDH Spicer, A. P.; Kaback, L. A.; Smith, T. J.; Seldin, M. F.: Molecularcloning and characterization of the human and mouse UDP- glucose dehydrogenasegenes. J. Biol. Chem. 273: 25117- 25124, 1998. 3 B b

GAM2071 371 UGDH Walsh, E. C.; Stainier, D. Y. R.: UDP- glucose dehydrogenase requiredfor cardiac valve formation in zebrafish. Science 293: 1670- 1674,2001. 3 B b

GAM2071 371 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 B b

GAM2071 371 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 B b

GAM2071 371 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 B b

GAM2071 371 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 B b

GAM2071 371 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000. 3 B b

GAM2071 371 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine 3 B b
l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et
l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938.

GAM2071 371 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. 3 B b
G.: Two distinct phenotypes caused by two differentmissense mutations in the
same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999.

GAM2071 371 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, 3 B b
F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL)
disease with pheochromocytoma in the Black Forest region ofGermany: evidence
for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM2071 371 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 3 B b
Arch.Neurol. 28: 67- 68, 1973.

GAM2071 371 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 3 B b
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM2071 371 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 3 B b
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM2071 371 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 3 B b
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM2071 371 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 3 B b
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell,
J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.;
Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the
von Hippel- Lindau disease tumorsuppressor gene: correlations with
phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM2071 371 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 B b
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification
of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM2071 371 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 B b
disease. J.A.M.A. 178: 280- 282, 1961.

GAM2071 371 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 B b
peculiar vascular new growth, probably primarily retinal,affecting both
eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM2071 371 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 B b
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N.
A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of
the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of
allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM2071 371 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 B b
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E.
R.: Identification of intragenic mutations in thevon Hippel- Lindau disease
tumour suppressor gene and correlation withdisease phenotype. Hum. Molec.
Genet. 3: 1303- 1308, 1994.

GAM2071 371 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's 3 B b
disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928.

GAM2071 371 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- 3 B b
expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin.
Genet. 45: 104- 106, 1994.

GAM2071 371 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p 3 B b
involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region
of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65,

1988.

GAM2071 371 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459-6463, 1995. 3 B b

GAM2071 371 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995. 3 B b

GAM2071 371 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001. 3 B b

GAM2071 371 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995. 3 B b

GAM2071 371 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell107: 43- 54, 2001. 3 B b

GAM2071 371 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 B b

GAM2071 371 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 3 B b

GAM2071 371 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin TRiC. Molec. Cell 1051- 1061, 1999. 3 B b

GAM2071 371 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof von Hippel- Lindau disease. Radiology 133: 289- 295, 1979. 3 B b

GAM2071 371 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331, 1979. 3 B b

GAM2071 371 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel-Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001. 3 B b

GAM2071 371 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with hydrocephalus as a complication of cerebellar hemangioblastoma:identification of pro157leu mutation in the VHL gene. J. Hum. Genet. 45:47- 51, 2000. 3 B b

GAM2071 371 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C Thomas (pub.) 1946. 3 B b

GAM2071 371 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989. 3 B b

GAM2071 371 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg. 3 B b

Path. 18: 1254- 1260, 1994.

GAM2071 371 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.; Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999. 3 B b

GAM2071 371 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 B b

GAM2071 371 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 B b

GAM2071 371 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 B b

GAM2071 371 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 B b

GAM2071 371 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991. 3 B b

GAM2071 371 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992. 3 B b

GAM2071 371 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997. 3 B b

GAM2071 371 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984. 3 B b

GAM2071 371 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968. 3 B b

GAM2071 371 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 B b

GAM2071 371 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986. 3 B b

GAM2071 371 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour, phaeochromocytoma and the von Hippel- Lindau complex:two distinctive neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987. 3 B b

GAM2071 371 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: Familial pheochromocytoma associated with a novel mutation inthe von Hippel- Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996. 3 B b

GAM2071 371 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam: 3 B b

North Holland (pub.) 14: 1972. Pp. 241- 259.

GAM2071 371 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors 3 B b in livers with targeted inactivation of the von Hippel- Lindautumor suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001.

GAM2071 371 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 3 B b retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022- 1034, 1971.

GAM2071 371 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 3 B b hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8: 601- 606,1967.

GAM2071 371 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, 3 B b D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas. Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994.

GAM2071 371 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; 3 B b McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.; Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma only. J. Med. Genet. 37: 939- 943,2000.

GAM2071 371 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 3 B b Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips, C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet. 106: 425- 431, 2000.

GAM2071 371 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 B b von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM2071 371 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; 3 B b Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002.

GAM2071 371 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; 3 B b Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989.

GAM2071 371 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - 3 B b clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976.

GAM2071 371 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, 3 B b P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990.

GAM2071 371 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid 3 B b body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982.

GAM2071 371 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; 3 B b Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986.

GAM2071 371 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995. 3 B b

GAM2071 371 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996. 3 B b

GAM2071 371 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 3 B b

GAM2071 371 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL-mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001. 3 B b

GAM2071 371 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 3 B b

GAM2071 371 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-regulated prolyl hydroxylation. Science 292: 468- 472, 2001. 3 B b

GAM2071 371 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 B b

GAM2071 371 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 3 B b

GAM2071 371 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 B b

GAM2071 371 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 B b

GAM2071 371 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 B b

GAM2071 371 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 B b

GAM2071 371 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 B b

GAM2071 371 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 B b

GAM2071 371 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-581, 1995. 3 B b

GAM2071 371 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of 3 B b

the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995.

GAM2071 371 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 B b

GAM2071 371 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel-Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 B b

GAM2071 371 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 B b

GAM2071 371 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 B b

GAM2071 371 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel-Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 B b

GAM2071 371 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 B b

GAM2071 371 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 B b

GAM2071 371 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317-1320, 1993. 3 B b

GAM2071 371 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 B b

GAM2071 371 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 B b

GAM2071 371 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 B b

GAM2071 371 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 B b

GAM2071 371 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002. 3 B b

GAM2071 371 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 B b

GAM2071 371 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3 B b

3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990.

GAM2071 371 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 B b

GAM2071 371 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 B b

GAM2071 371 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 B b

GAM2071 371 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 B b

GAM2071 371 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 B b

GAM2071 371 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 B b

GAM2071 371 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 B b

GAM2071 371 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 B b

GAM2071 371 WISP1 Pennica, D.; Swanson, T. A.; Welsh, J. W.; Roy, M. A.; Lawrence,D. A.; Lee, J.; Brush, J.; Taneyhill, L. A.; Deuel, B.; Lew, M.; Watanabe,C.; Cohen, R. L.; Melhem, M. F.; Finley, G. G.; Quirke, P.; Goddard,A. D.; Hillan, K. J.; Gurney, A. L.; Botstein, D.; Levine, A. J.:WISP genes are members of the connective tissue growth factor familythat are up- regulated in Wnt- 1- transformed cells and aberrantly expressedin human colon tumors. Proc. Nat. Acad. Sci. 95: 14717- 14722, 1998. 3 B c

GAM2071 371 WISP1 Tanaka, S.; Sugimachi, K.; Saeki, H.; Kinoshita, J.; Ohga, T.;Shimada, M.; Maehara, Y.; Sugimachi, K.: A novel variant of WISP1lacking a von Willebrand type C module overexpressed in scirrhousgastric carcinoma. Oncogene 20: 5525- 5532, 2001. 3 B c

GAM2071 371 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with 3 B b

XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000.

GAM2071 371 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 B b

GAM2071 371 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 3 B b

GAM2071 371 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995. 3 B b

GAM2071 371 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 3 B b

GAM2071 371 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 B b

GAM2071 371 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 B b

GAM2071 371 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997. 3 B b

GAM2071 371 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995. 3 B b

GAM2071 371 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma. CancerRes. 39: 3119- 3128, 1979. 3 B b

GAM2071 371 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a follicular lymphoma cell line carrying a t(14;18)chromosomal translocation. Int. J. Cancer 39: 785- 788, 1987. 3 B b

GAM2071 371 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. A.: STS map of genes and anonymous DNA fragments on human chromosome18 using a panel of somatic cell hybrids. Genomics 15: 387- 391,1993. 3 B b

GAM2071 371 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710- 717, 1988. 3 B b

GAM2071 371 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human chromosome and its expression in various tissues. Science 227:1038- 1040, 1985. 3 B b

GAM2071 371 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal reassignment: YACs containing both YES1 and thymidylatesynthase map to the short arm of chromosome 18. Genomics 15: 442- 445,1993. 3 B b

GAM2071 371 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c- 3 B b

yes gene. Molec. Cell. Biol. 7: 41- 47, 1987.

GAM2071 371 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; 3 B b
Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to
chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985.

GAM2608 245 ABCC3 Belinsky, M. G.; Bain, L. J.; Balsara, B. B.; Testa, J. R.; Kruh,G. D.: 6 A c
Characterization of MOAT- C and MOAT- D, new members of theMRP/cMOAT
subfamily of transporter proteins. J. Nat. Cancer Inst. 90:1735- 1741, 1998.

GAM2608 245 ABCC3 Fromm, M. F.; Leake, B.; Roden, D. M.; Wilkinson, G. R.; Kim, R.B.: Human 6 A c
MRP3 transporter: identification of the 5- prime flankingregion, genomic
organization and alternative splice variants. Biochim.Biophys. Acta 1415:
369- 374, 1999.

GAM2608 245 ABCC3 Kiuchi, Y.; Suzuki, H.; Hirohashi, T.; Tyson, C. A.; Sugiyama,Y.: cDNA 6 A c
cloning and inducible expression of human multidrug resistanceassociated
protein 3 (MRP3). FEBS Lett. 433: 149- 152, 1998.

GAM2608 245 ABCC3 Konig, J.; Rost, D.; Cui, Y.; Keppler, D.: Characterization ofthe human 6 A c
multidrug resistance protein isoform MRP3 localized to thebasolateral
hepatocyte membrane. Hepatology 29: 1156- 1163, 1999.

GAM2608 245 ABCC3 Kool, M.; van der Linden, M.; de Haas, M.; Scheffer, G. L.; deVree, J. M. 6 A c
L.; Smith, A. J.; Jansen, G.; Peters, G. J.; Ponne, N.;Scheper, R. J.; Oude
Elferink, R. P. J.; Baas, F.; Borst, P.: MRP3,an organic anion transporter
able to transport anti- cancer drugs. Proc.Nat. Acad. Sci. 96: 6914- 6919,
1999.

GAM2608 245 ABCC3 Ortiz, D. F.; Li, S.; Iyer, R.; Zhang, X.; Novikoff, P.; Arias,I. M.: MRP3, 6 A c
a new ATP- binding cassette protein localized to thecanalicular domain of
the hepatocyte. Am. J. Physiol. 276: G1493- G1500,1999.

GAM2608 245 ABCC3 Uchiumi, T.; Hinoshita, E.; Haga, S.; Nakamura, T.; Tanaka, T.;Toh, S.; 6 A c
Furukawa, M.; Kawabe, T.; Wada, M.; Kagotani, K.; Okumura,K.; Kohno, K.;
Akiyama, S.; Kuwano, M.: Isolation of a novel humancanalicular multispecific
organic anion transporter, cMOAT2/MRP3,and its expression in cisplatin-
resistant cancer cells with decreasedATP- dependent drug transport. Biochem.
Biophys. Res. Commun. 252:103- 110, 1998.

GAM2608 245 BACE Cai, H.; Wang, Y.; McCarthy, D.; Wen, H.; Borchelt, D. R.; Price,D. L.; 6 A c
Wong, P. C.: BACE1 is the major beta- secretase for generationof A- beta
peptides by neurons. Nature Neurosci. 4: 233- 234, 2001.

GAM2608 245 BACE De Strooper, B.; Konig, G.: A firm base for drug development. Nature 6 A c
402:471- 472, 1999.

GAM2608 245 BACE Fan, W.; Bennett, B. D.; Babu- Khan, S.; Luo, Y.; Louis, J.- C.;McCaleb, M.; 6 A c
Citron, M.; Vassar, R.; Richards, W. G.: Response toSaunders et al. (1999).
Science 286: 1255a, 1999. Note: ElectronicPublication.

GAM2608 245 BACE Haniu, M.; Denis, P.; Young, Y.; Mendiaz, E. A.; Fuller, J.; Hui,J. O.; 6 A c
Bennett, B. D.; Kahn, S.; Ross, S.; Burgess, T.; Katta, V.;Rogers, G.;
Vassar, R.; Citron, M.: Characterization of Alzheimer'sbeta- secretase
protein BACE: a pepsin family member with unusual properties. J.Biol. Chem.
275: 21099- 21106, 2000.

GAM2608 245 BACE Hong, L.; Koelsch, G.; Lin, X.; Wu, S.; Terzyan, S.; Ghosh, A.K.; Zhang, X. 6 A c
C.; Tang, J.: Structure of the protease domain of memapsin2 (beta-
secretase) complexed with inhibitor. Science 290: 150- 153,2000.

GAM2608 245 BACE Hussain, I.; Powell, D.; Howlett, D. R.; Tew, D. G.; Meek, T. D.;Chapman, 6 A c
C.; Gloger, I. S.; Murphy, K. E.; Southan, C. D.; Ryan, D.M.; Smith, T. S.;
Simmons, D. L.; Walsh, F. S.; Dingwall, C.; Christie,G.: Identification of a

novel aspartic protease (asp2) as beta- secretase Molec.Cell Neurosci. 14: 419- 427, 1999.

GAM2608 245 BACE Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643- 648, 2001. 6 A c

GAM2608 245 BACE Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.- H.; Goldstein, L. S.: Axonal transport of amyloid precursor protein is mediated by directbinding to the kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000. 6 A c

GAM2608 245 BACE Luo, Y.; Bolon, B.; Kahn, S.; Bennett, B. D.; Babu- Khan, S.; Denis,P.; Fan, W.; Kha, H.; Zhang, J.; Gong, Y.; Martin, L.; Louis, J.- C.;Yan, Q.; Richards, W. G.; Citron, M.; Vassar, R.: Mice deficientin BACE1, the Alzheimer's beta- secretase, have normal phenotype andabolished beta- amyloid generation. Nature Neurosci. 4: 231- 232,2001. 6 A c

GAM2608 245 BACE Nicolaou, M.; Song, Y.- Q.; Sato, C. A.; Orlacchio, A.; Kawarai,T.; Medeiros, H.; Liang, Y.; Sorbi, S.; Richard, E.; Rogaev, E. I.;Moliaka, Y.; Bruni, A. C.; Jorge, R.; Percy, M.; Duara, R.; Farrer,L. A.; St George- Hyslop, P.; Rogaeva, E. A.: Mutations in the openreading frame of the beta- site APP cleaving enzyme (BACE) locus arenot a common cause of Alzheimer's disease. Neurogenetics 3: 203- 206,2001. 6 A c

GAM2608 245 BACE Roberds, S. L.; Anderson, J.; Basi, G.; Bienkowski, M. J.; Branstetter,D. G.; Chen, K. S.; Freedman, S. B.; Frigon, N. L.; Games, D.; Hu,K.; Johnson- Wood, K.; Kappenman, K. E.; and 20 others: BACE knockoutmice are healthy despite lacking the primary beta- secretase activityin brain: implications for Alzheimer's disease therapeutics. Hum.Molec. Genet. 10: 1317- 1324, 2001. 6 A c

GAM2608 245 BACE Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a BACE homolog, BACE2, reside in the obligate Down syndromeregion of chromosome 21. Science 286: 1255a, 1999. Note: ElectronicPublication. 6 A c

GAM2608 245 BACE Sinha, S.; Anderson, J. P.; Barbour, R.; Basi, G. S.; Caccavello,R.; Davis, D.; Doan, M.; Dovey, H. F.; Frigon, N.; Hong, J.; Jacobson- Croak,K.; Jewett, N.; and 15 others: Purification and cloning of amyloidprecursor protein beta- secretase from human brain. Nature 402: 537- 540,1999. 6 A c

GAM2608 245 BACE Vassar, R.; Bennett, B. D.; Babu- Khan, S.; Kahn, S.; Mendiaz,E. A.; Dents, P.; Taplow, D. B.; Ross, S.; Amaranta, P.; Loeloff,R.; Luo, Y.; Fisher, S.; and 12 others: Beta- secretase cleavageof Alzheimer's amyloid precursor protein by the transmembrane asparticprotease BACE. Science 286: 735- 741, 1999. 6 A c

GAM2608 245 BACE Yan, R.; Bienkowski, M. J.; Shuck, M. E.; Miao, H.; Tory, M. C.;Pauley, A. M.; Brashler, J. R.; Stratman, N. C.; Mathews, W. R.; Buhl,A. E.; Carter, D. B.; Tomasselli, A. G.; Parodi, L. A.; Heinrikson,R. L.; Gurney, M. E.: Membrane- anchored aspartyl protease with Alzheimer'sdisease beta- secretase activity. Nature 402: 533- 536, 1999. 6 A c

GAM2608 245 DMN Mizuno, Y.; Thompson, T. G.; Guyon, J. R.; Lidov, H. G. W.; Brosius,M.; Imamura, M.; Ozawa, E.; Watkins, S. C.; Kunkel, L. M.: Desmuslin,an intermediate filament protein that interacts with alpha- dystrobrevinand desmin. Proc. Nat. Acad. Sci. 98: 6156- 6161, 2001. 6 A c

GAM2608 245 DMN Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new 6 A c

cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM2608 245 FBXL3A Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal,M.; Pagano, M.: Identification of a family of human F- box proteins. Curr.Biol. 9: 1177- 1179, 1999. 6 A c

GAM2608 245 FBXL3A Chiaur, D. S.; Murthy, S.; Cenciarelli, C.; Parks, W.; Loda, M.;Inghirami, G.; Demetrick, D.; Pagano, M.: Five human genes encodingF- box proteins: chromosome mapping and analysis in human tumors. Cytogenet.Cell Genet. 88: 255- 258, 2000. 6 A c

GAM2608 245 FBXL3A Winston, J. T.; Koepp, D. M.; Zhu, C.; Elledge, S. J.; Harper,J. W.: A family of mammalian F- box proteins. Curr. Biol. 9: 1180- 1182,1999. 6 A c

GAM2608 245 GRIA1 Gregor, P.; Reeves, R. H.; Jabs, E. W.; Yang, X.; Dackowski, W.;Rochelle, J. M.; Brown, R. H., Jr.; Haines, J. L.; O'Hara, B. F.;Uhl, G. R.; Seldin, M. F.: Chromosomal localization of glutamatereceptor genes: relationship to familial amyotrophic lateral sclerosisand other neurological disorders of mice and humans. Proc. Nat. Acad.Sci. 90: 3053- 3057, 1993. 6 A c

GAM2608 245 GRIA1 Lee, H.- K.; Barbarosie, M.; Kameyama, K.; Bear, M. F.; Huganir,R. L.: Regulation of distinct AMPA receptor phosphorylation sitesduring bidirectional synaptic plasticity. Nature 405: 955- 959, 2000. 6 A c

GAM2608 245 GRIA1 Mack, V.; Burnashev, N.; Kaiser, K. M. M.; Rozov, A.; Jensen, V.;Hvalby, O.; Seeburg, P. H.; Sakmann, B.; Sprengel, R.: Conditionalrestoration of hippocampal synaptic potentiation in GluR- A- deficientmice. Science 292: 2501- 2504, 2001. 6 A c

GAM2608 245 GRIA1 Puckett, C.; Gomez, C. M.; Korenberg, J. R.; Tung, H.; Meier, T.J.; Chen, X. N.; Hood, L.: Molecular cloning and chromosomal localizationof one of the human glutamate receptor genes. Proc. Nat. Acad. Sci. 88:7557- 7561, 1991. 6 A c

GAM2608 245 GRIA1 Shi, S.- H.; Hayashi, Y.; Petralla, R. S.; Zaman, S. H.; Wenthold,R. J.; Svoboda, K.; Malinow, R.: Rapid spine delivery and redistributionof AMPA receptors after synaptic NMDA receptor activation. Science 284:1811- 1816, 1999. 6 A c

GAM2608 245 GRIA1 Sun, W.; Ferrer- Montiel, A. V.; Schinder, A. F.; McPherson, J.P.; Evans, G. A.; Montal, M.: Molecular cloning, chromosomal mapping,and functional expression of human brain glutamate receptors. Proc.Nat. Acad. Sci. 89: 1443- 1447, 1992. 6 A c

GAM2608 245 GRIA1 Warrington, J. A.; Bailey, S. K.; Armstrong, E.; Aprelikova, O.;Alitalo, K.; Dolganov, G. M.; Wilcox, A. S.; Sikela, J. M.; Wolfe,S. F.; Lovett, M.; Wasmuth, J. J.: A radiation hybrid map of 18 growthfactor, growth factor receptor, hormone receptor, or neurotransmitterreceptor genes on the distal region of the long arm of chromosome5. Genomics 13: 803- 808, 1992. 6 A c

GAM2608 245 GRIA1 Zamanillo, D.; Sprengel, R.; Hvalby, O.; Jensen, V.; Burnashev,N.; Rozov, A.; Kaiser, K. M. M.; Koster, H. J.; Borchardt, T.; Worley,P.; Lubke, J.; Frotscher, M.; Kelly, P. H.; Sommer, B.; Andersen,P.; Seeburg, P. H.; Sakmann, B.: Importance of AMPA receptors forhippocampal synaptic plasticity but not for spatial learning. Science 284:1805- 1811, 1999. 6 A c

GAM2608 245 HPSE Baker, E.; Crawford, J.; Sutherland, G. R.; Freeman, C.; Parish,C. R.; Hulett, M. D.: Human HPA endoglycosidase heparanase. ChromosomeRes. 7: 319 only, 1999. 6 A c

GAM2608 245 HPSE Hulett, M. D.; Freeman, C.; Hamdorf, B. J.; Baker, R. T.; Harris,M. J.; Parish, C. R.: Cloning of mammalian heparanase, an importantenzyme in tumor invasion and metastasis. Nature Med. 5: 803- 809,1999. 6 A c

GAM2608 245 HPSE Kussie, P. H.; Hulmes, J. D.; Ludwig, D. L.; Patel, S.; Navarro,E. C.; Seddon, A. P.; Giorgio, N. A.; Bohlen, P: Cloning and functionalexpression of a human heparanase gene. Biochem. Biophys. Res. Commun. 261:183- 187, 1999. 6 A c

GAM2608 245 HPSE Toyoshima, M.; Nakajima, M.: Human heparanase: purification, characterization,cloning, and expression. J. Biol. Chem. 274: 24153- 24160, 1999. 6 A c

GAM2608 245 HPSE Vlodavsky, I.; Friedmann, Y.; Elkin, M.; Aingorn, H.; Atzmon, R.;Ishai-Michaeli, R.; Bitan, M.; Pappo, O.; Peretz, T.; Michal, I.;Spector, L.; Pecker, I.: Mammalian heparanase: gene cloning, expressionand function in tumor progression and metastasis. Nature Med. 5:793- 802, 1999. 6 A c

GAM2608 245 ITPKB Erneux, C.; Roeckel, N.; Takazawa, K.; Mailleux, P.; Vassart, G.;Mattei, M. G.: Localization of the genes for human inositol 1,4,5- trisphosphate3-kinase A (ITPKA) and B (ITPKB) to chromosome regions 15q14- q21 and1q41-q43, respectively, by in situ hybridization. Genomics 14:546- 547, 1992. 6 A c

GAM2608 245 ITPKB Takazawa, K.; Perret, J.; Dumont, J. E.; Erneux, C.: Molecularcloning and expression of a new putative inositol 1,4,5- trisphosphate3- kinase isoenzyme. Biochem. J. 278: 883- 886, 1991. 6 A c

GAM2608 245 LAMP1 Bermingham, N. A.; Martin, J. E.; Fisher, E. M. C.: The mouselysosomal membrane protein 1 gene as a candidate for the motorneurondegeneration (mnd) locus. Genomics 32: 266- 271, 1996. 6 A c

GAM2608 245 LAMP1 Howe, C. L.; Granger, B. L.; Hull, M.; Green, S. A.; Gabel, C.A.; Helenius, A.; Mellman, I.: Derived protein sequence, oligosaccharides,and membrane insertion of the 120- kDa lysosomal membrane glycoprotein(lgp120): identification of a highly conserved family of lysosomalmembrane glycoproteins. Proc. Nat. Acad. Sci. 85: 7577- 7581, 1988. 6 A c

GAM2608 245 LAMP1 Mattei, M.- G.; Matterson, J.; Chen, J. W.; Williams, M. A.; Fukuda,M.: Two human lysosomal membrane glycoproteins, h- lamp- 1 and h- lamp- 2,are encoded by genes localized to chromosome 13q34 and chromosomeXq24- 25, respectively. J. Biol. Chem. 265: 7548- 7551, 1990. 6 A c

GAM2608 245 LAMP1 Schleutker, J.; Haataja, L.; Renlund, M.; Puhakka, L.; Viitala,J.; Peltonen, L.; Aula, P.: Confirmation of the chromosomal localizationof human lamp genes and their exclusion as candidate genes for Salladisease. Hum. Genet. 88: 95- 97, 1991. 6 A c

GAM2608 245 LAMP1 Viitala, J.; Carlsson, S. R.; Siebert, P. D.; Fukuda, M.: Molecularcloning of cDNAs encoding lamp A, a human lysosomal membrane glycoproteinwith apparent M(r) about 120,000. Proc. Nat. Acad. Sci. 85: 3743- 3747,1988. 6 A c

GAM2608 245 MAP3K8 Aoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima,K.: The human cot proto- oncogene encodes two protein serine/threoninekinases with different transforming activities by alternative initiationof translation. J. Biol. Chem. 268: 22723- 22732, 1993. 6 A c

GAM2608 245 MAP3K8 Chan, A. M.- L.; Chedid, M.; McGovern, E. S.; Popescu, N. C.; Miki,T.; Aaronson, S. A.: Expression cDNA cloning of a serine kinase transforminggene. Oncogene 8: 1329- 1333, 1993. 6 A c

GAM2608 245 MAP3K8 Miyoshi, J.; Higashi, T.; Mukai, H.; Ohuchi, T.; Kakunaga, T.:Structure and transforming potential of the human cot oncogene encodinga putative protein kinase. Molec. Cell. Biol. 11: 4088- 4096, 1991. 6 A c

GAM2608 245 MAP3K8 Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.: The murine cotproto-oncogene: genome structure and tissue- specific expression. Jpn.J. Cancer Res. 84: 518- 525, 1993. 6 A c

GAM2608 245 MASP1 Dahl, M. R.; Thiel, S.; Matsushita, M.; Fujita, T.; Willis, A.C.; 6 A c
Christensen, T.; Vorup- Jensen, T.; Jensenius, J. C.: MASP- 3 andits
association with distinct complexes of the mannan- binding lectincomplement
activation pathway. Immunity 15: 127- 135, 2001.

GAM2608 245 MASP1 Endo, Y.; Sato, T.; Matsushita, M.; Fujita, T.: Exon structureof the gene 6 A c
encoding the human mannose- binding protein- associatedserine protease light
chain: comparison with complement C1r and C1sgenes. Int. Immun. 8: 1355-
1358, 1996.

GAM2608 245 MASP1 Matsushita, M.; Thiel, S.; Jensenius, J. C.; Terai, I.; Fujita,T.: 6 A c
Proteolytic activities of two types of mannose- binding lectin-
associatedserine protease. J. Immun. 165: 2637- 2642, 2000.

GAM2608 245 MASP1 Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.: Molecular characterizationof 6 A c
a novel serine protease involved in activation of the complementsystem by
mannose- binding protein. Int. Immun. 6: 665- 669, 1994.

GAM2608 245 MASP1 Takada, F.; Seki, N.; Matsuda, Y.; Takayama, Y.; Kawakami, M.:Localization 6 A c
of the genes for the 100- kDa complement- activating componentsof Ra-
reactive factor (CRARF and Crarf) to human 3q27- q28 and mouse16B2- B3.
Genomics 25: 757- 759, 1995.

GAM2608 245 MASP1 Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M.: A new memberof the C1s 6 A
c
family of complement proteins found in a bactericidal factor,Ra- reactive
factor, in human serum. Biochem. Biophys. Res. Commun. 196:1003- 1009, 1993.

GAM2608 245 MASP1 Takayama, Y.; Takada, F.; Nowatari, M.; Kawakami, M.; Matsu- ura,N.: Gene 6 A c
structure of the P100 serine- protease component of the humanRa- reactive
factor. Molec. Immun. 36: 505- 514, 1999.

GAM2608 245 NEDD4 Harvey, K. F.; Dinudom, A.; Cook, D. I.; Kumar, S.: The Nedd4- likeprotein 6 A c
KIAA0439 is a potential regulator of the epithelial sodiumchannel. J. Biol.
Chem. 276: 8597- 8601, 2001.

GAM2608 245 NEDD4 Imhof, M. O.; McDonnell, D. P.: Yeast RSP5 and its human homologhRPF1 6 A c
potentiate hormone- dependent activation of transcription byhuman
progesterone and glucocorticoid receptors. Molec. Cell. Biol. 16:2594- 2605,
1996.

GAM2608 245 NEDD4 Kumar, S.; Harvey, K. F.; Kinoshita, M.; Copeland, N. G.; Noda,M.; Jenkins, 6 A c
N. A.: cDNA cloning, expression analysis, and mappingof the mouse Nedd4
gene. Genomics 40: 435- 443, 1997.

GAM2608 245 NEDD4 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 6 A c
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM2608 245 NR1I2 Bertilsson, G.; Heidrich, J.; Svensson, K.; Asman, M.; Jendeberg,L.; Sydow- 6 A c
Backman, M.; Ohlsson, R.; Postlind, H.; Blomquist, P.; Berkenstam,A.:
Identification of a human nuclear receptor defines a new signalingpathway
for CYP3A induction. Proc. Nat. Acad. Sci. 95: 12208- 12213,1998.

GAM2608 245 NR1I2 Blumberg, B.; Sabbagh, W., Jr.; Juguilon, H.; Bolado, J., Jr.;van Meter, C. 6 A c
M.; Ong, E. S.; Evans, R. M.: SXR, a novel steroidand xenobiotic- sensing
nuclear receptor. Genes Dev. 12: 3195- 3205,1998.

GAM2608 245 NR1I2 Lehmann, J. M.; McKee, D. D.; Watson, M. A.; Willson, T. M.; Moore,J. T.; 6 A c
Kliewer, S. A.: The human orphan nuclear receptor PXR is activatedby
compounds that regulate CYP3A4 gene expression and cause drug interactions.
J.Clin. Invest. 102: 1016- 1023, 1998.

GAM2608 245 NR1I2 Synold, T. W.; Dussault, I.; Forman, B. M.: The orphan nuclearreceptor SXR 6 A c

coordinately regulates drug metabolism and efflux. NatureMed. 7: 584- 590, 2001.

GAM2608 245 NR1I2 Watkins, R. E.; Wisely, G. B.; Moore, L. B.; Collins, J. L.; Lambert,M. H.; 6 A c Williams, S. P.; Willson, T. M.; Kliewer, S. A.; Redinbo, M.R.: The human nuclear xenobiotic receptor PXR: structural determinantsof directed promiscuity. Science 292: 2329- 2333, 2001.

GAM2608 245 NR1I2 Xie, W.; Barwick, J. L.; Downes, M.; Blumberg, B.; Simon, C. M.;Nelson, M. 6 A c C.; Neuschwander- Tetri, B. A.; Brunt, E. M.; Guzelian,P. S.; Evans, R. M.: Humanized xenobiotic response in mice expressingnuclear receptor SXR. Nature 406: 435- 439, 2000.

GAM2608 245 NR1I2 Zhang, J.; Kuehl, P.; Green, E. D.; Touchman, J. W.; Watkins, P.B.; Daly, 6 A c A.; Hall, S. D.; Maurel, P.; Relling, M.; Brimer, C.; Yasuda,K.; Wrighton, S. A.; Hancock, M.; Kim, R. B.; Strom, S.; Thummel,K.; Russell, C. G.; Hudson, J. R., Jr.; Schuetz, E. G.; Boguski, M.S.: The human pregnane X receptor: genomic structure and identificationand functional characterization of natural allelic variants. Pharmacogenetics 11:555- 572, 2001.

GAM2608 245 PDE4D Bolger, G. B.; Erdogan, S.; Jones, R. E.; Loughney, K.; Scotland,G.; 6 A c Hoffmann, R.; Wilkinson, I.; Farrell, C.; Houslay, M. D.: Characterizationof five different proteins produced by alternatively spliced mRNAsfrom the human cAMP- specific phosphodiesterase PDE4D gene. Biochem.J. 328: 539- 548, 1997.

GAM2608 245 PDE4D Dudai, Y.; Jan, Y.- N.; Byers, D.; Quinn, W. G.; Benzer, S.: dunce,a mutant 6 A c of Drosophila deficient in learning. Proc. Nat. Acad. Sci. 73:1684- 1688, 1976.

GAM2608 245 PDE4D Hansen, G.; Jin, S.- L. C.; Umetsu, D. T.; Conti, M.: Absence ofmuscarinic 6 A c cholinergic airway responses in mice deficient in the cyclicnucleotide phosphodiesterase PDE4D. Proc. Nat. Acad. Sci. 97: 6751- 6756,2000.

GAM2608 245 PDE4D Jin, S.- L. C.; Richard, F. J.; Kuo, W.- P.; D'Ercole, A. J.; Conti,M.: 6 A c Impaired growth and fertility of cAMP- specific phosphodiesterasePDE4D- deficient mice. Proc. Nat. Acad. Sci. 96: 11998- 12003, 1999.

GAM2608 245 PDE4D Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 6 A c Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM2608 245 PDE4D Szpirer, C.; Szpirer, J.; Riviere, M.; Swinnen, J.; Vicini, E.;Conti, M.: 6 A c Chromosomal localization of the human and rat genes (PDE4Dand PDE4B) encoding the cAMP- specific phosphodiesterases 3 and 4. Cytogenet.Cell Genet. 69: 11- 14, 1995.

GAM2608 245 RAB5A Bucci, C.; Parton, R. G.; Mather, I. H.; Stunnenberg, H.; Simons,K.; 6 A c Hoflack, B.; Zerial, M.: The small GTPase rab5 functions as aregulatory factor in the early endocytic pathway. Cell 70: 715- 728,1992.

GAM2608 245 RAB5A Lanzetti, L.; Rybin, V.; Malabarba, M. G.; Christoforidis, S.;Scita, G.; 6 A c Zerial, M.; Di Fiore, P. P.: The Eps8 protein coordinatesEGF receptor signalling through Rac and trafficking through Rab5. Nature 408:374- 377, 2000.

GAM2608 245 RAB5A Rousseau- Merck, M. F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: 6 A c Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350- 354, 1991.

GAM2608 245 RAB5A Stenmark, H.; Vitale, G.; Ullrich, O.; Zerial, M.: Rabaptin- 5is a direct 6 A c effector of the small GTPase Rab5 in endocytic membranefusion. Cell 83: 423-

432, 1995.

GAM2608 245 RAB5A Xiao, G.- H.; Shoarinejad, F.; Jin, F.; Golemis, E. A.; Yeung, R.S.: The 6 A c
tuberous sclerosis 2 gene product, tuberin, functions asa Rab5 GTPase
activating protein (GAP) in modulating endocytosis. J.Biol. Chem. 272: 6097-
6100, 1997.

GAM2608 245 RAB5A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes 6 A c
encode a family of GTP- binding proteins related to yeastYPT1 and SEC4
products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989.

GAM2608 245 ROCK2 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 6 A c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM2608 245 ROCK2 Nakamura, M.; Nagano, T.; Chikama, T.; Nishida, T.: Role of thesmall GTP- 6 A c
binding protein Rho in epithelial cell migration in therabbit cornea.
Invest. Ophthal. Vis. Sci. 42: 941- 947, 2001.

GAM2608 245 ROCK2 Rao, P. V.; Deng, P.- F.; Kumar, J.; Epstein, D. L.: Modulationof aqueous 6 A c
humor outflow facility by the Rho kinase- specific inhibitorY- 27632.
Invest. Ophthal. Vis. Sci. 42: 1029- 1037, 2001.

GAM2608 245 ROCK2 Takahashi, N.; Tuiki, H.; Saya, H.; Kaibuchi, K.: Localizationof the gene 6 A c
coding for ROCK II/Rho kinase on human chromosome 2p24. Genomics 55:235-
237, 1999.

GAM2608 245 SIM2 Chen, H.; Chrast, R.; Rossier, C.; Gos, A.; Antonarakis, S. E.;Kudoh, J.; 6 A c
Yamaki, A.; Shindoh, N.; Maeda, H.; Minoshima, S.; Shimizu,N.: Single-
minded and Down syndrome? (Letter) Nature Genet. 10:9- 10, 1995.

GAM2608 245 SIM2 Chrast, R.; Scott, H. S.; Madani, R.; Huber, L.; Wolfer, D. P.;Prinz, M.; 6 A c
Aguzzi, A.; Lipp, H.- P.; Antonarakis, S. E.: Mice trisomicfor a bacterial
artificial chromosome with the single- minded 2 gene(Sim2) show phenotypes
similar to some of those present in the partialtrisomy 16 mouse models of
Down syndrome. Hum. Molec. Genet. 9:1853- 1864, 2000.

GAM2608 245 SIM2 Dahmane, N.; Charron, G.; Lopes, C.; Yaspo, M.- L.; Maunoury, C.;Decorte, 6 A c
L.; Sinet, P.- M.; Bloch, B.; Delabar, J.- M.: Down syndrome- criticalregion
contains a gene homologous to Drosophila sim expressed duringrat and human
central nervous system development. Proc. Nat. Acad.Sci. 92: 9191- 9195,
1995.

GAM2608 245 SIM2 Ema, M.; Ikegami, S.; Hosoya, T.; Mimura, J.; Ohtani, H.; Nakao,K.; 6 A c
Inokuchi, K.; Katsuki, M.; Fujii- Kuriyama, Y.: Mild impairmentof learning
and memory in mice overexpressing the mSim2 gene locatedon chromosome 16: an
animal model of Down's syndrome. Hum. Molec.Genet. 8: 1409- 1415, 1999.

GAM2608 245 SIM2 Moffett, P.; Dayo, M.; Reece, M.; McCormick, M. K.; Pelletier,J.: 6 A c
Characterization of msim, a murine homologue of the Drosophilasim
transcription factor. Genomics 35: 144- 155, 1996.

GAM2608 245 SIM2 Muenke, M.; Bone, L. J.; Mitchell, H. F.; Hart, I.; Walton, K.;Hall- 6 A c
Johnson, K.; Ippel, E. F.; Dietz- Band, J.; Kvaloy, K.; Fan, C.- M.;Tessier-
Lavigne, M.; Patterson, D.: Physical mapping of the
holoprosencephalycritical region in 21q22.3, exclusion of SIM2 as a
candidate genefor holoprosencephaly, and mapping of SIM2 to a region of
chromosome21 important for Down syndrome. Am. J. Hum. Genet. 57: 1074-
1079,1995.

GAM2608 245 SIM2 Yamaki, A.; Noda, S.; Kudoh, J.; Shindoh, N.; Maeda, H.; Minoshima,S.; 6 A c
Kawasaki, K.; Shimizu, Y.; Shimizu, N.: The mammalian single- minded(SIM)

gene: mouse cDNA structure and diencephalic expression indicatea candidate gene for Down syndrome. Genomics 35: 136- 143, 1996.

GAM2608 245 TTID Hauser, M. A.; Horrigan, S. K.; Salmikangas, P.; Torian, U. M.;Viles, K. D.; 6 A c Dancel, R.; Tim, R. W.; Taivainen, A.; Bartoloni, L.;Gilchrist, J. M.; Stajich, J. M.; Gaskell, P. C.; Gilbert, J. R.;Vance, J. M.; Pericak- Vance, M. A.; Carpen, O.; Westbrook, C. A.;Speer, M. C.: Myotilin is mutated in limb girdle muscular dystrophy1A. Hum. Molec. Genet. 9: 2141- 2147, 2000.

GAM2608 245 TTID Salmikangas, P.; Mykkanen, O.- M.; Gronholm, M.; Heiska, L.; Kere,J.; 6 A c Carpen, O.: Myotilin, a novel sarcomeric protein with two Ig- likedomains, is encoded by a candidate gene for limb- girdle muscular dystrophy. Hum.Molec. Genet. 8: 1329- 1336, 1999.

GAM3027 242 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 3 A c Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.: Identification of Bach2 as a B- cell- specific partner for smallMaf proteins that negatively regulate the immunoglobulin heavy chaingene 3- prime enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM3027 242 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 3 A c Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB- basic leucine zipper transcription factors that interact withMafK and regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083- 6095, 1996.

GAM3027 242 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, 3 A c A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.; Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene 19: 3739- 3749, 2000.

GAM3027 242 CCRL1 Gosling, J.; Dairaghi, D. J.; Wang, Y.; Hanley, M.; Talbot, D.;Miao, Z.; 3 A c Schall, T. J.: Cutting edge: identification of a novelchemokine receptor that binds dendritic cell- and T cell- active chemokinesincluding ELC, SLC, and TECK. J. Immun. 164: 2851- 2856, 2000.

GAM3027 242 CCRL1 Khoja, H.; Wang, G.; Ng, C.- T. L.; Tucker, J.; Brown, T.; Shyamala,V.: 3 A c Cloning of CCRL1, an orphan seven transmembrane receptor relatedto chemokine receptors, expressed abundantly in the heart. Gene 246:229- 238, 2000.

GAM3027 242 CCRL1 Schweickart, V. L.; Epp, A.; Raport, C. J.; Gray, P. W.: CCR11is a 3 A c functional receptor for the monocyte chemoattractant proteinfamily of chemokines. J. Biol. Chem. 275: 9550- 9556, 2000. Note:Erratum: J. Biol. Chem. 276: 856 only, 2001.

GAM3027 242 CSPG4 Behm, F. G.; Smith, F. O.; Raimondi, S. C.; Pui, C.- H.; Bernstein,I. D.: 3 A c Human homologue of the rat chondroitin sulfate proteoglycan,NG2, detected by monoclonal antibody 7.1, identifies childhood acutelymphoblastic leukemias with t(4;11)(q21;q23) or t(11;19)(q23;p13)and MLL gene rearrangements. Blood 87: 1134- 1139, 1996.

GAM3027 242 CSPG4 Pluschke, G.; Vanek, M.; Evans, A.; Dittmar, T.; Schmid, P.; Itin,P.; 3 A c Filardo, E. J.; Reisfeld, R. A.: Molecular cloning of a humanmelanoma-associated chondroitin sulfate proteoglycan. Proc. Nat.Acad. Sci. 93: 9710- 9715, 1996.

GAM3027 242 CSPG4 Rettig, W. J.; Dracopoli, N. C.; Goetzger, T. A.; Spengler, B.A.; Biedler, 3 A c J. L.; Oettgen, H. F.; Old, L. J.: Somatic cell geneticanalysis of human cell surface antigens: chromosomal assignments andregulation of expression in rodent- human hybrid cells. Proc. Nat.Acad. Sci. 81: 6437- 6441, 1984.

GAM3027 242 CSPG4 Rettig, W. J.; Real, F. X.; Spengler, B. A.; Biedler, J. L.; Old,L. J.: 3 A c
Human melanoma proteoglycan: expression in hybrids controlledby intrinsic and extrinsic signals. Science 231: 1281- 1284, 1986.

GAM3027 242 CSPG4 Smith, F. O.; Rauch, C.; Williams, D. E.; March, C. J.; Arthur,D.; Hilden, 3 A c
J.; Lampkin, B. C.; Buckley, J. D.; Buckley, C. V.; Woods,W. G.; Dinndorf, P. A.; Sorensen, P.; Kersey, J.; Hammond, D.; Bernstein,I. D.: The human homologue of rat NG2, a chondroitin sulfate proteoglycan,is not expressed on the cell surface of normal hematopoietic cellsbut is expressed by acute myeloid leukemia blasts from poor- prognosispatients with abnormalities of chromosome band 11q23. Blood 87:1123- 1133, 1996.

GAM3027 242 ITPR1 Matsumoto, M.; Nakagawa, T.; Inoue, T.; Nagata, E.; Tanaka, K.;Takano, H.; 3 A c
Minowa, O.; Kuno, J.; Sakakibara, S.; Yamada, M.; Yoneshima,H.; Miyawaki, A; Fukuichi, T.; Furuichi, T.; Okano, H.; Mikoshiba,K.; Noda, T.: Ataxia and epileptic seizures in mice lacking type1 inositol 1,4,5- triphosphate receptor. Nature 379: 168- 171, 1996.

GAM3027 242 ITPR1 Nucifora, F. C., Jr.; Li, S.- H.; Danoff, S.; Ullrich, A.; Ross,C. A.: 3 A c
Molecular cloning of a cDNA for the human inositol 1,4,5- trisphosphatereceptor type 1, and the identification of a third alternatively splicedvariant. Molec. Brain Res. 32: 291- 296, 1995.

GAM3027 242 ITPR1 Ozcelik, T.; Suedhof, T. C.; Francke, U.: The genes for inositol1,4,5- 3 A c
triphosphate receptors 1 (ITPR1) and 3 (ITPR3) are localizedon human chromosomes 3p and 6pter- p21, respectively. (Abstract) Cytogenet.Cell Genet. 58: 1880, 1991.

GAM3027 242 ITPR1 Yamada, N.; Makino, Y.; Clark, R. A.; Pearson, D. W.; Mattei, M.- G.;Guenet, 3 A c
J.- L.; Ohama, E.; Fujino, I.; Miyawaki, A.; Furuichi, T.;Mikoshiba, K.: Human inositol 1,4,5- triphosphate type- 1 receptor,InsP3R1: structure, function, regulation of expression and chromosomallocalization. Biochem. J. 302: 781- 790, 1994.

GAM3027 242 MEST Ferguson- Smith, A. C.; Cattanach, B. M.; Barton, S. C.; Beechey,C. V.; 3 A c
Surani, M. A.: Embryological and molecular investigationsof parental imprinting on mouse chromosome 7. Nature 351: 667- 670,1991.

GAM3027 242 MEST Kaneko- Ishino, T.; Kuroiwa, Y.; Miyoshi, N.; Kohda, T.; Suzuki,R.; 3 A c
Yokoyama, M.; Viville, S.; Barton, S. C.; Ishino, F.; Surani,M. A.: Peg1/Mest imprinted gene on chromosome 6 identified by cDNAsubtraction hybridization. Nature Genet. 11: 52- 59, 1995.

GAM3027 242 MEST Kobayashi, S.; Kohda, T.; Miyoshi, N.; Kuroiwa, Y.; Aisaka, K.;Tsutsumi, O.; 3 A c
Kaneko- Ishino, T.; Ishino, F.: Human PEG1/MEST, animprinted gene on chromosome 7. Hum. Molec. Genet. 6: 781- 786, 1997.

GAM3027 242 MEST Kobayashi, S.; Uemura, H.; Kohda, T.; Nagai, T.; Chinen, Y.; Naritomi,K.; 3 A c
Kinoshita, E.; Ohashi, H.; Imaizumi, K.; Tsukahara, M.; Sugio,Y.; Tonoki, H.; Kishino, T.; Tanaka, T.; Yamada, M.; Tsutsumi, O.;Niikawa, N.; Kaneko- Ishino, T.; Ishino, F.: No evidence of PEG1/MESTgene mutations in Silver- Russell syndrome patients. Am. J. Med. Genet. 104:225- 231, 2001.

GAM3027 242 MEST Kosaki, K.; Kosaki, R.; Craigen, W. J.; Matsuo, N.: Isoform- 3 A c
specificimprinting of the human PEG1/MEST gene. (Letter) Am. J. Hum. Genet. 66:309- 312, 2000.

GAM3027 242 MEST Kotzot, D.; Schmitt, S.; Bernasconi, F.; Robinson, W. P.; Lurie,I. W.; 3 A c
Ilyina, H.; Mehes, K.; Hamel, B. C. J.; Otten, B. J.; Hergersberg,M.; Werder, E.; Shoenle, E.; Schinzel, A.: Uniparental disomy 7 inSilver- Russell syndrome and primordial growth retardation. Hum. Molec.Genet. 4:

583- 587, 1995.

GAM3027 242 MEST Lefebvre, L.; Viville, S.; Barton, S. C.; Ishino, F.; Keverne,E. B.; Surani, 3 A c
M. A.: Abnormal maternal behaviour and growth retardationassociated with
loss of the imprinted gene Mest. Nature Genet. 20:163- 169, 1998.

GAM3027 242 MEST Lefebvre, L.; Viville, S.; Barton, S. C.; Ishino, F.; Surani, M.A.: Genomic 3 A c
structure and parent- of- origin- specific methylation ofPeg1. Hum. Molec.
Genet. 6: 1907- 1915, 1997.

GAM3027 242 MEST Nishita, Y.; Yoshida, I.; Sado, T.; Takagi, N.: Genomic imprintingand 3 A c
chromosomal localization of the human MEST gene. Genomics 36:539- 542, 1996.

GAM3027 242 MEST Riesewijk, A. M.; Blagitko, N.; Schinzel, A. A.; Hu, L.; Schulz,U.; Hamel, 3 A c
B. C. J.; Ropers, H.- H.; Kalscheuer, V. M.: Evidence againsta major role of
PEG1/MEST Silver- Russell syndrome. Europ. J. Hum.Genet. 6: 114- 120, 1998.

GAM3027 242 MEST Riesewijk, A. M.; Hu, L.; Schulz, U.; Tariverdian, G.; Hoglund,P.; Kere, J.; 3 A c
Ropers, H.- H.; Kalscheuer, V. M.: Monoallelic expressionof human PEG1/MEST
is paralleled by parent- specific methylation infetuses. Genomics 42: 236-
244, 1997.

GAM3027 242 MEST Sado, T.; Nakajima, N.; Tada, M.; Takagi, N.: A novel mesoderm- specificcDNA 3 A c
isolated from a mouse embryonal carcinoma cell line. Dev. GrowthDiffer. 35:
551- 560, 1993.

GAM3027 242 NEK2 Arama, E.; Yanai, A.; Kilfin, G.; Bernstein, A.; Motro, B.: MurineNIMA- 3 A c
related kinases are expressed in patterns suggesting distinctfunctions in
gametogenesis and a role in the nervous system. Oncogene 16:1813- 1823,
1998.

GAM3027 242 NEK2 Fry, A. M.; Meraldi, P.; Nigg, E. A.: A centrosomal function forthe human 3 A c
Nek2 protein kinase, a member of the NIMA family of cellcycle regulators.
EMBO J. 17: 470- 481, 1998.

GAM3027 242 NEK2 Schultz, S. J.; Fry, A. M.; Sutterlin, C.; Ried, T.; Nigg, E. A.: Cell 3 A c
cycle- dependent expression of Nek2, a novel human protein kinaserelated to
the NIMA mitotic regulator of Aspergillus nidulans. CellGrowth Diff. 5: 625-
635, 1994.

GAM3027 242 NEK2 Schultz, S. J.; Nigg, E. A.: Identification of 21 novel humanprotein 3 A c
kinases, including 3 members of a family related to the cellcycle regulator
nimA of Aspergillus nidulans. Cell Growth Diff. 4:821- 830, 1993.

GAM3027 242 PPP2R5C McCright, B.; Brothman, A. R.; Virshup, D. M.: Assignment of humanprotein 3 A c
phosphatase 2A regulatory subunit genes B56- alpha, B56- beta,B56- gamma,
B56- delta, and B56- epsilon (PPP2R5A- - PPP2R5E), highly expressedin muscle
and brain, to chromosome regions 1q41, 11q12, 3p21, 6p21.1,and 7p11.2- to-
p12. Genomics 36: 168- 170, 1996.

GAM3027 242 PPP2R5C McCright, B.; Virshup, D. M.: Identification of a new family ofprotein 3 A c
phosphatase 2A regulatory subunits. J. Biol. Chem. 270:26123- 26128, 1995.

GAM3027 242 PPP2R5C Muneer, S.; Ramalingam, V.; Wyatt, R.; Schultz, R. A.; Minna, J.D.; 3 A c
Kamibayashi, C.: Genomic organization and mapping of the geneencoding the
PP2A B56- gamma regulatory subunit. Genomics 79: 344- 348,2002.

GAM3027 242 RAB30 Chen, D.; Guo, J.; Miki, T.; Tachibana, M.; Gahl, W. A.: Molecularcloning of 3 A c
two novel rab genes from human melanocytes. Gene 174:129- 134, 1996.

GAM3027 242 RAB30 Scott, A. F.: Personal Communication. Baltimore, Md. 2/26/2001. 3 A c

GAM3027 242 RFXAP Durand, B.; Sperisen, P.; Emery, P.; Barras, E.; Zufferey, M.;Mach, B.; 3 A c
Reith, W.: RFXAP, a novel subunit of the RFX DNA bindingcomplex is mutated
in MHC class II deficiency. EMBO J. 16: 1045- 1055,1997.

GAM3027 242 RFXAP Mach, B.: Personal Communication. Geneva, Switzerland 10/28/1998. 3 A c

GAM3027 242 RFXAP Mach, B.; Steimle, V.; Martinez- Soria, E.; Reith, W.: Regulationof MHC class II genes: lessons from a disease. Annu. Rev. Immun. 14:301- 331, 1996. 3 A c

GAM3027 242 RFXAP Nekrep, N.; Jabrane- Ferrat, N.; Peterlin, B. M.: Mutations inthe bare lymphocyte syndrome define critical steps in the assemblyof the regulatory factor X complex. Molec. Cell Biol. 20: 4455- 4461,2000. 3 A c

GAM3027 242 RFXAP Schwartz, R. S.: The case of the bare lymphocyte syndrome: trackingdown faulty transcription factors. (Editorial) New Eng. J. Med. 337:781- 783, 1997. 3 A c

GAM3027 242 RFXAP Steimle, V.; Durand, B.; Barras, E.; Zufferey, M.; Hadam, M. R.;Mach, B.; Reith, W.: A novel DNA binding- regulatory factor is mutatedin primary MHC class II deficiency (bare lymphocyte syndrome). GenesDev. 9: 1021- 1032, 1995. 3 A c

GAM3027 242 RFXAP Touraine, J. L.; Betuel, H.: Immunodeficiency diseases and expressionof HLA antigens. Hum. Immun. 2: 147- 153, 1981. 3 A c

GAM3027 242 RFXAP Touraine, J. L.; Betuel, H.; Souillet, G.; Jeune, M.: Combinedimmunodeficiency disease associated with absence of cell- surface HLA- Aand - B antigens. J. Pediat. 93: 47- 51, 1978. 3 A c

GAM3027 242 RFXAP Villard, J.; Lisowska- Grospierre, B.; van den Elsen, P.; Fischer,A.; Reith, W.; Mach, B.: Mutation of RFXAP, a regulator of MHC classII genes, in primary MHC class II deficiency. New Eng. J. Med. 337:748- 753, 1997. 3 A c

GAM3027 242 RNGTT Pillutla, R. C.; Shimamoto, A.; Furuichi, Y.; Shatkin, A. J.:Human mRNA capping enzyme (RNGTT) and cap methyltransferase (RNMT)map to 6q16 and 18p11.22- p11.23, respectively. Genomics 54: 351- 353,1998. 3 A c

GAM3027 242 RNGTT Tsukamoto, T.; Shibagaki, Y.; Murakoshi, T.; Suzuki, M.; Nakamura,A.; Gotoh, H.; Mizumoto, K.: Cloning and characterization of twohuman cDNAs encoding the mRNA capping enzyme. Biochem. Biophys. Res.Commun. 243: 101- 108, 1998. 3 A c

GAM3027 242 RNGTT Yamada- Okabe, T.; Doi, R.; Shimmi, O.; Arisawa, M.; Yamada- Okabe,H.: Isolation and characterization of a human cDNA for mRNA 5- prime-cappingenzyme. Nucleic Acids Res. 26: 1700- 1706, 1998. 3 A c

GAM3027 242 RNGTT Yue, Z.; Maldonado, E.; Pillutla, R.; Cho, H.; Reinberg, D.; Shatkin,A. J.: Mammalian capping enzyme complements mutant Saccharomycescerevisiae lacking mRNA guanylyltransferase and selectively bindsthe elongating form of RNA polymerase II. Proc. Nat. Acad. Sci. 94:12898- 12903, 1997. 3 A c

GAM3027 242 SLC7A6 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 3 A c

GAM3027 242 SLC7A6 Torrents, D.; Estevez, R.; Pineda, M.; Fernandez, E.; Lloberas,J.; Shi, Y.- B.; Zorzano, A.; Palacin, M.: Identification and characterizationof a membrane protein (y(+)L amino acid transporter- 1) that associateswith 4F2hc to encode the amino acid transport activity y(+)L: a candidategene for lysinuric protein intolerance. J. Biol. Chem. 273: 32437- 32445,1998. 3 A c

GAM3027 242 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994. 3 A c

GAM3027 242 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human 3 A c

synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM3027 242 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 3 A c
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand
characterization of the mouse homolog of SYT, a gene implicatedin the
development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM3027 242 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 3 A c
G.: Mapping and characterization of the mouse and humanSS18 genes, two human
SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-
319, 2001.

GAM3027 242 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 A c
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene
family with several members transcribed in normaltestis and human cancer.
Int. J. Cancer 72: 965- 971, 1997.

GAM3027 242 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 A c
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand
prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM3027 242 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 A c
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J.
Nat. Cancer Inst. 91: 974- 975, 1999.

GAM3027 242 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 A c
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX
synovial sarcoma translocation proteins and co- localizationwith the SNF
protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM3027 242 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 A c
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in
synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM3027 242 TPK1 Nosaka, K.; Onozuka, M.; Kakazu, N.; Hibi, S.; Nishimura, H.; Nishino,H.; 3 A c
Abe, T.: Isolation and characterization of a human thiamine
pyrophosphokinasecDNA. Biochem. Biophys. Acta 1517: 293- 297, 2001.

GAM3027 242 TPK1 Nosaka, K.; Onozuka, M.; Nishino, H.; Nishimura, H.; Kawasaki,Y.; Ueyama, 3 A c
H.: Molecular cloning and expression of a mouse thiaminpyrophosphokinase
cDNA. J. Biol. Chem. 274: 34129- 34133, 1999.

GAM3027 242 TPK1 Zhao, R.; Gao, F.; Goldman, I. D.: Molecular cloning of humanthiamin 3 A c
pyrophosphokinase. Biochim. Biophys. Acta 1517: 320- 322,2001.

GAM3027 242 TRIM9 Li, Y.; Chin, L.- S.; Weigel, C.; Li, L.: Spring, a novel RINGfinger protein 3 A c
that regulates synaptic vesicle exocytosis. J. Biol.Chem. 276: 40824- 40833,
2001.

GAM3027 242 TRIM9 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; 3 A c
Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci,
S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell
compartments. EMBO J. 20: 2140- 2151, 2001.

GAM3229 221 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- 3 C c
glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to
chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989.

GAM3229 221 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion 3 C c
data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract)
Cytogenet. Cell Genet. 51: 994 only, 1989.

GAM3229 221 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma 3 C c
alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple
method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.

GAM3229 221 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986. 3 C c

GAM3229 221 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988. 3 C c

GAM3229 221 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999. 3 C c

GAM3229 221 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 C c

GAM3229 221 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999. 3 C c

GAM3229 221 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664- 1666, 1999. 3 C c

GAM3229 221 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 3 C b

GAM3229 221 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994. 3 C b

GAM3229 221 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: Chromosomal mapping of human adenylyl cyclase genestype III, type V and type VI. Hum. Genet. 94: 69- 73, 1994. 3 C b

GAM3229 221 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001. 3 C b

GAM3229 221 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001. 3 C b

GAM3229 221 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998. 3 C b

GAM3229 221 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: Identificationand characterization of STK12/Aik2: a human gene related to auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147- 152,1998. 3 C b

GAM3229 221 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism, OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001. 3 C b

GAM3229 221 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand characterization of genes associated with chromosome- 6 mediatedtumor suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996. 3 C b

GAM3229 221 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a novel non- lens member of the beta- gamma- crystallin superfamily,is associated with the control of tumorigenicity in human malignantmelanoma. Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997. 3 C b

GAM3229 221 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA cloning, expression, subcellular localization, and chromosomalassignment of mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem. Biophys. Res. Commun. 244: 285- 292, 1998. 3 C b

GAM3229 221 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof the aurora- and Ipl1- like midbody- associated protein mitotic kinasein human cancer cells. Cancer Res. 58: 4811- 4816, 1998. 3 C b

GAM3229 221 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian Genome 9: 715- 720, 1998. 3 C b

GAM3229 221 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human melanoma cell lines controlled by introduction of human chromosome6. Science 247: 568- 571, 1990. 3 C b

GAM3229 221 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89: 3962- 3966,1992. 3 C c

GAM3229 221 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat. Acad. Sci. 96: 4378- 4383, 1999. 3 C c

GAM3229 221 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988. 3 C c

GAM3229 221 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990. 3 C c

GAM3229 221 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 (CED- 4 homolog) regulates programmed cell death in mammaliandevelopment. Cell 94: 727- 737, 1998. 3 C b

GAM3229 221 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749, 1999. 3 C b

GAM3229 221 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248- 258, 2000. 3 C b

GAM3229 221 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 deficiency and neural tube closure defects are found in fogmice. Proc. Nat. Acad. Sci. 98: 9683- 9687, 2001. 3 C b

GAM3229 221 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic 3 C b

protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253, 1999.

GAM3229 221 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002. 3 C b

GAM3229 221 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001. 3 C b

GAM3229 221 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998. 3 C b

GAM3229 221 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998. 3 C b

GAM3229 221 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 3 C b

GAM3229 221 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 C c

GAM3229 221 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 C c

GAM3229 221 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 C c

GAM3229 221 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and Drosophila. Genomics 26: 101- 106, 1995. 3 C b

GAM3229 221 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer protein delta- COP, encoded by the archain gene, is conservedacross diverse eukaryotes. Mammalian Genome 7: 784- 786, 1996. 3 C b

GAM3229 221 ARHGEF7 Bagrodia, S.; Taylor, S. J.; Jordon, K. A.; Van Aelst, L.; Cerione,R. A.: A novel regulator of p21- activated kinases. J. Biol. Chem. 273:23633- 23636, 1998. 3 C c

GAM3229 221 ARHGEF7 Manser, E.; Loo, T.- H.; Koh, C.- G.; Zhao, Z.- S.; Chen, X.- Q.; Tan,L.; Tan, I.; Leung, T.; Lim, L.: PAK kinases are directly coupledto the PIX family of nucleotide exchange factors. Molec. Cell 1:183- 192, 1998. 3 C c

GAM3229 221 ARHGEF7 Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 3 C c

GAM3229 221 ARHGEF7 Oh, W. K.; Yoo, J. C.; Jo, D.; Song, Y. H.; Kim, M. G.; Park, D.: Cloning of a SH3 domain- containing proline- rich protein, p85SPR,and its localization in focal adhesion. Biochem. Biophys. Res. Commun. 235:794- 798, 1997. 3 C c

GAM3229 221 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; 3 C b
Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the
beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990.

GAM3229 221 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: 3 C b
Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11
near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec.
Genet. 16: 401- 405, 1990.

GAM3229 221 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K- 3 C b
ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics
6:697- 699, 1990.

GAM3229 221 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: 3 C b
Identification of a putative isoform of the Na,K- ATPase beta
subunit:primary structure and tissue- specific expression. J. Biol. Chem.
164:4613- 4618, 1989.

GAM3229 221 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: 3 C b
Identification of a cDNA clone specific for the neural adhesionmolecule
AMOG. J. Neurosci. Res. 22: 113- 119, 1989.

GAM3229 221 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re- 3 C c
evaluation of 'reactive lymphoid hyperplasia of the uvea':
animmunohistochemical and molecular analysis of 10 cases. Ophthalmology
107:151- 158, 2000.

GAM3229 221 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 3 C c
mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999.

GAM3229 221 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. 3 C c
J.Clin. Path. 48: 395- 397, 1995.

GAM3229 221 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; 3 C c
Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T.
W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of
NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001.

GAM3229 221 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; 3 C c
Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not
its cellular homologue, activates NF- kappa- B transcriptionfactor and c-
Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999.

GAM3229 221 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- 3 C c
Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.;
Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in
t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types
Cell 96: 35- 45, 1999.

GAM3229 221 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic 3 C c
study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer
Genet. Cytogenet. 58: 35- 38, 1992.

GAM3229 221 BDKRB1 Bachvarov, D. R.; Hess, J. F.; Menke, J. G.; Larrivee, J.- F.; Marceau,F.: 3 C c
Structure and genomic organization of the human B(1) receptorgene for kinins
(BDKRB1). Genomics 33: 374- 381, 1996.

GAM3229 221 BDKRB1 Chai, K. X.; Ni, A.; Wang, D.; Ward, D. C.; Chao, J.; Chao, L.: Genomic DNA 3 C c
sequence, expression, and chromosomal localization ofthe human B1 bradykinin
receptor gene BDKRB1. Genomics 31: 51- 57,1996.

GAM3229 221 BDKRB1 MacNeil, T.; Bierilo, K. K.; Menke, J. G.; Hess, J. F.: Cloningand 3 C c
pharmacological characterization of a rabbit bradykinin B- 1 receptor.
Biochim.Biophys. Acta 1264: 223- 228, 1995.

GAM3229 221 BDKRB1 Menke, J. G.; Borkowski, J. A.; Bierilo, K. K.; MacNeil, T.; Derrick,A. W.; 3 C c
Schneck, K. A.; Ransom, R. W.; Strader, C. D.; Linemeyer, D.L.; Hess, J. F.:
Expression cloning of a human B1 bradykinin receptor. J.Biol. Chem. 269:
21583- 21586, 1994.

GAM3229 221 BDKRB1 Yang, X.; Polgar, P.: Genomic structure of the human bradykininB(1) receptor 3 C c
gene and preliminary characterization of its regulatoryregions. Biochem.
Biophys. Res. Commun. 222: 718- 725, 1996.

GAM3229 221 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 C c
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM3229 221 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 C c
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM3229 221 CAPN5 Dear, N.; Matena, K.; Vingron, M.; Boehm, T.: A new subfamilyof vertebrate 3 C c
calpains lacking a calmodulin- like domain: implicationsfor calpain
regulation and evolution. Genomics 45: 175- 184, 1997.

GAM3229 221 CAPN5 Mugita, N.; Kumura, Y.; Ogawa, M.; Saya, H.; Nakao, M.: Identificationof a 3 C c
novel, tissue- specific calpain htra- 3; a human homologue of
theCaenorhabditis elegans sex determination gene. Biochem. Biophys.Res.
Commun. 239: 845- 850, 1997.

GAM3229 221 CASP10 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 C b
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM3229 221 CASP10 Park, W. S.; Lee, J. H.; Shin, M. S.; Park, J. Y.; Kim, H. S.;Lee, J. H.; 3 C b
Kim, Y. S.; Lee, S. N.; Xiao, W.; Park, C. H.; Lee, S.H.; Yoo, N. J.; Lee,
J. Y.: Inactivating mutations of the caspase- 10gene in gastric cancer.
Oncogene 21: 2919- 2925, 2002.

GAM3229 221 CASP10 Shin, M. S.; Kim, H. S.; Kang, C. S.; Park, W. S.; Kim, S. Y.;Lee, S. N.; 3 C b
Lee, J. H.; Park, J. Y.; Jang, J. J.; Kim, C. W.; Kim,S. H.; Lee, J. Y.;
Yoo, N. J.; Lee, S. H.: Inactivating mutationsof CASP10 gene in non- Hodgkin
lymphomas. Blood 99: 4094- 4099, 2002.

GAM3229 221 CASP10 Vincenz, C.; Dixit, V. M.: Fas- associated death domain proteininterleukin- 3 C b
1- beta- converting enzyme 2 (FLICE2), an ICE/Ced- 3 homologue,is proximally
involved in CD95- and p55- mediated death signaling. J.Biol. Chem. 272:
6578- 6583, 1997.

GAM3229 221 CASP10 Wang, J.; Chun, H. J.; Wong, W.; Spencer, D. M.; Lenardo, M. J.: Caspase- 10 3 C b
is an initiator caspase in death receptor signaling. Proc.Nat. Acad. Sci.
98: 13884- 13888, 2001.

GAM3229 221 CASP10 Wang, J.; Zheng, L.; Lobito, A.; Chan, F. K.; Dale, J.; Sneller,M.; Yao, X.; 3 C b
Puck, J. M.; Straus, S. E.; Lenardo, M. J.: Inheritedhuman caspase 10
mutations underlie defective lymphocyte and dendriticcell apoptosis in
autoimmune lymphoproliferative syndrome type II. Cell 98:47- 58, 1999.

GAM3229 221 CHEK1 Chen, P.; Luo, C.; Deng, Y.; Ryan, K.; Register, J.; Margosiak,S.; Tempczyk- 3 C c
Russell, A.; Nguyen, B.; Myers, P.; Lundgren, K.; Kan,C.- C.; O'Connor, P.
M.: The 1.7- angstrom crystal structure of humancell cycle checkpoint kinase
Chk1: implications for Chk1 regulation. Cell 100:681- 692, 2000.

GAM3229 221 CHEK1 Flaggs, G.; Plug, A. W.; Dunks, K. M.; Mundt, K. E.; Ford, J. C.;Quiggle, M. 3 C c
R. E.; Taylor, E. M.; Westphal, C. H.; Ashley, T.; Hoekstra,M. F.; Carr, A.

M.: Atm- dependent interactions of a mammalian Chk1homolog with meiotic chromosomes. Curr. Biol. 7: 977- 986, 1997.

GAM3229 221 CHEK1 Liu, Q.; Guntuku, S.; Cui, X.- S.; Matsuoka, S.; Cortez, D.; Tamai,K.; Luo, 3 C c
G.; Carattini- Rivera, S.; DeMayo, F.; Bradley, A.; Donehower,L. A.;
Elledge, S. J.: Chk1 is an essential kinase that is regulatedby Atr and
required for the G2/M DNA damage checkpoint. Genes Dev. 14:1448- 1459, 2000.

GAM3229 221 CHEK1 Sanchez, Y.; Wong, C.; Thoma, R. S.; Richman, R.; Wu, Z.; Piwnica- Worms,H.; 3 C c
Elledge, S. J.: Conservation of the Chk1 checkpoint pathway inmammals:
linkage of DNA damage to Cdk regulation through Cdc25. Science 277:1497-
1501, 1997.

GAM3229 221 CHEK1 Takai, H.; Tominaga, K.; Motoyama, N.; Minamishima, Y. A.; Nagahama,H.; 3 C c
Tsukiyama, T.; Ikeda, K.; Nakayama, K.; Nakanishi, M.; Nakayama,K.: Aberrant
cell cycle checkpoint function and early embryonic deathin Chk1- /- mice.
Genes Dev. 14: 1439- 1447, 2000.

GAM3229 221 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, 3 C b
G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.;
Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.;
Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for
Muckle- Wells syndrome and familial cold urticaria:a novel mutation
underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002.

GAM3229 221 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, 3 C b
E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile
neurological cutaneous and articular syndromeis caused by mutations in
CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes.
Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM3229 221 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. 3 C b
D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes
familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature
Genet. 29: 301- 305, 2001.

GAM3229 221 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 C b
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM3229 221 CLECSF11 Arce, I.; Roda- Navarro, P.; Montoya, M. C.; Hernanz- Falcon, P.;Puig- 3 C c
Kroger, A.; Fernandez- Ruiz, E.: Molecular and genomic characterizationof
human DLEC, a novel member of the C- type lectin receptor gene
familypreferentially expressed on monocyte- derived dendritic cells.
Europ.J. Immun. 31: 2733- 2740, 2001.

GAM3229 221 CLECSF11 Dzionek, A.; Sohma, Y.; Nagafune, J.; Cella, M.; Colonna, M.; Facchetti,F.; 3 C c
Gunther, G.; Johnston, I.; Lanzavecchia, A.; Nagasaka, T.; Okada,T.; Vermi,
W.; Winkels, G.; Yamamoto, T.; Zysk, M.; Yamaguchi, Y.;Schmitz, J.: BDCA- 2,
a novel plasmacytoid dendritic cell- specifictype II C- type lectin,
mediates antigen capture and is a potent inhibitorof interferon alpha/beta
induction. J. Exp. Med. 194: 1823- 1834,2001.

GAM3229 221 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 C b
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.:
Identification of a novel, dendritic cell- associated molecule,dectin- 1, by
subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM3229 221 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 3 C b

GAM3229 221 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 3 C b

GAM3229 221 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 3 C b

GAM3229 221 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359, 1997. 3 C c

GAM3229 221 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix Biol. 18: 319- 324, 1999. 3 C c

GAM3229 221 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of the gene encoding human cartilage associatedprotein (CRTAP). Cytogenet. Cell Genet. 87: 191- 194, 1999. 3 C c

GAM3229 221 CST Ishida, N.; Ito, M.; Yoshioka, S.; Sun- Wada, G.- H.; Kawakita, M.: Functional expression of human Golgi CMP- sialic acid transporterin the Golgi complex of a transporter- deficient Chinese hamster ovarycell mutant. J. Biochem. 124: 171- 178, 1998. 3 C b

GAM3229 221 CST Ishida, N.; Miura, N.; Yoshioka, S.; Kawakita, M.: Molecular cloningand characterization of a novel isoform of the human UDP- galactosetransporter, and of related complementary DNAs belonging to the nucleotide- sugartransporter gene family. J. Biochem. 120: 1074- 1078, 1996. 3 C b

GAM3229 221 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996. 3 C b

GAM3229 221 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989. 3 C b

GAM3229 221 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000. 3 C b

GAM3229 221 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. L.: The contribution of genetically determined oxidationstatus to inter- individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983. 3 C b

GAM3229 221 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986. 3 C b

GAM3229 221 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. Endocr. 3: 1399- 1408, 1989. 3 C b

GAM3229 221 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human 3 C b

P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the 3- prime nontranslated region, and localization ofgene to chromosome 15. J. Exp. Path. 3: 1- 17, 1987.

GAM3229 221 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996. 3 C b

GAM3229 221 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 C b

GAM3229 221 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 3 C b

GAM3229 221 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O- deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 3 C b

GAM3229 221 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva- based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 3 C b

GAM3229 221 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002. 3 C b

GAM3229 221 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 3 C c

GAM3229 221 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 C c

GAM3229 221 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 3 C c

GAM3229 221 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 C b

GAM3229 221 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 C b

GAM3229 221 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4- alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 C b

GAM3229 221 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000. 3 C c

GAM3229 221 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461- 3 C c

8466, 1998.

GAM3229 221 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997. 3 C c

GAM3229 221 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998. 3 C c

GAM3229 221 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. W.: Chromosomal localization and racial distributionof the polymorphic human dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352, 1988. 3 C c

GAM3229 221 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies three RFLPs. Nucleic Acids Res. 15: 5501 only,1987. 3 C c

GAM3229 221 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: Chromosomal localization and racial distribution of the polymorphichDHFR- psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985. 3 C c

GAM3229 221 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; Nienhuis, A. W.: Chromosomal organization of the human dihydrofolatereductase genes: dispersion, selective amplification and a novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984. 3 C c

GAM3229 221 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in dihydrofolatereductase that confer resistance to methotrexate: potential for clinicalapplication. Hum. Mutat. 11: 259- 263, 1998. 3 C c

GAM3229 221 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: Intronless human dihydrofolate reductase genes are derivedfrom processed RNA molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982. 3 C c

GAM3229 221 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association with variation in protein structure. Science 220: 1125- 1129,1983. 3 C c

GAM3229 221 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 757 and 807- 812, 1975. 3 C c

GAM3229 221 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5. Molec. Cell. Biol. 4: 2010- 2016, 1984. 3 C c

GAM3229 221 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater-Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med. 310: 789- 790, 1984. 3 C c

GAM3229 221 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986. 3 C c

GAM3229 221 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: Human dihydrofolate reductase gene is located in chromosome 5and is unlinked to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984. 3 C c

GAM3229 221 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human dihydrofolate reductase gene to band q23 of chromosome 5and of related pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85, 1985. 3 C c

GAM3229 221 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; Attardi, G.: Chromosomal location of the normal human DHFRgene and of its 3 C c

amplified copies in methotrexate resistant cell variants.(Abstract) Cytogenet. Cell Genet. 37: 534 only, 1984.

GAM3229 221 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 10/7/1983. 3 C c

GAM3229 221 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: Amplification of the human dihydrofolate reductase gene viadouble minutes is initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000. 3 C c

GAM3229 221 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976. 3 C c

GAM3229 221 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)-formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967. 3 C c

GAM3229 221 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, D. J.; Muir, W. J.: Schizophrenia and affective disorders- -cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001. 3 C c

GAM3229 221 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 355:771- 772, 2000. 3 C c

GAM3229 221 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 3 C c

GAM3229 221 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 3 C c

GAM3229 221 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000. 3 C c

GAM3229 221 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990. 3 C c

GAM3229 221 DUSP7 Groom, L. A.; Sneddon, A. A.; Alessi, D. R.; Dowd, S.; Keyse, S.M.: Differential regulation of the MAP, SAP and RK/p38 kinases byPyst1, a novel cytosolic dual- specificity phosphatase. EMBO J. 15:3621- 3632, 1996. 3 C c

GAM3229 221 DUSP7 Muda, M.; Boschert, U.; Dickinson, R.; Martinou, J.- C.; Martinou,I.; Camps, M.; Schlegel, W.; Arkinstall, S.: MKP- 3, a novel cytosolicprotein- tyrosine phosphatase that exemplifies a new class of mitogen- activatedprotein kinase phosphatase. J. Biol. Chem. 271: 4319- 4326, 1996. 3 C c

GAM3229 221 DUSP7 Smith, A.; Price, C.; Cullen, M.; Muda, M.; King, A.; Ozanne, B.;Arkinstall, S.; Ahsworth, A.: Chromosomal localization of three humandual specificity phosphatase genes (DUSP4, DUSP6, and DUSP7). Genomics 42:524- 527, 1997. 3 C c

GAM3229 221 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.: Neurodevelopmental delay, motor abnormalities and cognitive deficitsin transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001. 3 C b

GAM3229 221 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the 3 C b

Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262-265, 1997.

GAM3229 221 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A 3 C b potassium channel mutation in weaver mice implicates membraneexcitability in granule cell differentiation. Nature Genet. 11:126- 129, 1995.

GAM3229 221 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; 3 C b Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk gene from 'the Down syndrome critical region' of chromosome 21. Biochem.Biophys. Res. Commun. 225: 92- 99, 1996.

GAM3229 221 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, 3 C b M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.; Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in transgenic mice implicates minibrain in learningdefects associated with Down syndrome. Nature Genet. 16: 28- 36,1997.

GAM3229 221 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to 3 C b chromosome 16, localizes to the nucleus, and can form multimers. Biochem.Biophys. Res. Commun. 231: 640- 644, 1997.

GAM3229 221 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; 3 C b Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.; Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the Drosophila minibrain gene: human homologue maps to 21q22.2in the Down syndrome 'critical region.' Genomics 38: 331- 339, 1996.

GAM3229 221 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, 3 C b I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein kinase family involved in postembryonic neurogenesisin Drosophila. Neuron 14: 287- 301, 1995.

GAM3229 221 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for 3 C c tissue factor (coagulation factor III) is localized onhuman chromosome 1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985.

GAM3229 221 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to 3 C c human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985.

GAM3229 221 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional 3 C c assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat. Cell Molec. Genet. 14: 407- 410, 1988.

GAM3229 221 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional 3 C c analysis of the human tissue factor promoter and inductionby serum. Proc. Nat. Acad. Sci. 87: 2254- 2258, 1990.

GAM3229 221 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: 3 C c Completesequence of the human tissue factor gene, a highly regulated cellularreceptor that initiates the coagulation protease cascade. Biochemistry 28:1755- 1762, 1989.

GAM3229 221 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; 3 C c Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand mapping of RFLPs for human tissue factor (HTF) to chromosome 1p. NucleicAcids Res. 15: 9098 only, 1987.

GAM3229 221 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; 3 C c Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA sequenceand chromosome localization of the gene. Biochemistry 26: 5234-5238,1987.

GAM3229 221 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; 3 C c

Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA clones coding for human tissue factor: primary structureof the protein and cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987.

GAM3229 221 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of 3 C c tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad. Sci. 94: 6922- 6926, 1997.

GAM3229 221 FABP2 Baier, L. J.; Sacchettini, J. C.; Knowler, W. C.; Eads, J.; Paolisso,G.; 3 C c Tataranni, P. A.; Mochizuki, H.; Bennett, P. H.; Bogardus, C.;Prochazka, M.: An amino acid substitution in the human intestinalfatty acid binding protein is associated with increased fatty acidbinding, increased fat oxidation, and insulin resistance. J. Clin.Invest. 95: 1281- 1287, 1995.

GAM3229 221 FABP2 Carlsson, M.; Orho- Melander, M.; Hedenbro, J.; Almgren, P.; Groop,L. C.: 3 C c The T54 allele of the intestinal fatty acid- binding protein2 is associated with a parental history of stroke. J. Clin. Endocr.Metab. 85: 2801- 2804, 2000.

GAM3229 221 FABP2 Georgopoulos, A.; Aras, O.; Tsai, M. Y.: Codon- 54 polymorphismof the fatty 3 C c acid- binding protein 2 gene is associated with elevationof fasting and postprandial triglyceride in type 2 diabetes. J. Clin.Endocr. Metab. 85: 3155- 3160, 2000.

GAM3229 221 FABP2 Hegele, R. A.; Harris, S. B.; Hanley, A. J. G.; Sadikian, S.; Connelly,P. 3 C c W.; Zinman, B.: Genetic variation of intestinal fatty acid- bindingprotein associated with variation in body mass in aboriginal Canadians. J.Clin. Endocr. Metab. 81: 4334- 4337, 1996.

GAM3229 221 FABP2 Polymeropoulos, M. H.; Rath, D. S.; Xiao, H.; Merril, C. R.: 3 C c Trinucleotiderepeat polymorphism at the human intestinal fatty acid binding proteingene (FABP2). Nucleic Acids Res. 18: 7198 only, 1991.

GAM3229 221 FABP2 Prochazka, M.; Lillioja, S.; Tait, J. F.; Knowler, W. C.; Mott,D. M.; 3 C c Spraul, M.; Bennett, P. H.; Bogardus, C.: Linkage of chromosomalmarkers on 4q with a putative gene determining maximal insulin actionin Pima Indians. Diabetes 42: 514- 519, 1993.

GAM3229 221 FABP2 Sipilainen, R.; Uusitupa, M.; Heikkinen, S.; Rissanen, A.; Laakso,M.: 3 C c Variants in the human intestinal fatty acid binding protein 2gene in obese subjects. J. Clin. Endocr. Metab. 82: 2629- 2632, 1997.

GAM3229 221 FABP2 Sparkes, R. S.; Mohandas, T.; Heinzmann, C.; Gordon, J. I.; Klisak,I.; 3 C c Zollman, S.; Sweetser, D. A.; Ragunathan, L.; Winokur, S.; Lusis,A. J.: Human fatty acid binding protein assignments intestinal to4q28- 4q31 and liver to 2p11. (Abstract) Cytogenet. Cell Genet. 46:697 only, 1987.

GAM3229 221 FABP2 Sweetser, D. A.; Birkenmeier, E. H.; Klisak, I. J.; Zollman, S.;Sparkes, R. 3 C c S.; Mohandas, T.; Lusis, A. J.; Gordon, J. I.: The humanand rodent intestinal fatty acid binding protein genes: a comparativeanalysis of their structure, expression, and linkage relationships. J.Biol. Chem. 262: 16060- 16071, 1987.

GAM3229 221 FABP2 Weber, J. L.; Kwitek, A. E.; May, P. E.; Polymeropoulos, M.:Dinucleotide 3 C c repeat polymorphism at the D12S43 locus. Nucleic AcidsRes. 18: 4637 only, 1990.

GAM3229 221 FABP2 Weber, J. L.; May, P. E.: Abundant class of human DNA polymorphismswhich can 3 C c be typed using the polymerase chain reaction. Am. J. Hum.Genet. 44: 388- 396, 1989.

GAM3229 221 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: 3 C b

Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995.

GAM3229 221 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 3 C b

GAM3229 221 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665- 1672, 1990. 3 C b

GAM3229 221 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681- 1685, 1993. 3 C b

GAM3229 221 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 3 C b

GAM3229 221 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 3 C b

GAM3229 221 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 3 C b

GAM3229 221 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001. 3 C b

GAM3229 221 FHIT Barnes, L. D.; Garrison, P. N.; Siprashvili, Z.; Guranowski, A.;Robinson, A. K.; Ingram, S. W.; Croce, C. M.; Ohta, M.; Huebner, K.: Fhit, a putative tumor suppressor in humans, is a dinucleoside 5- prime,5- tripleprime- P(1),P(3)- triphosphate hydrolase. Biochemistry 35: 11529- 11535,1996. 3 C c

GAM3229 221 FHIT Bernar, J.; Funderburk, S. J.; Sparkes, R. S.: The inducible fragilesite on chromosome 3. (Letter) Hum. Genet. 66: 373 only, 1984. 3 C c

GAM3229 221 FHIT Cohen, A. J.; Li, F. P.; Berg, S.; Marchetto, D. J.; Tsai, S.;Jacobs, S. C.; Brown, R. S.: Hereditary renal- cell carcinoma associatedwith chromosomal translocation. New Eng. J. Med. 301: 592- 595, 1979. 3 C c

GAM3229 221 FHIT Dumon, K. R.; Ishii, H.; Fong, L. Y. Y.; Zanesi, N.; Fidanza, V.;Mancini, R.; Vecchione, A.; Baffa, R.; Trapasso, F.; During, M. J.;Huebner, K.; Croce, C. M.: FHIT gene therapy prevents tumor developmentin Fhit- deficient mice. Proc. Nat. Acad. Sci. 98: 3346- 3351, 2001. 3 C c

GAM3229 221 FHIT Fong, L. Y. Y.; Fidanza, V.; Zanesi, N.; Lock, L. F.; Siracusa,L. D.; Mancini, R.; Siprashvili, Z.; Ottey, M.; Martin, S. E.; Druck,T.; McCue, P. A.; Croce, C. M.; Huebner, K.: Muir- Torre- like syndromein Fhit- deficient mice. Proc. Nat. Acad. Sci. 97: 4742- 4747, 2000. 3 C c

GAM3229 221 FHIT Gemmill, R. M.; West, J. D.; Boldog, F.; Tanaka, N.; Robinson,L. J.; Smith, D. I.; Li, F.; Drabkin, H. A.: The hereditary renalcell carcinoma 3;8 translocation fuses FHIT to a patched- related gene,TRC8. Proc. Nat. Acad. Sci. 95: 9572- 9577, 1998. 3 C c

GAM3229 221 FHIT Geurts, J. M.; Schoenmakers, E. F.; Roijer, E.; Stenman, G.; Vande Ven, W. J. M.: Expression of reciprocal hybrid transcripts ofHMGIC and FHIT in a pleomorphic adenoma of the parotid gland. CancerRes. 57: 13- 17, 1997. 3 C c

GAM3229 221 FHIT Inoue, H.; Ishii, H.; Alder, H.; Snyder, E.; Druck, T.; Huebner,K.; Croce, 3 C c

C. M.: Sequence of the FRA3B common fragile region: implicationsfor the mechanism of FHIT deletion. Proc. Nat. Acad. Sci. 94: 14584- 14589,1997.

GAM3229 221 FHIT Lee, S.- H.; Kim, W.- H.; Kim, H.- K.; Woo, K.- M.; Nam, H.- S.; Kim,H.- S.; Kim, J.- G.; Cho, M.- H.: Altered expression of the fragilehistidine triad gene in primary gastric adenocarcinomas. Biochem.Biophys. Res. Commun. 284: 850- 855, 2001. 3 C c

GAM3229 221 FHIT Markkanen, A.; Heinonen, K.; Knuutila, S.; de la Chapelle, A.: Methotrexate- induced increase in gap formation in human chromosomeband 3p14. Hereditas 96: 317- 319, 1982. 3 C c

GAM3229 221 FHIT Markkanen, A.; Knuutila, S.; de la Chapelle, A.: Inducible fragilesite on chromosome 3. (Letter) Hum. Genet. 65: 217 only, 1983. 3 C c

GAM3229 221 FHIT Morikawa, H.; Nakagawa, Y.; Hashimoto, K.; Niki, M.; Egashira,Y.; Hirata, I.; Katsu, K.; Akao, Y.: Frequent altered expressionof fragile histidine triad protein in human colorectal adenomas. Biochem.Biophys. Res. Commun. 278: 205- 210, 2000. 3 C c

GAM3229 221 FHIT Ohta, M.; Inoue, H.; Cotticelli, M. G.; Kastury, K.; Baffa, R.;Palazzo, J.; Siprashvili, Z.; Mori, M.; McCue, P.; Druck, T.; Croce,C. M.; Huebner, K.: The FHIT gene, spanning the chromosome 3p14.2fragile site and renal carcinoma- associated t(3;8) breakpoint, isabnormal in digestive tract cancers. Cell 84: 587- 597, 1996. 3 C c

GAM3229 221 FHIT Rassool, F. V.; Le Beau, M. M.; Shen, M.- L.; Neilly, M. E.; Espinosa,R., III; Ong, S. T.; Boldog, F.; Drabkin, H.; McCarroll, R.; McKeithan,T. W.: Direct cloning of DNA sequences from the common fragile siteregion at chromosome band 3p14.2. Genomics 35: 109- 117, 1996. 3 C c

GAM3229 221 FHIT Rudduck, C.; Franzen, G.: A new heritable fragile site on humanchromosome 3. Hereditas 98: 297- 299, 1983. 3 C c

GAM3229 221 FHIT Shi, Y.; Zou, M.; Farid, N. R.; Paterson, M. C.: Associationof FHIT (fragile histidine triad), a candidate tumour suppressor gene,with the ubiquitin-conjugating enzyme hUBC9. Biochem. J. 352: 443- 448,2000. 3 C c

GAM3229 221 FHIT Shiraishi, T.; Druck, T.; Mimori, K.; Flomenberg, J.; Berk, L.;Alder, H.; Miller, W.; Huebner, K.; Croce, C. M.: Sequence conservationat human and mouse orthologous common fragile regions, FRA3B/FHITand Fra14A2/Fhit. Proc. Nat. Acad. Sci. 98: 5722- 5727, 2001. 3 C c

GAM3229 221 FHIT Sozzi, G.; Veronese, M. L.; Negrini, M.; Baffa, R.; Cotticelli,M. G.; Inoue, H.; Tornielli, S.; Pilotti, S.; De Gregorio, L.; Pastorino,U.; Pierotti, M. A.; Ohta, M.; Huebner, K.; Croce, C. M.: The FHITgene at 3p14.2 is abnormal in lung cancer. Cell 85: 17- 26, 1996. 3 C c

GAM3229 221 FHIT Stein, C. K.; Glover, T. W.; Palmer, J. L.; Glisson, B. S.: Directcorrelation between FRA3B expression and cigarette smoking. GenesChromosomes Cancer 34: 333- 340, 2002. 3 C c

GAM3229 221 FHIT Virgilio, L.; Shuster, M.; Gollin, S. M.; Veronese, M. L.; Ohta,M.; Huebner, K.; Croce, C. M.: FHIT gene alterations in head andneck squamous cell carcinomas. Proc. Nat. Acad. Sci. 93: 9770- 9775,1996. 3 C c

GAM3229 221 FHIT Wang, N.; Perkins, K. L.: Involvement of band 3p14 in t(3;8)hereditary renal carcinoma. Cancer Genet. Cytogenet. 11: 479- 481,1984. 3 C c

GAM3229 221 FHIT Wegner, R.- D.: A new inducible fragile site on chromosome 3 (p14.2)in human lymphocytes. Hum. Genet. 63: 297- 298, 1983. 3 C c

GAM3229 221 FHIT Wegner, R.- D.: Reply to the letter of A. Markkanen, S. Knuutila,and A. de la Chapelle. (Letter) Hum. Genet. 65: 218 only, 1983. 3 C c

GAM3229 221 FHIT Zanesi, N.; Fidanza, V.; Fong, L. Y.; Mancini, R.; Druck, T.;Valtieri, M.; 3 C c

Rudiger, T.; McCue, P. A.; Croce, C. M.; Huebner, K.: The tumor spectrum in FHIT- deficient mice. Proc. Nat. Acad. Sci. 98:10250- 10255, 2001.

GAM3229 221 FSTL3 Bartholin, L.; Maguer- Satta, V.; Hayette, S.; Martel, S.; Gadoux,M.; 3 C c
Bertrand, S.; Corbo, L.; Lamadon, C.; Morera, A.- M.; Magaud, J.- P.;Rimokh, R.: FLRG, an activin- binding protein, is a new target ofTGF- beta transcription activation through Smad proteins. Oncogene 20:5409- 5419, 2001.

GAM3229 221 FSTL3 Hayette, S.; Gadoux, M.; Martel, S.; Bertrand, S.; Tigaud, I.;Magaud, J.- 3 C c
P.; Rimokh, R.: FLRG (follistatin- related gene), a newtarget of chromosomal rearrangement in malignant blood disorders. Oncogene 16:2949- 2954, 1998.

GAM3229 221 FSTL3 Rimokh, R.; Berger, F.; Delsol, G.; Charrin, C.; Bertheas, M. F.;Ffrench, 3 C c
M.; Garoscio, M.; Felman, P.; Coiffier, C.; Bryon, P. A.: Rearrangement and overexpression of the BCL- 1/PRAD- 1 gene in intermediatelymphocytic lymphomas and in t(11q13)- bearing leukemias. Blood 81:3063- 3067, 1993.

GAM3229 221 FSTL3 Tortoriello, D. V.; Sidis, Y.; Holtzman, D. A.; Holmes, W. E.;Schneyer, A. 3 C c
L.: Human follistatin- related protein: a structuralhomologue of follistatin with nuclear localization. Endocrinology 142:3426- 3434, 2001.

GAM3229 221 FSTL3 Tsuchida, K.; Arai, K. Y.; Kuramoto, Y.; Yamakawa, N.; Hasegawa,Y.; Sugino, 3 C c
H.: Identification and characterization of a novel follistatin- likeprotein as a binding protein for the TGF- beta family. J. Biol. Chem. 275:40788- 40796, 2000.

GAM3229 221 GAN Bomont, P.; Cavalier, L.; Blondeau, F.; Ben Hamida, C.; Belal,S.; Tazir, M.; 3 C c
Demir, E.; Topaloglu, H.; Korinthenberg, R.; Tuysuz,B.; Landrieu, P.; Hentati, F.; Koenig, M.: The gene encoding gigaxonin,a new member of the cytoskeletal BTB/kelch repeat family, is mutatedin giant axonal neuropathy. Nature Genet. 26: 370- 374, 2000.

GAM3229 221 GAN Bousquet, O.; Basseville, M.; Vila- Porcile, E.; Billette de Villemeur,T.; 3 C c
Hauw, J.- J.; Landrieu, P.; Portier, M.- M.: Aggregation of a subpopulationof vimentin filaments in cultured human skin fibroblasts derived frompatients with giant axonal neuropathy. Cell. Motil. Cytoskeleton 33:115- 129, 1996.

GAM3229 221 GAN Kuhlenbaumer, G.; Young, P.; Oberwittler, C.; Hunermund, G.; Schirmacher,A.; 3 C c
Domschke, K.; Ringelstein, B.; Stogbauer, F.: Giant axonal neuropathy(GAN): case report and two novel mutations in the gigaxonin gene. Neurology 58:1273- 1276, 2002. Note: Erratum: Neurology 58: 1444, 2002.

GAM3229 221 GAN Pena, S. D.: Giant axonal neuropathy: an inborn error of organizationof 3 C c
intermediate filaments. Muscle Nerve 5: 166- 172, 1982.

GAM3229 221 GAN Prineas, J. W.; Ouvrier, R. A.; Wright, R. G.; Walsh, J. C.; McLeod,J. G.: 3 C c
Giant axonal neuropathy: a generalized disorder of cytoplasmicmicrofilament formation. J. Neuropath. Exp. Neurol. 35: 458- 470,1976.

GAM3229 221 GAN Treiber- Held, S.; Budjarjo- Welim, H.; Riemann, D.; Richter, 3 C c
J.;Kretzschmar, H. A.; Hanefeld, F.: Giant axonal neuropathy: a generalizeddisorder of intermediate filaments with longitudinal grooves in thehair. Neuropediatrics 25: 89- 93, 1994.

GAM3229 221 GLO1 Bakker, E.; Pearson, P. L.; Meera Khan, P.; Schreuder, G. M. T.;Madan, K.: 3 C c
Orientation of major histocompatibility (MHC) genes relativeto the centromere of human chromosome 6. Clin. Genet. 15: 198- 202,1979.

GAM3229 221 GLO1 Bender, K.; Grzeschik, K. H.: Assignment of the genes for humanglyoxalase I 3 C c
to chromosome 6 and for human esterase D to chromosome13. Cytogenet. Cell Genet. 16: 93- 96, 1976.

GAM3229 221 GLO1 Beretta, M.; Schiliro, G.; Russo, A.; Barbujani, G.; Mazzetti,P.; Russo, G.; 3 C c
Barrai, I.: A new rare variant of the glyoxalase Isystem of the red cell:
GLO- Sicily. Am. J. Hum. Genet. 35: 1042- 1047,1983.

GAM3229 221 GLO1 Blanche, H.; Zoghbi, H. Y.; Jabs, E. W.; de Gouyon, B.; Zunec,R.; Dausset, 3 C c
J.; Cann, H. M.: A centromere- based genetic map of theshort arm of human
chromosome 6. Genomics 9: 420- 428, 1991.

GAM3229 221 GLO1 Carter, N. D.; West, C. M.; Bernard, J. M.; Farid, N. R.; Larsen,B.; 3 C c
Marshall, W. H.: Linkage of glyoxalase I and HLA in two
Newfoundlandcommunities. Hum. Hered. 28: 397- 400, 1978.

GAM3229 221 GLO1 Giblett, E. R.; Lewis, M.: Gene linkage studies on glyoxalaseI. Cytogenet. 3 C c
Cell Genet. 16: 313 only, 1976.

GAM3229 221 GLO1 Goldman, D.; O'Brien, S. J.; Lucas- Derse, S.; Dean, M.: Linkagemapping of 3 C c
human polymorphic proteins identified by two- dimensionalelectrophoresis.
Genomics 11: 875- 884, 1991.

GAM3229 221 GLO1 Hansen, H. E.; Eriksen, B.: HLA- GLO linkage analysis in 57 3 C c
informativefamilies. Hum. Hered. 29: 355- 360, 1979.

GAM3229 221 GLO1 Karlsson, S.; Arnason, A.; Jensson, O.: GLO polymorphism in Iceland.Hum. 3 C c
Hered. 30: 383- 385, 1980.

GAM3229 221 GLO1 Kavathas, P.; DeMars, R.: A new variant glyoxalase I allele thatis readily 3 C c
detectable in stimulated lymphocytes and lymphoblastoidcell lines but not in
circulating lymphocytes or erythrocytes. Am.J. Hum. Genet. 33: 935- 945,
1981.

GAM3229 221 GLO1 Kompf, J.; Bissbort, S.; Gussmann, S.; Ritter, H.: Polymorphismof red cell 3 C c
glyoxalase I (E.C.4.4.1.5), a new genetic marker in man:investigation of 169
mother- child combinations. Humangenetik 27:141- 143, 1975.

GAM3229 221 GLO1 Kompf, J.; Bissbort, S.; Ritter, H.: Red cell glyoxalase I 3 C c
(E.C.4.4.1.5):formal genetics and linkage relations. Humangenetik 28: 249-
251,1975.

GAM3229 221 GLO1 Kompf, J.; Siebert, G.; Ritter, H.; Heilbronner, H.; Schunter,F.; Wernet, 3 C c
P.; Gupta, D.; Moeller, H.: Data on linkage relationsbetween GLO and 21-
hydroxylase. Hum. Genet. 54: 419- 420, 1980.

GAM3229 221 GLO1 Meo, T.; Douglas, T.; Rijnbeek, A.- M.: Glyoxalase I polymorphismin the 3 C c
mouse: a new genetic marker linked to H- 2. Science 198:311- 313, 1977.

GAM3229 221 GLO1 Olaisen, B.; Gedde- Dahl, T., Jr.; Thorsby, E.: Localization ofthe human GLO 3 C c
gene locus. Hum. Genet. 32: 301- 304, 1976.

GAM3229 221 GLO1 Parr, C. W.; Bagster, I. A.; Welch, S. G.: Human red cell glyoxalaseI 3 C c
polymorphism. Biochem. Genet. 15: 109- 114, 1977.

GAM3229 221 GLO1 Reinsmoen, N. L.; Friend, P. S.; Miller, W. V.; Burgdorf, A.;Giblett, E. R.; 3 C c
Yunis, E. J.: Inheritance of recombinant HLA- GLOhaplotype suggesting the
gene sequence. Nature 267: 276- 278, 1977.

GAM3229 221 GLO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 C c
New York: Oxford Univ. Press (pub.) 1988.

GAM3229 221 GLO1 Rubinstein, P.; Suciu- Foca, N.: Glyoxalase 1: a possible 'null'allele. Hum. 3 C c
Hered. 29: 217- 220, 1979.

GAM3229 221 GLO1 Schimandle, C. M.; Vander Jagt, D. L.: Isolation and kineticanalysis of the 3 C c
multiple forms of glyoxalase- 1 from human erythrocytes.Arch. Biochem.
Biophys. 195: 261- 268, 1979.

GAM3229 221 GLO1 Sparkes, R. S.; Sparkes, M. C.; Crist, M.; Anderson, C. E.: GlyoxalaseI 3 C c
'null' allele in a new family: identification by abnormal segregationpattern
and quantitative assay. Hum. Genet. 64: 146- 147, 1983.

GAM3229 221 GLO1 Teng, Y. S.; Tan, S. G.; Lopez, C. G.: Red cell glyoxalase land placental soluble aconitase polymorphisms in the three major ethnicgroups of Malaysia. Jpn. J. Hum. Genet. 23: 211- 215, 1978. 3 C c

GAM3229 221 GLO1 Whittington, J. E.; Keats, B. J. B.; Jackson, J. F.; Currier,R. D.; Terasaki, P. I.: Linkage studies on glyoxalase I (GLO), pepsinogen(PG), spinocerebellar ataxia (SCA1), and HLA. Cytogenet. Cell Genet. 28:145- 150, 1980. 3 C c

GAM3229 221 GLO1 Ziegler, A.; Fonatsch, C.; Kompf, J.: Mapping of the locus forglyoxalase 1 (GLO1) on human chromosome 6 using mutant cell lines.(Abstract) Cytogenet. Cell Genet. 40: 787 only, 1985. 3 C c

GAM3229 221 GRIN2A Hardingham, G. E.; Fukunaga, Y.; Bading, H.: Extrasynaptic NMDARsoppose synaptic NMDARs by triggering CREB shut- off and cell deathpathways. Nature Neurosci. 5: 405- 414, 2002. 3 C c

GAM3229 221 GRIN2A Hess, S. D.; Daggett, L. P.; Crona, J.; Deal, C.; Lu, C.- C.; Urrutia,A.; Chavez- Noriega, L.; Ellis, S. B.; Johnson, E. C.; Velicelebi,G.: Cloning and functional characterization of human heteromericN- methyl- D- aspartate receptors. J. Pharm. Exp. Ther. 278: 808- 816,1996. 3 C c

GAM3229 221 GRIN2A Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani,H.; Yokoi, M.; Akazawa, C.; Shigemoto, R.; Mizuno, N.; Masu, M.; Nakanishi,S.: Molecular characterization of the family of the N- methyl- D- aspartatereceptor subunits. J. Biol. Chem. 268: 2836- 2843, 1993. 3 C c

GAM3229 221 GRIN2A Kalsi, G.; Whiting, P.; Le Bourdelles, B.; Callen, D.; Barnard,E. A.; Gurling, H.: Localization of the human NMDAR2D receptor subunitgene (GRIN2D) to 19q13.1- qter, the NMDAR2A subunit gene to 16p13.2(GRIN2A), and the NMDAR2C subunit gene (GRIN2C) to 17q24- q25 usingsomatic cell hybrid and radiation hybrid mapping panels. Genomics 47:423- 425, 1998. 3 C c

GAM3229 221 GRIN2A Monyer, H.; Sprengel, R.; Schoepfer, R.; Herb, A.; Higuchi, M.;Lomeli, H.; Burnashev, N.; Sakmann, B.; Seeburg, P. H.: HeteromericNMDA receptors: molecular and functional distinction of subtypes. Science 256:1217- 1221, 1992. 3 C c

GAM3229 221 GRIN2A Sakimura, K.; Kutsuwada, T.; Ito, I.; Manabe, T.; Takayama, C.;Kushiya, E.; Yagi, T.; Aizawa, S.; Inoue, Y.; Sugiyama, H.; Mishina,M.: Reduced hippocampal LTP and spatial learning in mice lackingNMDA receptor epsilon 1 subunit. Nature 373: 151- 155, 1995. 3 C c

GAM3229 221 GRIN2A Sprengel, R.; Suchanek, B.; Amico, C.; Brusa, R.; Burnashev, N.;Rozov, A.; Hvalby, O.; Jensen, V.; Paulsen, O.; Andersen, P.; Kim,J. J.; Thompson, R. F.; Sun, W.; Webster, L. C.; Grant, S. G. N.;Eilers, J.; Konnerth, A.; Li, J.; McNamara, J. O.; Seeburg, P. H.: Importance of the intracellular domain of NR2 subunits for NMDAreceptor function in vivo. Cell 92: 279- 289, 1998. 3 C c

GAM3229 221 GRIN2A Takano, H.; Onodera, O.; Tanaka, H.; Mori, H.; Sakimura, K.; Hori,T.; Kobayashi, H.; Mishina, M.; Tsuji, S.: Chromosomal localizationof the epsilon- 1, epsilon- 3, and zeta- 1 subunit genes of the humanNMDA receptor channel. Biochem. Biophys. Res. Commun. 197: 922- 926,1993. 3 C c

GAM3229 221 HOXB2 Davenne, M.; Maconochie, M. K.; Neun, R.; Pattyn, A.; Chambon,P.; Krumlauf, R.; Rijli, F. M.: Hoxa2 and Hoxb2 control dorsoventralpatterns of neuronal development in the rostral hindbrain. Neuron 22:677- 691, 1999. 3 C c

GAM3229 221 HOXB2 Pollock, R. A.; Sreenath, T.; Ngo, L.; Bieberich, C. J.: Gainof function mutations for paralogous Hox genes: implications for theevolution of Hox gene function. Proc. Nat. Acad. Sci. 92: 4492- 4496,1995. 3 C c

GAM3229 221 HOXB2 Vieille- Grosjean, I.; Huber, P.: Transcription factor GATA- 1 regulateshuman HOXB2 gene expression in erythroid cells. J. Biol. Chem. 270:4544- 4550, 1995. 3 C c

GAM3229 221 HSPA5 Hendershot, L. M.; Valentine, V. A.; Lee, A. S.; Morris, S. W.;Shapiro, D. N.: Localization of the gene encoding human BiP/GRP78,the endoplasmic reticulum cognate of the HSP70 family, to chromosome9q34. Genomics 20: 281- 284, 1994. 3 C c

GAM3229 221 HSPA5 Law, M. L.; Seeliger, M. B.; Lee, A. S.; Kao, F. T.: Genetic mappingof the structural gene coding for a glucose- regulated protein (GRP78)of 78k- dalton to the long arm of human chromosome 9. (Abstract) Cytogenet.Cell Genet. 37: 518- 519, 1984. 3 C c

GAM3229 221 HSPA5 Lee, A. S.; Delegeane, A. M.; Baker, V.; Chow, P. C.: Transcriptionalregulation of two genes specifically induced by glucose starvationin hamster mutant fibroblast cell line. J. Biol. Chem. 258: 597- 603,1983. 3 C c

GAM3229 221 HSPA5 Lee, A. S.; Delegeane, A.; Scharff, D.: Highly conserved glucose- regulatedprotein in hamster and chicken cells: preliminary characterizationof its cDNA clone. Proc. Nat. Acad. Sci. 78: 4922- 4925, 1981. 3 C c

GAM3229 221 HSPA5 Muresan, Z.; Arvan, P.: Enhanced binding to the molecular chaperoneBiP slows thyroglobulin export from the endoplasmic reticulum. Molec.Endocr. 12: 458- 467, 1998. 3 C c

GAM3229 221 HSPA5 Womack, J. E.: Personal Communication. College Station, Texas 2/26/1990. 3 C c

GAM3229 221 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998. 3 C b

GAM3229 221 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol- Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay. Genomics 54: 278- 286, 1998. 3 C b

GAM3229 221 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated in response to DNA damage. EMBO J. 17: 2055- 2066,1998. 3 C b

GAM3229 221 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999. 3 C b

GAM3229 221 ICAM1 Ballantyne, C. M.; Kozak, C. A.; O'Brien, W. E.; Beaudet, A. L.: Assignment of the gene for intercellular adhesion molecule- 1 (Icam- 1)to proximal mouse chromosome 9. Genomics 9: 547- 550, 1991. 3 C c

GAM3229 221 ICAM1 Bella, J.; Kolatkar, P. R.; Marlor, C. W.; Greve, J. M.; Rossmann,M. G.: The structure of the two amino- terminal domains of human ICAM- 1suggests how it functions as a rhinovirus receptor and as an LFA- 1integrin ligand. Proc. Nat. Acad. Sci. 95: 4140- 4145, 1998. 3 C c

GAM3229 221 ICAM1 Bellamy, R.; Kwiatkowski, D.; and Hill, A. V. S.: Absence of anassociation between intercellular adhesion molecule 1, complementreceptor 1 and interleukin 1 receptor antagonist gene polymorphismsand severe malaria in a West African population. Trans. R. Soc. Trop.Med. Hyg. 92: 312- 316, 1998. 3 C c

GAM3229 221 ICAM1 Craig, A.; Fernandez- Reyes, D.; Mesri, M.; McDowall, A.; Altieri,D. C.; Hogg, N.; Newbold, C.: A functional analysis of a naturalvariant of intercellular adhesion molecule- 1 (ICAM- 1- Kilifi). Hum.Molec. Genet. 9: 3 C c

525- 530, 2000.

GAM3229 221 ICAM1 Fernandez- Reyes, D.; Craig, A. G.; Kyes, S. A.; Peshu, N.; Snow,R. W.; 3 C c
Berendt, A. R.; Marsh, K.; Newbold, C. I.: A high frequencyAfrican coding
polymorphism in the N- terminal domain of ICAM- 1 predisposingto cerebral
malaria in Kenya. Hum. Molec. Genet. 6: 1357- 1360, 1997.

GAM3229 221 ICAM1 Greve, J. M.; Davis, G.; Meyer, A. M.; Forte, C. P.; Yost, S. C.;Marlor, C. 3 C c
W.; Kamarck, M. E.; McClelland, A.: The major human rhinovirusreceptor is
ICAM- 1. Cell 56: 839- 847, 1989.

GAM3229 221 ICAM1 Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. 3 C c
Phys. 111: 272- 277, 1999.

GAM3229 221 ICAM1 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, 3 C c
M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B
cells. Europ. J. Immun. 15: 103- 106, 1985.

GAM3229 221 ICAM1 Le Beau, M. M.; Ryan, D., Jr.; Pericak- Vance, M. A.: Report ofthe committee 3 C c
on the genetic constitution of chromosomes 18 and 19. Cytogenet.Cell Genet.
51: 338- 357, 1989.

GAM3229 221 ICAM1 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in 3 C c
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM3229 221 ICAM1 Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot- 3 C c
Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow
cytometricanalysis of conjunctival epithelium in ocular rosacea and
keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000.

GAM3229 221 ICAM1 Prieto, J.; Takei, F.; Gendelman, R.; Christenson, B.; Biberfeld,P.; 3 C c
Patarroyo, M.: MALA- 2, mouse homologue of human adhesion moleculeICAM- 1
(CD54). Europ. J. Immun. 19: 1551- 1557, 1989.

GAM3229 221 ICAM1 Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal 3 C c
mouse chromosome 9 linkage map that further defines linkagegroups homologous
with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685,
1991.

GAM3229 221 ICAM1 Simmons, D.; Makgoba, M. W.; Seed, B.: ICAM, an adhesion ligandof LFA- 1, is 3 C c
homologous to the neural cell adhesion molecule NCAM. Nature 331:624- 627,
1988.

GAM3229 221 ICAM1 Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H.K.; Smith, C. 3 C c
W.; Bradley, A.; Beaudet, A. L.: Inflammatory and immuneresponses are
impaired in mice deficient in intercellular adhesionmolecule 1. Proc. Nat.
Acad. Sci. 90: 8529- 8533, 1993.

GAM3229 221 ICAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 C c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM3229 221 ICAM1 Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; 3 C c
Takeuchi, T.: Regulation of human leukocyte antigenexpression in human
conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999.

GAM3229 221 IGFBP5 Allander, S. V.; Larsson, C.; Ehrenborg, E.; Suwanichkul, A.; Weber,G.; 3 C c
Morris, S. L.; Bajalica, S.; Kiefer, M. C.; Luthman, H.; Powell,D. R.:
Characterization of the chromosomal gene and promoter forhuman insulin- like
growth factor binding protein- 5. J. Biol. Chem. 269:10891- 10898, 1994.

GAM3229 221 IGFBP5 Kou, K.; James, P. L.; Clemmons, D. R.; Copeland, N. G.; Gilbert,D. J.; 3 C c
Jenkins, N. A.; Rotwein, P.: Identification of two clustersof mouse insulin-

like growth factor binding protein genes on chromosomes1 and 11. Genomics 21: 653- 655, 1994.

GAM3229 221 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 C b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM3229 221 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 C b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM3229 221 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 C b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814-
819, 1992.

GAM3229 221 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 C b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang,
Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell-
derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87:
7512- 7516, 1990.

GAM3229 221 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 3 C b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract)
Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM3229 221 IL19 Blumberg, H.; Conklin, D.; Xu, W.; Grossmann, A.; Brender, T.;Carollo, S.; 3 C c
Eagan, M.; Foster, D.; Haldeman, B. A.; Hammond, A.;Haugen, H.; Jelinek, L.;
and 14 others: Interleukin 20: discovery,receptor identification, and role
in epidermal function. Cell 104:9- 19, 2001.

GAM3229 221 IL19 Gallagher, G.; Dickensheets, H.; Eskdale, J.; Izotova, L. S.; 3 C c
Mirochnitchenko,O. V.; Peat, J. D.; Vazquez, N.; Pestka, S.; Donnelly, R.
P.; Kotenko,S. V.: Cloning, expression and initial characterisation of
interleukin- 19(IL- 19), a novel homologue of human interleukin- 10 (IL-
10). GenesImmunity 1: 442- 450, 2000.

GAM3229 221 IL1A Bailly, S.; di Giovine, F. S.; Blakemore, A. I. F.; Duff, G. W.: Genetic 3 C c
polymorphism of human interleukin- 1- alpha. Europ. J. Immun. 23:1240- 1245,
1993.

GAM3229 221 IL1A Boultwood, J.; Breckon, G.; Birch, D.; Cox, R.: Chromosomal localizationof 3 C c
murine interleukin- 1 alpha and beta genes. Genomics 5: 481- 485,1989.

GAM3229 221 IL1A Cox, A.; Camp, N. J.; Cannings, C.; di Giovine, F. S.; Dale, M.;Worthington, 3 C c
J.; John, S.; Ollier, W. E. R.; Silman, A. J.; Duff,G. W.: Combined sib- TDT
and TDT provide evidence for linkage of theinterleukin- 1 gene cluster to
erosive rheumatoid arthritis. Hum.Molec. Genet. 8: 1707- 1713, 1999.

GAM3229 221 IL1A Cox, A.; Camp, N. J.; Nicklin, M. J. H.; di Giovine, F. S.; Duff,G. W.: An 3 C c
analysis of linkage disequilibrium in the interleukin- 1gene cluster, using
a novel grouping method for multiallelic markers. Am.J. Hum. Genet. 62:
1180- 1188, 1998.

GAM3229 221 IL1A Diehl, S. R.; Wang, Y.; Brooks, C. N.; Burmeister, J. A.; Califano,J. V.; 3 C c
Wang, S.; Schenkein, H. A.: Linkage disequilibrium of interleukin- 1genetic
polymorphisms with early- onset periodontitis. J. Periodont. 70:418- 430,
1999.

GAM3229 221 IL1A Du, Y.; Dodel, R. C.; Eastwood, B. J.; Bales, K. R.; Gao, F.; Lohmuller,F.; 3 C c
Muller, U.; Kurz, A.; Zimmer, R.; Evans, R. M.; Hake, A.; Gasser,T.; Oertel,
W. H.; Griffin, W. S. T.; Paul, S. M.; Farlow, M. R.:Association of an
interleukin 1- alpha polymorphism with Alzheimer'sdisease. Neurology 55:
480- 484, 2000.

GAM3229 221 IL1A Furutani, Y.; Notake, M.; Fukui, T.; Ohue, M.; Nomura, H.; Yamada,M.; 3 C c
Nakamura, S.: Complete nucleotide sequence of the gene for humaninterleukin

1 alpha. Nucleic Acids Res. 14: 3167- 3179, 1986.

GAM3229 221 IL1A Gray, P. W.; Glaister, D.; Chen, E.; Goeddel, D. V.; Pennica, D.: Two 3 C c
interleukin 1 genes in the mouse: cloning and expression ofthe cDNA for
murine interleukin 1- beta. J. Immun. 137: 3644- 3648,1986.

GAM3229 221 IL1A Grimaldi, L. M. E.; Casadei, V. M.; Ferri, C.; Veglia, F.; Licastro,F.; 3 C c
Annoni, G.; Biunno, I.; De Bellis, G.; Sorbi, S.; Mariani, C.;Canal, N.;
Griffin, W. S. T.: Association of early- onset Alzheimer'sdisease with an
interleukin- 1- alpha gene polymorphism. Ann. Neurol. 47:361- 365, 2000.

GAM3229 221 IL1A Hogquist, K. A.; Nett, M. A.; Unanue, E. R.; Chaplin, D. D.:Interleukin 1 is 3 C c
processed and released during apoptosis. Proc. Nat.Acad. Sci. 88: 8485-
8489, 1991.

GAM3229 221 IL1A Hurwitz, A.; Loukides, J.; Ricciarelli, E.; Botero, L.; Katz,E.; McAllister, 3 C c
J. M.; Garcia, J. E.; Rohan, R.; Adashi, E. Y.; Hernandez,E. R.: Human
intraovarian interleukin- 1 (IL- 1) system: highly compartmentalizedand
hormonally dependent regulation of the genes encoding IL- 1, itsreceptor,
and its receptor antagonist. J. Clin. Invest. 89: 1746- 1754,1992.

GAM3229 221 IL1A Ki, C.- S.; Na, D. L.; Kim, D. K.; Kim, H. J.; Kim, J.- W.: Lackof 3 C c
association of the interleukin- 1- alpha gene polymorphism with
Alzheimer'sdisease in a Korean population. (Letter) Ann. Neurol. 49: 817-
818,2001.

GAM3229 221 IL1A Kolsch, H.; Ptok, U.; Bagli, M.; Papassotiropoulos, A.; Schmitz,S.; Barkow, 3 C c
K.; Kockler, M.; Rao, M. L.; Maier, W.; Heun, R.: Genepolymorphisms of
interleukin- 1- alpha influence the course of Alzheimer'sdisease. (Letter)
Ann. Neurol. 49: 818- 819, 2001.

GAM3229 221 IL1A Kornman, K. S.; Crane, A.; Wang, H.- Y.; di Giovine, F. S.; Newman,M. G.; 3 C c
Pirk, F. W.; Wilson, T. G., Jr.; Higginbottom, F. L.; Duff,G. W.: The
interleukin- 1 genotype as a severity factor in adult periodontaldisease. J.
Clin. Periodont. 24: 72- 77, 1997.

GAM3229 221 IL1A Lafage, M.; Maroc, N.; Dubreuil, P.; de Waal Malefijt, R.; Pebusque,M.- J.; 3 C c
Carcassonne, Y.; Mannoni, P.: The human interleukin- 1- alphagene is located
on the long arm of chromosome 2 at band q13. Blood 73:104- 107, 1989.

GAM3229 221 IL1A Lord, P. C. W.; Wilmoth, L. M. G.; Mizel, S. B.; McCall, C. E.: Expression 3 C c
of interleukin- 1 alpha and beta genes by human bloodpolymorphonuclear
leukocytes. J. Clin. Invest. 87: 1312- 1321, 1991.

GAM3229 221 IL1A McGeer, P. L.; McGeer, E. G.: Polymorphisms in inflammatory genesand the 3 C c
risk of Alzheimer disease. Arch. Neurol. 58: 1790- 1792,2001.

GAM3229 221 IL1A Modi, W. S.; Masuda, A.; Yamada, M.; Oppenheim, J. J.; Matsushima,K.; 3 C c
O'Brien, S. J.: Chromosomal localization of the human interleukin1 alpha
(IL- 1- alpha) gene. Genomics 2: 310- 314, 1988.

GAM3229 221 IL1A Mosley, B.; Urdal, D. L.; Prickett, K. S.; Larsen, A.; Cosman,D.; Conlon, P. 3 C c
J.; Gillis, S.; Dower, S. K.: The interleukin- 1 receptorbinds the human
interleukin- 1- alpha precursor but not the interleukin- 1- betaprecursor.
J. Biol. Chem. 262: 2941- 2944, 1987.

GAM3229 221 IL1A Murphy, G. M., Jr.; Claassen, J. D.; DeVoss, J. J.; Pascoe, N.;Taylor, J.; 3 C c
Tinklenberg, J. R.; Yesavage, J. A.: Rate of cognitivedecline in AD is
accelerated by the interleukin- 1- alpha - 889 *1 allele. Neurology 56:1595-
1597, 2001.

GAM3229 221 IL1A Nicklin, M. J. H.; Weith, A.; Duff, G. W.: A physical map ofthe region 3 C c
encompassing the human interleukin- 1- alpha, interleukin- 1- beta,and
interleukin- 1 receptor antagonist genes. Genomics 19: 382- 384,1994.

GAM3229 221 IL1A Nicoll, J. A. R.; Mrak, R. E.; Graham, D. I.; Stewart, J.; Wilcock,G.; 3 C c
MacGowan, S.; Esiri, M. M.; Murray, L. S.; Dewar, D.; Love, S.;Moss, T.;
Griffin, W. S. T.: Association of interleukin- 1 gene polymorphismswith
Alzheimer's disease. Ann. Neurol. 47: 365- 368, 2000.

GAM3229 221 IL1A Rogers, J.: An IL- 1- alpha susceptibility polymorphism in 3 C c
Alzheimer'sdisease: new fuel for the inflammation hypothesis. (Editorial)
Neurology 55:464- 465, 2000.

GAM3229 221 IL1A Sabatino, M.; Boyce, B.; Aufdemorte, T.; Bonewald, L.; Mundy,G. R.: 3 C c
Infusions of recombinant human interleukins 1 alpha and 1beta cause
hypercalcemia in normal mice. Proc. Nat. Acad. Sci. 85:5235- 5239, 1988.

GAM3229 221 IL1A Silver, A. R. J.; Masson, W. K.; George, A. M.; Adam, J.; Cox,R.: The Il- 1 3 C c
alpha and beta genes are closely linked (less than 70kb) on mouse chromosome
2. Somat. Cell Molec. Genet. 16: 549- 556,1990.

GAM3229 221 KCNE3 Abbott, G. W.; Butler, M. H.; Bendahhou, S.; Dalakas, M. C.; Ptacek,L. J.; 3 C c
Goldstein, S. A. N.: MiRP2 forms potassium channels in skeletalmuscle with
Kv3.4 and is associated with periodic paralysis. Cell 104:217- 231, 2001.

GAM3229 221 KCNE3 Abbott, G. W.; Sesti, F.; Splawski, I.; Buck, M. E.; Lehmann, M.H.; Timothy, 3 C c
K. W.; Keating, M. T.; Goldstein, S. A. N.: MiRP1 formsI(Kr) potassium
channels with HERG and is associated with cardiacarrhythmia. Cell 97: 175-
187, 1999.

GAM3229 221 KCNE3 Schroeder, B. C.; Waldegger, S.; Fehr, S.; Bleich, M.; Warth, R.;Greger, R.; 3 C c
Jentsch, T. J.: A constitutively open potassium channelformed by KCNQ1 and
KCNE3. Nature 403: 196- 199, 2000.

GAM3229 221 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; 3 C b
Malherbe, P.: Cloning and functional expression of human kynurenine3-
monooxygenase. FEBS Lett. 410: 407- 412, 1997.

GAM3229 221 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; 3 C b
Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.:
Characterization ofa novel human opsin gene with wide tissue expression and
identificationof embedded and flanking genes on chromosome 1q43. Genomics
72:203- 208, 2001.

GAM3229 221 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 C c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM3229 221 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 C c
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22
suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci.
98: 10374- 10379, 2001.

GAM3229 221 MAPT Abel, K. J.; Boehnke, M.; Prahalad, M.; Ho, P.; Flejter, W. L.;Watkins, M.; 3 C c
VanderStoep, J.; Chandrasekharappa, S. C.; Collins, F.S.; Glover, T. W.;
Weber, B. L.: A radiation hybrid map of the BRCA1region of chromosome 17q12-
q21. Genomics 17: 632- 641, 1993.

GAM3229 221 MAPT Alonso, A. D. C.; Grundke- Iqbal, I.; Iqbal, K.: Alzheimer's 3 C c
diseasehyperphosphorylated tau sequesters normal tau into tangles of
filamentsand disassembles microtubules. Nature Med. 2: 783- 787, 1996.

GAM3229 221 MAPT Arima, K.; Kowalska, A.; Hasegawa, M.; Mukoyama, M.; Watanabe,R.; Kawai, M.; 3 C
c

Takahashi, K.; Iwatsubo, T.; Tabira, T.; Sunohara,N.: Two brothers with
frontotemporal dementia and parkinsonism withan N279K mutation of the tau

gene. Neurology 54: 1787- 1795, 2000.

GAM3229 221 MAPT Baker, M.; Litvan, I.; Houlden, H.; Adamson, J.; Dickson, D.; Perez- Tur,J.; 3 C c
Hardy, J.; Lynch, T.; Bigio, E.; Hutton, M.: Association of anextended
haplotype in the tau gene with progressive supranuclear palsy. Hum.Molec.
Genet. 8: 711- 715, 1999.

GAM3229 221 MAPT Brown, J.; Lantos, P. L.; Roques, P.; Fidani, L.; Rossor, M. N.: Familial 3 C c
dementia with swollen achromatic neurons and corticobasalinclusion bodies: a
clinical and pathological study. J. Neurol. Sci. 135:21- 30, 1996.

GAM3229 221 MAPT Clark, L. N.; Poorkaj, P.; Wszolek, Z.; Geschwind, D. H.; Nasreddine,Z. S.; 3 C c
Miller, B.; Li, D.; Payami, H.; Awert, F.; Markopoulou, K.;Andreadis, A.;
D'Souza, I.; Lee, V. M.- Y.; Reed, L.; Trojanowski,J. Q.; Zhukareva, V.;
Bird, T.; Schellenberg, G.; Wilhelmsen, K. C.: Pathogenic implications of
mutations in the tau gene in pallido- ponto- nigraldegeneration and related
neurodegenerative disorders linked to chromosome17. Proc. Nat. Acad. Sci.
95: 13103- 13107, 1998.

GAM3229 221 MAPT Connell, J. W.; Gibb, G. M.; Betts, J. C.; Blackstock, W. P.; Gallo,J.- M.; 3 C c
Lovestone, S.; Hutton, M.; Anderton, B. H.: Effects of FTDP- 17mutations on
the in vitro phosphorylation of tau by glycogen synthasekinase 3- beta
identified by mass spectrometry demonstrate certainmutations exert long-
range conformational changes. FEBS Lett. 493:40- 44, 2001.

GAM3229 221 MAPT Conrad, C.; Andreadis, A.; Trojanowski, J. Q.; Dickson,D. W.; Kang,D.; Chen, 3 C c
X.; Weiderholt, W.; Hansen, L.; Masliah, E.; Thal, L. J.;Katzman, R.; Xia,
Y.; Saitoh, T.: Genetic evidence for the involvementof tau in progressive
supranuclear palsy. Ann. Neurol. 41: 277- 281,1997.

GAM3229 221 MAPT Conrad, C.; Vianna, C.; Freeman, M.; Davies, P.: A polymorphicgene nested 3 C c
within an intron of the tau gene: implications for Alzheimer'sdisease. Proc.
Nat. Acad. Sci. 99: 7751- 7756, 2002.

GAM3229 221 MAPT Delisle, M. B.; Murrell, J. R.; Richardson, R.; Trofatter, J.A.; Rascol, O.; 3 C c
Soulages, X.; Mohr, M.; Calvas, P.; Ghetti, B.: Amutation at codon 279
(N279K) in exon 10 of the tau gene causes atauopathy with dementia and
supranuclear palsy. Acta Neuropath. 98:62- 77, 1999.

GAM3229 221 MAPT Donlon, T. A.; Harris, P.; Neve, R. L.: Localization of microtubule- 3 C c
associatedprotein tau (MTBT1) to chromosome 17q21. (Abstract) Cytogenet.
CellGenet. 46: 607, 1987.

GAM3229 221 MAPT Goedert, M.; Crowther, R. A.; Spillantini, M. G.: Tau mutationscause 3 C c
frontotemporal dementias. Neuron 21: 955- 958, 1998.

GAM3229 221 MAPT Goedert, M.; Spillantini, M. G.; Potier, M. C.; Ulrich, J.; Crowther,R. A.: 3 C c
Cloning and sequencing of the cDNA encoding an isoform ofmicrotubule-
associated protein tau containing four tandem repeats:differential
expression of tau protein mRNAs in human brain. EMBOJ. 8: 393- 399, 1989.

GAM3229 221 MAPT Goedert, M.; Wischik, C. M.; Crowther, R. A.; Walker, J. E.; Klug,A.: 3 C c
Cloning and sequencing of the cDNA encoding a core protein ofthe paired
helical filament of Alzheimer disease: identification asthe microtubule-
associated protein tau. Proc. Nat. Acad. Sci. 85:4051- 4055, 1988.

GAM3229 221 MAPT Goode, B. L.; Chau, M.; Denis, P. E.; Feinstein, S. C.: Structuraland 3 C c
functional differences between 3- repeat and 4- repeat tau
isoforms:implications for normal tau function and the onset of
neurodegenerativedisease. J. Biol. Chem. 275: 38182- 38189, 2000.

GAM3229 221 MAPT Gotz, J.; Chen, F.; van Dorpe, J.; Nitsch, R. M.: Formation 3 C c
ofneurofibrillary tangles in P301L tau transgenic mice induced by A-

beta42fibrils. Science 293: 1491- 1495, 2001.

GAM3229 221 MAPT Heutink, P.: Untangling tau- related dementia. Hum. Molec. Genet. 9:979- 986, 2000. 3 C c

GAM3229 221 MAPT Heutink, P.; Stevens, M.; Rizzu, P.; Bakker, E.; Kros, J. M.;Tibben, A.; Niermeijer, M. F.; van Duijn, C. M.; Oostra, B. A.; vanSwieten, J. C.: Hereditary frontotemporal dementia is linked to chromosome17q21- q22: a genetic and clinicopathological study of three Dutchfamilies. Ann. Neurol. 41: 150- 159, 1997. 3 C c

GAM3229 221 MAPT Hiesberger, T.; Trommsdorff, M.; Howell, B. W.; Goffinet, A.;Mumby, M. C.; Cooper, J. A.; Herz, J.: Direct binding of reelin toVLDL receptor and apoE receptor 2 induces tyrosine phosphorylationof disabled- 1 and modulates tau phosphorylation. Neuron 24: 481- 489,1999. 3 C c

GAM3229 221 MAPT Hong, M.; Zhukareva, V.; Vogelsberg- Ragaglia, V.; Wszolek, Z.;Reed, L.; Miller, B. I.; Geschwind, D. H.; Bird, T. D.; McKeel, D.;Goate, A.; Morris, J. C.; Wilhelmsen, K. C.; Schellenberg, G. D.;Trojanowski, J. Q.; Lee, V. M.- Y.: Mutation- specific functional impairmentsin distinct tau isoforms of hereditary FTDP- 17. Science 282: 1914- 1917,1998. 3 C c

GAM3229 221 MAPT Hutton, M.: Missense and splice site mutations in tau associatedwith FTDP- 17: multiple pathogenic mechanisms. Neurology 56 (suppl.4): S21- S25, 2001. 3 C c

GAM3229 221 MAPT Hutton, M.; Lendon, C. L.; Rizzu, P.; Baker, M.; Froelich, S.;Houlden, H.; Pickering- Brown, S.; Chakraverty, S.; Isaacs, A.; Grover,A.; Hackett, J.; Adamson, J.; and 39 others: Association of missenseand 5- prime- splice- site mutations in tau with the inherited dementiaFTDP- 17. Nature 393: 702- 705, 1998. 3 C c

GAM3229 221 MAPT Iijima, M.; Tabira, T.; Poorkaj, P.; Schellenberg, G. D.; Trojanowski,J. Q.; Lee, V. M.; Schmidt, M. L.; Takahashi, K.; Nabika, T.; Matsumoto,T.; Yamashita, Y.; Yoshioka, S.; Ishino, H.: A distinct familialpresenile dementia with a novel missense mutation in the tau gene. Neuroreport 10:497- 501, 1999. 3 C c

GAM3229 221 MAPT Ishihara, T.; Hong, M.; Zhang, B.; Nakagawa, Y.; Lee, M. K.; Trojanowski,J. Q.; Lee, V. M.- Y.: Age- dependent emergence and progression ofa tauopathy in transgenic mice overexpressing the shortest human tauisoform. Neuron 24: 751- 762, 1999. 3 C c

GAM3229 221 MAPT Janssen, J. C.; Warrington, E. K.; Morris, H. R.; Lantos, P.;Brown, J.; Revesz, T.; Wood, N.; Khan, M. N.; Cipolotti, L.; Fox,N. C.; Rossor, M. N.: Clinical features of frontotemporal dementiadue to the intronic tau 10 +16 mutation. Neurology 58: 1161- 1168,2002. 3 C c

GAM3229 221 MAPT Jiang, Z.; Cote, J.; Kwon, J. M.; Goate, A. M.; Wu, J. Y.: Aberrantsplicing of tau pre- mRNA caused by intronic mutations associated withthe inherited dementia frontotemporal dementia with Parkinsonism linkedto chromosome 17. Molec. Cell. Biol. 20: 4036- 4048, 2000. 3 C c

GAM3229 221 MAPT Lewis, J.; Dickson, D. W.; Lin, W.- L.; Chisholm, L.; Corral, A.;Jones, G.; Yen, S.- H.; Sahara, N.; Skipper, L.; Yager, D.; Eckman,C.; Hardy, J.; Hutton, M.; McGowan, E.: Enhanced neurofibrillarydegeneration in transgenic mice expressing mutant tau and APP. Science 293:1487- 1491, 2001. 3 C c

GAM3229 221 MAPT Lewis, J.; McGowan, E.; Rockwood, J.; Melrose, H.; Nacharaju,P.; Van Slegtenhorst, M.; Gwinn- Hardy, K.; Murphy, M. P.; Baker, M.;Yu, X.; Duff, K.; Hardy, J.; Corral, A.; Lin, W.- L.; Yen, S.- H.; Dickson,D. W.; Davies, P.; Hutton, M.: Neurofibrillary tangles, amyotrophyand progressive motor disturbance in mice expressing mutant (P301L)tau protein. Nature Genet. 25: 3 C c

402- 405, 2000. Note: Erratum: NatureGenet. 26: 127 only, 2000.

GAM3229 221 MAPT Lippa, C. F.; Zhukareva, V.; Kawarai, T.; Uryu, K.; Shafiq, M.;Nee, L. E.; Grafman, J.; Liang, Y.; St George- Hyslop, P. H.; Trojanowski,J. Q.; Lee, V. M.- Y.: Frontotemporal dementia with novel tau pathologyand a glu342val tau mutation. Ann. Neurol. 48: 850- 858, 2000. 3 C c

GAM3229 221 MAPT Litvan, I.; Baker, M.; Hutton, M.: Tau genotype: no effect ononset, symptom severity, or survival in progressive supranuclear palsy. Neurology 57:138- 140, 2001. 3 C c

GAM3229 221 MAPT Lu, P.- J.; Wulf, G.; Zhou, X. Z.; Davies, P.; Lu, K. P.: Theprolyl isomerase Pin1 restores the function of Alzheimer- associatedphosphorylated tau protein. Nature 399: 784- 788, 1999. 3 C c

GAM3229 221 MAPT Martin, E. R.; Scott, W. K.; Nance, M. A.; Watts, R. L.; Hubble,J. P.; Koller, W. C.; Lyons, K.; Pahwa, R.; Stern, M. B.; Colcher,A.; Hiner, B. C.; Jankovic, J.; and 20 others: Association of single- nucleotidepolymorphisms of the Tau gene with late- onset Parkinson disease. J.A.M.A. 286:2245- 2250, 2001. 3 C c

GAM3229 221 MAPT Murrell, J. R.; Spillantini, M. G.; Zolo, P.; Guazzelli, M.; Smith,M. J.; Hasegawa, M.; Redi, F.; Crowther, R. A.; Pietrini, P.; Ghetti,B.; Goedert, M.: Tau gene mutation G389R causes a tauopathy withabundant Pick body- like inclusions and axonal deposits. J. Neuropath.Exp. Neurol. 58: 1207- 1226, 1999. 3 C c

GAM3229 221 MAPT Nagase, T.; Ishikawa, K.; Kikuno, R.; Hirosawa, M.; Nomura, N.;Ohara, O.: Prediction of the coding sequences of unidentified humangenes. XV. The complete sequences of 100 new cDNA clones from brainwhich code for large proteins in vitro. DNA Res. 6: 337- 345, 1999. 3 C c

GAM3229 221 MAPT Neumann, M.; Schulz- Schaeffer, W.; Crowther, R. A.; Smith, M.J.; Spillantini, M. G.; Goedert, M.; Kretzschmar, H. A.: Pick's diseaseassociated with the novel tau gene mutation K369I. Ann. Neurol. 50:503- 513, 2001. 3 C c

GAM3229 221 MAPT Neve, R. L.; Harris, P.; Kosik, K. S.; Kurnit, D. M.; Donlon,T. A.: Identification of cDNA clones for the human microtubule- associatedprotein tau and chromosomal localization of the genes for tau andmicrotubule- associated protein 2. Molec. Brain Res. 1: 271- 280,1986. 3 C c

GAM3229 221 MAPT Pickering- Brown, S.; Baker, M.; Yen, S.- H.; Liu, W.- K.; Hasegawa,M.; Cairns, N.; Lantos, P. L.; Rossor, M.; Iwatsubo, T.; Davies, Y.;Allsop, D.; Furlong, R.; Owen, F.; Hardy, J.; Mann, D.; Hutton, M.: Pick's disease is associated with mutations in the tau gene. Ann.Neurol. 48: 859- 867, 2000. 3 C c

GAM3229 221 MAPT Poorkaj, P.: Personal Communication. Seattle, Wash. 11/10/1998. 3 C c

GAM3229 221 MAPT Poorkaj, P.; Bird, T. D.; Wijsman, E.; Nemens, E.; Garruto, R.M.; Anderson, L.; Andreadis, A.; Wiederholt, W. C.; Raskind, M.; Schellenberg,G. D.: Tau is a candidate gene for chromosome 17 frontotemporal dementia. Ann.Neurol. 43: 815- 825, 1998. 3 C c

GAM3229 221 MAPT Poorkaj, P.; Kas, A.; D'Souza, I.; Zhou, Y.; Pham, Q.; Stone,M.; Olson, M. V.; Schellenberg, G. D.: A genomic sequence analysisof the mouse and human microtubule- associated protein tau. MammalianGenome 12: 700- 712, 2001. 3 C c

GAM3229 221 MAPT Rapoport, M.; Dawson, H. N.; Binder, L. I.; Vitek, M. P.; Ferreira,A.: Tau is essential to beta- amyloid- induced neurotoxicity. Proc.Nat. Acad. Sci. 99: 6364- 6369, 2002. 3 C c

GAM3229 221 MAPT Rizzu, P.; Van Swieten, J. C.; Joosse, M.; Hasegawa, M.; Stevens,M.; Tibben, A.; Niermeijer, M. F.; Hillebrand, M.; Ravid, R.; Oostra,B. A.; Goedert, M.; 3 C c

van Duijn, C. M.; Heutink, P.: High prevalenceof mutations in the microtubule- associated protein tau in a populationstudy of frontotemporal dementia in the Netherlands. Am. J. Hum.Genet. 64: 414- 421, 1999.

GAM3229 221 MAPT Spillantini, M. G.; Murrell, J. R.; Goedert, M.; Farlow, M. R.;Klug, A.; Ghetti, B.: Mutation in the tau gene in familial multiplesystem tauopathy with presenile dementia. Proc. Nat. Acad. Sci. 95:7737- 7741, 1998. 3 C c

GAM3229 221 MAPT Spillantini, M. G.; Yoshida, H.; Rizzini, C.; Lantos, P. L.; Khan,N.; Rossor, M. N.; Goedert, M.; Brown, J.: A novel tau mutation (N296N)in familial dementia with swollen achromatic neurons and corticobasalinclusion bodies. Ann. Neurol. 48: 939- 943, 2000. 3 C c

GAM3229 221 MAPT Stambolic, V.; Ruel, L.; Woodgett, J. R.: Lithium inhibits glycogensynthase kinase- 3 activity and mimics Wingless signalling in intactcells. Curr. Biol. 6: 1664- 1668, 1996. Note: Erratum: Curr. Biol.7: 196 only, 1997. 3 C c

GAM3229 221 MAPT Stamer, K.; Vogel, R.; Thies, E.; Mandelkow, E.; Mandelkow, E.- M.: Tau blocks traffic of organelles, neurofilaments, and APP vesiclesin neurons and enhances oxidative stress. J. Cell Biol. 156: 1051- 1063,2002. 3 C c

GAM3229 221 MAPT Varani, L.; Hasegawa, M.; Spillantini, M. G.; Smith, M. J.; Murrell,J. R.; Ghetti, B.; Klug, A.; Goedert, M.; Varani, G.: Structure oftau exon 10 splicing regulatory element RNA and destabilization bymutations of frontotemporal dementia and parkinsonism linked to chromosome17. Proc. Nat. Acad. Sci. 96: 8229- 8234, 1999. 3 C c

GAM3229 221 MAPT Verpillat, P.; Camuzat, A.; Hannequin, D.; Thomas- Anterion, C.;Puel, M.; Belliard, S.; Dubois, B.; Didic, M.; Michel, B.- F.; Lacomblez,L.; Moreaud, O.; Sellal, F.; Golfier, V.; Campion, D.; Clerget- Darpoux,F.; Brice, A.: Association between the extended tau haplotype andfrontotemporal dementia. Arch. Neurol. 59: 935- 939, 2002. 3 C c

GAM3229 221 MAPT Wilhelmsen, K. C.; Lynch, T.; Pavlou, E.; Higgins, M.; Hygaard,T. G.: Localization of disinhibition- dementia- parkinsonism- amyotrophycomplex to 17q21- 22. Am. J. Hum. Genet. 55: 1159- 1165, 1994. 3 C c

GAM3229 221 MAPT Yasuda, M.; Yokoyama, K.; Nakayasu, T.; Nishimura, Y.; Matsui,M.; Yokoyama, T.; Miyoshi, K.; Tanaka, C.: A Japanese patient withfrontotemporal dementia and parkinsonism by a tau P301S mutation. Neurology 55:1224- 1227, 2000. 3 C c

GAM3229 221 MAPT Zhukareva, V.; Mann, D.; Pickering- Brown, S.; Uryu, K.; Shuck,T.; Shah, K.; Grossman, M.; Miller, B. L.; Hulette, C. M.; Feinstein,S. C.; Trojanowski, J. Q.; Lee, V. M.- Y.: Sporadic Pick's disease:a tauopathy characterized by a spectrum of pathological tau isoformsin gray and white matter. Ann. Neurol. 51: 730- 739, 2002. 3 C c

GAM3229 221 MICB Diefenbach, A.; Jensen, E. R.; Jamieson, A. M.; Raulet, D. H.:Rae1 and H60 ligands of the NKG2D receptor stimulate tumour immunity. Nature 413:165- 171, 2001. 3 C b

GAM3229 221 MICB Fischer, G.; Perez- Rodriguez, M.; Arguello, J. R.; Cox, S. T.;McWhinnie, A.; Travers, P. J.; Madrigal, J. A.: Three novel MICBalleles. Tissue Antigens 55: 166- 170, 2000. 3 C b

GAM3229 221 MICB Girardi, M.; Oppenheim, D. E.; Steele, C. R.; Lewis, J. M.; Glusac,E.; Filler, R.; Hobby, P.; Sutton, B.; Tigelaar, R. E.; Hayday, A.C.: Regulation of cutaneous malignancy by gamma- delta T cells. Science 294:605- 609, 2001. 3 C b

GAM3229 221 MICB Groh, V.; Bahram, S.; Bauer, S.; Herman, A.; Beauchamp, M.; Spies,T.: Cell stress- regulated human major histocompatibility complexclass I gene expressed in gastrointestinal epithelium. Proc. Nat.Acad. Sci. 93: 12445- 12450, 1996. 3 C b

GAM3229 221 MICB Groh, V.; Steinle, A.; Bauer, S.; Spies, T.: Recognition of stress- 3 C b
inducedMHC molecules by intestinal epithelial gamma- delta T cells. Science
279:1737- 1740, 1998.

GAM3229 221 MICB Nalabolu, S. R.; Shukla, H.; Nallur, G.; Parimoo, S.; Weissman,S. M.: Genes 3 C b
in a 220- kb region spanning the TNF cluster in humanMHC. Genomics 31: 215-
222, 1996.

GAM3229 221 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 C c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator.
J. Biol. Chem. 275: 5308- 5317, 2000.

GAM3229 221 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 C c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation
of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer
Res. 56: 3446- 3450, 1996.

GAM3229 221 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 C c
bindingprotein, an LXXLL motif- containing protein, functions as a
generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM3229 221 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 C c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-
H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor,
ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for
ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol.
Chem. 274: 34283- 34293, 1999.

GAM3229 221 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 C c
that integrate nuclear receptor signaling through CREB- bindingprotein.
Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM3229 221 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 C c
coding sequences of unidentified human genes. V. The codingsequences of 40
new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM3229 221 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 C c
J. K.: Isolation and characterization of peroxisomeproliferator- activated
receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.
Biol. Chem. 275: 13510- 13516, 2000.

GAM3229 221 NEDD4 Harvey, K. F.; Dinudom, A.; Cook, D. I.; Kumar, S.: The Nedd4- likeprotein 3 C c
KIAA0439 is a potential regulator of the epithelial sodiumchannel. J. Biol.
Chem. 276: 8597- 8601, 2001.

GAM3229 221 NEDD4 Imhof, M. O.; McDonnell, D. P.: Yeast RSP5 and its human homologhRPF1 3 C c
potentiate hormone- dependent activation of transcription byhuman
progesterone and glucocorticoid receptors. Molec. Cell. Biol. 16:2594- 2605,
1996.

GAM3229 221 NEDD4 Kumar, S.; Harvey, K. F.; Kinoshita, M.; Copeland, N. G.; Noda,M.; Jenkins, 3 C c
N. A.: cDNA cloning, expression analysis, and mappingof the mouse Nedd4
gene. Genomics 40: 435- 443, 1997.

GAM3229 221 NEDD4 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 3 C c
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM3229 221 NEUROD1 Fajans, S. S.; Bell, G. I.; Polonsky, K. S.: Molecular mechanismsand 3 C c
clinical pathophysiology of maturity- onset diabetes of the young. NewEng.
J. Med. 345: 971- 980, 2001.

GAM3229 221 NEUROD1 Lee, J. E.; Hollenberg, S. M.; Snider, L.; Turner, D. L.; Lipnick,N.; 3 C c

Weintraub, H.: Conversion of Xenopus ectoderm into neurons byNeuroD, a basic helix- loop- helix protein. Science 268: 836- 844,1995.

GAM3229 221 NEUROD1 Liu, M.; Pleasure, S. J.; Collins, A. E.; Noebels, J. L.; Naya,F. J.; Tsai, M.- J.; Lowenstein, D. H.: Loss of BETA2/NeuroD leadsto malformation of the dentate gyrus and epilepsy. Proc. Nat. Acad.Sci. 97: 865- 870, 2000. 3 C c

GAM3229 221 NEUROD1 Malecki, M. T.; Jhala, U. S.; Antonellis, A.; Fields, L.; Doria,A.; Orban, T.; Saad, M.; Warram, J. H.; Montminy, M.; Krolewski, A.S.: Mutations in NEUROD1 are associated with the development of type2 diabetes mellitus. Nature Genet. 23: 323- 328, 1999. 3 C c

GAM3229 221 NEUROD1 Naya, F. J.; Huang, H.- P.; Qiu, Y.; Mutoh, H.; DeMayo, F. J.; Leiter,A. B.; Tsai, M.- J.: Diabetes, defective pancreatic morphogenesis,and abnormal enteroendocrine differentiation in BETA2/neurod- deficientmice. Genes Dev. 11: 2323- 2334, 1997. 3 C c

GAM3229 221 NEUROD1 Naya, F. J.; Stellrecht, C. M.; Tsai, M. J.: Tissue- specific regulationof the insulin gene by a novel basic helix- loop- helix transcriptionfactor. Genes Dev. 9: 1009- 1019, 1995. 3 C c

GAM3229 221 NEUROD1 Tamimi, R.; Steingrimsson, E.; Copeland, N. G.; Dyer- Montgomery,K.; Lee, J. E.; Hernandez, R.; Jenkins, N. A.; Tapscott, S. J.: TheNEUROD gene maps to human chromosome 2q32 and mouse chromosome 2. Genomics 34:418- 421, 1996. 3 C c

GAM3229 221 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of NAD(P)H:quinonereductase by dietary antioxidants: possible role in protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77: 5216- 5220,1980. 3 C c

GAM3229 221 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.; Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of the long arm of human chromosome 16. Genomics 10:308- 312, 1991. 3 C c

GAM3229 221 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983. 3 C c

GAM3229 221 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum. Genet. 53: 189- 193, 1980. 3 C c

GAM3229 221 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578, 1988. 3 C c

GAM3229 221 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic variation in the prevalence of a common NAD(P)Hquinone oxidoreductase polymorphism and its implications for anti- cancerchemotherapy. Brit. J. Cancer 76: 852- 854, 1997. 3 C c

GAM3229 221 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further evidence for the regional localization of human APRT and DIA4on chromosome 16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984. 3 C c

GAM3229 221 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe increased susceptibility of individuals with a polymorphism inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat. Acad. Sci. 96: 8150- 8155, 1999. 3 C c

GAM3229 221 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA- 3 C c

4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980.

GAM3229 221 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. 3 C c
P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1)
gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382-
7389, 1998.

GAM3229 221 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; 3 C c
Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.;
Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.;
Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological
malignancy, is associated with the NQO1 609C- T mutationand rapid fractional
excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997.

GAM3229 221 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 C c
New York: Oxford Univ. Press (pub.) 1988.

GAM3229 221 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to 3 C c
cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999.

GAM3229 221 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, 3 C c
P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene
expression in human colon carcinoma cells: characterization ofa mutation
which modulates DT- diaphorase activity and mitomycin sensitivity.
CancerRes. 52: 797- 802, 1992.

GAM3229 221 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; 3 C c
Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H:
quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997.

GAM3229 221 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, 3 C c
S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and
long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese
workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998.

GAM3229 221 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the 3 C c
loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes.
Leukemia Res. 22: 105- 113, 1998.

GAM3229 221 OPRM1 Befort, K.; Filliol, D.; Decaillot, F. M.; Gaveriaux- Ruff, C.;Hoehe, M. R; 3 C c
Kieffer, B. L.: A single nucleotide polymorphic mutationin the human mu-
opioid receptor severely impairs receptor signaling. J.Biol. Chem. 276:
3130- 3137, 2001.

GAM3229 221 OPRM1 Bond, C.; LaForge, K. S.; Tian, M.; Melia, D.; Zhang, S.; Borg,L.; Gong, J.; 3 C c
Schluger, J.; Strong, J. A.; Leal, S. M.; Tischfield,J. A.; Kreek, M. J.;
Yu, L.: Single- nucleotide polymorphism in thehuman mu opioid receptor gene
alters beta- endorphin binding and activity:possible implications for opiate
addiction. Proc. Nat. Acad. Sci. 95:9608- 9613, 1998.

GAM3229 221 OPRM1 Chen, Y.; Mestek, A.; Liu, J.; Hurley, J. A.; Yu, L.: Molecularcloning and 3 C c
functional expression of a mu- opioid receptor from ratbrain. Molec. Pharm.
44: 8- 12, 1993.

GAM3229 221 OPRM1 He, L.; Fong, J.; von Zastrow, M.; Whistler, J. L.: Regulationof opioid 3 C c
receptor trafficking and morphine tolerance by receptoroligomerization. Cell
108: 271- 282, 2002.

GAM3229 221 OPRM1 Hoehe, M. R.; Kopke, K.; Wendel, B.; Rohde, K.; Flachmeier, C.;Kidd, K. K.; 3 C c
Berrettini, W. H.; Church, G. M.: Sequence variabilityand candidate gene
analysis in complex disease: association of muopioid receptor gene variation
with substance dependence. Hum. Molec.Genet. 9: 2895- 2908, 2000.

GAM3229 221 OPRM1 Hollt, V.: A polymorphism (A118G) in the mu- opioid receptor geneaffects the 3 C c

response to morphine- 6- glucuronide in humans. Pharmacogenetics 12:1- 2, 2002.

GAM3229 221 OPRM1 Kozak, C. A.; Filie, J.; Adamson, M. C.; Chen, Y.; Yu, L.: Murinechromosomal location of the mu and kappa opioid receptor genes. Genomics 21:659- 661, 1994. 3 C c

GAM3229 221 OPRM1 LaForge, K. S.; Yuferov, V.; Kreek, M. J.: Opioid receptor andpeptide gene polymorphisms: potential implications for addictions. Europ.J. Pharm. 410: 249- 268, 2000. 3 C c

GAM3229 221 OPRM1 Lotsch, J.; Skarke, C.; Grosch, S.; Darimont, J.; Schmidt, H.;Geisslinger, G.: The polymorphism A118G of the human mu- opioid receptorgene decreases the pupil constrictory effect of morphine- 6- glucuronidebut not that of morphine. Pharmacogenetics 12: 3- 9, 2002. 3 C c

GAM3229 221 OPRM1 Mansour, A.; Fox, C. A.; Burke, S.; Akil, H.; Watson, S. J.:Immunohistochemical localization of the clone mu opioid receptor inthe rat CNS. J. Chem. Neuroanat. 8: 283- 305, 1995. 3 C c

GAM3229 221 OPRM1 Meyer, U. A.: Pharmacogenetics and adverse drug reactions. Lancet 356:1667- 1671, 2000. 3 C c

GAM3229 221 OPRM1 Mogil, J. S.: The genetic mediation of individual differencesin sensitivity to pain and its inhibition. Proc. Nat. Acad. Sci. 96:7744- 7751, 1999. 3 C c

GAM3229 221 OPRM1 Uhl, G. R.; Sora, I.; Wang, Z.: The mu opiate receptor as a candidategene for pain: polymorphisms, variations in expression, nociception,and opiate responses. Proc. Nat. Acad. Sci. 96: 7752- 7755, 1999. 3 C c

GAM3229 221 OPRM1 Wang, J.- B.; Johnson, P. S.; Persico, A. M.; Hawkins, A. L.; Griffin,C. A.; Uhl, G. R.: Human mu opiate receptor: cDNA and genomic clones,pharmacologic characterization and chromosomal assignment. FEBS Lett. 338:217- 222, 1994. 3 C c

GAM3229 221 OPRM1 Wu, D.; Kang, Y.- S.; Bickel, U.; Pardridge, W. M.: Blood- brainbarrier permeability to morphine- 6- glucuronide is markedly reducedcompared with morphine. Drug Metab. Dispos. 25: 768- 771, 1997. 3 C c

GAM3229 221 OPRM1 Zubieta, J.- K.; Smith, Y. R.; Bueller, J. A.; Xu, Y.; Kilbourn,M. R.; Jewett, D. M.; Meyer, C. R.; Koeppe, R. A.; Stohler, C. S.: Regional mu opioid receptor regulation of sensory and affectivedimensions of pain. Science 293: 311- 315, 2001. 3 C c

GAM3229 221 OSM Miles, S. A.; Martinez- Maza, O.; Rezai, A.; Magpantay, L.; Kishimoto,T.; Nakamura, S.; Radka, S. F.; Linsley, P. S.: Oncostatin M as apotent mitogen for AIDS- Kaposi's sarcoma- derived cells. Science 255:1432- 1434, 1992. 3 C c

GAM3229 221 OSM Modur, V.; Feldhaus, M. J.; Weyrich, A. S.; Jicha, D. L.; Prescott,S. M.; Zimmerman, G. A.; McIntyre, T. M.: Oncostatin M is a proinflammatorymediator: in vivo effects correlate with endothelial cell expressionof inflammatory cytokines and adhesion molecules. J. Clin. Invest. 100:158- 168, 1997. 3 C c

GAM3229 221 OSM Nair, B. C.; DeVico, A. L.; Nakamura, S.; Copeland, T. D.; Chen,Y.; Patel, A.; O'Neil, T.; Oroszlan, S.; Gallo, R. C.; Sarngadharan,M. G.: Identification of a major growth factor for AIDS- Kaposi'ssarcoma cells as oncostatin M. Science 255: 1430- 1432, 1992. 3 C c

GAM3229 221 OSM Rose, T. M.; Bruce, A. G.: Oncostatin M is a member of a cytokinefamily that includes leukemia- inhibitory factor, granulocyte colony- stimulatingfactor, and interleukin 6. Proc. Nat. Acad. Sci. 88: 8641- 8645,1991. 3 C c

GAM3229 221 OSM Rose, T. M.; Lagrou, M. J.; Fransson, I.; Werelius, B.; Delattre,O.; Thomas, G.; de Jong, P. J.; Todaro, G. J.; Dumanski, J. P.: Thegenes for oncostatin 3 C c

M (OSM) and leukemia inhibitory factor (LIF)are tightly linked on human chromosome 22. Genomics 17: 136- 140,1993.

GAM3229 221 OSM Schwaller, J.; Parganas, E.; Wang, D.; Cain, D.; Aster, J. C.;Williams, I. R.; Lee, C.- K.; Gerthner, R.; Kitamura, T.; Frantsve,J.; Anastasiadou, E.; Loh, M. L.; Levy, D. E.; Ihle, J. N.; Gilliland,D. G.: Stat5 is essential for the myelo- and lymphoproliferativedisease induced by TEL/JAK2. Molec. Cell 6: 693- 704, 2000. 3 C c

GAM3229 221 OSM Zarling, J. M.; Shoyab, M.; Marquardt, H.; Hanson, M. B.; Lioubin,M. N.; Todaro, G. J.: Oncostatin M: a growth regulator produced bydifferentiated histiocytic lymphoma cells. Proc. Nat. Acad. Sci. 83:9739- 9743, 1986. 3 C c

GAM3229 221 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991. 3 C b

GAM3229 221 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine nucleotide synthesis on human chromosome 4 are closelylinked and divergently transcribed. J. Biol. Chem. 269: 5313- 5321,1994. 3 C b

GAM3229 221 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of three human multifunctional de novo purine biosyntheticgenes by functional complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920, 1990. 3 C b

GAM3229 221 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C b

GAM3229 221 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C b

GAM3229 221 PCDHB16 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997. 3 C c

GAM3229 221 PCDHB16 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of the coding sequences of unidentified human genes. XVIII.The complete sequences of 100 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 273- 281, 2000. 3 C c

GAM3229 221 PCDHB16 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGA12 Matsuyoshi, N.; Imamura, S.: Multiple cadherins are expressedin human fibroblasts. Biochem. Biophys. Res. Commun. 235: 355- 358,1997. 3 C c

GAM3229 221 PCDHGA12 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998. 3 C c

GAM3229 221 PCDHGA12 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene 3 C c

clusters. Genome Res. 11: 389- 404, 2001.

GAM3229 221 PCDHGA3 Wu, Q.; Maniatis, T.: A striking organization of a large familyof human neural cadherin like cell adhesion genes. Cell 97: 779- 790,1999. 3 C c

GAM3229 221 PCDHGA3 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGA5 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997. 3 C c

GAM3229 221 PCDHGA5 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGA8 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C c

GAM3229 221 PCDHGA8 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGB4 Matsuyoshi, N.; Imamura, S.: Multiple cadherins are expressedin human fibroblasts. Biochem. Biophys. Res. Commun. 235: 355- 358,1997. 3 C c

GAM3229 221 PCDHGB4 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGB7 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997. 3 C c

GAM3229 221 PCDHGB7 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGC3 Sago, H.; Kitagawa, M.; Obata, S.; Mori, N.; Taketani, S.; Rochelle,J. M.; Seldin, M. F.; Davidson, M.; St. John, T.; Suzuki, S. T.:Cloning, expression, and chromosomal localization of a novel cadherin-relatedprotein, protocadherin- 3. Genomics 29: 631- 640, 1995. 3 C c

GAM3229 221 PCDHGC3 Sano, K.; Tanihara, H.; Heimark, R. L.; Obata, S.; Davidson, M.;St. John, T.; Taketani, S.; Suzuki, S.: Protocadherins: a large familyof cadherin-related molecules in central nervous system. EMBO J. 12:2249- 2256, 1993. 3 C c

GAM3229 221 PCDHGC3 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 C c

GAM3229 221 PCDHGC4 Wu, Q.; Maniatis, T.: A striking organization of a large familyof human neural cadherin like cell adhesion genes. Cell 97: 779- 790,1999. 3 C c

GAM3229 221 PCDHGC4 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C c

Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM3229 221 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 3 C b
an ethanol- responsive potential modulator of guanine nucleotide-
bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM3229 221 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 C b
Cloning and characterization of the rat and human phosducin- likeprotein
genes: structure, expression and chromosomal localization. Biochim.Biophys.
Acta 1444: 346- 354, 1999.

GAM3229 221 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to 3 C c
two putative mammalian circadian regulators, mper1 andmper2, to light. Cell
91: 1055- 1064, 1997.

GAM3229 221 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM3229 221 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; 3 C c
Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and
mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531-
2534, 1999.

GAM3229 221 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of 3 C c
clock operative in the mammalian forebrain. Science 293:506- 509, 2001.

GAM3229 221 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; 3 C c
Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.;
Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock.
Science 288: 1013- 1019, 2000.

GAM3229 221 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; 3 C c
Reppert, S. M.: Two period homologs: circadian expression andphotic
regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997.

GAM3229 221 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; 3 C c
Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial
advanced sleep phase syndrome. Science 291: 1040- 1043,2001.

GAM3229 221 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; 3 C c
Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the
mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694,
2001.

GAM3229 221 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; 3 C c
Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the
mammalian circadian clock. Nature 400: 169- 173,1999.

GAM3229 221 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; 3 C b
Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx
activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C.
Genomics 47: 323- 324, 1998.

GAM3229 221 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, 3 C b
S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to
human chromosome 21q22.3. Genomics 41: 193- 200,1997.

GAM3229 221 PLA2G2D Ishizaki, J.; Suzuki, N.; Higashino, K.; Yokota, Y.; Ono, T.; Kawamoto,K.; 3 C c
Fujii, N.; Arita, H.; Hanasaki, K.: Cloning and characterizationof novel

mouse and human secretory phospholipase A(2)s. J. Biol.Chem. 274: 24973-24979, 1999.

GAM3229 221 PLA2G2D Shakhov, A. N.; Rubtsov, A. V.; Lyakhov, I. G.; Tumanov, A. V.;Nedospasov, S. A.: SPLASH (PLA(2)IID), a novel member of phospholipaseA2 family, is associated with lymphotoxin- deficiency. Genes Immun. 1:191- 199, 2000. 3 C c

GAM3229 221 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component of the steroid receptor complex: cloning of thecDNA and further characterization. J. Biol. Chem. 268: 12303- 12310,1993. 3 C b

GAM3229 221 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem. 267: 5503- 5507, 1992. 3 C b

GAM3229 221 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151 only, 1997. 3 C b

GAM3229 221 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; J.- E.: The structure and complete nucleotide sequenceof the human cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996. 3 C b

GAM3229 221 PRM2 Cho, C.; Willis, W. D.; Goulding, E. H.; Jung- Ha, H.; Choi, Y.- C.;Hecht, N. B.; Eddy, E. M.: Haploinsufficiency of protamine- 1 or - 2causes infertility in mice. Nature Genet. 28: 82- 86, 2001. 3 C c

GAM3229 221 PRM2 Domenjoud, L.; Fronia, C.; Uhde, F.; Engel, W.: Sequence of humanprotamine 2 cDNA. Nucleic Acids Res. 16: 7733 only, 1988. 3 C c

GAM3229 221 PRM2 Reeves, R. H.; Gearhart, J. D.; Hecht, N. B.; Yelick, P.; Johnson,P.; O'Brien, S. J.: The gene encoding protamine 1 is located on chromosome16 in humans and near the proximal end of mouse chromosome 16, whereit is tightly linked to protamine 2. (Abstract) Cytogenet. Cell Genet. 46:680 only, 1987. 3 C c

GAM3229 221 PRM2 Reeves, R. H.; Gearhart, J. D.; Hecht, N. B.; Yelick, P.; Johnson,P.; O'Brien, S. J.: The gene encoding protamine 1 is located on humanchromosome 16, and near the proximal end of mouse chromosome 16 whereit is tightly linked to the gene encoding protamine 2. J. Hered. 80:442- 446, 1989. 3 C c

GAM3229 221 PRM2 Viguie, F.; Domenjoud, L.; Rousseau- Merck, M.- F.; Dadoune, J.- P.;Chevaillier, P.: Chromosomal localization of the human protaminegenes, PRM1 and PRM2, to 16p13.3 by in situ hybridization. Hum. Genet. 85:171- 174, 1990. 3 C c

GAM3229 221 PSME3 Albertsen, H. M.; Smith, S. A.; Mazoyer, S.; Fujimoto, E.; Stevens,J.; Williams, B.; Rodriguez, P.; Cropp, C. S.; Slijepcevic, P.; Carlson,M.; Robertson, M.; Bradley, P.; Lawrence, E.; Harrington, T.; MeiSheng, Z.; Hoopes, R.; Sternberg, N.; Brothman, A.; Callahan, R.;Ponder, B. A. J.; White, R.: A physical map and candidate genes inthe BRCA1 region on chromosome 17q12- 21. Nature Genet. 7: 472- 479,1994. 3 C c

GAM3229 221 PSME3 Kandil, E.; Kohda, K.; Ishibashi, T.; Tanaka, K.; Kasahara, M.: PA28 subunits of the mouse proteasome: primary structures and chromosomallocalization of the genes. Immunogenetics 46: 337- 344, 1997. 3 C c

GAM3229 221 PSME3 Nikaido, T.; Shimada, K.; Shibata, M.; Hata, M.; Sakamoto, M.;Takasaki, Y.; Sato, C.; Takahashi, T.; Nishida, Y.: Cloning and nucleotidesequence of cDNA for Ki antigen, a highly conserved nuclear proteindetected with sera from patients with systemic lupus erythematosus. Clin.Exp. Immun. 79: 209- 214, 1990. 3 C c

GAM3229 221 PVR Gromeier, M.; Solecki, D.; Patel, D. D.; Wimmer, E.: Expressionof the human 3 C c

poliovirus receptor/CD155 gene during development ofthe central nervous system: implications for the pathogenesis of poliomyelitis. Virology 273:248- 257, 2000.

GAM3229 221 PVR He, Y.; Bowman, V. D.; Mueller, S.; Bator, C. M.; Bella, J.; Peng,X.; Baker, T. S.; Wimmer, E.; Kuhn, R. J.; Rossmann, M. G.: Interactionof the poliovirus receptor with poliovirus. Proc. Nat. Acad. Sci. 97:79- 84, 2000. 3 C c

GAM3229 221 PVR Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka,N.; Takeuchi, K.; Takegami, T.; Nomoto, A.: The poliovirus receptorprotein is produced both as membrane- bound and secreted forms. EMBOJ. 9: 3217- 3224, 1990. 3 C c

GAM3229 221 PVR Koike, S.; Taya, C.; Kurata, T.; Abe, S.; Ise, I.; Yonekawa, H.;Nomoto, A.: Transgenic mice susceptible to poliovirus. Proc. Nat.Acad. Sci. 88: 951- 955, 1991. 3 C c

GAM3229 221 PVR Mendelsohn, C. L.; Wimmer, E.; Racaniello, V. R.: Cellular receptorfor poliovirus: molecular cloning, nucleotide sequence, and expressionof a new member of the immunoglobulin superfamily. Cell 56: 855- 865,1989. 3 C c

GAM3229 221 PVR Mendelsohn, C.; Johnson, B.; Lionetti, K. A.; Nobis, P.; Wimmer,E.; Racaniello, V. R.: Transformation of a human poliovirus receptorgene into mouse cells. Proc. Nat. Acad. Sci. 83: 7845- 7849, 1986. 3 C c

GAM3229 221 PVR Miller, D. A.; Miller, O. J.; Dev, V. G.; Hashmi, S.; Tantravahi,R. R.; Medrano, L.; Green, H.: Human chromosome 19 carries a poliovirusreceptor gene. Cell 1: 167- 174, 1974. 3 C c

GAM3229 221 PVR Schonk, D.; van Dijk, P.; Riegmann, P.; Trapman, J.; Holm, C.;Willcocks, T. C.; Sillekens, P.; van Venrooij, W.; Wimmer, E.; Geurtsvan Kessel, A.; Ropers, H.- H.; Wieringa, B.: Assignment of sevengenes to distinct intervals on the midportion of human chromosome19q surrounding the myotonic dystrophy gene region. Cytogenet. CellGenet. 54: 15- 19, 1990. 3 C c

GAM3229 221 PVR Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal mouse chromosome 9 linkage map that further defines linkagegroups homologous with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685, 1991. 3 C c

GAM3229 221 PVR Shepley, M. P.; Sherry, B.; Weiner, H. L.: Monoclonal antibodyidentification of a 100- kDa membrane protein in HeLa cells and humanspinal cord involved in poliovirus attachment. Proc. Nat. Acad. Sci. 85:7743- 7747, 1988. 3 C c

GAM3229 221 PVR Siddique, T.; Bartlett, R. J.; McKinney, R.; Hung, W.- Y.; Bruns,G.; Wilfert, C.; Roses, A. D.: The poliovirus sensitivity (PVS) ison chromosome 19q13- qter. (Abstract) Cytogenet. Cell Genet. 40:745 only, 1985. 3 C c

GAM3229 221 PVR Siddique, T.; McKinney, R.; Hung, W.- Y.; Bartlett, R. J.; Bruns,G.; Mohandas, T. K.; Ropers, H.- H.; Wilfert, C.; Roses, A. D.: Thepoliovirus sensitivity (PVS) gene is on chromosome 19q12- q13.2. Genomics 3:156- 160, 1988. 3 C c

GAM3229 221 PVR Solecki, D. J.; Gromeier, M.; Mueller, S.; Bernhardt, G.; Wimmer,E.: Expression of the human poliovirus receptor/CD155 gene is activatedby Sonic hedgehog. J. Biol. Chem. 277: 25697- 25702, 2002. 3 C c

GAM3229 221 PVR Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993. 3 C c

GAM3229 221 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in 3 C b

RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993.

GAM3229 221 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 3 C b
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA
amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM3229 221 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. 3 C b
Med. 339: 1775- 1777, 1998.

GAM3229 221 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand 3 C b
molecular genetics. Blood Rev. 8: 199- 212, 1994.

GAM3229 221 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; 3 C b
Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood
group polymorphism as determined by Southern analysis. Blood 78:2747- 2752,
1991.

GAM3229 221 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and 3 C b
its association with universal edema of the fetus, icterusgravis neonatorum
and anemia of the newborn. J. Pediat. 1: 269- 309,1932.

GAM3229 221 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies 3 C b
in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989.

GAM3229 221 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with 3 C b
sickle cell disease. Transfusion 37: 357- 361, 1997.

GAM3229 221 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 C b

GAM3229 221 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the 3 C b
human RH locus: a family study of the red- cell Evans phenotypereveals a
transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59:
825- 833, 1996.

GAM3229 221 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular 3 C b
definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J.
Hum. Genet. 58: 133- 142, 1996.

GAM3229 221 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of 3 C b
Rh blood group genes: association between restrictionfragment length
polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994.

GAM3229 221 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine 3 C b
years and some observations on the biochemistry and geneticsof the system.
Transfusion Med. Rev. 3: 1- 12, 1989.

GAM3229 221 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh 3 C b
genes revealed by analysis of unrelated donors with therare D- - phenotype.
Am. J. Hum. Genet. 59: 1066- 1073, 1996.

GAM3229 221 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, 3 C b
J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by
alternative splicing. Blood 80: 1074- 1078, 1992.

GAM3229 221 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; 3 C b
Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the
human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929,
1992.

GAM3229 221 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; 3 C b
Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE
genotyping for correct blood group determination inchronically transfused
patients. Transfusion 39: 852- 855, 1999.

GAM3229 221 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its 3 C b
possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A.
116:825- 827, 1941.

GAM3229 221 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; 3 C b
Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.:
Prenatal diagnosis of fetal RhD status by molecular analysisof maternal
plasma. New Eng. J. Med. 339: 1734- 1738, 1998.

GAM3229 221 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; 3 C b
Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases
of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome
1. Am. J. Med. Genet. 104: 250- 256, 2001.

GAM3229 221 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, 3 C b
E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J.
Clin. Invest. 100: 373- 379, 1997.

GAM3229 221 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 C b
153:771- 772, 1944.

GAM3229 221 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 C b
ed.): 1975.

GAM3229 221 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 3 C b
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII)
category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM3229 221 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 3 C b
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral
transduction of K562 cells establishes the molecular basisof Rh blood group
antigens. Blood 87: 2968- 2973, 1996.

GAM3229 221 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 3 C b
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang.
58: 50- 55, 1990.

GAM3229 221 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 3 C b
Blood 95: 3662- 3668, 2000.

GAM3229 221 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 3 C b
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393,
1999.

GAM3229 221 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 3 C b
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311,
2002.

GAM3229 221 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 C b

GAM3229 221 S100A1 Engelkamp, D.; Schafer, B. W.; Mattei, M. G.; Erne, P.; Heizmann,C. W.: Six 3 C c
S100 genes are clustered on human chromosome 1q21: identificationof two
genes coding for the two previously unreported calcium- bindingproteins
S100D and S100E. Proc. Nat. Acad. Sci. 90: 6547- 6551, 1993.

GAM3229 221 S100A1 Herrera, G. A.; Turbat- Herrera, E. A.; Lott, R. L.: S- 100 3 C c
proteinexpression by primary and metastatic adenocarcinomas. Am. J.
Clin.Path. 89: 168- 176, 1988.

GAM3229 221 S100A1 Isobe, T.; Tsugira, A.; Okuyama, T.: Amino acid sequence of thesubunit 3 C c
structure of bovine brain S- 100 protein (PAP 1- b). J. Neurochem. 30:921-
923, 1978.

GAM3229 221 S100A1 Moore, B. W.: A soluble protein characteristic of the nervoussystem. 3 C c
Biochem. Biophys. Res. Commun. 19: 739- 744, 1965.

GAM3229 221 S100A1 Morii, K.; Tanaka, R.; Takahashi, Y.; Minoshima, S.; Fukuyama,R.; Shimizu, 3 C c
N.; Kuwano, R.: Structure and chromosome assignmentof human S100 alpha and
beta subunit genes. Biochem. Biophys. Res.Commun. 175: 185- 191, 1991.

GAM3229 221 S100A1 Most, P.; Bernotat, J.; Ehlermann, P.; Pleger, S. T.; Reppel, M.;Borries, 3 C c

M.; Niroomand, F.; Pieske, B.; Janssen, P. M. L.; Eschenhagen,T.; Karczewski, P.; Smith, G. L.; Koch, W. J.; Katus, H. A.; Remppis,A.: S100A1: a regulator of myocardial contractility. Proc. Nat.Acad. Sci. 98: 13889-13894, 2001.

GAM3229 221 S100A1 Schafer, B. W.; Wicki, R.; Engelkamp, D.; Mattei, M.- G.; Heizmann,C. W.: 3 C c
Isolation of a YAC clone covering a cluster of nine S100 geneson human chromosome 1q21: rationale for a new nomenclature of theS100 calcium-binding protein family. Genomics 25: 638- 643, 1995.

GAM3229 221 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, 3 C b
P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001.

GAM3229 221 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- 3 C b
linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002.

GAM3229 221 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. 3 C b
C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000.

GAM3229 221 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; 3 C b
Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999.

GAM3229 221 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; 3 C b
Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001.

GAM3229 221 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; 3 C b
Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001.

GAM3229 221 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. 3 C b
A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five-base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000.

GAM3229 221 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene 3 C b
for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001.

GAM3229 221 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, 3 C b
H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002.

GAM3229 221 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; 3 C b
Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X-linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398-1407,2001.

GAM3229 221 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked 3 C b
recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic

evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999.

GAM3229 221 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001. 3 C b

GAM3229 221 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996. 3 C b

GAM3229 221 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001. 3 C b

GAM3229 221 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 C b

GAM3229 221 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996. 3 C b

GAM3229 221 SIGLEC5 Cornish, A. L.; Freeman, S.; Forbes, G.; Ni, J.; Zhang, M.; Cepeda,M.; Gentz, R.; Augustus, M.; Carter, K. C.; Crocker, P. R.: Characterizationof siglec- 5, a novel glycoprotein expressed on myeloid cells relatedto CD33. Blood 92: 2123- 2132, 1998. 3 C c

GAM3229 221 SIGLEC5 Kim, H.- S.: Assignment of the human OB binding protein- 2 gene(CD33L2) to chromosome 19q13.3 by radiation hybrid mapping. Cytogenet.Cell Genet. 84: 96 only, 1999. 3 C c

GAM3229 221 SIGLEC5 Patel, N.; Brinkman- Van der Linden, E. C. M.; Altmann, S. W.; Gish,K.; Balasubramanian, S.; Timans, J. C.; Peterson, D.; Bell, M. P.;Bazan, J. F.; Varki, A.; Kastelein, R. A.: OB- BP1/Siglec- 6: a leptin- and sialic acid-binding protein of the immunoglobulin superfamily. J.Biol. Chem. 274: 22729-22738, 1999. 3 C c

GAM3229 221 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 3 C b

GAM3229 221 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 3 C b

GAM3229 221 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 3 C b

GAM3229 221 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human intestine:biology and function. Gastroenterology 113: 332- 340, 1997. 3 C b

GAM3229 221 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563-566, 1994. 3 C b

GAM3229 221 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 3 C b

GAM3229 221 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998. 3 C b

GAM3229 221 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet. 103: 411- 414, 1998. 3 C b

GAM3229 221 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses and phylogenetic characterization of the ZIP family of metalion transport proteins. J. Membr. Biol. 166: 1- 7, 1998. 3 C c

GAM3229 221 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping within the epidermal differentiation complex. Genomics 62:272- 280, 1999. 3 C c

GAM3229 221 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC fragmentation map of 1q21. Genomics 49: 200- 208, 1998. 3 C c

GAM3229 221 SLC6A12 Borden, L. A.; Smith, K. E.; Gustafson, E. L.; Branchek, T. A.;Weinshank, R. L.: Cloning and expression of a betaine/GABA transporterfrom human brain. J. Neurochem. 64: 977- 984, 1995. 3 C c

GAM3229 221 SLC6A12 Rasola, A.; Galietta, L. J. V.; Barone, V.; Romeo, G.; Bagnasco,S.: Molecular cloning and functional characterization of a GABA/betainetransporter from human kidney. FEBS Lett. 373: 229- 233, 1995. 3 C c

GAM3229 221 SLC6A12 Yamauchi, A.; Uchida, S.; Kwon, H. M.; Preston, A. S.; Robey, R.B.; Garcia- Perez, A.; Burg, M. B.; Handler, J. S.: Cloning of a Na(+)and Cl(-)- dependent betaine transporter that is regulated by hypertonicity. J.Biol. Chem. 267: 649- 652, 1992. 3 C c

GAM3229 221 SLC7A5 Gaugitsch, H. W.; Prieschl, E. E.; Kalthoff, F.; Huber, N. E.;Baumruker, T.: A novel transiently expressed, integral membrane proteinlinked to cell activation: molecular cloning via the rapid degradationsignal AUUUA. J. Biol. Chem 267: 11267- 11273, 1992. 3 C c

GAM3229 221 SLC7A5 Kanai, Y.; Segawa, H.; Miyamoto, K.; Uchino, H.; Takeda, H.; Endou,H.: Expression cloning and characterization of a transporter forlarge neutral amino acids activated by the heavy chain of 4F2 antigen(CD98). J. Biol. Chem. 273: 23629- 23632, 1998. 3 C c

GAM3229 221 SLC7A5 Maglott, D. R.; Durkin, A. S.; Lane, S. A.; Callen, D. F.; Feldblyum,T. V.; Nierman, W. C.: The gene for membrane protein E16 (D16S469E)maps to human chromosome 16q24.3 and is expressed in human brain,thymus, and retina. Genomics 23: 303- 304, 1994. 3 C c

GAM3229 221 SLC7A5 Mastroberardino, L.; Spindler, B.; Pfeiffer, R.; Skelly, P. J.;Loffing, J.; Shoemaker, C. B.; Verrey, F.: Amino- acid transport byheterodimers of 4F2hc/CD98 and members of a permease family. Nature 395:288- 291, 1998. 3 C c

GAM3229 221 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998. 3 C c

GAM3229 221 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic 3 C c

organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle-membranefusion processes. Hum. Genet. 108: 211- 215, 2001.

GAM3229 221 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle- 3 C c
membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells.
Biochem. Biophys. Res. Commun. 231: 808- 812, 1997.

GAM3229 221 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel 3 C c
syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in
non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996.

GAM3229 221 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: 3 C c
Identification of three new splice variants of the SNARE proteinSNAP- 23.
Biochem. Biophys. Res. Commun. 285: 320- 327, 2001.

GAM3229 221 SP110 Kadereit, S.; Gewert, D. R.; Galabru, J.; Hovanessian, A. G.; Meurs,E. F.: 3 C c
Molecular cloning of two new interferon- induced, highly relatednuclear
phosphoproteins. J. Biol. Chem. 268: 24432- 24441, 1993.

GAM3229 221 SP110 Welsh, G. I.; Kadereit, S.; Coccia, E. M.; Hovanessian, A. G.;Meurs, E. F.: 3 C c
Colocalization within the nucleolus of two highly relatedIFN- induced human
nuclear phosphoproteins with nucleolin. Exp. CellRes. 250: 62- 74, 1999.

GAM3229 221 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 3 C b
L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and
SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human
synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM3229 221 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 3 C b
J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and
SSX2, encoding proteins with homology to the Kruppel- associatedbox in human
synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM3229 221 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 3 C b
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand
characterization of the mouse homolog of SYT, a gene implicatedin the
development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM3229 221 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 3 C b
G.: Mapping and characterization of the mouse and humanSS18 genes, two human
SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-
319, 2001.

GAM3229 221 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 C b
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene
family with several members transcribed in normaltestis and human cancer.
Int. J. Cancer 72: 965- 971, 1997.

GAM3229 221 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 C b
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand
prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM3229 221 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 C b
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J.
Nat. Cancer Inst. 91: 974- 975, 1999.

GAM3229 221 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 C b
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX
synovial sarcoma translocation proteins and co- localizationwith the SNF
protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM3229 221 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 C b
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in

synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM3229 221 TAF11 Birck, C.; Poch, O.; Romier, C.; Ruff, M.; Mengus, G.; Lavigne,A.- C.; Davidson, I.; Moras, D.: Human TAFII28 and TAFII18 interactthrough a histone fold encoded by atypical evolutionary conservedmotifs also found in the SPT3 family. Cell 94: 239- 249, 1998. 3 C c

GAM3229 221 TAF11 Mengus, G.; May, M.; Jacq, X.; Staub, A.; Tora, L.; Chambon, P.;Davidson, I.: Cloning and characterization of hTAFII18, hTAFII20and hTAFII28: three subunits of the human transcription factor TFIID. EMBOJ. 14: 1520- 1531, 1995. 3 C c

GAM3229 221 TAL1 Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 3 C b

GAM3229 221 TAL1 Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 C b

GAM3229 221 TAL1 Begley, C. G.; Aplan, P. D.; Davey, M. P.; Nakahara, K.; Tchorz,K.; Kurtzberg, J.; Hershfield, M. S.; Haynes, B. F.; Cohen, D. I.;Waldmann, T. A.; Kirsch, I. R.: Chromosomal translocation in a humanleukemic stem- cell line disrupts the T- cell antigen receptor delta- chaindiversity region and results in a previously unreported fusion transcript. Proc.Nat. Acad. Sci. 86: 2031- 2035, 1989. 3 C b

GAM3229 221 TAL1 Begley, C. G.; Visvader, J.; Green, A. R.; Aplan, P. D.; Metcalf,D.; Kirsch, I. R.; Gough, N. M.: Molecular cloning and chromosomallocalization of the murine homolog of the human helix- loop- helix geneSCL. Proc. Nat. Acad. Sci. 88: 869- 873, 1991. 3 C b

GAM3229 221 TAL1 Finger, L. R.; Kagan, J.; Christopher, G.; Kurtzberg, J.; Hershfield,M. S.; Nowell, P. C.; Croce, C. M.: Involvement of the TCL5 geneon human chromosome 1 in T- cell leukemia and melanoma. Proc. Nat.Acad. Sci. 86: 5039- 5043, 1989. 3 C b

GAM3229 221 TAL1 Gottgens, B.; Barton, L. M.; Chapman, M. A.; Sinclair, A. M.; Knudsen,B.; Grafham, D.; Gilbert, J. G. R.; Rogers, J.; Bentley, D. R.; Green,A. R.: Transcriptional regulation of the stem cell leukemia gene(SCL)- - comparative analysis of five vertebrate SCL loci. Genome Res. 12:749- 759, 2002. 3 C b

GAM3229 221 TAL1 Gottgens, B.; Gilbert, J. G.; Barton, L. M.; Grafham, D.; Rogers,J.; Bentley, D. R.; Green, A. R.: Long- range comparison of humanand mouse SCL loci: localized regions of sensitivity to restrictionendonucleases correspond precisely with peaks of conserved noncodingsequences. Genome Res. 11: 87- 97, 2001. 3 C b

GAM3229 221 TAL1 Kocher, O.; Cheresh, P.; Lee, S. W.: Identification and partialcharacterization of a novel membrane- associated protein (MAP17) up-regulatedin human carcinomas and modulating cell replication and tumor growth. Am.J. Path. 149: 493- 500, 1996. 3 C b

GAM3229 221 TAL1 Kozak, M.: An analysis of 5- prime- noncoding sequences from 699vertebrate messenger RNAs. Nucleic Acids Res. 15: 8125- 8148, 1987. 3 C b

GAM3229 221 TAL1 Kurtzberg, J.; Bigner, S. H.; Hershfield, M. S.: Establishmentof the DU.528 human lymphohemopoietic stem cell line. J. Exp. Med. 162:1561- 1578, 1985. 3 C b

GAM3229 221 TAL1 Robb, L.; Lyons, I.; Li, R.; Hartley, L.; Kontgen, F.; Harvey,R. P.; 3 C b

Metcalf, D.; Begley, C. G.: Absence of yolk sac hematopoiesisfrom mice with a targeted disruption of the scl gene. Proc. Nat.Acad. Sci. 92: 7075- 7079, 1995.

GAM3229 221 TAL1 Shivdasani, R. A.; Mayer, E. L.; Orkin, S. H.: Absence of bloodformation in mice lacking the T- cell leukaemia oncoprotein tal- 1/SCL. Nature 373:432-434, 1995. 3 C b

GAM3229 221 TAL1 Sinclair, A. M.; Bench, A. J.; Bloor, A. J. C.; Li, J.; Gottgens,B.; Stanley, M. L.; Miller, J.; Piltz, S.; Hunter, S.; Nacheva, E.P.; Sanchez, M.- J.; Green, A. R.: Rescue of the lethal scl- /- phenotypeby the human SCL locus. Blood 99: 3931- 3938, 2002. 3 C b

GAM3229 221 TAL1 Williams, M.; Lyu, M. S.; Yang, Y. L.; Lin, E. P.; Dunbrack, R.;Birren, B.; Cunningham, J.; Hunter, K.: Ier5, a novel member of theslow- kinetics immediate- early genes. Genomics 44: 327- 334, 1999. 3 C b

GAM3229 221 TAL1 Xia, Y.; Brown, L.; Yang, C. Y.- C.; Tsou Tsan, J.; Siciliano,M. J.; Espinosa, R., III; Le Beau, M. M.; Baer, R. J.: TAL2, a helix- loop-helixgene activated by the (7;9)(q34;q32) translocation in human T-cellleukemia. Proc. Nat. Acad. Sci. 88: 11416- 11420, 1991. 3 C b

GAM3229 221 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459-467, 1998. 3 C c

GAM3229 221 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 C c

GAM3229 221 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 C c

GAM3229 221 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 C c

GAM3229 221 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 C c

GAM3229 221 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 C c

GAM3229 221 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496-1498, 2002. 3 C c

GAM3229 221 TEAD3 Jacquemin, P.; Chen, Z.; Martial, J. A.; Davidson, I.: Genomicstructure and chromosomal mapping of the mouse transcription factorTEF- 5 (Tead3) gene. Mammalian Genome 10: 632- 634, 1999. 3 C c

GAM3229 221 TEAD3 Jacquemin, P.; Depetris, D.; Mattei, M.- G.; Martial, J. A.; Davidson,I.: Localization of human transcription factor TEF- 4 and TEF- 5 (TEAD2,TEAD3) genes to chromosomes 19q13.3 and 6p21.2 using fluorescencein situ hybridization and radiation hybrid analysis. Genomics 55:127- 129, 1999. 3 C c

GAM3229 221 TEAD3 Jacquemin, P.; Martial, J. A.; Davidson, I.: Human TEF- 5 is preferentiallyexpressed in placenta and binds to multiple functional 3 C c

elements ofthe human chorionic somatomammotropin- B gene enhancer. J. Biol. Chem. 272:12928- 12937, 1997.

GAM3229 221 TEAD3 Jiang, S.- W.; Wu, K.; Eberhardt, N. L.: Human placental TEF- 3 C c
5transactivates the human chorionic somatomammotropin gene enhancer. Molec.Endocr. 13: 879- 889, 1999.

GAM3229 221 TES Tatarelli, C.; Linnenbach, A.; Mimori, K.; Croce, C. M.: Characterizationof 3 C c
the human TESTIN gene localized in the FRA7G region at 7q31.2. Genomics 68:1- 12, 2000.

GAM3229 221 TES Tobias, E. S.; Hurlstone, A. F. L.; MacKenzie, E.; McFarlane, R.;Black, D. 3 C c
M.: The TES gene at 7q31.1 is methylated in tumours andencodes a novel growth- suppressing LIM domain protein. Oncogene 20:2844- 2853, 2001.

GAM3229 221 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 3 C b
B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999.

GAM3229 221 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 C b
B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997.

GAM3229 221 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 C b
B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997.

GAM3229 221 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 C b
B W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM3229 221 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 C b
B decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997.

GAM3229 221 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 C b
B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997.

GAM3229 221 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 C b
B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM3229 221 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 C b
B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM3229 221 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 C b
B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM3229 221 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 C b
B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.

GAM3229 221 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 C c

Thiopurinemethyltransferase pharmacogenetics: alternative molecular diagnosisand preliminary data from Northern Portugal. Pharmacogenetics 9:257- 261, 1999.

GAM3229 221 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 C c
McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM3229 221 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 C c
Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof thiopurine methyltransferase alleles in Caucasian and Asian populations. Pharmacogenetics 9:37- 42, 1999.

GAM3229 221 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 C c
mercaptopurine metabolism, toxic effects, and dosagerequirement in a thiopurine methyltransferase- deficient child withacute lymphocytic leukemia. J. Pediat. 119: 985- 989, 1991.

GAM3229 221 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 C c
Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM3229 221 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 C c
Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine methyltransferase:molecular cloning and expression of T84 colon carcinoma cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM3229 221 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 C c
thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747- 749, 1993.

GAM3229 221 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 C c
Evans, W. E.: A single point mutation leading to loss of catalyticactivity in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953, 1995.

GAM3229 221 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 C c
variation in response to 6- mercaptopurine for childhoodacute lymphoblastic leukaemia. Lancet 336: 225- 229, 1990.

GAM3229 221 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 C c
azathioprine toxicity: relationship to thiopurine methyltransferasegenetic polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM3229 221 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 C c
Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in thiopurine methyltransferase pharmacogenetics: evidencefor allele specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773- 776, 1999.

GAM3229 221 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human 3 C c
thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon splice junction mutation that results in lossof activity. J. Clin. Invest. 101: 1036- 1044, 1998.

GAM3229 221 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; 3 C c
Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.; Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997.

GAM3229 221 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; 3 C c
Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine methyltransferase pharmacogenetics: human gene cloningand characterization

of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996.

GAM3229 221 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: 3 C c
Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by
mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic
polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997.

GAM3229 221 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; 3 C c
Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency:
two nucleotide transitions define the most prevalent mutantallele associated
with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694-
702, 1996.

GAM3229 221 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine 3 C c
pharmacogenetics:monogenic inheritance of erythrocyte thiopurine
methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980.

GAM3229 221 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, 3 C c
psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994.

GAM3229 221 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; 3 C c
Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired
nociception and pain sensation in mice lacking the capsaicinreceptor.
Science 288: 306- 313, 2000.

GAM3229 221 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. 3 C c
D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the
pain pathway. Nature 389: 816- 824, 1997.

GAM3229 221 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, 3 C c
A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release
the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411:
957- 962, 2001.

GAM3229 221 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity 3 C c
to 'hot' chili peppers. Cell 108: 421- 430, 2002.

GAM3229 221 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, 3 C c
A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related
osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor.
Cell 103: 525- 535, 2000.

GAM3229 221 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated 3 C c
by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J.
Neurophysiol. 76: 1858- 1869, 1996.

GAM3229 221 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel 3 C c
activity by protein kinase C. Nature 408: 985- 990, 2000.

GAM3229 221 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand 3 C c
multiple presentations of the oral irritant zingerone: relationshipto
frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996.

GAM3229 221 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith 3 C c
capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994.

GAM3229 221 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand 3 C c
pleasantness for the capsaicin burn between chili likers and non-
likers:implications for liking development. Chem. Senses 18: 471- 482, 1993.

GAM3229 221 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; 3 C c
McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.;
Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic
cystinosis gene (CTNS): complete sequencing of a200- kb segment and
discovery of a novel gene within the common cystinosis- causingdeletion.

Genome Res. 10: 165- 173, 2000.

GAM3229 221 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002. 3 C c

GAM3229 221 TUFT1 Bashir, M. M.; Abrams, W. R.; Tucker, T.; Sellinger, B.; Budarf,M.; Emanuel, B.; Rosenbloom, J.: Molecular cloning and characterizationof the bovine and human tuftelin genes. Connect. Tissue Res. 39:13- 24, 1998. 3 C c

GAM3229 221 TUFT1 Deutsch, D.: Structure and function of enamel gene products. Anat.Rec. 224: 189- 210, 1989. 3 C c

GAM3229 221 TUFT1 Deutsch, D.; Palmon, A.; Dafni, L.; Fisher, L.; Termine, J. D.;Young, M.: Cloning, sequencing, and characterization of tuftelin:a novel acidic enamel protein. Connect. Tissue Res. 27: 121 only,1992. 3 C c

GAM3229 221 TUFT1 Deutsch, D.; Palmon, A.; Fisher, L. W.; Kolodny, N.; Termine, J.D.; Young, M. F.: Sequencing of bovine enamelin (tuftelin), a novelacidic enamel protein. J. Biol. Chem. 266: 16021- 16028, 1991. 3 C c

GAM3229 221 TUFT1 Deutsch, D.; Palmon, A.; Young, M. F.; Selig, S.; Kearns, W. G.;Fisher, L. W.: Mapping of the human tuftelin (TUFT1) gene to chromosome1 by fluorescence in situ hybridization. (Abstract) Mammalian Genome 5:461- 462, 1994. 3 C c

GAM3229 221 TUFT1 MacDougall, M.; Simmons, D.; Dodds, A.; Knight, C.; Luan, X.; Zeichner-David,M.; Zhang, C.; Ryu, O. H.; Qian, Q.; Simmer, J. P.; Hu, C.- C.: Cloning,characterization, and tissue expression pattern of mouse tuftelincDNA. J. Dent. Res. 77: 1970- 1978, 1998. 3 C c

GAM3229 221 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 C c

GAM3229 221 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 C c

GAM3229 221 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 C c

GAM3229 221 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 C c

GAM3229 221 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000. 3 C c

GAM3229 221 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938. 3 C c

GAM3229 221 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. 3 C c

G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999.

GAM3229 221 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, 3 C c
F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM3229 221 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 3 C c
Arch.Neurol. 28: 67- 68, 1973.

GAM3229 221 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 3 C c
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM3229 221 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 3 C c
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM3229 221 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 3 C c
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM3229 221 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 3 C c
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell, J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.; Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the von Hippel- Lindau disease tumorsuppressor gene: correlations with phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM3229 221 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 C c
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM3229 221 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 C c
disease. J.A.M.A. 178: 280- 282, 1961.

GAM3229 221 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 C c
peculiar vascular new growth, probably primarily retinal,affecting both eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM3229 221 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 C c
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM3229 221 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 C c
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E. R.: Identification of intragenic mutations in thevon Hippel- Lindau disease tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994.

GAM3229 221 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's 3 C c
disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928.

GAM3229 221 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- 3 C c
expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994.

GAM3229 221 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p 3 C c
involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988.

GAM3229 221 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, 3 C c
S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the

effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459-
6463, 1995.

GAM3229 221 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. 3 C c
P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.:
Inhibition of transcription elongation by the VHL tumor suppressorprotein.
Science 269: 1402- 1406, 1995.

GAM3229 221 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; 3 C c
Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W.
M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple
endocrine neoplasia type 2 display distinctbiochemical and clinical
phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001.

GAM3229 221 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; 3 C c
Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P.
A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-
oncogene and the von Hippel- Lindau disease tumoursuppressor gene in
sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937,
1995.

GAM3229 221 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, 3 C c
J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian,
Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.;
Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans
EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate
HIF by prolyl hydroxylation. Cell107: 43- 54, 2001.

GAM3229 221 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 C c

GAM3229 221 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of 3 C c
cancer. Science 278: 1043- 1050, 1997.

GAM3229 221 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of 3 C c
the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin
TRiC. Molec. Cell 1051- 1061, 1999.

GAM3229 221 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof 3 C c
von Hippel- Lindau disease. Radiology 133: 289- 295, 1979.

GAM3229 221 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three 3 C c
generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331,
1979.

GAM3229 221 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- 3 C c
Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001.

GAM3229 221 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with 3 C c
hydrocephalus as a complication of cerebellar
hemangioblastoma:identification of pro157leu mutation in the VHL gene. J.
Hum. Genet. 45:47- 51, 2000.

GAM3229 221 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C 3 C c
Thomas (pub.) 1946.

GAM3229 221 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a 3 C c
patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989.

GAM3229 221 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of 3 C c
middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg.
Path. 18: 1254- 1260, 1994.

GAM3229 221 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; 3 C c
Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.;
Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic

renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999.

GAM3229 221 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 C c

GAM3229 221 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 C c

GAM3229 221 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 C c

GAM3229 221 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 C c

GAM3229 221 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991. 3 C c

GAM3229 221 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992. 3 C c

GAM3229 221 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997. 3 C c

GAM3229 221 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984. 3 C c

GAM3229 221 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968. 3 C c

GAM3229 221 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 C c

GAM3229 221 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986. 3 C c

GAM3229 221 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour, phaeochromocytoma and the von Hippel- Lindau complex:two distinctive neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987. 3 C c

GAM3229 221 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: Familial pheochromocytoma associated with a novel mutation inthe von Hippel- Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996. 3 C c

GAM3229 221 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam: North Holland (pub.) 14: 1972. Pp. 241- 259. 3 C c

GAM3229 221 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors in livers with targeted inactivation of the von Hippel- Lindautumor suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001. 3 C c

GAM3229 221 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 3 C c
retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022-
1034, 1971.

GAM3229 221 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 3 C c
hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8:
601- 606,1967.

GAM3229 221 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, 3 C c
D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing
of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas.
Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994.

GAM3229 221 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; 3 C c
McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.;
Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von
Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma
only. J. Med. Genet. 37: 939- 943,2000.

GAM3229 221 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 3 C c
Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips,
C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in
families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet.
106: 425- 431, 2000.

GAM3229 221 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 C c
von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve
the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM3229 221 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; 3 C c
Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.:
Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by
pVHL. Nature 417: 975- 978, 2002.

GAM3229 221 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; 3 C c
Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease-
- a combination of adrenal pheochromocytoma and ipsilateralrenal cell
carcinoma: a case report. Surgery 105: 436- 441, 1989.

GAM3229 221 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - 3 C c
clinicaland pathological manifestations in 9 families with 50 affected
members. Arch.Intern. Med. 136: 769- 777, 1976.

GAM3229 221 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, 3 C c
P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch,
K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M.
M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel-
Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640,
1990.

GAM3229 221 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid 3 C c
body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic
study. Arch. Path. Lab. Med. 106: 235- 239, 1982.

GAM3229 221 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; 3 C c
Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel-
Lindaudisease. Brain 109: 1297- 1310, 1986.

GAM3229 221 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression 3 C c
by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995.

GAM3229 221 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: 3 C c
Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau

protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996.

GAM3229 221 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 3 C c

GAM3229 221 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL-mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001. 3 C c

GAM3229 221 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 3 C c

GAM3229 221 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-regulated prolyl hydroxylation. Science 292: 468- 472, 2001. 3 C c

GAM3229 221 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 C c

GAM3229 221 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 3 C c

GAM3229 221 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 C c

GAM3229 221 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 C c

GAM3229 221 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 C c

GAM3229 221 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 C c

GAM3229 221 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 C c

GAM3229 221 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 C c

GAM3229 221 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-581, 1995. 3 C c

GAM3229 221 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 C c

GAM3229 221 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three 3 C c

pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989.

GAM3229 221 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3 C c
3p deletion in renal cell carcinoma cells from a patientwith von Hippel-
Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987.

GAM3229 221 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary 3 C c
cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J.
Obstet. Gynec. 163: 596- 598, 1990.

GAM3229 221 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand 3 C c
sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991.

GAM3229 221 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel- 3 C c
Lindau disease. New Eng. J. Med. 275: 950- 959, 1966.

GAM3229 221 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 C c

GAM3229 221 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease 3 C c
affecting 43 members of a single kindred. Medicine 68: 1- 29,1989.

GAM3229 221 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; 3 C c
Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li,
H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.;
Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.;
Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A.
C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of
the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317-
1320, 1993.

GAM3229 221 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; 3 C c
Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau
tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad.
Sci. 93: 1770- 1775, 1996.

GAM3229 221 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, 3 C c
K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with
pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992.

GAM3229 221 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. 3 C c
ActaOphthal. 4: 193- 226, 1927.

GAM3229 221 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel 3 C c
mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424,
1994.

GAM3229 221 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; 3 C c
Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of
chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene
21: 1117- 1122, 2002.

GAM3229 221 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. 3 C c
J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G.
R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33:
120- 127, 1996.

GAM3229 221 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; 3 C c
Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.;
Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome
3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990.

GAM3229 221 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; 3 C c
Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau
disease locus to a small region of chromosome 3pby genetic linkage analysis.

Genomics 10: 957- 960, 1991.

GAM3229 221 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 C c

GAM3229 221 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 C c

GAM3229 221 VNN1 Aurrand- Lions, M.; Galland, F.; Bazin, H.; Zakharyev, V. M.; Imhof,B. A.; Naquet, P.: Vanin- 1, a novel GPI- linked perivascular moleculeinvolved in thymus homing. Immunity 5: 391- 405, 1996. 3 C c

GAM3229 221 VNN1 Galland, F.; Malergue, F.; Bazin, H.; Mattei, M. G.; Aurrand- Lions,M.; Theillet, C.; Naquet, P.: Two human genes related to murine vanin- 1are located on the long arm of human chromosome 6. Genomics 53:203- 213, 1998. 3 C c

GAM3229 221 VNN1 Grimmond, S.; Van Hateren, N.; Siggers, P.; Arkell, R.; Larder,R.; Soares, M. B.; de Fatima Bonaldo, M.; Smith, L.; Tymowska- Lalanne,Z.; Wells, C.; Greenfield, A.: Sexually dimorphic expression of proteasenexin- 1 and vanin- 1 in the developing mouse gonad prior to overt differentiationsuggests a role in mammalian sexual development. Hum. Molec. Genet. 9:1553- 1560, 2000. 3 C c

GAM3229 221 VNN1 Martin, F.; Malergue, F.; Pitari, G.; Philippe, J. M.; Philips,S.; Chabret, C.; Granjeaud, S.; Mattei, M. G.; Mungall, A. J.; Naquet,P.; Galland, F.: Vanin genes are clustered (human 6q22- 24 and mouse10A2B1) and encode isoforms of pantetheinase ectoenzymes. Immunogenetics 53:296- 306, 2001. 3 C c

GAM3229 221 VNN1 Pitari, G.; Malergue, F.; Martin, F.; Philippe, J. M.; Massucci,M. T.; Chabret, C.; Maras, B.; Dupre, S.; Naquet, P.; Galland, F.: Pantetheinase activity of membrane- bound vanin- 1: lack of free cysteaminein tissues of vanin- 1 deficient mice. FEBS Lett. 483: 149- 154, 2000. 3 C c

GAM3229 221 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 C c

GAM3229 221 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 C c

GAM3229 221 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 C c

GAM3229 221 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 C c

GAM3229 221 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly 3 C c

defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997.

GAM3229 221 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 3 C b

GAM3229 221 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 C b

GAM3229 221 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 3 C b

GAM3229 221 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995. 3 C b

GAM3229 221 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 3 C b

GAM3229 221 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 C b

GAM3229 221 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 C b

GAM3229 221 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997. 3 C b

GAM3229 221 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995. 3 C b

GAM3298 259 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998. 6 A c

GAM3298 259 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 6 A c

GAM3298 259 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994. 6 A c

GAM3298 259 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal brain type I adenylyl cyclase. Genomics 16: 473- 478,1993. 6 A c

GAM3298 259 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.: Altered sensory processing in the somatosensory cortex of the mutantmouse barrelless. Science 271: 1864- 1867, 1996. 6 A c

GAM3298 259 ADCY7 Hellevuo, K.; Berry, R.; Sikela, J. M.; Tabakoff, B.: Localizationof the gene for a novel human adenylyl cyclase (ADCY7) to chromosome16. Hum. Genet. 6 A c

95: 197- 200, 1995.

GAM3298 259 ADCY7 Hellevuo, K.; Yoshimura, M.; Kao, M.; Hoffman, P. L.; Cooper, D.M. F.; Tabakoff, B.: A novel adenylyl cyclase sequence cloned fromthe human erythroleukemia cell line. Biochem. Biophys. Res. Commun. 192:311- 318, 1993. 6 A c

GAM3298 259 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: Apolipoprotein L gene family: tissue- specific expression,splicing, promoter regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001. 6 A c

GAM3298 259 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya- Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a new human high density lipoprotein apolipoproteinexpressed by the pancreas: identification, cloning, characterization,and plasma distribution of apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997. 6 A c

GAM3298 259 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.; Bahn, S.: Gene expression analysis in schizophrenia:reproducible up- regulation of several members of the apolipoproteinL family located in a high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat. Acad. Sci. 99: 4680- 4685, 2002. 6 A c

GAM3298 259 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The apolipoprotein L gene cluster has emerged recently in evolutionand is expressed in human vascular tissue. Genomics 79: 539- 546,2002. 6 A c

GAM3298 259 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman apolipoprotein L gene cluster: identification, classification,and sites of distribution. Genomics 74: 71- 78, 2001. 6 A c

GAM3298 259 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 6 A c

GAM3298 259 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 6 A c

GAM3298 259 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 6 A c

GAM3298 259 ASB1 Hirosawa, M.; Nagase, T.; Ishikawa, K.; Kikuno, R.; Nomura, N.;Ohara, O.: Characterization of cDNA clones selected by the GeneMarkanalysis from size- fractionated cDNA libraries from human brain. DNARes. 6: 329- 336, 1999. 6 A c

GAM3298 259 ASB1 Kile, B. T.; Viney, E. M.; Willson, T. A.; Brodnicki, T. C.; Cancilla,M. R.; Herlihy, A. S.; Croker, B. A.; Baca, M.; Nicola, N. A.; Hilton,D. J.; Alexander, W. S.: Cloning and characterization of the genesencoding the ankyrin repeat and SOCS box- containing proteins Asb- 1,Asb- 2, Asb- 3, and Asb- 4. Gene 258: 31- 41, 2000. 6 A c

GAM3298 259 ATF5 Pati, D.; Meistrich, M. L.; Plon, S. E.: Human Cdc34 and Rad6Bubiquitin- conjugating enzymes target repressors of cyclic AMP- inducedtranscription for proteolysis. Molec. Cell. Biol. 19: 5001- 5013,1999. 6 A c

GAM3298 259 ATF5 Peters, C. S.; Liang, X.; Li, S.; Kannan, S.; Peng, Y.; Taub, R.;Diamond, R. H.: ATF- 7, a novel bZIP protein, interacts with the PRL- 1protein- tyrosine phosphatase. J. Biol. Chem. 276: 13718- 13726, 2001. 6 A c

GAM3298 259 ATF5 White, J. H.; McIlhinney, R. A. J.; Wise, A.; Ciruela, F.; Chan,W.- Y.; 6 A c

Emson, P. C.; Billinton, A.; Marshall, F. H.: The GABA- B receptorinteracts directly with the related transcription factors CREB2 andATFx. Proc. Nat. Acad. Sci. 97: 13967- 13972, 2000.

GAM3298 259 CD28 Aruffo, A.; Seed, B.: Molecular cloning of a CD28 cDNA by a high- 6 A c
efficiencyCOS cell expression system. Proc. Nat. Acad. Sci. 84: 8573-
8577,1987.

GAM3298 259 CD28 Buonavista, N.; Balzano, C.; Pontarotti, P.; Le Paslier, D.; Golstein,P.: 6 A c
Molecular linkage of the human CTLA4 and CD28 Ig- superfamilygenes in yeast
artificial chromosomes. Genomics 13: 856- 861, 1992.

GAM3298 259 CD28 Howard, T. A.; Rochelle, J. M.; Seldin, M. F.: Cd28 and Ctla- 4,two related 6 A c
members of the Ig supergene family, are tightly linkedon proximal mouse
chromosome 1. Immunogenetics 33: 74- 76, 1991.

GAM3298 259 CD28 Lafage- Pochitaloff, M.; Costello, R.; Couez, D.; Simonetti, J.;Mannoni, P.; 6 A c
Mawas, C.; Olive, D.: Human CD28 and CTLA- 4 Ig superfamilygenes are located
on chromosome 2 at bands q33- q34. Immunogenetics 31:198- 201, 1990.

GAM3298 259 CD28 Lee, K. P.; Taylor, C.; Petryniak, B.; Turka, L. A.; June, C. H.;Thompson, 6 A c
C. B.: The genomic organization of the CD28 gene: implicationsfor the
regulation of CD28 mRNA expression and heterogeneity. J.Immun. 145: 344-
352, 1990.

GAM3298 259 CD28 Lesslauer, W.; Gmunder, H.; Bohlen, P.: Purification and N- terminalamino 6 A c
acid sequence of the human T90/44 (CD28) antigen. Immunogenetics 27:388-
391, 1988.

GAM3298 259 CD28 Okkenhaug, K.; Wu, L.; Garza, K. M.; La Rose, J.; Khoo, W.; Odermatt,B.; 6 A c
Mak, T. W.; Ohashi, P. S.; Rottapel, R.: A point mutation inCD28
distinguishes proliferative signals from survival signals. NatureImmun. 2:
325- 332, 2001.

GAM3298 259 CD68 Holness, C. L.; Simmons, D. L.: Molecular cloning of CD68, a humanmacrophage 6 A c
marker related to lysosomal glycoproteins. Blood 81:1607- 1613, 1993.

GAM3298 259 CD68 Jones, E.; Quinn, C. M.; See, C. G.; Montgomery, D. S.; Ford, M.J.; Kolble, 6 A c
K.; Gordon, S.; Greaves, D. R.: The linked human elongationinitiation factor
4A1 (EIF4A1) and CD68 genes map to chromosome 17p13. Genomics 53:248- 250,
1998.

GAM3298 259 COPA Chow, V. T. K.; Quek, H. H.: HEP- COP, a novel human gene whoseproduct is 6 A c
highly homologous to the alpha- subunit of the yeast coatomerprotein
complex. Gene 169: 223- 227, 1996.

GAM3298 259 COPA Presley, J. F.; Ward, T. H.; Pfeifer, A. C.; Siggia, E. D.; Phair,R. D.; 6 A c
Lippincott- Schwartz, J.: Dissection of COPI and Arf1 dynamicsin vivo and
role in Golgi membrane transport. Nature 417: 187- 193,2002.

GAM3298 259 COPA Quek, H. H.; Chow, V. T. K.: Genomic organization and mappingof the human 6 A c
HEP- COP gene (COPA) to 1q. Cytogenet. Cell Genet. 76:139- 143, 1997.

GAM3298 259 COPA Quek, H. H.; Chow, V. T. K.: Molecular and cellular studies ofthe human 6 A c
homolog of the 160- kD alpha- subunit of the coatomer proteincomplex. DNA
Cell Biol. 16: 275- 280, 1997.

GAM3298 259 DDOST Kelleher, D. J.; Kreibich, G.; Gilmore, R.: 6 A c
Oligosaccharyltransferaseactivity is associated with a protein complex
composed of ribophorinsI and II and a 48 kd protein. Cell 69: 55- 65, 1992.

GAM3298 259 DDOST Yamagata, T.; Tsuru, T.; Momoi, M. Y.; Suwa, K.; Nozaki, Y.; Mukasa,T.; 6 A c
Ohashi, H.; Fukushima, Y.; Momoi, T.: Genome organization ofhuman 48- kDa
oligosaccharyltransferase (DDOST). Genomics 45: 535- 540,1997.

GAM3298 259 DDX9 Abdelhaleem, M. M.; Hameed, S.; Klassen, D.; Greenberg, A. H.:Leukophysin: 6 A c

an RNA helicase A- related molecule identified in cytotoxicT cell granules and vesicles. J. Immun. 156: 2026- 2035, 1996.

GAM3298 259 DDX9 Lee, C. G.; Hurwitz, J.: A new RNA helicase isolated from HeLacells that catalytically translocates in the 3- prime to 5- prime direction. J.Biol. Chem. 267: 4398- 4407, 1992. 6 A c

GAM3298 259 DDX9 Lee, C.- G.; Eki, T.; Okumura, K.; da Costa Soares, V.; Hurwitz,J.: Molecular analysis of the cDNA and genomic DNA encoding mouseRNA helicase A. Genomics 47: 365- 371, 1998. 6 A c

GAM3298 259 DDX9 Lee, C.- G.; Hurwitz, J.: Human RNA helicase A is homologous tothe maleless protein of Drosophila. J. Biol. Chem. 268: 16822- 16830,1993. 6 A c

GAM3298 259 DDX9 Zhang, S.; Grosse, F.: Domain structure of human nuclear DNA helicaseII (RNA helicase A). J. Biol. Chem. 272: 11487- 11494, 1997. 6 A c

GAM3298 259 DDX9 Zhang, S.; Maacke, H.; Grosse, F.: Molecular cloning of the geneencoding nuclear DNA helicase II: a bovine homologue of human RNAhelicase A and Drosophila Mle protein. J. Biol. Chem. 270: 16422- 16427,1995. 6 A c

GAM3298 259 EIF2C1 Koesters, R.; Adams, V.; Betts, D.; Moos, R.; Schmid, M.; Siermann,A.; Hassam, S.; Weitz, S.; Lichter, P.; Heitz, P. U.; von Knebel Doeberitz,M.; Briner, J.: Human eukaryotic initiation factor EIF2C1 gene: cDNAsequence, genomic organization, localization to chromosomal bands1q34- p35, and expression. Genomics 61: 210- 218, 1999. 6 A c

GAM3298 259 EIF2C1 Martinez, J.; Patkaniowska, A.; Urlaub, H.; Luhrmann, R.; Tuschi,T.: Single- stranded antisense siRNAs guide target RNA cleavage inRNAi. Cell 110: 563- 574, 2002. 6 A c

GAM3298 259 ERBB3 Carraway, K. L., III; Sliwkowski, M. X.; Akita, R.; Platko, J.V.; Guy, P. M.; Nuijens, A.; Diamonti, A. J.; Vandlen, R. L.; Cantley,L. C.; Cerione, R. A.: The erbB3 gene product is a receptor for heregulin. J.Biol. Chem. 269: 14303- 14306, 1994. 6 A c

GAM3298 259 ERBB3 Cho, H.- S.; Leahy, D. J.: Structure of the extracellular regionof HER3 reveals an interdomain tether. Science 297: 1330- 1333, 2002. 6 A c

GAM3298 259 ERBB3 Kraus, M. H.; Issing, W.; Miki, T.; Popescu, N. C.; Aaronson, S.A.: Isolation and characterization of ERBB3, a third member of theERBB/epidermal growth factor receptor family: evidence for overexpressionin a subset of human mammary tumors. Proc. Nat. Acad. Sci. 86: 9193- 9197,1989. 6 A c

GAM3298 259 ERBB3 Plowman, G. D.; Whitney, G. S.; Neubauer, M. G.; Green, J. M.;McDonald, V. L.; Todaro, G. J.; Shoyab, M.: Molecular cloning andexpression of an additional epidermal growth factor receptor- relatedgene. Proc. Nat. Acad. Sci. 87: 4905- 4909, 1990. 6 A c

GAM3298 259 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 6 A c

GAM3298 259 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 6 A c

GAM3298 259 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 6 A c

GAM3298 259 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998. 6 A c

GAM3298 259 GLO1 Bakker, E.; Pearson, P. L.; Meera Khan, P.; Schreuder, G. M. T.;Madan, K.: 6 A c
Orientation of major histocompatibility (MHC) genes relativeto the
centromere of human chromosome 6. Clin. Genet. 15: 198- 202,1979.

GAM3298 259 GLO1 Bender, K.; Grzeschik, K. H.: Assignment of the genes for humanglyoxalase I 6 A c
to chromosome 6 and for human esterase D to chromosome13. Cytogenet. Cell
Genet. 16: 93- 96, 1976.

GAM3298 259 GLO1 Beretta, M.; Schiliro, G.; Russo, A.; Barbujani, G.; Mazzetti,P.; Russo, G.; 6 A c
Barrai, I.: A new rare variant of the glyoxalase Isystem of the red cell:
GLO- Sicily. Am. J. Hum. Genet. 35: 1042- 1047,1983.

GAM3298 259 GLO1 Blanche, H.; Zoghbi, H. Y.; Jabs, E. W.; de Gouyon, B.; Zunec,R.; Dausset, 6 A c
J.; Cann, H. M.: A centromere- based genetic map of theshort arm of human
chromosome 6. Genomics 9: 420- 428, 1991.

GAM3298 259 GLO1 Carter, N. D.; West, C. M.; Bernard, J. M.; Farid, N. R.; Larsen,B.; 6 A c
Marshall, W. H.: Linkage of glyoxalase I and HLA in two
Newfoundlandcommunities. Hum. Hered. 28: 397- 400, 1978.

GAM3298 259 GLO1 Giblett, E. R.; Lewis, M.: Gene linkage studies on glyoxalaseI. Cytogenet. 6 A c
Cell Genet. 16: 313 only, 1976.

GAM3298 259 GLO1 Goldman, D.; O'Brien, S. J.; Lucas- Derse, S.; Dean, M.: Linkagemapping of 6 A c
human polymorphic proteins identified by two- dimensionalelectrophoresis.
Genomics 11: 875- 884, 1991.

GAM3298 259 GLO1 Hansen, H. E.; Eriksen, B.: HLA- GLO linkage analysis in 57 6 A c
informativefamilies. Hum. Hered. 29: 355- 360, 1979.

GAM3298 259 GLO1 Karlsson, S.; Arnason, A.; Jensson, O.: GLO polymorphism in Iceland.Hum. 6 A c
Hered. 30: 383- 385, 1980.

GAM3298 259 GLO1 Kavathas, P.; DeMars, R.: A new variant glyoxalase I allele thatis readily 6 A c
detectable in stimulated lymphocytes and lymphoblastoidcell lines but not in
circulating lymphocytes or erythrocytes. Am.J. Hum. Genet. 33: 935- 945,
1981.

GAM3298 259 GLO1 Kompf, J.; Bissbort, S.; Gussmann, S.; Ritter, H.: Polymorphismof red cell 6 A c
glyoxalase I (E.C.4.4.1.5), a new genetic marker in man:investigation of 169
mother- child combinations. Humangenetik 27:141- 143, 1975.

GAM3298 259 GLO1 Kompf, J.; Bissbort, S.; Ritter, H.: Red cell glyoxalase I 6 A c
(E.C.4.4.1.5):formal genetics and linkage relations. Humangenetik 28: 249-
251,1975.

GAM3298 259 GLO1 Kompf, J.; Siebert, G.; Ritter, H.; Heilbronner, H.; Schunter,F.; Wernet, 6 A c
P.; Gupta, D.; Moeller, H.: Data on linkage relationsbetween GLO and 21-
hydroxylase. Hum. Genet. 54: 419- 420, 1980.

GAM3298 259 GLO1 Meo, T.; Douglas, T.; Rijnbeek, A.- M.: Glyoxalase I polymorphismin the 6 A c
mouse: a new genetic marker linked to H- 2. Science 198:311- 313, 1977.

GAM3298 259 GLO1 Olaisen, B.; Gedde- Dahl, T., Jr.; Thorsby, E.: Localization ofthe human GLO 6 A c
gene locus. Hum. Genet. 32: 301- 304, 1976.

GAM3298 259 GLO1 Parr, C. W.; Bagster, I. A.; Welch, S. G.: Human red cell glyoxalaseI 6 A c
polymorphism. Biochem. Genet. 15: 109- 114, 1977.

GAM3298 259 GLO1 Reinsmoen, N. L.; Friend, P. S.; Miller, W. V.; Burgdorf, A.;Giblett, E. R.; 6 A c
Yunis, E. J.: Inheritance of recombinant HLA- GLOhaplotype suggesting the
gene sequence. Nature 267: 276- 278, 1977.

GAM3298 259 GLO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 6 A c
New York: Oxford Univ. Press (pub.) 1988.

GAM3298 259 GLO1 Rubinstein, P.; Suciu- Foca, N.: Glyoxalase 1: a possible 'null'allele. Hum. 6 A c
Hered. 29: 217- 220, 1979.

GAM3298 259 GLO1 Schimandle, C. M.; Vander Jagt, D. L.: Isolation and kineticanalysis of the multiple forms of glyoxalase- 1 from human erythrocytes.Arch. Biochem. Biophys. 195: 261- 268, 1979. 6 A c

GAM3298 259 GLO1 Sparkes, R. S.; Sparkes, M. C.; Crist, M.; Anderson, C. E.: Glyoxalasel 'null' allele in a new family: identification by abnormal segregationpattern and quantitative assay. Hum. Genet. 64: 146- 147, 1983. 6 A c

GAM3298 259 GLO1 Teng, Y. S.; Tan, S. G.; Lopez, C. G.: Red cell glyoxalase land placental soluble aconitase polymorphisms in the three major ethnicgroups of Malaysia. Jpn. J. Hum. Genet. 23: 211- 215, 1978. 6 A c

GAM3298 259 GLO1 Whittington, J. E.; Keats, B. J. B.; Jackson, J. F.; Currier,R. D.; Terasaki, P. I.: Linkage studies on glyoxalase I (GLO), pepsinogen(PG), spinocerebellar ataxia (SCA1), and HLA. Cytogenet. Cell Genet. 28:145- 150, 1980. 6 A c

GAM3298 259 GLO1 Ziegler, A.; Fonatsch, C.; Kompf, J.: Mapping of the locus forglyoxalase 1 (GLO1) on human chromosome 6 using mutant cell lines.(Abstract) Cytogenet. Cell Genet. 40: 787 only, 1985. 6 A c

GAM3298 259 GPR6 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation of three novel human genes encoding G protein- coupledreceptors. DNA Cell Biol. 14: 25- 35, 1995. 6 A c

GAM3298 259 GPR6 Song, Z.- H.; Modi, W.; Bonner, T. I.: Molecular cloning and chromosomallocalization of human genes encoding three closely related G protein- coupledreceptors. Genomics 28: 347- 349, 1995. 6 A c

GAM3298 259 GPRK7 Chen, C.- K.; Zhang, K.; Church- Kopish, J.; Huang, W.; Zhang, H.;Chen, Y.- J.; Frederick, J. M.; Baehr, W.: Characterization of humanGRK7 as a potential cone opsin kinase. Molec. Vision 7: 305- 313,2001. 6 A c

GAM3298 259 GPRK7 Haribabu, B.; Snyderman, R.: Identification of additional membersof human G- protein- coupled receptor kinase multigene family. Proc.Nat. Acad. Sci. 90: 9398- 9402, 1993. 6 A c

GAM3298 259 GPRK7 Slentz- Kesler, K.; Moore, J. T.; Lombard, M.; Zhang, J.; Hollingsworth,R.; Weiner, M. P.: Identification of the human Mnk2 gene (MKNK2)through protein interaction with estrogen receptor beta. Genomics 69:63- 71, 2000. 6 A c

GAM3298 259 GPRK7 Waskiewicz, A. J.; Flynn, A.; Proud, C. G.; Cooper, J. A.: Mitogen- activatedprotein kinases activate the serine/threonine kinases Mnk1 and Mnk2. EMBOJ. 16: 1909- 1920, 1997. 6 A c

GAM3298 259 GPRK7 Weiss, E. R.; Ducceschi, M. H.; Horner, T. J.; Li, A.; Craft, C.M.; Osawa, S.: Species- specific differences in expression of G- protein- coupledreceptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells:implications for cone cell phototransduction. J. Neurosci. 21: 9175- 9184,2001. 6 A c

GAM3298 259 IFIT4 de Veer, M. J.; Sim, H.; Whisstock, J. C.; Devenish, R. J.; Ralph,S. J.: IFI60/ISG60/IFIT4, a new member of the human IFI54/IFIT2 familyof interferon- stimulated genes. Genomics 54: 267- 277, 1998. 6 A c

GAM3298 259 IFIT4 Yu, M.; Tong, J.- H.; Mao, M.; Kan, L.- X.; Liu, M.- M.; Sun, Y.- W.;Fu, G.; Jing, Y.- K.; Yu, L.; Lepaslier, D.; Lanotte, M.; Wang, Z.- Y.;Chen, Z.; Waxman, S.; Wang, Y.- X.; Tan, J.- Z.; Chen, S.- J.: Cloningof a gene (RIG- G) associated with retinoic acid- induced differentiationof acute promyelocytic leukemia cells and representing a new memberof a family of interferon- stimulated genes. Proc. Nat. Acad. Sci. 94:7406- 7411, 1997. 6 A c

GAM3298 259 IFIT4 Zhu, H.; Cong, J.- P.; Shenk, T.: Use of differential display analysisto 6 A c

assess the effect of human cytomegalovirus infection on the accumulationof cellular RNAs: induction of interferon- responsive RNAs. Proc.Nat. Acad. Sci. 94: 13985- 13990, 1997.

GAM3298 259 IL12RB2 Chua, A. O.; Chizzonite, R.; Desai, B. B.; Truitt, T. P.; Nunes,P.; Minetti, 6 A c
L. J.; Warrier, R. R.; Presky, D. H.; Levine, J. F.;Gately, M. K.; Gubler, U.: Expression cloning of a human IL- 12 receptorcomponent: a new member of the cytokine receptor superfamily withstrong homology to gp130. J. Immun. 153: 128- 136, 1994.

GAM3298 259 IL12RB2 Kim, J.; Uyemura, K.; Van Dyke, M. K.; Legaspi, A. J.; Rea, T.H.; Shuai, K.; 6 A c
Modlin, R. L.: A role for IL- 12 receptor expressionand signal transduction in host defense in leprosy. J. Immun. 167:779- 786, 2001.

GAM3298 259 IL12RB2 Morton, S. M.; Bocaccio, I.; Depetris, D.; Mattei, M.; Dessein,A.: 6 A c
Assignment of IL12RB2 to human chromosome 1p31.3- p31.2 betweenD1S230 and D1S198. Cytogenet. Cell Genet. 79: 282- 283, 1997.

GAM3298 259 IL12RB2 Presky, D. H.; Yang, H.; Minetti, L. J.; Chua, A. O.; Nabavi, N.;Wu, C.- Y.; 6 A c
Gately, M. K.; Gubler, U.: A functional interleukin 12receptor complex is composed of two beta- type cytokine receptor subunits. Proc.Nat. Acad. Sci. 93: 14002- 14007, 1996.

GAM3298 259 IL12RB2 Yamamoto, K.; Kobayashi, H.; Miura, O.; Hirosawa, S.; Miyasaka,N.: 6 A c
Assignment of IL12RB1 and IL12RB2, interleukin- 12 receptor beta- 1and beta- 2 chains, to human chromosome 19 band p13.1 and chromosome1 band p31.2, respectively, by in situ hybridization. Cytogenet.Cell Genet. 77: 257- 258, 1997.

GAM3298 259 INPP5B Janne, P. A.; Dutra, A. S.; Dracopoli, N. C.; Charnas, L. R.; Puck,J. M.; 6 A c
Nussbaum, R. L.: Localization of the 75- kDa inositol polyphosphate- 5- phosphatase(INPP5B) to human chromosome band 1p34. Cytogenet. Cell Genet. 66:164- 166, 1994.

GAM3298 259 INPP5B Janne, P. A.; Rochelle, J. M.; Martin- DeLeon, P. A.; Stambolian,D.; Seldin, 6 A c
M. F.; Nussbaum, R. L.: Mapping of the 75- kDa inositolpolyphosphate- 5- phosphatase (Inpp5b) to distal mouse chromosome 4and its exclusion as a candidate gene for dysgenetic lens. Genomics 28:280- 285, 1995.

GAM3298 259 INPP5B Ross, T. S.; Jefferson, A. B.; Mitchell, C. A.; Majerus, P. W.: Cloning and 6 A c
expression of human 75- kDa inositol polyphosphate- 5- phosphatase.J. Biol. Chem. 266: 20283- 20289, 1991.

GAM3298 259 IRAK4 Li, S.; Strelow, A.; Fontana, E. J.; Wesche, H.: IRAK- 4: a novelmember of 6 A c
the IRAK family with the properties of an IRAK- kinase. Proc.Nat. Acad. Sci. 99: 5567- 5572, 2002.

GAM3298 259 IRAK4 Scanlan, M. J.; Gordon, J. D.; Williamson, B.; Stockert, E.; Bander,N. H.; 6 A c
Jongeneel, V.; Gure, A. O.; Jager, D.; Jager, E.; Knuth, A.;Chen, Y.- T.; Old, L. J.: Antigens recognized by autologous antibodyin patients with renal- cell carcinoma. Int. J. Cancer 83: 456- 464,1999.

GAM3298 259 IRAK4 Scott, A. F.: Personal Communication. Baltimore, Md. 4/25/2002. 6 A c

GAM3298 259 IRAK4 Suzuki, N.; Suzuki, S.; Duncan, G. S.; Millar, D. G.; Wada, T.;Mirtsos, C.; 6 A c
Takada, H.; Wakeham, A.; Itie, A.; Li, S.; Penninger,J. M.; Wesche, H.; Ohashi, P. S.; Mak, T. W.; Yeh, W.- C.: Severeimpairment of interleukin- 1 and Toll- like receptor signalling in micelacking IRAK- 4. Nature 416: 750- 754, 2002.

GAM3298 259 ITK Cheng, G.; Ye, Z.- S.; Baltimore, D.: Binding of Bruton's tyrosinekinase to 6 A c
Fyn, Lyn, or Hck through a Src homology 3 domain- mediatedinteraction. Proc. Nat. Acad. Sci. 91: 8152- 8155, 1994.

GAM3298 259 ITK Gibson, S.; Leung, B.; Squire, J. A.; Hill, M.; Arima, N.; Goss,P.; Hogg, 6 A c
D.; Mills, G. B.: Identification, cloning, and characterizationof a novel
human T- cell- specific tyrosine kinase located at the hematopoietincomplex
on chromosome 5q. Blood 82: 1561- 1572, 1993.

GAM3298 259 ITK Janis, E. M.; Siliciano, J. D.; Isaac, D. D.; Griffin, C. A.; Hawkins,A. L.; 6 A c
Kozak, C. A.; Desiderio, S.: Mapping of the gene for the tyrosinekinase Itk
to a region of conserved synteny between mouse chromosome11 and human
chromosome 5q. Genomics 23: 269- 271, 1994.

GAM3298 259 ITK Schaeffer, E. M.; Debnath, J.; Yap, G.; McVicar, D.; Liao, X. C.;Littman, D. 6 A c
R.; Sher, A.; Varmus, H. E.; Lenardo, M. J.; Schwartzberg,P. L.: Requirement
for Tec kinases Rlk and Itk in T cell receptorsignaling and immunity.
Science 284: 638- 641, 1999.

GAM3298 259 ITK Woods, M. L.; Kivens, W. J.; Adelsman, M. A.; Qiu, Y.; August,A.; Shimizu, 6 A c
Y.: A novel function for the Tec family tyrosine kinaseItk in activation of
beta- 1 integrins by the T- cell receptor. EMBOJ. 20: 1232- 1244, 2001.

GAM3298 259 KCNA7 Bardien- Kruger, S.; Wulff, H.; Arieff, Z.; Brink, P.; Chandy, K.G.; 6 A c
Corfield, V.: Characterisation of the human voltage- gated potassiumchannel
gene, KCNA7, a candidate gene for inherited cardiac disorders,and its
exclusion as cause of progressive familial heart block I (PFHBI). Europ.J.
Hum. Genet. 10: 36- 43, 2002.

GAM3298 259 KCNA7 Kalman, K.; Nguyen, A.; Tseng- Crank, J.; Dukes, I. D.; Chandy,G.; Hustad, 6 A c
C. M.; Copeland, N. G.; Jenkins, N. A.; Mohrenweiser,H.; Brandriff, B.;
Cahalan, M.; Gutman, G. A.; Chandy, K. G.: Genomicorganization, chromosomal
localization, tissue distribution, and biophysicalcharacterization of a
novel mammalian Shaker- related voltage- gatedpotassium channel, Kv1.7. J.
Biol. Chem. 273: 5851- 5857, 1998.

GAM3298 259 KCNA7 McPherson, J. D.; Wasmuth, J. J.; Chandy, K. G.; Swanson, R.; Dethlefs,B.; 6 A c
Chandy, G.; Wymore, R.; Ghanshani, S.: Chromosomal localizationof 7
potassium channel genes. (Abstract) Cytogenet. Cell Genet. 58:1979 only,
1991.

GAM3298 259 KIF3B Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 6 A c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM3298 259 KIF3B Nonaka, S.; Tanaka, Y.; Okada, Y.; Takeda, S.; Harada, A.; Kanai,Y.; Kido, 6 A c
M.; Hirokawa, N.: Randomization of left- right asymmetrydue to loss of nodal
cilia generating leftward flow of extraembryonicfluid in mice lacking KIF3B
motor protein. Cell 95: 829- 837, 1998.

GAM3298 259 KIF3B Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.: KIF3A/B: aheterodimeric 6 A c
kinesin superfamily protein that works as a microtubuleplus end- directed
motor for membrane organelle transport. J. CellBiol. 130: 1387- 1399, 1995.

GAM3298 259 MAP3K8 Aoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima,K.: 6 A c
The human cot proto- oncogene encodes two protein serine/threoninekinases
with different transforming activities by alternative initiationof
translation. J. Biol. Chem. 268: 22723- 22732, 1993.

GAM3298 259 MAP3K8 Chan, A. M.- L.; Chedid, M.; McGovern, E. S.; Popescu, N. C.; Miki,T.; 6 A c
Aaronson, S. A.: Expression cDNA cloning of a serine kinase
transforminggene. Oncogene 8: 1329- 1333, 1993.

GAM3298 259 MAP3K8 Miyoshi, J.; Higashi, T.; Mukai, H.; Ohuchi, T.; Kakunaga, T.:Structure and 6 A c

transforming potential of the human cot oncogene encodinga putative protein kinase. Molec. Cell. Biol. 11: 4088- 4096, 1991.

GAM3298 259 MAP3K8 Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.: The murine cotproto- 6 A c
oncogene: genome structure and tissue- specific expression. Jpn.J. Cancer Res. 84: 518- 525, 1993.

GAM3298 259 MSH3 Akiyama, Y.; Tsubouchi, N.; Yuasa, Y.: Frequent somatic mutationsof hMSH3 6 A c
with reference to microsatellite instability in hereditarynonpolyposis colorectal cancer. Biochem. Biophys. Res. Commun. 236:248- 252, 1997.

GAM3298 259 MSH3 de Wind, N.; Dekker, M.; Claij, N.; Jansen, L.; van Klink, Y.;Radman, M.; 6 A c
Riggins, G.; van der Valk, M.; van't Wout, K.; te Riele,H.: HNPCC- like cancer predisposition in mice through simultaneousloss of Msh3 and Msh6 mismatch- repair protein functions. Nature Genet. 23:359- 362, 1999.

GAM3298 259 MSH3 Drummond, J. T.; Genschel, J.; Wolf, E.; Modrich, P.: DHFR/MSH3amplification 6 A c
in methotrexate- resistant cells alters the hMutS- alpha/hMutS- betaratio and reduces the efficiency of base- base mismatch repair. Proc.Nat. Acad. Sci. 94: 10144- 10149, 1997.

GAM3298 259 MSH3 Fujii, H.; Shimada, T.: Isolation and characterization of cDNAclones derived 6 A c
from the divergently transcribed gene in the regionupstream from the human dihydrofolate reductase gene. J. Biol. Chem. 264:10057- 10064, 1989.

GAM3298 259 MSH3 Inokuchi, K.; Ikejima, M.; Watanabe, A.; Nakajima, E.; Orimo, H.;Nomura, T.; 6 A c
Shimada, T.: Loss of expression of the human MSH3 genein hematological malignancies. Biochem. Biophys. Res. Commun. 214:171- 179, 1995.

GAM3298 259 MSH3 Linton, J. P.; Yen, J. Y.- J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; 6 A c
Kellems, R. E.; Crouse, G. F.: Dual bidirectional promotersat the mouse dhfr locus: cloning and characterization of two mRNAclasses of the divergently transcribed Rep- 1 gene. Molec. Cell. Biol. 9:3058- 3072, 1989.

GAM3298 259 MSH3 Marra, G.; Iaccarino, I.; Lettieri, T.; Roscilli, G.; Delmastro,P.; Jiricny, 6 A c
J.: Mismatch repair deficiency associated with overexpressionof the MSH3 gene. Proc. Nat. Acad. Sci. 95: 8568- 8573, 1998.

GAM3298 259 MSH3 Nakajima, E.; Orimo, H.; Ikejima, M.; Shimada, T.: Nine- bp 6 A c
repeatpolymorphism in exon 1 of the hMSH3 gene. Jpn. J. Hum. Genet. 40:343- 345, 1995.

GAM3298 259 MSH3 Risinger, J. I.; Umar, A.; Boyd, J.; Berchuck, A.; Kunkel, T. A.;Barrett, J. 6 A c
C.: Mutation of MSH3 in endometrial cancer and evidencefor its functional role in heteroduplex repair. Nature Genet. 14:102- 109, 1996.

GAM3298 259 MSH3 Smith, M. L.; Mitchell, P. J.; Crouse, G. F.: Analysis of themouse Dhfr/Rep- 6 A c
3 major promoter region by using linker- scanning andinternal deletion mutations and DNase I footprinting. Molec. Cell.Biol. 10: 6003- 6012, 1990.

GAM3298 259 MSH3 Watanabe, A.; Ikejima, M.; Suzuki, N.; Shimada, T.: Genomic organizationand 6 A c
expression of the human MSH3 gene. Genomics 31: 311- 318, 1996.

GAM3298 259 MSH3 Yin, J.; Kong, D.; Wang, S.; Zou, T.- T. Souza, R. F.; Smolinski,K. N.; 6 A c
Lynch, P. M.; Hamilton, S. R.; Sugimura, H.; Powell, S. M.;Young, J.; Abraham, J. M.; Meltzer, S. J.: Mutation of hMSH3 andhMSH6 mismatch repair genes in genetically unstable human colorectaland gastric carcinomas. Hum. Mutat. 10: 474- 478, 1997.

GAM3298 259 MVP Bareiss, P.; Christmann, D.; Beissel, J.: Formes familiales dusyndrome 6 A c
'click et souffle meso- telesystoliques' avec anomalies dela cinetique ventriculaire gauche. Arch. Mal. Coeur 69: 71- 81, 1976.

GAM3298 259 MVP Bareiss, P.; Christmann, D.; Stork, D.; Warter, J.: Prolapsusvalvulaire 6 A c
mitral familial et syncopes par tachycardic ventriculaire. Arch.Mal. Coeur

70: 85- 91, 1977.

GAM3298 259 MVP BonTempo, C. P.; Ronan, J. A., Jr.; de Leon, A. C., Jr.; Twigg,H. L.: 6 A c
Radiographic appearance of the thorax in systolic- click latesystolic murmur
syndrome. Am. J. Cardiol. 36: 27- 31, 1975.

GAM3298 259 MVP Cohen, M. E.; Badal, D. W.; Kilpatrick, A.; Reed, E. W.; White,P. D.: The 6 A c
high familial prevalence of neurocirculatory asthenia(anxiety neurosis,
effort syndrome). Am. J. Hum. Genet. 3: 126- 158,1961.

GAM3298 259 MVP Cooper, M. J.; Abinader, E. G.: Family history in assessing therisk for 6 A c
progression of mitral valve prolapse: report of a kindred. Am.J. Dis. Child.
135: 647- 649, 1981.

GAM3298 259 MVP Darsee, J. R.; Mikolich, J. R.; Nicoloff, N. B.; Lesser, L. E.: Prevalence 6 A c
of mitral valve prolapse in presumably healthy youngmen. Circulation 59:
619- 622, 1979.

GAM3298 259 MVP Devereux, R. B.; Brown, W. T.; Kramer- Fox, R.; Sachs, I.: Inheritanceof 6 A c
mitral valve prolapse: effect of age and sex on gene expression. Ann.Intern.
Med. 97: 826- 832, 1982.

GAM3298 259 MVP Disse, S.; Abergel, E.; Berrebi, A.; Houot, A.- M.; Le Heuzey, J.- 6 A c
Y.;Diebold, B.; Guize, L.; Carpentier, A.; Corvol, P.; Jeunemaitre, X.:
Mapping of a first locus for autosomal dominant myxomatous mitral-
valveprolapse to chromosome 16p11.2- p12.1. Am. J. Hum. Genet. 65: 1242-
1251,1999.

GAM3298 259 MVP Fortuin, N. J.; Strahan, N. V.; Come, P. C.; Humphries, J. O.;Murphy, E. A.: 6 A c
Inheritance of the mitral valve prolapse syndrome.(Abstract) Clin. Res. 25:
470A only, 1977.

GAM3298 259 MVP Gooch, A. S.; Vicencio, F.; Maranhao, V.; Goldberg, H.: Arrhythmiasand left 6 A c
ventricular asynergy in the prolapsing mitral leaflet syndrome. Am.J.
Cardiol. 29: 611- 620, 1972.

GAM3298 259 MVP Henney, A. M.; Tsipouras, P.; Schwartz, R. C.; Child, A. H.; Devereux,R. B.; 6 A c
Leech, G. J.: Genetic evidence that mutations in the COL1A1,COL1A2, COL3A1,
or COL5A2 collagen genes are not responsible for mitralvalve prolapse. Brit.
Heart J. 61: 292- 299, 1989.

GAM3298 259 MVP Hunt, D.; Sloman, G.: Prolapse of the posterior leaflet of themitral valve 6 A c
occurring in eleven members of a family. Am. Heart J. 78:149- 153, 1969.

GAM3298 259 MVP Hutchins, G. M.; Moore, G. W.; Skoog, D. K.: The associationof floppy mitral 6 A c
valve with disjunction of the mitral annulus fibrosus. NewEng. J. Med. 314:
535- 541, 1986.

GAM3298 259 MVP Kramer, R.; Devereux, R. B.; Brown, W. T.; Sachs, I.: Inheritanceof mitral 6 A c
valve prolapse: autosomal dominant with variable expression.(Abstract) Am.
J. Hum. Genet. 33: 82A only, 1981.

GAM3298 259 MVP Lange, C.; Walther, W.; Schwabe, H.; Stein, U.: Cloning and initialanalysis 6 A c
of the human multidrug resistance- related MVP/LRP gene promoter.
Biochem.Biophys. Res. Commun. 278: 125- 133, 2000.

GAM3298 259 MVP Malcolm, A. D.: Mitral valve prolapse associated with other disorders:casual 6 A c
coincidence, common link, or fundamental genetic disturbance? Brit.Heart J.
53: 353- 362, 1985.

GAM3298 259 MVP Procacci, P. M.; Savran, S. V.; Schreiter, S. L.; Bryson, A. L.: Prevalence 6 A c
of clinical mitral valve prolapse in 1169 young women. NewEng. J. Med. 294:
1086- 1088, 1976.

GAM3298 259 MVP Pyeritz, R. E.; Woppel, M. A.: Progressive mitral valve dysfunctionin the 6 A c
Marfan syndrome. (Abstract) Am. J. Cardiol. 49: 900 only,1982.

GAM3298 259 MVP Rice, G. P. A.; Borghner, D. R.; Stiller, C.; Ebers, G. C.: Familialstroke 6 A c
syndrome associated with mitral valve prolapse. Ann. Neurol. 7:130- 134,
1980.
GAM3298 259 MVP Rizzon, P.; Biasco, G.; Brindicci, G.; Mauro, F.: Familial syndromeof 6 A c
midsystolic click and late systolic murmur. Brit. Heart J. 35:245- 259,
1973.
GAM3298 259 MVP Rogan, K.; Sears- Rogan, P.; Virmani, R.; Pyeritz, R. E.: Familialmyxomatous 6 A c
valvular disease. Am. J. Cardiol. 63: 1149- 1151, 1989.
GAM3298 259 MVP Salomon, J.; Shah, P. M.; Heinle, R. A.: Thoracic skeletal abnormalitiesin 6 A c
mitral valve prolapse. Am. J. Cardiol. 36: 32- 36, 1975.
GAM3298 259 MVP Sbarbaro, J. A.; Mehlman, D. J.; Wu, L.; Brooks, H. L.: A prospectivestudy 6 A c
of mitral valvular prolapse in young men. Chest 75: 555- 559,1979.
GAM3298 259 MVP Scheffer, G. L.; Wijngaard, P. L. J.; Flens, M. J.; Izquierdo,M. A.; Slovak, 6 A c
M. L.; Pinedo, H. M.; Meijer, C. J. L. M.; Clevers,H. C.; Scheper, R. J.:
The drug resistance- related protein LRP isthe human major vault protein.
Nature Med. 1: 578- 582, 1995.
GAM3298 259 MVP Schutte, J. E.; Gaffney, F. A.; Blend, L.; Blomqvist, C. G.:Distinctive 6 A c
anthropometric characteristics of women with mitral valveprolapse. Am. J.
Med. 71: 533- 538, 1981.
GAM3298 259 MVP Shappell, S. D.; Marshall, C. E.; Brown, R. E.; Bruce, T. A.:Sudden death 6 A c
and the familial occurrence of mid- systolic click, latesystolic murmur
syndrome. Circulation 48: 1128- 1134, 1973.
GAM3298 259 MVP Shell, W. E.; Walton, J. A.; Clifford, M. E.; Willis, P. W., III: The 6 A c
familial occurrence of the syndrome of mid- late systolic clickand late
systolic murmur. Circulation 39: 327- 337, 1969.
GAM3298 259 MVP Sreenivasan, V. V.; Liebman, J.; Linton, D. S.; Downs, T. D.:Posterior 6 A c
mitral regurgitation in girls possibly due to posteriorpapillary muscle
dysfunction. Pediatrics 42: 276- 290, 1968.
GAM3298 259 MVP Stannard, M.; Rigo, S. J.: Prolapse of the posterior leafletof the mitral 6 A c
valve: chromosome studies in three sisters. Am. HeartJ. 75: 282- 283, 1968.
GAM3298 259 MVP Stannard, M.; Sloman, J. G.; Hare, W. S. C.; Goble, A. J.: Prolapseof the 6 A c
posterior leaflet of the mitral valve. A clinical, familial,and
cineangiographic study. Brit. Med. J. 3: 71- 74, 1967.
GAM3298 259 MVP Towbin, J. A.: Toward an understanding of the cause of mitralvalve prolapse. 6 A c
(Editorial) Am. J. Hum. Genet. 65: 1238- 1241, 1999.
GAM3298 259 MVP Venkatesh, A.; Pauls, D. L.; Crowe, R.; Noyes, R., Jr.; Van Valkenburg,C.; 6 A c
Martins, J. B.; Kerber, R. E.: Mitral valve prolapse in anxietyneurosis
(panic disorder). Am. Heart J. 100: 302- 305, 1980.
GAM3298 259 MVP Weiss, A. N.; Mimbs, J. W.; Ludbrook, P. A.; Sobel, B. E.: 6 A c
Echocardiographicdetection of mitral valve prolapse: exclusion of false
positive diagnosisand determination of inheritance. Circulation 52: 1091-
1096, 1975.
GAM3298 259 MVP Winters, S. J.; Schreiner, B.; Griggs, R. C.; Rowley, P. T.; Nanda,N. C.: 6 A c
Familial mitral valve prolapse and myotonic dystrophy. Ann.Intern. Med. 85:
19- 22, 1976.
GAM3298 259 MVP Wordsworth, P.; Ogilvie, D.; Akhras, F.; Jackson, G.; Sykes, B.: Genetic 6 A c
segregation analysis of familial mitral valve prolapse showsno linkage of
fibrillar collagen genes. Brit. Heart J. 61: 300- 306,1989.
GAM3298 259 NCOA3 Anzick, S. L.; Kononen, J.; Walker, R. L.; Azorsa, D. O.; Tanner,M. M.; 6 A c
Guan, X.- Y.; Sauter, G.; Kallioniemi, O.- P.; Trent, J. M.;Meltzer, P. S.:

AIB1, a steroid receptor coactivator amplified inbreast and ovarian cancer. Science 277: 965- 968, 1997.

GAM3298 259 NCOA3 Bai, J.; Uehara, Y.; Montell, D. J.: Regulation of invasive cellbehavior by 6 A c taiman, a Drosophila protein related to AIB1, a steroidreceptor coactivator amplified in breast cancer. Cell 103: 1047- 1058,2000.

GAM3298 259 NCOA3 Chen, H.; Lin, R. J.; Schiltz, R. L.; Chakravarti, D.; Nash, A.;Nagy, L.; 6 A c Privalsky, M. L.; Nakatani, Y.; Evans, R. M.: Nuclear receptorcoactivator ACTR is a novel histone acetyltransferase and forms amultimeric activation complex with P/CAF and CBP/p300. Cell 90:569- 580, 1997.

GAM3298 259 NCOA3 Demarest, S. J.; Martinez- Yamout, M.; Chung, J.; Chen, H.; Xu,W.; Dyson, H. 6 A c J.; Evans, R. M.; Wright, P. E.: Mutual synergisticfolding in recruitment of CBP/p300 by p160 nuclear receptor coactivators. Nature 415:549- 553, 2002.

GAM3298 259 NCOA3 Guan, X.- Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 6 A c Hybrid selection of transcribed sequences from microdissectedDNA: isolation of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer Res. 56: 3446- 3450, 1996.

GAM3298 259 NCOA3 Shirazi, S. K.; Bober, M. A.; Coetzee, G. A.: Polymorphic exonicCAG 6 A c microsatellites in the gene amplified in breast cancer (AIB1 gene). Clin.Genet. 54: 102- 103, 1998.

GAM3298 259 NCOA3 Takeshita, A.; Cardona, G. R.; Koibuchi, N.; Suen, C.- S.; Chin,W. W.: TRAM- 6 A c 1, a novel 160- kDa thyroid hormone receptor activatormolecule, exhibits distinct properties from steroid receptor coactivator- 1. J.Biol. Chem. 272: 27629- 27634, 1997.

GAM3298 259 NEDD4L Chen, H.; Ross, C. A.; Wang, N.; Huo, Y.; MacKinnon, D. F.; Potash,J. B.; 6 A c Simpson, S. G.; McMahon, F. J.; DePaulo, J. R., Jr.; McInnis,M. G.: NEDD4L on human chromosome 18q21 has multiple forms of transcriptsand is a homologue of the mouse Nedd4- 2 gene. Europ. J. Hum. Genet. 9:922- 930, 2001.

GAM3298 259 NEDD4L Erdeniz, N.; Rothstein, R.: Rsp5, a ubiquitin- protein ligase,is involved in 6 A c degradation of the single- stranded- DNA binding proteinRfa1 in Saccharomyces cerevisiae. Molec. Cell. Biol. 20: 224- 232,2000.

GAM3298 259 NEDD4L Harvey, K. F.; Dinudom, A.; Cook, D. I.; Kumar, S.: The Nedd4- likeprotein 6 A c KIAA0439 is a potential regulator of the epithelial sodiumchannel. J. Biol. Chem. 276: 8597- 8601, 2001.

GAM3298 259 NEDD4L Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; 6 A c Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VIII. 78 new cDNAclones from brain which code for large proteins in vitro. DNA Res. 4:307- 313, 1997.

GAM3298 259 NKTR Anderson, S. K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, 6 A c J. R.: A cyclophilin- related protein involved in thefunction of natural killer cells. Proc. Nat. Acad. Sci. 90: 542- 546,1993.

GAM3298 259 NKTR Frey, J. L.; Bino, T.; Kantor, R. R. S.; Segal, D. M.; Giardina,S. L.; 6 A c Roder, J.; Anderson, S.; Ortaldo, J. R.: Mechanism of targetcell recognition by natural killer cells: characterization of a noveltriggering molecule restricted to CD3- large granular lymphocytes. J.Exp. Med. 174: 1527- 1536, 1991.

GAM3298 259 NKTR Rinfret, A.; Anderson, S. K.: IL- 2 regulates the expression ofthe NK- TR 6 A c gene via an alternate RNA splicing mechanism. Molec. Immun. 30:1307- 1313, 1993.

GAM3298 259 NKTR Simons- Evelyn, M.; Young, H. A.; Anderson, S. K.: Characterizationof the 6 A c

mouse Nktr gene and promoter. Genomics 40: 94- 100, 1997.

GAM3298 259 NKTR Young, H. A.; Jenkins, N. A.; Copeland, N. G.; Simek, S.; Lerman,M. I.; 6 A c
Zbar, B.; Glenn, G.; Ortaldo, J. R.; Anderson, S. K.: Localizationof a novel
natural killer triggering receptor locus to human chromosome3p23- p21 and
mouse chromosome 9. Genomics 16: 548- 549, 1993.

GAM3298 259 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 6 A c
Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM3298 259 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 6 A c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM3298 259 PIK3R2 Janssen, J. W. G.; Schleithoff, L.; Bartram, C. R.; Schulz, A.S.: An 6 A c
oncogenic fusion product of the phosphatidylinositol 3- kinasep85- beta
subunit and HUMORF8, a putative deubiquitinating enzyme. Oncogene 16:1767-
1772, 1998.

GAM3298 259 PIK3R2 Otsu, M.; Hiles, I.; Gout, I.; Fry, M. J.; Ruiz- Larrea, F.; Panayotou,G.; 6 A c
Thompson, A.; Dhand, R.; Hsuan, J.; Totty, N.; Smith, A. D.; Morgan,S. J.;
Courtneidge, S. A.; Parker, P. J.; Waterfield, M. D.: Characterizationof two
85 kd proteins that associate with receptor tyrosine kinases,middle-
T/pp60(c- src) complexes, and PI3- kinase. Cell 65: 91- 104,1991.

GAM3298 259 PIK3R2 Volinia, S.; Patracchini, P.; Otsu, M.; Hiles, I.; Gout, I.; Calzolari,E.; 6 A c
Bernardi, F.; Rooke, L.; Waterfield, M. D.: Chromosomal localizationof human
p85- alpha, a subunit of phosphatidylinositol 3- kinase, andits homologue
p85- beta. Oncogene 7: 789- 793, 1992.

GAM3298 259 PPP6C Bastians, H.; Krebber, H.; Vetrie, D.; Hoheisel, J.; Lichter, P.;Ponstingl, 6 A c
H.; Joos, S.: Localization of the novel serine/threonineprotein phosphatase
6 gene (PPP6C) to human chromosome Xq22.3. Genomics 41:296- 297, 1997.

GAM3298 259 PPP6C Bastians, H.; Ponstingl, H.: The novel human protein 6 A c
serine/threoninephosphatase 6 is a functional homologue of budding yeast
Sit4p andfission yeast ppe1, which are involved in cell cycle regulation.
J.Cell Sci. 109: 2865- 2874, 1996.

GAM3298 259 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 6 A c
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene
PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal
instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM3298 259 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 6 A c
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY)
to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet.
76: 49- 52, 1997.

GAM3298 259 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 6 A c
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated
protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of
all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM3298 259 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 6 A c
Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly,
F.: Characterization of new mutations in the codingsequence and 5- prime-
untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum.

Genet. 108: 148- 155, 2001.

GAM3298 259 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 6 A c
Molecular cloning and expression of human prostacyclin synthase.
Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM3298 259 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 6 A c
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.;
Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences,
gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42,
1996.

GAM3298 259 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 6 A c
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM3298 259 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 6 A c
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase
(PTGIS): genomic organization, chromosomal localization,and promoter
activity. Genomics 36: 296- 304, 1996.

GAM3298 259 SLC17A5 Aula, N.; Salomaki, P.; Timonen, R.; Verheijen, F.; Mancini, G.;Mansson, J.- 6 A c
E.; Aula, P.; Peltonen, L.: The spectrum of SLC17A5- genemutations resulting
in free sialic acid- storage diseases indicatessome genotype- phenotype
correlation. Am. J. Hum. Genet. 67: 832- 840,2000.

GAM3298 259 SLC17A5 Berra, B.; Gornati, R.; Rapelli, S.; Gatti, R.; Mancini, G. M.S.; Ciana, G.; 6 A c
Bembi, B.: Infantile sialic acid storage disease:biochemical studies. Am. J.
Med. Genet. 58: 24- 31, 1995.

GAM3298 259 SLC17A5 Biancheri, R.; Verbeek, E.; Rossi, A.; Gaggero, R.; Roccatagliata,L.; Gatti, 6 A c
R.; van Diggelen, O.; Verheijen, F. W.; Mancini, G. M.S.: An Italian severe
Salla disease variant associated with a SLC17A5mutation earlier described in
infantile sialic acid storage disease. Clin.Genet. 61: 443- 447, 2002.

GAM3298 259 SLC17A5 Cameron, P. D.; Dubowitz, V.; Besley, G. T. N.; Fensom, A. H.:Sialic acid 6 A c
storage disease. Arch. Dis. Child. 65: 314- 315, 1990.

GAM3298 259 SLC17A5 Haataja, L.; Schleutker, J.; Laine, A.- P.; Renlund, M.; Savontaus,M.- L.; 6 A c
Dib, C.; Weissenbach, J.; Peltonen, L.; Aula, P.: The geneticlocus for free
sialic acid storage disease maps to the long arm ofchromosome 6. Am. J. Hum.
Genet. 54: 1042- 1049, 1994.

GAM3298 259 SLC17A5 Lemyre, E.; Russo, P.; Melancon, S. B.; Gagne, R.; Potier, M.;Lambert, M.: 6 A c
Clinical spectrum of infantile free sialic acid storagedisease. Am. J. Med.
Genet. 82: 385- 391, 1999.

GAM3298 259 SLC17A5 Mancini, G. M. S.; Beerens, C. E. M. T.; Aula, P. P.; Verheijen,F. W.: 6 A c
Sialic acid storage diseases: a multiple lysosomal transportdefect for
acidic monosaccharides. J. Clin. Invest. 87: 1329- 1335,1991.

GAM3298 259 SLC17A5 Schleutker, J.; Laine, A.- P.; Haataja, L.; Renlund, M.; Weissenbach,J.; 6 A c
Aula, P.; Peltonen, L.: Linkage disequilibrium utilized to establisha
refined genetic position of the Salla disease locus on 6q14- q15. Genomics
27:286- 292, 1995.

GAM3298 259 SLC17A5 Schleutker, J.; Leppanen, P.; Mansson, J.- E.; Erikson, A.; Weissenbach,J.; 6 A c
Peltonen, L.; Aula, P.: Lysosomal free sialic acid storage disorderswith
different phenotypic presentations- - infantile- form sialic acidstorage
disease and Salla disease- - represent allelic disorders on6q14- 15. Am. J.
Hum. Genet. 57: 893- 901, 1995.

GAM3298 259 SLC17A5 Tondeur, M.; Libert, J.; Vamos, E.; Van Hoof, F.; Thomas, G. H.;Strecker, 6 A c
G.: Infantile form of sialic acid storage disorder:
clinical,ultrastructural, and biochemical studies in two siblings. Europ.J.

Pediat. 139: 142- 147, 1982.

GAM3298 259 SLC17A5 Verheijen, F. W.; Verbeek, E.; Aula, N.; Beerens, C. E. M. T.;Havelaar, A. C.; Joosse, M.; Peltonen, L.; Aula, P.; Galjaard, H.;van der Spek, P. J.; Mancini, G. M. S.: A new gene, encoding an aniontransporter, is mutated in sialic acid storage diseases. Nature Genet. 23:462- 465, 1999. 6 A c

GAM3298 259 SLC31A1 Eisses, J. F.; Kaplan, J. H.: Molecular characterization of hCTR1,the human copper uptake protein. J. Biol. Chem. 277: 29162- 29171,2002. 6 A c

GAM3298 259 SLC31A1 Klomp, A. E. M.; Tops, B. B. J.; van den Berg, I. E. T.; Berger,R.; Klomp, L. W. J.: Biochemical characterization and subcellularlocalization of human copper transporter 1 (hCTR1). Biochem. J. 364:497- 505, 2002. 6 A c

GAM3298 259 SLC31A1 Kuo, Y.- M.; Zhou, B.; Cosco, D.; Gitschier, J.: The copper transporterCTR1 provides an essential function in mammalian embryonic development. Proc.Nat. Acad. Sci. 98: 6836- 6841, 2001. 6 A c

GAM3298 259 SLC31A1 Lee, J.; Pena, M. M. O.; Nose, Y.; Thiele, D. J.: Biochemicalcharacterization of the human copper transporter Ctr1. J. Biol. Chem. 277:4380- 4387, 2002. 6 A c

GAM3298 259 SLC31A1 Lee, J.; Prohaska, J. R.; Thiele, D. J.: Essential role for mammaliancopper transporter Ctr1 in copper homeostasis and embryonic development. Proc.Nat. Acad. Sci. 98: 6842- 6847, 2001. 6 A c

GAM3298 259 SLC31A1 Moller, L. B.; Petersen, C.; Lund, C.; Horn, N.: Characterizationof the hCTR1 gene: genomic organization, functional expression, andidentification of a highly homologous processed gene. Gene 257:13- 22, 2000. 6 A c

GAM3298 259 SLC31A1 Zhou, B.; Gitschier, J.: hCTR1: a human gene for copper uptakeidentified by complementation in yeast. Proc. Nat. Acad. Sci. 94:7481- 7486, 1997. 6 A c

GAM3298 259 SMARCD2 Ring, H. Z.; Vameghi- Meyers, V.; Wang, W.; Crabtree, G. R.; Francke,U.: Five SWI/SNF- related, matrix- associated, actin- dependent regulatorof chromatin (SMARC) genes are dispersed in the human genome. Genomics 51:140- 143, 1998. 6 A c

GAM3298 259 SMARCD2 Wang, W.; Xue, Y.; Zhou, S.; Kuo, A.; Cairns, B. R.; Crabtree,G. R.: Diversity and specialization of mammalian SWI/SNF complexes. GenesDev. 10: 2117- 2130, 1996. 6 A c

GAM3298 259 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence insitu hybridization. Genomics 36: 527- 529, 1996. 6 A c

GAM3298 259 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence homologue of staufen is an RNA- binding protein thatis associated with polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell. Biol. 19: 2212- 2219, 1999. 6 A c

GAM3298 259 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19: 2220- 2230, 1999. 6 A c

GAM3298 259 TEM7 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in mice and humans. Cancer Res. 61: 6649- 6655, 2001. 6 A c

GAM3298 259 TEM7 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.; Kinzler, K. W.: Genes expressed in human tumor endothelium. Science 289:1197- 1202, 2000. 6 A c

GAM3298 259 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 6 A c

A Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997.

GAM3298 259 TNFRSF10 Pan, G.; O'Rourke, K.; Chinnaiyan, A. M.; Gentz, R.; Ebner, R.;Ni, J.; 6 A c A Dixit, V. M.: The receptor for the cytotoxic ligand TRAIL. Science 276:111- 113, 1997.

GAM3298 259 TNFRSF10 Degli- Esposti, M. A.; Dougall, W. C.; Smolak, P. J.; Waugh, J.Y.; Smith, C. 6 A c D A.; Goodwin, R. G.: The novel receptor TRAIL- R4 inducesNF- kappa- B and protects against TRAIL- mediated apoptosis, yet retainsan incomplete death domain. Immunity 7: 813- 820, 1997.

GAM3298 259 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 6 A c D Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997.

GAM3298 259 TNFRSF10 Pan, G.; Ni, J.; Yu, G.; Wei, Y.- F.; Dixit, V. M.: TRUNDD, a newmember of 6 A c D the TRAIL receptor family that antagonizes TRAIL signalling. FEBSLett. 424: 41- 45, 1998.

GAM3298 259 TRPM1 Duncan, L. M.; Deeds, J.; Hunter, J.; Shao, J.; Holmgren, L. M.;Woolf, E. 6 A c A.; Tepper, R. I.; Shyjan, A. W.: Down- regulation of thenovel gene melastatin correlates with potential for melanoma metastasis. CancerRes. 58: 1515- 1520, 1998.

GAM3298 259 TRPM1 Fang, D.; Setaluri, V.: Expression and up- regulation of 6 A c alternativelyspliced transcripts of melastatin, a melanoma metastasis- related gene,in human melanoma cells. Biochem. Biophys. Res. Commun. 279: 53- 61,2000.

GAM3298 259 TRPM1 Hunter, J. J.; Shao, J.; Smutko, J. S.; Dussault, B. J.; Nagle,D. L.; Woolf, 6 A c E. A.; Holmgren, L. M.; Moore, K. J.; Shyjan, A. W.: Chromosomal localization and genomic characterization of the mousemelastatin gene (Mlsn1). Genomics 54: 116- 123, 1998.

GAM3298 259 TRPM1 Xu, X. Z.; Moebius, F.; Gill, D. L.; Montell, C.: Regulation ofmelastatin, a 6 A c TRP- related protein, through interaction with a cytoplasmicisoform. Proc. Nat. Acad. Sci. 98: 10692- 10697, 2001.

GAM3298 259 UPK1B Finch, J. L.; Webb, G. C.; Evdokiou, A; Cowled, P. A.: 6 A c Chromosomallocalization of the human urothelial tetraspan gene, UPK1B, to 3q13.3- q21and detection of a Taq1 polymorphism. Genomics 40: 501- 503, 1997.

GAM3298 259 UPK1B Yu, J.; Lin, J.- H.; Wu, X.- R.; Sun, T.- T.: Uroplakins Ia and Ib,two major 6 A c differentiation products of bladder epithelium, belong toa family of four transmembrane domain (4TM) proteins. J. Cell Biol. 125:171- 182, 1994.

GAM3298 259 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. 6 A c M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001.

GAM3298 259 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; 6 A c Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979.

GAM3298 259 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; 6 A c Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr.

Metab. 82: 3356- 3360, 1997.

GAM3298 259 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; 6 A c
Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.;
Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age
related penetrance but no increased overall mortality. J.Med. Genet. 38:
508- 514, 2001.

GAM3298 259 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; 6 A c
Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau
syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab.
85: 4568- 4574, 2000.

GAM3298 259 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine 6 A c
l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et
l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938.

GAM3298 259 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. 6 A c
G.: Two distinct phenotypes caused by two differentmissense mutations in the
same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999.

GAM3298 259 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, 6 A c
F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL)
disease with pheochromocytoma in the Black Forest region ofGermany: evidence
for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM3298 259 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 6 A c
Arch.Neurol. 28: 67- 68, 1973.

GAM3298 259 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 6 A c
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM3298 259 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 6 A c
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM3298 259 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 6 A c
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM3298 259 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 6 A c
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell,
J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.;
Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the
von Hippel- Lindau disease tumorsuppressor gene: correlations with
phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM3298 259 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 6 A c
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification
of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM3298 259 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 6 A c
disease. J.A.M.A. 178: 280- 282, 1961.

GAM3298 259 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 6 A c
peculiar vascular new growth, probably primarily retinal,affecting both
eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM3298 259 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 6 A c
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N.
A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of
the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of
allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM3298 259 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 6 A c
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E.
R.: Identification of intragenic mutations in thevon Hippel- Lindau disease

tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994.

GAM3298 259 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928. 6 A c

GAM3298 259 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non-expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994. 6 A c

GAM3298 259 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988. 6 A c

GAM3298 259 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459-6463, 1995. 6 A c

GAM3298 259 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995. 6 A c

GAM3298 259 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001. 6 A c

GAM3298 259 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995. 6 A c

GAM3298 259 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell107: 43- 54, 2001. 6 A c

GAM3298 259 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 6 A c

GAM3298 259 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 6 A c

GAM3298 259 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin TRiC. Molec. Cell 1051- 1061, 1999. 6 A c

GAM3298 259 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof von Hippel- Lindau disease. Radiology 133: 289- 295, 1979. 6 A c

GAM3298 259 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331, 1979. 6 A c

GAM3298 259 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel-Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001. 6 A c

GAM3298 259 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with 6 A c
hydrocephalus as a complication of cerebellar
hemangioblastoma:identification of pro157leu mutation in the VHL gene. J.
Hum. Genet. 45:47- 51, 2000.

GAM3298 259 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C 6 A c
Thomas (pub.) 1946.

GAM3298 259 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a 6 A c
patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989.

GAM3298 259 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of 6 A c
middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg.
Path. 18: 1254- 1260, 1994.

GAM3298 259 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; 6 A c
Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.;
Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic
renal cell carcinoma: definition of a risk factorfor VHL patients to develop
an RCC. Hum. Mutat. 13: 464- 475, 1999.

GAM3298 259 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; 6 A c
De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred
with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359-
363, 1997.

GAM3298 259 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; 6 A c
Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney
cancer gene suppresses growth and functionswith VHL in a common pathway.
Oncogene 21: 3507- 3516, 2002.

GAM3298 259 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von 6 A c
Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988.

GAM3298 259 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, 6 A c
T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary
cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995.

GAM3298 259 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, 6 A c
M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.:
Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one
mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991.

GAM3298 259 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; 6 A c
Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther,
M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.:
Screening for von Hippel- Lindau disease by DNA polymorphismanalysis.
J.A.M.A. 267: 1226- 1231, 1992.

GAM3298 259 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; 6 A c
Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston
Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in
VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997.

GAM3298 259 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: 6 A c
Segregation and linkage analyses of von Hippel Lindau diseaseamong 220
descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984.

GAM3298 259 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: 6 A c
histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66:
693- 705,1968.

GAM3298 259 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 6 A c

GAM3298 259 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a 6 A c

Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986.

GAM3298 259 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid 6 A c
tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour,
phaeochromocytoma and the von Hippel- Lindau complex:two distinctive
neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987.

GAM3298 259 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: 6 A c
Familial pheochromocytoma associated with a novel mutation inthe von Hippel-
Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996.

GAM3298 259 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; 6 A c
Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam:
North Holland (pub.) 14: 1972. Pp. 241- 259.

GAM3298 259 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors 6 A c
in livers with targeted inactivation of the von Hippel- Lindautumor
suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001.

GAM3298 259 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 6 A c
retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022-
1034, 1971.

GAM3298 259 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 6 A c
hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8:
601- 606,1967.

GAM3298 259 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, 6 A c
D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing
of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas.
Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994.

GAM3298 259 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; 6 A c
McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.;
Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von
Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma
only. J. Med. Genet. 37: 939- 943,2000.

GAM3298 259 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 6 A c
Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips,
C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in
families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet.
106: 425- 431, 2000.

GAM3298 259 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 6 A c
von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve
the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM3298 259 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; 6 A c
Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.:
Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by
pVHL. Nature 417: 975- 978, 2002.

GAM3298 259 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; 6 A c
Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease-
- a combination of adrenal pheochromocytoma and ipsilateralrenal cell
carcinoma: a case report. Surgery 105: 436- 441, 1989.

GAM3298 259 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - 6 A c
clinicaland pathological manifestations in 9 families with 50 affected
members. Arch.Intern. Med. 136: 769- 777, 1976.

GAM3298 259 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, 6 A c
P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch,

K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990.

GAM3298 259 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982. 6 A c

GAM3298 259 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986. 6 A c

GAM3298 259 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995. 6 A c

GAM3298 259 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996. 6 A c

GAM3298 259 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998. 6 A c

GAM3298 259 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL-mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001. 6 A c

GAM3298 259 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998. 6 A c

GAM3298 259 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-regulated prolyl hydroxylation. Science 292: 468- 472, 2001. 6 A c

GAM3298 259 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 6 A c

GAM3298 259 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 6 A c

GAM3298 259 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 6 A c

GAM3298 259 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 6 A c

GAM3298 259 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 6 A c

GAM3298 259 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 6 A c

1994.

GAM3298 259 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell 6 A c
carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992.

GAM3298 259 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the 6 A c
VHL gene is associated exclusively with the developmentof non- papillary
renal cell carcinomas. J. Path. 179: 157- 161, 1996.

GAM3298 259 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. 6 A c
J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-
581, 1995.

GAM3298 259 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of 6 A c
the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science
269: 1444- 1446, 1995.

GAM3298 259 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; 6 A c
Wullich, B.; Schempp, W.: Cytogenetic studies on three
pheochromocytomasderived from patients with von Hippel- Lindau syndrome.
Hum. Genet. 82:127- 130, 1989.

GAM3298 259 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 6 A c
3p deletion in renal cell carcinoma cells from a patientwith von Hippel-
Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987.

GAM3298 259 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary 6 A c
cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J.
Obstet. Gynec. 163: 596- 598, 1990.

GAM3298 259 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand 6 A c
sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991.

GAM3298 259 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel- 6 A c
Lindau disease. New Eng. J. Med. 275: 950- 959, 1966.

GAM3298 259 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 6 A c

GAM3298 259 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease 6 A c
affecting 43 members of a single kindred. Medicine 68: 1- 29,1989.

GAM3298 259 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; 6 A c
Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li,
H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.;
Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.;
Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A.
C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of
the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317-
1320, 1993.

GAM3298 259 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; 6 A c
Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau
tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad.
Sci. 93: 1770- 1775, 1996.

GAM3298 259 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, 6 A c
K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with
pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992.

GAM3298 259 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. 6 A c
ActaOphthal. 4: 193- 226, 1927.

GAM3298 259 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel 6 A c
mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424,
1994.

GAM3298 259 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; 6 A c

Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002.

GAM3298 259 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 6 A c

GAM3298 259 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 6 A c

GAM3298 259 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 6 A c

GAM3298 259 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 6 A c

GAM3298 259 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 6 A c

GAM3298 259 WEE1 Heald, R.; McLoughlin, M.; McKeon, F.: Human wee1 maintains mitotictiming by protecting the nucleus from cytoplasmically activated cdc2kinase. Cell 74: 463- 474, 1993. 6 A c

GAM3298 259 WEE1 Igarashi, M.; Nagata, A.; Jinno, S.; Suto, K.; Okayama, H.: Wee1(+)- likegene in human cells. Nature 353: 80- 83, 1991. 6 A c

GAM3298 259 WEE1 Taviaux, S. A.; Demaille, J. G.: Localization of human cell cycleregulatory genes CDC25C to 5q31 and WEE1 to 11p15.3- 11p.15.1 by fluorescencein situ hybridization. Genomics 15: 194- 196, 1993. 6 A c

GAM3298 259 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 6 A c

GAM3298 259 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 6 A c

GAM3298 259 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 6 A c

GAM3298 259 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995. 6 A c

GAM3298 259 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 6 A c

GAM3298 259 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 6 A c

GAM3298 259 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; 6 A c
McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand
purification of two distinct complexes containing the five RAD51paralogs.
Genes Dev. 15: 3296- 3307, 2001.

GAM3298 259 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; 6 A c
Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional
candidate. Genomics 41: 84- 92, 1997.

GAM3298 259 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: 6 A c
Localization to chromosome 7q36.1 of the human XRCC2 gene,determining
sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995.

GAM3418 291 ADAM19 Hirohata, S.; Seldin, M. F.; Apte, S. S.: Chromosomal assignmentof two ADAM 3 A c
genes, TACE (ADAM17) and MLTNB (ADAM19), to human chromosomes2 and 5,
respectively, and of Mltnb to mouse chromosome 11. Genomics 54:178- 179,
1998.

GAM3418 291 ADAM19 Inoue, D.; Reid, M.; Lum, L.; Kratzschmar, J.; Weskamp, G.; Myung,Y. M.; 3 A c
Baron, R.; Blobel, C. P.: Cloning and initial characterizationof mouse
meltrin beta and analysis of the expression of four metalloprotease-
disintegrinsin bone cells. J. Biol. Chem. 273: 4180- 4187, 1998.

GAM3418 291 ESRRG Eudy, J. D.; Yao, S.; Weston, M. D.; Ma- Edmonds, M.; Talmadge,C. B.; Cheng, 3 A c
J. J.; Kimberling, W. J.; Sumegi, J.: Isolation ofa gene encoding a novel
member of the nuclear receptor superfamilyfrom the critical region of Usher
syndrome type IIa at 1q41. Genomics 50:382- 384, 1998.

GAM3418 291 ESRRG Greschik, H.; Wurtz, J.- M.; Sanglier, S.; Bourguet, W.; van Dorsselaer,A.; 3 A c
Moras, D.; Renaud, J.- P.: Structural and functional evidencefor ligand-
independent transcriptional activation by the estrogen- relatedreceptor 3.
Molec. Cell 9: 303- 313, 2002.

GAM3418 291 ESRRG Heard, D. J.; Norby, P. L.; Holloway, J.; Vissing, H.: Human ERR- gamma,a 3 A c
third member of the estrogen receptor- related receptor (ERR) subfamilyof
orphan nuclear receptors: tissue- specific isoforms are expressedduring
development in the adult. Molec. Endocr. 14: 382- 392, 2000.

GAM3418 291 ESRRG Hong, H.; Yang, L.; Stallcup, M. R.: Hormone- independent 3 A c
transcriptionalactivation and coactivator binding by novel orphan nuclear
receptorERR3. J. Biol. Chem. 274: 22618- 22626, 1999.

GAM3418 291 HTR7 Bard, J. A.; Zgombick, J.; Adham, N.; Vaysse, P.; Branchek, T.A.; Weinshank, 3 A c
R. L.: Cloning of a novel human serotonin receptor(5- HT- 7) positively
linked to adenylate cyclase. J. Biol. Chem. 268:23422- 23426, 1993.

GAM3418 291 HTR7 Gelernter, J.; Rao, P. A.; Pauls, D. L.; Hamblin, M. W.; Sibley,D. R.; Kidd, 3 A c
K. K.: Assignment of the 5HT7 receptor gene (HTR7) tochromosome 10q and
exclusion of genetic linkage with Tourette syndrome. Genomics 26:207- 209,
1995.

GAM3418 291 HTR7 Kenakin, T. P.; Bond, R. A.; Bonner, T. I.: II. Definition ofpharmacological 3 A c
receptors. Pharm. Rev. 44: 351- 362, 1992.

GAM3418 291 HTR7 Lassig, J. P.; Vachirasomtoon, K.; Hartzell, K.; Leventhal, M.;Courchesne, 3 A c
E.; Courchesne, R.; Lord, C.; Leventhal, B. L.; Cook,E. H., Jr.: Physical
mapping of the serotonin 5- HT(7) receptor gene(HTR7) to chromosome 10 and
pseudogene (HTR7P) to chromosome 12, andtesting of linkage disequilibrium
between HTR7 and autistic disorder. Am.J. Med. Genet. 88: 472- 475, 1999.

GAM3418 291 HTR7 Ruat, M.; Traiffort, E.; Leurs, R.; Tardivel- Lacombe, J.; Diaz,J.; Arrang, 3 A c
J.- M.; Schwartz, J.- C.: Molecular cloning, characterization,and

localization of a high- affinity serotonin receptor (5- HT- 7) activatingcAMP formation. Proc. Nat. Acad. Sci. 90: 8547- 8551, 1993.

GAM3418 291 HTR7 Tsou, A.; Kosaka, A.; Bach, C.; Zuppan, P.; Yee, C.; Tom, L.; Alvarez,R.; Ramsey, S.; Bonhaus, D. W.; Stefanich, E.; Jakeman, L.; Eglen,R. M.; Chan, H. W.: Cloning and expression of a 5- hydroxytryptamine- 7receptor positively coupled to adenylyl cyclase. J. Neurochem. 63:456- 464, 1994. 3 A c

GAM3418 291 MAPK14 Adams, R. H.; Porras, A.; Alonso, G.; Jones, M.; Vintersten, K.;Panelli, S.; Valladares, A.; Perez, L.; Klein, R.; Nebreda, A. R.: Essential role of p38- alpha MAP kinase in placental but not embryoniccardiovascular development. Molec. Cell 6: 109- 116, 2000. 3 A c

GAM3418 291 MAPK14 Bulavin, D. V.; Higashimoto, Y.; Popoff, I. J.; Gaarde, W. A.;Basrur, V.; Potapova, O.; Appella, E.; Fornace, A. J., Jr.: Initiationof a G2/M checkpoint after ultraviolet radiation requires p38 kinase. Nature 411:102- 107, 2001. 3 A c

GAM3418 291 MAPK14 Ge, B.; Gram, H.; Di Padova, F.; Huang, B.; New, L.; Ulevitch,R. J.; Luo, Y.; Han, J.: MAPKK- independent activation of p38- alphamediated by TAB1- dependent autophosphorylation of p38- alpha. Science 295:1291- 1294, 2002. 3 A c

GAM3418 291 MAPK14 Goedert, M.; Hasegawa, J.; Craxton, M.; Leversha, M. A.; Clegg,S.: Assignment of the human stress- activated protein kinase- 3 gene(SAPK3) to chromosome 22q13.3 by fluorescence in situ hybridization. Genomics 41:501- 502, 1997. 3 A c

GAM3418 291 MAPK14 Han, J.; Lee, J.- D.; Bibbs, L.; Ulevitch, R. J.: A MAP kinasetargeted by endotoxin and hyperosmolarity in mammalian cells. Science 265:808- 811, 1994. 3 A c

GAM3418 291 MAPK14 Kim, D. H.; Feinbaum, R.; Alloing, G.; Emerson, F. E.; Garsin,D. A.; Inoue, H.; Tanaka- Hino, M.; Hisamoto, N.; Matsumoto, K.; Tan,M.- W.; Ausubel, F. M.: A conserved p38 MAP kinase pathway in Caenorhabditiselegans innate immunity. Science 297: 623- 626, 2002. 3 A c

GAM3418 291 MAPK14 Kumar, S.; McLaughlin, M. M.; McDonnell, P. C.; Lee, J. C.; Livi,G. P.; Young, P. R.: Human mitogen- activated protein kinase CSBP1,but not CSBP2, complements a hog1 deletion in yeast. J. Biol. Chem. 270:29043- 29046, 1995. 3 A c

GAM3418 291 MAPK14 Lee, J. C.; Laydon, J. T.; McDonnell, P. C.; Gallagher, T. F.;Kumar, S.; Green, D.; McNulty, D.; Blumenthal, M. J.; Heys, J. R.;Landvatter, S. W.; Stickler, J. E.; McLaughlin, M. M.; Siemens, I.R.; Fisher, S. M.; Livi, G. P.; White, J. R.; Adams, J. L.; Young,P. R.: A protein kinase involved in the regulation of inflammatorycytokine biosynthesis. Nature 372: 739- 746, 1994. 3 A c

GAM3418 291 MAPK14 Liao, P.; Georgakopoulos, D.; Kovacs, A.; Zheng, M.; Lerner, D.;Pu, H.; Saffitz, J.; Chien, K.; Xiao, R.- P.; Kass, D. A.; Wang, Y.: The in vivo role of p38 MAP kinases in cardiac remodeling and restrictivecardiomyopathy. Proc. Nat. Acad. Sci. 98: 12283- 12288, 2001. 3 A c

GAM3418 291 MAPK14 Maizels, E. T.; Mukherjee, A.; Sithanandam, G.; Peters, C. A.;Cottom, J.; Mayo, K. E.; Hunzicker- Dunn, M.: Developmental regulationof mitogen- activated protein kinase- activated kinases- 2 and - 3 (MAPKAPK- 2/- 3)in vivo during corpus luteum formation in the rat. Molec. Endocr. 15:716- 733, 2001. 3 A c

GAM3418 291 MAPK14 McDonnell, P. C.; DiLella, A. G.; Lee, J. C.; Young, P. R.: Localizationof the human stress responsive MAP kinase- like CSAIDs binding protein(CSBP) gene to chromosome 6p21.3/21.2. Genomics 29: 301- 302, 1995. 3 A c

GAM3418 291 MAPK14 New, L.; Jiang, Y.; Zhao, M.; Liu, K.; Zhu, W.; Flood, L. J.;Kato, Y.; 3 A c

Parry, G. C. N.; Han, J.: PRAK, a novel protein kinaseregulated by the p38 MAP kinase. EMBO J. 17: 3372- 3384, 1998.

GAM3418 291 MAPK14 Ni, H.; Wang, X. S.; Diener, K.; Yao, Z.: MAPKAPK5, a novel mitogen- 3 A c
activated protein kinase (MAPK)- activated protein kinase, is a substrate ofthe extracellular- regulated kinase (ERK) and p38 kinase. Biochem.Biophys. Res. Commun. 243: 492- 496, 1998.

GAM3418 291 MAPK14 Takekawa, M.; Maeda, T.; Saito, H.: Protein phosphatase 2C- alphainhibits 3 A c
the human stress- responsive p38 and JNK MAPK pathways. EMBOJ. 17: 4744- 4752, 1998.

GAM3418 291 MAPK14 Tamura, K.; Sudo, T.; Senftleben, U.; Dadak, A. M.; Johnson, R.;Karin, M.: 3 A c
Requirement for p38- alpha in erythropoietin expression:a role for stress kinases in erythropoiesis. Cell 102: 221- 231,2000.

GAM3418 291 MAPK14 Zervos, A. S.; Faccio, L.; Gatto, J. P.; Kyriakis, J. M.; Brent,R.: Mxi2, a 3 A c
mitogen- activated protein kinase that recognizes andphosphorylates Max protein. Proc. Nat. Acad. Sci. 92: 10531- 10534,1995.

GAM3418 291 OGG1 Aburatani, H.; Hippo, Y.; Ishida, T.; Takashima, R.; Matsuba, C.;Kodama, T.; 3 A c
Takao, M.; Yasui, A.; Yamamoto, K.; Asano, M.; Fukasawa,K.; Yoshinari, T.; Inoue, H.; Ohtsuka, E.; Nishimura, S.: Cloningand characterization of mammalian 8- hydroxyguanine- specific DNA glycosylase/apurinic,apyrimidinic lyase, a functional mutM homologue. Cancer Res. 57:2151- 2156, 1997.

GAM3418 291 OGG1 Arai, K.; Morishita, K.; Shinmura, K.; Kohno, T.; Kim, S.- R.; Nohmi,T.; 3 A c
Taniwaki, M.; Ohwada, S.; Yokota, J.: Cloning of a human homologof the yeast OGG1 gene that is involved in the repair of oxidativeDNA damage. Oncogene 14: 2857- 2861, 1997.

GAM3418 291 OGG1 Audebert, M.; Chevillard, S.; Levalois, C.; Gyapay, G.; Vieillefond,A.; 3 A c
Klijanienko, J.; Vielh, P.; El Naggar, A. K.; Oudard, S.; Boiteux,S.; Radicella, J. P.: Alterations of the DNA repair gene OGG1 inhuman clear cell carcinomas of the kidney. Cancer Res. 60: 4740- 4744,2000.

GAM3418 291 OGG1 Bjoras, M.; Luna, L.; Johnsen, B.; Hoff, E.; Haug, T.; Rognes,T.; Seeberg, 3 A c
E.: Opposite base- dependent reactions of a human baseexcision repair enzyme on DNA containing 7,8- dihydro- 8- oxoguanineand abasic sites. EMBO J. 16: 6314- 6322, 1997.

GAM3418 291 OGG1 Ishida, T.; Hippo, Y.; Nakahori, Y.; Matsushita, I.; Kodama, T.;Nishimura, 3 A c
S.; Aburatani, H.: Structure and chromosome location ofhuman OGG1. Cytogenet. Cell Genet. 85: 232- 236, 1999.

GAM3418 291 OGG1 Kohno, T.; Shinmura, K.; Tosaka, M.; Tani, M.; Kim, S.- R.; Sugimura,H.; 3 A c
Nohmi, T.; Kasai, H.; Yokota, J.: Genetic polymorphisms and alternativesplicing of the hOGG1 gene, that is involved in the repair of 8- hydroxyguanineindamaged DNA. Oncogene 16: 3219- 3225, 1998.

GAM3418 291 OGG1 Kuo, F. C.; Sklar, J.: Augmented expression of a human gene for8- oxoguanine 3 A c
DNA glycosylase (MutM) in B lymphocytes of the dark zonein lymph node germinal centers. J. Exp. Med. 186: 1547- 1556, 1997.

GAM3418 291 OGG1 Lu, R.; Nash, H. M.; Verdine, G. L.: A mammalian DNA repair enzymethat 3 A c
excises oxidatively damaged guanines maps to a locus frequentlylost in lung cancer. Curr. Biol. 7: 397- 407, 1997.

GAM3418 291 OGG1 Radicella, J. P.; Dherin, C.; Desmaze, C.; Fox, M. S.; Boiteux,S.: Cloning 3 A c
and characterization of hOGG1, a human homolog of theOGG1 gene of Saccharomyces cerevisiae. Proc. Nat. Acad. Sci. 94:8010- 8015, 1997.

GAM3418 291 OGG1 Roldan- Arjona, T.; Wei, Y.- F.; Carter, K. C.; Klungland, A.; Anselmino,C.; 3 A c
Wang, R.- P.; Augustus, M.; Lindahl, T.: Molecular cloning andfunctional

expression of a human cDNA encoding the antimutator enzyme8- hydroxyguanine-DNA glycosylase. Proc. Nat. Acad. Sci. 94: 8016- 8020,1997.

GAM3418 291 OGG1 Rosenquist, T. A.; Zharkov, D. O.; Grollman, A. P.: Cloning 3 A c
andcharacterization of a mammalian 8- oxoguanine DNA glycosylase. Proc.Nat. Acad. Sci. 94: 7429- 7434, 1997.

GAM3418 291 OGG1 Tani, M.; Shinmura, K.; Kohno, T.; Shiroishi, T.; Wakama, S.;Kim, S.- R.; 3 A c
Nohmi, T.; Kasai, H.; Takenoshita, S.; Nagamachi, Y.;Yokota, J.: Genomic structure and chromosomal localization of themouse Ogg1 gene that is involved in the repair of 8- hydroxyguaninein DNA damage. Mammalian Genome 9: 32- 37, 1998.

GAM3418 291 PCDH12 Ludwig, D.; Lorenz, J.; Dejana, E.; Bohlen, P.; Hicklin, D. J.;Witte, L.; 3 A c
Pytowski, B.: cDNA cloning, chromosomal mapping, and expressionanalysis of human VE- cadherin- 2. Mammalian Genome 11: 1030- 1033,2000.

GAM3418 291 PCDH12 Telo, P.; Breviario, F.; Huber, P.; Panzeri, C.; Dejana, E.: 3 A c
Identificationof a novel cadherin (vascular endothelial cadherin- 2) located at intercellularjunctions in endothelial cells. J. Biol. Chem. 273: 17565-17572,1998.

GAM3418 291 PCDH12 Wu, Q.; Maniatis, T.: Large exons encoding multiple ectodomainsare a 3 A c
characteristic feature of protocadherin genes. Proc. Nat. Acad.Sci. 97: 3124- 3129, 2000.

GAM3418 291 POLS Walowsky, C.; Fitzhugh, D. J.; Castano, I. B.; Ju, J. Y.; Levin,N. A.; 3 A c
Christman, M. F.: The topoisomerase- related function geneTRF4 affects cellular sensitivity to the antitumor agent camptothecin. J.Biol. Chem. 274: 7302- 7308, 1999.

GAM3418 291 POLS Wang, Z.; Castano, I. B.; De Las Penas, A.; Adams, C.; Christman,M. F.: Pol 3 A c
kappa: a DNA polymerase required for sister chromatidcohesion. Science 289: 774- 779, 2000.

GAM3418 291 SWAP70 Borggrefe, T.; Masat, L.; Wabl, M.; Riwar, B.; Cattoretti, G.;Jessberger, 3 A c
R.: Cellular, intracellular, and developmental expressionpatterns of murine SWAP- 70. Europ. J. Immun. 29: 1812- 1822, 1999.

GAM3418 291 SWAP70 Borggrefe, T.; Wabl, M.; Akhmedov, A. T.; Jessberger, R.: A B- cell- 3 A c
specificDNA recombination complex. J. Biol. Chem. 273: 17025- 17035, 1998.

GAM3418 291 SWAP70 Masat, L.; Caldwell, J.; Armstrong, R.; Khoshnevisan, H.; Jessberger,R.; 3 A c
Herndier, B.; Wabl, M.; Ferrick, D.: Association of SWAP- 70 withthe B cell antigen receptor complex. Proc. Nat. Acad. Sci. 97: 2180- 2184,2000.

GAM3418 291 SWAP70 Masat, L.; Liddell, R. A.; Mock, B. A.; Kuo, W.- L.; Jessberger,R.; Wabl, 3 A c
M.; Morse, H. C., III: Mapping of the SWAP70 gene to mousechromosome 7 and human chromosome 11p15. Immunogenetics 51: 16- 19,2000.

GAM3418 291 SWAP70 Shinohara, M.; Terada, Y.; Iwamatsu, A.; Shinohara, A.; Mochizuki,N.; 3 A c
Higuchi, M.; Gotoh, Y.; Ihara, S.; Nagata, S.; Itoh, H.; Fukui,Y.; Jessberger, R.: SWAP- 70 is a guanine- nucleotide- exchange factorthat mediates signalling of membrane ruffling. Nature 416: 759- 763,2002.

GAM3418 291 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. 3 A c
F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM3418 291 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 A c
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of

fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM3418 291 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 A c

GAM3418 291 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 A c

GAM3418 291 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 A c

GAM3431 356 CD59 Acosta, J.; Hettinga, J.; Fluckiger, R.; Krumrei, N.; Goldfine,A.; Angarita, L.; Halperin, J.: Molecular basis for a link betweencomplement and the vascular complications of diabetes. Proc. Nat.Acad. Sci. 97: 5450- 5455, 2000. 6 A c

GAM3431 356 CD59 Bickmore, W. A.; Longbottom, D.; Oghene, K.; Fletcher, J. M.; vanHeyningen, V.: Colocalization of the human CD59 gene to 11p13 withthe MIC11 cell surface antigen. Genomics 17: 129- 135, 1993. 6 A c

GAM3431 356 CD59 Davies, A.; Simmons, D. L.; Hale, G.; Harrison, R. A.; Tighe, H.;Lachmann, P. J.; Waldmann, H.: CD59, an LY- 6- like protein expressedin human lymphoid cells, regulates the action of the complement membraneattack complex on homologous cells. J. Exp. Med. 170: 637- 654, 1989. 6 A c

GAM3431 356 CD59 Forsberg, U. H.; Bazil, V.; Stefanova, I.; Schroder, J.: Genefor human CD59 (likely Ly- 6 homologue) is located on the short armof chromosome 11. Immunogenetics 30: 188- 193, 1989. 6 A c

GAM3431 356 CD59 Harada, R.; Okada, N.; Fujita, T.; Okada, H.: Purification of1F5 antigen that prevents complement attack on homologous cell membranes. J.Immun. 144: 1823- 1828, 1990. 6 A c

GAM3431 356 CD59 Heckl- Ostreicher, B.; Ragg, S.; Drechsler, M.; Scherthan, H.; Royer-Pokora,B.: Localization of the human CD59 gene by fluorescence in situ hybridizationand pulsed- field gel electrophoresis. Cytogenet. Cell Genet. 63:144- 146, 1993. 6 A c

GAM3431 356 CD59 Holt, D. S.; Botto, M.; Bygrave, A. E.; Hanna, S. M.; Walport,M. J.; Morgan, B. P.: Targeted deletion of the CD59 gene causes spontaneousintravascular hemolysis and hemoglobinuria. Blood 98: 442- 449, 2001. 6 A c

GAM3431 356 CD59 Holt, D. S.; Powell, M. B.; Rushmere, N. K.; Morgan, B. P.: Genomicstructure and chromosome location of the gene encoding mouse CD59. Cytogenet.Cell Genet. 89: 264- 267, 2000. 6 A c

GAM3431 356 CD59 Huppi, K.; Duncan, R.; Potter, M.: Myc- 1 is centromeric to thelinkage group Ly- 6- Sis- Gdc- 1 on mouse chromosome 15. Immunogenetics 27:215- 219, 1988. 6 A c

GAM3431 356 CD59 Kamiura, S.; Nolan, C. M.; Meruelo, D.: Long- range physical mapof the Ly- 6 complex: mapping the Ly- 6 multigene family by field- inversionand two-dimensional gel electrophoresis. Genomics 12: 89- 105, 1992. 6 A c

GAM3431 356 CD59 LeClair, K. P.; Rabin, M.; Nesbitt, M. N.; Pravtcheva, D.; Ruddle,F. H.; Palfree, R. G. E.; Bothwell, A.: Murine Ly- 6 multigene familyis located on 6 A c

chromosome 15. Proc. Nat. Acad. Sci. 84: 1638- 1642,1987.

GAM3431 356 CD59 Low, M. G.; Saltiel, A. R.: Structural and functional roles ofglycosyl- 6 A c
phosphatidylinositol in membranes. Science 239: 268- 275,1988.

GAM3431 356 CD59 Mahoney, J. F.; Urakaze, M.; Hall, S.; DeGasperi, R.; Chang, H.- 6 A c
M.;Sugiyama, E.; Warren, C. D.; Borowitz, M.; Nicholson- Weller, A.;
Rosse,W. F.; Yeh, E. T. H.: Defective glycosylphosphatidylinositol
anchorsynthesis in paroxysmal nocturnal hemoglobinuria granulocytes. Blood
79:1400- 1403, 1992.

GAM3431 356 CD59 Mao, M.; Yu, M.; Tong, J.- H.; Ye, J.; Zhu, J.; Huang, Q.- H.; Fu,G.; Yu, 6 A c
L.; Zhao, S.- Y.; Waxman, S.; Lanotte, M.; Wang, Z.- Y.; Tan,J.- Z.; Chan,
S.- J.; Chen, Z.: RIG- E, a human homolog of the murineLy- 6 family, is
induced by retinoic acid during the differentiationof acute promyelocytic
leukemia cell. Proc. Nat. Acad. Sci. 93:5910- 5914, 1996.

GAM3431 356 CD59 Meri, S.; Morgan, B. P.; Davies, A.; Daniels, R. H.; Olavesen,M. G.; 6 A c
Waldmann, H.; Lachmann, P. J.: Human protectin (CD59), an18,000- 20,000 MW
complement lysis restricting factor, inhibits C5b- 8catalysed insertion of
C9 into lipid bilayers. Immunology 71: 1- 9,1990.

GAM3431 356 CD59 Meri, S.; Morgan, B. P.; Wing, M.; Jones, J.; Davies, A.; Podack,E.; 6 A c
Lachmann, P. J.: Human protectin (CD59), an 18- 20- kD homologouscomplement
restriction factor, does not restrict perforin- mediatedlysis. J. Exp. Med.
172: 367- 370, 1990.

GAM3431 356 CD59 Motoyama, N.; Okada, N.; Yamashina, M.; Okada, H.: Paroxysmalnocturnal 6 A c
hemoglobinuria due to hereditary nucleotide deletion inthe HRF20 (CD59)
gene. Europ. J. Immun. 22: 2669- 2673, 1992.

GAM3431 356 CD59 Okada, N.; Harada, R.; Fujiita, T.; Okada, H.: A novel membraneglycoprotein 6 A c
capable of inhibiting membrane attack by homologous complement. Int.Immun.
1: 205- 208, 1989.

GAM3431 356 CD59 Ono, H.; Kuno, Y.; Tanaka, H.; Yamashina, M.; Tsuyoshi, T.; Kondo,N.; Orii, 6 A c
T.: A case of paroxysmal nocturnal hemoglobinuria withoutdeficiency of
decay- accelerating factor on erythrocytes. Blood 75:1746- 1747, 1990.

GAM3431 356 CD59 Petranka, J. G.; Fleenor, D. E.; Sykes, K.; Kaufman, R. E.; Rosse,W. F.: 6 A c
Structure of the CD59- encoding gene: further evidence of arelationship to
murine lymphocyte antigen Ly- 6 protein. Proc. Nat.Acad. Sci. 89: 7876-
7879, 1992.

GAM3431 356 CD59 Rosse, W. F.: Personal Communication. Durham, N. C. 6/3/1993. 6 A c

GAM3431 356 CD59 Rosse, W. F.; Parker, C. J.: Paroxysmal nocturnal hemoglobinuria. 6 A c
Clin.Haemat. 14: 105- 125, 1985.

GAM3431 356 CD59 Rother, R. P.; Rollins, S. A.; Mennone, J.; Chodera, A.; Fidel,S. A.; 6 A c
Bessler, M.; Hillmen, P.; Squinto, S. P.: Expression of
recombinanttransmembrane CD59 in paroxysmal nocturnal hemoglobinuria B
cellsconfers resistance to human complement. Blood 84: 2604- 2611, 1994.

GAM3431 356 CD59 Tone, M.; Walsh, L. A.; Waldmann, H.: Gene structure of humanCD59 and 6 A c
demonstration that discrete mRNAs are generated by
alternativepolyadenylation. J. Molec. Biol. 227: 971- 976, 1992.

GAM3431 356 CD59 Walsh, L. A.; Tone, M.; Thiru, S.; Waldmann, H.: The CD59 antigen- - 6 A c
amultifunctional molecule. Tissue Antigens 40: 213- 220, 1992.

GAM3431 356 CD59 Woodroofe, M. N.; Tunnacliffe, A.; Pym, B.; Goodfellow, P. N.;Walsh, F. S.: 6 A c
Human muscle cell surface antigen 16- 3A5 is encodedby a gene on chromosome
11. Somat. Cell Molec. Genet. 10: 535- 540,1984.

GAM3431 356 CD59 Yamashina, M.; Ueda, E.; Kinoshita, T.; Takami, T.; Ojima, A.;Ono, H.; 6 A c

Tanaka, H.; Kondo, N.; Orii, T.; Okada, N.; Okada, H.; Inoue,K.; Kitani, T.: Inherited complete deficiency of 20- kilodalton homologousrestriction factor (CD59) as a cause of paroxysmal nocturnal hemoglobinuria. NewEng. J. Med. 323: 1184- 1189, 1990.

GAM3431 356 PSCD3 Ferguson, K. M.; Kavran, J. M.; Sankaran, V. G.; Fournier, E.;Isakoff, S. J.; Skolnik, E. Y.; Lemmon, M. A.: Structural basis fordiscrimination of 3-phosphoinositides by pleckstrin homology domains. Molec.Cell 6: 373- 384, 2000. 6 A c

GAM3431 356 PSCD3 Franco, M.; Boretto, J.; Robineau, S.; Monier, S.; Goud, B.; Chardin,P.; Chavrier, P.: ARNO3, a Sec7- domain guanine nucleotide exchangefactor for ADP ribosylation factor 1, is involved in the control ofGolgi structure and function. Proc. Nat. Acad. Sci. 95: 9926- 9931,1998. 6 A c

GAM3431 356 PSCD3 Klarlund, J. K.; Guilherme, A.; Holik, J. J.; Virbasius, J. V.;Chawla, A.; Czech, M. P.: Signaling by phosphoinositide- 3,4,5- triphosphatethrough proteins containing pleckstrin and Sec7 homology domains. Science 275:1927-1930, 1997. 6 A c

GAM3431 356 PSCD3 Lietzke, S. E.; Bose, S.; Cronin, T.; Klarlund, J.; Chawla, A.;Czech, M. P.; Lambright, D. G.: Structural basis of 3- phosphoinositiderecognition by pleckstrin homology domains. Molec. Cell 6: 385- 394,2000. 6 A c

GAM3431 356 PSCD3 Venkateswarlu, K.; Gunn- Moore, F.; Oatey, P. B.; Tavare, J. M.;Cullen, P. J.: Nerve growth factor- and epidermal growth factor-stimulatedtranslocation of the ADP- ribosylation factor- exchange factor GRP1to the plasma membrane of PC12 cells requires activation of phosphatidylinositol3- kinase and the GRP1 pleckstrin homology domain. Biochem. J. 335:139- 146, 1998. 6 A c

GAM3431 356 RELN D'Arcangelo, G.: Personal Communication. Nutley, N. J. 6/2/1995. 6 A c

GAM3431 356 RELN D'Arcangelo, G.; Homayouni, R.; Keshvara, L.; Rice, D. S.; Sheldon,M.; Curran, T.: Reelin is a ligand for lipoprotein receptors. Neuron 24:471-479, 1999. 6 A c

GAM3431 356 RELN D'Arcangelo, G.; Miao, G. G.; Chen, S.- C.; Soares, H. D.; Morgan,J. I.; Curran, T.: A protein related to extracellular matrix proteinsdeleted in the mouse mutant reeler. Nature 374: 719- 723, 1995. 6 A c

GAM3431 356 RELN DeSilva, U.; D'Arcangelo, G.; Braden, V. V.; Chen, J.; Miao, G.G.; Curran, T.; Green, E. D.: The human reelin gene: isolation, sequencing,and mapping on chromosome 7. Genome Res. 7: 157- 164, 1997. 6 A c

GAM3431 356 RELN Green, M. C.: Catalog of mutant genes and polymorphic loci.In:Lyon, M. F.; Searle, A. G.: Genetic Variants and Strains of the LaboratoryMouse. Oxford: Oxford Univ. Press (pub.) (2nd ed.): 1989. 6 A c

GAM3431 356 RELN Hack, I.; Bancila, M.; Loulier, K.; Carroll, P.; Cremer, H.: Reelinis a detachment signal in tangential chain- migration during postnatalneurogenesis. Nature Neurosci. 5: 939- 945, 2002. 6 A c

GAM3431 356 RELN Hiesberger, T.; Trommsdorff, M.; Howell, B. W.; Goffinet, A.; Mumby,M. C.; Cooper, J. A.; Herz, J.: Direct binding of reelin to VLDLreceptor and apoE receptor 2 induces tyrosine phosphorylation of disabled- 1and modulates tau phosphorylation. Neuron 24: 481- 489, 1999. 6 A c

GAM3431 356 RELN Hirotsune, S.; Takahara, T.; Sasaki, N.; Hirose, K.; Yoshiki, A.;Ohashi, T.; Kusakabe, M.; Murakami, Y.; Muramatsu, M.; Watanabe, S.;Nakao, K.; Katsuki, M.; Hayashizaki, Y.: The reeler gene encodesa protein with an EGF- like motif expressed by pioneer neurons. NatureGenet. 10: 77- 83, 1995. 6 A c

GAM3431 356 RELN Hong, S. E.; Shugart, Y. Y.; Huang, D. T.; Al Shahwan, S.; Grant,P. E.; 6 A c

Hourihane, J. O.; Martin, N. D. T.; Walsh, C. A.: Autosomalrecessive lissencephaly with cerebellar hypoplasia is associated withhuman RELN mutations. Nature Genet. 26: 93- 96, 2000. Note: Erratum:Nature Genet. 27: 225 only, 2001.

GAM3431 356 RELN Hourihane, J. O.; Bennett, C. P.; Chaudhuri, R.; Robb, S. A.;Martin, N. D. 6 A c
T.: A sibship with a neuronal migration defect, cerebellarhypoplasia and congenital lymphedema. Neuropediatrics 24: 43- 46,1993.

GAM3431 356 RELN Impagnatiello, F.; Guidotti, A. R.; Pesold, C.; Dwivedi, Y.; Caruncho,H.; 6 A c
Pisu, M. G.; Uzunov, D. P.; Smalheiser, N. R.; Davis, J. M.; Pandey,G. N.; Pappas, G. D.; Tueting, P.; Sharma, R. P.; Costa, E.: A decreaseof reelin expression as a putative vulnerability factor in schizophrenia. Proc.Nat. Acad. Sci. 95: 15718- 15723, 1998.

GAM3431 356 RELN Magdaleno, S.; Keshvara, L.; Curran, T.: Rescue of ataxia andpreplate 6 A c
splitting by ectopic expression of reelin in reeler mice. Neuron 33:573- 586, 2002.

GAM3431 356 RELN Royaux, I.; Lambert de Rouvroit, C.; D'Arcangelo, G.; Demirov,D.; Goffinet, 6 A c
A. M.: Genomic organization of the mouse reelin gene. Genomics 46:240- 250, 1997.

GAM3431 356 RELN Trommsdorff, M.; Gotthardt, M.; Hiesberger, T.; Shelton, J.; Stockinger,W.; 6 A c
Nimpf, J.; Hammer, R. E.; Richardson, J. A.; Herz, J.: Reeler/Disabled- likedisruption of neuronal migration in knockout mice lacking the VLDLreceptor and ApoE receptor 2. Cell 97: 689- 701, 1999.

GAM3431 356 RELN Yip, J. W.; Yip, Y. P. L.; Nakajima, K.; Capriotti, C.: Reelincontrols 6 A c
position of autonomic neurons in the spinal cord. Proc.Nat. Acad. Sci. 97: 8612- 8616, 2000.

GAM3431 356 RNGTT Pillutla, R. C.; Shimamoto, A.; Furuichi, Y.; Shatkin, A. J.:Human mRNA 6 A c
capping enzyme (RNGTT) and cap methyltransferase (RNMT)map to 6q16 and 18p11.22- p11.23, respectively. Genomics 54: 351- 353,1998.

GAM3431 356 RNGTT Tsukamoto, T.; Shibagaki, Y.; Murakoshi, T.; Suzuki, M.; Nakamura,A.; Gotoh, 6 A c
H.; Mizumoto, K.: Cloning and characterization of twohuman cDNAs encoding the mRNA capping enzyme. Biochem. Biophys. Res.Commun. 243: 101- 108, 1998.

GAM3431 356 RNGTT Yamada- Okabe, T.; Doi, R.; Shimmi, O.; Arisawa, M.; Yamada- Okabe,H.: 6 A c
Isolation and characterization of a human cDNA for mRNA 5- prime- cappingenzyme. Nucleic Acids Res. 26: 1700- 1706, 1998.

GAM3431 356 RNGTT Yue, Z.; Maldonado, E.; Pillutla, R.; Cho, H.; Reinberg, D.; Shatkin,A. J.: 6 A c
Mammalian capping enzyme complements mutant Saccharomycescerevisiae lacking mRNA guanylyltransferase and selectively bindsthe elongating form of RNA polymerase II. Proc. Nat. Acad. Sci. 94:12898- 12903, 1997.

GAM3431 356 SLC25A12 Crackower, M. A.; Sinasac, D. S.; Lee, J. R.; Herbrick, J.- A.;Tsui, L.- C.; 6 A c
Scherer, S. W.: Assignment of the SLC25A12 gene codingfor the human calcium- binding mitochondrial solute carrier proteinaralar to human chromosome 2q24. Cytogenet. Cell Genet. 87: 197- 198,1999.

GAM3431 356 SLC25A12 del Arco, A.; Satrustegui, J.: Molecular cloning of aralar, anew member of 6 A c
the mitochondrial carrier superfamily that binds calciumand is present in human muscle and brain. J. Biol. Chem. 273: 23327- 23334,1998.

GAM3431 356 SLC25A12 Sanz, R.; del Arco, A.; Ayuso, C.; Ramos, C.; Satrustegui, J.:Assignment of 6 A c
the calcium- binding mitochondrial carrier Aralar 1 gene(SLC25A12) to human chromosome band 2q31 by in situ hybridization. Cytogenet.Cell Genet. 89: 143- 144, 2000.

GAM3499 226 CCND2 Inaba, T.; Matsushime, H.; Valentine, M.; Roussel, M. F.; Sherr,C. J.; Look, 3 A c

A. T.: Genomic organization, chromosomal localization,and independent expression of human cyclin D genes. Genomics 13:565- 574, 1992.

GAM3499 226 CCND2 Kim, H. A.; Pomeroy, S. L.; Whoriskey, W.; Pawlitzky, I.; Benowitz,L. I.; Sicinski, P.; Stiles, C. D.; Roberts, T. M.: A developmentallyregulated switch directs regenerative growth of Schwann cells throughcyclin D1. Neuron 26: 405- 416, 2000. 3 A c

GAM3499 226 CCND2 Xiong, Y.; Menninger, J.; Beach, D.; Ward, D. C.: Molecular cloningand chromosomal mapping of CCND genes encoding human D- type cyclins. Genomics 13:575- 584, 1992. 3 A c

GAM3499 226 CLCN6 Brandt, S.; Jentsch, T. J.: ClC- 6 and ClC- 7 are two novel broadlyexpressed members of the CLC chloride channel family. FEBS Lett. 377:15- 20, 1995. 3 A c

GAM3499 226 CLCN6 Eggermont, J.; Buyse, G.; Voets, T.; Tytgat, J.; De Smedt, H.;Droogmans, G.: Alternative splicing of ClC- 6 (a member of the ClCchloride- channel family) transcripts generates three truncated isoformsone of which, ClC- 6c, is kidney- specific. Biochem. J. 325: 269- 276,1997. 3 A c

GAM3499 226 CLCN6 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994. 3 A c

GAM3499 226 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila-relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997. 3 A c

GAM3499 226 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998. 3 A c

GAM3499 226 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994. 3 A c

GAM3499 226 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997. 3 A c

GAM3499 226 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993. 3 A c

GAM3499 226 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997. 3 A c

GAM3499 226 GP2 Fukuoka, S.- I.; Freedman, S. D.; Scheele, G. A.: A single geneencodes membrane- bound and free forms of GP- 2, the major glycoproteinin pancreatic secretory (zymogen) granule membranes. Proc. Nat. Acad.Sci. 88: 2898- 2902, 1991. 3 A c

GAM3499 226 GP2 Fukuoka, S.- I.; Freedman, S. D.; Yu, H.; Sukhatme, V. P.; Scheele,G. A.: GP- 2/THP gene family encodes self- binding glycosylphosphatidylinositol-anchoredproteins in apical secretory compartments of pancreas and kidney. Proc.Nat. Acad. Sci. 89: 1189- 1193, 1992. 3 A c

GAM3499 226 GP2 Fukuoka, S.- I.; Suzuki, M.; Okabayashi, K.; Takahashi, E.: Assignmentof 3 A c

pancreatic zymogen granule membrane protein GP2 (GP2) to humanchromosome band 9q21.11 to q21.2 by in situ hybridization. Cytogenet.Cell Genet. 79: 231- 232, 1997.

GAM3499 226 GP2 Wong, S. M. E.; Lowe, A. W.: Sequence of the cDNA encoding humanGP- 2, the major membrane protein in the secretory granule of the exocrinepancreas. Gene 171: 311- 312, 1996. 3 A c

GAM3499 226 MCF2 Anson, D. S.; Blake, D. J.; Winship, P. R.; Birnbaum, D.; Brownlee,G. G.: Nullisomic deletion of the mcf.2 transforming gene in twohaemophilia B patients. EMBO J. 7: 2795- 2799, 1988. 3 A c

GAM3499 226 MCF2 Eva, A.; Aaronson, S. A.: Isolation of a new human oncogene froma diffuse B- cell lymphoma. Nature 316: 273- 275, 1985. 3 A c

GAM3499 226 MCF2 Eva, A.; Vecchio, G.; Rao, C. D.; Tronick, S. R.; Aaronson, S.A.: The predicted DBL oncogene product defines a distinct class oftransforming proteins. Proc. Nat. Acad. Sci. 85: 2061- 2065, 1988. 3 A c

GAM3499 226 MCF2 Galland, F.; Stefanova, M.; Lafage, M.; Birnbaum, D.: Localizationof the 5- prime end of the MCF2 oncogene to human chromosome 15q15- q23.Cytogenet. Cell Genet. 60: 114- 116, 1992. 3 A c

GAM3499 226 MCF2 Grant, S. G.; Mattei, M.- G.; Galland, F.; Stephenson, D. A.; Keitz,B. T.; Birnbaum, D.; Chapman, V. M.: Localization of the mouse Mcf- 2(Dbl) protooncogene within a conserved linkage group on the mouseX chromosome. Cytogenet. Cell Genet. 54: 175- 181, 1990. 3 A c

GAM3499 226 MCF2 Nguyen, C.; Pontarotti, P.; Birnbaum, D.; Chimini, G.; Rey, J.A.; Mattei, J.- F.; Jordan, B. R.: Large scale physical mapping inthe q27 region of the human X chromosome: the coagulation factor IXgene and the mcf.2 transforming sequence are separated by at most270 kilobase pairs and are surrounded by several 'HTF islands.' EMBOJ. 6: 3285- 3289, 1987. 3 A c

GAM3499 226 MCF2 Nguyen, C.; Poustka, A.- M.; Djabali, M.; Roux, D.; Mattei, J.- F.;Lehrach, H.; Jordan, B. R.: Large- scale mapping and chromosome jumpingin the q27 region of the human X chromosome. Genomics 5: 298- 303,1989. 3 A c

GAM3499 226 MCF2 Noguchi, T.; Mattei, M.- G.; Oberle, I.; Planche, J.; Imbert, J.;Pelassy, C.; Birg, F.; Birnbaum, D.: Localization of the mcf.2 transformingsequence to the X chromosome. EMBO J. 6: 1301- 1307, 1987. 3 A c

GAM3499 226 MCF2 Ron, D.; Tronick, S. R.; Aaronson, S. A.; Eva, A.: Molecular cloningand characterization of the human DBL proto- oncogene: evidence thatits overexpression is sufficient to transform NIH/3T3 cells. EMBOJ. 7: 2465- 2473, 1988. 3 A c

GAM3499 226 MCF2 Srivastava, S. K.; Wheelock, R. H. P.; Aaronson, S. A.; Eva, A.: Identification of the protein encoded by the human diffuse B- celllymphoma (dbl) oncogene. Proc. Nat. Acad. Sci. 83: 8868- 8872, 1986. 3 A c

GAM3499 226 MCF2 Tronick, S. R.; McBride, O. W.; Popescu, N. C.; Eva, A.: Chromosomallocalization of DBL oncogene sequences. Genomics 5: 546- 553, 1989. 3 A c

GAM3499 226 MYH11 Castilla, L. H.; Garrett, L.; Adya, N.; Orlic, D.; Dutra, A.; Anderson,S.; Owens, J.; Eckhaus, M.; Bodine, D.; Liu, P. P.: The fusion geneCbfb- MYH11 blocks myeloid differentiation and predisposes mice toacute myelomonocytic leukaemia. (Letter) Nature Genet. 23: 144- 146,1999. 3 A c

GAM3499 226 MYH11 Deng, Z.; Liu, P.; Marlton, P.; Claxton, D. F.; Lane, S.; Callen,D. F.; Collins, F. S.; Siciliano, M. J.: Smooth muscle myosin heavychain locus (MYH11) maps to 16p13.13- p13.12 and establishes a newregion of conserved synteny between human 16p and mouse 16. Genomics 18:156- 159, 1993. 3 A c

GAM3499 226 MYH11 Liu, P.; Tarle, S. A.; Hajra, A.; Claxton, D. F.; Marlton, P.;Freedman, M.; 3 A c
Siciliano, M. J.; Collins, F. S.: Fusion between transcriptionfactor CBF-
beta/PEBP2- beta and a myosin heavy chain in acute myeloidleukemia. Science
261: 1041- 1044, 1993.

GAM3499 226 MYH11 Matsuoka, R.; Yoshida, M. C.; Furutani, Y.; Imamura, S.; Kanda,N.; 3 A c
Yanagisawa, M.; Masaki, T.; Takao, A.: Human smooth muscle myosinheavy chain
gene mapped to chromosomal region 16q12. Am. J. Med.Genet. 46: 61- 67, 1993.

GAM3499 226 MYH11 Matsuoka, R.; Yoshida, M. C.; Kanda, N.; Furutani, Y.; Bruns, G.;Yanagisawa, 3 A c
M.; Masaki, T.; Takao, A.: Human smooth muscle myosinheavy- chain gene
mapped to chromosomal region 16q12.1- q12.2. (Abstract) Cytogenet.Cell
Genet. 58: 2000- 2001, 1991.

GAM3499 226 NRIP1 Cavailles, V.; Dauvois, S.; Horset, L. F.; Lopez, G.; Hoare, S.;Kushner, P. 3 A c
J.; Parker, M. G.: Nuclear factor RIP140 modulates transcriptionalactivation
by the estrogen receptor. EMBO J. 14: 3741- 3751, 1995.

GAM3499 226 NRIP1 Katsanis, N.; Ives, J. H.; Groet, J.; Nizetic, D.; Fisher, E. M.C.: 3 A c
Localisation of receptor interacting protein 140 (RIP140) within100 kb of
D21S13 on 21q11, a gene- poor region of the human genome. Hum.Genet. 102:
221- 223, 1998.

GAM3499 226 ORC4L Eki, T.; Dean, F. B.; Kohda, A.; Okumura, K.; Abe, M.; Murakami,Y.; Ishiai, 3 A c
M.; Satomoto, K.; Hurwitz, J.; O'Donnell, M.; Hanaoka,F.: Assignment1 of the
homologue of the yeast origin recognitioncomplex subunit ORC4 (ORC4L) to
human chromosome band 2q22- q23 byin situ hybridization and somatic cell
hybrid analysis. Cytogenet.Cell Genet. 81: 89- 90, 1998.

GAM3499 226 ORC4L Quintana, D. G.; Hou, Z.; Thome, K. C.; Hendricks, M.; Saha, P.;Dutta, A.: 3 A c
Identification of HsORC4, a member of the human originof replication
recognition complex. J. Biol. Chem. 272: 28247- 28251,1997.

GAM3499 226 PTK2 Andre, E.; Becker- Andre, M.: Expression of an N- terminally truncatedform 3 A c
of human focal adhesion kinase in brain. Biochem. Biophys. Res.Commun. 190:
140- 147, 1993.

GAM3499 226 PTK2 Fiedorek, F. T., Jr.; Kay, E. S.: Mapping of the focal adhesionkinase (Fadk) 3 A c
gene to mouse chromosome 15 and human chromosome 8. MammalianGenome 6: 123-
126, 1995.

GAM3499 226 PTK2 Polte, T. R.; Hanks, S. K.: Interaction between focal adhesionkinase and 3 A c
Crk- associated tyrosine kinase substrate p130- Cas. Proc.Nat. Acad. Sci.
92: 10678- 10682, 1995.

GAM3499 226 PTK2 Schaller, M. D.; Borgman, C.; Cobb, B. S.; Vines, R. R.; Reynolds,A. B.; 3 A c
Parsons, J. T.: pp125(FAK), a structurally distinctive protein-
tyrosinekinase associated with focal adhesions. Proc. Nat. Acad. Sci.
89:5192- 5196, 1992.

GAM3499 226 RAD18 Hoege, C.; Pfander, B.; Moldovan, G.- L.; Pyrowolakis, G.; Jentsch,S.: RAD6- 3 A c
dependent DNA repair is linked to modification of PCNA byubiquitin and SUMO.
Nature 419: 135- 141, 2002.

GAM3499 226 RAD18 Tateishi, S.; Sakuraba, Y.; Masuyama, S.; Inoue, H.; Yamaizumi,M.: 3 A c
Dysfunction of human Rad18 results in defective postreplicationrepair and
hypersensitivity to multiple mutagens. Proc. Nat. Acad.Sci. 97: 7927- 7932,
2000.

GAM3499 226 TLR3 Alexopoulou, L.; Holt, A. C.; Medzhitov, R.; and Flavell, R. A.: Recognition 3 A c
of double stranded RNA and activation of NFKB by Toll- likereceptor 3.
Nature 413: 732- 738, 2001.

GAM3499 226 TLR3 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; 3 A c

Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress different Toll- like receptors and respond to different microbialantigens. J. Exp. Med. 194: 863- 869, 2001.

GAM3499 226 TLR3 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.; Mantovani, A.: Differential expression and regulation of Toll- likereceptors (TLR) in human leukocytes: selective expression of TLR3in dendritic cells. J. Immun. 164: 5998- 6004, 2000. 3 A c

GAM3499 226 TLR3 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A family of human receptors structurally related to DrosophilaToll. Proc. Nat. Acad. Sci. 95: 588- 593, 1998. 3 A c

GAM3499 226 ZNF36 Rousseau- Merck, M.- F.; Duro, D.; Berger, R.; Thiesen, H. J.: Chromosomallocalization of two KOX zinc finger genes on chromosome bands 7q21- q22. Ann.Genet. 38: 81- 84, 1995. 3 A c

GAM3499 226 ZNF36 Tommerup, N.; Aagaard, L.; Lund, C. L.; Boel, E.; Baxendale, S.;Bates, G. P.; Lehrach, H.; Vissing, H.: A zinc- finger gene ZNF141mapping at 4p16.3/D4S90 is a candidate gene for the Wolf- Hirschhorn(4p-) syndrome. Hum. Molec. Genet. 2: 1571- 1575, 1993. 3 A c

GAM3499 226 ZNF36 Tommerup, N.; Vissing, H.: Isolation and fine mapping of 16 novelhuman zinc finger- encoding cDNAs identify putative candidate genesfor developmental and malignant disorders. Genomics 27: 259- 264,1995. 3 A c

GAM3770 241 AMFR Hirono, Y.; Fushida, S.; Yonemura, Y.; Yamamoto, H.; Watanabe,H.; Raz, A.: Expression of autocrine motility factor receptor correlateswith disease progression in human gastric cancer. Brit. J. Cancer 74:2003- 2007, 1996. 3 C c

GAM3770 241 AMFR Huang, B.; Xie, Y.; Raz, A.: Identification of an upstream regionthat controls the transcription of the human autocrine motility factorreceptor. Biochem. Biophys. Res. Commun. 212: 727- 742, 1995. 3 C c

GAM3770 241 AMFR Silletti, S.; Yao, J.; Sanford, J.; Mohammed, A. N.; Otto, T.;Wolman, S. R.; Raz, A.: Autocrine motility factor receptor in humanbladder carcinoma: gene expression, loss of cell- contact regulationand chromosomal mapping. Int. J. Oncol. 3: 801- 807, 1993. 3 C c

GAM3770 241 AMFR Watanabe, H.; Carmi, P.; Hogan, V.; Raz, T.; Silletti, S.; Nabi,I. R.; Raz, A.: Purification of human tumor cell autocrine motilityfactor and molecular cloning of its receptor. J. Biol. Chem. 266:13442- 13448, 1991. 3 C c

GAM3770 241 CD1D Balk, S. P.; Burke, S.; Polischuk, J. E.; Frantz, M. E.; Yang,L.; Porcelli, S.; Colgan, S. P.; Blumberg, R. S.: Beta- 2- microglobulin- independentMHC class Ib molecule expressed by human intestinal epithelium. Science 265:259- 262, 1994. 3 C c

GAM3770 241 CD1D Benlagha, K.; Kyin, T.; Beavis, A.; Teyton, L.; Bendelac, A.:A thymic precursor to NK T cell lineage. Science 296: 553- 555, 2002. 3 C c

GAM3770 241 CD1D Bradbury, A.; Milstein, C.; Kozak, C. A.: Chromosomal localizationof Cd1d genes in the mouse. Somat. Cell Molec. Genet. 17: 93- 96,1991. 3 C c

GAM3770 241 CD1D Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S controls the trafficking and maturation of MHC class IImolecules in dendritic cells. J. Cell Biol. 147: 775- 790, 1999. 3 C c

GAM3770 241 CD1D Honey, K.; Benlagha, K.; Beers, C.; Forbush, K.; Teyton, L.; Kleijmeer,M. J.; Rudensky, A. Y.; Bendelac, A.: Thymocyte expression of cathepsinL is essential for NKT cell development. Nature Immun. 7Oct, 2002.Note: Advance Electronic Publication. 3 C c

GAM3770 241 CD1D Jayawardena- Wolf, J.; Benlagha, K.; Chiu, Y.- H.; Mehr, R.; Bendelac,A.: 3 C c
CD1d endosomal trafficking is independently regulated by an intrinsicCD1d-
encoded tyrosine motif and by the invariant chain. Immunity 15:897- 908,
2001.

GAM3770 241 CD1D MacDonald, H. R.: T before NK. Science 296: 481- 482, 2002. 3 C c

GAM3770 241 CD1D Nieuwenhuis, E. E. S.; Matsumoto, T.; Exley, M.; Schleipman, R.A.; Glickman, 3 C c
J.; Bailey, D. T.; Corazza, N.; Colgan, S. P.; Onderdonk,A. B.; Blumberg, R.
S.: CD1d- dependent macrophage- mediated clearanceof Pseudomonas aeruginosa
from lung. Nature Med. 8: 588- 593, 2002.

GAM3770 241 CD1D Park, S.- H.; Bendelac, A.: CD1- restricted T- cell responses andmicrobial 3 C c
infection. Nature 406: 788- 792, 2000.

GAM3770 241 CD1D Pellicci, D. G.; Hammond, K. J. L.; Uldrich, A. P.; Baxter, A.G.; Smyth, M. 3 C c
J.; Godfrey, D. I.: A natural killer T (NKT) cell developmentalpathway
involving a thymus- dependent NK1.1(-)CD4(+) CD1d- dependentprecursor
stage. J. Exp. Med. 195: 835- 844, 2002.

GAM3770 241 CD1D Prigozy, T. I.; Naidenko, O.; Qasba, P.; Elewaut, D.; Brossay,L.; Khurana, 3 C c
A.; Natori, T.; Koezuka, Y.; Kulkarni, A.; Kronenberg,M.: Glycolipid antigen
processing for presentation by CD1d molecules. Science 291:664- 667, 2001.

GAM3770 241 CD1D Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; 3 C c
Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.;
Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell
selection and maturation by cathepsin S. Immunity 15:909- 919, 2001.

GAM3770 241 CD1D Shi, F.- D.; Flodstrom, M.; Balasa, B.; Kim, S. H.; Van Gunst,K.; 3 C c
Strominger, J. L.; Wilson, S. B.; Sarvetnick, N.: Germ line deletionof the
CD1 locus exacerbates diabetes in the NOD mouse. Proc. Nat.Acad. Sci. 98:
6777- 6782, 2001.

GAM3770 241 CD1D Zeng, Z.- H.; Castano, A. R.; Segelke, B. W.; Stura, E. A.; Peterson,P. A.; 3 C c
Wilson, I. A.: Crystal structure of mouse CD1: an MHC- likefold with a large
hydrophobic binding groove. Science 277: 339- 345,1997.

GAM3770 241 CUL3 Du, M.; Sansores- Garcia, L.; Zu, Z.; Wu, K. K.: Cloning and 3 C c
expressionanalysis of a novel salicylate suppressible gene, Hs- CUL- 3, a
memberof cullin/Cdc53 family. J. Biol. Chem. 273: 24289- 24292, 1998.

GAM3770 241 CUL3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM3770 241 CUL3 Kipreos, E. T.; Lander, L. E.; Wing, J. P.; He, W. W.; Hedgecock,E. M.: cul- 3 C c
1 is required for cell cycle exit in C. elegans and identifiesa novel gene
family. Cell 85: 829- 839, 1996.

GAM3770 241 CUL3 Michel, J. J.; Xiong, Y.: Human CUL- 1, but not other cullin familymembers, 3 C c
selectively interacts with SKP1 to form a complex with SKP2and cyclin A.
Cell Growth Differ. 9: 435- 449, 1998.

GAM3770 241 CYLN2 Hoogenraad, C. C.; Eussen, B. H. J.; Langeveld, A.; van Haperen,R.; 3 C c
Winterberg, S.; Wouters, C. H.; Grosveld, F.; De Zeeuw, C. I.;Galjart, N.:
The murine CYLN2 gene: genomic organization, chromosomelocalization, and
comparison to the human gene that is located withinthe 7q11.23 Williams
syndrome critical region. Genomics 53: 348- 358,1998.

GAM3770 241 CYLN2 Hoogenraad, C. C.; Koekkoek, B.; Akhmanova, A.; Krugers, H.; Dortland,B.; 3 C c
Miedema, M.; van Alphen, A.; Kistler, W. M.; Jaegle, M.; Koutsourakis,M.;
Van Camp, N.; Verhoye, M.; van der Linden, A.; Kaverina, I.; Grosveld,F.; De

Zeeuw, C. I.; Galjart, N.: Targeted mutation of Cyln2 in theWilliams syndrome critical region links CLIP- 115 haploinsufficiencyto neurodevelopmental abnormalities in mice. Nature Genet. 32: 116- 127,2002. Note: Erratum: Nature Genet. 32: 331 only, 2002.

GAM3770 241 CYLN2 Osborne, L. R.; Martindale, D.; Scherer, S. W.; Shi, X.- M.; Huizenga,J.; 3 C c Heng, H. H. Q.; Costa, T.; Pober, B.; Lew, L.; Brinkman, J.; Rommens,J.; Koop, B.; Tsui, L.- C.: Identification of genes from a 500- kbregion at 7q11.23 that is commonly deleted in Williams syndrome patients. Genomics 36:328- 336, 1996.

GAM3770 241 GALNT2 Bennett, E. P.; Weghuis, D. O.; Merkx, G.; Geurts van Kessel, A.;Eiberg, H.; 3 C c Clausen, H.: Genomic organization and chromosomal localizationof three members of the UDP- N- acetylgalactosamine:polypeptide N- acetylgalactosaminyltransferasefamily. Glycobiology 8: 547- 555, 1998.

GAM3770 241 GALNT2 White, T.; Bennett, E. P.; Takio, K.; Sorensen, T.; Bonding, N.;Clausen, H.: 3 C c Purification and cDNA cloning of a human UDP- N- acetyl- alpha- D- galactosamine:polypeptideN- acetylgalactosaminyltransferase. J. Biol. Chem. 270: 24156- 24165,1995.

GAM3770 241 GLRA3 Kingsmore, S. F.; Suh, D.; Seldin, M. F.: Genetic mapping of theglycine 3 C c receptor alpha- 3 subunit on mouse chromosome 8. MammalianGenome 5: 831- 832, 1994.

GAM3770 241 GLRA3 Kuhse, J.; Schmieden, V.; Betz, H.: Identification and functionalexpression 3 C c of a novel ligand binding subunit of the inhibitory glycinereceptor. J. Biol. Chem. 265: 22317- 22320, 1990.

GAM3770 241 GLRA3 Nikolic, Z.; Laube, B.; Weber, R. G.; Lichter, P.; Kioschis, P.;Poustka, A.; 3 C c Mulhardt, C.; Becker, C.- M.: The human glycine receptorsubunit alpha- 3: GLRA3 gene structure, chromosomal localization, andfunctional characterization of alternative transcripts. J. Biol.Chem. 273: 19708- 19714, 1998.

GAM3770 241 HMGB3 Vaccari, T.; Beltrame, M.; Ferrari, S.; Bianchi, M. E.: Hmg4,a new member of 3 C c the Hmg1/2 gene family. Genomics 49: 247- 252, 1998.

GAM3770 241 HMGB3 Wilke, K.; Wiemann, S.; Gaul, R.; Gong, W.; Poustka, A.: Isolationof human 3 C c and mouse HMG2a cDNAs: evidence for an HMG2a- specific 3- primeuntranslated region. Gene 198: 269- 274, 1997.

GAM3770 241 KIF5A Hamlin, P. J.; Jones, P. F.; Leek, J. P.; Bransfield, K.; Lench,N. J.; 3 C c Aldersley, M. A.; Howdle, P. D.; Markham, A. F.; Robinson,P. A.: Assignment of GALGT encoding beta- 1,4N- acetylgalactosaminyl- transferase(GalNAc- T) and KIF5A encoding neuronal kinesin (D12S1889) to humanchromosome band 12q13 by assignment to ICI YAC 26EG10 and in situhybridization. Cytogenet. Cell Genet. 82: 267- 268, 1998.

GAM3770 241 KIF5A Niclas, J.; Navone, F.; Hom- Booher, N.; Vale, R. D.: Cloning 3 C c andlocalization of a conventional kinesin motor expressed exclusivelyin neurons. Neuron 12: 1059- 1072, 1994.

GAM3770 241 NCF4 Bravo, J.; Karathanassis, D.; Pacold, C. M.; Pacold, M. E.; Ellson,C. D.; 3 C c Anderson, K. E.; Butler, P. J. G.; Lavenir, I.; Perisic, O.;Hawkins, P. T.; Stephens, L.; Williams, R. L.: The crystal structureof the PX domain from p40- phox bound to phosphatidylinositol 3- phosphate. Molec.Cell 829- 839, 2001.

GAM3770 241 NCF4 Zhan, S.; Vazquez, N.; Zhan, S.; Wientjes, F. B.; Budarf, M. L.;Schrock, E.; 3 C c Ried, T.; Green, E. D.; Chanock, S. J.: Genomic structure,chromosomal localization, start of transcription, and tissue expressionof the human p40-

phox, a new component of the nicotinamide adeninedinucleotide phosphate-oxidase complex. Blood 88: 2714- 2721, 1996.

GAM3770 241 PITPN Dickeson, S. K.; Helmkamp, G. M., Jr.; Yarbrough, L. R.: Sequenceof a human cDNA encoding phosphatidylinositol transfer protein andoccurrence of a related sequence in widely divergent eukaryotes. Gene 142:301- 305, 1994. 3 C c

GAM3770 241 PITPN Dickeson, S. K.; Lim, C. N.; Schuyler, G. T.; Dalton, T. P.; Helmkamp,G. M., Jr.; Yarbrough, L. R.: Isolation and sequence of cDNA clonesencoding rat phosphatidylinositol transfer protein. J. Biol. Chem. 264:16557- 16564, 1989. 3 C c

GAM3770 241 PITPN Fitzgibbon, J.; Pilz, A.; Gayther, S.; Appukuttan, B.; Dulai, K.S.; Delhanty, J. D. A.; Helmkamp, G. M., Jr.; Yarbrough, L. R.; Hunt,D. M.: Localization of the gene encoding human phosphatidylinositoltransfer protein (PITPN) to 17p13.3: a gene showing homology to theDrosophila retinal degeneration B gene (rdgB). Cytogenet. Cell Genet. 67:205- 207, 1994. 3 C c

GAM3770 241 PITPN Hamilton, B. A.; Smith, D. J.; Mueller, K. L.; Kerrebrock, A. W.;Bronson, R. T.; van Berkel, V.; Daly, M. J.; Kruglyak, L.; Reeve,M. P.; Nemhauser, J. L.; Hawkins, T. L.; Rubin, E. M.; Lander, E.S.: The vibrator mutation causes neurodegeneration via reduced expressionof PITP- alpha: positional complementation cloning and extragenic suppression. Neuron 18:711- 722, 1997. 3 C c

GAM3770 241 PITPN Hay, J. C.; Martin, T. F. J.: Phosphatidylinositol transfer proteinrequired for ATP- dependent priming of Ca(2+)- activated secretion. Nature 366:572-575, 1993. 3 C c

GAM3770 241 PITPN Vihtelic, T. S.; Goebl, M.; Milligan, S.; O'Tousa, J. E.; Hyde,D. R.: Localization of Drosophila retinal degeneration B, a membrane-associatedphosphatidylinositol transfer protein. J. Cell Biol. 122: 1013-1022,1993. 3 C c

GAM3770 241 PITPN Wirtz, K. W. A.: Phospholipid transfer proteins. Annu. Rev. Biochem. 60:73- 99, 1991. 3 C c

GAM3770 241 RUNX3 Avraham, K. B.; Levanon, D.; Negreanu, V.; Bernstein, Y.; Groner,Y.; Copeland, N. G.; Jenkins, N. A.: Mapping of the mouse homologof the human runt domain gene, AML2, to the distal region of mousechromosome 4. Genomics 25: 603- 605, 1995. 3 C c

GAM3770 241 RUNX3 Bae, S.- C.; Takahashi, E.; Zhang, Y. W.; Ogawa, E.; Shigesada,K.; Namba, Y.; Satake, M.; Ito, Y.: Cloning, mapping and expressionof PEBP2- alpha- C, a third gene encoding the mammalian Runt domain. Gene 159:245- 248, 1995. 3 C c

GAM3770 241 RUNX3 Inoue, K,; Ozaki, S.; Shiga, T.; Ito, K.; Masuda, T.; Okado, N.;Iseda, T.; Kawaguchi, S.; Ogawa, M.; Bae, S.- C.; Yamashita, N.; Itohara,S.; Kudo, N.; Ito, Y.: Runx3 controls the axonal projection of proprioceptivedorsal root ganglion neurons. Nature Neurosci. 23Sept, 2002. Note:Advance Electronic Publication. 3 C c

GAM3770 241 RUNX3 Levanon, D.; Negreanu, V.; Bernstein, Y.; Bar- Am, I.; Avivi, L.;Groner, Y.: AML1, AML2, and AML3, the human members of the runt domaingene- family: cDNA structure, expression, and chromosomal localization. Genomics 23:425- 432, 1994. 3 C c

GAM3770 241 RUNX3 Li, Q.- L.; Ito, K.; Sakakura, C.; Fukamachi, H.; Inoue, K.; Chi,X.- Z.; Lee, K.- Y.; Nomura, S.; Lee, C.- W.; Han, S.- B.; Kim, H.- M.;Kim, W.- J.; and 15 others: Causal relationship between the lossof RUNX3 expression and gastric cancer. Cell 109: 113- 124, 2002. 3 C c

GAM3770 241 RUNX3 Wijmenga, C.; Speck, N. A.; Dracopoli, N. C.; Hofker, M. H.; Liu,P.; 3 C c

Collins, F. S.: Identification of a new murine runt domain- containinggene, Cbfa3, and localization of the human homolog, CBFA3, to chromosome1p35- pter. Genomics 26: 611- 614, 1995.

GAM3770 241 SIT Hubener, C.; Mincheva, A.; Lichter, P.; Schraven, B.; Bruyns, E.: Complete 3 C c sequence, genomic organization, and chromosomal localizationof the human gene encoding the SHP2- interacting transmembrane adaptorprotein (SIT). Immunogenetics 53: 337- 341, 2001.

GAM3770 241 SIT Marie- Cardine, A.; Kirchgessner, H.; Bruyns, E.; Shevchenko, A.;Mann, M.; 3 C c Autschbach, F.; Ratnofsky, S.; Meuer, S.; Schraven, B.:SHP2- interacting transmembrane adaptor protein (SIT), a novel disulfide- linkeddimer regulating human T cell activation. J. Exp. Med. 189: 1181- 1194,1999.

GAM3770 241 SMN1 Battaglia, G.; Princivalle, A.; Forti, F.; Lizier, C.; Zeviani,M.: 3 C c Expression of the SMN gene, the spinal muscular atrophy determininggene, in the mammalian central nervous system. Hum. Molec. Genet. 6:1961- 1971, 1997.

GAM3770 241 SMN1 Brahe, C.; Servidei, S.; Zappata, S.; Ricci, E.; Tonali, P.; Neri,G.: 3 C c Genetic homogeneity between childhood- onset and adult- onset autosomalrecessive spinal muscular atrophy. Lancet 346: 741- 742, 1995.

GAM3770 241 SMN1 Burglen, L.; Amiel. J.; Viollet, L.; Lefebvre, S.; Burlet, P.;Clermont, O.; 3 C c Raclin, V.; Landrieu, P.; Verloes, A.; Munnich, A.;Melki, J.: Survival motor neuron gene deletion in the arthrogryposismultiplex congenita- spinal muscular atrophy association. J. Clin.Invest. 98: 1130- 1132, 1996.

GAM3770 241 SMN1 Burglen, L.; Lefebvre, S.; Clermont, O.; Burlet, P.; Viollet, L.;Cruaud, C.; 3 C c Munnich, A.; Melki, J.: Structure and organization ofthe human survival motor neurone (SMN) gene. Genomics 32: 479- 482,1996.

GAM3770 241 SMN1 Burglen, L.; Spiegel, R.; Ignatius, J.; Cobben, J. M.; Landrieu,P.; 3 C c Lefebvre, S.; Munnich, A.; Melki, J.: SMN gene deletion in variantof infantile spinal muscular atrophy. (Letter) Lancet 346: 316- 317,1995.

GAM3770 241 SMN1 Bussaglia, E.; Clermont, O.; Tizzano, E.; Lefebvre, S.; Burglen,L.; Cruaud, 3 C c C.; Urtizberea, J. A.; Colomer, J.; Munnich, A.; Baiget,M.; Melki, J.: A frame- shift deletion in the survival motor neurongene in Spanish spinal muscular atrophy patients. Nature Genet. 11:335- 337, 1995.

GAM3770 241 SMN1 Callebaut, I.; Mornon, J. P.: The human EBNA- 2 coactivator p100:multidomain 3 C c organization and relationship to the staphylococcal nucleasefold and to the tudor protein involved in Drosophila melanogasterdevelopment. Biochem. J. 321: 125- 132, 1997.

GAM3770 241 SMN1 Campbell, L.; Daniels, R. J.; Dubowitz, V.; Davies, K. E.: Maternalmosaicism 3 C c for a second mutational event in a type I spinal muscularatrophy family. Am. J. Hum. Genet. 63: 37- 44, 1998.

GAM3770 241 SMN1 Campbell, L.; Hunter, K. M. D.; Mohaghegh, P.; Tinsley, J. M.;Brasch, M. A.; 3 C c Davies, K. E.: Direct interaction of Smn with dp103,a putative RNA helicase: a role for Smn in transcription regulation? Hum.Molec. Genet. 9: 1093- 1100, 2000.

GAM3770 241 SMN1 Chen, K.- L.; Wang, Y. L.; Rennert, H.; Joshi, I.; Mills, J. K.;Leonard, D. 3 C c G. B.; Wilson, R. B.: Duplications and de novo deletionsof the SMNt gene demonstrated by fluorescence- based carrier testingfor spinal muscular atrophy. Am. J. Med. Genet. 85: 463- 469, 1999.

GAM3770 241 SMN1 Cobben, J. M.; van der Steege, G.; Grootscholten, P.; de Visser,M.; 3 C c Scheffer, H.; Buys, C. H. C. M.: Deletions of the survival motorneuron gene in unaffected siblings of patients with spinal muscularatrophy. Am. J. Hum. Genet. 57: 805- 808, 1995.

GAM3770 241 SMN1 Coovert, D. D.; Le, T. T.; McAndrew, P. E.; Strasswimmer, J.;Crawford, T. O.; Mendell, J. R.; Coulson, S. E.; Androphy, E. J.;Prior, T. W.; Burghes, A. H. M.: The survival motor neuron proteinin spinal muscular atrophy. Hum. Molec. Genet. 6: 1205- 1214, 1997. 3 C c

GAM3770 241 SMN1 Coovert, D. D.; Le, T. T.; Morris, G. E.; Man, N. T.; Kralewski,M.; Sendtner, M.; Burghes, A. H. M.: Does the survival motor neuronprotein (SMN) interact with Bcl- 2? (Letter) J. Med. Genet. 37: 536- 539,2000. 3 C c

GAM3770 241 SMN1 DiDonato, C. J.; Chen, X.- N.; Noya, D.; Korenberg, J. R.; Nadeau,J. H.; Simard, L. R.: Cloning, characterization, and copy numberof the murine survival motor neuron gene: homolog of the spinal muscularatrophy-determining gene. Genome Res. 7: 339- 352, 1997. 3 C c

GAM3770 241 SMN1 DiDonato, C. J.; Morgan, K.; Carpten, J. D.; Fuerst, P.; Ingraham,S. E.; Prescott, G.; McPherson, J. D.; Wirth, B.; Zerres, K.; Hurko,O.; Wasmuth, J. J.; Mendell, J. R.; Burghes, A. H. M.; Simard, L.R.: Association between Ag1- CA alleles and severity of autosomalrecessive proximal spinal muscular atrophy. Am. J. Hum. Genet. 55:1218- 1229, 1994. 3 C c

GAM3770 241 SMN1 Feldkotter, M.; Schwarzer, V.; Wirth, R.; Wienker, T. F.; Wirth,B.: Quantitative analyses of SMN1 and SMN2 based on real- time lightCyclerPCR: fast and highly reliable carrier testing and prediction of severityof spinal muscular atrophy. Am. J. Hum. Genet. 70: 358- 368, 2002. 3 C c

GAM3770 241 SMN1 Friesen, W. J.; Massenet, S.; Paushkin, S.; Wyce, A.; Dreyfuss,G.: SMN, the product of the spinal muscular atrophy gene, binds preferentiallyto dimethylarginine- containing protein targets. Molec. Cell 7: 1111-1117,2001. 3 C c

GAM3770 241 SMN1 Frugier, T.; Tiziano, F. D.; Cifuentes- Diaz, C.; Miniou, P.; Roblot,N.; Dierich, A.; Le Meur, M.; Melki, J.: Nuclear targeting defectof SMN lacking the C- terminus in a mouse model of spinal muscularatrophy. Hum. Molec. Genet. 9: 849- 858, 2000. 3 C c

GAM3770 241 SMN1 Gambardella, A.; Mazzei, R.; Toscano, A.; Annesi, G.; Pasqua,A.; Annesi, F.; Quattrone, F.; Oliveri, R. L.; Valentino, P.; Bono,F.; Aguglia, U.; Zappia, M.; Vita, G.; Quattrone, A.: Spinal muscularatrophy due to an isolated deletion of exon 8 of the telomeric survivalmotor neuron gene. Ann. Neurol. 44: 836- 839, 1998. 3 C c

GAM3770 241 SMN1 Hahnen, E.; Schonling, J.; Rudnik- Schoneborn, S.; Raschke, H.;Zerres, K.; Wirth, B.: Missense mutations in exon 6 of the survivalmotor neuron gene in patients with spinal muscular atrophy (SMA). Hum.Molec. Genet. 6: 821- 825, 1997. 3 C c

GAM3770 241 SMN1 Hahnen, E.; Schonling, J.; Rudnik- Schoneborn, S.; Zerres, K.;Wirth, B.: Hybrid survival motor neuron genes in patients with autosomalrecessive spinal muscular atrophy: new insights into molecular mechanismsresponsible for the disease. Am. J. Hum. Genet. 59: 1057- 1065, 1996. 3 C c

GAM3770 241 SMN1 Hannus, S.; Buhler, D.; Romano, M.; Seraphin, B.; Fischer, U.: The Schizosaccharomyces pombe protein Yab8p and a novel factor,Yip1p, share structural and functional similarity with the spinalmuscular atrophy-associated proteins SMN and SIP1. Hum. Molec. Genet. 9:663- 674, 2000. 3 C c

GAM3770 241 SMN1 Hsieh- Li, H. M.; Chang, J.- G.; Jong, Y.- J.; Wu, M.- H.; Wang, N.M.; Tsai, C. H.; Li, H.: A mouse model for spinal muscular atrophy. NatureGenet. 24: 66- 70, 2000. 3 C c

GAM3770 241 SMN1 Jablonka, S.; Bandilla, M.; Wiese, S.; Buhler, D.; Wirth, B.;Sendtner, M.; Fischer, U.: Co- regulation of survival of motor neuron(SMN) protein and its 3 C c

interactor SIP1 during development and in spinalmuscular atrophy. Hum. Molec. Genet. 10: 497- 505, 2001.

GAM3770 241 SMN1 Lefebvre, S.; Burglen, L.; Reboullet, S.; Clermont, O.; Burlet,P.; Viollet, L.; Benichou, B.; Cruaud, C.; Millasseau, P.; Zeviani,M.; Le Paslier, D.; Frezal, J.; Cohen, D.; Weissenbach, J.; Munnich,A.; Melki, J.: Identification and characterization of a spinal muscularatrophy- determining gene. Cell 80: 155- 165, 1995. 3 C c

GAM3770 241 SMN1 Liu, Q.; Dreyfuss, G.: A novel nuclear structure containing thesurvival of motor neurons protein. EMBO J. 15: 3555- 3565, 1996. 3 C c

GAM3770 241 SMN1 Liu, Q.; Fischer, U.; Wang, F.; Dreyfuss, G.: The spinal muscularatrophy disease gene product, SMN, and its associated protein SIP1are in a complex with spliceosomal snRNP proteins. Cell 90: 1013- 1021,1997. 3 C c

GAM3770 241 SMN1 Lorson, C. L.; Androphy, E. J.: The domain encoded by exon 2of the survival motor neuron protein mediates nucleic acid binding. Hum.Molec. Genet. 7: 1269- 1275, 1998. 3 C c

GAM3770 241 SMN1 Lorson, C. L.; Hahnen, E.; Androphy, E. J.; Wirth, B.: A singlenucleotide in the SMN gene regulates splicing and is responsible forspinal muscular atrophy. Proc. Nat. Acad. Sci. 96: 6307- 6311, 1999. 3 C c

GAM3770 241 SMN1 Lorson, C. L.; Strasswimmer, J.; Yao, J.- M.; Baleja, J. D.; Hahnen,E.; Wirth, B.; Le, T.; Burghes, A. H. M.; Androphy, E. J.: SMN oligomerizationdefect correlates with spinal muscular atrophy severity. Nature Genet. 19:63- 66, 1998. 3 C c

GAM3770 241 SMN1 Matthijs, G.; Schollen, E.; Legius, E.; Devriendt, K.; Goemans,N.; Kayserili, H.; Apak, M. Y.; Cassiman, J.- J.: Unusual molecularfindings in autosomal recessive spinal muscular atrophy. J. Med.Genet. 33: 469- 474, 1996. 3 C c

GAM3770 241 SMN1 McAndrew, P. E.; Parsons, D. W.; Simard, L. R.; Rochette, C.;Ray, P. N.; Mendell, J. R.; Prior, T. W.; Burghes, A. H.: Identificationof proximal spinal muscular atrophy carriers and patients by analysisof SMNT and SMNC gene copy number. Am. J. Hum. Genet. 60: 1411- 1422,1997. 3 C c

GAM3770 241 SMN1 Meister, G.; Buhler, D.; Laggerbauer, B.; Zobawa, M.; Lottspeich,F.; Fischer, U.: Characterization of a nuclear 20S complex containingthe survival of motor neurons (SMN) protein and a specific subsetof spliceosomal Sm proteins. Hum. Molec. Genet. 9: 1977- 1986, 2000. 3 C c

GAM3770 241 SMN1 Mohaghegh, P.; Rodrigues, N. R.; Owen, N.; Ponting, C. P.; Le,T. T.; Burghes, A. H. M.; Davies, K. E.: Analysis of mutations inthe tudor domain of the survival motor neuron protein SMN. Europ.J. Hum. Genet. 7: 519- 525, 1999. 3 C c

GAM3770 241 SMN1 Monani, U. R.; Lorson, C. L.; Parsons, D. W.; Prior, T. W.; Androphy,E. J.; Burghes, A. H. M.; McPherson, J. D.: A single nucleotide differencethat alters splicing patterns distinguishes the SMA gene SMN1 fromthe copy gene SMN2. Hum. Molec. Genet. 8: 1177- 1183, 1999. 3 C c

GAM3770 241 SMN1 Mourelatos, Z.; Abel, L.; Yong, J.; Kataoka, N.; Dreyfuss, G.: SMN interacts with a novel family of hnRNP and spliceosomal proteins. EMBOJ. 20: 5443- 5452, 2001. 3 C c

GAM3770 241 SMN1 Owen, N.; Doe, C. L.; Mellor, J.; Davies, K. E.: Characterizationof the Schizosaccharomyces pombe orthologue of the human survivalmotor neuron (SMN) protein. Hum. Molec. Genet. 9: 675- 684, 2000. 3 C c

GAM3770 241 SMN1 Pagliardini, S.; Giavazzi, A.; Setola, V.; Lizier, C.; Di Luca,M.; DeBiasi, S.; Battaglia, G.: Subcellular localization and axonaltransport of the 3 C c

survival motor neuron (SMN) protein in the developingrat spinal cord. Hum. Molec. Genet. 9: 47- 56, 2000.

GAM3770 241 SMN1 Parsons, D. W.; McAndrew, P. E.; Iannaccone, S. T.; Mendell, J.R.; Burghes, A. H. M.; Prior, T. W.: Intragenic telSMN mutations:frequency, distribution, evidence of a founder effect, and modificationof the spinal muscular atrophy phenotype by cenSMN copy number. Am.J. Hum. Genet. 63: 1712- 1723, 1998. 3 C c

GAM3770 241 SMN1 Parsons, D. W.; McAndrew, P. E.; Monani, U. R.; Mendell, J. R.;Burghes, A. H. M.; Prior, T. W.: An 11 base pair duplication in exon6 of the SMN gene produces a type I spinal muscular atrophy (SMA)phenotype: further evidence for SMN as the primary SMA- determininggene. Hum. Molec. Genet. 5: 1727- 1732, 1996. 3 C c

GAM3770 241 SMN1 Pellizzoni, L.; Kataoka, N.; Charroux, B.; Dreyfuss, G.: A novelfunction for SMN, the spinal muscular atrophy gene product, in pre- mRNAsplicing. Cell 95: 615- 624, 1998. 3 C c

GAM3770 241 SMN1 Rodrigues, N. R.; Owen, N.; Talbot, K.; Ignatius, J.; Dubowitz,V.; Davies, K. E.: Deletions in the survival motor neuron gene on5q13 in autosomal recessive spinal muscular atrophy. Hum. Molec.Genet. 4: 631- 634, 1995. 3 C c

GAM3770 241 SMN1 Rossoll, W.; Kroning, A.- K.; Ohndorf, U.- M.; Steegborn, C.; Jablonka,S.; Sendtner, M.: Specific interaction of Smn, the spinal muscularatrophy determining gene product, with hnRNP- R and gry- rbp/hnRNP- Q:a role for Smn in RNA processing in motor axons? Hum. Molec. Genet. 11:93- 105, 2002. 3 C c

GAM3770 241 SMN1 Simard, L. R.; Rochette, C.; Semionov, A.; Morgan, K.; Vanasse,M.: SMN(T) and NAIP mutations in Canadian families with spinal muscularatrophy (SMA): genotype/phenotype correlations with disease severity. Am.J. Med. Genet. 72: 51- 58, 1997. 3 C c

GAM3770 241 SMN1 Sossi, V.; Giuli, A.; Vitali, T.; Tiziano, F.; Mirabella, M.;Antonelli, A.; Neri, G.; Brahe, C.: Premature termination mutationsin exon 3 of the SMN1 gene are associated with exon skipping and arelatively mild SMA phenotype. Europ. J. Hum. Genet. 9: 113- 120,2001. 3 C c

GAM3770 241 SMN1 Stewart, H.; Wallace, A.; McGaughran, J.; Mountford, R.; Kingston,H.: Molecular diagnosis of spinal muscular atrophy. Arch. Dis. Child. 78:531- 535, 1998. 3 C c

GAM3770 241 SMN1 Talbot, K.; Ponting, C. P.; Theodosiou, A. M.; Rodrigues, N. R.;Surtees, R.; Mountford, R.; Davies, K. E.: Missense mutation clusteringin the survival motor neuron gene: a role for a conserved tyrosineand glycine rich region of the protein in RNA metabolism? Hum. Molec.Genet. 6: 497- 500, 1997. 3 C c

GAM3770 241 SMN1 van der Steege, G.; Grootschloten, P. M.; Cobben, J. M.; Zappata,S.; Scheffer, H.; den Dunnen, J. T.; van Ommen, G.- J. B.; Brahe, C.;Buys, C. H. C. M.: Apparent gene conversions involving the SMN genein the region of the spinal muscular atrophy locus on chromosome 5. Am.J. Hum. Genet. 59: 834- 838, 1996. 3 C c

GAM3770 241 SMN1 Viollet, L.; Bertrandy, S.; Bueno Brunialti, A. L.; Lefebvre,S.; Burlet, P.; Clermont, O.; Cruaud, C.; Guenet, J.- L.; Munnich,A.; Melki, J.: cDNA isolation, expression, and chromosomal localizationof the mouse survival motor neuron gene (Smn). Genomics 40: 185- 188,1997. 3 C c

GAM3770 241 SMN1 Wang, C. H.; Xu, J.; Carter, T. A.; Ross, B. M.; Dominski, M.K.; Bellcross, C. A.; Penchaszadeh, G. K.; Munsat, T. L.; Gilliam,T. C.: Characterization of survival motor neuron (SMNT) gene deletionsin asymptomatic carriers of spinal muscular atrophy. Hum. Molec.Genet. 5: 359- 365, 1996. 3 C c

GAM3770 241 SMN1 Wang, J.; Dreyfuss, G.: A cell system with targeted disruptionof the SMN 3 C c

gene: functional conservation of the SMN protein and dependenceof Gemin2 on SMN. J. Biol. Chem. 276: 9599- 9605, 2001.

GAM3770 241 SMN1 Wirth, B.: An update of the mutation spectrum of the survivalmotor neuron gene (SMN1) in autosomal recessive spinal muscular atrophy(SMA). Hum. Mutat. 15: 228- 237, 2000. 3 C c

GAM3770 241 SMN1 Wirth, B.; Hahnen, E.; Morgan, K.; DiDonato, C. J.; Dadze, A.;Rudnik-Schoneborn, S.; Simard, L. R.; Zerres, K.; Burghes, A. H. M.: Allelic association and deletions in autosomal recessive proximalspinal muscular atrophy: association of marker genotype with diseaseseverity and candidate cDNAs. Hum. Molec. Genet. 4: 1273- 1284, 1995. 3 C c

GAM3770 241 SMN1 Wirth, B.; Herz, M.; Wetter, A.; Moskau, S.; Hahnen, E.; Rudnik-Schoneborn,S.; Wienker, T.; Zerres, K.: Quantitative analysis of survival motorneuron copies: identification of subtle SMN1 mutations in patientswith spinal muscular atrophy, genotype- phenotype correlation, andimplications for genetic counseling. Am. J. Hum. Genet. 64: 1340- 1356,1999. 3 C c

GAM3770 241 SMN1 Wirth, B.; Schmidt, T.; Hahnen, E.; Rudnik- Schoneborn, S.; Krawczak,M.; Muller- Myhsok, B.; Schonling, J.; Zerres, K.: De novo rearrangementsfound in 2% of index patients with spinal muscular atrophy: mutationalmechanisms, parental origin, mutation rate, and implications for geneticcounseling. Am. J. Hum. Genet. 61: 1102- 1111, 1997. 3 C c

GAM3770 241 SMN1 Young, P. J.; Man, N.; Lorson, C. L.; Le, T. T.; Androphy, E.J.; Burghes, A. H. M.; Morris, G. E.: The exon 2b region of the spinalmuscular atrophy protein, SMN, is involved in self- association andSIP1 binding. Hum. Molec. Genet. 9: 2869- 2877, 2000. 3 C c

GAM3770 241 TCEA1 Aso, T.; Lane, W. S.; Conaway, J. W.; Conaway, R. C.: Elongin(SIII): a multisubunit regulator of elongation by RNA polymerase II. Science 269:1439-1443, 1995. 3 C c

GAM3770 241 TCEA1 Astrom, A.- K.; Voz, M. L.; Kas, K.; Roijer, E.; Wedell, B.; Mandahl,N.; Van de Ven, W.; Mark, J.; Stenman, G.: Conserved mechanism ofPLAG1 activation in salivary gland tumors with and without chromosome8q12 abnormalities: identification of SII as a new fusion partnergene. Cancer Res. 59: 918- 923, 1999. 3 C c

GAM3770 241 TCEA1 DiMarco, S. P.; Glover, T. W.; Miller, D. E.; Reines, D.; Warren,S. T.: Transcription elongation factor SII (TCEA) maps to human chromosome3p22-p21.3. Genomics 36: 185- 188, 1996. 3 C c

GAM3770 241 TCEA1 Park, H.; Baek, K.; Jeon, C.; Agarwal, K.; Yoo, O.: Characterizationof the gene encoding the human transcriptional elongation factor TFIIS. Gene 139:263- 267, 1994. 3 C c

GAM3770 241 TCEA1 Reines, D.: Nascent RNA cleavage by transcription elongation complexes.In:Conaway, R. C.; Conaway, J. W. (eds.): Transcription: Mechanismsand Regulation. New York: Raven Press 1994. Pp. 263- 278. 3 C c

GAM3770 241 TCEA1 Thomas, M. J.; Platas, A. A.; Hawley, D. K.: Transcriptional fidelityand proofreading by RNA polymerase II. Cell 93: 627- 637, 1998. 3 C c

GAM3770 241 UBE4A Koegl, M.; Hoppe, T.; Schlenker, S.; Ulrich, H. D.; Mayer, T. U.;Jentsch, S.: A novel ubiquitination factor, E4, is involved in multiubiquitinchain assembly. Cell 96: 635- 644, 1999. 3 C c

GAM3770 241 UBE4A Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 3 C c

GAM3770 241 VIPR1 Couvineau, A.; Rouyer- Fessard, C.; Darmoul, D.; Maoret, J.- J.;Carrero, I.; 3 C c
Ogier- Denis, E.; Laburthe, M.: Human intestinal VIPreceptor: cloning and
functional expression of two cDNA encoding proteinswith different N-
terminal domains. Biochem. Biophys. Res. Commun. 200:769- 776, 1994.

GAM3770 241 VIPR1 Hashimoto, H.; Nishino, A.; Shintani, N.; Hagihara, N.; Copeland,N. G.; 3 C c
Jenkins, N. A.; Yamamoto, K.; Matsuda, T.; Ishihara, T.; Nagata,S.; Baba,
A.: Genomic organization and chromosomal location of themouse vasoactive
intestinal polypeptide 1 (VPAC- 1) receptor. Genomics 58:90- 93, 1999.

GAM3770 241 VIPR1 Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 C c
M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor,
and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991.

GAM3770 241 VIPR1 Sreedharan, S. P.; Huang, J.- X.; Cheung, M.- C.; Goetzl, E. J.:Structure, 3 C c
expression, and chromosomal localization of the type Ihuman vasoactive
intestinal peptide receptor gene. Proc. Nat. Acad.Sci. 92: 2939- 2943, 1995.

GAM3770 241 VIPR1 Sreedharan, S. P.; Patel, D. R.; Huang, J.- X.; Goetzl, E. J.:Cloning and 3 C c
functional expression of a human neuroendocrine vasoactiveintestinal peptide
receptor. Biochem. Biophys. Res. Commun. 193:546- 553, 1993.

GAM3770 241 VIPR1 Sreedharan, S. P.; Robichon, A.; Peterson, K. E.; Goetzl, E. J.: Cloning and 3 C c
expression of the human vasoactive intestinal peptidereceptor. Proc. Nat.
Acad. Sci. 88: 4986- 4990, 1991.

GAM3770 241 VIPR1 Vassart, G.: Personal Communication. Brussels, Belgium 1/15/1992. 3 C c

GAM3770 241 VIPR1 Wenger, G. D.: Personal Communication. Columbus, Ohio 8/3/1993. 3 C c

GAM3770 281 ABCD2 Broccardo, C.; Troffer- Charlier, N.; Savary, S.; Mandel, J. L.;Chimini, G.: 3 C c
Exon organisation of the mouse gene encoding the adrenoleukodystrophyrelated
protein (ALDRP). Europ. J. Hum. Genet. 6: 638- 641, 1998.

GAM3770 281 ABCD2 Lombard- Platet, G.; Savary, S.; Sarde, C.- O.; Mandel, J.- L.; Chimini,G.: 3 C c
A close relative of the adrenoleukodystrophy (ALD) gene codesfor a
peroxisomal protein with a specific expression pattern. Proc.Nat. Acad. Sci.
93: 1265- 1269, 1996.

GAM3770 281 ABCD2 Netik, A.; Forss- Petter, S.; Holzinger, A.; Molzer, B.; Unterrainer,G.; 3 C c
Berger, J.: Adrenoleukodystrophy- related protein can compensatefunctionally
for adrenoleukodystrophy protein deficiency (X- ALD):implications for
therapy. Hum. Molec. Genet. 8: 907- 913, 1999.

GAM3770 281 ABCD2 Savary, S.; Troffer- Charlier, N.; Gyapay, G.; Mattei, M.- G.; Chimini,G.: 3 C c
Chromosomal localization of the adrenoleukodystrophy- relatedgene in man and
mice. Europ. J. Hum. Genet. 5: 99- 101, 1997.

GAM3770 281 AKAP2 Dong, F.; Feldmesser, M.; Casadevall, A.; Rubin, C. S.: 3 C c
Molecularcharacterization of a cDNA that encodes six isoforms of a novel
murineA kinase anchor protein. J. Biol. Chem. 273: 6533- 6541, 1998.

GAM3770 281 AKAP2 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XIII. The completesequences of 100
new cDNA clones from brain which code for large proteinsin vitro. DNA Res.
6: 63- 70, 1999.

GAM3770 281 AMPD3 Eddy, R. L.; Mahnke- Zizelman, D. K.; Bausch- Jurken, M. T.; Sabina,R. L.; 3 C c
Shows, T. B.: Distribution of the AMP deaminase multigenefamily within the
human genome: assignment of the AMPD2 to chromosome1p21- p34 and AMPD3 to
chromosome 11p13- pter. (Abstract) Human GenomeMapping Workshop 93 24 only,
1993.

GAM3770 281 AMPD3 Ogasawara, N.; Goto, H.; Yamada, Y.; Nishigaki, I.; Itoh, T.; Hasegawa,I.; 3 C c

Park, K. S.: Deficiency of AMP deaminase in erythrocytes. Hum.Genet. 75: 15-18, 1987.

GAM3770 281 AMPD3 Sermsuvitayawong, K.; Wang, X.; Nagabukuro, A.; Matsuda, Y.; Morisaki,H.; 3 C c
Toyama, K.; Mukai, T.; Morisaki, T.: Genomic organization ofAmpd3, heart-type AMPD gene, located in mouse chromosome 7. MammalianGenome 8: 767- 769, 1997.

GAM3770 281 AMPD3 Yamada, Y.; Goto, H.; Ogasawara, N.: A point mutation responsiblefor human 3 C c
erythrocyte AMP deaminase deficiency. Hum. Molec. Genet. 3:331- 334, 1994.

GAM3770 281 AMPD3 Yamada, Y.; Goto, H.; Ogasawara, N.: Cloning and nucleotide sequenceof the 3 C c
cDNA encoding human erythrocyte- specific AMP deaminase. Biochim.Biophys. Acta 1171: 125- 128, 1992.

GAM3770 281 BRF2 Cabart, P.; Murphy, S.: BRFU, a TFIIB- like factor, is directlyrecruited to 3 C c
the TATA- box of polymerase III small nuclear RNA genepromoters through its interaction with TATA- binding protein. J. Biol.Chem. 276: 43056- 43064, 2001.

GAM3770 281 BRF2 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 C c
TFIIIB activities direct RNA polymerase III transcription fromTATA-containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM3770 281 BSN Gundelfinger, E.: Personal Communication. Madgeburg, FRG. 1/8/1999. 3 C c

GAM3770 281 BSN Hashida, H.; Goto, J.; Zhao, N.; Takahashi, N.; Hirai, M.; Kanazawa,I.; 3 C c
Sakaki, Y.: Cloning and mapping of ZNF231, a novel brain- specificgene encoding neuronal double zinc finger protein whose expressionis enhanced in a neurodegenerative disorder, multiple system atrophy(MSA). Genomics 54: 50-58, 1998.

GAM3770 281 BSN Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VIII. 78 new cDNAclones from brain which code for large proteins in vitro. DNA Res. 4:307- 313, 1997.

GAM3770 281 BSN tom Dieck, S.; Sanmarti- Vila, L.; Langnaese, K.; Richter, K.; Kindler,S.; 3 C c
Soyke, A.; Wex, H.; Smalla, K.- H.; Kampf, U.; Franzer, J.- T.;Stumm, M.; Garner, C. C.; Gundelfinger, E. D.: Bassoon, a novel zinc-fingerCAG/glutamine- repeat protein selectively localized at the active zoneof presynaptic nerve terminals. J. Cell Biol. 142: 499- 509, 1998.

GAM3770 281 BSN Winter, c.; tom Dieck, S.; Boeckers, T. M.; Bockmann, J.; Kampf,U.; 3 C c
Sanmarti- Vila, L.; Langnaese, K.; Altrock, W.; Stumm, M.; Soyke,A.; Wieacker, P.; Garner, C. C.; Gundelfinger, E. D.: The presynapticcytomatrix protein Bassoon: sequence and chromosomal localizationof the human BSN gene. Genomics 57: 389- 397, 1999.

GAM3770 281 CD1A Albertson, D. G.; Fishpool, R.; Sherrington, P.; Nacheva, E.; Milstein,C.: 3 C c
Sensitive and high resolution in situ hybridization to humanchromosomes using biotin labelled probes: assignment of the humanthymocyte CD1 antigen genes to chromosome 1. EMBO J. 7: 2801- 2805,1988.

GAM3770 281 CD1A Balk, S. P.; Bleicher, P. A.; Terhorst, C.: Isolation and characterizationof 3 C c
a cDNA and gene coding for a fourth CD1 molecule. Proc. Nat. Acad.Sci. 86: 252- 256, 1989.

GAM3770 281 CD1A Calabi, F.; Milstein, C.: A novel family of human major 3 C c
histocompatibilitycomplex- related genes not mapping to chromosome 6. Nature 323: 540- 543,1986.

GAM3770 281 CD1A Martin, L. H.; Calabi, F.; Lefebvre, F.- A.; Bilsland, C. A. G.;Milstein, 3 C c
C.: Structure and expression of the human thymocyte antigensCD1a, CD1b, and

CD1c. Proc. Nat. Acad. Sci. 84: 9189- 9193, 1987.

GAM3770 281 CD1A Martin, L. H.; Calabi, F.; Milstein, C.: Isolation of CD1 genes:a family of 3 C c
major histocompatibility complex- related differentiationantigens. Proc.
Nat. Acad. Sci. 83: 9154- 9158, 1986.

GAM3770 281 CD1A Moseley, W. S.; Watson, M. L.; Kingsmore, S. F.; Seldin, M. F.: CD1 defines 3 C c
conserved linkage group border between human chromosomes1 and mouse
chromosomes 1 and 3. Immunogenetics 30: 378- 382, 1989.

GAM3770 281 CD1A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on 3 C c
mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human
DNA. Hum. Molec. Genet. 1: 613- 620,1992.

GAM3770 281 CD1A Park, S.- H.; Bendelac, A.: CD1- restricted T- cell responses andmicrobial 3 C c
infection. Nature 406: 788- 792, 2000.

GAM3770 281 CD1A Yu, C. Y.; Milstein, C.: A physical map linking the five CD1 humanthymocyte 3 C c
differentiation antigen genes. EMBO J. 8: 3727- 3732, 1989.

GAM3770 281 CD1A Zeng, Z.- H.; Castano, A. R.; Segelke, B. W.; Stura, E. A.; Peterson,P. A.; 3 C c
Wilson, I. A.: Crystal structure of mouse CD1: an MHC- likefold with a large
hydrophobic binding groove. Science 277: 339- 345,1997.

GAM3770 281 CDH5 Bussemakers, M. J. G.; van Bokhoven, A.; Voller, M.; Smit, F. P.;Schalken, 3 C c
J. A.: The genes for the calcium- dependent cell adhesionmolecules P- and
E- cadherin are tandemly arranged in the human genome. Biochem.Biophys. Res.
Commun. 203: 1291- 1294, 1994.

GAM3770 281 CDH5 Carmeliet, P.; Lampugnani, M.- G.; Moons, L.; Breviario, F.; Compernolle,V.; 3 C c
Bono, F.; Balconi, G.; Spagnuolo, R.; Oosthuyse, B.; Dewerchin,M.; Zanetti,
A.; Angellilo, A.; and 11 others: Targeted deficiencyof cytosolic truncation
of the VE- cadherin gene in mice impairs VEGF- mediatedendothelial survival
and angiogenesis. Cell 98: 147- 157, 1999.

GAM3770 281 CDH5 Huber, P.; Dalmon, J.; Engiles, J.; Breviario, F.; Gory, S.; Siracusa,L. D.; 3 C c
Buchberg, A. M.; Dejana, E.: Genomic structure and chromosomalmapping of the
mouse VE- cadherin gene (Cdh5). Genomics 32: 21- 28,1996.

GAM3770 281 CDH5 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 3 C c
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting
cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM3770 281 CDH5 Salomon, D.; Ayalon, O.; Patel- King, R.; Hynes, R. O.; Geiger,B.: 3 C c
Extrajunctional distribution of N- cadherin in cultured humanendothelial
cells. J. Cell Sci. 102: 7- 17, 1992.

GAM3770 281 CDO1 Hosokawa, Y.; Matsumoto, A.; Oka, J.; Itakura, H.; Yamaguchi, K.: Isolation 3 C c
and characterization of a cDNA for rat liver cysteinedioxygenase. Biochem.
Biophys. Res. Commun. 168: 473- 478, 1990.

GAM3770 281 CDO1 Jeremiah, S.; McCann, K. P.; Williams, A. C.; Ramsden, D. B.; Pilz,A. J.; 3 C c
Fox, M. F.; Povey, S.: Chromosomal localisation of genes codingfor human and
mouse liver cytosolic cysteine dioxygenase. Ann. Hum.Genet. 60: 29- 33,
1996.

GAM3770 281 CDO1 McCann, K. P.; Akbari, M. T.; Williams, A. C.; Ramsden, D. B.:Human cysteine 3 C c
dioxygenase type I: primary structure derived frombase sequencing of cDNA.
Biochim. Biophys. Acta 1209: 107- 110, 1994.

GAM3770 281 CDO1 Ramsden, D. B.; Kapadi, A.; Fitch, N. J. S.; Farmer, M. J.; Bennett,P.; 3 C c
Williams, A. C.: Human cysteine dioxygenase type I (CDO- I; EC1.13.11.20):
5- prime flanking region and intron- exon structure ofthe gene. Molec. Path.
50: 269- 271, 1997.

GAM3770 281 GABRE Davies, P. A.; Hanna, M. C.; Hales, T. G.; Kirkness, E. F.: Insensitivityto 3 C c

anaesthetic agents conferred by a class of GABA(A) receptor subunit. Nature 385:820- 823, 1997.

GAM3770 281 GABRE Sinkkonen, S. T.; Hanna, M. C.; Kirkness, E. F.; Korpi, E. R.:GABA- A 3 C c
receptor epsilon and theta subunits display unusual structuralvariation between species and are enriched in the rat locus ceruleus. J.Neurosci. 20: 3588- 3595, 2000.

GAM3770 281 GABRE Wilke, K.; Gaul, R.; Klauck, S. M.; Poustka, A.: A gene in humanchromosome 3 C c
band Xq28 (GABRE) defines a putative new subunit classof the GABA(A) neurotransmitter receptor. Genomics 45: 1- 10, 1997.

GAM3770 281 GATM Bianchi, M. C.; Tosetti, M.; Fornai, F.; Alessandri, M. G.; Cipriani,P.; De 3 C c
Vito, G.; Canapicchi, R.: Reversible brain creatine deficiencyin two sisters with normal blood creatine level. Ann. Neurol. 47:511- 513, 2000.

GAM3770 281 GATM Humm, A.; Fritsche, E.; Mann, K.; Gohl, M.; Huber, R.: Recombinantexpression 3 C c
and isolation of human L- arginine:glycine amidinotransferaseand identification of its active- site cysteine residue. Biochem.J. 322: 771- 776, 1997.

GAM3770 281 GATM Humm, A.; Huber, R.; Mann, K.: The amino acid sequences of humanand pig L- 3 C c

arginine:glycine amidinotransferase. FEBS Lett. 339: 101- 107,1994.

GAM3770 281 GATM Item, C. B.; Stockler- Ipsiroglu, S.; Stromberger, C.; Muhl, A.;Alessandri, 3 C c
M. G.; Bianchi, M. C.; Tosetti, M.; Fornai, F.; Cioni,G.: Arginine:glycine amidinotransferase deficiency: the third inbornerror of creatine metabolism in humans. Am. J. Hum. Genet. 69: 1127- 1133,2001.

GAM3770 281 ID4 Pagliuca, A.; Bartoli, P. C.; Saccone, S.; Valle, G. D.; Lania,L.: Molecular 3 C c
cloning of ID4, a novel dominant negative helix- loop- helixhuman gene on chromosome 6p21.3- p22. Genomics 27: 200- 203, 1995.

GAM3770 281 ID4 Rigolet, M.; Rich, T.; Gross- Morand, M.- S.; Molina- Gomes, D.; Viegas- 3 C c
Pequignot,E.; Junien, C.: cDNA cloning, tissue distribution and chromosomallocalization of the human ID4 gene. DNA Res. 5: 309- 313, 1998.

GAM3770 281 IL6R Kluck, P. M. C.; Wiegant, J.; Jansen, R. P. M.; Bolk, M. W. J.;Raap, A. K.; 3 C c
Willemze, R.; Landegent, J. E.: The human interleukin- 6receptor alpha- chain gene is localized on chromosome 1 band q21. Hum.Genet. 90: 542- 544, 1993.

GAM3770 281 IL6R Szpirer, J.; Szpirer, C.; Riviere, M.; Houart, C.; Baumann, M.;Fey, G. H.; 3 C c
Poli, V.; Cortese, R.; Islam, M. Q.; Levan, G.: The interleukin- 6- dependentDNA- binding protein gene (transcription factor 5: TCF5) maps to humanchromosome 20 and rat chromosome 3, the IL6 receptor locus (IL6R)to human chromosome 1 and rat chromosome 2, and the rat IL6 gene torat chromosome 4. Genomics 10: 539- 546, 1991.

GAM3770 281 IL6R Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.;Seed, B.; 3 C c
Taniguchi, T.; Hirano, T.; Kishimoto, T.: Cloning and expressionof the human interleukin- 6 (BSF- 2/IFN- beta- 2) receptor. Science 241:825- 828, 1988.

GAM3770 281 INHBB Brown, C. W.; Houston- Hawkins, D. E.; Woodruff, T. K.; Matzuk,M. M.: 3 C c
Insertion of Inhbb into the Inhba locus rescues the Inhba- nullphenotype and reveals new activin functions. Nature Genet. 25: 453- 457,2000.

GAM3770 281 INHBB Lafuse, W. P.; Zwilling, B. S.: Localization of the inhibin beta- Bgene on 3 C c
mouse chromosome 1. Mammalian Genome 4: 399- 400, 1993.

GAM3770 281 INHBB Matzuk, M. M.; Kumar, T. R.; Vassalli, A.; Bickenbach, J. R.; Roop,D. R.; 3 C c
Jaenisch, R.; Bradley, A.: Functional analysis of activinsduring mammalian development. Nature 374: 354- 356, 1995.

GAM3770 281 INHBB Mellor, S. L.; Cranfield, M.; Ries, R.; Pedersen, J.; Cancilla,B.; de Kretser, D.; Groome, N. P.; Mason, A. J.; Risbridger, G. P.: Localization of activin beta(A)- , beta(B)- , and beta(C)- subunitsin human prostate and evidence for formation of new activin heterodimersof beta(C)- subunit. J. Clin. Endocr. Metab. 85: 4851- 4858, 2000. 3 C c

GAM3770 281 INHBB Salmenkivi, K.; Arola, J.; Voutilainen, R.; Ilvesmaki, V.; Haglund,C.; Kahri, A. I.; Heikkila, P.; Liu, J.: Inhibin/activin beta- B-subunitexpression in pheochromocytomas favors benign diagnosis. J. Clin.Endocr. Metab. 86: 2231- 2235, 2001. 3 C c

GAM3770 281 INHBB Schrewe, H.; Gendron- Maguire, M.; Harbison, M. L.; Gridley, T.: Mice homozygous for a null mutation of activin beta B are viableand fertile. Mech. Dev. 47: 43- 51, 1994. 3 C c

GAM3770 281 OSR1 Daigo, Y.; Isomura, M.; Nishiwaki, T.; Tamari, M.; Ishikawa, S.;Kai, M.; Murata, Y.; Takeuchi, K.; Yamane, Y.; Hayashi, R.; Minami,M.; Fujino, M. A.; Hojo, Y.; Uchiyama, I.; Takagi, T.; Nakamura, Y.: Characterization of a 1200- kb genomic segment of chromosome 3p22- p21.3. DNARes. 6: 37- 44, 1999. 3 C c

GAM3770 281 OSR1 Tamari, M.; Daigo, Y.; Nakamura, Y.: Isolation and characterizationof a novel serine threonine kinase gene on chromosome 3q22- 21.3. J.Hum. Genet. 44: 116- 120, 1999. 3 C c

GAM3770 281 PCOLN3 Halila, R.; Apostolou, S.; Winqvist, R.; Callen, D.; Prockop, D.J.; Peltonen, L.: Isolation and genomic assignment of a candidatecDNA clone for type III procollagen N- proteinase. (Abstract) Am.J. Hum. Genet. 51 (suppl.): A128 only, 1992. 3 C c

GAM3770 281 PCOLN3 Halila, R.; Peltonen, L.; Prockop, D. J.: Isolation of a candidatecDNA clone for type III procollagen N- proteinase from human placentalcDNA library. (Abstract) Am. J. Hum. Genet. 45 (suppl.): A192 only,1989. 3 C c

GAM3770 281 PCOLN3 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994. 3 C c

GAM3770 281 PCOLN3 Scott, I. C.; Halila, R.; Jenkins, J. M.; Mehan, S.; Apostolou,S.; Winqvist, R.; Callen, D. F.; Prockop, D. J.; Peltonen, L.; Kadler,K. E.: Molecular cloning, expression and chromosomal localizationof a human gene encoding a 33 kDa putative metallopeptidase (PRSM1). Gene 174:135- 143, 1996. 3 C c

GAM3770 281 PGF Carmeliet, P.; Moons, L.; Luttun, A.; Vincenti, V.; Compernolle,V.; De Mol, M.; Wu, Y.; Bono, F.; Devy, L.; Beck, H.; Scholz, D.;Acker, T.; and 17 others: Synergism between vascular endothelialgrowth factor and placental growth factor contributes to angiogenesisand plasma extravasation in pathological conditions. Nature Med. 7:575- 583, 2001. 3 C c

GAM3770 281 PGF Luttun, A.; Tjwa, M.; Moons, L.; Wu, Y.; Angelillo- Scherrer, A.;Liao, F.; Nagy, J. A.; Hooper, A.; Priller, J.; De Klerck, B.; Compernolle,V.; Daci, E.; and 10 others: Revascularization of ischemic tissuesby PlGF treatment, and inhibition of tumor angiogenesis, arthritisand atherosclerosis by anti-Flt1. Nature Med. 8: 831- 840, 2002. 3 C c

GAM3770 281 PGF Maglione, D.; Guerriero, V.; Viglietto, G.; Delli- Bovi, P.; Persico,M. G.: Isolation of a human placenta cDNA coding for a protein relatedto the vascular permeability factor. Proc. Nat. Acad. Sci. 88: 9267- 9271,1991. 3 C c

GAM3770 281 PGF Mattei, M.- G.; Borg, J.- P.; Rosnet, O.; Marme, D.; Birnbaum, D.: Assignment of vascular endothelial growth factor (VEGF) and placentagrowth 3 C c

factor (PLGF) genes to human chromosome 6p12- p21 and 14q24- q31regions, respectively. Genomics 32: 168- 169, 1996.

GAM3770 281 PRSS7 Haworth, J. C.; Gourley, B.; Hadorn, B.; Sumida, C.: Malabsorptionand growth failure due to intestinal enterokinase deficiency. J.Pediat. 78: 481- 490, 1971. 3 C c

GAM3770 281 PRSS7 Haworth, J. C.; Hadorn, B.; Gourley, B.; Prasad, A.; Troesch, V.: Intestinal enterokinase deficiency: occurrence in two sibs and agedependency of clinical expression. Arch. Dis. Child. 50: 277- 282,1975. 3 C c

GAM3770 281 PRSS7 Holzinger, A.; Maier, E. M.; Buck, C.; Mayerhofer, P. U.; Kappler,M.; Haworth, J. C.; Moroz, S. P.; Hadorn, H.- B.; Sadler, J. E.; Roscher,A. A.: Mutations in the proenteropeptidase gene are the molecularcause of congenital enteropeptidase deficiency. Am. J. Hum. Genet. 70:20- 25, 2002. 3 C c

GAM3770 281 PRSS7 Kitamoto, Y.; Veile, R. A.; Donis- Keller, H.; Sadler, J. E.: cDNAsequence and chromosomal localization of human enterokinase, the proteolyticactivator of trypsinogen. Biochemistry 34: 4562- 4568, 1995. 3 C c

GAM3770 281 PRSS7 Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D. W.; Sadler, J. E.:Enterokinase, the initiator of intestinal digestion, is a mosaic proteasecomposed of a distinctive assortment of domains. Proc. Nat. Acad.Sci. 91: 7588- 7592, 1994. 3 C c

GAM3770 281 RFC1 Bunz, F.; Kobayashi, R.; Stillman, B.: cDNAs encoding the largesubunit of human replication factor C. Proc. Nat. Acad. Sci. 90:11014- 11018, 1993. 3 C b

GAM3770 281 RFC1 Lossie, A. C.; Haugen, B. R.; Wood, W. M.; Camper, S. A.; Gordon,D. F.: Chromosomal localization of the large subunit of mouse replicationfactor C in the mouse and human. Mammalian Genome 6: 58- 59, 1995. 3 C b

GAM3770 281 RFC1 Luckow, B.; Bunz, F.; Stillman, B.; Lichter, P.; Schutz, G.: Cloning,expression, and chromosomal localization of the 140- kilodalton subunitof replication factor C from mice and humans. Molec. Cell. Biol. 14:1626- 1634, 1994. 3 C b

GAM3770 281 RFC1 Pennaneach, V.; Salles- Passador, I.; Munshi, A.; Brickner, H.;Regazzoni, K.; Dick, F.; Dyson, N.; Chen, T.- T.; Wang, J. Y. J.; Fotedar,R.; Fotedar, A.: The large subunit of replication factor C promotescell survival after DNA damage in an LxCxE motif- and Rb- dependentmanner. Molec. Cell 7: 715- 727, 2001. 3 C b

GAM3770 281 RFC1 Uchiumi, F.; Ohta, T.; Tanuma, S.: Replication factor C recognizes5- prime- phosphate ends of telomeres. Biochem. Biophys. Res. Commun. 229:310- 315, 1996. 3 C b

GAM3770 281 RFC1 Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin,J.: BASC, a super complex of BRCA1- associated proteins involved inthe recognition and repair of aberrant DNA structures. Genes Dev. 14:927- 939, 2000. 3 C b

GAM3770 281 RNH Lee, F. S.; Fox, E. A.; Zhou, H.- M.; Strydom, D. J.; Vallee, B.L.: Primary structure of human placental ribonuclease inhibitor. Biochemistry 27:8545- 8553, 1988. 3 C c

GAM3770 281 RNH Weremowicz, S.; Fox, E. A.; Morton, C. C.; Vallee, B. L.: Theplacental ribonuclease inhibitor (RNH) gene is located on chromosomesubband 11p15.5. Genomics 8: 717- 721, 1990. 3 C c

GAM3770 281 RNH Zneimer, S. M.; Crawford, D.; Schneider, N. R.; Beutler, B.: Mappingof the human ribonuclease inhibitor gene (RNH) to chromosome 11p15by in situ hybridization. Genomics 8: 175- 178, 1990. 3 C c

GAM3770 281 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: 3 C c

Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001.

GAM3770 281 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 C c

GAM3770 281 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 C c

GAM3770 281 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999. 3 C c

GAM3770 281 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001. 3 C c

GAM3770 281 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001. 3 C c

GAM3770 281 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five- base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000. 3 C c

GAM3770 281 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001. 3 C c

GAM3770 281 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002. 3 C c

GAM3770 281 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001. 3 C c

GAM3770 281 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999. 3 C c

GAM3770 281 SURF4 Belden, W. J.; Barlowe, C.: Role of Erv29p in collecting solublesecretory proteins into ER- derived transport vesicles. Science 294:1528- 1531, 2001. 3 C c

GAM3770 281 SURF4 Duhig, T.; Ruhrberg, C.; Mor, O.; Fried, M.: The human surfeitlocus. Genomics 52: 72- 78, 1998. 3 C c

GAM3770 281 SURF4 Reeves, J. E.; Fried, M.: The surf- 4 gene encodes a novel 30 kDaintegral membrane protein. Molec. Membr. Biol. 12: 201- 208, 1995. 3 C c

GAM3770 281 TNFRSF1B Baker, E.; Chen, L. Z.; Smith, C. A.; Callen, D. F.; Goodwin, R.;Sutherland, G. R.: Chromosomal location of the human tumor necrosisfactor receptor 3 C c

genes. Cytogenet. Cell Genet. 57: 117- 118, 1991.

GAM3770 281 TNFRSF1B Beltinger, C. P.; White, P. S.; Maris, J. M.; Sulman, E. P.; Jensen,S. J.; 3 C c
LePaslier, D.; Stallard, B. J.; Goeddel, D. V.; de Sauvage,F. J.; Brodeur,
G. M.: Physical mapping and genomic structure ofthe human TNFR2 gene.
Genomics 35: 94- 100, 1996.

GAM3770 281 TNFRSF1B Bruce, A. J.; Boling, W.; Kindy, M. S.; Peschon, J.; Kraemer, P.J.; 3 C c
Carpenter, M. K.; Holtsberg, F. W.; Mattson, M. P.: Altered neuronaland
microglial responses to excitotoxic and ischemic brain injuryin mice lacking
TNF receptors. Nature Med. 2: 788- 794, 1996.

GAM3770 281 TNFRSF1B Chan, F. K.- M.; Chun, H. J.; Zheng, L.; Siegel, R. M.; Bui, K.L.; Lenardo, 3 C c
M. J.: A domain in TNF receptors that mediates ligand- independentreceptor
assembly and signaling. Science 288: 2351- 2354, 2000.

GAM3770 281 TNFRSF1B Geurts, J. M. W.; Janssen, R. G. J. H.; van Greevenbroek, M. M.J.; van der 3 C c
Kallen, C. J. H.; Cantor, R. M.; Bu, X.; Aouizerat, B.E.; Allayee, H.;
Rotter, J. I.; de Bruin, T. W. A.: Identificationof TNFRSF1B as a novel
modifier gene in familial combined hyperlipidemia. Hum.Molec. Genet. 9:
2067- 2074, 2000.

GAM3770 281 TNFRSF1B Glenn, C. L.; Wang, W. Y. S.; Benjafield, A. V.; Morris, B. J.: Linkage and 3 C c
association of tumor necrosis factor receptor 2 locuswith hypertension,
hypercholesterolemia and plasma shed receptor. Hum.Molec. Genet. 9: 1943-
1949, 2000.

GAM3770 281 TNFRSF1B Kaufman, B. A.; White, P. S.; Steinbrueck, T.; Donis- Keller, H.;Brodeur, G. 3 C c
M.: Linkage mapping of the tumor necrosis factor receptor2 (TNFR2) gene to
1p36.2 using the single- strand conformation polymorphismtechnique. Hum.
Genet. 94: 418- 422, 1994.

GAM3770 281 TNFRSF1B Kemper, O.; Derre, J.; Cherif, D.; Engelmann, H.; Wallach, D.;Berger, R.: 3 C c
The gene for the type II (p75) tumor necrosis factorreceptor (TNF- RII) is
localized on band 1p36.2- p36.3. Hum. Genet. 87:623- 624, 1991.

GAM3770 281 TNFRSF1B Li, X.; Yang, Y.; Ashwell, J. D.: TNF- RII and c- IAP1 mediate 3 C c
ubiquitinationand degradation of TRAF2. Nature 416: 345- 349, 2002.

GAM3770 281 TNFRSF1B Milatovich, A.; Song, K.; Heller, R. A.; Francke, U.: Tumor necrosisfactor 3 C c
receptor genes, TNFR1 and TNFR2, on human chromosomes 12 and1. Somat. Cell
Molec. Genet. 17: 519- 523, 1991.

GAM3770 281 TNFRSF1B Santee, S. M.; Owen- Schaub, L. B.: Human tumor necrosis factorreceptor 3 C c
p75/80 (CD120b) gene structure and promoter characterization. J.Biol. Chem.
271: 21151- 21159, 1996.

GAM3770 281 TNFRSF1B Sashio, H.; Tamura, K.; Ito, R.; Yamamoto, Y.; Bamba, H.; Kosaka,T.; Fukui, 3 C c
S.; Sawada, K.; Fukuda, Y.; Tamura, K.; Satomi, M.; Shimoyama,T.; Furuyama,
J.: Polymorphisms of the TNF gene and the TNF receptorsuperfamily member 1B
gene are associated with susceptibility to ulcerativecolitis and Crohn's
disease, respectively. Immunogenetics 53: 1020- 1027,2002.

GAM3770 281 TNFRSF1B Schall, T. J.; Lewis, M.; Koller, K. J.; Lee, A.; Rice, G. C.;Wong, G. H. 3 C c
W.; Gatanaga, T.; Granger, G. A.; Lentz, R.; Raab, H.;Kohr, W. J.; Goeddel,
D. V.: Molecular cloning and expression ofa receptor for human tumor
necrosis factor. Cell 61: 361- 370, 1990.

GAM3770 281 TNFRSF1B Van Ostade, X.; Vandenabeele, P.; Everaerdt, B.; Loetscher, H.;Gentz, R.; 3 C c
Brockhaus, M.; Lesslauer, W.; Tavernier, J.; Brouckaert,P.; Fiers, W.: Human
TNF mutants with selective activity on the p55receptor. Nature 361: 266-
269, 1993.

GAM3770 281 TNFRSF1B White, P. S.; Maris, J. M.; Beltinger, C.; Sulman, E.; Marshall,H. N.; 3 C c

Fujimori, M.; Kaufman, B. A.; Biegel, J. A.; Allen, C.; Hilliard,C.; Valentine, M. B.; Look, A. T.; Enomoto, H.; Sakiyama, S.; Brodeur,G. M.: A region of consistent deletion in neuroblastoma maps withinhuman chromosome 1p36.2- 36.3. Proc. Nat. Acad. Sci. 92: 5520- 5524,1995.

GAM3770 281 TRPM2 Bertrand, P.; Poirier, J.; Oda, T.; Finch, C. E.; Pasinetti, G.M.: 3 C c
Association of apolipoprotein E genotype with brain levels ofapolipoprotein E and apolipoprotein J (clusterin) in Alzheimer disease. Molec.Brain Res. 33: 174- 178, 1995.

GAM3770 281 TRPM2 Birkenmeier, E. H.; Letts, V. A.; Frankel, W. N.; Magenheimer,B. S.; Calvet, 3 C c
J. P.: Sulfated glycoprotein- 2 (Sgp- 2) maps to mousechromosome 14. Mammalian Genome 4: 131- 132, 1993.

GAM3770 281 TRPM2 Danik, M.; Chabot, J.- G.; Hassan- Gonzalez, D.; Suh, M.; Quirion,R.: 3 C c
Localization of sulfated glycoprotein- 2/clusterin mRNA in therat brain by in situ hybridization. J. Comp. Neurol. 334: 209- 227,1993.

GAM3770 281 TRPM2 de Silva, H. V.; Harmony, J. A. K.; Stuart, W. D.; Gil, C. M.;Robbins, J.: 3 C c
Apolipoprotein J: structure and tissue distribution. Biochemistry 29:5380- 5389, 1990.

GAM3770 281 TRPM2 de Silva, H. V.; Stuart, W. D.; Park, Y. B.; Mao, S. J. T.; Gil,C. M.; 3 C c
Wetterau, J. R.; Busch, S. J.; Harmony, J. A. K.: Purificationand characterization of apolipoprotein J. J. Biol. Chem. 265: 14292- 14297,1990.

GAM3770 281 TRPM2 Dietzsch, E.; Murphy, B. F.; Kirszbaum, L.; Walker, I. D.; Garson,O. M.: 3 C c
Regional localization of the gene for clusterin (SP- 40,40;gene symbol CLI) to human chromosome 8p12- p21. Cytogenet. Cell Genet. 61:178- 179, 1992.

GAM3770 281 TRPM2 Dragunow, M.; Preston, K.; Dodd, J.; Young, D.; Lawlor, P.; Christie,D.: 3 C c
Clusterin accumulates in dying neurons following status epilepticus. Molec.Brain Res. 32: 279- 290, 1995.

GAM3770 281 TRPM2 Duguid, J. R.; Bohmont, C. W.; Liu, N.; Tourtellotte, W. W.: Changesin brain 3 C c
gene expression shared by scrapie and Alzheimer disease. Proc.Nat. Acad. Sci. 86: 7260- 7264, 1989.

GAM3770 281 TRPM2 Fink, T. M.; Zimmer, M.; Tschopp, J.; Etienne, J.; Jenne, D. E.;Lichter, P.: 3 C c
Human clusterin (CLI) maps to 8p21 in proximity to thelipoprotein lipase (LPL) gene. Genomics 16: 526- 528, 1993.

GAM3770 281 TRPM2 Han, B. H.; DeMattos, R. B.; Dugan, L. L.; Kim- Han, J. S.; Brendza,R. P.; 3 C c
Fryer, J. D.; Kierson, M.; Cirrito, J.; Quick, K.; Harmony,J. A. K.; Aronow, B. J.; Holtzman, D. M.: Clusterin contributes tocaspase- 3- independent brain injury following neonatal hypoxia- ischemia. NatureMed. 7: 338- 343, 2001.

GAM3770 281 TRPM2 Hara, Y.; Wakamori, M.; Ishii, M.; Maeno, E.; Nishida, M.; Yoshida,T.; 3 C c
Yamada, H.; Shimizu, S.; Mori, E.; Kudoh, J.; Shimizu, S.; Kurose,H.; Okada, Y.; Imoto, K.; Mori, Y.: LTRPC2 Ca(2+)- permeable channelactivated by changes in redox status confers susceptibility to celldeath. Molec. Cell 9: 163- 173, 2002.

GAM3770 281 TRPM2 Harteneck, C.; Plant, T. D.; Schultz, G.: From worm to man: threesubfamilies 3 C c
of TRP channels. Trends Neurosci. 23: 159- 166, 2000.

GAM3770 281 TRPM2 Jenne, D. E.; Tschopp, J.: Clusterin: the intriguing guises ofa widely 3 C c
expressed glycoprotein. Trends Biochem. Sci. 17: 154- 159,1992.

GAM3770 281 TRPM2 Kamboh, M. I.; Harmony, J. A. K.; Sepehrnia, B.; Nwankwo, M.;Ferrell, R. E.: 3 C c
Genetic studies of human apolipoproteins. XX. Geneticpolymorphism of apolipoprotein J and its impact on quantitative lipidtraits in normolipidemic subjects. Am. J. Hum. Genet. 49: 1167- 1173,1991.

GAM3770 281 TRPM2 Kirszbaum, L.; Sharpe, J. A.; Murphy, B.; d'Apice, A. J. F.; Classon,B.; 3 C c
Hudson, P.; Walker, I. D.: Molecular cloning and characterizationof the
novel, human complement- associated protein, SP- 40,40: a linkbetween the
complement and reproductive systems. EMBO J. 8: 711- 718,1989.

GAM3770 281 TRPM2 Kudoh, J.; Nagamine, K.; Asakawa, S.; Abe, I.; Kawasaki, K.; Maeda,H.; 3 C c
Tsujimoto, S.; Minoshima, S.; Ito, F.; Shimizu, N.: Localizationof 16 exons
to a 450- kb region involved in the autoimmune polyglandulardisease type I
(APECED) on human chromosome 21q22.3. DNA Res. 4:45- 52, 1997.

GAM3770 281 TRPM2 Murphy, B. F.; Kirszbaum, L.; Walker, I. D.; d'Apice, A. J. F.: SP- 40,40, a 3 C c
newly identified normal human serum protein found inthe SC5b- 9 complex of
complement and in the immune deposits in glomerulonephritis. J.Clin. Invest.
81: 1858- 1864, 1988.

GAM3770 281 TRPM2 Nagamine, K.; Kudoh, J.; Minoshima, S.; Kawasaki, K.; Asakawa,S.; Ito, F.; 3 C c
Shimizu, N.: Molecular cloning of a novel putative Ca(2+)channel protein
(TRPC7) highly expressed in brain. Genomics 54:124- 131, 1998.

GAM3770 281 TRPM2 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. 3 C c
J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly
oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J.
Clin. Invest. 99: 2005- 2019, 1997.

GAM3770 281 TRPM2 O'Bryan, M. K.; Baker, H. W. G.; Saunders, J. R.; Kirszbaum, L.;Walker, I. 3 C c
D.; Hudson, P.; Liu, D. Y.; Glew, M. D.; d'Apice, A. J.F.; Murphy, B. F.:
Human seminal clusterin (SP- 40,40): isolationand characterization. J. Clin.
Invest. 85: 1477- 1486, 1990.

GAM3770 281 TRPM2 Perraud, A.- L.; Fleig, A.; Dunn, C. A.; Bagley, L. A.; Launay,P.; Schmitz, 3 C c
C.; Stokes, A. J.; Zhu, Q.; Bessman, M. J.; Penner, R.;Kinet, J.- P.;
Scharenberg, A. M.: ADP- ribose gating of the calcium- permeableLTRPC2
channel revealed by Nudix motif homology. Nature 411: 595- 599,2001.

GAM3770 281 TRPM2 Purrello, M.; Bettuzzi, S.; Di Pietro, C.; Mirabile, E.; Di Blasi,M.; 3 C c
Rimini, R.; Grzeschik, K.- H.; Ingletti, C.; Corti, A.; Sichel,G.: The gene
for SP- 40,40, human homolog of rat sulfated glycoprotein2, rat clusterin,
and rat testosterone- repressed prostate message2, maps to chromosome 8.
Genomics 10: 151- 156, 1991.

GAM3770 281 TRPM2 Sano, Y.; Inamura, K.; Miyake, A.; Mochizuki, S.; Yokoi, H.; Matsushime,H.; 3 C c
Furuichi, K.: Immunocyte Ca(2+) influx system mediated by LTRPC2. Science
293:1327- 1330, 2001.

GAM3770 281 TRPM2 Slawin, K.; Sawczuk, I. S.; Olsson, C. A.; Buttyan, R.: 3 C c
Chromosomalassignment of the human homologue encoding SGP- 2. Biochem.
Biophys.Res. Commun. 172: 160- 164, 1990.

GAM3770 281 TRPM2 Tobe, T.; Minoshima, S.; Yamase, S.; Choi, N.- H.; Tomita, M.;Shimizu, N.: 3 C c
Assignment of a human serum glycoprotein SP- 40,40 gene(CLI) to chromosome
8. Cytogenet. Cell Genet. 57: 193- 195, 1991.

GAM3770 281 TRPM2 Wong, P.; Pineault, J.; Lakins, J.; Taillefer, D.; Leger, J.;Wang, C.; 3 C c
Tenniswood, M.: Genomic organization and expression ofthe rat TRPM- 2
(clusterin) gene, a gene implicated in apoptosis. J.Biol. Chem. 268: 5021-
5031, 1993.

GAM3770 281 TRPM2 Wong, P.; Taillefer, D.; Lakins, J.; Pineault, J.; Chader, G.;Tenniswood, 3 C c
M.: Molecular characterization of human TRPM- 2/clusterin,a gene associated
with sperm maturation, apoptosis and neurodegeneration. Europ.J. Biochem.
221: 917- 925, 1994.

GAM3770 281 UCHL1 Day, I. N. M.; Hinks, L. J.; Thompson, R. J.: The structure ofthe gene 3 C c

encoding protein gene product 9.5 (PGP9.5), a neuron- specificubiquitin C-terminal hydrolase. Biochem. J. 268: 521- 524, 1990.

GAM3770 281 UCHL1 Day, I. N. M.; Thompson, R. J.: Molecular cloning of cDNA codingfor human PGP 9.5 protein: a novel cytoplasmic marker for neuronesand neuroendocrine cells. FEBS Lett. 210: 157- 160, 1987. 3 C c

GAM3770 281 UCHL1 Doran, J. F.; Jackson, P.; Kynoch, P.; Thompson, R. J.: Isolationof PGP 9.5, a new human neurone- specific protein detected by highresolution two-dimensional electrophoresis. J. Neurochem. 40: 1542- 1547,1983. 3 C c

GAM3770 281 UCHL1 Edwards, Y. H.; Fox, M. F.; Povey, S.; Hinks, L. J.; Day, I. N.M.; Thompson, R. J.: The gene for human neuron specific ubiquitinC- terminal hydrolase maps to chromosome 4p14. (Abstract) Cytogenet.Cell Genet. 58: 1886- 1887, 1991. 3 C c

GAM3770 281 UCHL1 Kurihara, L. J.; Kikuchi, T.; Wada, K.; Tilghman, S. M.: Lossof Uch- L1 and Uch- L3 leads to neurodegeneration, posterior paralysisand dysphagia. Hum. Molec. Genet. 10: 1963- 1970, 2001. 3 C c

GAM3770 281 UCHL1 Kurihara, L. J.; Semenova, E.; Levorse, J. M.; Tilghman, S. M.: Expression and functional analysis of Uch- L3 during mouse development. Molec.Cell. Biol. 20: 2498- 2504, 2000. 3 C c

GAM3770 281 UCHL1 Leroy, E.; Boyer, R.; Auburger, G.; Leube, B.; Ulm, G.; Mezey,E.; Harta, G.; Brownstein, M. J.; Jonnalagada, S.; Chernova, T.; Dehejia,A.; Lavedan, C.; Gasser, T.; Steinbach, P. J.; Wilkinson, K. D.; Polymeropoulos,M. H.: The ubiquitin pathway in Parkinson's disease. (Letter) Nature 395:451- 452, 1998. 3 C c

GAM3770 281 UCHL1 Lincoln, S.; Vaughan, J.; Wood, N.; Baker, M.; Adamson, J.; Gwinn- Hardy,K.; Lynch, T.; Hardy, J.; Farrer, M.: Low frequency of pathogenicmutations in the ubiquitin carboxy- terminal hydrolase gene in familialParkinson's disease. Neuroreport 10: 427- 429, 1999. 3 C c

GAM3770 281 UCHL1 MacDonald, M. E.: Gadzooks! Nature Genet. 23: 10- 11, 1999. 3 C c

GAM3770 281 UCHL1 Saigoh, K.; Wang, Y.- L.; Suh, J.- G.; Yamanishi, T.; Sakai, Y.;Kiyosawa, H.; Harada, T.; Ichihara, N.; Wakana, S.; Kikuchi, T.; Wada,K.: Intragenic deletion in the gene encoding ubiquitin carboxy- terminalhydrolase in gad mice. Nature Genet. 23: 47- 51, 1999. 3 C c

GAM3770 281 UCHL1 Suh, J. G.; Yamanishi, T.; Matsui, K.; Tanaka, K.; Wada, K.:Mapping of the gracile axonal dystrophy (gad) gene to a region betweenD5Mit197 and D5Mit113 on proximal mouse chromosome 5. Genomics 27:549- 551, 1995. 3 C c

GAM3770 281 UCHL1 Wilkinson, K. D.; Lee, K. M.; Deshpande, S.; Duerksen- Hughes,P.; Boss, J. M.; Pohl, J.: The neuron- specific protein PGP 9.5 isa ubiquitin carboxyl-terminal hydrolase. Science 246: 670- 672, 1989. 3 C c

GAM3770 281 UCHL1 Yamazaki, K.; Wakasugi, N.; Tomita, T.; Kikuchi, T.; Mukoyama,M.; Ando, K.: Gracile axonal dystrophy (GAD), a new neurologicalmutant in the mouse. Proc. Soc. Exp. Biol. Med. 187: 209- 215, 1988. 3 C c

GAM5227 299 A2M Anonymous: Freely associating. (Editorial) Nature Genet. 22:1- 2, 1999. 1 B c

GAM5227 299 A2M Bell, G. I.; Rall, L. B.; Sanchez- Pescador, R.; Merryweather, J.P.; Scott, J.; Eddy, R. L.; Shows, T. B.: Human alpha- 2- macroglobulingene is located on chromosome 12. Somat. Cell Molec. Genet. 11:285- 289, 1985. 1 B c

GAM5227 299 A2M Bergqvist, D.; Nilsson, I. M.: Hereditary alpha- 2- macroglobulindeficiency. Scand. J. Haemat. 23: 433- 436, 1979. 1 B c

GAM5227 299 A2M Blacker, D.; Crystal, A. S.; Wilcox, M. A.; Laird, N. M.; Tanzi,R. E.: Reply to Rudrasingham et al. Nature Genet. 22: 21- 22, 1999. 1 B c

GAM5227 299 A2M Blacker, D.; Wilcox, M. A.; Laird, N. M.; Rodes, L.; Horvath, S.M.; Go, R. 1 B c

C. P.; Perry, R.; Watson, B., Jr.; Bassett, S. S.; McInnis,M. G.; Albert, M. S.; Hyman, B. T.; Tanzi, R. E.: Alpha- 2 macroglobulinis genetically associated with Alzheimer disease. Nature Genet. 19:357- 360, 1998.

GAM5227 299 A2M David, F.; Kan, C. C.; Lucotte, G.: Two Taq I RFLPs for humanalpha- 2 macroglobulin (alpha- 2M) using a full length cDNA probe. NucleicAcids Res. 15: 374 only, 1987. 1 B c

GAM5227 299 A2M Devriendt, K.; Zhang, J.; van Leuven, F.; van den Berghe, H.; Cassiman,J. J.; Marynen, P.: A cluster of alpha 2- macroglobulin- related genes(alpha 2 M) on human chromosome 12p: cloning of the pregnancy- zoneprotein gene and an alpha 2M pseudogene. Gene 81: 325- 334, 1989. 1 B c

GAM5227 299 A2M Dow, D. J.; Lindsey, N.; Cairns, N. J.; Brayne, C.; Robinson, D.;Huppert, F. A.; Paykel, E. S.; Xuereb, J.; Wilcock, G.; Whittaker,J. L.; Rubinsztein, D. C.: Alpha- 2 macroglobulin polymorphism andAlzheimer disease risk in the UK. (Letter) Nature Genet. 22: 16- 17,1999. 1 B c

GAM5227 299 A2M Fukushima, Y.; Bell, G. I.; Shows, T. B.: The polymorphic humanalpha- 2- macroglobulin gene (A2M) is located in chromosome region 12p12.3- p13.3. Cytogenet.Cell Genet. 48: 58- 59, 1988. 1 B c

GAM5227 299 A2M Gallango, M. L.; Castillo, O.: Alpha- 2- macroglobulin polymorphism:a new genetic system detected by immuno- electrophoresis. J. Immunogenet. 1:147- 151, 1974. 1 B c

GAM5227 299 A2M Hilliker, C.; Overbergh, L.; Petit, P.; Van Leuven, F.; Van denBerghe, H.: Assignment of mouse alpha- 2- macroglobulin gene to chromosome6 band F1- G3. Mammalian Genome 3: 469- 471, 1992. 1 B c

GAM5227 299 A2M Kan, C.- C.; Solomon, E.; Belt, K. T.; Chain, A. C.; Hiorns, L.R.; Fey, G.: Nucleotide sequence of cDNA encoding human alpha- 2- macroglobulinand assignment of the chromosomal locus. Proc. Nat. Acad. Sci. 82:2282- 2286, 1985. 1 B c

GAM5227 299 A2M Leikola, J.; Fudenberg, H. H.; Kasukawa, R.; Milgrom, F.: A newgenetic polymorphism of human serum: alpha(2) macroglobulin (AL- M). Am.J. Hum. Genet. 24: 134- 144, 1972. 1 B c

GAM5227 299 A2M Liao, A.; Nitsch, R. M.; Greenberg, S. M.; Finckh, U.; Blacker,D.; Albert, M.; Rebeck, G. W.; Gomez- Isla, T.; Clatworthy, A.; Binetti,G.; Hock, C.; Mueller- Thomsen, T.; Mann, U.; Zuchowski, K.; Beisiegel,U.; Staehelin, H.; Growdon, J. H.; Tanzi, R. E.; Hyman, B. T.: Geneticassociation of an alpha- 2- macroglobulin (val1000ile) polymorphismand Alzheimer's disease. Hum. Molec. Genet. 7: 1953- 1956, 1998. 1 B c

GAM5227 299 A2M Marynen, P.; Bell, G. I.; Cavalli- Sforza, L. L.: Three RFLPsassociated with the human alpha- 2- macroglobulin gene (A2M). NucleicAcids Res. 13: 8287 only, 1985. 1 B c

GAM5227 299 A2M Marynen, P.; Zhang, J.; Devriendt, K.; Cassiman, J.- J.: Alpha- 2- macroglobulin,pregnancy zone protein and an alpha- 2- macroglobulin pseudogene mapto chromosome 12p12.2- p13. (Abstract) Cytogenet. Cell Genet. 51:1040 only, 1989. 1 B c

GAM5227 299 A2M Matthijs, G.; Devriendt, K.; Cassiman, J.- J.; van den Berghe,H.; Marynen, P.: Structure of the human alpha- 2 macroglobulin geneand its promotor (sic). Biochem. Biophys. Res. Commun. 184: 596- 603,1992. 1 B c

GAM5227 299 A2M Matthijs, G.; Marynen, P. A.: A deletion polymorphism in thehuman alpha- 2- macroglobulin (A2M) gene. Nucleic Acids Res. 19: 5102only, 1991. 1 B c

GAM5227 299 A2M Matthijs, G.; Marynen, P.: A deletion polymorphism in the humanalpha- 2- macroglobulin (A2M) gene. Nucleic Acids Res. 19: 5102 only,1991. 1 B c

GAM5227 299 A2M Poller, W.; Barth, J.; Voss, B.: Detection of an alteration ofthe alpha- 2- 1 B c
macroglobulin gene in a patient with chronic lung diseaseand serum alpha- 2-
macroglobulin deficiency. Hum. Genet. 83: 93- 96,1989.

GAM5227 299 A2M Poller, W.; Faber, J.- P.; Klobeck, G.; Olek, K.: Cloning of thehuman alpha- 1 B c
2- macroglobulin gene and detection of mutations in twofunctional domains:
the bait region and the thiolester site. Hum.Genet. 88: 313- 319, 1992.

GAM5227 299 A2M Rogaeva, E. A.; Premkumar, S.; Grubber, J.; Serneels, L.; Scott,W. K.; 1 B c
Kawarai, T.; Song, Y.; Hill, D. M.; Abou- Donia, S. M.; Martin,E. R.; Vance,
J. J.; Yu, G.; and 18 others: An alpha- 2- macroglobulininsertion- deletion
polymorphism in Alzheimer disease. (Letter) NatureGenet. 22: 19- 21, 1999.

GAM5227 299 A2M Rudrasingham, V.; Wavrant- De Vrieze, F.; Lambert, J.- C.; Chakraverty,S.; 1 B c
Kehoe, P.; Crook, R.; Amouyel, P.; Wu, W.; Rice, F.; Perez- Tur,J.; Frigard,
B.; Morris, J. C.; and 11 others: Alpha- 2 macroglobulingene and Alzheimer
disease. (Letter) Nature Genet. 22: 17- 19, 1999.

GAM5227 299 A2M Sottrup- Jensen, L.; Stepanik, T. M.; Kristensen, T.; Lonblad,P. B.; Jones, 1 B c
C. M.; Wierzbicki, D. M.; Magnusson, S.; Domdey, H.;Wetsel, R. A.; Lundwall,
A.; Tack, B. F.; Fey, G. H.: Common evolutionaryorigin of alpha- 2-
macroglobulin and complement components C3 and C4. Proc.Nat. Acad. Sci. 82:
9- 13, 1985.

GAM5227 299 A2M Umans, L.; Serneels, L.; Hilliker, C.; Stas, L.; Overbergh, L.;De Strooper, 1 B c
B.; Van Leuven, F.; Van den Berghe, H.: Molecular cloningof the mouse gene
coding for alpha- 2- macroglobulin and targeting ofthe gene in embryonic
stem cells. Genomics 22: 519- 529, 1994.

GAM5227 299 A2M Umans, L.; Serneels, L.; Overbergh, L.; Lorent, K.; Van Leuven,F.; Van den 1 B c
Berghe, H.: Targeted inactivation of the mouse alpha- 2- macroglobulingene.
J. Biol. Chem. 270: 19778- 19785, 1995.

GAM5227 299 A2M Webb, D. J.; Wen, J.; Lysiak, J. J.; Umans, L.; Van Leuven, F.;Gonias, S. 1 B c
L.: Murine alpha- macroglobulins demonstrate divergentactivities as
neutralizers of transforming growth factor- beta andas inducers of nitric
oxide synthesis: a possible mechanism for theendotoxin insensitivity of the
alpha- 2- macroglobulin gene knock- outmouse. J. Biol. Chem. 271: 24982-
24988, 1996.

GAM5227 299 AMPD2 Bausch- Jurken, M. T.; Mahnke- Zizelman, D. K.; Morisaki, T.; Sabina,R. L.: 1 B c
Molecular cloning of AMP deaminase isoform L. J. Biol. Chem. 267:22407-
22413, 1992.

GAM5227 299 AMPD2 Eddy, R. L.; Mahnke- Zizelman, D. K.; Bausch- Jurken, M. T.; Sabina,R. L.; 1 B c
Shows, T. B.: Distribution of the AMP deaminase multigenefamily within the
human genome: assignment of the AMPD2 to chromosome1p21- p34 and AMPD3 to
chromosome 11p13- pter. (Abstract) Human GenomeMapping Workshop 93 24, 1993.

GAM5227 299 AMPD2 Mahnke- Zizelman, D. K.; Van den Bergh, F.; Bausch- Jurken, M. T.;Eddy, R.; 1 B c
Sait, S.; Shows, T. B.; Sabina, R. L.: Cloning, sequenceand characterization
of the human AMPD2 gene: evidence for transcriptionalregulation by two
closely spaced promoters. Biochim. Biophys. Acta 1308:122- 132, 1996.

GAM5227 299 AMPD2 Moseley, W. S.; Morisaki, T.; Sabina, R. L.; Holmes, E. W.; Seldin,M. F.: 1 B c
Ampd- 2 maps to distal mouse chromosome 3 in linkage with Ampd- 1. Genomics
6:572- 574, 1990.

GAM5227 299 ANXA5 Demange, P.; Voges, D.; Benz, J.; Liemann, S.; Gottig, P.; Berendes,R.; 1 B c
Burger, A.; Huber, R.: Annexin V: the key to understanding ionselectivity
and voltage regulation? Trends Biochem. Sci. 19: 272- 276,1994.

GAM5227 299 ANXA5 Funakoshi, T.; Heimark, R. L.; Hendrickson, L. E.; McMullen, B.A.; Fujikawa, 1 B c

K.: Human placental anticoagulant protein: isolationand characterization. Biochemistry 26: 5572- 5578, 1987.

GAM5227 299 ANXA5 Grundmann, U.; Abel, K.- J.; Bohn, H.; Lobermann, H.; Lottspeich,F.; Kupper, 1 B c
H.: Characterization of cDNA encoding human placentalanticoagulant protein (PP4): homology with the lipocortin family. Proc.Nat. Acad. Sci. 85: 3708-3712, 1988.

GAM5227 299 ANXA5 Kaplan, R.; Jaye, M.; Burgess, W. H.; Schlaepfer, D. D.; Haigler,H. T.: 1 B c
Cloning and expression of cDNA for human endonexin II, a Ca(2+)and phospholipid binding protein. J. Biol. Chem. 263: 8037- 8043,1988.

GAM5227 299 ANXA5 Modi, W. S.; Seuanez, H. N.; Jaye, M.; Haigler, H. J.; Kaplan,R.; O'Brien, 1 B c
S. J.: The human endonexin II (ENX2) gene is locatedat 4q28- q32. Cytogenet. Cell Genet. 52: 167- 169, 1989.

GAM5227 299 ANXA5 Modi, W. S.; Seuanez, H.; Jaye, M.; Kaplan, R.; Haigler, H.; O'Brien,S. J.: 1 B c
Chromosomal mapping of the endonexin II gene. (Abstract) Cytogenet.Cell Genet. 51: 1046, 1989.

GAM5227 299 ANXA5 Rodriguez- Garcia, M. I.; Kozak, C. A.; Morgan, R. O.; Fernandez,M. P.: 1 B c
Mouse annexin V chromosomal localization, cDNA sequence conservation,and molecular evolution. Genomics 31: 151- 157, 1996.

GAM5227 299 ANXA5 Tait, J. F.; Frankenberry, D. A.; Shiang, R.; Murray, J. C.; Adler,D. A.; 1 B c
Disteche, C. M.: Chromosomal localization of the human genefor annexin V (placental anticoagulant protein I) to 4q26- q28. Cytogenet.Cell Genet. 57: 187- 192, 1991.

GAM5227 299 BAX Apte, S. S.; Mattei, M.- G.; Olsen, B. R.: Mapping of human BAXgene to 1 B c
chromosome 19q13.3- q13.4 and isolation of a novel alternativelyspliced transcript, BAX- delta. Genomics 26: 592- 594, 1995.

GAM5227 299 BAX Cartron, P.- F.; Oliver, L.; Martin, S.; Moreau, C.; LeCabellec,M.- T.; 1 B c
Jezequel, P.; Meflah, K.; Vallette, F. M.: The expressionof a new variant of the pro- apoptotic molecule Bax, Bax- psi, is correlatedwith an increased survival of glioblastoma multiforme patients. Hum.Molec. Genet. 11: 675-687, 2002.

GAM5227 299 BAX Chong, M. J.; Murray, M. R.; Gosink, E. C.; Russell, H. R. C.;Srinivasan, 1 B c
A.; Kapsetaki, M.; Korsmeyer, S. J.; McKinnon, P. J.:Atm and Bax cooperate in ionizing radiation- induced apoptosis in thecentral nervous system. Proc. Nat. Acad. Sci. 97: 889- 894, 2000.

GAM5227 299 BAX Chou, D.; Miyashita, T.; Mohrenweiser, H. W.; Ueki, K.; Kastury,K.; Druck, 1 B c
T.; von Deimling, A.; Huebner, K.; Reed, J. C.; Louis,D. N.: The BAX gene maps to the glioma candidate region at 19q13.3,but is not altered in human gliomas. Cancer Genet. Cytogenet. 88:136- 140, 1996.

GAM5227 299 BAX Deckwerth, T. L.; Elliott, J. L.; Knudson, C. M.; Johnson, E. M.,Jr.; 1 B c
Snider, W. D.; Korsmeyer, S. J.: BAX is required for neuronaldeath after trophic factor deprivation and during development. Neuron 17:401- 411, 1996.

GAM5227 299 BAX Knudson, C. M.; Tung, K. S. K.; Tourtellotte, W. G.; Brown, G.A. J.; 1 B c
Korsmeyer, S. J.: Bax- deficient mice with lymphoid hyperplasiaand male germ cell death. Science 270: 96- 99, 1995.

GAM5227 299 BAX LeBlanc, H.; Lawrence, D.; Varfolomeev, E.; Totpal, K.; Morlan,J.; Schow, 1 B c
P.; Fong, S.; Schwall, R.; Sinicropi, D.; Ashkenazi, A.: Tumor- cell resistance to death receptor- induced apoptosis throughmutational inactivation of the proapoptotic Bcl- 2 homolog Bax. NatureMed. 8: 274- 281, 2002.

GAM5227 299 BAX Li, Q. J.; Ashraf, M. F.; Shen, D.; Green, W. R.; Stark, W. J.;Chan, C.- C; 1 B c

O'Brien, T. P.: The role of apoptosis in the pathogenesisof Fuchs endothelial dystrophy of the cornea. Arch. Ophthal. 119:1597- 1604, 2001.

GAM5227 299 BAX Lindsten, T.; Ross, A. J.; King, A.; Zong, W.- X.; Rathmell, J.C.; Shiels, H. A.; Ulrich, E.; Waymire, K. G.; Mahar, P.; Frauwirth,K.; Chen, Y.; Wei, M.; and 9 others: The combined functions ofproapoptotic Bcl- 2 family members Bak and Bax are essential for normaldevelopment of multiple tissues. Molec. Cell 6: 1389- 1399, 2000. 1 B c

GAM5227 299 BAX Marzo, I.; Brenner, C.; Zamzami, N.; Jurgensmeier, J. M.; Susin,S. A.; Vieira, H. L. A.; Prevost, M.- C.; Xie, Z.; Matsuyama, S.; Reed,J. C.; Kroemer, G.: Bax and adenine nucleotide translocator cooperatein the mitochondrial control of apoptosis. Science 281: 2027- 2031,1998. 1 B c

GAM5227 299 BAX Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 1 B c

GAM5227 299 BAX Matsuda, Y.; Kusano, H.; Tsujimoto, Y.: Chromosomal assignmentof the Bcl2- related genes, Bcl2l and Bax, in the mouse and rat. Cytogenet.Cell Genet. 74: 107- 110, 1996. 1 B c

GAM5227 299 BAX Meijerink, J. P. P.; Mensink, E. J. B. M.; Wang, K.; Sedlak, T.W.; Sloetjes, A. W.; de Witte, T.; Waksman, G.; Korsmeyer, S. J.:Hematopoietic malignancies demonstrate loss- of- function mutationsof BAX. Blood 91: 2991- 2997, 1998. 1 B c

GAM5227 299 BAX Miyashita, T.; Reed, J. C.: Tumor suppressor p53 is a directtranscriptional activator of the human bax gene. Cell 80: 293- 299,1995. 1 B c

GAM5227 299 BAX Oltvai, Z. N.; Milliman, C. L.; Korsmeyer, S. J.: Bcl- 2 heterodimersin vivo with a conserved homolog, Bax, that accelerates programmedcell death. Cell 74: 609- 619, 1993. 1 B c

GAM5227 299 BAX Perez, G. I.; Robles, R.; Knudson, C. M.; Flaws, J. A.; Korsmeyer,S. J.; Tilly, J. L.: Prolongation of ovarian lifespan into advancedchronological age by Bax- deficiency. Nature Genet. 21: 200- 203,1999. 1 B c

GAM5227 299 BAX Rampino, N.; Yamamoto, H.; Ionov, Y.; Li, Y.; Sawai, H.; Reed,J. C.; Perucho, M.: Somatic frameshift mutations in the BAX genein colon cancers of the microsatellite mutator phenotype. Science 275:967- 969, 1997. 1 B c

GAM5227 299 BAX Shimizu, S.; Narita, M.; Tsujimoto, Y.: Bcl- 2 family proteinsregulate the release of apoptogenic cytochrome c by the mitochondrialchannel VDAC. Nature 399: 483- 487, 1999. 1 B c

GAM5227 299 BAX Sugino, N.; Suzuki, T.; Kashida, S.; Karube, A.; Takiguchi, S.;Kato, H.: Expression of Bcl- 2 and Bax in the human corpus luteumduring the menstrual cycle in early pregnancy: regulation by humanchorionic gonadotropin. J. Clin. Endocr. Metab. 85: 4379- 4386, 2000. 1 B c

GAM5227 299 BAX Suzuki, M.; Youle, R. J.; Tjandra, N.: Structure of Bax: coregulationof dimer formation and intracellular localization. Cell 103: 645- 654,2000. 1 B c

GAM5227 299 BAX Vaskivuo, T. E.; Anttonen, M.; Herva, R.; Billig, H.; Dorland,M.; Te Velde, E. R.; Stenback, F.; Heikinheimo, M.; Tapanainen, J.S.: Survival of human ovarian follicles from fetal to adult life:apoptosis, apoptosis- related proteins, and transcription factor GATA- 4. J.Clin. Endocr. Metab. 86: 3421- 3429, 2001. 1 B c

GAM5227 299 BAX Wei, M. C.; Zong, W.- X.; Cheng, E. H.- Y.; Lindsten, T.; Panoutsakopoulou,V.; Ross, A. J.; Roth, K. A.; MacGregor, G. R.; Thompson, 1 B c

C. B.; Korsmeyer,S. J.: Proapoptotic BAX or BAK: a requisite gateway to mitochondrialdysfunction and death. Science 292: 727- 730, 2001.

GAM5227 299 BAX Zhang, L.; Yu, J.; Park, B. H.; Kinzler, K. W.; Vogelstein, B.: Role of BAX 1 B c in the apoptotic response to anticancer agents. Science 290:989- 992, 2000.

GAM5227 299 BMP8 DiLeone, R. J.; King, J. A.; Storm, E. E.; Copeland, N. G.; Jenkins,N. A.; 1 B c Kingsley, D. M.: The Bmp8 gene is expressed in developingskeletal tissue and maps near the achondroplasia locus on mouse chromosome4. Genomics 40: 196- 198, 1997.

GAM5227 299 BMP8 Ozkaynak, E.; Schnegelsberg, P. N. J.; Jin, D. F.; Clifford, G.M.; Warren, 1 B c F. D.; Drier, E. A.; Oppermann, H.: Osteogenic protein- 2:a new member of the transforming growth factor- beta superfamily expressedin early embryogenesis. J. Biol. Chem. 267: 25220- 25227, 1992.

GAM5227 299 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a 1 B c membrane- associated C- type lectin that exhibits CD4- independentbinding of human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad. Sci. 89: 8356- 8360, 1992.

GAM5227 299 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis 1 B c for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR. Science 294: 2163- 2166, 2001.

GAM5227 299 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van 1 B c Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S. L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC- SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans- infection of T cells. Cell 100: 587- 597,2000.

GAM5227 299 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. 1 B c F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000.

GAM5227 299 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related 1 B c gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000.

GAM5227 299 CD34 Cheng, J.; Baumhueter, S.; Cacalano, G.; Carver- Moore, K.; Thibodeaux,H.; 1 B c Thomas, R.; Broxmeyer, H. E.; Cooper, S.; Hague, N.; Moore, M.;Lasky, L. A.: Hematopoietic defects in mice lacking the sialomucinCD34. Blood 87: 479- 490, 1996.

GAM5227 299 CD34 He, X.- Y.; Antao, V. P.; Basila, D.; Marx, J. C.; Davis, B. R.: Isolation 1 B c and molecular characterization of the human CD34 gene. Blood 79:2296- 2302, 1992.

GAM5227 299 CD34 Howell, S. M.; Molgaard, H. V.; Greaves, M. F.; Spurr, N. K.:Localisation of 1 B c the gene coding for the haemopoietic stem cell antigenCD34 to chromosome 1q32. Hum. Genet. 87: 625- 627, 1991.

GAM5227 299 CD34 Okuno, Y.; Iwasaki, H.; Huettner, C. S.; Radomska, H. S.; Gonzalez,D. A.; 1 B c Tenen, D. G.; Akashi, K.: Differential regulation of the humanand murine CD34 genes in hematopoietic stem cells. Proc. Nat. Acad.Sci. 99: 6246- 6251, 2002.

GAM5227 299 CD34 Satterthwaite, A. B.; Burn, T. C.; Le Beau, M. M.; Tenen, D. G.: Structure 1 B c of the gene encoding CD34, a human hematopoietic stemcell antigen. Genomics 12: 788- 794, 1992.

GAM5227 299 CD34 Simmons, D. L.; Satterthwaite, A. B.; Tenen, D. G.; Seed, B.:Molecular 1 B c cloning of a cDNA encoding CD34, a sialomucin of human hematopoieticstem

cells. J. Immun. 148: 267- 271, 1992.

GAM5227 299 CD34 Sutherland, D. R.; Stewart, A. K.; Keating, A.: CD34 antigen:molecular features and potential clinical applications. Stem Cells 11(suppl. 3): 50- 57, 1993. 1 B c

GAM5227 299 CD34 Sutherland, D. R.; Watt, S. M.; Dowden, G.; Karhi, K.; Baker, M.A.; Greaves, M. F.; Smart, J. E.: Structural and partial amino acidsequence analysis of the human hemopoietic progenitor cell antigenCD34. Leukemia 2: 793- 803, 1988. 1 B c

GAM5227 299 CD34 Tenen, D. G.; Satterthwaite, A. B.; Borson, R.; Simmons, D.; Eddy,R. L.; Shows, T. B.: Chromosome 1 localization of the gene for CD34,a surface antigen of human stem cells. Cytogenet. Cell Genet. 53:55- 57, 1990. 1 B c

GAM5227 299 CDH16 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999. 1 B c

GAM5227 299 CDH16 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck, P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with a protein related to the cadherin superfamily. Science 264:430- 433, 1994. 1 B c

GAM5227 299 CDH16 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, D. F.: Localization of human cadherin genes to chromosomeregions exhibiting cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998. 1 B c

GAM5227 299 CDH16 Thomson, R. B.; Igarashi, P.; Biemesderfer, D.; Kim, R.; Abu- Alfa,A.; Soleimani, M.; Aronson, P. S.: Isolation and cDNA cloning ofKsp- cadherin, a novel kidney- specific member of the cadherin multigenefamily. J. Biol. Chem. 270: 17594- 17601, 1995. 1 B c

GAM5227 299 CDH16 Thomson, R. B.; Ward, D. C.; Quaggin, S. E.; Igarashi, P.; Muckler,Z. E.; Aronson, P. S.: cDNA cloning and chromosomal localizationof the human and mouse isoforms of Ksp- cadherin. Genomics 51: 445- 451,1998. 1 B c

GAM5227 299 CPD McGwire, G. B.; Tan, F.; Michel, B.; Rehli, M.; Skidgel, R. A.: Identification of a membrane- bound carboxypeptidase as the mammalianhomolog of duck gp180, a hepatitis B virus- binding protein. LifeSci. 60: 715- 724, 1997. 1 B c

GAM5227 299 CPD Riley, D. A.; Tan, F.; Miletich, D. J.; Skidgel, R. A.: Chromosomallocalization of the genes for human carboxypeptidase D (CPD) and theactive 50- kilodalton subunit of human carboxypeptidase N (CPN1). Genomics 50:105- 108, 1998. 1 B c

GAM5227 299 CPD Tan, F.; Rehli, M.; Krause, S. W.; Skidgel, R. A.: Sequence ofhuman carboxypeptidase D reveals it to be a member of the regulatorycarboxypeptidase family with three tandem active site domains. Biochem.J. 327: 81- 87, 1997. 1 B c

GAM5227 299 CXADR Bergelson, J. M.; Cunningham, J. A.; Droguett, G.; Kurt- Jones,E. A.; Krithivas, A.; Hong, J. S.; Horwitz, M. S.; Crowell, R. L.;Finberg, R. W.: Isolation of a common receptor for coxsackie B virusesand adenoviruses 2 and 5. Science 275: 1320- 1323, 1997. 1 B c

GAM5227 299 CXADR Bowles, K. R.; Gibson, J.; Wu, J.; Shaffer, L. G.; Towbin, J. A.;Bowles, N. E.: Genomic organization and chromosomal localizationof the human Coxsackievirus B- adenovirus receptor gene. Hum. Genet. 105:354- 359, 1999. 1 B c

GAM5227 299 CXADR Carson, S. D.; Chapman, N. N.; Tracy, S. M.: Purification of theputative coxsackievirus B receptor from HeLa cells. Biochem. Biophys.Res. Commun. 233: 325- 328, 1997. 1 B c

GAM5227 299 CXADR Griffin, L. D.; Kearney, D.; Ni, J.; Jaffe, R.; Fricker, F. J.;Webber, S.; 1 B c
Demmler, G.; Gelb, B. D.; Towbin, J. A.: Analysis offormalin- fixed and
frozen myocardial autopsy samples for viral genomein childhood myocarditis
and dilated cardiomyopathy with endocardialfibroelastosis using polymerase
chain reaction (PCR). Cardiovasc.Path. 4: 3- 11, 1995.

GAM5227 299 CXADR Martin, A. B.; Webber, S.; Fricker, F. J.; Jaffe, R.; Demmler,G.; Kearney, 1 B c
D.; Zhang, Y.- H.; Bodurtha, J.; Gelb, B.; Ni, J.; Bricker,J. T.; Towbin, J.
A.: Acute myocarditis: rapid diagnosis by PCR inchildren. Circulation 90:
330- 339, 1994.

GAM5227 299 CXADR Pauschinger, M.; Bowles, N. E.; Fuentes- Garcia, F. J.; Pham, V.;Kuhl, U.; 1 B c
Schwimmbeck, P. L.; Schultheiss, H.- P.; Towbin, J. A.:Detection of
adenoviral genome in the myocardium of adult patientswith idiopathic left
ventricular dysfunction. Circulation 99: 1348- 1354,1999.

GAM5227 299 CXADR Tomko, R. P.; Xu, R.; Philipson, L.: HCAR and MCAR: the humanand mouse 1 B c
receptors for subgroup C adenoviruses and group B coxsackieviruses.
Proc.Nat. Acad. Sci. 94: 3352- 3356, 1997.

GAM5227 299 DAG1 Arahata, K.; Hayashi, Y. K.; Mizuno, Y.; Yoshida, M.; Ozawa, E.: Dystrophin- 1 B c
associated glycoprotein and dystrophin co- localisationat sarcolemma in
Fukuyama congenital muscular dystrophy. (Letter) Lancet 342:623- 624, 1993.

GAM5227 299 DAG1 Campanelli, J. T.; Roberds, S. L.; Campbell, K. P.; Scheller, R.H.: A role 1 B c
for dystrophin- associated glycoproteins and utrophin inagrin- induced AChR
clustering. Cell 77: 663- 674, 1994.

GAM5227 299 DAG1 Cao, W.; Henry, M. D.; Borrow, P.; Yamada, H.; Elder, J. H.; Ravkov,E. V.; 1 B c
Nichol, S. T.; Compans, R. W.; Campbell, K. P.; Oldstone, M.B. A.:
Identification of alpha- dystroglycan as a receptor for
lymphocyticchoriomeningitis virus and Lassa fever virus. Science 282: 2079-
2081,1998.

GAM5227 299 DAG1 Cohn, R. D.; Henry, M. D.; Michele, D. E.; Barresi, R.; Saito,F.; Moore, S. 1 B c
A.; Flanagan, J. D.; Skwarchuk, M. W.; Robbins, M. E.;Mendell, J. R.;
Williamson, R. A.; Campbell, K. P.: Disruption ofDag1 in differentiated
skeletal muscle reveals a role for dystroglycanin muscle regeneration. Cell
110: 639- 648, 2002.

GAM5227 299 DAG1 Cote, P. D.; Moukhles, H.; Lindenbaum, M.; Carbonetto, S.: Chimaericmice 1 B c
deficient in dystroglycans develop muscular dystrophy and havedisrupted
myoneural synapses. Nature Genet. 23: 338- 342, 1999.

GAM5227 299 DAG1 Gee, S. H.; Montanaro, F.; Lindenbaum, M. H.; Carbonetto, S.:Dystroglycan- 1 B c
alpha, a dystrophin- associated glycoprotein, is a functionalagrin receptor.
Cell 77: 675- 686, 1994.

GAM5227 299 DAG1 Gorecki, D. C.; Derry, J. M. J.; Barnard, E. A.: Dystroglycan:brain 1 B c
localisation and chromosome mapping in the mouse. Hum. Molec.Genet. 3: 1589-
1597, 1994.

GAM5227 299 DAG1 Hayashi, Y. K.; Ogawa, M.; Tagawa, K.; Noguchi, S.; Ishihara, T.;Nonaka, I.; 1 B c
Arahata, K.: Selective deficiency of alpha- dystroglycanin Fukuyama- type
congenital muscular dystrophy. Neurology 57: 115- 121,2001.

GAM5227 299 DAG1 Henry, M. D.; Campbell, K. P.: A role for dystroglycan in basementmembrane 1 B c
assembly. Cell 95: 859- 970, 1998.

GAM5227 299 DAG1 Ibraghimov- Beskrovnaya, O.; Ervasti, J. M.; Leveille, C. J.; Slaughter,C. 1 B c
A.; Sernett, S. W.; Campbell, K. P.: Primary structure of dystrophin-
associatedglycoproteins linking dystrophin to the extracellular matrix.

Nature 355:696- 702, 1992.

GAM5227 299 DAG1 Ibraghimov- Beskrovnaya, O.; Milatovich, A.; Ozcelik, T.; Yang,B.; Francke, 1 B c
U.; Campbell, K. P.: Dystroglycan: tissue distribution,human muscle cDNA,
genomic structure and chromosome mapping. (Abstract) Am.J. Hum. Genet. 51
(suppl.): A130 only, 1992.

GAM5227 299 DAG1 Ibraghimov- Beskrovnaya, O.; Milatovich, A.; Ozcelik, T.; Yang,B.; Koepnick, 1 B c
K.; Francke, U.; Campbell, K. P.: Human dystroglycan:skeletal muscle cDNA,
genomic structure, origin of tissue specificisoforms and chromosomal
localization. Hum. Molec. Genet. 2: 1651- 1657,1993.

GAM5227 299 DAG1 Ma, J.; Nastuk, M. A.; McKechnie, B. A.; Fallon, J. R.: The agrinreceptor: 1 B c
localization in the postsynaptic membrane, interaction withagrin, and
relationship to the acetylcholine receptor. J. Biol. Chem. 268:25108- 25117,
1993.

GAM5227 299 DAG1 Matsumura, K.; Nonaka, I.; Campbell, K. P.: Abnormal expressionof 1 B c
dystrophin- associated proteins in Fukuyama- type congenital
musculardystrophy. Lancet 341: 521- 522, 1993.

GAM5227 299 DAG1 Matsumura, K.; Tome, F. M. S.; Collin, H.; Azibi, K.; Chaouch,M.; Kaplan, 1 B c
J.- C.; Fardeau, M.; Campbell, K. P.: Deficiency of the50K dystrophin-
associated glycoprotein in severe childhood autosomalrecessive muscular
dystrophy. Nature 359: 320- 322, 1992.

GAM5227 299 DAG1 Matsumura, K.; Tome, F. M. S.; Ionasescu, V.; Ervasti, J. M.;Anderson, R. 1 B c
D.; Romero, N. B.; Simon, D.; Recan, D.; Kaplan, J.- C.;Fardeau, M.;
Campbell, K. P.: Deficiency of dystrophin- associatedproteins in Duchenne
muscular dystrophy patients lacking COOH- terminaldomains of dystrophin. J.
Clin. Invest. 92: 866- 871, 1993.

GAM5227 299 DAG1 Michele, D. E.; Barresi, R.; Kanagawa, M.; Saito, F.; Cohn, R.D.; Satz, J. 1 B c
S.; Dollar, J.; Nishino, I.; Kelley, R. I.; Somer, H.;Straub, V.; Mathews,
K. D.; Moore, S. A.; Campbell, K. P.: Post- translationaldisruption of
dystroglycan- ligand interactions in congenital musculardystrophies. Nature
418: 417- 422, 2002.

GAM5227 299 DAG1 Moore, S. A.; Saito, F.; Chen, J.; Michele, D. E.; Henry, M. D.;Messing, A.; 1 B c
Cohn, R. D.; Ross- Barta, S. E.; Westra, S.; Williamson,R. A.; Hoshi, T.;
Campbell, K. P.: Deletion of brain dystroglycanrecapitulates aspects of
congenital muscular dystrophy. Nature 418:422- 425, 2002.

GAM5227 299 DAG1 Rambukkana, A.; Yamada, H.; Zanazzi, G.; Mathus, T.; Salzer, J.L.; 1 B c
Yurchenco, P. D.; Campbell, K. P.; Fischetti, V. A.: Role ofalpha-
dystroglycan as a Schwann cell receptor for Mycobacterium leprae. Science
282:2076- 2078, 1998.

GAM5227 299 DAG1 Sealock, R.; Froehner, S. C.: Dystrophin- associated proteinsand synapse 1 B c
formation: is alpha- dystroglycan the agrin receptor? Cell 77:617- 619,
1994.

GAM5227 299 DAG1 Spear, P. G.: A welcome mat for leprosy and Lassa fever. Science 282:1999- 1 B c
2000, 1998.

GAM5227 299 DAG1 Tinsley, J. M.; Blake, D. J.; Zuellig, R. A.; Davies, K. E.:Increasing 1 B c
complexity of the dystrophin- associated protein complex. Proc.Nat. Acad.
Sci. 91: 8307- 8313, 1994.

GAM5227 299 DAG1 Williamson, R. A.; Henry, M. D.; Daniels, K. J.; Hrstka, R. F.;Lee, J. C.; 1 B c
Sunada, Y.; Ibraghimov- Beskrovnaya, O.; Campbell, K. P.: Dystroglycan is
essential for early embryonic development: disruptionof Reichert's membrane
in Dag1- null mice. Hum. Molec. Genet. 6:831- 841, 1997.

GAM5227 299 DAG1 Yamada, H.; Denzer, A. J.; Hori, H.; Tanaka, T.; Anderson, L.V. B.; Fujita, 1 B c
S.; Fukuta- Ohi, H.; Shimizu, T.; Ruegg, M. A.; Matsumura,K.: Dystroglycan
is a dual receptor for agrin and laminin- 2 in Schwanncell membrane. J.
Biol. Chem. 271: 23418- 23423, 1996.

GAM5227 299 DAG1 Yamada, H.; Saito, F.; Fukuta- Ohi, H.; Zhong, D.; Hase, A.; Arai,K.; 1 B c
Okuyama, A.; Maekawa, R.; Shimizu, T.; Matsumura, K.: Processingof beta-
dystroglycan by matrix metalloproteinase disrupts the linkbetween the
extracellular matrix and cell membrane via the dystroglycancomplex. Hum.
Molec. Genet. 10: 1563- 1569, 2001.

GAM5227 299 DGCR2 Augusseau, S.; Jouk, S.; Jalbert, P.; Prieur, M.: DiGeorge syndromeand 22q11 1 B c
rearrangements. (Letter) Hum. Genet. 74: 206 only, 1986.

GAM5227 299 DGCR2 Bartsch, O.; Wagner, A.; Hinkel, G. K.; Lichtner, P.; Murken, 1 B c
J.;Schuffenhauer, S.: No evidence for chromosomal microdeletions atthe
second DiGeorge syndrome locus on 10p near D10S585. (Letter) Am.J. Med.
Genet. 83: 425- 426, 1999.

GAM5227 299 DGCR2 Daw, S. C. M.; Taylor, C.; Kraman, M.; Call, K.; Mao, J.; Schuffenhauer,S.; 1 B c
Meitinger, T.; Lipson, T.; Goodship, J.; Scambler, P.: A commonregion of 10p
deleted in DiGeorge and velocardiofacial syndromes. NatureGenet. 13: 458-
461, 1996.

GAM5227 299 DGCR2 Demczuk, S.; Aledo, R.; Zucman, J.; Delattre, O.; Desmaze, C.;Dauphinot, L.; 1 B c
Jalbert, P.; Rouleau, G. A.; Thomas, G.; Aurias, A.: Cloning of a balanced
translocation breakpoint in the DiGeorge syndromecritical region and
isolation of a novel potential adhesion receptorgene in its vicinity. Hum.
Molec. Genet. 4: 551- 558, 1995.

GAM5227 299 DGCR2 Hasegawa, T.; Hasegawa, Y.; Aso, T.; Koto, S.; Nagai, T.; Tsuchiya,Y.; Kim, 1 B c
K. C.; Ohashi, H.; Wakui, K.; Fukushima, Y.: HDR
syndrome(hypoparathyroidism, sensorineural deafness, renal dysplasia)
associatedwith del(10)(p13). Am. J. Med. Genet. 73: 416- 418, 1997.

GAM5227 299 DGCR2 Lichtner, P.; Konig, R.; Hasegawa, T.; Van Esch, H.; Meitinger,T.; 1 B c
Schuffenhauer, S.: An HDR (hypoparathyroidism, deafness, renaldysplasia)
syndrome locus maps distal to the DiGeorge syndrome regionon 10p13/14. J.
Med. Genet. 37: 33- 37, 2000.

GAM5227 299 DGCR2 Schuffenhauer, S.; Lichtner, P.; Peykar- Derakhshandeh, P.; Murken,J.; Haas, 1 B c
O. A.; Back, E.; Wolff, G.; Zabel, B.; Barisic, I.; Rauch,A.; Borochowitz,
Z.; Dallapiccola, B.; Ross, M.; Meitinger, T.: Deletionmapping on chromosome
10p and definition of a critical region forthe second DiGeorge syndrome
locus (DGS2). Europ. J. Hum. Genet. 6:213- 225, 1998.

GAM5227 299 DGCR2 Van Esch, H.; Groenen, P.; Daw, S.; Poffyn, A.; Holvoet, M.; Scambler,P.; 1 B c
Fryns, J.- P.; Van de Ven, W.; Devriendt, K.: Partial DiGeorgesyndrome in
two patients with a 10p rearrangement. Clin. Genet. 55:269- 276, 1999.

GAM5227 299 DGCR2 Wadey, R.; Daw, S.; Taylor, C.; Atif, U.; Kamath, S.; Halford,S.; O'Donnell, 1 B c
H.; Wilson, D.; Goodship, J.; Burn, J.; Scambler, P.: Isolation of a gene
encoding an integral membrane protein from thevicinity of a balanced
translocation breakpoint associated with DiGeorgesyndrome. Hum. Molec.
Genet. 4: 1027- 1033, 1995.

GAM5227 299 E2F3 Cloud, J. E.; Rogers, C.; Reza, T. L.; Ziebold, U.; Stone, J. R.;Picard, M. 1 B c
H.; Caron, A. M.; Bronson, R. T.; Lees, J. A.: Mutantmouse models reveal the
relative roles of E2F1 and E2F3 in vivo. Molec.Cell. Biol. 22: 2663- 2672,
2002.

GAM5227 299 E2F3 He, Y.; Armanious, M. K.; Thomas, M. J.; Cress, W. D.: Identificationof E2F- 1 B c

3B, an alternative form of E2F- 3 lacking a conserved N- terminalregion. Oncogene 19: 3422- 3433, 2000.

GAM5227 299 E2F3 Lees, J. A.; Saito, M.; Vidal, M.; Valentine, M.; Look, T.; Harlow,E.; Dyson, N.; Helin, K.: The retinoblastoma protein binds to a familyof E2F transcription factors. Molec. Cell. Biol. 13: 7813- 7825,1993. 1 B c

GAM5227 299 E2F3 Leone, G.; Sears, R.; Huang, E.; Rempel, R.; Nuckolls, F.; Park,C.- H.; Giangrande, P.; Wu, L.; Saavedra, H. I.; Field, S. J.; Thompson,M. A.; Yang, H.; Fujiwara, Y.; Greenberg, M. E.; Orkin, S.; Smith,C.; Nevins, J. R.: Myc requires distinct E2F activities to induceS phase and apoptosis. Molec. Cell 8: 105- 113, 2001. 1 B c

GAM5227 299 E2F3 Wu, L.; Timmers, C.; Maiti, B.; Saavedra, H. I.; Sang, L.; Chong,G. T.; Nuckolls, F.; Giangrande, P.; Wright, F. A.; Field, S. J.;Greenberg, M. E.; Orkin, S.; Nevins, J. R.; Robinson, M. L.; Leone,G.: The E2F1- 3 transcription factors are essential for cellular proliferation. Nature 414:457- 462, 2001. 1 B c

GAM5227 299 EGFR Aden, D. P.; Knowles, B. B.: Cell surface antigens coded for bythe human chromosome 7. Immunogenetics 3: 209- 211, 1976. 1 B c

GAM5227 299 EGFR Carlin, C. R.; Aden, D. P.; Knowles, B. B.: S6 is the human receptorfor epidermal growth factor (EGF). (Abstract) Cytogenet. Cell Genet. 32:256 only, 1982. 1 B c

GAM5227 299 EGFR Carlin, C. R.; Knowles, B. B.: Identity of human epidermal growthfactor (EGF) receptor with glycoprotein SA- 7: evidence for differentialphosphorylation of the two components of the EGF receptor from A431cells. Proc. Nat. Acad. Sci. 79: 5026- 5030, 1982. 1 B c

GAM5227 299 EGFR Carpenter, G.: Properties of the receptor for epidermal growthfactor. Cell 37: 357- 358, 1984. 1 B c

GAM5227 299 EGFR Chen, B.; Bronson, R. T.; Klaman, L. D.; Hampton, T. G.; Wang,J.; Green, P. J.; Magnuson, T.; Douglas, P. S.; Morgan, J. P.; Neel,B. G.: Mice mutant for Egfr and Shp2 have defective cardiac semilunarvalvulogenesis. Nature Genet. 24: 296- 299, 2000. 1 B c

GAM5227 299 EGFR Davies, R. L.; Grosse, V. A.; Kucherlapati, R.; Bothwell, M.:Genetic analysis of epidermal growth factor action: assignment ofhuman epidermal growth factor receptor gene to chromosome 7. Proc.Nat. Acad. Sci. 77: 4188- 4192, 1980. 1 B c

GAM5227 299 EGFR Downward, J.; Yarden, Y.; Mayes, E.; Scrace, G.; Totty, N.; Stockwell,P.; Ullrich, A.; Schlessinger, J.; Waterfield, M. D.: Close similarityof epidermal growth factor receptor and v- erb- B oncogene protein sequences. Nature 307:521- 527, 1984. 1 B c

GAM5227 299 EGFR Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich,A.; Waterfield, M.: The human EGF receptor gene: structure of the110 kb locus and identification of sequences regulating its transcription. OncogeneRes. 1: 375- 396, 1987. 1 B c

GAM5227 299 EGFR Henn, W.; Blin, N.; Zang, K. D.: Polysomy of chromosome 7 is correlatedwith overexpression of the erbB oncogene in human glioblastoma celllines. Hum. Genet. 74: 104- 106, 1986. 1 B c

GAM5227 299 EGFR Kondo, I.; Shimizu, N.: Mapping of the human gene for epidermalgrowth factor receptor (EGFR) on the p13- q22 region of chromosome7. Cytogenet. Cell Genet. 35: 9- 14, 1983. 1 B c

GAM5227 299 EGFR Kramer, A.; Yang, F.- C.; Snodgrass, P.; Li, X.; Scammell, T. E.;Davis, F. C.; Weitz, C. J.: Regulation of daily locomotor activityand sleep by 1 B c

hypothalamic EGF receptor signaling. Science 294: 2511- 2515,2001.

GAM5227 299 EGFR Lanzetti, L.; Rybin, V.; Malabarba, M. G.; Christoforidis, S.;Scita, G.; Zerial, M.; Di Fiore, P. P.: The Eps8 protein coordinatesEGF receptor signalling through Rac and trafficking through Rab5. Nature 408:374- 377, 2000. 1 B c

GAM5227 299 EGFR Maciag, T.: The human epidermal growth factor receptor- kinasecomplex. Trends Biochem. Sci. 7: 1- 2, 1982. 1 B c

GAM5227 299 EGFR Pai, R.; Soreghan, B.; Szabo, I. L.; Pavelka, M.; Baatar, D.;Tarnawski, A. S.: Prostaglandin E2 transactivates EGF receptor: anovel mechanism for promoting colon cancer growth and gastrointestinalhypertrophy. Nature Med. 8: 289- 293, 2002. 1 B c

GAM5227 299 EGFR Privalsky, M. L.; Ralston, R.; Bishop, J. M.: The membrane glycoproteinencoded by the retroviral oncogene v- erb- B is structurally relatedto tyrosine- specific protein kinases. Proc. Nat. Acad. Sci. 81:704- 707, 1984. 1 B c

GAM5227 299 EGFR Reynolds, F. H., Jr.; Todaro, G. J.; Fryling, C.; Stephenson,J. R.: Human transforming growth factors induce tyrosine phosphorylationof EGF receptors. Nature 292: 259- 262, 1981. 1 B c

GAM5227 299 EGFR Shimizu, N.; Behzadian, M. A.; Shimizu, Y.: Genetics of cellsurface receptors for bioactive polypeptides: binding of epidermalgrowth factor is associated with the presence of human chromosome7 in human- mouse cell hybrids. Proc. Nat. Acad. Sci. 77: 3600- 3604,1980. 1 B c

GAM5227 299 EGFR Sibilia, M.; Fleischmann, A.; Behrens, A.; Stingl, L.; Carroll,J.; Watt, F. M.; Schlessinger, J.; Wagner, E. F.: The EGF receptorprovides an essential survival signal for SOS- dependent skin tumordevelopment. Cell 102: 211- 220, 2000. 1 B c

GAM5227 299 EGFR Silver, J.; Whitney, J. B., III; Kozak, C.; Hollis, G.; Kirsch,I.: Erbb is linked to the alpha- globin locus on mouse chromosome11. Molec. Cell. Biol. 5: 1784- 1786, 1985. 1 B c

GAM5227 299 EGFR Spurr, N. K.; Goodfellow, P. N.; Solomon, E.; Parkar, M.; Vennstrom,B.; Bodmer, W. F.: Mapping of cellular oncogenes; erb B on chromosome7. (Abstract) Cytogenet. Cell Genet. 37: 590 only, 1984. 1 B c

GAM5227 299 EGFR Spurr, N. K.; Solomon, E.; Jansson, M.; Sheer, D.; Goodfellow,P. N.; Bodmer, W. F.; Vennstrom, B.: Chromosomal localisation ofthe human homologues to the oncogenes erbA and B. EMBO J. 3: 159- 163,1984. 1 B c

GAM5227 299 EGFR Thaung, C.; West, K.; Clark, B. J.; McKie, L.; Morgan, J. E.;Arnold, K.; Nolan, P. M.; Peters, J.; Hunter, A. J.; Brown, S. D.M.; Jackson, I. J.; Cross, S. H.: Novel ENU- induced eye mutationsin the mouse: models for human eye disease. Hum. Molec. Genet. 11:755- 767, 2002. 1 B c

GAM5227 299 EGFR Ullrich, A.; Coussens, L.; Hayflick, J. S.; Dull, T. J.; Gray,A.; Tam, A. W.; Lee, J.; Yarden, Y.; Libermann, T. A.; Schlessinger,J.; Downward, J.; Mayes, E. L. V.; Whittle, N.; Waterfield, M. D.;Seeburg, P. H.: Human epidermal growth factor receptor cDNA sequenceand aberrant expression of the amplified gene in A431 epidermoid carcinomacells. Nature 309: 418- 425, 1984. 1 B c

GAM5227 299 EGFR Verveer, P. J.; Wouters, F. S.; Reynolds, A. R.; Bastiaens, P.I. H.: Quantitative imaging of lateral ErbB1 receptor signal propagationin the plasma membrane. Science 290: 1567- 1570, 2000. 1 B c

GAM5227 299 EGFR Wakeling, E. L.; Abu- Amero, S. N.; Stanier, P.; Preece, M. A.;Moore, G. E.: Human EGFR, a candidate gene for the Silver- Russellsyndrome, is 1 B c

biallelically expressed in a wide range of fetal tissues. Europ.J. Hum. Genet. 6: 158- 164, 1998.

GAM5227 299 EGFR Yang, E.- B.; Wang, D.- F.; Mack, P.; Cheng, L.- Y.: Genistein,a tyrosine kinase inhibitor, reduces EGF- induced EGF receptor internalizationand degradation in human hepatoma HepG2 cells. Biochem. Biophys.Res. Commun. 224: 309- 317, 1996. 1 B c

GAM5227 299 FZD4 Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.;Hirai, M.; Katoh, M.: Molecular cloning and characterization of humanfrizzled- 4 on chromosome 11q14- q21. Biochem. Biophys. Res. Commun. 264:955- 961, 1999. 1 B c

GAM5227 299 FZD4 Robitaille, J.; MacDonald, M. L. E.; Kaykas, A.; Sheldahl, L. C.;Zeisler, J.; Dube, M.- P.; Zhang, L.- H.; Singaraja, R. R.; Guernsey,D. L.; Zhang, B.; Siebert, L. F.; Hoskin- Mott, A.; Trese, M. T.; Pimstone,S. N.; Shastry, B. S.; Moon, R. T.; Hayden, M. R.; Goldberg, Y. P.;Samuels, M. E.: Mutant frizzled- 4 disrupts retinal angiogenesis infamilial exudative vitreoretinopathy. Nature Genet. 32: 326- 330,2002. 1 B c

GAM5227 299 GCLM Gipp, J. J.; Bailey, H. H.; Mulcahy, R. T.: Cloning and sequencingof the cDNA for the light subunit of human liver gamma- glutamylcysteinesynthetase and relative mRNA levels for heavy and light subunits inhuman normal tissues. Biochem. Biophys. Res. Commun. 206: 584- 589,1995. 1 B c

GAM5227 299 GCLM Huang; C.- S.; Anderson; M. E.; Meister, A.: Amino acid sequenceand function of the light subunit of rat kidney gamma- glutamylcysteinesynthetase. J. Biol. Chem. 268: 20578- 20583, 1993. 1 B c

GAM5227 299 GCLM Rozet, J.- M.; Gerber, S.; Perrault, I.; Calvas, P.; Souied, E.;Chatelin, S.; Viegas- Pequignot, E.; Molina- Gomez, D.; Munnich, A.;Kaplan, J.: Structure and refinement of the physical mapping of thegamma-glutamylcysteine ligase regulatory subunit (GLCLR) gene to chromosome1pp22.1 within the critically deleted region of human malignant mesothelioma. Cytogenet.Cell Genet. 82: 91- 94, 1998. 1 B c

GAM5227 299 GCLM Sierra- Rivera, E.; Dasouki, M.; Summar, M. L.; Krishnamani, M.R. S.; Meredith, M.; Rao, P. N.; Phillips, J. A., III; Freeman, M.L.: Assignment of the human gene (GLCLR) that encodes the regulatorysubunit of gamma-glutamylcysteine synthetase to chromosome 1p21. Cytogenet.Cell Genet. 72: 252- 254, 1996. 1 B c

GAM5227 299 GCLM Tsuchiya, K.; Mulcahy, R. T.; Reid, L. L.; Disteche, C. M.; Kavanagh,T. J.: Mapping of the glutamate- cysteine ligase catalytic subunitgene (GLCLC) to human chromosome 6p12 and mouse chromosome 9D- E andof the regulatory subunit gene (GLCLR) to human chromosome 1p21- p22and mouse chromosome 3H1-3. Genomics 30: 630- 632, 1995. 1 B c

GAM5227 299 GPR4 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation of three novel human genes encoding G protein- coupledreceptors. DNA Cell Biol. 14: 25- 35, 1995. 1 B c

GAM5227 299 GPR4 Mahadevan, M. S.; Baird, S.; Bailly, J. E.; Shutler, G. G.; Sabourin,L. A.; Tsilfidis, C.; Neville, C. E.; Narang, M.; Korneluk, R. G.: Isolation of a novel G protein- coupled receptor (GPR4) localizedto chromosome 19q13.3. Genomics 30: 84- 88, 1995. 1 B c

GAM5227 299 GPR4 Ye, R. D.; Prossnitz, E. R.; Zou, A.; Cochrane, C. G.: Characterizationof a human cDNA that encodes a functional receptor for platelet activatingfactor. Biochem. Biophys. Res. Commun. 180: 105- 111, 1991. 1 B c

GAM5227 299 GPR4 Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina,K. L.; 1 B c

Kabarowski, J. H. S.; Witte, O. N.; Xu, Y.: Sphingosylphosphorylcholineand lysophosphatidylcholine are ligands for the G protein- coupledreceptor GPR4. J. Biol. Chem. 276: 41325- 41335, 2001.

GAM5227 299 GSPT1 Hoshino, S.; Miyazawa, H.; Enomoto, T.; Hanaoka, F.; Kikuchi, Y.;Kikuchi, A.; Ui, M.: A human homologue of the yeast GST1 gene codesfor a GTP- binding protein and is expressed in a proliferation- dependentmanner in mammalian cells. EMBO J. 8: 3807- 3814, 1989. 1 B c

GAM5227 299 GSPT1 Kikuchi, Y.; Shimatake, H.; Kikucki, A.: A yeast gene requiredfor the G1- to- S transition encodes a protein containing an A- kinasetarget site and GTPase domain. EMBO J. 7: 1175- 1182, 1988. 1 B c

GAM5227 299 GSPT1 Ozawa, K.; Murakami, Y.; Eki, T.; Yokoyama, K.; Soeda, E.; Hoshino,S.; Ui, M.; Hanaoka, F.: Mapping of the human GSPT1 gene, a humanhomolog of the yeast GST1 gene, to chromosomal band 16p13.1. Somat.Cell Molec. Genet. 18: 189- 194, 1992. 1 B c

GAM5227 299 HAS2 Spicer, A. P.; Augustine, M. L.; McDonald, J. A.: Molecular cloningand characterization of a putative mouse hyaluronan synthase. J.Biol. Chem. 271: 23400- 23406, 1996. 1 B c

GAM5227 299 HAS2 Spicer, A. P.; Seldin, M. F.; Olsen, A. S.; Brown, N.; Wells, D.E.; Doggett, N. A.; Itano, N.; Kimata, K.; Inazawa, J.; McDonald,J. A.: Chromosomal localization of the human and mouse hyaluronansynthase genes. Genomics 41: 493- 497, 1997. 1 B c

GAM5227 299 HAS2 Watanabe, K.; Yamaguchi, Y.: Molecular identification of a putativehuman hyaluronan synthase. J. Biol. Chem. 271: 22945- 22948, 1996. 1 B c

GAM5227 299 HS3ST2 Liu, J.; Shworak, N. W.; Sinay, P.; Schwartz, J. J.; Zhang, L.;Fritze, L. M.; Rosenberg, R. D.: Expression of heparan sulfate D- glucosaminyl3- O- sulfotransferase isoforms reveals novel substrate specificities. J.Biol. Chem. 274: 5185- 5192, 1999. 1 B c

GAM5227 299 HS3ST2 Shworak, N. W.; Liu, J.; Petros, L. M.; Zhang, L.; Kobayashi, M.;Copeland, N. G.; Jenkins, N. A.; Rosenberg, R. D.: Multiple isoformsof heparan sulfate D- glucosaminyl 3- O- sulfotransferase: isolation,characterization, and expression of human cDNAs and identificationof distinct genomic loci. J. Biol. Chem. 274: 5170- 5184, 1999. 1 B c

GAM5227 299 IHH Chen, L.; Li, C.; Qiao, W.; Xu, X.; Deng, C.: A ser365- cys mutationof fibroblast growth factor receptor 3 in mouse downregulates Ihh/PTHrPsignals and causes severe achondroplasia. Hum. Molec. Genet. 10:457- 465, 2001. 1 B c

GAM5227 299 IHH Gao, B.; Guo, J.; She, C.; Shu, A.; Yang, M.; Tan, Z.; Yang, X.;Guo, S.; Feng, G.; He, L.: Mutations in IHH, encoding Indian hedgehog,cause brachydactyly type A- 1. Nature Genet. 28: 386- 388, 2001. 1 B c

GAM5227 299 IHH Hebrok, M.; Kim, S. K.; St Jacques, B.; McMahon, A. P.; Melton,D. A.: Regulation of pancreas development by hedgehog signaling. Development 127:4905- 4913, 2000. 1 B c

GAM5227 299 IHH Lanske, B.; Karaplis, A. C.; Lee, K.; Luz, A.; Vortkamp, A.; Pirro,A.; Karperien, M.; Defize, L. H. K.; Ho, C.; Mulligan, R. C.; Abou- Samra,A.- B.; Juppner, H.; Segre, G. V.; Kronenberg, H. M.: PTH/PTHrP receptorin early development and Indian hedgehog- regulated bone growth. Science 273:663- 666, 1996. 1 B c

GAM5227 299 IHH Leek, J. P.; Moynihan, T. P.; Anwar, R.; Bonthron, D. T.; Markham,A. F.; Lench, N. J.: Assignment of Indian hedgehog (IHH) to humanchromosome bands 2q33- q35 by in situ hybridization. Cytogenet. CellGenet. 76: 187- 188, 1997. 1 B c

GAM5227 299 IHH Marigo, V.; Roberts, D. J.; Lee, S. M. K.; Tsukurov, O.; Levi,T.; Gastier, 1 B c
J. M.; Epstein, D. J.; Gilbert, D. J.; Copeland, N. G.;Seidman, C. E.;
Jenkins, N. A.; Seidman, J. G.; McMahon, A. P.; Tabin,C.: Cloning,
expression, and chromosomal location of SHH and IHH:two human homologues of
the Drosophila segment polarity gene hedgehog. Genomics 28:44- 51, 1995.

GAM5227 299 IHH Porter, J. A.; Young, K. E.; Beachy, P. A.: Cholesterol modificationof 1 B c
hedgehog signaling proteins in animal development. Science 274:255- 259,
1996.

GAM5227 299 IHH Vortkamp, A.; Lee, K.; Lanske, B.; Segre, G. V.; Kronenberg, H.M.; Tabin, C. 1 B c
J.: Regulation of rate of cartilage differentiationby Indian hedgehog and
PTH- related protein. Science 273: 613- 622,1996.

GAM5227 299 IHH Zhang, X. M.; Ramalho- Santos, M.; McMahon, A. P.: Smoothened mutantsreveal 1 B c
redundant roles for Shh and Ihh signaling including regulationof L/R
asymmetry by the mouse node. Cell 105: 781- 792, 2001.

GAM5227 299 IL1F8 Kumar, S.; McDonnell, P. C.; Lehr, R.; Tierney, L.; Tzimas, M.N.; Griswold, 1 B c
D. E.; Capper, E. A.; Tal- Singer, R.; Wells, G. I.;Doyle, M. L.; Young, P.
R.: Identification and initial characterizationof four novel members of the
interleukin- 1 family. J. Biol. Chem. 275:10308- 10314, 2000.

GAM5227 299 IL1F8 Smith, D. E.; Renshaw, B. R.; Ketchem, R. R.; Kubin, M.; Garka,K. E.; Sims, 1 B c
J. E.: Four new members expand the interleukin- 1 superfamily. J.Biol. Chem.
275: 1169- 1175, 2000.

GAM5227 299 IL1R1 Copeland, N. G.; Silan, C. M.; Kingsley, D. M.; Jenkins, N. A.;Cannizzaro, 1 B c
L. A.; Croce, C. M.; Huebner, K.; Sims, J. E.: Chromosomallocation of murine
and human IL- 1 receptor genes. Genomics 9: 44- 50,1991.

GAM5227 299 IL1R1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 1 B c
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp)
on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM5227 299 IL1R1 Dower, S. K.; Kronheim, S. R.; Hopp, T. P.; Cantrell, M.; Deeley,M.; Gillis, 1 B c
S.; Henney, C. S.; Urdal, D. L.: The cell surface receptorsfor interleukin-
1(alpha) and interleukin- 1(beta) are identical. Nature 324:266- 268, 1986.

GAM5227 299 IL1R1 Sims, J. E.; Acres, R. B.; Grubin, C. E.; McMahan, C. J.; Wignall,J. M.; 1 B c
March, C. J.; Dower, S. K.: Cloning the interleukin 1 receptorfrom human T
cells. Proc. Nat. Acad. Sci. 86: 8946- 8950, 1989.

GAM5227 299 IL1RAP Dale, M.; Hammond, D. W.; Cox, A.; Nicklin, M. J. H.: The humangene encoding 1 B c
the interleukin- 1 receptor accessory protein (IL1RAP)maps to chromosome
3q28 by fluorescence in situ hybridization andradiation hybrid mapping.
Genomics 47: 325- 326, 1998.

GAM5227 299 IL1RAP Huang, J.; Gao, X.; Li, S.; Cao, Z.: Recruitment of IRAK to theinterleukin 1 1 B c
receptor complex requires interleukin 1 receptor accessoryprotein. Proc.
Nat. Acad. Sci. 94: 12829- 12832, 1997.

GAM5227 299 IL1RAP Wesche, H.; Korherr, C.; Kracht, M.; Falk, W.; Resch, K.; Martin,M. U.: The 1 B c
interleukin- 1 receptor accessory protein (IL- 1RAcP) isessential for IL- 1-
induced activation of interleukin- 1 receptor- associatedkinase (IRAK) and
stress- activated protein kinases (SAP kinases). J.Biol. Chem. 272: 7727-
7731, 1997.

GAM5227 299 LDLR Aalto- Setala, K.; Helve, E.; Kovanen, P. T.; Kontula, K.: Finnishtype of 1 B c
low density lipoprotein receptor gene mutation (FH- Helsinki)deletes exons
encoding the carboxy- terminal part of the receptor andcreates an
internalization- defective phenotype. J. Clin. Invest. 84:499- 505, 1989.

GAM5227 299 LDLR Aalto- Setala, K.; Koivisto, U.- M.; Miettinen, T. A.; Gylling, 1 B c

H.;Kesaniemi, Y. A.; Savolainen, M.; Pyorala, K.; Ebeling, T.; Mononen,I.; Turtola, H.; Viikari, J.; Kontula, K.: Prevalence and geographicaldistribution of major LDL receptor gene rearrangements in Finland. J.Intern. Med. 231: 227- 234, 1992.

GAM5227 299 LDLR Agnello, V.; Abel, G.; Elfahal, M.; Knight, G. B.; Zhang, Q.- X.: Hepatitis 1 B c C virus and other flaviviridae viruses enter cells vialow density lipoprotein receptor. Proc. Nat. Acad. Sci. 96: 12766- 12771,1999.

GAM5227 299 LDLR Allen, J. M.; Thompson, G. R.; Myant, N. B.; Steiner, R.; Oakley,C. M.: 1 B c Cardiovascular complications of homozygous familial hypercholesterolaemia. Brit.Heart J. 44: 361- 368, 1980.

GAM5227 299 LDLR Benlian, P.; Amselem, S.; Loux, N.; Pastier, D.; Giraud, G.; deGennes, J. 1 B c L.; Turpin, G.; Monnier, L.; Rieu, D.; Douste- Blazy, P.;Dastugue, B.; Goossens, M.; Junien, C.: A LDL receptor gene homozygousmutation: PCR amplification, direct genomic sequencing, associatedhaplotype, rapid screening for frequency. Ann. Genet. 33: 65- 69,1990.

GAM5227 299 LDLR Bertolini, S.; Lelli, N.; Coviello, D. A.; Ghisellini, M.; Masturzo,P.; 1 B c Tiozzo, R.; Elicio, N.; Gaddi, A.; Calandra, S.: A large deletionin the LDL receptor gene- - the cause of familial hypercholesterolemiain three Italian families: a study that dates back to the 17th century(FH- Pavia). Am. J. Hum. Genet. 51: 123- 134, 1992.

GAM5227 299 LDLR Betard, C.; Kessling, A. M.; Roy, M.; Chamberland, A.; Lussier- Cacan,S.; 1 B c Davignon, J.: Molecular genetic evidence for a founder effectin familial hypercholesterolemia among French Canadians. Hum. Genet. 88:529- 536, 1992.

GAM5227 299 LDLR Boehnke, M.; Arnheim, N.; Li, H.; Collins, F. S.: Fine- structuregenetic 1 B c mapping of human chromosomes using the polymerase chain reactionon single sperm: experimental design considerations. Am. J. Hum.Genet. 45: 21- 32, 1989.

GAM5227 299 LDLR Brink, P. A.; Steyn, L. T.; Coetzee, G. A.; van der Westhuyzen,D. R.: 1 B c Familial hypercholesterolemia in South African Afrikaners:PvuII and StuI DNA polymorphisms in the LDL- receptor gene consistentwith a predominating founder gene effect. Hum. Genet. 77: 32- 35,1987.

GAM5227 299 LDLR Brown, M. S.; Goldstein, J. L.: Analysis of a mutant strain ofhuman 1 B c fibroblasts with a defect in the internalization of receptor- boundlow density lipoproteins. Cell 9: 663- 674, 1976.

GAM5227 299 LDLR Brown, M. S.; Goldstein, J. L.: Familial hypercholesterolemia:defective 1 B c binding of lipoproteins to cultured fibroblasts associatedwith impaired regulation of 3- hydroxy- 3- methylglutaryl coenzyme atreductase activity. Proc. Nat. Acad. Sci. 71: 788- 792, 1974.

GAM5227 299 LDLR Brown, M. S.; Goldstein, J. L.: Receptor- mediated endocytosis:insights from 1 B c the lipoprotein receptor system. Proc. Nat. Acad. Sci. 76:3330- 3337, 1979.

GAM5227 299 LDLR Davis, C. G.; Lehrman, M. A.; Russell, D. W.; Anderson, R. G.W.; Brown, M. 1 B c S.; Goldstein, J. L.: The J.D. mutation in familialhypercholesterolemia: amino acid substitution in cytoplasmic domainimpedes internalization of LDL receptors. Cell 45: 15- 24, 1986.

GAM5227 299 LDLR De Braekeleer, M.: Hereditary disorders in Saguenay- Lac- St- Jean(Quebec, 1 B c Canada). Hum. Hered. 41: 141- 146, 1991.

GAM5227 299 LDLR Defesche, J. C.; Kastelein, J. J. P.: Molecular epidemiologyof familial 1 B c hypercholesterolaemia. (Letter) Lancet 352: 1643- 1644,1998.

GAM5227 299 LDLR Defesche, J. C.; van de Ree, M. A.; Kastelein, J. J. P.; van Diermen,D. E.; 1 B c Janssens, N. W. E.; van Doormaal, J. J.; Hayden, M. R.: Detectionof the

pro664- to- leu mutation in the low- density lipoprotein receptorand its relation to lipoprotein(a) levels in patients with familialhypercholesterolemia of Dutch ancestry from The Netherlands and Canada. Clin.Genet. 42: 273- 280, 1992.

GAM5227 299 LDLR Defesche, J. C.; van Diermen, D. E.; Lansberg, P. J.; Lamping,R. J.; Reymer, P. W. A.; Hayden, M. R.; Kastelein, J. J. P.: SouthAfrican founder mutations in the low- density lipoprotein receptorgene causing familial hypercholesterolemia in the Dutch population. Hum.Genet. 92: 567- 570, 1993. 1 B c

GAM5227 299 LDLR Durst, R.; Colombo, R.; Shpitzen, S.; Ben Avi, L.; Friedlander,Y.; Wexler, R.; Raal, F. J.; Marais, D. A.; Defesche, J. C.; Mandelshtam,M. Y.; Kotze, M. J.; Leitersdorf, E.; Meiner, V.: Recent origin andspread of a common Lithuanian mutation, G197del LDLR, causing familialhypercholesterolemia: positive selection is not always necessary toaccount for disease incidence among Ashkenazi Jews. Am. J. Hum. Genet. 68:1172- 1188, 2001. 1 B c

GAM5227 299 LDLR Ekstrom, U.; Abrahamson, M.; Floren, C.- H.; Tollig, H.; Wettrell,G.; Nilsson, G.; Sun, X.- M.; Soutar, A. K.; Nilsson- Ehle, P.: Anindividual with a healthy phenotype in spite of a pathogenic LDL receptormutation (C240F). Clin. Genet. 55: 332- 339, 1999. 1 B c

GAM5227 299 LDLR Elston, R. C.; Namboodiri, K. K.; Go, R. C. P.; Siervogel, R.M.; Glueck, C. J.: Probable linkage between essential familial hypercholesterolemiaand third complement component (C3). Cytogenet. Cell Genet. 16:294- 297, 1976. 1 B c

GAM5227 299 LDLR Esser, V.; Russell, D. W.: Transport- deficient mutations in thelow density lipoprotein receptor: alterations in the cysteine- richand cysteine- poor regions of the protein block intracellular transport. J.Biol. Chem. 263: 13276- 13281, 1988. 1 B c

GAM5227 299 LDLR Feussner, G.; Dobmeyer, J.; Nissen, H.; Hansen, T. S.: UnusualXanthomas in a young patient with heterozygous familial hypercholesterolemiaand type III hyperlipoproteinemia. Am. J. Med. Genet. 65: 149- 154,1996. 1 B c

GAM5227 299 LDLR Francke, U.; Brown, M. S.; Goldstein, J. L.: Assignment of thehuman gene for the low density lipoprotein receptor to chromosome19: synteny of a receptor, a ligand, and a genetic disease. Proc.Nat. Acad. Sci. 81: 2826- 2830, 1984. 1 B c

GAM5227 299 LDLR Frank, S. L.; Taylor, B. A.; Lusis, A. J.: Linkage of the mouseLDL receptor gene on chromosome 9. Genomics 5: 646- 648, 1989. 1 B c

GAM5227 299 LDLR Fumeron, F.; Grandchamp, B.; Fricker, J.; Krempf, M.; Wolf, L.- M.;Khayat, M.- C.; Boiffard, O.; Apfelbaum, M.: Presence of the FrenchCanadian deletion in a French patient with familial hypercholesterolemia.(Letter) New Eng. J. Med. 326: 69 only, 1992. 1 B c

GAM5227 299 LDLR Gilbert, W.: Genes- in- pieces revisited. Science 228: 823- 824,1985. 1 B c

GAM5227 299 LDLR Goldfarb, L. G.; Petersen, R. B.; Tabaton, M.; Brown, P.; LeBlanc,A. C.; Montagna, P.; Cortelli, P.; Julien, J.; Vital, C.; Pendelbury,W. W.; Haltia, M.; Wills, P. R.; and 9 others: Fatal familial insomniaand familial Creutzfeldt- Jakob disease: disease phenotype determinedby a DNA polymorphism. Science 258: 806- 808, 1992. 1 B c

GAM5227 299 LDLR Goldstein, J. L.; Brown, M. S.; Stone, N. J.: Genetics of theLDL receptor: evidence that the mutations affecting binding and internalizationare allelic. Cell 12: 629- 641, 1977. 1 B c

GAM5227 299 LDLR Goldstein, J. L.; Dana, S. E.; Brunschede, G. Y.; Brown, M. S.: Genetic heterogeneity in familial hypercholesterolemia: evidencefor two different mutations affecting functions of low- density lipoproteinreceptor. Proc. Nat. Acad. Sci. 72: 1092- 1096, 1975. 1 B c

GAM5227 299 LDLR Graadt van Roggen, F.; van der Westhuyzen, D. R.; Marais, A. D.;Gevers, W.; 1 B c
Coetzee, G. A.: Low density lipoprotein receptor foundermutations in
Afrikaner familial hypercholesterolaemic patients: acomparison of two
geographical areas. Hum. Genet. 88: 204- 208, 1991.

GAM5227 299 LDLR Gudnason, V.; King- Underwood, L.; Seed, M.; Sun, X.- M.; Soutar,A. K.; 1 B c
Humphries, S. E.: Identification of recurrent and novel mutationsin exon 4
of the LDL receptor gene in patients with familial hypercholesterolemiain
the United Kingdom. Arteriosclerosis Thromb. 13: 56- 63, 1993.

GAM5227 299 LDLR Gudnason, V.; Sigurdsson, G.; Nissen, H.; Humphries, S. E.: Commonfounder 1 B c
mutation in the LDL receptor gene causing familial hypercholesterolemiain
the Icelandic population. Hum. Mutat. 10: 36- 44, 1997.

GAM5227 299 LDLR Henderson, H. E.; Berger, G. M. B.; Marais, A. D.: A new LDLreceptor gene 1 B c
deletion mutation in the South African population. Hum.Genet. 80: 371- 374,
1988.

GAM5227 299 LDLR Hobbs, H. H.: Personal Communication. Dallas, Tex. 12/1/1990. 1 B c

GAM5227 299 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: Molecular geneticsof the LDL 1 B c
receptor gene in familial hypercholesterolemia. Hum. Mutat. 1:445- 466,
1992.

GAM5227 299 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.; Russell, D. W.:Deletion of 1 B c
exon encoding cysteine- rich repeat of low density lipoproteinreceptor
alters its binding specificity in a subject with
familialhypercholesterolemia. J. Biol. Chem. 261: 13114- 13120, 1986.

GAM5227 299 LDLR Hobbs, H. H.; Brown, M. S.; Russell, D. W.; Davignon, J.; Goldstein,J. L.: 1 B c
Deletion in the gene for the low- density- lipoprotein receptorin a majority
of French Canadians with familial hypercholesterolemia. NewEng. J. Med. 317:
734- 737, 1987.

GAM5227 299 LDLR Hobbs, H. H.; Lehrman, M. A.; Yamamoto, T.; Russell, D. W.: Polymorphismand 1 B c
evolution of Alu sequences in the human low density lipoproteinreceptor
gene. Proc. Nat. Acad. Sci. 82: 7651- 7655, 1985.

GAM5227 299 LDLR Hobbs, H. H.; Leitersdorf, E.; Goldstein, J. L.; Brown, M. S.;Russell, D. 1 B c
W.: Multiple CRM- mutations in familial hypercholesterolemia:evidence for
13 alleles, including four deletions. J. Clin. Invest. 81:909- 917, 1988.

GAM5227 299 LDLR Hobbs, H. H.; Leitersdorf, E.; Leffert, C. C.; Cryer, D. R.; Brown,M. S.; 1 B c
Goldstein, J. L.: Evidence for a dominant gene that
suppresseshypercholesterolemia in a family with defective low density
lipoproteinreceptors. J. Clin. Invest. 84: 656- 664, 1989.

GAM5227 299 LDLR Hobbs, H. H.; Russell, D. W.; Brown, M. S.; Goldstein, J. L.:The LDL 1 B c
receptor locus in familial hypercholesterolemia: mutationalanalysis of a
membrane protein. Annu. Rev. Genet. 24: 133- 170, 1990.

GAM5227 299 LDLR Horsthemke, B.; Beisiegel, U.; Dunning, A.; Havinga, J. R.; Williamson,R.; 1 B c
Humphries, S.: Unequal crossing- over between two Alu- repetitiveDNA
sequences in the low- density- lipoprotein- receptor gene: a
possiblemechanism for the defect in a patient with familial
hypercholesterolaemia. Europ.J. Biochem. 164: 77- 81, 1987.

GAM5227 299 LDLR Horsthemke, B.; Dunning, A.; Humphries, S.: Identification ofdeletions in 1 B c
the human low density lipoprotein receptor gene. J.Med. Genet. 24: 144- 147,
1987.

GAM5227 299 LDLR Horsthemke, B.; Kessling, A. M.; Seed, M.; Wynn, V.; Williamson,R.; 1 B c
Humphries, S. E.: Identification of a deletion in the low densitylipoprotein
(LDL) receptor gene in a patient with familial hypercholesterolaemia.

Hum.Genet. 71: 75- 78, 1985.

GAM5227 299 LDLR Jensen, H. K.; Jensen, T. G.; Faergeman, O.; Jensen, L. G.; Andresen,B. S.; 1 B c
Corydon, M. J.; Andreasen, P. H.; Hansen, P. S.; Heath, F.;Bolund, L.;
Gregersen, N.: Two mutations in the same low- densitylipoprotein receptor
allele act in synergy to reduce receptor functionin heterozygous familial
hypercholesterolemia. Hum. Mutat. 9: 437- 444,1997.

GAM5227 299 LDLR Jensen, J. M.; Kruse, T. A.; Brorholt- Petersen, J. U.; Christiansen,T. M.; 1 B c
Jensen, H. K.; Kolvraa, S.; Faergeman, O.: Linking genotypeto aorto-
coronary atherosclerosis: a model using familial hypercholesterolemiaand
aorto- coronary calcification. Ann. Hum. Genet. 63: 511- 520,1999.

GAM5227 299 LDLR Kajinami, K.; Fujita, H.; Koizumi, J.; Mabuchi, H.; Takeda, R.;Ohta, M.: 1 B c
Genetically determined mild type of familial hypercholesterolemiaincluding
normocholesterolemic patients: FH- Tonami- 2. Circulation 80(suppl. 2): 278
only, 1989.

GAM5227 299 LDLR Kajinami, K.; Mabuchi, H.; Itoh, H.; Michishita, I.; Takeda, M.;Wakasugi, 1 B c
T.; Koizumi, J.; Takeda, R.: New variant of low densitylipoprotein receptor
gene FH- Tonami. Arteriosclerosis 8: 187- 192,1988.

GAM5227 299 LDLR Khachadurian, A. K.: The inheritance of essential familial 1 B c
hypercholesterolemia. Am.J. Med. 37: 402- 407, 1964.

GAM5227 299 LDLR Kingsley, D. M.; Krieger, M.: Receptor- mediated endocytosis oflow density 1 B c
lipoprotein: somatic cell mutants define multiple genesrequired for
expression of surface- receptor activity. Proc. Nat.Acad. Sci. 81: 5454-
5458, 1984.

GAM5227 299 LDLR Knight, B. L.; Gavigan, S. J. P.; Soutar, A. K.; Patel, D. D.: Defective 1 B c
processing and binding of low- density lipoprotein receptorsin fibroblasts
from a familial hypercholesterolaemic subject. Europ.J. Biochem. 179: 693-
698, 1989.

GAM5227 299 LDLR Knoblauch, H.; Muller- Myhsok, B.; Busjahn, A.; Ben Avi, L.; Bahring,S.; 1 B c
Baron, H.; Heath, S. C.; Uhlmann, R.; Faulhaber, H.- D.; Shpitzen,S.; Aydin,
A.; Reshef, A.; and 11 others: A cholesterol- loweringgene maps to
chromosome 13q. Am. J. Hum. Genet. 66: 157- 166, 2000.

GAM5227 299 LDLR Koivisto, U.- M.; Hubbard, A. L.; Mellman, I.: A novel cellularphenotype for 1 B c
familial hypercholesterolemia due to a defect in polarizedtargeting of LDL
receptor. Cell 105: 575- 585, 2001.

GAM5227 299 LDLR Koivisto, U.- M.; Turtola, H.; Aalto- Setala, K.; Top, B.; Frants,R. R.; 1 B c
Kovanen, P. T.; Syvanen, A.- C.; Kontula, K.: The
familialhypercholesterolemia (FH)- North Karelia mutation of the low
densitylipoprotein receptor gene deletes seven nucleotides of exon 6 andis a
common cause of FH in Finland. J. Clin. Invest. 90: 219- 228,1992.

GAM5227 299 LDLR Koivisto, U.- M.; Viikari, J. S.; Kontula, K.: Molecular characterizationof 1 B c
minor gene rearrangements in Finnish patients with heterozygousfamilial
hypercholesterolemia: identification of two common missensemutations
(Gly823- to- Asp and Leu380- to- His) and eight rare mutationsof the LDL
receptor gene. Am. J. Hum. Genet. 57: 789- 797, 1995.

GAM5227 299 LDLR Komuro, I.; Kato, H.; Nakagawa, T.; Takahashi, K.; Mimori, A.;Takeuchi, F.; 1 B c
Nishida, Y.; Miyamoto, T.: Case report: the longest- livedpatient with
homozygous familial hypercholesterolemia secondary toa defect in
internalization of the LDL receptor. Am. J. Med. Sci. 294:341- 345, 1987.

GAM5227 299 LDLR Kotze, M. J.; Langenhoven, E.; Retief, A. E.; Steyn, K.; Marais,M. P.; 1 B c
Grobbelaar, J. J.; Oosthuizen, C. J. J.; Weich, H. F. H.; Benade,A. J. S.:

Haplotype associations of three DNA polymorphisms at thehuman low density lipoprotein receptor gene locus in familial hypercholesterolemia. J.Med. Genet. 24: 750- 755, 1987.

GAM5227 299 LDLR Kotze, M. J.; Langenhoven, E.; Warnich, L.; du Plessis, L.; Retief,A. E.: 1 B c
The molecular basis and diagnosis of familial hypercholesterolaemiain South African Afrikaners. Ann. Hum. Genet. 55: 115- 121, 1991.

GAM5227 299 LDLR Kotze, M. J.; Theart, L.; Peeters, A.; Langenhoven, E.: A denovo duplication 1 B c
in the low density lipoprotein receptor gene. Hum.Mutat. 6: 181- 183, 1995.

GAM5227 299 LDLR Kotze, M. J.; Warnich, L.; Langenhoven, E.; du Plessis, L.; Retief,A. E.: An 1 B c
exon 4 mutation identified in the majority of South Africanfamilial hypercholesterolaemics. J. Med. Genet. 27: 298- 302, 1990.

GAM5227 299 LDLR Landsberger, D.; Meiner, V.; Reshef, A.; Levy, Y.; van der Westhuyzen,D. R.; 1 B c
Coetzee, G. A.; Leitersdorf, E.: A nonsense mutation in theLDL receptor gene leads to familial hypercholesterolemia in the Druzesect. Am. J. Hum. Genet. 50: 427- 433, 1992.

GAM5227 299 LDLR Langlois, S.: Personal Communication. Vancouver, British Columbia,Canada 1 B c
1989.

GAM5227 299 LDLR Langlois, S.; Kastelein, J. J. P.; Hayden, M. R.: Characterizationof six 1 B c
partial deletions in the low- density- lipoprotein (LDL) receptorgene causing familial hypercholesterolemia (FH). Am. J. Hum. Genet. 43:60- 68, 1988.

GAM5227 299 LDLR Lee, W. K.; Haddad, L.; Macleod, M. J.; Dorrance, A. M.; Wilson,D. J.; 1 B c
Gaffney, D.; Dominiczak, M. H.; Packard, C. J.; Day, I. N.;Humphries, S. E.; Dominiczak, A. F.: Identification of a common lowdensity lipoprotein receptor mutation (C163Y) in the West of Scotland. J.Med. Genet. 35: 573- 578, 1998.

GAM5227 299 LDLR Lehrman, M. A.; Goldstein, J. L.; Brown, M. S.; Russell, D. W.;Schneider, W. 1 B c
J.: Internalization- defective LDL receptors producedby genes with nonsense and frameshift mutations that truncate thecytoplasmic domain. Cell 41: 735- 743, 1985.

GAM5227 299 LDLR Lehrman, M. A.; Goldstein, J. L.; Russell, D. W.; Brown, M. S.: Duplication 1 B c
of seven exons in LDL receptor gene caused by Alu- Alurecombination in a subject with familial hypercholesterolemia. Cell 48:827- 835, 1987.

GAM5227 299 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Alu- Alu 1 B c
recombination deletes splice acceptor sites and producessecreted low density lipoprotein receptor in a subject with familialhypercholesterolemia. J. Biol. Chem. 262: 3354- 3361, 1987.

GAM5227 299 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Exon- Alu 1 B c
recombination deletes 5 kilobases from the low densitylipoprotein receptor gene, producing a null phenotype in familialhypercholesterolemia. Proc. Nat. Acad. Sci. 83: 3679- 3683, 1986.

GAM5227 299 LDLR Lehrman, M. A.; Schneider, W. J.; Sudhof, T. C.; Brown, M. S.;Goldstein, J. 1 B c
L.; Russell, D. W.: Mutation in LDL receptor: Alu- Alurecombination deletes exons encoding transmembrane and cytoplasmicdomains. Science 227: 140- 146, 1985.

GAM5227 299 LDLR Leitersdorf, E.; Hobbs, H. H.: Personal Communication. Dallas,Tex. 12/1990. 1 B c

GAM5227 299 LDLR Leitersdorf, E.; Hobbs, H. H.; Fourie, A. M.; Jacobs, M.; vander Westhuyzen, 1 B c
D. R.; Coetzee, G. A.: Deletion in the first cysteine- richrepeat of low- density lipoprotein receptor impairs its transport butnot lipoprotein binding in fibroblasts from a subject with familialhypercholesterolemia.

Proc. Nat. Acad. Sci. 85: 7912- 7916, 1988.

GAM5227 299 LDLR Leitersdorf, E.; Tobin, E. J.; Davignon, J.; Hobbs, H. H.: Commonlow- 1 B c
density lipoprotein receptor mutations in the French Canadianpopulation. J.
Clin. Invest. 85: 1014- 1023, 1990.

GAM5227 299 LDLR Leitersdorf, E.; van der Westhuyzen, D. R.; Coetzee, G. A.; Hobbs,H. H.: Two 1 B c
common low density lipoprotein receptor gene mutationscause familial
hypercholesterolemia in Afrikaners. J. Clin. Invest. 84:954- 961, 1989.

GAM5227 299 LDLR Lelli, N.; Ghisellini, M.; Calandra, S.; Gaddi, A.; Ciarrocchi,A.; Coviello, 1 B c
D. A.; Bertolini, S.: Duplication of exons 13, 14 and15 of the LDL- receptor
gene in a patient with heterozygous familialhypercholesterolemia. Hum.
Genet. 86: 359- 362, 1991.

GAM5227 299 LDLR Leren, T. P.; Solberg, K.; Rodningen, O. K.; Tonstad, S.; Ose,L.: Two 1 B c
founder mutations in the LDL receptor gene in Norwegian
familialhypercholesterolemia subjects. Atherosclerosis 111: 175- 182, 1994.

GAM5227 299 LDLR Li, H.; Gyllensten, U. B.; Cui, X.; Saiki, R. K.; Erlich, H. A.;Arnheim, N.: 1 B c
Amplification and analysis of DNA sequences in singlehuman sperm and diploid
cells. Nature 335: 414- 417, 1988.

GAM5227 299 LDLR Lindgren, V.; Luskey, K. L.; Russell, D. W.; Francke, U.: Humangenes 1 B c
involved in cholesterol metabolism: chromosomal mapping of theloci for the
low density lipoprotein receptor and 3- hydroxy- 3- methylglutaryl-
coenzymeA reductase with cDNA probes. Proc. Nat. Acad. Sci. 82: 8567-
8571,1985.

GAM5227 299 LDLR Loux, N.; Benlian, P.; Pastier, D.; Boileau, C.; Cambou, J. P.;Monnier, L.; 1 B c
Percheron, C.; Junien, C.: Recurrent mutation at aa792 in the LDL receptor
gene in a French patient. Hum. Genet. 87:373- 375, 1991.

GAM5227 299 LDLR Ma, Y. H.; Betard, C.; Roy, M.; Davignon, J.; Kessling, A. M.: 1 B c
Identification of a second 'French Canadian' LDL receptor gene deletionand
development of a rapid method to detect both deletions. Clin.Genet. 36: 219-
228, 1989.

GAM5227 299 LDLR Maartmann- Moe, K.; Wang, H. S.; Donald, L. J.; Hamerton, J. L.;Berg, K.: 1 B c
Data from hybrid cell lines raise the possibility thatfactors controlling
the low density lipoprotein receptor activitymay reside on human chromosome
21, 5 or both. (Abstract) Cytogenet.Cell Genet. 32: 295- 296, 1982.

GAM5227 299 LDLR Mandelshtam, M.; Chakir, K.; Shevtsov, S.; Golubkov, V.; Skobeleva,N.; 1 B c
Lipovetsky, B.; Konstantinov, V.; Denisenko, A.; Gaitskhoki, V.;Schwartz,
E.: Prevalence of Lithuanian mutation among St. PetersburgJews with familial
hypercholesterolemia. Hum. Mutat. 12: 255- 258,1998.

GAM5227 299 LDLR Meiner, V.; Landsberger, D.; Berkman, N.; Reshef, A.; Segal, P.;Seftel, H. 1 B c
C.; van der Westhuyzen, D. R.; Jeenah, M. S.; Coetzee,G. A.; Leitersdorf,
E.: A common Lithuanian mutation causing familialhypercholesterolemia in
Ashkenazi Jews. Am. J. Hum. Genet. 49: 443- 449,1991.

GAM5227 299 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamoto, A.: Analysisof a recycling- 1 B c
impaired mutant of low density lipoprotein receptorin familial
hypercholesterolemia. J. Biol. Chem. 264: 16584- 16590,1989.

GAM5227 299 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamura, T.; Yamamoto,A.: A point 1 B c
mutation of low- density- lipoprotein receptor causingrapid degradation of
the receptor. Europ. J. Biochem. 210: 1- 7,1992.

GAM5227 299 LDLR Moorjani, S.; Roy, M.; Torres, A.; Betard, C.; Gagne, C.; Lambert,M.; Brun, 1 B c
D.; Davignon, J.; Lupien, P.: Mutations of low- density- lipoprotein-
receptorgene, variation in plasma cholesterol, and expression of

coronaryheart disease in homozygous familial hypercholesterolaemia. Lancet 341:1303- 1306, 1993.

GAM5227 299 LDLR Oppenheim, A.; Friedlander, Y.; Dann, E. J.; Berkman, N.; Schwartz,S. P.; 1 B c
Leitersdorf, E.: Hypercholesterolemia in five Israeli Christian-Arabkindreds is caused by the 'Lebanese' allele at the low density lipoproteinreceptor gene locus and by an additional independent major factor. Hum.Genet. 88: 75- 84, 1991.

GAM5227 299 LDLR Pisciotta, L.; Cantafora, A.; De Stefano, F.; Langheim, S.; Calandra,S.; 1 B c
Bertolini, S.: A 'de novo' mutation of the LDL- receptor geneas the cause of familial hypercholesterolemia. Biochim. Biophys.Acta 1587: 7- 11, 2002.

GAM5227 299 LDLR Rodningen, O. K.; Rosby, O.; Tonstad, S.; Ose, L.; Berg, K.; Leren,T. P.: A 1 B c
9.6 kilobase deletion in the low density lipoprotein receptorgene in Norwegian familial hypercholesterolemia subjects. Clin. Genet. 42:288- 295, 1992.

GAM5227 299 LDLR Rubinsztein, D. C.; Coetzee, G. A.; Marais, A. D.; Leitersdorf,E.; Seftel, 1 B c
H. C.; van der Westhuyzen, D. R.: Identification andproperties of the proline- 644- to- leucine mutant LDL receptor in SouthAfricans of Indian origin. J. Lipid Res. 33: 1647- 1655, 1992.

GAM5227 299 LDLR Rudiger, N. S.; Heinsvig, E. M.; Hansen, F. A.; Faergeman, O.;Bolund, L.; 1 B c
Gregersen, N.: DNA deletions in the low density lipoprotein(LDL) receptor gene in Danish families with familial hypercholesterolemia. Clin.Genet. 39: 451- 462, 1991.

GAM5227 299 LDLR Ruffner, D. E.; Sprung, C. N.; Minghetti, P. P.; Gibbs, P. E.M.; Dugaiczyk, 1 B c
A.: Invasion of the human albumin- alpha- fetoproteingene family by Alu, Kpn, and two novel repetitive DNA elements. Molec.Biol. Evol. 4: 1- 9, 1987.

GAM5227 299 LDLR Russell, D. W.; Lehrman, M. A.; Sudhof, T. C.; Yamamoto, T.; Davis,C. G.; 1 B c
Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: The LDL receptorin familial hypercholesterolemia: use of human mutations to dissecta membrane protein. Cold Spring Harbor Symp. Quant. Biol. 51: 811- 819,1986.

GAM5227 299 LDLR Russell, D. W.; Schneider, W. J.; Yamamoto, T.; Luskey, K. L.;Brown, M. S.; 1 B c
Goldstein, J. L.: Domain map of the LDL receptor: sequencehomology with the epidermal growth factor precursor. Cell 37: 577- 585,1984.

GAM5227 299 LDLR Savov, A.; Angelicheva, D.; Balassopoulou, A.; Jordanova, A.;Noussia- 1 B c
Arvanitakis, S.; Kalaydjieva, L.: Double mutant alleles:are they rare? Hum. Molec. Genet. 4: 1169- 1171, 1995.

GAM5227 299 LDLR Schuster, H.; Manke, C.; Fischer, J.; Keller, C.; Wolfram, G.;Zollner, N.: 1 B c
Identification of the valine 408 to methionine mutationin the LDL receptor in a Greek patient with homozygous familial hypercholesterolemia. Clin.Genet. 48: 90- 92, 1995.

GAM5227 299 LDLR Schuster, H.; Ostwald, P.; Keller, P.; Wolfram, G.; Keller, C.: 1 B c
Identification of the serine- 156 to leucine mutation in the low-densitylipoprotein receptor in a German family with familial hypercholesterolemia. Clin.Investig. 71: 172- 175, 1993.

GAM5227 299 LDLR Seftel, H. C.; Baker, S. G.; Sandler, M. P.; Forman, M. B.; Joffe,B. I.; 1 B c
Mendelsohn, D.; Jenkins, T.; Mieny, C. J.: A host of hypercholesterolaemichomozygotes in South Africa. Brit. Med. J. 281: 633- 636, 1980.

GAM5227 299 LTA Aggarwal, B. B.; Eessalu, T. E.; Hass, P. E.: Characterizationof receptors 1 B c
for human tumour necrosis factor and their regulationby gamma- interferon. Nature 318: 665- 667, 1985.

GAM5227 299 LTA Evans, A. M.; Petersen, J. W.; Sekhon, G. S.; DeMars, R.: Mappingof 1 B c
prolactin and tumor necrosis factor- beta genes on human chromosome6p using
lymphoblastoid cell deletion mutants. Somat. Cell Molec.Genet. 15: 203- 213,
1989.

GAM5227 299 LTA Gray, P. W.; Aggarwal, B. B.; Benton, C. V.; Bringman, T. S.; Henzel,W. J.; 1 B c
Jarrett, J. A.; Leung, D. W.; Moffat, B.; Ng, P.; Svedersky,L. P.;
Palladino, M. A.; Nedwin, G. E.: Cloning and expression ofcDNA for human
lymphotoxin, a lymphokine with tumour necrosis activity. Nature 312:721-
724, 1984.

GAM5227 299 LTA Jongeneel, C. V.; Briant, L.; Udalova, I. A.; Sevin, A.; Nedospasov,S. A.; 1 B c
Cambon- Thomsen, A.: Extensive genetic polymorphism in thehuman tumor
necrosis factor region and relation to extended HLA haplotypes. Proc.Nat.
Acad. Sci. 88: 9717- 9721, 1991.

GAM5227 299 LTA Koss, K.; Satsangi, J.; Fanning, G. C.; Welsh, K. I.; Jewell, D.P.: Cytokine 1 B c
(TNF- alpha, LT- alpha, and IL- 10) polymorphisms in inflammatorybowel
diseases and normal controls: differential effects on productionand allele
frequencies. Genes Immun. 1: 185- 190, 2000.

GAM5227 299 LTA Spies, T.; Blanck, G.; Bresnahan, M.; Sands, J.; Strominger, J.L.: A new 1 B c
cluster of genes within the human major histocompatibilitycomplex. Science
243: 214- 217, 1989.

GAM5227 299 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; 1 B c
Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.;
Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2
purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363-
18367,1996.

GAM5227 299 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof 1 B c
leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature
372: 179- 182, 1994.

GAM5227 299 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; 1 B c
Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol.
Nature 384: 39- 43, 1996.

GAM5227 299 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 1 B c
specifictranscriptional regulation of human leukotriene B4 receptor gene.
J.Exp. Med. 192: 413- 420, 2000.

GAM5227 299 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 1 B c
chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM5227 299 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 1 B c
Leukotrienes and lipoxins: structures, biosynthesis,and biological effects.
Science 237: 1171- 1176, 1987.

GAM5227 299 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 1 B c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene
and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-
130, 1997.

GAM5227 299 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 1 B c
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature
387:620- 624, 1997.

GAM5227 299 MAP4K2 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 1 B c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.;
Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.;
Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the

2.8- Mb region containing the multiple endocrineneoplasia type 1 locus. Genome Res. 7: 725- 735, 1997.

GAM5227 299 MAP4K2 Katz, P.; Whalen, G.; Kehrl, J. H.: Differential expression ofa novel protein kinase in human B lymphocytes: preferential localizationin the germinal center. J. Biol. Chem. 269: 16802- 16809, 1994. 1 B c

GAM5227 299 MAP4K2 Pombo, C. M.; Kehrl, J. H.; Sanchez, I.; Katz, P.; Avruch, J.;Zon, L. I.; Woodgett, J. R.; Force, T.; Kyriakis, J. M.: Activationof the SAPK pathway by the human STE20 homologue germinal centre kinase. Nature 377:750- 754, 1995. 1 B c

GAM5227 299 MAP4K2 Ren, M.; Zeng, J.; De Lemos- Chiarandini, C.; Rosenfeld, M.; Adesnik,M.; Sabatini, D. D.: In its active form, the GTP- binding proteinrab8 interacts with a stress- activated protein kinase. Proc. Nat.Acad. Sci. 93: 5151- 5155, 1996. 1 B c

GAM5227 299 MLLT3 Nakamura, T.; Alder, H.; Gu, Y.; Prasad, R.; Canaani, O.; Kamada,N.; Gale, R. P.; Lange, B.; Crist, W. M.; Nowell, P. C.; Croce, C.M.; Canaani, E.: Genes on chromosomes 4, 9, and 19 involved in 11q23abnormalities in acute leukemia share sequence homology and/or commonmotifs. Proc. Nat. Acad. Sci. 90: 4631- 4635, 1993. 1 B c

GAM5227 299 MLLT3 Strissel, P. L.; Strick, R.; Tomek, R. J.; Roe, B. A.; Rowley,J. D.; Zeleznik- Le, N. J.: DNA structural properties of AF9 are similarto MLL and could act as recombination hot spots resulting in MLL/AF9translocations and leukemogenesis. Hum. Molec. Genet. 9: 1671- 1679,2000. 1 B c

GAM5227 299 MXI1 Albarosa, R.; DiDonato, S.; Finocchiaro, G.: Redefinition of thecoding sequence of the MXI1 gene and identification of a polymorphicrepeat in the 3- prime non- coding region that allows the detectionof loss of heterozygosity of chromosome 10q25 in glioblastomas. Hum.Genet. 95: 709- 711, 1995. 1 B c

GAM5227 299 MXI1 Eagle, L. R.; Yin, X.; Brothman, A. R.; Williams, B. J.; Atkin,N. B.; Prochownik, E. V.: Mutation of the MXI1 gene in prostate cancer. NatureGenet. 9: 249- 255, 1995. 1 B c

GAM5227 299 MXI1 Edelhoff, S.; Ayer, D. E.; Zervos, A. S.; Steingrimsson, E.; Jenkins,N. A.; Copeland, N. G.; Eisenman, R. N.; Brent, R.; Disteche, C. M.: Mapping of two genes encoding members of a distinct subfamily ofMAX interacting proteins: MAD to human chromosome 2 and mouse chromosome6, and MXI1 to chromosome 10 and mouse chromosome 19. Oncogene 9:665- 668, 1994. 1 B c

GAM5227 299 MXI1 Li, X.- J.; Wang, D.- Y.; Zhu, Y.; Guo, R.- J.; Wang, X.- D.; Lubomir,K.; Mukai, K.; Sasaki, H.; Yoshida, H.; Oka, T.; Machinami, R.; Shinmura,K.; Tanaka, M.; Sugimura, H.: Mxi1 mutations in human neurofibrosarcomas. Jpn.J. Cancer Res. 90: 740- 746, 1999. 1 B c

GAM5227 299 MXI1 Prochownik, E. V.; Grove, L. E.; Deubler, D.; Zhu, X. L.; Stephenson,R. A.; Rohr, L. R.; Yin, X.; Brothman, A. R.: Commonly occurringloss and mutation of the MXI1 gene in prostate cancer. Genes ChromosomesCancer 22: 295- 304, 1998. 1 B c

GAM5227 299 MXI1 Schreiber- Agus, N.; Meng, Y.; Hoang, T.; Hou, H., Jr.; Chen, K.;Greenberg, R.; Cordon- Cardo, C.; Lee, H.- W.; DePinho, R. A.: Roleof Mxi1 in ageing organ systems and the regulation of normal and neoplasticgrowth. Nature 393: 483- 487, 1998. 1 B c

GAM5227 299 MXI1 Shapiro, D. N.; Valentine, V.; Eagle, L.; Yin, X.; Morris, S. W.;Prochownik, E. V.: Assignment of the human MAD and MXI1 genes tochromosomes 2p12- p13 and 10q24- q25. Genomics 23: 282- 285, 1994. 1 B c

GAM5227 299 MXI1 Steingrimsson, E.; Sawadogo, M.; Gilbert, D. J.; Zervos, A. S.;Brent, R.; 1 B c
Blanar, M. A.; Fisher, D. E.; Copeland, N. G.; Jenkins,N. A.: Murine chromosomal location of five bHLH- Zip transcriptionfactor genes. Genomics 28: 179- 183, 1995.

GAM5227 299 MXI1 Wechsler, D. S.; Hawkins, A. L.; Li, X.; Jabs, E. W.; Griffin,C. A.; Dang, 1 B c
C. V.: Localization of the human Mxi1 transcriptionfactor gene (MXI1) to chromosome 10q24- q25. Genomics 21: 669- 672,1994.

GAM5227 299 MXI1 Wechsler, D. S.; Shelly, C. A.; Dang, C. V.: Genomic organizationof human 1 B c
MXI1, a putative tumor suppressor gene. Genomics 32: 466- 470,1996.

GAM5227 299 MXI1 Zervos, A. S.; Gyuris, J.; Brent, R.: Mxi1, a protein that 1 B c
specificallyinteracts with Max to bind Myc- Max recognition sites. Cell 72: 223- 232,1993. Note: Erratum: Cell 79: 389 only, 1994.

GAM5227 299 NCOR2 Chen, J. D.; Evans, R. M.: A transcriptional co- repressor thatinteracts 1 B b
with nuclear hormone receptors. Nature 377: 454- 457, 1995.

GAM5227 299 NCOR2 Fischle, W.; Dequiedt, F.; Hendzel, M. J.; Guenther, M. G.; Lazar,M. A.; 1 B b
Voelter, W.; Verdin, E.: Enzymatic activity associated withclass II HDACs is dependent on a multiprotein complex containing HDAC3and SMRT/N- CoR. Molec. Cell 9: 45- 57, 2002.

GAM5227 299 NCOR2 Horlein, A. J.; Naar, A. M.; Heinzel, T.; Torchia, J.; Gloss, B.;Kurokawa, 1 B b
R.; Ryan, A.; Kamel, Y.; Soderstrom, M.; Glass, C. K.; Rosenfeld,M. G.: Ligand- independent repression by the thyroid hormone receptormediated by a nuclear receptor co- repressor. Nature 377: 397- 403,1995.

GAM5227 299 NCOR2 Hu, X.; Lazar, M. A.: The CoRNR motif controls the recruitmentof 1 B b
corepressors by nuclear hormone receptors. Nature 402: 93- 96,1999.

GAM5227 299 NCOR2 Jiang, Q.; Galiegue- Zouitina, S.; Roumier, C.; Hildebrand, M. P.;Thomas, 1 B b
S.; Coignet, L. J.: Genomic organization and refined mappingof the human nuclear corepressor 2 (NCOR2)/ silencing mediator ofretinoid and thyroid hormone receptor (SMRT) gene on chromosome 12q24.3. Cytogenet.Cell Genet. 92: 217- 220, 2001.

GAM5227 299 NCOR2 Ordentlich, P.; Downes, M.; Xie, W.; Genin, A.; Spinner, N. B.;Evans, R. M.: 1 B b
Unique forms of human and mouse nuclear receptor corepressorSMRT. Proc. Nat. Acad. Sci. 96: 2639- 2644, 1999.

GAM5227 299 NGB Burmester, T.; Weich, B.; Reinhardt, S.; Hankeln, T.: A vertebrateglobin 1 B c
expressed in the brain. Nature 407: 520- 523, 2000.

GAM5227 299 NGB Moens, L.; Dewilde, S.: Globins in the brain. Nature 407: 461- 462,2000. 1 B c

GAM5227 299 NME2 Backer, J. M.; Mendola, C. E.; Kovesdi, I.; Fairhurst, J. L.; O'Hara,B.; 1 B c
Eddy, R. L., Jr.; Shows, T. B.; Mathew, S.; Murty, V. V. V. S.;Chaganti, R. S. K.: Chromosomal localization and nucleoside diphosphatekinase activity of human metastasis- suppressor genes NM23- 1 and NM23- 2. Oncogene 8:497- 502, 1993.

GAM5227 299 NME2 Chandrasekharappa, S. C.; Gross, L. A.; King, S. E.; Collins, F.S.: The 1 B c
human NME2 gene lies within 18kb of NME1 in chromosome 17. GenesChromosomes Cancer 6: 245- 248, 1993.

GAM5227 299 NME2 Gilles, A. M.; Presecan, E.; Vonica, A.; Lascu, I.: Nucleosidediphosphate 1 B c
kinase from human erythrocytes: structural characterizationof the two polypeptide chains responsible for heterogeneity of thehexameric enzyme. J. Biol. Chem. 266: 8784- 8789, 1991.

GAM5227 299 NME2 Kelsell, D. P.; Black, D. M.; Solomon, E.; Spurr, N. K.: Localizationof a 1 B c
second NM23 gene, NME2, to chromosome 17q21- q22. Genomics 17:522- 524, 1993.

GAM5227 299 NME2 Leone, A.; McBride, O. W.; Weston, A.; Wang, M. G.; Anglard, P.;Cropp, C. S.; Goepel, J. R.; Lidereau, R.; Callahan, R.; Marston Linehan,W.; Rees, R. C.; Harris, C. C.; Liotta, L. A.; Steeg, P. S.: Somaticallelic deletion of nm23 in human cancer. Cancer Res. 51: 2490- 2493,1991. 1 B c

GAM5227 299 NME2 Stahl, J. A.; Leone, A.; Rosengard, A. M.; Porter, L.; King, C.R.; Steeg, P. S.: Identification of a second human nm23 gene, nm23- H2. CancerRes. 51: 445- 449, 1991. 1 B c

GAM5227 299 PFKFB3 Chesney, J.; Mitchell, R.; Benigni, F.; Bacher, M.; Spiegel, L.;Al- Abed, Y.; Han, J. H.; Metz, C.; Bucala, R.: An inducible geneproduct for 6-phosphofructo- 2- kinase with an AU- rich instability element:role in tumor cell glycolysis and the Warburg effect. Proc. Nat.Acad. Sci. 96: 3047- 3052, 1999. 1 B c

GAM5227 299 PFKFB3 Manzano, A.; Rosa, J. L.; Ventura, F.; Perez, J. X.; Nadal, M.;Estivill, X.; Ambrosio, S.; Gil, J.; Bartrons, R.: Molecular cloning,expression, and chromosomal localization of a ubiquitously expressedhuman 6- phosphofructo-2- kinase/fructose- 2,6- bisphosphatase gene (PFKFB3). Cytogenet.Cell Genet. 83: 214- 217, 1998. 1 B c

GAM5227 299 PFKFB3 Nicholl, J.; Hamilton, J. A.; Sutherland, G. R.; Sutherland, R.L.; Watts, C. K. W.: The third human isoform of 6- phosphofructo- 2- kinase/fructose- 2,6-bisphosphatase(PFKFB3) map position 10p14- p15. Chromosome Res. 5: 150 only, 1997. 1 B c

GAM5227 299 PFKFB3 Sakai, A.; Kato, M.; Fukasawa, M.; Ishiguro, M.; Furuya, E.; Sakakibara,R.: Cloning of cDNA encoding for a novel isozyme of fructose 6- phosphate,2-kinase/fructose2,6- bisphosphatase from human placenta. J. Biochem. 119: 506- 511,1996. 1 B c

GAM5227 299 PFKFB3 Sakakibara, R.; Kato, M.; Okamura, N.; Nakagawa, T.; Komada, Y.;Tominaga, N.; Shimojo, M.; Fukasawa, M.: Characterization of a humanplacental fructose- 6- phosphate,2- kinase/fructose- 2,6- bisphosphatase. J.Biochem. 122: 122- 128, 1997. 1 B c

GAM5227 299 PFKFB3 Warburg, O.: On the origin of cancer cells. Science 123: 309- 314,1956. 1 B c

GAM5227 299 PLXNA2 Maestrini, E.; Tamagnone, L.; Longati, P.; Cremona, O.; Gulisano,M.; Bione, S.; Tamanini, F.; Neel, B. G.; Toniolo, D.; Comoglio, P.M.: A family of transmembrane proteins with homology to the MET- hepatocytegrowth factor receptor. Proc. Nat. Acad. Sci. 93: 674- 678, 1996. 1 B c

GAM5227 299 PLXNA2 Tamagnone, L.; Artigiani, S.; Chen, H.; He, Z.; Ming, G.; Song,H.; Chedotal, A.; Winberg, M. L.; Goodman, C. S.; Poo, M.; Tessier- Lavigne,M.; Comoglio, P. M.: Plexins are a large family of receptors fortransmembrane, secreted, and GPI- anchored semaphorins in vertebrates. Cell 99:71- 80, 1999. 1 B c

GAM5227 299 PODXL Kershaw, D. B.; Beck, S. G.; Wharram, B. L.; Wiggins, J. E.; Goyal,M.; Thomas, P. E.; Wiggins, R. C.: Molecular cloning and characterizationof human podocalyxin- like protein: orthologous relationship to rabbitPCLP1 and rat podocalyxin. J. Biol. Chem. 272: 15708- 15714, 1997. 1 B c

GAM5227 299 PODXL Kershaw, D. B.; Wiggins, J. E.; Wharram, B. L.; Wiggins, R. C.: Assignment of the human podocalyxin- like protein (PODXL) gene to7q32- q33. Genomics 45: 239- 240, 1997. 1 B c

GAM5227 299 POU2F2 Deans, Z.; Dawson, S. J.; Xie, J.; Young, A. P.; Wallace, D.; Latchman,D. S.: Differential regulation of the two neuronal nitric- oxide synthasegene promoters by the Oct- 2 transcription factor. J. Biol. Chem. 271:32153-32158, 1996. 1 B c

GAM5227 299 POU2F2 Ko, H.- S.; Fast, P.; McBride, W.; Staudt, L. M.: A human proteinspecific for the immunoglobulin octamer DNA motif contains a functionalhomeobox domain. Cell 55: 135- 144, 1988. 1 B c

GAM5227 299 POU2F2 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001. 1 B c

GAM5227 299 POU2F2 Siracusa, L. D.; Rosner, M. H.; Vigano, M. A.; Gilbert, D. J.;Staudt, L. M.; Copeland, N. G.; Jenkins, N. A.: Chromosomal locationof the octamer transcription factors, Otf- 1, Otf- 2, and Otf- 3, definesmultiple Otf- 3- related sequences dispersed in the mouse genome. Genomics 10:313- 326, 1991. 1 B c

GAM5227 299 POU2F2 Staudt, L. M.; Clerc, R. G.; Singh, H.; LeBowitz, J. H.; Sharp,P. A.; Baltimore, D.: Cloning of a lymphoid- specific cDNA encodinga protein binding the regulatory octamer DNA motif. Science 241:577- 580, 1988. 1 B c

GAM5227 299 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: Chromosomalassignment of the interferon- inducible double- stranded RNA- dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse chromosome17 E2. Genomics 16: 765- 767, 1993. 1 B c

GAM5227 299 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human interferon- gamma mRNA autoregulates its translation througha pseudoknot that activates the interferon- inducible protein kinasePKR. Cell 108: 221- 232, 2002. 1 B c

GAM5227 299 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR) encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and differences from its mouse homolog. Genomics 36:197- 201, 1996. 1 B c

GAM5227 299 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: sequence of the human interferon- inducible RNA- dependent proteinkinase (PKR) deduced from genomic clones. Gene 178: 191- 193, 1996. 1 B c

GAM5227 299 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand characterization of the human double- stranded RNA- activated proteinkinase induced by interferon. Cell 62: 379- 390, 1990. 1 B c

GAM5227 299 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds preferentially to Huntington's disease (HD) transcriptsand is activated in HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001. 1 B c

GAM5227 299 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. G.; Williams, B. R. G.: Localization of the human interferon- induced,ds- RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics 16:768- 770, 1993. 1 B c

GAM5227 299 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein. Science 285: 107- 110, 1999. 1 B c

GAM5227 299 PSG7 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999. 1 B c

GAM5227 299 PSG7 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by 1 B c

fluorescence in situ hybridization. Genomics 12:773- 779, 1992.

GAM5227 299 PSG7 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.; Georgescu,A.; 1 B c
Carrano, A.; Hammarstrom, S.: Gene organization of the pregnancy-
specificglycoprotein region on human chromosome 19: assembly and analysisof
a 700- kb cosmid contig spanning the region. Genomics 23: 659- 668,1994.

GAM5227 299 PSG7 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The 1 B c
pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19:
fine structure of the 11 PSG genes and identificationof 6 new genes forming
a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics
23: 669- 684, 1994.

GAM5227 299 PSG7 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, 1 B c
H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.;
Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly
linked on the long arm of chromosome 19 and arecoordinately expressed.
Biochem. Biophys. Res. Commun. 167: 848- 859,1990.

GAM5227 299 PSG7 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades- 1 B c
Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan,
K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the
carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772,
1992.

GAM5227 299 PSG7 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 1 B c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM5227 299 PSG7 Tynan, K.; Olsen, A.; Trask, B.; de Jong, P.; Thompson, J.; Zimmermann,W.; 1 B c
Carrano, A.; Mohrenweiser, H.: Assembly and analysis of cosmidcontigs in the
CEA- gene family region of human chromosome 19. NucleicAcids Res. 20: 1629-
1636, 1992.

GAM5227 299 RAMP3 Aiyar, N.; Rand, K.; Elshourbagy, N. A.; Zeng, Z.; Adamou, J. E.;Bergsma, D. 1 B c
J.; Li, Y.: A cDNA encoding the calcitonin gene- relatedpeptide type 1
receptor. J. Biol. Chem. 271: 11325- 11329, 1996.

GAM5227 299 RAMP3 Christopoulos, G.; Perry, K. J.; Morfis, M.; Tilakaratne, N.; Gao,Y.; 1 B c
Fraser, N. J.; Main, M. J.; Foord, S. M.; Sexton, P. M.: Multipleamylin
receptors arise from receptor activity- modifying protein interactionwith
the calcitonin receptor gene product. Molec. Pharm. 56: 235- 242,1999.

GAM5227 299 RAMP3 Derst, C.; Engel, H.; Grzeschik, K.- H.; Daut, J.: Genomic structureand 1 B c
chromosome mapping of human and mouse RAMP genes. Cytogenet.Cell Genet. 90:
115- 118, 2000.

GAM5227 299 RAMP3 Foord, S. M.; Marshall, F. H.: RAMPs: accessory proteins for 1 B c
seventransmembrane domain receptors. Trends Pharm. Sci. 20: 184- 187,1999.

GAM5227 299 RAMP3 McLatchie, L. M.; Fraser, N. J.; Main, M. J.; Wise, A.; Brown,J.; Thompson, 1 B c
N.; Solari, R.; Lee, M. G.; Foord, S. M.: RAMPs regulatethe transport and
ligand specificity of the calcitonin- receptor- likereceptor. Nature 393:
333- 339, 1998.

GAM5227 299 RELN D'Arcangelo, G.: Personal Communication. Nutley, N. J. 6/2/1995. 1 B c

GAM5227 299 RELN D'Arcangelo, G.; Homayouni, R.; Keshvara, L.; Rice, D. S.; Sheldon,M.; 1 B c
Curran, T.: Reelin is a ligand for lipoprotein receptors. Neuron 24:471-
479, 1999.

GAM5227 299 RELN D'Arcangelo, G.; Miao, G. G.; Chen, S.- C.; Soares, H. D.; Morgan,J. I.; 1 B c

Curran, T.: A protein related to extracellular matrix proteinsdeleted in the mouse mutant reeler. Nature 374: 719- 723, 1995.

GAM5227 299 RELN DeSilva, U.; D'Arcangelo, G.; Braden, V. V.; Chen, J.; Miao, G.G.; Curran, T.; Green, E. D.: The human reelin gene: isolation, sequencing,and mapping on chromosome 7. Genome Res. 7: 157- 164, 1997. 1 B c

GAM5227 299 RELN Green, M. C.: Catalog of mutant genes and polymorphic loci.In:Lyon, M. F.; Searle, A. G.: Genetic Variants and Strains of the LaboratoryMouse. Oxford: Oxford Univ. Press (pub.) (2nd ed.): 1989. 1 B c

GAM5227 299 RELN Hack, I.; Bancila, M.; Loulier, K.; Carroll, P.; Cremer, H.: Reelinis a detachment signal in tangential chain- migration during postnatalneurogenesis. Nature Neurosci. 5: 939- 945, 2002. 1 B c

GAM5227 299 RELN Hiesberger, T.; Trommsdorff, M.; Howell, B. W.; Goffinet, A.; Mumby,M. C.; Cooper, J. A.; Herz, J.: Direct binding of reelin to VLDLreceptor and apoE receptor 2 induces tyrosine phosphorylation of disabled- 1and modulates tau phosphorylation. Neuron 24: 481- 489, 1999. 1 B c

GAM5227 299 RELN Hirotsune, S.; Takahara, T.; Sasaki, N.; Hirose, K.; Yoshiki, A.;Ohashi, T.; Kusakabe, M.; Murakami, Y.; Muramatsu, M.; Watanabe, S.;Nakao, K.; Katsuki, M.; Hayashizaki, Y.: The reeler gene encodesa protein with an EGF- like motif expressed by pioneer neurons. NatureGenet. 10: 77- 83, 1995. 1 B c

GAM5227 299 RELN Hong, S. E.; Shugart, Y. Y.; Huang, D. T.; Al Shahwan, S.; Grant,P. E.; Hourihane, J. O.; Martin, N. D. T.; Walsh, C. A.: Autosomalrecessive lissencephaly with cerebellar hypoplasia is associated withhuman RELN mutations. Nature Genet. 26: 93- 96, 2000. Note: Erratum:Nature Genet. 27: 225 only, 2001. 1 B c

GAM5227 299 RELN Hourihane, J. O.; Bennett, C. P.; Chaudhuri, R.; Robb, S. A.;Martin, N. D. T.: A sibship with a neuronal migration defect, cerebellarhypoplasia and congenital lymphedema. Neuropediatrics 24: 43- 46,1993. 1 B c

GAM5227 299 RELN Impagnatiello, F.; Guidotti, A. R.; Pesold, C.; Dwivedi, Y.; Caruncho,H.; Pisu, M. G.; Uzunov, D. P.; Smalheiser, N. R.; Davis, J. M.; Pandey,G. N.; Pappas, G. D.; Tueting, P.; Sharma, R. P.; Costa, E.: A decreaseof reelin expression as a putative vulnerability factor in schizophrenia. Proc.Nat. Acad. Sci. 95: 15718- 15723, 1998. 1 B c

GAM5227 299 RELN Magdaleno, S.; Keshvara, L.; Curran, T.: Rescue of ataxia andpreplate splitting by ectopic expression of reelin in reeler mice. Neuron 33:573- 586, 2002. 1 B c

GAM5227 299 RELN Royaux, I.; Lambert de Rouvroit, C.; D'Arcangelo, G.; Demirov,D.; Goffinet, A. M.: Genomic organization of the mouse reelin gene. Genomics 46:240- 250, 1997. 1 B c

GAM5227 299 RELN Trommsdorff, M.; Gotthardt, M.; Hiesberger, T.; Shelton, J.; Stockinger,W.; Nimpf, J.; Hammer, R. E.; Richardson, J. A.; Herz, J.: Reeler/Disabled- likedisruption of neuronal migration in knockout mice lacking the VLDLreceptor and ApoE receptor 2. Cell 97: 689- 701, 1999. 1 B c

GAM5227 299 RELN Yip, J. W.; Yip, Y. P. L.; Nakajima, K.; Capriotti, C.: Reelincontrols position of autonomic neurons in the spinal cord. Proc.Nat. Acad. Sci. 97: 8612- 8616, 2000. 1 B c

GAM5227 299 SLC17A7 Aihara, Y.; Mashima, H.; Onda, H.; Hisano, S.; Kasuya, H.; Hori,T.; Yamada, S.; Tomura, H.; Yamada, Y.; Inoue, I.; Kojima, I.; Takeda,J.: Molecular cloning of a novel brain- type Na(+)- dependent inorganicphosphate cotransporter. J. Neurochem. 74: 2622- 2625, 2000. 1 B b

GAM5227 299 SLC17A7 Bellocchio, E. E.; Reimer, R. J.; Fremeau, R. T., Jr.; Edwards,R. H.: Uptake 1 B b

of glutamate into synaptic vesicles by an inorganicphosphate transporter. Science 289: 957- 960, 2000.

GAM5227 299 SLC17A7 Ni, B.; Du, Y.; Wu, X.; DeHoff, B. S.; Rosteck, P. R., Jr.; Paul,S. M.: 1 B b
Molecular cloning, expression, and chromosomal localizationof a human brain-specific Na(+)- dependent inorganic phosphate cotransporter. J.Neurochem. 66: 2227- 2238, 1996.

GAM5227 299 SLC17A7 Takamori, S.; Rhee, J. S.; Rosenmund, C.; Jahn, R.: Identificationof a 1 B b
vesicular glutamate transporter that defines a glutamatergicphenotype in neurons. Nature 407: 189- 194, 2000.

GAM5227 299 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 1 B c
L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM5227 299 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 1 B c
J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM5227 299 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 1 B c
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand characterization of the mouse homolog of SYT, a gene implicatedin the development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM5227 299 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 1 B c
G.: Mapping and characterization of the mouse and humanSS18 genes, two human SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-319, 2001.

GAM5227 299 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 1 B c
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene family with several members transcribed in normaltestis and human cancer. Int. J. Cancer 72: 965- 971, 1997.

GAM5227 299 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 1 B c
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM5227 299 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 1 B c
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J. Nat. Cancer Inst. 91: 974- 975, 1999.

GAM5227 299 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 1 B c
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX synovial sarcoma translocation proteins and co- localizationwith the SNF protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM5227 299 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 1 B c
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM5227 299 TLE2 Artavanis- Tsakonas, S.; Matsuono, K.; Fortini, M.: Notch signaling. Science 1 B c
268:225- 232, 1995.

GAM5227 299 TLE2 Liu, Y.; Dehni, G.; Purcell, K. J.; Sokolow, J.; Carcangiu, M.L.; Artavanis- 1 B c
Tsakonas, S.; Stifani, S.: Epithelial expression andchromosomal location of human TLE genes: implications for Notch signalingand neoplasia. Genomics 31: 58- 64, 1996.

GAM5227 299 TNNC1 Bermingham, N.; Hernandez, D.; Balfour, A.; Gilmour, F.; Martin,J. E.; 1 B c
Fisher, E. M. C.: Mapping TNNC1, the gene that encodes cardiactroponin I in

the human and mouse. Genomics 30: 620- 622, 1995.

GAM5227 299 TNNC1 Roher, A.; Lieska, N.; Spitz, W.: The amino acid sequence of humancardiac troponin- C. Muscle Nerve 9: 73- 77, 1986. 1 B c

GAM5227 299 TNNC1 Romero- Herrera, A. E.; Castillo, O.; Lehmann, H.: Human skeletalmuscle proteins: the primary structure of troponin C. J. Molec. Evol. 8:251- 270, 1976. 1 B c

GAM5227 299 TNNC1 Schreier, T.; Kedes, L.; Gahlmann, R.: Cloning, structural analysis,and expression of the human slow twitch skeletal muscle/cardiac troponinC gene. J. Biol. Chem. 265: 21247- 21253, 1990. 1 B c

GAM5227 299 TNNC1 Song, W. J.: Personal Communication. Ann Arbor, Mich. 1/17/1997. 1 B c

GAM5227 299 TNNC1 Song, W.- J.; Van Keuren, M. L.; Drabkin, H. A.; Cypser, J. R.;Gemmill, R. M.; Kurnit, D. M.: Assignment of the human slow twitchskeletal muscle/cardiac troponin C gene (TNNC1) to human chromosome3p21.3- 3p14.3 using somatic cell hybrids. Cytogenet. Cell Genet. 75:36- 37, 1996. 1 B c

GAM5227 299 TNNC1 Townsend, P. J.; Yacoub, M. H.; Barton, P. J. R.: Assignment ofthe human cardiac/slow skeletal muscle troponin C gene (TNNC1) betweenD3S3118 and GCT4B10 on the short arm of chromosome 3 by somatic cellhybrid analysis. Ann. Hum. Genet. 61: 375- 377, 1997. 1 B c

GAM5227 299 TRPS1 Hatamura, I.; Kanauchi, Y.; Takahara, M.; Fujiwara, M.; Muragaki,Y.; Ooshima, A.; Ogino, T.: A nonsense mutation in TRPS1 in a Japanesefamily with tricho- rhino- phalangeal syndrome type I. (Letter) Clin.Genet. 59: 366- 367, 2001. 1 B b

GAM5227 299 TRPS1 Hilton, M. J.; Sawyer, J. M.; Gutierrez, L.; Hogart, A.; Kung,T. C.; Wells, D. E.: Analysis of novel and recurrent mutations responsiblefor the tricho- rhino- phalangeal syndromes. J. Hum. Genet. 47: 103- 106,2002. 1 B b

GAM5227 299 TRPS1 Hou, J.; Parrish, J.; Ludecke, H.- J.; Sapru, M.; Wang, Y.; Chen,W.; Hill, A.; Siegel- Bartelt, J.; Northrup, H.; Elder, F. F. B.; Chinault,C.; Horsthemke, B.; Wagner, M. J.; Wells, D. E.: A 4- megabase YACcontig that spans the Langer- Giedion syndrome region on human chromosome8q24.1: use in refining the location of the trichorhinophalangealsyndrome and multiple exostoses genes (TRPS1 and EXT1). Genomics 29:87- 97, 1995. 1 B b

GAM5227 299 TRPS1 Kobayashi, H.; Hino, M.; Shimodahira, M.; Iwakura, T.; Ishihara,T.; Ikekubo, K.; Ogawa, Y.; Nakao, K.; Kurahachi, H.: Missense mutationof TRPS1 in a family of tricho- rhino- phalangeal syndrome type III. Am.J. Med. Genet. 107: 26- 29, 2002. 1 B b

GAM5227 299 TRPS1 Ludecke, H.- J.; Schaper, J.; Meinecke, P.; Momeni, P.; Gross, S.;von Holtum, D.; Hirche, H.; Abramowicz, M. J.; Albrecht, B.; Apacik,C.; Christen, H.- J.; Claussen, U.; and 28 others: Genotypic andphenotypic spectrum in tricho- rhino- phalangeal syndrome types I andIII. Am. J. Hum. Genet. 68: 81- 91, 2001. 1 B b

GAM5227 299 TRPS1 Ludecke, H.- J.; Wagner, M. J.; Nardmann, J.; La Pillo, B.; Parrish,J. E.; Willems, P. J.; Haan, E. A.; Frydman, M.; Hamers, G. J. H.;Wells, D. E.; Horsthemke, B.: Molecular dissection of a contiguousgene syndrome: localization of the genes involved in the Langer- Giedionsyndrome. Hum. Molec. Genet. 4: 31- 36, 1995. 1 B b

GAM5227 299 TRPS1 Momeni, P.; Glockner, G.; Schmidt, O.; von Holtum, D.; Albrecht,B.; Gillessen- Kaesbach, G.; Hennekam, R.; Meinecke, P.; Zabel, B.;Rosenthal, A.; Horsthemke, B.; Ludecke, H.- J.: Mutations in a newgene, encoding a zinc- finger protein, cause tricho- rhino- phalangealsyndrome type I. Nature Genet. 24: 71- 74, 2000. 1 B b

GAM5227 299 TSTA3 Lenzerini, L.; Benatti, U.; Morelli, A.; Pontremoli, S.; De Flora,A.; Piazza, A.; Rinaldi, A.; Filippi, G.; Siniscalco, M.: Geneticvariation in the quantitative levels of an NADP(H)- binding protein(FX) in human erythrocytes. Blood 57: 209- 217, 1981. 1 B c

GAM5227 299 TSTA3 Morelli, A.; De Flora, A.: Isolation and partial characterizationof an NADP- and NADPH- binding protein from human erythrocytes. Arch.Biochem. Biophys. 179: 698- 705, 1977. 1 B c

GAM5227 299 TSTA3 Sullivan, F. X.; Kumar, R.; Kriz, R.; Stahl, M.; Xu, G.- Y.; Rouse,J.; Chang, X.; Boodhoo, A.; Potvin, B.; Cumming, D. A.: Molecularcloning of human GDP- mannose 4,6- dehydratase and reconstitution ofGDP- fucose biosynthesis in vitro. J. Biol. Chem. 273: 8193- 8202,1998. 1 B c

GAM5227 299 TSTA3 Tonetti, M.; Sturla, L.; Bisso, A.; Benatti, U.; De Flora, A.:Synthesis of GDP- L- fucose by the human FX protein. J. Biol. Chem. 271:27274- 27279, 1996. 1 B c

GAM5346 319 ARNT2 Hirose, K.; Morita, M.; Ema, M.; Mimura, J.; Hamada, H.; Fujii,H.; Saijo, Y.; Gotoh, O.; Sogawa, K.; Fujii- Kuriyama, Y.: cDNA cloningand tissue-specific expression of a novel basic helix- loop- helix/PASfactor (Arnt2) with close sequence similarity to the aryl hydrocarbonreceptor nuclear translocator (Arnt). Molec. Cell. Biol. 16: 1706- 1713,1996. 3 B c

GAM5346 319 ARNT2 Keith, B.; Adelman, D. M.; Simon, M. C.: Targeted mutation ofthe murine arylhydrocarbon receptor nuclear translocator 2 (Arnt2)gene reveals partial redundancy with Arnt. Proc. Nat. Acad. Sci. 98:6692- 6697, 2001. 3 B c

GAM5346 319 ARNT2 Michaud, J. L.; DeRossi, C.; May, N. R.; Holdener, B. C.; Fan,C.- M.: ARNT2 acts as the dimerization partner of SIM1 for the developmentof the hypothalamus. Mech. Dev. 90: 253- 261, 2000. 3 B c

GAM5346 319 ARNT2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B c

GAM5346 319 BVES Andree, B.; Hillemann, T.; Kessler- Ieckson, G.; Schmitt- John, T.;Jockusch, H.; Arnold, H.- H.; Brand, T.: Isolation and characterizationof the novel Popeye gene family expressed in skeletal muscle and heart. Dev.Biol. 223: 371- 382, 2000. 3 B c

GAM5346 319 BVES Reese, D. E.; Bader, D. M.: Cloning and expression of hbves, anovel and highly conserved mRNA expressed in the developing and adultheart and skeletal muscle in the human. Mammalian Genome 10: 913- 915,1999. 3 B c

GAM5346 319 BVES Reese, D. E.; Zavaljevski, M.; Streiff, N. L.; Bader, D.: Bves:a novel gene expressed during coronary blood vessel development. Dev.Biol. 209: 159- 171, 1999. 3 B c

GAM5346 319 CAMK2A Bayer, K.- U.; De Koninck, P.; Leonard, A. S.; Hell, J. W.; Schulman,H.: Interaction with the NMDA receptor locks CaMKII in an activeconformation. Nature 411: 801- 805, 2001. 3 B c

GAM5346 319 CAMK2A Chen, C.; Rainnie, D. G.; Greene, R. W.; Tonegawa, S.: Abnormalfear response and aggressive behavior in mutant mice deficient foralpha- calcium-calmodulin kinase II. Science 266: 291- 294, 1994. 3 B c

GAM5346 319 CAMK2A Cho, Y. H.; Giese, K. P.; Tanila, H.; Silva, A. J.; Eichenbaum,H.: Abnormal hippocampal spatial representations in alpha- CaMKII(T286A)and CREB(alpha-delta-) mice. Science 279: 867- 869, 1998. 3 B c

GAM5346 319 CAMK2A Frankland, P. W.; O'Brien, C.; Ohno, M.; Kirkwood, A.; Silva, A.J.: Alpha- 3 B c
CaMKII- dependent plasticity in the cortex is required forpermanent memory.
Nature 411: 309- 313, 2001.

GAM5346 319 CAMK2A Giese, K. P.; Federov, N. B.; Filipkowski, R. K.; Silva, A. J.: 3 B c
Autophosphorylation at thr286 of the alpha calcium- calmodulin kinaseII in
LTP and learning. Science 279: 870- 873, 1998.

GAM5346 319 CAMK2A Glazewski, S.; Chen, C.- M.; Silva, A.; Fox, K.: Requirement foralpha- 3 B c
CaMKII in experience- dependent plasticity of the barrel cortex. Science
272:421- 423, 1996.

GAM5346 319 CAMK2A Gordon, J. A.; Cioffi, D.; Silva, A. J.; Stryker, M. P.: Deficientplasticity 3 B c
in the primary visual cortex of alpha- calcium/calmodulin- dependentprotein
kinase II mutant mice. Neuron 17: 491- 499, 1996.

GAM5346 319 CAMK2A Justice, M. J.; Gilbert, D. J.; Kinzler, K. W.; Vogelstein, B.;Buchberg, A. 3 B c
M.; Ceci, J. D.; Matsuda, Y.; Chapman, V. M.; Patriotis,C.; Makris, A.;
Tsichlis, P. N.; Jenkins, N. A.; Copeland, N. G.:A molecular genetic linkage
map of mouse chromosome 18 reveals extensivelinkage conservation with human
chromosomes 5 and 18. Genomics 13:1281- 1288, 1992.

GAM5346 319 CAMK2A Karcher, R. L.; Roland, J. T.; Zappacosta, F.; Huddleston, M. J.;Annan, R. 3 B c
S.; Carr, S. A.; Gelfand, V. I.: Cell cycle regulationof myosin- V by
calcium/calmodulin- dependent protein kinase II. Science 293:1317- 1320,
2001.

GAM5346 319 CAMK2A Matsumoto, Y.; Maller, J. L.: Calcium, calmodulin, and CaMKIIrequirement for 3 B c
initiation of centrosome duplication in Xenopus eggextracts. Science 295:
499- 502, 2002.

GAM5346 319 CAMK2A Rotenberg, A.; Mayford, M.; Hawkins, R. D.; Kandel, E. R.; Muller,R. U.: 3 B c
Mice expressing activated CaMKII lack low frequency LTP anddo not form
stable place cells in the CA1 region of the hippocampus. Cell 87:1351- 1361,
1996.

GAM5346 319 CAMK2A Silva, A. J.; Rosahl, T. W.; Chapman, P. F.; Marowitz, Z.; Friedman,E.; 3 B c
Frankland, P. W.; Cestari, V.; Cioffi, D.; Sudhof, T. C.; Bourtchuladze,R.:
Impaired learning in mice with abnormal short- lived plasticity. Curr.Biol.
6: 1509- 1518, 1996.

GAM5346 319 CHRNA3 Anand, R.; Lindstrom, J.: Chromosomal localization of seven 3 B c
neuronalnicotinic acetylcholine receptor subunit genes in humans. Genomics
13:962- 967, 1992.

GAM5346 319 CHRNA3 Boulter, J.; O'Shea- Greenfield, A.; Duvoisin, R. M.; Connolly,J. G.; Wada, 3 B c
E.; Jensen, A.; Gardner, P. D.; Ballivet, M.; Deneris,E. S.; McKinnon, D.;
Heinemann, S.; Patrick, J.: Alpha3, alpha5 andbeta4: three members of the
rat neuronal nicotinic acetylcholine receptor- relatedgene family form a
gene cluster. J. Biol. Chem. 265: 4472- 4482,1990.

GAM5346 319 CHRNA3 Duga, S.; Solda, G.; Asselta, R.; Bonati, M. T.; Dalpra, L.; Malcovati,M.; 3 B c
Tenchini, M. L.: Characterization of the genomic structure ofthe human
neuronal nicotinic acetylcholine receptor CHRNA5/A3/B4 genecluster and
identification of novel intragenic polymorphisms. J.Hum. Genet. 46: 640-
648, 2001.

GAM5346 319 CHRNA3 Elliott, K. J.; Ellis, S. B.; Berckhan, K. J.; Urrutia, A.; Chavez- 3 B c
Noriega,L. E.; Johnson, E. C.; Velicelebi, G.; Harpold, M. M.:
Comparativestructure of human neuronal alpha(2)- alpha(7) and beta(2)-
beta(4)nicotinic acetylcholine receptor subunits and functional expressionof
the alpha(2), alpha(3), alpha(4), alpha(7), beta(2), and beta(4)subunits. J.

Molec. Neurosci. 7: 217- 228, 1996.

GAM5346 319 CHRNA3 Eng, C. M.; Kozak, C. A.; Beaudet, A. L.; Zoghbi, H. Y.: Mappingof multiple 3 B c
subunits of the neuronal nicotinic acetylcholine receptorto chromosome 15 in
man and chromosome 9 in mouse. Genomics 9: 278- 282,1991.

GAM5346 319 CHRNA3 Flora, A.; Schulz, R.; Benfante, R.; Battaglioli, E.; Terzano,S.; Clementi, 3 B c
F.; Fornasari, D.: Transcriptional regulation of thehuman alpha5 nicotinic
receptor subunit gene in neuronal and non- neuronaltissues. Europ. J. Pharm.
393: 85- 95, 2000.

GAM5346 319 CHRNA3 Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.: Molecularcloning of 3 B c
human neuronal nicotinic receptor alpha(3)- subunit. Neurosci.Lett. 111:
351- 356, 1990.

GAM5346 319 CHRNA3 Groot Kormelink, P. J.; Luyten, W. H. M. L.: Cloning and sequenceof full- 3 B c
length cDNAs encoding the human neuronal nicotinic acetylcholinereceptor
(nAChR) subunits beta- 3 and beta- 4 and expression of sevennAChR subunits
in the human neuroblastoma cell line SH- SY5Y and/orIMR- 32. FEBS Lett. 400:
309- 314, 1997.

GAM5346 319 CHRNA3 Khakh, B. S.; Zhou, X.; Sydes, J.; Galligan, J. J.; Lester, H.A.: State- 3 B c
dependent cross- inhibition between transmitter- gated cationchannels.
Nature 406: 405- 410, 2000.

GAM5346 319 CHRNA3 Mihovilovic, M.; Roses, A. D.: Expression of mRNAs in human thymuscoding for 3 B
c
the alpha- 3 subunit of a neuronal acetylcholine receptor. Exp.Neurol. 111:
175- 180, 1991.

GAM5346 319 CHRNA3 Raimondi, E.; Rubboli, F.; Moralli, D.; Chini, B.; Fornasari,D.; Tarroni, 3 B c
P.; De Carli, L.; Clementi, F.: Chromosomal localizationand physical linkage
of the genes encoding the human alpha- 3, alpha- 5,and beta- 4 neuronal
nicotinic receptor subunits. Genomics 12: 849- 850,1992.

GAM5346 319 CHRNA3 Rempel, N.; Heyers, S.; Engels, H.; Sleegers, E.; Steinlein, O.K.: The 3 B c
structures of the human neuronal nicotinic acetylcholinereceptor beta- 2-
and alpha- 3- subunit genes (CHRNB2 and CHRNA3). Hum.Genet. 103: 645- 653,
1998.

GAM5346 319 CHRNA3 Xu, W.; Gelber, S.; Orr- Urtreger, A.; Armstrong, D.; Lewis, R.A.; Ou, C.- 3 B c
N.; Patrick, J.; Role, L.; De Biasi, M.; Beaudet, A. L.: Megacystis,
mydriasis, and ion channel defect in mice lacking thealpha- 3 neuronal
nicotinic acetylcholine receptor. Proc. Nat. Acad.Sci. 96: 5746- 5751, 1999.

GAM5346 319 DDX11 Amann, J.; Kidd, V. J.; Lahti, J. M.: Characterization of putativehuman 3 B c
homologues of the yeast chromosome transmission fidelity gene,CHL1. J. Biol.
Chem. 272: 3823- 3832, 1997.

GAM5346 319 DDX11 Amann, J.; Valentine, M.; Kidd, V. J.; Lahti, J. M.: Localizationof Chl1- 3 B c
related helicase genes to human chromosome regions 12p11 and12p13:
similarity between parts of these genes and conserved humantelomeric-
associated DNA. Genomics 32: 260- 265, 1996.

GAM5346 319 DDX11 Frank, S.; Werner, S.: The human homologue of the yeast CHL1 geneis a novel 3 B c
keratinocyte growth factor- regulated gene. J. Biol. Chem. 271:24337- 24340,
1996.

GAM5346 319 DMRT1 Burtis, K. C.; Baker, B. S.: Drosophila doublesex gene controlssomatic 3 B c
sexual differentiation by producing alternatively splicedmRNAs encoding
related sex- specific polypeptides. Cell 56: 997- 1010,1989.

GAM5346 319 DMRT1 McDonald, M. T.; Flejter, W.; Sheldon, S.; Putzi, M. J.; Gorski,J. L.: XY 3 B c
sex reversal and gonadal dysgenesis due to 9p24 monosomy. Am.J. Med. Genet.

73: 321- 326, 1997.

GAM5346 319 DMRT1 Muroya, K.; Okuyama, T.; Goishi, K.; Ogiso, Y.; Fukuda, S.; Kameyama,J.; 3 B c
Sato, H.; Suzuki, Y.; Terasaki, H.; Gomyo, H.; Wakui, K.; Fukushima,Y.;
Ogata, T.: Sex- determining gene(s) on distal 9p: clinical andmolecular
studies in six cases. J. Clin. Endocr. Metab. 85: 3094- 3100,2000.

GAM5346 319 DMRT1 Raymond, C. S.; Shamu, C. E.; Shen, M. M.; Seifert, K. J.; Hirsch,B.; 3 B c
Hodgkin, J.; Zarkower, D.: Evidence for evolutionary conservationof sex-
determining genes. Nature 391: 691- 695, 1998.

GAM5346 319 DMRT1 Shan, Z.; Zabel, B.; Trautmann, U.; Hillig, U.; Ottolenghi, C.;Wang, Y.; 3 B c
Haaf, T.: FISH mapping of the sex- reversal region on humanchromosome 9p in
two XY females and in primates. Europ. J. Hum. Genet. 8:167- 173, 2000.

GAM5346 319 DMRT1 Shen, M. M.; Hodgkin, J.: mab- 3, a gene required for sex- specificyolk 3 B c
protein expression and a male- specific lineage in C. elegans. Cell 54:1019-
1031, 1988.

GAM5346 319 DMRT1 Smith, C. A.; McClive, P. J.; Western, P. S.; Reed, K. J.; Sinclair,A. H.: 3 B c
Conservation of a sex- determining gene. (Letter) Nature 402:601- 602, 1999.

GAM5346 319 DMRT1 Veitia, R.; Nunes, M.; Brauner, R.; Doco- Fenzy, M.; Joanny- Flinois,O.; 3 B c
Jaubert, F.; Lortat- Jacob, S.; Fellous, M.; McElreavey, K.: Deletionsof
distal 9p associated with 46,XY male to female sex reversal: definitionof
the breakpoints at 9p23.3- p24.1. Genomics 41: 271- 274, 1997.

GAM5346 319 EIF4EL3 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 B c
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM5346 319 EIF4EL3 Rom, E.; Kim, H. C.; Gingras, A.- C.; Marcotrigiano, J.; Favre,D.; Olsen, 3 B c
H.; Burley, S. K.; Sonenberg, N.: Cloning and characterizationof 4EHP, a
novel mammalian eIF4E- related cap- binding protein. J.Biol. Chem. 273:
13104- 13109, 1998.

GAM5346 319 FLRT2 Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; 3 B c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VIII. 78 new cDNAclones from brain
which code for large proteins in vitro. DNA Res. 4:307- 313, 1997.

GAM5346 319 FLRT2 Lacy, S. E.; Bonnemann, C. G.; Buzney, E. A.; Kunkel, L. M.: 3 B c
Identificationof FLRT1, FLRT2, and FLRT3: a novel family of transmembrane
leucine- richrepeat proteins. Genomics 62: 417- 426, 1999.

GAM5346 319 IARS Nichols, R. C.; Blinder, J.; Pai, S. I.; Ge, Q.; Targoff, I. N.;Plotz, P. 3 B c
H.; Liu, P.: Assignment of two human autoantigen genes:isoleucyl- tRNA
synthetase locates to 9q21 and lysyl- tRNA synthetaselocates to 16q23- q24.
Genomics 36: 210- 213, 1996.

GAM5346 319 IARS Nichols, R. C.; Raben, N.; Boerkoel, C. F.; Plotz, P. H.: Humanisoleucyl- 3 B c
tRNA synthetase: sequence of the cDNA, alternative mRNAsplicing, and the
characteristics of an unusually long C- terminalextension. Gene 155: 299-
304, 1995.

GAM5346 319 ITPKB Erneux, C.; Roeckel, N.; Takazawa, K.; Mailleux, P.; Vassart, G.;Mattei, M. 3 B c
G.: Localization of the genes for human inositol 1,4,5- trisphosphate3-
kinase A (ITPKA) and B (ITPKB) to chromosome regions 15q14- q21 and1q41-
q43, respectively, by in situ hybridization. Genomics 14:546- 547, 1992.

GAM5346 319 ITPKB Takazawa, K.; Perret, J.; Dumont, J. E.; Erneux, C.: Molecularcloning and 3 B c

expression of a new putative inositol 1,4,5- trisphosphate3- kinase isoenzyme. Biochem. J. 278: 883- 886, 1991.

GAM5346 319 MME Barker, P. E.; Shipp, M. A.; D'Adamio, L.; Masteller, E. L.; Reinherz,E. L.: 3 B c
The common acute lymphoblastic leukemia antigen gene mapsto chromosomal region 3(q21- q27). J. Immun. 142: 283- 287, 1989.

GAM5346 319 MME D'Adamio, L.; Shipp, M. A.; Masteller, E. L.; Reinherz, E. L.:Organization 3 B c
of the gene encoding common acute lymphoblastic leukemiaantigen (neutral endopeptidase 24.11): multiple miniexons and separate5- prime untranslated regions. Proc. Nat. Acad. Sci. 86: 7103- 7107,1989.

GAM5346 319 MME Debiec, H.; Guigonis, V.; Mougenot, B.; Decobert, F.; Haymann,J.- P.; 3 B c
Bensman, A.; Deschenes, G.; Ronco, P. M.: Antenatal membranousglomerulonephritis due to anti- neutral endopeptidase antibodies. NewEng. J. Med. 346: 2053- 2060, 2002.

GAM5346 319 MME Iwata, N.; Tsubuki, S.; Takaki, Y.; Shirotani, K.; Lu, B.; Gerard,N. P.; 3 B c
Gerard, C.; Hama, E.; Lee, H.- J.; Saido, T. C.: Metabolicregulation of brain A- beta by neprilysin. Science 292: 1550- 1552,2001.

GAM5346 319 MME Letarte, M.; Vera, S.; Tran, R.; Addis, J. B. L.; Onizuka, R. 3 B c
J.;Quackenbush, E. J.; Jongeneel, C. V.; McInnes, R. R.: Common acutelymphocytic leukemia antigen is identical to neutral endopeptidase. J.Exp. Med. 168: 1247- 1253, 1988.

GAM5346 319 MME Shipp, M. A.; Vijayaraghavan, J.; Schmidt, E. V.; Masteller, E.L.; D'Adamio, 3 B c
L.; Hersh, L. B.; Reinherz, E. L.: Common acute lymphoblasticleukemia antigen (CALLA) is active neutral endopeptidase 24.11 ('enkephalinase'):direct evidence by cDNA transfection analysis. Proc. Nat. Acad. Sci. 86:297- 301, 1989.

GAM5346 319 MME Tran- Paterson, R.; Willard, H. F.; Letarte, M.: The common 3 B c
acutelymphoblastic leukemia antigen (neutral endopeptidase- - 3.4.24.11)gene is located on human chromosome 3. Cancer Genet. Cytogenet. 42:129- 134, 1989.

GAM5346 319 MYF5 Braun, T.; Bober, E.; Winter, B.; Rosenthal, N.; Arnold, H. H.: Myf- 6, a 3 B c
new member of the human gene family of myogenic determinationfactors: evidence for a gene cluster on chromosome 12. EMBO J. 9:821- 831, 1990.

GAM5346 319 MYF5 Braun, T.; Grzeschik, K.- H.; Bober, E.; Arnold, H.- H.: The MYFgenes, a 3 B c
group of human muscle determining factors, are localizedon different human chromosomes.(Abstract) Cytogenet. Cell Genet. 51:969, 1989.

GAM5346 319 MYF5 Cupelli, L.; Renault, B.; Leblanc- Straceski, J.; Banks, A.; Ward,D.; 3 B c
Kucherlapati, R. S.; Krauter, K.: Assignment of the human myogenicfactors 5 and 6 (MYF5, MYF6) gene cluster to 12q21 by in situ hybridizationand physical mapping of the locus between D12S350 and D12S106. Cytogenet.Cell Genet. 72: 250- 251, 1996.

GAM5346 319 MYF5 Ott, M.- O.; Bober, E.; Lyons, G.; Arnold, H.- H.; Buckingham, M.: Early 3 B c
expression of the myogenic regulatory gene, Myf- 5, in precursorcells of skeletal muscle in the mouse embryo. Development 111:1097- 1107, 1991.

GAM5346 319 MYF5 Rudnicki, M. A.; Schnegelsberg, P. N. J.; Stead, R. H.; Braun,T.; Arnold, 3 B c
H.- H.; Jaenisch, R.: MyoD or Myf- 5 is required for theformation of skeletal muscle. Cell 75: 1351- 1359, 1993.

GAM5346 319 NOTCH2 Gao, X.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Gridley,T.: 3 B c
Assignment of the murine Notch2 and Notch3 genes to chromosomes3 and 17. Genomics 49: 160- 161, 1998.

GAM5346 319 NOTCH2 Katsanis, N.; Fitzgibbon, J.; Fisher, E. M. C.: Paralogy 3 B c

mapping:identification of a region in the human MHC triplicated onto humanchromosomes 1 and 9 allows the prediction and isolation of novel PBXand NOTCH loci. Genomics 35: 101- 108, 1996.

GAM5346 319 NOTCH2 Larsson, C.; Lardelli, M.; White, I.; Lendahl, U.: The human NOTCH1,2, and 3 3 B c genes are located at chromosome positions 9q34, 1p13- p11,and 19p13.2- p13.1 in regions of neoplasia- associated translocation. Genomics 24:253- 258, 1994.

GAM5346 319 PTBP1 Charlet- B., N.; Logan, P.; Singh, G.; Cooper, T. A.: Dynamic 3 B c antagonismbetween ETR- 3 and PTB regulates cell type- specific alternative splicing. Molec.Cell 9: 649- 658, 2002.

GAM5346 319 PTBP1 Ghetti, A.; Pinol- Roma, S.; Michael, W. M.; Morandi, C.; Dreyfuss,G.: HNRNP 3 B c I, the polypyrimidine tract- binding protein: distinct nuclearlocalization and association with hnRNAs. Nucleic Acids Res. 20:3671- 3678, 1992.

GAM5346 319 PTBP1 Raimondi, E.; Romanelli, M. G.; Moralli, D.; Gamberi, C.; Russo,M. P.; 3 B c Morandi, C.: Assignment of the human gene encoding heterogeneousnuclear RNA ribonucleoprotein I (PTB) to chromosome 14q23- q24.1. Genomics 27:553- 555, 1995.

GAM5346 319 PTBP1 Romanelli, M. G.; Lorenzi, P.; Morandi, C.: Organization of thehuman gene 3 B c encoding heterogeneous nuclear ribonucleoprotein type I(hnRNP I) and characterization of hnRNP I related pseudogene. Gene 255:267- 272, 2000.

GAM5346 319 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 3 B c Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime- untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001.

GAM5346 319 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 3 B c Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM5346 319 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 3 B c Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996.

GAM5346 319 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 3 B c synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM5346 319 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 3 B c M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996.

GAM5346 319 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: 3 B c Strand- specific postreplicative processing of mammalian telomeres. Science 293:2462- 2465, 2001.

GAM5346 319 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: 3 B c Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet. 17: 236- 239, 1997.

GAM5346 319 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres 3 B c contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17: 231- 235, 1997.

GAM5346 319 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 B c the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2.

Molec. Cell 8: 351- 361, 2001.

GAM5346 319 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 B c
Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell
97: 503- 514, 1999.

GAM5346 319 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered 3 B c
telomere state, not telomere loss. Science 295: 2446- 2449,2002.

GAM5346 319 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; 3 B c
McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization
of the transcribed human telomere repeat binding factor2 gene and
comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163,
1998.

GAM5346 319 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman 3 B c
telomeres from end- to- end fusions. Cell 92: 401- 413, 1998.

GAM5346 319 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 B c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human
telomeres. Nature Genet. 25: 347- 352, 2000.

GAM5385 218 ATRN Duke- Cohan, J. S.; Gu, J.; McLaughlin, D. F.; Xu, Y.; Freeman,G. J.; 6 A c
Schlossman, S. F.: Attractin (DPPT- L), a member of the CUBfamily of cell
adhesion and guidance proteins, is secreted by activatedhuman T lymphocytes
and modulates immune cell interactions. Proc.Nat. Acad. Sci. 95: 11336-
11341, 1998.

GAM5385 218 ATRN Gunn, T. M.; Miller, K. A.; He, L.; Hyman, R. W.; Davis, R. W.;Azarani, A.; 6 A c
Schlessman, S. F.; Duke- Cohan, J. S.; Barsh, G. S.:The mouse mahogany locus
encodes a transmembrane form of human attractin. Nature 398:152- 156, 1999.

GAM5385 218 ATRN He, L.; Gunn, T. M.; Bouley, D. M.; Lu, X.- Y.; Watson, S. J.; Schlossman,S. 6 A c
F.; Duke- Cohan, J. S.; Barsh, G. S.: A biochemical function forattractin in
agouti- induced pigmentation and obesity. Nature Genet. 27:40- 47, 2001.

GAM5385 218 ATRN Nagle, D. L.; McGrail, S. H.; Vitale, J.; Woolf, E. A.; Dussault,B. J., Jr.; 6 A c
DiRocco, L.; Holmgren, L.; Montagno, J.; Bork, P.; Huszar,D.; Fairchild-
Huntress, V.; Ge, P.; Keilty, J.; Ebelling, C.; Baldini,L.; Gilchrist, J.;
Burr, P.; Carlson, G. A.; Moore, K. J.: The mahoganyprotein is a receptor
involved in suppression of obesity. Nature 398:148- 151, 1999.

GAM5385 218 ATRN Tang, W.; Gunn, T. M.; McLaughlin, D. F.; Barsh, G. S.; Schlossman,S. F.; 6 A c
Duke- Cohan, J. S.: Secreted and membrane attractin resultfrom alternative
splicing of the human ATRN gene. Proc. Nat. Acad.Sci. 97: 6025- 6030, 2000.

GAM5385 218 CISH Uchida, K.; Yoshimura, A.; Inazawa, J.; Yanagisawa, K.; Osada,H.; Masuda, 6 A c
A.; Saito, T.; Takahashi, T.; Miyajima, A.; Takahashi,T.: Molecular cloning
of CISH, chromosome assignment to 3p21.3, andanalysis of expression in fetal
and adult tissues. Cytogenet. CellGenet. 78: 209- 212, 1997.

GAM5385 218 CISH Yoshimura, A.; Ohkubo, T.; Kiguchi, T.; Jenkins, N. A.; Gilbert,D. J.; 6 A c
Copeland, N. G.; Hara, T.; Miyajima, A.: A novel cytokine- inducible gene
CIS, encodes an SH2- containing protein that binds to tyrosine-
phosphorylatedinterleukin 3 and erythropoietin receptors. EMBO J. 14: 2816-
2826,1995.

GAM5385 218 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, 6 A c
D. J.; Muir, W. J.: Schizophrenia and affective disorders- -
cosegretationwith a translocation at chromosome 1q42 that directly disrupts
brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum.
Genet. 69:428- 433, 2001.

GAM5385 218 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 6 A c

355:771- 772, 2000.

GAM5385 218 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 6 A c

GAM5385 218 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 6 A c

GAM5385 218 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000. 6 A c

GAM5385 218 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990. 6 A c

GAM5385 218 EPB49 Azim, A. C.; Knoll, J. H. M.; Beggs, A. H.; Chisti, A. H.: Isoformcloning, actin binding, and chromosomal localization of human erythroiddematin, a member of the villin superfamily. J. Biol. Chem. 270:17407- 17413, 1995. 6 A c

GAM5385 218 EPB49 Azim, A. C.; Marfatia, S. M.; Korsgren, C.; Dotimas, E.; Cohen,C. M.; Chishti, A. H.: Human erythrocyte dematin and protein 4.2(pallidin) are ATP binding proteins. Biochemistry 35: 3001- 3006,1996. 6 A c

GAM5385 218 EPB49 Chishti, A. H.; Faquin, W.; Wu, C.- C.; Branton, D.: Purificationof erythrocyte dematin (protein 4.9) reveals an endogenous proteinkinase that modulates actin- bundling activity. J. Biol. Chem. 264:8985- 8991, 1989. 6 A c

GAM5385 218 EPB49 Gilligan, D. M.; Bennett, V.: The junctional complex of the membraneskeleton. Seminars Hemat. 30: 74- 83, 1993. 6 A c

GAM5385 218 EPB49 Khanna, R.; Chang, S. H.; Andrabi, S.; Azam, M.; Kim, A.; Rivera,A.; Brugnara, C.; Low, P. S.; Liu, S.- C.; Chishti, A. H.: Headpiecedomain of dematin is required for the stability of the erythrocytemembrane. Proc. Nat. Acad. Sci. 99: 6637- 6642, 2002. 6 A c

GAM5385 218 EPB49 Peters, L. L.; Eicher, E. M.; Azim, A. C.; Chishti, A. H.: Thegene encoding the erythrocyte membrane skeleton protein dematin (Epb4.9)maps to mouse chromosome 14. Genomics 26: 634- 635, 1995. 6 A c

GAM5385 218 EPB49 Rana, A. P.; Ruff, P.; Maalouf, G. J.; Speicher, D. W.; Chishti,A. H.: Cloning of human erythroid dematin reveals another memberof the villin family. Proc. Nat. Acad. Sci. 90: 6651- 6655, 1993. 6 A c

GAM5385 218 FBLN1 Argraves, W. S.; Dickerson, K.; Burgess, W. H.; Ruoslahti, E.:Fibulin, a novel protein that interacts with the fibronectin receptor- betasubunit cytoplasmic domain. Cell 58: 623- 629, 1989. 6 A c

GAM5385 218 FBLN1 Korenberg, J. R.; Chen, X.- N.; Tran, H.; Argraves, W. S.: Localizationof the human gene for fibulin- 1 (FBLN1) to chromosome band 22q13.3.Cytogenet. Cell Genet. 68: 192- 193, 1995. 6 A c

GAM5385 218 FBLN1 Mattei, M.- G.; Pan, T.- C.; Zhang, R.- Z.; Timpl, R.; Chu, M.- L.: The fibulin- 1 gene (FBLN1) is located on human chromosome 22 andon mouse chromosome 15. Genomics 22: 437- 438, 1994. 6 A c

GAM5385 218 FCGR1A Maresco, D. L.; Chang, E.; Theil, K. S.; Francke, U.; Anderson,C. L.: The three genes of the human FCGR1 gene family encoding Fc- gamma- RIflank the centromere of chromosome 1 at 1p12 and 1q21. Cytogenet.Cell Genet. 73: 157- 163, 1996. 6 A c

GAM5385 218 FCGR1A Oakey, R. J.; Howard, T. A.; Hogarth, P. M.; Tani, K.; Seldin,M. F.: 6 A c
Chromosomal mapping of the high affinity Fc- gamma receptorgene.
Immunogenetics 35: 279- 282, 1992.

GAM5385 218 FCGR1A Osman, N.; Kozak, C. A.; McKenzie, I. F. C.; Hogarth, P. M.: Structureand 6 A c
mapping of the gene encoding mouse high affinity Fc- gamma- RI
andchromosomal location of the human Fc- gamma- RI gene. J. Immun. 148:1570-
1575, 1992.

GAM5385 218 FCGR1A Pearse, R. N.; Feinman, R.; Ravetch, J. V.: Characterization ofthe promoter 6 A c
of the human gene encoding the high- affinity IgG receptor:transcriptional
induction by gamma- interferon is mediated throughcommon DNA response
elements. Proc. Nat. Acad. Sci. 88: 11305- 11309,1991.

GAM5385 218 FCGR1A Takai, S.; Kasama, M.; Yamada, K.; Kai, N.; Hirayama, N.; Namiki,H.; 6 A c
Taniyama, T.: Human high- affinity Fc- gamma- RI (CD64) gene mappedto
chromosome 1q21.2- q21.3 by fluorescence in situ hybridization. Hum.Genet.
93: 13- 15, 1994.

GAM5385 218 FCGR1A van de Winkel, J. G. J.; de Wit, T. P. M.; Ernst, L. K.; Capel,P. J. A.; 6 A c
Ceuppens, J. L.: Molecular basis for a familial defectin phagocyte
expression of IgG receptor I (CD64). J. Immun. 154:2896- 2903, 1995.

GAM5385 218 GRHPR Cramer, S. D.; Ferree, P. M.; Lin, K.; Milliner, D. S.; Holmes,R. P.: The 6 A c
gene encoding hydroxypyruvate reductase (GRHPR) is mutatedin patients with
primary hyperoxaluria type II. Hum. Molec. Genet. 8:2063- 2069, 1999.

GAM5385 218 GRHPR Rumsby, G.; Cregeen, D. P.: Identification and expression of acDNA for human 6 A c
hydroxypyruvate/glyoxylate reductase. Biochim. Biophys.Acta 1446: 383- 388,
1999.

GAM5385 218 GRHPR Webster, K. E.; Ferree, P. M.; Holmes, R. P.; Cramer, S. D.: 6 A c
Identificationof missense, nonsense, and deletion mutations in the GRHPR
gene inpatients with primary hyperoxaluria type II (PH2). Hum. Genet.
107:176- 185, 2000.

GAM5385 218 HLA-G Bodmer, J. G.; Marsh, S. G. E.; Albert, E.: Nomenclature for factorsof the 6 A c
HLA system, 1989. Immun. Today 11: 3- 10, 1990.

GAM5385 218 HLA-G Ellis, S. A.; Palmer, M. S.; McMichael, A. J.: Human trophoblastand the 6 A c
choriocarcinoma cell line BeWo express a truncated HLA classI molecule. J.
Immun. 144: 731- 735, 1990.

GAM5385 218 HLA-G Geraghty, D. E.; Koller, B. H.; Orr, H. T.: A human major 6 A c
histocompatibilitycomplex class I gene that encodes a protein with a
shortened cytoplasmicsegment. Proc. Nat. Acad. Sci. 84: 9145- 9149, 1987.

GAM5385 218 HLA-G Geraghty, D. E.; Pei, J.; Lipsky, B.; Hansen, J. A.; Taillon- Miller,P.; 6 A c
Bronson, S. K.; Chaplin, D. D.: Cloning and physical mappingof the HLA class
I region spanning the HLA- E- to- HLA- F interval byusing yeast artificial
chromosomes. Proc. Nat. Acad. Sci. 89: 2669- 2673,1992.

GAM5385 218 HLA-G Hurks, H. M. H.; Valter, M. M.; Wilson, L.; Hilgert, I.; van denElsen, P. 6 A c
J.; Jager, M. J.: Uveal melanoma: no expression of HLA- G. Invest.Ophthal.
Vis. Sci. 42: 3081- 3084, 2001.

GAM5385 218 HLA-G Kirszenbaum, M.; Moreau, P.; Gluckman, E.; Dausset, J.; Carosella,E.: An 6 A c
alternatively spliced form of HLA- G mRNA in human trophoblastsand evidence
for the presence of HLA- G transcript in adult lymphocytes. Proc.Nat. Acad.
Sci. 91: 4209- 4213, 1994.

GAM5385 218 HLA-G Lila, N.; Carpentier, A.; Amrein, C.; Khalil- Daher, I.; Dausset,J.; 6 A c
Carosella, E. D.: Implication of HLA- G molecule in heart- graftacceptance.
Lancet 355: 2138 only, 2000.

GAM5385 218 HLA-G McAlpine, P. J.: Personal Communication. Winnipeg, Manitoba,Canada 6 A c 6/22/1988.

GAM5385 218 HLA-G Morales, P.; Corell, A.; Martinez- Laso, J.; Martin- Villa, J. M.;Varela, P.; Paz- Artal, E.; Allende, L.- M.; Arnaiz- Villena, A.: Threenew HLA- G alleles and their linkage disequilibria with HLA- A. Immunogenetics 38:323-331, 1993. 6 A c

GAM5385 218 HLA-G Onno, M.; Guillaudeux, T.; Amiot, L.; Renard, I.; Drenou, B.;Hirel, B.; Girr, M.; Semana, G.; Le Bouteiller, P.; Fauchet, R.:The HLA- G gene is expressed at a low mRNA level in different humancells and tissues. Human Immun. 41: 79- 86, 1994. 6 A c

GAM5385 218 HLA-G Paul, P.; Rouas- Freiss, N.; Khalil- Daher, I.; Moreau, P.; Riteau,B.; Le Gal, F. A.; Avril, M. F.; Dausset, J.; Guillet, J. G.; Carosella,E. D.: HLA-G expression in melanoma: a way for tumor cells to escapefrom immunosurveillance. Proc. Nat. Acad. Sci. 95: 4510- 4515, 1998. 6 A c

GAM5385 218 HLA-G Rodriguez de Cordoba, S.; Lublin, D. M.; Rubinstein, P.; Atkinson,J. P.: Human genes for three complement components that regulatethe activation of C3 are tightly linked. J. Exp. Med. 161: 1189- 1195,1985. 6 A c

GAM5385 218 HLA-G Rouas- Freiss, N.; Marchal, R. E.; Kirszenbaum, M.; Dausset, J.;Carosella, E. D.: The alpha1 domain of HLA- G1 and HLA- G2 inhibitscytotoxicity induced by natural killer cells: is HLA- G the publicligand for natural killer cell inhibitory receptors? Proc. Nat. Acad.Sci. 94: 5249- 5254, 1997. 6 A c

GAM5385 218 HLA-G Schmidt, C. M.; Orr, H. T.: A physical linkage map of HLA- A,- G, - 7.5p, and - F. Hum. Immun. 31: 180- 185, 1991. 6 A c

GAM5385 218 HLA-G Van Leeuwen, A.: Di- allelic allo- antigenic systems on human T-lymphocytesubsets. Thesis: London Hospital Medical College (pub.) 1982. 6 A c

GAM5385 218 HLA-G Walker, I. D.; Sandrin, M. S.; Hogarth, P. M.; Sutton, V. R.;McKenzie, I. F. C.: Expression of Qa alloantigens on peripheral Tcells: the relationship of the Qa- m2, 7, 8, 9 specificities. Immunogenetics 24:90- 94, 1986. 6 A c

GAM5385 218 HLA-G Yokoyama, W. M.: The mother- child union: the case of missing- selfand protection of the fetus. Proc. Nat. Acad. Sci. 94: 5998- 6000,1997. 6 A c

GAM5385 218 ITGAL Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P. G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome 16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991. 6 A c

GAM5385 218 ITGAL Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. C.: Chromosomal location of the genes encoding the leukocyteadhesion receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988. 6 A c

GAM5385 218 ITGAL Fischer, A.; Durandy, A.; Sterkers, G.; Griscelli, C.: Role ofthe LFA- 1 molecule in cellular interactions required for antibodyproduction in humans. J. Immun. 136: 3198- 3203, 1986. 6 A c

GAM5385 218 ITGAL Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cell retentionin the splenic marginal zone. Science 297: 409- 412, 2002. 6 A c

GAM5385 218 ITGAL Marlin, S. D.; Morton, C. C.; Anderson, D. C.; Springer, T. A.: LFA- 1 immunodeficiency disease: definition of the genetic defectand chromosomal mapping of alpha and beta subunits of the lymphocytefunction- associated antigen 1 (LFA- 1) by complementation in hybridcells. J. Exp. Med. 164: 855-867, 1986. 6 A c

GAM5385 218 ITGAL Pischel, K. D.; Marlin, S. D.; Springer, T. A.; Woods, V. L., Jr.;Bluestein, H. G.: Polymorphism of lymphocyte function- associatedantigen- 1 6 A c

demonstrated by a lupus patient's alloantiserum. J. Clin.Invest. 79: 1607-1614, 1987.

GAM5385 218 ITGAL Sanchez- Madrid, F.; Nagy, J.; Robbins, E.; Simon, P.; Springer,T. A.: A human leukocyte differentiation antigen family with distinctalpha subunits and a common beta subunit: the lymphocyte function- associatedantigen (LFA-1), the C3bi complement receptor (OKM1/Mac- 1), and thep150,95 molecule. J. Exp. Med. 158: 1785- 1803, 1983. 6 A c

GAM5385 218 LMO4 Arber, S.; Halder, G.; Caroni, P.: Muscle LIM protein, a novelessential regulator of myogenesis, promotes myogenic differentiation. Cell 79:221-231, 1994. 6 A c

GAM5385 218 LMO4 Fung, Y. W.; Wang, R. X.; Heng, H. H. Q.; Liew, C. C.: Mappingof a human LIM protein (CLP) to human chromosome 11p15.1 by fluorescencein situ hybridization. Genomics 28: 602- 603, 1995. 6 A c

GAM5385 218 LMO4 Weiskirchen, R.; Pino, J. D.; Macalma, T.; Bister, K.; Beckerle,M. C.: The cysteine- rich protein family of highly related LIM domainproteins. J. Biol. Chem. 270: 28946- 28954, 1995. 6 A c

GAM5385 218 MEF2B Hobson, G. M.; Krahe, R.; Garcia, E.; Siciliano, M. J.; Funanage,V. L.: Regional chromosomal assignments for four members of the MADSdomain transcription enhancer factor 2 (MEF2) gene family to humanchromosomes 15q26, 19p12, 5q14, and 1q12- q23. Genomics 29: 704- 711,1995. 6 A c

GAM5385 218 MEF2B Pollock, R.; Treisman, R.: Human SRF- related proteins: DNA-bindingproperties and potential regulatory targets. Genes Dev. 5: 2327-2341,1991. 6 A c

GAM5385 218 MEF2B Youn, H.- D.; Sun, L.; Prywes, R.; Liu, J. O.: Apoptosis of T cellsmediated by Ca(2+)- induced release of the transcription factor MEF2. Science 286:790- 793, 1999. 6 A c

GAM5385 218 MEF2B Yu, Y.- T.; Breitbart, R. E.; Smoot, L. B.; Lee, Y.; Mahdavi, V.;Nadal-Ginard, B.: Human myocyte- specific enhancer factor 2 comprisesa group of tissue- restricted MADS box transcription factors. GenesDev. 6: 1783- 1798, 1992. 6 A c

GAM5385 218 NR2F2 Ladias, J. A. A.; Karathanasis, S. K.: Regulation of the apolipoproteinAI gene by ARP- 1, a novel member of the steroid receptor superfamily. Science 251:561- 565, 1991. 6 A c

GAM5385 218 NR2F2 Modi, W. S.; Seuanez, H.; Mietus- Snyder, M.; O'Brien, S. J.; Karathanasis,S. K.: Chromosomal localization of the ARP- 1 gene to 15q26. (Abstract) Cytogenet.Cell Genet. 58: 1995 only, 1991. 6 A c

GAM5385 218 NR2F2 Pereira, F. A.; Qiu, Y.; Zhou, G.; Tsai, M.- J.; Tsai, S. Y.: Theorphan nuclear receptor COUP- TFII is required for angiogenesis andheart development. Genes Dev. 13: 1037- 1049, 1999. 6 A c

GAM5385 218 NR2F2 Qiu, Y.; Krishnan, V.; Zeng, Z.; Gilbert, D. J.; Copeland, N. G.;Gibson, L.; Yang- Feng, T.; Jenkins, N. A.; Tsai, M.- J.; Tsai, S. Y.: Isolation, characterization, and chromosomal localization of mouseand human COUP- TF I and II genes. Genomics 29: 240- 246, 1995. 6 A c

GAM5385 218 NR2F2 Widom, R. L.; Ladias, J. A. A.; Kouidou, S.; Karathanasis, S. K.: Synergistic interactions between transcription factors control expressionof the apolipoprotein AI gene in liver cells. Molec. Cell. Biol. 11:677- 687, 1991. 6 A c

GAM5385 218 PAX7 Barr, F. G.; Nauta, L. E.; Davis, R. J.; Schafer, B. W.; Nycum,L. M.; Biegel, J. A.: In vivo amplification of the PAX3- FKHR andPAX7- FKHR fusion genes in alveolar rhabdomyosarcoma. Hum. Molec.Genet. 5: 15- 21, 1996. 6 A c

GAM5385 218 PAX7 Burri, M.; Tromvoukis, Y.; Bopp, D.; Frigerio, G.; Noll, M.: Conservationof 6 A c
the paired domain in metazoans and its structure in three isolatedhuman
genes. EMBO J. 8: 1183- 1190, 1989.
GAM5385 218 PAX7 Gruss, P.; Walther, C.: Pax in development. Cell 69: 719- 722,1992. 6 A c
GAM5385 218 PAX7 Pilz, A. J.; Povey, S.; Gruss, P.; Abbott, C. M.: Mapping of thehuman 6 A c
homologs of the murine paired- box- containing genes. MammalianGenome 4: 78-
82, 1993.
GAM5385 218 PAX7 Schafer, B. W.; Mattei, M. G.: The human paired domain gene PAX7(Hup1) maps 6 A
c
to chromosome 1p35- 1p36.2. Genomics 17: 249- 251, 1993.
GAM5385 218 PAX7 Seale, P.; Sabourin, L. A.; Girgis- Gabardo, A.; Mansouri, A.; Gruss,P.; 6 A c
Rudnicki, M. A.: Pax7 is required for the specification of myogenicsatellite
cells. Cell 102: 777- 786, 2000.
GAM5385 218 PAX7 Shapiro, D. N.; Sublett, J. E.; Li, B.; Valentine, M. B.; Morris,S. W.; 6 A c
Noll, M.: The gene for PAX7, a member of the paired- box- containinggenes,
is localized on human chromosome arm 1p36. Genomics 17: 767- 769,1993.
GAM5385 218 PAX7 Stapleton, P.; Weith, A.; Urbanek, P.; Kozmik, Z.; Busslinger,M.: 6 A c
Chromosomal localization of seven PAX genes and cloning of anovel family
member, PAX- 9. Nature Genet. 3: 292- 298, 1993.
GAM5385 218 PAX7 Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: 6 A c
Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes
Cancer 5: 299- 310, 1992.
GAM5385 218 RASD1 Fang, M.; Jaffrey, S. R.; Sawa, A.; Ye, K.; Luo, X.; Snyder, S.H.: Dexras1: 6 A c
a G protein specifically coupled to neuronal nitricoxide synthase via CAPON.
Neuron 28: 183- 193, 2000.
GAM5385 218 RASD1 Kemppainen, R. J.; Behrend, E. N.: Dexamethasone rapidly inducesa novel Ras 6 A c
superfamily member- related gene in AtT- 20 cells. J. Biol.Chem. 273: 3129-
3131, 1998.
GAM5385 218 RASD1 Tu, Y.; Wu, C.: Cloning, expression and characterization of anovel human 6 A c
Ras- related protein that is regulated by glucocorticoidhormone. Biochim.
Biophys. Acta 1489: 452- 456, 1999.
GAM5385 218 RGS2 Akazawa, K.; Yamane, S.; Shiota, H.; Naito, E.: A case of 6 A c
retinoblastomaassociated with Rieger's anomaly and 13q deletion. Jpn. J.
Ophthal. 25:321- 325, 1981.
GAM5385 218 RGS2 Legius, E.; de Die- Smulders, C. E. M.; Verbraak, F.; Habex, H.;Decorte, R.; 6 A c
Marynen, P.; Fryns, J. P.; Cassiman, J. J.: Geneticheterogeneity in Rieger
eye malformation. J. Med. Genet. 31: 340- 341,1994.
GAM5385 218 RGS2 Phillips, J. C.; Del Bono, E. A.; Haines, J. L.; Pralea, A. M.;Cohen, J. S.; 6 A c
Greff, L. J.; Wiggs, J. L.: A second locus for Riegersyndrome maps to
chromosome 13q14. Am. J. Hum. Genet. 59: 613- 619,1996.
GAM5385 218 RGS2 Siderovski, D. P.; Blum, S.; Forsdyke, R. E.; Forsdyke, D. R.:A set of human 6 A c
putative lymphocyte G0/G1 switch genes includes geneshomologous to rodent
cytokine and zinc finger protein- encoding genes. DNACell Biol. 9: 579- 587,
1990.
GAM5385 218 RGS2 Siderovski, D. P.; Heximer, S. P.; Forsdyke, D. R.: A human geneencoding a 6 A c
putative basic helix- loop- helix phosphoprotein whose mRNAincreases rapidly
in cycloheximide- treated blood mononuclear cells. DNACell Biol. 13: 125-
147, 1994.
GAM5385 218 RGS2 Sinnarajah, S.; Dessauer, C. W.; Srikumar, D.; Chen, J.; Yuen,J.; Yilma, S.; 6 A c

Dennis, J. C.; Morrison, E. E.; Vodyanoy, V.; Kehrl,J. H.: RGS2 regulates signal transduction in olfactory neurons byattenuating activation of adenylyl cyclase III. Nature 409: 1051- 1055,2001.

GAM5385 218 RGS2 Stathacopoulos, R. A.; Bateman, J. B.; Sparkes, R. S.; Hepler,R. S.: The Rieger syndrome and a chromosome 13 deletion. J. Pediat.Ophthal. Strabismus 24: 198- 203, 1987. 6 A c

GAM5385 218 RGS2 Wu, H.- K.; Heng, H. H. Q.; Shi, X.- M.; Forsdyke, D. R.; Tsui, L.- C.;Mak, T. W.; Minden, M. D.; Siderovski, D. P.: Differential expressionof a basic helix- loop- helix phosphoprotein gene, G0S8, in acute leukemiaand localization to human chromosome 1q31. Leukemia 9: 1291- 1298,1995. 6 A c

GAM5385 218 SCAMP3 Singleton, D. R.; Wu, T. T.; Castle, J. D.: Three mammalian SCAMPs(secretory carrier membrane proteins) are highly related productsof distinct genes having similar subcellular distributions. J. CellSci. 110: 2099- 2107, 1997. 6 A c

GAM5385 218 SCAMP3 Winfield, S. L.; Tayebi, N.; Martin, B. M.; Ginns, E. I.; Sidransky,E.: Identification of three additional genes contiguous to the glucocerebrosidaselocus on chromosome 1q21: implications for Gaucher disease. GenomeRes. 7: 1020- 1026, 1997. 6 A c

GAM5385 218 UBL3 Chadwick, B. P.; Kidd, T.; Sgouros, J.; Ish- Horowicz, D.; Frischauf,A.- M.: Cloning, mapping and expression of UBL3, a novel ubiquitin- likegene. Gene 233: 189- 195, 1999. 6 A c

GAM5385 218 UBL3 Hodges, M.; Tissot, C.; Freemont, P. S. Protein regulation:tag wrestling with relatives of ubiquitin. Curr. Biol. 8: R749- R752,1998. 6 A c

GAM5385 218 XT3 Nash, S. R.; Giros, B.; Kingsmore, S. F.; Kim, K. M.; El- Mestikawy,S.; Dong, Q.; Fumagalli, F.; Seldin, M. F.; Caron, M. G.: Cloning,gene structure and genomic localization of an orphan transporter frommouse kidney with six alternatively- spliced isoforms. Receptors Channels 6:113- 128, 1998. 6 A c

GAM5385 218 XT3 Scott, A. F.: Personal Communication. Baltimore, Md. 2/5/2001. 6 A c

GAM7052 296 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989. 3 C c

GAM7052 296 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989. 3 C c

GAM7052 296 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987. 3 C c

GAM7052 296 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986. 3 C c

GAM7052 296 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988. 3 C c

GAM7052 296 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999. 3 C c

GAM7052 296 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human 3 C c

genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM7052 296 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM 3 C c protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999.

GAM7052 296 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664- 1666, 1999. 3 C c

GAM7052 296 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 3 C c

GAM7052 296 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994. 3 C c

GAM7052 296 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: Chromosomal mapping of human adenylyl cyclase genestype III, type V and type VI. Hum. Genet. 94: 69- 73, 1994. 3 C c

GAM7052 296 AGTPBP1 Fernandez- Gonzalez, A.; La Spada, A. R.; Treadaway, J.; Higdon,J. C.; Harris, B. S.; Sidman, R. L.; Morgan, J. I.; Zuo, J.: Purkinjecell degeneration (pcd) phenotypes caused by mutations in the axotomy- inducedgene, Nna1. Science 295: 1904- 1906, 2002. 3 C c

GAM7052 296 AGTPBP1 Harris, A.; Morgan, J. I.; Pecot, M.; Soumare, A.; Osborne, A.;Soares, H. D.: Regenerating motor neurons express Nna1, a novel ATP/GTP- bindingprotein related to zinc carboxypeptidases. Molec. Cell. Neurosci. 16:578- 596, 2000. 3 C c

GAM7052 296 AGTPBP1 Kikuno, R.; Nagase, T.; Ishikawa, K.; Hirosawa, M.; Miyajima, N.;Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of unidentified human genes. XIV. The complete sequencesof 100 new cDNA clones from brain which code for large proteins invitro. DNA Res. 6: 197- 205, 1999. 3 C c

GAM7052 296 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89: 3962- 3966,1992. 3 C c

GAM7052 296 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat. Acad. Sci. 96: 4378- 4383, 1999. 3 C c

GAM7052 296 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988. 3 C c

GAM7052 296 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990. 3 C c

GAM7052 296 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 C c

GAM7052 296 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding 3 C c

sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996.

GAM7052 296 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule- 3 C c interacting protein, recognizes the basolateral sortingsignal of amyloid precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998.

GAM7052 296 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene 3 C c structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996.

GAM7052 296 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem 3 C c arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997.

GAM7052 296 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: 3 C c an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999.

GAM7052 296 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, 3 C c A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and Drosophila. Genomics 26: 101- 106, 1995.

GAM7052 296 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer 3 C c protein delta- COP, encoded by the archain gene, is conservedacross diverse eukaryotes. Mammalian Genome 7: 784- 786, 1996.

GAM7052 296 CACNG6 Burgess, D. L.; Gefrides, L. A.; Foreman, P. J.; Noebels, J. L.: A cluster 3 C c of three novel Ca(2+) channel gamma subunit genes on chromosome19q13.4: evolution and expression profile of the gamma subunit genefamily. Genomics 71: 339- 350, 2001.

GAM7052 296 CACNG6 Chu, P.- J.; Robertson, H. M.; Best, P. M.: Calcium channel gammasubunits 3 C c provide insights into the evolution of this gene family. Gene 280:37- 48, 2001.

GAM7052 296 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 C c cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM7052 296 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 C c Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG) is located on human chromosome 5q23 and a syntenicregion of mouse chromosome 13. Genomics 31: 257- 260, 1996.

GAM7052 296 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a 3 C c member of a multigene family. Genomics 52: 332- 341, 1998.

GAM7052 296 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a 3 C c new member of the MTG8/ETO gene family, maps on 20q11region and is deleted in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998.

GAM7052 296 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; 3 C c Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic fusion protein forms a complex with a novel member of theMTG8(ETO/CDR) family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998.

GAM7052 296 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. 3 C c J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis machinery through a novel motif, the F- box. Cell 86:263- 274, 1996.

GAM7052 296 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; 3 C c Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene (CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics

24:27- 33, 1994.

GAM7052 296 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F 3 C c
maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6:
149- 150, 1995.

GAM7052 296 CDC6 Saha, P.; Chen, J.; Thome, K. C.; Lawlis, S. J.; Hou, Z.- H.; Hendricks,M.; 3 C c
Parvin, J. D.; Dutta, A.: Human CDC6/Cdc18 associates with Orc1and cyclin-
cdk and is selectively eliminated from the nucleus at theonset of S phase.
Molec. Cell. Biol. 18: 2758- 2767, 1998.

GAM7052 296 CDC6 Williams, R. S.; Shohet, R. V.; Stillman, B.: A human proteinrelated to 3 C c
yeast Cdc6p. Proc. Nat. Acad. Sci. 94: 142- 147, 1997.

GAM7052 296 CDC6 Yan, Z.; DeGregori, J.; Shohet, R.; Leone, G.; Stillman, B.; Nevins,J. R.; 3 C c
Williams, R. S.: Cdc6 is regulated by E2F and is essentialfor DNA
replication in mammalian cells. Proc. Nat. Acad. Sci. 95:3603- 3608, 1998.

GAM7052 296 CDC6 Yan, Z.; Fedorov, S. A.; Mumby, M. C.; Williams, R. S.: PR48,a novel 3 C c
regulatory subunit of protein phosphatase 2A, interacts withCdc6 and
modulates DNA replication in human cells. Molec. Cell. Biol. 20:1021- 1029,
2000.

GAM7052 296 CDH11 Hoffman, I.; Balling, R.: Chromosomal localization of the murinecadherin- 3 C c
11. Mammalian Genome 6: 304 only, 1995.

GAM7052 296 CDH11 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, 3 C c
D. F.: Localization of human cadherin genes to chromosomeregions exhibiting
cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998.

GAM7052 296 CDH11 Okazaki, M.; Takeshita, S.; Kawai, S.; Kikuno, R.; Tsujimura, A.;Kudo, A.; 3 C c
Amann, E.: Molecular cloning and characterization of OB- cadherin,a new
member of cadherin family expressed in osteoblasts. J. Biol.Chem. 269:
12092- 12098, 1994.

GAM7052 296 CDH11 Tanihara, H.; Sano, K.; Heimark, R. L.; St. John, T.; Suzuki, S.: Cloning of 3 C c
five human cadherins clarifies characteristic featuresof cadherin
extracellular domain and provides further evidence fortwo structurally
different types of cadherin. Cell Adhes. Commun. 2:15- 26, 1994.

GAM7052 296 CHRNB4 Elliott, K. J.; Ellis, S. B.; Berckhan, K. J.; Urrutia, A.; Chavez- 3 C c
Noriega,L. E.; Johnson, E. C.; Velicelebi, G.; Harpold, M. M.:
Comparativestructure of human neuronal alpha(2)- alpha(7) and beta(2)-
beta(4)nicotinic acetylcholine receptor subunits and functional expressionof
the alpha(2), alpha(3), alpha(4), alpha(7), beta(2), and beta(4)subunits. J.
Molec. Neurosci. 7: 217- 228, 1996.

GAM7052 296 CHRNB4 Groot Kormelink, P. J.; Luyten, W. H. M. L.: Cloning and sequenceof full- 3 C c
length cDNAs encoding the human neuronal nicotinic acetylcholinereceptor
(nAChR) subunits beta- 3 and beta- 4 and expression of sevennAChR subunits
in the human neuroblastoma cell line SH- SY5Y and/orIMR- 32. FEBS Lett. 400:
309- 314, 1997.

GAM7052 296 CHRNB4 Khakh, B. S.; Zhou, X.; Sydes, J.; Galligan, J. J.; Lester, H.A.: State- 3 C c
dependent cross- inhibition between transmitter- gated cationchannels.
Nature 406: 405- 410, 2000.

GAM7052 296 CHRNB4 Raimondi, E.; Rubboli, F.; Moralli, D.; Chini, B.; Fornasari, D.;Tarroni, 3 C c
P.; De Carli, L.; Clementi, F.: Chromosomal localizationand physical linkage
of the genes encoding the human alpha- 3, alpha- 5,and beta- 4 neuronal
nicotinic receptor subunits. Genomics 12: 849- 850,1992.

GAM7052 296 CHRNB4 Tarroni, P.; Rubboli, F.; Chini, B.; Zwart, R.; Oortgiesen, M.;Sher, E.; 3 C c
Clementi, F.: Neuronal- type nicotinic receptors in humanneuroblastoma and

small- cell lung carcinoma cell lines. FEBS Lett. 312:66- 70, 1992.

GAM7052 296 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, 3 C c
G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.;
Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.;
Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for
Muckle- Wells syndrome and familial cold urticaria:a novel mutation
underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002.

GAM7052 296 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, 3 C c
E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile
neurological cutaneous and articular syndromeis caused by mutations in
CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes.
Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM7052 296 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. 3 C c
D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes
familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature
Genet. 29: 301- 305, 2001.

GAM7052 296 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- 3 C c
H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu,
S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes
expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed
sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci.
95: 8175- 8180, 1998.

GAM7052 296 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, 3 C c
T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.:
Identification of a novel, dendritic cell- associated molecule,dectin- 1, by
subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000.

GAM7052 296 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 3 C c
37, 2001.

GAM7052 296 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: 3 C c
Cloning of human dectin- 1, a novel C- type lectin- like receptorgene
expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001.

GAM7052 296 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification 3 C c
of a human homologue of the dendritic cell- associatedC- type lectin- 1,
dectin- 1. Gene 272: 51- 60, 2001.

GAM7052 296 CRSP6 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, 3 C c
Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC
complexes indicates novel pathways for the functionof nuclear receptors and
diverse mammalian activators. Molec. Cell 3:361- 370, 1999.

GAM7052 296 CRSP6 Jiang, Y.- W.; Veschambre, P.; Erdjument- Bromage, H.; Tempst, P.;Conaway, 3 C c
J. W.; Conaway, R. C.; Kornberg, R. D.: Mammalian mediatorof transcriptional
regulation and its possible role as an end- pointof signal transduction
pathways. Proc. Nat. Acad. Sci. 95: 8538- 8543,1998.

GAM7052 296 CRSP6 Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R.: The transcriptionalcofactor 3 C c
complex CRSP is required for activity of the enhancer- bindingprotein Sp1.
Nature 397: 446- 450, 1999.

GAM7052 296 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, 3 C c
J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal
localization and evidence for alternative splicing. NucleicAcids Res. 16:
5783- 5795, 1988.

GAM7052 296 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major 3 C c

phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988.

GAM7052 296 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. 3 C c
Lancet 355: 979- 983, 2000.

GAM7052 296 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; 3 C c
Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996.

GAM7052 296 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; 3 C c
Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999.

GAM7052 296 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 3 C c
12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4- alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001.

GAM7052 296 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; 3 C c
Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000.

GAM7052 296 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 3 C c
40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461- 8466, 1998.

GAM7052 296 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that 3 C c
functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997.

GAM7052 296 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, 3 C c
S.: Molecular cloning and characterization of human caspase- activatedDNase. Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998.

GAM7052 296 DLST Ali, G.; Wasco, W.; Cai, X.; Szabo, P.; Sheu, K.- F. R.; Cooper,A. J. L.; 3 C c
Gaston, S. M.; Gusella, J. F.; Tanzi, R. E.; Blass, J. P.: Isolation, characterization, and mapping of gene encoding dihydrolipoylsuccinyltransferase (E2k) of human alpha- ketoglutarate dehydrogenasecomplex. Somat. Cell Molec. Genet. 20: 99- 105, 1994.

GAM7052 296 DLST Nakano, K.; Matuda, S.; Sakamoto, T.; Takase, C.; Nakagawa, S.;Ohta, S.; 3 C c
Ariyama, T.; Inazawa, J.; Abe, T.; Miyata, T.: Human dihydrolipoamidesuccinyltransferase: cDNA cloning and localization on chromosome 14q24.2- q24.3.Biochim. Biophys. Acta 1216: 360- 368, 1993.

GAM7052 296 DLST Nakano, K.; Takase, C.; Sakamoto, T.; Ohta, S.; Nakagawa, S.; Ariyama,T.; 3 C c
Inazawa, J.; Abe, T.; Matuda, S.: An unspliced cDNA for humandihydrolipoamide succinyltransferase: characterization and mappingof the gene to chromosome 14q24.2- q24.3. Biochem. Biophys. Res.Commun. 196: 527- 533, 1993.

GAM7052 296 DLST Patel, M. S.; Harris, R. A.: Mammalian alpha- keto acid 3 C c
dehydrogenasecomplexes: gene regulation and genetic defects. FASEB J. 9: 1164- 1172,1995.

GAM7052 296 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, 3 C c
T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and

desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995.

GAM7052 296 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, 3 C c
H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin.
J. Biol. Chem. 269: 26295- 26302, 1994.

GAM7052 296 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The 3 C c
desmocollins of human foreskin epidermis: identification and
chromosomalassignment of a third gene and expression patterns of the three
isoforms. J.Invest. Derm. 105: 314- 321, 1995.

GAM7052 296 DYRK1A Altafaj, X.; Dierssen, M.; Baamonde, C.; Marti, E.; Visa, J.; Guimera,J.; 3 C c
Oset, M.; Gonzalez, J. R.; Florez, J.; Fillat, C.; Estivill, X.:
Neurodevelopmental delay, motor abnormalities and cognitive deficitsin
transgenic mice overexpressing Dyrk1A (minibrain), a murine modelof Down's
syndrome. Hum. Molec. Genet. 10: 1915- 1923, 2001.

GAM7052 296 DYRK1A Chen, H.; Antonarakis, S. E.: Localisation of a human homologueof the 3 C c
Drosophila mnb and rat Dyrk genes to chromosome 21q22.2. Hum.Genet. 99: 262-
265, 1997.

GAM7052 296 DYRK1A Patil, N.; Cox, D. R.; Bhat, D.; Faham, M.; Myers, R. M.; Peterson,A. S.: A 3 C c
potassium channel mutation in weaver mice implicates membraneexcitability in
granule cell differentiation. Nature Genet. 11:126- 129, 1995.

GAM7052 296 DYRK1A Shindoh, N.; Kudoh, J.; Maeda, H.; Yamaki, A.; Minoshima, S.; Shimizu,Y.; 3 C c
Shimizu, N.: Cloning of a human homolog of the Drosophila minibrain/ratDyrk
gene from 'the Down syndrome critical region' of chromosome 21.
Biochem.Biophys. Res. Commun. 225: 92- 99, 1996.

GAM7052 296 DYRK1A Smith, D. J.; Stevens, M. E.; Sudanagunta, S. P.; Bronson, R. T.;Makhinson, 3 C c
M.; Watabe, A. M.; O'Dell, T. J.; Fung, J.; Weier, H.- U.G.; Cheng, J.- F.;
Rubin, E. M.: Functional screening of 2 Mb of humanchromosome 21q22.2 in
transgenic mice implicates minibrain in learningdefects associated with Down
syndrome. Nature Genet. 16: 28- 36,1997.

GAM7052 296 DYRK1A Song, W.- J.; Chung, S.- H.; Kurnit, D. M.: The murine Dyrk proteinmaps to 3 C c
chromosome 16, localizes to the nucleus, and can form multimers.
Biochem.Biophys. Res. Commun. 231: 640- 644, 1997.

GAM7052 296 DYRK1A Song, W.- J.; Sternberg, L. R.; Kasten- Sportes, C.; Van Keuren,M. L.; 3 C c
Chung, S.- H.; Slack, A. C.; Miller, D. E.; Glover, T. W.; Chiang,P.- W.;
Lou, L.; Kurnit, D. M.: Isolation of human and murine homologuesof the
Drosophila minibrain gene: human homologue maps to 21q22.2in the Down
syndrome 'critical region.' Genomics 38: 331- 339, 1996.

GAM7052 296 DYRK1A Tejedor, F.; Zhu, X. R.; Kaltenbach, E.; Ackermann, A.; Baumann,A.; Canal, 3 C c
I.; Heisenberg, M.; Fischbach, K. F.; Pongs, O.: Minibrain:a new protein
kinase family involved in postembryonic neurogenesisin Drosophila. Neuron
14: 287- 301, 1995.

GAM7052 296 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- 3 C b
elongationfactor 2 kinase (calmodulin- dependent protein kinase III)
antibodiesin patients with systemic lupus erythematosus. Biochem.
Biophys.Res. Commun. 293: 1073- 1076, 2002.

GAM7052 296 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 3 C b
Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C.
R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein
kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat.
Acad. Sci. 94: 4884- 4889, 1997.

GAM7052 296 F2RL2 Duperat, V. G.; Jacquelin, B.; Boisseau, P.; Arveiler, B.; Nurden,A. T.: 3 C c
Protease- activated receptor genes are clustered on 5q13. Blood 92:25- 31,
1998.

GAM7052 296 F2RL2 Ishihara, H.; Connolly, A. J.; Zeng, D.; Kahn, M. L.; Zheng, Y.W.; Timmons, 3 C c
C.; Tram, T.; Coughlin, S. R.: Protease- activated receptor3 is a second
thrombin receptor in humans. Nature 386: 502- 506,1997.

GAM7052 296 F2RL2 Kahn, M. L.; Zheng, Y. W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 C c
Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system
for platelet activation. Nature 394: 690- 694, 1998.

GAM7052 296 F2RL2 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 C c
M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin.
Nature 404: 609- 613, 2000.

GAM7052 296 F2RL2 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 C c
Role of thrombin signalling in platelets in haemostasis andthrombosis.
Nature 413: 74- 78, 2001.

GAM7052 296 F2RL2 Schmidt, V.; Wainer, J.; Bahou, W.: Identification and characterizationof 3 C c
the human proteolytically activated receptor- 3 (PAR- 3) gene withinthe PAR
gene cluster by positional mapping. (Abstract) Blood (suppl.1) 90: 284a
only, 1997.

GAM7052 296 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for 3 C c
tissue factor (coagulation factor III) is localized onhuman chromosome
1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985.

GAM7052 296 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to 3 C c
human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985.

GAM7052 296 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional 3 C c
assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat.
Cell Molec. Genet. 14: 407- 410, 1988.

GAM7052 296 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional 3 C c
analysis of the human tissue factor promoter and inductionby serum. Proc.
Nat. Acad. Sci. 87: 2254- 2258, 1990.

GAM7052 296 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: 3 C c
Completesequence of the human tissue factor gene, a highly regulated
cellularreceptor that initiates the coagulation protease cascade.
Biochemistry 28:1755- 1762, 1989.

GAM7052 296 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; 3 C c
Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand
mapping of RFLPs for human tissue factor (HTF) to chromosome 1p.
NucleicAcids Res. 15: 9098 only, 1987.

GAM7052 296 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; 3 C c
Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA
sequenceand chromosome localization of the gene. Biochemistry 26: 5234-
5238,1987.

GAM7052 296 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; 3 C c
Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA
clones coding for human tissue factor: primary structureof the protein and
cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987.

GAM7052 296 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of 3 C c
tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad.
Sci. 94: 6922- 6926, 1997.

GAM7052 296 FABP2 Baier, L. J.; Sacchettini, J. C.; Knowler, W. C.; Eads, J.; Paolisso,G.; 3 C c

Tataranni, P. A.; Mochizuki, H.; Bennett, P. H.; Bogardus, C.;Prochazka, M.: An amino acid substitution in the human intestinalfatty acid binding protein is associated with increased fatty acidbinding, increased fat oxidation, and insulin resistance. J. Clin.Invest. 95: 1281- 1287, 1995.

GAM7052 296 FABP2 Carlsson, M.; Orho- Melander, M.; Hedenbro, J.; Almgren, P.; Groop,L. C.: 3 C c
The T54 allele of the intestinal fatty acid- binding protein2 is associated with a parental history of stroke. J. Clin. Endocr.Metab. 85: 2801- 2804, 2000.

GAM7052 296 FABP2 Georgopoulos, A.; Aras, O.; Tsai, M. Y.: Codon- 54 polymorphismof the fatty 3 C c
acid- binding protein 2 gene is associated with elevationof fasting and postprandial triglyceride in type 2 diabetes. J. Clin.Endocr. Metab. 85: 3155- 3160, 2000.

GAM7052 296 FABP2 Hegele, R. A.; Harris, S. B.; Hanley, A. J. G.; Sadikian, S.; Connelly,P. 3 C c
W.; Zinman, B.: Genetic variation of intestinal fatty acid- bindingprotein associated with variation in body mass in aboriginal Canadians. J.Clin. Endocr. Metab. 81: 4334- 4337, 1996.

GAM7052 296 FABP2 Polymeropoulos, M. H.; Rath, D. S.; Xiao, H.; Merril, C. R.: 3 C c
Trinucleotiderepeat polymorphism at the human intestinal fatty acid binding proteingene (FABP2). Nucleic Acids Res. 18: 7198 only, 1991.

GAM7052 296 FABP2 Prochazka, M.; Lillioja, S.; Tait, J. F.; Knowler, W. C.; Mott,D. M.; 3 C c
Spraul, M.; Bennett, P. H.; Bogardus, C.: Linkage of chromosomalmarkers on 4q with a putative gene determining maximal insulin actionin Pima Indians. Diabetes 42: 514- 519, 1993.

GAM7052 296 FABP2 Sipilainen, R.; Uusitupa, M.; Heikkinen, S.; Rissanen, A.; Laakso,M.: 3 C c
Variants in the human intestinal fatty acid binding protein 2gene in obese subjects. J. Clin. Endocr. Metab. 82: 2629- 2632, 1997.

GAM7052 296 FABP2 Sparkes, R. S.; Mohandas, T.; Heinzmann, C.; Gordon, J. I.; Klisak,I.; 3 C c
Zollman, S.; Sweetser, D. A.; Ragunathan, L.; Winokur, S.; Lusis,A. J.: Human fatty acid binding protein assignments intestinal to4q28- 4q31 and liver to 2p11. (Abstract) Cytogenet. Cell Genet. 46:697 only, 1987.

GAM7052 296 FABP2 Sweetser, D. A.; Birkenmeier, E. H.; Klisak, I. J.; Zollman, S.;Sparkes, R. 3 C c
S.; Mohandas, T.; Lusis, A. J.; Gordon, J. I.: The humanand rodent intestinal fatty acid binding protein genes: a comparativeanalysis of their structure, expression, and linkage relationships. J.Biol. Chem. 262: 16060- 16071, 1987.

GAM7052 296 FABP2 Weber, J. L.; Kwitek, A. E.; May, P. E.; Polymeropoulos, M.:Dinucleotide 3 C c
repeat polymorphism at the D12S43 locus. Nucleic AcidsRes. 18: 4637 only, 1990.

GAM7052 296 FABP2 Weber, J. L.; May, P. E.: Abundant class of human DNA polymorphismswhich can 3 C c
be typed using the polymerase chain reaction. Am. J. Hum.Genet. 44: 388- 396, 1989.

GAM7052 296 FANCE Buchwald, M.: Complementation groups: one or more per gene? NatureGenet. 11: 3 C c
228- 230, 1995.

GAM7052 296 FANCE de Winter, J. P.; Leveille, F.; van Berkel, C. G. M.; Rooimans,M. A.; van 3 C c
der Weel, L.; Steltenpool, J.; Demuth, I.; Morgan, N. V.;Alon, N.; Bosnoyan-Collins, L.; Lightfoot, J.; Leegwater, P. A.; Waisfisz,Q.; Komatsu, K.; Arwert, F.; Pronk, J. C.; Mathew, C. G.; Digweed,M.; Buchwald, M.; Joenje, H.: Isolation of a cDNA representing theFanconi anemia complementation group

E gene. Am. J. Hum. Genet. 67:1306- 1308, 2000. Note: Erratum: Am. J. Hum. Genet. 67: 1365 only,2000.

GAM7052 296 FANCE Joenje, H.: Fanconi anaemia complementation groups in Germanyand The Netherlands. Hum. Genet. 97: 280- 282, 1996. 3 C c

GAM7052 296 FANCE Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G.M.; Rooimans, M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J.J. P.; Buchwald, M.; Arwert, F.: Classification of Fanconi anemiapatients by complementation analysis: evidence for a fifth geneticsubtype. Blood 86: 2156- 2160, 1995. 3 C c

GAM7052 296 FANCE Joenje, H.; Oostra, A. B.; Wijker, M.; di Summa, F. M.; van Berkel,C. G. M.; Rooimans, M. A.; Ebell, W.; van Weel, M.; Pronk, J. C.;Buchwald, M.; Arwert, F.: Evidence for at least eight Fanconi anemiagenes. Am. J. Hum. Genet. 61: 940- 944, 1997. 3 C c

GAM7052 296 FANCE Pace, P.; Johnson, M.; Tan, W. M.; Mosedale, G.; Sng, C.; Hoatlin,M.; de Winter, J.; Joenje, H.; Gergely, F.; Patel, K. J.: FANCE:the link between Fanconi anaemia complex assembly and activity. EMBOJ. 21: 3414- 3423, 2002. 3 C c

GAM7052 296 FANCE Waisfisz, Q.; Saar, K.; Morgan, N. V.; Altay, C.; Leegwater, P.A.; de Winter, J. P.; Komatsu, K.; Evans, G. R.; Wegner, R.- D.; Reis,A.; Joenje, H.; Arwert, F.; Mathew, C. G.; Pronk, J. C.; Digweed,M.: The Fanconi anemia group E gene, FANCE, maps to chromosome 6p. Am.J. Hum. Genet. 64: 1400- 1405, 1999. 3 C c

GAM7052 296 FANCE Wegner, R.- D.; Henrichs, I.; Joenje, H.; Schroeder- Kurth, T.:Fanconi anemia complementation group E: clinical and cytogenetic dataof the first patient. Clin. Genet. 50: 479- 482, 1996. 3 C c

GAM7052 296 FCGR2A Grundy, H. O.; Peltz, G.; Barsh, G.; Moore, K.; Golbus, M. S.;Lebo, R. V.: Immunoglobulin G Fc receptor II and Fc receptor IIIgenes map to chromosome 1 by spot- blot chromosome analysis. (Abstract) Am.J. Hum. Genet. 43: A145, 1988. 3 C c

GAM7052 296 FCGR2A Grundy, H. O.; Peltz, G.; Moore, K. W.; Golbus, M. S.; Jackson,L. G.; Lebo, R. V.: The polymorphic Fc- gamma receptor II gene mapsto human chromosome 1q. Immunogenetics 29: 331- 339, 1989. 3 C c

GAM7052 296 FCGR2A Hibbs, M. L.; Bonadonna, L.; Scott, B. M.; McKenzie, I. F. C.;Hogarth, P. M.: Molecular cloning of a human immunoglobulin G Fcreceptor. Proc. Nat. Acad. Sci. 85: 2240- 2244, 1988. 3 C c

GAM7052 296 FCGR2A Hibbs, M. L.; Hogarth, P. M.; McKenzie, I. F. C.: The mouse Ly- 17locus identifies a polymorphism of the Fc receptor. Immunogenetics 22:335- 348, 1985. 3 C c

GAM7052 296 FCGR2A Lebo, R. V.; Lynch, E. D.; Wiegant, J.; Moore, K.; Trounstine,M.; van der Ploeg, M.: Multicolor fluorescence in situ hybridizationand pulsed field electrophoresis dissect CMT1B gene region. Hum.Genet. 88: 13- 20, 1991. 3 C c

GAM7052 296 FCGR2A Moser, K. L.; Neas, B. R.; Salmon, J. E.; Yu, H.; Gray- McGuire,C.; Asundi, N.; Bruner, G. R.; Fox, J.; Kelly, J.; Henshall, S.; Bacino,D.; Dietz, M.; Hogue, R.; Koelsch, G.; Nightingale, L.; Shaver, T.;Abdou, N. I.; Albert, D. A.; Carson, C.; Petri, M.; Treadwell, E.L.; James, J. A.; Harley, J. B.: Genome scan of human systemic lupuserythematosus: evidence for linkage on chromosome 1q in African- Americanpedigrees. Proc. Nat. Acad. Sci. 95: 14869- 14874, 1998. 3 C c

GAM7052 296 FCGR2A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human DNA. Hum. Molec. Genet. 1: 613- 620,1992. 3 C c

GAM7052 296 FCGR2A Peltz, G. A.; Grundy, H. O.; Lebo, R. V.; Yssel, H.; Barsh, G.S.; Moore, K. 3 C c

W.: Human Fc- gamma- RIII: cloning, expression, and identificationof the chromosomal locus of two Fc receptors for IgG. Proc. Nat.Acad. Sci. 86: 1013- 1017, 1989.

GAM7052 296 FCGR2A Qiu, W. Q.; de Bruin, D.; Brownstein, B. H.; Pearse, R.; Ravetch,J. V.: 3 C c
Organization of the human and mouse low- affinity Fc- gamma- Rgenes: duplication and recombination. Science 248: 732- 735, 1990.

GAM7052 296 FCGR2A Salmon, J. E.; Millard, S.; Schachter, L. A.; Arnett, F. C.; Ginzler,E. M.; 3 C c
Gourley, M. F.; Ramsey- Goldman, R.; Peterson, M. G. E.; Kimberly,R. P.: Fc-gamma- RIIA alleles are heritable risk factors for lupusnephritis in African Americans. J. Clin. Invest. 97: 1348- 1354,1996.

GAM7052 296 FCGR2A Sammartino, L.; Webber, L. M.; Hogarth, P. M.; McKenzie, I. F.C.; Garson, O. 3 C c
M.: Assignment of the gene coding for human FcRII(CD32) to bands q23q24 on chromosome 1. Immunogenetics 28: 380- 381,1988.

GAM7052 296 FCGR2A Stein, M.- P.; Edberg, J. C.; Kimberly, R. P.; Mangan, E. K.; Bharadwaj,D.; 3 C c
Mold, C.; Du Clos, T. W.: C- reactive protein binding to Fc- gamma- RIIaon human monocytes and neutrophils is allele- specific. J. Clin. Invest. 105:369- 376, 2000.

GAM7052 296 FCGR2A Unkeless, J. C.: Function and heterogeneity of human Fc receptorsfor 3 C c
immunoglobulin G. J. Clin. Invest. 83: 355- 361, 1989.

GAM7052 296 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 C c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM7052 296 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 C c
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001.

GAM7052 296 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome 3 C c
assignment by polymerase chain reaction techniques: assignmentof the oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990.

GAM7052 296 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator 3 C c
of the hair growth cycle: evidence from targeted and spontaneousmutations. Cell 78: 1017- 1025, 1994.

GAM7052 296 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 3 C c
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM7052 296 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; 3 C c
Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and the bcl.1 locus are contained within one megabase in bandq13 of chromosome 11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988.

GAM7052 296 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes 3 C c
a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8: 3487- 3495, 1988.

GAM7052 296 G2A Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y.: 3 C c
Lysophosphatidylcholine as a ligand for the immunoregulatory receptorG2A. Science 293: 702- 705, 2001.

GAM7052 296 G2A Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.;Harvill, E. 3 C c
T.; Jensen, E. R.; Miller, J. F.; Witte, O. N.: Micelacking the orphan G protein- coupled receptor G2A develop a late- onsetautoimmune syndrome. Immunity 14: 561- 571, 2001.

GAM7052 296 G2A Weng, Z.; Fluckiger, A.- C.; Nisitani, S.; Wahl, M. I.; Le, L. Q.;Hunter, C. 3 C c

A.; Fernal, A. A.; le Beau, M. M.; Witte, O. N.: A DNAdamage and stress inducible G protein- coupled receptor blocks cellsin G2/M. Proc. Nat. Acad. Sci. 95: 12334- 12339, 1998.

GAM7052 296 GFER Francavilla, A.; Hagiya, M.; Porter, K. A.; Polimeno, L.; Ihara,I.; Starzl, T. E.: Augmenter of liver regeneration: its place inthe universe of hepatic growth factors. Hepatology 20: 747- 757,1994. 3 C c

GAM7052 296 GFER Giorda, R.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sakai, H.; Michaelson,J.; Francavilla, A.; Starzl, T. E.; Trucco, M.: Analysis of the structureand expression of the augmenter of liver regeneration (ALR) gene. Molec.Med. 2: 97- 108, 1996. 3 C c

GAM7052 296 GFER Hagiya, M.; Francavilla, A.; Polimeno, L.; Ihara, I.; Sakai, H.;Seki, T.; Shimonishi, M.; Porter, K. A.; Starzl, T. E.: Cloning andsequence analysis of the rat augmenter of liver regeneration (ALR)gene: expression of biologically active recombinant ALR and demonstrationof tissue distribution. Proc. Nat. Acad. Sci. 91: 8142- 8146, 1994.Note: Erratum Proc. Nat. Acad. Sci. 92, p. 3076 only, 1995. 3 C c

GAM7052 296 GFER Lisowsky, T.; Weinstat- Saslow, D. L.; Barton, N.; Reeders, S. T.;Schneider, M. C.: A new human gene located in the PKD1 region ofchromosome 16 is a functional homologue to ERV1 of yeast. Genomics 29:690- 697, 1995. 3 C c

GAM7052 296 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N- acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001. 3 C c

GAM7052 296 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2- epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313- 24318,1997. 3 C c

GAM7052 296 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 C c

GAM7052 296 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997. 3 C c

GAM7052 296 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase gene (GNE). J. Hum. Genet. 47: 77- 79, 2002. 3 C c

GAM7052 296 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999. 3 C c

GAM7052 296 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993. 3 C c

GAM7052 296 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001. 3 C c

GAM7052 296 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal 3 C c

myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981.

GAM7052 296 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; 3 C c Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002.

GAM7052 296 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N- acetylglucosamine 2- epimerase gene define the disease sialuriaand the allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999. 3 C c

GAM7052 296 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; 3 C c Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N-acetylneuraminic acid biosynthesis of rat liver: molecularcloning and functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N-acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997.

GAM7052 296 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification 3 C c of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989.

GAM7052 296 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a 3 C c second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987.

GAM7052 296 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, 3 C c J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a novel secretin- like human G- protein- coupledreceptor gene. Genomics 55: 296- 305, 1999.

GAM7052 296 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; 3 C c van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected with mRNA differential display using human melanoma celllines with different metastatic potential. FEBS Lett. 446: 292- 298,1999.

GAM7052 296 HTR1E Levy, F. O.; Gudermann, T.; Birnbaumer, M.; Kaumann, A. J.; Birnbaumer,L.: 3 C c Molecular cloning of a human gene (S31) encoding a novel serotoninreceptor mediating inhibition of adenylyl cyclase. FEBS Lett. 296:201- 206, 1992.

GAM7052 296 HTR1E Levy, F. O.; Holtgreve- Grez, H.; Tasken, K.; Solberg, R.; Ried,T.; 3 C c Gudermann, T.: Assignment of the gene encoding the 5- HT- 1E serotoninreceptor (S31) (locus HTR1E) to human chromosome 6q14- q15. Genomics 22:637- 640, 1994.

GAM7052 296 HTR1E McAllister, G.; Charlesworth, A.; Snodin, C.; Beer, M. S.; Noble,A. J.; 3 C c Middlemiss, D. N.; Iversen, L. L.; Whiting, P.: Molecularcloning of a serotonin receptor from human brain (5HT1E): a fifth5HT1- like subtype. Proc. Nat. Acad. Sci. 89: 5517- 5521, 1992.

GAM7052 296 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human 3 C c homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998.

GAM7052 296 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol- 3 C c Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay. Genomics 54: 278- 286, 1998.

GAM7052 296 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved 3 C c fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated in response to DNA damage. EMBO J. 17: 2055- 2066,1998.

GAM7052 296 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe 3 C c Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999.

GAM7052 296 IFNAR2 Croze, E.; Russell- Harde, D.; Wagner, T. C.; Pu, H.; Pfeffer, L.M.; Perez, 3 C c

H. D.: The human type I interferon receptor: identificationof the interferon beta- specific receptor- associated phosphoprotein. J.Biol. Chem. 271: 33165- 33168, 1996.

GAM7052 296 IFNAR2 Croze, E.; Usacheva, A.; Asarnow, D.; Minshall, R.D.; Perez, H.D.;Colamonici, O.: Receptor for activated C- kinase (RACK- 1), a WD motif-containingprotein, specifically associates with the human type I IFN receptor. J.Immun. 165: 5127- 5132, 2000. 3 C c

GAM7052 296 IFNAR2 Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.;Pitha, P.; Colamonici, O. R.: Cloning and expression of a long formof the beta subunit of the interferon alpha/beta receptor that isrequired for signaling. J. Biol. Chem. 270: 21606- 21611, 1995. 3 C c

GAM7052 296 IFNAR2 Lutfalla, G.; Holland, S. J.; Cinato, E.; Monneron, D.; Reboul,J.; Rogers, N. C.; Smith, J. M.; Stark, G. R.; Gardiner, K.; Mogensen,K. E.; Kerr, I. M.; Uze, G.: Mutant U5A cells are complemented byan interferon- alpha/beta receptor subunit generated by alternativeprocessing of a new member of a cytokine receptor gene cluster. EMBOJ. 14: 5100- 5108, 1995. 3 C c

GAM7052 296 IFNAR2 Novick, D.; Cohen, B.; Rubinstein, M.: The human interferon alpha/betareceptor: characterization and molecular cloning. Cell 77: 391-400,1994. 3 C c

GAM7052 296 IFNAR2 Platanias, L. C.; Uddin, S.; Domanski, P.; Colamonici, O. R.:Differences in interferon alpha and beta signaling: interferon betaselectively induces the interaction of the alpha and beta(L) subunitsof the type I interferon receptor. J. Biol. Chem. 271: 23630- 23633,1996. 3 C c

GAM7052 296 IFNAR2 Raz, R.; Cheung, K.; Ling, L.; Levy, D. E.: Three distinct locion human chromosome 21 contribute to interferon- alpha/beta responsiveness. Somat.Cell Molec. Genet. 21: 139- 145, 1995. 3 C c

GAM7052 296 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like growth factor- I and cognitive function inhealthy older men. J. Clin. Endocr. Metab. 84: 471- 475, 1999. 3 C c

GAM7052 296 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993. 3 C c

GAM7052 296 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and absence of association with stature among African Pygmies. Hum.Genet. 85: 349- 354, 1990. 3 C c

GAM7052 296 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for insulin- like growth factors I and II and for epidermalgrowth factor in man. (Abstract) Am. J. Hum. Genet. 36: 133S only,1984. 3 C c

GAM7052 296 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of genes for insulin- like growth factors I and II and epidermalgrowth factor. Nature 310: 781- 784, 1984. 3 C c

GAM7052 296 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of recombinant human insulin- like growth factor I(IGF- I) therapy on the growth hormone- IGF system of a patient witha partial IGF- I gene deletion. J. Clin. Endocr. Metab. 84: 1611- 1616,1999. 3 C c

GAM7052 296 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of the growth hormone receptor in children with idiopathicshort stature. New Eng. J. Med. 333: 1093- 1098, 1995. 3 C c

GAM7052 296 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; 3 C c
Froesch, E. R.: Small stature and insulin- like growth factors:prolonged
treatment of mini- poodles with recombinant human insulin- likegrowth factor
I. Acta Endocr. 121: 456- 464, 1989.

GAM7052 296 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. 3 C c
S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating
concentrations of insulin- like growth factor- I and riskof breast cancer.
Lancet 351: 1393- 1396, 1998.

GAM7052 296 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: 3 C c
Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding
protein- 3, and prostate- specific antigen as predictorsof clinical prostate
cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000.

GAM7052 296 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; 3 C c
Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith,
D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival
signaling in retinal endothelial cells: direct correlationwith clinical
retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001.

GAM7052 296 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer 3 C c
prevention. Lancet 351: 1373- 1375, 1998.

GAM7052 296 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; 3 C c
Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J.
S.: The human gene encoding insulin- like growthfactor I is located on
chromosome 12. Hum. Genet. 69: 157- 160, 1985.

GAM7052 296 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, 3 C c
J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic
linkage map of mouse chromosome 10: localizationof eighteen molecular
markers using a single interspecific backcross. Genetics 125:855- 866, 1990.

GAM7052 296 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete 3 C c
characterization of the human IGF- I nucleotide sequenceisolated from a
newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986.

GAM7052 296 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; 3 C c
Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated
blood pressure and enhanced myocardial contractilityin mice with severe IGF-
1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996.

GAM7052 296 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: 3 C c
Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat.
Acad. Sci. 80: 2216- 2220, 1983.

GAM7052 296 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; 3 C c
Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand
implications for cell type- specific growth. Nature 364: 208- 213,1993.

GAM7052 296 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: 3 C c
Mice carrying null mutations of the genes encoding insulin- likegrowth
factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993.

GAM7052 296 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like 3 C c
growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83:
9343- 9347, 1986.

GAM7052 296 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human 3 C c
genes for insulin- like growth factors I and II and epidermalgrowth factor
are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively.
Cytogenet.Cell Genet. 41: 245- 249, 1986.

GAM7052 296 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 3 C c
1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2
(IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985.

GAM7052 296 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. 3 C c
D.: Growth characteristics and response to growth hormonetherapy in patients
with hypochondroplasia: genetic linkage of theinsulin- like growth factor I
gene at chromosome 12q23 to the diseasein a subgroup of these patients.
Clin. Endocr. 34: 265- 274, 1991.

GAM7052 296 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: 3 C c
IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin
association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999.

GAM7052 296 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, 3 C c
M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene
expression sustains hypertrophy and regeneration insenescent skeletal
muscle. Nature Genet. 27: 195- 200, 2001.

GAM7052 296 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like 3 C c
growth factor 1 regulates the location, stability,and transcriptional
activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000.

GAM7052 296 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, 3 C c
S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal
embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993.

GAM7052 296 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the 3 C c
protein which binds insulin- like growth factor in human serum. Europ.J.
Biochem. 172: 421- 425, 1988.

GAM7052 296 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; 3 C c
Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith,
R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the
insulin- like growth factor I receptor and its ligandin relation to type 2
diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000.

GAM7052 296 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed 3 C c
in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986.

GAM7052 296 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; 3 C c
Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I)
reduces hyperglycaemia in patients with extremeinsulin resistance.
Diabetologia 34: 675- 679, 1991.

GAM7052 296 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; 3 C c
Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a
Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999.

GAM7052 296 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. 3 C c
E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma:
chemical and biological properties, partial sequenceanalysis, and
relationship to other somatomedins. Biochemistry 19:790- 797, 1980.

GAM7052 296 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like 3 C c
growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58,
1991.

GAM7052 296 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- 3 C c
like growth factor genes: chromosome organization andassociation with
disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984.

GAM7052 296 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: 3 C c
Localization of insulin- like growth factor genes to human chromosomes11 and

12. Nature 310: 784- 786, 1984.

GAM7052 296 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of 3 C c
the human insulin- like growth factor I gene using asingle synthetic DNA
probe. EMBO J. 3: 361- 364, 1984.

GAM7052 296 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; 3 C c
Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-
resistantdiabetic ketoacidosis with insulin- like growth factor I in an
adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-
857,1992.

GAM7052 296 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; 3 C c
Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic
variation in the gene for insulin- like growth factor- 1and low birthweight.
Lancet 359: 1036- 1037, 2002.

GAM7052 296 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand 3 C c
assays that somatomedin- C and insulin- like growth factor- Iare similar to
each other and different from other somatomedins. J.Clin. Endocr. Metab. 50:
206- 208, 1980.

GAM7052 296 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish 3 C c
Osteoporosis Prevention Study: Effect of sex hormone replacementon the
insulin- like growth factor system and bone mineral: a cross- sectionaland
longitudinal study in 595 perimenopausal women participating inthe Danish
osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999.

GAM7052 296 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. 3 C c
L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy
on body composition and insulin resistance in IGF- Igene deletion. J. Clin.
Endocr. Metab. 85: 1407- 1411, 2000.

GAM7052 296 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 3 C c
Intrauterine growth retardation and postnatal growth failureassociated with
deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335:
1363- 1367, 1996.

GAM7052 296 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 3 C c
regional localization of human genes for insulin- like growthfactors I
(IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell
Genet. 40: 782 only, 1985.

GAM7052 296 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 3 C c
growth factors and bone mineral density in African Americanand white girls.
J. Pediat. 137: 826- 832, 2000.

GAM7052 296 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 3 C c
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM7052 296 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel 3 C c
genes. Trends Pharm. Sci. 14: 434, 1993.

GAM7052 296 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; 3 C c
Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe
pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011-
1017, 1996.

GAM7052 296 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; 3 C c
Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an
inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166-
1170, 1995.

GAM7052 296 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: 3 C c
Targeted overactivity of beta cell KATP channels induces profoundneonatal diabetes. Cell 100: 645- 654, 2000.

GAM7052 296 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: 3 C c
Homozygositymapping, to chromosome 11p, of the gene for familial persistent hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421, 1995.

GAM7052 296 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward 3 C c
rectifier Kir6.2 also leads to familial persistent hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812, 1996.

GAM7052 296 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, 3 C c
T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium channels in hypoxia- induced generalized seizure. Science 292:1543- 1546, 2001.

GAM7052 296 KLRC3 Adamkiewicz, T. V.; McSherry, C.; Bach, F. H.; Houchins, J. P.: Natural 3 C c
killer lectin- like receptors have divergent carboxy- termini,distinct from C- type lectins. Immunogenetics 39: 218, 1994.

GAM7052 296 KLRC3 Plougastel, B.; Trowsdale, J.: Sequence analysis of a 62- kb 3 C c
regionoverlapping the human KLRC cluster of genes. Genomics 49: 193- 199,1998.

GAM7052 296 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand 3 C c
characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000.

GAM7052 296 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; 3 C c
Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000.

GAM7052 296 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein 3 C c
kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990.

GAM7052 296 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. 3 C c
F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994.

GAM7052 296 MEF2A Breitbart, R. E.; Liang, C.; Smoot, L. B.; Laheru, D. A.; Mahdavi,V.; Nadal- 3 C c
Ginard, B.: A fourth human MEF2 transcription factor, hMEF2D,is an early marker of the myogenic lineage. Development 118: 1095- 1106,1993.

GAM7052 296 MEF2A Hobson, G. M.; Krahe, R.; Garcia, E.; Siciliano, M. J.; Funanage,V. L.: 3 C c
Regional chromosomal assignments for four members of the MADSdomain transcription enhancer factor 2 (MEF2) gene family to humanchromosomes 15q26, 19p12, 5q14, and 1q12- q23. Genomics 29: 704- 711,1995.

GAM7052 296 MEF2A Mao, Z.; Bonni, A.; Xia, F.; Nadal- Vicans, M.; Greenberg, M. E.: Neuronal 3 C c
activity- dependent cell survival mediated by transcriptionfactor MEF2. Science 286: 785- 790, 1999.

GAM7052 296 MEF2A Martin, J. F.; Miano, J. M.; Hustad, C. M.; Copeland, N. G.; Jenkins,N. A.; 3 C c
Olson, E. N.: A Mef2 gene that generates a muscle- specificisoform via alternative mRNA splicing. Molec. Cell. Biol. 14: 1647- 1656,1994.

GAM7052 296 MEF2A Molkentin, J. D.; Black, B. L.; Martin, J. F.; Olson, E. N.: 3 C c
Cooperativeactivation of muscle gene expression by MEF2 and myogenic bHLH

proteins. Cell 83:1125- 1136, 1995.

GAM7052 296 MEF2A Naya, F. J.; Black, B. L.; Wu, H.; Bassel- Duby, R.; Richardson,J. A.; Hill, J. A.; Olson, E. N.: Mitochondrial deficiency and cardiacsudden death in mice lacking the MEF2A transcription factor. NatureMed. 15Oct, 2002. Note: Advance Electronic Publication. 3 C c

GAM7052 296 MEF2A Pollock, R.; Treisman, R.: Human SRF- related proteins: DNA-bindingproperties and potential regulatory targets. Genes Dev. 5: 2327-2341,1991. 3 C c

GAM7052 296 MEF2A Suzuki, E.; Lowry, J.; Sonoda, G.; Testa, J. R.; Walsh, K.: Structuresand chromosome locations of the human MEF2A gene and a pseudogeneMEF2AP. Cytogenet. Cell Genet. 73: 244- 249, 1996. 3 C c

GAM7052 296 MEF2A Yu, Y.- T.; Breitbart, R. E.; Smoot, L. B.; Lee, Y.; Mahdavi, V.;Nadal-Ginard, B.: Human myocyte- specific enhancer factor 2 comprisesa group of tissue- restricted MADS box transcription factors. GenesDev. 6: 1783- 1798, 1992. 3 C c

GAM7052 296 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: Cloning and characterization of RAP250, a novel nuclear receptorcoactivator. J. Biol. Chem. 275: 5308- 5317, 2000. 3 C c

GAM7052 296 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: Hybrid selection of transcribed sequences from microdissectedDNA: isolation of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer Res. 56: 3446- 3450, 1996. 3 C c

GAM7052 296 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor-bindingprotein, an LXXLL motif- containing protein, functions as a generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000. 3 C c

GAM7052 296 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor, ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol. Chem. 274: 34283- 34293, 1999. 3 C c

GAM7052 296 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators that integrate nuclear receptor signaling through CREB- bindingprotein. Molec. Cell. Biol. 20: 5048- 5063, 2000. 3 C c

GAM7052 296 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. V. The codingsequences of 40 new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 3: 17- 24, 1996. 3 C c

GAM7052 296 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, J. K.: Isolation and characterization of peroxisomeproliferator- activated receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J. Biol. Chem. 275: 13510- 13516, 2000. 3 C c

GAM7052 296 NHLH1 Begley, C. G.; Lipkowitz, S.; Gobel, V.; Mahon, K. A.; Bertness,V.; Green, A. R.; Gough, N. M.; Kirsch, I. R.: Molecular characterizationof NSCL, a gene encoding a helix- loop- helix protein expressed in thedeveloping nervous system. Proc. Nat. Acad. Sci. 89: 38- 42, 1992. 3 C c

GAM7052 296 NHLH1 Brown, L.; Espinosa, R., III; Le Beau, M. M.; Siciliano, M. J.;Baer, R.: HEN1 and HEN2: a subgroup of basic helix- loop- helix genesthat are coexpressed in a human neuroblastoma. Proc. Nat. Acad. Sci. 89:8492- 8496, 1992. 3 C c

GAM7052 296 NHLH1 Cogliati, T.; Good, D. J.; Haigney, M.; Delgado- Romero, P.; Eckhaus,M. A.; 3 C c
Koch, W. J.; Kirsch, I. R.: Predisposition to arrhythmia andautonomic
dysfunction in Nhlh1- deficient mice. Molec. Cell. Biol. 22:4977- 4983,
2002.

GAM7052 296 NHLH1 Lipkowitz, S.; Gobel, V.; Varterasian, M. L.; Nakahara, K.; Tchorz,K.; 3 C c
Kirsch, I. R.: A comparative structural characterization of thehuman NSCL- 1
and NSCL- 2 genes: two basic helix- loop- helix genes expressedin the
developing nervous system. J. Biol. Chem. 267: 21065- 21071,1992.

GAM7052 296 NHLH1 Mullick, A.; Groulx, N.; Trasler, D.; Gros, P.: Nhlh1, a basichelix- loop- 3 C c
helix transcription factor, is very tightly linked to themouse looptail (Lp)
mutation. Mammalian Genome 6: 700- 704, 1995.

GAM7052 296 NUFIP1 Bardoni, B.; Giglio, S.; Schenck, A.; Rocchi, M.; Mandel, J. L.: Assignment 3 C c
of NUFIP1 (nuclear FMRP interacting protein 1) gene tochromosome 13q14 and
assignment of a pseudogene to chromosome 6q12. Cytogenet.Cell Genet. 89: 11-
13, 2000.

GAM7052 296 NUFIP1 Bardoni, B.; Schenck, A.; Mandel, J. L.: A novel RNA- binding nuclearprotein 3 C c
that interacts with the fragile X mental retardation (FMR1)protein. Hum.
Molec. Genet. 8: 2557- 2566, 1999.

GAM7052 296 NUMA1 Compton, D. A.; Szilak, I.; Cleveland, D. W.: Primary structureof NuMA, an 3 C c
intranuclear protein that defines a novel pathway forsegregation of proteins
at mitosis. J. Cell Biol. 116: 1395- 1408,1992.

GAM7052 296 NUMA1 Lydersen, B. K.; Pettijohn, D. E.: Human- specific nuclear proteinthat 3 C c
associates with the polar region of the mitotic apparatus: distributionin a
human/hamster hybrid cell. Cell 22: 489- 499, 1980.

GAM7052 296 NUMA1 Merdes, A.; Ramyar, K.; Vechio, J. D.; Cleveland, D. W.: A complexof NuMA 3 C c
and cytoplasmic dynein is essential for mitotic spindle assembly. Cell
87:447- 458, 1996.

GAM7052 296 NUMA1 Sparks, C. A.; Bangs, P. L.; McNeil, G. P.; Lawrence, J. B.; Fey,E. G.: 3 C c
Assignment of the nuclear mitotic apparatus protein NuMA geneto human
chromosome 11q13. Genomics 17: 222- 224, 1993.

GAM7052 296 NUMA1 Wells, R. A.; Catzavelos, C.; Kamel- Reid, S.: Fusion of retinoicacid 3 C c
receptor alpha to NuMA, the nuclear mitotic apparatus protein,by a variant
translocation in acute promyelocytic leukaemia. NatureGenet. 17: 109- 113,
1997.

GAM7052 296 NUMA1 Wiese, C.; Wilde, A.; Moore, M. S.; Adam, S. A.; Merdes, A.; Zheng,Y.: Role 3 C c
of importin- beta in coupling Ran to downstream targets inmicrotubule
assembly. Science 291: 653- 656, 2001.

GAM7052 296 NUMA1 Yang, C. H.; Lambie, E. J.; Snyder, M.: NuMA: an unusually longcoiled- coil 3 C c
related protein in the mammalian nucleus. J. Cell Biol. 116:1303- 1317,
1992.

GAM7052 296 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM7052 296 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM7052 296 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to 3 C c

two putative mammalian circadian regulators, mper1 andmper2, to light. Cell 91: 1055- 1064, 1997.

GAM7052 296 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM7052 296 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; 3 C c
Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531- 2534, 1999.

GAM7052 296 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of 3 C c
clock operative in the mammalian forebrain. Science 293:506- 509, 2001.

GAM7052 296 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; 3 C c
Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.; Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock. Science 288: 1013- 1019, 2000.

GAM7052 296 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; 3 C c
Reppert, S. M.: Two period homologs: circadian expression andphotic regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997.

GAM7052 296 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; 3 C c
Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial advanced sleep phase syndrome. Science 291: 1040- 1043,2001.

GAM7052 296 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; 3 C c
Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694, 2001.

GAM7052 296 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; 3 C c
Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the mammalian circadian clock. Nature 400: 169- 173,1999.

GAM7052 296 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. 3 C c
W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol 3- kinase catalytic subunit that associates withp85 and is expressed predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997.

GAM7052 296 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, 3 C c
E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J. H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002.

GAM7052 296 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; 3 C c
Nakagawara, A.: Identification and chromosome assignment of ahuman gene encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997.

GAM7052 296 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; 3 C c
Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.: p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat. Acad. Sci. 94: 4330- 4335, 1997.

GAM7052 296 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; 3 C c
Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C. Genomics 47: 323- 324, 1998.

GAM7052 296 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, 3 C c

S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to human chromosome 21q22.3. Genomics 41: 193- 200,1997.

GAM7052 296 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; 3 C c Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 2002.

GAM7052 296 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- 3 C c cell coactivator of octamer- binding transcription factors. Nature 373:360- 362, 1995.

GAM7052 296 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: 3 C c Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell- specific coactivator of octamer- binding transcription factors1 and 2, to 11q23.1 by somatic cell hybridization and in situ hybridization. Genomics 33:143- 145, 1996.

GAM7052 296 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism 3 C c of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995.

GAM7052 296 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; 3 C c Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001.

GAM7052 296 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. 3 C c Immun. 9: 373- 398, 1991.

GAM7052 296 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell- 3 C c specificcoactivator that stimulates immunoglobulin promoter activity throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995.

GAM7052 296 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; 3 C c Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B, BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853- 864, 2000.

GAM7052 296 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; 3 C c Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor integrity, and rhodopsin dephosphorylation in mice lackingboth protein phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21: 8605- 8614, 2001.

GAM7052 296 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; 3 C c Nathans, J.: Identification and characterization of a conservedfamily of protein serine/threonine phosphatases homologous to Drosophilaretinal degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997.

GAM7052 296 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 C c Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component of the steroid receptor complex: cloning of thecDNA and further characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM7052 296 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 C c characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem. 267: 5503- 5507, 1992.

GAM7052 296 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 C c E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151 only, 1997.

GAM7052 296 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 C c J.- E.: The structure and complete nucleotide sequenceof the human

cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM7052 296 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 C c
Chromosomalassignment of the interferon- inducible double- stranded RNA-
dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse
chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM7052 296 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human 3 C c
interferon- gamma mRNA autoregulates its translation througha pseudoknot
that activates the interferon- inducible protein kinasePKR. Cell 108: 221-
232, 2002.

GAM7052 296 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; 3 C c
Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR)
encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and
differences from its mouse homolog. Genomics 36:197- 201, 1996.

GAM7052 296 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: 3 C c
sequence of the human interferon- inducible RNA- dependent proteinkinase
(PKR) deduced from genomic clones. Gene 178: 191- 193, 1996.

GAM7052 296 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; 3 C c
Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand
characterization of the human double- stranded RNA- activated proteinkinase
induced by interferon. Cell 62: 379- 390, 1990.

GAM7052 296 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; 3 C c
Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds
preferentially to Huntington's disease (HD) transcriptsand is activated in
HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001.

GAM7052 296 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. 3 C c
G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-
RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics
16:768- 770, 1993.

GAM7052 296 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: 3 C c
Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein.
Science 285: 107- 110, 1999.

GAM7052 296 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 C c
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.:
Genomicorganization, comparative analysis, and genetic polymorphisms of
thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733,
2001.

GAM7052 296 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 C c
Chen, S. G.: Expression and structural characterizationof the recombinant
human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM7052 296 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 C c
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.;
Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-
deficient mice is associated with upregulation of thenovel PrP- like protein
doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM7052 296 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 C c
T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin
the prion- like protein gene (Prnd) and their implications inhuman prion
diseases, Alzheimer's disease and other neurological disorders. Hum.Genet.
109: 319- 325, 2001.

GAM7052 296 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 C c

P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-glycosylated, glycosylphosphatidylinositol- anchored protein:expression in testis and ectopic production in the brains of Prnp(0/0)mice predisposed to Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM7052 296 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 915, 1999. 3 C c

GAM7052 296 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime-untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001. 3 C c

GAM7052 296 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994. 3 C c

GAM7052 296 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996. 3 C c

GAM7052 296 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996. 3 C c

GAM7052 296 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996. 3 C c

GAM7052 296 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999. 3 C c

GAM7052 296 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000. 3 C c

GAM7052 296 RBM8A Conklin, D. C.; Rixon, M. W.; Kuestner, R. E.; Maurer, M. F.; Whitmore,T. E.; Millar, R. P.: Cloning and gene expression of a novel humanribonucleoprotein. Biochim. Biophys. Acta 1492: 465- 469, 2000. 3 C c

GAM7052 296 RBM8A Kataoka, N.; Yong, J.; Kim, V. N.; Velazquez, F.; Perkinson, R.A.; Wang, F.; Dreyfuss, G.: Pre- mRNA splicing imprints mRNA in thenucleus with a novel RNA- binding protein that persists in the cytoplasm. Molec.Cell 6: 673- 682, 2000. 3 C c

GAM7052 296 RBM8A Salicioni, A. M.; Xi. M.; Vanderveer, L. A.; Balsara, B.; Testa,J. R.; Dunbrack, R. L., Jr.; Godwin, A. K.: Identification and structuralanalysis of human RBM8A and RBM8B: two highly conserved RNA- bindingmotif proteins that interact with OVCA1, a candidate tumor suppressor. Genomics 69:54- 62, 2000. 3 C c

GAM7052 296 RBM8A Zhao, X.- F.; Nowak, N. J.; Shows, T. B.; Aplan, P. D.: MAGOH interactswith a novel RNA- binding protein. Genomics 63: 145- 148, 2000. 3 C c

GAM7052 296 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993. 3 C c

GAM7052 296 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 3 C c
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA
amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM7052 296 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. 3 C c
Med. 339: 1775- 1777, 1998.

GAM7052 296 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand 3 C c
molecular genetics. Blood Rev. 8: 199- 212, 1994.

GAM7052 296 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; 3 C c
Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood
group polymorphism as determined by Southern analysis. Blood 78:2747- 2752,
1991.

GAM7052 296 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and 3 C c
its association with universal edema of the fetus, icterusgravis neonatorum
and anemia of the newborn. J. Pediat. 1: 269- 309,1932.

GAM7052 296 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies 3 C c
in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989.

GAM7052 296 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with 3 C c
sickle cell disease. Transfusion 37: 357- 361, 1997.

GAM7052 296 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 C c

GAM7052 296 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the 3 C c
human RH locus: a family study of the red- cell Evans phenotypereveals a
transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59:
825- 833, 1996.

GAM7052 296 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular 3 C c
definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J.
Hum. Genet. 58: 133- 142, 1996.

GAM7052 296 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of 3 C c
Rh blood group genes: association between restrictionfragment length
polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994.

GAM7052 296 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine 3 C c
years and some observations on the biochemistry and geneticsof the system.
Transfusion Med. Rev. 3: 1- 12, 1989.

GAM7052 296 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh 3 C c
genes revealed by analysis of unrelated donors with therare D- - phenotype.
Am. J. Hum. Genet. 59: 1066- 1073, 1996.

GAM7052 296 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, 3 C c
J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by
alternative splicing. Blood 80: 1074- 1078, 1992.

GAM7052 296 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; 3 C c
Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the
human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929,
1992.

GAM7052 296 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; 3 C c
Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE
genotyping for correct blood group determination inchronically transfused
patients. Transfusion 39: 852- 855, 1999.

GAM7052 296 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its 3 C c
possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A.
116:825- 827, 1941.

GAM7052 296 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; 3 C c

Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal plasma. New Eng. J. Med. 339: 1734- 1738, 1998.

GAM7052 296 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; 3 C c
Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome 1. Am. J. Med. Genet. 104: 250- 256, 2001.

GAM7052 296 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, 3 C c
E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J. Clin. Invest. 100: 373- 379, 1997.

GAM7052 296 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 C c
153:771- 772, 1944.

GAM7052 296 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 C c
ed.): 1975.

GAM7052 296 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 3 C c
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII) category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM7052 296 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 3 C c
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral transduction of K562 cells establishes the molecular basisof Rh blood group antigens. Blood 87: 2968- 2973, 1996.

GAM7052 296 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 3 C c
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang. 58: 50- 55, 1990.

GAM7052 296 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 3 C c
Blood 95: 3662- 3668, 2000.

GAM7052 296 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 3 C c
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393, 1999.

GAM7052 296 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 3 C c
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311, 2002.

GAM7052 296 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 C c

GAM7052 296 RNF3 Beck, S.; Hanson, I.; Kelly, A.; Pappin, D. J.; Trowsdale, J.:A homologue of 3 C c
the Drosophila female sterile homeotic (fsh) gene inthe class II region of the human MHC. DNA Sequence 2: 203- 210, 1992.

GAM7052 296 RNF3 Denis, G. V.; Green, M. R.: A novel, mitogen- activated nuclearkinase is 3 C c
related to a Drosophila developmental regulator. GenesDev. 10: 261- 271, 1996.

GAM7052 296 RNF3 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, 3 C c
N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994.

GAM7052 296 RNF3 Okamoto, N.; Ando, A.; Kawai, J.; Yoshiwara, T.; Tsuji, K.; Inoko,H.: 3 C c
Orientation of HLA- DNA gene and identification of a CpG island-associatedgene adjacent to DNA in human major histocompatibility complex classII region. Hum. Immun. 32: 221- 228, 1991.

GAM7052 296 RNF3 Thorpe, K. L.; Abdulla, S.; Kaufman, J.; Trowsdale, J.; Beck, S.: Phylogeny 3 C c
and structure of the RING3 gene. Immunogenetics 44:391- 396, 1996.

GAM7052 296 RPH3AL Kotake, K.; Ozaki, N.; Mizuta, M.; Sekiya, S.; Inagaki, N.; Seino,S.: Noc2, a putative zinc finger protein involved in exocytosis inendocrine cells. J. Biol. Chem. 272: 29407- 29410, 1997. 3 C c

GAM7052 296 RPH3AL Smith, J. S.; Tachibana, I.; Allen, C.; Chiappa, S. A.; Lee, H.K.; McIver, B.; Jenkins, R. B.; Raffel, C.: Cloning of a human ortholog(RPH3AL) of (RNO)Rph3al from a candidate 17p13.3 medulloblastoma tumorsuppressor locus. Genomics 59: 97- 101, 1999. 3 C c

GAM7052 296 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two scleroderma autoimmune antigens that copurify with human ribonucleaseP. Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997. 3 C b

GAM7052 296 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: Autoantigenic properties of some protein subunits of catalyticallyactive complexes of human ribonuclease P. RNA 4: 407- 417, 1998. 3 C b

GAM7052 296 SAS Jankowski, S. A.; De Jong, P.; Meltzer, P. S.: Genomic structureof SAS, a member of the transmembrane 4 superfamily amplified in humansarcomas. Genomics 25: 501- 506, 1995. 3 C c

GAM7052 296 SAS Meltzer, P. S.; Jankowski, S. A.; Dal Cin, P.; Sandberg, A. A.;Paz, I. B.; Coccia, M. A.; Smith, S. H.: Identification and cloningof a novel amplified DNA sequence in human malignant fibrous histiocytomaderived from a region of chromosome 12 frequently rearranged in softtissue tumors. (Abstract) Cytogenet. Cell Genet. 58: 1979 only,1991. 3 C c

GAM7052 296 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 C c

GAM7052 296 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 C c

GAM7052 296 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 C c

GAM7052 296 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999. 3 C c

GAM7052 296 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001. 3 C c

GAM7052 296 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001. 3 C c

GAM7052 296 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five- base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000. 3 C c

GAM7052 296 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001. 3 C c

GAM7052 296 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002. 3 C c

GAM7052 296 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001. 3 C c

GAM7052 296 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999. 3 C c

GAM7052 296 SHC1 Almind, K.; Ahlgren, M. G.; Hansen, T.; Urhammer, S. A.; Clausen,J. O.; Pedersen, O.: Discovery of a Met300Val variant in Shc andstudies of its relationship to birth weight and length, impaired insulinsecretion, insulin resistance, and type 2 diabetes mellitus. J. Clin.Endocr. Metab. 84: 2241- 2244, 1999. 3 C c

GAM7052 296 SHC1 Harun, R. B.; Smith, K. K.; Leek, J. P.; Markham, A. F.; Norris,A.; Morrison, J. F. J.: Characterization of human SHC p66 cDNA andits processed pseudogene mapping to Xq12- q13.1. Genomics 42: 349- 352,1997. 3 C c

GAM7052 296 SHC1 Huebner, K.; Kastury, K.; Druck, T.; Salcini, A. E.; Lanfrancone,L.; Pelicci, G.; Lowenstein, E.; Li, W.; Park, S.- H.; Cannizzaro,L.; Pelicci, P. G.; Schlessinger, J.: Chromosome locations of genesencoding human signal transduction adapter proteins, Nck (NCK), Shc(SHC1), and Grb2 (GRB2). Genomics 22: 281- 287, 1994. 3 C c

GAM7052 296 SHC1 McGlade, J.; Cheng, A.; Pelicci, G.; Pelicci, P. G.; Pawson, T.: Shc proteins are phosphorylated and regulated by the v- src and v- fpsprotein- tyrosine- kinases. Proc. Nat. Acad. Sci. 89: 8869- 8873, 1992. 3 C c

GAM7052 296 SHC1 Migliaccio, E.; Giorgio, M.; Mele, S.; Pelicci, G.; Reboldi, P.;Pandolfi, P. P.; Lanfrancone, L.; Pelicci, P. G.: The p66(shc) adaptorprotein controls oxidative stress response and life span in mammals. Nature 402:309- 313, 1999. 3 C c

GAM7052 296 SHC1 Nemoto, S.; Finkel, T.: Redox regulation of forkhead proteinsthrough a p66shc- dependent signaling pathway. Science 295: 2450- 2452,2002. 3 C c

GAM7052 296 SHC1 Pelicci, G.; Lanfrancone, L.; Grignani, F.; McGlade, J.; Cavallo,F.; Forni, G.; Nicoletti, I.; Grignani, F.; Pawson, T.; Pelicci, P.G.: A novel transforming protein (SHC) with an SH2 domain is implicatedin mitogenic signal transduction. Cell 70: 93- 104, 1992. 3 C c

GAM7052 296 SHC1 Yulug, I. G.; Egan, S. E.; See, C. G.; Fisher, E. M. C.: A humanSHC- related sequence maps to chromosome 17, the SHC gene maps to chromosome1. Hum. Genet. 96: 245- 248, 1995. 3 C c

GAM7052 296 SHC1 Zhang, L.; Camerini, V.; Bender, T. P.; Ravichandran, K. S.: Anonredundant role for the adapter protein Shc in thymic T cell development. NatureImmun. 3: 749- 755, 2002. 3 C c

GAM7052 296 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human intestine:biology and function. Gastroenterology 113: 332- 340, 1997. 3 C c

GAM7052 296 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; 3 C c

Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning of a mammalian proton- coupled oligopeptide transporter. Nature 368:563-566, 1994.

GAM7052 296 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal H(+)/peptide cotransporter: cloning, functional expression,and chromosomal localization. J. Biol. Chem. 270: 6456- 6463, 1995. 3 C c

GAM7052 296 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855-862, 2000. 3 C c

GAM7052 296 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein that promotes cytochrome c- dependent caspase activation byeliminating IAP inhibition. Cell 102: 33- 42, 2000. 3 C c

GAM7052 296 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000. 3 C c

GAM7052 296 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509-3517, 2002. 3 C c

GAM7052 296 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 C c

GAM7052 296 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.: A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates caspase activity and apoptosis. Nature 410:112- 116, 2001. 3 C c

GAM7052 296 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO, a mammalian protein that promotes apoptosis by bindingto and antagonizing IAP proteins. Cell 102: 43- 53, 2000. 3 C c

GAM7052 296 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012, 2000. 3 C c

GAM7052 296 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998. 3 C c

GAM7052 296 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle-membranefusion processes. Hum. Genet. 108: 211- 215, 2001. 3 C c

GAM7052 296 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle-membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells. Biochem. Biophys. Res. Commun. 231: 808- 812, 1997. 3 C c

GAM7052 296 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996. 3 C c

GAM7052 296 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: Identification of three new splice variants of the SNARE proteinSNAP- 23. Biochem. Biophys. Res. Commun. 285: 320- 327, 2001. 3 C c

GAM7052 296 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, 3 C c

D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459- 467, 1998.

GAM7052 296 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? 3 C c Immunogenetics 53:719- 723, 2001.

GAM7052 296 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the 3 C c Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000.

GAM7052 296 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; 3 C c Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997.

GAM7052 296 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles 3 C c for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996.

GAM7052 296 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; 3 C c Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002.

GAM7052 296 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; 3 C c Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496- 1498, 2002.

GAM7052 296 TERF1 Broccoli, D.; Chong, L.; Oelmann, S.; Fernald, A. A.; Marziliano,N.; van 3 C c Steensel, B.; Kipling, D.; Le Beau, M. M.; de Lange, T.:Comparison of the human and mouse genes encoding the telomeric protein,TRF1: chromosomal localization, expression and conserved protein domains. Hum.Molec. Genet. 6: 69- 76, 1997.

GAM7052 296 TERF1 Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.;Hanish, 3 C c J.; Tempst, P.; de Lange, T.: A human telomeric protein. Science 270:1663- 1667, 1995.

GAM7052 296 TERF1 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 C c the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001.

GAM7052 296 TERF1 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 C c Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999.

GAM7052 296 TERF1 Kim, S.; Kaminker, P.; Campisi, J.: TIN2, a new regulator of telomerelength 3 C c in human cells. Nature Genet. 23: 405- 412, 1999.

GAM7052 296 TERF1 Marcand, S.; Gilson, E.; Shore, D.: A protein- counting mechanismfor 3 C c telomere length regulation in yeast. Science 275: 986- 990, 1997.

GAM7052 296 TERF1 Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M.: TRF1 is a 3 C c critical trans- acting factor required for de novo telomereformation in human cells. Hum. Molec. Genet. 9: 2639- 2650, 2000.

GAM7052 296 TERF1 Young, A. C.; Chavez, M.; Giambernardi, T. A.; Mattern, V.; McGill,J. R.; 3 C c Harris, J. M.; Sarosdy, M. F.; Patel, P.; Sakaguchi, A. Y.: Organization and expression of human telomere repeat binding factorgenes. Somat. Cell Molec. Genet. 23: 275- 286, 1997.

GAM7052 296 TERF1 Zakian, V. A.: Telomeres: beginning to understand the end. Science 270:1601- 3 C c 1607, 1995.

GAM7052 296 THRA Anderson, L. A.; Friedman, L.; Osborne- Lawrence, S.; Lynch, E.;Weissenbach, J.; Bowcock, A.; King, M.- C.: High- density genetic mapof the BRCA1 region of chromosome 17q12- q21. Genomics 17: 618- 623,1993. 3 C c

GAM7052 296 THRA Benbrook, D.; Pfahl, M.: A novel thyroid hormone receptor encodedby a cDNA clone from a human testis library. Science 238: 788- 791,1987. 3 C c

GAM7052 296 THRA Bernal, J.; Refetoff, S.; DeGroot, L. J.: Abnormalities of triiodothyroninebinding to lymphocyte and fibroblast nuclei from a patient with peripheraltissue resistance to thyroid hormone action. J. Clin. Endocr. Metab. 47:1266- 1272, 1978. 3 C c

GAM7052 296 THRA Dayton, A. I.; Selden, J. R.; Laws, G.; Dorney, D. J.; Finan, J.;Tripputi, P.; Emanuel, B. S.; Rovera, G.; Nowell, P. C.; Croce, C.M.: A human c- erbA oncogene homologue is closely proximal to thechromosome 17 breakpoint in acute promyelocytic leukemia. Proc. Nat.Acad. Sci. 81: 4495- 4499, 1984. 3 C c

GAM7052 296 THRA Debuire, B.; Henry, C.; Benaissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, P.; Stehelin, D.: Sequencing the erbA geneof avian erythroblastosis virus reveals a new type of oncogene. Science 224:1456- 1459, 1984. 3 C c

GAM7052 296 THRA Ferro, M. T.; San Roman, C.: Constitutional t(15;17). CancerGenet. Cytogenet. 4: 89- 91, 1981. 3 C c

GAM7052 296 THRA Gullberg, H.; Rudling, M.; Forrest, D.; Angelin, B.; Vennstrom,B.: Thyroid hormone receptor beta- deficient mice show complete lossof the normal cholesterol 7- alpha- hydroxylase (CYP7A) response tothyroid hormone but display enhanced resistance to dietary cholesterol. Molec.Endocr. 14: 1739- 1749, 2000. 3 C c

GAM7052 296 THRA Ichikawa, K.; Hughes, I. A.; Horwitz, A. L.; DeGroot, L. J.: Characterizationof nuclear thyroid hormone receptors of cultured skin fibroblastsfrom patients with resistance to thyroid hormone. Metabolism 36:392- 399, 1987. 3 C c

GAM7052 296 THRA Iskaros, J.; Pickard, M.; Evans, I.; Sinha, A.; Hardiman, P.; Ekins,R.: Thyroid hormone receptor gene expression in first trimester humanfetal brain. J. Clin. Endocr. Metab. 85: 2620- 2623, 2000. 3 C c

GAM7052 296 THRA Jansson, M.; Philipson, L.; Vennstrom, B.: Isolation and characterizationof multiple human genes homologous to the oncogenes of avian erythroblastosisvirus. EMBO J. 2: 561- 565, 1983. 3 C c

GAM7052 296 THRA Jhanwar, S. C.; Chaganti, R. S. K.; Croce, C. M.: Germ- line chromosomallocalization of human c- erb- A oncogene. Somat. Cell Molec. Genet. 11:99- 102, 1985. 3 C c

GAM7052 296 THRA Kaneshige, M.; Suzuki, H.; Kaneshige, K.; Cheng, J.; Wimbrow,H.; Barlow, C.; Willingham, M. C.; Cheng, S.: A targeted dominantnegative mutation of the thyroid hormone alpha- 1 receptor causes increasedmortality, infertility, and dwarfism in mice. Proc. Nat. Acad. Sci. 98:15095- 15100, 2001. 3 C c

GAM7052 296 THRA Laudet, V.; Begue, A.; Henry- Duthoit, C.; Joubel, A.; Martin,P.; Stehelin, D.; Saule, S.: Genomic organization of the human thyroidhormone receptor alpha (c- erbA- 1) gene. Nucleic Acids Res. 19: 1105- 1112,1991. 3 C c

GAM7052 296 THRA Le Beau, M. M.; Westbrook, C. A.; Diaz, M. O.; Rowley, J. D.;Oren, M.: Translocation of the p53 gene in t(15;17) in acute promyelocyticleukaemia. Nature 316: 826- 828, 1985. 3 C c

GAM7052 296 THRA Mathieu- Mahul, D.; Xu, D. Q.; Saule, S.; Lidereau, R.; Galibert,F.; Berger, R.; Mauchauffe, M.; Larsen, C. J.: An EcoRI restrictionfragment length polymorphism (RFLP) in the human c- erb A locus. Hum.Genet. 71: 41- 44, 3 C c

1985.

GAM7052 296 THRA McCabe, C. J.; Gittoes, N. J.; Sheppard, M. C.; Franklyn, J. A.: Thyroid 3 C c
receptor alpha- 1 and alpha- 2 mutations in nonfunctioningpituitary tumors.
J. Clin. Endocr. Metab. 84: 649- 653, 1999.

GAM7052 296 THRA Menezes- Ferreira, M. M.; Eil, C.; Wortsman, J.; Weintraub, B.D.: Decreased 3 C c
nuclear uptake of [125- I]triiodo- L- thyronine in fibroblastsfrom patients
with peripheral thyroid hormone resistance. J. Clin.Endocr. Metab. 59: 1081-
1087, 1984.

GAM7052 296 THRA Mitelman, F.; Manolov, G.; Manolova, Y.; Billstrom, R.; Heim,S.; 3 C c
Kristoffersson, U.; Mandahl, N.; Ferro, M. T.; San Roman, C.:High resolution
chromosome analysis of constitutional and acquiredt(15;17) maps c- erbA to
subband 17q11.2. Cancer Genet. Cytogenet. 22:95- 98, 1986.

GAM7052 296 THRA Miyajima, N.; Horiuchi, R.; Shibuya, Y.; Fukushige, S.; Matsubara,K.; 3 C c
Toyoshima, K.; Yamamoto, T.: Two erbA homologs encoding proteinswith
different T(3) binding capacities are transcribed from oppositeDNA strands
of the same genetic locus. Cell 57: 31- 39, 1989.

GAM7052 296 THRA Nagaya, T.; Nomura, Y.; Fujieda, M.; Seo, H.: Heterodimerizationpreferences 3 C c
of thyroid hormone receptor alpha isoforms. Biochem.Biophys. Res. Commun.
226: 426- 430, 1996.

GAM7052 296 THRA Nakai, A.; Seino, S.; Sakurai, A.; Szilak, I.; Bell, G. I.; DeGroot,L. J.: 3 C c
Characterization of a thyroid hormone receptor expressed inhuman kidney and
other tissues. Proc. Nat. Acad. Sci. 85: 2781- 2785,1988.

GAM7052 296 THRA Ng, L.; Rusch, A.; Amma, L. L.; Nordstrom, K.; Erway, L. C.; Vennstrom,B.; 3 C c
Forrest, D.: Suppression of the deafness and thyroid dysfunctionin Thrb-
null mice by an independent mutation in the Thra thyroid hormonereceptor
gene. Hum. Molec. Genet. 10: 2701- 2708, 2001.

GAM7052 296 THRA Puzianowska- Kuznicka, M.; Krystyniak, A.; Madej, A.; Cheng, S.- Y.;Nauman, 3 C c
J.: Functionally impaired TR mutants are present in thyroidpapillary cancer.
J. Clin. Endocr. Metab. 87: 1120- 1128, 2002.

GAM7052 296 THRA Refetoff, S.; DeGroot, L. J.; Benard, B.; DeWind, L. T.: Studiesof a sibship 3 C c
with apparent hereditary resistance to the intracellularaction of thyroid
hormone. Metabolism 21: 723- 756, 1972.

GAM7052 296 THRA Rider, S. H.; Bailey, C. J.; Voss, R.; Sheer, D.; Hiorns, L. R.;Solomon, E.: 3 C c
RFLP for the human erb- A1 gene. Nucleic Acids Res. 15:863 only, 1987.

GAM7052 296 THRA Sakurai, A.; Nakai, A.; DeGroot, L. J.: Expression of three formsof thyroid 3 C c
hormone receptor in human tissues. Molec. Endocr. 3:392- 399, 1989.

GAM7052 296 THRA Sap, J.; Munoz, A.; Damm, K.; Goldberg, Y.; Ghysdael, J.; Leutz,A.; Beug, 3 C c
H.; Vennstrom, B.: The c- erb- A protein is a high- affinityreceptor for
thyroid hormone. Nature 324: 635- 640, 1986.

GAM7052 296 THRA Sheer, D.; Sheppard, D. M.; Le Beau, M.; Rowley, J. D.; San Roman,C.; 3 C c
Solomon, E.: Localization of the oncogene c- erbA1 immediatelyproximal to
the acute promyelocytic leukaemia breakpoint on chromosome17. Ann. Hum.
Genet. 49: 167- 171, 1985.

GAM7052 296 THRA Spurr, N. K.; Goodfellow, P. N.; Sheer, D.; Bodmer, W. F.; Vennstrom,B.: 3 C c
Mapping of cellular oncogenes: ERBA1 is on chromosome 17. (Abstract)
Cytogenet.Cell Genet. 37: 591 only, 1984.

GAM7052 296 THRA Spurr, N. K.; Solomon, E.; Jansson, M.; Sheer, D.; Goodfellow,P. N.; Bodmer, 3 C c
W. F.; Vennstrom, B.: Chromosomal localisation ofthe human homologues to the
oncogenes erbA and B. EMBO J. 3: 159- 163,1984.

GAM7052 296 THRA Thompson, C. C.; Weinberger, C.; Lebo, R.; Evans, R. M.: Identificationof a 3 C c

novel thyroid hormone receptor expressed in the mammalian centralnervous system. Science 237: 1610- 1614, 1987.

GAM7052 296 THRA Weinberger, C.; Thompson, C. C.; Ong, E. S.; Lebo, R.; Gruol,D. J.; Evans, 3 C c R. M.: The c- erb- A gene encodes a thyroid hormone receptor. Nature 324:641- 646, 1986.

GAM7052 296 THRA Zabel, B. U.; Fournier, R. E. K.; Lalley, P. A.; Naylor, S. L.;Sakaguchi, A. 3 C c Y.: Cellular homologs of the avian erythroblastosisvirus erb- A and erb- B genes are syntenic in mouse but asyntenic inman. Proc. Nat. Acad. Sci. 81: 4874- 4878, 1984.

GAM7052 296 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, 3 C c M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020- 4027, 1998.

GAM7052 296 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. 3 C c R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature 410: 1099- 1103, 2001.

GAM7052 296 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; 3 C c Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress different Toll- like receptors and respond to different microbialantigens. J. Exp. Med. 194: 863- 869, 2001.

GAM7052 296 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; 3 C c Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.; Mantovani, A.: Differential expression and regulation of Toll- likereceptors (TLR) in human leukocytes: selective expression of TLR3in dendritic cells. J. Immun. 164: 5998- 6004, 2000.

GAM7052 296 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A 3 C c family of human receptors structurally related to DrosophilaToll. Proc. Nat. Acad. Sci. 95: 588- 593, 1998.

GAM7052 296 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; 3 C c Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and 13 others: Dominant and recessive deafnesscaused by mutations of a novel gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277- 284, 2002.

GAM7052 296 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; 3 C c Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M. H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant, progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002.

GAM7052 296 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 3 C c B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999.

GAM7052 296 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 C c B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997.

GAM7052 296 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 C c B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi,

A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997.

GAM7052 296 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 C c B W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM7052 296 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 C c B decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997.

GAM7052 296 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 C c B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997.

GAM7052 296 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 C c B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM7052 296 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 C c B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM7052 296 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 C c B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM7052 296 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 C c B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141- 143, 1997.

GAM7052 296 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 C c Thiopurinemethyltransferase pharmacogenetics: alternative molecular diagnosisand preliminary data from Northern Portugal. Pharmacogenetics 9:257- 261, 1999.

GAM7052 296 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 C c McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM7052 296 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 C c Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof thiopurine methyltransferase alleles in Caucasian and Asian populations. Pharmacogenetics 9:37- 42, 1999.

GAM7052 296 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 C c mercaptopurine metabolism, toxic effects, and dosagerequirement in a thiopurine methyltransferase- deficient child withacute lymphocytic leukemia. J. Pediat. 119: 985- 989, 1991.

GAM7052 296 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 C c Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM7052 296 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 C c Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine methyltransferase:molecular cloning and expression of T84 colon carcinoma cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM7052 296 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 C c

thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-749, 1993.

GAM7052 296 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 C c Evans, W. E.: A single point mutation leading to loss of catalyticactivity in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953, 1995.

GAM7052 296 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 C c variation in response to 6- mercaptopurine for childhoodacute lymphoblastic leukaemia. Lancet 336: 225- 229, 1990.

GAM7052 296 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute 3 C c azathioprine toxicity: relationship to thiopurine methyltransferasegenetic polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989.

GAM7052 296 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; 3 C c Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in thiopurine methyltransferase pharmacogenetics: evidencefor allele specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773-776, 1999.

GAM7052 296 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human 3 C c thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon splice junction mutation that results in lossof activity. J. Clin. Invest. 101: 1036- 1044, 1998.

GAM7052 296 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; 3 C c Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.; Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997.

GAM7052 296 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; 3 C c Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine methyltransferase pharmacogenetics: human gene cloningand characterization of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996.

GAM7052 296 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: 3 C c Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997.

GAM7052 296 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; 3 C c Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694-702, 1996.

GAM7052 296 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine 3 C c pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980.

GAM7052 296 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, 3 C c H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor-associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF-kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997.

GAM7052 296 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, 3 C c H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661-14664, 1996.

GAM7052 296 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; 3 C c

Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999.

GAM7052 296 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997. 3 C c

GAM7052 296 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994. 3 C c

GAM7052 296 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000. 3 C c

GAM7052 296 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the pain pathway. Nature 389: 816- 824, 1997. 3 C c

GAM7052 296 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 3 C c

GAM7052 296 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity to 'hot' chili peppers. Cell 108: 421- 430, 2002. 3 C c

GAM7052 296 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000. 3 C c

GAM7052 296 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996. 3 C c

GAM7052 296 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel activity by protein kinase C. Nature 408: 985- 990, 2000. 3 C c

GAM7052 296 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand multiple presentations of the oral irritant zingerone: relationshipto frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996. 3 C c

GAM7052 296 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994. 3 C c

GAM7052 296 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand pleasantness for the capsaicin burn between chili likers and non- likers:implications for liking development. Chem. Senses 18: 471- 482, 1993. 3 C c

GAM7052 296 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000. 3 C c

GAM7052 296 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the 3 C c

vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002.

GAM7052 296 UPK1B Finch, J. L.; Webb, G. C.; Evdokiou, A; Cowled, P. A.: 3 C c
Chromosomallocalization of the human urothelial tetraspan gene, UPK1B, to 3q13.3- q21and detection of a Taq1 polymorphism. Genomics 40: 501- 503, 1997.

GAM7052 296 UPK1B Yu, J.; Lin, J.- H.; Wu, X.- R.; Sun, T.- T.: Uroplakins Ia and Ib,two major 3 C c
differentiation products of bladder epithelium, belong toa family of four transmembrane domain (4TM) proteins. J. Cell Biol. 125:171- 182, 1994.

GAM7052 296 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. 3 C c
M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001.

GAM7052 296 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; 3 C c
Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979.

GAM7052 296 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; 3 C c
Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997.

GAM7052 296 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; 3 C c
Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001.

GAM7052 296 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; 3 C c
Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000.

GAM7052 296 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine 3 C c
l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938.

GAM7052 296 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. 3 C c
G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999.

GAM7052 296 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, 3 C c
F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM7052 296 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 3 C c
Arch.Neurol. 28: 67- 68, 1973.

GAM7052 296 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 3 C c
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM7052 296 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 3 C c
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM7052 296 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 3 C c
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM7052 296 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 3 C c
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell, J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.;

Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the von Hippel- Lindau disease tumorsuppressor gene: correlations with phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM7052 296 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 C c
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM7052 296 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 C c
disease. J.A.M.A. 178: 280- 282, 1961.

GAM7052 296 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 C c
peculiar vascular new growth, probably primarily retinal,affecting both eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM7052 296 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 C c
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.; Maher, E. R.: Molecular genetic investigations of the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM7052 296 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 C c
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E. R.: Identification of intragenic mutations in thevon Hippel- Lindau disease tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994.

GAM7052 296 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's 3 C c
disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928.

GAM7052 296 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- 3 C c
expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994.

GAM7052 296 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p 3 C c
involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988.

GAM7052 296 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, 3 C c
S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459- 6463, 1995.

GAM7052 296 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. 3 C c
P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995.

GAM7052 296 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; 3 C c
Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001.

GAM7052 296 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; 3 C c
Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto- oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995.

GAM7052 296 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, 3 C c
J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian,
Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.;
Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans
EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate
HIF by prolyl hydroxylation. Cell107: 43- 54, 2001.

GAM7052 296 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 C c

GAM7052 296 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of 3 C c
cancer. Science 278: 1043- 1050, 1997.

GAM7052 296 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of 3 C c
the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin
TRiC. Molec. Cell 1051- 1061, 1999.

GAM7052 296 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof 3 C c
von Hippel- Lindau disease. Radiology 133: 289- 295, 1979.

GAM7052 296 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three 3 C c
generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331,
1979.

GAM7052 296 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- 3 C c
Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001.

GAM7052 296 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with 3 C c
hydrocephalus as a complication of cerebellar
hemangioblastoma:identification of pro157leu mutation in the VHL gene. J.
Hum. Genet. 45:47- 51, 2000.

GAM7052 296 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C 3 C c
Thomas (pub.) 1946.

GAM7052 296 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a 3 C c
patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989.

GAM7052 296 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of 3 C c
middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg.
Path. 18: 1254- 1260, 1994.

GAM7052 296 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; 3 C c
Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.;
Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic
renal cell carcinoma: definition of a risk factorfor VHL patients to develop
an RCC. Hum. Mutat. 13: 464- 475, 1999.

GAM7052 296 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; 3 C c
De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred
with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359-
363, 1997.

GAM7052 296 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; 3 C c
Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney
cancer gene suppresses growth and functionswith VHL in a common pathway.
Oncogene 21: 3507- 3516, 2002.

GAM7052 296 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von 3 C c
Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988.

GAM7052 296 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, 3 C c
T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary
cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995.

GAM7052 296 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, 3 C c
M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.:

Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991.

GAM7052 296 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; 3 C c
Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992.

GAM7052 296 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; 3 C c
Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997.

GAM7052 296 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: 3 C c
Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984.

GAM7052 296 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: 3 C c
histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968.

GAM7052 296 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 C c

GAM7052 296 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a 3 C c
Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986.

GAM7052 296 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid 3 C c
tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour, phaeochromocytoma and the von Hippel- Lindau complex:two distinctive neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987.

GAM7052 296 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: 3 C c
Familial pheochromocytoma associated with a novel mutation inthe von Hippel-Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996.

GAM7052 296 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; 3 C c
Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam: North Holland (pub.) 14: 1972. Pp. 241- 259.

GAM7052 296 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors 3 C c
in livers with targeted inactivation of the von Hippel- Lindautumor suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001.

GAM7052 296 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis 3 C c
retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022-1034, 1971.

GAM7052 296 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar 3 C c
hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8: 601- 606,1967.

GAM7052 296 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, 3 C c
D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas. Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994.

GAM7052 296 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; 3 C c
McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.; Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma only. J. Med. Genet. 37: 939- 943,2000.

GAM7052 296 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 3 C c
Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips,

C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet. 106: 425- 431, 2000.

GAM7052 296 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 C c
von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM7052 296 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; 3 C c
Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002.

GAM7052 296 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; 3 C c
Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989.

GAM7052 296 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - 3 C c
clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976.

GAM7052 296 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, 3 C c
P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990.

GAM7052 296 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid 3 C c
body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982.

GAM7052 296 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; 3 C c
Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986.

GAM7052 296 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression 3 C c
by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995.

GAM7052 296 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: 3 C c
Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996.

GAM7052 296 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a 3 C c
biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998.

GAM7052 296 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; 3 C c
Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL- mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001.

GAM7052 296 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; 3 C c
Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel- Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998.

GAM7052 296 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; 3 C c
Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-

regulated prolyl hydroxylation. Science 292: 468- 472, 2001.

GAM7052 296 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 C c

GAM7052 296 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 3 C c

GAM7052 296 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel- Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 C c

GAM7052 296 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 C c

GAM7052 296 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 C c

GAM7052 296 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 C c

GAM7052 296 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 C c

GAM7052 296 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 C c

GAM7052 296 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573- 581, 1995. 3 C c

GAM7052 296 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 C c

GAM7052 296 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 C c

GAM7052 296 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel- Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 C c

GAM7052 296 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 C c

GAM7052 296 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 C c

GAM7052 296 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel- Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 C c

GAM7052 296 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 C c

GAM7052 296 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 C c

GAM7052 296 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, 3 C c

H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317- 1320, 1993.

GAM7052 296 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 C c

GAM7052 296 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 C c

GAM7052 296 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 C c

GAM7052 296 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 C c

GAM7052 296 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002. 3 C c

GAM7052 296 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 C c

GAM7052 296 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 3 C c

GAM7052 296 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 C c

GAM7052 296 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 C c

GAM7052 296 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 C c

GAM7080 399 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989. 3 C c

GAM7080 399 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989. 3 C c

GAM7080 399 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple 3 C c

method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987.

GAM7080 399 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human 3 C c
plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene
family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.

GAM7080 399 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: 3 C c
Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new
alleles and allele frequencies in Caucasians and in Americanblacks. Hum.
Hered. 38: 267- 272, 1988.

GAM7080 399 ABCB9 Allikmets, R.; Gerrard, B.; Hutchinson, A.; Dean, M.: Characterizationof the 3 C c
human ABC superfamily: isolation and mapping of 21 new genesusing the
expressed sequence tags database. Hum. Molec. Genet. 5:1649- 1655, 1996.

GAM7080 399 ABCB9 Zhang, F.; Zhang, W.; Liu, L.; Fisher, C. L.; Hui, D.; Childs,S.; Dorovini- 3 C c
Zis, K.; Ling, V.: Characterization of ABCB9, an ATPbinding cassette protein
associated with lysosomes. J. Biol. Chem. 275:23287- 23294, 2000.

GAM7080 399 ADRA2B Hein, L.; Altman, J. D.; Kobilka, B. K.: Two functionally distinctalpha- 2- 3 C c
adrenergic receptors regulate sympathetic neurotransmission. Nature 402:181-
184, 1999.

GAM7080 399 ADRA2B Heinonen, P.; Koulu, M.; Pesonen, U.; Karvonen, M. K.; Rissanen,A.; Laakso, 3 C c
M.; Valve, R.; Uusitupa, M.; Scheinin, M.: Identificationof a three- amino
acid deletion in the alpha- 2B- adrenergic receptorthat is associated with
reduced basal metabolic rate in obese subjects. J.Clin. Endocr. Metab. 84:
2429- 2433, 1999.

GAM7080 399 ADRA2B Lomasney, J. W.; Lorenz, W.; Allen, L. F.; King, K.; Regan, J.W.; Yang- 3 C c
Feng, T. L.; Caron, M. G.; Lefkowitz, R. J.: Expansion ofthe alpha- 2-
adrenergic receptor family: cloning and characterizationof a human alpha- 2-
adrenergic receptor subtype, the gene for whichis located on chromosome 2.
Proc. Nat. Acad. Sci. 87: 5094- 5098,1990.

GAM7080 399 ADRA2B Regan, J. W.; Kobilka, T. S.; Yang- Feng, T. L.; Caron, M. G.; Lefkowitz,R. 3 C c
J.; Kobilka, B. K.: Cloning and expression of a human kidney cDNAfor an
alpha- 2- adrenergic receptor subtype. Proc. Nat. Acad. Sci. 85:6301- 6305,
1988.

GAM7080 399 ATRN Duke- Cohan, J. S.; Gu, J.; McLaughlin, D. F.; Xu, Y.; Freeman,G. J.; 3 C c
Schlossman, S. F.: Attractin (DPPT- L), a member of the CUBfamily of cell
adhesion and guidance proteins, is secreted by activatedhuman T lymphocytes
and modulates immune cell interactions. Proc.Nat. Acad. Sci. 95: 11336-
11341, 1998.

GAM7080 399 ATRN Gunn, T. M.; Miller, K. A.; He, L.; Hyman, R. W.; Davis, R. W.;Azarani, A.; 3 C c
Schlessman, S. F.; Duke- Cohan, J. S.; Barsh, G. S.:The mouse mahogany locus
encodes a transmembrane form of human attractin. Nature 398:152- 156, 1999.

GAM7080 399 ATRN He, L.; Gunn, T. M.; Bouley, D. M.; Lu, X.- Y.; Watson, S. J.; Schlossman,S. 3 C c
F.; Duke- Cohan, J. S.; Barsh, G. S.: A biochemical function forattractin in
agouti- induced pigmentation and obesity. Nature Genet. 27:40- 47, 2001.

GAM7080 399 ATRN Nagle, D. L.; McGrail, S. H.; Vitale, J.; Woolf, E. A.; Dussault,B. J., Jr.; 3 C c
DiRocco, L.; Holmgren, L.; Montagno, J.; Bork, P.; Huszar,D.; Fairchild-
Huntress, V.; Ge, P.; Keilty, J.; Ebelling, C.; Baldini,L.; Gilchrist, J.;
Burr, P.; Carlson, G. A.; Moore, K. J.: The mahoganyprotein is a receptor
involved in suppression of obesity. Nature 398:148- 151, 1999.

GAM7080 399 ATRN Tang, W.; Gunn, T. M.; McLaughlin, D. F.; Barsh, G. S.; Schlossman,S. F.; 3 C c
Duke- Cohan, J. S.: Secreted and membrane attractin resultfrom alternative
splicing of the human ATRN gene. Proc. Nat. Acad.Sci. 97: 6025- 6030, 2000.

GAM7080 399 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; 3 C c
Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.:
Identification of Bach2 as a B- cell- specific partner for smallMaf proteins
that negatively regulate the immunoglobulin heavy chaingene 3- prime
enhancer. EMBO J. 17: 5734- 5743, 1998.

GAM7080 399 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; 3 C c
Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-
basic leucine zipper transcription factors that interact withMafK and
regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-
6095, 1996.

GAM7080 399 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, 3 C c
A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.;
Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B
cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene
19: 3739- 3749, 2000.

GAM7080 399 BFSP2 Conley, Y. P.; Erturk, D.; Keverline, A.; Mah, T. S.; Keravala,A.; Barnes, 3 C c
L. R.; Bruchis, A.; Hess, J. F.; FitzGerald, P. G.; Weeks,D. E.; Ferrell, R.
E.; Gorin, M. B.: A juvenile- onset, progressivecataract locus on chromosome
3q21- q22 is associated with a missensemutation in the beaded filament
structural protein- 2. Am. J. Hum.Genet. 66: 1426- 1431, 2000.

GAM7080 399 BFSP2 Hess, J. F.; Casselman, J. T.; FitzGerald, P. G.: Chromosomallocations of 3 C c
the genes for the beaded filament proteins CP 115 andCP 47. Curr. Eye Res.
14: 11- 18, 1995.

GAM7080 399 BFSP2 Hess, J. F.; Casselman, J. T.; FitzGerald, P. G.: Gene structureand cDNA 3 C c
sequence identify the beaded filament protein CP49 as a highlydivergent type
I intermediate filament protein. J. Biol. Chem. 271:6729- 6735, 1996.

GAM7080 399 BFSP2 Jakobs, P. M.; Hess, J. F.; FitzGerald, P. G.; Kramer, P.; Weleber,R. G.; 3 C c
Litt, M.: Autosomal- dominant congenital cataract associatedwith a deletion
mutation in the human beaded filament protein geneBFSP2. Am. J. Hum. Genet.
66: 1432- 1436, 2000.

GAM7080 399 BSN Gundelfinger, E.: Personal Communication. Madgeburg, FRG. 1/8/1999. 3 C c

GAM7080 399 BSN Hashida, H.; Goto, J.; Zhao, N.; Takahashi, N.; Hirai, M.; Kanazawa,I.; 3 C c
Sakaki, Y.: Cloning and mapping of ZNF231, a novel brain- specificgene
encoding neuronal double zinc finger protein whose expressionis enhanced in
a neurodegenerative disorder, multiple system atrophy(MSA). Genomics 54: 50-
58, 1998.

GAM7080 399 BSN Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding
sequences of unidentified human genes. VIII. 78 new cDNAclones from brain
which code for large proteins in vitro. DNA Res. 4:307- 313, 1997.

GAM7080 399 BSN tom Dieck, S.; Sanmarti- Vila, L.; Langnaese, K.; Richter, K.; Kindler,S.; 3 C c
Soyke, A.; Wex, H.; Smalla, K.- H.; Kampf, U.; Franzer, J.- T.;Stumm, M.;
Garner, C. C.; Gundelfinger, E. D.: Bassoon, a novel zinc-
fingerCAG/glutamine- repeat protein selectively localized at the active
zoneof presynaptic nerve terminals. J. Cell Biol. 142: 499- 509, 1998.

GAM7080 399 BSN Winter, c.; tom Dieck, S.; Boeckers, T. M.; Bockmann, J.; Kampf,U.; 3 C c
Sanmarti- Vila, L.; Langnaese, K.; Altrock, W.; Stumm, M.; Soyke,A.;
Wieacker, P.; Garner, C. C.; Gundelfinger, E. D.: The presynapticcytomatrix
protein Bassoon: sequence and chromosomal localizationof the human BSN gene.
Genomics 57: 389- 397, 1999.

GAM7080 399 CALB2 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.; Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of the long arm of human chromosome 16. Genomics 10:308- 312, 1991. 3 C c

GAM7080 399 CALB2 Parmentier, M.; Passage, E.; Vassart, G.; Mattei, M.- G.: The humancalbindin D28k (CALB1) and calretinin (CALB2) genes are located at8q21.3- q22.1 and 16q22- q23, respectively, suggesting a common duplicationwith the carbonic anhydrase isozyme loci. Cytogenet. Cell Genet. 57:41- 43, 1991. 3 C c

GAM7080 399 CALB2 Parmentier, M.; Szpirer, J.; Levan, G.; Vassart, G.: The humangenes for calbindin 27 and 29 kDa proteins are located on chromosomes8 and 16, respectively. Cytogenet. Cell Genet. 52: 85- 87, 1989. 3 C c

GAM7080 399 CALB2 Schiffmann, S. N.; Cheron, G.; Lohof, A.; d'Alcantara, P.; Meyer,M.; Parmentier, M.; Schurmans, S.: Impaired motor coordination andPurkinje cell excitability in mice lacking calretinin. Proc. Nat.Acad. Sci. 96: 5257- 5262, 1999. 3 C c

GAM7080 399 CAST Inazawa, J.; Nakagawa, H.; Misawa, S.; Abe, T.; Minoshima, S.;Fukuyama, R.; Maki, M.; Murachi, T.; Hatanaka, M.; Shimizu, N.: Assignmentof the human calpastatin gene (CAST) to chromosome 5 at region q14- q22.Cytogenet. Cell Genet. 54: 156- 158, 1990. 3 C c

GAM7080 399 CAST Inazawa, J.; Nakagawa, H.; Misawa, S.; Abe, T.; Minoshima, S.;Fukuyama, R.; Maki, M.; Murachi, T.; Hatanaka, M.; Shimizu, N.: Assignmentof the human calpastatin gene (CAST) to chromosome 5 at region q15- q21.(Abstract) Cytogenet. Cell Genet. 58: 1898 only, 1991. 3 C c

GAM7080 399 CAST Mimori, T.; Suganuma, K.; Tanami, Y.; Nojima, T.; Matsumura, M.;Fujii, T.; Yoshizawa, T.; Suzuki, K.; Akizuki, M.: Autoantibodiesto calpastatin (an endogenous inhibitor for calcium- dependent neutralprotease, calpain) in systemic rheumatic diseases. Proc. Nat. Acad.Sci. 92: 7267- 7271, 1995. 3 C c

GAM7080 399 CAST Pontremoli, S.; Salamino, F.; Sparatore, B.; De Tullio, R.; Pontremoli,R.; Melloni, E.: Characterization of the calpastatin defect in erythrocytesfrom patients with essential hypertension. Biochem. Biophys. Res.Commun. 157: 867- 874, 1988. 3 C c

GAM7080 399 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, D. J.; Muir, W. J.: Schizophrenia and affective disorders- - cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001. 3 C c

GAM7080 399 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 355:771- 772, 2000. 3 C c

GAM7080 399 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001. 3 C c

GAM7080 399 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970. 3 C c

GAM7080 399 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000. 3 C c

GAM7080 399 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, 3 C c
G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced
autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM7080 399 DMP1 Aplin, H. M.; Hirst, K. L.; Crosby, A. H.; Dixon, M. J.: Mappingof the human 3 C c
dentin matrix acidic phosphoprotein gene (DMP1) to thedentinogenesis
imperfecta type II critical region at chromosome 4q21. Genomics 30:347- 349,
1995.

GAM7080 399 DMP1 George, A.; Sabsay, B.; Simonian, P. A.; Veis, A.: Characterizationof a 3 C c
novel dentin matrix acidic phosphoprotein: implications for inductionof
biomineralization . J. Biol. Chem. 268: 12624- 12630, 1993.

GAM7080 399 DMP1 Hirst, K. L.; Simmons, D.; Feng, J.; Aplin, H.; Dixon, M. J.; MacDougall,M.: 3 C c
Elucidation of the sequence and the genomic organization of thehuman dentin
matrix acidic phosphoprotein 1 (DMP1) gene: exclusionof the locus from a
causative role in the pathogenesis of dentinogenesisimperfecta type II.
Genomics 42: 38- 45, 1997.

GAM7080 399 DMP1 MacDougall, M.; DuPont, B. R.; Simmons, D.; Leach, R. J.: Assignmentof DMP1 3 C c
to human chromosome 4 band q21 by in situ hybridization. Cytogenet.Cell.
Genet. 74: 189 only, 1996.

GAM7080 399 DNMT3A Baylin, S. B.; Herman, J. G.; Graff, J. R.; Vertino, P. M.; Issa,J. P.: 3 C c
Alterations in DNA methylation: a fundamental aspect of neoplasia.
Adv.Cancer Res. 72: 141- 196, 1998.

GAM7080 399 DNMT3A Lei, H.; Oh, S. P.; Okano, M.; Juttermann, R.; Goss, K. A.; Jaenisch,R.; Li, 3 C c
E.: De novo DNA cytosine methyltransferase activities inmouse embryonic stem
cells. Development 122: 3195- 3205, 1996.

GAM7080 399 DNMT3A Lyko, F.; Ramsahoye, B. H.; Kashevsky, H.; Tudor, M.; Mastrangelo,M.- A.; 3 C c
Orr- Weaver, T. L.; Jaenisch, R.: Mammalian (cytosine- 5)
methyltransferasescause genomic DNA methylation and lethality in Drosophila.
NatureGenet. 23: 363- 366, 1999.

GAM7080 399 DNMT3A Okano, M.; Bell, D. W.; Haber, D. A.; Li, E.: DNA methyltransferasesDnmt3a 3 C c
and Dnmt3b are essential for de novo methylation and mammaliandevelopment.
Cell 99: 247- 257, 1999.

GAM7080 399 DNMT3A Okano, M.; Xie, S.; Li, E.: Cloning and characterization of afamily of novel 3 C c
mammalian DNA (cytosine- 5) methyltransferases. (Letter) NatureGenet. 19:
219- 220, 1998.

GAM7080 399 DNMT3A Robertson, K. D.; Uzvolgyi, E.; Liang, G.; Talmadge, C.; Sumegi,J.; 3 C c
Gonzales, F. A.; Jones, P. A.: The human DNA methyltransferases(DNMTs) 1, 3a
and 3b: coordinate mRNA expression in normal tissuesand overexpression in
tumors. Nucleic Acids Res. 27: 2291- 2298,1999.

GAM7080 399 DNMT3A Xie, S.; Wang, Z.; Okano, M.; Nogami, M.; Li, Y.; He, W.- W.; Okumura,K.; 3 C c
Li, E.: Cloning, expression and chromosome locations of the humanDNMT3 gene
family. Gene 236: 87- 95, 1999.

GAM7080 399 EHF Kas, K.; Finger, E.; Grall, F.; Gu, X.; Akbarali, Y.; Boltax, J.;Weiss, A.; 3 C c
Oettgen, P.; Kapeller, R.; Libermann, T. A.: ESE- 3, anovel member of an
epithelium- specific Ets transcription factor subfamily,demonstrates
different target gene specificity from ESE- 1. J. Biol.Chem. 275: 2986-
2998, 2000.

GAM7080 399 EHF Kleinbaum, L. A.; Duggan, C.; Ferreira, E.; Coffey, G. P.; Buttice,G.; 3 C c
Burton, F. H.: Human chromosomal localization, tissue/tumor expression,and
regulatory function of the ets family gene EHF. Biochem. Biophys.Res.
Commun. 264: 119- 126, 1999.

GAM7080 399 EPHA3 Boyd, A. W.; Ward, L. D.; Wicks, I. P.; Simpson, R. J.; Salvaris,E.; Wilks, A.; Welch, K.; Loudovaris, M.; Rockman, S.; Busmanis, I.: Isolation and characterization of a novel receptor- type proteintyrosine kinase (hek) from a human pre- B cell line. J. Biol. Chem. 267:3262- 3267, 1992. 3 C c

GAM7080 399 EPHA3 Fox, G. M.; Holst, P. L.; Chute, H. T.; Lindberg, R. A.; Janssen,A. M.; Basu, R.; Welcher, A. A.: cDNA cloning and tissue distributionof five human EPH- like receptor protein- tyrosine kinases. Oncogene 10:897- 905, 1995. 3 C c

GAM7080 399 EPHA3 Wicks, I. P.; Lapsys, N. M.; Baker, E.; Campbell, L. J.; Boyd,A. W.; Sutherland, G. R.: Localization of a human receptor tyrosinekinase (ETK1) to chromosome region 3p11.2. Genomics 19: 38- 41, 1994. 3 C c

GAM7080 399 EPHA3 Wicks, I. P.; Wilkinson, D.; Salvaris, E.; Boyd, A. W.: Molecularcloning of HEK, the gene encoding a receptor tyrosine kinase expressedby human lymphoid tumor cell lines. Proc. Nat. Acad. Sci. 89: 1611- 1615,1992. 3 C c

GAM7080 399 ERBB2IP Borg, J.- P.; Marchetto, S.; Le Bivic, A.; Ollendorff, V.; Jaulin-Bastard,F.; Saito, H.; Fournier, E.; Adelaide, J.; Margolis, B.; Birnbaum,D.: ERBIN: a basolateral PDZ protein that interacts with the mammalianERBB2/HER2 receptor. Nature Cell Biol. 2: 407- 414, 2000. 3 C c

GAM7080 399 ERBB2IP Favre, B.; Fontao, L.; Koster, J.; Shafaatian, R.; Jaunin, F.;Saurat, J.-H.; Sonnenberg, A.; Borradori, L.: The hemidesmosomalprotein bullous pemphigoid antigen 1 and the integrin beta- 4 subunitbind to ERBIN: molecular cloning of multiple alternative splice variantsof ERBIN and analysis of their tissue expression. J. Biol. Chem. 276:32427- 32436, 2001. 3 C c

GAM7080 399 ERBB2IP Huang, Y. Z.; Wang, Q.; Xiong, W. C.; Mei, L.: Erbin is a proteinconcentrated at postsynaptic membranes that interacts with PSD- 95. J.Biol. Chem. 276: 19318- 19326, 2001. 3 C c

GAM7080 399 FRAT2 Saitoh, T.; Moriwaki, J.; Koike, J.; Takagi, A.; Miwa, T.; Shiokawa,K.; Katoh, M.: Molecular cloning and characterization of FRAT2, encodinga positive regulator of the WNT signaling pathway. Biochem. Biophys.Res. Commun. 281: 815- 820, 2001. 3 C c

GAM7080 399 FRAT2 Yost, C.; Farr, G. H., III; Pierce, S. B.; Ferkey, D. M.; Chen,M. M.; Kimelman, D.: GBP, an inhibitor of GSK- 3, is implicated inXenopus development and oncogenesis. Cell 93: 1031- 1041, 1998. 3 C c

GAM7080 399 GFRA1 Eng, C.; Myers, S. M.; Kogon, M. D.; Sanicola, M.; Hession, C.;Cate, R. L.; Mulligan, L. M.: Genomic structure and chromosomal localizationof the human GDNFR- alpha gene. Oncogene 16: 597- 601, 1998. 3 C c

GAM7080 399 GFRA1 GFR- alpha Nomenclature Committee: Nomenclature of GPI- linkedreceptors for the GDNF ligand family. Neuron 19: 485 only, 1997. 3 C c

GAM7080 399 GFRA1 Gorodinsky, A.; Zimonjic, D. B.; Popescu, N. C.; Milbrandt, J.: Assignment of the GDNF family receptor alpha- 1 (GFRA1) to humanchromosome band 10q26 by in situ hybridization. Cytogenet. Cell Genet. 78:289- 290, 1997. 3 C c

GAM7080 399 GFRA1 Jing, S.; Wen, D.; Yu, Y.; Holst, P. L.; Luo, Y.; Fang, M.; Tamir,R.; Antonio, L.; Hu, Z.; Cupples, R.; Louis, J.- C.; Hu, S.; Altrock,B. W.; Fox, G. M.: GDNF- induced activation of the Ret protein tyrosinekinase is mediated by GDNFR- alpha, a novel receptor for GDNF. Cell 85:1113- 1124, 1996. 3 C c

GAM7080 399 GFRA1 Paratcha, G.; Ledda, F.; Baars, L.; Coulpier, M.; Besset, V.; Anders,J.; Scott, R.; Ibanez, C. F.: Released GFR- alpha- 1 potentiates downstreamsignaling, neuronal survival, and differentiation via a novel mechanismof recruitment of c- Ret to lipid rafts. Neuron 29: 171- 184, 2001. 3 C c

GAM7080 399 GFRA1 Puliti, A.; Cinti, R.; Seri, M.; Ceccherini, I.; Romeo, G.: Assignmentof 3 C c
mouse Gfra1, the homologue of a new human HSCR candidate gene,to the
telomeric region of mouse chromosome 19. Cytogenet. Cell Genet. 78:291- 294,
1997.

GAM7080 399 GFRA1 Shefelbine, S. E.; Khorana, S.; Schultz, P. N.; Huang, E.; Thobe,N.; Hu, Z. 3 C c
J.; Fox, G. M.; Jing, S.; Cote, G. J.; Gagel, R. F.: Mutationalanalysis of
the GDNF/RET- GDNFR- alpha signaling complex in a kindredwith vesicoureteral
reflux. Hum. Genet. 102: 474- 478, 1998.

GAM7080 399 GNAQ Adams, J. W.; Sakata, Y.; Davis, M. G.; Sah, V. P.; Wang, Y.; Liggett,S. B.; 3 C c
Chien, K. R.; Brown, J. H.; Dorn, G. W., II: Enhanced G- alpha- qsignaling:
a common pathway mediates cardiac hypertrophy and apoptoticheart failure.
Proc. Nat. Acad. Sci. 95: 10140- 10145, 1998.

GAM7080 399 GNAQ Dong, Q.; Shenker, A.; Way, J.; Haddad, B. R.; Lin, K.; Hughes,M. R.; 3 C c
McBride, O. W.; Spiegel, A. M.; Battey, J.: Molecular cloningof human G-
alpha(q) cDNA and chromosomal localization of the G- alpha(q)gene (GNAQ) and
a processed pseudogene. Genomics 30: 470- 475, 1995.

GAM7080 399 GNAQ Gabbeta, J.; Yang, X.; Kowalska, M. A.; Sun, L.; Dhanasekaran,N.; Rao, A. 3 C c
K.: Platelet signal transduction defect with G- alphasubunit dysfunction and
diminished G- alpha(q) in a patient with abnormalplatelet responses. Proc.
Nat. Acad. Sci. 94: 8750- 8755, 1997.

GAM7080 399 GNAQ Offermanns, S.; Hashimoto, K.; Watanabe, M.; Sun, W.; Kurihara,H.; Thompson, 3 C c

R. F.; Inoue, Y.; Kano, M.; Simon, M. I.: Impairedmotor coordination and
persistent multiple climbing fiber innervationof cerebellar Purkinje cells
in mice lacking G- alpha- q. Proc. Nat.Acad. Sci. 94: 14089- 14094, 1997.

GAM7080 399 GNAQ Offermanns, S.; Toombs, C. F.; Hu, Y.- H.; Simon, M. I.: Defectiveplatelet 3 C c
activation in G- alpha- q- deficient mice. Nature 389: 183- 186,1997.

GAM7080 399 GNAQ Offermanns, S.; Zhao, L.- P.; Gohla, A.; Sarosi, I.; Simon, M. I.;Wilkie, T. 3 C c
M.: Embryonic cardiomyocyte hypoplasia and craniofacialdefects in G- alpha-
q/G- alpha- 11- mutant mice. EMBO J. 17: 4304- 4312,1998.

GAM7080 399 GNAQ Oyesiku, N. M.; Evans, C.- O.; Brown, M. R.; Blevins, L. S.; Tindall,G. T.; 3 C c
Parks, J. S.: Pituitary adenomas: screening for G- alpha- qmutations. J.
Clin. Endocr. Metab. 82: 4184- 4188, 1997.

GAM7080 399 GNAQ Rao, A. K.; Koike, K.; Willis, J.; Daniel, J. L.; Beckett, C.;Hassel, B.; 3 C c
Day, H. J.; Smith, J. B.; Holmsen, H.: Platelet secretiondefect associated
with impaired liberation of arachidonic acid andnormal myosin light chain
phosphorylation. Blood 64: 914- 921, 1984.

GAM7080 399 GNAQ Santagata, S.; Boggon, T. J.; Baird, C. L.; Gomez, C. A.; Zhao,J.; Shan, W. 3 C c
S.; Myszka, D. G.; Shapiro, L.: G- protein signalingthrough tubby proteins.
Science 292: 2041- 2050, 2001.

GAM7080 399 GRM4 Barbon, A.; Ferraboli, S.; Barlati, S.: Assignment of the humanmetabotropic 3 C c
glutamate receptor gene GRM4 to chromosome 6 band p21.3by radiation hybrid
mapping. Cytogenet. Cell Genet. 88: 210 only,2000.

GAM7080 399 GRM4 Gerlai, R.; Roder, J. C.; Hampson, D. R.: Altered spatial learningand memory 3 C c
in mice lacking the mGluR4 subtype of metabotropic glutamatereceptor. Behav.
Neurosci. 112: 525- 532, 1998.

GAM7080 399 GRM4 Makoff, A.; Lelchuk, R.; Oxer, M.; Harrington, K.; Emson, P.:Molecular 3 C c
characterization and localization of human metabotropicglutamate receptor
type 4. Molec. Brain Res. 37: 239- 248, 1996.

GAM7080 399 GRM4 Pekhletski, R.; Gerlai, R.; Overstreet, L. S.; Huang, X. P.; Agopyan,N.; 3 C c

Slater, N. T.; Abramow- Newerly, W.; Roder, J. C.; Hampson, D.R.: Impaired cerebellar synaptic plasticity and motor performancein mice lacking the mGluR4 subtype of metabotropic glutamate receptor. J.Neurosci. 16: 6364- 6373, 1996.

GAM7080 399 GRM4 Wu, S.; Wright, R. A.; Rockey, P. K.; Burgett, S. G.; Arnold, J.S.; Rosteck, 3 C c
P. R., Jr.; Johnson, B. G.; Schoepp, D. D.; Belagaje,R. M.: Group III human metabotropic glutamate receptors 4, 7 and8: molecular cloning, functional expression, and comparison of pharmacologicalproperties in RGT cells. Molec. Brain Res. 53: 88- 97, 1998.

GAM7080 399 GRPR Bolton, P.; Powell, J.; Rutter, M.; Buckle, V.; Yates, J. R. W.;Ishikawa- 3 C c
Brush, Y.; Monaco, A. P.: Autism, mental retardation, multipleexostoses and short stature in a female with 46,X,t(X;8)(p22.13;q22.1). Psychiat.Genet. 5: 51- 55, 1995.

GAM7080 399 GRPR Ishikawa- Brush, Y.; Powell, J. F.; Bolton, P.; Miller, A. P.; Francis,F.; 3 C c
Willard, H. F.; Lehrach, H.; Monaco, A. P.: Autism and multipleexostoses associated with an X;8 translocation occurring within theGRPR gene and 3-prime to the SDC2 gene. Hum. Molec. Genet. 6: 1241- 1250,1997.

GAM7080 399 GRPR Maslen, G. L.; Boyd, Y.: Comparative mapping of the Grpr locuson the X 3 C c
chromosomes of man and mouse. Genomics 17: 106- 109, 1993.

GAM7080 399 GRPR Schantz, L. J.; Naylor, S. L.; Giladi, E.; Spindel, E. R.: Assignmentof the 3 C c
GRP receptor gene to the human X chromosome. (Abstract) Cytogenet.Cell Genet. 58: 2085- 2086, 1991.

GAM7080 399 GRPR Shiraishi, M.; Alitalo, T.; Sekiya, T.: The chromosomal organizationof the 3 C c
human endogenous retrovirus- like sequence HERV- H: clusteringof the HERV- H sequences in a 300- kb region close to the GRPR locuson the X chromosome. DNA Res. 3: 425- 429, 1996.

GAM7080 399 GRPR Shriver, S. P.; Bourdeau, H. A.; Gubish, C. T.; Tirpak, D. L.;Davis, A. L. 3 C c
G.; Luketich, J. D.; Siegfried, J. M.: Sex- specificexpression of gastrin-releasing peptide receptor: relationship tosmoking history and risk of lung cancer. J. Nat. Cancer Inst. 92:24- 33, 2000.

GAM7080 399 GRPR Spindel, E. R.; Giladi, E.; Brehm, P.; Goodman, R. H.; Segerson,T. P.: 3 C c
Cloning and functional characterization of a complementaryDNA encoding the murine fibroblast bombesin/gastrin- releasing peptidereceptor. Molec. Endocr. 4: 1956- 1963, 1990.

GAM7080 399 GSTM3 Campbell, E.; Takahashi, Y.; Abramovitz, M.; Peretz, M.; Listowsky,I.: A 3 C c
distinct human testis and brain mu- class glutathione S-transferase:molecular cloning and characterization of a form present even in individualslacking hepatic type mu isoenzymes. J. Biol. Chem. 265: 9188- 9193,1990.

GAM7080 399 GSTM3 Gough, A. C.; Zhong, S.; Wolf, C. R.; Spurr, N. K.: Chromosomeassignment of 3 C c
the human glutathione S- transferase mu- 3 gene (GSTM3)to chromosome 1 by gene specific polymerase chain reaction. Cytogenet.Cell Genet. 65: 111- 114, 1994.

GAM7080 399 GSTM3 Inskip, A.; Elexperu- Camiruaga, J.; Buxton, N.; Dias, P. S.; MacIntosh,J.; 3 C c
Campbell, D.; Jones, P. W.; Yengi, L.; Talbot, J. A.; Strange,R. C.; Fryer, A. A.: Identification of polymorphism at the glutathioneS- transferase, GSTM3 locus: evidence for linkage with GSTM1*A. Biochem.J. 312: 713- 716, 1995.

GAM7080 399 GSTM3 Pearson, W. R.; Vorachek, W. R.; Xu, S.; Berger, R.; Hart, I.;Vannais, D.; 3 C c
Patterson, D.: Identification of class- mu glutathionetransferase genes

GSTM1- GSTM5 on human chromosome 1p13. Am. J. Hum.Genet. 53: 220- 233, 1993.

GAM7080 399 GSTM3 Van Cong, N.; Laisney, V.; Gross, M. S.; Frezal, J.: Glutathione- S- 3 C c
transferases- - tissuesdistribution, number of loci, polymorphism,
chromosome localization.(Abstract) Cytogenet. Cell Genet. 37: 554, 1984.

GAM7080 399 HTR2C Brennan, T. J.; Seeley, W. W.; Kilgard, M.; Schreiner, C. E.; Tecott,L. H.: 3 C c
Sound- induced seizures in serotonin 5- HT- 2C receptor mutantmice. Nature
Genet. 16: 387- 390, 1997.

GAM7080 399 HTR2C Gurevich, I.; Tamir, H.; Arango, V.; Dwork, A. J.; Mann, J. J.;Schmauss, C.: 3 C c
Altered editing of serotonin 2C receptor pre- mRNA inthe prefrontal cortex
of depressed suicide victims. Neuron 34: 349- 356,2002.

GAM7080 399 HTR2C Hall, C. S.: Genetic differences in fatal audiogenic seizures:between two 3 C c
inbred strains of house mice. J. Hered. 38: 3- 6, 1947.

GAM7080 399 HTR2C Heisler, L. K.; Cowley, M. A.; Tecott, L. H.; Fan, W.; Low, M.J.; Smart, J. 3 C c
L.; Rubinstein, M.; Tatro, J. B.; Marcus, J. N.; Holstege,H.; Lee, C. E.;
Cone, R. D.; Elmquist, J. K.: Activation of centralmelanocortin pathways by
fenfluramine. Science 297: 609- 611, 2002.

GAM7080 399 HTR2C Holmes, C.; Arranz, M. J.; Powell, J. F.; Collier, D. A.; Lovestone,S.: 5- 3 C c
HT- 2A and 5- HT- 2C receptor polymorphisms and psychopathologyin late onset
Alzheimer's disease. Hum. Molec. Genet. 7: 1507- 1509,1998.

GAM7080 399 HTR2C Lappalainen, J.; Zhang, L.; Dean, M.; Oz, M.; Ozaki, N.; Yu, D.;Virkkunen, 3 C c
M.; Weight, F.; Linnoila, M.; Goldman, D.: Identification,expression, and
pharmacology of a cys(23)- ser(23) substitution inthe human 5- HT(2C)
receptor gene (HTR2C). Genomics 27: 274- 279,1995.

GAM7080 399 HTR2C Milatovich, A.; Hsieh, C.- L.; Bonaminio, G.; Tecott, L.; Julius,D.; 3 C c
Francke, U.: Serotonin receptor 1c gene assigned to X chromosomein human
(band q24) and mouse (bands D- F4). Hum. Molec. Genet. 1:681- 684, 1992.

GAM7080 399 HTR2C Tecott, L. H.; Sun, L. M.; Akana, S. F.; Strack, A. M.; Lowenstein,D. H.; 3 C c
Dallman, M. F.; Julius, D.: Eating disorder and epilepsy inmice lacking 5-
HT2C serotonin receptors. Nature 374: 542- 546, 1995.

GAM7080 399 ICA1 Gaedigk, R.; Duncan, A. M. V.; Miyazaki, I.; Robinson, B. H.; Dosch,H.- M.: 3 C c
ICA1 encoding p69, a protein linked to the development oftype 1 diabetes,
maps to human chromosome 7p22. Cytogenet. Cell Genet. 66:274- 276, 1994.

GAM7080 399 ICA1 Gaedigk, R.; Karges, W.; Hui, M. F.; Scherer, S. W.; Dosch, H.- M.: Genomic 3 C c
organization and transcript analysis of ICAp69, a targetantigen in diabetic
autoimmunity. Genomics 38: 382- 391, 1996.

GAM7080 399 ICA1 Pietropaolo, M.; Castano, L.; Babu, S.; Buelow, R.; Kuo, Y.- L.S.; Martin, 3 C c
S.; Martin, A.; Powers, A. C.; Prochazka, M.; Naggert,J.; Leiter, E. H.;
Eisenbarth, G. S.: Islet cell autoantigen 69 kD(ICA69): molecular cloning
and characterization of a novel diabetes- associatedautoantigen. J. Clin.
Invest. 92: 359- 371, 1993.

GAM7080 399 IL24 Blumberg, H.; Conklin, D.; Xu, W.; Grossmann, A.; Brender, T.;Carollo, S.; 3 C c
Eagan, M.; Foster, D.; Haldeman, B. A.; Hammond, A.;Haugen, H.; Jelinek, L.;
and 14 others: Interleukin 20: discovery,receptor identification, and role
in epidermal function. Cell 104:9- 19, 2001.

GAM7080 399 IL24 Huang, E. Y.; Madireddi, M. T.; Gopalkrishnan, R. V.; Leszczyniecka,M.; Su, 3 C c
Z.; Lebedeva, I. V.; Kang, D.; Jiang, H.; Lin, J. J.; Alexandre,D.; Chen,
Y.; Vozhilla, N.: and 9 others: Genomic structure, chromosomallocalization
and expression profile of a novel melanoma differentiationassociated (mda-
7) gene with cancer specific growth suppressing andapoptosis inducing
properties. Oncogene 20: 7051- 7063, 2001.

GAM7080 399 IL24 Jiang, H.; Lin, J. J.; Su, Z.- Z.; Goldstein, N. I.; Fisher, P.B.: 3 C c
Subtraction hybridization identifies a novel melanoma
differentiationassociated gene, mda- 7, modulated during human melanoma
differentiation,growth and progression. Oncogene 11: 2477- 2486, 1995.

GAM7080 399 IL24 Jiang, H.; Su, Z.- Z.; Lin, J. J.; Goldstein, N. I.; Young, C. S.H.; Fisher, 3 C c
P. B.: The melanoma differentiation associated gene mda- 7suppresses cancer
cell growth. Proc. Nat. Acad. Sci. 93: 9160- 9165,1996.

GAM7080 399 IL24 Su, Z.; Madireddi, M. T.; Lin, J. J.; Young, C. S. H.; Kitada,S.; Reed, J. 3 C c
C.; Goldstein, N. I.; Fisher, P. B.: The cancer growthsuppressor gene mda- 7
selectively induces apoptosis in human breastcancer cells and inhibits tumor
growth in nude mice. Proc. Nat. Acad.Sci. 95: 14400- 14405, 1998.

GAM7080 399 IL6ST Chow, D.; He, X.; Snow, A. L.; Rose- John, S.; Garcia, K. C.: Structureof an 3 C c
extracellular gp130 cytokine receptor signaling complex. Science 291:2150-
2155, 2001.

GAM7080 399 IL6ST Hirota, H.; Chen, J.; Betz, U. A. K.; Rajewsky, K.; Gu, Y.; Ross,J., Jr.; 3 C c
Muller, W.; Chien, K. R.: Loss of a gp130 cardiac musclecell survival
pathway is a critical event in the onset of heart failureduring biochemical
stress. Cell 97: 189- 198, 1999.

GAM7080 399 IL6ST Kidd, V. J.; Nesbitt, J. E.; Fuller, G. M.: Chromosomal localizationof the 3 C c
IL- 6 receptor signal transducing subunit, gp130 (IL6ST). Somat.Cell Molec.
Genet. 18: 477- 483, 1992.

GAM7080 399 IL6ST Kishimoto, T.; Taga, T.; Akira, S.: Cytokine signal transduction. Cell 3 C c
76:253- 262, 1994.

GAM7080 399 IL6ST Rodriguez, C.; Grosgeorge, J.; Nguyen, V. C.; Gaudray, P.; Theillet,C.: 3 C c
Human gp130 transducer chain gene (IL6ST) is localized to chromosomeband
5q11 and possesses a pseudogene on chromosome band 17p11. Cytogenet.Cell
Genet. 70: 64- 67, 1995.

GAM7080 399 IL6ST Tebbutt, N. C.; Giraud, A. S.; Inglese, M.; Jenkins, B.; Waring,P.; Clay, F. 3 C c
J.; Malki, S.; Alderman, B. M.; Grail, D.; Hollande,F.; Heath, J. K.; Ernst,
M.: Reciprocal regulation of gastrointestinalhomeostasis by SHP2 and STAT-
mediated trefoil gene activation in gp130mutant mice. Nature Med. 8: 1089-
1097, 2002.

GAM7080 399 KCNQ2 Berkovic, S. F.; Kennerson, M. L.; Howell, R. A.; Scheffer, I.E.; Hwang, P. 3 C c
A.; Nicholson, G. A.: Phenotypic expression of benignfamilial neonatal
convulsions linked to chromosome 20. Arch. Neurol. 51:1125- 1128, 1994.

GAM7080 399 KCNQ2 Biervert, C.; Schroeder, B. C.; Kubisch, C.; Berkovic, S. F.; Propping,P.; 3 C c
Jentsch, T. J.; Steinlein, O. K.: A potassium channel mutationin neonatal
human epilepsy. Science 279: 406- 409, 1998.

GAM7080 399 KCNQ2 Biervert, C.; Steinlein, O. K.: Structural and mutational analysisof KCNQ2, 3 C c
the major gene locus for benign familial neonatal convulsions. Hum.Genet.
104: 234- 240, 1999.

GAM7080 399 KCNQ2 Cooper, E. C.; Aldape, K. D.; Abosch, A.; Barbaro, N. M.; Berger,M. S.; 3 C c
Peacock, W. S.; Jan, Y. N.; Jan, L. Y.: Colocalization andcoassembly of two
human brain M- type potassium channel subunits thatare mutated in epilepsy.
Proc. Nat. Acad. Sci. 97: 4914- 4919, 2000.

GAM7080 399 KCNQ2 Dedek, K.; Kunath, B.; Kananura, C.; Reuner, U.; Jentsch, T. J.;Steinlein, 3 C c
O. K.: Myokymia and neonatal epilepsy caused by a mutationin the voltage
sensor of the KCNQ2 K(+) channel. Proc. Nat. Acad.Sci. 98: 12272- 12277,
2001.

GAM7080 399 KCNQ2 del Giudice, E. M.; Coppola, G.; Scuccimarra, G.; Cirillo, G.;Bellini, G.; 3 C c

Pascotto, A.: Benign familial neonatal convulsions (BFNC)resulting from mutation of the KCNQ2 voltage sensor. Europ. J. Hum.Genet. 8: 994- 997, 2000.

GAM7080 399 KCNQ2 Singh, N. A.; Charlier, C.; Stauffer, D.; DuPont, B. R.; Leach,R. J.; Melis, R.; Ronen, G. M.; Bjerre, I.; Quattlebaum, T.; Murphy,J. V.; McHarg, M. L.; Gagnon, D.; Rosales, T. O.; Peiffer, A.; Anderson,V. E.; Leppert, M.: A novel potassium channel gene, KCNQ2, is mutatedin an inherited epilepsy of newborns. Nature Genet. 18: 25- 29, 1998. 3 C c

GAM7080 399 KCNQ2 Wang, H.- S.; Pan, Z.; Shi, W.; Brown, B. S.; Wymore, R. S.; Cohen,I. S.; Dixon, J. E.; McKinnon, D.: KCNQ2 and KCNQ3 potassium channelsubunits: molecular correlates of the M- channel. Science 282: 1890- 1893,1998. 3 C c

GAM7080 399 KCNQ2 Wang, Q.; Curren, M. E.; Splawski, I.; Burn, T. C.; Millholland,J. M.; VanRaay, T. J.; Shen, J.; Timothy, K. W.; Vincent, G. M.; deJager, T.; Schwartz, P. J.; Towbin, J. A.; Moss, A. J.; Atkinson,D. L.; Landes, G. M.; Connors, T. D.; Keating, M. T.: Positionalcloning of a novel potassium channel gene: KVLQT1 mutations causecardiac arrhythmias. Nature Genet. 12: 17- 23, 1996. 3 C c

GAM7080 399 KCNQ2 Yang, W.- P.; Levesque, P. C.; Little, W. A.; Conder, M. L.; Ramakrishnan,P.; Neubauer, M. G.; Blanar, M. A.: Functional expression of twoKvLQT1- related potassium channels responsible for an inherited idiopathicepilepsy. J. Biol. Chem. 273: 19419- 19423, 1998. 3 C c

GAM7080 399 NBS1 Carlomagno, F.; Chang- Claude, J.; Dunning, A. M.; Ponder, B. A.J.: Determination of the frequency of the common 675del5 Nijmegenbreakage syndrome mutation in the German population: no associationwith risk of breast cancer. Genes Chromosomes Cancer 25: 393- 395,1999. 3 C c

GAM7080 399 NBS1 Carney, J. P.; Maser, R. S.; Olivares, H.; Davis, E. M.; Le Beau,M.; Yates, J. R., III; Hays, L.; Morgan, W. F.; Petrini, J. H. J.: The hMre11/hRad50 protein complex and Nijmegen breakage syndrome:linkage of double- strand break repair to the cellular DNA damage response. Cell 93:477- 486, 1998. 3 C c

GAM7080 399 NBS1 Chen, H. T.; Bhandoola, A.; Difilippantonio, M. J.; Zhu, J.; Brown,M. J.; Tai, X.; Rogakou, E. P.; Brotz, T. M.; Bonner, W. M.; Ried,T.; Nussenzweig, A.: Response to RAG- mediated V(D)J cleavage by NBS1and gamma- H2AX. Science 290: 1962- 1964, 2000. 3 C c

GAM7080 399 NBS1 Falck, J.; Petrini, J. H. J.; Williams, B. R.; Lukas, J.; Bartek,J.: The DNA damage- dependent intra- S phase checkpoint is regulatedby parallel pathways. Nature Genet. 30: 290- 294, 2002. 3 C c

GAM7080 399 NBS1 Gatei, M.; Young, D.; Cerosaletti, K. M.; Desai- Mehta, A.; Spring,K.; Kozlov, S.; Lavin, M. F.; Gatti, R. A.; Concannon, P.; Khanna,K.: ATM- dependent phosphorylation of nibrin in response to radiationexposure. Nature Genet. 25: 115- 119, 2000. 3 C c

GAM7080 399 NBS1 Kleier, S.; Herrmann, M.; Wittwer, B.; Varon, R.; Reis, A.; Horst,J.: Clinical presentation and mutation identification in the NBS1gene in a boy with Nijmegen breakage syndrome. Clin. Genet. 57:384- 387, 2000. 3 C c

GAM7080 399 NBS1 Lim, D.- S.; Kim, S.- T.; Xu, B.; Maser, R. S.; Lin, J.; Petrini,J. H. J.; Kastan, M. B.: ATM phosphorylates p95/nbs1 in an S- phasecheckpoint pathway. Nature 404: 613- 617, 2000. 3 C c

GAM7080 399 NBS1 Lombard, D. B.; Guarente, L.: Nijmegen breakage syndrome diseaseprotein and MRE11 at PML nuclear bodies and meiotic telomeres. CancerRes. 60: 2331- 2334, 2000. 3 C c

GAM7080 399 NBS1 Maser, R. S.; Zinkel, R.; Petrini, J. H. J.: An alternative modeof 3 C c

translation permits production of a variant NBS1 protein from thecommon Nijmegen breakage syndrome allele. Nature Genet. 27: 417- 421,2001.

GAM7080 399 NBS1 Matsuura, S.; Tauchi, H.; Nakamura, A.; Kondo, N.; Sakamoto, S.;Endo, S.; 3 C c Smeets, D.; Solder, B.; Belohradsky, B. H.; Der Kaloustian,V. M.; Oshimura, M.; Isomura, M.; Nakamura, Y.; Komatsu, K.: Positionalcloning of the gene for Nijmegen breakage syndrome. Nature Genet. 19:179- 181, 1998.

GAM7080 399 NBS1 Petersen, S.; Casellas, R.; Reina- San- Martin, B.; Chen, H. 3 C c T.;Difilippantonio, M. J.; Wilson, P. C.; Hanitsch, L.; Celeste, A.;Muramatsu, M.; Pilch, D. R.; Redon, C.; Ried, T.; Bonner, W. M.; Honjo,T.; Nussenzweig, M. C.; Nussenzweig, A.: AID is required to initiateNbs1/gamma- H2AX focus formation and mutations at sites of class switching. Nature 414:660- 665, 2001.

GAM7080 399 NBS1 Stracker, T. H.; Carson, C. T.; Weitzman, M. D.: Adenovirus 3 C c oncoproteinsinactivate the Mre11- Rad50- NBS1 DNA repair complex. Nature 418:348- 352, 2002.

GAM7080 399 NBS1 Tauchi, H.; Matsuura, S.; Isomura, M.; Kinjo, T.; Nakamura, A.;Sakamoto, S.; 3 C c Kondo, N.; Endo, S.; Komatsu, K.; Nakamura, Y.: Sequenceanalysis of an 800- kb genomic DNA region on chromosome 8q21 that containsthe Nijmegen breakage syndrome gene, NBS1. Genomics 55: 242- 247,1999.

GAM7080 399 NBS1 Tekin, M.; Dogu, F.; Tacyildiz, N.; Akar, E.; Ikinciogullari,A.; Ogur, G.; 3 C c Yavuz, G.; Babacan, E.; Akar, N.: 657del5 mutationin the NBS1 gene is associated with Nijmegen breakage syndrome ina Turkish family. Clin. Genet. 62: 84- 88, 2002.

GAM7080 399 NBS1 Varon, R.; Reis, A.; Henze, G.; Einsiedel, H. G.; Sperling, K.;Seeger, K.: 3 C c Mutations in the Nijmegen breakage syndrome gene (NBS1)in childhood acute lymphoblastic leukemia (ALL). Cancer Res. 61:3570- 3572, 2001.

GAM7080 399 NBS1 Varon, R.; Vissinga, C.; Platzer, M.; Cerosaletti, K. M.; Chrzanowska,K. H.; 3 C c Saar, K.; Beckmann, G.; Seemanova, E.; Cooper, P. R.; Nowak,N. J.; Stumm, M.; Weemaes, C. M. R.; Gatti, R. A.; Wilson, R. K.;Digweed, M.; Rosenthal, A.; Sperling, K.; Concannon, P.; Reis, A.: Nibrin, a novel DNA double- strand break repair protein, is mutatedin Nijmegen breakage syndrome. Cell 93: 467- 476, 1998.

GAM7080 399 NBS1 Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin,J.: BASC, a 3 C c super complex of BRCA1- associated proteins involved inthe recognition and repair of aberrant DNA structures. Genes Dev. 14:927- 939, 2000.

GAM7080 399 NBS1 Wilda, M.; Demuth, I.; Concannon, P.; Sperling, K.; Hameister,H.: Expression 3 C c pattern of the Nijmegen breakage syndrome gene, Nbs1,during murine development. Hum. Molec. Genet. 9: 1739- 1744, 2000.

GAM7080 399 NBS1 Wu, X.; Ranganathan, V.; Weisman, D. S.; Heine, W. F.; Ciccone,D. N.; 3 C c O'Neill, T. B.; Crick, K. E.; Pierce, K. A.; Lane, W. S.; Rathbun,G.; Livingston, D. M.; Weaver, D. T.: ATM phosphorylation of Nijmegenbreakage syndrome protein is required in a DNA damage response. Nature 405:477- 482, 2000.

GAM7080 399 NBS1 Zhao, S.; Weng, Y.- C.; Yuan, S.- S. F.; Lin, Y.- T.; Hsu, H.- C.;Lin, S.- 3 C c C. J.; Gerbino, E.; Song, M.; Zdzienicka, M. Z.; Gatti, R.A.; Shay, J. W.; Ziv, Y.; Shiloh, Y.; Lee, E. Y.- H. P.: Functionallink between ataxia- telangiectasia and Nijmegen breakage syndromegene products. Nature 405: 473- 477, 2000.

GAM7080 399 NBS1 Zhong, Q.; Chen, C.- F.; Li, S.; Chen, Y.; Wang, C.- C.; Xiao, J.;Chen, P.- 3 C c L.; Sharp, Z. D.; Lee, W.- H.: Association of BRCA1 withthe hRad50- hMre11-

p95 complex and the DNA damage response. Science 285:747- 750, 1999.

GAM7080 399 NBS1 Zhu, J.; Petersen, S.; Tessarollo, L.; Nussenzweig, A.: Targeteddisruption 3 C c
of the Nijmegen breakage syndrome gene NBS1 leads to earlyembryonic
lethality in mice. Curr. Biol. 11: 105- 109, 2001.

GAM7080 399 NBS1 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 C c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human
telomeres. Nature Genet. 25: 347- 352, 2000.

GAM7080 399 OGG1 Aburatani, H.; Hippo, Y.; Ishida, T.; Takashima, R.; Matsuba, C.;Kodama, T.; 3 C c
Takao, M.; Yasui, A.; Yamamoto, K.; Asano, M.; Fukasawa,K.; Yoshinari, T.;
Inoue, H.; Ohtsuka, E.; Nishimura, S.: Cloningand characterization of
mammalian 8- hydroxyguanine- specific DNA glycosylase/apurinic,apyrimidinic
lyase, a functional mutM homologue. Cancer Res. 57:2151- 2156, 1997.

GAM7080 399 OGG1 Arai, K.; Morishita, K.; Shinmura, K.; Kohno, T.; Kim, S.- R.; Nohmi,T.; 3 C c
Taniwaki, M.; Ohwada, S.; Yokota, J.: Cloning of a human homologof the yeast
OGG1 gene that is involved in the repair of oxidativeDNA damage. Oncogene
14: 2857- 2861, 1997.

GAM7080 399 OGG1 Audebert, M.; Chevillard, S.; Levalois, C.; Gyapay, G.; Vieillefond,A.; 3 C c
Klijanienko, J.; Vielh, P.; El Naggar, A. K.; Oudard, S.; Boiteux,S.;
Radicella, J. P.: Alterations of the DNA repair gene OGG1 inhuman clear cell
carcinomas of the kidney. Cancer Res. 60: 4740- 4744,2000.

GAM7080 399 OGG1 Bjoras, M.; Luna, L.; Johnsen, B.; Hoff, E.; Haug, T.; Rognes,T.; Seeberg, 3 C c
E.: Opposite base- dependent reactions of a human baseexcision repair enzyme
on DNA containing 7,8- dihydro- 8- oxoguanineand abasic sites. EMBO J. 16:
6314- 6322, 1997.

GAM7080 399 OGG1 Ishida, T.; Hippo, Y.; Nakahori, Y.; Matsushita, I.; Kodama, T.;Nishimura, 3 C c
S.; Aburatani, H.: Structure and chromosome location ofhuman OGG1.
Cytogenet. Cell Genet. 85: 232- 236, 1999.

GAM7080 399 OGG1 Kohno, T.; Shinmura, K.; Tosaka, M.; Tani, M.; Kim, S.- R.; Sugimura,H.; 3 C c
Nohmi, T.; Kasai, H.; Yokota, J.: Genetic polymorphisms and
alternativesplicing of the hOGG1 gene, that is involved in the repair of 8-
hydroxyguaninein damaged DNA. Oncogene 16: 3219- 3225, 1998.

GAM7080 399 OGG1 Kuo, F. C.; Sklar, J.: Augmented expression of a human gene for8- oxoguanine 3 C c
DNA glycosylase (MutM) in B lymphocytes of the dark zonein lymph node
germinal centers. J. Exp. Med. 186: 1547- 1556, 1997.

GAM7080 399 OGG1 Lu, R.; Nash, H. M.; Verdine, G. L.: A mammalian DNA repair enzymethat 3 C c
excises oxidatively damaged guanines maps to a locus frequentlylost in lung
cancer. Curr. Biol. 7: 397- 407, 1997.

GAM7080 399 OGG1 Radicella, J. P.; Dherin, C.; Desmaze, C.; Fox, M. S.; Boiteux,S.: Cloning 3 C c
and characterization of hOGG1, a human homolog of theOGG1 gene of
Saccharomyces cerevisiae. Proc. Nat. Acad. Sci. 94:8010- 8015, 1997.

GAM7080 399 OGG1 Roldan- Arjona, T.; Wei, Y.- F.; Carter, K. C.; Klungland, A.; Anselmino,C.; 3 C c
Wang, R.- P.; Augustus, M.; Lindahl, T.: Molecular cloning andfunctional
expression of a human cDNA encoding the antimutator enzyme8- hydroxyguanine-
DNA glycosylase. Proc. Nat. Acad. Sci. 94: 8016- 8020,1997.

GAM7080 399 OGG1 Rosenquist, T. A.; Zharkov, D. O.; Grollman, A. P.: Cloning 3 C c
andcharacterization of a mammalian 8- oxoguanine DNA glycosylase. Proc.Nat.
Acad. Sci. 94: 7429- 7434, 1997.

GAM7080 399 OGG1 Tani, M.; Shinmura, K.; Kohno, T.; Shiroishi, T.; Wakama, S.;Kim, S.- R.; 3 C c
Nohmi, T.; Kasai, H.; Takenoshita, S.; Nagamachi, Y.;Yokota, J.: Genomic
structure and chromosomal localization of themouse Ogg1 gene that is

involved in the repair of 8- hydroxyguaninein DNA damage. Mammalian Genome 9: 32- 37, 1998.

GAM7080 399 OLIG2 Lu, Q. R.; Park, J. K.; Noll, E.; Chan, J. A.; Alberta, J.; Yuk,D.; Alzamora, M. G.; Louis, D. N.; Stiles, C. D.; Rowitch, D. H.;Black, P. M.: Oligodendrocyte lineage genes (OLIG) as molecular markersfor human glial brain tumors. Proc. Nat. Acad. Sci. 98: 10851- 10856,2001. 3 C c

GAM7080 399 OLIG2 Lu, Q. R.; Sun, T.; Zhu, Z.; Ma, N.; Garcia, M.; Stiles, C. D.;Rowitch, D. H.: Common developmental requirement for Olig functionindicates a motor neuron/oligodendrocyte connection. Cell 109: 75- 86,2002. 3 C c

GAM7080 399 OLIG2 Lu, Q. R.; Yuk, D.; Alberta, J. A.; Zhu, Z.; Pawlitzky, I.; Chan,J.; McMahon, A. P.; Stiles, C. D.; Rowitch, D. H.: Sonic hedgehog-regulatedoligodendrocyte lineage genes encoding bHLH proteins in the mammaliancentral nervous system. Neuron 25: 317- 329, 2000. 3 C c

GAM7080 399 OLIG2 Raff, M. C.; Miller, R. H.; Noble, M.: A glial progenitor cellthat develops in vitro into an astrocyte or an oligodendrocyte dependingon culture medium. Nature 303: 390- 396, 1983. 3 C c

GAM7080 399 OLIG2 Zhou, Q.; Anderson, D. J.: The bHLH transcription factors OLIG2and OLIG1 couple neuronal and glial subtype specification. Cell 109:61- 73, 2002. 3 C c

GAM7080 399 OLIG2 Zhou, Q.; Wang, S.; Anderson, D. J.: Identification of a novelfamily of oligodendrocyte lineage- specific basic helix- loop- helixtranscription factors. Neuron 25: 331- 343, 2000. 3 C c

GAM7080 399 PPEF1 Montini, E.; Rugarli, E. I.; Van de Vosse, E.; Andolfi, G.; Mariani,M.; Puca, A. A.; Consalez, G. G.; den Dunnen, J. T.; Ballabio, A.;Franco, B.: A novel human serine- threonine phosphatase related tothe Drosophila retinal degeneration C (rdgC) gene is selectively expressedin sensory neurons of neural crest origin. Hum. Molec. Genet. 6:1137- 1145, 1997. 3 C c

GAM7080 399 PPEF1 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor integrity, and rhodopsin dephosphorylation in mice lackingboth protein phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21: 8605- 8614, 2001. 3 C c

GAM7080 399 PPEF1 van de Vosse, E.; Franco, B.; van der Bent, P.; Montini, E.; Orth,U.; Hanauer, A.; Tijmes, N.; van Ommen, G.- J. B.; Ballabio, A.; denDunnen, J. T.; Bergen, A. A. B.: Exclusion of PPEF as the gene causingX- linked juvenile retinoschisis. Hum. Genet. 101: 235- 237, 1997. 3 C c

GAM7080 399 RAB6A Rousseau- Merck, M.- F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350- 354, 1991. 3 C c

GAM7080 399 RAB6A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes encode a family of GTP- binding proteins related to yeastYPT1 and SEC4 products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989. 3 C c

GAM7080 399 TBCD Martin, L.; Fanarraga, M. L.; Aloria, K.; Zabala, J. C.: Tubulinfolding cofactor D is a microtubule destabilizing protein. FEBS Lett. 470:93- 95, 2000. 3 C c

GAM7080 399 TBCD Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999. 3 C c

GAM7080 399 TBL1X Bassi, M. T.; Ramesar, R. S.; Caciotti, B.; Winship, I. M.; DeGrandi, A.; 3 C c

Riboni, M.; Townes, P. L.; Beighton, P.; Ballabio, A.;Borsani, G.: X- linked late- onset sensorineural deafness caused bya deletion involving OA1 and a novel gene containing WD- 40 repeats. Am.J. Hum. Genet. 64: 1604- 1616, 1999.

GAM7080 399 TBL1X Converse, P. J.: Personal Communication. Baltimore, Md. 8/24/2001. 3 C c

GAM7080 399 TBL1X Disteche, C. M.; Dinulos, M. B.; Bassi, M. T.; Elliott, R. W.;Rugarli, E. I.: Mapping of the murine Tbl1 gene reveals a new rearrangementbetween mouse and human X chromosomes. Mammalian Genome 9: 1062- 1064,1998. 3 C c

GAM7080 399 TBL1X Dong, X.; Tsuda, L.; Zavitz, K. H.; Lin, M.; Li, S.; Carthew, R.W.; Zipursky, S. L.: ebi regulates epidermal growth factor receptorsignaling pathways in Drosophila. Genes Dev. 13: 954- 965, 1999. 3 C c

GAM7080 399 TBL1X Emes, R. D.; Ponting, C. P.: A new sequence motif linking lissencephaly,Treacher Collins and oral- facial- digital type 1 syndromes, microtubuledynamics and cell migration. Hum. Molec. Genet. 10: 2813- 2820, 2001. 3 C c

GAM7080 399 TBL1X Matsuzawa, S.; Reed, J. C.: Siah- 1, SIP, and Ebi collaborate ina novel pathway for beta- catenin degradation linked to p53 responses. Molec.Cell 7: 915- 926, 2001. 3 C c

GAM7080 399 TBL1X Zhang, J.; Kalkum, M.; Chait, B. T.; Roeder, R. G.: The N- CoR- HDAC3nuclear receptor corepressor complex inhibits the JNK pathway throughthe integral subunit GPS2. Molec. Cell 9: 611- 623, 2002. 3 C c

GAM7080 399 TCF3 Bain, G.; Robanus Maandag, E. C.; Izon, D. J.; Amsen, D.; Kruisbeek,A. M.; Weintraub, B. C.; Krop, I.; Schlissel, M. S.; Feeney, A. J.;van Roon, M.; van der Valk, M.; te Riele, H. P. J.; Berns, A.; Murre,C.: E2A proteins are required for proper B cell development and initiationof immunoglobulin gene rearrangements. Cell 79: 885- 892, 1994. 3 C c

GAM7080 399 TCF3 El Ghouzzi, V.; Legeai- Mallet, L.; Aresta, S.; Benoist, C.; Munnich,A.; de Gunzburg, J.; Bonaventure, J.: Saethre- Chotzen mutations causeTWIST protein degradation or impaired nuclear location. Hum. Molec.Genet. 9: 813- 819, 2000. 3 C c

GAM7080 399 TCF3 Henthorn, P.; Kiledjian, M.; Kadesch, T.: Two distinct transcriptionfactors that bind the immunoglobulin enhancer mu- E5/kappa- E2 motif. Science 247:467- 470, 1990. 3 C c

GAM7080 399 TCF3 Honda, H.; Inaba, T.; Suzuki, T.; Oda, H.; Ebihara, Y.; Tsuiji,K.; Nakahata, T.; Ishikawa, T.; Yazaki, Y.; Hirai, H.: Expressionof E2A- HLF chimeric protein induced T- cell apoptosis, B- cell maturationarrest, and development of acute lymphoblastic leukemia. Blood 93:2780- 2790, 1999. 3 C c

GAM7080 399 TCF3 Hunger, S. P.: Chromosomal translocations involving the E2A genein acute lymphoblastic leukemia: clinical features and molecular pathogenesis. Blood 87:1211- 1224, 1996. 3 C c

GAM7080 399 TCF3 Inaba, T.; Roberts, W. M.; Shapiro, L. H.; Jolly, K. W.; Raimondi,S. C.; Smith, S. D.; Look, A. T.: Fusion of the leucine zipper geneHLF to the E2A gene in human acute B- lineage leukemia. Science 257:531- 534, 1992. 3 C c

GAM7080 399 TCF3 Kamps, M. P.; Murre, C.; Sun, X.; Baltimore, D.: A new homeoboxgene contributes the DNA binding domain of the t(1;19) translocationprotein in pre- B ALL. Cell 60: 547- 555, 1990. 3 C c

GAM7080 399 TCF3 Mellentin, J. D.; Murre, C.; Donlon, T. A.; McCaw, P. S.; Smith,S. D.; Carroll, A. J.; McDonald, M. E.; Baltimore, D.; Cleary, M.L.: The gene for enhancer binding proteins E12/E47 lies at the t(1;19)breakpoint in acute leukemias. Science 246: 379- 382, 1989. 3 C c

GAM7080 399 TCF3 Murre, C.; McCaw, P. S.; Baltimore, D. :Cell 56: 777- 783, 1989. 3 C c

GAM7080 399 TCF3 Nourse, J.; Mellentin, J. D.; Galili, N.; Wilkinson, J.; Stanbridge,E.; Smith, S. D.; Cleary, M. L.: Chromosomal translocation t(1;19)results in synthesis of a homeobox fusion mRNA that codes for a potentialchimeric transcription factor. Cell 60: 535- 545, 1990. 3 C c

GAM7080 399 TCF3 Smith, K. S.; Rhee, J. W.; Naumovski, L.; Cleary, M. L.: Disrupteddifferentiation and oncogenic transformation of lymphoid progenitorsin E2A- HLF transgenic mice. Molec. Cell. Biol. 19: 4443- 4451, 1999. 3 C c

GAM7080 399 TCF3 Sun, X.- H.: Constitutive expression of the Id1 gene impairs mouseB cell development. Cell 79: 893- 900, 1994. 3 C c

GAM7080 399 TCF3 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993. 3 C c

GAM7080 399 TCF3 Zhuang, Y.; Soriano, P.; Weintraub, H.: The helix- loop- helixgene E2A is required for B cell formation. Cell 79: 875- 884, 1994. 3 C c

GAM7080 399 TNFSF15 Migone, T.- S.; Zhang, J.; Luo, X.; Zhuang, L.; Chen, C.; Hu, B.;Hong, J. S.; Perry, J. W.; Chen, S.- F.; Zhou, J. X. H.; Cho, Y. H.;Ullrich, S.; and 14 others: TL1A is a TNF- like ligand for DR3 andTR6/DcR3 and functions as a T cell costimulator. Immunity 16: 479- 492,2002. 3 C c

GAM7080 399 TNFSF15 Tan, K. B.; Harrop, J.; Reddy, M.; Young, P.; Terrett, J.; Emery,J.; Moore, G.; Truneh, A.: Characterization of a novel TNF- like ligandand recently described TNF ligand and TNF receptor superfamily genesand their constitutive and inducible expression in hematopoietic andnon- hematopoietic cells. Gene 204: 35- 46, 1997. 3 C c

GAM7080 399 TNFSF15 Yue, T.- L.; Ni, J.; Romanic, A. M.; Gu, J.- L.; Keller, P.; Wang,C.; Kumar, S.; Yu, G.; Hart, T. K.; Wang, X.; Xia, Z.; DeWolf, W.E., Jr.; Feuerstein, G. Z.: TL1, a novel tumor necrosis factor- likecytokine, induces apoptosis in endothelial cells: involvement of activationof stress protein kinases (stress- activated protein kinase and p38mitogen- activated protein kinase) and caspase- 3- like protease. J.Biol. Chem. 274: 1479- 1486, 1999. 3 C c

GAM7080 399 TNFSF15 Zhai, Y.; Ni, J.; Jiang, G.- W.; Lu, J.; Xing, L.; Lincoln, C.;Carter, K. C.; Janat, F.; Kozak, D.; Xu, S.; Rojas, L.; Aggarwal,B. B.; Ruben, S.; Li, L.- Y.; Gentz, R.; Yu, G.- L.: VEGI, a novelcytokine of the tumor necrosis factor family, is an angiogenesis inhibitorthat suppresses the growth of colon carcinomas in vivo. FASEB J. 13:181- 189, 1999. 3 C c

GAM7080 399 TXNRD1 Gasdaska, J. R.; Gasdaska, P. Y.; Gallegos, A.; Powis, G.: Humanthioredoxin reductase gene localization to chromosomal position 12q23- q24.1and mRNA distribution in human tissue. Genomics 37: 257- 259, 1996. 3 C c

GAM7080 399 TXNRD1 Gasdaska, P. Y.; Gasdaska, J. R.; Cochran, S.; Powis, G.: Cloningand sequencing of a human thioredoxin reductase. FEBS Lett. 373:5- 9, 1995. 3 C c

GAM7080 399 TXNRD1 Gladyshev, V. N.; Jeang, K.- T.; Stadtman, T. C.: Selenocysteine,identified as the penultimate C- terminal residue in human T- cell thioredoxinreductase, corresponds to TGA in the human placental gene. Proc.Nat. Acad. Sci. 93: 6146- 6151, 1996. 3 C c

GAM7080 399 TXNRD1 Gorlatov, S. N.; Stadtman, T. C.: Human thioredoxin reductasefrom HeLa cells: selective alkylation of selenocysteine in the proteininhibits enzyme activity and reduction with NADPH influences affinityto heparin. Proc. Nat. 3 C c

Acad. Sci. 95: 8520- 8525, 1998.

GAM7080 399 UBL1 Boddy, M. N.; Howe, K.; Etkin, L. D.; Solomon, E.; Freemont, P.S.: PIC 1, a novel ubiquitin- like protein which interacts with thePML component of a multiprotein complex that is disrupted in acutepromyelocytic leukaemia. Oncogene 13: 971- 982, 1996. 3 C c

GAM7080 399 UBL1 Desterro, J. M. P.; Rodriguez, M. S.; Hay, R. T.: SUMO- 1 modificationof I- kappa- B- alpha inhibits NF- kappa- B activation. Molec. Cell 2:233- 239, 1998. 3 C c

GAM7080 399 UBL1 Lapenta, V.; Chiurazzi, P.; van der Spek, P.; Pizzuti, A.; Hanaoka,F.; Brahe, C.: SMT3A, a human homologue of the S. cerevisiae SMT3gene, maps to chromosome 21qter and defines a novel gene family. Genomics 40:362- 366, 1997. 3 C c

GAM7080 399 UBL1 Mao, Y.; Sun, M.; Desai, S. D.; Liu, L. F.: SUMO- 1 conjugationto topoisomerase I: a possible repair response to topoisomerase- mediatedDNA damage. Proc. Nat. Acad. Sci. 97: 4046- 4051, 2000. 3 C c

GAM7080 399 UBL1 Okura, T.; Gong, L.; Kamitani, T.; Wada, T.; Okura, I.; Wei, C.- F.;Chang, H.- M.; Yeh, E. T. H.: Protection against Fas/APO- 1- and tumornecrosis factor- mediated cell death by a novel protein, sentrin. J.Immun. 157: 4277- 4281, 1996. 3 C c

GAM7080 399 UBL1 Shen, Z.; Pardington- Purtymun, P. E.; Comeaux, J. C.; Moyzis, R.K.; Chen, D. J.: UBL1, a human ubiquitin- like protein associatingwith human RAD51/RAD52 proteins. Genomics 36: 271- 279, 1996. 3 C c

GAM7080 399 ZNF10 Huebner, K.; Druck, T.; Croce, C. M.; Thiesen, H. J.: Twenty- sevennonoverlapping zinc finger cDNAs from human T cells map to nine differentchromosomes with apparent clustering. Am. J. Hum. Genet. 48: 726- 740,1991. 3 C c

GAM7080 399 ZNF10 Rousseau- Merck, M.- F.; Hillion, J.; Jonveaux, P.; Couillin, P.;Seite, P.; Thiesen, H.- J.; Berger, R.: Chromosomal localization of9 KOX zinc finger genes: physical linkages suggest clustering of KOXgenes on chromosomes 12, 16, and 19. Hum. Genet. 92: 583- 587, 1993. 3 C c

GAM7553 354 ADORA3 Liang, B. T.; Jacobson, K. A.: A physiological role of the adenosineA3 receptor: sustained cardioprotection. Proc. Nat. Acad. Sci. 95:6995- 6999, 1998. 6 A c

GAM7553 354 ADORA3 Monitto, C. L.; Levitt, R. C.; DiSilvestre, D.; Holroyd, K. J.: Localization of the A(3) adenosine receptor gene (ADORA3) to humanchromosome 1p. Genomics 26: 637- 638, 1995. 6 A c

GAM7553 354 ADORA3 Sajjadi, F. G.; Firestein, G. S.: cDNA cloning and sequence analysisof the human A3 adenosine receptor. Biochim. Biophys. Acta 1179:105- 107, 1993. 6 A c

GAM7553 354 ADORA3 Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and genome organization of mammalian G- protein- coupled receptors. Genomics 18:175- 184, 1993. 6 A c

GAM7553 354 ADORA3 Zhao, Z.; Ravid, S.; Ravid, K.: Chromosomal mapping of the mouseA3 adenosine receptor gene, Adora3. Genomics 30: 118- 119, 1995. 6 A c

GAM7553 354 ADORA3 Zhou, Q.- Y.; Li, C.; Olah, M. E.; Johnson, R. A.; Stiles, G. L.;Civelli, O.: Molecular cloning and characterization of an adenosinereceptor: the A3 adenosine receptor. Proc. Nat. Acad. Sci. 89: 7432- 7436,1992. 6 A c

GAM7553 354 BIG1 Mansour, S. J.; Skaug, J.; Zhao, X.- H.; Giordano, J.; Scherer,S. W.; Melancon, P.: p200 ARF- GEP1: a Golgi- localized guanine nucleotideexchange 6 A c

protein whose Sec7 domain is targeted by the drug brefeldinA. Proc. Nat. Acad. Sci. 96: 7968- 7973, 1999.

GAM7553 354 BIG1 Morinaga, N.; Moss, J.; Vaughan, M.: Cloning and expression ofa cDNA 6 A c
encoding a bovine brain brefeldin A- sensitive guanine nucleotide-
exchangeprotein for ADP- ribosylation factor. Proc. Nat. Acad. Sci. 94:
12926- 12931,1997.

GAM7553 354 BIG1 Morinaga, N.; Tsai, S.- C.; Moss, J.; Vaughan, M.: Isolation ofa brefeldin 6 A c
A- inhibited guanine nucleotide- exchange protein for ADPribosylation factor
(ARF) 1 and ARF3 that contains a Sec7- like domain. Proc.Nat. Acad. Sci. 93:
12856- 12860, 1996.

GAM7553 354 BIG1 Togawa, A.; Morinaga, N.; Ogasawara, M.; Moss, J.; Vaughan, M.: Purification 6 A c
and cloning of a brefeldin A- inhibited guanine nucleotide- exchangeprotein
for ADP- ribosylation factors. J. Biol. Chem. 274: 12308- 12315,1999.

GAM7553 354 CASP7 Barrett, A. J.; Rawlings, N. D.: Evolutionary lines of cysteinepeptidases. 6 A c
Biol. Chem. 382: 727- 733, 2001.

GAM7553 354 CASP7 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 6 A c
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM7553 354 CASP7 Fernandes- Alnemri, T.; Takahashi, A.; Armstrong, R.; Krebs, J.;Fritz, L.; 6 A c
Tomaselli, K. J.; Wang, L.; Yu, Z.; Croce, C. M.; Salveson,G.; Earnshaw, W.
C.; Litwack, G.; Alnemri, E. S.: Mch3, a novel humanapoptotic cysteine
protease highly related to CPP32. Cancer Res. 55:6045- 6052, 1995.

GAM7553 354 CASP7 Riedl, S. J.; Fuentes- Prior, P.; Renatus, M.; Kairies, N.; Krapp,S.; Huber, 6 A c
R.; Salvesen, G. S.; Bode, W.: Structural basis for theactivation of human
procaspase- 7. Proc. Nat. Acad. Sci. 98: 14790- 14795,2001.

GAM7553 354 CASP7 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; 6 A c
Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes,
CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem.
Biophys. Res. Commun. 225: 983- 989, 1996.

GAM7553 354 CAV1 Drab, M.; Verkade, P.; Elger, M.; Kasper, M.; Lohn, M.; Lauterbach,B.; 6 A c
Menne, J.; Lindschau, C.; Mende, F.; Luft, F. C.; Schedl, A.;Haller, H.;
Kurzchalia, T. V.: Loss of caveolae, vascular dysfunction,and pulmonary
defects in caveolin- 1 gene- disrupted mice. Science 293:2449- 2452, 2001.

GAM7553 354 CAV1 Engelman, J. A.; Zhang, X. L.; Galbiati, F.; Lisanti, M. P.: 6 A c
Chromosomallocalization, genomic organization, and developmental expression
ofthe murine caveolin gene family (Cav- 1, - 2, and - 3): Cav- 1 and Cav-
2genes map to a known tumor suppressor locus (6- A2/7q31). FEBS Lett.
429:330- 336, 1998.

GAM7553 354 CAV1 Engelman, J. A.; Zhang, X. L.; Lisanti, M. P.: Genes encodinghuman caveolin- 6 A c
1 and - 2 are co- localized to the D7S522 locus (7q31.1),a known fragile
site (FRA7G) that is frequently deleted in human cancers. FEBSLett. 436:
403- 410, 1998.

GAM7553 354 CAV1 Engelman, J. A.; Zhang, X.; Galbiati, F.; Volonte, D.; Sotgia,F.; Pestell, 6 A c
R. G.; Minetti, C.; Scherer, P. E.; Okamoto, T.; Lisanti,M. P.: Molecular
genetics of the caveolin gene family: implicationsfor human cancers,
diabetes, Alzheimer disease, and muscular dystrophy. Am.J. Hum. Genet. 63:
1578- 1587, 1998.

GAM7553 354 CAV1 Feron, O.; Dessy, C.; Moniotte, S.; Desager, J.- P.; Balligand,J.- L.: 6 A c

Hypercholesterolemia decreases nitric oxide production bypromoting the interaction of caveolin and endothelial nitric oxidesynthase. J. Clin. Invest. 103: 897- 905, 1999.

GAM7553 354 CAV1 Giordano, S.; Ponzetto, C.; Di Renzo, M. F.; Cooper, C. S.; Comoglio,P. M.: 6 A c
Tyrosine kinase receptor indistinguishable from the c- metprotein. Nature 339: 155- 156, 1989.

GAM7553 354 CAV1 Glenney, J. R., Jr.: The sequence of human caveolin reveals identitywith 6 A c
VIP21, a component of transport vesicles. FEBS Lett. 314: 45- 48,1992.

GAM7553 354 CAV1 Kurzchalia, T. V.; Dupree, P.; Parton, R. G.; Kellner, R.; Virta,H.; 6 A c
Lehnert, M.; Simons, K.: VIP21, a 21- kD membrane protein is anintegral component of trans- Golgi- network- derived transport vesicles. J.Cell Biol. 118 1003- 1014, 1992.

GAM7553 354 CAV1 Mouillet- Richard, S.; Ermonval, M.; Chebassier, C.; Laplanche,J. L.; 6 A c
Lehmann, S.; Launay, J. M.; Kellermann, O.: Signal transductionthrough prion protein. Science 289: 1925- 1928, 2000.

GAM7553 354 CAV1 Razani, B.; Engelman, J. A.; Wang, X. B.; Schubert, W.; Zhang,X. L.; Marks, 6 A c
C. B.; Macaluso, F.; Russell, R. G.; Li, M.; Pestell,R. G.; Di Vizio, D.; Hou, H., Jr.; Kneitz, B.; Lagaud, G.; Christ,G. J.; Edelmann, W.; Lisanti, M. P.: Caveolin- 1 null mice are viablebut show evidence of hyperproliferative and vascular abnormalities. J.Biol. Chem. 276: 38121- 38138, 2001.

GAM7553 354 CAV1 Scherer, P. E.; Okamoto, T.; Chun, M.; Nishimoto, I.; Lodish,H. F.; Lisanti, 6 A c
M. P.: Identification, sequence, and expression ofcaveolin- 2 defines a caveolin gene family. Proc. Nat. Acad. Sci. 93:131- 135, 1996.

GAM7553 354 CAV1 Scherer, P. E.; Tang, Z.; Chun, M.; Sargiacomo, M.; Lodish, H.F.; Lisanti, 6 A c
M. P.: Caveolin isoforms differ in their N- terminalprotein sequence and subcellular distribution: identification andepitope mapping of an isoform- specific monoclonal antibody probe. J.Biol. Chem. 270 16395- 16401, 1995.

GAM7553 354 CAV1 Tahir, S. A.; Yang, G.; Ebara, S.; Timme, T. L.; Satoh, T.; Li,L.; Goltsov, 6 A c
A.; Ittmann, M.; Morrisett, J. D.; Thompson, T. C.:Secreted caveolin- 1 stimulates cell survival/clonal growth and contributesto metastasis in androgen- insensitive prostate cancer. Cancer Res. 61:3882- 3885, 2001.

GAM7553 354 CAV1 Wary, K. K.; Mariotti, A.; Zurzolo, C.; Giancotti, F. G.: A requirementfor 6 A c
caveolin- 1 and associated kinase Fyn in integrin signaling andanchorage- dependent cell growth. Cell 94: 625- 634, 1998.

GAM7553 354 CAV1 Yang, G.; Truong, L. D.; Timme, T. L.; Ren, C.; Wheeler, T. M.;Park, S. H.; 6 A c
Nasu, Y.; Bangma, C. H.; Kattan, M. W.; Scardino, P.T.; Thompson, T. C.: Elevated expression of caveolin is associatedwith prostate and breast cancer. Clin. Cancer Res. 4: 1873- 1880,1998.

GAM7553 354 CAV1 Zhao, Y.- Y.; Liu, Y.; Stan, R.- V.; Fan, L.; Gu, Y.; Dalton, N.;Chu, P.- 6 A c
H.; Peterson, K.; Ross, J., Jr.; Chien, K. R.: Defects incaveolin- 1 cause dilated cardiomyopathy and pulmonary hypertensionin knockout mice. Proc. Nat. Acad. Sci. 99: 11375- 11380, 2002.

GAM7553 354 CCKBR Beinborn, M.; Lee, Y.- M.; McBride, E. W.; Quinn, S. M.; Kopin,A. S.: A 6 A c
single amino acid of the cholecystokinin- B/gastrin receptordetermines specificity for non- peptide antagonists. Nature 362:348- 350, 1993.

GAM7553 354 CCKBR Huppi, K.; Siwarski, D.; Pisegna, J. R.; Wank, S.: Chromosomallocalization 6 A c
of the gastric and brain receptors for cholecystokinin(CCKAR and CCKBR) in human and mouse. Genomics 25: 727- 729, 1995.

GAM7553 354 CCKBR Lee, Y.- M.; Beinborn, M.; McBride, E. W.; Lu, M.; Kolakowski, L.F., Jr.; 6 A c

Kopin, A. S.: The human brain cholecystokinin- B/gastrinreceptor: cloning and characterization. J. Biol. Chem. 268: 8164- 8169,1993.

GAM7553 354 CCKBR Pisegna, J. R.; de Weerth, A.; Huppi, K.; Wank, S. A.: Molecularcloning of the human brain and gastric cholecystokinin receptor: structure,functional expression and chromosomal localization. Biochem. Biophys.Res. Commun. 189: 296- 303, 1992. 6 A c

GAM7553 354 CCKBR Samuelson, L. C.; Isakoff, M. S.; Lacourse, K. A.: Localizationof the murine cholecystokinin A and B receptor genes. MammalianGenome 6: 242- 246, 1995. 6 A c

GAM7553 354 CCKBR Zimonjic, D. B.; Popescu, N. C.; Matsui, T.; Ito, M.; Chihara,K.: Localization of the human cholecystokinin- B/gastrin receptorgene (CCKBR) to chromosome 11p15.5- p15.4 by fluorescence in situ hybridization.Cytogenet. Cell Genet. 65: 184- 185, 1994. 6 A c

GAM7553 354 CLK2 Hanes, J.; von der Kammer, H.; Klaudiny, J.; Scheit, K. H.: Characterizationby cDNA cloning of two new human protein kinases: evidence by sequencecomparison of a new family of mammalian protein kinases. J. Molec.Biol. 244: 665- 672, 1994. 6 A c

GAM7553 354 CLK2 Nothwang, H. G.; Kim, H. G.; Aoki, J.; Geisterfer, M.; Kubart,S.; Wegner, R. D.; van Moers, A.; Ashworth, L. K.; Haaf, T.; Bell,J.; Arai, H.; Tommerup, N.; Ropers, H. H.; Wirth, J.: Functionalhemizygosity of PAFAH1B3 due to a PAFAH1B3- CLK2 fusion gene in a femalewith mental retardation, ataxia and atrophy of the brain. Hum. Molec.Genet. 10: 797- 806, 2001. 6 A c

GAM7553 354 CLK2 Talmadge, C. B.; Finkernagel, S.; Sumegi, J.; Sciorra, L.; Rabinow,L.: Chromosomal mapping of three human LAMMER protein- kinase- encodinggenes. Hum. Genet. 103: 523- 524, 1998. 6 A c

GAM7553 354 CLK2 Tsujikawa, M.; Kurahashi, H.; Tanaka, T.; Okada, M.; Yamamoto,S.; Maeda, N.; Watanabe, H.; Inoue, Y.; Kiridoshi, A.; Matsumoto,K.; Ohashi, Y.; Kinoshita, S.; Shimomura, Y.; Nakamura, Y.; Tano,Y.: Homozygosity mapping of a gene responsible for gelatinous drop- likecorneal dystrophy to chromosome 1p. Am. J. Hum. Genet. 63: 1073- 1077,1998. 6 A c

GAM7553 354 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 6 A c

GAM7553 354 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 6 A c

GAM7553 354 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 6 A c

GAM7553 354 DNMT3A Baylin, S. B.; Herman, J. G.; Graff, J. R.; Vertino, P. M.; Issa,J. P.: Alterations in DNA methylation: a fundamental aspect of neoplasia. Adv.Cancer Res. 72: 141- 196, 1998. 6 A c

GAM7553 354 DNMT3A Lei, H.; Oh, S. P.; Okano, M.; Juttermann, R.; Goss, K. A.; Jaenisch,R.; Li, E.: De novo DNA cytosine methyltransferase activities inmouse embryonic stem cells. Development 122: 3195- 3205, 1996. 6 A c

GAM7553 354 DNMT3A Lyko, F.; Ramsahoye, B. H.; Kashevsky, H.; Tudor, M.; Mastrangelo,M.- A.; Orr- Weaver, T. L.; Jaenisch, R.: Mammalian (cytosine- 5) methyltransferasescause genomic DNA methylation and lethality in Drosophila. NatureGenet. 23: 363- 366, 1999. 6 A c

GAM7553 354 DNMT3A Okano, M.; Bell, D. W.; Haber, D. A.; Li, E.: DNA methyltransferasesDnmt3a and Dnmt3b are essential for de novo methylation and mammaliandevelopment. 6 A c

Cell 99: 247- 257, 1999.

GAM7553 354 DNMT3A Okano, M.; Xie, S.; Li, E.: Cloning and characterization of afamily of novel 6 A c
mammalian DNA (cytosine- 5) methyltransferases. (Letter) NatureGenet. 19:
219- 220, 1998.

GAM7553 354 DNMT3A Robertson, K. D.; Uzvolgyi, E.; Liang, G.; Talmadge, C.; Sumegi,J.; 6 A c
Gonzales, F. A.; Jones, P. A.: The human DNA methyltransferases(DNMTs) 1, 3a
and 3b: coordinate mRNA expression in normal tissuesand overexpression in
tumors. Nucleic Acids Res. 27: 2291- 2298,1999.

GAM7553 354 DNMT3A Xie, S.; Wang, Z.; Okano, M.; Nogami, M.; Li, Y.; He, W.- W.; Okumura,K.; 6 A c
Li, E.: Cloning, expression and chromosome locations of the humanDNMT3 gene
family. Gene 236: 87- 95, 1999.

GAM7553 354 EMP1 Ben Porath, I.; Kozak, C. A.; Benvenisty, N.: Chromosomal mappingof Tmp 6 A c
(Emp1), Xmp (Emp2), and Ymp (Emp3), genes encoding membraneproteins related
to Pmp22. Genomics 49: 443- 447, 1998.

GAM7553 354 EMP1 Ben- Porath, I.; Benvenisty, N.: Characterization of a tumor- 6 A c
associatedgene, a member of a novel family of genes encoding membrane
glycoproteins. Gene 183:69- 75, 1996.

GAM7553 354 EMP1 Chen, Y.; Medvedev, A.; Ruzanov, P.; Marvin, K. W.; Jetten, A.M.: cDNA 6 A c
cloning, genomic structure, and chromosome mapping of thehuman epithelial
membrane protein CL- 20 gene (EMP1), a member of thePMP22 family. Genomics
41: 40- 48, 1997.

GAM7553 354 EMP1 Liehr, T.; Kuhlenbaumer, G.; Wulf, P.; Taylor, V.; Suter, U.; 6 A c
VanBroeckhoven, C.; Lupski, J. R.; Claussen, U.; Rautenstrauss, B.:Regional
localization of the human epithelial membrane protein genes1, 2, and 3
(EMP1, EMP2, EMP3) to 12p12.3, 16p13.2, and 19q13.3. Genomics 58:106- 108,
1999.

GAM7553 354 EMP1 Marvin, K. W.; Fujimoto, W.; Jetten, A. M.: Identification 6 A c
andcharacterization of a novel squamous cell- associated gene relatedto
PMP22. J. Biol. Chem. 270: 28910- 28916, 1995.

GAM7553 354 EMP1 Ruegg, C. L.; Wu, H.; Fagnoni, F. F.; Engleman, E. G.; Laus, R.: B4B, a 6 A c
novel growth- arrest gene, is expressed by a subset of progenitor/pre-
Blymphocytes negative for cytoplasmic mu- chain. J. Immun. 157: 72- 80,1996.

GAM7553 354 GATA6 Laitinen, M. P. E.; Anttonen, M.; Ketola, I.; Wilson, D. B.; Ritvos,O.; 6 A c
Butzow, R.; Heikinheimo, M.: Transcription factors GATA- 4 andGATA- 6 and a
GATA family cofactor, FOG- 2, are expressed in human ovaryand sex cord-
derived ovarian tumors. J. Clin. Endocr. Metab. 85:3476- 3483, 2000.

GAM7553 354 GATA6 Morrisey, E. E.; Tang, Z.; Sigrist, K.; Lu, M. M.; Jiang, F.; Ip,H. S.; 6 A c
Parmacek, M. S.: GATA6 regulates HNF4 and is required fordifferentiation of
visceral endoderm in the mouse embryo. Genes Dev. 12:3579- 3590, 1998.

GAM7553 354 GATA6 Suzuki, E.; Evans, T.; Lowry, J.; Truong, L.; Bell, D. W.; Testa,J. R.; 6 A c
Walsh, K.: The human GATA- 6 gene: structure, chromosomal location,and
regulation of expression by tissue- specific and mitogen- responsivesignals.
Genomics 38: 283- 290, 1996.

GAM7553 354 GRIA1 Gregor, P.; Reeves, R. H.; Jabs, E. W.; Yang, X.; Dackowski, W.;Rochelle, J. 6 A c
M.; Brown, R. H., Jr.; Haines, J. L.; O'Hara, B. F.;Uhl, G. R.; Seldin, M.
F.: Chromosomal localization of glutamatereceptor genes: relationship to
familial amyotrophic lateral sclerosisand other neurological disorders of
mice and humans. Proc. Nat. Acad.Sci. 90: 3053- 3057, 1993.

GAM7553 354 GRIA1 Lee, H.- K.; Barbarosie, M.; Kameyama, K.; Bear, M. F.; Huganir,R. L.: 6 A c
Regulation of distinct AMPA receptor phosphorylation sitesduring

bidirectional synaptic plasticity. Nature 405: 955- 959, 2000.

GAM7553 354 GRIA1 Mack, V.; Burnashev, N.; Kaiser, K. M. M.; Rozov, A.; Jensen, V.;Hvalby, O.; 6 A c
Seeburg, P. H.; Sakmann, B.; Sprengel, R.: Conditionalrestoration of
hippocampal synaptic potentiation in GluR- A- deficientmice. Science 292:
2501- 2504, 2001.

GAM7553 354 GRIA1 Puckett, C.; Gomez, C. M.; Korenberg, J. R.; Tung, H.; Meier, T.J.; Chen, X. 6 A c
N.; Hood, L.: Molecular cloning and chromosomal localizationof one of the
human glutamate receptor genes. Proc. Nat. Acad. Sci. 88:7557- 7561, 1991.

GAM7553 354 GRIA1 Shi, S.- H.; Hayashi, Y.; Petralla, R. S.; Zaman, S. H.; Wenthold,R. J.; 6 A c
Svoboda, K.; Malinow, R.: Rapid spine delivery and redistributionof AMPA
receptors after synaptic NMDA receptor activation. Science 284:1811- 1816,
1999.

GAM7553 354 GRIA1 Sun, W.; Ferrer- Montiel, A. V.; Schinder, A. F.; McPherson, J.P.; Evans, G. 6 A c
A.; Montal, M.: Molecular cloning, chromosomal mapping,and functional
expression of human brain glutamate receptors. Proc.Nat. Acad. Sci. 89:
1443- 1447, 1992.

GAM7553 354 GRIA1 Warrington, J. A.; Bailey, S. K.; Armstrong, E.; Aprelikova, O.;Alitalo, K.; 6 A c
Dolganov, G. M.; Wilcox, A. S.; Sikela, J. M.; Wolfe,S. F.; Lovett, M.;
Wasmuth, J. J.: A radiation hybrid map of 18 growthfactor, growth factor
receptor, hormone receptor, or neurotransmitterreceptor genes on the distal
region of the long arm of chromosome5. Genomics 13: 803- 808, 1992.

GAM7553 354 GRIA1 Zamanillo, D.; Sprengel, R.; Hvalby, O.; Jensen, V.; Burnashev,N.; Rozov, 6 A c
A.; Kaiser, K. M. M.; Koster, H. J.; Borchardt, T.; Worley,P.; Lubke, J.;
Frotscher, M.; Kelly, P. H.; Sommer, B.; Andersen,P.; Seeburg, P. H.;
Sakmann, B.: Importance of AMPA receptors forhippocampal synaptic plasticity
but not for spatial learning. Science 284:1805- 1811, 1999.

GAM7553 354 HOXB8 Greer, J. M.; Capecchi, M. R.: Hoxb8 is required for normal groomingbehavior 6 A b
in mice. Neuron 33: 23- 34, 2002.

GAM7553 354 HOXB8 van den Akker, E.; Reijnen, M.; Korving, J.; Brouwer, A.; Meijlink,F.; 6 A b
Deschamps, J.: Targeted inactivation of Hoxb8 affects survivalof a spinal
ganglion and causes aberrant limb reflexes. Mech. Dev. 89:103- 114, 1999.

GAM7553 354 HPSE Baker, E.; Crawford, J.; Sutherland, G. R.; Freeman, C.; Parish,C. R.; 6 A c
Hulett, M. D.: Human HPA endoglycosidase heparanase. ChromosomeRes. 7: 319
only, 1999.

GAM7553 354 HPSE Hulett, M. D.; Freeman, C.; Hamdorf, B. J.; Baker, R. T.; Harris,M. J.; 6 A c
Parish, C. R.: Cloning of mammalian heparanase, an importantenzyme in tumor
invasion and metastasis. Nature Med. 5: 803- 809,1999.

GAM7553 354 HPSE Kussie, P. H.; Hulmes, J. D.; Ludwig, D. L.; Patel, S.; Navarro,E. C.; 6 A c
Seddon, A. P.; Giorgio, N. A.; Bohlen, P: Cloning and functionalexpression
of a human heparanase gene. Biochem. Biophys. Res. Commun. 261:183- 187,
1999.

GAM7553 354 HPSE Toyoshima, M.; Nakajima, M.: Human heparanase: purification, 6 A c
characterization,cloning, and expression. J. Biol. Chem. 274: 24153- 24160,
1999.

GAM7553 354 HPSE Vlodavsky, I.; Friedmann, Y.; Elkin, M.; Aingorn, H.; Atzmon, R.;Ishai- 6 A c
Michaeli, R.; Bitan, M.; Pappo, O.; Peretz, T.; Michal, I.;Spector, L.;
Pecker, I.: Mammalian heparanase: gene cloning, expressionand function in
tumor progression and metastasis. Nature Med. 5:793- 802, 1999.

GAM7553 354 HSD3B1 Bain, P. A.; Meisler, M. H.; Taylor, B. A.; Payne, A. H.: Thegenes encoding 6 A c
gonadal and nongonadal forms of 3- beta- hydroxysteroiddehydrogenase/delta-

5- delta- 4 isomerase are closely linked on mousechromosome 3. Genomics 16: 219- 223, 1993.

GAM7553 354 HSD3B1 Berube, D.; Luu The, V.; Lachance, Y.; Gagne, R.; Labrie, F.:Assignment of the human 3 beta- hydroxysteroid dehydrogenase gene (HSDB3)to the p13 band of chromosome 1. Cytogenet. Cell Genet. 52: 199- 200,1989. 6 A c

GAM7553 354 HSD3B1 Morissette, J.; Rheaume, E.; Leblanc, J.- F.; Luu- The, V.; Labrie,F.; Simard, J.: Genetic linkage mapping of HSD3B1 and HSD3B2 encodinghuman types I and II 3- beta- hydroxysteroid dehydrogenase/delta- 5- delta- 4- isomeraseclose to D1S514 and the centromeric D1Z5 locus. Cytogenet. CellGenet. 69: 59- 62, 1995. 6 A c

GAM7553 354 HSD3B1 Morrison, N.; Nickson, D. A.; McBride, M. W.; Mueller, U. W.; Boyd,E.; Sutcliffe, R. G.: Regional chromosomal assignment of human 3- beta- hydroxy- 5- enesteroid dehydrogenase to 1p13.1 by non- isotopic in situ hybridisation.Hum. Genet. 87: 223- 225, 1991. 6 A c

GAM7553 354 HSD3B1 Rheaume, E.; Leblanc, J. F.; Lachance, Y.; Labrie, F.; Simard,J.: Detection of frequent BglII polymorphism by polymerase chainreaction and TaqI restriction fragment length polymorphism for 3- beta- hydroxysteroiddehydrogenase/delta- 5- delta- 4 isomerase at the human HSDB3 locus (1p11- p13).Hum. Genet. 87: 753- 754, 1991. 6 A c

GAM7553 354 HSD3B1 Rheaume, E.; Simard, J.; Morel, Y.; Mebarki, F.; Zachmann, M.;Forest, M. G.; New, M. I.; Labrie, F.: Congenital adrenal hyperplasiadue to point mutations in the type II 3- beta- hydroxysteroid dehydrogenasegene. Nature Genet. 1: 239- 245, 1992. 6 A c

GAM7553 354 IARS Nichols, R. C.; Blinder, J.; Pai, S. I.; Ge, Q.; Targoff, I. N.;Plotz, P. H.; Liu, P.: Assignment of two human autoantigen genes:isoleucyl- tRNA synthetase locates to 9q21 and lysyl- tRNA synthetaselocates to 16q23- q24. Genomics 36: 210- 213, 1996. 6 A c

GAM7553 354 IARS Nichols, R. C.; Raben, N.; Boerkoel, C. F.; Plotz, P. H.: Humanisoleucyl- tRNA synthetase: sequence of the cDNA, alternative mRNAsplicing, and the characteristics of an unusually long C- terminalextension. Gene 155: 299- 304, 1995. 6 A c

GAM7553 354 IL22RA2 Dumoutier, L.; Lejeune, D.; Colau, D.; Renauld, J. C.: Cloningand characterization of IL- 22 binding protein, a natural antagonistof IL- 10- related T cell- derived inducible factor/IL 22. J. Immun. 166:7090- 7095, 2001. 6 A c

GAM7553 354 IL22RA2 Kotenko, S. V.; Izotova, L. S.; Mirochnitchenko, O. V.; Esterova,E.; Dickensheets, H.; Donnelly, R. P.; Pestka, S.: Identification,cloning, and characterization of a novel soluble receptor that bindsIL- 22 and neutralizes its activity. J. Immun. 166: 7096- 7103, 2001. 6 A c

GAM7553 354 IL22RA2 Xu, W.; Presnell, S. R.; Parrish- Novak, J.; Kindsvogel, W.; Jaspers,S.; Chen, Z.; Dillon, SR.; Gao, Z.; Gilbert, T.; Madden, K.; Schlutsmeyer,S.; Yao, L.; and 11 others: A soluble class II cytokine receptor,IL- 22RA2, is a naturally occurring IL- 22 antagonist. Proc. Nat. Acad.Sci. 98: 9511- 9516, 2001. 6 A c

GAM7553 354 KCNE3 Abbott, G. W.; Butler, M. H.; Bendahhou, S.; Dalakas, M. C.; Ptacek,L. J.; Goldstein, S. A. N.: MiRP2 forms potassium channels in skeletalmuscle with Kv3.4 and is associated with periodic paralysis. Cell 104:217- 231, 2001. 6 A c

GAM7553 354 KCNE3 Abbott, G. W.; Sesti, F.; Splawski, I.; Buck, M. E.; Lehmann, M.H.; Timothy, K. W.; Keating, M. T.; Goldstein, S. A. N.: MiRP1 formsI(Kr) potassium channels with HERG and is associated with cardiacarrhythmia. Cell 97: 175- 6 A c

187, 1999.

GAM7553 354 KCNE3 Schroeder, B. C.; Waldegger, S.; Fehr, S.; Bleich, M.; Warth, R.;Greger, R.; 6 A c
Jentsch, T. J.: A constitutively open potassium channelformed by KCNQ1 and
KCNE3. Nature 403: 196- 199, 2000.

GAM7553 354 MFAP1 Horrigan, S. K.; Rich, C. B.; Streeten, B. W.; Li, Z.- Y.; Foster,J. A.: 6 A c
Characterization of an associated microfibril protein throughrecombinant DNA
techniques. J. Biol. Chem. 267: 10087- 10095, 1992.

GAM7553 354 MFAP1 Liu, W.; Faraco, J.; Qian, C.; Francke, U.: The gene for microfibril- 6 A c
associatedprotein- 1 (MFAP1) is located several megabases centromeric to
FBN1and is not mutated in Marfan syndrome. Hum. Genet. 99: 578- 584,1997.

GAM7553 354 MFAP1 Yeh, H.; Chow, M.; Abrams, W. R.; Fan, J.; Foster, J.; Mitchell,H.; Muenke, 6 A c
M.; Rosenbloom, J.: Structure of the human gene encodingthe associated
microfibrillar protein (MFAP1) and localization tochromosome 15q15- q21.
Genomics 23: 443- 449, 1994.

GAM7553 354 MYEOV Janssen, J. W. G.; Imoto, I.; Inoue, J.; Shimada, Y.; Ueda, M.;Imamura, M.; 6 A c
Bartram, C. R.; Inazawa, J.: MYEOV, a gene at 11q13,is coamplified with
CCND1, but epigenetically inactivated in a subsetof esophageal squamous cell
carcinomas. J. Hum. Genet. 47: 460- 464,2002.

GAM7553 354 MYEOV Janssen, J. W. G.; Vaandrager, J.- W.; Heuser, T.; Jauch, A.; Kluin,P. M.; 6 A c
Geelen, E.; Bergsagel, P. L.; Kuehl, W. M.; Drexler, H. G.;Otsuki, T.;
Bartram, C. R.; Schuuring, E.: Concurrent activationof a novel putative
transforming gene, myeov, and cyclin D1 in a subsetof multiple myeloma cell
lines with t(11;14)(q13;q32). Blood 95:2691- 2698, 2000.

GAM7553 354 PCSK1 Cool, D. R.; Normant, E.; Shen, F.; Chen, H.- C.; Pannell, L.; Zhang,Y.; 6 A c
Loh, Y. P.: Carboxypeptidase E is a regulated secretory pathwaysorting
receptor: genetic obliteration leads to endocrine disordersin Cpe(fat) mice.
Cell 88: 73- 83, 1997.

GAM7553 354 PCSK1 Copeland, N. G.; Gilbert, D. J.; Chretien, M.; Seidah, N. G.; Jenkins,N. A.: 6 A c
Regional localization of three convertases, PC1 (Nec- 1), PC2(Nec- 2), and
furin (Fur), on mouse chromosomes. Genomics 13: 1356- 1358,1992.

GAM7553 354 PCSK1 Jackson, R. S.; Creemers, J. W. M.; Ohagi, S.; Raffin- Sanson, M.- 6 A c
L.;Sanders, L.; Montague, C. T.; Hutton, J. C.; O'Rahilly, S.: Obesityand
impaired prohormone processing associated with mutations in thehuman
prohormone convertase 1 gene. Nature Genet. 16: 303- 306, 1997.

GAM7553 354 PCSK1 Naggert, J. K.; Fricker, L. D.; Varlamov, O.; Nishina, P. M.; Rouille,Y.; 6 A c
Steiner, D. F.; Carroll, R. J.; Paigen, B. J.; Leiter, E.
H.:Hyperproinsulinaemia in obese fat/fat mice associated with a
carboxypeptidaseE mutation which reduces enzyme activity. Nature Genet. 10:
135- 142,1995.

GAM7553 354 PCSK1 O'Rahilly, S.; Gray, H.; Humphreys, P. J.; Krook, A.; Polonsky,K. S.; White, 6 A c
A.; Gibson, S.; Taylor, K.; Carr, C.: Brief report:impaired processing of
prohormones associated with abnormalities ofglucose homeostasis and adrenal
function. New Eng. J. Med. 333:1386- 1390, 1995.

GAM7553 354 PCSK1 Ohagi, S.; Sakaguchi, H.; Sanke, T.; Tatsuta, H.; Hanabusa, T.;Nanjo, K.: 6 A c
Human prohormone convertase 3 gene: exon- intron organizationand molecular
scanning for mutations in Japanese subjects with NIDDM. Diabetes 45:897-
901, 1996.

GAM7553 354 PCSK1 Seidah, N. G.; Mattei, M. G.; Gaspar, L.; Benjannet, S.; Mbikay,M.; 6 A c
Chretien, M.: Chromosomal assignments of the genes for
neuroendocrineconvertase PC1 (NEC1) to human 5q15- 21, neuroendocrine

convertasePC2 (NEC2) to human 20p11.1- 11.2, and furin (mouse 7[D1- E2] region). Genomics 11:103- 107, 1991.

GAM7553 354 PIK4CB Meyers, R.; Cantley, L. C.: Cloning and characterization of awortmannin- 6 A c
sensitive human phosphatidylinositol 4- kinase. J. Biol.Chem. 272: 4384-
4390, 1997.

GAM7553 354 PIK4CB Nakanishi, S.; Catt, K. J.; Balla, T.: A wortmannin- 6 A c
sensitivephosphatidylinositol 4- kinase that regulates hormone- sensitive
poolsof inositolphospholipids. Proc. Nat. Acad. Sci. 92: 5317- 5321, 1995.

GAM7553 354 PIK4CB Saito, T.; Seki, N.; Ishii, H.; Ohira, M.; Hayashi, A.; Kozuma,S.; Hori, T.: 6 A c
Complementary DNA cloning and chromosomal mapping ofa novel
phosphatidylinositol kinase gene. DNA Res. 4: 301- 305, 1997.

GAM7553 354 PIK4CB Suzuki, K.; Hirano, H.; Okutomi, K.; Suzuki, M.; Kuga, Y.; Fujiwara,T.; 6 A c
Kanemoto, N.; Isono, K.; Horie, M.: Identification and characterizationof a
novel human phosphatidylinositol 4- kinase. DNA Res. 4: 273- 280,1997.

GAM7553 354 STAM Asao, H.; Sasaki, Y.; Arita, T.; Tanaka, N.; Endo, K.; Kasai, H.;Takeshita, 6 A c
T; Endo, Y.; Fujita, T.; Sugamura, K.: Hrs is associatedwith STAM, a signal-
transducing adaptor molecule: its suppressiveeffect on cytokine- induced
cell growth. J. Biol. Chem. 272: 32785- 32791,1997.

GAM7553 354 STAM Takeshita, T.; Arita, T.; Asao, H.; Tanaka, N.; Higuchi, M.; Kuroda,H.; 6 A c
Kaneko, K.; Munakata, H.; Endo, Y.; Fujita, T.; Sugamura, K.:Cloning of a
novel signal- transducing adaptor molecule containingan SH3 domain and ITAM.
Biochem. Biophys. Res. Commun. 225: 1035- 1039,1996.

GAM7553 354 TACSTD2 Calabrese, G.; Crescenzi, C.; Morizio, E.; Palka, G.; Guerra, E.;Alberti, 6 A c
S.: Assignment of TACSTD1 (alias TROP1, M4S1) to human chromosome2p21 and
refinement of mapping of TACSTD2 (alias TROP2, M1S1) to humanchromosome 1p32
by in situ hybridization. Cytogenet. Cell Genet. 92:164- 165, 2001.

GAM7553 354 TACSTD2 Fornaro, M.; Dell'Arciprete, R.; Stella, M.; Bucci, C.; Nutini,M.; Capri, M. 6 A c
G.; Alberti, S.: Cloning of the gene encoding Trop- 2,a cell- surface
glycoprotein expressed by human carcinomas. Int. J.Cancer 62: 610- 618,
1995.

GAM7553 354 TACSTD2 Linnenbach, A. J.; Seng, B. A.; Wu, S.; Robbins, S.; Scollon, M.;Pyrc, J. 6 A c
J.; Druck, T.; Huebner, K.: Retroposition in a family ofcarcinoma-
associated antigen genes. Molec. Cell Biol. 13: 1507- 1515,1993.

GAM7553 354 TACSTD2 Linnenbach, A. J.; Wojcierowski, J.; Wu, S.; Pyrc, J. J.; Ross,A. H.; 6 A c
Dietzschold, B.; Speicher, D.; Koprowski, H.: Sequence investigationof the
major gastrointestinal tumor- associated antigen gene family,GA733. Proc.
Nat. Acad. Sci. 86: 27- 31, 1989.

GAM7553 354 TACSTD2 Ren, Z.; Lin, P.- Y.; Klintworth, G. K.; Iwata, F.; Munier, F. 6 A c
L.;Schorderet, D. F.; El Matri, L.; Theendakara, V.; Basti, S.; Reddy,M.;
Hejtmancik, J. F.: Allelic and locus heterogeneity in autosomalrecessive
gelatinous drop- like corneal dystrophy. Hum. Genet. 110:568- 577, 2002.

GAM7553 354 TACSTD2 Tsujikawa, M.; Kurahashi, H.; Tanaka, T.; Nishida, K.; Shimomura,Y.; Tano, 6 A c
Y.; Nakamura, Y.: Identification of the gene responsiblefor gelatinous drop-
like corneal dystrophy. Nature Genet. 21: 420- 423,1999.

GAM7553 354 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; 6 A c
Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.;
Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1
are associated with human left- right lateralitydefects. Nature Genet. 26:
365- 369, 2000.

GAM7553 354 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: 6 A c

Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989.

GAM7553 354 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002. 6 A c

GAM7553 354 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991. 6 A c

GAM7553 354 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997. 6 A c

GAM7553 354 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996. 6 A c

GAM7553 354 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995. 6 A c

GAM7553 354 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in vertebratedevelopment. Trends Genet. 16: 303- 309, 2000. 6 A c

GAM7553 354 TNFSF8 Cerutti, A.; Schaffer, A.; Goodwin, R. G.; Shah, S.; Zan, H.; Ely,S.; Casali, P.: Engagement of CD153 (CD30 ligand) by CD30- positiveT cells inhibits class switch DNA recombination and antibody productionin human IgD- positive IgM- positive B cells. J. Immun. 165: 786- 794,2000. 6 A c

GAM7553 354 TNFSF8 Croager, E. J.; Abraham, L. J.: Characterisation of the humanCD30 ligand gene structure. Biochim. Biophys. Acta 1353: 231- 235,1997. 6 A c

GAM7553 354 TNFSF8 Smith, C. A.; Gruss, H.- J.; Davis, T.; Anderson, D.; Farrah, T.;Baker, E.; Sutherland, G. R.; Brannan, C. I.; Copeland, N. G.; Jenkins,N. A.; Grabstein, K. H.; Gliniak, B.; and 9 others: CD30 antigen,a marker for Hodgkin's lymphoma, is a receptor whose ligand definesan emerging family of cytokines with homology to TNF. Cell 73: 1349- 1360,1993. 6 A c

GAM7553 354 UBE4A Koegl, M.; Hoppe, T.; Schlenker, S.; Ulrich, H. D.; Mayer, T. U.;Jentsch, S.: A novel ubiquitination factor, E4, is involved in multiubiquitinchain assembly. Cell 96: 635- 644, 1999. 6 A c

GAM7553 354 UBE4A Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 6 A c

GAM7776 246 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989. 3 C b

GAM7776 246 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989. 3 C b

GAM7776 246 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987. 3 C b

GAM7776 246 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene 3 C b

family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986.

GAM7776 246 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: 3 C b
Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988.

GAM7776 246 ABCC11 Bera, T. K.; Lee, S.; Salvatore, G.; Lee, B.; Pastan, I.: MRP8,a new member 3 C c
of ABC transporter superfamily, identified by EST databasemining and gene prediction program, is highly expressed in breastcancer. Molec. Med. 7: 509- 516, 2001.

GAM7776 246 ABCC11 Tammur, J.; Prades, C.; Arnould, I.; Rzhetsky, A.; Hutchinson,A.; Adachi, 3 C c
M.; Schuetz, J. D.; Swoboda, K. J.; Ptacek, L. J.; Rosier,M.; Dean, M.; Allikmets, R.: Two new genes from the human ATP- bindingcassette transporter superfamily, ABCC11 and ABCC12, tandemly duplicatedon chromosome 16q12. Gene 273: 89- 96, 2001.

GAM7776 246 ABCC11 Yabuuchi, H.; Shimizu, H.; Takayanagi, S.; Ishikawa, T.: Multiplesplicing 3 C c
variants of two new human ATP- binding cassette transporters,ABCC11 and ABCC12. Biochem. Biophys. Res. Commun. 288: 933- 939,2001.

GAM7776 246 ABCD3 Gartner, J.; Kearns, W.; Pearson, P.; Valle, D.: Characterizationand 3 C c
localization of the human 70- kD peroxisomal membrane protein (PMP70)gene. (Abstract) Am. J. Hum. Genet. 51 (suppl.): A168, 1992.

GAM7776 246 ABCD3 Gartner, J.; Kearns, W.; Rosenberg, C.; Pearson, P.; Copeland,N. G.; 3 C c
Gilbert, D. J.; Jenkins, N. A.; Valle, D.: Localization ofthe 70- kDa peroxisomal membrane protein to human 1p21- p22 and mouse

GAM7776 246 ABCD3 Gartner, J.; Obie, C.; Watkins, P.; Valle, D.: Restoration ofperoxisome 3 C c
biogenesis in a peroxisome- deficient mammalian cell lineby expression of either the 35 kDa or the 70 kDa peroxisomal membraneproteins. J. Inherit. Metab. Dis. 17: 327- 329, 1994.

GAM7776 246 ABCD3 Genomics 15: 412- 414, 1993.3. Gartner, J.; Moser, H.; Valle, D.: Mutations 3 C c
in the 70K peroxisomalmembrane protein gene in Zellweger syndrome. Nature Genet. 1: 16- 23,1992.

GAM7776 246 ABCD3 Moser, A. B.; Rasmussen, M.; Naidu, S.; Watkins, P. A.; McGuinness,M.; 3 C c
Hajra, A. K.; Chen, G.; Raymond, G.; Liu, A.; Gordon, D.; Garnaas,K.; Walton, D. S.; Skjedal, O. H.; Guggenheim, M. A.; Jackson, L.G.; Elias, E. R.; Moser, H. W.: Phenotype of patients with peroxisomaldisorders subdivided into sixteen complementation groups. J. Pediat. 127:13- 22, 1995.

GAM7776 246 ABCD3 Paton, B. C.; Heron, S. E.; Nelson, P. V.; Morris, C. P.; Poulos,A.: Absence 3 C c
of mutations raises doubts about the role of the 70- kDperoxisomal membrane protein in Zellweger syndrome. (Letter) Am.J. Hum. Genet. 60: 1535- 1539, 1997.

GAM7776 246 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- 3 C b
TS6, and ADAM- TS7, novel members of a new family of zinc metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.

GAM7776 246 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C b
Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM7776 246 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM 3 C b
protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999.

GAM7776 246 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; 3 C b
Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.;
Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of
aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664-
1666, 1999.

GAM7776 246 ADCY6 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 C b
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian
Genome 6: 111- 113, 1995.

GAM7776 246 ADCY6 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 C b
members are randomly located on different chromosomes. Hum.Genet. 94: 527-
529, 1994.

GAM7776 246 ADCY6 Haber, N.; Stengel, D.; Defer, N.; Roeckel, N.; Mattei, M.- G.;Hanoune, J.: 3 C b
Chromosomal mapping of human adenylyl cyclase genestype III, type V and type
VI. Hum. Genet. 94: 69- 73, 1994.

GAM7776 246 ADORA2A Chen, J.- F.; Huang, Z.; Ma, J.; Zhu, J.; Moratalla, R.; Standaert,D.; 3 C c
Moskowitz, M. A.; Fink, J. S.; Schwarzschild, M. A.: A2A adenosinereceptor
deficiency attenuates brain injury induced by transient focalischemia in
mice. J. Neurosci. 19: 9192- 9200, 1999.

GAM7776 246 ADORA2A Gaudray, P.: Personal Communication. Nice, France 6/1/1994. 3 C c

GAM7776 246 ADORA2A Gusella, J. F.: Personal Communication. Boston, Mass. 4/17/1994. 3 C c

GAM7776 246 ADORA2A Le, F.; Townsend- Nicholson, A.; Baker, E.; Sutherland, G. R.; Schofield,P. 3 C c
R.: Characterization and chromosomal localization of the humanA2a adenosine
receptor gene: ADORA2A. Biochem. Biophys. Res. Commun. 223:461- 467, 1996.

GAM7776 246 ADORA2A Ledent, C.; Vaugeois, J.- M.; Schiffmann, S. N.; Pedrazzini, T.;El Yacoubi, 3 C c
M. E.; Vanderhaeghen, J.- J.; Costentin, J.; Heath, J.K.; Vassart, G.;
Parmentier, M.: Aggressiveness, hypoalgesia andhigh blood pressure in mice
lacking the adenosine A2a receptor. Nature 388:674- 678, 1997.

GAM7776 246 ADORA2A Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 C c
M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor,
and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991. Note:
Erratum: Genomics 23: 305 only, 1994.

GAM7776 246 ADORA2A MacCollin, M.; Peterfreund, R.; MacDonald, M.; Fink, J. S.; Gusella,J.: 3 C c
Mapping of a human A2a adenosine receptor (ADORA2) to chromosome22. Genomics
20: 332- 333, 1994.

GAM7776 246 ADORA2A Ohta, A.; Sitkovsky, M.: Role of G- protein- coupled adenosine receptorsin 3 C c
downregulation of inflammation and protection from tissue damage. Nature
916- 920,2001.

GAM7776 246 ADORA2A Szepetowski, P.; Perucca- Lostanlen, D.; Gaudray, P.: Mapping genesaccording 3 C c
to their amplification status in tumor cells: contributionto the map of
11q13. Genomics 16: 745- 750, 1993.

GAM7776 246 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; 3 C c
Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive
dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad.
Sci. 99: 9990- 9995, 2002.

GAM7776 246 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; 3 C c
Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor:
functional expression and chromosomal assignment to 7p21. J.Biochem. 116:
845- 851, 1994.

GAM7776 246 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, 3 C c

C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994.

GAM7776 246 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 3 C c

GAM7776 246 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95- 101, 1997. 3 C c

GAM7776 246 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779- 782, 2000. 3 C c

GAM7776 246 AIM1 Fukamachi, S.; Shimada, A.; Shima, A.: Mutations in the gene encodingB, a novel transporter protein, reduce melanin content in medaka. NatureGenet. 28: 381- 385, 2001. 3 C c

GAM7776 246 AIM1 Harada, M.; Li, Y. F.; El- Gamil, M.; Rosenberg, S. A.; Robbins,P. F.: Use of an in vitro immunoselected tumor line to identify sharedmelanoma antigens recognized by HLA- A*0201- restricted T cells. CancerRes. 61: 1089- 1094, 2001. 3 C c

GAM7776 246 AIM1 Katayama, H.; Ota, T.; Morita, K.; Terada, Y.; Suzuki, F.; Katoh,O.; Tatsuka, M.: Human AIM- 1: cDNA cloning and reduced expressionduring endomitosis in megakaryocyte- lineage cells. Gene 224: 1- 7,1998. 3 C c

GAM7776 246 AIM1 Kimura, M.; Matsuda, Y.; Yoshioka, T.; Sumi, N.; Okano, Y.: Identificationand characterization of STK12/Aik2: a human gene related to auroraof Drosophila and yeast IPL1. Cytogenet. Cell Genet. 82: 147- 152,1998. 3 C c

GAM7776 246 AIM1 Newton, J. M.; Cohen- Barak, O.; Hagiwara, N.; Gardner, J. M.; Davisson,M. T.; King, R. A.; Brilliant, M. H.: Mutations in the human orthologueof the mouse underwhite gene (uw) underlie a new form of oculocutaneousalbinism, OCA4. Am. J. Hum. Genet. 69: 981- 988, 2001. 3 C c

GAM7776 246 AIM1 Ray, M. E.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: Isolationand characterization of genes associated with chromosome- 6 mediatedtumor suppression in human malignant melanoma. Oncogene 12: 2527- 2533,1996. 3 C c

GAM7776 246 AIM1 Ray, M. E.; Wistow, G.; Su, Y. A.; Meltzer, P. S.; Trent, J. M.: AIM1, a novel non- lens member of the beta- gamma- crystallin superfamily,is associated with the control of tumorigenicity in human malignantmelanoma. Proc. Nat. Acad. Sci. 94: 3229- 3234, 1997. 3 C c

GAM7776 246 AIM1 Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara,M.; Gilbert, D. J.; Jenkins, N. A.; Copeland, N. G.; Yagita, H.; Okumura,K.: cDNA cloning, expression, subcellular localization, and chromosomalassignment of mammalian aurora homologues, aurora- related kinase (ARK)1 and 2. Biochem. Biophys. Res. Commun. 244: 285- 292, 1998. 3 C c

GAM7776 246 AIM1 Tatsuka, M.; Katayama, H.; Ota, T.; Tanaka, T.; Odashima, S.; Suzuki,F.; Terada, Y.: Multinuclearity and increased ploidy caused by overexpressionof the aurora- and Ipl1- like midbody- associated protein mitotic kinasein human cancer cells. Cancer Res. 58: 4811- 4816, 1998. 3 C c

GAM7776 246 AIM1 Teichmann, U.; Ray, M. E.; Ellison, J.; Graham, C.; Wistow, G.;Meltzer, P. 3 C c
S.; Trent, J. M.; Pavan, W. J.: Cloning and tissue expressionof the mouse
ortholog of AIM1, a beta- gamma- crystallin superfamilymember. Mammalian
Genome 9: 715- 720, 1998.

GAM7776 246 AIM1 Trent, J. M.; Stanbridge, E. J.; McBride, H. L.; Meese, E. U.;Casey, G.; 3 C c
Araujo, D. E.; Witkowski, C. M.; Nagle, R. B.: Tumorigenicityin human
melanoma cell lines controlled by introduction of human chromosome6. Science
247: 568- 571, 1990.

GAM7776 246 ALOX15 Funk, C. D.; Funk, L. B.; FitzGerald, G. A.; Samuelsson, B.: 3 C c
Characterizationof human 12- lipoxygenase genes. Proc. Nat. Acad. Sci. 89:
3962- 3966,1992.

GAM7776 246 ALOX15 Kelavkar, U. P.; Badr, K. F.: Effects of mutant p53 expressionon human 15- 3 C c
lipoxygenase- promoter activity and murine 12/15- lipoxygenasegene
expression: evidence that 15- lipoxygenase is a mutator gene. Proc.Nat.
Acad. Sci. 96: 4378- 4383, 1999.

GAM7776 246 ALOX15 Sigal, E.; Craik, C. S.; Highland, E.; Grunberger, D.; Costello,L. L.; 3 C c
Dixon, R. A. F.; Nadel, J. A.: Molecular cloning and primarystructure of
human 15- lipoxygenase. Biochem. Biophys. Res. Commun. 157:457- 464, 1988.

GAM7776 246 ALOX15 Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.;Tanabe, T.: 3 C c
Cloning and sequence analysis of the cDNA for arachidonate12- lipoxygenase
of porcine leukocytes. Proc. Nat. Acad. Sci. 87:2142- 2146, 1990.

GAM7776 246 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 3 C b
(CED- 4 homolog) regulates programmed cell death in mammaliandevelopment.
Cell 94: 727- 737, 1998.

GAM7776 246 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of 3 C b
Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749,
1999.

GAM7776 246 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: 3 C b
Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248-
258, 2000.

GAM7776 246 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 3 C b
deficiency and neural tube closure defects are found in fogmice. Proc. Nat.
Acad. Sci. 98: 9683- 9687, 2001.

GAM7776 246 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic 3 C b
protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by
fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253,
1999.

GAM7776 246 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, 3 C b
P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.;
Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.:
Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of
the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002.

GAM7776 246 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- 3 C b
Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.;
Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf-
1 in malignant melanoma. Nature 409: 207- 211, 2001.

GAM7776 246 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: 3 C b
Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization.
Molec.Cell 1: 949- 957, 1998.

GAM7776 246 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; 3 C b

Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998.

GAM7776 246 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997. 3 C b

GAM7776 246 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: Apolipoprotein L gene family: tissue- specific expression,splicing, promoter regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001. 3 C c

GAM7776 246 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya-Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a new human high density lipoprotein apolipoproteinexpressed by the pancreas: identification, cloning, characterization,and plasma distribution of apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997. 3 C c

GAM7776 246 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.; Bahn, S.: Gene expression analysis in schizophrenia:reproducible up-regulation of several members of the apolipoproteinL family located in a high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat. Acad. Sci. 99: 4680- 4685, 2002. 3 C c

GAM7776 246 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The apolipoprotein L gene cluster has emerged recently in evolutionand is expressed in human vascular tissue. Genomics 79: 539- 546,2002. 3 C c

GAM7776 246 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman apolipoprotein L gene cluster: identification, classification,and sites of distribution. Genomics 74: 71- 78, 2001. 3 C c

GAM7776 246 APPBP2 Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002. 3 C b

GAM7776 246 APPBP2 Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;Ohara, O.; Tanaka, A.; Kotani, H.; Miyajima, N.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. VI. The codingsequences of 80 new genes (KIAA0201- KIAA0280) deduced by analysisof cDNA clones from cell line KG- 1 and brain. DNA Res. 3: 321- 329,1996. 3 C b

GAM7776 246 APPBP2 Zheng, P.; Eastman, J.; Vande Pol, S.; Pimplikar, S. W.: PAT1,a microtubule-interacting protein, recognizes the basolateral sortingsignal of amyloid precursor protein. Proc. Nat. Acad. Sci. 95: 14745- 14750,1998. 3 C b

GAM7776 246 AQP6 Ma, T.; Yang, B.; Kuo, W.- L.; Verkman, A. S.: cDNA cloning andgene structure of a novel water channel expressed exclusively in humankidney: evidence for a gene cluster of aquaporins at chromosome locus12q13. Genomics 35: 543- 550, 1996. 3 C c

GAM7776 246 AQP6 Ma, T.; Yang, B.; Umenishi, F.; Verkman, A. S.: Closely spacedtandem arrangement of AQP2, AQP5, and AQP6 genes in a 27- kilobasesegment at chromosome locus 12q13. Genomics 43: 387- 389, 1997. 3 C c

GAM7776 246 AQP6 Yasui, M.; Kwon, T.- H.; Knepper, M. A.; Nielsen, S.; Agre, P.:Aquaporin- 6: an intracellular vesicle water channel protein in renalepithelia. Proc. Nat. Acad. Sci. 96: 5808- 5813, 1999. 3 C c

GAM7776 246 ARCN1 Radice, P.; Pensotti, V.; Jones, C.; Perry, H.; Pierotti, M. A.;Tunnacliffe, A.: The human archain gene, ARCN1, has highly conservedhomologs in rice and Drosophila. Genomics 26: 101- 106, 1995. 3 C c

GAM7776 246 ARCN1 Tunnacliffe, A.; van de Vrugt, H.; Pensotti, V.; Radice, P.: Thecoatomer protein delta- COP, encoded by the archain gene, is conservedacross diverse eukaryotes. Mammalian Genome 7: 784- 786, 1996. 3 C c

GAM7776 246 ATP1B2 Gloor, S.; Antonicek, H.; Sweadner, K. J.; Pagliusi, S.; Frank,R.; Moos, M.; Schachner, M.: The adhesion molecule on glia (AMOG)is a homologue of the beta subunit of the Na,K- ATPase. J. Cell Biol. 110:165- 174, 1990. 3 C b

GAM7776 246 ATP1B2 Hsieh, C.- L.; Cheng- Deutsch, A.; Gloor, S.; Schachner, M.; Francke,U.: Assignment of Amog (adhesion molecule on glia) gene to mousechromosome 11 near Zfp- 3 and Asgr- 1,2 and to human chromosome 17. Somat.Cell Molec. Genet. 16: 401- 405, 1990. 3 C b

GAM7776 246 ATP1B2 Malo, D.; Schurr, E.; Levenson, R.; Gros, P.: Assignment of Na,K-ATPasebeta- (2)- subunit gene (Atpb- 2) to mouse chromosome 11. Genomics 6:697- 699, 1990. 3 C b

GAM7776 246 ATP1B2 Martin- Vasallo, P.; Dackowski, P.; Emanuel, J. R.; Levenson, R.: Identification of a putative isoform of the Na,K- ATPase beta subunit:primary structure and tissue- specific expression. J. Biol. Chem. 164:4613- 4618, 1989. 3 C b

GAM7776 246 ATP1B2 Pagliusi, S.; Antonicek, H.; Gloor, S.; Frank, R.; Moos, M.; Schachner,M.: Identification of a cDNA clone specific for the neural adhesionmolecule AMOG. J. Neurosci. Res. 22: 113- 119, 1989. 3 C b

GAM7776 246 BACE2 Acquati, F.; Accarino, M.; Nucci, C.; Fumagalli, P.; Jovine, L.;Ottolenghi, S.; Taramelli, R.: The gene encoding DRAP (BACE2), aglycosylated transmembrane protein of the aspartic protease family,maps to the Down syndrome critical region. FEBS Lett. 468: 59- 64,2000. 3 C c

GAM7776 246 BACE2 Bennett, B. D.; Babu- Khan, S.; Loeloff, R.; Louis, J.- C.; Curran,E.; Citron, M.; Vassar, R.: Expression analysis of BACE2 in brainand peripheral tissues. J. Biol. Chem. 275: 20647- 20651, 2000. 3 C c

GAM7776 246 BACE2 Saunders, A. J.; Kim, T.- W.; Tanzi, R. E.: BACE maps to chromosome11 and a BACE homolog, BACE2, reside in the obligate Down syndromeregion of chromosome 21. Science 286: 1255A only, 1999. 3 C c

GAM7776 246 BACE2 Solans, A.; Estivill, X.; de la Luna, S.: A new aspartyl proteaseon 21q22.3, BACE2, is highly similar to Alzheimer's amyloid precursorprotein beta-secretase. Cytogenet. Cell Genet. 89: 177- 184, 2000. 3 C c

GAM7776 246 BACE2 Xin, H.; Stephans, J. C.; Duan, X.; Harrowe, G.; Kim, E.; Grieshammer,U.; Kingsley, C.; Giese, K.: Identification of a novel aspartic- likeprotease differentially expressed in human breast cancer cell lines. Biochim.Biophys. Acta 1501: 125- 137, 2000. 3 C c

GAM7776 246 BCL10 Cockerham, G. C.; Hidayat, A. A.; Bijwaard, K. E.; Sheng, Z.- M.: Re-evaluation of 'reactive lymphoid hyperplasia of the uvea': animmunohistochemical and molecular analysis of 10 cases. Ophthalmology 107:151- 158, 2000. 3 C b

GAM7776 246 BCL10 Fakruddin, J. M.; Chaganti, R. S. K.; Murty, V. V. V. S.: Lackof BCL10 mutations in germ cell tumors and B cell lymphomas. Cell 97:683- 688, 1999. 3 C b

GAM7776 246 BCL10 Isaacson, P. G.; Spencer, J.: The biology of low grade MALT lymphoma. J.Clin. Path. 48: 395- 397, 1995. 3 C b

GAM7776 246 BCL10 Ruland, J.; Duncan, G. S.; Elia, A.; del Barco Barrantes, I.; Nguyen,L.; Plyte, S.; Millar, D. G.; Bouchard, D.; Wakeham, A.; Ohashi, P.S.; Mak, T. W.: Bcl10 is a positive regulator of antigen receptor- inducedactivation of NF- kappa- B and neural tube closure. Cell 104: 33- 42,2001. 3 C b

GAM7776 246 BCL10 Thome, M.; Martinon, F.; Hofmann, K.; Rubio, V.; Steiner, V.; Schneider,P.; 3 C b
Mattmann, C.; Tschopp, J.: Equine herpesvirus- 2 E10 gene product,but not
its cellular homologue, activates NF- kappa- B transcriptionfactor and c-
Jun N- terminal kinase. J. Biol. Chem. 274: 9962- 9968,1999.

GAM7776 246 BCL10 Willis, T. G.; Jadayel, D. M.; Du, M.- Q.; Peng, H.; Perry, A. R.;Abdul- 3 C b
Rauf, M.; Price, H.; Karran, L.; Majekodunmi, O.; Wlodarska,I.; Pan, L.;
Crook, T.; Hamoudi, R.; Isaacson, P. G.; Dyer, M. J.S.: Bcl10 is involved in
t(1;14)(p22;q32) of MALT B cell lymphomaand mutated in multiple tumor types
Cell 96: 35- 45, 1999.

GAM7776 246 BCL10 Wotherspoon, A. C.; Pan, L. X.; Diss, T. C.; Isaacson, P. G.:Cytogenetic 3 C b
study of B- cell lymphoma of mucosa- associated lymphoidtissue. Cancer
Genet. Cytogenet. 58: 35- 38, 1992.

GAM7776 246 BDP1 Kelter, A.- R.; Herchenbach, J.; Wirth, B.: The transcription factor- 3 C b
likenuclear regulator (TFNR) contains a novel 55- amino- acid motif
repeatednine times and maps closely to SMN1. Genomics 70: 315- 326, 2000.

GAM7776 246 BDP1 Schramm, L.; Pendergrast, P. S.; Sun, Y.; Hernandez, N.: Differenthuman 3 C b
TFIIB activities direct RNA polymerase III transcription fromTATA-
containing and TATA- less promoters. Genes Dev. 14: 2650- 2663,2000.

GAM7776 246 CAMLG Bram, R. J.; Crabtree, G. R.: Calcium signalling in T cells stimulatedby a 3 C b
cyclophilin B- binding protein. Nature 371: 355- 358, 1994.

GAM7776 246 CAMLG Bram, R. J.; Valentine, V.; Shapiro, D. N.; Jenkins, N. A.; Gilbert,D. J.; 3 C b
Copeland, N. G.: The gene for calcium- modulating cyclophilinligand (CAMLG)
is located on human chromosome 5q23 and a syntenicregion of mouse chromosome
13. Genomics 31: 257- 260, 1996.

GAM7776 246 CASP2 Bergeron, L.; Perez, G. I.; Macdonald, G.; Shi, L.; Sun, Y.; Jurisicova,A.; 3 C c
Varmuza, S.; Latham, K. E.; Flaws, J. A.; Salter, J. C. M.; Hara,H.;
Moskowitz, M. A.; Li, E.; Greenberg, A.; Tilly, J. L.; Yuan, J.: Defects in
regulation of apoptosis in caspase- 2- deficient mice. GenesDev. 12: 1304-
1314, 1998.

GAM7776 246 CASP2 Kumar, S.; Kinoshita, M.; Noda, M.; Copeland, N. G.; Jenkins, N.A.: 3 C c
Induction of apoptosis by the mouse Nedd2 gene, which encodesa protein
similar to the product of the Caenorhabditis elegans celldeath gene ced- 3
and the mammalian IL- 1- beta- converting enzyme. GenesDev. 8: 1613- 1626,
1994.

GAM7776 246 CASP2 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 3 C c
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM7776 246 CASP2 Kumar, S.; White, D. L.; Takai, S.; Turczynowicz, S.; Juttner,C. A.; Hughes, 3 C c
T. P.: Apoptosis regulatory gene NEDD2 maps to humanchromosome segment 7q34-
35, a region frequently affected in haematologicalneoplasms. Hum. Genet. 95:
641- 644, 1995.

GAM7776 246 CASP2 Lassus, P.; Opitz- Araya, X.; Lazebnik, Y.: Requirement for caspase- 2in 3 C c
stress- induced apoptosis before mitochondrial permeabilization. Science
297:1352- 1354, 2002.

GAM7776 246 CASP2 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; 3 C c
Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes,
CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem.
Biophys. Res. Commun. 225: 983- 989, 1996.

GAM7776 246 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 C b
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.

P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte activation caused by caspase- 8 mutations lead to humanimmunodeficiency. Nature 419: 395- 399, 2002.

GAM7776 246 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.; Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a novel human apoptotic cysteine protease containingtwo FADD- like domains. Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996. 3 C b

GAM7776 246 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager, V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002. 3 C b

GAM7776 246 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999. 3 C b

GAM7776 246 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: Expanded polyglutamine in the Machado- Joseph disease proteininduces cell death in vitro and in vivo. Nature Genet. 13: 196- 202,1996. 3 C b

GAM7776 246 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to the murine syntenic region on chromosome 1B- proximalC by in situ hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998. 3 C b

GAM7776 246 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: Caspase- 8 is required for cell death induced by expanded polyglutaminerepeats. Neuron 22: 623- 633, 1999. 3 C b

GAM7776 246 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet, O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.; Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1, and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998. 3 C b

GAM7776 246 CBFA2T2 Calabi, F.; Cilli, V.: CBFA2T1, a gene rearranged in human leukemia,is a member of a multigene family. Genomics 52: 332- 341, 1998. 3 C c

GAM7776 246 CBFA2T2 Fracchiolla, N. S.; Colombo, G.; Finelli, P.; Maiolo, A. T.; Neri,A.: EHT, a new member of the MTG8/ETO gene family, maps on 20q11region and is deleted in acute myeloid leukemias. (Letter) Blood 92:3481- 3484, 1998. 3 C c

GAM7776 246 CBFA2T2 Kitabayashi, I.; Ida, K.; Morohoshi, F.; Yokoyama, A.; Mitsuhashi,N.; Shimizu, K.; Nomura, N.; Hayashi, Y.; Ohki, M.: The AML1- MTG8leukemic fusion protein forms a complex with a novel member of theMTG8(ETO/CDR) family, MTGR1. Molec. Cell. Biol. 18: 846- 858, 1998. 3 C c

GAM7776 246 CCNF Bai, C.; Sen, P.; Hofmann, K.; Ma, L.; Goebl, M.; Harper, J. W.;Elledge, S. J.: SKP1 connects cell cycle regulators to the ubiquitinproteolysis machinery through a novel motif, the F- box. Cell 86:263- 274, 1996. 3 C c

GAM7776 246 CCNF Kraus, B.; Pohlschmidt, M.; Leung, A. L. S.; Germino, G. G.; Snarey,A.; Schneider, M. C.; Reeders, S. T.; Frischauf, A.- M.: A novel cyclingene (CCNF) in the region of the polycystic kidney disease gene (PKD1). Genomics 24:27- 33, 1994. 3 C c

GAM7776 246 CCNF Obermayr, F.; Sutherland, H. F.; Kraus, B.; Frischauf, A.- M.:Mouse cyclin F maps to a conserved linkage group on mouse chromosome17. Mammalian Genome 6: 149- 150, 1995. 3 C c

GAM7776 246 CD209 Curtis, B. M.; Scharnowske, S.; Watson, A. J.: Sequence and expressionof a membrane- associated C- type lectin that exhibits CD4- independentbinding of human immunodeficiency virus envelope glycoprotein gp120. Proc.Nat. Acad. Sci. 89: 8356- 8360, 1992. 3 C b

GAM7776 246 CD209 Feinberg, H.; Mitchell, D. A.; Drickamer, K.; Weis, W. I.: Structuralbasis for selective recognition of oligosaccharides by DC- SIGN andDC- SIGNR. Science 294: 2163- 2166, 2001. 3 C b

GAM7776 246 CD209 Geijtenbeek, T. B. H.; Kwon, D. S.; Torensma, R.; van Vliet, S.J.; van Duijnhoven, G. C. F.; Middel, J.; Cornelissen, I. L. M. H.A.; Nottet, H. S. L. M.; KewalRamani, V. N.; Littman, D. R.; Figdor,C. G.; van Kooyk, Y.: DC-SIGN, a dendritic cell- specific HIV- 1- bindingprotein that enhances trans-infection of T cells. Cell 100: 587- 597,2000. 3 C b

GAM7776 246 CD209 Geijtenbeek, T. B. H.; Torensma, R.; van Vliet, S. J.; van Duijnhoven,G. C. F.; Adema, G. J.; van Kooyk, Y.; Figdor, C. G.: Identificationof DC- SIGN, a novel dendritic cell- specific ICAM- 3 receptor that supportsprimary immune responses. Cell 100: 575- 585, 2000. 3 C b

GAM7776 246 CD209 Soilleux, E. J.; Barten, R.; Trowsdale, J.: Cutting edge: DC- SIGN;a related gene, DC- SIGNR; and CD23 form a cluster on 19p13. J. Immun. 165:2937- 2942, 2000. 3 C b

GAM7776 246 CDC6 Saha, P.; Chen, J.; Thome, K. C.; Lawlis, S. J.; Hou, Z.- H.; Hendricks,M.; Parvin, J. D.; Dutta, A.: Human CDC6/Cdc18 associates with Orc1and cyclin-cdk and is selectively eliminated from the nucleus at theonset of S phase. Molec. Cell. Biol. 18: 2758- 2767, 1998. 3 C b

GAM7776 246 CDC6 Williams, R. S.; Shohet, R. V.; Stillman, B.: A human proteinrelated to yeast Cdc6p. Proc. Nat. Acad. Sci. 94: 142- 147, 1997. 3 C b

GAM7776 246 CDC6 Yan, Z.; DeGregori, J.; Shohet, R.; Leone, G.; Stillman, B.; Nevins,J. R.; Williams, R. S.: Cdc6 is regulated by E2F and is essentialfor DNA replication in mammalian cells. Proc. Nat. Acad. Sci. 95:3603- 3608, 1998. 3 C b

GAM7776 246 CDC6 Yan, Z.; Fedorov, S. A.; Mumby, M. C.; Williams, R. S.: PR48,a novel regulatory subunit of protein phosphatase 2A, interacts withCdc6 and modulates DNA replication in human cells. Molec. Cell. Biol. 20:1021- 1029, 2000. 3 C b

GAM7776 246 CDH17 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999. 3 C c

GAM7776 246 CDH17 Dantzig, A. H.; Hoskins, J.; Tabas, L. B.; Bright, S.; Shepard,R. L.; Jenkins, I. L.; Duckworth, D. C.; Sportsman, J. R.; Mackensen,D.; Rosteck, P. R., Jr.; Skatrud, P. L.: Association of intestinalpeptide transport with a protein related to the cadherin superfamily. Science 264:430- 433, 1994. 3 C c

GAM7776 246 CDH17 Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias,J.; Callen, D. F.: Localization of human cadherin genes to chromosomeregions exhibiting cancer- related loss of heterozygosity. Genomics 49:467- 471, 1998. 3 C c

GAM7776 246 CIAS1 Dode, C.; Le Du, N.; Cuisset, L.; Letourneur, F.; Berthelot, J.- M.;Vaudour, G.; Meyrier, A.; Watts, R. A.; Scott, D. G. I.; Nicholls,A.; Granel, B.; Frances, C.; Garcier, F.; Edery, P.; Boulinguez, S.;Domergues, J.- P.; Delpech, M.; Grateau, G.: New mutations of CIAS1that are responsible for Muckle- Wells syndrome and familial cold urticaria:a novel mutation underlies both syndromes. Am. J. Hum. Genet. 70:1498- 1506, 2002. 3 C b

GAM7776 246 CIAS1 Feldmann, J.; Prieur, A.- M.; Quartier, P.; Berquin, P.; Certain,S.; Cortis, E.; Teillac- Hamel, D.; Fischer, A.; de Saint Basile, G.: Chronic infantile 3 C b

neurological cutaneous and articular syndromeis caused by mutations in CIAS1, a gene highly expressed in polymorphonuclearcells and chondrocytes. Am. J. Hum. Genet. 71: 198- 203, 2002.

GAM7776 246 CIAS1 Hoffman, H. M.; Mueller, J. L.; Broide, D. H.; Wanderer, A. A.;Kolodner, R. D.: Mutation of a new gene encoding a putative pyrin- likeprotein causes familial cold autoinflammatory syndrome and Muckle- Wellssyndrome. Nature Genet. 29: 301- 305, 2001. 3 C b

GAM7776 246 CIAS1 Mao, M.; Fu, G.; Wu, J.- S.; Zhang, Q.- H.; Zhou, J.; Kan, L.- X.;Huang, Q.- H.; He, K.- L.; Gu, B.- W.; Han, Z.- G.; Shen, Y.; Gu, J.;Yu, Y.- P.; Xu, S.- H.; Wang, Y.- X.; Chen, S.- J.; Chen, Z.: Identificationof genes expressed in human CD34+ hematopoietic stem/progenitor cellsby expressed sequence tags and efficient full- length cDNA cloning. Proc.Nat. Acad. Sci. 95: 8175- 8180, 1998. 3 C b

GAM7776 246 CLECSF12 Ariizumi, K.; Shen, G.- L.; Shikano, S.; Xu, S.; Ritter, R., III;Kumamoto, T.; Edelbaum, D.; Morita, A.; Bergstresser, P. R.; Takashima,A.: Identification of a novel, dendritic cell- associated molecule,dectin- 1, by subtractive cDNA cloning. J. Biol. Chem. 275: 20157- 20167,2000. 3 C c

GAM7776 246 CLECSF12 Brown, G. D.; Gordon, S.: A new receptor for beta- glucans. Nature 413:36- 37, 2001. 3 C c

GAM7776 246 CLECSF12 Hernanz- Falcon, P.; Arce, I.; Roda- Navarro, P.; Fernandez- Ruiz,E.: Cloning of human dectin- 1, a novel C- type lectin- like receptorgene expressed on dendritic cells. Immunogenetics 53: 288- 295, 2001. 3 C c

GAM7776 246 CLECSF12 Yokota, K.; Takashima, A.; Bergstresser, P. R.; Ariizumi, K.:Identification of a human homologue of the dendritic cell- associatedC- type lectin- 1, dectin- 1. Gene 272: 51- 60, 2001. 3 C c

GAM7776 246 CLNS1A Anguita, J.; Chalfant, M. L.; Civan, M. M.; Coca- Prados, M.: Molecularcloning of the human volume- sensitive chloride conductance regulatoryprotein, pI(Cln), from ocular ciliary epithelium. Biochem. Biophys.Res. Commun. 208: 89- 95, 1995. 3 C c

GAM7776 246 CLNS1A Buyse, G.; De Greef, C.; Raeymaekers, L.; Droogmans, G.; Nilius,B.; Eggermont, J.: The ubiquitously expressed pI(Cln) protein formshomomeric complexes in vitro. Biochem. Biophys. Res. Commun. 218:822- 827, 1996. 3 C c

GAM7776 246 CLNS1A Nagl, U. O.; Erdel, M.; Schmarda, A.; Seri, M.; Pinggera, G. M.;Gschwentner, M.; Duba, C.; Galietta, L. J. V.; Deetjen, P.; Utermann,G.; Paulmichl, M.: Chromosomal localization of the genes (CLNS1Aand CLNS1B) coding for the swelling- dependent chloride channel I(Cln). Genomics 38:438- 441, 1996. 3 C c

GAM7776 246 CLNS1A Schwartz, R. S.; Rybicki, A. C.; Nagel, R. L.: Molecular cloningand expression of a chloride channel- associated protein pI(Cln) inhuman young red blood cells: association with actin. Biochem. J. 327:609- 616, 1997. 3 C c

GAM7776 246 CNN2 Cheng, J.- F.; Boyartchuk, V.; Zhu, Y.: Isolation and mapping ofhuman chromosome 21 cDNA: progress in constructing a chromosome 21expression map. Genomics 23: 75- 84, 1994. 3 C b

GAM7776 246 CNN2 Masuda, H.; Tanaka, K.; Takagi, M.; Ohgami, K.; Sakamaki, T.; Shibata,N.; Takahashi, K.: Molecular cloning and characterization of humannon- smooth muscle calponin. J. Biochem. 120: 415- 424, 1996. 3 C b

GAM7776 246 CNP Bernier, L.; Colman, D. R.; D'Eustachio, P.: Chromosomal locationsof genes encoding 2- prime,3- prime cyclic nucleotide 3- prime- phosphodiesteraseand glial fibrillary acidic protein in the mouse. J. Neurosci. Res. 20:497- 504, 1988. 3 C c

GAM7776 246 CNP Bifulco, M.; Laezza, C.; Stingo, S.; Wolff, J.: 2- prime,3- prime- 3 C c

cyclicnucleotide 3- prime- phosphodiesterase: a membrane- bound, microtubule- associatedprotein and membrane anchor for tubulin. Proc. Nat. Acad. Sci. 99:1807- 1812, 2002.

GAM7776 246 CNP Douglas, A. J.; Fox, M. F.; Abbott, C. M.; Hinks, L. J.; Sharpe,G.; Povey, 3 C c
S.; Thompson, R. J.: Structure and chromosomal localizationof the human 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasegene. Ann. Hum. Genet. 56: 243- 254, 1992.

GAM7776 246 CNP Douglas, A. J.; Fox, M. F.; Hinks, L. J.; Povey, S.; Thompson,R. J.: 3 C c
Localization of the myelin specific enzyme 2- prime,3- prime- cyclicnucleotide- 3- prime- phosphohydrolase to 17q21. (Abstract) Cytogenet.Cell Genet. 58: 2004 only, 1991.

GAM7776 246 CNP Kurihara, T.; Monoh, K.; Sakimura, K.; Takahashi, Y.: Alternativesplicing of 3 C c
mouse brain 2- prime,3- prime- cyclic nucleotide 3- prime- phosphodiesterasemRNA. Biochem. Biophys. Res. Commun. 170: 1074- 1081, 1990.

GAM7776 246 CNP Monoh, K.; Kurihara, T.; Takahashi, Y.; Ichikawa, T.; Kumanishi,T.; Hayashi, 3 C c
S.; Minoshima, S.; Shimizu, N.: Structure, expressionand chromosomal localization of the gene encoding human 2- prime,3- prime- cyclic- nucleotide3- prime- phosphodiesterase. Gene 129: 297- 301, 1993.

GAM7776 246 CNP Sprinkle, T. J.; Kouri, R. E.; Fain, P. D.; Stoming, T. A.; Whitney,J. B., 3 C c
III: Chromosomal mapping of the human CNP gene using a meioticcrossover DNA panel, PCR, and allele- specific probes. Genomics 16:542- 545, 1993.

GAM7776 246 CNP Sprinkle, T. J.; Lanclos, K. D.; Lapp, D. F.: Assignment of thehuman 2- 3 C c
prime,3- prime- cyclic nucleotide 3- prime- phosphohydrolase geneto chromosome 17. Genomics 13: 877- 880, 1992.

GAM7776 246 CNP Vogel, U. S.; Thompson, R. J.: Molecular structure, localization,and 3 C c
possible functions of the myelin- associated enzyme 2- prime,3- prime- cyclicnucleotide 3- prime- phosphodiesterase. J. Neurochem. 50: 1667- 1677,1988.

GAM7776 246 CRSP6 Ito, M.; Yuan, C.- X.; Malik, S.; Gu, W.; Fondell, J. D.; Yamamura,S.; Fu, 3 C c
Z.- Y.; Zhang, X.; Qin, J.; Roeder, R. G.: Identity betweenTRAP and SMCC complexes indicates novel pathways for the functionof nuclear receptors and diverse mammalian activators. Molec. Cell 3:361- 370, 1999.

GAM7776 246 CRSP6 Jiang, Y.- W.; Veschambre, P.; Erdjument- Bromage, H.; Tempst, P.;Conaway, 3 C c
J. W.; Conaway, R. C.; Kornberg, R. D.: Mammalian mediatorof transcriptional regulation and its possible role as an end- pointof signal transduction pathways. Proc. Nat. Acad. Sci. 95: 8538- 8543,1998.

GAM7776 246 CRSP6 Ryu, S.; Zhou, S.; Ladurner, A. G.; Tjian, R.: The transcriptionalcofactor 3 C c
complex CRSP is required for activity of the enhancer- bindingprotein Sp1. Nature 397: 446- 450, 1999.

GAM7776 246 CRTAP Castagnola, P.; Gennari, M.; Morello, R.; Tonachini, L.; Marin,O.; Gaggero, 3 C b
A.; Cancedda, R.: Cartilage associated protein (CASP)is a novel developmentally regulated chick embryo protein. J. CellSci. 110: 1351- 1359, 1997.

GAM7776 246 CRTAP Morello, R.; Tonachini, L.; Monticone, M.; Viggiano, L.; Rocchi,M.; 3 C b
Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of Crtap encoding the mouse cartilage associatedprotein. Matrix Biol. 18: 319- 324, 1999.

GAM7776 246 CRTAP Tonachini, L.; Morello, R.; Monticone, M.; Skaug, J.; Scherer,S. W.; 3 C b
Cancedda, R.; Castagnola, P.: cDNA cloning, characterizationand chromosome mapping of the gene encoding human cartilage associatedprotein (CRTAP).

Cytogenet. Cell Genet. 87: 191- 194, 1999.

GAM7776 246 CSNK2A2 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation 3 C c
of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297:
1700- 1703, 2002.

GAM7776 246 CSNK2A2 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; 3 C c
Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine
392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292,
2001.

GAM7776 246 CSNK2A2 Lozeman, F. J.; Litchfield, D. W.; Piening, C.; Takio, K.; Walsh,K. A.; 3 C c
Krebs, E. G.: Isolation and characterization of human cDNAclones encoding
the alpha and the alpha- prime subunits of casein kinaseII. Biochemistry 29:
8436- 8447, 1990.

GAM7776 246 CSNK2A2 Xu, X.; Toselli, P. A.; Russell, L. D.; Seldin, D. C.: Globozoospermiain 3 C c
mice lacking the casein kinase II alpha- prime catalytic subunit.
NatureGenet. 23: 118- 121, 1999.

GAM7776 246 CSNK2A2 Yang- Feng, T. L.; Naiman, T.; Kopatz, I.; Eli, D.; Dafni, N.; Canaani,D.: 3 C c
Assignment of the human casein kinase II alpha- prime subunitgene (CSNK2A1)
to chromosome 16p13.2- p13.3. Genomics 19: 173 only,1994.

GAM7776 246 CSNK2A2 Yang- Feng, T. L.; Zheng, K.; Kopatz, I.; Naiman, T.; Canaani, D.: Mapping 3 C c
of the human casein kinase II catalytic subunit genes: twoloci carrying the
homologous sequences for the alpha subunit. NucleicAcids Res. 19: 7125-
7129, 1991.

GAM7776 246 CTF1 Bordet, T.; Lesbordes, J.- C.; Rouhani, S.; Castelnau- Ptakhine,L.; 3 C b
Schmalbruch, H.; Haase, G.; Kahn, A.: Protective effects of cardiotrophin-
1adenoviral gene transfer on neuromuscular degeneration in transgenicALS
mice. Hum. Molec. Genet. 10: 1925- 1933, 2001.

GAM7776 246 CTF1 Pennica, D.; Arce, V.; Swanson, T. A.; Vejsada, R.; Pollock, R.A.; Armanini, 3 C b
M.; Dudley, K.; Phillips, H. S..; Rosenthal, A.; Kato,A. C.; Henderson, C.
E.: Cardiotrophin- 1, a cytokine present in embryonicmuscle, supports long-
term survival of spinal motoneurons. Neuron 17:63- 74, 1996.

GAM7776 246 CTF1 Pennica, D.; King, K. L.; Shaw, K. J.; Luis, E.; Rullamas, J.;Luoh, S.- M.; 3 C b
Darbonne, W. C.; Knutzon, D. S.; Yen, R.; Chien, K. R.;Baker, J. B.; Wood,
W. I.: Expression cloning of cardiotrophin 1,a cytokine that induces cardiac
myocyte hypertrophy. Proc. Nat. Acad.Sci. 92: 1142- 1146, 1995.

GAM7776 246 CTF1 Pennica, D.; Swanson, T. A.; Shaw, K. J.; Kuang, W.- J.; Gray, C.L.; Beatty, 3 C b
B. G.; Wood, W. I.: Human cardiotrophin- 1: protein andgene structure,
biological and binding activities, and chromosomallocalization. Cytokine 8:
183- 189, 1996.

GAM7776 246 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; 3 C b
Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H,
L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245,
1997.

GAM7776 246 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; 3 C b
Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S
controls the trafficking and maturation of MHC class IImolecules in
dendritic cells. J. Cell Biol. 147: 775- 790, 1999.

GAM7776 246 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. 3 C b
J.; Chapman, H. A.: Structure and chromosomal assignmentof the human
cathepsin K gene. Genomics 41: 258- 262, 1997.

GAM7776 246 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; 3 C b

Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.; Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell selection and maturation by cathepsin S. Immunity 15:909- 919, 2001.

GAM7776 246 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: 3 C b
Molecular cloning and expression of human alveolar macrophagecathepsin S, an elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992.

GAM7776 246 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; 3 C b
Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization, gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536, 1994.

GAM7776 246 CXCL16 Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G.: A 3 C c
transmembrane CXC chemokine is a ligand for HIV- coreceptor Bonzo. NatureImmun. 1: 298- 304, 2000.

GAM7776 246 CXCL16 Shimaoka, T.; Kume, N.; Minami, M.; Hayashida, K.; Kataoka, H.;Kita, T.; 3 C c
Yonehara, S.: Molecular cloning of a novel scavenger receptorfor oxidized low density lipoprotein, SR- PSOX, on macrophages. J.Biol. Chem. 275: 40663- 40666, 2000.

GAM7776 246 CXCL16 Wilbanks, A.; Zondlo, S. C.; Murphy, K.; Mak, S.; Soler, D.; Langdon,P.; 3 C c
Andrew, D. P.; Wu, L.; Briskin, M.: Expression cloning of theSTRL33/BONZO/TYMSTR ligand reveals elements of CC, CXC, CX3C chemokines. J.Immun. 166: 5145- 5154, 2001.

GAM7776 246 CYP1A2 Buters, J. T. M.; Tang, B.- K.; Pineau, T.; Gelboin, H. V.; Kimura,S.; 3 C b
Gonzalez, F. J.: Role of CYP1A2 in caffeine pharmacokineticsand metabolism: studies using mice deficient in CYP1A2. Pharmacogenetics 6:291- 296, 1996.

GAM7776 246 CYP1A2 Butler, M. A.; Iwasaki, M.; Guengerich, F. P.; Kadlubar, F. F.: Human 3 C b
cytochrome P- 450(PA) (P- 450IA2), the phenacetin O- deethylase,is primarily responsible for the hepatic 3- demethylation of caffeineand N- oxidation of carcinogenic arylamines. Proc. Nat. Acad. Sci. 86:7696- 7700, 1989.

GAM7776 246 CYP1A2 Christiansen, L.; Bygum, A.; Jensen, A.; Thomsen, K.; Brandrup,F.; Horder, 3 C b
M.; Petersen, N. E.: Association between CYP1A2 polymorphismand susceptibility to porphyria cutanea tarda. Hum. Genet. 107:612- 614, 2000.

GAM7776 246 CYP1A2 Devonshire, H. W.; Kong, I.; Cooper, M.; Sloan, T. P.; Idle, J.R.; Smith, R. 3 C b
L.: The contribution of genetically determined oxidationstatus to inter-individual variation in phenacetin disposition. Brit.J. Clin. Pharm. 16: 157- 166, 1983.

GAM7776 246 CYP1A2 Guengerich, F. P.; Distlerath, L. M.; Reilly, P. E. B.; Wolff,T.; Shimada, 3 C b
T.; Umbenhauer, D. R.; Martin, M. V.: Human- liver cytochromesP- 450 involved in polymorphisms of drug oxidation. Xenobiotica 16:367- 378, 1986.

GAM7776 246 CYP1A2 Ikeya, K.; Jaiswal, A. K.; Owens, R. A.; Jones, J. E.; Nebert,D. W.; Kimura, 3 C b
S.: Human CYP1A2: sequence, gene structure, comparisonwith the mouse and rat orthologous gene, and differences in liver1A2 mRNA expression. Molec. Endocr. 3: 1399- 1408, 1989.

GAM7776 246 CYP1A2 Jaiswal, A. K.; Nebert, D. W.; McBride, O. W.; Gonzalez, F. J.: Human 3 C b
P(3)450: cDNA and complete protein sequence, repetitive Alusequences in the 3- prime nontranslated region, and localization ofgene to chromosome 15. J. Exp. Path. 3: 1- 17, 1987.

GAM7776 246 CYP1A2 Liang, H.- C. L.; Li, H.; McKinnon, R. A.; Duffy, J. J.; Potter,S. S.; Puga, 3 C b
A.; Nebert, D. W.: Cyp1a2(- /-) null mutant mice developnormally but show deficient drug metabolism. Proc. Nat. Acad. Sci. 93:1671- 1676, 1996.

GAM7776 246 CYP1A2 Nebert, D. W.: Personal Communication. Bethesda, Md. 2/3/1988. 3 C b

GAM7776 246 CYP1A2 Paolini, M.; Cantelli- Forti, G.; Perocco, P.; Pedulli, G. F.;Abdel- Rahman, S. Z.; Legator, M. S.: Co- carcinogenic effect of beta- carotene.(Letter) Nature 398: 760- 761, 1999. 3 C b

GAM7776 246 CYP1A2 Sesardic, D.; Boobis, A. R.; Edwards, R. J.; Davies, D. S.: Aform of cytochrome P450 in man, orthologous to form d in the rat,catalyses the O-deethylation of phenacetin and is inducible by cigarettesmoking. Brit. J. Clin. Pharm. 26: 363- 372, 1988. 3 C b

GAM7776 246 CYP1A2 Tantcheva- Poor, I.; Zaigler, M.; Rietbrock, S.; Fuhr, U.: Estimationof cytochrome P- 450 CYP1A2 activity in 863 healthy Caucasians usinga saliva-based caffeine test. Pharmacogenetics 9: 131- 144, 1999. 3 C b

GAM7776 246 CYP1A2 Wooding, S. P.; Watkins, W. S.; Bamshad, M. J.; Dunn, D. M.; Weiss,R. B.; Jorde, L. B.: DNA sequence variation in a 3.7- kb noncodingsequence 5- prime of the CYP1A2 gene: implications for human populationhistory and natural selection. Am. J. Hum. Genet. 71: 528- 542, 2002. 3 C b

GAM7776 246 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988. 3 C b

GAM7776 246 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988. 3 C b

GAM7776 246 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. Lancet 355: 979- 983, 2000. 3 C b

GAM7776 246 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene: molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230, 1998. 3 C b

GAM7776 246 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii-Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in humanpolymorphonuclear leukocytes: cDNA cloning and expression of leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993. 3 C b

GAM7776 246 CYP8B1 Eggertsen, G.; Olin, M.; Andersson, U.; Ishida, H.; Kubota, S.;Hellman, U.; Okuda, K.- I.; Bjorkhem, I.: Molecular cloning and expressionof rabbit sterol 12- alpha- hydroxylase. J. Biol. Chem. 271: 32269- 32275,1996. 3 C b

GAM7776 246 CYP8B1 Gafvels, M.; Olin, M.; Chowdhary, B. P.; Raudsepp, T.; Andersson,U.; Persson, B.; Jansson, M.; Bjorkhem, I.; Eggertsen, G.: Structureand chromosomal assignment of the sterol 12- alpha- hydroxylase gene(CYP8B1) in human and mouse: eukaryotic cytochrome P- 450 gene devoidof introns. Genomics 56: 184- 196, 1999. 3 C b

GAM7776 246 CYP8B1 Zhang, M.; Chiang, J. Y. L.: Transcriptional regulation of thehuman sterol 12- alpha- hydroxylase gene (CYP8B1): roles of hepatocytenuclear factor 4-alpha in mediating bile acid repression. J. Biol.Chem. 276: 41690- 41699, 2001. 3 C b

GAM7776 246 DFFB Judson, H.; van Roy, N.; Strain, L.; Vandesompele, J.; Van Gele,M.; Speleman, F.; Bonthron, D. T.: Structure and mutation analysisof the gene encoding DNA fragmentation factor 40 (caspase- activatednuclease), a candidate neuroblastoma tumour suppressor gene. Hum.Genet. 106: 406- 413, 2000. 3 C b

GAM7776 246 DFFB Liu, X.; Li, P.; Widlak, P.; Zou, H.; Luo, X.; Garrard, W. T.;Wang, X.: The 40- kDa subunit of DNA fragmentation factor inducesDNA fragmentation and 3 C b

chromatin condensation during apoptosis. Proc.Nat. Acad. Sci. 95: 8461-
8466, 1998.

GAM7776 246 DFFB Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that 3 C b
functions downstream of caspase- 3 to trigger DNA fragmentationduring
apoptosis. Cell 89: 175- 184, 1997.

GAM7776 246 DFFB Mukae, N.; Enari, M.; Sakahira, H.; Fukuda, Y.; Inazawa, J.; Toh,H.; Nagata, 3 C b
S.: Molecular cloning and characterization of human caspase- activatedDNase.
Proc. Nat. Acad. Sci. 95: 9123- 9128, 1998.

GAM7776 246 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Modi, W. S.;Nienhuis, A. 3 C b
W.: Chromosomal localization and racial distributionof the polymorphic human
dihydrofolate reductase pseudogene (DHFRPI). Am.J. Hum. Genet. 42: 345- 352,
1988.

GAM7776 246 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: A novel 3 C b
form of human polymorphism involving the hDHFR- psi- 1pseudogene identifies
three RFLPs. Nucleic Acids Res. 15: 5501 only,1987.

GAM7776 246 DHFR Anagnou, N. P.; Antonarakis, S. E.; O'Brien, S. J.; Nienhuis, A.W.: 3 C b
Chromosomal localization and racial distribution of the polymorphichDHFR-
psi- 1 pseudogene. (Abstract) Clin. Res. 33: 328A only, 1985.

GAM7776 246 DHFR Anagnou, N. P.; O'Brien, S. J.; Shimada, T.; Nash, W. G.; Chen,M.- J.; 3 C b
Nienhuis, A. W.: Chromosomal organization of the human
dihydrofolatereductase genes: dispersion, selective amplification and a
novel formof polymorphism. Proc. Nat. Acad. Sci. 81: 5170- 5174, 1984.

GAM7776 246 DHFR Blakley, R. L.; Sorrentino, B. P.: In vitro mutations in 3 C b
dihydrofolatereductase that confer resistance to methotrexate: potential for
clinicalapplication. Hum. Mutat. 11: 259- 263, 1998.

GAM7776 246 DHFR Chen, M.- J.; Shimada, T.; Moulton, A. D.; Harrison, M.; Nienhuis,A. W.: 3 C b
Intronless human dihydrofolate reductase genes are derivedfrom processed RNA
molecules. Proc. Nat. Acad. Sci. 79: 7435- 7439,1982.

GAM7776 246 DHFR Craik, C. S.; Rutter, W. J.; Fletterick, R.: Splice junctions:association 3 C b
with variation in protein structure. Science 220: 1125- 1129,1983.

GAM7776 246 DHFR Erbe, R. W.: Inborn errors of folate metabolism. New Eng. J.Med. 293: 753- 3 C b
757 and 807- 812, 1975.

GAM7776 246 DHFR Funanage, V. L.; Myoda, T. T.; Moses, P. A.; Cowell, H. R.: Assignmentof the 3 C b
human dihydrofolate reductase gene to the q11- q22 region ofchromosome 5.
Molec. Cell. Biol. 4: 2010- 2016, 1984.

GAM7776 246 DHFR Hoffbrand, A. V.; Tripp, E.; Jackson, B. F. A.; Luck, W. E.; Frater- 3 C b
Schroder,M.: Hereditary abnormal transcobalamin II previously diagnosed
ascongenital dihydrofolate reductase deficiency. (Letter) New Eng.J. Med.
310: 789- 790, 1984.

GAM7776 246 DHFR Killary, A. M.; Leach, R. J.; Moran, R. G.; Fournier, R. E. K.: Assignment 3 C b
of genes encoding dihydrofolate reductase and hexosaminidaseB to Mus
musculus chromosome 13. Somat. Cell Molec. Genet. 12: 641- 648,1986.

GAM7776 246 DHFR Maurer, B. J.; Barker, P. E.; Masters, J. N.; Ruddle, F. H.; Attardi,G.: 3 C b
Human dihydrofolate reductase gene is located in chromosome 5and is unlinked
to the related pseudogenes. Proc. Nat. Acad. Sci. 81:1484- 1488, 1984.

GAM7776 246 DHFR Maurer, B. J.; Carlock, L.; Wasmuth, J.; Attardi, G.: Assignmentof human 3 C b
dihydrofolate reductase gene to band q23 of chromosome 5and of related
pseudogene psiHD1 to chromosome 3. Somat. Cell Molec.Genet. 11: 79- 85,
1985.

GAM7776 246 DHFR Maurer, B.; Barker, P. E.; Masters, J. N.; D'Eustachio, P.; Ruddle,F. H.; 3 C b

Attardi, G.: Chromosomal location of the normal human DHFRgene and of its amplified copies in methotrexate resistant cell variants.(Abstract) Cytogenet. Cell Genet. 37: 534 only, 1984.

GAM7776 246 DHFR Myoda, T. T.; Funanage, V. L.: Personal Communication. Wilmington,Del. 3 C b 10/7/1983.

GAM7776 246 DHFR Singer, M. J.; Mesner, L. D.; Friedman, C. L.; Trask, B. J.; Hamlin,J. L.: 3 C b Amplification of the human dihydrofolate reductase gene viadouble minutes is initiated by chromosome breaks. Proc. Nat. Acad.Sci. 97: 7921- 7926, 2000.

GAM7776 246 DHFR Tauro, G. P.; Danks, D. M.; Rowe, P. B.; Van der Weyden, M. B.;Schwarz, M. 3 C b A.; Collins, V. L.; Neal, B. W.: Dihydrofolate reductasedeficiency causing megaloblastic anemia in two families. New Eng.J. Med. 294: 466- 470, 1976.

GAM7776 246 DHFR Walters, T. R.: Congenital megaloblastic anemia responsive toN(5)- 3 C b formyltetrahydrofolic acid administration. J. Pediat. 70: 686- 687,1967.

GAM7776 246 DIAPH2 Banfi, S.; Borsani, G.; Bulfone, A.; Ballabio, A.: Drosophila- 3 C c relatedexpressed sequences. Hum. Molec. Genet. 6: 1745- 1753, 1997.

GAM7776 246 DIAPH2 Bione, S.; Sala, C.; Manzini, C.; Arrigo, G.; Zuffardi, O.; Banfi,S.; 3 C c Borsani, G.; Jonveaux, P.; Philippe, C.; Zuccotti, M.; Ballabio,A.; Toniolo, D.: A human homologue of the Drosophila melanogasterdiaphanous gene is disrupted in a patient with premature ovarian failure:evidence for conserved function in oogenesis and implications forhuman sterility. Am. J. Hum. Genet. 62: 533- 541, 1998.

GAM7776 246 DIAPH2 Castrillon, D. H.; Wasserman, S. A.: Diaphanous is required forcytokinesis 3 C c in Drosophila and shares domains of similarity with theproducts of the limb deformity gene. Development 120: 3367- 3377,1994.

GAM7776 246 DIAPH2 Lynch, E. D.; Lee, M. K.; Morrow, J. E.; Welcsh, P. L.; Leon, P.E.; King, 3 C c M.- C.: Nonsyndromic deafness DFNA1 associated with mutationof the human homolog of the Drosophila gene diaphanous. Science 278:1315- 1318, 1997.

GAM7776 246 DIAPH2 Philippe, C.; Cremers, F. P. M.; Chery, M.; Bach, I.; Abbadi, N.;Ropers, H. 3 C c H.; Gilgenkrantz, S.: Physical mapping of DNA markersin the q13- q22 region of the human X chromosome. Genomics 17: 147- 152,1993.

GAM7776 246 DIAPH2 Sala, C.; Arrigo, G.; Torri, G.; Martinazzi, F.; Riva, P.; Larizza,L.; 3 C c Philippe, C.; Jonveaux, P.; Sloan, F.; Labella, T.; Toniolo, D.: Eleven X chromosome breakpoints associated with premature ovarianfailure (POF) map to a 15- Mb YAC contig spanning Xq21. Genomics 40:123- 131, 1997.

GAM7776 246 DISC1 Blackwood, D. H. R.; Fordyce, A.; Walker, M. T.; St. Clair, D.M.; Porteous, 3 C c D. J.; Muir, W. J.: Schizophrenia and affective disorders- - cosegretationwith a translocation at chromosome 1q42 that directly disrupts brain- expressedgenes: clinical and P300 findings in a family. Am. J. Hum. Genet. 69:428- 433, 2001.

GAM7776 246 DISC1 Blackwood, D.: P300, a state and a trait marker in schizophrenia. Lancet 3 C c 355:771- 772, 2000.

GAM7776 246 DISC1 Ekelund, J.; Hovatta, I.; Parker, A.; Paunio, T.; Varilo, T.; Martin,R.; 3 C c Suhonen, J.; Ellonen, P.; Chan, G.; Sinsheimer, J. S.; Sobel,E.; Juvonen, H.; Arajarvi, R.; Partonen, T.; Suvisaari, J.; Lonnqvist,J.; Meyer, J.; Peltonen, L.: Chromosome 1 loci in Finnish schizophreniafamilies. Hum. Molec. Genet. 10: 1611- 1617, 2001.

GAM7776 246 DISC1 Jacobs, P. A.; Brunton, M.; Frackiewicz, A.; Newton, M.; Cook,P. J. L.; 3 C c Robson, E. B.: Studies on a family with three cytogeneticmarkers. Ann. Hum. Genet. 33: 325- 336, 1970.

GAM7776 246 DISC1 Millar, J. K.; Wilson- Annan, J. C.; Anderson, S.; Christie, S.;Taylor, M. 3 C c

S.; Semple, C. A. M.; Devon, R. S.; St. Clair, D. M.; Muir,W. J.; Blackwood, D. H. R.; Porteous, D. J.: Disruption of two novelgenes by a translocation co- segregating with schizophrenia. Hum.Molec. Genet. 9: 1415- 1423, 2000.

GAM7776 246 DISC1 St. Clair, D.; Blackwood, D.; Muir, W.; Carothers, A.; Walker,M.; Spowart, 3 C c
G.; Gosden, C.; Evans, H. J.: Association within a familyof a balanced autosomal translocation with major mental illness. Lancet 336:13- 16, 1990.

GAM7776 246 DNAH11 Arnold, G. L.; Bixler, D.; Girod, D.: Probable autosomal 3 C c
recessiveinheritance of polysplenia, situs inversus and cardiac defects inan Amish family. Am. J. Med. Genet. 16: 35- 42, 1983.

GAM7776 246 DNAH11 Brueckner, M.; D'Eustachio, P.; Horwich, A. L.: Linkage mappingof a mouse 3 C c
gene, iv, that controls left- right asymmetry of the heartand viscera. Proc. Nat. Acad. Sci. 86: 5035- 5038, 1989.

GAM7776 246 DNAH11 Chapelin, C.; Duriez, N.; Magnino, F.; Goossens, M.; Escudier,E.; Amselem, 3 C c
S.: Isolation of several human axonemal dynein heavychain genes: genomic structure of the catalytic site, phylogeneticanalysis and chromosomal assignment. FEBS Lett. 412: 325- 330, 1997.

GAM7776 246 DNAH11 Hanzlik, A. J.; Binder, M.; Layton, W. M.; Rowe, L.; Layton, M.;Taylor, B. 3 C c
A.; Osemlak, M. M.; Richards, J. E.; Kurnit, D. M.; Stewart,G. D.: The murine situs inversus viscerum (iv) gene responsiblefor visceral asymmetry is linked tightly to the Igh- C cluster on chromosome12. Genomics 7: 389- 393, 1990.

GAM7776 246 DNAH11 McGrath, J.; Horwich, A. L.; Brueckner, M.: Duplication/deficiencymapping of 3 C c
situs inversus viscerum (iv), a gene that determines left- rightasymmetry in the mouse. Genomics 14: 643- 648, 1992.

GAM7776 246 DNAH11 Nonaka, S.; Shiratori, H.; Saijoh, Y.; Hamada, H.: Determinationof left- 3 C c
right patterning of the mouse embryo by artificial nodal flow. Nature 418:96- 99, 2002.

GAM7776 246 DNAH11 Okada, Y.; et al.; et al: Abnormal nodal flow precedes situs inversusin iv 3 C c
and inv mice. Molec. Cell 4: 459- 468, 1999.

GAM7776 246 DNAH11 Supp, D. M.; Witte, D. P.; Potter, S. S.; Brueckner, M.: Mutationof an 3 C c
axonemal dynein affects left- right asymmetry in inversus viscerummice. Nature 389: 963- 966, 1997.

GAM7776 246 DNAH11 Supp, D.; et al.; et al: Targeted deletion of the ATP bindingdomain of left- 3 C c
right dynein confirms its role in specifying developmentof left- right asymmetries. Development 126: 5495- 5504, 1999.

GAM7776 246 DSC3 Amagai, M.; Wang, Y.; Minoshima, S.; Kawamura, K.; Green, K. J.;Nishikawa, 3 C c
T.; Shimizu, N.: Assignment of the human genes for desmocollin3 (DSC3) and desmocollin 4 (DSC4) to chromosome 18q12. Genomics 25:330- 332, 1995.

GAM7776 246 DSC3 Kawamura, K.; Watanabe, K.; Suzuki, T.; Yamakawa, T.; Kamiyama,T.; Nakagawa, 3 C c
H.; Tsurufuji, S.: cDNA cloning and expression of anovel human desmocollin. J. Biol. Chem. 269: 26295- 26302, 1994.

GAM7776 246 DSC3 King, I. A.; Sullivan, K. H.; Bennett, R., Jr.; Buxton, R. S.:The 3 C c
desmocollins of human foreskin epidermis: identification and chromosomalassignment of a third gene and expression patterns of the three isoforms. J.Invest. Derm. 105: 314- 321, 1995.

GAM7776 246 EBAF Burdine, R. D.; Schier, A. F.: Conserved and divergent mechanismsin left- 3 C c
right axis formation. Genes Dev. 14: 763- 776, 2000.

GAM7776 246 EBAF Kosaki, K.; Bassi, M. T.; Kosaki, R.; Lewin, M.; Belmont, J.; Schauer,G.; 3 C c
Casey, B.: Characterization and mutation analysis of human LEFTYA and LEFTY

B, homologues of murine genes implicated in left- rightaxis development. Am. J. Hum. Genet. 64: 712- 721, 1999.

GAM7776 246 EBAF Kothapalli, R.; Buyuksal, I.; Wu, S.- Q.; Chegini, N.; Tabibzadeh,S.: 3 C c
Detection of ebaf, a novel human gene of the transforming growthfactor beta superfamily: association of gene expression with endometrialbleeding. J. Clin. Invest. 99: 2342- 2350, 1997.

GAM7776 246 EBAF Meno, C.; Itoh, Y.; Saijoh, Y.; Matsuda, Y.; Tashiro, K.; Kuhara,S.; Hamada, 3 C c
H.: Two closely- related left- right asymmetrically expressedgenes, lefty- 1 and lefty- 2: their distinct expression domains, chromosomallinkage and direct neuralizing activity in Xenopus embryos. GenesCells 2: 513- 524, 1997.

GAM7776 246 EBAF Meno, C.; Saijoh, Y.; Fujii, H.; Ikeda, M.; Yokoyama, T.; Yokoyama,M.; 3 C c
Toyoda, Y.; Hamada, H.: Left- right asymmetric expression of theTGF- beta-family member lefty in mouse embryos. Nature 381: 151- 155,1996.

GAM7776 246 EBAF Meno, C.; Shimono, A.; Saijoh, Y.; Yashiro, K.; Mochida, K.; Ohishi,S.; 3 C c
Noji, S.; Kondoh, H.; Hamada, H.: Lefty- 1 is required for left-rightdetermination as a regulator of lefty- 2 and nodal. Cell 94: 287-297,1998.

GAM7776 246 EBAF Tabibzadeh, S.; Mason, J. M.; Shea, W.; Cai, Y.; Murray, M. J.;Lessey, B.: 3 C c
Dysregulated expression of ebaf, a novel molecular defectin the endometria of patients with infertility. J. Clin. Endocr.Metab. 85: 2526- 2536, 2000.

GAM7776 246 EEF2K Arora, S.; Yang, J.- M.; Craft, J.; Hait, W.: Detection of anti- 3 C c
elongationfactor 2 kinase (calmodulin- dependent protein kinase III) antibodiesin patients with systemic lupus erythematosus. Biochem. Biophys.Res. Commun. 293: 1073- 1076, 2002.

GAM7776 246 EEF2K Ryazanov, A. G.; Ward, M. D.; Mendola, C. E.; Pavur, K. S.; Dorovkov,M. V.; 3 C c
Wiedmann, M.; Erdjument- Bromage, H.; Tempst, P.; Parmer, T.G.; Prostko, C. R.; Germino, F. J.; Hait, W. N.: Identification ofa new class of protein kinases represented by eukaryotic elongationfactor- 2 kinase. Proc. Nat. Acad. Sci. 94: 4884- 4889, 1997.

GAM7776 246 EHD1 Di Fiore, P. P.; Pelicci, P. G.; Sorkin, A.: EH: a novel protein- 3 C c
proteininteraction domain potentially involved in intracellular sorting. TrendsBiochem. Sci. 22: 411- 413, 1997.

GAM7776 246 EHD1 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 3 C c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.; Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.; Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the 2.8- Mb region containing the multiple endocrineneoplasia type 1 locus. Genome Res. 7: 725- 735, 1997.

GAM7776 246 EHD1 Haider, N. B.; Searby, C.; Galperin, E.; Mintz, L.; Horowitz, M.;Stone, E. 3 C c
M.; Sheffield, V. C.: Evaluation and molecular characterizationof EHD1, a candidate gene for Bardet- Biedl syndrome 1 (BBS1). Gene 240:227- 232, 1999.

GAM7776 246 EHD1 Mintz, L.; Galperin, E.; Pasmanik- Chor, M.; Tulzinsky, S.; Bromberg,Y.; 3 C c
Kozak, C. A.; Joyner, A.; Fein, A.; Horowitz, M.: EHD1- - an EH- domain-containingprotein with a specific expression pattern. Genomics 59: 66-76,1999.

GAM7776 246 EHD1 Rotem- Yehudar, R.; Galperin, E.; Horowitz, M.: Association ofinsulin- like 3 C c
growth factor 1 receptor with EHD1 and SNAP29. J. Biol.Chem. 276: 33054-33060, 2001.

GAM7776 246 EIF2S3 Ehrmann, I. E.; Ellis, P. S.; Mazeyrat, S.; Duthie, S.; Brockdorff,N.; 3 C c

Mattei, M. G.; Gavin, M. A.; Affara, N. A.; Brown, G. M.; Simpson,E.; Mitchell, M. J.; Scott, D. M.: Characterization of genes encodingtranslation initiation factor eIF- 2- gamma in mouse and human: sexchromosome localization, escape from X- inactivation and evolution. Hum.Molec. Genet. 7: 1725- 1737, 1998.

GAM7776 246 EIF2S3 Gasper, N. J.; Kinzy, T. G.; Scherer, B. J.; Humbelin, M.; Hershey,J. W. B.; 3 C c
Merrick, W. C.: Translation initiation factor eIF- 2: cloningand expression of the human cDNA encoding the gamma- subunit. J. Biol.Chem. 269: 3415- 3422, 1994.

GAM7776 246 EPHA8 Chan, J.; Watt, V. M.: Eek and erk, new members of the eph subclassof 3 C c
receptor protein- tyrosine kinases. Oncogene 6: 1057- 1061, 1991.

GAM7776 246 EPHA8 Park, S.; Frisen, J.; Barbacid, M.: Aberrant axonal projectionsin mice 3 C c
lacking EphA8 (Eek) tyrosine protein kinase receptors. EMBOJ. 16: 3106- 3114, 1997.

GAM7776 246 EZH1 Abel, K. J.; Brody, L. C.; Valdes, J. M.; Erdos, M. R.; McKinley,D. R.; 3 C c
Castilla, L. H.; Merajver, S. D.; Couch, F. J.; Friedman, L.S.; Ostermeyer, E. A.; Lynch, E. D.; King, M.- C.; Welcsh, P. L.; Osborne- Lawrence,S.; Spillman, M.; Bowcock, A. M.; Collins, F. S.; Weber, B. L.: Characterizationof EZH1, a human homolog of Drosophila enhancer of zeste near BRCA1. Genomics 37:161- 171, 1996.

GAM7776 246 EZH1 Cardoso, C.; Mignon, C.; Hetet, G.; Grandchamps, B.; Fontes, M.;Colleaux, 3 C c
L.: The human EZH2 gene: genomic organisation and revisedmapping in 7q35 within the critical region for malignant myeloid disorders. Europ.J. Hum. Genet. 8: 174- 180, 2000.

GAM7776 246 EZH1 Cardoso, C.; Timsit, S.; Villard, L.; Khrestchatisky, M.; Fontes,M.; 3 C c
Colleaux, L.: Specific interaction between the XNP/ATR- X geneproduct and the SET domain of the human EZH2 protein. Hum. Molec.Genet. 7: 679- 684, 1998.

GAM7776 246 EZH1 Chen, H.; Rossier, C.; Antonarakis, S. E.: Cloning of a humanhomolog of the 3 C c
Drosophila enhancer of zeste gene (EZH2) that mapsto chromosome 21q22.2. Genomics 38: 30- 37, 1996.

GAM7776 246 EZH1 Dohner, K.; Brown, J.; Hehmann, U.; Hetzel, C.; Stewart, J.; Lowther,G.; 3 C c
Scholl, C.; Frohling, S.; Cuneo, A.; Tsui, L. C.; Lichter, P.;Scherer, S. W.; Dohner, H.: Molecular cytogenetic characterizationof a critical region in bands 7q35- q36 commonly deleted in malignantmyeloid disorders. Blood 92: 4031- 4035, 1998.

GAM7776 246 EZH1 Laible, G.; Haynes, A. R.; Lebersorger, A.; O'Carroll, D.; Mattei,M.- G.; 3 C c
Denny, P.; Brown, S. D. M.; Jenuwein, T.: The murine polycomb- groupgenes Ezh1 and Ezh2 map close to Hox gene clusters on mouse chromosomes11 and 6. Mammalian Genome 10: 311- 314, 1999.

GAM7776 246 EZH1 Varambally, S.; Dhanasekaran, S. M.; Zhou, M.; Barrette, T. R.;Kumar- Sinha, 3 C c
C.; Sanda, M. G.; Ghosh, D.; Pienta, K. J.; Sewalt, R.G. A. B.; Otte, A. P.; Rubin, M. A.; Chinnaiyan, A. M.: The polycombgroup protein EZH2 is involved in progression of prostate cancer. Nature 419:624- 629, 2002.

GAM7776 246 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; 3 C b
Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998.

GAM7776 246 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, 3 C b
M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000.

GAM7776 246 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: 3 C b
Role of thrombin signalling in platelets in haemostasis andthrombosis.
Nature 413: 74- 78, 2001.

GAM7776 246 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; 3 C b
Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand
characterization of human protease- activated receptor 4. Proc.Nat. Acad.
Sci. 95: 6642- 6646, 1998.

GAM7776 246 F3 Carson, S. D.; Henry, W. M.; Haley, L.; Byers, M.; Shows, T.:The gene for 3 C c
tissue factor (coagulation factor III) is localized onhuman chromosome
1pter- 1p21. (Abstract) Cytogenet. Cell Genet. 40:600 only, 1985.

GAM7776 246 F3 Carson, S. D.; Henry, W. M.; Shows, T. B.: Tissue factor genelocalized to 3 C c
human chromosome 1 (1pter- 1p21). Science 229: 991- 993,1985.

GAM7776 246 F3 Kao, F.- T.; Hartz, J.; Horton, R.; Nemerson, Y.; Carson, S. D.: Regional 3 C c
assignment of human tissue factor gene (F3) to chromosome1p21- p22. Somat.
Cell Molec. Genet. 14: 407- 410, 1988.

GAM7776 246 F3 Mackman, N.; Fowler, B. J.; Edgington, T. S.; Morrissey, J. H.: Functional 3 C c
analysis of the human tissue factor promoter and inductionby serum. Proc.
Nat. Acad. Sci. 87: 2254- 2258, 1990.

GAM7776 246 F3 Mackman, N.; Morrissey, J. H.; Fowler, B.; Edgington, T. S.: 3 C c
Completesequence of the human tissue factor gene, a highly regulated
cellularreceptor that initiates the coagulation protease cascade.
Biochemistry 28:1755- 1762, 1989.

GAM7776 246 F3 Scarpati, E. M.; Sadler, J. E.; O'Connell, P.; Nakamura, Y.; Leppert,M.; 3 C c
Ballard, L.; Lathrop, G. M.; Lalouel, J.- M.; White, R.: Identificationand
mapping of RFLPs for human tissue factor (HTF) to chromosome 1p.
NucleicAcids Res. 15: 9098 only, 1987.

GAM7776 246 F3 Scarpati, E. M.; Wen, D.; Broze, G. J., Jr.; Miletich, J. P.; 3 C c
Flandermeyer,R. R.; Siegel, N. R.; Sadler, J. E.: Human tissue factor: cDNA
sequenceand chromosome localization of the gene. Biochemistry 26: 5234-
5238,1987.

GAM7776 246 F3 Spicer, E. K.; Horton, R.; Bloem, L.; Bach, R.; Williams, K. R.;Guha, A.; 3 C c
Kraus, J.; Lin, T.- C.; Nemerson, Y.; Konigsberg, W. H.:Isolation of cDNA
clones coding for human tissue factor: primary structureof the protein and
cDNA. Proc. Nat. Acad. Sci. 84: 5148- 5152, 1987.

GAM7776 246 F3 Toomey, J. R.; Kratzer, K. E.; Lasky, N. M.; Broze, G. J., Jr.: Effect of 3 C c
tissue factor deficiency on mouse and tumor development. Proc.Nat. Acad.
Sci. 94: 6922- 6926, 1997.

GAM7776 246 FABP2 Baier, L. J.; Sacchettini, J. C.; Knowler, W. C.; Eads, J.; Paolisso,G.; 3 C c
Tataranni, P. A.; Mochizuki, H.; Bennett, P. H.; Bogardus, C.;Prochazka, M.:
An amino acid substitution in the human intestinalfatty acid binding protein
is associated with increased fatty acidbinding, increased fat oxidation, and
insulin resistance. J. Clin.Invest. 95: 1281- 1287, 1995.

GAM7776 246 FABP2 Carlsson, M.; Orho- Melander, M.; Hedenbro, J.; Almgren, P.; Groop,L. C.: 3 C c
The T54 allele of the intestinal fatty acid- binding protein2 is associated
with a parental history of stroke. J. Clin. Endocr.Metab. 85: 2801- 2804,
2000.

GAM7776 246 FABP2 Georgopoulos, A.; Aras, O.; Tsai, M. Y.: Codon- 54 polymorphismof the fatty 3 C c
acid- binding protein 2 gene is associated with elevationof fasting and
postprandial triglyceride in type 2 diabetes. J. Clin.Endocr. Metab. 85:
3155- 3160, 2000.

GAM7776 246 FABP2 Hegele, R. A.; Harris, S. B.; Hanley, A. J. G.; Sadikian, S.; Connelly,P. W.; Zinman, B.: Genetic variation of intestinal fatty acid- bindingprotein associated with variation in body mass in aboriginal Canadians. J.Clin. Endocr. Metab. 81: 4334- 4337, 1996. 3 C c

GAM7776 246 FABP2 Polymeropoulos, M. H.; Rath, D. S.; Xiao, H.; Merril, C. R.: Trinucleotiderepeat polymorphism at the human intestinal fatty acid binding proteingene (FABP2). Nucleic Acids Res. 18: 7198 only, 1991. 3 C c

GAM7776 246 FABP2 Prochazka, M.; Lillioja, S.; Tait, J. F.; Knowler, W. C.; Mott,D. M.; Spraul, M.; Bennett, P. H.; Bogardus, C.: Linkage of chromosomalmarkers on 4q with a putative gene determining maximal insulin actionin Pima Indians. Diabetes 42: 514- 519, 1993. 3 C c

GAM7776 246 FABP2 Sipilainen, R.; Uusitupa, M.; Heikkinen, S.; Rissanen, A.; Laakso,M.: Variants in the human intestinal fatty acid binding protein 2gene in obese subjects. J. Clin. Endocr. Metab. 82: 2629- 2632, 1997. 3 C c

GAM7776 246 FABP2 Sparkes, R. S.; Mohandas, T.; Heinzmann, C.; Gordon, J. I.; Klisak,I.; Zollman, S.; Sweetser, D. A.; Ragunathan, L.; Winokur, S.; Lusis,A. J.: Human fatty acid binding protein assignments intestinal to4q28- 4q31 and liver to 2p11. (Abstract) Cytogenet. Cell Genet. 46:697 only, 1987. 3 C c

GAM7776 246 FABP2 Sweetser, D. A.; Birkenmeier, E. H.; Klisak, I. J.; Zollman, S.;Sparkes, R. S.; Mohandas, T.; Lusis, A. J.; Gordon, J. I.: The humanand rodent intestinal fatty acid binding protein genes: a comparativeanalysis of their structure, expression, and linkage relationships. J.Biol. Chem. 262: 16060- 16071, 1987. 3 C c

GAM7776 246 FABP2 Weber, J. L.; Kwitek, A. E.; May, P. E.; Polymeropoulos, M.:Dinucleotide repeat polymorphism at the D12S43 locus. Nucleic AcidsRes. 18: 4637 only, 1990. 3 C c

GAM7776 246 FABP2 Weber, J. L.; May, P. E.: Abundant class of human DNA polymorphismswhich can be typed using the polymerase chain reaction. Am. J. Hum.Genet. 44: 388- 396, 1989. 3 C c

GAM7776 246 FANCE Buchwald, M.: Complementation groups: one or more per gene? NatureGenet. 11: 228- 230, 1995. 3 C c

GAM7776 246 FANCE de Winter, J. P.; Leveille, F.; van Berkel, C. G. M.; Rooimans,M. A.; van der Weel, L.; Steltenpool, J.; Demuth, I.; Morgan, N. V.;Alon, N.; Bosnoyan-Collins, L.; Lightfoot, J.; Leegwater, P. A.; Waisfisz,Q.; Komatsu, K.; Arwert, F.; Pronk, J. C.; Mathew, C. G.; Digweed,M.; Buchwald, M.; Joenje, H.: Isolation of a cDNA representing theFanconi anemia complementation group E gene. Am. J. Hum. Genet. 67:1306- 1308, 2000. Note: Erratum: Am. J. Hum. Genet. 67: 1365 only,2000. 3 C c

GAM7776 246 FANCE Joenje, H.: Fanconi anaemia complementation groups in Germanyand The Netherlands. Hum. Genet. 97: 280- 282, 1996. 3 C c

GAM7776 246 FANCE Joenje, H.; Lo Ten Foe, J. R.; Oostra, A. B.; van Berkel, C. G.M.; Rooimans, M. A.; Schroeder- Kurth, T.; Wegner, R.- D.; Gille, J.J. P.; Buchwald, M.; Arwert, F.: Classification of Fanconi anemiapatients by complementation analysis: evidence for a fifth geneticsubtype. Blood 86: 2156- 2160, 1995. 3 C c

GAM7776 246 FANCE Joenje, H.; Oostra, A. B.; Wijker, M.; di Summa, F. M.; van Berkel,C. G. M.; Rooimans, M. A.; Ebell, W.; van Weel, M.; Pronk, J. C.;Buchwald, M.; Arwert, F.: Evidence for at least eight Fanconi anemiagenes. Am. J. Hum. Genet. 61: 940- 944, 1997. 3 C c

GAM7776 246 FANCE Pace, P.; Johnson, M.; Tan, W. M.; Mosedale, G.; Sng, C.; Hoatlin,M.; de Winter, J.; Joenje, H.; Gergely, F.; Patel, K. J.: FANCE:the link between Fanconi anaemia complex assembly and activity. EMBOJ. 21: 3414- 3423, 2002. 3 C c

GAM7776 246 FANCE Waisfisz, Q.; Saar, K.; Morgan, N. V.; Altay, C.; Leegwater, P.A.; de Winter, J. P.; Komatsu, K.; Evans, G. R.; Wegner, R.- D.; Reis,A.; Joenje, H.; Arwert, F.; Mathew, C. G.; Pronk, J. C.; Digweed,M.: The Fanconi anemia group E gene, FANCE, maps to chromosome 6p. Am.J. Hum. Genet. 64: 1400- 1405, 1999. 3 C c

GAM7776 246 FANCE Wegner, R.- D.; Henrichs, I.; Joenje, H.; Schroeder- Kurth, T.:Fanconi anemia complementation group E: clinical and cytogenetic dataof the first patient. Clin. Genet. 50: 479- 482, 1996. 3 C c

GAM7776 246 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995. 3 C c

GAM7776 246 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 3 C c

GAM7776 246 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665- 1672, 1990. 3 C c

GAM7776 246 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681- 1685, 1993. 3 C c

GAM7776 246 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 3 C c

GAM7776 246 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 3 C c

GAM7776 246 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 3 C c

GAM7776 246 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001. 3 C c

GAM7776 246 FCGR2A Grundy, H. O.; Peltz, G.; Barsh, G.; Moore, K.; Golbus, M. S.;Lebo, R. V.: Immunoglobulin G Fc receptor II and Fc receptor IIIgenes map to chromosome 1 by spot- blot chromosome analysis. (Abstract) Am.J. Hum. Genet. 43: A145, 1988. 3 C c

GAM7776 246 FCGR2A Grundy, H. O.; Peltz, G.; Moore, K. W.; Golbus, M. S.; Jackson,L. G.; Lebo, R. V.: The polymorphic Fc- gamma receptor II gene mapsto human chromosome 1q. Immunogenetics 29: 331- 339, 1989. 3 C c

GAM7776 246 FCGR2A Hibbs, M. L.; Bonadonna, L.; Scott, B. M.; McKenzie, I. F. C.;Hogarth, P. M.: Molecular cloning of a human immunoglobulin G Fcreceptor. Proc. Nat. Acad. Sci. 85: 2240- 2244, 1988. 3 C c

GAM7776 246 FCGR2A Hibbs, M. L.; Hogarth, P. M.; McKenzie, I. F. C.: The mouse Ly- 17locus identifies a polymorphism of the Fc receptor. Immunogenetics 22:335- 348, 1985. 3 C c

GAM7776 246 FCGR2A Lebo, R. V.; Lynch, E. D.; Wiegant, J.; Moore, K.; Trounstine,M.; van der Ploeg, M.: Multicolor fluorescence in situ hybridizationand pulsed field electrophoresis dissect CMT1B gene region. Hum.Genet. 88: 13- 20, 1991. 3 C c

GAM7776 246 FCGR2A Moser, K. L.; Neas, B. R.; Salmon, J. E.; Yu, H.; Gray- McGuire,C.; Asundi, N.; Bruner, G. R.; Fox, J.; Kelly, J.; Henshall, S.; Bacino,D.; Dietz, M.; Hogue, R.; Koelsch, G.; Nightingale, L.; Shaver, T.;Abdou, N. I.; Albert, D. A.; Carson, C.; Petri, M.; Treadwell, E.L.; James, J. A.; Harley, J. B.: Genome scan of human systemic lupuserythematosus: evidence for linkage on chromosome 1q in African- Americanpedigrees. Proc. Nat. Acad. Sci. 95: 14869- 14874, 1998. 3 C c

GAM7776 246 FCGR2A Oakey, R. J.; Watson, M. L.; Seldin, M. F.: Construction of aphysical map on mouse and human chromosome 1: comparison of 13 Mbof mouse and 11 Mb of human DNA. Hum. Molec. Genet. 1: 613- 620,1992. 3 C c

GAM7776 246 FCGR2A Peltz, G. A.; Grundy, H. O.; Lebo, R. V.; Yssel, H.; Barsh, G.S.; Moore, K. W.: Human Fc- gamma- RIII: cloning, expression, and identificationof the chromosomal locus of two Fc receptors for IgG. Proc. Nat.Acad. Sci. 86: 1013- 1017, 1989. 3 C c

GAM7776 246 FCGR2A Qiu, W. Q.; de Bruin, D.; Brownstein, B. H.; Pearse, R.; Ravetch,J. V.: Organization of the human and mouse low- affinity Fc- gamma- Rgenes: duplication and recombination. Science 248: 732- 735, 1990. 3 C c

GAM7776 246 FCGR2A Salmon, J. E.; Millard, S.; Schachter, L. A.; Arnett, F. C.; Ginzler,E. M.; Gourley, M. F.; Ramsey- Goldman, R.; Peterson, M. G. E.; Kimberly,R. P.: Fc-gamma- RIIA alleles are heritable risk factors for lupusnephritis in African Americans. J. Clin. Invest. 97: 1348- 1354,1996. 3 C c

GAM7776 246 FCGR2A Sammartino, L.; Webber, L. M.; Hogarth, P. M.; McKenzie, I. F.C.; Garson, O. M.: Assignment of the gene coding for human FcRII(CD32) to bands q23q24 on chromosome 1. Immunogenetics 28: 380- 381,1988. 3 C c

GAM7776 246 FCGR2A Stein, M.- P.; Edberg, J. C.; Kimberly, R. P.; Mangan, E. K.; Bharadwaj,D.; Mold, C.; Du Clos, T. W.: C- reactive protein binding to Fc- gamma- RIIaon human monocytes and neutrophils is allele- specific. J. Clin. Invest. 105:369- 376, 2000. 3 C c

GAM7776 246 FCGR2A Unkeless, J. C.: Function and heterogeneity of human Fc receptorsfor immunoglobulin G. J. Clin. Invest. 83: 355- 361, 1989. 3 C c

GAM7776 246 FEZ1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999. 3 C b

GAM7776 246 FEZ1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 C b

GAM7776 246 FGF5 Dionne, C. A.; Kaplan, R.; Seuanez, H.; O'Brien, S. J.; Jaye, M.: Chromosome assignment by polymerase chain reaction techniques: assignmentof the oncogene FGF- 5 to human chromosome 4. Biotechniques 8: 190- 194,1990. 3 C b

GAM7776 246 FGF5 Hebert, J. M.; Rosenquist, T.; Gotz, J.; Martin, G. R.: FGF5 asa regulator of the hair growth cycle: evidence from targeted and spontaneousmutations. Cell 78: 1017- 1025, 1994. 3 C b

GAM7776 246 FGF5 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992. 3 C b

GAM7776 246 FGF5 Nguyen, C.; Roux, D.; Mattei, M.- G.; de Lapeyriere, O.; Goldfarb,M.; 3 C b

Birnbaum, D.; Jordan, B. R.: The FGF- related oncogenes hst andint.2, and the bcl.1 locus are contained within one megabase in bandq13 of chromosome 11, while the fgf.5 oncogene maps to 4q21. Oncogene 3:703- 708, 1988.

GAM7776 246 FGF5 Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.: The human FGF- 5 oncogeneencodes a novel protein related to fibroblast growth factors. Molec.Cell. Biol. 8: 3487- 3495, 1988. 3 C b

GAM7776 246 FHL2 Chan, K. K.; Tsui, S. K. W.; Lee, S. M. Y.; Luk, S. C. W.; Liew,C. C.; Fung, K. P.; Waye, M. M. Y.; Lee, C. Y.: Molecular cloningand characterization of FHL2, a novel LIM domain protein preferentiallyexpressed in human heart. Gene 210: 345- 350, 1998. 3 C b

GAM7776 246 FHL2 Genini, M.; Schwalbe, P.; Scholl, F. A.; Remppis, A.; Mattei, M.-G.;Schafer, B. W.: Subtractive cloning and characterization of DRAL,a novel LIM- domain protein down- regulated in rhabdomyosarcoma. DNACell Biol. 16: 433- 442, 1997. 3 C b

GAM7776 246 FHL2 Morgan, M. J.; Madgwick, A. J. A.: Slim defines a novel familyof LIM-proteins expressed in skeletal muscle. Biochem. Biophys. Res.Commun. 225: 632- 638, 1996. 3 C b

GAM7776 246 FHL2 Tanahashi, H.; Tabira, T.: Alzheimer's disease- associated presenilin2 interacts with DRAL, an LIM- domain protein. Hum. Molec. Genet. 9:2281-2289, 2000. 3 C b

GAM7776 246 FOXO1A Anderson, M. J.; Shelton, G. D.; Cavenee, W. K.; Arden, K. C.:Embryonic expression of the tumor- associated PAX3- FKHR fusion proteininterferes with the developmental functions of Pax3. Proc. Nat. Acad.Sci. 98: 1589- 1594, 2001. 3 C c

GAM7776 246 FOXO1A Anderson, M. J.; Viars, C. S.; Czekay, S.; Cavenee, W. K.; Arden,K. C.: Cloning and characterization of three human forkhead genesthat comprise an FKHR- like gene subfamily. Genomics 47: 187- 199,1998. 3 C c

GAM7776 246 FOXO1A Barr, F. G.; Galili, N.; Holick, J.; Biegel, J. A.; Rovera, G.;Emanuel, B. S.: Rearrangement of the PAX3 paired box gene in thepaediatric solid tumor alveolar rhabdomyosarcoma. Nature Genet. 3:113- 117, 1993. 3 C c

GAM7776 246 FOXO1A Davis, R. J.; Barr, F. G.: Fusion genes resulting from alternativechromosomal translocations are overexpressed by gene- specific mechanismsin alveolar rhabdomyosarcoma. Proc. Nat. Acad. Sci. 94: 8047-8051,1997. 3 C c

GAM7776 246 FOXO1A Fredericks, W. J.; Galili, N.; Mukhopadhyay, S.; Rovera, G.; Bennicelli,J.; Barr, F. G.; Rauscher, F. J., III: The PAX3- FKHR fusion proteincreated by the t(2;13) translocation in alveolar rhabdomyosarcomasis a more potent transcriptional activator than PAX3. Molec. Cell.Biol. 15: 1522- 1535, 1995. 3 C c

GAM7776 246 FOXO1A Galili, N.; Davis, R. J.; Fredericks, W. J.; Mukhopadhyay, S.;Rauscher, F. J., III; Emanuel, B. S.; Rovera, G.; Barr, F. G.: Fusionof a fork head domain gene to PAX3 in the solid tumour alveolar rhabdomyosarcoma. NatureGenet. 5: 230- 235, 1993. 3 C c

GAM7776 246 FOXO1A Khan, J.; Bittner, M. L.; Saal, L. H.; Teichmann, U.; Azorsa, D.O.; Gooden, G. C.; Pavan, W. J.; Trent, J. M.; Meltzer, P. S.: cDNAmicroarrays detect activation of a myogenic transcription programby the PAX3- FKHR fusion oncogene. Proc. Nat. Acad. Sci. 96: 13264- 13269,1999. 3 C c

GAM7776 246 FOXO1A Medema, R. H.; Kops, G. J. P. L.; Bos, J. L.; Burgering, B. M.T.: AFX- like forkhead transcription factors mediate cell- cycle regulationby Ras and PKB through p27(kip1). Nature 404: 782- 787, 2000. 3 C c

GAM7776 246 FOXO1A Nakae, J.; Biggs, W. H., III; Kitamura, T.; Cavenee, W. K.; Wright,C. V. E.; 3 C c

Arden, K. C.; Accili, D.: Regulation of insulin actionand pancreatic beta-cell function by mutated alleles of the gene encodingforkhead transcription factor Foxo1. Nature Genet. 32: 245- 253,2002.

GAM7776 246 FOXO1A Scheidler, S.; Fredericks, W. J.; Rauscher, F. J., III; Barr,F. G.; Vogt, P. K.: The hybrid PAX3- FKHR fusion protein of alveolarrhabdomyosarcoma transforms fibroblasts in culture. Proc. Nat. Acad.Sci. 93: 9805- 9809, 1996. 3 C c

GAM7776 246 FOXO1A Sublett, J. E.; Jeon, I- S.; Shapiro, D. N.: The alveolar rhabdomyosarcomaPAX3/FKHR fusion protein is a transcriptional activator. Oncogene 11:545- 552, 1995. 3 C c

GAM7776 246 FOXO1A Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes Cancer 5: 299- 310, 1992. 3 C c

GAM7776 246 FSHPRH1 Aittomaki, K.; Lucena, J. L. D.; Pakarinen, P.; Sistonen, P.; Tapanainen,J.; Gromoll, J.; Kaskikari, R.; Sankila, E.- M.; Lehvaslaiho, H.; Engel,A. R.; Nieschlag, E.; Huhtaniemi, I.; de la Chapelle, A.: Mutationin the follicle-stimulating hormone receptor gene causes hereditaryhypergonadotropic ovarian failure. Cell 82: 959- 968, 1995. 3 C c

GAM7776 246 FSHPRH1 Roberts, R. G.; Kendall, E.; Vetrie, D.; Bobrow, M.: Sequenceand chromosomal location of a human homologue of LRPR1, an FSH primaryresponse gene. Genomics 37: 122- 124, 1996. 3 C c

GAM7776 246 FSHPRH1 Slegtenhorst- Eegdeman, K. E.; Post, M.; Baarends, W. M.; Themmen,A. P. N.; Grootegoed, J. A.: Regulation of gene expression in Sertolicells by follicle- stimulating hormone (FSH): cloning and characterizationof LRPR1, a primary response gene encoding a leucine- rich protein. Molec.Cell. Endocr. 108: 115- 124, 1995. 3 C c

GAM7776 246 FZD4 Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.;Hirai, M.; Katoh, M.: Molecular cloning and characterization of humanfrizzled- 4 on chromosome 11q14- q21. Biochem. Biophys. Res. Commun. 264:955- 961, 1999. 3 C c

GAM7776 246 FZD4 Robitaille, J.; MacDonald, M. L. E.; Kaykas, A.; Sheldahl, L. C.;Zeisler, J.; Dube, M.- P.; Zhang, L.- H.; Singaraja, R. R.; Guernsey,D. L.; Zhang, B.; Siebert, L. F.; Hoskin- Mott, A.; Trese, M. T.; Pimstone,S. N.; Shastry, B. S.; Moon, R. T.; Hayden, M. R.; Goldberg, Y. P.;Samuels, M. E.: Mutant frizzled- 4 disrupts retinal angiogenesis infamilial exudative vitreoretinopathy. Nature Genet. 32: 326- 330,2002. 3 C c

GAM7776 246 G2A Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y.: Lysophosphatidylcholine as a ligand for the immunoregulatory receptorG2A. Science 293: 702- 705, 2001. 3 C c

GAM7776 246 G2A Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.;Harvill, E. T.; Jensen, E. R.; Miller, J. F.; Witte, O. N.: Micelacking the orphan G protein- coupled receptor G2A develop a late- onsetautoimmune syndrome. Immunity 14: 561- 571, 2001. 3 C c

GAM7776 246 G2A Weng, Z.; Fluckiger, A.- C.; Nisitani, S.; Wahl, M. I.; Le, L. Q.;Hunter, C. A.; Fernal, A. A.; le Beau, M. M.; Witte, O. N.: A DNAdamage and stress inducible G protein- coupled receptor blocks cellsin G2/M. Proc. Nat. Acad. Sci. 95: 12334- 12339, 1998. 3 C c

GAM7776 246 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; 3 C c

Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N-acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001.

GAM7776 246 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2-epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313-24318,1997. 3 C c

GAM7776 246 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 C c

GAM7776 246 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997. 3 C c

GAM7776 246 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase gene (GNE). J. Hum. Genet. 47: 77- 79, 2002. 3 C c

GAM7776 246 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999. 3 C c

GAM7776 246 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993. 3 C c

GAM7776 246 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001. 3 C c

GAM7776 246 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981. 3 C c

GAM7776 246 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002. 3 C c

GAM7776 246 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N-acetylglucosamine 2- epimerase gene define the disease sialuriaand the allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999. 3 C c

GAM7776 246 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N-acetylneuraminic acid biosynthesis of rat liver: molecularcloning and functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N-acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997. 3 C c

GAM7776 246 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989. 3 C c

GAM7776 246 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987. 3 C c

GAM7776 246 GPR4 Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng,H. H. Q.; Marchese, A.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd,B. F.: Isolation of three novel human genes encoding G protein- coupledreceptors. DNA Cell Biol. 14: 25- 35, 1995. 3 C c

GAM7776 246 GPR4 Mahadevan, M. S.; Baird, S.; Bailly, J. E.; Shutler, G. G.; Sabourin,L. A.; 3 C c
Tsilfidis, C.; Neville, C. E.; Narang, M.; Korneluk, R. G.: Isolation of a
novel G protein- coupled receptor (GPR4) localizedto chromosome 19q13.3.
Genomics 30: 84- 88, 1995.

GAM7776 246 GPR4 Ye, R. D.; Prossnitz, E. R.; Zou, A.; Cochrane, C. G.: Characterizationof a 3 C c
human cDNA that encodes a functional receptor for platelet activatingfactor.
Biochem. Biophys. Res. Commun. 180: 105- 111, 1991.

GAM7776 246 GPR4 Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina,K. L.; 3 C c
Kabarowski, J. H. S.; Witte, O. N.; Xu, Y.: Sphingosylphosphorylcholineand
lysophosphatidylcholine are ligands for the G protein- coupledreceptor GPR4.
J. Biol. Chem. 276: 41325- 41335, 2001.

GAM7776 246 GPR56 Liu, M.; Parker, R. M. C.; Darby, K.; Eyre, H. J.; Copeland, N.G.; Crawford, 3 C b
J.; Gilbert, D. J.; Sutherland, G. R.; Jenkins, N. A.;Herzog, H.: GPR56, a
novel secretin- like human G- protein- coupledreceptor gene. Genomics 55:
296- 305, 1999.

GAM7776 246 GPR56 Zendman, A. J. W.; Cornelissen, I. M. H. A.; Weidle, U. H.; Ruiter,D. J.; 3 C b
van Muijen, G. N. P.: TM7XN1, a novel human EGF- TM7- like cDNA,detected
with mRNA differential display using human melanoma celllines with different
metastatic potential. FEBS Lett. 446: 292- 298,1999.

GAM7776 246 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; 3 C b
Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann,
S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is
fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in
three cases of myelodysplastic syndrome/acutemyeloid leukemia with a
deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000.

GAM7776 246 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain- 3 C b
containingGTPase- activating protein for Rho and Cdc42 associates with
focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996.

GAM7776 246 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C b
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM7776 246 GRINL1A Roginski, R. S.; Mohan Raj, B. K.; Finkernagel, S. W.; Sciorra,L. J.: 3 C b
Assignment of an ionotropic glutamate receptor- like gene (GRINL1A)to human
chromosome 15q22.1 by in situ hybridization. Cytogenet.Cell Genet. 93: 143-
144, 2001.

GAM7776 246 GRINL1A Wydner, K. S.; Mohan Raj, B. K.; Sciorra, L. J.; Roginski, R. S.: The mouse 3 C b
orthologue of the human ionotropic glutamate receptor- likegene (GRINL1A)
maps to mouse chromosome 9. Cytogenet. Cell Genet. 95:240- 241, 2001.

GAM7776 246 GSTM1 Board, P. G.: Biochemical genetics of glutathione- S- transferasein man. Am. 3 C c
J. Hum. Genet. 33: 36- 43, 1981.

GAM7776 246 GSTM1 Board, P.; Coggan, M.; Johnston, P.; Ross, V.; Suzuki, T.; Webb,G.: Genetic 3 C c
heterogeneity of the human glutathione transferases:a complex of gene
families. Pharm. Therap. 48: 357- 369, 1990.

GAM7776 246 GSTM1 Chen, C.- L.; Liu, Q.; Relling, M. V.: Simultaneous characterizationof 3 C c
glutathione S- transferase M1 and T1 polymorphisms by polymerasechain
reaction in American whites and blacks. Pharmacogenetics 6:187- 191, 1996.

GAM7776 246 GSTM1 DeJong, J. L.; Chang, C.- M.; Whang- Peng, J.; Knutsen, T.; Tu, C.- P.D.: 3 C c
The human liver glutathione S- transferase gene superfamily: expressionand
chromosome mapping of an H(b) subunit cDNA. Nucleic Acids Res. 16:8541-

8554, 1988.

GAM7776 246 GSTM1 DeJong, J. L.; Mohandas, T.; Tu, C.- P. D.: The human H(b) (mu)class 3 C c
glutathione S- transferases are encoded by a dispersed gene family.
Biochem.Biophys. Res. Commun. 180: 15- 22, 1991.

GAM7776 246 GSTM1 Godschalk, R. W. L.; Dallinga, J. W.; Wikman, H.; Risch, A.; Kleinjans,J. C. 3 C c
S.; Bartsch, H.; Van Schooten, F.- J.: Modulation of DNA andprotein adducts
in smokers by genetic polymorphisms in GSTM1, GSTT1,NAT1 and NAT2.
Pharmacogenetics 11: 389- 398, 2001.

GAM7776 246 GSTM1 Harada, S.; Abei, M.; Tanaka, N.; Agarwal, D. P.; Goedde, H. W.: Liver 3 C c
glutathione S- transferase polymorphism in Japanese and itspharmacogenetic
importance. Hum. Genet. 75: 322- 325, 1987.

GAM7776 246 GSTM1 Islam, M. Q.; Platz, A.; Szpirer, J.; Szpirer, C.; Levan, G.; Mannervik,B.: 3 C c
Chromosomal localization of human glutathione transferase genesof classes
alpha, mu and pi. Hum. Genet. 82: 338- 342, 1989.

GAM7776 246 GSTM1 Lee, K. A.; Kim, S. H.; Woo, H. Y.; Hong, Y. J.; Cho, H. C.: 3 C c
Increasedfrequencies of glutathione S- transferase (GSTM1 and GSTT1) gene
deletionsin Korean patients with acquired aplastic anemia. Blood 98: 3483-
3485,2001.

GAM7776 246 GSTM1 Mannervik, B.: The isozymes of glutathione transferase. Adv.Enzym. Relat. 3 C c
Areas Molec. Biol. 57: 357- 417, 1985.

GAM7776 246 GSTM1 Mannervik, B.; Awasthi, Y. C.; Board, P. G.; Hayes, J. D.; Dillio, C.; 3 C c
Ketterer, B.; Listowsky, I.; Morgenstern, R.; Muramatsu,M.; Pearson, W. R.;
Pickett, C. B.; Sato, K.; Widersten, M.; Wolf,R. C.: Nomenclature for human
glutathione transferases. (Letter) Biochem.J. 282: 305- 306, 1992.

GAM7776 246 GSTM1 McLellan, R. A.; Oscarson, M.; Alexandrie, A.- K.; Seidegard, J.;Evans, D. 3 C c
A. P.; Rannug, A.; Ingelman- Sundberg, M.: Characterizationof a human
glutathione S- transferase mu cluster containing a duplicatedGSTM1 gene that
causes ultrarapid enzyme activity. Molec. Pharm. 52:958- 965, 1997.

GAM7776 246 GSTM1 Pearson, W. R.; Vorachek, W. R.; Xu, S.; Berger, R.; Hart, I.;Vannais, D.; 3 C c
Patterson, D.: Identification of class- mu glutathionetransferase genes
GSTM1- GSTM5 on human chromosome 1p13. Am. J. Hum.Genet. 53: 220- 233, 1993.

GAM7776 246 GSTM1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 C c
New York: Oxford Univ. Press (pub.) 1988.

GAM7776 246 GSTM1 Scott, E. M.; Wright, R. C.: Variability of glutathione S- transferaseof 3 C c
human erythrocytes. Am. J. Hum. Genet. 32: 115- 117, 1980.

GAM7776 246 GSTM1 Seidegard, J.; Pero, R. W.; Markowitz, M. M.; Roush, G.; Miller,D. G.; 3 C c
Beattie, E. J.: Isoenzyme(s) of glutathione transferase (classmu) as a
marker for the susceptibility to lung cancer: a follow upstudy.
Carcinogenesis 11: 33- 36, 1990.

GAM7776 246 GSTM1 Seidegard, J.; Pero, R. W.; Miller, D. G.; Beattie, E. J.: Aglutathione 3 C c
transferase in human leukocytes as a marker for the susceptibilityto lung
cancer. Carcinogenesis 7: 751- 753, 1986.

GAM7776 246 GSTM1 Seidegard, J.; Vorachek, W. R.; Pero, R. W.; Pearson, W. R.:Hereditary 3 C c
differences in the expression of the human glutathionetransferase active on
trans- stilbene oxide are due to a gene deletion. Proc.Nat. Acad. Sci. 85:
7293- 7297, 1988.

GAM7776 246 GSTM1 Strange, R. C.; Davis, B. A.; Faulder, C. G.; Cotton, W.; Bain,A. D.; 3 C c
Hopkinson, D. A.; Hume, R.: The human glutathione S-
transferases:developmental aspects of the GST1, GST2, and GST3 loci.
Biochem.Genet. 23: 1011- 1028, 1985.

GAM7776 246 GSTM1 Strange, R. C.; Faulder, C. G.; Davis, B. A.; Hume, R.; Brown,J. A. H.; 3 C c
Cotton, W.; Hopkinson, D. A.: The human glutathione S- transferases:studies
on the tissue distribution and genetic variation of the GST1,GST2 and GST3
isozymes. Ann. Hum. Genet. 48: 11- 20, 1984.

GAM7776 246 GSTM1 Strange, R. C.; Matharoo, B.; Faulder, G. C.; Jones, P.; Cotton,W.; Elder, 3 C c
J. B.; Deakin, M.: The human glutathione S- transferases:a case- control
study of the incidence of the GST1 0 phenotype in patientswith
adenocarcinoma. Carcinogenesis 12: 25- 28, 1991.

GAM7776 246 GSTM1 van Poppel, G.; de Vogel, N.; van Bladeren, P. J.; Kok, F. J.: Increased 3 C c
cytogenetic damage in smokers deficient in glutathioneS- transferase isozyme
mu. Carcinogenesis 13: 303- 305, 1992.

GAM7776 246 GSTM1 Xu, S.; Wang, Y.; Roe, B.; Pearson, W. R.: Characterization ofthe human 3 C c
class mu glutathione S- transferase gene cluster and theGSTM1 deletion. J.
Biol. Chem. 273: 3517- 3527, 1998.

GAM7776 246 GSTM1 Zhong, S.; Wolf, C. R.; Spurr, N. K.: Chromosomal assignmentand linkage 3 C c
analysis of the human glutathione S- transferase mu- gene(GSTM1) using
intron specific polymerase chain reaction. Hum. Genet. 90:435- 439, 1992.

GAM7776 246 GSTM1 Zhong, S.; Wyllie, A. H.; Barnes, D.; Wolf, C. R.; Spurr, N. K.: 3 C c
Relationship between the GSTM1 genetic polymorphism and susceptibilityto
bladder, breast and colon cancer. Carcinogenesis 14: 1821- 1824,1993.

GAM7776 246 GSTM4 Comstock, K. E.; Johnson, K. J.; Rifenbery, D.; Henner, W. D.:Isolation and 3 C c
analysis of the gene and cDNA for a human mu class glutathioneS-
transferase, GSTM4. J. Biol. Chem. 268: 16958- 16965, 1993.

GAM7776 246 GSTM4 Ross, V. L.; Board, P. G.: Molecular cloning and heterologousexpression of 3 C c
an alternatively spliced human mu class glutathioneS- transferase
transcript. Biochem. J. 294: 373- 380, 1993.

GAM7776 246 GSTM4 Ross, V. L.; Board, P. G.; Webb, G. C.: Chromosomal mapping ofthe human mu 3 C
c
class glutathione S- transferases to 1p13. Genomics 18:87- 91, 1993.

GAM7776 246 GSTM4 Taylor, J. B.; Oliver, J.; Sherrington, R.; Pemble, S. E.: Structureof human 3 C c
glutathione S- transferase class mu genes. Biochem. J. 274:587- 593, 1991.

GAM7776 246 GYG Barbetti, F.; Rocchi, M.; Bossolasco, M.; Cordera, R.; Sbraccia,P.; Finelli, 3 C b
P.; Consalez, G. G.: The human skeletal muscle glycogeningene: cDNA, tissue
expression, and chromosomal localization. Biochem.Biophys. Res. Commun. 220:
72- 77, 1996.

GAM7776 246 GYG Lomako, J.; Mazuruk, K.; Lomako, W. M.; Alonso, M. D.; Whelan,W. J.; 3 C b
Rodriguez, I. R.: The human intron- containing gene for glycogeninmaps to
chromosome 3, band q24. Genomics 33: 519- 522, 1996.

GAM7776 246 GYG Mu, J.; Skurat, A. V.; Roach, P. J.: Glycogenin- 2, a novel self- 3 C b
glucosylatingprotein involved in liver glycogen biosynthesis. J. Biol. Chem.
272:27589- 27597, 1997.

GAM7776 246 GYG Viskupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; DePaoli- Roach, A.A.; Roach, P. 3 C b
J.: Rabbit skeletal muscle glycogenin. Molecular cloningand production of
fully functional protein in Escherichia coli. J.Biol. Chem. 267: 25759-
25763, 1992.

GAM7776 246 HEPH Anderson, G. J.; Murphy, T. L.; Cowley, L.; Evans, B. A.; Halliday,J. W.; 3 C c
McLaren, G. D.: Mapping the gene for sex- linked anemia: aninherited defect
of intestinal iron absorption in the mouse. Genomics 48:34- 39, 1998.

GAM7776 246 HEPH Bannerman, R. M.: Genetic defects of iron transport. Fed. Proc. 35:2281- 3 C c
2285, 1976.

GAM7776 246 HEPH Edwards, J. A.; Hoke, J. E.; Mattioli, M.; Reichlin, M.: 3 C c
Ferritindistribution and synthesis in sex- linked anemia. J. Lab. Clin. Med.
90:68- 76, 1977.

GAM7776 246 HEPH Falconer, D. S.; Isaacson, J. H.: The genetics of sex- linked anaemiain the 3 C c
mouse. Genet. Res. 3: 248- 250, 1962.

GAM7776 246 HEPH Grewal, M. S.: A sex- linked anaemia in the mouse. Genet. Res. 3:238- 247, 3 C c
1962.

GAM7776 246 HEPH Lee, G. R.; Nacht, S.; Lukens, J. N.; Cartwright, G. E.: Ironmetabolism in 3 C c
copper- deficient swine. J. Clin. Invest. 47: 2058- 2069,1968.

GAM7776 246 HEPH Vulpe, C. D.; Kuo, Y.- M.; Murphy, T. L.; Cowley, L.; Askwith, C.;Libina, 3 C c
N.; Gitschier, J.; Anderson, G. J.: Hephaestin, a ceruloplasminhomologue
implicated in intestinal iron transport, is defective inthe sla mouse.
Nature Genet. 21: 195- 199, 1999.

GAM7776 246 HTR1D Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S. J.; Duncan,A. M. V.; 3 C c
Rozmahel, R.; Yang, Y.; Mengod, G.; Palacios, J. M.; O'Dowd,B. F.:
Characterization of the human 5- hydroxytryptamine(1B) receptor. J.Biol.
Chem. 267: 5735- 5738, 1992.

GAM7776 246 HTR1D Libert, F.; Passage, E.; Parmentier, M.; Simons, M.- J.; Vassart,G.; Mattei, 3 C c
M.- G.: Chromosomal mapping of A1 and A2 adenosine receptors,VIP receptor,
and a new subtype of serotonin receptor. Genomics 11:225- 227, 1991.

GAM7776 246 HTR1D Weinshank, R. L.; Zgombick, J. M.; Macchi, M. J.; Branchek, T.A.; Hartig, P. 3 C c
R.: Human serotonin 1D receptor is encoded by a subfamilyof two distinct
genes: 5- HT(1D- alpha) and 5- HT(1D- beta). Proc. Nat.Acad. Sci. 89: 3630-
3634, 1992.

GAM7776 246 HTR1D Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; 3 C c
Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and
genome organization of mammalian G- protein- coupled receptors. Genomics
18:175- 184, 1993.

GAM7776 246 HUS1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human 3 C c
homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of
homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster.
Genomics 54: 424- 436, 1998.

GAM7776 246 HUS1 Dominguez, O.; Ashhab, Y.; Sabater, L.; Belloso, E.; Caro, P.;Pujol- 3 C c
Borrell, R.: Cloning of ARE- containing genes by AU- motif- directeddisplay.
Genomics 54: 278- 286, 1998.

GAM7776 246 HUS1 Kostrub, C. F.; Knudsen, K.; Subramani, S.; Enoch, T.: Hus1p,a conserved 3 C c
fission yeast checkpoint protein, interacts with Rad1pand is phosphorylated
in response to DNA damage. EMBO J. 17: 2055- 2066,1998.

GAM7776 246 HUS1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe 3 C c
Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol.
Chem. 274: 567- 570, 1999.

GAM7776 246 ICAM1 Ballantyne, C. M.; Kozak, C. A.; O'Brien, W. E.; Beaudet, A. L.: Assignment 3 C c
of the gene for intercellular adhesion molecule- 1 (Icam- 1)to proximal
mouse chromosome 9. Genomics 9: 547- 550, 1991.

GAM7776 246 ICAM1 Bella, J.; Kolatkar, P. R.; Marlor, C. W.; Greve, J. M.; Rossmann,M. G.: The 3 C c
structure of the two amino- terminal domains of human ICAM- 1suggests how it
functions as a rhinovirus receptor and as an LFA- 1integrin ligand. Proc.
Nat. Acad. Sci. 95: 4140- 4145, 1998.

GAM7776 246 ICAM1 Bellamy, R.; Kwiatkowski, D.; and Hill, A. V. S.: Absence of anassociation 3 C c
between intercellular adhesion molecule 1, complementreceptor 1 and

interleukin 1 receptor antagonist gene polymorphismsand severe malaria in a West African population. Trans. R. Soc. Trop.Med. Hyg. 92: 312- 316, 1998.

GAM7776 246 ICAM1 Craig, A.; Fernandez- Reyes, D.; Mesri, M.; McDowall, A.; Altieri,D. C.; Hogg, N.; Newbold, C.: A functional analysis of a naturalvariant of intercellular adhesion molecule- 1 (ICAM- 1- Kilifi). Hum.Molec. Genet. 9: 525- 530, 2000. 3 C c

GAM7776 246 ICAM1 Fernandez- Reyes, D.; Craig, A. G.; Kyes, S. A.; Peshu, N.; Snow,R. W.; Berendt, A. R.; Marsh, K.; Newbold, C. I.: A high frequencyAfrican coding polymorphism in the N- terminal domain of ICAM- 1 predisposingto cerebral malaria in Kenya. Hum. Molec. Genet. 6: 1357- 1360, 1997. 3 C c

GAM7776 246 ICAM1 Greve, J. M.; Davis, G.; Meyer, A. M.; Forte, C. P.; Yost, S. C.;Marlor, C. W.; Kamarck, M. E.; McClelland, A.: The major human rhinovirusreceptor is ICAM- 1. Cell 56: 839- 847, 1989. 3 C c

GAM7776 246 ICAM1 Hill, A. V. S.: The immunogenetics of resistance to malaria. Proc.Assoc. Am. Phys. 111: 272- 277, 1999. 3 C c

GAM7776 246 ICAM1 Katz, F. E.; Parkar, M.; Stanley, K.; Murray, L. J.; Clark, E.A.; Greaves, M. F.: Chromosome mapping of cell membrane antigensexpressed on activated B cells. Europ. J. Immun. 15: 103- 106, 1985. 3 C c

GAM7776 246 ICAM1 Le Beau, M. M.; Ryan, D., Jr.; Pericak- Vance, M. A.: Report ofthe committee on the genetic constitution of chromosomes 18 and 19. Cytogenet.Cell Genet. 51: 338- 357, 1989. 3 C c

GAM7776 246 ICAM1 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in the splenic marginal zone. Science 297: 409- 412, 2002. 3 C c

GAM7776 246 ICAM1 Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot-Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow cytometricanalysis of conjunctival epithelium in ocular rosacea and keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000. 3 C c

GAM7776 246 ICAM1 Prieto, J.; Takei, F.; Gendelman, R.; Christenson, B.; Biberfeld,P.; Patarroyo, M.: MALA- 2, mouse homologue of human adhesion moleculeICAM- 1 (CD54). Europ. J. Immun. 19: 1551- 1557, 1989. 3 C c

GAM7776 246 ICAM1 Seldin, M. F.; Saunders, A. M.; Rochelle, J. M.; Howard, T. A.: A proximal mouse chromosome 9 linkage map that further defines linkagegroups homologous with segments of human chromosomes 11, 15, and 19. Genomics 9:678- 685, 1991. 3 C c

GAM7776 246 ICAM1 Simmons, D.; Makgoba, M. W.; Seed, B.: ICAM, an adhesion ligandof LFA- 1, is homologous to the neural cell adhesion molecule NCAM. Nature 331:624- 627, 1988. 3 C c

GAM7776 246 ICAM1 Sligh, J. E., Jr.; Ballantyne, C. M.; Rich, S. S.; Hawkins, H.K.; Smith, C. W.; Bradley, A.; Beaudet, A. L.: Inflammatory and immuneresponses are impaired in mice deficient in intercellular adhesionmolecule 1. Proc. Nat. Acad. Sci. 90: 8529- 8533, 1993. 3 C c

GAM7776 246 ICAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993. 3 C c

GAM7776 246 ICAM1 Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; Takeuchi, T.: Regulation of human leukocyte antigenexpression in human conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999. 3 C c

GAM7776 246 IGF1 Aleman, A.; Verhaar, H. J. J.; De Haan, E. H. F.; De Vries, W.R.; Samson, M. 3 C c

M.; Drent, M. L.; Van Der Veen, E. A.; Koppeschaar,H. P. F.: Insulin- like growth factor- I and cognitive function inhealthy older men. J. Clin. Endocr. Metab. 84: 471- 475, 1999.

GAM7776 246 IGF1 Baker, J.; Liu, J.- P.; Robertson, E. J.; Efstratiadis, A.: Roleof insulin- like growth factors in embryonic and postnatal growth. Cell 75:73- 82, 1993. 3 C c

GAM7776 246 IGF1 Bowcock, A.; Sartorelli, V.: Polymorphism and mapping of the IGF1gene, and absence of association with stature among African Pygmies. Hum.Genet. 85: 349- 354, 1990. 3 C c

GAM7776 246 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Chromosomal mappingof loci for insulin- like growth factors I and II and for epidermalgrowth factor in man. (Abstract) Am. J. Hum. Genet. 36: 133S only,1984. 3 C c

GAM7776 246 IGF1 Brissenden, J. E.; Ullrich, A.; Francke, U.: Human chromosomalmapping of genes for insulin- like growth factors I and II and epidermalgrowth factor. Nature 310: 781- 784, 1984. 3 C c

GAM7776 246 IGF1 Camacho- Hubner, C.; Woods, K. A.; Miraki- Moud, F.; Hindmarsh, P.C.; Clark, A. J.; Hansson, Y.; Johnston, A.; Baxter, R. C.; Savage,M. O.: Effects of recombinant human insulin- like growth factor I(IGF- I) therapy on the growth hormone- IGF system of a patient witha partial IGF- I gene deletion. J. Clin. Endocr. Metab. 84: 1611- 1616,1999. 3 C c

GAM7776 246 IGF1 Goddard, A. D.; Covello, R.; Luoh, S.- M.; Clackson, T.; Attie,K. M.; Gesundheit, N.; Rundle, A. C.; Wells, J. A.; Carlsson, L. M.S.: Mutations of the growth hormone receptor in children with idiopathicshort stature. New Eng. J. Med. 333: 1093- 1098, 1995. 3 C c

GAM7776 246 IGF1 Guler, H.- P.; Binz, K.; Eigenmann, E.; Jaggi, S.; Zimmermann, D.;Zapf, J.; Froesch, E. R.: Small stature and insulin- like growth factors:prolonged treatment of mini- poodles with recombinant human insulin- likegrowth factor I. Acta Endocr. 121: 456- 464, 1989. 3 C c

GAM7776 246 IGF1 Hankinson, S. E.; Willett, W. C.; Colditz, G. A.; Hunter, D. J.;Michaud, D. S.; Deroo, B.; Rosner, B.; Speizer, F. E.; Pollak, M.: Circulating concentrations of insulin- like growth factor- I and riskof breast cancer. Lancet 351: 1393- 1396, 1998. 3 C c

GAM7776 246 IGF1 Harman, S. M.; Metter, E. J.; Blackman, M. R.; Landis, P. K.;Carter, H. B.: Serum levels of insulin- like growth factor I (IGF- I),IGF- II, IGF- binding protein- 3, and prostate- specific antigen as predictorsof clinical prostate cancer. J. Clin. Endocr. Metab. 85: 4258- 4265,2000. 3 C c

GAM7776 246 IGF1 Hellstrom, A.; Perruzzi, C.; Ju, M.; Engstrom, E.; Hard, A.- L.;Liu, J.- L.; Albertsson- Wikland, K.; Carlsson, B.; Niklasson, A.; Sjodell,L.; LeRoith, D.; Senger, D. R.; Smith, L. E. H.: Low IGF- I suppressesVEGF- survival signaling in retinal endothelial cells: direct correlationwith clinical retinopathy of prematurity. Proc. Nat. Acad. Sci. 98:5804- 5808, 2001. 3 C c

GAM7776 246 IGF1 Holly, J.: Insulin- like growth factor- I and new opportunitiesfor cancer prevention. Lancet 351: 1373- 1375, 1998. 3 C c

GAM7776 246 IGF1 Hoppener, J. W. M.; de Pagter- Holthuizen, P.; Geurts van Kessel,A. H. M.; Jansen, M.; Kittur, S. D.; Antonarakis, S. E.; Lips, C.J. M.; Sussenbach, J. S.: The human gene encoding insulin- like growthfactor I is located on chromosome 12. Hum. Genet. 69: 157- 160, 1985. 3 C c

GAM7776 246 IGF1 Justice, M. J.; Siracusa, L. D.; Gilbert, D. J.; Heisterkamp,N.; Groffen, J.; Chada, K.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: A genetic linkage map of mouse chromosome 10: localizationof eighteen molecular markers using a single interspecific backcross. Genetics 125:855- 866, 1990. 3 C c

GAM7776 246 IGF1 Le Bouc, Y.; Dreyer, D.; Jaeger, F.; Binoux, M.; Sondermeyer,P.: Complete characterization of the human IGF- I nucleotide sequenceisolated from a newly constructed adult liver cDNA library. FEBSLett. 196: 108- 112, 1986. 3 C c

GAM7776 246 IGF1 Lembo, G.; Rockman, H. A.; Hunter, J. J.; Steinmetz, H.; Koch,W. J.; Ma, L.; Printz, M. P.; Ross, J., Jr.; Chien, K. R.; Powell- Braxton,L.: Elevated blood pressure and enhanced myocardial contractilityin mice with severe IGF- 1 deficiency. J. Clin. Invest. 98: 2648- 2655,1996. 3 C c

GAM7776 246 IGF1 Li, C. H.; Yamashiro, D.; Gospodarowicz, D.; Kaplan, S. L.; VanVliet, G.: Total synthesis of insulin- like growth factor I (somatomedinC). Proc. Nat. Acad. Sci. 80: 2216- 2220, 1983. 3 C c

GAM7776 246 IGF1 Lin, S.- C.; Lin, C. R.; Gukovsky, I.; Lusis, A. J.; Sawchenko,P. E.; Rosenfeld, M. G.: Molecular basis of the little mouse phenotypeand implications for cell type- specific growth. Nature 364: 208- 213,1993. 3 C c

GAM7776 246 IGF1 Liu, J.- P.; Baker, J.; Perkins, A. S.; Robertson, E. J.; Efstratiadis,A.: Mice carrying null mutations of the genes encoding insulin- likegrowth factor I (Igf- 1) and type 1 IGF receptor (Igf1r). Cell 75:59- 72, 1993. 3 C c

GAM7776 246 IGF1 Mathews, L. S.; Norstedt, G.; Palmiter, R. D.: Regulation ofinsulin- like growth factor I gene expression by growth hormone. Proc.Nat. Acad. Sci. 83: 9343- 9347, 1986. 3 C c

GAM7776 246 IGF1 Morton, C. C.; Byers, M. G.; Nakai, H.; Bell, G. I.; Shows, T.B.: Human genes for insulin- like growth factors I and II and epidermalgrowth factor are located on 12q22- q24.1, 11p15, and 4q25- q27, respectively. Cytogenet.Cell Genet. 41: 245- 249, 1986. 3 C c

GAM7776 246 IGF1 Morton, C.; Rall, L.; Bell, G.; Shows, T.: Human insulin- likegrowth factor- 1 (IGF1) is encoded at 12q22- q24.1, and insulin- likegrowth factor- 2 (IGF2) is at 11p15. (Abstract) Cytogenet. Cell Genet. 40:703 only, 1985. 3 C c

GAM7776 246 IGF1 Mullis, P. E.; Patel, M. S.; Brickell, P. M.; Hindmarsh, P. C.;Brook, C. G. D.: Growth characteristics and response to growth hormonetherapy in patients with hypochondroplasia: genetic linkage of theinsulin- like growth factor I gene at chromosome 12q23 to the diseasein a subgroup of these patients. Clin. Endocr. 34: 265- 274, 1991. 3 C c

GAM7776 246 IGF1 Musaro, A.; McCullagh, K. J. A.; Naya, F. J.; Olson, E. N.; Rosenthal,N.: IGF- 1 induces skeletal myocyte hypertrophy through calcineurinin association with GATA- 2 and NF- ATc1. Nature 400: 581- 585, 1999. 3 C c

GAM7776 246 IGF1 Musaro, A.; McCullagh, K.; Paul, A.; Houghton, L.; Dobrowolny,G.; Molinaro, M.; Barton, E. R.; Sweeney, H. L.; Rosenthal, N.: LocalizedIgf- 1 transgene expression sustains hypertrophy and regeneration insenescent skeletal muscle. Nature Genet. 27: 195- 200, 2001. 3 C c

GAM7776 246 IGF1 Playford, M. P.; Bicknell, D.; Bodmer, W. F.; Macaulay, V. M.: Insulin- like growth factor 1 regulates the location, stability,and transcriptional activity of beta- catenin. Proc. Nat. Acad. Sci. 97:12103- 12108, 2000. 3 C c

GAM7776 246 IGF1 Powell- Braxton, L.; Hollingshead, P.; Warburton, C.; Dowd, M.;Pitts- Meek, S.; Dalton, D.; Gillett, N.; Stewart, T. A.: IGF- I isrequired for normal embryonic growth in mice. Genes Dev. 7: 2609- 2617,1993. 3 C c

GAM7776 246 IGF1 Rapp, R.; Deger, A.; Blum, W.; Koch, R.; Weber, U.: Characterizationof the protein which binds insulin- like growth factor in human serum. Europ.J. Biochem. 172: 421- 425, 1988. 3 C c

GAM7776 246 IGF1 Rasmussen, S. K.; Lautier, C.; Hansen, L.; Echwald, S. M.; Hansen,T.; Ekstrom, C. T.; Urhammer, S. A.; Borch- Johnsen, K.; Grigorescu,F.; Smith, R. J.; Pedersen, O.: Studies of the variability of thegenes encoding the 3 C c

insulin- like growth factor I receptor and its ligandin relation to type 2 diabetes mellitus. J. Clin. Endocr. Metab. 85:1606- 1610, 2000.

GAM7776 246 IGF1 Rotwein, P.: Two insulin- like growth factor I messenger RNAsare expressed in human liver. Proc. Nat. Acad. Sci. 83: 77- 81, 1986. 3 C c

GAM7776 246 IGF1 Schoenle, E. J.; Zenobi, P. D.; Torresani, T.; Werder, E. A.;Zachmann, M.; Froesch, E. R.: Recombinant human insulin- like growthfactor I (rhIGF I) reduces hyperglycaemia in patients with extremeinsulin resistance. Diabetologia 34: 675- 679, 1991. 3 C c

GAM7776 246 IGF1 Semsarian, C.; Wu, M.- J.; Ju, Y.- K.; Marciniec, T.; Yeoh, T.;Allen, D. G.; Harvey, R. P.; Graham, R. M.: Skeletal muscle hypertrophyis mediated by a Ca(2+)- dependent calcineurin signalling pathway. Nature 400:576- 581, 1999. 3 C c

GAM7776 246 IGF1 Svoboda, M. E.; Van Wyk, J. J.; Klapper, D. G.; Fellows, R. E.;Grissom, F. E.; Schleuter, R. J.: Purification of somatomedin- C fromhuman plasma: chemical and biological properties, partial sequenceanalysis, and relationship to other somatomedins. Biochemistry 19:790- 797, 1980. 3 C c

GAM7776 246 IGF1 Taylor, B. A.; Grieco, D.: Localization of the gene encodinginsulin- like growth factor I on mouse chromosome 10. Cytogenet. CellGenet. 56: 57- 58, 1991. 3 C c

GAM7776 246 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Insulin- like growth factor genes: chromosome organization andassociation with disease. (Abstract) Am. J. Hum. Genet. 36: 121Sonly, 1984. 3 C c

GAM7776 246 IGF1 Tricoli, J. V.; Rall, L. B.; Scott, J.; Bell, G. I.; Shows, T.B.: Localization of insulin- like growth factor genes to human chromosomes11 and 12. Nature 310: 784- 786, 1984. 3 C c

GAM7776 246 IGF1 Ullrich, A.; Berman, C. H.; Dull, T. J.; Gray, A.; Lee, J. M.: Isolation of the human insulin- like growth factor I gene using asingle synthetic DNA probe. EMBO J. 3: 361- 364, 1984. 3 C c

GAM7776 246 IGF1 Usala, A.- L.; Madigan, T.; Burguera, B.; Sinha, M. K.; Caro, J.F.; Cunningham, P.; Powell, J. G.; Butler, P. C.: Treatment of insulin-resistantdiabetic ketoacidosis with insulin- like growth factor I in an adolescentwith insulin- dependent diabetes. New Eng. J. Med. 327: 853-857,1992. 3 C c

GAM7776 246 IGF1 Vaessen, N.; Janssen, J. A.; Heutink, P.; Hofman, A.; Lamberts,S. W. J.; Oostra, B. A.; Pols, H. A. P.; van Duijn, C. M.: Associationbetween genetic variation in the gene for insulin- like growth factor- 1and low birthweight. Lancet 359: 1036- 1037, 2002. 3 C c

GAM7776 246 IGF1 Van Wyk, J. J.; Svoboda, M. E.; Underwood, L. E.: Evidence fromradioligand assays that somatomedin- C and insulin- like growth factor- Iare similar to each other and different from other somatomedins. J.Clin. Endocr. Metab. 50: 206- 208, 1980. 3 C c

GAM7776 246 IGF1 Vestergaard, P.; Hermann, A.P.; Orskov, H.; Mosekilde, L.; TheDanish Osteoporosis Prevention Study: Effect of sex hormone replacementon the insulin- like growth factor system and bone mineral: a cross- sectionaland longitudinal study in 595 perimenopausal women participating inthe Danish osteoporosis prevention study. J. Clin. Endocr. Metab. 84:2286- 2290, 1999. 3 C c

GAM7776 246 IGF1 Woods, K. A.; Camacho- Hubner, C.; Bergman, R. N.; Barter, D.;Clark, A. J. L.; Savage, M. O.: Effects of insulin- like growth factorI (IGF- I) therapy on body composition and insulin resistance in IGF- Igene deletion. J. Clin. Endocr. Metab. 85: 1407- 1411, 2000. 3 C c

GAM7776 246 IGF1 Woods, K. A.; Camacho- Hubner, C.; Savage, M. O.; Clark, A. J.L.: 3 C c

Intrauterine growth retardation and postnatal growth failureassociated with deletion of the insulin- like growth factor I gene. NewEng. J. Med. 335: 1363- 1367, 1996.

GAM7776 246 IGF1 Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.; Francke, U.: Sub- 3 C c
regional localization of human genes for insulin- like growthfactors I (IGF1) and II (IGF2) by in situ hybridization. (Abstract) Cytogenet.Cell Genet. 40: 782 only, 1985.

GAM7776 246 IGF1 Yanovski, J. A.; Sovik, K. N.; Nguyen, T. T.; Sebring, N. G.:Insulin- like 3 C c
growth factors and bone mineral density in African Americanand white girls. J. Pediat. 137: 826- 832, 2000.

GAM7776 246 IGF1 Zhu, J.; Kahn, C. R.: Analysis of a peptide hormone- receptorinteraction in 3 C c
the yeast two- hybrid system. Proc. Nat. Acad. Sci. 94:13063- 13068, 1997.

GAM7776 246 IGLL1 Kudo, A.; Melchers, F.: A second gene, Vpre- B in the lambda 5locus of the 3 C c
mouse, which appears to be selectively expressed in pre- Blymphocytes. EMBO J. 6: 2267- 2272, 1987.

GAM7776 246 IGLL1 Mattei, M.- G.; Fumoux, F.; Roeckel, N.; Fougereau, M.; Schiff,C.: The human 3 C c
pre- B- specific lambda- like cluster is located in the22q11.2- 22q12.3 region, distal to the IgC- lambda locus. Genomics 9:544- 546, 1991.

GAM7776 246 IGLL1 Minegishi, Y.; Coustan- Smith, E.; Wang, Y.- H.; Cooper, M. D.; Campana,D.; 3 C c
Conley, M. E.: Mutations in the human lambda- 5/14.1 gene resultin B cell deficiency and agammaglobulinemia. J. Exp. Med. 187: 71- 77,1998.

GAM7776 246 IGLL1 Pillai, S.; Baltimore, D.: The omega and iota surrogate immunoglobulinlight 3 C c
chains. Curr. Top. Microbiol. Immun. 137: 136- 139, 1988.

GAM7776 246 IGLL1 Sakaguchi, N.; Melchers, F.: Lambda 5, a new light- chain- relatedlocus 3 C c
selectively expressed in pre- B lymphocytes. Nature 324: 579- 582,1986.

GAM7776 246 IGLL1 Schiff, C.; Milili, M.; Fougereau, M.: Isolation of early 3 C c
immunoglobulinlambda- like gene transcripts in human fetal liver. Europ. J. Immun. 19:1873- 1878, 1989.

GAM7776 246 IL11 Du, X. X.; Williams, D. A.: Interleukin- 11: a multifunctionalgrowth factor 3 C b
derived from the hematopoietic microenvironment. Blood 83:2023- 2030, 1994.

GAM7776 246 IL11 Du, X.; Williams, D. A.: Interleukin- 11: review of molecular,cell biology, 3 C b
and clinical use. Blood 89: 3897- 3908, 1997.

GAM7776 246 IL11 McKinley, D.; Wu, Q.; Yang- Feng, T.; Yang, Y.- C.: Genomic sequenceand 3 C b
chromosomal location of human interleukin- 11 gene (IL11). Genomics 13:814- 819, 1992.

GAM7776 246 IL11 Paul, S. R.; Bennett, F.; Calvetti, J. A.; Kelleher, K.; Wood,C. R.; O'Hara, 3 C b
R. M., Jr.; Leary, A. C.; Sibley, B.; Clark, S. C.;Williams, D. A.; Yang, Y.- C.: Molecular cloning of a cDNA encodinginterleukin 11, a stromal cell- derived lymphopoietic and hematopoieticcytokine. Proc. Nat. Acad. Sci. 87: 7512- 7516, 1990.

GAM7776 246 IL11 Yang- Feng, T. L.; Gibson, L.; Yang, Y. C.: Assignment of the geneencoding 3 C b
human interleukin- 11 to chromosome 19q13.3- q13.4. (Abstract) Cytogenet.Cell Genet. 58: 2027 only, 1991.

GAM7776 246 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, 3 C b
sequence, expression, and processing of the interleukin 16precursor. Proc. Nat. Acad. Sci. 94: 5273- 5277, 1997.

GAM7776 246 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 3 C b
381: 30 only, 1996.

GAM7776 246 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 3 C b
16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics

49:704- 706, 1999.

GAM7776 246 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. 3 C b
C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte
chemoattractant factor: association of biologic functionwith CD4 expression.
Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994.

GAM7776 246 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human 3 C b
lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128:
2569- 2574, 1982.

GAM7776 246 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS 3 C b
human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311-
314, 1993.

GAM7776 246 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; 3 C b
Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M.
E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945-
1954, 1995.

GAM7776 246 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; 3 C b
Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure
and function between human and murine IL- 16. J. Immun. 160:5945- 5954,
1998.

GAM7776 246 IL21R Asao, H.; Okuyama, C.; Kumaki, S.; Ishii, N.; Tsuchiya, S.; Foster,D.; 3 C c
Sugamura, K.: Cutting edge: the common gamma- chain is an
indispensablesubunit of the IL- 21 receptor complex. J. Immun. 167: 1- 5,
2001.

GAM7776 246 IL21R Kasaian, M. T.; Whitters, M. J.; Carter, L. L.; Lowe, L. D.; Jussif,J. M.; 3 C c
Deng, B.; Johnson, K. A.; Witek, J. S.; Senices, M.; Konz,R. F.; Wurster, A.
L.; Donaldson, D. D.; Collins, M.; Young, D. A.;Grusby, M. J.: IL- 21 limits
NK cell responses and promotes antigen- specificT cell activation: a
mediator of the transition from innate to adaptiveimmunity. Immunity 16:
559- 569, 2002.

GAM7776 246 IL21R Ozaki, K.; Kikly, K.; Michalovich, D.; Young, P. R.; Leonard, W.J.: Cloning 3 C c
of a type I cytokine receptor most related to the IL- 2receptor beta chain.
Proc. Nat. Acad. Sci. 97: 11439- 11444, 2000.

GAM7776 246 IL21R Parrish- Novak, J.; Dillon, S. R.; Nelson, A.; Hammond, A.; Sprecher,C.; 3 C c
Gross, J. A.; Johnston, J.; Madden, K.; Xu, W.; West, J.; Schrader,S.;
Burkhead, S.; and 26 others: Interleukin 21 and its receptorare involved in
NK cell expansion and regulation of lymphocyte function. Nature 408:57- 63,
2000.

GAM7776 246 IL21R Ueda, C.; Akasaka, T.; Kurata, M.; Maesako, Y.; Nishikori, M.;Ichinohasama, 3 C c
R.; Imada, K.; Uchiyama, T.; Ohno, H.: The gene forinterleukin- 21 receptor
is the partner of BCL6 in t(13;16)(q27;p11),which is recurrently observed in
diffuse large B- cell lymphoma. Oncogene 21:368- 376, 2002.

GAM7776 246 IL5RA Geijsen, N.; Uings, I. J.; Pals, C.; Armstrong, J.; McKinnon, 3 C c
M.;Raaijmakers, J. A. M.; Lammers, J.- W. J.; Koenderman, L.; Coffer,P. J.:
Cytokine- specific transcriptional regulation through an IL- 5R-
alphainteracting protein. Science 293: 1136- 1138, 2001.

GAM7776 246 IL5RA Gough, N. M.; Rakar, S.: Localization of the IL- 5 receptor geneto the 3 C c
distal half of murine chromosome 6 using recombinant inbredstrains of mice.
Genomics 12: 855- 856, 1992.

GAM7776 246 IL5RA Isobe, M.; Kumura, Y.; Murata, Y.; Takaki, S.; Tominaga, A.; Takatsu,K.; 3 C c
Ogita, Z.: Localization of the gene encoding the alpha subunitof human

interleukin- 5 receptor (IL5RA) to chromosome region 3p24- 3p26. Genomics 14:755- 758, 1992.

GAM7776 246 IL5RA Jacob, C. O.; Mykytyn, K.; Varcony, T.; Drabkin, H. A.: Mappingof the interleukin 5 receptor gene to human chromosome 3p25- p26 andto mouse chromosome 6 close to the Raf- 1 locus with polymorphic tandemrepeat sequences. Mammalian Genome 4: 435- 439, 1993. 3 C c

GAM7776 246 IL5RA Sun, Z.; Yergeau, D. A.; Tuypens, T.; Tavernier, J.; Paul, C. C.;Baumann, M. A.: Tenen, D. G.; Ackerman, S. J.: Identification andcharacterization of a functional promoter region in the human eosinophilIL- 5 receptor alpha subunit gene. J. Biol. Chem. 270: 1462- 1471,1995. 3 C c

GAM7776 246 IL5RA Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden,J.; Fiers, W.; Plaetinck, G.: A human high affinity interleukin- 5receptor (IL5R) is composed of an IL5- specific alpha chain and a betachain shared with the receptor for GM- CSF. Cell 66: 1175- 1184, 1991. 3 C c

GAM7776 246 IL5RA Tavernier, J.; Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.;Devos, R.: Molecular basis of the membrane- anchored and two solubleisoforms of the human interleukin 5 receptor alpha subunit. Proc.Nat. Acad. Sci. 89: 7041- 7045, 1992. 3 C c

GAM7776 246 IL5RA Zhang, J.; Kuvelkar, R.; Cheewatrakoolpong, B.; Williams, S.; Egan,R. W.; Billah, M. M.: Evidence for multiple promoters of the humanIL- 5 receptor alpha subunit gene: a novel 6- base pair element determinescell- specific promoter function. J. Immun. 15: 5412- 5421, 1997. 3 C c

GAM7776 246 JRK Morita, R.; Miyazaki, E.; Fong, C. G.; Chen, X.- N.; Korenberg,J. R.; Delgado- Escueta, A. V.; Yamakawa, K.: JH8, a gene highly homologousto the mouse jerky gene, maps to the region for childhood absenceepilepsy on 8q24. Biochem. Biophys. Res. Commun. 248: 307- 314, 1998. 3 C b

GAM7776 246 JRK Toth, M.; Grimsby, J.; Buzsaki, G.; Donovan, G. P.: Epilepticseizures caused by inactivation of a novel gene, jerky, related tocentromere binding protein- B in transgenic mice. Nature Genet. 11:71- 75, 1995. Note: Erratum: Nature Genet. 12: 110 only, 1996. 3 C b

GAM7776 246 KCNJ11 Chandy, K. G.; Gutman, G. A.: Nomenclature for mammalian potassiumchannel genes. Trends Pharm. Sci. 14: 434, 1993. 3 C b

GAM7776 246 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P., IV; Wang, C.- Z.; Aguilar- Bryan,L.; Bryan, J.; Seino, S.: A family of sulfonylurea receptors determinesthe pharmacological properties of ATP- sensitive K(+) channels. Neuron 16:1011- 1017, 1996. 3 C b

GAM7776 246 KCNJ11 Inagaki, N.; Gonoi, T.; Clement, J. P.; Namba, N.; Inazawa, J.;Gonzalez, G.; Aguilar- Bryan, L.; Seino, S.; Bryan, J.: Reconstitutionof I(KATP): an inward rectifier subunit plus the sulfonylurea receptor. Science 270:1166- 1170, 1995. 3 C b

GAM7776 246 KCNJ11 Koster, J. C.; Marshall, B. A.; Ensor, N.; Corbett, J. A.; Nichols,C. G.: Targeted overactivity of beta cell KATP channels induces profoundneonatal diabetes. Cell 100: 645- 654, 2000. 3 C b

GAM7776 246 KCNJ11 Thomas, P. M.; Cote, G. J.; Hallman, D. M.; Mathew, P. M.: Homozygositymapping, to chromosome 11p, of the gene for familial persistent hyperinsulinemichypoglycemia of infancy. Am. J. Hum. Genet. 56: 416- 421, 1995. 3 C b

GAM7776 246 KCNJ11 Thomas, P.; Ye, Y.; Lightner, E.: Mutation of the pancreatic isletinward rectifier Kir6.2 also leads to familial persistent 3 C b

hyperinsulinemichypoglycemia of infancy. Hum. Molec. Genet. 5: 1809- 1812, 1996.

GAM7776 246 KCNJ11 Yamada, K.; Ji, J. J.; Yuan, H.; Miki, T.; Sata, S.; Horimoto,N.; Shimizu, T.; Seino, S.; Inagaki, N.: Protective role of ATP- sensitivepotassium channels in hypoxia- induced generalized seizure. Science 292:1543- 1546, 2001. 3 C b

GAM7776 246 KLRD1 Braud, V. M.; Allan, D. S. J.; O'Callaghan, C. A.; Soderstrom,K.; D'Andrea, A.; Ogg, G. S.; Lazetic, S.; Young, N. T.; Bell, J.I.; Phillips, J. H.; Lanier, L. L.; McMichael, A. J.: HLA- E bindsto natural killer cell receptors CD94/NKG2A, B and C. Nature 391:795- 799, 1998. 3 C c

GAM7776 246 KLRD1 Chang, C.; Rodriguez, A.; Carretero, M.; Lopez- Botet, M.; Phillips,J. H.; Lanier, L. L.: Molecular characterization of human CD94: atype II membrane glycoprotein related to the C- type lectin superfamily. Europ.J. Immun. 25: 2433- 2437, 1995. 3 C c

GAM7776 246 KLRD1 Lazetic, S.; Chang, C.; Houchins, J. P.; Lanier, L. L.; Phillips,J. H.: Human natural killer cell receptors involved in MHC classI recognition are disulfide- linked heterodimers of CD94 and NKG2 subunits. J.Immun. 157: 4741- 4745, 1996. 3 C c

GAM7776 246 KLRD1 Plougastel, B.; Trowsdale, J.: Sequence analysis of a 62- kb regionoverlapping the human KLRC cluster of genes. Genomics 49: 193- 199,1998. 3 C c

GAM7776 246 KLRD1 Rodriguez, A.; Carretero, M.; Glienke, J.; Bellon, T.; Ramirez,A.; Lehrach, H.; Francis, F.; Lopez- Botet, M.: Structure of the humanCD94 C- type lectin gene. Immunogenetics 47: 305- 309, 1998. 3 C c

GAM7776 246 KMO Alberati- Giani, D.; Cesura, A. M.; Broger, C.; Warren, W. D.; Rover,S.; Malherbe, P.: Cloning and functional expression of human kynurenine3- monooxygenase. FEBS Lett. 410: 407- 412, 1997. 3 C b

GAM7776 246 KMO Halford, S.; Freedman, M. S.; Bellingham, J.; Inglis, S. L.; Poopalasundaram,S.; Soni, B. G.; Foster, R. G.; Hunt, D. M.: Characterization ofa novel human opsin gene with wide tissue expression and identificationof embedded and flanking genes on chromosome 1q43. Genomics 72:203- 208, 2001. 3 C b

GAM7776 246 LNK Li, Y.; He, X.; Schembri- King, J.; Jakes, S.; Hayashi, J.: Cloningand characterization of human Lnk, an adaptor protein with pleckstrinhomology and Src homology 2 domains that can inhibit T cell activation. J.Immun. 164: 5199- 5206, 2000. 3 C c

GAM7776 246 LNK Takaki, S.; Sauer, K.; Iritani, B. M.; Chien, S.; Ebihara, Y.;Tsuji, K.; Takatsu, K.; Perlmutter, R. M.: Control of B cell productionby the adaptor protein Lnk: definition of a conserved family of signal- modulatingproteins. Immunity 13: 599- 609, 2000. 3 C c

GAM7776 246 LTB4R Akbar, G. K. M.; Dasari, V. R.; Webb, T. E.; Ayyanathan, K.; Pillarisetti,K.; Sandhu, A. K.; Athwal, R. S.; Daniel, J. L.; Ashby, B.; Barnard,E. A.; Kunapuli, S. P.: Molecular cloning of a novel P2 purinoceptorfrom human erythroleukemia cells. J. Biol. Chem. 271: 18363- 18367,1996. 3 C b

GAM7776 246 LTB4R Chen, X.- S.; Sheller, J. R.; Johnson, E. N.; Funk, C. D.: Roleof leukotrienes revealed by targeted disruption of 5- lipoxygenasegene. Nature 372: 179- 182, 1994. 3 C b

GAM7776 246 LTB4R Devchand, P. R.; Keller, H.; Peters, J. M.; Vazquez, M.; Gonzalez,F. J.; Wahli, W.: The PPAR alpha- leukotriene B4 pathway to inflammationcontrol. 3 C b

Nature 384: 39- 43, 1996.

GAM7776 246 LTB4R Kato, K.; Yokomizo, T.; Izumi, T.; Shimizu, T.: Cell- 3 C b
specifictranscriptional regulation of human leukotriene B4 receptor gene.
J.Exp. Med. 192: 413- 420, 2000.

GAM7776 246 LTB4R Owman, C.; Nilsson, C.; Lolait, S. J.: Cloning of cDNA encodinga putative 3 C b
chemoattractant receptor. Genomics 37: 187- 194, 1996.

GAM7776 246 LTB4R Samuelsson, B.; Dahlen, S. E.; Lindgren, J. A.; Rouzer, C. A.;Serhan, C. N.: 3 C b
Leukotrienes and lipoxins: structures, biosynthesis,and biological effects.
Science 237: 1171- 1176, 1987.

GAM7776 246 LTB4R Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C b
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene
and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-
130, 1997.

GAM7776 246 LTB4R Yokomizo, T.; Izumi, T.; Chang, K.; Takuwa, Y.; Shimizu, T.: AG- protein- 3 C b
coupled receptor for leukotriene B4 that mediates chemotaxis. Nature
387:620- 624, 1997.

GAM7776 246 LYZ Camara, V. M.; Harding, J. W.; Prieur, D. J.: Inherited lysozymedeficiency 3 C b
in rabbits: the absence of a primary isozyme of lysozymeas the cause of the
condition. Lab. Invest. 63: 544- 550, 1990.

GAM7776 246 LYZ Canet, D.; Sunde, M.; Last, A. M.; Miranker, A.; Spencer, A.; Robinson,C. 3 C b
V.; Dobson, C. M.: Mechanistic studies of the folding of humanlysozyme and
the origin of amyloidogenic behavior in its disease- relatedvariants.
Biochemistry 38: 6419- 6427, 1999.

GAM7776 246 LYZ Dayhoff, M. O.: Atlas of Protein Sequence and Structure. Lactalbuminand 3 C b
Lysozyme. Washington: National Biomedical Research Foundation(pub.) 5:
1972. Pp. D133- D140.

GAM7776 246 LYZ Fleming, A.: On a remarkable bacteriolytic element found in tissuesand 3 C b
secretions. Proc. Roy. Soc. Ser. B. 93: 306- 317, 1922.

GAM7776 246 LYZ Fleming, A.; Allison, V. D.: Observations on a bacteriolytic 3 C b
substance('lysozyme') found in secretions and tissues. Brit. J. Exp. Path.
3:252- 260, 1922.

GAM7776 246 LYZ Greenwald, R. A.; Cantor, J. O.; Prieur, D. J.; Young, D. M.:Composition of 3 C b
cartilage from lysozyme- deficient rabbits. Biochim.Biophys. Acta 385: 435-
437, 1975.

GAM7776 246 LYZ Neufeld, E. L.: Personal Communication. Bethesda, Maryland 1972. 3 C b

GAM7776 246 LYZ Pepys, M. B.; Hawkins, P. N.; Booth, D. R.; Vigushin, D. M.; Tennent,G. A.; 3 C b
Soutar, A. K.; Totty, N.; Nguyen, O.; Blake, C. C. F.; Terry,C. J.; Feest,
T. G.; Zalin, A. M.; Hsuan, J. J.: Human lysozyme genemutations cause
hereditary systemic amyloidosis. Nature 362: 553- 557,1993.

GAM7776 246 LYZ Peters, C. W. B.; Kruse, U.; Pollwein, R.; Grzeschik, K.- H.; Sippel,A. E.: 3 C b
The human lysozyme gene: sequence organization and chromosomallocalization.
(Abstract) Cytogenet. Cell Genet. 51: 1059 only, 1989.

GAM7776 246 LYZ Prieur, D. J.: Personal Communication. Pullman, Washington 5/13/1975. 3 C b

GAM7776 246 LYZ Prieur, D. J.; Olson, H. M.; Young, D. M.: Lysozyme deficiency- - 3 C b
aninherited disorder of rabbits. Am. J. Path. 77: 283- 296, 1974.

GAM7776 246 LYZ Spitznagel, J. K.; Cooper, M. R.; McCall, A. E.; DeChatelet, L.R.; Welsh, I. 3 C b
R.: Selective deficiency of granules associated withlysozyme and lactoferrin
in human polymorphs (PMN) with reduced microbicidalcapacity. (Abstract) J.
Clin. Invest. 51: 93A only, 1972.

GAM7776 246 LYZ Taniyama, Y.; Kuroki, R.; Omura, F.; Seko, C.; Kikuchi, M.: Evidencefor 3 C b

intramolecular disulfide bond shuffling in the folding of mutanthuman lysozyme. J. Biol. Chem. 266: 6456- 6461, 1991.

GAM7776 246 LYZ Yoshimura, K.; Toibana, A.; Nakahama, K.: Human lysozyme: sequencingof a cDNA, and expression and secretion by Saccharomyces cerevisiae. Biochem.Biophys. Res. Commun. 150: 794- 801, 1988. 3 C b

GAM7776 246 LYZ Zalin, A. M.; Jones, S.; Fitch, N. J. S.; Ramsden, D. B.: Familialnephropathic non- neuropathic amyloidosis: clinical features, immunohistochemistryand chemistry. Quart. J. Med. 81: 945- 956, 1991. 3 C b

GAM7776 246 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999. 3 C c

GAM7776 246 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001. 3 C c

GAM7776 246 MAK Matsushime, H.; Jinno, A.; Takagi, N.; Shibuya, M.: A novel mammalianprotein kinase gene (mak) is highly expressed in testicular germ cellsat and after meiosis. Molec. Cell. Biol. 10: 2261- 2268, 1990. 3 C b

GAM7776 246 MAK Taketo, M.; Jinno, A.; Yamaguchi, S.; Matushime, H.; Shibuya, M.;Seldin, M. F.: Mouse Mak gene for male germ cell- associated kinasemaps to chromosome 13. Genomics 19: 397- 398, 1994. 3 C b

GAM7776 246 MDM2 Boyd, M. T.; Vlatkovic, N.; Haines, D. S.: A novel cellular protein(MTBP) binds to MDM2 and induces a G1 arrest that is suppressed byMDM2. J. Biol. Chem. 275: 31883- 31890, 2000. 3 C c

GAM7776 246 MDM2 Bueso- Ramos, C. E.; Yang, Y.; deLeon, E.; McCown, P.; Stass, S.A.; Albitar, M.: The human MDM- 2 oncogene is overexpressed in leukemias. Blood 82:2617- 2623, 1993. 3 C c

GAM7776 246 MDM2 Bureau, J. F.; Bihl, F.; Brahic, M.; Le Paslier, D.: The genecoding for interferon- gamma is linked to the D12S335 and D12S313 microsatellitesand to the MDM2 gene. Genomics 28: 109- 112, 1995. 3 C c

GAM7776 246 MDM2 Buschmann, T.; Fuchs, S. Y.; Lee, C.- G.; Pan, Z.- Q.; Ronai, Z.: SUMO- 1 modification of Mdm2 prevents its self- ubiquitination andincreases Mdm2 ability to ubiquitinate p53. Cell 101: 753- 762, 2000.Note: Erratum: Cell 107: 549 only, 2001. 3 C c

GAM7776 246 MDM2 de Oca Luna, R. M.; Tabor, A. D.; Eberspaecher, H.; Hulboy, D.L.; Worth, L. L.; Colman, M. S.; Finlay, C. A.; Lozano, G.: The organizationand expression of the mdm2 gene. Genomics 33: 352- 357, 1996. 3 C c

GAM7776 246 MDM2 Fakharzadeh, S.; Trusko, S. P.; George, D. L.: Tumorigenic potentialassociated with enhanced expression of a gene that is amplified ina mouse tumor cell line. EMBO J. 10: 1565- 1569, 1991. 3 C c

GAM7776 246 MDM2 Freedman, D. A.; Epstein, C. B.; Roth, J. C.; Levine, A. J.: Agenetic approach to mapping the p53 binding site in the MDM2 protein. Molec.Med. 3: 248- 259, 1997. 3 C c

GAM7776 246 MDM2 Fuchs, S. Y.; Adler, V.; Buschmann, T.; Yin, Z.; Wu, X.; Jones,S. N.; Ronai, Z.: JNK targets p53 ubiquitination and degradationin nonstressed cells. Genes Dev. 12: 2658- 2663, 1998. 3 C c

GAM7776 246 MDM2 Mayo, L. D.; Donner, D. B.: A phosphatidylinositol 3- kinase/Aktpathway promotes translocation of Mdm2 from the cytoplasm to the nucleus. Proc.Nat. Acad. Sci. 98: 11598- 11603, 2001. 3 C c

GAM7776 246 MDM2 Mitchell, E. L. D.; White, G. R. M.; Santibanez- Koref, M. F.;Varley, J. M.; 3 C c
Heighway, J.: Mapping of gene loci in the q13- q15region of chromosome 12.
Chromosome Res. 3: 261- 262, 1995.

GAM7776 246 MDM2 Momand, J.; Zambetti, G. P.; Olson, D. C.; George, D. L.; Levine,A. J.: The 3 C c
mdm- 2 oncogene product forms a complex with the p53 proteinand inhibits
p53- mediated transactivation. Cell 69: 1237- 1245, 1992.

GAM7776 246 MDM2 Oliner, J. D.; Kinzler, K. W.; Meltzer, P. S.; George, D. L.;Vogelstein, B.: 3 C c
Amplification of a gene encoding a p53- associatedprotein in human sarcomas.
Nature 358: 80- 83, 1992.

GAM7776 246 MDM2 Ries, S.; Biederer, C.; Woods, D.; Shifman, O.; Shirasawa, S.;Sasazuki, T.; 3 C c
McMahon, M.; Oren, M.; McCormick, F.: Opposing effectsof Ras on p53:
transcriptional activation of mdm2 and induction ofp19(ARF). Cell 103: 321-
330, 2000.

GAM7776 246 MDM2 Shenoy, S. K.; McDonald, P. H.; Kohout, T. A.; Lefkowitz, R. J.: Regulation 3 C c
of receptor fate by ubiquitination of activated beta- 2- adrenergicreceptor
and beta- arrestin. Science 294: 1307- 1313, 2001.

GAM7776 246 MDM2 Shieh, S.- Y.; Ikeda, M.; Taya, Y.; Prives, C.: DNA damage- 3 C c
inducedphosphorylation of p53 alleviates inhibition by MDM2. Cell 91: 325-
334,1997.

GAM7776 246 MDM2 Testa, J. R.; Bellacosa, A.: AKT plays a central role in tumorigenesis. 3 C c
Proc.Nat. Acad. Sci. 98: 10983- 10985, 2001.

GAM7776 246 MDM2 Xiao, Z.- X.; Chen, J.; Levine, A. J.; Modjtahedi, N.; Xing, J.;Sellers, W. 3 C c
R.; Livingston, D. M.: Interaction between the retinoblastomaprotein and the
oncoprotein MDM2. Nature 375: 694- 698, 1995.

GAM7776 246 MDM2 Zhang, Y.; Xiong, Y.: A p53 amino- terminal nuclear export signalinhibited 3 C c
by DNA damage- induced phosphorylation. Science 292: 1910- 1915,2001.

GAM7776 246 MDM4 Parant, J.; Chavez- Reyes, A.; Little, N. A.; Yan, W.; Reinke, V.;Jochemsen, 3 C c
A. G.; Lozano, G.: Rescue of embryonic lethality in Mdm4- nullmice by loss
of Trp53 suggests a nonoverlapping pathway with MDM2to regulate p53. Nature
Genet. 29: 92- 95, 2001.

GAM7776 246 MDM4 Shvarts, A.; Bazuine, M.; Dekker, P.; Ramos, Y. F. M.; Steegenga,W. T.; 3 C c
Merckx, G.; van Ham, R. C. A.; van der Houven van Oordt, W.;van der Eb, A.
J.; Jochemsen, A. G.: Isolation and identificationof the human homolog of a
new p53- binding protein, Mdmx. Genomics 43:34- 42, 1997.

GAM7776 246 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 C c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator.
J. Biol. Chem. 275: 5308- 5317, 2000.

GAM7776 246 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 C c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation
of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer
Res. 56: 3446- 3450, 1996.

GAM7776 246 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 C c
bindingprotein, an LXXLL motif- containing protein, functions as a
generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM7776 246 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 C c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-
H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor,
ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for
ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol.
Chem. 274: 34283- 34293, 1999.

GAM7776 246 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 C c
that integrate nuclear receptor signaling through CREB- bindingprotein.
Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM7776 246 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 C c
coding sequences of unidentified human genes. V. The codingsequences of 40
new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM7776 246 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 C c
J. K.: Isolation and characterization of peroxisomeproliferator- activated
receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.
Biol. Chem. 275: 13510- 13516, 2000.

GAM7776 246 NONO Brown, C. J.; Carrel, L.; Willard, H. F.: Expression of genesfrom the human 3 C b
active and inactive X chromosomes. Am. J. Hum. Genet. 60:1333- 1343, 1997.

GAM7776 246 NONO Dong, B.; Horowitz, D. S.; Kobayashi, R.; Krainer, A. R.: Purificationand 3 C b
cDNA cloning of HeLa cell p54(nrb), a nuclear protein with twoRNA
recognition motifs and extensive homology to human splicing factorPSF and
Drosophila NONA/BJ6. Nucleic Acids Res. 21: 4085- 4092, 1993.

GAM7776 246 NONO Nelson, D. L.; Ballabio, A.; Cremers, F.; Monaco, A. P.; Schlessinger,D.: 3 C b
Report of the sixth international workshop on X chromosome mapping1995.
Cytogenet. Cell Genet. 71: 308- 342, 1995.

GAM7776 246 NONO Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller,U.: AFX1 and 3 C b
p54(nrb): fine mapping, genomic structure, and exclusionas candidate genes
of X- linked dystonia parkinsonism. Hum. Genet. 100:569- 572, 1997.

GAM7776 246 NQO1 Benson, A. M.; Hunkeler, M. J.; Talalay, P.: Increase of 3 C c
NAD(P)H:quinonereductase by dietary antioxidants: possible role in
protection againstcarcinogenesis and toxicity. Proc. Nat. Acad. Sci. 77:
5216- 5220,1980.

GAM7776 246 NQO1 Chen, L. Z.; Harris, P. C.; Apostolou, S.; Baker, E.; Holman, K.;Lane, S. 3 C c
A.; Nancarrow, J. K.; Whitmore, S. A.; Stallings, R. L.;Hildebrand, C. E.;
Richards, R. I.; Sutherland, G. R.; Callen, D.F.: A refined physical map of
the long arm of human chromosome 16. Genomics 10:308- 312, 1991.

GAM7776 246 NQO1 Edwards, Y. H.; Hopkinson, D. A.; Carritt, B.: A genetic characterizationof 3 C c
the human diaphorase- 4 deficiency. Ann. Hum. Genet. 47: 97- 105,1983.

GAM7776 246 NQO1 Grzeschik, K.- H.: Assignment of a structural gene for a fourthhuman 3 C c
diaphorase (DIA- 4) to chromosome 16 in man- mouse somatic cellhybrids. Hum.
Genet. 53: 189- 193, 1980.

GAM7776 246 NQO1 Jaiswal, A. K.; McBride, O. W.; Adesnik, M.; Nebert, D. W.: Humandioxin- 3 C c
inducible cytosolic NAD(P)H:menadione oxidoreductase: cDNAsequence and
localization of gene to chromosome 16. J. Biol. Chem. 263:13572- 13578,
1988.

GAM7776 246 NQO1 Kelsey, K. T.; Ross, D.; Traver, R. D.; Christiani, D. C.; Zuo,Z. F.; Spitz, 3 C c
M. R.; Wang, M.; Xu, X.; Lee, B. K.; Schwartz, B. S.;Wiencke, J. K.: Ethnic
variation in the prevalence of a common NAD(P)Hquinone oxidoreductase
polymorphism and its implications for anti- cancerchemotherapy. Brit. J.
Cancer 76: 852- 854, 1997.

GAM7776 246 NQO1 Lavinha, J.; Morrison, N.; Glasgow, L.; Ferguson- Smith, M. A.:Further 3 C c
evidence for the regional localization of human APRT and DIA4on chromosome
16. (Abstract) Cytogenet. Cell Genet. 37: 517 only,1984.

GAM7776 246 NQO1 Moran, J. L.; Siegel, D.; Ross, D.: A potential mechanism underlyingthe 3 C c
increased susceptibility of individuals with a polymorphism

inNAD(P)H:quinone oxidoreductase 1 (NQO1) to benzene toxicity. Proc.Nat. Acad. Sci. 96: 8150- 8155, 1999.

GAM7776 246 NQO1 Povey, S.; Wilson, D.; Edwards, Y. H.: Assignment of a human diaphorase(DIA- 4) to chromosome 16. Ann. Hum. Genet. 43: 349- 353, 1980. 3 C c

GAM7776 246 NQO1 Radjendirane, V.; Joseph, P.; Lee, Y.- H.; Kimura, S.; Klein- Szanto,A. J. P.; Gonzalez, F. J.; Jaiswal, A. K.: Disruption of the DT diaphorase(NQO1) gene in mice leads to increased menadione toxicity. J. Biol.Chem. 273: 7382- 7389, 1998. 3 C c

GAM7776 246 NQO1 Rothman, N.; Smith, M. T.; Hayes, R. B.; Traver, R. D.; Hoener,B.; Campleman, S.; Li, G. L.; Dosemeci, M.; Linet, M.; Zhang, L.;Xi, L.; Wacholder, S.; Lu, W.; Meyer, K. B.; Titenko- Holland, N.;Stewart, J. T.; Yin, S.; Ross, D.: Benzene poisoning, a risk factorfor hematological malignancy, is associated with the NQO1 609C- T mutationand rapid fractional excretion of chlorzoxazone. Cancer Res. 57:2839- 2842, 1997. 3 C c

GAM7776 246 NQO1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 C c

GAM7776 246 NQO1 Smith, M. T.: Benzene, NQO1, and genetic susceptibility to cancer.(Commentary) Proc. Nat. Acad. Sci. 96: 7624- 7626, 1999. 3 C c

GAM7776 246 NQO1 Traver, R. D.; Horikoshi, T.; Danenberg, K. D.; Stadlbauer, T.H.; Danenberg, P. V.; Ross, D.; Gibson, N. W.: NAD(P)H:quinone oxidoreductasegene expression in human colon carcinoma cells: characterization ofa mutation which modulates DT- diaphorase activity and mitomycin sensitivity. CancerRes. 52: 797- 802, 1992. 3 C c

GAM7776 246 NQO1 Traver, R. D.; Siegel, D.; Beall, H. D.; Phillips, R. M.; Gibson,N. W.; Franklin, W. A.; Ross, D.: Characterization of a polymorphismin NAD(P)H: quinone oxidoreductase (DT- diaphorase). Brit. J. Cancer 75:69- 75, 1997. 3 C c

GAM7776 246 NQO1 Zhang, L.; Rothman, N.; Wang, Y.; Hayes, R. B.; Li, G.; Dosemeci,M.; Yin, S.; Kolachana, P.; Titenko- Holland, N.; Smith, M. T.: Increasedaneusomy and long arm deletion of chromosomes 5 and 7 in the lymphocytesof Chinese workers exposed to benzene. Carcinogenesis 19: 1955- 1961,1998. 3 C c

GAM7776 246 NQO1 Zhang, L.; Wang, Y.; Shang, N.; Smith, M. T.: Benzene metabolitesinduce the loss of long arm deletion of chromosomes 5 and 7 in humanlymphocytes. Leukemia Res. 22: 105- 113, 1998. 3 C c

GAM7776 246 NR2E1 Jackson, A.; Panayiotidis, P.; Foroni, L.: The human homologueof the Drosophila tailless gene (TLX): characterization and mappingto a region of common deletion in human lymphoid leukemia on chromosome6q21. Genomics 50: 34- 43, 1998. 3 C c

GAM7776 246 NR2E1 Monaghan, A. P.; Bock, D.; Gass, P.; Schwager, A.; Wolfer, D. P.;Lipp, H.- P.; Schutz, G.: Defective limbic system in mice lackingthe tailless gene. Nature 390: 515- 517, 1997. 3 C c

GAM7776 246 NR2E1 Yu, R. T.; McKeown, M.; Evans, R. M.; Umesono, K.: Relationshipbetween Drosophila gap gene tailless and a vertebrate nuclear receptorTlx. Nature 370: 375- 379, 1994. 3 C c

GAM7776 246 NUMA1 Compton, D. A.; Szilak, I.; Cleveland, D. W.: Primary structureof NuMA, an intranuclear protein that defines a novel pathway forsegregation of proteins at mitosis. J. Cell Biol. 116: 1395- 1408,1992. 3 C c

GAM7776 246 NUMA1 Lydersen, B. K.; Pettijohn, D. E.: Human- specific nuclear proteinthat associates with the polar region of the mitotic apparatus: distributionin a human/hamster hybrid cell. Cell 22: 489- 499, 1980. 3 C c

GAM7776 246 NUMA1 Merdes, A.; Ramyar, K.; Vechio, J. D.; Cleveland, D. W.: A complexof NuMA 3 C c

and cytoplasmic dynein is essential for mitotic spindle assembly. Cell 87:447- 458, 1996.

GAM7776 246 NUMA1 Sparks, C. A.; Bangs, P. L.; McNeil, G. P.; Lawrence, J. B.; Fey,E. G.: 3 C c Assignment of the nuclear mitotic apparatus protein NuMA geneto human chromosome 11q13. Genomics 17: 222- 224, 1993.

GAM7776 246 NUMA1 Wells, R. A.; Catzavelos, C.; Kamel- Reid, S.: Fusion of retinoicacid 3 C c receptor alpha to NuMA, the nuclear mitotic apparatus protein,by a variant translocation in acute promyelocytic leukaemia. NatureGenet. 17: 109- 113, 1997.

GAM7776 246 NUMA1 Wiese, C.; Wilde, A.; Moore, M. S.; Adam, S. A.; Merdes, A.; Zheng,Y.: Role 3 C c of importin- beta in coupling Ran to downstream targets inmicrotubule assembly. Science 291: 653- 656, 2001.

GAM7776 246 NUMA1 Yang, C. H.; Lambie, E. J.; Snyder, M.: NuMA: an unusually longcoiled- coil 3 C c related protein in the mammalian nucleus. J. Cell Biol. 116:1303- 1317, 1992.

GAM7776 246 ORC1L Eki, T.; Okumura, K.; Amin, A.; Ishiai, M.; Abe, M.; Nogami, M.;Taguchi, H.; 3 C b Hurwitz, J.; Murakami, Y.; Hanaoka, F.: Mapping of thehuman homologue (ORC1L) of the yeast origin recognition complex subunit1 gene to chromosome band 1p32. Genomics 36: 559- 561, 1996.

GAM7776 246 ORC1L Gavin, K. A.; Hidaka, M.; Stillman, B.: Conserved initiator proteinsin 3 C b eukaryotes. Science 270: 1667- 1671, 1995.

GAM7776 246 ORC1L Mendez, J.; Zou- Yang, H.; Kim, S.- Y.; Hidaka, M.; Tansey, W. P.;Stillman, 3 C b B.: Human origin recognition complex large subunit is degradedby ubiquitin-mediated proteolysis after initiation of DNA replication. Molec.Cell 9: 481-491, 2002.

GAM7776 246 ORC1L Ohtani, K.; DeGregori, J.; Leone, G.; Herendeen, D. R.; Kelly,T. J.; Nevins, 3 C b J. R.: Expression of the HsOrc1 gene, a human ORC1homolog, is regulated by cell proliferation via the E2F transcriptionfactor. Molec. Cell. Biol. 16: 6977- 6984, 1996.

GAM7776 246 P2RY1 Ayyanathan, K.; Naylor, S. L.; Kunapuli, S. P.: Structural 3 C c characterizationand fine chromosomal mapping of the human P2Y(1) purinergic receptorgene (P2RY1). Somat. Cell Molec. Genet. 22: 419- 424, 1996.

GAM7776 246 P2RY1 Ayyanathan, K.; Webbs, T. E.; Sandhu, A. K.; Athwal, R. S.; Barnard,E. A.; 3 C c Kunapuli, S. P.: Cloning and chromosomal localization of thehuman P2Y1 purinoceptor. Biochem. Biophys. Res. Commun. 218: 783- 788,1996.

GAM7776 246 P2RY1 Leon, C.; Hechler, B.; Freund, M.; Eckly, A.; Vial, C.; Ohlmann,P.; Dierich, 3 C c A.; LeMeur, M.; Cazenave, J.- P.; Gachet, C.: Defectiveplatelet aggregation and increased resistance to thrombosis in purinergicP2Y1 receptor- null mice. J. Clin. Invest. 104: 1731- 1737, 1999.

GAM7776 246 P2RY1 Leon, C.; Hechler, B.; Vial, C.; Leray, C.; Cazenave, J.- P.; Gachet,C.: The 3 C c P2Y(1) receptor is an ADP receptor antagonized by ATP andexpressed in platelets and megakaryoblastic cells. FEBS Letts. 403:26- 30, 1997.

GAM7776 246 P2RY1 Leon, C.; Vial, C.; Cazenave, J.- P.; Gachet, C.: Cloning and sequencingof a 3 C c human cDNA encoding endothelial P2Y1 purinoceptor. Gene 171:295- 297, 1996.

GAM7776 246 P2RY1 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C c Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-130, 1997.

GAM7776 246 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack 3 C b of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary

cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991.

GAM7776 246 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; 3 C b
Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine
nucleotide synthesis on human chromosome 4 are closelylinked and divergently
transcribed. J. Biol. Chem. 269: 5313- 5321,1994.

GAM7776 246 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of 3 C b
three human multifunctional de novo purine biosyntheticgenes by functional
complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920,
1990.

GAM7776 246 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C b
Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding
sequences of unidentified human genes. VII. The completesequences of 100 new
cDNA clones from brain which can code for largeproteins in vitro. DNA Res.
4: 141- 150, 1997.

GAM7776 246 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM7776 246 PCDHB16 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel 3 C c
cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913,
1997.

GAM7776 246 PCDHB16 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of 3 C c
the coding sequences of unidentified human genes. XVIII.The complete
sequences of 100 new cDNA clones from brain which codefor large proteins in
vitro. DNA Res. 7: 273- 281, 2000.

GAM7776 246 PCDHB16 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM7776 246 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 C b
protocadherin- beta one- exon gene families show high
evolutionaryconservation, despite the difference in gene number. FEBS Lett.
495:120- 125, 2001.

GAM7776 246 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C b
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.:
Comparative DNA sequence analysis of mouse and human protocadheringene
clusters. Genome Res. 11: 389- 404, 2001.

GAM7776 246 PDZK1 Custer, M.; Spindler, B.; Verrey, F.; Murer, H.; Biber, J.: Identificationof 3 C b
a new gene product (diphor- 1) regulated by dietary phosphate. Am.J.
Physiol. 273: F801- F806, 1997.

GAM7776 246 PDZK1 Ikemoto, M.; Arai, H.; Feng, D.; Tanaka, K.; Aoki, J.; Dohmae,N.; Takio, K.; 3 C b
Adachi, H.; Tsujimoto, M.; Inoue, K.: Identificationof a PDZ- domain-
containing protein that interacts with the scavengerreceptor class B type I.
Proc. Nat. Acad. Sci. 97: 6538- 6543, 2000.

GAM7776 246 PDZK1 Kocher, O.; Comella, N.; Gilchrist, A.; Pal, R.; Tognazzi, K.;Brown, L. F.; 3 C b
Knoll, J. H. M.: PDZK1, a novel PDZ domain- containingprotein up- regulated
in carcinomas and mapped to chromosome 1q21,interacts with cMOAT (MRP2), the
multidrug resistance- associated protein. Lab.Invest. 79: 1161- 1170, 1999.

GAM7776 246 PDZK1 Kocher, O.; Comella, N.; Tognazzi, K.; Brown, L. F.: Identificationand 3 C b
partial characterization of PDZK1: a novel protein containingPDZ interaction

domains. Lab. Invest. 78: 117- 125, 1998.

GAM7776 246 PDZK1 Wang, S.; Yue, H.; Derin, R. B.; Guggino, W. B.; Li, M.: Accessoryprotein facilitated CFTR- CFTR interaction, a molecular mechanism topotentiate the chloride channel activity. Cell 103: 169- 179, 2000. 3 C b

GAM7776 246 PDZK1 White, K. E.; Biber, J.; Murer, H.; Econs, M. J.: A PDZ domain-containingprotein with homology to Diphor- 1 maps to human chromosome 1q21. Ann.Hum. Genet. 62: 287- 290, 1998. 3 C b

GAM7776 246 PER2 Albrecht, U.; Sun, Z. S.; Eichele, G.; Lee, C. C.: A differentialresponse to two putative mammalian circadian regulators, mper1 andmper2, to light. Cell 91: 1055- 1064, 1997. 3 C b

GAM7776 246 PER2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C b

GAM7776 246 PER2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531-2534, 1999. 3 C b

GAM7776 246 PER2 Reick, M.; Garcia, J. A.; Dudley, C.; McKnight, S. L.: NPAS2:an analog of clock operative in the mammalian forebrain. Science 293:506- 509, 2001. 3 C b

GAM7776 246 PER2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.; Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock. Science 288: 1013- 1019, 2000. 3 C b

GAM7776 246 PER2 Shearman, L. P.; Zylka, M. J.; Weaver, D. R.; Kolakowski, L. F.,Jr.; Reppert, S. M.: Two period homologs: circadian expression andphotic regulation in the suprachiasmatic nuclei. Neuron 19: 1261- 1269,1997. 3 C b

GAM7776 246 PER2 Toh, K. L.; Jones, C. R.; He, Y.; Eide, E. J.; Hinz, W. A.; Virshup,D. M.; Ptacek, L. J.; Fu, Y.- H.: An hPer2 phosphorylation site mutationin familial advanced sleep phase syndrome. Science 291: 1040- 1043,2001. 3 C b

GAM7776 246 PER2 Zheng, B.; Albrecht, U.; Kaasik, K.; Sage, M.; Lu, W.; Vaishnav,S.; Li, Q.; Sun, Z. S.; Eichele, G.; Bradley, A.; Lee, C. C.: Nonredundantroles of the mPer1 and mPer2 genes in the mammalian circadian clock. Cell 105:683- 694, 2001. 3 C b

GAM7776 246 PER2 Zheng, B.; Larkin, D. W.; Albrecht, U.; Sun, Z. S.; Sage, M.; Eichele,G.; Lee, C. C.; Bradley, A.: The mPer2 gene encodes a functionalcomponent of the mammalian circadian clock. Nature 400: 169- 173,1999. 3 C b

GAM7776 246 PIK3CD Chantry, D.; Vojtek, A.; Kashishian, A.; Holtzman, D. A.; Wood,C.; Gray, P. W.; Cooper, J. A.; Hoekstra, M. F.: p110- delta, a novelphosphatidylinositol 3- kinase catalytic subunit that associates withp85 and is expressed predominantly in leukocytes. J. Biol. Chem. 272:19236- 19241, 1997. 3 C b

GAM7776 246 PIK3CD Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.;Peskett, E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Waterfield, M.D.; Smith, A. J. H.; Vanhaesebroeck, B.: Impaired B and T cell antigenreceptor signaling in p110- delta PI 3- kinase mutant mice. Science 297:1031- 1034, 2002. 3 C b

GAM7776 246 PIK3CD Seki, N.; Nimura, Y.; Ohira, M.; Saito, T.; Ichimiya, S.; Nomura,N.; Nakagawara, A.: Identification and chromosome assignment of ahuman gene encoding a novel phosphatidylinositol- 3 kinase. DNA Res. 4:355- 358, 1997. 3 C b

GAM7776 246 PIK3CD Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne,P. H.; 3 C b

Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield,M. D.: p110- delta, a novel phosphoinositide 3- kinase in leukocytes. Proc.Nat. Acad. Sci. 94: 4330- 4335, 1997.

GAM7776 246 PKNOX1 Berthelsen, J.; Viggiano, L.; Schulz, H.; Ferretti, E.; Consalez,G. G.; Rocchi, M.; Blasi, F.: PKNOX1, a gene encoding PREP1, a newregulator of Pbx activity, maps on human chromosome 21q22.3 and murinechromosome 17B/C. Genomics 47: 323- 324, 1998. 3 C b

GAM7776 246 PKNOX1 Chen, H.; Rossier, C.; Nakamura, Y.; Lynn, A.; Chakravarti, A.;Antonarakis, S. E.: Cloning of a novel homeobox- containing gene,PKNOX1, and mapping to human chromosome 21q22.3. Genomics 41: 193- 200,1997. 3 C b

GAM7776 246 PON1 Adkins, S.; Gan, K. N.; Mody, M.; La Du, B. N.: Molecular basisfor the polymorphic forms of human serum paraoxonase/arylesterase:glutamine or arginine at position 191, for the respective A and Ballozymes. Am. J. Hum. Genet. 52: 598- 608, 1993. 3 C b

GAM7776 246 PON1 Antikainen, M.; Murtomaki, S.; Syvanne, M.; Pahlman, R.; Tahvanainen,E.; Jauhiainen, M.; Frick, M. H.; Ehnholm, C.: The gln- arg191 polymorphismof the human paraoxonase gene (HUMPONA) is not associated with therisk of coronary artery disease in Finns. J. Clin. Invest. 98: 883- 885,1996. 3 C b

GAM7776 246 PON1 Augustinsson, K.- B.; Henricson, B.: A genetically controlled esterasein rat plasma. Biochim. Biophys. Acta 124: 323- 331, 1966. 3 C b

GAM7776 246 PON1 Barbieri, M.; Bonafe, M.; Marfella, R.; Ragno, E.; Giugliano, D.;Franceschi, C.; Paolisso, G.: LL- paraoxonase genotype is associatedwith a more severe degree of homeostasis model assessment IR in healthysubjects. J. Clin. Endocr. Metab. 87: 222- 225, 2002. 3 C b

GAM7776 246 PON1 Brophy, V. H.; Jampsa, R. L.; Clendenning, J. B.; McKinstry, L.A.; Jarvik, G. P.; Furlong, C. E.: Effects of 5- prime regulatory- regionpolymorphisms on paraoxonase- gene (PON1) expression. Am. J. Hum.Genet. 68: 1428- 1436, 2001. 3 C b

GAM7776 246 PON1 Cherry, N.; Mackness, M.; Durrington, P.; Povey, A.; Dippnall,M.; Smith, T.; Mackness, B.: Paraoxonase (PON1) polymorphisms infarmers attributing ill health to sheep dip. Lancet 359: 763- 764,2002. 3 C b

GAM7776 246 PON1 Clendenning, J. B.; Humbert, R.; Green, E. D.; Wood, C.; Traver,D.; Furlong, C. E.: Structural organization of the human PON1 gene. Genomics 35:586- 589, 1996. 3 C b

GAM7776 246 PON1 Coates, P. M.; Mestriner, M. A.; Hopkinson, D. A.: A preliminaryinterpretation of the esterase isozymes of human tissues. Ann. Hum.Genet. 39: 1- 20, 1975. 3 C b

GAM7776 246 PON1 Davies, H. G.; Richter, R. J.; Keifer, M.; Broomfield, C. A.; Sowalla,J.; Furlong, C. E.: The effect of the human serum paraoxonase polymorphismis reversed with diazoxon, soman and sarin. Nature Genet. 14: 334- 336,1996. 3 C b

GAM7776 246 PON1 Deakin, S.; Leviev, I.; Nicaud, V.; Meynet, M.- C. B.; Tiret, L.;James, R. W.: Paraoxonase- 1 L55M polymorphism is associated withan abnormal oral glucose tolerance test and differentiates high riskcoronary disease families. J. Clin. Endocr. Metab. 87: 1268- 1273,2002. 3 C b

GAM7776 246 PON1 Eckerson, H. W.; Romson, J.; Wyte, C.; La Du, B. N.: The humanserum paraoxonase polymorphism: identification of phenotypes by theirresponse to salts. Am. J. Hum. Genet. 35: 214- 227, 1983. 3 C b

GAM7776 246 PON1 Eckerson, H. W.; Wyte, C. M.; La Du, B. N.: The human serum paraoxonase/arylesterasepolymorphism. Am. J. Hum. Genet. 35: 1126- 1136, 1983. 3 C b

GAM7776 246 PON1 Eiberg, H.; Mohr, J.: Linkage relations of the paraoxonase polymorphismwith 43 marker systems. (Abstract) Cytogenet. Cell Genet. 25: 150,1979. 3 C b

GAM7776 246 PON1 Eiberg, H.; Mohr, J.; Schmiegelow, K.; Nielsen, L. S.; Williamson,R.: Linkage relationships of paraoxonase (PON) with other markers:indication of PON- cystic fibrosis synteny. Clin. Genet. 28: 265- 271,1985. 3 C b

GAM7776 246 PON1 Furlong, C. E.; Richter, R. J.; Chapline, C.; Crabb, J. W.: Purificationof rabbit and human serum paraoxonase. Biochemistry 30: 10133- 10140,1991. 3 C b

GAM7776 246 PON1 Furlong, C. E.; Richter, R. J.; Seidel, S. L.; Motulsky, A. G.: Role of genetic polymorphism of human plasma paraoxonase/arylesterasein hydrolysis of the insecticide metabolites chlorpyrifos oxon andparaoxon. Am. J. Hum. Genet. 43: 230- 238, 1988. 3 C b

GAM7776 246 PON1 Garin, M.- C. B.; James, R. W.; Dussoix, P.; Blanche, H.; Passa,P.; Froguel, P.; Ruiz, J.: Paraoxonase polymorphism met- leu54 isassociated with modified serum concentrations of the enzyme: a possiblelink between the paraoxonase gene and increased risk of cardiovasculardisease in diabetes. J. Clin. Invest. 99: 62- 66, 1997. 3 C b

GAM7776 246 PON1 Geldmacher- von Mallinckrodt, M.: Polymorphism of human serumparaoxonase. Hum. Genet. 45 (suppl. 1): 65- 68, 1978. 3 C b

GAM7776 246 PON1 Geldmacher- von Mallinckrodt, M.; Lindorft, H. H.; Petenyi, M.;Flugel, M.; Fischer, T.; Hiller, T.: Genetisch determinierter Polymorphismusde menschlichen Serum- Paroxonase (E.C.3.1.1.2). Humangenetik 17:331- 335, 1973. 3 C b

GAM7776 246 PON1 Hassett, C.; Richter, R. J.; Humbert, R.; Chapline, C.; Crabb,J. W.; Omiecinski, C. J.; Furlong, C. E.: Characterization of cDNAclones encoding rabbit and human serum paraoxonase: the mature proteinretains its signal sequence. Biochemistry 30: 10141- 10149, 1991. 3 C b

GAM7776 246 PON1 Humbert, R.; Adler, D. A.; Disteche, C. M.; Hassett, C.; Omiecinski,C. J.; Furlong, C. E.: The molecular basis of the human serum paraoxonaseactivity polymorphism. Nature Genet. 3: 73- 76, 1993. 3 C b

GAM7776 246 PON1 Ito, T.; Yasue, H.; Yoshimura, M.; Nakamura, S.; Nakayama, M.;Shimasaki, Y.; Harada, E.; Mizuno, Y.; Kawano, H.; Ogawa, H.: Paraoxonasegene gln192- to-arg (Q192R) polymorphism is associated with coronaryartery spasm. Hum. Genet. 110: 89- 94, 2002. 3 C b

GAM7776 246 PON1 Kao, Y.- L.; Donaghue, K.; Chan, A.; Knight, J.; Silink, M.: Avariant of paraoxonase (PON1) gene is associated with diabetic retinopathyin IDDM. J. Clin. Endocr. Metab. 83: 2589- 2592, 1998. 3 C b

GAM7776 246 PON1 La Du, B. N.: The human serum paraoxonase/arylesterase polymorphism.(Editorial) Am. J. Hum. Genet. 43: 227- 229, 1988. 3 C b

GAM7776 246 PON1 Li, W.- F.; Furlong, C. E.; Costa, L. G.: Paraoxonase protectsagainst chlorpyrifos toxicity in mice. Toxic. Lett. 76: 219- 226,1995. 3 C b

GAM7776 246 PON1 Li, W.- F.; Matthews, C.; Disteche, C. M.; Costa, L. G.; Furlong,C. E.: Paraoxonase (Pon1) gene in mice: sequencing, chromosomal localizationand developmental expression. Pharmacogenetics 7: 137- 144, 1997. 3 C b

GAM7776 246 PON1 Mackness, B.; Mackness, M. I.; Arrol, S.; Turkie, W.; Durrington,P. N.: Effect of the human serum paraoxonase 55 and 192 genetic polymorphismson the protection by high density lipoprotein against low densitylipoprotein oxidative modification. FEBS Lett. 423: 57- 60, 1998. 3 C b

GAM7776 246 PON1 Mochizuki, H.; Scherer, S. W.; Xi, T.; Nickle, D. C.; Majer, M.;Huizenga, J. J.; Tsui, L.- C.; Prochazka, M.: Human PON2 gene at 7q21.3:cloning, multiple 3 C b

mRNA forms, and missense polymorphisms in the codingsequence. Gene 213: 149-157, 1998.

GAM7776 246 PON1 Mueller, R. F.; Hornung, S.; Furlong, C. E.; Anderson, J.; Giblett,E. R.; Motulsky, A. G.: Plasma paraoxonase polymorphism: a new enzymeassay, population, family, biochemical, and linkage studies. Am.J. Hum. Genet. 35: 393- 408, 1983. 3 C b

GAM7776 246 PON1 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J. Clin. Invest. 99: 2005- 2019, 1997. 3 C b

GAM7776 246 PON1 Neel, J. V.; Tanis, R. J.; Migliazza, E. C.; Spielman, R. S.;Salzano, F. M.; Oliver, W. J.; Morrow, M.; Bachofer, S.: Geneticstudies of the Macushi and Wapishana Indians. I. Rare genetic variantsand a 'private polymorphism' of esterase A. Hum. Genet. 36: 81- 108,1977. 3 C b

GAM7776 246 PON1 Nielsen, A.; Eiberg, H.; Mohr, J.: Number of loci responsiblefor the inheritance of high and low activity of paraoxonase. Clin.Genet. 29: 216-221, 1986. 3 C b

GAM7776 246 PON1 Odawara, M.; Tachi, Y.; Yamashita, K.: Paraoxonase polymorphismGln192- Arg is associated with coronary heart disease in Japanese noninsulin-dependentdiabetes mellitus. J. Clin. Endocr. Metab. 82: 2257- 2260, 1997. 3 C b

GAM7776 246 PON1 Ortigoza- Ferado, J.; Richter, R. J.; Hornung, S. K.; Motulsky,A. G.; Furlong, C. E.: Paraoxon hydrolysis in human serum mediatedby a genetically variable arylesterase and albumin. Am. J. Hum. Genet. 36:295- 305, 1984. 3 C b

GAM7776 246 PON1 Paolisso, G.; Manzella, D.; Tagliamonte, M. R.; Barbieri, M.;Marfella, R.; Zito, G.; Bonafe, M.; Giugliano, D.; Franceschi, C.;Varricchio, M.: The BB-paraoxonase genotype is associated with impairedbrachial reactivity after acute hypertriglyceridemia in healthy subjects. J.Clin. Endocr. Metab. 86: 1078- 1082, 2001. 3 C b

GAM7776 246 PON1 Playfer, J. R.; Eze, L. C.; Bullen, M. F.; Evans, D. A. P.: Geneticpolymorphism and interethnic variability of plasma paroxonase activity. J.Med. Genet. 13: 337- 342, 1976. 3 C b

GAM7776 246 PON1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 C b

GAM7776 246 PON1 Schmiegelow, K.; Eiberg, H.; Tsui, L.- C.; Buchwald, M.; Phelan,P. D.; Williamson, R.; Warwick, W.; Niebuhr, E.; Mohr, J.; Schwartz,M.; Koch, C.: Linkage between the loci for cystic fibrosis and paraoxonase. Clin.Genet. 29: 374- 377, 1986. 3 C b

GAM7776 246 PON1 Serrato, M.; Marian, A. J.: A variant of human paraoxonase/arylesterase(HUMPONA) gene is a risk factor for coronary artery disease. J. Clin.Invest. 96: 3005- 3008, 1995. 3 C b

GAM7776 246 PON1 Shih, D. M.; Gu, L.; Xia, Y.- R.; Navab, M.; Li, W.- F.; Hama, S.;Castellani, L. W.; Furlong, C. E.; Costa, L. G.; Fogelman, A. M.;Lusis, A. J.: Mice lacking serum paraoxonase are susceptible to organophosphatetoxicity and atherosclerosis. Nature 394: 284- 287, 1998. 3 C b

GAM7776 246 PON1 Simpson, N. E.: Serum arylesterase levels of activity in twinsand their parents. Am. J. Hum. Genet. 23: 375- 382, 1971. 3 C b

GAM7776 246 PON1 Sorenson, R. C.; Primo- Parmo, S. L.; Camper, S.; La Du, B. N.: The genetic mapping and gene structure of mouse paraoxonase/arylesterase. Genomics 30:431- 438, 1995. 3 C b

GAM7776 246 PON1 Tashian, R. E.: Genetic variation and evolution of the carboxylicesterases and carbonic anhydrases of primate erythrocytes. Am. J.Hum. Genet. 17: 257-272, 1965. 3 C b

GAM7776 246 PON1 Tashian, R. E.; Shaw, M. W.: Inheritance of an erythrocyte acetylesterasevariant of man. Am. J. Hum. Genet. 14: 295- 300, 1962. 3 C b

GAM7776 246 PON1 Tsui, L.- C.; Buchwald, M.; Barker, D.; Braman, J. C.; Knowlton,R.; Schumm, J. W.; Eiberg, H.; Mohr, J.; Kennedy, D.; Plavsic, N.;Zsiga, M.; Markiewicz, D.; Akots, G.; Brown, V.; Helms, C.; Gravius,T.; Parker, C.; Rediker, K.; Donis- Keller, H.: Cystic fibrosis locusdefined by a genetically linked polymorphic DNA marker. Science 230:1054- 1057, 1985. 3 C b

GAM7776 246 PON1 Watson, C. E.; Draganov, D. I.; Billecke, S. S.; Bisgaier, C.L.; La Du, B. N.: Rabbits possess a serum paraoxonase polymorphismsimilar to the human Q192R. Pharmacogenetics 11: 123- 134, 2001. 3 C b

GAM7776 246 PON1 Yamasaki, Y.; Sakamoto, K.; Watada, H.; Kajimoto, Y.; Hori, M.: The arg- 192 isoform of paraoxonase with low sarin- hydrolyzing activityis dominant in the Japanese. Hum. Genet. 101: 67- 68, 1997. 3 C b

GAM7776 246 POU2AF1 Casellas, R.; Jankovic, M.; Meyer, G.; Gazumyan, A.; Luo, Y.; Roeder,R. G.; Nussenzweig, M. C.: OcaB is required for normal transcriptionand V(D)J recombination of a subset of immunoglobulin kappa genes. Cell 110:575- 585, 2002. 3 C b

GAM7776 246 POU2AF1 Gstaiger, M.; Knoepfel, L.; Georgiev, O.; Schaffner, W.; Hovens,C. M.: A B- cell coactivator of octamer- binding transcription factors. Nature 373:360-362, 1995. 3 C b

GAM7776 246 POU2AF1 Junker, S.; Brondum- Nielsen, K.; Newell, J. W.; Matthias, P.; Tommerup,N.: Assignment of the human gene for Oct- binding factor- 1 (OBF1),a B- cell-specific coactivator of octamer- binding transcription factors1 and 2, to 11q23.1 by somatic cell hybridization and in situ hybridization. Genomics 33:143- 145, 1996. 3 C b

GAM7776 246 POU2AF1 Luo, Y.; Roeder, R. G.: Cloning, functional characterization,and mechanism of action of the B- cell- specific transcriptional activatorOCA- B. Molec. Cell. Biol. 15: 4115- 4124, 1995. 3 C b

GAM7776 246 POU2AF1 Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink,A. G.; Matthias, P.: B cell development and immunoglobulin gene transcriptionin the absence of Oct- 2 and OBF- 1. Nature Immun. 2: 69- 74, 2001. 3 C b

GAM7776 246 POU2AF1 Staudt, L. M.; Lenardo, M. J.: Immunoglobulin gene transcription. Ann.Rev. Immun. 9: 373- 398, 1991. 3 C b

GAM7776 246 POU2AF1 Strubin, M.; Newell, J. W.; Matthias, P.: OBF- 1, a novel B cell-specificcoactivator that stimulates immunoglobulin promoter activity throughassociation with octamer- binding proteins. Cell 80: 497- 506, 1995. 3 C b

GAM7776 246 POU2AF1 Tomilin, A.; Remenyi, A.; Lins, K.; Bak, H.; Leidel, S.; Vriend,G.; Wilmanns, M.; Scholer, H. R.: Synergism with the coactivatorOBF- 1 (OCA- B, BOB- 1) is mediated by a specific POU dimer configuration. Cell 103:853-864, 2000. 3 C b

GAM7776 246 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor integrity, and rhodopsin dephosphorylation in mice lackingboth protein phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21: 8605- 8614, 2001. 3 C b

GAM7776 246 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; Nathans, J.: Identification and characterization of a conservedfamily of 3 C b

protein serine/threonine phosphatases homologous to Drosophilaretinal degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997.

GAM7776 246 PPID Kieffer, L. J.; Seng, T. W.; Li, W.; Osterman, D. G.; Handschumacher,R. E.; 3 C c
Bayney, R. M.: Cyclophilin- 40, a protein with homology tothe P59 component of the steroid receptor complex: cloning of thecDNA and further characterization. J. Biol. Chem. 268: 12303- 12310,1993.

GAM7776 246 PPID Kieffer, L. J.; Thalhammer, T.; Handschumacher, R. E.: Isolationand 3 C c
characterization of a 40- kDa cyclophilin- related protein. J.Biol. Chem. 267: 5503- 5507, 1992.

GAM7776 246 PPID Ratajczak, T.; Woollatt, E.; Kumar, P.; Ward, B. K.; Minchin, R.F.; Baker, 3 C c
E.: Cyclophilin 40 (PPID) gene map position 4q31.3. ChromosomeRes. 5: 151 only, 1997.

GAM7776 246 PPID Yokoi, H.; Shimizu, Y.; Anazawa, H.; Lefebvre, C. A.; Korneluk,R. G.; Ikeda; 3 C c
J.- E.: The structure and complete nucleotide sequenceof the human cyclophilin 40 (PPID) gene. Genomics 35: 448- 455, 1996.

GAM7776 246 PRKR Barber, G. N.; Edelhoff, S.; Katze, M. G.; Disteche, C. M.: 3 C b
Chromosomalassignment of the interferon- inducible double- stranded RNA-dependentprotein kinase (PRKR) to human chromosome 2p21- p22 and mouse chromosome17 E2. Genomics 16: 765- 767, 1993.

GAM7776 246 PRKR Ben- Asouli, Y.; Banai, Y.; Pel- Or, Y.; Shir, A.; Kaempfer, R.:Human 3 C b
interferon- gamma mRNA autoregulates its translation througha pseudoknot that activates the interferon- inducible protein kinasePKR. Cell 108: 221-232, 2002.

GAM7776 246 PRKR Kuhen, K. L.; Shen, X.; Carlisle, E. R.; Richardson, A.L.; Weier,H.- U. G.; 3 C b
Tanaka, H.; Samuel, C. E.: Structural organization of thehuman gene (PKR) encoding an interferon- inducible RNA- dependent proteinkinase (PKR) and differences from its mouse homolog. Genomics 36:197- 201, 1996.

GAM7776 246 PRKR Kuhen, K. L.; Shen, X.; Samuel, C. E.: Mechanism of interferonaction: 3 C b
sequence of the human interferon- inducible RNA- dependent proteinkinase (PKR) deduced from genomic clones. Gene 178: 191- 193, 1996.

GAM7776 246 PRKR Meurs, E.; Chong, K.; Galabru, J.; Shaun, N.; Thomas, S. B.; Kerr,I. M.; 3 C b
Williams, B. R. G.; Hovanessian, A. G.: Molecular cloningand characterization of the human double- stranded RNA- activated proteinkinase induced by interferon. Cell 62: 379- 390, 1990.

GAM7776 246 PRKR Peel, A. L.; Rao, R. V.; Cottrell, B. A.; Hayden, M. R.; Ellerby,L. M.; 3 C b
Bredesen, D. E.: Double- stranded RNA- dependent protein kinase,PKR, binds preferentially to Huntington's disease (HD) transcriptsand is activated in HD tissue. Hum. Molec. Genet. 10: 1531- 1538,2001.

GAM7776 246 PRKR Squire, J.; Meurs, E. F.; Chong, K. L.; McMillan, N. A. J.; Hovanessian,A. 3 C b
G.; Williams, B. R. G.: Localization of the human interferon- induced,ds-RNA activated p68 kinase gene (PRKR) to chromosome 2p21- p22. Genomics 16:768- 770, 1993.

GAM7776 246 PRKR Taylor, D. R.; Shi, S. T.; Romano, P. R.; Barber, G. N.; Lal, M.M. C.: 3 C b
Inhibition of the interferon- inducible protein kinase PKRby HCV E2 protein. Science 285: 107- 110, 1999.

GAM7776 246 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 C b
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.:
Genomicorganization, comparative analysis, and genetic polymorphisms of thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733, 2001.

GAM7776 246 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 C b
Chen, S. G.: Expression and structural characterizationof the recombinant
human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM7776 246 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 C b
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.;
Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-
deficient mice is associated with upregulation of thenovel PrP- like protein
doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM7776 246 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 C b
T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin
the prion- like protein gene (Prnd) and their implications inhuman prion
diseases, Alzheimer's disease and other neurological disorders. Hum.Genet.
109: 319- 325, 2001.

GAM7776 246 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 C b
P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-
glycosylated, glycosylphosphatidylinositol- anchored protein:expression in
testis and ectopic production in the brains of Prnp(0/0)mice predisposed to
Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM7776 246 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 C b
915, 1999.

GAM7776 246 PRPF31 Al- Maghtheh, M.; Vithana, E.; Tarttelin, E.; Jay, M.; Evans, K.;Moore, T.; 3 C c
Bhattacharya, S.; Inglehearn, C. F.: Evidence for a majorretinitis
pigmentosa locus on 19q13.4 (RP11), and association witha unique bimodal
expressivity phenotype. Am. J. Hum. Genet. 59:864- 871, 1996.

GAM7776 246 PRPF31 Vithana, E. N.; Abu- Safieh, L.; Allen, M. J.; Carey, A.; Papaioannou,M.; 3 C c
Chakarova, C.; Al- Maghtheh, M.; Ebenezer, N. D.; Willis, C.; Moore,A. T.;
Bird, A. C.; Hunt, D. M.; Bhattacharya, S. S.: A human homologof yeast pre-
mRNA splicing gene, PRP31, underlies autosomal dominantretinitis pigmentosa
on chromosome 19q13.4 (RP11). Molec. Cell 8:375- 381, 2001.

GAM7776 246 PRPF31 Weidenhammer, E. M.; Singh, M.; Ruiz- Noriega, M.; Woolford, J.L., Jr.: The 3 C c
PRP31 gene encodes a novel protein required for pre- mRNAsplicing in
Saccharomyces cerevisiae. Nucleic Acids Res. 24: 1164- 1170,1996.

GAM7776 246 PSMD9 Thomas, M. K.; Yao, K.- M.; Tenser, M. S.; Wong, G. G.; Habener,J. F.: 3 C c
Bridge- 1, a novel PDZ- domain coactivator of E2A- mediated regulationof
insulin gene transcription. Molec. Cell. Biol. 19: 8492- 8504,1999.

GAM7776 246 PSMD9 Watanabe, T. K.; Saito, A.; Suzuki, M.; Fujiwara, T.; Takahashi,E.; 3 C c
Slaughter, C. A.; DeMartino, G. N.; Hendil, K. B.; Chung, C. H.;Tanahashi,
N.; Tanaka, K.: cDNA cloning and characterization of ahuman proteasomal
modulator subunit, p27 (PSMD9). Genomics 50: 241- 250,1998.

GAM7776 246 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; 3 C b
Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly,
F.: Characterization of new mutations in the codingsequence and 5- prime-
untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum.
Genet. 108: 148- 155, 2001.

GAM7776 246 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: 3 C b
Molecular cloning and expression of human prostacyclin synthase.
Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994.

GAM7776 246 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; 3 C b
Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.;
Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences,

gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996.

GAM7776 246 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin 3 C b
synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996.

GAM7776 246 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, 3 C b
M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996.

GAM7776 246 PTK2 Andre, E.; Becker- Andre, M.: Expression of an N- terminally truncatedform 3 C b
of human focal adhesion kinase in brain. Biochem. Biophys. Res.Commun. 190: 140- 147, 1993.

GAM7776 246 PTK2 Fiedorek, F. T., Jr.; Kay, E. S.: Mapping of the focal adhesionkinase (Fadk) 3 C b
gene to mouse chromosome 15 and human chromosome 8. MammalianGenome 6: 123- 126, 1995.

GAM7776 246 PTK2 Polte, T. R.; Hanks, S. K.: Interaction between focal adhesionkinase and 3 C b
Crk- associated tyrosine kinase substrate p130- Cas. Proc.Nat. Acad. Sci. 92: 10678- 10682, 1995.

GAM7776 246 PTK2 Schaller, M. D.; Borgman, C.; Cobb, B. S.; Vines, R. R.; Reynolds,A. B.; 3 C b
Parsons, J. T.: pp125(FAK), a structurally distinctive protein- tyrosinekinase associated with focal adhesions. Proc. Nat. Acad. Sci. 89:5192- 5196, 1992.

GAM7776 246 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; 3 C b
Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab- family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600, 1999.

GAM7776 246 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation 3 C b
of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2. Gene 241: 133- 141, 2000.

GAM7776 246 RAB4A Barbosa, M. D. F. S.; Johnson, S. A.; Achey, K.; Gutierrez, M.;Wakeland, E. 3 C c
K.; Zerial, M.; Kingsmore, S. F.: The Rab protein family:genetic mapping of six Rab genes in the mouse. Genomics 30: 439- 444,1995.

GAM7776 246 RAB4A Rousseau- Merck, M.- F.; Zahraoui, A.; Touchot, N.; Tavitian, A.;Berger, R.: 3 C c
Chromosome assignment of four RAS- related RAB genes. Hum.Genet. 86: 350- 354, 1991.

GAM7776 246 RAB4A Zahraoui, A.; Touchot, N.; Chardin, P.; Tavitian, A.: The humanrab genes 3 C c
encode a family of GTP- binding proteins related to yeastYPT1 and SEC4 products involved in secretion. J. Biol. Chem. 264:12394- 12401, 1989.

GAM7776 246 RBL2 Baldi, A.; Boccia, V.; Claudio, P. P.; De Luca, A.; Giordano, A.: Genomic 3 C c
structure of the human retinoblastoma- related Rb2/p130 gene. Proc.Nat. Acad. Sci. 93: 4629- 4632, 1996.

GAM7776 246 RBL2 Mayol, X.; Grana, X.; Baldi, A.; Sang, N.; Hu, Q.; Giordano, A.: Cloning of 3 C c
a new member of the retinoblastoma gene family (pRb2)which binds to the E1A transforming domain. Oncogene 8: 2561- 2566,1993.

GAM7776 246 RBL2 Yeung, R. S.; Bell, D. W.; Testa, J. R.; Mayol, X.; Baldi, A.;Grana, X.; 3 C c
Klinga- Levan, K.; Knudson, A. G.; Giordano, A.: The retinoblastoma- relatedgene, RB2, maps to human chromosome 16q12 and rat chromosome 19. Oncogene 8:3465- 3468, 1993.

GAM7776 246 RGS3 Chatterjee, T. K.; Eapen, A.; Kanis, A. B.; Fisher, R. A.: 3 C c
Genomicorganization, 5- prime- flanking region, and chromosomal

localizationof the human RGS3 gene. Genomics 45: 429- 433, 1997.

GAM7776 246 RGS3 Druey, K. M.; Blumer, K. J.; Kang, V. H.; Kehrl, J. H.: Inhibitionof G- 3 C c
protein- mediated MAP kinase activation by a new mammalian genefamily.
Nature 379: 742- 746, 1996.

GAM7776 246 RGS3 Lu, Q.; Sun, E. E.; Klein, R. S.; Flanagan, J. G.: Ephrin- B 3 C c
reversesignaling is mediated by a novel PDZ- RGS protein and selectively
inhibitsG protein- coupled chemoattraction. Cell 105: 69- 79, 2001.

GAM7776 246 RHD Arce, M. A.; Thompson, E. S.; Wagner, S.; Coyne, K. E.; Ferdman,B. A.; 3 C b
Lublin, D. M.: Molecular cloning of RhD cDNA derived froma gene present in
RhD- positive, but not RhD- negative individuals. Blood 82:651- 655, 1993.

GAM7776 246 RHD Bennett, P. R.; Le Van Kim, C.; Colin, Y.; Warwick, R. M.; Cherif- Zahar,B.; 3 C b
Fisk, N. M.; Cartron, J.- P.: Prenatal determination of fetalRhD type by DNA
amplification. New Eng. J. Med. 329: 607- 610, 1993.

GAM7776 246 RHD Bowman, J. M.: RhD hemolytic disease of the newborn. (Editorial) NewEng. J. 3 C b
Med. 339: 1775- 1777, 1998.

GAM7776 246 RHD Cartron, J.- P.: Defining the Rh blood group antigens: biochemistryand 3 C b
molecular genetics. Blood Rev. 8: 199- 212, 1994.

GAM7776 246 RHD Colin, Y.; Cherif- Zahar, B.; Le Van Kim, C.; Raynal, V.; Van Huffel,V.; 3 C b
Cartron, J.- P.: Genetic basis of the RhD- positive and RhD- negativeblood
group polymorphism as determined by Southern analysis. Blood 78:2747- 2752,
1991.

GAM7776 246 RHD Diamond, L. K.; Blackfan, K. D.; Baty, J. M.: Erythroblastosisfetalis and 3 C b
its association with universal edema of the fetus, icterusgravis neonatorum
and anemia of the newborn. J. Pediat. 1: 269- 309,1932.

GAM7776 246 RHD du Toit, E. D.; Martell, R. W.; Botha, I.; Kriel, C. J.: Anti- Dantibodies 3 C b
in the Rh- positive mothers. S. Afr. Med. J. 75: 452,1989.

GAM7776 246 RHD Garratty, G.: Severe reactions associated with transfusion ofpatients with 3 C b
sickle cell disease. Transfusion 37: 357- 361, 1997.

GAM7776 246 RHD Huang, C.- H.: Personal Communication. New York City, N. Y. 10/11/1996. 3 C b

GAM7776 246 RHD Huang, C.- H.; Chen, Y.; Reid, M.; Ghosh, S.: Genetic recombinationat the 3 C b
human RH locus: a family study of the red- cell Evans phenotypereveals a
transfer of exons 2- 6 from the RHD to the RHCE gene. Am.J. Hum. Genet. 59:
825- 833, 1996.

GAM7776 246 RHD Huang, C.- H.; Reid, M. E.; Chen, Y.; Coghlan, G.; Okubo, Y.:Molecular 3 C b
definition of red cell Rh haplotypes by tightly linked SphIRFLPs. Am. J.
Hum. Genet. 58: 133- 142, 1996.

GAM7776 246 RHD Hyland, C. A.; Wolter, L. C.; Liew, Y. W.; Saul, A.: A Southernanalysis of 3 C b
Rh blood group genes: association between restrictionfragment length
polymorphism patterns and Rh serotypes. Blood 83:566- 572, 1994.

GAM7776 246 RHD Issitt, P. D.: The Rh blood group system, 1988: eight new antigensin nine 3 C b
years and some observations on the biochemistry and geneticsof the system.
Transfusion Med. Rev. 3: 1- 12, 1989.

GAM7776 246 RHD Kemp, T. J.; Poulter, M.; Carritt, B.: A recombination hot spotin the Rh 3 C b
genes revealed by analysis of unrelated donors with therare D- - phenotype.
Am. J. Hum. Genet. 59: 1066- 1073, 1996.

GAM7776 246 RHD Le Van Kim, C.; Cherif- Zahar, B.; Raynal, V.; Mouro, I.; Lopez,M.; Cartron, 3 C b
J. P.; Colin, Y.: Multiple Rh messenger RNA isoformsare produced by
alternative splicing. Blood 80: 1074- 1078, 1992.

GAM7776 246 RHD Le Van Kim, C.; Mouro, I.; Cherif- Zahar, B.; Raynal, V.; Cherrier,C.; 3 C b
Cartron, J.- P.; Colin, Y.: Molecular cloning and primary structureof the

human blood group RhD polypeptide. Proc. Nat. Acad. Sci. 89:10925- 10929, 1992.

GAM7776 246 RHD Legler, T. J.; Eber, S. W.; Lakomek, M.; Lynen, R.; Maas, J. H.;Pekrun, A.; 3 C b
Repas- Humpe, M.; Schroter, W.; Kohler, M.: Applicationof RHD and RHCE genotyping for correct blood group determination inchronically transfused patients. Transfusion 39: 852- 855, 1999.

GAM7776 246 RHD Levine, P.; Katzin, E. M.; Burnham, L.: Isoimmunization in pregnancy:its 3 C b
possible bearing on the etiology of erythroblastosis foetalis. J.A.M.A. 116:825- 827, 1941.

GAM7776 246 RHD Lo, Y. M. D.; Hjelm, N. M.; Fidler, C.; Sargent, I. L.; Murphy,M. F.; 3 C b
Chamberlain, P. F.; Poon, P. M. K.; Redman, C. W. G.; Wainscoat,J. S.: Prenatal diagnosis of fetal RhD status by molecular analysisof maternal plasma. New Eng. J. Med. 339: 1734- 1738, 1998.

GAM7776 246 RHD Miyoshi, O.; Yabe, R.; Wakui, K.; Fukushima, Y.; Koizumi, S.;Uchikawa, M.; 3 C b
Kajii, T.; Numakura, C.; Takahashi, S.; Hayasaka, K.;Niikawa, N.: Two cases of mosaic RhD blood- group phenotypes and paternalisodisomy for chromosome 1. Am. J. Med. Genet. 104: 250- 256, 2001.

GAM7776 246 RHD Okuda, H.; Kawano, M.; Iwamoto, S.; Tanaka, M.; Seno, T.; Okubo,Y.; Kajii, 3 C b
E.: The RHD gene is highly detectable in RhD- negativeJapanese donors. J. Clin. Invest. 100: 373- 379, 1997.

GAM7776 246 RHD Race, R. R.: An 'incomplete' antibody in human serum. (Letter) Nature 3 C b
153:771- 772, 1944.

GAM7776 246 RHD Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 C b
ed.): 1975.

GAM7776 246 RHD Rouillac, C.; Le Van Kim, C.; Beolet, M.; Cartron, J.- P.; Colin,Y.: Leu110- 3 C b
to- pro substitution in the RhD polypeptide is responsiblefor the D(VII) category blood group phenotype. Am. J. Hemat. 49:87- 88, 1995.

GAM7776 246 RHD Smythe, J. S.; Avent, N. D.; Judson, P. A.; Parsons, S. F.; Martin,P. G.; 3 C b
Anstee, D. J.: Expression of RHD and RHCE gene products usingretroviral transduction of K562 cells establishes the molecular basisof Rh blood group antigens. Blood 87: 2968- 2973, 1996.

GAM7776 246 RHD Spanos, T.; Karageorga, M.; Ladis, V.; Peristeri, J.; Hatziliami,A.; 3 C b
Kattamis, C.: Red cell alloantibodies in patients with thalassemia. VoxSang. 58: 50- 55, 1990.

GAM7776 246 RHD Wagner, F. F.; Flegel, W. A.: RHD gene deletion occurred in theRhesus box. 3 C b
Blood 95: 3662- 3668, 2000.

GAM7776 246 RHD Wagner, F. F.; Gassner, C.; Muller, T. H.; Schonitzer, D.; Schunter,F.; 3 C b
Flegel, W. A.: Molecular basis of weak D phenotypes. Blood 93:385- 393, 1999.

GAM7776 246 RHD Wagner, F. F.; Ladewig, B.; Angert, K. S.; Heymann, G. A.; Eicher,N. I.; 3 C b
Flegel, W. A.: The DAU allele cluster of the RHD gene. Blood 100:306- 311, 2002.

GAM7776 246 RHD Wiener, A. S.: The Rh series of allelic genes. Science 100:595- 597, 1944. 3 C b

GAM7776 246 RPH3AL Kotake, K.; Ozaki, N.; Mizuta, M.; Sekiya, S.; Inagaki, N.; Seino,S.: Noc2, 3 C b
a putative zinc finger protein involved in exocytosis inendocrine cells. J. Biol. Chem. 272: 29407- 29410, 1997.

GAM7776 246 RPH3AL Smith, J. S.; Tachibana, I.; Allen, C.; Chiappa, S. A.; Lee, H.K.; McIver, 3 C b
B.; Jenkins, R. B.; Raffel, C.: Cloning of a human ortholog(RPH3AL) of (RNO)Rph3al from a candidate 17p13.3 medulloblastoma tumorsuppressor locus. Genomics 59: 97- 101, 1999.

GAM7776 246 RPP30 Eder, P. S.; Kekuda, R.; Stolc, V.; Altman, S.: Characterizationof two scleroderma autoimmune antigens that copurify with human ribonucleaseP. Proc. Nat. Acad. Sci. 94: 1101- 1106, 1997. 3 C b

GAM7776 246 RPP30 Jarrous, N.; Eder, P. S.; Guerrier- Takada, C.; Hoog, C.; Altman,S.: Autoantigenic properties of some protein subunits of catalyticallyactive complexes of human ribonuclease P. RNA 4: 407- 417, 1998. 3 C b

GAM7776 246 SAS Jankowski, S. A.; De Jong, P.; Meltzer, P. S.: Genomic structureof SAS, a member of the transmembrane 4 superfamily amplified in humansarcomas. Genomics 25: 501- 506, 1995. 3 C b

GAM7776 246 SAS Meltzer, P. S.; Jankowski, S. A.; Dal Cin, P.; Sandberg, A. A.;Paz, I. B.; Coccia, M. A.; Smith, S. H.: Identification and cloningof a novel amplified DNA sequence in human malignant fibrous histiocytomaderived from a region of chromosome 12 frequently rearranged in softtissue tumors. (Abstract) Cytogenet. Cell Genet. 58: 1979 only,1991. 3 C b

GAM7776 246 SCD Cohen, P.; Miyazaki, M.; Socci, N. D.; Hagge- Greenberg, A. Liedtke,W.; Soukas, A. A.; Sharma, R.; Hudgins, L. C.; Ntambi, J. M.; Friedman,J. M.: Role for stearoyl- CoA desaturase- 1 in leptin- mediated weightloss. Science 297: 240- 243, 2002. 3 C c

GAM7776 246 SCD Li, J.; Ding, S.- F.; Habib, N. A.; Fermor, B. F.; Wood, C. B.;Gilmour, R. S.: Partial characterization of a cDNA for human stearoyl- CoAdesaturase and changes in its mRNA expression in some normal and malignanttissues. Int. J. Cancer 57: 348- 352, 1994. 3 C c

GAM7776 246 SCD Ntambi, J. M.; Miyazaki, M.; Stoehr, J. P.; Lan, H.; Kendziorski,C. M.; Yandell, B. S.; Song, Y.; Cohen, P.; Friedman, J. M.; Attie,A. D.: Loss of stearoyl- CoA desaturase- 1 function protects mice againstadiposity. Proc. Nat. Acad. Sci. 99: 11482- 11486, 2002. 3 C c

GAM7776 246 SCD Thiede, M. A.; Ozols, J.; Strittmatter, P.: Construction and sequenceof cDNA for rat liver stearyl coenzyme A desaturase. J. Biol. Chem. 261:13230- 13235, 1986. 3 C c

GAM7776 246 SCD Zhang, L.; Ge, L.; Parimoo, S.; Stenn, K.; Prouty, S. M.: Humanstearoyl- CoA desaturase: alternative transcripts generated from asingle gene by usage of tandem polyadenylation sites. Biochem. J. 340:255- 264, 1999. 3 C c

GAM7776 246 SCD Zheng, Y.; Eilertsen, K. J.; Ge, L.; Zhang, L.; Sundberg, J. P.;Prouty, S. M.; Stenn, K. S.; Parimoo, S.: Scd1 is expressed in sebaceousglands and is disrupted in the asebia mouse. (Letter) Nature Genet. 23:268- 270, 1999. 3 C c

GAM7776 246 SCN2B Bolino, A.; Seri, M.; Caroli, F.; Eubanks, J.; Srinivasan, J.;Mandich, P.; Schenone, A.; Quattrone, A.; Romeo, G.; Catterall, W.A.; Devoto, M.: Exclusion of the SCN2B gene as candidate for CMT4B. Europ.J. Hum. Genet. 6: 629- 634, 1998. 3 C c

GAM7776 246 SCN2B Eubanks, J.; Srinivasan, J.; Dinulos, M. B.; Disteche, C. M.; Catterall,W. A.: Structure and chromosomal localization of the beta2 subunitof the human brain sodium channel. Neuroreport 8: 2775- 2779, 1997. 3 C c

GAM7776 246 SCN2B Imai, K.; Kingsley, D. M.: Mouse chromosome 9. Mammalian Genome 5:S139- S153, 1994. 3 C c

GAM7776 246 SCN2B Isom, L. L.; Ragsdale, D. S.; De Jongh, K. S.; Westenbroek, R.E.; Reber, B. F. X.; Scheuer, T.; Catterall, W. A.: Structure andfunction of the beta- 2 subunit of brain sodium channels, a transmembraneglycoprotein with a CAM motif. Cell 83: 433- 442, 1995. 3 C c

GAM7776 246 SCN2B Jones, J. M.; Meisler, M. H.; Isom, L. L.: Scn2b, a voltage- gatedsodium 3 C c

channel beta- 2 gene on mouse chromosome 9. Genomics 34: 258- 259,1996.

GAM7776 246 SEDL Christie, P. T.; Curley, A.; Nesbit, M. A.; Chapman, C.; Genet,S.; Harper, P. S.; Keeling, S. L.; Wilkie, A. O. M.; Winter, R. M.;Thakker, R. V.: Mutational analysis in X- linked spondyloepiphysealdysplasia tarda. J. Clin. Endocr. Metab. 86: 3233- 3236, 2001. 3 C b

GAM7776 246 SEDL Fiedler, J.; Bittner, M.; Puhl, W.; Brenner, R. E.: Mutationsin the X- linked spondyloepiphyseal dysplasia tarda (SEDL) coding sequenceare not a common cause of early primary osteoarthritis in men. (Letter) Clin.Genet. 62: 94- 95, 2002. 3 C b

GAM7776 246 SEDL Gecz, J.; Hillman, M. A.; Gedeon, A. K.; Cox, T. C.; Baker, E.;Mulley, J. C.: Gene structure and expression study of the SEDL genefor spondyloepiphyseal dysplasia tarda. Genomics 69: 242- 251, 2000. 3 C b

GAM7776 246 SEDL Gedeon, A. K.; Colley, A.; Jamieson, R.; Thompson, E. M.; Rogers,J.; Sillence, D.; Tiller, G. E.; Mulley, J. C.; Gecz, J.: Identificationof the gene (SEDL) causing X- linked spondyloepiphyseal dysplasia tarda. NatureGenet. 22: 400- 404, 1999. 3 C b

GAM7776 246 SEDL Gedeon, A. K.; Tiller, G. E.; Le Merrer, M.; Heuertz, S.; Tranebjaerg,L.; Chitayat, D.; Robertson, S.; Glass, I. A.; Savarirayan, R.; Cole,W. G.; Rimoin, D. L.; Kousseff, B. G.; Ohashi, H.; Zabel, B.; Munnich,A.; Gecz, J.; Mulley, J. C.: The molecular basis of X- linked spondyloepiphysealdysplasia tarda. Am. J. Hum. Genet. 68: 1386- 1397, 2001. 3 C b

GAM7776 246 SEDL Grunebaum, E.; Arpaia, E.; MacKenzie, J. J.; Fitzpatrick, J.; Ray,P. N.; Roifman, C. M.: A missense mutation in the SEDL gene resultsin delayed onset of X linked spondyloepiphyseal dysplasia in a largepedigree. (Letter) J. Med. Genet. 38: 409- 411, 2001. 3 C b

GAM7776 246 SEDL Mumm, S.; Christie, P. T.; Finnegan, P.; Jones, J.; Dixon, P. H.;Pannett, A. A. J.; Harding, B.; Gottesman, G. S.; Thakker, R. V.;Whyte, M. P.: A five- base pair deletion in the sedlin gene causesspondyloepiphyseal dysplasia tarda in a six- generation Arkansas kindred. J.Clin. Endocr. Metab. 85: 3343- 3347, 2000. 3 C b

GAM7776 246 SEDL Mumm, S.; Zhang, X.; Vacca, M.; D'Esposito, M.; Whyte, M. P.:The sedlin gene for spondyloepiphyseal dysplasia tarda escapes X- inactivationand contains a non- canonical splice site. Gene 273: 285- 293, 2001. 3 C b

GAM7776 246 SEDL Takahashi, T.; Takahashi, I.; Tsuchida, S.; Oyama, K.; Komatsu,M.; Saito, H.; Takada, G.: An SEDL gene mutation in a Japanese kindredof X- linked spondyloepiphyseal dysplasia tarda. (Letter) Clin. Genet. 61:319- 320, 2002. 3 C b

GAM7776 246 SEDL Tiller, G. E.; Hannig, V. L.; Dozier, D.; Carrel, L.; Trevarthen,K. C.; Wilcox, W. R.; Mundlos, S.; Haines, J. L.; Gedeon, A. K.; Gecz,J.: A recurrent RNA- splicing mutation in the SEDL gene causes X- linkedspondyloepiphyseal dysplasia tarda. Am. J. Hum. Genet. 68: 1398- 1407,2001. 3 C b

GAM7776 246 SEDL Whyte, M. P.; Gottesman, G. S.; Eddy, M. C.; McAlister, W. H.: X- linked recessive spondyloepiphyseal dysplasia tarda: clinicaland radiographic evolution in a 6- generation kindred and review ofthe literature. Medicine 78: 9- 25, 1999. 3 C b

GAM7776 246 SERPINB9 Bladergroen, B. A.; Strik, M. C. M.; Bovenschen, N.; van Berkum,O.; Scheffer, G. L.; Meijer, C. J. L. M.; Hack, C. E.; Kummer, J.A.: The granzyme B inhibitor, protease inhibitor 9, is mainly expressedby dendritic cells and at immune- privileged sites. J. Immun. 166:3218- 3225, 2001. 3 C b

GAM7776 246 SERPINB9 Eyre, H. J.; Sun, J.; Sutherland, G. R.; Bird, P.: Chromosomalmapping of the 3 C b

gene (PI9) encoding the intracellular serpin proteinaseinhibitor 9 to 6p25 by fluorescence in situ hybridization. Genomics 37:406- 408, 1996.

GAM7776 246 SERPINB9 Krieg, S. A.; Krieg, A. J.; Shapiro, D. J.: A unique downstreamestrogen responsive unit mediates estrogen induction of proteinaseinhibitor- 9, a cellular inhibitor of IL- 1- beta- converting enzyme (caspase1). Molec. Endocr. 15: 1971- 1982, 2001. 3 C b

GAM7776 246 SERPINB9 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995. 3 C b

GAM7776 246 SERPINB9 Sun, J.; Bird, C. H.; Sutton, V.; McDonald, L.; Coughlin, P. B.;De Jong, T. A.; Trapani, J. A.; Bird, P. I.: A cytosolic granzymeB inhibitor related to the viral apoptotic regulator cytokine responsemodifier A is present in cytotoxic lymphocytes. J. Biol. Chem. 271:27802- 27809, 1996. 3 C b

GAM7776 246 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 3 C c

GAM7776 246 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 3 C c

GAM7776 246 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 3 C c

GAM7776 246 SIL Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe transactivation domain induces bony abnormalities and cooperateswith LMO1 to generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419, 1997. 3 C b

GAM7776 246 SIL Aplan, P. D.; Lombardi, D. P.; Ginsberg, A. M.; Cossman, J.; Bertness,V. L.; Kirsch, I. L.: Disruption of the human SCL locus by 'illegitimate'V- (D)- J recombinase activity. Science 250: 1426- 1429, 1990. 3 C b

GAM7776 246 SIL Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992. 3 C b

GAM7776 246 SIL Brown, L.; Cheng, J.- T.; Chen, Q.; Siciliano, M. J.; Crist, W.;Buchanan, G.; Baer, R.: Site- specific recombination of the tal- 1gene is a common occurrence in human T- cell leukemia. EMBO J. 9:3343- 3351, 1990. 3 C b

GAM7776 246 SIL Collazo- Garcia, N.; Scherer, P.; Aplan, P. D.: Cloning and characterizationof a murine SIL gene. Genomics 30: 506- 513, 1995. 3 C b

GAM7776 246 SIL Izraeli, S.; Lowe, L. A.; Bertness, V. L.; Good, D. J.; Dorward,D. W.; Kirsch, I. R.; Kuehn, M. R.: The SIL gene is required formouse embryonic axial development and left- right specification. Nature 399:691- 694, 1999. 3 C b

GAM7776 246 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.; Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998. 3 C c

GAM7776 246 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea 3 C c

transporter in the human kidney. FEBS Lett. 386: 156- 160,1996.

GAM7776 246 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; 3 C c
Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.;
Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2
is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157-
2164, 2001.

GAM7776 246 SLC15A1 Adibi, S. A.: The oligopeptide transporter (Pept- 1) in human 3 C b
intestine:biology and function. Gastroenterology 113: 332- 340, 1997.

GAM7776 246 SLC15A1 Fei, Y. - J.; Kanai, Y.; Nussberger, S.; Ganapathy, V.; Leibach,F. H.; 3 C b
Romero, M. F.; Singh, S. K.; Boron, W. F.; Hediger, M. A.:Expression cloning
of a mammalian proton- coupled oligopeptide transporter. Nature 368:563-
566, 1994.

GAM7776 246 SLC15A1 Liang, R.; Fei, Y.- J.; Prasad, P. D.; Ramamoorthy, S.; Han, H.;Yang- Feng, 3 C b
T. L.; Hediger, M. A.; Ganapathy, V.; Leibach, F. H.:Human intestinal
H(+)/peptide cotransporter: cloning, functional expression,and chromosomal
localization. J. Biol. Chem. 270: 6456- 6463, 1995.

GAM7776 246 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Cooper, C. B.; Schnetkamp, P. P.: cDNA 3 C b
cloning of the human retinal rod Na- Ca + K exchanger: comparisonwith a
revised bovine sequence. Invest. Ophthal. Vis. Sci. 39: 435- 440,1998.

GAM7776 246 SLC24A1 Tucker, J. E.; Winkfein, R. J.; Murthy, S. K.; Friedman, J. S.;Walter, M. 3 C b
A.; Demetrick, D. J.; Schnetkamp, P. P. M.: Chromosomallocalization and
genomic organization of the human retinal rod Na- Ca+Kexchanger. Hum. Genet.
103: 411- 414, 1998.

GAM7776 246 SLC39A1 Eng, B. H.; Guerinot, M. L.; Eide, D.; Saier, M. H., Jr.: Sequenceanalyses 3 C b
and phylogenetic characterization of the ZIP family of metalion transport
proteins. J. Membr. Biol. 166: 1- 7, 1998.

GAM7776 246 SLC39A1 Lioumi, M.; Ferguson, C. A.; Sharpe, P. T.; Freeman, T.; Marenholz,I.; 3 C b
Mischke, D.; Heizmann, C.; Ragoussis, J.: Isolation and characterizationof
human and mouse ZIRTL, a member of the IRT1 family of transporters,mapping
within the epidermal differentiation complex. Genomics 62:272- 280, 1999.

GAM7776 246 SLC39A1 Lioumi, M.; Olavesen, M. G.; Nizetic, D.; Ragoussis, J.: High- resolutionYAC 3 C b
fragmentation map of 1q21. Genomics 49: 200- 208, 1998.

GAM7776 246 SLC6A3 Byerley, W.; Hoff, M.; Holik, J.; Caron, M. G.; Giros, B.: VNTRpolymorphism 3 C c
for the human dopamine transporter gene (DAT1). Hum.Molec. Genet. 2: 335,
1993.

GAM7776 246 SLC6A3 Cook, E. H., Jr.; Stein, M. A.; Krasowski, M. D.; Cox, N. J.; Olkon,D. M.; 3 C c
Kieffer, J. E.; Leventhal, B. L.: Association of attention- deficitdisorder
and the dopamine transporter gene. Am. J. Hum. Genet. 56:993- 998, 1995.

GAM7776 246 SLC6A3 Doucette- Stamm, L.; Blakely, D. J.; Tian, J.; Mockus, S.; Mao,J.: 3 C c
Population genetic study of the human dopamine transporter gene(DAT1).
Genet. Epidemiol. 12: 303- 308, 1995.

GAM7776 246 SLC6A3 Gainetdinov, R. R.; Wetsel, W. C.; Jones, S. R.; Levin, E. D.;Jaber, M.; 3 C c
Caron, M. G.: Role of serotonin in the paradoxical calmingeffect of
psychostimulants on hyperactivity. Science 283: 397- 401,1999.

GAM7776 246 SLC6A3 Gelernter, J.; Vandenbergh, D.; Kruger, S. D.; Pauls, D. L.; Kurlan,R.; 3 C c
Pakstis, A. J.; Kidd, K. K.; Uhl, G.: The dopamine transporterprotein gene
(SLC6A3): primary linkage mapping and linkage studiesin Tourette syndrome.
Genomics 30: 459- 463, 1995.

GAM7776 246 SLC6A3 Gill, M.; Daly, G.; Heron, S.; Hawi, Z.; Fitgerald, M.: Confirmationof 3 C c
association between attention deficit hyperactivity disorder anda dopamine

transporter polymorphism. Molec. Psychiat. 2: 311- 313,1997.

GAM7776 246 SLC6A3 Giros, B.; El Mestikawy, S.; Godinot, N.; Zheng, K.; Han, H.; Yang- Feng,T.; 3 C c
Caron, M. G.: Cloning, pharmacological characterization, andchromosome
assignment of the human dopamine transporter. Molec. Pharm. 42:383- 390,
1992.

GAM7776 246 SLC6A3 Giros, B.; Jaber, M.; Jones, S. R.; Wightman, R. M.; Caron, M.G.: 3 C c
Hyperlocomotion and indifference to cocaine and amphetamine inmice lacking
the dopamine receptor. Nature 370: 606- 612, 1996.

GAM7776 246 SLC6A3 Goldman, D.: Dopamine transporter, alcoholism and other diseases. NatureMed. 3 C c
1: 624- 625, 1995.

GAM7776 246 SLC6A3 Kurlan, R.; Behr, J.; Medved, L.; Shoulson, I.; Pauls, D.; Kidd,J. R.; Kidd, 3 C c
K. K.: Familial Tourette's syndrome: report of a largepedigree and potential
for linkage analysis. Neurology 36: 772- 776,1986.

GAM7776 246 SLC6A3 Lerman, C.; Caporaso, N. E.; Audrain, J.; Main, D.; Bowman, E.D.; Lockshin, 3 C c
B.; Boyd, N. R.; Shields, P. G.: Evidence suggestingthe role of specific
genetic factors in cigarette smoking. HealthPsych. 18: 14- 20, 1999.

GAM7776 246 SLC6A3 Lossie, A. C.; Vandenbergh, D. J.; Uhl, G. R.; Camper, S. A.:Localization of 3 C c
the dopamine transporter gene, Dat1, on mouse chromosome

GAM7776 246 SLC6A3 Mammalian Genome 5: 117- 118, 1994.13. Sabol, S. Z.; Nelson, M. L.; Fisher, 3 C c
C.; Gunzerath, L.; Brody,C. L.; Hu, S.; Sirota, L. A.; Marcus, S. E.;
Greenberg, B. D.; Lucas,F. R., IV; Benjamin, J.; Murphy, D. L.; Hamer, D.
H.: A genetic associationfor cigarette smoking behavior. Health Psych. 18:
7- 13, 1999.

GAM7776 246 SLC6A3 Tiihonen, J.; Kuikka, J.; Bergstrom, K.; Hakola, P.; Karhu, J.;Ryynanen, O.- 3 C c
P.; Fohr, J.: Altered striatal dopamine re- uptake sitedensities in
habitually violent and non- violent alcoholics. NatureMed. 1: 654- 657,
1995.

GAM7776 246 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Hawkins, A. L.; Griffin, C.A.; Li, X.; 3 C c
Jabs, E. W.; Uhl, G. R.: Human dopamine transporter gene(DAT1) maps to
chromosome 5p15.3 and displays a VNTR. Genomics 14:1104- 1106, 1992.

GAM7776 246 SLC6A3 Vandenbergh, D. J.; Persico, A. M.; Uhl, G. R.: A human dopaminetransporter 3 C c
cDNA predicts reduced glycosylation, displays a novelrepetitive element and
provides racially- dimorphic TaqI RFLPs. Molec.Brain Res. 15: 161- 166,
1992.

GAM7776 246 SLC6A3 Waldman, I. D.; Rowe, D. C.; Abramowitz, A.; Kozel, S. T.; Mohr,J. H.; 3 C c
Sherman, S. L.; Cleveland, H. H.; Sanders, M. L.; Gard, J.M. C.; Stever, C.:
Association and linkage of the dopamine transportergene and attention-
deficit hyperactivity disorder in children: heterogeneityowing to diagnostic
subtype and severity. Am. J. Hum. Genet. 63:1767- 1776, 1998.

GAM7776 246 SMAC Chai, J.; Du, C.; Wu, J.- W.; Kyin, S.; Wang, X.; Shi, Y.: Structuraland 3 C b
biochemical basis of apoptotic activation by Smac/DIABLO. Nature 406:855-
862, 2000.

GAM7776 246 SMAC Du, C.; Fang, M.; Li, Y.; Li, L.; Wang, X.: Smac, a mitochondrialprotein 3 C b
that promotes cytochrome c- dependent caspase activation byeliminating IAP
inhibition. Cell 102: 33- 42, 2000.

GAM7776 246 SMAC Liu, Z.; Sun, C.; Olejniczak, E. T.; Meadows, R. P.; Betz, S. F.;Oost, T.; 3 C b
Herrmann, J.; Wu, J. C.; Fesik, S. W.: Structural basisfor binding of
Smac/DIABLO to the XIAP BIR3 domain. Nature 408:1004- 1008, 2000.

GAM7776 246 SMAC Okada, H.; Suh, W.- K.; Jin, J.; Woo, M.; Du, C.; Elia, A.; Duncan,G. S.; 3 C b

Wakeham, A.; Itie, A.; Lowe, S. W.; Wang, X.; Mak, T. W.:Generation and characterization of Smac/DIABLO- deficient mice. Molec.Cell. Biol. 22: 3509-3517, 2002.

GAM7776 246 SMAC Scott, A. F.: Personal Communication. Baltimore, Md. 8/18/2000. 3 C b

GAM7776 246 SMAC Srinivasula, S. M.; Hegde, R.; Saleh, A.; Datta, P.; Shiozaki,E.; Chai, J.; Lee, R.- A.; Robbins, P. D.; Fernandes- Alnemri, T.; Shi,Y.; Alnemri, E. S.: A conserved XIAP- interaction motif in caspase- 9and Smac/DIABLO regulates caspase activity and apoptosis. Nature 410:112- 116, 2001. 3 C b

GAM7776 246 SMAC Verhagen, A. M.; Ekert, P. G.; Pakusch, M.; Silke, J.; Connolly,L. M.; Reid, G. E.; Moritz, R. L.; Simpson, R. J.; Vaux, D. L.: Identificationof DIABLO, a mammalian protein that promotes apoptosis by bindingto and antagonizing IAP proteins. Cell 102: 43- 53, 2000. 3 C b

GAM7776 246 SMAC Wu, G.; Chai, J.; Suber, T. L.; Wu, J.- W.; Du, C.; Wang, X.; Shi,Y.: Structural basis of IAP recognition by Smac/DIABLO. Nature 408:1008- 1012, 2000. 3 C b

GAM7776 246 SNAP23 Guo, Z.; Turner, C.; Castle, D.: Relocation of the t- SNARE SNAP- 23from lamellipodia- like cell surface projections regulates compoundexocytosis in mast cells. Cell 94: 537- 548, 1998. 3 C c

GAM7776 246 SNAP23 Lazo, P. A.; Nadal, M.; Ferrer, M.; Area, E.; Hernandez- Torres,J.; Nabokina, S. M.; Mollinedo, F.; Estivill, X.: Genomic organization,chromosomal localization, alternative splicing, and isoforms of thehuman synaptosome- associated protein- 23 gene implicated in vesicle-membranefusion processes. Hum. Genet. 108: 211- 215, 2001. 3 C c

GAM7776 246 SNAP23 Mollinedo, F.; Lazo, P. A.: Identification of two isoforms ofthe vesicle-membrane fusion protein SNAP- 23 in human neutrophils andHL- 60 cells. Biochem. Biophys. Res. Commun. 231: 808- 812, 1997. 3 C c

GAM7776 246 SNAP23 Ravichandran, V.; Chawla, A.; Roche, P. A.: Identification ofa novel syntaxin- and synaptobrevin/VAMP- binding protein, SNAP- 23,expressed in non- neuronal tissues. J. Biol. Chem. 271: 13300- 13303,1996. 3 C c

GAM7776 246 SNAP23 Shukla, A.; Corydon, T. J.; Nielsen, S.; Hoffmann, H. J.; Dahl,R.: Identification of three new splice variants of the SNARE proteinSNAP- 23. Biochem. Biophys. Res. Commun. 285: 320- 327, 2001. 3 C c

GAM7776 246 SPN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM-dependent movement of CD43 defines a novelprotein complex distal to the immunological synapse. Immunity 15:739- 750, 2001. 3 C b

GAM7776 246 SPN Baecher, C. M.; Dorfman, K. S.; Mattei, M.- G.; Frelinger, J. G.: cDNA cloning and localization of the mouse leukosialin gene (Ly48)to chromosome 7. Immunogenetics 31: 307- 314, 1990. 3 C b

GAM7776 246 SPN Bazil, V.; Strominger, J. L.: CD43, the major sialoglycoproteinof human leukocytes, is proteolytically cleaved from the surface ofstimulated lymphocytes and granulocytes. Proc. Nat. Acad. Sci. 90:3792- 3796, 1993. 3 C b

GAM7776 246 SPN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe immunological synapse is mediated by phosphorylation- regulatedrelocation of the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001. 3 C b

GAM7776 246 SPN Pallant, A.; Eskenazi, A.; Mattei, M.- G.; Fournier, R. E. K.; Carlsson,S. R.; Fukuda, M.; Frelinger, J. G.: Characterization of cDNAs encodinghuman leukosialin and localization of the leukosialin gene to chromosome16. Proc. Nat. Acad. Sci. 86: 1328- 1332, 1989. 3 C b

GAM7776 246 SPN Park, J. K.; Rosenstein, Y. J.; Remold- O'Donnell, E.; Bierer, B.E.; Rosen, 3 C b

F. S.; Burakoff, S. J.: Enhancement of T- cell activationby the CD43 molecule whose expression is defective in Wiskott- Aldrichsyndrome. Nature 350: 706- 709, 1991.

GAM7776 246 SPN Rosenstein, Y.; Park, J. K.; Hahn, W. C.; Rosen, F. S.; Bierer,B. E.; 3 C b
Burakoff, S. J.: CD43, a molecule defective in Wiskott- Aldrichsyndrome, binds ICAM- 1. Nature 354: 233- 235, 1991.

GAM7776 246 SPN Schmid, K.; Hediger, M. A.; Brossmer, R.; Collins, J. H.; Haupt,H.; Marti, 3 C b
T.; Offner, G. D.; Schaller, J.; Takagaki, K.; Walsh, M.T.; Schwick, H. G.; Rosen, F. S.; Remold- O'Donnell, E.: Amino acidsequence of human plasma galactoglycoprotein: identity with the extracellularregion of CD43 (sialophorin). Proc. Nat. Acad. Sci. 89: 663- 667,1992.

GAM7776 246 SPN Shelley, C. S.; Carroll, M. C.; Davis, A. E., III; Bruns, G. A.P.; 3 C b
Whitehead, A. S.; Finberg, R.; Remold- O'Donnell, E.; Rosen, F.S.: Human sialophorin: cDNA cloning and gene location. (Abstract) FASEBJ. 2: A1659 only, 1988.

GAM7776 246 SPN Shelley, C. S.; Remold- O'Donnell, E.; Davis, A. E., III; Bruns,G. A. P.; 3 C b
Rosen, F. S.; Carroll, M. C.; Whitehead, A. S.: Molecularcharacterization of sialophorin (CD43), the lymphocyte surface sialoglycoproteindefective in Wiskott- Aldrich syndrome. Proc. Nat. Acad. Sci. 86:2819- 2823, 1989.

GAM7776 246 SPN Shelley, C. S.; Remold- O'Donnell, E.; Rosen, F. S.; Whitehead,A. S.: 3 C b
Structure of the human sialophorin (CD43) gene: identificationof features atypical of genes encoding integral membrane proteins. Biochem.J. 270: 569- 576, 1990.

GAM7776 246 SPN van den Berg, T. K.; Nath, D.; Ziltener, H. J.; Vestweber, D.;Fukuda, M.; 3 C b
van Die, I.; Crocker, P. R.: Cutting edge: CD43 functionsas a T cell counterreceptor for the macrophage adhesion receptor sialoadhesin(Siglec- 1). J. Immun. 166: 3637- 3640, 2001.

GAM7776 246 SRRM2 Blencowe, B. J.; Bauren, G.; Eldridge, A. G.; Issner, R.; Nickerson,J. A.; 3 C c
Rosonina, E.; Sharp, P. A.: The SRm160/300 splicing coactivatorsubunits. RNA 6: 111- 120, 2000.

GAM7776 246 SRRM2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM7776 246 SRRM2 Sawada, Y.; Miura, Y.; Umeki, K.; Tamaoki, T.; Fujinaga, K.; Ohtaki,S.: 3 C c
Cloning and characterization of a novel RNA- binding protein SRL300with RS domains. Biochim. Biophys. Acta 1492: 191- 195, 2000.

GAM7776 246 SS18 Clark, J.; Rocques, P. J.; Crew, A. J.; Gill, S.; Shipley, J.;Chan, A. M.- 3 C b
L.; Gusterson, B. A.; Cooper, C. S.: Identification ofnovel genes, SYT and SSX, involved in the t(X;18)(p11.2;q11.2) translocationfound in human synovial sarcoma. Nature Genet. 7: 502- 508, 1994.

GAM7776 246 SS18 Crew, A. J.; Clark, J.; Fisher, C.; Gill, S.; Grimer, R.; Chand,A.; Shipley, 3 C b
J.; Gusterson, B. A.; Cooper, C. S.: Fusion of SYT totwo genes, SSX1 and SSX2, encoding proteins with homology to the Kruppel- associatedbox in human synovial sarcoma. EMBO J. 14: 2333- 2340, 1995.

GAM7776 246 SS18 de Bruijn, D. R. H.; Baats, E.; Zechner, U.; de Leeuw, B.; Balemans,M.; Olde 3 C b
Weghuis, D.; Hirning- Folz, U.; Geurts van Kessel, A.: Isolationand characterization of the mouse homolog of SYT, a gene implicatedin the development of human synovial sarcomas. Oncogene 13: 643- 648,1996.

GAM7776 246 SS18 de Bruijn, D. R. H.; Kater- Baats, E.; Eleveld, M.; Merkx, G.; vanKessel, A. 3 C b
G.: Mapping and characterization of the mouse and humanSS18 genes, two human
SS18- like genes and a mouse Ss18 pseudogene. Cytogenet.Cell Genet. 92: 310-
319, 2001.

GAM7776 246 SS18 Gure, A. O.; Tureci, O.; Sahin, U.; Tsang, S.; Scanlan, M. J.;Jager, E.; 3 C b
Knuth, A.; Pfreundschuh, M.; Old, L. J.; Chen, Y.- T.:SSX: a multigene
family with several members transcribed in normaltestis and human cancer.
Int. J. Cancer 72: 965- 971, 1997.

GAM7776 246 SS18 Kawai, A.; Woodruff, J.; Healey, J. H.; Brennan, M. F.; Antonescu,C. R.; 3 C b
Ladanyi, M.: SYT- SSX gene fusion as a determinant of morphologyand
prognosis in synovial sarcoma. New Eng. J. Med. 338: 153- 160,1998.

GAM7776 246 SS18 Skytting, B.; Nilsson, G.; Brodin, B.; Xie, Y.; Lundeberg, J.;Uhlen, M.; 3 C b
Larsson, O.: A novel fusion gene, SYT- SSX4, in synovialsarcoma. (Letter) J.
Nat. Cancer Inst. 91: 974- 975, 1999.

GAM7776 246 SS18 Thaete, C.; Brett, D.; Monaghan, P.; Whitehouse, S.; Rennie, G.;Rayner, E.; 3 C b
Cooper, C. S.; Goodwin, G.: Functional domains of theSYT and SYT- SSX
synovial sarcoma translocation proteins and co- localizationwith the SNF
protein BRM in the nucleus. Hum. Molec. Genet. 8: 585- 591,1999.

GAM7776 246 SS18 Yang, K.; Lui, W.- O.; Xie, Y.; Zhang, A.; Skytting, B.; Mandahl,N.; 3 C b
Larsson, C.; Larsson, O.: Co- existence of SYT- SSX1 and SYT- SSX2fusions in
synovial sarcomas. Oncogene 21: 4181- 4190, 2002.

GAM7776 246 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- 3 C b
strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence
insitu hybridization. Genomics 36: 527- 529, 1996.

GAM7776 246 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence 3 C b
homologue of staufen is an RNA- binding protein thatis associated with
polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell.
Biol. 19: 2212- 2219, 1999.

GAM7776 246 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: 3 C b
Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein
which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19:
2220- 2230, 1999.

GAM7776 246 STE Aksoy, I. A.; Wood, T. C.; Weinshilboum, R.: Human liver 3 C b
estrogensulfotransferase: identification by cDNA cloning and expression.
Biochem.Biophys. Res. Commun. 200: 1621- 1629, 1994.

GAM7776 246 STE Bernier, F.; Leblanc, G.; Labrie, F.; Luu- The, V.: Structure ofhuman 3 C b
estrogen and aryl sulfotransferase gene: two mRNA species issuedfrom a
single gene. J. Biol. Chem. 269: 28200- 28205, 1994.

GAM7776 246 STE Her, C.; Aksoy, I. A.; Kimura, S.; Brandriff, B. F.; Wasmuth, J.J.; 3 C b
Weinshilboum, R. M.: Human estrogen sulfotransferase gene (STE):cloning,
structure, and chromosomal localization. Genomics 29: 16- 23,1995.

GAM7776 246 STE Weinshilboum, R. M.; Otterness, D. M.; Aksoy, I. A.; Wood, T. C.;Her, C.; 3 C b
Raftogianis, R. B.: Sulfotransferase molecular biology:cDNAs and genes.
FASEB J. 11: 3- 14, 1997.

GAM7776 246 STE Weinshilboum, R.: Personal Communication. Rochester, Minn. 10/9/1995. 3 C b

GAM7776 246 TAL1 Aplan, P. D.; Jones, C. A.; Chervinsky, D. S.; Zhao, X.; Ellsworth,M.; Wu, 3 C c
C.; McGuire, E. A.; Gross, K. W.: An scl gene product lackingthe
transactivation domain induces bony abnormalities and cooperateswith LMO1 to
generate T- cell malignancies in transgenic mice. EMBOJ. 16: 2408- 2419,
1997.

GAM7776 246 TAL1 Aplan, P. D.; Lombardi, D. P.; Reaman, G. H.; Sather, H. N.; Hammond,G. D.; 3 C c
Kirsch, I. R.: Involvement of the putative hematopoietic transcriptionfactor SCL in T- cell acute lymphoblastic leukemia. Blood 79: 1327- 1333,1992.

GAM7776 246 TAL1 Begley, C. G.; Aplan, P. D.; Davey, M. P.; Nakahara, K.; Tchorz,K.; 3 C c
Kurtzberg, J.; Hershfield, M. S.; Haynes, B. F.; Cohen, D. I.;Waldmann, T. A.; Kirsch, I. R.: Chromosomal translocation in a humanleukemic stem- cell line disrupts the T- cell antigen receptor delta- chaindiversity region and results in a previously unreported fusion transcript. Proc.Nat. Acad. Sci. 86: 2031- 2035, 1989.

GAM7776 246 TAL1 Begley, C. G.; Visvader, J.; Green, A. R.; Aplan, P. D.; Metcalf,D.; Kirsch, 3 C c
I. R.; Gough, N. M.: Molecular cloning and chromosomallocalization of the murine homolog of the human helix- loop- helix geneSCL. Proc. Nat. Acad. Sci. 88: 869- 873, 1991.

GAM7776 246 TAL1 Finger, L. R.; Kagan, J.; Christopher, G.; Kurtzberg, J.; Hershfield,M. S.; 3 C c
Nowell, P. C.; Croce, C. M.: Involvement of the TCL5 geneon human chromosome 1 in T- cell leukemia and melanoma. Proc. Nat.Acad. Sci. 86: 5039- 5043, 1989.

GAM7776 246 TAL1 Gottgens, B.; Barton, L. M.; Chapman, M. A.; Sinclair, A. M.; Knudsen,B.; 3 C c
Grafham, D.; Gilbert, J. G. R.; Rogers, J.; Bentley, D. R.; Green,A. R.: Transcriptional regulation of the stem cell leukemia gene(SCL)- - comparative analysis of five vertebrate SCL loci. Genome Res. 12:749- 759, 2002.

GAM7776 246 TAL1 Gottgens, B.; Gilbert, J. G.; Barton, L. M.; Grafham, D.; Rogers,J.; 3 C c
Bentley, D. R.; Green, A. R.: Long- range comparison of humanand mouse SCL loci: localized regions of sensitivity to restrictionendonucleases correspond precisely with peaks of conserved noncodingsequences. Genome Res. 11: 87- 97, 2001.

GAM7776 246 TAL1 Kocher, O.; Cheresh, P.; Lee, S. W.: Identification and 3 C c
partialcharacterization of a novel membrane- associated protein (MAP17) up-regulatedin human carcinomas and modulating cell replication and tumor growth. Am.J. Path. 149: 493- 500, 1996.

GAM7776 246 TAL1 Kozak, M.: An analysis of 5- prime- noncoding sequences from 699vertebrate 3 C c
messenger RNAs. Nucleic Acids Res. 15: 8125- 8148, 1987.

GAM7776 246 TAL1 Kurtzberg, J.; Bigner, S. H.; Hershfield, M. S.: Establishmentof the DU.528 3 C c
human lymphohemopoietic stem cell line. J. Exp. Med. 162:1561- 1578, 1985.

GAM7776 246 TAL1 Robb, L.; Lyons, I.; Li, R.; Hartley, L.; Kontgen, F.; Harvey,R. P.; 3 C c
Metcalf, D.; Begley, C. G.: Absence of yolk sac hematopoiesisfrom mice with a targeted disruption of the scl gene. Proc. Nat.Acad. Sci. 92: 7075- 7079, 1995.

GAM7776 246 TAL1 Shivdasani, R. A.; Mayer, E. L.; Orkin, S. H.: Absence of bloodformation in 3 C c
mice lacking the T- cell leukaemia oncoprotein tal- 1/SCL. Nature 373:432-434, 1995.

GAM7776 246 TAL1 Sinclair, A. M.; Bench, A. J.; Bloor, A. J. C.; Li, J.; Gottgens,B.; 3 C c
Stanley, M. L.; Miller, J.; Piltz, S.; Hunter, S.; Nacheva, E.P.; Sanchez, M.- J.; Green, A. R.: Rescue of the lethal scl- /- phenotypeby the human SCL locus. Blood 99: 3931- 3938, 2002.

GAM7776 246 TAL1 Williams, M.; Lyu, M. S.; Yang, Y. L.; Lin, E. P.; Dunbrack, R.;Birren, B.; 3 C c
Cunningham, J.; Hunter, K.: Ier5, a novel member of theslow- kinetics immediate- early genes. Genomics 44: 327- 334, 1999.

GAM7776 246 TAL1 Xia, Y.; Brown, L.; Yang, C. Y.- C.; Tsou Tsan, J.; Siciliano,M. J.; 3 C c

Espinosa, R., III; Le Beau, M. M.; Baer, R. J.: TAL2, a helix- loop-helixgene activated by the (7;9)(q34;q32) translocation in human T-cellleukemia. Proc. Nat. Acad. Sci. 88: 11416- 11420, 1991.

GAM7776 246 TAPBP Herberg, J. A.; Sgouros, J.; Jones, T.; Copeman, J.; Humphray,S. J.; Sheer, D.; Cresswell, P.; Beck, S.; Trowsdale, J.: Genomicanalysis of the Tapasin gene, located close to the TAP loci in theMHC. Europ. J. Immun. 28: 459-467, 1998. 3 C b

GAM7776 246 TAPBP Mayer, W. E.; Klein, J.: Is tapasin a modified Mhc class I molecule? Immunogenetics 53:719- 723, 2001. 3 C b

GAM7776 246 TAPBP Michalova, V.; Murray, B. W.; Sultmann, H.; Klein, J.: A contigmap of the Mhc class I genomic region in the zebrafish reveals ancientsynteny. J. Immun. 164: 5296- 5305, 2000. 3 C b

GAM7776 246 TAPBP Ortmann, B.; Copeman, J.; Lehner, P. J.; Sadasivan, B.; Herberg,J. A.; Grandea, A. G.; Riddell, S. R.; Tampe, R.; Spies, T.; Trowsdale,J.; Cresswell, P.: A critical role for tapasin in the assembly andfunction of multimeric MHC class I- TAP complexes. Science 277: 1306- 1309,1997. 3 C b

GAM7776 246 TAPBP Sadasivan, B.; Lehner, P. J.; Ortmann, B.; Spies, T.; Cresswell,P.: Roles for calreticulin and a novel glycoprotein, tapasin, inthe interaction of MHC class I molecules with TAP. Immunity 5: 103- 114,1996. 3 C b

GAM7776 246 TAPBP Teng, M. S.; Stephens, R.; Du Pasquier, L.; Freeman, T.; Lindquist,J. A.; Trowsdale, J.: A human TAPBP (TAPASIN)- related gene, TAPBP- R. Europ.J. Immun. 32: 1059- 1068, 2002. 3 C b

GAM7776 246 TAPBP Yabe, T.; Kawamura, S.; Sato, M.; Kashiwase, K.; Tanaka, H.; Ishikawa,Y.; Asao, Y.; Oyama, J.; Tsuruta, K.; Tokunaga, K.; Tadokoro, K.;Juji, T.: A subject with a novel type I bare lymphocyte syndromehas tapasin deficiency due to deletion of 4 exons by Alu- mediatedrecombination. Blood 100: 1496-1498, 2002. 3 C b

GAM7776 246 TAT Barton, D. E.; Yang- Feng, T. L.; Francke, U.: The human tyrosineaminotransferase gene mapped to the long arm of chromosome 16 (region16q22- q24) by somatic cell hybrid analysis and in situ hybridization. Hum.Genet. 72: 221- 224, 1986. 3 C c

GAM7776 246 TAT Beinfang, D. C.; Kuwabara, T.; Pueschel, S. M.: The Richner-Hanhartsyndrome: report of a case with associated tyrosinemia. Arch. Ophthal. 94:1133- 1137, 1976. 3 C c

GAM7776 246 TAT Bohnert, A.; Anton- Lamprecht, I.: Richner- Hanhart's syndrome:ultrastructural abnormalities of epidermal keratinization indicatinga causal relationship to high intracellular tyrosine levels. J. Invest.Derm. 79: 68- 74, 1982. 3 C c

GAM7776 246 TAT Buist, N.: Phenylketonuria and related problems.In: Nyhan, W.L.: Amino Acid Metabolism and Genetic Variation. New York: McGraw- Hill(pub.) 1967. Pp. 117 only. 3 C c

GAM7776 246 TAT Chitayat, D.; Balbul, A.; Hani, V.; Mamer, O. A.; Clow, C.; Scriver,C. R.: Hereditary tyrosinaemia type II in a consanguineous AshkenaziJewish family: intrafamilial variation in phenotype; absence of parentalphenotype effects on the fetus. J. Inherit. Metab. Dis. 15: 198- 203,1992. 3 C c

GAM7776 246 TAT Crovato, F.; Desirello, G.; Gatti, R.; Babbini, N.; Rebora, A.: Richner-Hanhart syndrome spares a plantar autograft. Arch. Derm. 121:539- 540, 1985. 3 C c

GAM7776 246 TAT Fellman, J. H.; Vanbellinghen, P. J.; Jones, R. T.; Koler, R. D.: Soluble and mitochondrial forms of tyrosine aminotransferase: relationshipto human tyrosinemia. Biochemistry 8: 615- 622, 1969. 3 C c

GAM7776 246 TAT Garibaldi, L. R.; Siliato, F.; De Martini, I.; Scarsi, M. R.; Romano,C.: 3 C c
Oculocutaneous tyrosinosis: report of two cases in the same family.
Helv.Paediat. Acta 32: 173- 180, 1977.

GAM7776 246 TAT Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.; Gerald,P. S.; 3 C c
Baden, H. P.: Tyrosinemia with plantar and palmar keratosisand keratitis. J.
Pediat. 83: 798- 805, 1973.

GAM7776 246 TAT Hanhart, E.: Neue Sonderformen von Keratosis palmo- plantaris,u.a. eine 3 C c
regelmaessig- dominante mit systematisierten Lipomen, ferner2 einfach-
rezessive mit Schwachsinn und z.T. mit Hornhautveraenderungendes Auges
(Ektodermatosyndrom). Dermatologica 94: 286- 308, 1947.

GAM7776 246 TAT Hunziker, N.: Richner- Hanhart syndrome and tyrosinemia type II. 3 C c
Dermatologica 160:180- 189, 1980.

GAM7776 246 TAT Kennaway, N. G.; Buist, N. R. M.: Metabolic studies in a patientwith hepatic 3 C c
cytosol tyrosine aminotransferase deficiency. Pediat.Res. 5: 287- 297, 1971.

GAM7776 246 TAT Muller, G.; Scherer, G.; Zentgraf, H.; Ruppert, S.; Herrmann,B.; Lehrach, 3 C c
H.; Schutz, G.: Isolation, characterization and chromosomalmapping of the
mouse tyrosine aminotransferase gene. J. Molec. Biol. 184:367- 373, 1985.

GAM7776 246 TAT Natt, E.; Kao, F.- T.; Rettenmeier, R.; Scherer, G.: Assignmentof the human 3 C c
tyrosine aminotransferase gene to chromosome 16. Hum.Genet. 72: 225- 228,
1986.

GAM7776 246 TAT Natt, E.; Kida, K.; Odievre, M.; Di Rocco, M.; Scherer, G.: Pointmutations 3 C c
in the tyrosine aminotransferase gene in tyrosinemia typeII. Proc. Nat.
Acad. Sci. 89: 9297- 9301, 1992.

GAM7776 246 TAT Natt, E.; Westphal, E.- M.; Toth- Fejel, S. E.; Magenis, R. E.;Buist, N. R. 3 C c
M.; Rettenmeier, R.; Scherer, G.: Inherited and de novodeletion of the
tyrosine aminotransferase gene locus at 16q22.1- q22.3in a patient with
tyrosinemia type II. Hum. Genet. 77: 352- 358,1987.

GAM7776 246 TAT Pelet, B.; Antener, I.; Faggioni, R.; Spahr, A.; Gautier, E.:Tyrosinemia 3 C c
without liver or renal damage with plantar and palmarkeratosis and keratitis
(hypertyrosinemia type II). Helv. Paediat.Acta 34: 177- 183, 1979.

GAM7776 246 TAT Rehak, A.; Selim, M. M.; Yadav, G.: Richner- Hanhart syndrome(tyrosinaemia- 3 C c
II) (report of four cases without ocular involvement). Brit.J. Derm. 104:
469- 475, 1981.

GAM7776 246 TAT Rettenmeier, R.; Natt, E.; Zentgraf, H.; Scherer, G.: Isolationand 3 C c
characterization of the human tyrosine aminotransferase gene. NucleicAcids
Res. 18: 3853- 3861, 1990.

GAM7776 246 TAT Richner, H.: Hornhautaffektion bei Keratoma palmare et plantarehereditarium. 3 C c
Klin. Mbl. Augenheilk. 100: 580- 588, 1938.

GAM7776 246 TAT Schmid, W.; Muller, G.; Schutz, G.; Gluecksohn- Waelsch, S.: Deletionsnear 3 C c
the albino locus on chromosome 7 of the mouse affect the levelof tyrosine
aminotransferase mRNA. Proc. Nat. Acad. Sci. 82: 2866- 2869,1985.

GAM7776 246 TAT Tallab, T.M.: Richner- Hanhart syndrome: importance of early diagnosisand 3 C c
early intervention. J. Am. Acad. Dermatol. 35: 857- 859, 1996.

GAM7776 246 TAT Ventura, G.; Biasini, G.; Petrozzi, M.: Cheratomia palmoplantaredissipatum 3 C c
associato a lesioni corneali in due fratelli. Boll. Oculist. 44:497- 510,
1965.

GAM7776 246 TAT Waardenburg, P. J.; Franceschetti, A.; Klein, D.: Genetics andOphthalmology. 3 C c
Springfield, Ill.: Charles C Thomas (pub.) 1:1961. Pp. 515- 517.

GAM7776 246 TAT Westphal, E.- M.; Natt, E.; Grimm, T.; Odievre, M.; Scherer, G.: The human 3 C c
tyrosine aminotransferase gene: characterization of restrictionfragment

length polymorphisms and haplotype analysis in a family withtyrosinemia type II. Hum. Genet. 79: 260- 264, 1988.

GAM7776 246 TCF2 Abbott, C.; Piaggio, G.; Ammendola, R.; Solomon, E.; Povey, S.;Gounari, F.; De Simone, V.; Cortese, R.: Mapping of the gene TCF2for the transcription factor LFB3 to human chromosome 17 by polymerasechain reaction. Genomics 8: 165- 167, 1990. 3 C c

GAM7776 246 TCF2 Bach, I.; Mattei, M.- G.; Cereghini, S.; Yaniv, M.: Two membersof an HNF1 homeoprotein family are expressed in human liver. NucleicAcids Res. 19: 3553- 3559, 1991. 3 C c

GAM7776 246 TCF2 Bingham, C.; Bulman, M. P.; Ellard, S.; Allen, L. I. S.; Lipkin,G. W.; van't Hoff, W. G.; Woolf, A. S.; Rizzoni, G.; Novelli, G.;Nicholls, A. J.; Hattersley, A. T.: Mutations in the hepatocyte nuclearfactor- 1- beta gene are associated with familial hypoplastic glomerulocystickidney disease. Am. J. Hum. Genet. 68: 219- 224, 2001. 3 C c

GAM7776 246 TCF2 Bingham, C.; Ellard, S.; Allen, L.; Bulman, M.; Shepherd, M.; Frayling,T.; Berry, P. J.; Clark, P. M.; Lindner, T.; Bell, G. I.; Ryffel,G. U.; Nicholls, A. J.; Hattersley, A. T.: Abnormal nephron developmentassociated with a frameshift mutation in the transcription factorhepatocyte nuclear factor- 1- beta. Kidney Int. 57: 898- 907, 2000. 3 C c

GAM7776 246 TCF2 Horikawa, Y.; Iwasaki, N.; Hara, M.; Furuta, H.; Hinokio, Y.; Cockburn,B. N.; Lindner, T.; Yamagata, K.; Ogata, M.; Tomonaga, O.; Kuroki,H.; Kasahara, T.; Iwamoto, Y.; Bell, G. I.: Mutation in hepatocytenuclear factor- 1- beta gene (TCF2) associated with MODY. (Letter) NatureGenet. 17: 384- 385, 1997. 3 C c

GAM7776 246 TCF2 Kaplan, B. S.; Gordon, I.; Pincott, J.; Barratt, T. M.: Familialhypoplastic glomerulocystic kidney disease: a definite entity withdominant inheritance. Am. J. Med. Genet. 34: 569- 573, 1989. 3 C c

GAM7776 246 TCF2 Lindner, T. H.; Njolstad, P. R.; Horikawa, Y.; Bostad, L.; Bell,G. I.; Sovik, O.: A novel syndrome of diabetes mellitus, renal dysfunctionand genital malformation associated with a partial deletion of thepseudo- POU domain of hepatocyte nuclear factor- 1- beta. Hum. Molec.Genet. 8: 2001- 2008, 1999. 3 C c

GAM7776 246 TCF2 Menzel, R.; Kaisaki, P. J.; Rjasanowski, I.; Heinke, P.; Kerner,W.; Menzel, S.: A low renal threshold for glucose in diabetic patientswith a mutation in the hepatocyte nuclear factor- 1- alpha (HNF- 1- alpha)gene. Diabet. Med. 15: 816- 820, 1998. 3 C c

GAM7776 246 TCF2 Nishigori, H.; Yamada, S.; Kohama, T.; Tomura, H.; Sho, K.; Horikawa,Y.; Bell, G. I.; Takeuchi, T.; Takeda, J.: Frameshift mutation, A263fsinsGG,in the hepatocyte nuclear factor- 1- beta gene associated with diabetesand renal dysfunction. Diabetes 47: 1354- 1355, 1998. 3 C c

GAM7776 246 TCF2 Rizzoni, G.; Loirat, C.; Levy, M.; Milanesi, C.; Zachello, G.;Mathieu, H.: Familial hypoplastic glomerulocystic kidney: a new entity? Clin.Nephrol. 18: 263- 268, 1982. 3 C c

GAM7776 246 TCF2 Wild, W.; Pogge von Strandmann, E.; Nastos, A.; Senkel, S.; Lingott-Frieg,A.; Bulman, M.; Bingham, C.; Ellard, S.; Hattersley, A. T.; Ryffel,G. U.: The mutated human gene encoding hepatocyte nuclear factor1- beta inhibits kidney formation in developing Xenopus embryos. Proc.Nat. Acad. Sci. 97: 4695- 4700, 2000. 3 C c

GAM7776 246 TDGF1 Bamford, R. N.; Roessler, E.; Burdine, R. D.; Saplakoglu, U.; delaCruz, J.; Splitt, M.; Towbin, J.; Bowers, P.; Marino, B.; Schier,A. F.; Shen, M. M.; Muenke, M.; Casey, B.: Loss- of- function mutationsin the EGF- CFC gene CFC1 3 C c

are associated with human left- right lateralitydefects. Nature Genet. 26: 365- 369, 2000.

GAM7776 246 TDGF1 Ciccodicola, A.; Dono, R.; Obici, S.; Simeone, A.; Zollo, M.; Persico,M. G.: 3 C c
Molecular characterization of a gene of the 'EGF family' expressedin undifferentiated human NTERA2 teratocarcinoma cells. EMBO J. 8:1987- 1991, 1989.

GAM7776 246 TDGF1 de la Cruz, J. M.; Bamford, R. N.; Burdine, R. D.; Roessler, E.;Barkovich, 3 C c
A. J.; Donnai, D.; Schier, A. F.; Muenke, M.: A loss- of- functionmutation in the CFC domain of TDGF1 is associated with human forebraindefects. Hum. Genet. 110: 422- 428, 2002.

GAM7776 246 TDGF1 Dono, R.; Montuori, N.; Rocchi, M.; De Ponti- Zilli, L.; Ciccodicola,A.; 3 C c
Persico, M. G.: Isolation and characterization of the CRIPTOautosomal gene and its X- linked related sequence. Am. J. Hum. Genet. 49:555- 565, 1991.

GAM7776 246 TDGF1 Liguori, G.; De Gregorio, L.; Tucci, M.; Lago, C. T.; Barra, A.;Dragani, T. 3 C c
A.; Persico, M.: Mapping of the mouse Tdgf1 gene andTdgf pseudogenes. Mammalian Genome 8: 502- 505, 1997.

GAM7776 246 TDGF1 Liguori, G.; Tucci, M.; Montuori, N.; Dono, R.; Lago, C. T.; Pacifico,F.; 3 C c
Armenante, F.; Persico, M. G.: Characterization of the mouseTdgf1 gene and Tdgf pseudogenes. Mammalian Genome 7: 344- 348, 1996.

GAM7776 246 TDGF1 Saccone, S.; Rapisarda, A.; Motta, S.; Dono, R.; Persico, G. M.;Della Valle, 3 C c
G.: Regional localization of the human EGF- like growthfactor CRIPTO gene (TDGF- 1) to chromosome 3p21. Hum. Genet. 95:229- 230, 1995.

GAM7776 246 TDGF1 Shen, M. M.; Schier, A. F.: The EGF- CFC gene family in 3 C c
vertebratedevelopment. Trends Genet. 16: 303- 309, 2000.

GAM7776 246 TERF1 Broccoli, D.; Chong, L.; Oelmann, S.; Fernald, A. A.; Marziliano,N.; van 3 C b
Steensel, B.; Kipling, D.; Le Beau, M. M.; de Lange, T.:Comparison of the human and mouse genes encoding the telomeric protein,TRF1: chromosomal localization, expression and conserved protein domains. Hum.Molec. Genet. 6: 69- 76, 1997.

GAM7776 246 TERF1 Chong, L.; van Steensel, B.; Broccoli, D.; Erdjument- Bromage, H.;Hanish, 3 C b
J.; Tempst, P.; de Lange, T.: A human telomeric protein. Science 270:1663- 1667, 1995.

GAM7776 246 TERF1 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 C b
the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2. Molec. Cell 8: 351- 361, 2001.

GAM7776 246 TERF1 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 C b
Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell 97: 503- 514, 1999.

GAM7776 246 TERF1 Kim, S.; Kaminker, P.; Campisi, J.: TIN2, a new regulator of telomerelength 3 C b
in human cells. Nature Genet. 23: 405- 412, 1999.

GAM7776 246 TERF1 Marcand, S.; Gilson, E.; Shore, D.: A protein- counting mechanismfor 3 C b
telomere length regulation in yeast. Science 275: 986- 990, 1997.

GAM7776 246 TERF1 Okabe, J.; Eguchi, A.; Masago, A.; Hayakawa, T.; Nakanishi, M.: TRF1 is a 3 C b
critical trans- acting factor required for de novo telomereformation in human cells. Hum. Molec. Genet. 9: 2639- 2650, 2000.

GAM7776 246 TERF1 Young, A. C.; Chavez, M.; Giambernardi, T. A.; Mattern, V.; McGill,J. R.; 3 C b
Harris, J. M.; Sarosdy, M. F.; Patel, P.; Sakaguchi, A. Y.: Organization and expression of human telomere repeat binding factorgenes. Somat. Cell Molec. Genet. 23: 275- 286, 1997.

GAM7776 246 TERF1 Zakian, V. A.: Telomeres: beginning to understand the end. Science 270:1601- 3 C b

1607, 1995.

GAM7776 246 TERF2 Bailey, S. M.; Cornforth, M. N.; Kurimasa, A.; Chen, D. J.; Goodwin,E. H.: 3 C c
Strand- specific postreplicative processing of mammalian telomeres. Science
293:2462- 2465, 2001.

GAM7776 246 TERF2 Bilaud, T.; Brun, C.; Ancelin, K.; Koering, C. E.; Laroche, T.;Gilson, E.: 3 C c
Telomeric localization of TRF2, a novel human teloboxprotein. Nature Genet.
17: 236- 239, 1997.

GAM7776 246 TERF2 Broccoli, D.; Smogorzewska, A.; Chong, L.; de Lange, T.: Humantelomeres 3 C c
contain two distinct Myb- related proteins, TRF1 and TRF2. NatureGenet. 17:
231- 235, 1997.

GAM7776 246 TERF2 Fairall, L.; Chapman, L.; Moss, H.; de Lange, T.; Rhodes, D.:Structure of 3 C c
the TRFH dimerization domain of the human telomeric proteinsTRF1 and TRF2.
Molec. Cell 8: 351- 361, 2001.

GAM7776 246 TERF2 Griffith, J. D.; Comeau, L.; Rosenfield, S.; Stansel, R. M.; Bianchi,A.; 3 C c
Moss, H.; de Lange, T.: Mammalian telomeres end in a large duplexloop. Cell
97: 503- 514, 1999.

GAM7776 246 TERF2 Karlseder, J.; Smogorzewska, A.; de Lange, T.: Senescence inducedby altered 3 C c
telomere state, not telomere loss. Science 295: 2446- 2449,2002.

GAM7776 246 TERF2 Sakaguchi, A. Y.; Padalecki, S. S.; Mattern, V.; Rodriguez, A.;Leach, R. J.; 3 C c
McGill, J. R.; Chavez, M.; Giambernardi, T. A.: Chromosomalsublocalization
of the transcribed human telomere repeat binding factor2 gene and
comparative mapping in the mouse. Somat. Cell Molec. Genet. 24:157- 163,
1998.

GAM7776 246 TERF2 van Steensel, B.; Smogorzewska, A.; de Lange, T.: TRF2 protectshuman 3 C c
telomeres from end- to- end fusions. Cell 92: 401- 413, 1998.

GAM7776 246 TERF2 Zhu, X.- D.; Kuster, B.; Mann, M.; Petrini, J. H. J.; de Lange,T.: Cell- 3 C c
cycle- regulated association of RAD50/MRE11/NBS1 with TRF2and human
telomeres. Nature Genet. 25: 347- 352, 2000.

GAM7776 246 TLR5 Chaudhary, P. M.; Ferguson, C.; Nguyen, V.; Nguyen, O.; Massa,H. F.; Eby, 3 C c
M.; Jasmin, A.; Trask, B. J.; Hood, L.; Nelson, P. S.: Cloning and
characterization of two Toll/interleukin- 1 receptor- likegenes TIL3 and
TIL4: evidence for a multi- gene receptor family inhumans. Blood 91: 4020-
4027, 1998.

GAM7776 246 TLR5 Hayashi, F.; Smith, K. D.; Ozinsky, A.,; Hawn, T. R.; Yi, E. C.;Goodlett, D. 3 C c
R.; Eng, J. K.; Akira, S.; Underhill, D. M.; Aderem,A.: The innate immune
response to bacterial flagellin is mediatedby Toll- like receptor 5. Nature
410: 1099- 1103, 2001.

GAM7776 246 TLR5 Kadowaki, N.; Ho, S.; Antonenko, S.; de Waal Malefyt, R.; Kastelein,R. A.; 3 C c
Bazan, F.; Liu, Y.- J.: Subsets of human dendritic cell precursorsexpress
different Toll- like receptors and respond to different microbialantigens.
J. Exp. Med. 194: 863- 869, 2001.

GAM7776 246 TLR5 Muzio, M.; Bosisio, D.; Polentarutti, N.; D'amico, G.; Stoppacciaro,A.; 3 C c
Mancinelli, R.; van't Veer, C.; Penton- Rol, G.; Ruco, L. P.; Allavena,P.;
Mantovani, A.: Differential expression and regulation of Toll- likereceptors
(TLR) in human leukocytes: selective expression of TLR3in dendritic cells.
J. Immun. 164: 5998- 6004, 2000.

GAM7776 246 TLR5 Rock, F. L.; Hardiman, G.; Timans, J. C.; Kastelein, R. A.; Bazan,J. F.: A 3 C c
family of human receptors structurally related to DrosophilaToll. Proc. Nat.
Acad. Sci. 95: 588- 593, 1998.

GAM7776 246 TMC1 Kurima, K.; Peters. L. M.; Yang, Y.; Riazuddin, S.; Ahmed, Z. M.;Naz, S.; 3 C b

Arnaud, D.; Drury, S.; Mo, J.; Makishima, T.; Ghosh, M.;Menon, P. S. N.; and 13 others: Dominant and recessive deafnesscaused by mutations of a novel gene, TMC1, required for cochlear hair- cellfunction. Nature Genet. 30: 277-284, 2002.

GAM7776 246 TMC1 Vreugde, S.; Erven, A.; Kros, C. J.; Marcotti, W.; Fuches, H.;Kurima, K.; 3 C b Wilcox, E. R.; Friedman, T. B.; Griffith, A. J.; Balling,R.; de Angelis, M. H.; Avraham, K. B.; Steel, K. P.: Beethoven, amouse model for dominant, progressive hearing loss DFNA36. NatureGenet. 30: 257- 258, 2002.

GAM7776 246 TNFRSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; 3 C b B Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999.

GAM7776 246 TNFRSF10 MacFarlane, M.; Ahmad, M.; Srinivasula, S. M.; Fernandes- Alnemri,T.; Cohen, 3 C b B G. M.; Alnemri, E. S.: Identification and molecular cloningof two novel receptors for the cytotoxic ligand TRAIL. J. Biol. Chem. 272:25417- 25420, 1997.

GAM7776 246 TNFRSF10 Marsters, S. A.; Sheridan, J. P.; Pitti, R. M.; Huang, A.; Skubatch,M.; 3 C b B Baldwin, D.; Yuan, J.; Gurney, A.; Goddard, A. D.; Godowski, P.;Ashkenazi, A.: A novel receptor for Apo2L/TRAIL contains a truncateddeath domain. Curr. Biol. 7: 1003- 1006, 1997.

GAM7776 246 TNFRSF10 Pai, S. I.; Wu, G. S.; Ozoren, N.; Wu, L.; Jen, J.; Sidransky,D.; El- Deiry, 3 C b B W. S.: Rare loss- of- function mutation of a death receptorgene in head and neck cancer. Cancer Res. 58: 3513- 3518, 1998.

GAM7776 246 TNFRSF10 Pan, G.; Ni, J.; Wei, Y.- F.; Yu, G.; Gentz, R.; Dixit, V. M.:An antagonist 3 C b B decoy receptor and a death domain- containing receptorfor TRAIL. Science 277: 815- 818, 1997.

GAM7776 246 TNFRSF10 Schneider, P.; Bodmer, J.- L.; Thome, M.; Hofmann, K.; Holler, N.;Tschopp, 3 C b B J.: Characterization of two receptors for TRAIL. FEBS Lett. 416:329- 334, 1997.

GAM7776 246 TNFRSF10 Screaton, G. R.; Mongkolsapaya, J.; Xu, X.- N.; Cowper, A. E.; McMichael,A. 3 C b B J.; Bell, J. I.: TRICK2, a new alternatively spliced receptorthat transduces the cytotoxic signal from TRAIL. Curr. Biol. 7:693- 696, 1997.

GAM7776 246 TNFRSF10 Sheridan, J. P.; Marsters, S. A.; Pitti, R. M.; Gurney, A.; Skubatch,M.; 3 C b B Baldwin, D.; Ramakrishnan, L.; Gray, C. L.; Baker, K.; Wood, W.I.; Goddard, A. D.; Godowski, P.; Ashkenazi, A.: Control of TRAIL- inducedapoptosis by a family of signaling and decoy receptors. Science 277:818- 821, 1997.

GAM7776 246 TNFRSF10 Walczak, H.; Degli- Esposti, M. A.; Johnson, R. S.; Smolak, P. J.;Waugh, J. 3 C b B Y.; Boiani, N.; Timour, M. S.; Gerhart, M. J.; Schooley,K. A.; Smith, C. A.; Goodwin, R. G.; Rauch, C. T.: TRAIL- R2: a novelapoptosis- mediating receptor for TRAIL. EMBO J. 16: 5386- 5397, 1997.

GAM7776 246 TNFRSF10 Wu, G. S.; Burns, T. F.; McDonald, E. R., III; Jiang, W.; Meng,R.; Krantz, 3 C b B I. D.; Kao, G.; Gan, D.- D.; Zhou, J.- Y.; Muschel, R.;Hamilton, S. R.; Spinner, N. B.; Markowitz, S.; Wu, G.; El- Deiry,W. S.: KILLER/DR5 is a DNA damage- inducible p53- regulated death receptorgene. Nature Genet. 17: 141-143, 1997.

GAM7776 246 TNFRSF9 Alderson, M. R.; Smith, C. A.; Tough, T. W.; Davis- Smith, T.; Armitage,R. 3 C c J.; Falk, B.; Roux, E.; Baker, E.; Sutherland, G. R.; Din, W. S.;Goodwin, R. G.: Molecular and biological characterization of human4- 1BB and its ligand. Europ. J. Immun. 24: 2219- 2227, 1994.

GAM7776 246 TNFRSF9 Kwon, B. S.; Weissman, S. M.: cDNA sequences of two inducibleT- cell genes. 3 C c
Proc. Nat. Acad. Sci. 86: 1963- 1967, 1989.

GAM7776 246 TNFRSF9 Loo, D. T.; Chalupny, N. J.; Bajorath, J.; Shuford, W. W.; Mittler,R. S.; 3 C c
Aruffo, A.: Analysis of 4- 1BBL and laminin binding to murine4- 1BB, a
member of the tumor necrosis factor receptor superfamily,and comparison with
human 4- 1BB. J. Biol. Chem. 272: 6448- 6456,1997.

GAM7776 246 TNFRSF9 Schwarz, H.; Arden, K.; Lotz, M.: CD137, a member of the tumornecrosis 3 C c
factor receptor family, is located on chromosome 1p36, ina cluster of
related genes, and colocalizes with several malignancies. Biochem.Biophys.
Res. Commun. 235: 699- 703, 1997.

GAM7776 246 TNFRSF9 Schwarz, H.; Blanco, F. J.; von Kempis, J.; Valbracht, J.; Lotz,M.: ILA, a 3 C c
member of the human nerve growth factor/tumor necrosisfactor receptor
family, regulates T- lymphocyte proliferation and survival. Blood 87:2839-
2845, 1996.

GAM7776 246 TNFRSF9 Schwarz, H.; Tuckwell, J.; Lotz, M.: A receptor induced by 3 C c
lymphocyteactivation (ILA): a new member of the human nerve- growth-
factor/tumor- necrosis- factorreceptor family. Gene 134: 295- 298, 1993.

GAM7776 246 TPMT Alves, S.; Prata, M.- J.; Ferreira, F.; Amorim, A.: 3 C b
Thiopurinemethyltransferase pharmacogenetics: alternative molecular
diagnosisand preliminary data from Northern Portugal. Pharmacogenetics
9:257- 261, 1999.

GAM7776 246 TPMT Ameyaw, M.- M.; Collie- Duguid, E. S. R.; Powrie, R. H.; Ofori- Adjei,D.; 3 C b
McLeod, H. L.: Thiopurine methyltransferase alleles in Britishand Ghanaian
populations. Hum. Molec. Genet. 8: 367- 370, 1999.

GAM7776 246 TPMT Collie- Duguid, E. S. R.; Pritchard, S. C.; Powrie, R. H.; Sludden,J.; 3 C b
Collier, D. A.; Li, T.; McLeod, H. L.: The frequency and distributionof
thiopurine methyltransferase alleles in Caucasian and Asian populations.
Pharmacogenetics 9:37- 42, 1999.

GAM7776 246 TPMT Evans, W. E.; Horner, M.; Chu, Y. Q.; Kalwinsky, D.; Roberts, W.M.: Altered 3 C b
mercaptopurine metabolism, toxic effects, and dosagerequirement in a
thiopurine methyltransferase- deficient child withacute lymphocytic
leukemia. J. Pediat. 119: 985- 989, 1991.

GAM7776 246 TPMT Hon, Y. Y.; Fessing, M. Y.; Pui, C.- H.; Relling, M. V.; Krynetski,E. Y.; 3 C b
Evans, W. E.: Polymorphism of the thiopurine S- methyltransferasegene in
African- Americans. Hum. Molec. Genet. 8: 371- 376, 1999.

GAM7776 246 TPMT Honchel, R.; Aksoy, I. A.; Szumlanski, C.; Wood, T. C.; Otterness,D. M.; 3 C b
Wieben, E. D.; Weinshilboum, R. M.: Human thiopurine
methyltransferase:molecular cloning and expression of T84 colon carcinoma
cell cDNA. Molec.Pharm. 43: 878- 887, 1993.

GAM7776 246 TPMT Klemetsdal, B.; Wist, E.; Aarbakke, J.: Gender difference in redblood cell 3 C b
thiopurine methyltransferase activity. Scand. J. Clin.Lab. Invest. 53: 747-
749, 1993.

GAM7776 246 TPMT Krynetski, E. Y.; Schuetz, J. D.; Galpin, A. J.; Pui, C.- H.; Relling,M. V.; 3 C b
Evans, W. E.: A single point mutation leading to loss of catalyticactivity
in human thiopurine S- methyltransferase. Proc. Nat. Acad.Sci. 92: 949- 953,
1995.

GAM7776 246 TPMT Lennard, L.; Lilleyman, J. S.; Van Loon, J.; Weinshilboum, R. M.: Genetic 3 C b
variation in response to 6- mercaptopurine for childhoodacute lymphoblastic
leukaemia. Lancet 336: 225- 229, 1990.

GAM7776 246 TPMT Lennard, L.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof acute azathioprine toxicity: relationship to thiopurine methyltransferasegenetic polymorphism. Clin. Pharm. Therap. 46: 149- 154, 1989. 3 C b

GAM7776 246 TPMT McLeod, H. L.; Pritchard, S. C.; Githang'a, J.; Indalo, A.; Ameyaw,M.- M.; Powrie, R. H.; Booth, L.; Collie- Duguid, E. S. R.: Ethnicdifferences in thiopurine methyltransferase pharmacogenetics: evidencefor allele specificity in Caucasian and Kenyan individuals. Pharmacogenetics 9:773- 776, 1999. 3 C b

GAM7776 246 TPMT Otterness, D. M.; Szumlanski, C. L.; Wood, T. C.; Weinshilboum,R. M.: Human thiopurine methyltransferase pharmacogenetics: kindredwith a terminal exon splice junction mutation that results in lossof activity. J. Clin. Invest. 101: 1036- 1044, 1998. 3 C b

GAM7776 246 TPMT Otterness, D.; Szumlanski, C.; Lennard, L. Klemetsdal, B.; Aarbakke,J.; Park- Hah, J. O.; Iven, H.; Schmiegelow, K.; Branum, E.; O'Brien,J.; Weinshilboum, R.: Human thiopurine methyltransferase pharmacogenetics:gene sequence polymorphisms. Clin. Pharm. Therap. 62: 60- 73, 1997. 3 C b

GAM7776 246 TPMT Szumlanski, C.; Otterness, D.; Her, C.; Lee, D.; Brandriff, B.;Kelsell, D.; Spurr, N.; Lennard, L.; Wieben, E.; Weinshilboum, R.: Thiopurine methyltransferase pharmacogenetics: human gene cloningand characterization of a common polymorphism. DNA Cell Biol. 15:17- 30, 1996. 3 C b

GAM7776 246 TPMT Tai, H.- L.; Krynetski, E. Y.; Schuetz, E. G.; Yanishevski, Y.;Evans, W. E.: Enhanced proteolysis of thiopurine S- methyltransferase(TPMT) encoded by mutant alleles in humans (TPMT*3A, TPMT*2): mechanismsfor the genetic polymorphism of TPMT activity. Proc. Nat. Acad. Sci. 94:6444- 6449, 1997. 3 C b

GAM7776 246 TPMT Tai, H.- L.; Krynetski, E. Y.; Yates, C. R.; Loennechen, T.; Fessing,M. Y.; Krynetskaia, N. F.; Evans, W. E.: Thiopurine S- methyltransferasedeficiency: two nucleotide transitions define the most prevalent mutantallele associated with loss of catalytic activity in Caucasians. Am.J. Hum. Genet. 58: 694- 702, 1996. 3 C b

GAM7776 246 TPMT Weinshilboum, R. M.; Sladek, S. L.: Mercaptopurine pharmacogenetics:monogenic inheritance of erythrocyte thiopurine methyltransferaseactivity. Am. J. Hum. Genet. 32: 651- 662, 1980. 3 C b

GAM7776 246 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor- associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF- kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997. 3 C c

GAM7776 246 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661- 14664, 1996. 3 C c

GAM7776 246 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.; Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted disruption of Traf5 gene causes defectsin CD40- and CD27- mediated lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999. 3 C c

GAM7776 246 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.: Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997. 3 C c

GAM7776 246 TRPM6 Schlingmann, K. P.; Weber, S.; Peters, M.; Nejsum, L. N.; Vitzthum,H.; 3 C b

Klingel, K.; Kratz, M.; Haddad, E.; Ristoff, E.; Dinour, D.; Syrrou,M.; Nielsen, S.; Sassen, M.; Waldegger, S.; Seyberth, H. W.; Konrad,M.: Hypomagnesemia with secondary hypocalcemia is caused by mutationsin TRPM6, a new member of the TRPM gene family. Nature Genet. 31:166- 170, 2002.

GAM7776 246 TRPM6 Walder, R. Y.; Landau, D.; Meyer, P.; Shalev, H.; Tsolia, M.; Borochowitz,Z.; Boettger, M. B.; Beck, G. E.; Englehardt, R. K.; Carmi, R.; Sheffield,V. C.: Mutation of TRPM6 causes familial hypomagnesemia with secondaryhypocalcemia. Nature Genet. 31: 171- 174, 2002. 3 C b

GAM7776 246 TRPM6 Walder, R. Y.; Shalev, H.; Brennan, T. M. H.; Carmi, R.; Elbedour,K.; Scott, D. A.; Hanauer, A.; Mark, A. L.; Patil, S.; Stone, E. M.;Sheffield, V. C.: Familial hypomagnesemia maps to chromosome 9q,not to the X chromosome: genetic linkage mapping and analysis of abalanced translocation breakpoint. Hum. Molec. Genet. 6: 1491- 1497,1997. 3 C b

GAM7776 246 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994. 3 C b

GAM7776 246 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000. 3 C b

GAM7776 246 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the pain pathway. Nature 389: 816- 824, 1997. 3 C b

GAM7776 246 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 3 C b

GAM7776 246 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity to 'hot' chili peppers. Cell 108: 421- 430, 2002. 3 C b

GAM7776 246 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000. 3 C b

GAM7776 246 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996. 3 C b

GAM7776 246 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel activity by protein kinase C. Nature 408: 985- 990, 2000. 3 C b

GAM7776 246 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand multiple presentations of the oral irritant zingerone: relationshipto frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996. 3 C b

GAM7776 246 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994. 3 C b

GAM7776 246 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand pleasantness for the capsaicin burn between chili likers and non- likers:implications for liking development. Chem. Senses 18: 471- 482, 1993. 3 C b

GAM7776 246 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. 3 C b

Genome Res. 10: 165- 173, 2000.

GAM7776 246 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002. 3 C b

GAM7776 246 UGDH Bontemps, Y.; Maquart, F.- X.; , Wegrowski, Y.: Human UDP-glucosedehydrogenase gene: complete cloning and transcription start mapping. Biochem.Biophys. Res. Commun. 275: 981- 985, 2000. 3 C b

GAM7776 246 UGDH Hempel, J.; Perozich, J.; Romovacek, H.; Hinich, A.; Kuo, I.; Feingold,D. S.: UDP- glucose dehydrogenase from bovine liver: primary structureand relationship to other dehydrogenases. Protein Sci. 3: 1074- 1080,1994. 3 C b

GAM7776 246 UGDH Marcu, O.; Stathakis, D. G.; Marsh, J. L.: Assignment of the UGDHlocus encoding UDP- glucose dehydrogenase to human chromosome band4p15.1 by radiation hybrid mapping. Cytogenet. Cell Genet. 86: 244- 245,1999. 3 C b

GAM7776 246 UGDH Spicer, A. P.; Kaback, L. A.; Smith, T. J.; Seldin, M. F.: Molecularcloning and characterization of the human and mouse UDP- glucose dehydrogenasegenes. J. Biol. Chem. 273: 25117- 25124, 1998. 3 C b

GAM7776 246 UGDH Walsh, E. C.; Stainier, D. Y. R.: UDP- glucose dehydrogenase requiredfor cardiac valve formation in zebrafish. Science 293: 1670- 1674,2001. 3 C b

GAM7776 246 UGT1A4 Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.;Yeatman, M. T.; Owens, I. S.: A novel complex locus UGT1 encodeshuman bilirubin, phenol, and other UDP- glucuronosyltransferase isozymeswith identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261,1992. 3 C c

GAM7776 246 UGT1A4 Ritter, J. K.; Crawford, J. M.; Owens, I. S.: Cloning of two humanliver bilirubin UDP- glucuronosyltransferase cDNAs with expressionin COS- 1 cells. J. Biol. Chem. 266: 1043- 1047, 1991. 3 C c

GAM7776 246 UGT1A4 Tukey, R. H.; Strassburg, C. P.: Human UDP-glucuronosyltransferases:metabolism, expression, and disease. Annu. Rev. Pharm. Toxicol. 40:581- 616, 2000. 3 C c

GAM7776 246 UGT1A8 Huang, Y.- H.; Galijatovic, A.; Nguyen, N.; Geske, D.; Beaton, D.;Green, J.; Green, M.; Peters, W. H.; Tukey, R. H.: Identificationand functional characterization of UDP- glucuronosyltransferases UGT1A8*1,UGT1A8*2 and UGT1A8*3. Pharmacogenetics 12: 287- 297, 2002. 3 C c

GAM7776 246 UGT1A8 Mojarrabi, B.; Mackenzie, P. I.: Characterization of two UDP glucuronosyltransferasesthat are predominantly expressed in human colon. Biochem. Biophys.Res. Commun. 247: 704- 709, 1998. 3 C c

GAM7776 246 UGT1A8 Ritter, J. K.; Chen, F.; Sheen, Y. Y.; Tran, H. M.; Kimura, S.;Yeatman, M. T.; Owens, I. S.: A novel complex locus UGT1 encodeshuman bilirubin, phenol, and other UDP- glucuronosyltransferase isozymeswith identical carboxyl termini. J. Biol. Chem. 267: 3257- 3261,1992. 3 C c

GAM7776 246 UGT1A8 Strassburg, C. P.; Manns, M. P.; Tukey, R. H.: Expression of theUDP-glucuronosyltransferase 1A locus in human colon: identificationand characterization of the novel extrahepatic UGT1A8. J. Biol. Chem. 273:8719-8726, 1998. 3 C c

GAM7776 246 UGT1A9 Findlay, K. A. B.; Kaptein, E.; Visser, T. J.; Burchell, B.: Characterizationof the uridine diphosphate- glucuronosyltransferase-catalyzing thyroidhormone glucuronidation in man. J. Clin. Endocr. Metab. 85: 2879- 2883,2000. 3 C c

GAM7776 246 UGT1A9 Harding, D.; Jeremiah, S. J.; Povey, S.; Burchell, B.: Chromosomalmapping of 3 C c

a human phenol UDP- glucuronosyltransferase, GNT1. Ann.Hum. Genet. 54: 17-21, 1990.

GAM7776 246 UGT1A9 Harding, D.; Jeremiah, S. J.; Povey, S.; Burchell, B.: PhenolUDP- glucuronosyltransferase is coded by a gene on human chromosome2. (Abstract) Cytogenet. Cell Genet. 51: 1011, 1989. 3 C c

GAM7776 246 UGT1A9 Wooster, R.; Sutherland, L.; Ebner, T.; Clarke, D.; Da Cruz e Silva,O.; Burchell, B.: Cloning and stable expression of a new member ofthe human liver phenol/bilirubin:UDP- glucuronosyltransferase cDNAfamily. Biochem. J. 278: 465- 469, 1991. 3 C c

GAM7776 246 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 C c

GAM7776 246 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 C c

GAM7776 246 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 C c

GAM7776 246 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 C c

GAM7776 246 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000. 3 C c

GAM7776 246 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938. 3 C c

GAM7776 246 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999. 3 C c

GAM7776 246 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence for a founder effect. Hum. Genet. 95: 551- 556,1995. 3 C c

GAM7776 246 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. Arch.Neurol. 28: 67- 68, 1973. 3 C c

GAM7776 246 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942. 3 C c

GAM7776 246 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures of phaeochromocytoma. Lancet I: 492- 494, 1970. 3 C c

GAM7776 246 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962. 3 C c

GAM7776 246 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell, 3 C c

J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.; Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the von Hippel- Lindau disease tumorsuppressor gene: correlations with phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM7776 246 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 C c Genotype- phenotype correlation in von Hippel- Lindaudisease: identification of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM7776 246 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 C c disease. J.A.M.A. 178: 280- 282, 1961.

GAM7776 246 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 C c peculiar vascular new growth, probably primarily retinal,affecting both eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM7776 246 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 C c K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM7776 246 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 C c F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E. R.: Identification of intragenic mutations in thevon Hippel- Lindau disease tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994.

GAM7776 246 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's 3 C c disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928.

GAM7776 246 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- 3 C c expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994.

GAM7776 246 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p 3 C c involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65, 1988.

GAM7776 246 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, 3 C c S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the VHL tumor suppressor gene product: localization, complex formation,and the effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459- 6463, 1995.

GAM7776 246 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. 3 C c P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.: Inhibition of transcription elongation by the VHL tumor suppressorprotein. Science 269: 1402- 1406, 1995.

GAM7776 246 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; 3 C c Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W. M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple endocrine neoplasia type 2 display distinctbiochemical and clinical phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001.

GAM7776 246 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; 3 C c Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto- oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937,

1995.

GAM7776 246 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian, Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.; Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate HIF by prolyl hydroxylation. Cell107: 43- 54, 2001. 3 C c

GAM7776 246 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 C c

GAM7776 246 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 3 C c

GAM7776 246 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin TRiC. Molec. Cell 1051- 1061, 1999. 3 C c

GAM7776 246 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof von Hippel- Lindau disease. Radiology 133: 289- 295, 1979. 3 C c

GAM7776 246 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331, 1979. 3 C c

GAM7776 246 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001. 3 C c

GAM7776 246 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with hydrocephalus as a complication of cerebellar hemangioblastoma:identification of pro157leu mutation in the VHL gene. J. Hum. Genet. 45:47- 51, 2000. 3 C c

GAM7776 246 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C Thomas (pub.) 1946. 3 C c

GAM7776 246 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989. 3 C c

GAM7776 246 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg. Path. 18: 1254- 1260, 1994. 3 C c

GAM7776 246 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.; Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999. 3 C c

GAM7776 246 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 C c

GAM7776 246 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 C c

GAM7776 246 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 C c

GAM7776 246 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 C c

GAM7776 246 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, 3 C c

M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991.

GAM7776 246 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992. 3 C c

GAM7776 246 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997. 3 C c

GAM7776 246 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984. 3 C c

GAM7776 246 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968. 3 C c

GAM7776 246 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 C c

GAM7776 246 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986. 3 C c

GAM7776 246 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour, phaeochromocytoma and the von Hippel- Lindau complex:two distinctive neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987. 3 C c

GAM7776 246 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: Familial pheochromocytoma associated with a novel mutation inthe von Hippel- Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996. 3 C c

GAM7776 246 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam: North Holland (pub.) 14: 1972. Pp. 241- 259. 3 C c

GAM7776 246 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors in livers with targeted inactivation of the von Hippel- Lindautumor suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001. 3 C c

GAM7776 246 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022- 1034, 1971. 3 C c

GAM7776 246 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8: 601- 606,1967. 3 C c

GAM7776 246 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas. Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994. 3 C c

GAM7776 246 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.; Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma only. J. Med. Genet. 37: 939- 943,2000. 3 C c

GAM7776 246 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; 3 C c

Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips, C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet. 106: 425- 431, 2000.

GAM7776 246 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: 3 C c von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001.

GAM7776 246 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; 3 C c Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002.

GAM7776 246 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; 3 C c Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989.

GAM7776 246 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - 3 C c clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976.

GAM7776 246 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, 3 C c P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990.

GAM7776 246 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid 3 C c body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982.

GAM7776 246 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; 3 C c Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel- Lindaudisease. Brain 109: 1297- 1310, 1986.

GAM7776 246 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression 3 C c by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995.

GAM7776 246 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: 3 C c Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996.

GAM7776 246 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a 3 C c biologicallyactive product of the von Hippel- Lindau gene arising from internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666, 1998.

GAM7776 246 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; 3 C c Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL- mediated destruction by proline hydroxylation: implicationsfor O(2) sensing. Science 292: 464- 468, 2001.

GAM7776 246 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; 3 C c Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel- Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998.

GAM7776 246 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; 3 C c Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.; Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting

of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-regulated prolyl hydroxylation. Science 292: 468- 472, 2001.

GAM7776 246 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 C c

GAM7776 246 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British family: clinicopathological features and recommendationsfor screening and follow- up. Quart. J. Med. 66: 233- 249, 1988. 3 C c

GAM7776 246 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-Lindau tumor suppressor gene in sporadic centralnervous system hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994. 3 C c

GAM7776 246 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during neuronal differentiation. Cancer Res. 60: 2820- 2824,2000. 3 C c

GAM7776 246 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961. 3 C c

GAM7776 246 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.; Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease: new strategies in early detection and treatment. Am.J. Med. 97: 158- 168, 1994. 3 C c

GAM7776 246 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992. 3 C c

GAM7776 246 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the VHL gene is associated exclusively with the developmentof non- papillary renal cell carcinomas. J. Path. 179: 157- 161, 1996. 3 C c

GAM7776 246 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-581, 1995. 3 C c

GAM7776 246 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 C c

GAM7776 246 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 C c

GAM7776 246 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel-Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 C c

GAM7776 246 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 C c

GAM7776 246 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 C c

GAM7776 246 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel-Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 C c

GAM7776 246 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 C c

GAM7776 246 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 C c

GAM7776 246 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; 3 C c

Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317- 1320, 1993.

GAM7776 246 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 C c

GAM7776 246 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 C c

GAM7776 246 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 C c

GAM7776 246 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 C c

GAM7776 246 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002. 3 C c

GAM7776 246 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 C c

GAM7776 246 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 3 C c

GAM7776 246 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 C c

GAM7776 246 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 C c

GAM7776 246 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 C c

GAM7776 246 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 C c

GAM7776 246 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple 3 C c

myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM7776 246 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 C c

GAM7776 246 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 C c

GAM7776 246 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 C c

GAM7776 246 WNT5A Clark, C. C.; Cohen, I.; Eichstetter, I.; Cannizzaro, L. A.; McPherson,J. D.; Wasmuth, J. J.; Iozzo, R. V.: Molecular cloning of the humanproto-oncogene Wnt- 5A and mapping of the gene (WNT5A) to chromosome3p14- p21. Genomics 18: 249- 260, 1993. 3 C c

GAM7776 246 WNT5A Gavin, B. J.; McMahon, J. A.; McMahon, A. P.: Expression of multiplenovel Wnt- 1/int- 1- related genes during fetal and adult mouse development. GenesDev. 4: 2319- 2332, 1990. 3 C c

GAM7776 246 WNT5A He, X.; Saint- Jeannet, J.- P.; Wang, Y.; Nathans, J.; Dawid, I.;Varmus, H.: A member of the frizzled protein family mediating axisinduction by Wnt- 5A. Science 275: 1652- 1654, 1997. 3 C c

GAM7776 246 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 3 C c

GAM7776 246 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 C c

GAM7776 246 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x-ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 3 C c

GAM7776 246 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. Genomics 26: 619- 622, 1995. 3 C c

GAM7776 246 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 3 C c

GAM7776 246 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 C c

GAM7776 246 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 C c

GAM7776 246 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; 3 C c
Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional
candidate. Genomics 41: 84- 92, 1997.

GAM7776 246 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: 3 C c
Localization to chromosome 7q36.1 of the human XRCC2 gene,determining
sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995.

GAM7776 246 YES1 Fukuhara, S.; Rowley, J. D.; Variakojis, D.; Sweet, D. L.: 3 C b
Chromosomeabnormalities in poorly differentiated lymphocytic lymphoma.
CancerRes. 39: 3119- 3128, 1979.

GAM7776 246 YES1 Ohno, H.; Fukuhara, S.; Takahashi, R.; Mihara, K.; Sugiyama, T.;Doi, S.; 3 C b
Uchino, H.; Toyoshima, K.: c- yes and bcl- 2 genes locatedon 18q21.3 in a
follicular lymphoma cell line carrying a t(14;18)chromosomal translocation.
Int. J. Cancer 39: 785- 788, 1987.

GAM7776 246 YES1 Overhauser, J.; Mewar, R.; Rojas, K.; Lia, K.; Kline, A. D.; Silverman,G. 3 C b
A.: STS map of genes and anonymous DNA fragments on human chromosome18 using
a panel of somatic cell hybrids. Genomics 15: 387- 391,1993.

GAM7776 246 YES1 Semba, K.; Nishizawa, M.; Satoh, H.; Fukushige, S.; Yoshida, M.C.; Sasaki, 3 C b
M.; Matsubara, K.; Yamamoto, T.; Toyoshima, K.: Nucleotidesequence and
chromosomal mapping of the human c- yes- 2 gene. Jpn.J. Cancer Res. 79: 710-
717, 1988.

GAM7776 246 YES1 Semba, K.; Yamanashi, Y.; Nishizawa, M.; Sukegawa, J.; Yoshida,M.; Sasaki, 3 C b
M.; Yamamoto, T.; Toyoshima, K.: Location of the c- yesgene on the human
chromosome and its expression in various tissues. Science 227:1038- 1040,
1985.

GAM7776 246 YES1 Silverman, G. A.; Kuo, W.- L.; Taillon- Miller, P.; Gray, J. W.:Chromosomal 3 C b
reassignment: YACs containing both YES1 and thymidylatesynthase map to the
short arm of chromosome 18. Genomics 15: 442- 445,1993.

GAM7776 246 YES1 Sukegawa, J.; Semba, K.; Yamanashi, Y.; Nishizawa, M.; Miyajima,N.; 3 C b
Yamamoto, T.; Toyoshima, K.: Characterization of cDNA clonesfor the human c-
yes gene. Molec. Cell. Biol. 7: 41- 47, 1987.

GAM7776 246 YES1 Yoshida, M. C.; Sasaki, M.; Mise, K.; Semba, K.; Nishizawa, M.;Yamamoto, T.; 3 C b
Toyoshima, K.: Regional mapping of the human proto- oncogenec- yes- 1 to
chromosome 18 at band q21.3. Jpn. J. Cancer Res. 76:559- 562, 1985.

GAM7809 398 APAF1 Cecconi, F.; Alvarez- Bolado, G.; Meyer, B. I.; Roth, K. A.; Gruss,P.: Apaf1 3 A c
(CED- 4 homolog) regulates programmed cell death in mammaliandevelopment.
Cell 94: 727- 737, 1998.

GAM7809 398 APAF1 Hahn, C.; Hirsch, B.; Jahnke, D.; Durkop, H.; Stein, H.: Threenew types of 3 A c
Apaf- 1 in mammalian cells. Biochem. Biophys. Res. Commun. 261:746- 749,
1999.

GAM7809 398 APAF1 Honarpour, N.; Du, C.; Richardson, J. A.; Hammer, R. E.; Wang,X.; Herz, J.: 3 A c
Adult Apaf- 1- deficient mice exhibit male infertility. Dev.Biol. 218: 248-
258, 2000.

GAM7809 398 APAF1 Honarpour, N.; Gilbert, S. L.; Lahn, B. T.; Wang, X.; Herz, J.: Apaf- 1 3 A c
deficiency and neural tube closure defects are found in fogmice. Proc. Nat.
Acad. Sci. 98: 9683- 9687, 2001.

GAM7809 398 APAF1 Kim, H.; Jung, Y. K.; Kwon, Y. K.; Park, S. H.: Assignment ofapoptotic 3 A c
protease activating factor- 1 gene (APAF1) to human chromosomeband 12q23 by
fluorescence in situ hybridization. Cytogenet. CellGenet. 87: 252- 253,
1999.

GAM7809 398 APAF1 Marsden, V. S.; O'Connor, L.; O'Reilly, L. A.; Silke, J.; Metcalf,D.; Ekert, 3 A c

P. G.; Huang, D. C. S.; Cecconi, F.; Kuida, K.; Tomaselli,K. J.; Roy, S.; Nicholson, D. W.; Vaux, D. L.; Bouillet, P.; Adams,J. M.; Strasser, A.: Apoptosis initiated by Bcl- 2- regulated caspaseactivation independently of the cytochrome c/Apaf- 1/caspase- 9 apoptosome. Nature 419:634- 637, 2002.

GAM7809 398 APAF1 Soengas, M. S.; Capodieci, P.; Polsky, D.; Mora, J.; Esteller,M.; Opitz- 3 A c
Araya, X.; McCombie, R.; Herman, J. G.; Gerald, W. L.; Lazebnik,Y. A.; Cordon- Cardo, C.; Lowe, S. W.: Inactivation of the apoptosiseffector Apaf- 1 in malignant melanoma. Nature 409: 207- 211, 2001.

GAM7809 398 APAF1 Srinivasula, S. M.; Ahmad, M.; Fernandes- Alnemri, T.; Alnemri,E. S.: 3 A c
Autoactivation of procaspase- 9 by Apaf- 1- mediated oligomerization. Molec.Cell 1: 949- 957, 1998.

GAM7809 398 APAF1 Yoshida, H.; Kong, Y.- Y.; Yoshida, R.; Elia, A. J.; Hakem, A.;Hakem, R.; 3 A c
Penninger, J. M.; Mak, T. W.: Apaf1 is required for mitochondrialpathways of apoptosis and brain development. Cell 94: 739- 750, 1998.

GAM7809 398 APAF1 Zou, H.; Henzel, W. J.; Liu, X.; Lutschg, A.; Wang, X.: APAF- 1,a human 3 A c
protein homologous to C. elegans CED- 4, participates in cytochromec-dependent activation of caspase- 3. Cell 90: 405- 413, 1997.

GAM7809 398 DDX11 Amann, J.; Kidd, V. J.; Lahti, J. M.: Characterization of putativehuman 3 A c
homologues of the yeast chromosome transmission fidelity gene,CHL1. J. Biol. Chem. 272: 3823- 3832, 1997.

GAM7809 398 DDX11 Amann, J.; Valentine, M.; Kidd, V. J.; Lahti, J. M.: Localizationof Chl1- 3 A c
related helicase genes to human chromosome regions 12p11 and12p13: similarity between parts of these genes and conserved humantelomeric-associated DNA. Genomics 32: 260- 265, 1996.

GAM7809 398 DDX11 Frank, S.; Werner, S.: The human homologue of the yeast CHL1 geneis a novel 3 A c
keratinocyte growth factor- regulated gene. J. Biol. Chem. 271:24337- 24340, 1996.

GAM7809 398 HNMT Aksoy, S.; Raftogianis, R.; Weinshilboum, R.: Human histamineN- 3 A c
methyltransferase gene: structural characterization and chromosomallocalization. Biochem. Biophys. Res. Commun. 219: 548- 554, 1996.

GAM7809 398 HNMT Preuss, C. V.; Wood, T. C.; Szumlanski, C. L.; Raftogianis, R.B.; Otterness, 3 A c
D. M.; Girard, B.; Scott, M. C.; Weinshilboum, R. M.: Human histamine N-methyltransferase pharmacogenetics: common geneticpolymorphisms that alter activity. Molec. Pharm. 53: 708- 717, 1998.

GAM7809 398 HNMT Price, R. A.; Scott, M. C.; Weinshilboum, R. M.: Genetic segregationanalysis 3 A c
of red blood cell (RBC) histamine N- methyltransferase (HNMT)activity. Genet. Epidemiol. 10: 123- 131, 1993.

GAM7809 398 HNMT Scott, M. C.; Van Loon, J. A.; Weinshilboum, R. M.: Pharmacogeneticsof N- 3 A c
methylation: heritability of human erythrocyte histamine N-methyltransferaseactivity. Clin. Pharm. Ther. 43: 256- 262, 1988.

GAM7809 398 HNMT Yamauchi, K.; Sekizawa, K.; Suzuki, H.; Nakazawa, H.; Ohkawara,Y.; Katayose, 3 A c
D.; Ohtsu, H.; Tamura, G.; Shibahara, S.; Takemura,M.; Maeyama, K.; Watanabe, T.; Sasaki, H.; Shirato, K.; Takishima,T.: Structure and function of human histamine N- methyltransferase:critical enzyme in histamine metabolism in airway. Am. J. Physiol. 267:L342- L349, 1994.

GAM7809 398 HNMT Yan, L.; Galinsky, R. E.; Bernstein, J. A.; Liggett, S. B.; Weinshilboum,R. 3 A c
M.: Histamine N- methyltransferase pharmacogenetics: associationof a common functional polymorphism with asthma. Pharmacogenetics 10:261- 266, 2000.

GAM7809 398 ITGB2 Abramson, J. S.; Mills, E. L.; Sawyer, M. K.; Regelmann, W. R.;Nelson, J. 3 A c
D.; Quie, P. G.: Recurrent infections and delayed separationof the umbilical

cord in an infant with abnormal phagocytic cell locomotionand oxidative response during particle phagocytosis. J. Pediat. 99:887- 894, 1981.

GAM7809 398 ITGB2 Akao, Y.; Utsumi, K. R.; Naito, K.; Ueda, R.; Takahashi, T.; Yamada,K.: 3 A c
Chromosomal assignments of genes coding for human leukocyte commonantigen, T- 200, and lymphocyte function- associated antigen 1, LFA- 1beta subunit. Somat. Cell Molec. Genet. 13: 273- 278, 1987.

GAM7809 398 ITGB2 Allende, L. M.; Hernandez, M.; Corell, A.; Garcia- Perez, M. A.;Varela, P.; 3 A c
Moreno, A.; Caragol, I.; Garcia- Martin, F.; Guillen- Perales,J.; Olive, T.; Espanol, T.; Arnaiz- Villena, A.: A novel CD18 genomicdeletion in a patient with severe leucocyte adhesion deficiency: apossible CD2/lymphocyte function- associated antigen- 1 functional associationin humans. Immunology 99: 440- 450, 2000.

GAM7809 398 ITGB2 Anderson, D. C.; Schmalstieg, F. C.; Finegold, M. J.; Hughes, B.J.; 3 A c
Rothlein, R.; Miller, L. J.; Kohl, S.; Tosi, M. F.; Jacobs, R.L.; Waldrop, T. C.; Goldman, A. S.; Shearer, W. T.; Springer, T. A.: The severe and moderate phenotypes of heritable Mac- 1, LFA- 1 deficiency:their quantitative definition and relation to leukocyte dysfunctionand clinical features. J. Infect. Dis. 152: 668- 689, 1985.

GAM7809 398 ITGB2 Anderson, D. C.; Springer, T. A.: Leukocyte adhesion deficiency:an inherited 3 A c
defect in the Mac- 1, LFA- 1, and p150,95 glycoproteins. Annu.Rev. Med. 38: 175- 194, 1987.

GAM7809 398 ITGB2 Arnaout, M. A.; Dana, N.; Gupta, S. K.; Tenen, D. G.; Fathallah,D. M.: Point 3 A c
mutations impairing cell surface expression of the commonbeta subunit (CD18) in a patient with leukocyte adhesion molecule(Leu- CAM) deficiency. J. Clin. Invest. 85: 977- 981, 1990.

GAM7809 398 ITGB2 Arnaout, M. A.; Pitt, J.; Cohen, H. J.; Melamed, J.; Rosen, F.S.; Colten, H. 3 A c
R.: Deficiency of a granulocyte- membrane glycoprotein(gp150) in a boy with recurrent bacterial infections. New Eng. J.Med. 306: 693- 699, 1982.

GAM7809 398 ITGB2 Arnaout, M. A.; Spits, H.; Terhorst, C.; Pitt, J.; Todd, R. F.,III: 3 A c
Deficiency of a leukocyte surface glycoprotein (LFA- 1) in twopatients with Mo1 deficiency: effects of cell activation on Mo1/LFA- 1surface expression in normal and deficient leukocytes. J. Clin. Invest. 74:1291- 1300, 1984.

GAM7809 398 ITGB2 Back, A. L.; Kerkering, M.; Baker, D.; Bauer, T. R.; Embree, L.J.; 3 A c
Hickstein, D. D.: A point mutation associated with leukocyteadhesion deficiency type 1 of moderate severity. Biochem. Biophys.Res. Commun. 193: 912- 918, 1993.

GAM7809 398 ITGB2 Back, A. L.; Kwok, W. W.; Hickstein, D. D.: Identification oftwo molecular 3 A c
defects in a child with leukocyte adherence deficiency. J.Biol. Chem. 267: 5482- 5487, 1992.

GAM7809 398 ITGB2 Bairoch, A.: Personal Communication. Geneva, Switzerland 5/13/1994. 3 A c

GAM7809 398 ITGB2 Barclay, A. N.; Birkeland, M. L.; Brown, M. H.; Beyers, A. D.;Davis, S. J.; 3 A c
Somoza, C.; Williams, A. F.: The Leukocyte AntigenFacts Book. New York: Academic Press (pub.) 1993. Pp. 124- 127and 140- 141.

GAM7809 398 ITGB2 Beatty, P. G.; Ochs, H. D.; Harlan, J. M.; Price, T. H.; Rosen,H.; Taylor, 3 A c
R. F.; Hansen, J. A.; Klebanoff, S. J.: Absence of monoclonal- antibody-definedprotein complex in a boy with abnormal leucocyte function. Lancet I:535- 537, 1984.

GAM7809 398 ITGB2 Bianchi, E.; Denti, S.; Granata, A.; Bossi, G.; Geginat, J.; Villa,A.; 3 A c
Rogge, L.; Pardi, R.: Integrin LFA- 1 interacts with the transcriptionalco-activator JAB1 to modulate AP- 1 activity. Nature 404: 617- 621,2000.

GAM7809 398 ITGB2 Bissenden, J. G.; Haeney, M. R.; Tarlow, M. J.; Thompson, R. A.: Delayed separation of the umbilical cord, severe widespread infections,and immunodeficiency. Arch. Dis. Child. 56: 397- 399, 1981. 3 A c

GAM7809 398 ITGB2 Boucheix, C.: Personal Communication. Villejuif, France 1/31/1987. 3 A c

GAM7809 398 ITGB2 Bowen, T. J.; Ochs, H. D.; Altman, L. C.; Price, T. H.; Van Epps,D. E.; Brautigan, D. L.; Rosin, R. E.; Perkins, W. D.; Babior, B.M.; Klebanoff, S. J.; Wedgwood, R. J.: Severe recurrent bacterialinfections associated with defective adherence and chemotaxis in twopatients with neutrophils deficient in a cell- associated glycoprotein. J.Pediat. 101: 932- 940, 1982. 3 A c

GAM7809 398 ITGB2 Bullard, D. C.; Scharffetter- Kochanek, K.; McArthur, M. J.; Chosay,J. G.; McBride, M. E.; Montgomery, C. A.; Beaudet, A. L.: A polygenicmouse model of psoriasiform skin disease in CD18- deficient mice. Proc.Nat. Acad. Sci. 93: 2116- 2121, 1996. 3 A c

GAM7809 398 ITGB2 Crowley, C. A.; Curnutte, J. T.; Rosin, R. E.; Andre- Schwartz,J.; Gallin, J. I.; Klempner, M.; Snyderman, R.; Southwick, F. S.;Stossel, T. P.; Babior, B. M.: An inherited abnormality of neutrophiladhesion: its genetic transmission and its association with a missingprotein. New Eng. J. Med. 302: 1163- 1168, 1980. 3 A c

GAM7809 398 ITGB2 Dana, N.; Clayton, L. K.; Tennen, D. G.; Pierce, M. W.; Lachmann,P. J.; Law, S. A.; Arnaout, M. A.: Leukocytes from four patientswith complete or partial Leu- CAM deficiency contain the common beta- subunitprecursor and beta-subunit messenger RNA. J. Clin. Invest. 79: 1010- 1015,1987. 3 A c

GAM7809 398 ITGB2 Dana, N.; Todd, R. F., III; Pitt, J.; Springer, T. A.; Arnaout,M. A.: Deficiency of a surface membrane glycoprotein (Mo1) in man. J.Clin. Invest. 73: 153- 159, 1984. 3 A c

GAM7809 398 ITGB2 Fischer, A.; Griscelli, C.; Friedrich, W.; Kubanek, B.; Levinsky,R.; Morgan, G.; Vossen, J.; Wagemaker, G.; Landais, P.: Bone- marrowtransplantation for immunodeficiencies and osteopetrosis: Europeansurvey, 1968- 1985. Lancet II: 1080- 1084, 1986. 3 A c

GAM7809 398 ITGB2 Fujita, K.; Kobayashi, K.; Kajii, T.: Impaired neutrophil adhesion:a new patient in a previously reported family. Acta Paediat. Jpn. 27:527- 534, 1985. 3 A c

GAM7809 398 ITGB2 Fujita, K.; Kobayashi, K.; Okino, F.: Juvenile rheumatoid arthritisin two siblings with congenital leucocyte adhesion deficiency. Europ.J. Pediat. 148: 118- 119, 1988. 3 A c

GAM7809 398 ITGB2 Harvath, L.; Andersen, B. R.: Defective initiation of oxidativemetabolism in polymorphonuclear leukocytes. New Eng. J. Med. 300:1130- 1135, 1979. 3 A c

GAM7809 398 ITGB2 Hayward, A. R.; Leonard, J.; Harvey, B. A. M.; Greenwood, M. C.;Wood, C. B. S.; Soothill, J. F.: Delayed separation of the umbilicalcord, widespread infections, and defective neutrophil mobility. Lancet I:1099- 1101, 1979. 3 A c

GAM7809 398 ITGB2 Hibbs, M. L.; Wardlaw, A. J.; Stacker, S. A.; Anderson, D. C.;Lee, A.; Roberts, T. M.; Springer, T. A.: Transfection of cells frompatients with leukocyte adhesion deficiency with an integrin betasubunit (CD18) restores lymphocyte function- associated antigen- 1 expressionand function. J. Clin. Invest. 85: 674- 681, 1990. 3 A c

GAM7809 398 ITGB2 Hogg, N.; Stewart, M. P.; Scarth, S. L.; Newton, R.; Shaw, J.M.; Law, S. K. A.; Klein, N.: A novel leukocyte adhesion deficiencycaused by expressed but nonfunctional beta- 2 integrins Mac- 1 and LFA- 1. J.Clin. Invest. 103: 97-106, 1999. 3 A c

GAM7809 398 ITGB2 Hynes, R. O.: Integrins: versatility, modulation and signalingin cell 3 A c

adhesion. Cell 69: 11- 25, 1992.

GAM7809 398 ITGB2 Kehrli, M. E., Jr.; Ackermann, M. R.; Shuster, D. E.; van derMaaten, M. J.; 3 A c
Schmalstieg, F. C.; Anderson, D. C.; Hughes, B. J.: Bovine leukocyte
adhesion deficiency: beta(2) integrin deficiencyin young Holstein cattle.
Am. J. Path. 140: 1489- 1492, 1992.

GAM7809 398 ITGB2 Kishimoto, T. K.; Hollander, N.; Roberts, T. M.; Anderson, D.C.; Springer, 3 A c
T. A.: Heterogeneous mutations in the beta subunitcommon to the LFA- 1, Mac-
1, and p150,95 glycoproteins cause leukocyteadhesion deficiency. Cell 50:
193- 202, 1987.

GAM7809 398 ITGB2 Kishimoto, T. K.; O'Connor, K.; Lee, A.; Roberts, T. M.; Springer,T. A.: 3 A c
Cloning of the beta subunit of the leukocyte adhesion proteins:homology to
an extracellular matrix receptor defines a novel supergenefamily. Cell 48:
681- 690, 1987.

GAM7809 398 ITGB2 Kobayashi, K.; Fujita, K.; Okino, F.; Kajii, T.: An abnormalityof neutrophil 3 A c
adhesion: autosomal recessive inheritance associatedwith missing neutrophil
glycoproteins. Pediatrics 73: 606- 610, 1984.

GAM7809 398 ITGB2 Krauss, J. C.; Mayo- Bond, L. A.; Rogers, C. E.; Weber, K. L.;Todd, R. F., 3 A c
III; Wilson, J. M.: An in vivo animal model of genetherapy for leukocyte
adhesion deficiency. J. Clin. Invest. 88:1412- 1417, 1991.

GAM7809 398 ITGB2 Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cellretention in 3 A c
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM7809 398 ITGB2 Marlin, S. D.; Morton, C. C.; Anderson, D. C.; Springer, T. A.: LFA- 1 3 A c
immunodeficiency disease: definition of the genetic defectand chromosomal
mapping of alpha and beta subunits of the lymphocytefunction- associated
antigen 1 (LFA- 1) by complementation in hybridcells. J. Exp. Med. 164: 855-
867, 1986.

GAM7809 398 ITGB2 Matsuura, S.; Kishi, F.; Tsukahara, M.; Nunoi, H.; Matsuda, I.;Kobayashi, 3 A c
K.; Kajii, T.: Leukocyte adhesion deficiency: identificationof novel
mutations in two Japanese patients with a severe form. Biochem.Biophys. Res.
Commun. 184: 1460- 1467, 1992.

GAM7809 398 ITGB2 Nelson, C.; Rabb, H.; Arnaout, M. A.: Genetic cause of leukocyteadhesion 3 A c
molecule deficiency: abnormal splicing and a missense mutationin a conserved
region of CD18 impair cell surface expression of beta- 2integrins. J. Biol.
Chem. 267: 3351- 3357, 1992.

GAM7809 398 ITGB2 Niethammer, D.; Dieterle, U.; Kleihauer, E.; Wildfeuer, A.; Haferkamp,O.; 3 A c
Hitzig, W. H.: An inherited defect in granulocyte function:
impairedchemotaxis, phagocytosis and intracellular killing of
microorganisms. Helv.Paediat. Acta 30: 537- 541, 1976.

GAM7809 398 ITGB2 Ostermann, G.; Weber, K. S. C.; Zernecke, A.; Schroder, A.; Weber,C.: JAM- 1 3 A c
is a ligand of the beta- 2 integrin LFA- 1 involved in
transendothelialmigration of leukocytes. Nature Immun. 3: 151- 158, 2002.

GAM7809 398 ITGB2 Petersen, M. B.; Slaugenhaupt, S. A.; Lewis, J. G.; Warren, A.C.; 3 A c
Chakravarti, A.; Antonarakis, S. E.: A genetic linkage map of27 markers on
human chromosome 21. Genomics 9: 407- 419, 1991.

GAM7809 398 ITGB2 Pierce, M. W.; Remold- O'Donnell, E.; Todd, R. F., III; Arnaout,M. A.: N- 3 A c
terminal sequence of human leukocyte glycoprotein Mo1: conservationacross
species and homology to platelet IIb/IIIa. Biochim. Biophys.Acta 874: 368-
371, 1986.

GAM7809 398 ITGB2 Rivera- Matos, I. R.; Rakita, R. M.; Mariscalco, M. M.; Elder,F. F. B.; 3 A c
Dreyer, S. A.; Cleary, T. G.: Leukocyte adhesion deficiencymimicking

Hirschsprung disease. J. Pediat. 127: 755- 757, 1995.

GAM7809 398 ITGB2 Rosmarin, A. G.; Caprio, D.; Levy, R.; Simkevich, C.: CD18 (beta- 2leukocyte 3 A c
integrin) promoter requires PU.1 transcription factor formyeloid activity.
Proc. Nat. Acad. Sci. 92: 801- 805, 1995.

GAM7809 398 ITGB2 Ross, G. D.: Clinical and laboratory features of patients withan inherited 3 A c
deficiency of neutrophil membrane complement receptortype 3 (CR3) and the
related membrane antigens LFA- 1 and p150,95. J.Clin. Immun. 6: 107- 113,
1986.

GAM7809 398 ITGB2 Ross, G. D.; Thompson, R. A.; Walport, M. J.; Springer, T. A.;Watson, J. V.; 3 A c
Ward, R. H. R.; Lida, J.; Newman, S. L.; Harrison,R. A.; Lachmann, P. J.:
Characterization of patients with an increasedsusceptibility to bacterial
infections and a genetic deficiency ofleukocyte membrane complement receptor
type three (CR3) and the relatedmembrane antigen LFA- 1. Blood 66: 882- 890,
1985.

GAM7809 398 ITGB2 Shuster, D. E.; Kehrli, M. E., Jr.; Ackermann, M. R.; Gilbert,R. O.: 3 A c
Identification and prevalence of a genetic defect that causesleukocyte
adhesion deficiency in Holstein cattle. Proc. Nat. Acad.Sci. 89: 9225- 9229,
1992.

GAM7809 398 ITGB2 Sligh, J. E., Jr.; Anderson, D. C.; Beaudet, A. L.: A mutationin the 3 A c
initiation codon of the CD18 gene in a patient with the moderatephenotype of
leukocyte adhesion deficiency. (Abstract) Am. J. Hum.Genet. 45 (suppl.):
A219, 1989.

GAM7809 398 ITGB2 Solomon, E.; Palmer, R. W.; Hing, S.; Law, S. K. A.: Regionallocalization of 3 A c
CD18, the beta- subunit of the cell surface adhesionmolecule LFA- 1, on
human chromosome 21 by in situ hybridization. Ann.Hum. Genet. 52: 123- 128,
1988.

GAM7809 398 ITGB2 Springer, T. A.; Miller, L. J.; Anderson, D. C.: p150,95, thethird member of 3 A c
the Mac- 1, LFA- 1 human leukocyte adhesion glycoproteinfamily. J. Immun.
136: 240- 245, 1986.

GAM7809 398 ITGB2 Springer, T. A.; Teplow, D. B.; Dreyer, W. J.: Sequence homologyof the LFA- 3 A c
1 and Mac- 1 leukocyte adhesion glycoproteins and unexpectedrelation to
leukocyte interferon. Nature 314: 540- 542, 1985.

GAM7809 398 ITGB2 Springer, T. A.; Thompson, W. S.; Miller, L. J.; Schmalstieg,F. C.; 3 A c
Anderson, D. C.: Inherited deficiency of the Mac- 1, LFA- 1,p150,95
glycoprotein family and its molecular basis. J. Exp. Med. 160:1901- 1918,
1984.

GAM7809 398 ITGB2 Suomalainen, H. A.; Gahmberg, C. G.; Patarroyo, M.; Beatty, P.G.; Schroder, 3 A c
J.: Genetic assignment of GP90, leukocyte adhesionglycoprotein to human
chromosome 21. Somat. Cell Molec. Genet. 12:297- 302, 1986.

GAM7809 398 ITGB2 Suomalainen, H. A.; Gahmberg, C. G.; Patarroyo, M.; Schroder,J.: GP90 (Leu- 3 A c
CAM antigen) is coded for by genes on chromosome 21.(Abstract) Cytogenet.
Cell Genet. 40: 755, 1985.

GAM7809 398 ITGB2 Taylor, G. M.; Williams, A.; D'Souza, S. W.; Fergusson, W. D.;Donnai, D.; 3 A c
Fennell, J.; Harris, R.: The expression of CD18 is increasedon trisomy 21
(Down syndrome) lymphoblastoid cells. Clin. Exp. Immun. 71:324- 328, 1988.

GAM7809 398 ITGB2 Todd, R. F., III; Freyer, D. R.: The CD11/CD18 leukocyte 3 A c
glycoproteindeficiency. Hemat. Oncol. Clin. North Am. 2: 13- 31, 1988.

GAM7809 398 ITGB2 van der Meer, J. W. M.; van Zwet, T. L.; van Furth, R.: New familialdefect 3 A c
in microbicidal function of polymorphonuclear leucocytes. Lancet II:630-
632, 1975.

GAM7809 398 ITGB2 Vazquez- Torres, A.; Jones- Carson, J.; Baumler, A. J.; Falkow,S.; Valdivia, R.; Brown, W.; Le, M.; Berggren, R.; Parks, W. T.; Fang,F. C.: Extraintestinal dissemination of Salmonella by CD18- expressingphagocytes. Nature 401: 804- 808, 1999. 3 A c

GAM7809 398 ITGB2 Vedder, N. B.; Winn, R. K.; Rice, C. L.; Chi, E. Y.; Arfors, K.- E.;Harlan, J. M.: A monoclonal antibody to the adherence- promoting leukocyteglycoprotein, CD18, reduces organ injury and improves survival fromhemorrhagic shock and resuscitation in rabbits. J. Clin. Invest. 81:939- 944, 1988. 3 A c

GAM7809 398 ITGB2 Wardlaw, A. J.; Hibbs, M. L.; Stacker, S. A.; Springer, T. A.: Distinct mutations in two patients with leukocyte adhesion deficiencyand their functional correlates. J. Exp. Med. 172: 335- 345, 1990. 3 A c

GAM7809 398 ITGB2 Weening, R. S.; Roos, D.; Weemaes, C. M. R.; Homan- Muller, J.W. T.; van Schaik, M. L. J.: Defective initiation of the metabolicstimulation in phagocytizing granulocytes: a new congenital defect. J.Lab. Clin. Med. 88: 757- 768, 1976. 3 A c

GAM7809 398 ITGB2 Weitzman, J. B.; Wells, C. E.; Wright, A. H.; Clark, P. A.; Law,S. K. A.: The gene organisation of the human beta- 2 integrin subunit(CD18). FEBS Lett. 294: 97- 103, 1991. 3 A c

GAM7809 398 ITGB2 Wilson, J. M.; Ping, A. J.; Krauss, J. C.; Mayo- Bond, L.; Rogers,C. E.; Anderson, D. C.; Todd, R. F., III: Correction of CD18- deficientlymphocytes by retrovirus- mediated gene transfer. Science 248: 1413- 1416,1990. 3 A c

GAM7809 398 ITGB2 Wilson, R. W.; Ballantyne, C. M.; Smith, C. W.; Montgomery, C.;Bradley, A.; O'Brien, W. E.; Beaudet, A. L.: Gene targeting yieldsa CD18- mutant mouse for study of inflammation. J. Immun. 151: 1571- 1578,1993. 3 A c

GAM7809 398 ITGB2 Yorifuji, T.; Wilson, R. W.; Beaudet, A. L.: Retroviral mediatedexpression of CD18 in normal and deficient human bone marrow progenitorcells. Hum. Molec. Genet. 2: 1443- 1448, 1993. 3 A c

GAM7809 398 MS4A6A Ishibashi, K.; Suzuki, M.; Sasaki, S.; Imai, M.: Identificationof a new multigene four- transmembrane family (MS4A) related to CD20,HTm4 and beta subunit of the high- affinity IgE receptor. Gene 264:87- 93, 2001. 3 A c

GAM7809 398 MS4A6A Liang, Y.; Tedder, T. F.: Identification of a CD20- , Fc- epsilon- RI- beta- relatedgene family: sixteen new MS4A family members expressed in human andmouse. Genomics 72: 119- 127, 2001. 3 A c

GAM7809 398 NFIB Geurts, J. M. W.; Schoenmakers, E. F. P. M.; Roijer, E.; Astrom,A.- K.; Stenman, G.; van de Ven, W. J. M.: Identification of NFIBas recurrent translocation partner gene of HMGIC in pleomorphic adenomas. Oncogene 16:865- 872, 1998. 3 A c

GAM7809 398 NFIB Qian, F.; Kruse, U.; Lichter, P.; Sippel, A. E.: Chromosomal localizationof the four genes (NFIA, B, C, and X) for the human transcriptionfactor nuclear factor I by FISH. Genomics 28: 66- 73, 1995. 3 A c

GAM7809 398 NTRK2 Bibel, M.; Barde, Y.- A.: Neurotrophins: key regulators of cellfate and cell shape in the vertebrate nervous system. Genes Dev. 14:2919- 2937, 2000. 3 A c

GAM7809 398 NTRK2 Bothwell, M.: p75(NTR): a receptor after all. Science 272: 506- 507,1996. 3 A c

GAM7809 398 NTRK2 Carter, B. D.; Lewin, G. R.: Neurotrophins live or let die: doesp75(NTR) decide? Neuron 18: 187- 190, 1997. 3 A c

GAM7809 398 NTRK2 Ip, N. Y.; Stitt, T. N.; Tapley, P.; Klein, R.; Glass, D. J.; Fandl,J.; Greene, L. A.; Barbacid, M.; Yancopoulos, G. D.: Similaritiesand differences in the way neurotrophins interact with the Trk receptorsin neuronal and nonneuronal cells. Neuron 10: 137- 149, 1993. 3 A c

GAM7809 398 NTRK2 Nakagawara, A.; Liu, X.- G.; Ikegaki, N.; White, P. S.; Yamashiro,D. J.; 3 A c
Nycum, L. M.; Biegel, J. A.; Brodeur, G. M.: Cloning and
chromosomallocalization of the human TRK- B tyrosine kinase receptor gene
(NTRK2). Genomics 25:538- 546, 1995.

GAM7809 398 NTRK2 Rico, B.; Xu, B.; Reichardt, L. F.: TrkB receptor signaling isrequired for 3 A c
establishment of GABAergic synapses in the cerebellum. NatureNeurosci. 5:
225- 233, 2002.

GAM7809 398 NTRK2 Slaugenhaupt, S. A.; Blumenfeld, A.; Liebert, C. B.; Mull, J.;Lucente, D. 3 A c
E.; Monahan, M.; Breakefield, X. O.; Maayan, C.; Parada,L.; Axelrod, F. B.;
Gusella, J. F.: The human gene for neurotrophictyrosine kinase receptor type
2 (NTRK2) is located on chromosome 9but is not the familial dysautonomia
gene. Genomics 25: 730- 732,1995.

GAM7809 398 NTRK2 Soppet, D.; Escandon, E.; Maragos, J.; Middlemas, D. S.; Reid,S. W.; Blair, 3 A c
J.; Burton, L. E.; Stanton, B. R.; Kaplan, D. R.; Hunter,T.; Nikolics, K.;
Parada, L. F.: The neurotrophic factors brain- derivedneurotrophic factor
and neurotrophin- 3 are ligands for the trkB tyrosinekinase receptor. Cell
65: 895- 903, 1991.

GAM7809 398 NTRK2 Squinto, S. P.; Stitt, S. N.; Aldrich, T. H.; Davis, S.; Bianco,S. M.; 3 A c
Radziejewski, C.; Glass, D. J.; Masiakowski, P.; Furth, M.E.; Valenzuela, D.
M.; DiStefano, P. S.; Yancopoulos, G. D.: trkBencodes a functional receptor
for brain- derived neurotrophic factorand neurotrophin- 3 but not nerve
growth factor. Cell 65: 885- 893,1991.

GAM7809 398 NTRK2 Valent, A.; Danglot, G.; Bernheim, A.: Mapping of the tyrosinekinase 3 A c
receptors trkA (NTRK1), trkB (NTRK2) and trkC (NTRK3) to humanchromosomes
1q22, 9q22 and 15q25 by fluorescence in situ hybridization. Europ.J. Hum.
Genet. 5: 102- 104, 1997.

GAM7809 398 PCLO Fenster, S. D.; Chung, W. J.; Zhai, R.; Cases- Langhoff, C.; Voss,B.; 3 A c
Garner, A. M.; Kaempf, U.; Kindler, S.; Gundelfinger, E. D.; Garner,C. C.:
Piccolo, a presynaptic zinc finger protein structurally relatedto Bassoon.
Neuron 25: 203- 214, 2000.

GAM7809 398 PCLO Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 A c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM7809 398 PDGFRB Abe, A.; Emi, N.; Tanimoto, M.; Terasaki, H.; Marunouchi, T.; Saito,H.: 3 A c
Fusion of the platelet- derived growth factor receptor beta toa novel gene
CEV14 in acute myelogenous leukemia after clonal evolution. Blood 90:4271-
4277, 1997.

GAM7809 398 PDGFRB Apperley, J. F.; Gardembas, M.; Melo, J. V.; Russell- Jones, R.;Bain, B. J.; 3 A c
Baxter, E. J.; Chase, A.; Chessells, J. M.; Colombat,M.; Dearden, C. E.;
Dimitrijevic, S.; Mahon, F.- X.; Marin, D.; Nikolova,Z.; Olavarria, E.;
Silberman, S.; Schultheis, B.; Cross, N. C. P.;Goldman, J. M.: Response to
imatinib mesylate in patients with chronicmyeloproliferative diseases with
rearrangements of the platelet- derivedgrowth factor receptor beta. New Eng.
J. Med. 347: 481- 487, 2002.

GAM7809 398 PDGFRB Buchberg, A. M.; Jenkins, N. A.; Copeland, N. G.: Localizationof the murine 3 A c
macrophage colony- stimulating factor gene to chromosome3 using
interspecific backcross analysis. Genomics 5: 363- 367, 1989.

GAM7809 398 PDGFRB Claesson- Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek,B.; 3 A c
Ostman, A.; Betsholtz, C.; Heldin, C.- H.: cDNA cloning and expressionof a

human platelet- derived growth factor (PDGF) receptor specificfor B- chain-containing PDGF molecules. Molec. Cell. Biol. 8: 3476- 3486,1988.

GAM7809 398 PDGFRB Escobedo, J. A.; Fried, V. A.; Daniel, T. O.; Williams, L. T.:Primary structure of the platelet- derived growth factor. (Abstract) Clin.Res. 34: 544A, 1986. 3 A c

GAM7809 398 PDGFRB Francke, U.; Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.:Chromosomal mapping of genes involved in growth control. Cold SpringHarbor Symp. Quant. Biol. 51: 855- 866, 1986. 3 A c

GAM7809 398 PDGFRB Golub, T. R.; Barker, G. F.; Lovett, M.; Gilliland, D. G.: Fusionof PDGF receptor beta to a novel ets- like gene, tel, in chronic myelomonocyticleukemia with t(5;12) chromosomal translocation. Cell 77: 307-316,1994. 3 A c

GAM7809 398 PDGFRB Gronwald, R. G. K.; Grant, F. J.; Haldeman, B. A.; Hart, C. E.;O'Hara, P. J.; Hagen, F. S.; Ross, R.; Bowen- Pope, D. F.; Murray,M. J.: Cloning and expression of a cDNA coding for the human platelet- derivedgrowth factor receptor: evidence for more than one receptor class. Proc.Nat. Acad. Sci. 85: 3435- 3439, 1988. 3 A c

GAM7809 398 PDGFRB How, G.- F.; Venkatesh, B.; Brenner, S.: Conserved linkage betweenthe puffer fish (Fugu rubripes) and human genes for platelet- derivedgrowth factor receptor and macrophage colony- stimulating factor receptor. GenomeRes. 6: 1185- 1191, 1996. 3 A c

GAM7809 398 PDGFRB Klinghoffer, R. A.; Mueting- Nelsen, P. F.; Faerman, A.; Shani,M.; Soriano, P.: The two PDGF receptors maintain conserved signalingin vivo despite divergent embryological functions. Molec. Cell 7:343- 354, 2001. 3 A c

GAM7809 398 PDGFRB Kulkarni, S.; Heath, C.; Parker, S.; Chase, A.; Iqbal, S.; Pocock,C. F.; Kaeda, J.; Cwynarski, K.; Goldman, J. M.; Cross, N. C. P.:Fusion of H4/D10S170 to the platelet- derived growth factor receptorbeta in BCR- ABL-negative myeloproliferative disorders with a t(5;10)(q33;q21). CancerRes. 60: 3592- 3598, 2000. 3 A c

GAM7809 398 PDGFRB Leal, F.; Williams, L. T.; Robbins, K. C.; Aaronson, S. A.: Evidencethat the v- sis gene product transforms by interaction with the receptorfor platelet-derived growth factor. Science 230: 327- 330, 1985. 3 A c

GAM7809 398 PDGFRB Magnusson, M. K.; Meade, K. E.; Brown, K. E., Arthur, D. C.; Krueger,L. A.; Barrett, A. J.; Dunbar, C. E.: Rabaptin- 5 is a novel fusionpartner to platelet- derived growth factor beta receptor in chronicmyelomonocytic leukemia. Blood 98: 2518- 2525, 2001. 3 A c

GAM7809 398 PDGFRB Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle,W.; Kraus, M.; Pierce, J.; Aaronson, S.: Isolation of a novel receptorcDNA establishes the existence of two PDGF receptor genes. Science 243:800- 804, 1989. 3 A c

GAM7809 398 PDGFRB Roberts, W. M.; Look, A. T.; Roussel, M. F.; Sherr, C. J.: Tandemlinkage of human CSF- 1 receptor (c- fms) and PDGF receptor genes. Cell 55:655- 661, 1988. 3 A c

GAM7809 398 PDGFRB Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof Huntingtin interacting protein 1 to platelet- derived growth factor-betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998. 3 A c

GAM7809 398 PDGFRB Steer, E. J.; Cross, N. C. P.: Myeloproliferative disorders withtranslocations of chromosome 5q31- 35: role of the platelet-derivedgrowth factor receptor beta. Acta Haemat. 107: 113- 122, 2002. 3 A c

GAM7809 398 PDGFRB Treacher Collins Syndrome Collaborative Group: Positional cloningof a gene 3 A c

involved in the pathogenesis of Treacher Collins syndrome. NatureGenet. 12: 130- 136, 1996.

GAM7809 398 PDGFRB Yarden, Y.; Escobedo, J. A.; Kuang, W.- J.; Yang- Feng, T. L.; Daniel,T. O.; 3 A c
Tremble, P. M.; Chen, E. Y.; Ando, M. E.; Harkins, R. N.; Francke,U.; Fried, V. A.; Ullrich, A.; Williams, L. T.: Structure of thereceptor for platelet-derived growth factor helps define a familyof closely related growth factor receptors. Nature 323: 226- 232,1986.

GAM7809 398 PDGFRB Yarden, Y.; Ullrich, A.: Growth factor receptor tyrosine kinases. Ann.Rev. 3 A c
Biochem. 57: 443- 478, 1988.

GAM7809 398 RECK Oh, J.; Takahashi, R.; Kondo, S.; Mizoguchi, A.; Adachi, E.; Sasahara,R. M.; 3 A c
Nishimura, S.; Imamura, Y.; Kitayama, H.; Alexander, D. B.;Ide, C.; Horan, T. P.; Arakawa, T.; Yoshida, H.; Nishikawa, S.; Itoh,Y.; Seiki, M.; Itohara, S.; Takahashi, C.; Noda, M.: The membrane- anchoredMMP inhibitor RECK is a key regulator of extracellular matrix integrityand angiogenesis. Cell 107: 789- 800, 2001.

GAM7809 398 RECK Takahashi, C.; Sheng, Z.; Horan, T. P.; Kitayama, H.; Maki, M.;Hitomi, K.; 3 A c
Kitaura, Y.; Takai, S.; Sasahara, R. M.; Horimoto, A.;Ikawa, Y.; Ratzkin, B. J.; Arakawa, T.; Noda, M.: Regulation of matrixmetalloproteinase- 9 and inhibition of tumor invasion by the membrane- anchoredglycoprotein RECK. Proc. Nat. Acad. Sci. 95: 13221- 13226, 1998.

GAM7809 398 SOX5 Connor, F.; Wright, E.; Denny, P.; Koopman, P.; Ashworth, A.:The Sry- 3 A c
related HMG box- containing gene Sox6 is expressed in the adulttestis and developing nervous system of the mouse. Nucleic AcidsRes. 23: 3365- 3372, 1995.

GAM7809 398 SOX5 Wunderle, V. M.; Critcher, R.; Ashworth, A.; Goodfellow, P. N.: Cloning and 3 A c
characterization of SOX5, a new member of the humanSOX gene family. Genomics 36: 354- 358, 1996.

GAM7809 398 TTK Abrieu, A.; Magnaghi- Jaulin, L.; Kahana, J. A.; Peter, M.; Castro,A.; 3 A c
Vigneron, S.; Lorca, T.; Cleveland, D. W.; Labbe, J.- C.: Mps1is a kinetochore- associated kinase essential for the vertebrate mitoticcheckpoint. Cell 106: 83- 93, 2001.

GAM7809 398 TTK Cahill, D. P.; da Costa, L. T.; Carson- Walter, E. B.; Kinzler,K. W.; 3 A c
Vogelstein, B.; Lengauer, C.: Characterization of MAD2B andother mitotic spindle checkpoint genes. Genomics 58: 181- 187, 1999.

GAM7809 398 TTK Fisk, H. A.; Winey, M.: The mouse Mps1p- like kinase regulatescentrosome 3 A c
duplication. Cell 106: 95- 104, 2001.

GAM7809 398 TTK Lauze, E.; Stoelcker, B.; Luca, F. C.; Weiss, E.; Schutz, A. R.;Winey, M.: 3 A c
Yeast spindle pole body duplication gene MPS1 encodesan essential dual specificity protein kinase. EMBO J. 14: 1655- 1663,1995.

GAM7809 398 TTK Lindberg, R. A.; Fischer, W. H.; Hunter, T.: Characterizationof a human 3 A c
protein threonine kinase isolated by screening an expressionlibrary with antibodies to phosphotyrosine. Oncogene 8: 351- 359,1993.

GAM7809 398 TTK Mills, G. B.; Schmandt, R.; McGill, M.; Amendola, A.; Hill, M.;Jacobs, K.; 3 A c
May, C.; Rodricks, A.- M.; Campbell, S.; Hogg, D.: Expressionof TTK, a novel human protein kinase, is associated with cell proliferation. J.Biol. Chem. 267: 16000- 16006, 1992.

GAM7933 203 ADAM10 Hattori, M.; Osterfield, M.; Flanagan, J. G.: Regulated cleavageof a 7 A c
contact- mediated axon repellent. Science 289: 1360- 1365, 2000.

GAM7933 203 ADAM10 Lunn, C. A.; Fan, X.; Dalie, B.; Miller, K.; Zavodny, P. J.; Narula,S. K.; 7 A c
Lundell, D.: Purification of ADAM 10 from bovine spleen asa TNFalpha

convertase. FEBS Lett. 400: 333- 335, 1997.

GAM7933 203 ADAM10 Wolfsberg, T. G.; Primakoff, P.; Myles, D. G.; White, J. M.: ADAM,a novel 7 A c
family of membrane proteins containing a disintegrin and
metalloproteasedomain: multipotential functions in cell- cell and cell-
matrix interactions. J.Cell Biol. 131: 275- 278, 1995.

GAM7933 203 ADAM10 Yamazaki, K.; Mizui, Y.; Tanaka, I.: Radiation hybrid mappingof human ADAM10 7 A
c
gene to chromosome 15. Genomics 45: 457- 459, 1997.

GAM7933 203 ADAMTS13 Bianchi, V.; Robles, R.; Alberio, L.; Furlan, M.; Lammle, B.:Von Willebrand 7 A c
factor- cleaving protease (ADAMTS13) in thrombocytopenicdisorders: a
severely deficient activity is specific for thromboticthrombocytopenic
purpura. Blood 100: 710- 713, 2002.

GAM7933 203 ADAMTS13 Fujikawa, K.; Suzuki, H.; McMullen, B.; Chung, D.: Purificationof human von 7 A c
Willebrand factor- cleaving protease and its identificationas a new member
of the metalloproteinase family. Blood 98: 1662- 1666,2001.

GAM7933 203 ADAMTS13 Furlan, M.; Robles, R.; Galbusera, M.; Remuzzi, G.; Kyrle, P. A.;Brenner, 7 A c
B.; Krause, M.; Scharrer, I.; Aumann, V.; Mittler, U.; Solenthaler,M.;
Lammle, B.: Von Willebrand factor- cleaving protease in
thromboticthrombocytopenic purpura and the hemolytic- uremic syndrome. New
Eng.J. Med. 339: 1578- 1584, 1998.

GAM7933 203 ADAMTS13 Furlan, M.; Robles, R.; Lammle, B.: Partial purification and 7 A c
characterizationof a protease from human plasma cleaving von Willebrand
factor tofragments produced by in vivo proteolysis. Blood 87: 4223-
4234,1996.

GAM7933 203 ADAMTS13 Furlan, M.; Robles, R.; Solenthaler, M.; Wassmer, M.; Sandoz, Pl;Lammle, B.: 7 A c

Deficient activity of von Willebrand factor- cleavingprotease in chronic
relapsing thrombotic thrombocytopenic purpura. Blood 89:3097- 3103, 1997.

GAM7933 203 ADAMTS13 Gerritsen, H. E.; Robles, R.; Lammle, B.; Furlan, M.: Partialamino acid 7 A c
sequence of purified von Willebrand factor- cleaving protease. Blood
98:1654- 1661, 2001.

GAM7933 203 ADAMTS13 Kokame, K.; Matsumoto, M.; Soejima, K.; Yagi, H.; Ishizashi, H.;Funato, M.; 7 A c
Tamai, H.; Konno, M.; Kamide, K.; Kawano, Y.; Miyata,T.; Fujimura, Y.:
Mutations and common polymorphisms in ADAMTS13gene responsible for von
Willebrand factor- cleaving protease activity. Proc.Nat. Acad. Sci. 99:
11902- 11907, 2002.

GAM7933 203 ADAMTS13 Levy, G. G.; Nichols, W. C.; Lian, E. C.; Foroud, T.; McClintick,J. N.; 7 A c
McGee, B. M.; Yang, A. Y.; Slemieniak, D. R.; Stark, K. R.;Gruppo, R.;
Sarode, R.; Shurin, S. B.; Chandrasekaran, V.; Stabler,S. P.; Sabio, H.;
Bouhassira, E. E.; Upshaw, J. D., Jr.; Ginsburg,D.; Tsai, H.- M.: Mutations
in a member of the ADAMTS gene familycause thrombotic thrombocytopenic
purpura. Nature 413: 488- 494,2001.

GAM7933 203 ADAMTS13 Tsai, H.- M.: Physiologic cleavage of von Willebrand factor bya plasma 7 A c
protease is dependent on its conformation and requires calciumion. Blood 87:
4235- 4244, 1996.

GAM7933 203 ADAMTS13 Tsai, H.- M.; Lian, E. C.- Y.: Antibodies to von Willebrand factor- 7 A c
cleavingprotease in acute thrombotic thrombocytopenic purpura. New Eng.
J.Med. 339: 1585- 1594, 1998.

GAM7933 203 CENTD1 Miura, K.; Jacques, K. M.; Stauffer, S.; Kubosaki, A.; Zhu, K.;Hirsch, D. 7 A c
S.; Resau, J.; Zheng, Y.; Randazzo, P. A.: ARAP1: a pointof convergence for

Arf and Rho signaling. Molec. Cell 9: 109- 119,2002.

GAM7933 203 CENTD1 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 7 A c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM7933 203 CRI1 Carim, L.; Sumoy, L.; Andreu, N.; Estivill, X.; Escarceller, M.: 7 A c
Identification and expression analysis of C15orf3, a novel geneon chromosome
15q21.1- q21.2. Cytogenet. Cell Genet. 88: 330- 332,2000.

GAM7933 203 CRI1 MacLellan, W. R.; Xiao, G.; Abdellatif, M.; Schneider, M. D.:A novel Rb- 7 A c
and p300- binding protein inhibits transactivation by MyoD. Molec.Cell.
Biol. 20: 8903- 8915, 2000.

GAM7933 203 CRI1 Miyake, S.; Sellers, W. R.; Safran, M.; Li, X.; Zhao, W.; Grossman,S. R.; 7 A c
Gan, J.; DeCaprio, J. A.; Adams, P. D.; Kaelin, W. G., Jr.: Cells degrade a
novel inhibitor of differentiation with E1A- likeproperties upon exiting the
cell cycle. Molec. Cell. Biol. 20: 8889- 8902,2000.

GAM7933 203 EZH1 Abel, K. J.; Brody, L. C.; Valdes, J. M.; Erdos, M. R.; McKinley,D. R.; 7 A c
Castilla, L. H.; Merajver, S. D.; Couch, F. J.; Friedman, L.S.; Ostermeyer,
E. A.; Lynch, E. D.; King, M.- C.; Welcsh, P. L.; Osborne- Lawrence,S.;
Spillman, M.; Bowcock, A. M.; Collins, F. S.; Weber, B. L.:
Characterizationof EZH1, a human homolog of Drosophila enhancer of zeste
near BRCA1. Genomics 37:161- 171, 1996.

GAM7933 203 EZH1 Cardoso, C.; Mignon, C.; Hetet, G.; Grandchamps, B.; Fontes, M.;Colleaux, 7 A c
L.: The human EZH2 gene: genomic organisation and revisedmapping in 7q35
within the critical region for malignant myeloid disorders. Europ.J. Hum.
Genet. 8: 174- 180, 2000.

GAM7933 203 EZH1 Cardoso, C.; Timsit, S.; Villard, L.; Khrestchatisky, M.; Fontes,M.; 7 A c
Colleaux, L.: Specific interaction between the XNP/ATR- X geneproduct and
the SET domain of the human EZH2 protein. Hum. Molec.Genet. 7: 679- 684,
1998.

GAM7933 203 EZH1 Chen, H.; Rossier, C.; Antonarakis, S. E.: Cloning of a humanhomolog of the 7 A c
Drosophila enhancer of zeste gene (EZH2) that mapsto chromosome 21q22.2.
Genomics 38: 30- 37, 1996.

GAM7933 203 EZH1 Dohner, K.; Brown, J.; Hehmann, U.; Hetzel, C.; Stewart, J.; Lowther,G.; 7 A c
Scholl, C.; Frohling, S.; Cuneo, A.; Tsui, L. C.; Lichter, P.;Scherer, S.
W.; Dohner, H.: Molecular cytogenetic characterizationof a critical region
in bands 7q35- q36 commonly deleted in malignantmyeloid disorders. Blood 92:
4031- 4035, 1998.

GAM7933 203 EZH1 Laible, G.; Haynes, A. R.; Lebersorger, A.; O'Carroll, D.; Mattei,M.- G.; 7 A c
Denny, P.; Brown, S. D. M.; Jenuwein, T.: The murine polycomb- groupgenes
Ezh1 and Ezh2 map close to Hox gene clusters on mouse chromosomes11 and 6.
Mammalian Genome 10: 311- 314, 1999.

GAM7933 203 EZH1 Varambally, S.; Dhanasekaran, S. M.; Zhou, M.; Barrette, T. R.;Kumar- Sinha, 7 A c
C.; Sanda, M. G.; Ghosh, D.; Pienta, K. J.; Sewalt, R.G. A. B.; Otte, A. P.;
Rubin, M. A.; Chinnaiyan, A. M.: The polycombgroup protein EZH2 is involved
in progression of prostate cancer. Nature 419:624- 629, 2002.

GAM7933 203 FGF2 Abraham, J. A.; Mergia, A.; Whang, J. L.; Tumolo, A.; Friedman,J.; Hjerild, 7 A c
K. A.; Gospodarowicz, D.; Fiddes, J. C.: Nucleotidesequence of a bovine
clone encoding the angiogenic protein, basicfibroblast growth factor.
Science 233: 545- 548, 1986.

GAM7933 203 FGF2 Abraham, J. A.; Whang, J. L.; Tumolo, A.; Mergia, A.; Friedman,J.; 7 A c

Gospodarowicz, D.; Fiddes, J. C.: Human basic fibroblast growthfactor: nucleotide sequence and genomic organization. EMBO J. 5:2523- 2528, 1986.

GAM7933 203 FGF2 Doniach, T.: Basic FGF as an inducer of anteroposterior neuralpattern. Cell 7 A c
83: 1067- 1070, 1995.

GAM7933 203 FGF2 Dono, R.; Texido, G.; Dussel, R.; Ehmke, H.; Zeller, R.: Impairedcerebral 7 A c
cortex development and blood pressure regulation in FGF2- deficientmice.
EMBO J. 17: 4213- 4225, 1998.

GAM7933 203 FGF2 Eckenstein, F. P.: Fibroblast growth factors in the nervous system. 7 A c
J.Neurobiol. 25: 1467- 1480, 1994.

GAM7933 203 FGF2 Fukushima, Y.; Byers, M. G.; Fiddes, J. C.; Shows, T. B.: Thehuman basic 7 A c
fibroblast growth factor gene (FGFB) is assigned to chromosome4q25.
Cytogenet. Cell Genet. 54: 159- 160, 1990.

GAM7933 203 FGF2 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; 7 A c
Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast
growth factor homologous factor 2 (FHF2): gene structure,expression and
mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated
by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63,
1999.

GAM7933 203 FGF2 Gritti, A.; Parati, E. A.; Cova, L.; Frolichsthal, P.; Galli, R.;Wanke, E.; 7 A c
Faravelli, L.; Morassutti, D. J.; Roisen, F.; Nickel, D.D.; Vescovi, A. L.:
Multipotential stem cells from the adult mousebrain proliferate and self-
renew in response to basic fibroblast growthfactor. J. Neurosci. 16: 1091-
1100, 1996.

GAM7933 203 FGF2 Johnson, R. L.; Tabin, C. J.: Molecular models for vertebratelimb 7 A c
development. Cell 90: 979- 990, 1997.

GAM7933 203 FGF2 Jung, J.; Zheng, M.; Goldfarb, M.; Zaret, K. S.: Initiation ofmammalian 7 A c
liver development from endoderm by fibroblast growth factors. Science
284:1998- 2003, 1999.

GAM7933 203 FGF2 Kawaguchi, H.; Nakamura, K.; Tabata, Y.; Ikada, Y.; Aoyama, I.;Anzai, J.; 7 A c
Nakamura, T.; Hiyama, Y.; Tamura, M.: Acceleration offracture healing in
nonhuman primates by fibroblast growth factor- 2. J.Clin. Endocr. Metab. 86:
875- 880, 2001.

GAM7933 203 FGF2 Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.: Cloning andexpression of 7 A c
cDNA encoding human basic fibroblast growth factor. FEBSLett. 213: 189- 194,
1987.

GAM7933 203 FGF2 Lafage- Pochitaloff, M.; Galland, F.; Simonetti, J.; Prats, H.;Mattei, M.- 7 A c
G.; Birnbaum, D.: The human basic fibroblast growth factorgene is located on
the long arm of chromosome 4 at bands q26- q27. OncogeneRes. 5: 241- 244,
1990.

GAM7933 203 FGF2 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; 7 A c
Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21
by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997.

GAM7933 203 FGF2 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 7 A c
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM7933 203 FGF2 Mergia, A.; Eddy, R.; Abraham, J. A.; Fiddes, J. C.; Shows, T.B.: The genes 7 A c
for basic and acidic fibroblast growth factors areon different human
chromosomes. Biochem. Biophys. Res. Commun. 138:644- 651, 1986.

GAM7933 203 FGF2 Montero, A.; Okada, Y.; Tomita, M.; Ito, M.; Tsurukami, H.; Nakamura,T.; 7 A c
Doetschman, T.; Coffin, J. D.; Hurley, M. M.: Disruption of thefibroblast
growth factor- 2 gene results in decreased bone mass andbone formation. J.

Clin. Invest. 105: 1085- 1093, 2000.

GAM7933 203 FGF2 Ortega, S.; Ittmann, M.; Tsang, S. H.; Ehrlich, M.; Basilico,C.: Neuronal 7 A c
defects and delayed wound healing in mice lacking fibroblastgrowth factor 2.
Proc. Nat. Acad. Sci. 95: 5672- 5677, 1998.

GAM7933 203 FGF2 Plotnikov, A. N.; Hubbard, S. R.; Schlessinger, J.; Mohammadi,M.: Crystal 7 A c
structures of two FGF- FGFR complexes reveal the determinantsof ligand-
receptor specificity. Cell 101: 413- 424, 2000.

GAM7933 203 FGF2 Plotnikov, A. N.; Schlessinger, J.; Hubbard, S. R.; Mohammadi,M.: Structural 7 A c
basis for FGF receptor dimerization and activation. Cell 98:641- 650, 1999.

GAM7933 203 FGF2 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. 7 A c
C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast
growth factor (FGF) homologous factors: new membersof the FGF family
implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850-
9857, 1996.

GAM7933 203 GABRP Hedblom, E.; Kirkness, E. F.: A novel class of GABA- A receptorsubunit in 7 A c
tissues of the reproductive system. J. Biol. Chem. 272:15346- 15350, 1997.

GAM7933 203 GABRP Whiting, P. J.; Bonnert, T. P.; McKernan, R. M.; Farrar, S.; leBourdelles, 7 A c
B.; Heavens, R. P.; Smith, D. W.; Hewson, L.; Rigby, M.R.; Sirinathsinghji,
D. J. S.; Thompson, S. A.; Wafford, K. A.: Molecularand functional diversity
of the expanding GABA- A receptor gene family. Ann.N.Y. Acad. Sci. 645- 653,
1999.

GAM7933 203 GDI2 Bachner, D.; Sedlacek, Z.; Korn, B.; Hameister, H.; Poustka, A.: Expression 7 A c
patterns of two human genes coding for different rabGDP- dissociation
inhibitors (GDIs), extremely conserved proteins involvedin cellular
transport. Hum. Molec. Genet. 4: 701- 708, 1995.

GAM7933 203 GDI2 Sedlacek, Z.; Konecki, D. S.; Korn, B.; Klauck, S. M.; Poustka,A.: 7 A c
Evolutionary conservation and genomic organization of XAP- 4,an Xq28 located
gene coding for a human rab GDP- dissociation inhibitor(GDI). Mammalian
Genome 5: 633- 639, 1995.

GAM7933 203 GDI2 Sedlacek, Z.; Munstermann, E.; Mincheva, A.; Lichter, P.; Poustka,A.: The 7 A c
human rab GDI beta gene with long retroposon- rich intronsmaps to 10p15 and
its pseudogene to 7p11- p13. Mammalian Genome 9:78- 80, 1998.

GAM7933 203 GDI2 Shisheva, A.; Sudhof, T. C.; Czech, M. P.: Cloning, characterization,and 7 A c
expression of a novel GDP dissociation inhibitor isoform fromskeletal
muscle. Molec. Cell. Biol. 14: 3459- 3468, 1994.

GAM7933 203 KCNMB4 Behrens, R.; Nolting, A.; Reimann, F.; Schwarz, M.; Waldschutz,R.; Pongs, 7 A c
O.: hKCNMB3 and hKCNMB4, cloning and characterizationof two members of the
large- conductance calcium- activated potassiumchannel beta subunit family.
FEBS Lett. 474: 99- 106, 2000.

GAM7933 203 KCNMB4 Brenner, R.; Jegla, T. J.; Wickenden, A.; Liu, Y.; Aldrich, R.W.: Cloning 7 A c
and functional characterization of novel large conductancecalcium- activated
potassium channel beta subunits, hKCNMB3 and hKCNMB4. J.Biol. Chem. 275:
6453- 6461, 2000.

GAM7933 203 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 7 A c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome
8p22 encodes a leucine- zipper protein, and itsexpression is altered in
multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM7933 203 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 7 A c
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22
suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci.

98: 10374- 10379, 2001.

GAM7933 203 MADH7 Dong, C.; Zhu, S.; Wang, T.; Yoon, W.; Li, Z.; Alvarez, R. J.;ten Dijke, P.; 7 A c White, B.; Wigley, F. M.; Goldschmidt- Clermont, P.J.: Deficient Smad7 expression: a putative molecular defect in scleroderma. Proc.Nat. Acad. Sci. 99: 3908- 3913, 2002.

GAM7933 203 MADH7 Kavsak, P.; Rasmussen, R. K.; Causing, C. G.; Bonni, S.; Zhu, H.;Thomsen, G. 7 A c H.; Wrana, J. L.: Smad7 binds to Smurf2 to form an E3ubiquitin ligase that targets the TGF- beta receptor for degradation. Molec.Cell 6: 1365- 1375, 2000.

GAM7933 203 MADH7 Lallemand, F.; Mazars, A.; Prunier, C.; Bertrand, F.; Kornprost,M.; Gallea, 7 A c S.; Roman- Roman, S.; Cherqui, G.; Atfi, A.: Smad7 inhibitsthe survival nuclear factor kappa- B and potentiates apoptosis in epithelialcells. Oncogene 20: 879- 884, 2001.

GAM7933 203 MADH7 Roijer, E.; Moren, A.; ten Dijke, P.; Stenman, G.: Assignmentof the Smad7 7 A c gene (MADH7) to human chromosome 18q21.1 by fluorescencein situ hybridization. Cytogenet. Cell Genet. 81: 189- 190, 1998.

GAM7933 203 MADH7 Topper, J. N.; Cai, J.; Qiu, Y.; Anderson, K. R.; Xu, Y.- Y.; Deeds,J. D.; 7 A c Feeley, R.; Gimeno, C. J.; Woolf, E. A.; Tayber, O.; Mays,G. G.; Sampson, B. A.; Schoen, F. J.; Gimbrone, M. A., Jr.; Falb,D.: Vascular MADs: two novel MAD- related genes selectively inducibleby flow in human vascular endothelium. Proc. Nat. Acad. Sci. 94:9314- 9319, 1997.

GAM7933 203 PLAG1 Astrom, A.- K.; Voz, M. L.; Kas, K.; Roijer, E.; Wedell, B.; Mandahl,N.; Van 7 A c de Ven, W.; Mark, J.; Stenman, G.: Conserved mechanism ofPLAG1 activation in salivary gland tumors with and without chromosome8q12 abnormalities: identification of SII as a new fusion partnergene. Cancer Res. 59: 918- 923, 1999.

GAM7933 203 PLAG1 Kas, K.; Roijer, E.; Voz, M.; Meyen, E.; Stenman, G.; Van de Ven,W. J. M.: A 7 A c 2- Mb YAC contig and physical map covering the chromosome8q12 breakpoint cluster region in pleomorphic adenomas of the salivaryglands. Genomics 43: 349- 358, 1997.

GAM7933 203 PLAG1 Kas, K.; Voz, M. L.; Roijer, E.; Astrom, A.- K.; Meyen, E.; Stenman,G.; Van 7 A c de Ven, W. J. M.: Promoter swapping between the genes fora novel zinc finger protein and beta- catenin in pleiomorphic adenomaswith t(3;8)(p21;q12) translocations. Nature Genet. 15: 170- 174,1997.

GAM7933 203 PPM1D Bulavin, D. V.; Demidov, O. N.; Saito, S.; Kauraniemi, P.; Phillips,C.; 7 A c Amundson, S. A.; Ambrosino, C.; Sauter, G.; Nebreda, A. R.; Anderson,C. W.; Kallioniemi, A.; Fornace, A. J., Jr.; Appella, E.: Amplificationof PPM1D in human tumors abrogates p53 tumor- suppressor activity. NatureGenet. 31: 210- 215, 2002.

GAM7933 203 PPM1D Fiscella, M.; Zhang, H.; Fan, S.; Sakaguchi, K.; Shen, S.; Mercer,W. E.; 7 A c Vande Woude, G. F.; O'Connor, P. M.; Appella, E.: Wip1, anovel human protein phosphatase that is induced in response to ionizingradiation in a p53- dependent manner. Proc. Nat. Acad. Sci. 94: 6048- 6053,1997.

GAM7933 203 PPM1D Li, J.; Yang, Y.; Peng, Y.; Austin, R. J.; van Eyndhoven, W. G.;Nguyen, K. 7 A c C. Q.; Gabriele, T.; McCurrach, M. E.; Marks, J. R.; Hoey,T.; Lowe, S. W.; Powers, S.: Oncogenic properties of PPM1D locatedwithin a breast cancer amplification epicenter at 17q23. Nature Genet. 31:133- 134, 2002.

GAM7933 203 PPM1D Nagase, T.; Seki, N.; Ishikawa, K.; Ohira, M.; Kawarabayasi, Y.;1. Fiscella, 7 A c M.; Zhang, H.; Fan, S.; Sakaguchi, K.; Shen, S.; Mercer,W. E.; Vande Woude, G. F.; O'Connor, P. M.; Appella, E.: Wip1, anovel human protein phosphatase

that is induced in response to ionizingradiation in a p53- dependent manner. Proc. Nat. Acad. Sci. 94: 6048- 6053,1997.

GAM7933 203 PPP1R3A Chen, Y. H.; Hansen, L.; Chen, M. X.; Bjorbaek, C.; Vestergaard,H.; Hansen, T.; Cohen, P. T. W.; Pedersen, O.: Sequence of the humanglycogen- associated regulatory subunit of type 1 protein phosphataseand analysis of its coding region and mRNA level in muscle from patientswith NIDDM. Diabetes 43: 1234- 1241, 1994. 7 A c

GAM7933 203 PPP1R3A Hansen, L.; Hansen, T.; Vestergaard, H.; Bjorbaek, C.; Echwald,S. M.; Clausen, J. O.; Chen, Y. H.; Chen, M. X.; Cohen, P. T. W.;Pedersen, O.: A widespread amino acid polymorphism at codon 905 ofthe glycogen- associated regulatory subunit of protein phosphatase- 1is associated with insulin resistance and hypersecretion of insulin. Hum.Molec. Genet. 4: 1313- 1320, 1995. 7 A c

GAM7933 203 PPP1R3A Hegele, R. A.; Harris, S. B.; Zinman, B.; Wang, J.; Cao, H.; Hanley,A. J. G.; Tsui, L.- C.; Scherer, S. W.: Variation in the AU(AT)- richelement within the 3- prime- untranslated region of PPP1R3 is associatedwith variation in plasma glucose in aboriginal Canadians. J. Clin.Endocr. Metab. 83: 3980- 3983, 1998. 7 A c

GAM7933 203 PPP1R3A Savage, D. B.; Agostini, M.; Barroso, I.; Gurnell, M.; Luan, J.;Meirhaeghe, A.; Harding, A.- H.; Ihrke, G.; Rajanayagam, O.; Soos,M. A.; George, S.; Berger, D.; and 9 others: Digenic inheritanceof severe insulin resistance in a human pedigree. Nature Genet. 31:379- 384, 2002. 7 A c

GAM7933 203 PPP1R3A Tang, P. M.; Bondor, J. A.; Swiderek, K. M.; DePaoli- Roach, A.A.: Molecular cloning and expression of the regulatory (RG1) subunitof the glycogen- associated protein phosphatase. J. Biol. Chem. 266:15782- 15789, 1991. 7 A c

GAM7933 203 PPT2 Gupta, P.; Soyombo, A. A.; Atashband, A.; Wisniewski, K. E.; Shelton,J. M.; Richardson, J. A.; Hammer, R. E.; Hofmann, S. L.: Disruptionof PPT1 or PPT2 causes neuronal ceroid lipofuscinosis in knockoutmice. Proc. Nat. Acad. Sci. 98: 13566- 13571, 2001. 7 A c

GAM7933 203 PPT2 Soyombo, A. A.; Hofmann, S. L.: Molecular cloning and expressionof palmitoyl- protein thioesterase 2 (PPT2), a homolog of lysosomalpalmitoyl- protein thioesterase with a distinct substrate specificity. J.Biol. Chem. 272: 27456- 27463, 1997. 7 A c

GAM7933 203 RECK Oh, J.; Takahashi, R.; Kondo, S.; Mizoguchi, A.; Adachi, E.; Sasahara,R. M.; Nishimura, S.; Imamura, Y.; Kitayama, H.; Alexander, D. B.;Ide, C.; Horan, T. P.; Arakawa, T.; Yoshida, H.; Nishikawa, S.; Itoh,Y.; Seiki, M.; Itohara, S.; Takahashi, C.; Noda, M.: The membrane- anchoredMMP inhibitor RECK is a key regulator of extracellular matrix integrityand angiogenesis. Cell 107: 789- 800, 2001. 7 A c

GAM7933 203 RECK Takahashi, C.; Sheng, Z.; Horan, T. P.; Kitayama, H.; Maki, M.;Hitomi, K.; Kitaura, Y.; Takai, S.; Sasahara, R. M.; Horimoto, A.;Ikawa, Y.; Ratzkin, B. J.; Arakawa, T.; Noda, M.: Regulation of matrixmetalloproteinase- 9 and inhibition of tumor invasion by the membrane- anchoredglycoprotein RECK. Proc. Nat. Acad. Sci. 95: 13221- 13226, 1998. 7 A c

GAM7933 203 SIAH1 Banfi, S.; Borsani, G.; Rossi, E.; Bernard, L.; Guffanti, A.; Rubboli,F.; Marchitiello, A.; Giglio, S.; Coluccia, E.; Zollo, M.; Zuffardi,O.; Ballabio, A.: Identification and mapping of human cDNAs homologousto Drosophila mutant genes through EST database searching. NatureGenet. 13: 167- 174, 1996. 7 A c

GAM7933 203 SIAH1 Hu, G.; Chung, Y.- L.; Glover, T.; Valentine, V.; Look, A T.; Fearon,E. R.: 7 A c

Characterization of human homologs of the Drosophila sevenin absentia (sina) gene. Genomics 46: 103- 111, 1997.

GAM7933 203 SIAH1 Liu, J.; Stevens, J.; Rote, C. A.; Yost, H. J.; Hu, Y.; Neufeld,K. L.; White, R. L.; Matsunami, N.: Siah- 1 mediates a novel beta-catenindegradation pathway linking p53 to the adenomatous polyposis coliprotein. Molec. Cell 7: 927- 936, 2001. 7 A c

GAM7933 203 SIAH1 Matsuzawa, S.; Reed, J. C.: Siah- 1, SIP, and Ebi collaborate ina novel pathway for beta- catenin degradation linked to p53 responses. Molec.Cell 7: 915- 926, 2001. 7 A c

GAM7933 203 SIAH1 Nemani, M.; Linares- Cruz, G.; Bruzzoni- Giovanelli, H.; Roperch,J.- P.; Tuynder, M.; Bougueleret, L.; Cherif, D.; Medhioub, M.; Pasturaud,P.; Alvaro, V.; der Sarkissan, H.; Cazes, L.; Le Paslier, D.; Le Gall,I.; Israeli, D.; Dausset, J.; Sigaux, F.; Chumakov, I.; Oren, M.;Calvo, F.; Amson, R. B.; Cohen, D.; Telerman, A.: Activation of thehuman homologue of the Drosophila SINA gene in apoptosis and tumorsuppression. Proc. Nat. Acad. Sci. 93: 9039- 9042, 1996. 7 A c

GAM7933 203 SIGLEC8 Floyd, H.; Ni, J.; Cornish, A. L.; Zeng, Z.; Liu, D.; Carter, K.C.; Steel, J.; Crocker, P. R.: Siglec- 8: a novel eosinophil- specificmember of the immunoglobulin superfamily. J. Biol. Chem. 275: 861- 866,2000. 7 A c

GAM7933 203 SIGLEC8 Foussias, G.; Yousef, G. M.; Diamandis, E. P.: Molecular characterizationof a Siglec8 variant containing cytoplasmic tyrosine- based motifs,and mapping of the Siglec8 gene. Biochem. Biophys. Res. Commun. 278:775- 781, 2000. 7 A c

GAM7933 203 SIGLEC8 Kikly, K. K.; Bochner, B. S.; Freeman, S. D.; Tan, K. B.; Gallagher,K. T.; D'alessio, K. J.; Holmes, S. D.; Abrahamson, J. A.; Erickson- Miller,C. L.; Murdock, P. R.; Tachimoto, H.; Schleimer, R. P.; White, J.R.: Identification of SAF- 2, a novel Siglec expressed on eosinophils,mast cells, and basophils. J. Allergy Clin. Immun. 105 1093- 1100,2000. 7 A c

GAM7933 203 SPG7 Casari, G.; De Fusco, M.; Ciarmatori, S.; Zeviani, M.; Mora, M.;Fernandez, P.; De Michele, G.; Filla, A.; Cocozza, S.; Marconi, R.;Durr, A.; Fontaine, B.; Ballabio, A.: Spastic paraplegia and OXPHOSimpairment caused by mutations in paraplegin, a nuclear- encoded mitochondrialmetalloprotease. Cell 93: 973- 983, 1998. 7 A c

GAM7933 203 SPG7 De Michele, G.; De Fusco, M.; Cavalcanti, F.; Filla, A.; Marconi,R.; Volpe, G.; Monticelli, A.; Ballabio, A.; Casari, G.; Cocozza,S.: A new locus for autosomal recessive hereditary spastic paraplegiamaps to chromosome 16q24.3. Am. J. Hum. Genet. 63: 135- 139, 1998. 7 A c

GAM7933 203 SPG7 Settasatian, C.; Whitmore, S. A.; Crawford, J.; Bilton, R. L.;Cleton-Jansen, A.- M.; Sutherland, G. R.; Callen, D. F.: Genomic structureand expression analysis of the spastic paraplegia gene, SPG7. Hum.Genet. 105: 139- 144, 1999. 7 A c

GAM7933 203 STXBP1 Fisher, R. J.; Pevsner, J.; Burgoyne, R. D.: Control of fusionpore dynamics during exocytosis by Munc18. Science 291: 875- 878,2001. 7 A c

GAM7933 203 STXBP1 Gengyo- Ando, K.; Kitayama, H.; Mukaida, M.; Ikawa, Y.: A murineneural-specific homolog corrects cholinergic defects in Caenorhabditiselegans unc-18 mutants. J. Neurosci. 16: 6695- 6702, 1996. 7 A c

GAM7933 203 STXBP1 Pevsner, J.; Hsu, S.- C.; Scheller, R. H.: n- Sec1: a neural-specificsyntaxin- binding protein. Proc. Nat. Acad. Sci. 91: 1445- 1449, 1994. 7 A c

GAM7933 203 STXBP1 Swanson, D. A.; Steel, J. M.; Valle, D.: Identification and characterizationof the human ortholog of rat STXBP1, a protein implicated in 7 A c

vesicletrafficking and neurotransmitter release. Genomics 48: 373- 376,1998.

GAM7933 203 STXBP1 Verhage, M.; Mala, A. S.; Plomp, J. J.; Brussaard, A. B.; Heeroma,J. H.; 7 A c
Vermeer, H.; Toonen, R. F.; Hammer, R. E.; van den Berg, T.K.; Missler, M.;
Geuze, H. J.; Sudhof, T. C.: Synaptic assembly ofthe brain in the absence of
neurotransmitter secretion. Science 287:864- 869, 2000.

GAM7933 203 TFAP2A Bauer, R.; Imhof, A.; Pscherer, A.; Kopp, H.; Moser, M.; Seegers,S.; 7 A c
Kerscher, M.; Tainsky, M. A.; Hofstaedter, F.; Buettner, R.:The genomic
structure of the human AP- 2 transcription factor. NucleicAcids Res. 22:
1413- 1420, 1994.

GAM7933 203 TFAP2A Buettner, R.; Kannan, P.; Imhof, A.; Bauer, R.; Yim, S. O.; Glockshuber,R.; 7 A c
Van Dyke, M. W.; Tainsky, M. A.: An alternatively spliced mRNAfrom the AP- 2
gene encodes a negative regulator of transcriptionalactivation by AP- 2.
Molec. Cell. Biol. 13: 4174- 4185, 1993.

GAM7933 203 TFAP2A Davies, A. F.; Mirza, G.; Flinter, F.; Ragoussis, J.: An 7 A c
interstitialdeletion of 6p24- p25 proximal to the FKHL7 locus and including
AP- 2- alphathat affects anterior eye chamber development. J. Med. Genet.
36:708- 710, 1999.

GAM7933 203 TFAP2A Gaynor, R. B.; Muchardt, C.; Xia, Y.; Klisak, I.; Mohandas, T.;Sparkes, R. 7 A c
S.; Lusis, A. J.: Localization of the gene for the DNA- bindingprotein AP- 2
to human chromosome 6p22.3- pter. Genomics 10: 1100- 1102,1991.

GAM7933 203 TFAP2A Schorle, H.; Meier, P.; Buchert, M.; Jaenisch, R.; Mitchell, P.J.: 7 A c
Transcription factor AP- 2 essential for cranial closure and
craniofacialdevelopment. Nature 381: 235- 238, 1996.

GAM7933 203 TFAP2A Warren, G.; Gordon, M.; Siracusa, L. D.; Buchberg, A. M.; Williams,T.: 7 A c
Physical and genetic localization of the gene encoding the AP-
2transcription factor to mouse chromosome 13. Genomics 31: 234- 237,1996.

GAM7933 203 TFAP2A Williams, T.; Admon, A.; Luscher, B.; Tjian, R.: Cloning and expressionof 7 A c
AP- 2, a cell- type- specific transcription factor that activatesinducible
enhancer elements. Genes Dev. 2: 1557- 1569, 1988.

GAM7933 203 TFAP2A Williamson, J. A.; Bosher, J. M.; Skinner, A.; Sheer, D.; Williams,T.; 7 A c
Hurst, H. C.: Chromosomal mapping of the human and mouse homologuesof two
new members of the AP- 2 family of transcription factors. Genomics 35:262-
264, 1996.

GAM7933 203 TFAP2A Zhang, J.; Hagopian- Donaldson, S.; Serbedzija, G.; Elsemore, J.;Plehn- 7 A c
Dujowich, D.; McMahon, A. P.; Flavell, R. A.; Williams, T.:Neural tube,
skeletal and body wall defects in mice lacking transcriptionfactor AP- 2.
Nature 381: 238- 241, 1996.

GAM7933 203 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. 7 A c
F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.;
Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and
high resolution restriction map of the2 megabase region containing the
Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM7933 203 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 7 A c
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple
myeloma is associated with increased expression and activatingmutations of
fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM7933 203 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, 7 A c
R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel
chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the
fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997.

GAM7933 203 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 7 A c

GAM7933 203 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 7 A c

GAM7957 297 ACE Amant, C.; Bauters, C.; Bodart, J.- C.; Lablanche, J.- M.; Grollier,G.; Danchin, N.; Hamon, M.; Richard, F.; Helbecque, N.; McFadden,E. P.; Amouyel, P.; Bertrand, M. E.: D allele of the angiotensinI- converting enzyme is a major risk factor for restenosis after coronarystenting. Circulation 96: 56- 60, 1997. 3 C c

GAM7957 297 ACE Arbustini, E.; Grasso, M.; Fasani, R.; Klersy, C.; Diegoli, M.;Porcu, E.; Banchieri, N.; Fortina, P.; Danesino, C.; Specchia, G.: Angiotensin converting enzyme gene deletion allele is independentlyand strongly associated with coronary atherosclerosis and myocardialinfarction. Brit. Heart J. 74: 584- 591, 1995. 3 C c

GAM7957 297 ACE Berge, K. E.; Berg, K.: No effect of insertion/deletion polymorphismat the ACE locus on normal blood pressure level or variability. Clin.Genet. 45: 169- 174, 1994. 3 C c

GAM7957 297 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: Insertion/deletion(I/D) polymorphism at the locus for angiotensin I- converting enzymeand myocardial infarction. Clin. Genet. 44: 292- 297, 1993. 3 C c

GAM7957 297 ACE Bohn, M.; Berge, K. E.; Bakken, A.; Erikssen, J.; Berg, K.: Insertion/deletion(I/D) polymorphism at the locus for angiotensin I- converting enzymeand parental history of myocardial infarction. Clin. Genet. 44:298- 301, 1993. 3 C c

GAM7957 297 ACE Brown, N. J.; Ray, W. A.; Snowden, M.; Griffin, M. R.: Black Americanshave an increased rate of angiotensin converting enzyme inhibitor- associatedangioedema. Clin. Pharmacol. Therapeutics 60: 8- 13, 1996. 3 C c

GAM7957 297 ACE Cambien, F.; Alhenc- Gelas, F.; Herbeth, B.; Andre, J. L.; Rakotovao,R.; Gonzales, M. F.; Allegrini, J.; Bloch, C.: Familial resemblanceof plasma angiotensin- converting enzyme level: the Nancy study. Am.J. Hum. Genet. 43: 774- 780, 1988. 3 C c

GAM7957 297 ACE Cambien, F.; Poirier, O.; Lecerf, L.; Evans, A.; Cambou, J.- P.;Arveiler, D.; Luc, G.; Bard, J.- M.; Bara, L.; Ricard, S.; Tiret, L.;Amouyel, P.; Alhenc- Gelas, F.; Soubrier, F.: Deletion polymorphismin the gene for angiotensin- converting enzyme is a potent risk factorfor myocardial infarction. Nature 359: 641- 644, 1992. 3 C c

GAM7957 297 ACE Doria, A.; Warram, J. H.; Krolewski, A. S.: Genetic predispositionto diabetic nephropathy: evidence for a role of the angiotensin I- convertingenzyme gene. Diabetes 43: 690- 695, 1994. 3 C c

GAM7957 297 ACE Ehlers, M. R. W.; Fox, E. A.; Strydom, D. J.; Riordan, J. F.:Molecular cloning of human testicular angiotensin- converting enzyme:the testis isozyme is identical to the C- terminal half of endothelialangiotensin- converting enzyme. Proc. Nat. Acad. Sci. 86: 7741- 7745,1989. 3 C c

GAM7957 297 ACE Esther, C. R., Jr.; Marino, E. M.; Howard, T. E.; Machaud, A.;Corvol, P.; 3 C c
Capecchi, M. R.; Bernstein, K. E.: The critical roleof tissue angiotensin-
converting enzyme as revealed by gene targetingin mice. J. Clin. Invest. 99:
2375- 2385, 1997.

GAM7957 297 ACE Evans, A. E.; Poirier, O.; Kee, F.; Lecerf, L.; McCrum, E.; Falconer,T.; 3 C c
Crane, J.; O'Rourke, D. F.; Cambien, F.: Polymorphisms of theangiotensin-
converting- enzyme gene in subjects who die from coronaryheart disease.
Quart. J. Med. 87: 211- 214, 1994.

GAM7957 297 ACE Exner, D. V.; Dries, D. L.; Domanski, M. J.; Cohn, J. N.: Lesserresponse to 3 C c
angiotensin- converting- enzyme inhibitor therapy in blackas compared with
white patients with left ventricular dysfunction. NewEng. J. Med. 344: 1351-
1357, 2001.

GAM7957 297 ACE Gardemann, A.; Fink, M.; Stricker, J.; Nguyen, Q. D.; Humme, J.;Katz, N.; 3 C c
Tillmanns, H.; Hehrlein, F. W.; Rau, M.; Haberbosch, W.: ACE I/D gene
polymorphism: presence of the ACE D allele increasesthe risk of coronary
artery disease in younger individuals. Atherosclerosis 139:153- 159, 1998.

GAM7957 297 ACE Gayagay, G.; Yu, B.; Hambly, B.; Boston, T.; Hahn, A.; Celermajer,D. S.; 3 C c
Trent, R. J.: Elite endurance athletes and the ACE I allele:the role of
genes in athletic performance. Hum. Genet. 103: 48- 50,1998.

GAM7957 297 ACE Hagaman, J. R.; Moyer, J. S.; Bachman, E. S.; Sibony, M.; Magyar,P. L.; 3 C c
Welch, J. E.; Smithies, O.; Krege, J. H.; O'Brien, D. A.:Angiotensin-
converting enzyme and male fertility. Proc. Nat. Acad.Sci. 95: 2552- 2557,
1998.

GAM7957 297 ACE Hamdi, H. K.; Reznik, J.; Castellon, R.; Atilano, S. R.; Ong,J. M.; Udar, 3 C c
N.; Tavis, J. H.; Aoki, A. M.; Nesburn, A. B.; Boyer,D. S.; Small, K. W.;
Brown, D. J.; Kenney, M. C.: Alu DNA polymorphismin ACE gene is protective
for age- related macular degeneration. Biochem.Biophys. Res. Commun. 295:
668- 672, 2002.

GAM7957 297 ACE Howard, T. E.; Shai, S. Y.; Langford, K. G.; Martin, B. M.; Bernstein,K. E.: 3 C c
Transcription of testicular angiotensin- converting enzyme(ACE) is initiated
within the 12th intron of the somatic ACE gene. Molec.Cell. Biol. 10: 4294-
4302, 1990.

GAM7957 297 ACE Huang, W.; Gallois, Y.; Bouby, N.; Bruneval, P.; Heudes, D.; Belair,M.- F.; 3 C c
Krege, J. H.; Menteton, P.; Marre, M.; Smithies, O.; Alhenc- Gelas,F.:
Genetically increased angiotensin I- converting enzyme level andrenal
complications in the diabetic mouse. Proc. Nat. Acad. Sci. 98:13330- 13334,
2001.

GAM7957 297 ACE Jeffery, S.; Malik, A. K. S.; Crosby, A.; Bland, M.; Eastwood,J. B.; Amoah- 3 C c
Danquah, J.; Acheampong, J. W.; Plange- Rhule, J.: Adominant relationship
between the ACE D allele and serum ACE levelsin a Ghanaian population.
(Letter) J. Med. Genet. 36: 869- 870, 1999.

GAM7957 297 ACE Jeunemaitre, X.; Lifton, R. P.; Hunt, S. C.; Williams, R. R.;Lalouel, J.- 3 C c
M.: Absence of linkage between the angiotensin convertingenzyme locus and
human essential hypertension. Nature Genet. 1:72- 75, 1992.

GAM7957 297 ACE Julier, C.; Delepine, M.; Keavney, B.; Terwilliger, J.; Davis,S.; Weeks, D. 3 C c
E.; Bui, T.; Jeunemaitre, X.; Velho, G.; Froguel, P.;Ratcliffe, P.; Corvol,
P.; Soubrier, F.; Lathrop, G. M.: Geneticsusceptibility for human familial
essential hypertension in a regionof homology with blood pressure linkage on
rat chromosome 10. Hum.Molec. Genet. 6: 2077- 2085, 1997.

GAM7957 297 ACE Keavney, B.; McKenzie, C.; Parish, S.; Palmer, A.; Clark, S.;Youngman, L.; 3 C c

Delepine, M.; Lathrop, M.; Peto, R.; Collins, R.: Large- scaletest of hypothesized associations between the angiotensin- converting-enzymeinsertion/deletion polymorphism and myocardial infarction in about5000 cases and 6000 controls. Lancet 355: 434- 442, 2000.

GAM7957 297 ACE Kehoe, P. G.; Russ, C.; McIlroy, S.; Williams, H.; Holmans, P.;Holmes, C.; 3 C c Liolitsa, D.; Vahidassr, D.; Powell, J.; McGleenon, B.;Liddell, M.; Plomin, R.; and 9 others: Variation in DCP1, encodingACE, is associated with susceptibility to Alzheimer disease. (Letter) NatureGenet. 21: 71- 72, 1999.

GAM7957 297 ACE Keramatipour, M.; McConnell, R. S.; Kirkpatrick, P.; Tebbs, S.;Furlong, R. 3 C c A.; Rubinsztein, D. C.: The ACE I allele is associatedwith increased risk for ruptured intracranial aneurysms. J. Med.Genet. 37: 498- 500, 2000.

GAM7957 297 ACE Krege, J. H.; John, S. W. M.; Langenbach, L. L.; Hodgin, J. B.;Hagaman, J. 3 C c R.; Bachman, E. S.; Jennette, J. C.; O'Brien, D. A.; Smithies,O.: Male-female differences in fertility and blood pressure in ACE- deficientmice. Nature 375: 146- 148, 1995.

GAM7957 297 ACE Kurtz, T. W.: The ACE of hearts. Nature 359: 588- 589, 1992. 3 C c

GAM7957 297 ACE Lindpaintner, K.; Lee, M.; Larson, M. G.; Rao, V. S; Pfeffer,M. A.; Ordovas, 3 C c J. M.; Schaefer, E. J.; Wilson, A. F.; Wilson, P.W. F.; Vasan, R. S.; Myers, R. H.; Levy, D.: Absence of associationor genetic linkage between the angiotensin- converting- enzyme geneand left ventricular mass. New Eng. J. Med. 334: 1023- 1028, 1996.

GAM7957 297 ACE Lindpaintner, K.; Pfeffer, M. A.; Kreutz, R.; Stampfer, M. J.;Grodstein, F.; 3 C c LaMotte, F.; Buring, J.; Hennekens, C. H.: A prospectiveevaluation of an angiotensin- converting- enzyme gene polymorphism andthe risk of ischemic heart disease. New Eng. J. Med. 332: 706- 711,1995.

GAM7957 297 ACE Marre, M.; Bernadet, P.; Gallois, Y.; Savagner, F.; Guyene, T.- T.;Hallab, 3 C c M.; Cambien, F.; Passa, P.; Alhenc- Gelas, F.: Relationshipsbetween angiotensin I converting enzyme gene polymorphism, plasmalevels, and diabetic retinal and renal complications. Diabetes 43:384- 388, 1994.

GAM7957 297 ACE Marre, M.; Jeunemaitre, X.; Gallois, Y.; Rodier, M.; Chatellier,G.; Sert, 3 C c C.; Dusselier, L.; Kahal, Z.; Chaillous, L.; Halimi, S.;Muller, A.; Sackmann, H.; Bauduceau, B.; Bled, F.; Passa, P.; Alhenc- Gelas,F.: Contribution of genetic polymorphism in the renin- angiotensinsystem to the development of renal complications in insulin- dependentdiabetes. J. Clin. Invest. 99: 1585- 1595, 1997.

GAM7957 297 ACE Mattei, M.- G.; Hubert, C.; Alhenc- Gelas, F.; Roeckel, N.; Corvol,P.; 3 C c Soubrier, F.: Angiotensin- I converting enzyme gene is on chromosome17. (Abstract) Cytogenet. Cell Genet. 51: 1041, 1989.

GAM7957 297 ACE Montgomery, H. E.; Clarkson, P.; Dollery, C. M.; Prasad, K.; Losi,M.- A.; 3 C c Hemingway, H.; Statters, D.; Jubb, M.; Girvain, M.; Varnava,A.; World, M.; Deanfield, J.; Talmud, P.; McEwan, J. R.; McKenna,W. J.; Humphries, S.: Association of angiotensin- converting enzymegene I/D polymorphism with change in left ventricular mass in responseto physical training. Circulation 96: 741- 747, 1997.

GAM7957 297 ACE Montgomery, H. E.; Marshall, R.; Hemingway, H.; Myerson, S.; Clarkson,P.; 3 C c Dollery, C.; Hayward, M.; Holliman, D. E.; Jubb, M.; World, M.;Thomas, E. L.; Brynes, A. E.; Saeed, N.; Barnard, M.; Bell, J. D.;Prasad, K.; Rayson, M.; Talmud, P. J.; Humphries, S. E.: Human genefor physical performance. (Letter) Nature 393: 221- 222, 1998.

GAM7957 297 ACE Ohishi, M.; Fujii, K.; Minamino, T.; Hagaki, J.; Kamitani, A.;Rakugi, H.; 3 C c

Zhao, Y.; Mikami, H.; Miki, T.; Ogihara, T.: A potentgenetic risk factor for restenosis. (Letter) Nature Genet. 5: 324- 325,1993.

GAM7957 297 ACE Oike, Y.; Hata, A.; Ogata, Y.; Numata, Y.; Shido, K.; Kondo, K.: Angiotensin converting enzyme as a genetic risk factor for coronaryartery spasm: implication in the pathogenesis of myocardial infarction. J.Clin. Invest. 96: 2975- 2979, 1995. 3 C c

GAM7957 297 ACE Okabe, T.; Fusisawa, M.; Yotsumoto, M.; Takaru, F.; Lanzillo,J. J.; Fanburg, B. L.: Familial elevation of serum angiotensin- convertingenzyme. Quart. J. Med. 216: 55- 61, 1985. 3 C c

GAM7957 297 ACE Pfeffer, M. A.; Braunwald, E.; Moye, L. A.; Basta, L.; Brown,E. J., Jr.; Cuddy, T. E.; Davis, B. R.; Geltman, E. M.; Goldman, S.;Flaker, G. C.; Klein, M.; Lamas, G. A.; Packer, M.; Rouleau, J.; Rouleau,J. L.; Rutherford, J.; Wertheimer, J. H.; Hawkins, C. M.: Effectof captopril on mortality and morbidity in patients with left ventricular dysfunction after myocardial infarction: results of the survival andventricular enlargement trial. New Eng. J. Med. 327: 669- 677, 1992. 3 C c

GAM7957 297 ACE Ramaraj, P.; Kessler, S. P.; Colmenares, C.; Sen, G. C.: Selectiverestoration of male fertility in mice lacking angiotensin-convertingenzymes by sperm- specific expression of the testicular isozyme. J.Clin. Invest. 102: 371- 378, 1998. 3 C c

GAM7957 297 ACE Rigat, B.; Hubert, C.; Alhenc- Gelas, F.; Cambien, F.; Corvol,P.; Soubrier, F.: An insertion/deletion polymorphism in the angiotensinI- converting enzyme gene accounting for half the variance of serumenzyme levels. J. Clin. Invest. 86: 1343- 1346, 1990. 3 C c

GAM7957 297 ACE Rigat, B.; Hubert, C.; Corvol, P.; Soubrier, F.: PCR detectionof the insertion/deletion polymorphism of the human angiotensin convertingenzyme gene (DCP1) (dipeptidylcarboxypeptidase 1). Nucleic AcidsRes. 20: 1433, 1992. 3 C c

GAM7957 297 ACE Ruiz, J.; Blanche, H.; Cohen, N.; Velho, G.; Cambien, F.; Cohen,D.; Passa, P.; Froguel, P.: Insertion/deletion polymorphism of theangiotensin-converting enzyme gene is strongly associated with coronaryheart disease in non- insulin- dependent diabetes mellitus. Proc. Nat.Acad. Sci. 91: 3662-3665, 1994. 3 C c

GAM7957 297 ACE Schachter, F.; Faure- Delanef, L.; Guenot, F.; Rouger, H.; Froguel,P.; Lesueur- Ginot, L.; Cohen, D.: Genetic associations with humanlongevity at the APOE and ACE loci. Nature Genet. 6: 29- 32, 1994. 3 C c

GAM7957 297 ACE Schmidt, S.; Schone, N.; Ritz, E.; Giesel, R.; Bergis, K.; Strojek,K.; Greszczak, W.; Schroter, W.; Willms, B. H. L.; Petzold, R.; Henrichs,H. R.; Rambausek, M.; Schwarzbeck, A.; Kohr, B.; Schneider, P.; Bosch,A.: Association of ACE gene polymorphism and diabetic nephropathy? KidneyInt. 47: 1176- 1181, 1995. 3 C c

GAM7957 297 ACE Schunkert, H.; Hense, H.- W.; Holmer, S. R.; Stender, M.; Perz,S.; Keil, U.; Lorell, B. H.; Riegger, G. A. J.: Association betweena deletion polymorphism of the angiotensin- converting- enzyme geneand left ventricular hypertrophy. New Eng. J. Med. 330: 1634- 1638,1994. 3 C c

GAM7957 297 ACE Singer, D. R. J.; Missouris, C. G.; Jeffery, S.: Angiotensin-convertingenzyme gene polymorphism: what to do about all the confusion? (Editorial) Circulation 94:236- 239, 1996. 3 C c

GAM7957 297 ACE Soubrier, F.; Alhenc- Gelas, F.; Hubert, C.; Allegrini, J.; John,M.; Tregear, G.; Corvol, P.: Two putative active centers in humanangiotensin I- 3 C c

converting enzyme revealed by molecular cloning. Proc.Nat. Acad. Sci. 85: 9386- 9390, 1988.

GAM7957 297 ACE Tarnow, L.; Cambien, F.; Rossing, P.; Nielsen, F. S.; Hansen,B. V.; Lecerf, 3 C c
L.; Poirier, O.; Danilov, S.; Parving, H.- H.: Lackof relationship between an insertion/deletion polymorphism in theangiotensin I- converting enzyme gene and diabetic nephropathy andproliferative retinopathy in IDDM patients. Diabetes 44: 489- 494,1995.

GAM7957 297 ACE Tiret, L.; Rigat, B.; Visvikis, S.; Breda, C.; Corvol, P.; Cambien,F.; 3 C c
Soubrier, F.: Evidence, from combined segregation and linkageanalysis, that a variant of the angiotensin I- converting enzyme (ACE)gene controls plasma ACE levels. Am. J. Hum. Genet. 51: 197- 205,1992.

GAM7957 297 ACE Vleming, L. J.; van der Pijl, J. W.; Lemkes, H. H. P. J.; Westendorp,R. G. 3 C c
J.; Maassen, J. A.; Daha, M. R.; van Es, L. A.; van Kooten,C.: The DD genotype of the ACE gene polymorphism is associated withprogression of diabetic nephropathy to end stage renal failure inIDDM. Clin. Nephrol. 51: 133- 140, 1999.

GAM7957 297 ACE Williams, A. G.; Rayson, M. P.; Jubb, M.; World, M.; Woods, D.R.; Hayward, 3 C c
M.; Martin, J.; Humphries, S. E.; Montgomery, H. E.:The ACE gene and muscle performance. Nature 403: 614 only, 2000.

GAM7957 297 ACE Winkelmann, B. R.; Nauck, M.; Klein, B.; Russ, A. P.; Bohm, B.O.; Siekmeier, 3 C c
R.; Ihnken, K.; Verho, M.; Gross, W.; Marz, W.: Deletionpolymorphism of the angiotensin I- converting enzyme gene is associatedwith increased plasma angiotensin- converting enzyme activity but notwith increased risk for myocardial infarction and coronary arterydisease. Ann. Intern. Med. 125: 19- 25, 1996.

GAM7957 297 ACE Woods, D.; Onambele, G.; Woledge, R.; Skelton, D.; Bruce, S.;Humphries, S. 3 C c
E.; Montgomery, H.: Angiotensin- I converting enzymegenotype- dependent benefit from hormone replacement therapy in isometricmuscle strength and bone mineral density. J. Clin. Endocr. Metab. 86:2200- 2204, 2001.

GAM7957 297 ACE Yoshida, H.; Mitarai, T.; Kawamura, T.; Kitajima, T.; Miyazaki,Y.; Nagasawa, 3 C c
R.; Kawaguchi, Y.; Kubo, H.; Ichikawa, I.; Sakai, O.: Role of the deletion polymorphism of the angiotensin convertingenzyme gene in the progression and therapeutic responsiveness of IgAnephropathy. J. Clin. Invest. 96: 2162- 2169, 1995.

GAM7957 297 ACE Yoshioka, T.; Xu, Y.; Yoshida, H.; Shiraga, H.; Muraki, T.; Ito,K.: Deletion 3 C c
polymorphism of the angiotensin converting enzyme genepredicts persistent proteinuria in Henoch- Schonlein purpura nephritis. Arch.Dis. Child. 79: 394- 399, 1998.

GAM7957 297 ACE Zhu, X.; Bouzekri, N.; Southam, L.; Cooper, R. S.; Adeyemo, A.;McKenzie, C. 3 C c
A.; Luke, A.; Chen, G.; Elston, R. C.; Ward, R.: Linkageand association analysis of angiotensin I- converting enzyme (ACE)- genepolymorphisms with ACE concentration and blood pressure. Am. J. Hum.Genet. 68: 1139- 1148, 2001.

GAM7957 297 ACE Zhu, X.; McKenzie, C. A.; Forrester, T.; Nickerson, D. A.; Broeckel,U.; 3 C c
Schunkert, H.; Doering, A.; Jacob, H. J.; Cooper, R. S.; Rieder,M. J.: Localization of a small genomic region associated with elevatedACE. Am. J. Hum. Genet. 67: 1144- 1153, 2000. Note: Erratum: Am.J. Hum. Genet. 67: 1365 only, 2000.

GAM7957 297 ADAMTS4 Hurskainen, T. L.; Hirohata, S.; Seldin, M. F.; Apte, S. S.: ADAM- TS5,ADAM- 3 C c
TS6, and ADAM- TS7, novel members of a new family of zinc

metalloproteases:general features and genomic distribution of the ADAM- TS family. J.Biol. Chem. 274: 25555- 25563, 1999.

GAM7957 297 ADAMTS4 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM7957 297 ADAMTS4 Tang, B. L.; Hong, W.: ADAMTS: a novel family of proteases withan ADAM 3 C c
protease domain and thrombospondin 1 repeats. FEBS Lett. 445:223- 225, 1999.

GAM7957 297 ADAMTS4 Tortorella, M. D.; Burn, T. C.; Pratta, M. A.; Abbaszade, I.; Hollis,J. M.; 3 C c
Liu, R.; Rosenfeld, S. A.; Copeland, R. A.; Decicco, C. P.;Wynn, R.; Rockwell, A.; Yang, F.; and 16 others: Purification andcloning of aggrecanase- 1: a member of the ADAMTS family of proteins. Science 284:1664- 1666, 1999.

GAM7957 297 ADAT1 Maas, S.; Gerber, A. P.; Rich, A.: Identification and characterizationof a 3 C c
human tRNA- specific adenosine deaminase related to the ADAR familyof pre- mRNA editing enzymes. Proc. Nat. Acad. Sci. 96: 8895- 8900,1999.

GAM7957 297 ADAT1 Maas, S.; Kim, Y.- G.; Rich, A.: Genomic clustering of tRNA- 3 C c
specificadenosine deaminase ADAT1 and two tRNA synthetases. Mammalian Genome 12:387- 393, 2001.

GAM7957 297 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, 3 C b
S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998.

GAM7957 297 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 C b
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995.

GAM7957 297 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 C b
members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994.

GAM7957 297 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; 3 C b
Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal brain type I adenylyl cyclase. Genomics 16: 473- 478,1993.

GAM7957 297 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- 3 C b
Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.: Altered sensory processing in the somatosensory cortex of the mutantmouse barrelless. Science 271: 1864- 1867, 1996.

GAM7957 297 AGRP Graham, M.; Shutter, J. R.; Sarmiento, U.; Sarosi, I.; Stark, K.L.: 3 C c
Overexpression of Agrt leads to obesity in transgenic mice. (Letter) NatureGenet. 17: 273- 274, 1997.

GAM7957 297 AGRP Katsuki, A.; Sumida, Y.; Gabazza, E. C.; Murashima, S.; Tanaka,T.; Furuta, 3 C c
M.; Araki- Sasaki, R.; Hori, Y.; Nakatani, K.; Yano, Y.;Adachi, Y.: Plasma levels of agouti- related protein are increasedin obese men. J. Clin. Endocr. Metab. 86: 1921- 1924, 2001.

GAM7957 297 AGRP Ollmann, M. M.; Wilson, B. D.; Yang, Y.- K.; Kerns, J. A.; Chen,Y.; Gantz, 3 C c
I.; Barsh, G. S.: Antagonism of central melanocortin receptorsin vitro and in vivo by agouti- related protein. Science 278: 135- 138,1997.

GAM7957 297 AGRP Shutter, J. R.; Graham, M.; Kinsey, A. C.; Scully, S.; Luthy, R.;Stark, K. 3 C c
L.: Hypothalamic expression of ART, a novel gene relatedto agouti, is up- regulated in obese and diabetic mutant mice. GenesDev. 11: 593- 602, 1997.

GAM7957 297 AHR Andersson, P.; McGuire, J.; Rubio, C.; Gradin, K.; Whitelaw, M.L.; Pettersson, S.; Hanberg, A.; Poellinger, L.: A constitutivelyactive dioxin/aryl hydrocarbon receptor induces stomach tumors. Proc.Nat. Acad. Sci. 99: 9990- 9995, 2002. 3 C c

GAM7957 297 AHR Ema, M.; Matsushita, N.; Sogawa, K.; Ariyama, T.; Inazawa, J.;Nemoto, T.; Ota, M.; Oshimura, M.; Fujii- Kuriyama, Y.: Human arylhydrocarbonreceptor: functional expression and chromosomal assignment to 7p21. J.Biochem. 116: 845- 851, 1994. 3 C c

GAM7957 297 AHR Le Beau, M. M.; Carver, L. A.; Espinosa, R., III; Schmidt, J. V.;Bradfield, C. A.: Chromosomal localization of the human AHR locusencoding the structural gene for the Ah receptor to 7p21- p15. Cytogenet.Cell Genet. 66: 172- 176, 1994. 3 C c

GAM7957 297 AHR Matikainen, T.; Perez, G. I.; Jurisicova, A.; Pru, J. K.; Schlezinger,J. J.; Ryu, H.- Y.; Laine, J.; Sakai, T.; Korsmeyer, S. J.; Casper,R. F.; Sherr, D. H.; Tilly, J. L.: Aromatic hydrocarbon receptor- drivenBax gene expression is required for premature ovarian failure causedby biohazardous environmental chemicals. Nature Genet. 28: 355- 360,2001. 3 C c

GAM7957 297 AHR Micka, J.; Milatovich, A.; Menon, A.; Grabowski, G. A.; Puga, A.;Nebert, D. W.: Human Ah receptor (AHR) gene: localization to 7p15and suggestive correlation of polymorphism with CYP1A1 inducibility. Pharmacogenetics 7:95- 101, 1997. 3 C c

GAM7957 297 AHR Shimizu, Y.; Nakatsuru, Y.; Ichinose, M.; Takahashi, Y.; Kume,H.; Mimura, J.; Fujii- Kuriyama, Y.; Ishikawa, T.: Benzo[a]pyrenecarcinogenicity is lost in mice lacking the aryl hydrocarbon receptor. Proc.Nat. Acad. Sci. 97: 779- 782, 2000. 3 C c

GAM7957 297 AIRE Aaltonen, J.; Bjorses, P.; Sandkuijl, L.; Perheentupa, J.; Peltonen,L.: An autosomal locus causing autoimmune disease: autoimmune polyglandulardisease type I assigned to chromosome 21. Nature Genet. 8: 83- 87,1994. 3 C b

GAM7957 297 AIRE Aaltonen, J.; Horelli- Kuitunen, N.; Fan, J.- B.; Bjorses, P.; Perheentupa,J.; Myers, R.; Palotie, A.; Peltonen, L.: High- resolution physicaland transcriptional mapping of the autoimmune polyendocrinopathy- candidiasis- ectodermaldystrophy locus on chromosome 21q22.3 by FISH. Genome Res. 7: 820- 829,1997. 3 C b

GAM7957 297 AIRE Ahonen, P.: Autoimmune polyendocrinopathy- - candidosis- - ectodermaldystrophy (APECED): autosomal recessive inheritance. Clin. Genet. 27:535- 542, 1985. 3 C b

GAM7957 297 AIRE Ahonen, P.; Myllarniemi, S.; Sipila, I.; Perheentupa, J.: Clinicalvariation of autoimmune polyendocrinopathy- candidiasis- ectodermaldystrophy (APECED) in a series of 68 patients. New Eng. J. Med. 322:1829- 1836, 1990. 3 C b

GAM7957 297 AIRE Arulanantham, K.; Kwyer, J. M.; Genel, M.: Evidence for defectiveimmunoregulation in the syndrome of familial candidiasis endocrinopathy. NewEng. J. Med. 300: 164- 168, 1979. 3 C b

GAM7957 297 AIRE Betterle, C.; Greggio, N. A.; Volpato, M.: Autoimmune polyglandularsyndrome type 1. J. Clin. Endocr. Metab. 83: 1049- 1055, 1998. 3 C b

GAM7957 297 AIRE Bjorses, P.; Aaltonen, J.; Vikman, A.; Perheentupa, J.; Ben- Zion,G.; Chiumello, G.; Dahl, N.; Heideman, P.; Hoorweg- Nijman, J. J. G.;Mathivon, L.; Mullis, P. E.; Pohl, M.; Ritzen, M.; Romeo, G.; Shapiro,M. S.; Smith, C. S.; Solyom, J.; Zlotogora, J.; Peltonen, L.: Genetichomogeneity of autoimmune polyglandular disease type I. Am. J. Hum.Genet. 59: 879- 886, 1996. 3 C b

GAM7957 297 AIRE Bjorses, P.; Halonen, M.; Palvimo, J. J.; Kolmer, M.; Aaltonen,J.; Ellonen, 3 C b
P.; Perheentupa, J.; Ulmanen, I.; Peltonen, L.: Mutationsin the AIRE gene:
effects on subcellular location and transactivationfunction of the
autoimmune polyendocrinopathy- candidiasis- ectodermaldystrophy protein. Am.
J. Hum. Genet. 66: 378- 392, 2000.

GAM7957 297 AIRE Bjorses, P.; Pelto- Huikko, M.; Kaukonen, J.; Aaltonen, J.; Peltonen,L.; 3 C b
Ulmanen, I.: Localization of the APECED protein in distinct
nuclearstructures. Hum. Molec. Genet. 8: 259- 266, 1999.

GAM7957 297 AIRE Blizzard, R. M.; Kyle, M. A.: Studies of the adrenal antigensand antibodies 3 C b
in Addison's disease. J. Clin. Invest. 42: 1653- 1660,1963.

GAM7957 297 AIRE Castells, S.; Fikrig, S.; Inamdar, S.; Orti, E.: Familial 3 C b
moniliasis,defective delayed hypersensitivity, and adrenocorticotropic
hormonedeficiency. J. Pediat. 79: 72- 79, 1971.

GAM7957 297 AIRE Cetani, F.; Barbesino, G.; Borsari, S.; Pardi, E.; Cianferotti,L.; Pinchera, 3 C b
A.; Marcocci, C.: A novel mutation of the autoimmuneregulator gene in an
Italian kindred with autoimmune polyendrocrinopathy- candidiasis-
ectodermaldystrophy, acting in a dominant fashion and strongly
cosegregatingwith hypothyroid autoimmune thyroiditis. J. Clin. Endocr.
Metab. 86:4747- 4752, 2001.

GAM7957 297 AIRE Cihakova, D.; Trebusak, K.; Heino, M.; Fadeyev, V.; Tiulpakov,A.; Battelino, 3 C b
T.; Tar, A.; Halasz, Z.; Blumel, P.; Tawfik, S.; Krohn,K.; Lebl, J.;
Peterson, P.; MEWPE- APECED Study Group: Novel AIREmutations and P450
cytochrome autoantibodies in Central and EasternEuropean patients with
APECED. Hum. Mutat. 18: 225- 232, 2001.

GAM7957 297 AIRE Clemente, M. G.; Obermayer- Straub, P.; Meloni, A.; Strassburg,C. P.; 3 C b
Arangino, V.; Tukey, R. H.; de Virgiliis, S.; Manns, M. P.: Cytochrome P450
1A2 is a hepatic autoantigen in autoimmune polyglandularsyndrome type 1. J.
Clin. Endocr. Metab. 82: 1353- 1361, 1997.

GAM7957 297 AIRE Craig, J. M.; Schiff, L. H.; Boone, J. E.: Chronic moniliasisassociated with 3 C b
Addison's disease. Am. J. Dis. Child. 89: 669- 684,1955.

GAM7957 297 AIRE Ekwall, O.; Hedstrand, H.; Haavik, J.; Perheentupa, J.; Betterle,C.; 3 C b
Gustafsson, J.; Husebye, E.; Rorsman, F.; Kampe, O.: Pteridin-
dependenthydroxylases as autoantigens in autoimmune polyendocrine
syndrometype I. J. Clin. Endocr. Metab. 85: 2944- 2950, 2000.

GAM7957 297 AIRE Finnish- German APECED Consortium: An autoimmune disease, APECED,caused by 3 C b
mutations in a novel gene featuring two PHD- type zinc- fingerdomains.
Nature Genet. 17: 399- 403, 1997.

GAM7957 297 AIRE Foz, M.; Mirada, A.; Guardia, J.: Endocrine disorders in a family.(Letter) 3 C b
Lancet II: 269 only, 1970.

GAM7957 297 AIRE Gass, J. D. M.: The syndrome of keratoconjunctivitis, superficialmoniliasis, 3 C b
idiopathic hypoparathyroidism and Addison's disease. Am.J. Ophthal. 54: 660-
674, 1962.

GAM7957 297 AIRE Gylling, M.; Tuomi, T.; Bjorses, P.; Kontiainen, S.; Partanen,J.; Christie, 3 C b
M. R.; Knip, M.; Perheentupa, J.; Miettinen, A.: Beta- cellautoantibodies,
human leukocyte antigen II alleles, and type 1 diabetesin autoimmune
polyendocrinopathy- candidiasis- ectodermal dystrophy. J.Clin. Endocr.
Metab. 85: 4434- 4440, 2000.

GAM7957 297 AIRE Hedstrand, H.; Ekwall, O.; Haavik, J.; Landgren, E.; Betterle,C.; 3 C b
Perheentupa, J.; Gustafsson, J.; Husebye, E.; Rorsman, F.; Kampe,O.:

Identification of tyrosine hydroxylase as an autoantigen in autoimmunepolyendocrine syndrome type I. Biochem. Biophys. Res. Commun. 267:456- 461, 2000.

GAM7957 297 AIRE Heino, M.; Peterson, P.; Kudoh, J.; Shimizu, N.; Antonarakis,S. E.; Scott, H. S.; Krohn, K.: APECED mutations in the autoimmuneregulator (AIRE) gene. Hum. Mutat. 18: 205- 211, 2001. 3 C b

GAM7957 297 AIRE Heino, M.; Scott, H. S.; Chen, Q.; Peterson, P.; Maenpaa, U.;Papasavvas, M.- P.; Mittaz, L.; Barras, C.; Rossier, C.; Chrousos,G. P.; Stratakis, C. A.; Nagamine, K.; Kudoh, J.; Shimizu, N.; Maclaren,N.; Antonarakis, S. E.; Krohn, K.: Mutation analyses of North AmericanAPS- 1 patients. Hum. Mutat. 13: 69- 74, 1999. 3 C b

GAM7957 297 AIRE Hendrix, T. R.: Personal Communication. Baltimore, Md. 1/14/1985. 3 C b

GAM7957 297 AIRE Hiekkala, H.: Idiopathic hypoparathyroidism, adrenal insufficiencyand moniliasis in children. Ann. Paediat. Fenn. 10: 213- 222, 1964. 3 C b

GAM7957 297 AIRE Hung, W.; Migeon, C. J.; Parrott, R. H.: A possible autoimmunebasis for Addison's disease in three siblings, one with idiopathichypoparathyroidism, pernicious anemia and superficial moniliasis. NewEng. J. Med. 269: 658- 663, 1963. 3 C b

GAM7957 297 AIRE Husebye, E. S.; Gebre- Medhin, G.; Tuomi, T.; Perheentupa, J.;Landin- Olsson, M.; Gustafsson, J.; Rorsman, F.; Kampe, O.: Autoantibodiesagainst aromatic L- amino acid decarboxylase in autoimmune polyendocrinesyndrome type I. J. Clin. Endocr. Metab. 82: 147- 150, 1997. 3 C b

GAM7957 297 AIRE Ishii, T.; Suzuki, Y.; Ando, N.; Matsuo, N.; Ogata, T.: Novelmutations of the autoimmune regulator gene in two siblings with autoimmunepolyendocrinopathy- candidiasis- ectodermal dystrophy. J. Clin. Endocr.Metab. 85: 2922- 2926, 2000. 3 C b

GAM7957 297 AIRE Kenny, F. M.; Holliday, M. D.: Hypoparathyroidism, moniliasis,Addison's and Hashimoto's disease. Hypercalcemia treated with intravenouslyadministered sodium sulfate. New Eng. J. Med. 271: 708- 713, 1964. 3 C b

GAM7957 297 AIRE Krohn, K.; Uibo, R.; Aavik, E.; Peterson, P.; Savilahti, K.:Identification by molecular cloning of an autoantigen associated withAddison's disease as steroid 17- alpha- hydroxylase. Lancet 339: 770- 773,1992. 3 C b

GAM7957 297 AIRE Kunin, A. S.; MacKay, B. R.; Burns, S. L.; Halberstam, M. J.:The syndrome of hypoparathyroidism and adrenocortical insufficiency,a possible sequel of hepatitis: case report and review of the literature. Am.J. Med. 34: 856- 866, 1963. 3 C b

GAM7957 297 AIRE Louria, D. B.; Shannon, D. C.; Johnson, G.; Caroline, L.; Okas,A.; Taschdjian, C.: The susceptibility to moniliasis in childrenwith endocrine hypofunction. Trans. Assoc. Am. Phys. 80: 236- 249,1967. 3 C b

GAM7957 297 AIRE Maclaren, N. K.; Riley, W. J.: Inherited susceptibility to autoimmuneAddison's disease is linked to human leukocyte antigens- DR3 and/orDR4, except when associated with type I autoimmune polyglandular syndrome. J.Clin. Endocr. Metab. 62: 455- 459, 1986. 3 C b

GAM7957 297 AIRE Maghnie, M.; Cosi, G.; Genovese, E.; Manca- Bitti, M. L.; Cohen,A.; Zecca, S.; Tinelli, C.; Gallucci, M.; Bernasconi, S.; Boscherini,B.; Severi, F.; Arico, M.: Central diabetes insipidus in childrenand young adults. New Eng. J. Med. 343: 998- 1007, 2000. 3 C b

GAM7957 297 AIRE Marieb, N. J.; Melby, J. C.; Lyall, S. S.: Isolated hypoaldosteronismassociated with idiopathic hypoparathyroidism. Arch. Intern. Med. 134:424- 429, 1974. 3 C b

GAM7957 297 AIRE McKusick, V. A.: Personal Communication. Baltimore, Md. 1985. 3 C b

GAM7957 297 AIRE Meloni, A.; Perniola, R.; Faa, V.; Corvaglia, E.; Cao, A.; Rosatelli,M. C.: Delineation of the molecular defects in the AIRE gene in autoimmunepolyendocrinopathy- candidiasis- ectodermal dystrophy patients fromSouthern Italy. J. Clin. Endocr. Metab. 87: 841- 846, 2002. 3 C b

GAM7957 297 AIRE Nagamine, K.; Peterson, P.; Scott, H. S.; Kudoh, J.; Minoshima,S.; Heino, M.; Krohn, K. J. E.; Lalioti, M. D.; Mullis, P. E.; Antonarakis,S. E.; Kawasaki, K.; Asakawa, S.; Ito, F.; Shimizu, N.: Positionalcloning of the APECED gene. Nature Genet. 17: 393- 398, 1997. 3 C b

GAM7957 297 AIRE Neufeld, M.; Maclaren, N. K.; Blizzard, R. M.: Two types of autoimmuneAddison's disease associated with different polyglandular autoimmune(PGA) syndromes. Medicine 60: 355- 362, 1981. 3 C b

GAM7957 297 AIRE Neufeld, M.; Maclaren, N.; Blizzard, R.: Autoimmune polyglandularsyndrome. Pediat. Ann. 9: 154- 162, 1980. 3 C b

GAM7957 297 AIRE Nithiyananthan, R.; Heward, J. M.; Allahabadia, A.; Barnett, A.H.; Franklyn, J. A.; Gough, S. C. L.: A heterozygous deletion ofthe autoimmune regulator (AIRE1) gene, autoimmune thyroid disease,and type 1 diabetes: no evidence for association. J. Clin. Endocr.Metab. 85: 1320- 1322, 2000. 3 C b

GAM7957 297 AIRE Pearce, S. H. S.; Cheetham, T.; Imrie, H.; Vaidya, B.; Barnes,N. D.; Bilous, R. W.; Carr, D.; Meeran, K.; Shaw, N. J.; Smith, C.S.; Toft, A. D.; Williams, G.; Kendall- Taylor, P.: A common and recurrent13- bp deletion in the autoimmune regulator gene in British kindredswith autoimmune polyendocrinopathy type 1. Am. J. Hum. Genet. 63:1675- 1684, 1998. 3 C b

GAM7957 297 AIRE Perheentupa, J.: Autoimmune polyendocrinopathy- candidosis- ectodermaldystrophy (APECED).In: Eriksson, A. W.; Forsius, H. R.; Nevanlinna,H. R.; Workman, P. L.; Norio, R. K.: Population Structure and GeneticDisorders. New York: Academic Press (pub.) 1980. Pp. 583- 587. 3 C b

GAM7957 297 AIRE Prader, A.: Personal Communication. Zurich, Switzerland 1972. 3 C b

GAM7957 297 AIRE Ramsay, C.; Winqvist, O.; Puhakka, L.; Halonen, M.; Moro, A.;Kampe, O.; Eskelin, P.; Pelto- Huikko, M.; Peltonen, L.: Aire deficientmice develop multiple features of APECED phenotype and show alteredimmune response. Hum. Molec. Genet. 11: 397- 409, 2002. 3 C b

GAM7957 297 AIRE Rinderle, C.; Christensen, H.- M.; Schweiger, S.; Lehrach, H.;Yaspo, M.- L.: AIRE encodes a nuclear protein co- localizing with cytoskeletalfilaments: altered sub- cellular distribution of mutants lacking PHDzinc fingers. Hum. Molec. Genet. 8: 277- 290, 1999. 3 C b

GAM7957 297 AIRE Rosatelli, M. C.; Meloni, A.; Meloni, A.; Devoto, M.; Cao, A.;Scott, H. S.; Peterson, P.; Heino, M.; Krohn, K. J.; Nagamine, K.;Kudoh, J.; Shimizu, N.; Antonarakis, S. E.: A common mutation inSardinian autoimmune polyendocrinopathy- candidiasis- ectodermal dystrophypatients. Hum. Genet. 103: 428- 434, 1998. 3 C b

GAM7957 297 AIRE Saenger, P.: Primary hypoaldosteronism due to zona glomerulosadefect. (Letter) New Eng. J. Med. 310: 1394 only, 1984. 3 C b

GAM7957 297 AIRE Saenger, P.; Levine, L. S.; Irvine, W. J.; Gottesdiener, K.; Rauh,W.; Sonino, N.; Chow, D.; New, M. I.: Progressive adrenal failurein polyglandular autoimmune disease. J. Clin. Endocr. Metab. 54:863- 868, 1982. 3 C b

GAM7957 297 AIRE Scott, H. S.; Heino, M.; Peterson, P.; Mittaz, L.; Lalioti, M.D.; Betterle, C.; Cohen, A.; Seri, M.; Lerone, M.; Romeo, G.; Collin,P.; Salo, M.; and 9 others: Common mutations in autoimmune polyendocrinopathy- candidiasis- ectodermaldystrophy patients of different origins. Molec. Endocr. 12: 1112- 3 C b

1119,1998.

GAM7957 297 AIRE Shapiro, M. S.; Zamir, R.; Weiss, E.; Radnay, J.; Shenkman, L.: The polyglandular deficiency syndrome: a new variant in PersianJews. J. Endocr. Invest. 10: 1- 7, 1987. 3 C b

GAM7957 297 AIRE Spinner, M. W.; Blizzard, R. M.; Childs, B.: Clinical and geneticalheterogeneity in idiopathic Addison's disease and hypoparathyroidism. J.Clin. Endocr. 28: 795- 804, 1968. 3 C b

GAM7957 297 AIRE Sweetnam, W. P.: Juvenile familial endocrinopathy. Lancet I:463- 465, 1966. 3 C b

GAM7957 297 AIRE Wang, C.- Y.; Davoodi- Semiromi, A.; Huang, W.; Connor, E.; Shi,J.- D.; She, J.- X.: Characterization of mutations in patients withautoimmune polyglandular syndrome type 1 (APS1). Hum. Genet. 103:681- 685, 1998. 3 C b

GAM7957 297 AIRE Whitaker, J. A.; Landing, B. H.; Esselborn, V. M.; Williams, R.R.: Syndrome of familial juvenile hypoadrenocorticism, hypoparathyroidismand superficial moniliasis. J. Clin. Endocr. 16: 1374- 1387, 1956. 3 C b

GAM7957 297 AIRE Wirfalt, A.: Genetic heterogeneity in autoimmune polyglandularfailure. Acta Med. Scand. 210: 7- 13, 1981. 3 C b

GAM7957 297 AIRE Zlotogora, J.; Shapiro, M. S.: Polyglandular autoimmune syndrometype I among Iranian Jews. J. Med. Genet. 29: 824- 826, 1992. 3 C b

GAM7957 297 ALDH3B1 Hsu, L. C.; Chang, W.- C.; Yoshida, A.: Cloning of a cDNA encodinghuman ALDH7, a new member of the aldehyde dehydrogenase family. Gene 151:285- 289, 1994. 3 C c

GAM7957 297 ALDH3B1 Hsu, L. C.; Chang, W.- C.; Yoshida, A.: Human aldehyde dehydrogenasegenes, ALDH7 and ALDH8: genomic organization and gene structure comparison. Gene 189:89- 94, 1997. 3 C c

GAM7957 297 ALPP Badger, K. S.; Sussman, H. H.: Structural evidence that humanliver and placental alkaline phosphatase isoenzymes are coded by differentgenes. Proc. Nat. Acad. Sci. 73: 2201- 2205, 1976. 3 C b

GAM7957 297 ALPP Beckman, L.; Beckman, G.; Christodoulou, C.; Ifekwunigwe, A.:Variations in human placental alkaline phosphatase. Acta Genet. Statist.Med. 17: 406- 412, 1967. 3 C b

GAM7957 297 ALPP Beckman, L.; Bjorling, G.; Christodoulou, C.: Pregnancy enzymesand placental polymorphism: alkaline phosphatase. Acta Genet. Statist.Med. 16: 59- 73, 1966. 3 C b

GAM7957 297 ALPP Boyer, S. H.: Alkaline phosphatase in human sera and placenta. Science 134:1002- 1004, 1961. 3 C b

GAM7957 297 ALPP Boyer, S. H.: Human organ alkaline phosphatases: discriminationby several means including starch gel electrophoresis of antienzyme- enzymesupernatant fluids. Ann. N.Y. Acad. Sci. 103: 938- 950, 1963. 3 C b

GAM7957 297 ALPP Donald, L. J.: The genetics of placental alkaline phosphatase:a possible 'null' allele. Ann. Hum. Genet. 38: 7- 18, 1974. 3 C b

GAM7957 297 ALPP Donald, L. J.; Robson, E. B.: Rare variants of placental alkalinephosphatase. Ann. Hum. Genet. 37: 303- 313, 1974. 3 C b

GAM7957 297 ALPP Edwards, J. H.; Wingham, J.: Data on linkage between the locusdetermining placental alkaline phosphatase and other markers. Ann.Hum. Genet. 30: 233- 237, 1967. 3 C b

GAM7957 297 ALPP Garattini, E.; Margolis, J.; Heimer, E.; Felix, A.; Udenfriend,S.: Human placental alkaline phosphatase in liver and intestine. Proc.Nat. Acad. Sci. 82: 6080- 6084, 1985. 3 C b

GAM7957 297 ALPP Gogolin, K. J.; Slaughter, C. A.; Harris, H.: Electrophoresisof enzyme- 3 C b

monoclonal antibody complexes: studies of human placentalalkaline phosphatase polymorphism. Proc. Nat. Acad. Sci. 78: 5061- 5065,1981.

GAM7957 297 ALPP Griffin, C. A.; Smith, M.; Henthorn, P. S.; Harris, H.; Weiss,M. J.; Raducha, M.; Emanuel, B. S.: Human placental and intestinalalkaline phosphatase genes map to 2q34- q37. Am. J. Hum. Genet. 41:1025- 1034, 1987. 3 C b

GAM7957 297 ALPP Henthorn, P. S.; Knoll, B. J.; Raducha, M.; Rothblum, K. N.; Slaughter,C.; Weiss, M.; Lafferty, M. A.; Fischer, T.; Harris, H.: Productsof two common alleles at the locus for human placental alkaline phosphatasediffer by seven amino acids. Proc. Nat. Acad. Sci. 83: 5597- 5601,1986. 3 C b

GAM7957 297 ALPP Henthorn, P. S.; Raducha, M.; Edwards, Y. H.; Weiss, M. J.; Slaughter,C.; Lafferty, M. A.; Harris, H.: Nucleotide and amino acid sequencesof human intestinal alkaline phosphatase: close homology to placentalalkaline phosphatase. Proc. Nat. Acad. Sci. 84: 1234- 1238, 1987. 3 C b

GAM7957 297 ALPP Kam, W.; Clauser, E.; Kim, Y. S.; Kan, Y. W.; Rutter, W. J.:Cloning, sequencing, and chromosomal localization of human term placentalalkaline phosphatase cDNA. Proc. Nat. Acad. Sci. 82: 8715- 8719,1985. 3 C b

GAM7957 297 ALPP Knoll, B. J.; Rothblum, K. N.; Longley, M.: Nucleotide sequenceof the human placental alkaline phosphatase gene: evolution of the5- prime flanking region by deletion/substitution. J. Biol. Chem. 263:12020- 12027, 1988. 3 C b

GAM7957 297 ALPP Lucarelli, P.; Scacchi, R.; Corbo, R. M.; Benincasa, A.; Palmarino,R.: Human placental alkaline phosphatase electrophoretic alleles:quantitative studies. Am. J. Hum. Genet. 34: 331- 336, 1982. 3 C b

GAM7957 297 ALPP Martin, D.; Spurr, N. K.; Trowsdale, J.: RFLP of the human placentalalkaline phosphatase gene (PLAP). Nucleic Acids Res. 15: 9104 only,1987. 3 C b

GAM7957 297 ALPP Martin, D.; Tucker, D. F.; Gorman, P.; Sheer, D.; Spurr, N. K.;Trowsdale, J.: The human placental alkaline phosphatase gene andrelated sequences map to chromosome 2 band q37. Ann. Hum. Genet. 51:145- 152, 1987. 3 C b

GAM7957 297 ALPP Millan, J. L.; Beckman, G.; Jeppsson, A.; Stigbrand, T.: Geneticvariants of placental alkaline phosphatase as detected by a monoclonalantibody. Hum. Genet. 60: 145- 149, 1982. 3 C b

GAM7957 297 ALPP Millan, J. L.; Stigbrand, T.: Antigenic determinants of humanplacental and testicular placental- like alkaline phosphatases as mappedby monoclonal antibodies. Europ. J. Biochem. 136: 1- 7, 1983. 3 C b

GAM7957 297 ALPP Palmarino, R.; Corbo, R. M.; Lucarelli, P.: Human placental alkalinephosphatase: analysis of genetically determined rare variants. Hum.Biol. 51: 341- 352, 1979. 3 C b

GAM7957 297 ALPP Raimondi, E.; Talarico, D.; Moro, L.; Rutter, W. J.; Della Valle,G.; De Carli, L.: Regional mapping of the human placental alkalinephosphatase gene (ALPP) to 2q37 by in situ hybridization. Cytogenet.Cell Genet. 47: 98- 99, 1988. 3 C b

GAM7957 297 ALPP Robinson, J. C.; Goldsmith, L. A.: Genetically determined variantsof serum alkaline phosphatase: a review. Vox Sang. 13: 289- 307,1967. 3 C b

GAM7957 297 ALPP Robson, E. B.; Harris, H.: Genetics of the alkaline phosphatasepolymorphism of the human placenta. Nature 207: 1257- 1259, 1965. 3 C b

GAM7957 297 ALPP Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. New York: Oxford Univ. Press (pub.) 1988. 3 C b

GAM7957 297 ALPP Slaughter, C. A.; Gogolin, K. J.; Coseo, M. C.; Meyer, L. J.;Lesko, J.; Harris, H.: Discrimination of human placental alkalinephosphatase allelic variants by monoclonal antibodies. Am. J. Hum.Genet. 35: 1- 20, 1983. 3 C b

GAM7957 297 ANKH Ho, A. M.; Johnson, M. D.; Kingsley, D. M.: Role of the mouseank gene in 3 C b

control of tissue calcification and arthritis. Science 289:265- 270, 2000.

GAM7957 297 ANKH Nurnberg, P.; Thiele, H.; Chandler, D.; Hohne, W.; Cunningham,M. L.; Ritter, 3 C b
H.; Leschik, G.; Uhlmann, K.; Mischung, C.; Harrop,K.; Goldblatt, J.;
Borochowitz, Z. U.; Kotzot, D.; Westermann, F.;Mundlos, S.; Braun, H.- S.;
Laing, N.; Tinschert, S.: Heterozygousmutations in ANKH, the human ortholog
of the mouse progressive ankylosisgene, result in craniometaphyseal
dysplasia. Nature Genet. 28: 37- 41,2001.

GAM7957 297 ANKH Nurnberg, P.; Tinschert, S.; Mrug, M.; Hampe, J.; Muller, C. R.;Fuhrmann, 3 C b
E.; Braun, H.- S.; Reis, A.: The gene for autosomal
dominantcraniometaphyseal dysplasia maps to chromosome 5q and is
distinctfrom the growth hormone- receptor gene. Am. J. Hum. Genet. 61: 918-
923,1997.

GAM7957 297 ANKH Reichenberger, E.; Tiziani, V.; Watanabe, S.; Park, L.; Ueki, Y.;Santanna, 3 C b
C.; Baur, S. T.; Shiang, R.; Grange, D. K.; Beighton, P.;Gardner, J.;
Hamersma, H.; Sellars, S.; Ramesar, R.; Lidral, A. C.;Sommer, A.; Raposo do
Amaral, C. M.; Gorlin, R. J.; Mulliken, J. B.;Olsen, B. R.: Autosomal
dominant craniometaphyseal dysplasia is causedby mutations in the
transmembrane protein ANK. Am. J. Hum. Genet. 68:1321- 1326, 2001.

GAM7957 297 AOAH Hagen, F. S.; Grant, F. J.; Kuijper, J. L.; Slaughter, C. A.; Moomaw,C. R.; 3 C c
Orth, K.; O'Hara, P. J.; Munford, R. S.: Expression and characterizationof
recombinant human acyloxyacyl hydrolase, a leukocyte enzyme thatdeacylates
bacterial lipopolysaccharides. Biochemistry 30: 8415- 8423,1991.

GAM7957 297 AOAH Whitmore, T. E.; Mathewes, S. L.; O'Hara, P. J.; Durnam, D. M.: Chromosomal 3 C c
localization of the acyloxyacyl hydrolase (AOAH) geneto 7p14- p12 using
fluorescence in situ hybridization. Genomics 21:457- 458, 1994.

GAM7957 297 APOL1 Duchateau, P. N.; Pullinger, C. R.; Cho, M. H.; Eng, C.; Kane,J. P.: 3 C c
Apolipoprotein L gene family: tissue- specific expression,splicing, promoter
regions; discovery of a new gene. J. Lipid Res. 42:620- 630, 2001.

GAM7957 297 APOL1 Duchateau, P. N.; Pullinger, C. R.; Orellana, R. E.; Kunitake,S. T.; Naya- 3 C c
Vigne, J.; O'Connor, P. M.; Malloy, M. J.; Kane, J. P.: Apolipoprotein L, a
new human high density lipoprotein apolipoproteinexpressed by the pancreas:
identification, cloning, characterization,and plasma distribution of
apolipoprotein L. J. Biol. Chem. 272:25576- 25582, 1997.

GAM7957 297 APOL1 Mimmack, M. L.; Ryan, M.; Baba, H.; Navarro- Ruiz, J.; Iritani,S.; Faull, R. 3 C c
L. M.; McKenna, P. J.; Jones, P. B.; Arai, H.; Starkey,M.; Emson, P. C.;
Bahn, S.: Gene expression analysis in schizophrenia:reproducible up-
regulation of several members of the apolipoproteinL family located in a
high- susceptibility locus for schizophreniaon chromosome 22. Proc. Nat.
Acad. Sci. 99: 4680- 4685, 2002.

GAM7957 297 APOL1 Monajemi, H.; Fontijn, R. D.; Pannekoek, H.; Horrevoets, A. J.G.: The 3 C c
apolipoprotein L gene cluster has emerged recently in evolutionand is
expressed in human vascular tissue. Genomics 79: 539- 546,2002.

GAM7957 297 APOL1 Page, N. M.; Butlin, D. J.; Lomthaisong, K.; Lowry, P. J.: Thehuman 3 C c
apolipoprotein L gene cluster: identification, classification,and sites of
distribution. Genomics 74: 71- 78, 2001.

GAM7957 297 ARNT2 Hirose, K.; Morita, M.; Ema, M.; Mimura, J.; Hamada, H.; Fujii,H.; Saijo, 3 C c
Y.; Gotoh, O.; Sogawa, K.; Fujii- Kuriyama, Y.: cDNA cloningand tissue-
specific expression of a novel basic helix- loop- helix/PASfactor (Arnt2)
with close sequence similarity to the aryl hydrocarbonreceptor nuclear
translocator (Arnt). Molec. Cell. Biol. 16: 1706- 1713,1996.

GAM7957 297 ARNT2 Keith, B.; Adelman, D. M.; Simon, M. C.: Targeted mutation ofthe murine arylhydrocarbon receptor nuclear translocator 2 (Arnt2)gene reveals partial redundancy with Arnt. Proc. Nat. Acad. Sci. 98:6692- 6697, 2001. 3 C c

GAM7957 297 ARNT2 Michaud, J. L.; DeRossi, C.; May, N. R.; Holdener, B. C.; Fan,C.- M.: ARNT2 acts as the dimerization partner of SIM1 for the developmentof the hypothalamus. Mech. Dev. 90: 253- 261, 2000. 3 C c

GAM7957 297 ARNT2 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C c

GAM7957 297 BCAR1 Brinkman, A.; van der Flier, S.; Kok, E. M.; Dorssers, L. C. J.: BCAR1, a human homologue of the adapter protein p130Cas, and antiestrogenresistance in breast cancer cells. J. Nat. Cancer Inst. 92: 112- 120,2000. 3 C c

GAM7957 297 BCAR1 Brugge, J. S.: Casting light on focal adhesions. Nature Genet. 19:309- 311, 1998. 3 C c

GAM7957 297 BCAR1 Chen, Z.; Friedrich, G. A.; Soriano, P.: Transcriptional enhancerfactor 1 disruption by a retroviral gene trap leads to heart defectsand embryonic lethality in mice. Genes Dev. 8: 2293- 2301, 1994. 3 C c

GAM7957 297 BCAR1 Dorssers, L. C. J.; van Agthoven, T.; Dekker, A.; van Agthoven,T. L. A.; Kok, E. M.: Induction of antiestrogen resistance in humanbreast cancer cells by random insertional mutagenesis using defectiveretroviruses: identification of bcar- 1, a common integration site. Molec.Endocr. 7: 870- 878, 1993. 3 C c

GAM7957 297 BCAR1 Honda, H.; Oda, H.; Nakamoto, T.; Honda, Z.; Sakai, R.; Suzuki,T.; Saito, T.; Nakamura, K.; Nakao, K.; Ishikawa, T.; Katsuki, M.;Yazaki, Y.; Hirai, H.: Cardiovascular anomaly, impaired actin bundlingand resistance to Src- induced transformation in mice lacking p130- Cas. NatureGenet. 19: 361- 365, 1998. 3 C c

GAM7957 297 BCAR1 Kanner, S. B.; Reynolds, A. B.; Wang, H. C.; Vines, R. R.; Parsons,J. T.: The SH2 and SH3 domains of pp60src direct stable associationwith tyrosine phosphorylated proteins p130 and p110. EMBO J. 10:1689- 1698, 1991. 3 C c

GAM7957 297 BCAR1 Kuo, C. T.; Morrisey, E. E.; Anandappa, R.; Sigrist, K.; Lu, M.M.; Parmacek, M. S.; Soudais, C.; Leiden, J. M.: GATA4 transcriptionfactor is required for ventral morphogenesis and heart tube formation. GenesDev. 11: 1048- 1060, 1997. 3 C c

GAM7957 297 BCAR1 Reynolds, A. B.; Kanner, S. B.; Wang, H. C.; Parsons, J. T.: Stableassociation of activated pp60src with two tyrosine- phosphorylatedcellular proteins. Molec. Cell. Biol. 9: 3951- 3958, 1989. 3 C c

GAM7957 297 BCAR1 Sakai, R.; Iwamatsu, A.; Hirano, N.; Ogawa, S.; Tanaka, T.; Mano,H.; Yazaki, Y.; Hirai, H.: A novel signaling molecule, p130, formsstable complexes in vivo with v- Crk and v- Src in a tyrosine phosphorylation- dependentmanner. EMBO J. 13: 3748- 3756, 1994. 3 C c

GAM7957 297 BCAR1 van der Flier, S.; Brinkman, A.; Look, M. P.; Kok, E. M.; Meijer- vanGelder, M. E.; Klijn, J. G. M.; Dorssers, L. C. J.; Foekens, J. A.: Bcar1/p130Cas protein and primary breast cancer: prognosis and responseto tamoxifen treatment. J. Nat. Cancer Inst. 92: 120- 127, 2000. 3 C c

GAM7957 297 BCAR1 Yoshida, K.; Taga, T.; Saito, M.; Suematsu, S.; Kumanogoh, A.;Tanaka, T.; Fujiwara, H.; Hirata, M.; Yamagami, T.; Nakahata, T.;Hirabayashi, T.; Yoneda, Y.; Tanaka, K.; Wang, W. Z.; Mori, C.; Shiota,K.; Yoshida, N.; 3 C c

Kishimoto, T.: Targeted disruption of gp130, a commonsignal transducer for the interleukin 6 family of cytokines, leadsto myocardial and hematological disorders. Proc. Nat. Acad. Sci. 93:407- 411, 1996.

GAM7957 297 BMP8 DiLeone, R. J.; King, J. A.; Storm, E. E.; Copeland, N. G.; Jenkins,N. A.; 3 C b
Kingsley, D. M.: The Bmp8 gene is expressed in developingskeletal tissue and maps near the achondroplasia locus on mouse chromosome4. Genomics 40: 196-198, 1997.

GAM7957 297 BMP8 Ozkaynak, E.; Schnegelsberg, P. N. J.; Jin, D. F.; Clifford, G.M.; Warren, 3 C b
F. D.; Drier, E. A.; Oppermann, H.: Osteogenic protein- 2:a new member of the transforming growth factor- beta superfamily expressedin early embryogenesis. J. Biol. Chem. 267: 25220- 25227, 1992.

GAM7957 297 CACNG1 Iles, D. E.; Segers, B.; Sengers, R. C. A.; Monsieurs, K.; Heytens,L.; 3 C c
Halsall, P. J.; Hopkins, P. M.; Ellis, F. R.; Hall- Curran, J.L.; Stewart, A. D.; Wieringa, B.: Genetic mapping of the beta- 1- and gamma- subunits of the human skeletal muscle L- type voltage- dependentcalcium channel on chromosome 17q and exclusion as candidate genesfor malignant hyperthermia susceptibility. Hum. Molec. Genet. 2:863- 868, 1993.

GAM7957 297 CACNG1 Iles, D. E.; Segers, B.; Weghuis, D. O.; Suikerbuijk, R.; Wieringa,B.: 3 C c
Localization of the gamma- subunit of the skeletal muscle L- typevoltage-dependent calcium channel gene (CACNLG) to human chromosomeband 17q24 by in situ hybridization and identification of a polymorphicrepetitive DNA sequence at the gene locus. Cytogenet. Cell Genet. 64:227- 230, 1993.

GAM7957 297 CACNG1 Powers, P. A.; Liu, S.; Hogan, K.; Gregg, R. G.: Molecular 3 C c
characterizationof the gene encoding the gamma subunit of the human skeletal muscle1,4- dihydropyridine- sensitive Ca(2+) channel (CACNLG), cDNA sequence,gene structure, and chromosomal location. J. Biol. Chem. 268: 9275-9279,1993.

GAM7957 297 CAP2 Bartuski, A. J.; Kamachi, Y.; Schick, C.; Overhauser, J.; Silverman,G. A.: 3 C c
Cytoplasmic antiproteinase 2 (PI8) and bomapin (PI10) mapto the serpin cluster at 18q21.3. Genomics 43: 321- 328, 1997.

GAM7957 297 CAP2 Huber, R.; Carrell, R. W.: Implications of the three- dimensionalstructure 3 C c
of alpha 1- antitrypsin for structure and function of serpins. Biochemistry 28:8951- 8966, 1989.

GAM7957 297 CAP2 Sprecher, C. A.; Morgenstern, K. A.; Mathewes, S.; Dahlen, J. R.;Schrader, 3 C c
S. K.; Foster, D. C.; Kisiel, W.: Molecular cloning, expression,and partial characterization of two novel members of the ovalbuminfamily of serine proteinase inhibitors. J. Biol. Chem. 270: 29854- 29861,1995.

GAM7957 297 CAPNS1 Arthur, J. S. C.; Elce, J. S.; Hegadorn, C.; Williams, K.; Greer,P. A.: 3 C c
Disruption of the murine calpain small subunit gene, Capn4:calpain is essential for embryonic development but not for cell growthand division. Molec. Cell. Biol. 20: 4474- 4481, 2000.

GAM7957 297 CAPNS1 Ohno, S.; Emori, Y.; Suzuki, K.: Nucleotide sequence of a cDNAcoding for the 3 C c
small subunit of human calcium- dependent protease. NucleicAcids Res. 14: 5559 only, 1986.

GAM7957 297 CAPNS1 Ohno, S.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Ohmi- Imajoh,S.; Suzuki, 3 C c
K.; Shimizu, Y.; Shimizu, N.: Four genes for the calpainfamily locate on four distinct human chromosomes. (Abstract) Cytogenet.Cell Genet. 51: 1054-1055, 1989.

GAM7957 297 CAPNS1 Ohno, S.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Shimizu, Y.;Ohmi- Imajoh, 3 C c
S.; Shimizu, N.; Suzuki, K.: Four genes for the calpainfamily locate on four

distinct human chromosomes. Cytogenet. CellGenet. 53: 225- 229, 1990.

GAM7957 297 CAPNS1 Sakihama, T.; Kakidani, H.; Zenita, K.; Yumoto, N.; Kikuchi, T.;Sasaki, T.; 3 C c
Kannagi, R.; Nakanishi, S.; Ohmori, M.; Takio, K.; Titani,K.; Murachi, T.: A
putative Ca(2+)- binding protein: structure ofthe light subunit of porcine
calpain elucidated by molecular cloningand protein sequence analysis. Proc.
Nat. Acad. Sci. 82: 6075- 6079,1985.

GAM7957 297 CARKL Phornphutkul, C.; Anikster, Y.; Huizing, M.; Braun, P.; Brodie,C.; Chou, J. 3 C b
Y.; Gahl, W. A.: The promoter of a lysosomal membranetransporter gene, CTNS,
binds Sp- 1, shares sequences with the promoterof an adjacent gene, CARKL,
and causes cystinosis if mutated in acritical region. Am. J. Hum. Genet. 69:
712- 721, 2001.

GAM7957 297 CARKL Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; 3 C b
McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.;
Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic
cystinosis gene (CTNS): complete sequencing of a200- kb segment and
discovery of a novel gene within the common cystinosis- causingdeletion.
Genome Res. 10: 165- 173, 2000.

GAM7957 297 CASP10 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 C c
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM7957 297 CASP10 Park, W. S.; Lee, J. H.; Shin, M. S.; Park, J. Y.; Kim, H. S.;Lee, J. H.; 3 C c
Kim, Y. S.; Lee, S. N.; Xiao, W.; Park, C. H.; Lee, S.H.; Yoo, N. J.; Lee,
J. Y.: Inactivating mutations of the caspase- 10gene in gastric cancer.
Oncogene 21: 2919- 2925, 2002.

GAM7957 297 CASP10 Shin, M. S.; Kim, H. S.; Kang, C. S.; Park, W. S.; Kim, S. Y.;Lee, S. N.; 3 C c
Lee, J. H.; Park, J. Y.; Jang, J. J.; Kim, C. W.; Kim,S. H.; Lee, J. Y.;
Yoo, N. J.; Lee, S. H.: Inactivating mutationsof CASP10 gene in non- Hodgkin
lymphomas. Blood 99: 4094- 4099, 2002.

GAM7957 297 CASP10 Vincenz, C.; Dixit, V. M.: Fas- associated death domain proteininterleukin- 3 C c
1- beta- converting enzyme 2 (FLICE2), an ICE/Ced- 3 homologue,is proximally
involved in CD95- and p55- mediated death signaling. J.Biol. Chem. 272:
6578- 6583, 1997.

GAM7957 297 CASP10 Wang, J.; Chun, H. J.; Wong, W.; Spencer, D. M.; Lenardo, M. J.: Caspase- 10 3 C c
is an initiator caspase in death receptor signaling. Proc.Nat. Acad. Sci.
98: 13884- 13888, 2001.

GAM7957 297 CASP10 Wang, J.; Zheng, L.; Lobito, A.; Chan, F. K.; Dale, J.; Sneller,M.; Yao, X.; 3 C c
Puck, J. M.; Straus, S. E.; Lenardo, M. J.: Inheritedhuman caspase 10
mutations underlie defective lymphocyte and dendriticcell apoptosis in
autoimmune lymphoproliferative syndrome type II. Cell 98:47- 58, 1999.

GAM7957 297 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 C c
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM7957 297 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 C c
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.

Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM7957 297 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 C c
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM7957 297 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 C c
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM7957 297 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 C c
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell
death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM7957 297 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 C c
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM7957 297 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 C c
Caspase- 8 is required for cell death induced by expanded
polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM7957 297 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 C c
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM7957 297 CD28 Aruffo, A.; Seed, B.: Molecular cloning of a CD28 cDNA by a high- 3 C b
efficiencyCOS cell expression system. Proc. Nat. Acad. Sci. 84: 8573-
8577,1987.

GAM7957 297 CD28 Buonavista, N.; Balzano, C.; Pontarotti, P.; Le Paslier, D.; Golstein,P.: 3 C b
Molecular linkage of the human CTLA4 and CD28 Ig- superfamilygenes in yeast
artificial chromosomes. Genomics 13: 856- 861, 1992.

GAM7957 297 CD28 Howard, T. A.; Rochelle, J. M.; Seldin, M. F.: Cd28 and Ctla- 4,two related 3 C b
members of the Ig supergene family, are tightly linkedon proximal mouse
chromosome 1. Immunogenetics 33: 74- 76, 1991.

GAM7957 297 CD28 Lafage- Pochitaloff, M.; Costello, R.; Couez, D.; Simonetti, J.;Mannoni, P.; 3 C b
Mawas, C.; Olive, D.: Human CD28 and CTLA- 4 Ig superfamilygenes are located
on chromosome 2 at bands q33- q34. Immunogenetics 31:198- 201, 1990.

GAM7957 297 CD28 Lee, K. P.; Taylor, C.; Petryniak, B.; Turka, L. A.; June, C. H.;Thompson, 3 C b
C. B.: The genomic organization of the CD28 gene: implicationsfor the
regulation of CD28 mRNA expression and heterogeneity. J.Immun. 145: 344-
352, 1990.

GAM7957 297 CD28 Lesslauer, W.; Gmunder, H.; Bohlen, P.: Purification and N- terminalamino 3 C b
acid sequence of the human T90/44 (CD28) antigen. Immunogenetics 27:388-
391, 1988.

GAM7957 297 CD28 Okkenhaug, K.; Wu, L.; Garza, K. M.; La Rose, J.; Khoo, W.; Odermatt,B.; 3 C b
Mak, T. W.; Ohashi, P. S.; Rottapel, R.: A point mutation inCD28
distinguishes proliferative signals from survival signals. NatureImmun. 2:
325- 332, 2001.

GAM7957 297 CD59 Acosta, J.; Hettinga, J.; Fluckiger, R.; Krumrei, N.; Goldfine,A.; Angarita, 3 C c
L.; Halperin, J.: Molecular basis for a link betweencomplement and the
vascular complications of diabetes. Proc. Nat.Acad. Sci. 97: 5450- 5455,

2000.

GAM7957 297 CD59 Bickmore, W. A.; Longbottom, D.; Oghene, K.; Fletcher, J. M.; vanHeyningen, V.: Colocalization of the human CD59 gene to 11p13 withthe MIC11 cell surface antigen. Genomics 17: 129- 135, 1993. 3 C c

GAM7957 297 CD59 Davies, A.; Simmons, D. L.; Hale, G.; Harrison, R. A.; Tighe, H.;Lachmann, P. J.; Waldmann, H.: CD59, an LY- 6- like protein expressedin human lymphoid cells, regulates the action of the complement membraneattack complex on homologous cells. J. Exp. Med. 170: 637- 654, 1989. 3 C c

GAM7957 297 CD59 Forsberg, U. H.; Bazil, V.; Stefanova, I.; Schroder, J.: Genefor human CD59 (likely Ly- 6 homologue) is located on the short armof chromosome 11. Immunogenetics 30: 188- 193, 1989. 3 C c

GAM7957 297 CD59 Harada, R.; Okada, N.; Fujita, T.; Okada, H.: Purification of1F5 antigen that prevents complement attack on homologous cell membranes. J.Immun. 144: 1823- 1828, 1990. 3 C c

GAM7957 297 CD59 Heckl- Ostreicher, B.; Ragg, S.; Drechsler, M.; Scherthan, H.; Royer-Pokora,B.: Localization of the human CD59 gene by fluorescence in situ hybridizationand pulsed- field gel electrophoresis. Cytogenet. Cell Genet. 63:144- 146, 1993. 3 C c

GAM7957 297 CD59 Holt, D. S.; Botto, M.; Bygrave, A. E.; Hanna, S. M.; Walport,M. J.; Morgan, B. P.: Targeted deletion of the CD59 gene causes spontaneousintravascular hemolysis and hemoglobinuria. Blood 98: 442- 449, 2001. 3 C c

GAM7957 297 CD59 Holt, D. S.; Powell, M. B.; Rushmere, N. K.; Morgan, B. P.: Genomicstructure and chromosome location of the gene encoding mouse CD59. Cytogenet.Cell Genet. 89: 264- 267, 2000. 3 C c

GAM7957 297 CD59 Huppi, K.; Duncan, R.; Potter, M.: Myc- 1 is centromeric to thelinkage group Ly- 6- Sis- Gdc- 1 on mouse chromosome 15. Immunogenetics 27:215- 219, 1988. 3 C c

GAM7957 297 CD59 Kamiura, S.; Nolan, C. M.; Meruelo, D.: Long- range physical mapof the Ly- 6 complex: mapping the Ly- 6 multigene family by field- inversionand two-dimensional gel electrophoresis. Genomics 12: 89- 105, 1992. 3 C c

GAM7957 297 CD59 LeClair, K. P.; Rabin, M.; Nesbitt, M. N.; Pravtcheva, D.; Ruddle,F. H.; Palfree, R. G. E.; Bothwell, A.: Murine Ly- 6 multigene familyis located on chromosome 15. Proc. Nat. Acad. Sci. 84: 1638- 1642,1987. 3 C c

GAM7957 297 CD59 Low, M. G.; Saltiel, A. R.: Structural and functional roles ofglycosyl-phosphatidylinositol in membranes. Science 239: 268- 275,1988. 3 C c

GAM7957 297 CD59 Mahoney, J. F.; Urakaze, M.; Hall, S.; DeGasperi, R.; Chang, H.-M.;Sugiyama, E.; Warren, C. D.; Borowitz, M.; Nicholson- Weller, A.; Rosse,W. F.; Yeh, E. T. H.: Defective glycosylphosphatidylinositol anchorsynthesis in paroxysmal nocturnal hemoglobinuria granulocytes. Blood 79:1400- 1403, 1992. 3 C c

GAM7957 297 CD59 Mao, M.; Yu, M.; Tong, J.- H.; Ye, J.; Zhu, J.; Huang, Q.- H.; Fu,G.; Yu, L.; Zhao, S.- Y.; Waxman, S.; Lanotte, M.; Wang, Z.- Y.; Tan,J.- Z.; Chan, S.- J.; Chen, Z.: RIG- E, a human homolog of the murineLy- 6 family, is induced by retinoic acid during the differentiationof acute promyelocytic leukemia cell. Proc. Nat. Acad. Sci. 93:5910- 5914, 1996. 3 C c

GAM7957 297 CD59 Meri, S.; Morgan, B. P.; Davies, A.; Daniels, R. H.; Olavesen,M. G.; Waldmann, H.; Lachmann, P. J.: Human protectin (CD59), an18,000- 20,000 MW complement lysis restricting factor, inhibits C5b- 8catalysed insertion of C9 into lipid bilayers. Immunology 71: 1- 9,1990. 3 C c

GAM7957 297 CD59 Meri, S.; Morgan, B. P.; Wing, M.; Jones, J.; Davies, A.; Podack,E.; Lachmann, P. J.: Human protectin (CD59), an 18- 20- kD homologouscomplement 3 C c

restriction factor, does not restrict perforin- mediatedlysis. J. Exp. Med. 172: 367- 370, 1990.

GAM7957 297 CD59 Motoyama, N.; Okada, N.; Yamashina, M.; Okada, H.: Paroxysmalnocturnal hemoglobinuria due to hereditary nucleotide deletion inthe HRF20 (CD59) gene. Europ. J. Immun. 22: 2669- 2673, 1992. 3 C c

GAM7957 297 CD59 Okada, N.; Harada, R.; Fujiita, T.; Okada, H.: A novel membraneglycoprotein capable of inhibiting membrane attack by homologous complement. Int.Immun. 1: 205- 208, 1989. 3 C c

GAM7957 297 CD59 Ono, H.; Kuno, Y.; Tanaka, H.; Yamashina, M.; Tsuyoshi, T.; Kondo,N.; Orii, T.: A case of paroxysmal nocturnal hemoglobinuria withoutdeficiency of decay- accelerating factor on erythrocytes. Blood 75:1746- 1747, 1990. 3 C c

GAM7957 297 CD59 Petranka, J. G.; Fleenor, D. E.; Sykes, K.; Kaufman, R. E.; Rosse,W. F.: Structure of the CD59- encoding gene: further evidence of arelationship to murine lymphocyte antigen Ly- 6 protein. Proc. Nat.Acad. Sci. 89: 7876- 7879, 1992. 3 C c

GAM7957 297 CD59 Rosse, W. F.: Personal Communication. Durham, N. C. 6/3/1993. 3 C c

GAM7957 297 CD59 Rosse, W. F.; Parker, C. J.: Paroxysmal nocturnal hemoglobinuria. Clin.Haemat. 14: 105- 125, 1985. 3 C c

GAM7957 297 CD59 Rother, R. P.; Rollins, S. A.; Mennone, J.; Chodera, A.; Fidel,S. A.; Bessler, M.; Hillmen, P.; Squinto, S. P.: Expression of recombinanttransmembrane CD59 in paroxysmal nocturnal hemoglobinuria B cellsconfers resistance to human complement. Blood 84: 2604- 2611, 1994. 3 C c

GAM7957 297 CD59 Tone, M.; Walsh, L. A.; Waldmann, H.: Gene structure of humanCD59 and demonstration that discrete mRNAs are generated by alternativepolyadenylation. J. Molec. Biol. 227: 971- 976, 1992. 3 C c

GAM7957 297 CD59 Walsh, L. A.; Tone, M.; Thiru, S.; Waldmann, H.: The CD59 antigen- - amultifunctional molecule. Tissue Antigens 40: 213- 220, 1992. 3 C c

GAM7957 297 CD59 Woodroofe, M. N.; Tunnacliffe, A.; Pym, B.; Goodfellow, P. N.;Walsh, F. S.: Human muscle cell surface antigen 16- 3A5 is encodedby a gene on chromosome 11. Somat. Cell Molec. Genet. 10: 535- 540,1984. 3 C c

GAM7957 297 CD59 Yamashina, M.; Ueda, E.; Kinoshita, T.; Takami, T.; Ojima, A.;Ono, H.; Tanaka, H.; Kondo, N.; Orii, T.; Okada, N.; Okada, H.; Inoue,K.; Kitani, T.: Inherited complete deficiency of 20- kilodalton homologousrestriction factor (CD59) as a cause of paroxysmal nocturnal hemoglobinuria. NewEng. J. Med. 323: 1184- 1189, 1990. 3 C c

GAM7957 297 CD68 Holness, C. L.; Simmons, D. L.: Molecular cloning of CD68, a humanmacrophage marker related to lysosomal glycoproteins. Blood 81:1607- 1613, 1993. 3 C c

GAM7957 297 CD68 Jones, E.; Quinn, C. M.; See, C. G.; Montgomery, D. S.; Ford, M.J.; Kolble, K.; Gordon, S.; Greaves, D. R.: The linked human elongationinitiation factor 4A1 (EIF4A1) and CD68 genes map to chromosome 17p13. Genomics 53:248- 250, 1998. 3 C c

GAM7957 297 CDH6 Chalmers, I. J.; Hofler, H.; Atkinson, M. J.: Mapping of a cadheringene cluster to a region of chromosome 5 subject to frequent allelicloss in carcinoma. Genomics 57: 160- 163, 1999. 3 C c

GAM7957 297 CDH6 Shimoyama, Y.; Gotoh, M.; Terasaki, T.; Kitajima, M.; Hirohashi,S.: Isolation and sequence analysis of human cadherin- 6 complementaryDNA for the full coding sequence and its expression in human carcinomacells. Cancer Res. 55: 2206- 2211, 1995. 3 C c

GAM7957 297 CDH6 Suzuki, S.; Sano, K.; Tanihara, H.: Diversity of the cadherinfamily: evidence for eight new cadherins in nervous tissue. CellRegul. 2: 261- 270, 3 C c

1991.

GAM7957 297 CEACAM5 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999. 3 C b

GAM7957 297 CEACAM5 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by fluorescence in situ hybridization. Genomics 12:773- 779, 1992. 3 C b

GAM7957 297 CEACAM5 Gold, P.; Freedman, S. O.: Demonstration of tumor- specific antigensin human colonic carcinomata by immunological tolerance and absorptiontechniques. J. Exp. Med. 121: 439- 462, 1965. 3 C b

GAM7957 297 CEACAM5 Kamarck, M. E.; Elting, J. J.; Hart, J. T.; Goebel, S. J.; Rae,P. M. M.; Nothdurft, M. A.; Nedwin, J. J.; Barnett, T. R.: Carcinoembryonicantigen family: expression in a mouse L- cell transfectant and characterizationof a partial cDNA in bacteriophage lambda- gt11. Proc. Nat. Acad.Sci. 84: 5350- 5354, 1987. 3 C b

GAM7957 297 CEACAM5 Nishi, M.; Inazawa, J.; Inoue, K.; Nakagawa, H.; Taniwaki, M.;Misawa, S.; Oikawa, S.; Nakazato, H.; Abe, T.: Regional chromosomalassignment of carcinoembryonic antigen gene (CEA) to chromosome 19at band q13.2. Cancer Genet. Cytogenet. 54: 77- 81, 1991. 3 C b

GAM7957 297 CEACAM5 Oikawa, S.; Nakazato, H.; Kosaki, G.: Primary structure of humancarcinoembryonic antigen (CEA) deduced from cDNA sequence. Biochem.Biophys. Res. Commun. 142: 511- 528, 1987. 3 C b

GAM7957 297 CEACAM5 Thompson, J. A.; Pande, H.; Paxton, R. J.; Shively, L.; Padma,A.; Simmer, R. L.; Todd, C. W.; Riggs, A. D.; Shively, J. E.: Molecularcloning of a gene belonging to the carcinoembryonic antigen gene familyand discussion of a domain model. Proc. Nat. Acad. Sci. 84: 2965- 2969,1987. 3 C b

GAM7957 297 CEACAM5 Thompson, J.; Zimmermann, W.: The carcinoembryonic antigen genefamily: structure, expression and evolution. Tumor Biol. 9: 63- 83,1988. 3 C b

GAM7957 297 CEACAM5 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades- Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan, K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772, 1992. 3 C b

GAM7957 297 CEACAM5 Willcocks, T. C.; Craig, I. W.: Characterization of the genomicorganization of human carcinoembryonic antigen (CEA): comparison withother family members and sequence analysis of 5- prime controllingregion. Genomics 8: 492- 500, 1990. 3 C b

GAM7957 297 CEACAM5 Willcocks, T. C.; Craig, S. P.; Coates, D.; Craig, I. W.: Codingsequences for carcinoembryonic antigen (CEA) assigned to human chromosome19q13. (Abstract) Cytogenet. Cell Genet. 46: 716 only, 1987. 3 C b

GAM7957 297 CEACAM5 Willcocks, T. C.; Craig, S. P.; Craig, I. W.: Assignment of thecoding sequence for carcinoembryonic antigen (CEA) and normal cross- reactingantigen (NCA) to human chromosome 19q13. Ann. Hum. Genet. 53: 141- 148,1989. 3 C b

GAM7957 297 CEACAM5 Zimmer, R.; Thomas, P.: Mutations in the carcinoembroyonic antigengene in 3 C b

colorectal cancer patients: implications on liver metastasis. CancerRes. 61: 2822- 2826, 2001.

GAM7957 297 CEACAM5 Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.: Isolationand 3 C b
characterization of cDNA clones encoding the human carcinoembryonicantigen reveal a highly conserved repeating structure. Proc. Nat.Acad. Sci. 84: 2960- 2964, 1987.

GAM7957 297 CEACAM5 Zimmermann, W.; Weber, B.; Ortlieb, B.; Rudert, F.; Schempp, W.;Fiebig, H.- 3 C b
H.; Shively, J. E.; von Kleist, S.; Thompson, J. A.: Chromosomallocalization of the carcinoembryonic antigen gene family and differentialexpression in various tumors. Cancer Res. 48: 2550- 2554, 1988.

GAM7957 297 CLCN7 Brandt, S.; Jentsch, T. J.: ClC- 6 and ClC- 7 are two novel broadlyexpressed 3 C c
members of the CLC chloride channel family. FEBS Lett. 377:15- 20, 1995.

GAM7957 297 CLCN7 Cleiren, E.; Benichou, O.; Van Hul, E.; Gram, J.; Bollerslav, J.;Singer, F. 3 C c
R.; Beaverson, K.; Aledo, A.; Whyte, M. P.; Yoneyama, T.;deVernejou, M.- C.; Van Hul, W.: Albers- Schonberg disease (autosomaldominant osteopetrosis, type II) results from mutations in the ClCN7chloride channel gene. Hum. Molec. Genet. 10: 2861- 2867, 2001.

GAM7957 297 CLCN7 Kornak, U.; Kasper, D.; Bosl, M. R.; Kaiser, E.; Schweizer, M.;Schulz, A.; 3 C c
Friedrich, W.; Delling, G.; Jentsch, T. J.: Loss of theClC- 7 chloride channel leads to osteopetrosis in mice and man. Cell 104:205- 215, 2001.

GAM7957 297 CPM Kas, K.; Schoenmakers, E. F. P. M.; Van de Ven, W. J. M.: Physicalmap 3 C c
location of the human carboxypeptidase M gene (CPM) distal toD12S375 and proximal to D12S8 at chromosome 12q15. Genomics 30:403- 405, 1995.

GAM7957 297 CPM Rehli, M.; Krause, S. W.; Kreutz, M.; Andreesen, R.: CarboxypeptidaseM is 3 C c
identical to the MAX.1 antigen and its expression is associatedwith monocyte to macrophage differentiation. J. Biol. Chem. 270:15644- 15649, 1995.

GAM7957 297 CPM Tan, F.; Chan, S. J.; Steiner, D. F.; Schilling, J. W.; Skidgel,R. A.: 3 C c
Molecular cloning and sequencing of the cDNA for human membrane-boundcarboxypeptidase M: comparison with carboxypeptidases A, B, H, andN. J. Biol. Chem. 264: 13165- 13170, 1989.

GAM7957 297 CRACC Boles, K. S.; Mathew, P. A.: Molecular cloning of CS1, a novelhuman natural 3 C b
killer cell receptor belonging to the CD2 subset ofthe immunoglobulin superfamily. Immunogenetics 52: 302- 307, 2001.

GAM7957 297 CRACC Bouchon, A.; Cella, M.; Grierson, H. L.; Cohen, J. I.; Colonna,M.: Cutting 3 C b
edge: activation of NK cell- mediated cytotoxicity bya SAP- independent receptor of the CD2 family. J. Immun. 167: 5517- 5521,2001.

GAM7957 297 CREB1 Barco, A.; Alarcon, J. M.; Kandel, E. R.: Expression of constitutivelyactive 3 C b
CREB protein facilitates the late phase of long- term potentiationby enhancing synaptic capture. Cell 108: 689- 703, 2002.

GAM7957 297 CREB1 Barton, C. H.; Ajioka, J. W.; Roach, T. I. A.; Blackwell, J. M.: Mapping 3 C b
Creb- 1 to chromosome 1 in the mouse. Genomics 14: 790- 792,1992.

GAM7957 297 CREB1 Barton, K.; Muthusamy, N.; Chanyangam, M.; Fischer, C.; Clendenin,C.; 3 C b
Leiden, J. M.: Defective thymocyte proliferation and IL- 2 productionin transgenic mice expressing a dominant- negative form of CREB. Nature 379:81-85, 1996.

GAM7957 297 CREB1 Carlezon, W. A., Jr.; Thome, J; Olson, V. G.; Lane- Ladd, S. B.;Brodkin, E. 3 C b
S.; Hiroi, N.; Duman, R. S.; Neve, R. L.; Nestler, E.J.: Regulation of cocaine reward by CREB. Science 282: 2272- 2275,1998.

GAM7957 297 CREB1 Cole, T. J.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Schutz,G.; 3 C b
Ruppert, S.: The mouse CREB (cAMP responsive element bindingprotein) gene:

structure, promoter analysis, and chromosomal localization. Genomics 13:974-982, 1992.

GAM7957 297 CREB1 Fentzke, R. C.; Korcarz, C. E.; Lang, R. M.; Lin, H.; Leiden, J.M.: Dilated cardiomyopathy in transgenic mice expressing a dominant- negativeCREB transcription factor in the heart. J. Clin. Invest. 101: 2415- 2426,1998. 3 C b

GAM7957 297 CREB1 Herzig, S.; Long, F.; Jhala, U. S.; Hedrick, S.; Quinn, R.; Bauer,A.; Rudolph, D.; Schutz, G.; Yoon, C.; Puigserver, P.; Spiegelman,B.; Montminy, M.: CREB regulates hepatic gluconeogenesis throughthe coactivator PGC- 1. Nature 413: 179- 183, 2001. 3 C b

GAM7957 297 CREB1 Hoeffler, J. P.; Meyer, T. E.; Yun, Y.; Jameson, J. L.; Habener,J. F.: Cyclic AMP- responsive DNA- binding protein: structure basedon a cloned placental cDNA. Science 242: 1430- 1433, 1988. 3 C b

GAM7957 297 CREB1 Kida, S.; Josselyn, S. A.; Pena de Ortiz, S.; Kogan, J. H.; Chevere,I.; Masushige, S.; Silva, A. J.: CREB required for the stabilityof new and reactivated fear memories. Nature Neurosci. 5: 348- 355,2002. 3 C b

GAM7957 297 CREB1 Mantamadiotis, T.; Lemberger, T.; Bleckmann, S. C.; Kern, H.;Kretz, O.; Villalba, A. M.; Tronche, F.; Kellendonk, C.; Gau, D.;Kapfhammer, J.; Otto, C.; Schmid, W.; Schutz, G.: Disruption of CREBfunction in brain leads to neurodegeneration. Nature Genet. 31:47- 54, 2002. 3 C b

GAM7957 297 CREB1 Montminy, M. R.; Bilezikjian, L. M.: Binding of a nuclear proteinto the cyclic- AMP response element of the somatostatin gene. Nature 328:175- 178, 1987. 3 C b

GAM7957 297 CREB1 Montminy, M. R.; Sevarino, K. A.; Wagner, J. A.; Mandel, G.; Goodman,R. H.: Identification of a cyclic- AMP- responsive element within therat somatostatin gene. Proc. Nat. Acad. Sci. 83: 6682- 6686, 1986. 3 C b

GAM7957 297 CREB1 Nguyen, L. Q.; Kopp, P.; Martinson, F.; Stanfield, K.; Roth, S.I.; Jameson, J. L.: A dominant negative CREB (cAMP response element- bindingprotein) isoform inhibits thyrocyte growth, thyroid- specific geneexpression, differentiation, and function. Molec. Endocr. 14: 1448- 1461,2000. 3 C b

GAM7957 297 CREB1 Parker, D.; Ferreri, K.; Nakajima, T.; LaMorte, V. J.; Evans,R.; Koerber, S. C.; Hoeger, C.; Montminy, M. R.: Phosphorylationof CREB at ser- 133 induces complex formation with CREB- binding proteinvia a direct mechanism. Molec. Cell. Biol. 16: 694- 703, 1996. 3 C b

GAM7957 297 CREB1 Radhakrishnan, I.; Perez- Alvarado, G. C.; Parker, D.; Dyson, H.J.; Montminy, M. R.; Wright, P. E.: Solution structure of the KIXdomain of CBP bound to the transactivation domain of CREB: a modelfor activator:coactivator interactions. Cell 91: 741- 752, 1997. 3 C b

GAM7957 297 CREB1 Solomou, E. E.; Juang, Y.- T.; Gourley, M. F.; Kammer, G. M.; Tsokos,G. C.: Molecular basis of deficient IL- 2 production in T cells frompatients with systemic lupus erythematosus. J. Immun. 166: 4216- 4222,2001. 3 C b

GAM7957 297 CREB1 Taylor, A. K.; Klisak, I.; Mohandas, T.; Sparkes, R. S.; Li, C.;Gaynor, R.; Lusis, A. J.: Assignment of the human gene for CREB1to chromosome 2q32.3-q34. Genomics 7: 416- 421, 1990. 3 C b

GAM7957 297 CROT Ferdinandusse, S.; Mulders, J.; IJlst, L.; Denis, S.; Dacremont,G.; Waterham, H. R.; Wanders, R. J. A.: Molecular cloning and expressionof human carnitine octanoyltransferase: evidence for its role in theperoxisomal beta-oxidation of branched- chain fatty acids. Biochem.Biophys. Res. Commun. 263: 213- 218, 1999. 3 C c

GAM7957 297 CROT van der Leij, F. R.; Huijkman, N. C. A.; Boomsma, C.; Kuipers,J. R. G.; Bartelds, B.: Genomics of the human carnitine acyltransferasegenes. Molec. 3 C c

Genet. Metab. 71: 139- 153, 2000.

GAM7957 297 CRY2 Freedman, M. S.; Lucas, R. J.; Soni, B.; von Schantz, M.; Munoz,M.; David- 3 C c
Gray, Z.; Foster, R.: Regulation of mammalian circadianbehavior by non- rod,
non- cone, ocular photoreceptors. Science 284:502- 504, 1999.

GAM7957 297 CRY2 Griffin, E. A., Jr.; Staknis, D.; Weitz, C. J.: Light- independentrole of 3 C c
CRY1 and CRY2 in the mammalian circadian clock. Science 286:768- 771, 1999.

GAM7957 297 CRY2 Hsu, D. S.; Zhao, X.; Zhao, S.; Kazantsev, A.; Wang, R.- P.; Todo,T.; Wei, 3 C c
Y.- F.; Sancar, A.: Putative human blue- light photoreceptorshCRY1 and hCRY2
are flavoproteins. Biochemistry 35: 13871- 13877,1996.

GAM7957 297 CRY2 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 C c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM7957 297 CRY2 Kobayashi, K.; Kanno, S.; Smit, B.; van der Horst, G. T. J.; Takao,M.; 3 C c
Yasui, A.: Characterization of photolyase/blue- light receptorhomologs in
mouse and human cells. Nucleic Acids Res. 26: 5086- 5092,1998.

GAM7957 297 CRY2 Kume, K.; Zylka, M. J.; Sriram, S.; Shearman, L. P.; Weaver, D.R.; Jin, X.; 3 C c
Maywood, E. S.; Hastings, M. H.; Reppert, S. M.: mCRY1and mCRY2 are
essential components of the negative limb of the circadianclock feedback
loop. Cell 98: 193- 205, 1999.

GAM7957 297 CRY2 Lucas, R. J.; Freedman, M. S.; Munoz, M.; Garcia- Fernandez, J.- M.;Foster, 3 C c
R. G.: Regulation of the mammalian pineal by non- rod, non- cone,ocular
photoreceptors. Science 284: 505- 507, 1999.

GAM7957 297 CRY2 Okamura, H.; Miyake, S.; Sumi, Y.; Yamaguchi, S.; Yasui, A.; Muijtjens,M.; 3 C c
Hoeijmakers, J. H. J.; van der Horst, G. T. J.: Photic inductionof mPer1 and
mPer2 in Cry- deficient mice lacking a biological clock. Science 286:2531-
2534, 1999.

GAM7957 297 CRY2 Shearman, L. P.; Sriram, S.; Weaver, D. R.; Maywood, E. S.; Chaves,I.; 3 C c
Zheng, B.; Kume, K.; Lee, C. C.; van der Horst, G. T. J.; Hastings,M. H.;
Reppert, S. M.: Interacting molecular loops in the mammaliancircadian clock.
Science 288: 1013- 1019, 2000.

GAM7957 297 CRY2 Thresher, R. J.; Vitaterna, M. H.; Miyamoto, Y.; Kazantsev, A.;Hsu, D. S.; 3 C c
Petit, C.; Selby, C. P.; Dawut, L.; Smithies, O.; Takahashi,J. S.; Sancar,
A.: Role of mouse cryptochrome blue- light photoreceptorin circadian
photoresponses. Science 282: 1490- 1494, 1998.

GAM7957 297 CRY2 van der Horst, G. T. J.; Muijtjens, M.; Kobayashi, K.; Takano,R.; Kanno, S.; 3 C c
Takao, M.; de Wit, J.; Verkerk, A.; Eker, A. P. M.;van Leenen, D.; Buijs,
R.; Bootsma, D.; Hoeijmakers, J. H. J.; Yasui,A.: Mammalian Cry1 and Cry2
are essential for maintenance of circadianrhythms. Nature 398: 627- 630,
1999.

GAM7957 297 CRY2 Yagita, K.; Tamanini, F.; van der Horst, G. T. J.; Okamura, H.: Molecular 3 C c
mechanisms of the biological clock in cultured fibroblasts. Science 292:278-
281, 2001.

GAM7957 297 CTSS Deussing, J.; Roth, W.; Rommerskirch, W.; Wiederanders, B.; vonFigura, K.; 3 C c
Peters, C.: The genes of the lysosomal cysteine proteinasescathepsin B, H,
L, and S map to different mouse chromosomes. MammalianGenome 8: 241- 245,
1997.

GAM7957 297 CTSS Driessen, C.; Bryant, R. A.; Lennon- Dumenil, A. M.; Villadangos,J. A.; 3 C c
Bryant, P. W.; Shi, G. P.; Chapman, H. A.; Ploegh, H. L.:Cathepsin S
controls the trafficking and maturation of MHC class IImolecules in

dendritic cells. J. Cell Biol. 147: 775- 790, 1999.

GAM7957 297 CTSS Gelb, B. D.; Shi, G.- P.; Heller, M.; Weremowicz, S.; Morton, C.;Desnick, R. 3 C c
J.; Chapman, H. A.: Structure and chromosomal assignmentof the human
cathepsin K gene. Genomics 41: 258- 262, 1997.

GAM7957 297 CTSS Riese, R. J.; Shi, G.- P.; Villadangos, J.; Stetson, D.; Driessen,C.; 3 C c
Lennon- Dumenil, A.- M.; Chu, C.- L.; Naumov, Y.; Behar, S. M.; Ploegh,H.;
Locksley, R.; Chapman, H. A.: Regulation of CD1 function andNK1.1+ T cell
selection and maturation by cathepsin S. Immunity 15:909- 919, 2001.

GAM7957 297 CTSS Shi, G.- P.; Munger, J. S.; Meara, J. P.; Rich, D. H.; Chapman,H. A.: 3 C c
Molecular cloning and expression of human alveolar macrophagecathepsin S, an
elastinolytic cysteine protease. J. Biol. Chem. 267:7258- 7262, 1992.

GAM7957 297 CTSS Shi, G.- P.; Webb, A. C.; Foster, K. E.; Knoll, J. H. M.; Lemere,C. A.; 3 C c
Munger, J. S.; Chapman, H. A.: Human cathepsin S: chromosomallocalization,
gene structure, and tissue distribution. J. Biol. Chem. 269:11530- 11536,
1994.

GAM7957 297 CYB561 McBride, O. W.; Yi, H. F.; Srivastava, M.: The human cytochromeb561 gene 3 C c
(CYB561) is located at 17q11- qter. Genomics 21: 662- 663,1994.

GAM7957 297 CYB561 Srivastava, M.: Genomic structure and expression of the humangene encoding 3 C c
cytochrome b(561), an integral protein of the cromaffingranule membrane. J.
Biol. Chem. 270: 22714- 22720, 1995.

GAM7957 297 CYP4F3 Kikuta, Y.; Kato, M.; Yamashita, Y.; Miyauchi, Y.; Tanaka, K.;Kamada, N.; 3 C c
Kusunose, M.: Human leukotriene B4 omega- hydroxylase(CYP4F3) gene:
molecular cloning and chromosomal localization. DNACell Biol. 17: 221- 230,
1998.

GAM7957 297 CYP4F3 Kikuta, Y.; Kusunose, E.; Endo, K.; Yamamoto, S.; Sogawa, K.; Fujii- 3 C c
Kuriyama,Y.; Kusunose, M.: A novel form of cytochrome P- 450 family 4 in
humanpolymorphonuclear leukocytes: cDNA cloning and expression of
leukotrieneB4 omega- hydroxylase. J. Biol. Chem. 268: 9376- 9380, 1993.

GAM7957 297 DAPP1 Dowler, S.; Currie, R. A.; Downes, C. P.; Alessi, D. R.: DAPP1:a dual 3 C b
adaptor for phosphotyrosine and 3- phosphoinositides. Biochem.J. 342: 7- 12,
1999.

GAM7957 297 DAPP1 Marshall, A. J.; Niiro, H.; Lerner, C. G.; Yun, T. J.; Thomas,S.; Disteche, 3 C b
C. M.; Clark, E. A.: A novel B lymphocyte- associatedadaptor protein, Bam32,
regulates antigen receptor signaling downstreamof phosphatidylinositol 3-
kinase. J. Exp. Med. 191: 1319- 1331, 2000.

GAM7957 297 DBCCR1 Habuchi, T.; Luscombe, M.; Elder, P. A.; Knowles, M. A.: Structureand 3 C b
methylation- based silencing of a gene (DBCCR1) within a candidatebladder
cancer tumor suppressor region at 9q32- q33. Genomics 48:277- 288, 1998.

GAM7957 297 DBCCR1 Habuchi, T.; Yoshida, O.; Knowles, M. A.: A novel candidate tumoursuppressor 3 C b
locus at 9q32- 33 in bladder cancer: localization of thecandidate region
within a single 840 kb YAC. Hum. Molec. Genet. 6:913- 919, 1997.

GAM7957 297 DBCCR1 Nishiyama, H.; Takahashi, T.; Kakehi, Y.; Habuchi, T.; Knowles,M. A.: 3 C b
Homozygous deletion at the 9q32- 33 candidate tumor suppressorlocus in
primary human bladder cancer. Genes Chromosomes Cancer 26:171- 175, 1999.

GAM7957 297 DCLRE1C Ma, Y.; Pannicke, U.; Schwarz, K.; Lieber, M. R.: Hairpin openingand 3 C c
overhang processing by an Artemis/DNA- dependent protein kinasecomplex in
nonhomologous end joining and V(D)J recombination. Cell 108:781- 794, 2002.

GAM7957 297 DCLRE1C Moshous, D.; Callebaut, I.; de Chasseval, R.; Corneo, B.; Cavazzana- 3 C c

Calvo,M.; Le Deist, F.; Tezcan, I.; Sanal, O.; Bertrand, Y.; Philippe, N.;Fischer, A.; de Villartay, J.- P.: Artemis, a novel DNA double-strandbreak repair/V(D)J recombination protein, is mutated in human severecombined immune deficiency. Cell 105: 177- 186, 2001.

GAM7957 297 DDOST Kelleher, D. J.; Kreibich, G.; Gilmore, R.: 3 C b
Oligosaccharyltransferaseactivity is associated with a protein complex composed of ribophorinsI and II and a 48 kd protein. Cell 69: 55- 65, 1992.

GAM7957 297 DDOST Yamagata, T.; Tsuru, T.; Momoi, M. Y.; Suwa, K.; Nozaki, Y.; Mukasa,T.; 3 C b
Ohashi, H.; Fukushima, Y.; Momoi, T.: Genome organization ofhuman 48- kDa oligosaccharyltransferase (DDOST). Genomics 45: 535- 540,1997.

GAM7957 297 DFFA Inohara, N.; Koseki, T.; Chen, S.; Wu, X.; Nunez, G.: CIDE, anovel family of 3 C b
cell death activators with homology to the 45 kDasubunit of the DNA fragmentation factor. EMBO J. 17: 2526- 2533,1998.

GAM7957 297 DFFA Leek, J. P.; Carr, I. M.; Bell, S. M.; Markham, A. F.; Lench, N.J.: 3 C b
Assignment of the DNA fragmentation factor gene (DFFA) to humanchromosome bands 1p36.3- p36.2 by in situ hybridization. Cytogenet.Cell Genet. 79: 212-213, 1997.

GAM7957 297 DFFA Liu, X.; Zou, H.; Slaughter, C.; Wang, X.: DFF, a heterodimericprotein that 3 C b
functions downstream of caspase- 3 to trigger DNA fragmentationduring apoptosis. Cell 89: 175- 184, 1997.

GAM7957 297 DGKI Ding, L.; Traer, E.; McIntyre, T. M.; Zimmerman, G. A.; Prescott,S. M.: The 3 C c
cloning and characterization of a novel human diacylglycerolkinase, DGK-iota. J. Biol. Chem. 273: 32746- 32752, 1998.

GAM7957 297 DGKI Masai, I.; Okazaki, A.; Hosoya, T.; Hotta, Y.: Drosophila 3 C c
retinaldegeneration A gene encodes an eye- specific diacylglycerol kinasewith cysteine- rich zinc- finger motifs and ankyrin repeats. Proc.Nat. Acad. Sci. 90: 11157- 11161, 1993.

GAM7957 297 DNASE2 Brook, J. D.; Shaw, D. J.; Meredith, A. L.; Bruns, G. A. P.; Harper,P. S.: 3 C b
Localisation of genetic markers and orientation of the linkagegroup on chromosome 19. Hum. Genet. 68: 282- 285, 1984.

GAM7957 297 DNASE2 Bruns, G. A. P.; Regina, V. M.; Gerald, P. S.: Lysosomal DNaseand chromosome 3 C b
19.(Abstract) J. Cell Biol. 83: 444a only, 1979.

GAM7957 297 DNASE2 Kawane, K.; Fukuyama, H.; Kondoh, G.; Takeda, J.; Ohsawa, Y.; Uchiyama,Y.; 3 C b
Nagata, S.: Requirement of DNase II for definitive erythropoiesisin the mouse fetal liver. Science 292: 1546- 1549, 2001.

GAM7957 297 DNASE2 Yasuda, T.; Nadano, D.; Sawazaki, K.; Kishi, K.: Genetic polymorphismof 3 C b
human deoxyribonuclease II (DNase II): low activity levels in urineand leukocytes are due to an autosomal recessive allele. Ann. Hum.Genet. 56: 1-10, 1992.

GAM7957 297 DNASE2 Yasuda, T.; Takeshita, H.; Iida, R.; Nakajima, T.; Hosomi, O.;Nakashima, Y.; 3 C b
Kishi, K.: Molecular cloning of the cDNA encodinghuman deoxyribonuclease II. J. Biol. Chem. 273: 2610- 2616, 1998.

GAM7957 297 DNASE2 Yasuda, T.; Takeshita, H.; Iida, R.; Nakajima, T.; Hosomi, O.;Nakashima, Y.; 3 C b
Mogi, K.; Kishi, K.: Chromosomal localization of ahuman deoxyribonuclease II gene (DNASE2) to 19p13.2- p13.1 using boththe polymerase chain reaction and fluorescence in situ hybridizationanalysis. Biochem. Biophys. Res. Commun. 244: 815- 818, 1998.

GAM7957 297 DSC1 King, I. A.; Arnemann, J.; Spurr, N. K.; Buxton, R. S.: Cloningof the cDNA 3 C b

(DSC1) coding for human type 1 desmocollin and its assignmentto chromosome 18. Genomics 18: 185- 194, 1993.

GAM7957 297 DSC1 Troyanovsky, S. M.; Eshkind, L. G.; Troyanovsky, R. B.; Leube,R. E.; Franke, W. W.: Contributions of cytoplasmic domains of desmosomalcadherins to desmosome assembly and intermediate filament anchorage. Cell 72:561- 574, 1993. 3 C b

GAM7957 297 DSC2 Arnemann, J.; Spurr, N. K.; Wheeler, G. N.; Parker, A. E.; Buxton,R. S.: Chromosomal assignment of the human genes coding for the majorproteins of the desmosome junction, desmoglein DGI (DSG), desmocollinsDGII/III (DSC), desmoplakins DPI/II (DSP), and plakoglobin DPIII (JUP). Genomics 10:640- 645, 1991. 3 C c

GAM7957 297 DSC2 Buxton, R. S.; Cowin, P.; Franke, W. W.; Garrod, D. R.; Green,K. J.; King, I. A.; Koch, P. J.; Magee, A. I.; Rees, D. A.; Stanley,J. R.; Steinberg, M. S.: Nomenclature of the desmosomal cadherins. J.Cell Biol. 121: 481- 483, 1993. 3 C c

GAM7957 297 DSC2 Buxton, R. S.; Wheeler, G. N.; Pidsley, S. C.; Marsden, M. D.;Adams, M. J.; Jenkins, N. A.; Gilbert, D. J.; Copeland, N. G.: Mousedesmocollin (Dsc3) and desmoglein (Dsg1) genes are closely linkedin the proximal region of chromosome 18. Genomics 21: 510- 516, 1994. 3 C c

GAM7957 297 DSC2 Greenwood, M. D.; Marsden, M. D.; Cowley, C. M. E.; Sahota, V.K.; Buxton, R. S.: Exon- intron organization of the human type 2 desmocollingene (DSC2): desmocollin gene structure is closer to 'classical' cadherinsthan to desmogleins. Genomics 44: 330- 335, 1997. 3 C c

GAM7957 297 DSC2 King, I. A.; Arnemann, J.; Spurr, N. K.; Buxton, R. S.: Cloningof the cDNA (DSC1) coding for human type 1 desmocollin and its assignmentto chromosome 18. Genomics 18: 185- 194, 1993. 3 C c

GAM7957 297 DTNB Blake, D. J.; Nawrotzki, R.; Loh, N. Y.; Gorecki, D. C.; Davies,K. E.: Beta- dystrobrevin, a member of the dystrophin- related proteinfamily. Proc. Nat. Acad. Sci. 95: 241- 246, 1998. 3 C c

GAM7957 297 DTNB Loh, N. Y.; Ambrose, H. J.; Guay- Woodford, L. M.; DasGupta, S.;Nawrotzki, R. A.; Blake, D. J.; Davies, K. E.: Genomic organizationand refined mapping of the mouse beta- dystrobrevin gene. MammalianGenome 9: 857- 862, 1998. 3 C c

GAM7957 297 DTNB Peters, M. F.; O'Brien, K. F.; Sadoulet- Puccio, H. M.; Kunkel,L. M.; Adams, M. E.; Froehner, S. C.: Beta- dystrobrevin, a new memberof the dystrophin family: identification, cloning, and protein associations. J.Biol. Chem. 272: 50:- 31561- 31569, 1997. 3 C c

GAM7957 297 DVL3 Bui, T. D.; Beier, D. R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; Kaklamanis, L.; Kearney, L.; Regan, R.; Sussman, D. J.; Harris,A. L.: cDNA cloning of a human dishevelled DVL- 3 gene, mapping to3q27, and expression in human breast and colon carcinomas. Biochem.Biophys. Res. Commun. 239: 510- 516, 1997. 3 C b

GAM7957 297 DVL3 Klingensmith, J.; Nusse, R.; Perrimon, N.: The Drosophila segmentpolarity gene dishevelled encodes a novel protein required for responseto wingless signal. Genes Dev. 8: 118- 130, 1994. 3 C b

GAM7957 297 DVL3 Pizzuti, A.; Amati, F.; Calabrese, G.; Mari, A.; Colosimo, A; Silani,V.; Giardino, L.; Ratti, A.; Penso, D.; Calza, L.; Palka, G.; Scarlato,G.; Novelli, G.; Dallapicolla, B.: cDNA characterization and chromosomalmapping of two human homologs of the Drosophila dishevelled polaritygene. Hum. Molec. Genet. 5: 953- 958, 1996. 3 C b

GAM7957 297 DVL3 Semenov, M. V.; Snyder, M.: Human dishevelled genes constitutea DHR- 3 C b

containing multigene family. Genomics 42: 302- 310, 1997.

GAM7957 297 EHD1 Di Fiore, P. P.; Pelicci, P. G.; Sorkin, A.: EH: a novel protein- 3 C c
proteininteraction domain potentially involved in intracellular sorting.
TrendsBiochem. Sci. 22: 411- 413, 1997.

GAM7957 297 EHD1 Guru, S. C.; Agarwal, S. K.; Manickam, P.; Olufemi, S.- E.; Crabtree,J. S.; 3 C c
Weisemann, J. M.; Kester, M. B.; Kim, Y. S.; Wang, Y.; Emmert- Buck,M. R.;
Liotta, L. A.; Spiegel, A. M.; Boguski, M. S.; Roe, B. A.;Collins, F. S.;
Marx, S. J.; Burns, L.; Chandrasekharappa, S. C.:A transcript map for the
2.8- Mb region containing the multiple endocrineneoplasia type 1 locus.
Genome Res. 7: 725- 735, 1997.

GAM7957 297 EHD1 Haider, N. B.; Searby, C.; Galperin, E.; Mintz, L.; Horowitz, M.;Stone, E. 3 C c
M.; Sheffield, V. C.: Evaluation and molecular characterizationof EHD1, a
candidate gene for Bardet- Biedl syndrome 1 (BBS1). Gene 240:227- 232, 1999.

GAM7957 297 EHD1 Mintz, L.; Galperin, E.; Pasmanik- Chor, M.; Tulzinsky, S.; Bromberg,Y.; 3 C c
Kozak, C. A.; Joyner, A.; Fein, A.; Horowitz, M.: EHD1- - an EH- domain-
containingprotein with a specific expression pattern. Genomics 59: 66-
76,1999.

GAM7957 297 EHD1 Rotem- Yehudar, R.; Galperin, E.; Horowitz, M.: Association ofinsulin- like 3 C c
growth factor 1 receptor with EHD1 and SNAP29. J. Biol.Chem. 276: 33054-
33060, 2001.

GAM7957 297 EIF1A Dever, T. E.; Wei, C.- L.; Benkowski, L. A.; Browning, K.; Merrick,W. C.; 3 C b
Hershey, J. W. B.: Determination of the amino acid sequenceof rabbit, human,
and wheat germ protein synthesis factor eIF- 4C bycloning and chemical
sequencing. J. Biol. Chem. 269: 3212- 3218,1994.

GAM7957 297 EIF1A Lahn, B. T.; Page, D. C.: Functional coherence of the human Ychromosome. 3 C b
Science 278: 675- 680, 1997.

GAM7957 297 EIF3S2 Asano, K.; Kinzy, T. G.; Merrick, W. C.; Hershey, J. W. B.: Conservationand 3 C b
diversity of eukaryotic translation initiation factor eIF3. J.Biol. Chem.
1101- 1109, 1997.

GAM7957 297 EIF3S2 Chen, R.- H.; Miettinen, P. J.; Maruoka, E. M.; Choy, L.; Derynck,R.: A WD- 3 C b
domain protein that is associated with and phosphorylatedby the type II TGF-
beta receptor. Nature 377: 548- 552, 1995.

GAM7957 297 EIF3S2 Galli- Stauber, C.; Raho, G.; Rossi, D.; Corona, D. F. V.; Pirola,B.; 3 C b
Bonaglia, M. C.; Zuffardi, O.; Sorrentino, V.: Genomic structureand
chromosomal location of the human TGF- beta- receptor interactingprotein- 1
(TRIP- 1) gene to 1p34.1. FEBS Lett. 426: 279- 282, 1998.

GAM7957 297 ELAVL2 Fletcher, C. F.; Okano, H. J.; Gilbert, D. J.; Yang, Y.; Yang,C.; Copeland, 3 C c
N. G.; Jenkins, N. A.; Darnell, R. B.: Mouse chromosomallocations of nine
genes encoding homologs of human paraneoplasticneurologic disorder antigens.
Genomics 45: 313- 319, 1997.

GAM7957 297 ELAVL2 Han, J.; Knops, J. F.; Longshore, J. W.; King, P. H.: Localizationof human 3 C c
elav- like neuronal protein 1 (Hel- N1) on chromosome 9p21by chromosome
microdissection polymerase chain reaction and fluorescencein situ
hybridization. Genomics 36: 189- 191, 1996.

GAM7957 297 ELAVL2 King, P. H.: Hel- N2: a novel isoform of Hel- N1 which is conservedin rat 3 C c
neural tissue and produced in early embryogenesis. Gene 151:261- 265, 1994.

GAM7957 297 ELAVL2 King, P. H.; Levine, T. D.; Fremeau, R. T., Jr.; Keene, J. D.:Mammalian 3 C c
homologs of Drosophila ELAV localized to a neuronal subsetcan bind in vitro
to the 3' UTR of mRNA encoding the Id transcriptionalrepressor. J. Neurosci.
14: 1943- 52, 1994.

GAM7957 297 EP300 Arany, Z.; Newsome, D.; Oldread, E.; Livingston, D. M.; Eckner,R.: A family 3 C c
of transcriptional adaptor proteins targeted by theE1A oncoprotein. Nature
374: 81- 84, 1995.

GAM7957 297 EP300 Arany, Z.; Sellers, W. R.; Livingston, D. M.; Eckner, R.: E1A- 3 C c
associatedp300 and CREB- associated CBP belong to a conserved family of
coactivators.(Letter) Cell 77: 799- 800, 1994.

GAM7957 297 EP300 Eckner, R.; Ewen, M. E.; Newsome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence, 3 C c
J. B.; Livingston, D. M.: Molecular cloning and functionalanalysis of the
adenovirus E1A- associated 300- kD protein (p300) revealsa protein with
properties of a transcriptional adaptor. Genes Dev. 15:869- 884, 1994.

GAM7957 297 EP300 Gayther, S. A.; Batley, S. J.; Linger, L.; Bannister, A.; Thorpe,K.; Chin, 3 C c
S.- F.; Daigo, Y.; Russell, P.; Wilson, A.; Sowter, H. M.;Delhanty, J. D.
A.; Ponder, B. A. J.; Kouzarides, T.; Caldas, C.:Mutations truncating the
EP300 acetylase in human cancers. NatureGenet. 24: 300- 303, 2000.

GAM7957 297 EP300 Hasan, S.; Hassa, P. O.; Imhof, R.; Hottiger, M. O.: 3 C c
Transcriptioncoactivator p300 binds PCNA and may have a role in DNA repair
synthesis. Nature 410:387- 391, 2001.

GAM7957 297 EP300 Hasan, S.; Stucki, M.; Hassa, P. O.; Imhof, R.; Gehrig, P.; Hunziker,P.; 3 C c
Hubscher, U.; Hottiger, M. O.: Regulation of human flap endonuclease-
1activity by acetylation through the transcriptional coactivator p300.
Molec.Cell 7: 1221- 1231, 2001.

GAM7957 297 EP300 Ida, K.; Kitabayashi, I.; Taki, T.; Taniwaki, M.; Noro, K.; Yamamoto,M.; 3 C c
Ohki, M.; Hayashi, Y.: Adenoviral E1A- associated protein p300is involved in
acute myeloid leukemia with t(11;22)(q23;q13). Blood 90:4699- 4704, 1997.

GAM7957 297 EP300 Lin, C. H.; Hare, B. J.; Wagner, G.; Harrison, S. C.; Maniatis,T.; Fraenkel, 3 C c
E.: A small domain of CBP/p300 binds diverse proteins:solution structure and
functional studies. Molec. Cell 8: 581- 590,2001.

GAM7957 297 EP300 Muraoka, M.; Konishi, M.; Kikuchi- Yanoshita, R.; Tanaka, K.; Shitara,N.; 3 C c
Chong, J.- M.; Iwama, T.; Miyaki, M.: p300 gene alterations incolorectal and
gastric carcinomas. Oncogene 12: 1565- 1569, 1996.

GAM7957 297 EP300 Nakashima, K.; Yanagisawa, M.; Arakawa, H.; Kimura, N.; Hisatsune,T.; 3 C c
Kawabata, M.; Miyazono, K.; Taga, T.: Synergistic signaling infetal brain by
STAT3- Smad1 complex bridged by p300. Science 284:479- 482, 1999.

GAM7957 297 EP300 Tini, M.; Benecke, A.; Um, S.- J.; Torchia, J.; Evans, R. M.; Chambon,P.: 3 C c
Association of CBP/p300 acetylase and thymine DNA glycosylaselinks DNA
repair and transcription. Molec. Cell 9: 265- 277, 2002.

GAM7957 297 EP300 Weaver, B. K.; Kumar, K. P.; Reich, N. C.: Interferon regulatoryfactor 3 and 3 C c
CREB- binding protein/p300 are subunits of double- strandedRNA- activated
transcription factor DRAF1. Molec. Cell. Biol. 18:1359- 1368, 1998.

GAM7957 297 EP300 Yao, T. P.; Oh, S. P.; Fuchs, M.; Zhou, N.- D.; Ch'ng, L.- E.; Newsome,D.; 3 C c
Bronson, R. T.; Li, E.; Livingston, D. M.; Eckner, R.: Gene dosage-
dependentembryonic development and proliferation defects in mice lacking
thetranscriptional integrator p300. Cell 93: 361- 372, 1998.

GAM7957 297 EPHB1 Contractor, A.; Rogers, C.; Maron, C.; Henkemeyer, M.; Swanson,G. T.; 3 C c
Heinemann, S. F.: Trans- synaptic Eph receptor- ephrin signalingin
hippocampal mossy fiber LTP. Science 296: 1864- 1869, 2002.

GAM7957 297 EPHB1 Cowan, C. A.; Yokoyama, N.; Bianchi, L. M.; Henkemeyer, M.; Fritzsch,B.: 3 C c
EphB2 guides axons at the midline and is necessary for normalvestibular
function. Neuron 26: 417- 430, 2000.

GAM7957 297 EPHB1 Tang, X. X.; Biegel, J. A.; Nycum, L. M.; Yoshioka, A.; Brodeur,G. M.; 3 C c

Pleasure, D. E.; Ikegaki, N.: cDNA cloning, molecular characterization,and chromosomal localization of NET (EPHT2), a human EPH- related receptorprotein- tyrosine kinase gene preferentially expressed in brain. :Genomics 29:426- 437, 1995.

GAM7957 297 F2RL3 Kahn, M. L.; Zheng, Y.- W.; Huang, W.; Bigornia, V.; Zeng, D.; Moff,S.; Farese, R. V., Jr.; Tam, C.; Coughlin, S. R.: A dual thrombinreceptor system for platelet activation. Nature 394: 690- 694, 1998. 3 C b

GAM7957 297 F2RL3 Nakanishi- Matsui, M.; Zheng, Y.- W.; Sulciner, D. J.; Weiss, E.J.; Ludeman, M. J.; Coughlin, S. R.: PAR3 is a cofactor for PAR4activation by thrombin. Nature 404: 609- 613, 2000. 3 C b

GAM7957 297 F2RL3 Sambrano, G. R.; Weiss, E. J.; Zheng, Y.- W.; Huang, W.; Coughlin,S. R.: Role of thrombin signalling in platelets in haemostasis andthrombosis. Nature 413: 74- 78, 2001. 3 C b

GAM7957 297 F2RL3 Xu, W.- F.; Andersen, H.; Whitmore, T. E.; Presnell, S. R.; Yee,D. P.; Ching, A.; Gilbert, T.; Davie, E. W.; Foster, D. C.: Cloningand characterization of human protease- activated receptor 4. Proc.Nat. Acad. Sci. 95: 6642- 6646, 1998. 3 C b

GAM7957 297 FCAR de Wit, T. P. M.; Morton, H. C.; Capel, P. J. A.; van de Winkel,J. G. J.: Structure of the gene for the human myeloid IgA Fc receptor(CD89). J. Immun. 155: 1203- 1209, 1995. 3 C c

GAM7957 297 FCAR Kremer, E. J.; Kalatzis, V.; Baker, E.; Callen, D. F.; Sutherland,G. R.; Maliszewski, C. R.: The gene for the human IgA Fc receptormaps to 19q13.4. Hum. Genet. 89: 107- 108, 1992. 3 C c

GAM7957 297 FCAR Maliszewski, C. R.; March, C. J.; Schoenborn, M. A.; Gimpel, S.;Shen, L.: Expression cloning of a human Fc receptor for IgA. J.Exp. Med. 172: 1665- 1672, 1990. 3 C c

GAM7957 297 FCAR Monteiro, R. C.; Hostoffer, R. W.; Cooper, M. D.; Bonner, J. R.;Gartland, G. L.; Kubagawa, H.: Definition of immunoglobulin A receptorson eosinophils and their enhanced expression in allergic individuals. J.Clin. Invest. 92: 1681- 1685, 1993. 3 C c

GAM7957 297 FCAR Narita, I.; Goto, S.; Saito, N.; Sakatsume, M.; Jin, S.; Omori,K.; Gejyo, F.: Genetic polymorphisms in the promoter and 5- primeUTR region of the Fc alpha receptor (CD89) are not associated witha risk of IgA nephropathy. J. Hum. Genet. 46: 694- 698, 2001. 3 C c

GAM7957 297 FCAR Pleass, R. J.; Andrews, P. D.; Kerr, M. A.; Woof, J. M.: Alternativesplicing of the human IgA Fc receptor CD89 in neutrophils and eosinophils. Biochem.J. 318: 771- 777, 1996. 3 C c

GAM7957 297 FCAR Shimokawa, T.; Tsuge, T.; Okumura, K.; Ra, C.: Identificationand characterization of the promoter for the gene encoding the humanmyeloid IgA Fc receptor (Fc- alpha- R, CD89). Immunogenetics 51: 945- 954,2000. 3 C c

GAM7957 297 FCAR Tsuge, T.; Shimokawa, T.; Horikoshi, S.; Tomino, Y.; Ra, C.: Polymorphismin promoter region of Fc- alpha receptor gene in patients with IgAnephropathy. Hum. Genet. 108: 128- 133, 2001. 3 C c

GAM7957 297 FCN2 Endo, Y.; Sato, Y.; Matsushita, M.; Fujita, T.: Cloning and characterizationof the human lectin P35 gene and its related gene. Genomics 36:515- 521, 1996. 3 C c

GAM7957 297 FCN2 Matsushita, M.; Endo, Y.; Taira, S.; Sato, Y.; Fujita, T.; Ichikawa,N.; Nakata, M.; Misuochi, T.: A novel human lectin with collagen- and fibrinogen- like domains which functions as an opsonin. J. Biol.Chem. 271: 2448- 2454, 1996. 3 C c

GAM7957 297 FGF2 Abraham, J. A.; Mergia, A.; Whang, J. L.; Tumolo, A.; Friedman,J.; Hjerild, 3 C c
K. A.; Gospodarowicz, D.; Fiddes, J. C.: Nucleotidesequence of a bovine
clone encoding the angiogenic protein, basicfibroblast growth factor.
Science 233: 545- 548, 1986.

GAM7957 297 FGF2 Abraham, J. A.; Whang, J. L.; Tumolo, A.; Mergia, A.; Friedman,J.; 3 C c
Gospodarowicz, D.; Fiddes, J. C.: Human basic fibroblast growthfactor:
nucleotide sequence and genomic organization. EMBO J. 5:2523- 2528, 1986.

GAM7957 297 FGF2 Doniach, T.: Basic FGF as an inducer of anteroposterior neuralpattern. Cell 3 C c
83: 1067- 1070, 1995.

GAM7957 297 FGF2 Dono, R.; Texido, G.; Dussel, R.; Ehmke, H.; Zeller, R.: Impairedcerebral 3 C c
cortex development and blood pressure regulation in FGF2- deficientmice.
EMBO J. 17: 4213- 4225, 1998.

GAM7957 297 FGF2 Eckenstein, F. P.: Fibroblast growth factors in the nervous system. 3 C c
J.Neurobiol. 25: 1467- 1480, 1994.

GAM7957 297 FGF2 Fukushima, Y.; Byers, M. G.; Fiddes, J. C.; Shows, T. B.: Thehuman basic 3 C c
fibroblast growth factor gene (FGFB) is assigned to chromosome4q25.
Cytogenet. Cell Genet. 54: 159- 160, 1990.

GAM7957 297 FGF2 Gecz, J.; Baker, E.; Donnelly, A.; Ming, J. E.; McDonald- McGinn,D. M.; 3 C c
Spinner, N. B.; Zackai, E. H.; Sutherland, G. R.; Mulley, J.C.: Fibroblast
growth factor homologous factor 2 (FHF2): gene structure,expression and
mapping to the Borjeson- Forssman- Lehmann syndrome regionin Xq26 delineated
by a duplication breakpoint in a BFLS- like patient. Hum.Genet. 104: 56- 63,
1999.

GAM7957 297 FGF2 Gritti, A.; Parati, E. A.; Cova, L.; Frolichsthal, P.; Galli, R.;Wanke, E.; 3 C c
Faravelli, L.; Morassutti, D. J.; Roisen, F.; Nickel, D.D.; Vescovi, A. L.:
Multipotential stem cells from the adult mousebrain proliferate and self-
renew in response to basic fibroblast growthfactor. J. Neurosci. 16: 1091-
1100, 1996.

GAM7957 297 FGF2 Johnson, R. L.; Tabin, C. J.: Molecular models for vertebratelimb 3 C c
development. Cell 90: 979- 990, 1997.

GAM7957 297 FGF2 Jung, J.; Zheng, M.; Goldfarb, M.; Zaret, K. S.: Initiation ofmammalian 3 C c
liver development from endoderm by fibroblast growth factors. Science
284:1998- 2003, 1999.

GAM7957 297 FGF2 Kawaguchi, H.; Nakamura, K.; Tabata, Y.; Ikada, Y.; Aoyama, I.;Anzai, J.; 3 C c
Nakamura, T.; Hiyama, Y.; Tamura, M.: Acceleration offracture healing in
nonhuman primates by fibroblast growth factor- 2. J.Clin. Endocr. Metab. 86:
875- 880, 2001.

GAM7957 297 FGF2 Kurokawa, T.; Sasada, R.; Iwane, M.; Igarashi, K.: Cloning andexpression of 3 C c
cDNA encoding human basic fibroblast growth factor. FEBSLett. 213: 189- 194,
1987.

GAM7957 297 FGF2 Lafage- Pochitaloff, M.; Galland, F.; Simonetti, J.; Prats, H.;Mattei, M.- 3 C c
G.; Birnbaum, D.: The human basic fibroblast growth factorgene is located on
the long arm of chromosome 4 at bands q26- q27. OncogeneRes. 5: 241- 244,
1990.

GAM7957 297 FGF2 Lovec, H.; Hartung, H.; Verdier, A.- S.; Mattei, M.- G.; Birnbaum,D.; 3 C c
Goldfarb, M.; Coulier, F.: Assignment of FGF13 to human chromosomeband Xq21
by in situ hybridization. Cytogenet. Cell Genet. 76: 183- 184,1997.

GAM7957 297 FGF2 Mattei, M.- G.; Pebusque, M.- J.; Birnbaum, D.: Chromosomal localizationsof 3 C c
mouse Fgf2 and Fgf5 genes. Mammalian Genome 2: 135- 137, 1992.

GAM7957 297 FGF2 Mergia, A.; Eddy, R.; Abraham, J. A.; Fiddes, J. C.; Shows, T.B.: The genes 3 C c

for basic and acidic fibroblast growth factors areon different human chromosomes. Biochem. Biophys. Res. Commun. 138:644- 651, 1986.

GAM7957 297 FGF2 Montero, A.; Okada, Y.; Tomita, M.; Ito, M.; Tsurukami, H.; Nakamura,T.; Doetschman, T.; Coffin, J. D.; Hurley, M. M.: Disruption of thefibroblast growth factor- 2 gene results in decreased bone mass andbone formation. J. Clin. Invest. 105: 1085- 1093, 2000. 3 C c

GAM7957 297 FGF2 Ortega, S.; Ittmann, M.; Tsang, S. H.; Ehrlich, M.; Basilico,C.: Neuronal defects and delayed wound healing in mice lacking fibroblastgrowth factor 2. Proc. Nat. Acad. Sci. 95: 5672- 5677, 1998. 3 C c

GAM7957 297 FGF2 Plotnikov, A. N.; Hubbard, S. R.; Schlessinger, J.; Mohammadi,M.: Crystal structures of two FGF- FGFR complexes reveal the determinantsof ligand-receptor specificity. Cell 101: 413- 424, 2000. 3 C c

GAM7957 297 FGF2 Plotnikov, A. N.; Schlessinger, J.; Hubbard, S. R.; Mohammadi,M.: Structural basis for FGF receptor dimerization and activation. Cell 98:641- 650, 1999. 3 C c

GAM7957 297 FGF2 Smallwood, P. M.; Munoz- Sanjuan, I.; Tong, P.; Macke, J. P.; Hendry,S. H. C.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans,J.: Fibroblast growth factor (FGF) homologous factors: new membersof the FGF family implicated in nervous system development. Proc.Nat. Acad. Sci. 93: 9850-9857, 1996. 3 C c

GAM7957 297 FUT6 Brinkman- Van der Linden, E. C. M.; Mollicone, R.; Oriol, R.; Larson,G.; Van den Eijnden, D. H.; Van Dijk, W.: A missense mutation inthe FUT6 gene results in total absence of alpha- 3- fucosylation ofhuman alpha- 1- acid glycoprotein. J. Biol. Chem. 271: 14492- 14495,1996. 3 C c

GAM7957 297 FUT6 Cameron, H. S.; Szczepaniak, D.; Weston, B. W.: Expression ofhuman chromosome 19p alpha- (1,3)- fucosyltransferase genes in normaltissues: alternative splicing, polyadenylation, and isoforms. J.Biol. Chem. 270: 20112- 20122, 1995. 3 C c

GAM7957 297 FUT6 Koszdin, K. L.; Bowen, B. R.: The cloning and expression of ahuman alpha-1,3 fucosyltransferase capable of forming the E- selectinligand. Biochem. Biophys. Res. Commun. 187: 152- 157, 1992. 3 C c

GAM7957 297 FUT6 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3 and 11q21. Genomics 26: 142- 146, 1995. 3 C c

GAM7957 297 FUT6 Mollicone, R.; Reguigne, I.; Fletcher, A.; Aziz, A.; Rustam, M.;Weston, B. W.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Molecular basisfor plasma alpha(1,3)- fucosyltransferase gene deficiency (FUT6). J.Biol. Chem. 269: 12662- 12671, 1994. 3 C c

GAM7957 297 FUT6 Pang, H.; Koda, Y.; Soejima, M.; Schlaphoff, T.; Du Toit, E. D.;Kimura, H.: Allelic diversity of the human plasma alpha(1,3)fucosyltransferasegene (FUT6). Ann. Hum. Genet. 63: 277- 284, 1999. 3 C c

GAM7957 297 FUT6 Schnyder- Candrian, S.; Borsig, L.; Moser, R.; Berger, E. G.: Localizationof alpha- 1,3- fucosyltransferase VI in Weibel- Palade bodies of humanendothelial cells. Proc. Nat. Acad. Sci. 97: 8369- 8374, 2000. 3 C c

GAM7957 297 FUT6 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple homologous sequences that determine expressionof the Lewis x, sialyl Lewis x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584, 1992. 3 C c

GAM7957 297 FZD2 Wang, Y.; Macke, J. P.; Abella, B. S.; Andreasson, K.; Worley,P.; Gilbert, 3 C c

D. J.; Copeland, N. G.; Jenkins, N. A.; Nathans, J.:A large family of putative transmembrane receptors homologous to theproduct of the Drosophila tissue polarity gene frizzled. J. Biol.Chem. 271: 4468- 4476, 1996.

GAM7957 297 FZD2 Zhao, Z. Y.; Lee, C. C.; Baldini, A.; Caskey, C. T.: A human homologueof the 3 C c Drosophila polarity gene frizzled has been identified and mappedto 17q21.1. Genomics 27: 370- 373, 1995.

GAM7957 297 GAS7 Ju, Y.- T.; Chang, A. C. Y.; She, B.- R.; Tsaur, M.- L.; Hwang, H.- M.;Chao, 3 C b C. C.- K.; Cohen, S. N.; Lin- Chao, S.: Gas7: a gene expressedpreferentially in growth- arrested fibroblasts and terminally differentiatedPurkinje neurons affects neurite formation. Proc. Nat. Acad. Sci. 95:11423- 11428, 1998.

GAM7957 297 GAS7 Kurtz, A.; Zimmer, A.: Interspecies fluorescence in situ 3 C b hybridizationfurther defines synteny homology between mouse chromosome 11 and humanchromosome 17. Mammalian Genome 6: 379- 380, 1995.

GAM7957 297 GAS7 Megonigal, M. D.; Cheung, N.- K. V.; Rappaport, E. F.; Nowell, P.C.; Wilson, 3 C b R. B.; Jones, D. H.; Addya, K.; Leonard, D. G. B.; Kushner,B. H.; Williams, T. M.; Lange, B. J.; Felix, C. A.: Detection ofleukemia- associated MLL-GAS7 translocation early during chemotherapywith DNA topoisomerase II inhibitors. Proc. Nat. Acad. Sci. 97:2814- 2819, 2000.

GAM7957 297 GCNT2 Bierhuizen, M. F. A.; Mattei, M.- G.; Fukuda, M.: Expression ofthe 3 C c developmental I antigen by a cloned human cDNA encoding a memberof a beta-1,6- N- acetylglucosaminyltransferase gene family. GenesDev. 7: 468- 478, 1993.

GAM7957 297 GCNT2 Lin- Chu, M.; Broadberry, R. E.; Okubo, Y.; Tanaka, M.: The i phenotypeand 3 C c congenital cataracts among Chinese in Taiwan (Letter) Transfusion 31:676-677, 1991.

GAM7957 297 GCNT2 Ogata, H.; Okubo, Y.; Akabane, T.: Phenotype i associated withcongenital 3 C c cataract in Japanese. Transfusion 19: 166- 168, 1979.

GAM7957 297 GCNT2 Olavesen, M. G.; Bentley, E.; Mason, R. V. F.; Stephens, R. J.;Ragoussis, 3 C c J.: Fine mapping of 39 ESTs on human chromosome 6p23- p25. Genomics 46:303-306, 1997.

GAM7957 297 GCNT2 Schwientek, T.; Nomoto, M.; Levery, S. B.; et al: Control of O- glycanbranch 3 C c formation. J. Biol. Chem. 274: 4504- 4512, 1999.

GAM7957 297 GCNT2 Yeh, J.- C.; Ong, E.; Fukuda, M.: Molecular cloning and expressionof a novel 3 C c beta- 1,6- N- acetylglucosaminyltransferase that forms core2, core 4, and I branches. J. Biol. Chem. 274: 3215- 3221, 1999.

GAM7957 297 GCNT2 Yu, L.- C.; Twu, Y.- C.; Chang, C.- Y.; Lin, M.: Molecular basisof the adult 3 C c i phenotype and the gene responsible for the expressionof the human blood group I antigen. Blood 98: 3840- 3845, 2001.

GAM7957 297 GNE Eisenberg, I.; Avidan, N.; Potikha, T.; Hochner, H.; Chen, M.;Olender, T.; 3 C c Barash, M.; Shemesh, M.; Sadeh, M.; Grabov- Nardini, G.;Shmilevich, I.; Friedmann, A.; Karpati, G.; Bradley, W. G.; Baumbach,L.; Lancet, D.; Ben Asher, E.; Beckmann, J. S.; Argov, Z.; Mitrani- Rosenbaum,S.: The UDP- N-acetylglucosamine 2- epimerase/N- acetylmannosamine kinasegene is mutated in recessive hereditary inclusion body myopathy. NatureGenet. 29: 83- 87, 2001.

GAM7957 297 GNE Hinderlich, S.; Stasche, R.; Zeitler, R.; Reutter, W.: A bifunctionalenzyme 3 C c catalyzes the first two steps in N- acetylneuraminic acid biosynthesisof rat liver: purification and characterization of UDP- N- acetylglucosamine2-epimerase/N- acetylmannosamine kinase. J. Biol. Chem. 272: 24313-24318,1997.

GAM7957 297 GNE Huizing, M.; Anikster, Y.: Personal Communication. Bethesda,Md. 1/10/2000. 3 C c

GAM7957 297 GNE Ikeuchi, T.; Asaka, T.; Saito, M.; Tanaka, H.; Higuchi, S.; Tanaka,K.; Saida, K.; Uyama, E.; Mizusawa, H.; Fukuhara, N.; Nonaka, I.;Takamori, M.; Tsuji, S.: Gene locus for autosomal recessive distalmyopathy with rimmed vacuoles maps to chromosome 9. Ann. Neurol. 41:432- 437, 1997. 3 C c

GAM7957 297 GNE Kayashima, T.; Matsuo, H.; Satoh, A.; Ohta, T.; Yoshiura, K.; Matsumoto,N.; Nakane, Y.; Niikawa, N.; Kishino, T.: Nonaka myopathy is causedby mutations in the UDP- N- acetylglucosamine- 2- epimerase/N- acetylmannosaminekinase gene (GNE). J. Hum. Genet. 47: 77- 79, 2002. 3 C c

GAM7957 297 GNE Keppler, O. T.; Hinderlich, S.; Langner, J.; Schwartz- Albiez, R.;Reutter, W.; Pawlita, M.: UDP- GlcNAc 2- epimerase: a regulator ofcell surface sialylation. Science 284: 1372- 1376, 1999. 3 C c

GAM7957 297 GNE Krasnewich, D. M.; Tietze, F.; Krause, W.; Pretzlaff, R.; Wenger,D. A.; Diwadkar, V.; Gahl, W. A.: Clinical and biochemical studiesin an American child with sialuria. Biochem. Med. Metab. Biol. 49:90- 96, 1993. 3 C c

GAM7957 297 GNE Leroy, J. G.; Seppala, R.; Huizing, M.; Dacremont, G.; De Simpel,H.; Van Coster, R. N.; Orvisky, E.; Krasnewich, D. M.; Gahl, W. A.: Dominant inheritance of sialuria, an inborn error of feedback inhibition. Am.J. Hum. Genet. 68: 1419- 1427, 2001. 3 C c

GAM7957 297 GNE Nonaka, I.; Sunohara, N.; Ishiura, S.; Satoyoshi, E.: Familialdistal myopathy with rimmed vacuole and lamellar (myeloid) body formation. J.Neurol. Sci. 51: 141- 155, 1981. 3 C c

GAM7957 297 GNE Schwarzkopf, M.; Knobeloch, K.- P.; Rohde, E.; Hinderlich, S.;Wiechens, N.; Lucka, L.; Horak, I.; Reutter, W.; Horstkorte, R.:Sialylation is essential for early development in mice. Proc. Nat.Acad. Sci. 99: 5267- 5270, 2002. 3 C c

GAM7957 297 GNE Seppala, R.; Lehto, V.- P.; Gahl, W. A.: Mutations in the humanUDP- N- acetylglucosamine 2- epimerase gene define the disease sialuriaand the allosteric site of the enzyme. Am. J. Hum. Genet. 64: 1563- 1569,1999. 3 C c

GAM7957 297 GNE Stasche, R.; Hinderlich, S.; Weise, C.; Effertz, K.; Lucka, L.;Moormann, P.; Reutter, W.: A bifunctional enzyme catalyzes the firsttwo steps in N- acetylneuraminic acid biosynthesis of rat liver: molecularcloning and functional expression of UDP- N- acetyl- glucosamine 2- epimerase/N- acetylmannosaminekinase. J. Biol. Chem. 272: 24319- 24324, 1997. 3 C c

GAM7957 297 GNE Weiss, P.; Tietze, F.; Gahl, W. A.; Seppala, R.; Ashwell, G.:Identification of the metabolic defect in sialuria. J. Biol. Chem. 264:17635- 17636, 1989. 3 C c

GAM7957 297 GNE Wilcken, B.; Don, N.; Greenaway, R.; Hammond, J.; Sosula, L.:Sialuria: a second case. J. Inherit. Metab. Dis. 10: 97- 102, 1987. 3 C c

GAM7957 297 GP2 Fukuoka, S.- I.; Freedman, S. D.; Scheele, G. A.: A single geneencodes membrane- bound and free forms of GP- 2, the major glycoproteinin pancreatic secretory (zymogen) granule membranes. Proc. Nat. Acad.Sci. 88: 2898- 2902, 1991. 3 C c

GAM7957 297 GP2 Fukuoka, S.- I.; Freedman, S. D.; Yu, H.; Sukhatme, V. P.; Scheele,G. A.: GP- 2/THP gene family encodes self- binding glycosylphosphatidylinositol-anchoredproteins in apical secretory compartments of pancreas and kidney. Proc.Nat. Acad. Sci. 89: 1189- 1193, 1992. 3 C c

GAM7957 297 GP2 Fukuoka, S.- I.; Suzuki, M.; Okabayashi, K.; Takahashi, E.: Assignmentof pancreatic zymogen granule membrane protein GP2 (GP2) to humanchromosome band 9q21.11 to q21.2 by in situ hybridization. Cytogenet.Cell Genet. 79: 231- 232, 1997. 3 C c

GAM7957 297 GP2 Wong, S. M. E.; Lowe, A. W.: Sequence of the cDNA encoding humanGP- 2, the 3 C c

major membrane protein in the secretory granule of the exocrinepancreas. Gene 171: 311- 312, 1996.

GAM7957 297 GPR1 Marchese, A.; Docherty, J. M.; Nguyen, T.; Heiber, M.; Cheng, R.;Heng, H. H. Q.; Tsui, L.- C.; Shi, X.; George, S. R.; O'Dowd, B. F.: Cloning of human genes encoding novel G protein- coupled receptors. Genomics 23:609- 618, 1994. 3 C b

GAM7957 297 GPR1 Poyner, D. R.; Hanley, M. R.: Molecular biology of peptide andglycoprotein hormone receptors.In: Brann, M. R.: Molecular Biologyof G- Protein- Coupled Receptors. Boston: Birkhaeuser (pub.) 1992.Pp. 198- 232. 3 C b

GAM7957 297 GPR1 Spiegel, A. M.: Genetic basis of endocrine disease: mutationsin G proteins and G protein- coupled receptors in endocrine disease. J.Clin. Endocr. Metab. 81: 2434- 2442, 1996. 3 C b

GAM7957 297 GRAF Borkhardt, A.; Bojesen, S.; Haas, O. A.; Fuchs, U.; Bartelheimer,D.; Loncarevic, I. F.; Bohle, R. M.; Harbott, J.; Repp, R.; Jaeger,U.; Viehmann, S.; Henn, T.; Korth, P.; Scharr, D.; Lampert, F.: Thehuman GRAF gene is fused to MLL in a unique t(5;11)(q31;q23) and bothalleles are disrupted in three cases of myelodysplastic syndrome/acutemyeloid leukemia with a deletion 5q. Proc. Nat. Acad. Sci. 97: 9168- 9173,2000. 3 C b

GAM7957 297 GRAF Hildebrand, J. D.; Taylor, J. M.; Parsons, T. J.: An SH3 domain- containingGTPase- activating protein for Rho and Cdc42 associates with focaladhesion kinase. Molec. Cell. Biol. 16: 3169- 3178, 1996. 3 C b

GAM7957 297 GRAF Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 C b

GAM7957 297 GTF2F1 Aso, T.; Tsai, P.; Kawaguchi, T.; Menninger, J. C.; Kitajima, S.;Yasukochi, Y.; Ward, D. C.; Weissman, S. M.: Assignment of the humanGTF2F1 gene to chromosome 19p13.3. Genomics 16: 252- 253, 1993. 3 C c

GAM7957 297 GTF2F1 Aso, T.; Vasavada, H. A.; Kawaguchi, T.; Germino, F. J.; Ganguly,S.; Kitajima, S.; Weissman, S. M.; Yasukochi, Y.: Characterizationof cDNA for the large subunit of the transcription initiation factorTFIIF. Nature 355: 461- 464, 1992. 3 C c

GAM7957 297 GTF2F1 Finkelstein, A.; Kostrub, C. F.; Li, J.; Chavez, D. P.; Wang, B.Q.; Fang, S. M.; Greenblatt, J.; Burton, Z. F.: A cDNA encoding RAP74,a general initiation factor for transcription by RNA polymerase II. Nature 355:464- 467, 1992. 3 C c

GAM7957 297 GTF2F1 Joliot, V.; Demma, M.; Prywes, R.: Interaction with RAP74 subunitof TFIIF is required for transcriptional activation by serum responsefactor. Nature 373: 632- 635, 1995. 3 C c

GAM7957 297 GTF2F1 Sopta, M.; Burton, Z. F.; Greenblatt, J.: Structure and associatedDNA- helicase activity of a general transcription initiation factorthat binds to RNA polymerase II. Nature 341: 410- 414, 1989. 3 C c

GAM7957 297 HIP1 Chopra, V. S.; Metzler, M.; Rasper, D. M.; Engqvist- Goldstein,A. E. Y.; Singaraja, R.; Gan, L.; Fichter, K. M.; McCutcheon, K.;Drubin, D.; Nicholson, D. W.; Hayden, M. R.: HIP12 is a non- proapoptoticmember of a gene family including HIP1, an interacting protein withhuntingtin. Mammalian Genome 11: 1006- 1015, 2000. 3 C b

GAM7957 297 HIP1 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager, V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and 3 C b

activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM7957 297 HIP1 Hackam, A. S.; Yassa, A. S.; Singaraja, R.; Metzler, M.; Gutekunst,C.- A.; 3 C b
Gan, L.; Warby, S.; Wellington, C. L.; Vaillancourt, J.; Chen,N.; Gervais, F. G.; Raymond, L.; Nicholson, D. W.; Hayden, M. R.:Huntingtin interacting protein 1 induces apoptosis via a novel caspase- dependentdeath effector domain. J. Biol. Chem. 275: 41299- 41308, 2000.

GAM7957 297 HIP1 Himmelbauer, H.; Wedemeyer, N.; Haaf, T.; Wanker, E. E.; Schalkwyk,L. C.; 3 C b
Lehrach, H.: IRS- PCR- based genetic mapping of the huntingtininteracting protein gene (HIP1) on mouse chromosome 5. MammalianGenome 9: 26- 31, 1998.

GAM7957 297 HIP1 Kalchman, M. A.; Koide, H. B.; McCutcheon, K.; Graham, R. K.; Nichol,K.; 3 C b
Nishiyama, K.; Kazemi- Esfarjani, P.; Lynn, F. C.; Wellington,C.; Metzler, M.; Goldberg, Y. P.; Kanazawa, I.; Gietz, R. D.; Hayden,M. R.: HIP1, a human homologue of S. cerevisiae Slap2, interactswith membrane- associated huntingtin in the brain. Nature Genet. 16:44- 53, 1997.

GAM7957 297 HIP1 Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof 3 C b
Huntingtin interacting protein 1 to platelet- derived growth factor- betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998.

GAM7957 297 HIP1 Waelter, S.; Scherzinger, E.; Hasenbank, R.; Nordhoff, E.; Lurz,R.; Goehler, 3 C b
H.; Gauss, C.; Sathasivam, K.; Bates, G. P.; Lehrach,H.; Wanker, E. E.: The huntingtin interacting protein HIP1 is a clathrinand alpha- adaptin- binding protein involved in receptor- mediated endocytosis. Hum.Molec. Genet. 10: 1807- 1817, 2001.

GAM7957 297 HIP1 Wanker, E. E.; Rovira, C.; Scherzinger, E.; Hasenbank, R.; Walter,S.; Tait, 3 C b
D.; Colicelli, J.; Lehrach, H.: HIP- I: a huntingtin interactingprotein isolated by the yeast two- hybrid system. Hum. Molec. Genet. 6:487- 495, 1997.

GAM7957 297 HIP1 Wedemeyer, N.; Peoples, R.; Himmelbauer, H.; Lehrach, H.; Francke,U.; 3 C b
Wanker, E. E.: Localization of the human HIP1 gene close to theelastin (ELN) locus on 7q11.23. Genomics 46: 313- 315, 1997.

GAM7957 297 HMGA2 Anand, A.; Chada, K.: In vivo modulation of Hmgic reduces obesity. 3 C c
NatureGenet. 24: 377- 380, 2000.

GAM7957 297 HMGA2 Arlotta, P.; Tai, A. K.- F.; Manfioletti, G.; Clifford, C.; Jay,G.; Ono, S. 3 C c
J.: Transgenic mice expressing a truncated form of thehigh mobility group I- C protein develop adiposity and an abnormallyhigh prevalence of lipomas. J. Biol. Chem. 275: 14394- 14400, 2000.

GAM7957 297 HMGA2 Ashar, H. R.; Cherath, L.; Przybysz, K. M.; Chada, K.: 3 C c
Genomiccharacterization of human HMGIC, a member of the accessory transcriptionfactor family found at translocation breakpoints in lipomas. Genomics 31:207- 214, 1996.

GAM7957 297 HMGA2 Ashar, H. R.; Schoenberg Fejzo, M.; Tkachenko, A.; Zhou, X.; Fletcher,J. A.; 3 C c
Weremowicz, S.; Morton, C. C.; Chada, K.: Disruption of thearchitectural factor HMGI- C: DNA- binding AT hook motifs fused in lipomasto distinct transcriptional regulatory domains. Cell 82: 57- 65,1995.

GAM7957 297 HMGA2 Chau, K.- Y.; Patel, U. A.; Lee, K.- L. D.; Lam, H.- Y. P.; Crane- 3 C c
Robinson,C.: The gene for the human architectural transcription factor HMGI- Cconsists of five exons each coding for a distinct functional element. NucleicAcids Res. 23: 4262- 4266, 1995.

GAM7957 297 HMGA2 Danforth, E., Jr.: Failure of adipocyte differentiation causestype II 3 C c

diabetes mellitus. Nature Genet. 26: 13 only, 2000.

GAM7957 297 HMGA2 Friedmann, M.; Holth, L. T.; Zoghbi, H. Y.; Reeves, R.: 3 C c
Organization,inducible- expression and chromosome localization of the human
HMG- I(Y)nonhistone protein gene. Nucleic Acids Res. 21: 4259- 4267, 1993.

GAM7957 297 HMGA2 Ishwad, C. S.; Shriver, M. D.; Lassige, D. M.; Ferrell, R. E.:The high 3 C c
mobility group I- C gene (HMGI- C): polymorphism and geneticlocalization.
Hum. Genet. 99: 103- 105, 1997.

GAM7957 297 HMGA2 Kazmierczak, B.; Dal Cin, P.; Wanschura, S.; Bartnitzke, S.; Vanden Berghe, 3 C c
H.; Bullerdiek, J.: Cloning and molecular characterizationof part of a new
gene fused to HMGIC in mesenchymal tumors. Am. J.Path. 152: 431- 435, 1998.

GAM7957 297 HMGA2 Kazmierczak, B.; Pohnke, Y.; Bullerdiek, J.: Fusion transcriptsbetween the 3 C c
HMGIC gene and RTVL- H- related sequences in mesenchymaltumors without
cytogenetic aberrations. Genomics 38: 223- 226, 1996.

GAM7957 297 HMGA2 Manfioletti, G.; Rustighi, A.; Mantovani, F.; Goodwin, G. H.;Giancotti, V.: 3 C c
Isolation and characterization of the gene codingfor murine high- mobility-
group protein HMGI- C. Gene 167: 249- 253,1995.

GAM7957 297 HMGA2 Mine, N.; Kurose, K.; Nagai, H.; Doi, D.; Ota, Y.; Yoneyama, K.;Konishi, H.; 3 C c
Araki, T.; Emi, M.: Gene fusion involving HMGIC is afrequent aberration in
uterine leiomyomas. J. Hum. Genet. 46: 408- 412,2001.

GAM7957 297 HMGA2 Nucci, M. R.; Weremowicz, S.; Neskey, D. M.; Sornberger, K.; Tallini,G.; 3 C c
Morton, C. C.; Quade, B. J.: Chromosomal translocation t(8;12)induces
aberrant HMGIC expression in aggressive angiomyxoma of thevulva. Genes
Chromosomes Cancer 32: 172- 176, 2001.

GAM7957 297 HMGA2 Petit, M. M. R.; Schoenmakers, E. F. P. M.; Huysmans, C.; Geurts,J. M. W.; 3 C c
Mandahl, N.; Van de Ven, W. J. M.: LHFP, a novel translocationpartner gene
of HMGIC in a lipoma, is a member of a new family ofLHFP- like genes.
Genomics 57: 438- 441, 1999.

GAM7957 297 HMGA2 Rohen, C.; Caselitz, J.; Stern, C.; Wanschura, S.; Schoenmakers,E. F.; Van 3 C c
de Ven, W. J.; Barnitzke, S.; Bullerdiek, J.: A hamartomaof the breast with
an aberration of 12q mapped to the MAR region byfluorescence in situ
hybridization. Genes Chromosomes Cancer 84:82- 84, 1995.

GAM7957 297 HMGA2 Schoenmakers, E. F. P. M.; Huysmans, C.; Van de Ven, W. J. M.: Allelic 3 C c
knockout of novel splice variants of human recombinationrepair gene RAD51B
in t(12;14) uterine leiomyomas. Cancer Res. 59:19- 23, 1999.

GAM7957 297 HMGA2 Schoenmakers, E. P. P. M.; Wanschura, S.; Mols, R.; Bullerdiek,J.; Van den 3 C c
Berghe, H.; Van de Ven, W. J. M.: Recurrent rearrangementsin the high
mobility group protein gene, HMGI- C, in benign mesenchymaltumours. Nature
Genet. 10: 436- 444, 1995.

GAM7957 297 HMGA2 Xiang, X.; Benson, K. F.; Chada, K.: Mini- mouse: disruption ofthe pygmy 3 C c
locus in a transgenic insertional mutant. Science 247:967- 969, 1990.

GAM7957 297 HMGA2 Zhou, X.; Benson, K. F.; Ashar, H. R.; Chada, K.: Mutation responsiblefor 3 C c
the mouse pygmy phenotype in the developmentally regulated factorHMGI- C.
Nature 377: 771- 774, 1995.

GAM7957 297 HRH1 Inoue, I.; Taniuchi, I.; Kitamura, D.; Jenkins, N. A.; Gilbert,D. J.; 3 C c
Copeland, N. G.; Watanabe, T.: Characteristics of the mousegenomic histamine
H1 receptor gene. Genomics 36: 178- 181, 1996.

GAM7957 297 HRH1 Jutel, M.; Watanabe, T.; Klunker, S.; Akdis, M.; Thomet, O. A.R.; 3 C c
Malolepszy, J.; Zak- Nejmark, T.; Koga, R.; Kobayashi, T.; Blaser,K.; Akdis,
C. A.: Histamine regulates T- cell and antibody responsesby differential
expression of H1 and H2 receptors. Nature 413: 420- 425,2001.

GAM7957 297 HRH1 Le Coniat, M.; Traiffort, E.; Ruat, M.; Arrang, J.- M.; Berger,R.: 3 C c
Chromosomal localization of the human histamine H1- receptor gene.
Hum.Genet. 94: 186- 188, 1994.

GAM7957 297 HRH1 Ma, R. Z.; Gao, J.; Meeker, N. D.; Fillmore, P. D.; Tung, K. S.K.; Watanabe, 3 C c
T.; Zachary, J. F.; Offner, H.; Blankenhorn, E. P.;Teuscher, C.:
Identification of Bphs, an autoimmune disease locus,as histamine receptor H-
1. Science 297: 620- 623, 2002.

GAM7957 297 HRH1 Yamashita, M.; Fukui, H.; Sugama, K.; Horio, Y.; Ito, S.; Mizuguchi,H.; 3 C c
Wada, H.: Expression cloning of a cDNA encoding the bovine histamineH1
receptor. Proc. Nat. Acad. Sci. 88: 11515- 11519, 1991.

GAM7957 297 HSPA5 Hendershot, L. M.; Valentine, V. A.; Lee, A. S.; Morris, S. W.;Shapiro, D. 3 C b
N.: Localization of the gene encoding human BiP/GRP78,the endoplasmic
reticulum cognate of the HSP70 family, to chromosome9q34. Genomics 20: 281-
284, 1994.

GAM7957 297 HSPA5 Law, M. L.; Seeliger, M. B.; Lee, A. S.; Kao, F. T.: Genetic mappingof the 3 C b
structural gene coding for a glucose- regulated protein (GRP78)of 78k-
dalton to the long arm of human chromosome 9. (Abstract) Cytogenet.Cell
Genet. 37: 518- 519, 1984.

GAM7957 297 HSPA5 Lee, A. S.; Delegeane, A. M.; Baker, V.; Chow, P. C.: 3 C b
Transcriptionalregulation of two genes specifically induced by glucose
starvationin hamster mutant fibroblast cell line. J. Biol. Chem. 258: 597-
603,1983.

GAM7957 297 HSPA5 Lee, A. S.; Delegeane, A.; Scharff, D.: Highly conserved glucose- 3 C b
regulatedprotein in hamster and chicken cells: preliminary
characterizationof its cDNA clone. Proc. Nat. Acad. Sci. 78: 4922- 4925,
1981.

GAM7957 297 HSPA5 Muresan, Z.; Arvan, P.: Enhanced binding to the molecular chaperoneBiP slows 3 C b
thyroglobulin export from the endoplasmic reticulum. Molec.Endocr. 12: 458-
467, 1998.

GAM7957 297 HSPA5 Womack, J. E.: Personal Communication. College Station, Texas 2/26/1990. 3 C b

GAM7957 297 IAPP Christmanson, L.; Rorsman, F.; Stenman, G.; Westermark, P.; Betsholtz,C.: 3 C b
The human islet amyloid polypeptide (IAPP) gene: organization,chromosomal
localization and functional identification of a promoterregion. FEBS Lett.
267: 160- 166, 1990.

GAM7957 297 IAPP Cockburn, D. C.; Holt, S. M.; Roberts, A. N.; Cooper, G. J. S.;Reid, K. B. 3 C b
M.; Boyd, Y.: Localization of the amylin locus to chromosome12. (Abstract)
Cytogenet. Cell Genet. 51: 977, 1989.

GAM7957 297 IAPP Cooper, G. J. S.; Leighton, B.; Dimitriadis, G. D.; Parry- Billings,M.; 3 C b
Kowalchuk, J. M.; Howland, K.; Rothbard, J. B.; Willis, A. C.;Reid, K. B.
M.: Amylin found in amyloid deposits in human type 2diabetes mellitus may be
a hormone that regulates glycogen metabolismin skeletal muscle. Proc. Nat.
Acad. Sci. 85: 7763- 7766, 1988.

GAM7957 297 IAPP Cooper, G. J.; Willis, A. C.; Clark, A.; Turner, R. C.; Sim, R.B.; Reid, K. 3 C b
B.: Purification and characterization of a peptide fromamyloid- rich
pancreases of type 2 diabetic patients. Proc. Nat. Acad.Sci. 84: 8628- 8632,
1987.

GAM7957 297 IAPP Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Sanke, 3 C b
T.; Steiner, D. F.; Shows, T. B.; Bell, G. I.: Localizationof the human
islet amyloid polypeptide gene (IAP) to chromosome 12p12.3.(Abstract)
Cytogenet. Cell Genet. 51: 997, 1989.

GAM7957 297 IAPP Harvey, A. M.: Medical students on the march: Brown, MacCallumand Opie. 3 C b
Johns Hopkins Med. J. 134: 330- 345, 1974.

GAM7957 297 IAPP Hoovers, J. M. N.; Redeker, E.; Speleman, F.; Hoppener, J. W. M.;Bhola, S.; 3 C b
Bliek, J.; van Roy, N.; Leschot, N. J.; Westerveld, A.;Mannens, M.: High-
resolution chromosomal localization of the humancalcitonin/CGRP/IAPP gene
family members. Genomics 15: 525- 529,1993.

GAM7957 297 IAPP Hoppener, J. W. M.; Oosterwijk, C.; van Hulst, K. L.; Verbeek,J. S.; Capel, 3 C b
P. J. A.; de Koning, E. J. P.; Clark, A.; Jansz, H.S.; Lips, C. J. M.:
Molecular physiology of the islet amyloid polypeptide(IAPP)/amylin gene in
man, rat, and transgenic mice. J. Cell. Biochem. 55S:39- 53, 1994.

GAM7957 297 IAPP Jaikaran, E. T. A. S.; Clark, A.: Islet amyloid and type 2 diabetes:from 3 C b
molecular misfolding to islet pathophysiology. Biochim. Biophys.Acta 1537:
179- 203, 2001.

GAM7957 297 IAPP Janson, J.; Soeller, W. C.; Roche, P. C.; Nelson, R. T.; Torchia,A. J.; 3 C b
Kreutter, D. K.; Butler, P. C.: Spontaneous diabetes mellitusin transgenic
mice expressing human islet amyloid polypeptide. Proc.Nat. Acad. Sci. 93:
7283- 7288, 1996.

GAM7957 297 IAPP Johnson, K. H.; O'Brien, T. D.; Betsholtz, C.; Westermark, P.: Islet 3 C b
amyloid, islet- amyloid polypeptide, and diabetes mellitus. NewEng. J. Med.
321: 513- 518, 1989.

GAM7957 297 IAPP Lorenzo, A.; Razzaboni, B.; Weir, G. C.; Yankner, B. A.: Pancreaticislet 3 C b
cell toxicity of amylin associated with type- 2 diabetes mellitus. Nature
368:756- 760, 1994.

GAM7957 297 IAPP Mosselman, S.; Hoppener, J. W. M.; Lips, C. J. M.; Jansz, H. S.: The 3 C b
complete islet amyloid polypeptide precursor is encoded by twoexons. FEBS
Lett. 247: 154- 158, 1989.

GAM7957 297 IAPP Mosselman, S.; Hoppener, J. W. M.; Zandberg, J.; van Mansfeld,A. D. M.; 3 C b
Geurts van Kessel, A. H. M.; Lips, C. J. M.; Jansz, H. S.: Islet amyloid
polypeptide: identification and chromosomal localizationof the human gene.
FEBS Lett. 239: 227- 232, 1988.

GAM7957 297 IAPP Nishi, M.; Sanke, T.; Seino, S.; Eddy, R. L.; Fan, Y.- S.; Byers,M. G.; 3 C b
Shows, T. B.; Bell, G. I.; Steiner, D. F.: Human islet amyloidpolypeptide
gene: complete nucleotide sequence, chromosomal localization,and
evolutionary history. Molec. Endocr. 3: 1775- 1781, 1989.

GAM7957 297 IAPP Opie, E. L.: On the relation of the chronic interstitial pancreatitisto the 3 C b
islands of Langerhans and to diabetes mellitus. J. Exp. Med. 5:397- 428,
1900.

GAM7957 297 IAPP Roberts, A. N.; Leighton, B.; Todd, J. A.; Cockburn, D.; Schofield,P. N.; 3 C b
Sutton, R.; Holt, S.; Boyd, Y.; Day, A. J.; Foot, E. A.; Willis,A. C.; Reid,
K. B. M.; Cooper, G. J. S.: Molecular and functionalcharacterization of
amylin, a peptide associated with type 2 diabetesmellitus. Proc. Nat. Acad.
Sci. 86: 9662- 9666, 1989.

GAM7957 297 IAPP Sanke, T.; Bell, G. I.; Sample, C.; Rubenstein, A. H.; Steiner,D. F.: An 3 C b
islet amyloid peptide is derived from an 89- amino acidprecursor by
proteolytic processing. J. Biol. Chem. 263: 17243- 17246,1988.

GAM7957 297 IAPP Verchere, C. B.; D'Alessio, D. A.; Palmiter, R. D.; Weir, G. C.;Bonner- 3 C b
Weir, S.; Baskin, D. G.; Kahn, S. E.: Islet amyloid formationassociated with
hyperglycemia in transgenic mice with pancreatic betacell expression of
human islet amyloid polypeptide. Proc. Nat. Acad.Sci. 93: 3492- 3496, 1996.

GAM7957 297 IAPP Westermark, P.; Engstrom, U.; Johnson, K. H.; Westermark, G. T.;Betsholtz, 3 C b

C.: Islet amyloid polypeptide: pinpointing amino acidresidues linked to amyloid fibril formation. Proc. Nat. Acad. Sci. 87:5036- 5040, 1990.

GAM7957 297 IFIT4 de Veer, M. J.; Sim, H.; Whisstock, J. C.; Devenish, R. J.; Ralph,S. J.: 3 C b
IFI60/ISG60/IFIT4, a new member of the human IFI54/IFIT2 familyof interferon- stimulated genes. Genomics 54: 267- 277, 1998.

GAM7957 297 IFIT4 Yu, M.; Tong, J.- H.; Mao, M.; Kan, L.- X.; Liu, M.- M.; Sun, Y.- W.;Fu, G.; 3 C b
Jing, Y.- K.; Yu, L.; Lepaslier, D.; Lanotte, M.; Wang, Z.- Y.;Chen, Z.; Waxman, S.; Wang, Y.- X.; Tan, J.- Z.; Chen, S.- J.: Cloningof a gene (RIG-G) associated with retinoic acid- induced differentiationof acute promyelocytic leukemia cells and representing a new memberof a family of interferon- stimulated genes. Proc. Nat. Acad. Sci. 94:7406- 7411, 1997.

GAM7957 297 IFIT4 Zhu, H.; Cong, J.- P.; Shenk, T.: Use of differential display analysisto 3 C b
assess the effect of human cytomegalovirus infection on the accumulationof cellular RNAs: induction of interferon- responsive RNAs. Proc.Nat. Acad. Sci. 94: 13985- 13990, 1997.

GAM7957 297 IFNAR1 Chany, C.; Vignal, M.; Couillin, P.; Van Cong, N.; Boue, J.; Boue,A.: 3 C c
Chromosomal localization of human genes governing the interferon-inducedantiviral state. Proc. Nat. Acad. Sci. 72: 3129- 3133, 1975.

GAM7957 297 IFNAR1 Cox, D. R.; Epstein, L. B.; Epstein, C. J.: Genes coding for sensitivityto 3 C c
interferon (IfRec) and soluble superoxide dismutase (SOD- 1) arelinked in mouse and man and map to mouse chromosome 16. Proc. Nat.Acad. Sci. 77: 2168-2172, 1980.

GAM7957 297 IFNAR1 De Clercq, E.; Edy, V. G.; Cassiman, J.- J.: Chromosome 21 doesnot code for 3 C c
an interferon receptor. Nature 264: 249- 251, 1976.

GAM7957 297 IFNAR1 Epstein, L. B.; Epstein, C. J.: Localization of the gene AVG forthe 3 C c
antiviral expression of immune and classical interferon to thedistal portion of the long arm of chromosome 21. J. Infect. Dis. 133(suppl.): A56- A62, 1976.

GAM7957 297 IFNAR1 Faltynek, C. R.; Branca, A. A.; McCandless, S.; Baglioni, 3 C c
C.:Characterization of an interferon receptor on human lymphoblastoidcells. Proc. Nat. Acad. Sci. 80: 3269- 3273, 1983.

GAM7957 297 IFNAR1 Fournier, A.; Zhang, Z. Q.; Tan, Y. H.: Human beta:alpha but notgamma 3 C c
interferon binding site is a product of the chromosome 21 interferonaction gene. Somat. Cell Molec. Genet. 11: 291- 295, 1985.

GAM7957 297 IFNAR1 Langer, J. A.; Rashidbaigi, A.; Lai, L.- W.; Patterson, D.; Jones,C.: 3 C c
Sublocalization on chromosome 21 of human interferon- alpha receptorgene and the gene for an interferon- gamma response protein. Somat.Cell Molec. Genet. 16: 231- 240, 1990.

GAM7957 297 IFNAR1 Lin, P.- F.; Slate, D. L.; Lawyer, F. C.; Ruddle, F. H.: Assignmentof the 3 C c
murine interferon sensitivity and cytoplasmic superoxide dismutasegenes to chromosome 16. Science 209: 285- 287, 1980.

GAM7957 297 IFNAR1 Lutfalla, G.; Gardiner, K.; Proudhon, D.; Vielh, E.; Uze, G.:The structure 3 C c
of the human interferon alpha/beta receptor gene. J.Biol. Chem. 267: 2802-2809, 1992.

GAM7957 297 IFNAR1 Lutfalla, G.; Roeckel, N.; Mogensen, K. E.; Mattei, M. G.; Uze,G.: 3 C c
Assignment of the human interferon- alpha receptor gene to chromosome21q22.1 by in situ hybridization. J. Interferon Res. 10: 515- 517,1990.

GAM7957 297 IFNAR1 Maroun, L. E.: Interferon action and chromosome 21 trisomy. (Letter) 3 C c
J.Theor. Biol. 86: 603- 606, 1980.

GAM7957 297 IFNAR1 Novick, D.; Cohen, B.; Rubinstein, M.: The human interferon 3 C c

alpha/betareceptor: characterization and molecular cloning. Cell 77: 391-400,1994.

GAM7957 297 IFNAR1 Raziuddin, A.; Sarkar, F. H.; Dutkowski, R.; Shulman, L.; Ruddle,F. H.; Gupta, S. L.: Receptors for human alpha and beta interferonbut not for gamma interferon are specified by human chromosome 21. Proc.Nat. Acad. Sci. 81: 5504- 5508, 1984. 3 C c

GAM7957 297 IFNAR1 Revel, M.; Bash, D.; Ruddle, F. H.: Antibodies to a cell- surfacecomponent coded by human chromosome 21 inhibit action of interferon. Nature 260:139-141, 1976. 3 C c

GAM7957 297 IFNAR1 Sarkar, F. H.; Gupta, S. L.: Receptors for human gamma interferon:binding and crosslinking of 125- I- labeled recombinant human gammainterferon to receptors on WISH cells. Proc. Nat. Acad. Sci. 81:5160- 5164, 1984. 3 C c

GAM7957 297 IFNAR1 Slate, D. L.; Ruddle, F. H.: Antibodies to chromosome 21 codedcell surface components can block response to human interferon. Cytogenet.Cell Genet. 22: 265- 269, 1978. 3 C c

GAM7957 297 IFNAR1 Slate, D. L.; Shulman, L.; Lawrence, J. B.; Revel, M.; Ruddle,F. H.: Presence of human chromosome 21 alone is sufficient for hybridcell sensitivity to human interferon. J. Virol. 25: 319- 325, 1978. 3 C c

GAM7957 297 IFNAR1 Takaoka, A.; Mitani, Y.; Suemori, H.; Sato, M.; Yokochi, T.; Noguchi,S.; Tanaka, N.; Taniguchi, T.: Cross talk between interferon- gammaand - alpha/beta signaling components in caveolar membrane domains. Science 288:2357- 2360, 2000. 3 C c

GAM7957 297 IFNAR1 Tan, Y. H.: Chromosome 21 and the cell growth inhibitory effectof human interferon preparations. Nature 260: 141- 143, 1976. 3 C c

GAM7957 297 IFNAR1 Tan, Y. H.; Schneider, E. L.; Tischfield, J.; Epstein, C. J.;Ruddle, F. H.: Human chromosome 21 dosage: effect on the expressionof the interferon induced antiviral state. Science 186: 61- 63, 1974. 3 C c

GAM7957 297 IFNAR1 Tan, Y. H.; Tischfield, J.; Ruddle, F. H.: The linkage of genesfor the human interferon- induced antiviral protein and indophenoloxidase- Btraits to chromosome G- 21. J. Exp. Med. 37: 317- 330, 1973. 3 C c

GAM7957 297 IFNAR1 Weil, J.; Tucker, G.; Epstein, L. B.; Epstein, C. J.: Interferoninduction of (2- prime- 5- prime) oligoisoadenylate synthetase in diploidand trisomy 21 human fibroblasts: relation to dosage of the interferonreceptor gene (IFRC). Hum. Genet. 65: 108- 111, 1983. 3 C c

GAM7957 297 IFNAR1 Wiranowska- Stewart, M.; Stewart, W. E., II: The role of humanchromosome 21 in sensitivity to interferons. J. Gen. Virol. 37:629- 633, 1977. 3 C c

GAM7957 297 IFNGR2 Bono, M. R.; Alcaide- Loridan, C.; Couillin, P.; Letouze, B.; Grisard,M. C.; Jouin, H.; Fellous, M.: Human chromosome 16 encodes a factorinvolved in induction of class II major histocompatibility antigensby interferon gamma. Proc. Nat. Acad. Sci. 88: 6077- 6081, 1991. 3 C b

GAM7957 297 IFNGR2 Bono, R.; Hatat, D.; Couillin, P.; Grisard, M. C.; Van Cong, N.;Fisher, D.; Fellous, M.: Receptor for human gamma interferon is specifiedby human chromosomes 6 and 21. (Abstract) Cytogenet. Cell Genet. 46:584, 1987. 3 C b

GAM7957 297 IFNGR2 Dorman, S. E.; Holland, S. M.: Mutation in the signal- transducingchain of the interferon- gamma receptor and susceptibility to mycobacterialinfection. J. Clin. Invest. 101: 2364- 2369, 1998. 3 C b

GAM7957 297 IFNGR2 Jung, V.; Rashidbaigi, A.; Jones, C.; Tischfield, J. A.; Shows,T. B.; Pestka, S.: Human chromosomes 6 and 21 are required for sensitivityto human interferon gamma. Proc. Nat. Acad. Sci. 84: 4151- 4155,1987. 3 C b

GAM7957 297 IFNGR2 Langer, J. A.; Rashidbaigi, A.; Lai, L.- W.; Patterson, D.; Jones,C.: 3 C b

Sublocalization on chromosome 21 of human interferon- alpha receptorgene and the gene for an interferon- gamma response protein. Somat.Cell Molec. Genet. 16: 231- 240, 1990.

GAM7957 297 IFNGR2 Mariano, T. M.; Muthukumaran, G.; Donnelly, R. J.; Wang, N.; Adamson,M. C.; 3 C b Pestka, S.; Kozak, C. A.: Genetic mapping of the gene forthe mouse interferon- gamma receptor signaling subunit to the distalend of chromosome 16. Mammalian Genome 7: 321- 322, 1996.

GAM7957 297 IFNGR2 Rhee, S.; Ebensperger, C.; Dembic, Z.; Pestka, S.: The structureof the gene 3 C b for the second chain of the human interferon- gamma receptor. J.Biol. Chem. 271: 28947- 28952, 1996.

GAM7957 297 IFNGR2 Soh, J.; Donnelly, R. J.; Mariano, T. M.; Cook, J. R.; Schwartz,B.; Pestka, 3 C b S.: Identification of a yeast artificial chromosome cloneencoding an accessory factor for the human interferon gamma receptor:evidence for multiple accessory factors. Proc. Nat. Acad. Sci. 90:8737- 8741, 1993.

GAM7957 297 IL10 Akbari, O.; Freeman, G. J.; Meyer, E. H.; Greenfield, E. A.; Chang,T. T.; 3 C c Sharpe, A. H.; Berry, G.; DeKruyff, R. H.; Umetsu, D. T.:Antigen- specific regulatory T cells develop via the ICOS- ICOS- ligandpathway and inhibit allergen- induced airway hyperreactivity. NatureMed. 8: 1024- 1032, 2002.

GAM7957 297 IL10 Cox, D. R.; Burmeister, M.; Price, E. R.; Kim, S.; Myers, R. M.: Radiation 3 C c hybrid mapping: a somatic cell genetic method for constructinghigh- resolution maps of mammalian chromosomes. Science 250: 245- 250,1990.

GAM7957 297 IL10 Crawley, J. B.; Williams, L. M.; Mander, T.; Brennan, F. M.; Foxwell,B. M.: 3 C c Interleukin- 10 stimulation of phosphatidylinositol 3- kinaseand p70 S6 kinase is required for the proliferative but not the antiinflammatoryeffects of the cytokine. J. Biol. Chem. 271: 16357- 16362, 1996.

GAM7957 297 IL10 Eskdale, J.; Gallagher, G.; Verweij, C. L.; Keijsers, V.; Westendorp,R. G. 3 C c J.; Huizinga, T. W. J.: Interleukin 10 secretion in relationto human IL- 10 locus haplotypes. Proc. Nat. Acad. Sci. 95: 9465- 9470,1998.

GAM7957 297 IL10 Eskdale, J.; Kube, D.; Tesch, H.; Gallagher, G.: Mapping of thehuman IL10 3 C c gene and further characterization of the 5- prime flankingsequence. Immunogenetics 46: 120- 128, 1997.

GAM7957 297 IL10 Farmer, M. A.; Sundberg, J. P.; Bristol, I. J.; Churchill, G. A.;Li, R.; 3 C c Elson, C. O.; Leiter, E. H.: A major quantitative trait locuson chromosome 3 controls colitis severity in IL- 10- deficient mice. Proc.Nat. Acad. Sci. 98: 13820- 13825, 2001.

GAM7957 297 IL10 Franchimont, D.; Martens, H.; Hagelstein, M.- T.; Louis, E.; Dewe,W.; 3 C c Chrousos, G. P.; Belaiche, J.; Geenen, V.: Tumor necrosis factoralpha decreases, and interleukin- 10 increases, the sensitivity ofhuman monocytes to dexamethasone: potential regulation of the glucocorticoidreceptor. J. Clin. Endocr. Metab. 84: 2834- 2839, 1999.

GAM7957 297 IL10 Gesser, B.; Leffers, H.; Jinquan, T.; Vestergaard, C.; Kirstein,N.; Sindet- 3 C c Pedersen, S.; Jensen, S. L.; Thestrup- Pedersen, K.; Larsen,C. G.: Identification of functional domains on human interleukin10. Proc. Nat. Acad. Sci. 94: 14620- 14625, 1997.

GAM7957 297 IL10 Gibson, A. W.; Edberg, J. C.; Wu, J.; Westendorp, R. G. J.; Huizinga,T. W. 3 C c J.; Kimberly, R. P.: Novel single nucleotide polymorphismsin the distal IL- 10 promoter affect IL- 10 production and enhance therisk of systemic lupus erythematosus. J. Immun. 166: 3915- 3922,2001.

GAM7957 297 IL10 Goudy, K.; Song, S.; Wasserfall, C.; Zhang, Y. C.; Kapturczak,M.; Muir, A.; 3 C c Powers, M.; Scott- Jorgensen, M.; Campbell- Thompson,M.; Crawford, J. M.;

Ellis, T. M.; Flotte, T. R.; Atkinson, M. A.: Adeno- associated virus vector- mediated IL- 10 gene delivery preventstype 1 diabetes in NOD mice. Proc. Nat. Acad. Sci. 98: 13913- 13918,2001.

GAM7957 297 IL10 Grove, J.; Daly, A. K.; Bassendine, M. F.; Gilvarry, E.; Day,C. P.: 3 C c
Interleukin 10 promoter region polymorphisms and susceptibilityto advanced alcoholic liver disease. Gut 46: 540- 545, 2000.

GAM7957 297 IL10 Kim, J. M.; Brannan, C. I.; Copeland, N. G.; Jenkins, N. A.; Khan,T. A.; 3 C c
Moore, K. W.: Structure of the mouse Il- 10 gene and chromosomallocalization of the mouse and human genes. J. Immun. 148: 3618- 3623,1992.

GAM7957 297 IL10 Kitagawa, N.; Goto, M.; Kurozumi, K.; Maruo, S.; Fukayama, M.;Naoe, T.; 3 C c
Yasukawa, M.; Hino, K.; Suzuki, T.; Todo, S.; Takada, K.: Epstein- Barr virus- encoded poly(A)- RNA supports Burkitt's lymphomagrowth through interleukin- 10 induction. EMBO J. 19: 6742- 6750,2000.

GAM7957 297 IL10 Kuhn, R.; Lohler, J.; Rennick, D.; Rajewsky, K.; Muller, K.:Interleukin- 10- 3 C c
deficient mice develop chronic enterocolitis. Cell 75:263- 274, 1993.

GAM7957 297 IL10 Lee, T.- S.; Chau, L.- Y.: Heme oxygenase- 1 mediates the anti- 3 C c
inflammatoryeffect of interleukin- 10 in mice. Nature Med. 8: 240- 246, 2002.

GAM7957 297 IL10 Meng, X.; Sawamura, D.; Tamai, K.; Hanada, K.; Ishida, H.; Hashimoto,I.: 3 C c
Keratinocyte gene therapy for systemic diseases: circulatinginterleukin 10 released from gene- transferred keratinocytes inhibitscontact hypersensitivity at distant areas of the skin. J. Clin. Invest. 101:1462- 1467, 1998.

GAM7957 297 IL10 Pinderski Oslund, L. J.; Hedrick, C. C.; Olvera, T.; Hagenbaugh,A.; Territo, 3 C c
M.; Berliner, J. A.; Fyfe, A. I.: Interleukin- 10 blocksatherosclerotic events in vitro and in vivo. Arterioscler. Thromb.Vasc. Biol. 19: 2847- 2853, 1999.

GAM7957 297 IL10 Rosenwasser, L. J.; Borish, L.: Genetics of atopy and asthma:the rationale 3 C c
behind promoter- based candidate gene studies (IL- 4 andIL- 10). Am. J. Resp. Crit. Care Med. 156: S152- S155, 1997.

GAM7957 297 IL10 Shin, H. D.; Winkler, C.; Stephens, J. C.; Bream, J.; Young, H.;Goedert, J. 3 C c
J.; O'Brien, T. R.; Vlahov, D.; Buchbinder, S.; Giorgi,J.; Rinaldo, C.; Donfield, S.; Willoughby, A.; O'Brien, S. J.; Smith,M. W.: Genetic restriction of HIV- 1 pathogenesis to AIDS by promoteralleles of IL10. Proc. Nat. Acad. Sci. 97: 14467- 14472, 2000.

GAM7957 297 IL10 Terkeltaub, R. A.: IL- 10: an 'immunologic scalpel' for 3 C c
atherosclerosis?(Editorial) Atheroscler. Thromb. Vasc. Biol. 19: 2823- 2825, 1999.

GAM7957 297 IL10 Turner, D. M.; Williams, D. M.; Sankaran, D.; Lazarus, M.; Sinnott,P. J.; 3 C c
Hutchinson, I. V.: An investigation of polymorphism in theinterleukin- 10 gene promoter. Europ. J. Immunogenet. 24: 1- 8, 1997.

GAM7957 297 IL10 Vieira, P.; de Waal- Malefyt, R.; Dang, M.- N.; Johnson, K. E.;Kastelein, 3 C c
R.; Fiorentino, D. F.; deVries, J. E.; Roncarolo, M.- G.;Mosmann, T. R.; Moore, K. W.: Isolation and expression of human cytokinesynthesis inhibitory factor cDNA clones: homology to Epstein- Barrvirus open reading frame BCRFI. Proc. Nat. Acad. Sci. 88: 1172- 1176,1991.

GAM7957 297 IL10 Westendorp, R. G. J.; Langermans, J. A. M.; Huizinga, T. W. G.;Elouali, A. 3 C c
H.; Boomsma, D. I.; Verweij, C. L.; Vandenbroucke, J.P.: Genetic influence on cytokine production and fatal meningococcaldisease. Lancet 349: 170- 173, 1997.

GAM7957 297 IL13RA1 Aman, M. J.; Tayebi, N.; Obiri, N. I.; Puri, R. K.; Modi, W. S.;Leonard, W. J.: cDNA cloning and characterization of the human interleukin13 receptor alpha chain. J. Biol. Chem. 271: 29265- 29270, 1996. 3 C b

GAM7957 297 IL13RA1 Guo, J.; Apiou , F.; Mellerin, M.- P.; Lebeau, B.; Jacques, Y.;Minvielle, S.: Chromosome mapping and expression of the human interleukin- 13receptor. Genomics 42: 141- 5, 1997. 3 C b

GAM7957 297 IL13RA1 Heinzmann, H.; Mao, X.- Q.; Akaiwa, M.; Kreomer, R. T.; Gao, P.- S.;Ohshima, K.; Umeshita, R.; Abe, Y.; Braun, S.; Yamashita, T.; Roberts,M. H.; Sugimoto, R.; and 20 others: Genetic variants of IL- 13 signallingand human asthma and atopy. Hum. Molec. Genet. 9: 549- 559, 2000. 3 C b

GAM7957 297 IL13RA1 Hilton, D. J.; Zhang, J.- G.; Metcalf, D.; Alexander, W. S.; Nicola,N. A.; Willson, T. A.: Cloning and characterization of a bindingsubunit of the interleukin 13 receptor that is also a component ofthe interleukin 4 receptor. Proc. Nat. Acad. Sci. 93: 497- 501, 1996. 3 C b

GAM7957 297 IL13RA1 Zurawski, S. M.; Vega, F., Jr.; Huyghe, B.; Zurawski, G.: Receptorsfor interleukin- 13 and interleukin- 4 are complex and share a novelcomponent that functions in signal transduction. EMBO J. 12: 2663- 2670,1993. 3 C b

GAM7957 297 IL18 Corbaz, A.; ten Hove, T.; Herren, S.; Graber, P.; Schwartsburd,B.; Belzer, I.; Harrison, J.; Plitz, T.; Kosco- Vilbois, M. H.; Kim,S.- H.; Dinarello, C. A.; Novick, D.; van Deventer, S.; Chvatchko,Y.: IL- 18- binding protein expression by endothelial cells and macrophagesis up- regulated during active Crohn's disease. J. Immun. 168: 3608- 3616,2002. 3 C c

GAM7957 297 IL18 Konishi, H.; Tsutsui, H.; Murakami, T.; Yumikura- Futatsugi, S.;Yamanaka, K.; Tanaka, M.; Iwakura, Y.; Suzuki, N.; Takeda, K.; Akira,S.; Nakanishi, K.; Mizutani, H.: IL- 18 contributes to the spontaneousdevelopment of atopic dermatitis- like inflammatory skin lesion independentlyof IgE/stat6 under specific pathogen- free conditions. Proc. Nat.Acad. Sci. 99: 11340- 11345, 2002. 3 C c

GAM7957 297 IL18 Nolan, K. F.; Greaves, D. R.; Waldmann, H.: The human interleukin18 gene IL18 maps to 11q22.2- q22.3, closely linked to the DRD2 genelocus and distinct from mapped IDDM loci. Genomics 51: 161- 163,1998. 3 C c

GAM7957 297 IL18 Okamoto, I.; Kohno, K.; Tanimoto, T.; Iwaki, K.; Ishihara, T.;Akamatsu, S.; Ikegami, H.; Kurimoto, M.: IL- 18 prevents the developmentof chronic graft- versus- host disease in mice. J. Immun. 164: 6067- 6074,2000. 3 C c

GAM7957 297 IL18 Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.;Tanimoto, T.; Torigoe, K.; Okura, T.; Nukada, Y.; Hattori, K.; Akita,K.; Namba, M.; Tanabe, F.; Konishi, K.; Fukuda, S.; Kurimoto, M.:Cloning of a new cytokine that induces IFN- gamma production by T cells. Nature 378:88- 91, 1995. 3 C c

GAM7957 297 IL18 Pizarro, T. T.; Michie, M. H.; Bentz, M.; Woraratanadharm, J.;Smith, M. F., Jr.; Foley, E.; Moskaluk, C. A.; Bickston, S. J.; Cominelli,F.: IL- 18, a novel immunoregulatory cytokine, is up- regulated inCrohn's disease: expression and localization in intestinal mucosalcells. J. Immun. 162: 6829- 6835, 1999. 3 C c

GAM7957 297 IL18 Reddy, P.; Teshima, T.; Kukuruga, M.; Ordemann, R.; Liu, C.; Lowler,K.; Ferrara, J. L. M.: Interleukin- 18 regulates acute graft- versus- hostdisease by enhancing Fas- mediated donor T cell apoptosis. J. Exp.Med. 194: 1433- 1440, 2001. 3 C c

GAM7957 297 IL18 Rothe, H.; Jenkins, N. A.; Copeland, N. G.; Kolb, H.: Active stageof autoimmune diabetes is associated with the expression of a novelcytokine, IGIF, which is located near Idd2. J. Clin. Invest. 99:469- 474, 1997. 3 C c

GAM7957 297 IL18 Sarvetnick, N.: IFN- gamma, IGIF, and IDDM. (Editorial) J. Clin.Invest. 99: 3 C c
371- 372, 1997.

GAM7957 297 IL18 Shida, K.; Shiratori, I.; Matsumoto, M.; Fukumori, Y.; Matsuhisa,A.; 3 C c
Kikkawa, S.; Tsuji, S.; Okamura, H.; Toyoshima, K.; Seya, T.:An alternative
form of IL- 18 in human blood plasma: complex formationwith IgM defined by
monoclonal antibodies. J. Immun. 166: 6671- 6679,2001.

GAM7957 297 IL18 Sugawara, S.; Uehara, A.; Nochi, T.; Yamaguchi, T.; Ueda, H.;Sugiyama, A.; 3 C c
Hanzawa, K.; Kumagai, K.; Okamura, H.; Takada, H.:Neutrophil proteinase 3-
mediated induction of bioactive IL- 18 secretionby human oral epithelial
cells. J. Immun. 167: 6568- 6575, 2001.

GAM7957 297 IL18 ten Hove, T.; Corbaz, A.; Amitai, H.; Aloni, S.; Belzer, I.; Graber,P.; 3 C c
Drillenburg, P.; van Deventer, S. J.; Chvatchko, Y.; Te Velde,A. A.:
Blockade of endogenous IL- 18 ameliorates TNBS- induced colitisby decreasing
local TNF- alpha production in mice. Gastroenterology 121:1372- 1379, 2001.

GAM7957 297 IL18 Vidal- Vanaclocha, F.; Fantuzzi, G.; Mendoza, L.; Fuentes, A. M.;Anasagasti, 3 C c
M. J.; Martin, J.; Carrascal, T.; Walsh, P.; Reznikov,L. L.; Kim, S.- H.;
Novick, D.; Rubinstein, M.; Dinarello, C. A.:IL- 18 regulates IL- 1- beta-
dependent hepatic melanoma metastasis viavascular cell adhesion molecule- 1.
Proc. Nat. Acad. Sci. 97: 734- 739,2000.

GAM7957 297 IL1R1 Copeland, N. G.; Silan, C. M.; Kingsley, D. M.; Jenkins, N. A.;Cannizzaro, 3 C b
L. A.; Croce, C. M.; Huebner, K.; Sims, J. E.: Chromosomallocation of murine
and human IL- 1 receptor genes. Genomics 9: 44- 50,1991.

GAM7957 297 IL1R1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 3 C b
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp)
on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM7957 297 IL1R1 Dower, S. K.; Kronheim, S. R.; Hopp, T. P.; Cantrell, M.; Deeley,M.; Gillis, 3 C b
S.; Henney, C. S.; Urdal, D. L.: The cell surface receptorsfor interleukin-
1(alpha) and interleukin- 1(beta) are identical. Nature 324:266- 268, 1986.

GAM7957 297 IL1R1 Sims, J. E.; Acres, R. B.; Grubin, C. E.; McMahan, C. J.; Wignall,J. M.; 3 C b
March, C. J.; Dower, S. K.: Cloning the interleukin 1 receptorfrom human T
cells. Proc. Nat. Acad. Sci. 86: 8946- 8950, 1989.

GAM7957 297 IL6R Kluck, P. M. C.; Wiegant, J.; Jansen, R. P. M.; Bolk, M. W. J.;Raap, A. K.; 3 C c
Willemze, R.; Landegent, J. E.: The human interleukin- 6receptor alpha-
chain gene is localized on chromosome 1 band q21. Hum.Genet. 90: 542- 544,
1993.

GAM7957 297 IL6R Szpirer, J.; Szpirer, C.; Riviere, M.; Houart, C.; Baumann, M.;Fey, G. H.; 3 C c
Poli, V.; Cortese, R.; Islam, M. Q.; Levan, G.: The interleukin- 6-
dependentDNA- binding protein gene (transcription factor 5: TCF5) maps to
humanchromosome 20 and rat chromosome 3, the IL6 receptor locus (IL6R)to
human chromosome 1 and rat chromosome 2, and the rat IL6 gene torat
chromosome 4. Genomics 10: 539- 546, 1991.

GAM7957 297 IL6R Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.;Seed, B.; 3 C c
Taniguchi, T.; Hirano, T.; Kishimoto, T.: Cloning and expressionof the human
interleukin- 6 (BSF- 2/IFN- beta- 2) receptor. Science 241:825- 828, 1988.

GAM7957 297 INHBC Hotten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.: Cloning ofa new member 3 C c
of the TGF- beta family: a putative new activin betaCchain. Biochem.
Biophys. Res. Commun. 206: 608- 613, 1995.

GAM7957 297 INHBC Ling, N.; Ying, S. Y.; Ueno, N.; Shimasaki, S.; Esch, F.; Hotta,M.; 3 C c
Guillemin, R.: Pituitary FSH is released by a heterodimer ofthe beta-
subunits from the two forms of inhibin. Nature 321: 779- 782,1986.

GAM7957 297 INHBC Mellor, S. L.; Cranfield, M.; Ries, R.; Pedersen, J.; Cancilla,B.; de Kretser, D.; Groome, N. P.; Mason, A. J.; Risbridger, G. P.: Localization of activin beta(A)- , beta(B)- , and beta(C)- subunitsin human prostate and evidence for formation of new activin heterodimersof beta(C)- subunit. J. Clin. Endocr. Metab. 85: 4851- 4858, 2000. 3 C c

GAM7957 297 INHBC Schmitt, J.; Hotten, G.; Jenkins, N. A.; Gilbert, D. J.; Copeland,N. G.; Pohl, J.; Schrewe, H.: Structure, chromosomal localization,and expression analysis of the mouse inhibin/activin betaC (Inhbc)gene. Genomics 32: 358- 366, 1996. 3 C c

GAM7957 297 INPP5B Janne, P. A.; Dutra, A. S.; Dracopoli, N. C.; Charnas, L. R.; Puck,J. M.; Nussbaum, R. L.: Localization of the 75- kDa inositol polyphosphate- 5- phosphatase(INPP5B) to human chromosome band 1p34. Cytogenet. Cell Genet. 66:164- 166, 1994. 3 C b

GAM7957 297 INPP5B Janne, P. A.; Rochelle, J. M.; Martin- DeLeon, P. A.; Stambolian,D.; Seldin, M. F.; Nussbaum, R. L.: Mapping of the 75- kDa inositolpolyphosphate- 5- phosphatase (Inpp5b) to distal mouse chromosome 4and its exclusion as a candidate gene for dysgenetic lens. Genomics 28:280- 285, 1995. 3 C b

GAM7957 297 INPP5B Ross, T. S.; Jefferson, A. B.; Mitchell, C. A.; Majerus, P. W.: Cloning and expression of human 75- kDa inositol polyphosphate- 5- phosphatase.J. Biol. Chem. 266: 20283- 20289, 1991. 3 C b

GAM7957 297 INPP5D Damen, J. E.; Liu, L.; Rosten, P.; Humphries, R. K.; Jefferson,A. B.; Majerus, P. W.; Krystal, G.: The 145- kDa protein induced toassociate with Shc by multiple cytokines is an inositol tetraphosphateand phosphatidylinositol 3,4,5- triphosphate 5- phosphatase. Proc.Nat. Acad. Sci. 93: 1689- 1693, 1996. 3 C b

GAM7957 297 INPP5D Drayer, A. L.; Pesesse, X.; De Smedt, F.; Woscholski, R.; Parker,P.; Erneux, C.: Cloning and expression of a human placenta inositol1,3,4,5- tetrakisphosphate and phosphatidylinositol 3,4,5- triphosphate5- phosphatase. Biochem. Biophys. Res. Commun. 225: 243- 249, 1996. 3 C b

GAM7957 297 INPP5D Helgason, C. D.; Damen, J. E.; Rosten, P.; Grewal, R.; Sorensen,P.; Chappel, S. M.; Borowski, A.; Jirik, F.; Krystal, G.; Humphries,R. K.: Targeted disruption of SHIP leads to hemopoietic perturbations,lung pathology, and a shortened life span. Genes Dev. 12: 1610- 1620,1998. 3 C b

GAM7957 297 INPP5D Huber, M.; Helgason, C. D.; Damen, J. E.; Liu, L.; Humphries, R.K.; Krystal, G.: The src homology 2- containing inositol phosphatase(SHIP) is the gatekeeper of mast cell degranulation. Proc. Nat. Acad.Sci. 95: 11330- 11335, 1998. 3 C b

GAM7957 297 INPP5D Kavanaugh, W. M.; Pot, D. A.; Chin, S. M.; Deuter- Reinhard, M.;Jefferson, A. B.; Norris, F. A.; Masiarz, F. R.; Cousens, L. S.; Majerus,P. W.; Williams, L. T.: Multiple forms of an inositol polyphosphate5- phosphatase form signaling complexes with Shc and Grb2. Curr. Biol. 6: 438- 445, 1996. 3 C b

GAM7957 297 INPP5D Lioubin, M. N.; Algate, P. A.; Tsai, S.; Carlberg, K.; Aebersold,R.; Rohrschneider, L. R.: p150(Ship), a signal transduction moleculewith inositol polyphosphate- 5- phosphatase activity. Genes Dev. 10:1084- 1095, 1996. 3 C b

GAM7957 297 INPP5D Liu, Q.; Amgen EST Program; Dumont, D. J.: Molecular cloningand chromosomal localization in human and mouse of the SH2- containinginositol phosphatase, INPP5D (SHIP). Genomics 39: 109- 112, 1997. 3 C b

GAM7957 297 INPP5D Liu, Q.; Shalaby, F.; Jones, J.; Bouchard, D.; Dumont, D. J.:The SH2- 3 C b

containing inositol polyphosphate 5- phosphatase, Ship, isexpressed during hematopoiesis and spermatogenesis. Blood 91: 2753- 2759,1998.

GAM7957 297 INPP5D Takeshita, S.; Namba, N.; Zhao, J. J.; Jiang, Y.; Genant, H. K.;Silva, M. J.; Brodt, M. D.; Helgason, C. D.; Kalesnikoff, J.; Rauh,M. J.; Humphries, R. K.; Krystal, G.; Teitelbaum, S. L.; Ross, F.P.: SHIP- deficient mice are severely osteoporotic due to increasednumbers of hyper- resorptive osteoclasts. Nature Med. 8: 943- 949,2002. 3 C b

GAM7957 297 INPP5D Wang, J.- W.; Howson, J. M.; Ghansah, T.; Desponts, C.; Ninos,J. M.; May, S. L.; Nguyen, K. H. T.; Toyama- Sorimachi, N.; Kerr, W.G.: Influence of SHIP on the NK repertoire and allogeneic bone marrowtransplantation. Science 295: 2094- 2097, 2002. 3 C b

GAM7957 297 INPP5D Ware, M. D.; Rosten, P.; Damen, J. E.; Liu, L.; Humphries, R.K.; Krystal, G.: Cloning and characterization of human SHIP, the145- kD inositol 5- phosphatase that associates with SHC after cytokinestimulation. Blood 88: 2833- 2840, 1996. 3 C b

GAM7957 297 IPP Chang- Yeh, A.; Jabs, E. W.; Li, X.; Dracopoli, N. C.; Huang, R.C. C.: The IPP gene is assigned to human chromosome 1p32- 1p22. Genomics 15:239- 241, 1993. 3 C b

GAM7957 297 IPP Chang- Yeh, A.; Mold, D. E.; Brilliant, M. H.; Huang, R. C. C.:The mouse intracisternal A particle- promoted placental gene retrotranspositionis mouse- strain- specific. Proc. Nat. Acad. Sci. 90: 292- 296, 1993. 3 C b

GAM7957 297 IPP Chang- Yeh, A.; Mold, D. E.; Huang, R. C. C.: Identification ofa novel murine IAP- promoted placenta- expressed gene. Nucleic AcidsRes. 19: 3667- 3672, 1991. 3 C b

GAM7957 297 IPP Mold, D. E.; Chang- Yeh, A.; Huang, R. C. C.: Cell lineage- specificexpression of the MIPP gene. Biochem. Biophys. Res. Commun. 177:1062- 1067, 1991. 3 C b

GAM7957 297 IRAK4 Li, S.; Strelow, A.; Fontana, E. J.; Wesche, H.: IRAK- 4: a novelmember of the IRAK family with the properties of an IRAK- kinase. Proc.Nat. Acad. Sci. 99: 5567- 5572, 2002. 3 C b

GAM7957 297 IRAK4 Scanlan, M. J.; Gordon, J. D.; Williamson, B.; Stockert, E.; Bander,N. H.; Jongeneel, V.; Gure, A. O.; Jager, D.; Jager, E.; Knuth, A.;Chen, Y.- T.; Old, L. J.: Antigens recognized by autologous antibodyin patients with renal- cell carcinoma. Int. J. Cancer 83: 456- 464,1999. 3 C b

GAM7957 297 IRAK4 Scott, A. F.: Personal Communication. Baltimore, Md. 4/25/2002. 3 C b

GAM7957 297 IRAK4 Suzuki, N.; Suzuki, S.; Duncan, G. S.; Millar, D. G.; Wada, T.;Mirtsos, C.; Takada, H.; Wakeham, A.; Itie, A.; Li, S.; Penninger,J. M.; Wesche, H.; Ohashi, P. S.; Mak, T. W.; Yeh, W.- C.: Severeimpairment of interleukin- 1 and Toll- like receptor signalling in micelacking IRAK- 4. Nature 416: 750- 754, 2002. 3 C b

GAM7957 297 ITGAL Callen, D. F.; Chen, L. Z.; Nancarrow, J.; Whitmore, S. A.; Apostolou,S.; Thompson, A. D.; Lane, S. A.; Stallings, R. L.; Hildebrand, C.E.; Harris, P. G.; Sutherland, G. R.: Current state of the physicalmap of human chromosome 16. (Abstract) Cytogenet. Cell Genet. 58:1998 only, 1991. 3 C b

GAM7957 297 ITGAL Corbi, A. L.; Larson, R. S.; Kishimoto, T. K.; Springer, T. A.;Morton, C. C.: Chromosomal location of the genes encoding the leukocyteadhesion receptors LFA- 1, Mac- 1 and p150,95: identification of a genecluster involved in cell adhesion. J. Exp. Med. 167: 1597- 1607,1988. 3 C b

GAM7957 297 ITGAL Fischer, A.; Durandy, A.; Sterkers, G.; Griscelli, C.: Role ofthe LFA- 1 molecule in cellular interactions required for antibodyproduction in humans. 3 C b

J. Immun. 136: 3198- 3203, 1986.

GAM7957 297 ITGAL Lu, T. T.; Cyster, J. G.: Integrin- mediated long- term B cell retentionin 3 C b
the splenic marginal zone. Science 297: 409- 412, 2002.

GAM7957 297 ITGAL Marlin, S. D.; Morton, C. C.; Anderson, D. C.; Springer, T. A.: LFA- 1 3 C b
immunodeficiency disease: definition of the genetic defectand chromosomal
mapping of alpha and beta subunits of the lymphocytefunction- associated
antigen 1 (LFA- 1) by complementation in hybridcells. J. Exp. Med. 164: 855-
867, 1986.

GAM7957 297 ITGAL Pischel, K. D.; Marlin, S. D.; Springer, T. A.; Woods, V. L., Jr.;Bluestein, 3 C b
H. G.: Polymorphism of lymphocyte function- associatedantigen- 1
demonstrated by a lupus patient's alloantiserum. J. Clin.Invest. 79: 1607-
1614, 1987.

GAM7957 297 ITGAL Sanchez- Madrid, F.; Nagy, J.; Robbins, E.; Simon, P.; Springer,T. A.: A 3 C b
human leukocyte differentiation antigen family with distinctalpha subunits
and a common beta subunit: the lymphocyte function- associatedantigen (LFA-
1), the C3bi complement receptor (OKM1/Mac- 1), and thep150,95 molecule. J.
Exp. Med. 158: 1785- 1803, 1983.

GAM7957 297 JPH2 Nishi, M.; Mizushima, A.; Nakagawara, K.; Takeshima, H.: Characterizationof 3 C c
human junctophilin subtype genes. Biochem. Biophys. Res. Commun. 273:920-
927, 2000.

GAM7957 297 JPH2 Takeshima, H.; Komazaki, S.; Nishi, M.; Iino, M.; Kangawa, K.:Junctophilins: 3 C c
a novel family of junctional membrane complex proteins. Molec.Cell 6: 11-
22, 2000.

GAM7957 297 KAI1 Baek, S. H.; Ohgi, K. A.; Rose, D. W.; Koo, E. H.; Glass, C. K.;Rosenfeld, 3 C b
M. G.: Exchange of N- CoR corepressor and Tip60 coactivatorcomplexes links
gene expression by NF- kappa- B and beta- amyloid precursorprotein. Cell
110: 55- 67, 2002.

GAM7957 297 KAI1 Dong, J.- T.; Isaacs, W. B.; Barrett, J. C.; Isaacs, J. T.: 3 C b
Genomicorganization of the human KAI1 metastasis- suppressor gene. Genomics
41:25- 32, 1997.

GAM7957 297 KAI1 Dong, J.- T.; Lamb, P. W.; Rinker- Schaeffer, C. W.; Vukanovic, J.;Ichikawa, 3 C b
T.; Isaacs, J. T.; Barrett, J. C.: KAI1, a metastasis suppressorgene for
prostate cancer on human chromosome 11p11.2. Science 268:884- 886, 1995.

GAM7957 297 KAI1 Guo, X.- Z.; Friess, H.; Di Mola, F. F.; Heinicke, J.- M.; Abou- Shady,M.; 3 C b
Graber, H. U.; Baer, H. U.; Zimmermann, A.; Korc, M.; Buchler,M. W.: KAI1, a
new metastasis suppressor gene, is reduced in metastatichepatocellular
carcinoma. Hepatology 28: 1481- 1488, 1998.

GAM7957 297 KAI1 Ichikawa, T.; Ichikawa, Y.; Dong, J.; Hawkins, A. L.; Griffin,C. A.; Isaacs, 3 C b
W. B.; Oshimura, M.; Barrett, J. C.; Isaacs, J. T.: Localization of
metastasis suppressor gene(s) for prostatic cancerto the short arm of human
chromosome 11. Cancer Res. 52: 3486- 3490,1992.

GAM7957 297 KAI1 Ichikawa, T.; Ichikawa, Y.; Isaacs, J. T.: Genetic factors andsuppression of 3 C b
metastatic ability of prostatic cancer. Cancer Res. 51:3788- 3792, 1991.

GAM7957 297 KAI1 Mashimo, T.; Watabe, M.; Hirota, S.; Hosobe, S.; Miura, K.; Tegtmeyer,P. J.; 3 C b
Rinker- Shaeffer, C. W.; Watabe, K.: The expression of theKAI1 gene, a tumor
metastasis suppressor, is directly activated byp53. Proc. Nat. Acad. Sci.
95: 11307- 11311, 1998.

GAM7957 297 KAI1 Miyazaki, T.; Kato, H.; Shitara, Y.; Yoshikawa, M.; Tajima, K.;Masuda, N.; 3 C b
Shouji, H.; Tsukada, K.; Nakajima, T.; Kuwano, H.: Mutationand expression of
the metastasis suppressor gene KAI1 in esophagealsquamous cell carcinoma.

Cancer 89: 955- 962, 2000.

GAM7957 297 KAI1 Virtaneva, K. I.; Angelisova, P.; Baumruker, T.; Horejsi, V.; Nevanlinna,H.; 3 C b
Schroder, J.: The genes for CD37, CD53, and R2, all members ofa novel gene family, are located on different chromosomes. Immunogenetics 37:461- 465, 1993.

GAM7957 297 KCNA7 Bardien- Kruger, S.; Wulff, H.; Arieff, Z.; Brink, P.; Chandy, K.G.; 3 C b
Corfield, V.: Characterisation of the human voltage- gated potassiumchannel gene, KCNA7, a candidate gene for inherited cardiac disorders,and its exclusion as cause of progressive familial heart block I (PFHBI). Europ.J. Hum. Genet. 10: 36- 43, 2002.

GAM7957 297 KCNA7 Kalman, K.; Nguyen, A.; Tseng- Crank, J.; Dukes, I. D.; Chandy,G.; Hustad, 3 C b
C. M.; Copeland, N. G.; Jenkins, N. A.; Mohrenweiser,H.; Brandriff, B.; Cahalan, M.; Gutman, G. A.; Chandy, K. G.: Genomicorganization, chromosomal localization, tissue distribution, and biophysicalcharacterization of a novel mammalian Shaker- related voltage- gatedpotassium channel, Kv1.7. J. Biol. Chem. 273: 5851- 5857, 1998.

GAM7957 297 KCNA7 McPherson, J. D.; Wasmuth, J. J.; Chandy, K. G.; Swanson, R.; Dethlefs,B.; 3 C b
Chandy, G.; Wymore, R.; Ghanshani, S.: Chromosomal localizationof 7 potassium channel genes. (Abstract) Cytogenet. Cell Genet. 58:1979 only, 1991.

GAM7957 297 KCNJ5 Ashford, M. L. J.; Bond, C. T.; Blair, T. A.; Adelman, J. P.:Cloning and 3 C b
functional expression of a rat heart KATP channel. Nature 370:456- 459, 1994.

GAM7957 297 KCNJ5 Bond, C. T.; Pessia, M.; Xia, X.- M.; Lagrutta, A.; Kavanaugh, M.P.; 3 C b
Adelman, J. P.: Cloning and expression of a family of inwardrectifier potassium channels. Receptors Channels 2: 183- 191, 1994.

GAM7957 297 KCNJ5 Tucker, S. J.; James, M. R.; Adelman, J. P.: Assignment of K(ATP)- 1,the 3 C b
cardiac ATP- sensitive potassium channel gene (KCNJ5), to humanchromosome 11q24. Genomics 28: 127- 128, 1995.

GAM7957 297 KCNJ5 Wickman, K.; Seldin, M. F.; Gendler, S. J.; Clapham, D. E.: 3 C b
Partialstructure, chromosome localization, and expression of the mouse Girk4gene. Genomics 40: 395- 401, 1997.

GAM7957 297 KCNK6 Chavez, R. A.; Gray, A. T.; Zhao, B. B.; Kindler, C. H.; Mazurek,M. J.; 3 C c
Mehta, Y.; Forsayeth, J. R.; Yost, C. S.: TWIK- 2, a new weakinward rectifying member of the tandem pore domain potassium channelfamily. J. Biol. Chem. 274: 7887- 7892, 1999.

GAM7957 297 KCNK6 Gray, A. T.; Kindler, C. H.; Sampson, E. R.; Yost, C. S.: Assignmentof KCNK6 3 C c
encoding the human weak inward rectifier potassium channelTWIK- 2 to chromosome band 19q13.1 by radiation hybrid mapping. Cytogenet.Cell Genet. 84: 190- 191, 1999.

GAM7957 297 KCNK6 Pountney, D. J.; Gulkarov, I.; Vega- Saenz de Miera, E.; Holmes,D.; 3 C c
Saganich, M.; Rudy, B.; Artman, M.; Coetzee, W. A.: Identificationand cloning of TWIK- originated similarity sequence (TOSS): a novelhuman 2- pore K(+) channel principal subunit. FEBS Lett. 450: 191- 196,1999.

GAM7957 297 KCNK6 Salinas, M.; Reyes, R.; Lesage, F.; Fosset, M.; Heurteaux, C.;Romey, G.; 3 C c
Lazdunski, M.: Cloning of a new mouse two- P domain channelsubunit and a human homologue with a unique pore structure. J. Biol.Chem. 274: 11751- 11760, 1999.

GAM7957 297 KCNMB3 Behrens, R.; Nolting, A.; Reimann, F.; Schwarz, M.; Waldschutz,R.; Pongs, 3 C b
O.: hKCNMB3 and hKCNMB4, cloning and characterizationof two members of the

large- conductance calcium- activated potassiumchannel beta subunit family. FEBS Lett. 474: 99- 106, 2000.

GAM7957 297 KCNMB3 Brenner, R.; Jegla, T. J.; Wickenden, A.; Liu, Y.; Aldrich, R.W.: Cloning and functional characterization of novel large conductancecalcium- activated potassium channel beta subunits, hKCNMB3 and hKCNMB4. J.Biol. Chem. 275: 6453- 6461, 2000. 3 C b

GAM7957 297 KCNMB3 Riazi, M. A.; Brinkman- Mills, P.; Johnson, A.; Naylor, S. L.; Minoshima,S.; Shimizu, N.; Baldini, A.; McDermid, H. E.: Identification ofa putative regulatory subunit of a calcium- activated potassium channelin the dup(3q) syndrome region and a related sequence on 22q11.2. Genomics 62:90- 94, 1999. 3 C b

GAM7957 297 KCNMB3 Uebele, V. N.; Lagrutta, A.; Wade, T.; Figueroa, D. J.; Liu, Y.;McKenna, E.; Austin, C. P.; Bennett, P. B.; Swanson, R.: Cloningand functional expression of two families of beta- subunits of thelarge conductance calcium- activated K(+) channel. J. Biol. Chem. 275:23211- 23218, 2000. 3 C b

GAM7957 297 KIF1B Gong, T.- W. L.; Burmeister, M.; Lomax, M. I.: The novel gene D4Mil1emaps to mouse chromosome 4 and human chromosome 1p36. Mammalian Genome 7:790- 791, 1996. 3 C b

GAM7957 297 KIF1B Nangaku, M.; Sato- Yoshitake, R.; Okada, Y.; Noda, Y.; Takemura,R.; Yamazaki, H.; Hirokawa, N.: KIF1B, a novel microtubule plus end- directedmonomeric motor protein for transport of mitochondria. Cell 79:1209- 1220, 1994. 3 C b

GAM7957 297 KIF1B Saito, M.; Hayashi, Y.; Suzuki, T.; Tanaka, H.; Hozumi, I.; Tsuji,S.: Linkage mapping of the gene for Charcot- Marie- Tooth disease type2 to chromosome 1p (CMT2A) and the clinical features of CMT2A. Neurology 49:1630- 1635, 1997. 3 C b

GAM7957 297 KIF1B Yang, H. W.; Chen, Y. Z.; Takita, J.; Soeda, E.; Piao, H. Y.; Hayashi,Y.: Genomic structure and mutational analysis of the human KIF1Bgene which is homozygously deleted in neuroblastoma at chromosome1p36.2. Oncogene 20: 5075- 5083, 2001. 3 C b

GAM7957 297 KIF1B Zhao, C.; Takita, J.; Tanaka, Y.; Setou, M.; Nakagawa, T.; Takeda,S.; Yang, H. W.; Terada, S.; Nakata, T.; Takei, Y.; Saito, M.; Tsuji,S.; Hayashi, Y.; Hirokawa, N.: Charcot- Marie- Tooth disease type 2Acaused by mutation in a microtubule motor KIF1B- beta. Cell 105:587- 597, 2001. 3 C b

GAM7957 297 KIF3B Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C b

GAM7957 297 KIF3B Nonaka, S.; Tanaka, Y.; Okada, Y.; Takeda, S.; Harada, A.; Kanai,Y.; Kido, M.; Hirokawa, N.: Randomization of left- right asymmetrydue to loss of nodal cilia generating leftward flow of extraembryonicfluid in mice lacking KIF3B motor protein. Cell 95: 829- 837, 1998. 3 C b

GAM7957 297 KIF3B Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.: KIF3A/B: aheterodimeric kinesin superfamily protein that works as a microtubuleplus end- directed motor for membrane organelle transport. J. CellBiol. 130: 1387- 1399, 1995. 3 C b

GAM7957 297 KLRG1 Butcher, S.; Arney, K. L.; Cook, G. P.: MAFA- L, an ITIM- containingreceptor encoded by the human NK cell gene complex and expressed bybasophils and NK cells. Europ. J. Immun. 28: 3755- 3762, 1998. 3 C c

GAM7957 297 KLRG1 Hanke, T.; Corral, L.; Vance, R. E.; Raulet, D. H.: 2F1 antigen,the mouse homolog of the rat 'mast cell function- associated antigen',is a lectin- 3 C c

like type II transmembrane receptor expressed by naturalkiller cells. Europ. J. Immun. 28: 4409- 4417, 1998.

GAM7957 297 KLRG1 Lamers, M. B. A. C.; Lamont, A. G.; Williams, D. H.: Human MAFAhas alternatively spliced variants. Biochim. Biophys. Acta 1399:209- 212, 1998. 3 C c

GAM7957 297 KLRG1 Voehringer, D.; Kaufmann, M.; Pircher, H.: Genomic structure,alternative splicing, and physical mapping of the killer cell lectin- likereceptor G1 gene (KLRG1), the mouse homologue of MAFA. Immunogenetics 52:206- 211, 2001. 3 C c

GAM7957 297 LDB3 Faulkner, G.; Pallavicini, A.; Formentin, E.; Comelli, A.; Ievolella,C.; Trevisan, S.; Bortoletto, G.; Scannapieco, P.; Salamon, M.; Mouly,V.; Valle, G.; Lanfranchi, G.: ZASP: a new Z- band alternatively splicedPDZ- motif protein. J. Cell Biol. 146: 465- 475, 1999. 3 C c

GAM7957 297 LDB3 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 C c

GAM7957 297 LDB3 Zhou, Q.; Ruiz- Lozano, P.; Martone, M. E.; Chen, J.: Cypher, astriated muscle- restricted PDZ and LIM domain- containing protein,binds to alpha-actinin- 2 and protein kinase C. J. Biol. Chem. 274:19807- 19813, 1999. 3 C c

GAM7957 297 LDLR Aalto- Setala, K.; Helve, E.; Kovanen, P. T.; Kontula, K.: Finnishtype of low density lipoprotein receptor gene mutation (FH- Helsinki)deletes exons encoding the carboxy- terminal part of the receptor andcreates an internalization- defective phenotype. J. Clin. Invest. 84:499- 505, 1989. 3 C b

GAM7957 297 LDLR Aalto- Setala, K.; Koivisto, U.- M.; Miettinen, T. A.; Gylling, H.;Kesaniemi, Y. A.; Savolainen, M.; Pyorala, K.; Ebeling, T.; Mononen,I.; Turtola, H.; Viikari, J.; Kontula, K.: Prevalence and geographicaldistribution of major LDL receptor gene rearrangements in Finland. J.Intern. Med. 231: 227- 234, 1992. 3 C b

GAM7957 297 LDLR Agnello, V.; Abel, G.; Elfahal, M.; Knight, G. B.; Zhang, Q.- X.: Hepatitis C virus and other flaviviridae viruses enter cells vialow density lipoprotein receptor. Proc. Nat. Acad. Sci. 96: 12766- 12771,1999. 3 C b

GAM7957 297 LDLR Allen, J. M.; Thompson, G. R.; Myant, N. B.; Steiner, R.; Oakley,C. M.: Cardiovascular complications of homozygous familial hypercholesterolaemia. Brit.Heart J. 44: 361- 368, 1980. 3 C b

GAM7957 297 LDLR Benlian, P.; Amselem, S.; Loux, N.; Pastier, D.; Giraud, G.; deGennes, J. L.; Turpin, G.; Monnier, L.; Rieu, D.; Douste- Blazy, P.;Dastugue, B.; Goossens, M.; Junien, C.: A LDL receptor gene homozygousmutation: PCR amplification, direct genomic sequencing, associatedhaplotype, rapid screening for frequency. Ann. Genet. 33: 65- 69,1990. 3 C b

GAM7957 297 LDLR Bertolini, S.; Lelli, N.; Coviello, D. A.; Ghisellini, M.; Masturzo,P.; Tiozzo, R.; Elicio, N.; Gaddi, A.; Calandra, S.: A large deletionin the LDL receptor gene- - the cause of familial hypercholesterolemiain three Italian families: a study that dates back to the 17th century(FH- Pavia). Am. J. Hum. Genet. 51: 123- 134, 1992. 3 C b

GAM7957 297 LDLR Betard, C.; Kessling, A. M.; Roy, M.; Chamberland, A.; Lussier- Cacan,S.; Davignon, J.: Molecular genetic evidence for a founder effectin familial hypercholesterolemia among French Canadians. Hum. Genet. 88:529- 536, 1992. 3 C b

GAM7957 297 LDLR Boehnke, M.; Arnheim, N.; Li, H.; Collins, F. S.: Fine- structuregenetic mapping of human chromosomes using the polymerase chain reactionon single sperm: experimental design considerations. Am. J. Hum.Genet. 45: 21- 32, 1989. 3 C b

GAM7957 297 LDLR Brink, P. A.; Steyn, L. T.; Coetzee, G. A.; van der Westhuyzen,D. R.: 3 C b
Familial hypercholesterolemia in South African Afrikaners:PvuII and StuI DNA
polymorphisms in the LDL- receptor gene consistentwith a predominating
founder gene effect. Hum. Genet. 77: 32- 35,1987.

GAM7957 297 LDLR Brown, M. S.; Goldstein, J. L.: Analysis of a mutant strain ofhuman 3 C b
fibroblasts with a defect in the internalization of receptor- boundlow
density lipoproteins. Cell 9: 663- 674, 1976.

GAM7957 297 LDLR Brown, M. S.; Goldstein, J. L.: Familial hypercholesterolemia:defective 3 C b
binding of lipoproteins to cultured fibroblasts associatedwith impaired
regulation of 3- hydroxy- 3- methylglutaryl coenzyme atreductase activity.
Proc. Nat. Acad. Sci. 71: 788- 792, 1974.

GAM7957 297 LDLR Brown, M. S.; Goldstein, J. L.: Receptor- mediated endocytosis:insights from 3 C b
the lipoprotein receptor system. Proc. Nat. Acad. Sci. 76:3330- 3337, 1979.

GAM7957 297 LDLR Davis, C. G.; Lehrman, M. A.; Russell, D. W.; Anderson, R. G.W.; Brown, M. 3 C b
S.; Goldstein, J. L.: The J.D. mutation in familialhypercholesterolemia:
amino acid substitution in cytoplasmic domainimpedes internalization of LDL
receptors. Cell 45: 15- 24, 1986.

GAM7957 297 LDLR De Braekeleer, M.: Hereditary disorders in Saguenay- Lac- St- Jean(Quebec, 3 C b
Canada). Hum. Hered. 41: 141- 146, 1991.

GAM7957 297 LDLR Defesche, J. C.; Kastelein, J. J. P.: Molecular epidemiologyof familial 3 C b
hypercholesterolaemia. (Letter) Lancet 352: 1643- 1644,1998.

GAM7957 297 LDLR Defesche, J. C.; van de Ree, M. A.; Kastelein, J. J. P.; van Diermen,D. E.; 3 C b
Janssens, N. W. E.; van Doormaal, J. J.; Hayden, M. R.: Detectionof the
pro664- to- leu mutation in the low- density lipoprotein receptorand its
relation to lipoprotein(a) levels in patients with
familialhypercholesterolemia of Dutch ancestry from The Netherlands and
Canada. Clin.Genet. 42: 273- 280, 1992.

GAM7957 297 LDLR Defesche, J. C.; van Diermen, D. E.; Lansberg, P. J.; Lamping,R. J.; Reymer, 3 C b
P. W. A.; Hayden, M. R.; Kastelein, J. J. P.: SouthAfrican founder mutations
in the low- density lipoprotein receptorgene causing familial
hypercholesterolemia in the Dutch population. Hum.Genet. 92: 567- 570, 1993.

GAM7957 297 LDLR Durst, R.; Colombo, R.; Shpitzen, S.; Ben Avi, L.; Friedlander,Y.; Wexler, 3 C b
R.; Raal, F. J.; Marais, D. A.; Defesche, J. C.; Mandelshtam,M. Y.; Kotze,
M. J.; Leitersdorf, E.; Meiner, V.: Recent origin andspread of a common
Lithuanian mutation, G197del LDLR, causing familialhypercholesterolemia:
positive selection is not always necessary toaccount for disease incidence
among Ashkenazi Jews. Am. J. Hum. Genet. 68:1172- 1188, 2001.

GAM7957 297 LDLR Ekstrom, U.; Abrahamson, M.; Floren, C.- H.; Tollig, H.; Wettrell,G.; 3 C b
Nilsson, G.; Sun, X.- M.; Soutar, A. K.; Nilsson- Ehle, P.: Anindividual
with a healthy phenotype in spite of a pathogenic LDL receptormutation
(C240F). Clin. Genet. 55: 332- 339, 1999.

GAM7957 297 LDLR Elston, R. C.; Namboodiri, K. K.; Go, R. C. P.; Siervogel, R.M.; Glueck, C. 3 C b
J.: Probable linkage between essential familial hypercholesterolemiaand
third complement component (C3). Cytogenet. Cell Genet. 16:294- 297, 1976.

GAM7957 297 LDLR Esser, V.; Russell, D. W.: Transport- deficient mutations in thelow density 3 C b
lipoprotein receptor: alterations in the cysteine- richand cysteine- poor
regions of the protein block intracellular transport. J.Biol. Chem. 263:
13276- 13281, 1988.

GAM7957 297 LDLR Feussner, G.; Dobmeyer, J.; Nissen, H.; Hansen, T. S.: UnusualXanthomas in a 3 C b
young patient with heterozygous familial hypercholesterolemiaand type III

hyperlipoproteinemia. Am. J. Med. Genet. 65: 149- 154,1996.

GAM7957 297 LDLR Francke, U.; Brown, M. S.; Goldstein, J. L.: Assignment of thehuman gene for 3 C b
the low density lipoprotein receptor to chromosome19: synteny of a receptor,
a ligand, and a genetic disease. Proc.Nat. Acad. Sci. 81: 2826- 2830, 1984.

GAM7957 297 LDLR Frank, S. L.; Taylor, B. A.; Lusis, A. J.: Linkage of the mouseLDL receptor 3 C b
gene on chromosome 9. Genomics 5: 646- 648, 1989.

GAM7957 297 LDLR Fumeron, F.; Grandchamp, B.; Fricker, J.; Krempf, M.; Wolf, L.- M.;Khayat, 3 C b
M.- C.; Boiffard, O.; Apfelbaum, M.: Presence of the FrenchCanadian deletion
in a French patient with familial hypercholesterolemia.(Letter) New Eng. J.
Med. 326: 69 only, 1992.

GAM7957 297 LDLR Gilbert, W.: Genes- in- pieces revisited. Science 228: 823- 824,1985. 3 C b

GAM7957 297 LDLR Goldfarb, L. G.; Petersen, R. B.; Tabaton, M.; Brown, P.; LeBlanc,A. C.; 3 C b
Montagna, P.; Cortelli, P.; Julien, J.; Vital, C.; Pendelbury,W. W.; Haltia,
M.; Wills, P. R.; and 9 others: Fatal familial insomniaand familial
Creutzfeldt- Jakob disease: disease phenotype determinedby a DNA
polymorphism. Science 258: 806- 808, 1992.

GAM7957 297 LDLR Goldstein, J. L.; Brown, M. S.; Stone, N. J.: Genetics of theLDL receptor: 3 C b
evidence that the mutations affecting binding and internalizationare
allelic. Cell 12: 629- 641, 1977.

GAM7957 297 LDLR Goldstein, J. L.; Dana, S. E.; Brunschede, G. Y.; Brown, M. S.: Genetic 3 C b
heterogeneity in familial hypercholesterolemia: evidencefor two different
mutations affecting functions of low- density lipoproteinreceptor. Proc.
Nat. Acad. Sci. 72: 1092- 1096, 1975.

GAM7957 297 LDLR Graadt van Roggen, F.; van der Westhuyzen, D. R.; Marais, A. D.;Gevers, W.; 3 C b
Coetzee, G. A.: Low density lipoprotein receptor foundermutations in
Afrikaner familial hypercholesterolaemic patients: acomparison of two
geographical areas. Hum. Genet. 88: 204- 208, 1991.

GAM7957 297 LDLR Gudnason, V.; King- Underwood, L.; Seed, M.; Sun, X.- M.; Soutar,A. K.; 3 C b
Humphries, S. E.: Identification of recurrent and novel mutationsin exon 4
of the LDL receptor gene in patients with familial hypercholesterolemiain
the United Kingdom. Arteriosclerosis Thromb. 13: 56- 63, 1993.

GAM7957 297 LDLR Gudnason, V.; Sigurdsson, G.; Nissen, H.; Humphries, S. E.: Commonfounder 3 C b
mutation in the LDL receptor gene causing familial hypercholesterolemiain
the Icelandic population. Hum. Mutat. 10: 36- 44, 1997.

GAM7957 297 LDLR Henderson, H. E.; Berger, G. M. B.; Marais, A. D.: A new LDLreceptor gene 3 C b
deletion mutation in the South African population. Hum.Genet. 80: 371- 374,
1988.

GAM7957 297 LDLR Hobbs, H. H.: Personal Communication. Dallas, Tex. 12/1/1990. 3 C b

GAM7957 297 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: Molecular geneticsof the LDL 3 C b
receptor gene in familial hypercholesterolemia. Hum. Mutat. 1:445- 466,
1992.

GAM7957 297 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.; Russell, D. W.:Deletion of 3 C b
exon encoding cysteine- rich repeat of low density lipoproteinreceptor
alters its binding specificity in a subject with
familialhypercholesterolemia. J. Biol. Chem. 261: 13114- 13120, 1986.

GAM7957 297 LDLR Hobbs, H. H.; Brown, M. S.; Russell, D. W.; Davignon, J.; Goldstein,J. L.: 3 C b
Deletion in the gene for the low- density- lipoprotein receptorin a majority
of French Canadians with familial hypercholesterolemia. NewEng. J. Med. 317:
734- 737, 1987.

GAM7957 297 LDLR Hobbs, H. H.; Lehrman, M. A.; Yamamoto, T.; Russell, D. W.: Polymorphismand 3 C b

evolution of Alu sequences in the human low density lipoproteinreceptor gene. Proc. Nat. Acad. Sci. 82: 7651- 7655, 1985.

GAM7957 297 LDLR Hobbs, H. H.; Leitersdorf, E.; Goldstein, J. L.; Brown, M. S.;Russell, D. W.: Multiple CRM- mutations in familial hypercholesterolemia:evidence for 13 alleles, including four deletions. J. Clin. Invest. 81:909- 917, 1988. 3 C b

GAM7957 297 LDLR Hobbs, H. H.; Leitersdorf, E.; Leffert, C. C.; Cryer, D. R.; Brown,M. S.; Goldstein, J. L.: Evidence for a dominant gene that suppresseshypercholesterolemia in a family with defective low density lipoproteinreceptors. J. Clin. Invest. 84: 656- 664, 1989. 3 C b

GAM7957 297 LDLR Hobbs, H. H.; Russell, D. W.; Brown, M. S.; Goldstein, J. L.:The LDL receptor locus in familial hypercholesterolemia: mutationalanalysis of a membrane protein. Annu. Rev. Genet. 24: 133- 170, 1990. 3 C b

GAM7957 297 LDLR Horsthemke, B.; Beisiegel, U.; Dunning, A.; Havinga, J. R.; Williamson,R.; Humphries, S.: Unequal crossing- over between two Alu- repetitiveDNA sequences in the low- density- lipoprotein- receptor gene: a possiblemechanism for the defect in a patient with familial hypercholesterolaemia. Europ.J. Biochem. 164: 77- 81, 1987. 3 C b

GAM7957 297 LDLR Horsthemke, B.; Dunning, A.; Humphries, S.: Identification ofdeletions in the human low density lipoprotein receptor gene. J.Med. Genet. 24: 144- 147, 1987. 3 C b

GAM7957 297 LDLR Horsthemke, B.; Kessling, A. M.; Seed, M.; Wynn, V.; Williamson,R.; Humphries, S. E.: Identification of a deletion in the low densitylipoprotein (LDL) receptor gene in a patient with familial hypercholesterolaemia. Hum.Genet. 71: 75- 78, 1985. 3 C b

GAM7957 297 LDLR Jensen, H. K.; Jensen, T. G.; Faergeman, O.; Jensen, L. G.; Andresen,B. S.; Corydon, M. J.; Andreasen, P. H.; Hansen, P. S.; Heath, F.;Bolund, L.; Gregersen, N.: Two mutations in the same low- densitylipoprotein receptor allele act in synergy to reduce receptor functionin heterozygous familial hypercholesterolemia. Hum. Mutat. 9: 437- 444,1997. 3 C b

GAM7957 297 LDLR Jensen, J. M.; Kruse, T. A.; Brorholt- Petersen, J. U.; Christiansen,T. M.; Jensen, H. K.; Kolvraa, S.; Faergeman, O.: Linking genotypeto aorto- coronary atherosclerosis: a model using familial hypercholesterolemiaand aorto- coronary calcification. Ann. Hum. Genet. 63: 511- 520,1999. 3 C b

GAM7957 297 LDLR Kajinami, K.; Fujita, H.; Koizumi, J.; Mabuchi, H.; Takeda, R.;Ohta, M.: Genetically determined mild type of familial hypercholesterolemiaincluding normocholesterolemic patients: FH- Tonami- 2. Circulation 80(suppl. 2): 278 only, 1989. 3 C b

GAM7957 297 LDLR Kajinami, K.; Mabuchi, H.; Itoh, H.; Michishita, I.; Takeda, M.;Wakasugi, T.; Koizumi, J.; Takeda, R.: New variant of low densitylipoprotein receptor gene FH- Tonami. Arteriosclerosis 8: 187- 192,1988. 3 C b

GAM7957 297 LDLR Khachadurian, A. K.: The inheritance of essential familial hypercholesterolemia. Am.J. Med. 37: 402- 407, 1964. 3 C b

GAM7957 297 LDLR Kingsley, D. M.; Krieger, M.: Receptor- mediated endocytosis oflow density lipoprotein: somatic cell mutants define multiple genesrequired for expression of surface- receptor activity. Proc. Nat.Acad. Sci. 81: 5454- 5458, 1984. 3 C b

GAM7957 297 LDLR Knight, B. L.; Gavigan, S. J. P.; Soutar, A. K.; Patel, D. D.: Defective processing and binding of low- density lipoprotein receptorsin fibroblasts from a familial hypercholesterolaemic subject. Europ.J. Biochem. 179: 693- 698, 1989. 3 C b

GAM7957 297 LDLR Knoblauch, H.; Muller- Myhsok, B.; Busjahn, A.; Ben Avi, L.; Bahring,S.; 3 C b
Baron, H.; Heath, S. C.; Uhlmann, R.; Faulhaber, H.- D.; Shpitzen,S.; Aydin,
A.; Reshef, A.; and 11 others: A cholesterol- loweringgene maps to
chromosome 13q. Am. J. Hum. Genet. 66: 157- 166, 2000.

GAM7957 297 LDLR Koivisto, U.- M.; Hubbard, A. L.; Mellman, I.: A novel cellularphenotype for 3 C b
familial hypercholesterolemia due to a defect in polarizedtargeting of LDL
receptor. Cell 105: 575- 585, 2001.

GAM7957 297 LDLR Koivisto, U.- M.; Turtola, H.; Aalto- Setala, K.; Top, B.; Frants,R. R.; 3 C b
Kovanen, P. T.; Syvanen, A.- C.; Kontula, K.: The
familialhypercholesterolemia (FH)- North Karelia mutation of the low
densitylipoprotein receptor gene deletes seven nucleotides of exon 6 andis a
common cause of FH in Finland. J. Clin. Invest. 90: 219- 228,1992.

GAM7957 297 LDLR Koivisto, U.- M.; Viikari, J. S.; Kontula, K.: Molecular characterizationof 3 C b
minor gene rearrangements in Finnish patients with heterozygousfamilial
hypercholesterolemia: identification of two common missensemutations
(Gly823- to- Asp and Leu380- to- His) and eight rare mutationsof the LDL
receptor gene. Am. J. Hum. Genet. 57: 789- 797, 1995.

GAM7957 297 LDLR Komuro, I.; Kato, H.; Nakagawa, T.; Takahashi, K.; Mimori, A.;Takeuchi, F.; 3 C b
Nishida, Y.; Miyamoto, T.: Case report: the longest- livedpatient with
homozygous familial hypercholesterolemia secondary toa defect in
internalization of the LDL receptor. Am. J. Med. Sci. 294:341- 345, 1987.

GAM7957 297 LDLR Kotze, M. J.; Langenhoven, E.; Retief, A. E.; Steyn, K.; Marais,M. P.; 3 C b
Grobbelaar, J. J.; Oosthuizen, C. J. J.; Weich, H. F. H.; Benade,A. J. S.:
Haplotype associations of three DNA polymorphisms at thehuman low density
lipoprotein receptor gene locus in familial hypercholesterolemia. J.Med.
Genet. 24: 750- 755, 1987.

GAM7957 297 LDLR Kotze, M. J.; Langenhoven, E.; Warnich, L.; du Plessis, L.; Retief,A. E.: 3 C b
The molecular basis and diagnosis of familial hypercholesterolaemiain South
African Afrikaners. Ann. Hum. Genet. 55: 115- 121, 1991.

GAM7957 297 LDLR Kotze, M. J.; Theart, L.; Peeters, A.; Langenhoven, E.: A denovo duplication 3 C b
in the low density lipoprotein receptor gene. Hum.Mutat. 6: 181- 183, 1995.

GAM7957 297 LDLR Kotze, M. J.; Warnich, L.; Langenhoven, E.; du Plessis, L.; Retief,A. E.: An 3 C b
exon 4 mutation identified in the majority of South Africanfamilial
hypercholesterolaemics. J. Med. Genet. 27: 298- 302, 1990.

GAM7957 297 LDLR Landsberger, D.; Meiner, V.; Reshef, A.; Levy, Y.; van der Westhuyzen,D. R.; 3 C b
Coetzee, G. A.; Leitersdorf, E.: A nonsense mutation in theLDL receptor gene
leads to familial hypercholesterolemia in the Druzesect. Am. J. Hum. Genet.
50: 427- 433, 1992.

GAM7957 297 LDLR Langlois, S.: Personal Communication. Vancouver, British Columbia,Canada 3 C b
1989.

GAM7957 297 LDLR Langlois, S.; Kastelein, J. J. P.; Hayden, M. R.: Characterizationof six 3 C b
partial deletions in the low- density- lipoprotein (LDL) receptorgene
causing familial hypercholesterolemia (FH). Am. J. Hum. Genet. 43:60- 68,
1988.

GAM7957 297 LDLR Lee, W. K.; Haddad, L.; Macleod, M. J.; Dorrance, A. M.; Wilson,D. J.; 3 C b
Gaffney, D.; Dominiczak, M. H.; Packard, C. J.; Day, I. N.;Humphries, S. E.;
Dominiczak, A. F.: Identification of a common lowdensity lipoprotein
receptor mutation (C163Y) in the West of Scotland. J.Med. Genet. 35: 573-
578, 1998.

GAM7957 297 LDLR Lehrman, M. A.; Goldstein, J. L.; Brown, M. S.; Russell, D. W.;Schneider, W. 3 C b

J.: Internalization- defective LDL receptors producedby genes with nonsense and frameshift mutations that truncate thecytoplasmic domain. Cell 41: 735-743, 1985.

GAM7957 297 LDLR Lehrman, M. A.; Goldstein, J. L.; Russell, D. W.; Brown, M. S.: Duplication 3 C b of seven exons in LDL receptor gene caused by Alu- Alurecombination in a subject with familial hypercholesterolemia. Cell 48:827- 835, 1987.

GAM7957 297 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Alu- Alu 3 C b recombination deletes splice acceptor sites and producessecreted low density lipoprotein receptor in a subject with familialhypercholesterolemia. J. Biol. Chem. 262: 3354- 3361, 1987.

GAM7957 297 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Exon- Alu 3 C b recombination deletes 5 kilobases from the low densitylipoprotein receptor gene, producing a null phenotype in familialhypercholesterolemia. Proc. Nat. Acad. Sci. 83: 3679- 3683, 1986.

GAM7957 297 LDLR Lehrman, M. A.; Schneider, W. J.; Sudhof, T. C.; Brown, M. S.;Goldstein, J. 3 C b L.; Russell, D. W.: Mutation in LDL receptor: Alu- Alurecombination deletes exons encoding transmembrane and cytoplasmicdomains. Science 227: 140- 146, 1985.

GAM7957 297 LDLR Leitersdorf, E.; Hobbs, H. H.: Personal Communication. Dallas,Tex. 12/1990. 3 C b

GAM7957 297 LDLR Leitersdorf, E.; Hobbs, H. H.; Fourie, A. M.; Jacobs, M.; vander Westhuyzen, 3 C b D. R.; Coetzee, G. A.: Deletion in the first cysteine- richrepeat of low-density lipoprotein receptor impairs its transport butnot lipoprotein binding in fibroblasts from a subject with familialhypercholesterolemia. Proc. Nat. Acad. Sci. 85: 7912- 7916, 1988.

GAM7957 297 LDLR Leitersdorf, E.; Tobin, E. J.; Davignon, J.; Hobbs, H. H.: Commonlow- 3 C b density lipoprotein receptor mutations in the French Canadianpopulation. J. Clin. Invest. 85: 1014- 1023, 1990.

GAM7957 297 LDLR Leitersdorf, E.; van der Westhuyzen, D. R.; Coetzee, G. A.; Hobbs,H. H.: Two 3 C b common low density lipoprotein receptor gene mutationscause familial hypercholesterolemia in Afrikaners. J. Clin. Invest. 84:954- 961, 1989.

GAM7957 297 LDLR Lelli, N.; Ghisellini, M.; Calandra, S.; Gaddi, A.; Ciarrocchi,A.; Coviello, 3 C b D. A.; Bertolini, S.: Duplication of exons 13, 14 and15 of the LDL- receptor gene in a patient with heterozygous familialhypercholesterolemia. Hum. Genet. 86: 359- 362, 1991.

GAM7957 297 LDLR Leren, T. P.; Solberg, K.; Rodningen, O. K.; Tonstad, S.; Ose,L.: Two 3 C b founder mutations in the LDL receptor gene in Norwegian familialhypercholesterolemia subjects. Atherosclerosis 111: 175- 182, 1994.

GAM7957 297 LDLR Li, H.; Gyllensten, U. B.; Cui, X.; Saiki, R. K.; Erlich, H. A.;Arnheim, N.: 3 C b Amplification and analysis of DNA sequences in singlehuman sperm and diploid cells. Nature 335: 414- 417, 1988.

GAM7957 297 LDLR Lindgren, V.; Luskey, K. L.; Russell, D. W.; Francke, U.: Humangenes 3 C b involved in cholesterol metabolism: chromosomal mapping of theloci for the low density lipoprotein receptor and 3- hydroxy- 3- methylglutaryl-coenzymeA reductase with cDNA probes. Proc. Nat. Acad. Sci. 82: 8567-8571,1985.

GAM7957 297 LDLR Loux, N.; Benlian, P.; Pastier, D.; Boileau, C.; Cambou, J. P.;Monnier, L.; 3 C b Percheron, C.; Junien, C.: Recurrent mutation at aa792 in the LDL receptor gene in a French patient. Hum. Genet. 87:373- 375, 1991.

GAM7957 297 LDLR Ma, Y. H.; Betard, C.; Roy, M.; Davignon, J.; Kessling, A. M.: 3 C b Identification of a second 'French Canadian' LDL receptor gene deletionand

development of a rapid method to detect both deletions. Clin.Genet. 36: 219-228, 1989.

GAM7957 297 LDLR Maartmann- Moe, K.; Wang, H. S.; Donald, L. J.; Hamerton, J. L.;Berg, K.: 3 C b
Data from hybrid cell lines raise the possibility thatfactors controlling the low density lipoprotein receptor activitymay reside on human chromosome 21, 5 or both. (Abstract) Cytogenet.Cell Genet. 32: 295- 296, 1982.

GAM7957 297 LDLR Mandelshtam, M.; Chakir, K.; Shevtsov, S.; Golubkov, V.; Skobeleva,N.; 3 C b
Lipovetsky, B.; Konstantinov, V.; Denisenko, A.; Gaitskhoki, V.;Schwartz, E.: Prevalence of Lithuanian mutation among St. PetersburgJews with familial hypercholesterolemia. Hum. Mutat. 12: 255- 258,1998.

GAM7957 297 LDLR Meiner, V.; Landsberger, D.; Berkman, N.; Reshef, A.; Segal, P.;Seftel, H. 3 C b
C.; van der Westhuyzen, D. R.; Jeenah, M. S.; Coetzee,G. A.; Leitersdorf, E.: A common Lithuanian mutation causing familialhypercholesterolemia in Ashkenazi Jews. Am. J. Hum. Genet. 49: 443- 449,1991.

GAM7957 297 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamoto, A.: Analysisof a recycling- 3 C b
impaired mutant of low density lipoprotein receptorin familial hypercholesterolemia. J. Biol. Chem. 264: 16584- 16590,1989.

GAM7957 297 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamura, T.; Yamamoto,A.: A point 3 C b
mutation of low- density- lipoprotein receptor causingrapid degradation of the receptor. Europ. J. Biochem. 210: 1- 7,1992.

GAM7957 297 LDLR Moorjani, S.; Roy, M.; Torres, A.; Betard, C.; Gagne, C.; Lambert,M.; Brun, 3 C b
D.; Davignon, J.; Lupien, P.: Mutations of low- density- lipoprotein-receptorgene, variation in plasma cholesterol, and expression of coronaryheart disease in homozygous familial hypercholesterolaemia. Lancet 341:1303- 1306, 1993.

GAM7957 297 LDLR Oppenheim, A.; Friedlander, Y.; Dann, E. J.; Berkman, N.; Schwartz,S. P.; 3 C b
Leitersdorf, E.: Hypercholesterolemia in five Israeli Christian-Arabkindreds is caused by the 'Lebanese' allele at the low density lipoproteinreceptor gene locus and by an additional independent major factor. Hum.Genet. 88: 75- 84, 1991.

GAM7957 297 LDLR Pisciotta, L.; Cantafora, A.; De Stefano, F.; Langheim, S.; Calandra,S.; 3 C b
Bertolini, S.: A 'de novo' mutation of the LDL- receptor geneas the cause of familial hypercholesterolemia. Biochim. Biophys.Acta 1587: 7- 11, 2002.

GAM7957 297 LDLR Rodningen, O. K.; Rosby, O.; Tonstad, S.; Ose, L.; Berg, K.; Leren,T. P.: A 3 C b
9.6 kilobase deletion in the low density lipoprotein receptorgene in Norwegian familial hypercholesterolemia subjects. Clin. Genet. 42:288- 295, 1992.

GAM7957 297 LDLR Rubinsztein, D. C.; Coetzee, G. A.; Marais, A. D.; Leitersdorf,E.; Seftel, 3 C b
H. C.; van der Westhuyzen, D. R.: Identification andproperties of the proline- 644- to- leucine mutant LDL receptor in SouthAfricans of Indian origin. J. Lipid Res. 33: 1647- 1655, 1992.

GAM7957 297 LDLR Rudiger, N. S.; Heinsvig, E. M.; Hansen, F. A.; Faergeman, O.;Bolund, L.; 3 C b
Gregersen, N.: DNA deletions in the low density lipoprotein(LDL) receptor gene in Danish families with familial hypercholesterolemia. Clin.Genet. 39: 451- 462, 1991.

GAM7957 297 LDLR Ruffner, D. E.; Sprung, C. N.; Minghetti, P. P.; Gibbs, P. E.M.; Dugaiczyk, 3 C b
A.: Invasion of the human albumin- alpha- fetoproteingene family by Alu, Kpn, and two novel repetitive DNA elements. Molec.Biol. Evol. 4: 1- 9, 1987.

GAM7957 297 LDLR Russell, D. W.; Lehrman, M. A.; Sudhof, T. C.; Yamamoto, T.; Davis,C. G.; 3 C b
Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: The LDL receptorin familial

hypercholesterolemia: use of human mutations to dissecta membrane protein. Cold Spring Harbor Symp. Quant. Biol. 51: 811- 819,1986.

GAM7957 297 LDLR Russell, D. W.; Schneider, W. J.; Yamamoto, T.; Luskey, K. L.;Brown, M. S.; 3 C b
Goldstein, J. L.: Domain map of the LDL receptor: sequencehomology with the epidermal growth factor precursor. Cell 37: 577- 585,1984.

GAM7957 297 LDLR Savov, A.; Angelicheva, D.; Balassopoulou, A.; Jordanova, A.;Noussia- 3 C b
Arvanitakis, S.; Kalaydjieva, L.: Double mutant alleles:are they rare? Hum. Molec. Genet. 4: 1169- 1171, 1995.

GAM7957 297 LDLR Schuster, H.; Manke, C.; Fischer, J.; Keller, C.; Wolfram, G.;Zollner, N.: 3 C b
Identification of the valine 408 to methionine mutationin the LDL receptor in a Greek patient with homozygous familial hypercholesterolemia. Clin.Genet. 48: 90- 92, 1995.

GAM7957 297 LDLR Schuster, H.; Ostwald, P.; Keller, P.; Wolfram, G.; Keller, C.: 3 C b
Identification of the serine- 156 to leucine mutation in the low-densitylipoprotein receptor in a German family with familial hypercholesterolemia. Clin.Investig. 71: 172- 175, 1993.

GAM7957 297 LDLR Seftel, H. C.; Baker, S. G.; Sandler, M. P.; Forman, M. B.; Joffe,B. I.; 3 C b
Mendelsohn, D.; Jenkins, T.; Mieny, C. J.: A host of hypercholesterolaemichomozygotes in South Africa. Brit. Med. J. 281: 633-636, 1980.

GAM7957 297 LZTS1 Ishii, H.; Baffa, R.; Numata, S.- I.; Murakumo, Y.; Rattan, S.;Inoue, H.; 3 C c
Mori, M.; Fidanza, V.; Alder, H.; Croce, C. M.: The FEZ1gene at chromosome 8p22 encodes a leucine- zipper protein, and itsexpression is altered in multiple human tumors. Proc. Nat. Acad.Sci. 96: 3928- 3933, 1999.

GAM7957 297 LZTS1 Ishii, H.; Vecchione, A.; Murakumo, Y.; Baldassarre, G.; Numata,S.; 3 C c
Trapasso, F.; Alder, H.; Baffa, R.; Croce, C. M.: FEZ1/LZTS1gene at 8p22 suppresses cancer cell growth and regulates mitosis. Proc.Nat. Acad. Sci. 98: 10374- 10379, 2001.

GAM7957 297 MAFF Dunham, I.; Shimizu, N.; Roe, B. A.; Chissoe, S.; Hunt, A. R.;Collins, J. 3 C c
E.; Bruskiewich, R.; Beare, D. M.; Clamp, M.; Smink, L.J.; Ainscough, R.; Almeida, J. P.; and 205 others: The DNA sequenceof human chromosome 22. Nature 402: 489- 495, 1999.

GAM7957 297 MAFF Inoue, T.; Kimura, T.; Azuma, C.; Inazawa, J.; Takemura, M.; Kikuchi,T.; 3 C c
Kubota, Y.; Ogita, K.; Saji, F.: Structural organization of thehuman oxytocin receptor gene. J. Biol. Chem. 269: 32451- 32456, 1994.

GAM7957 297 MAFF Kimura, T.; Ivell, R.; Rust, W.; Mizumoto, Y.; Ogita, K.; Kusui,C.; 3 C c
Matsumura, Y.; Azuma, C.; Murata, Y.: Molecular cloning of ahuman MafF homologue, which specifically binds to the oxytocin receptorgene in term myometrium. Biochem. Biophys. Res. Commun. 264: 86- 92,1999.

GAM7957 297 MAP3K9 Dorow, D. S.; Devereux, L.; Dietzsch, E.; De Kretser, T.: Identificationof a 3 C b
new family of human epithelial protein kinases containing twoleucine/isoleucine- zipper domains. Europ. J. Biochem. 213: 701-710,1993.

GAM7957 297 MAP3K9 Hanks, S. K.: Eukaryotic protein kinases. Curr. Opin. Struct.Biol. 1: 369- 3 C b
383, 1991.

GAM7957 297 MAP4 Chapin, S. J.; Bulinski, J. C.: Non- neuronal 210 x 10(3) M(r)microtubule- 3 C c
associated protein (MAP4) contains a domain homologousto the microtubule-binding domains of neuronal MAP2 and tau. J. CellSci. 98: 27- 36, 1991.

GAM7957 297 MAP4 Chapin, S. J.; Lue, C.- M.; Yu, M. T.; Bulinski, J. C.: 3 C c
Differentialexpression of alternatively spliced forms of MAP4: a repertoire

ofstructurally different microtubule- binding domains. Biochemistry 34:2289-2301, 1995.

GAM7957 297 MAP4 Mangan, M. E.; Olmsted, J. B.: The gene for microtubule- associatedprotein 4 (Mtap4) maps to the distal region of mouse chromosome 9. MammalianGenome 7: 918- 925, 1996. 3 C c

GAM7957 297 MAP4 West, R. R.; Tenbarge, K. M.; Olmsted, J. B.: A model for microtubule-associatedprotein 4 structure: domains defined by comparisons of human, mouse,and bovine sequences. J. Biol. Chem. 266: 21886- 21896, 1991. 3 C c

GAM7957 297 MCM4 Connelly, M. A.; Zhang, H.; Kieleczawa, J.; Anderson, C. W.: Thepromoters for human DNA- PK(cs) (PRKDC) and MCM4: divergently transcribedgenes located at chromosome 8 band q11. Genomics 47: 71- 83, 1998. 3 C b

GAM7957 297 MCM4 Hu, B.; Burkhart, R.; Schulte, D.; Musahl, C.; Knippers, R.: TheP1 family: a new class of nuclear mammalian proteins related to theyeast Mcm replication proteins. Nucleic Acids Res. 21: 5289- 5293,1993. 3 C b

GAM7957 297 MCM4 Ladenburger, E. M.; Fackelmayer, F. O.; Hameister, H.; Knippers,R.: MCM4 and PRKDC, human genes encoding proteins MCM4 and DNA- PKcs,are close neighbours located on chromosome 8q12- q13. Cytogenet. CellGenet. 77: 268- 270, 1997. 3 C b

GAM7957 297 MCM4 Musahl, C.; Schulte, D.; Burkhart, R.; Knippers, R.: A human homologueof the yeast replication protein Cdc21: interactions with other Mcmproteins. Europ. J. Biochem. 230: 1096- 1101, 1995. 3 C b

GAM7957 297 MCM4 Satoh, T.; Tsuruga, H.; Yabuta, N.; Ishidate, M., Jr.; Nojima,H.: Assignment of the human CDC21 (MCM4) gene to chromosome 8q11.2. Genomics 46:525- 526, 1997. 3 C b

GAM7957 297 MS4A2 Folster- Holst, R.; Moises, H. W.; Yang, L.; Fritsch, W.; Weissenbach,J.; Christophers, E.: Linkage between atopy and the IgE high- affinityreceptor gene at 11q13 in atopic dermatitis families. Hum. Genet. 102:236- 239, 1998. 3 C b

GAM7957 297 MS4A2 Hill, M. R.; Cookson, W. O. C. M.: A new variant of the beta subunitof the high- affinity receptor for immunoglobulin E (Fc- epsilon- RI- betaE237G): associations with measures of atopy and bronchial hyper- responsiveness. Hum.Molec. Genet. 5: 959- 962, 1996. 3 C b

GAM7957 297 MS4A2 Hizawa, N.; Yamaguchi, E.; Furuya, K.; Ohnuma, N.; Kodama, N.;Kojima, J.; Ohe, M.; Kawakami, Y.: Association between high serumtotal IgE levels and D11S97 on chromosome 11q13 in Japanese subjects. J.Med. Genet. 32: 363- 369, 1995. 3 C b

GAM7957 297 MS4A2 Hupp, K.; Siwarski, D.; Mock, B. A.; Kinet, J.- P.: Gene mappingof the three subunits of the high affinity FcR for IgE to mouse chromosomes1 and 19. J. Immun. 143: 3787- 3791, 1989. 3 C b

GAM7957 297 MS4A2 Kuster, H.; Zhang, L.; Brini, A. T.; MacGlashan, D. W. J.; Kinet,J.- P.: The gene and cDNA for the human high affinity immunoglobulinE receptor beta chain and expression of the complete human receptor. J.Biol. Chem. 267: 12782- 12787, 1992. 3 C b

GAM7957 297 MS4A2 Nagata, H.; Mutoh, H.; Kumahara, K.; Arimoto, Y.; Tomemori, T.;Sakurai, D.; Arase, K.; Ohno, K.; Yamakoshi, T.; Nakano, K.; Okawa,T.; Numata, T.; Konno, A.: Association between nasal allergy anda coding variant of the Fc-epsilon- RI- beta gene Glu237Gly in a Japanesepopulation. Hum. Genet. 109: 262- 266, 2001. 3 C b

GAM7957 297 MS4A2 Sandford, A. J.; Shirakawa, T.; Moffatt, M. F.; Daniels, S. E.;Ra, C.; Faux, J. A.; Young, R. P.; Nakamura, Y.; Lathrop, G. M.; Cookson,W. O. C. M.; Hopkin, J. M.: Localisation of atopy and beta subunitof high- affinity IgE receptor (FCER1) on chromosome 11q. Lancet 341:332- 334, 1993. 3 C b

GAM7957 297 MS4A2 Shirakawa, T.; Li, A.; Dubowitz, M.; Dekker, J. W.; Shaw, A. E.;Faux, J. A.; 3 C b
Ra, C.; Cookson, W. O. C. M.; Hopkin, J. M.: Associationbetween atopy and
variants of the beta subunit of the high- affinityimmunoglobulin E receptor.
Nature Genet. 7: 125- 130, 1994.

GAM7957 297 MS4A2 Shirakawa, T.; Mao, X.- Q.; Sasaki, S.; Enomoto, T.; Kawai, M.;Morimoto, K.; 3 C b
Hopkin, J.: Association between atopic asthma and acoding variant of Fc-
epsilon- RI- beta in a Japanese population. Hum.Molec. Genet. 5: 1129- 1130,
1996.

GAM7957 297 MS4A2 Szepetowski, P.; Gaudray, P.: FCER1B, a candidate gene for atopy,is located 3 C b
in 11q13 between CD20 and TCN1. Genomics 19: 399- 400,1994.

GAM7957 297 MSH3 Akiyama, Y.; Tsubouchi, N.; Yuasa, Y.: Frequent somatic mutationsof hMSH3 3 C b
with reference to microsatellite instability in hereditarynonpolyposis
colorectal cancer. Biochem. Biophys. Res. Commun. 236:248- 252, 1997.

GAM7957 297 MSH3 de Wind, N.; Dekker, M.; Claij, N.; Jansen, L.; van Klink, Y.;Radman, M.; 3 C b
Riggins, G.; van der Valk, M.; van't Wout, K.; te Riele,H.: HNPCC- like
cancer predisposition in mice through simultaneousloss of Msh3 and Msh6
mismatch- repair protein functions. Nature Genet. 23:359- 362, 1999.

GAM7957 297 MSH3 Drummond, J. T.; Genschel, J.; Wolf, E.; Modrich, P.: DHFR/MSH3amplification 3 C b
in methotrexate- resistant cells alters the hMutS- alpha/hMutS- betaratio
and reduces the efficiency of base- base mismatch repair. Proc.Nat. Acad.
Sci. 94: 10144- 10149, 1997.

GAM7957 297 MSH3 Fujii, H.; Shimada, T.: Isolation and characterization of cDNAclones derived 3 C b
from the divergently transcribed gene in the regionupstream from the human
dihydrofolate reductase gene. J. Biol. Chem. 264:10057- 10064, 1989.

GAM7957 297 MSH3 Inokuchi, K.; Ikejima, M.; Watanabe, A.; Nakajima, E.; Orimo, H.;Nomura, T.; 3 C b
Shimada, T.: Loss of expression of the human MSH3 genein hematological
malignancies. Biochem. Biophys. Res. Commun. 214:171- 179, 1995.

GAM7957 297 MSH3 Linton, J. P.; Yen, J. Y.- J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; 3 C b
Kellems, R. E.; Crouse, G. F.: Dual bidirectional promotersat the mouse dhfr
locus: cloning and characterization of two mRNAclasses of the divergently
transcribed Rep- 1 gene. Molec. Cell. Biol. 9:3058- 3072, 1989.

GAM7957 297 MSH3 Marra, G.; Iaccarino, I.; Lettieri, T.; Roscilli, G.; Delmastro,P.; Jiricny, 3 C b
J.: Mismatch repair deficiency associated with overexpressionof the MSH3
gene. Proc. Nat. Acad. Sci. 95: 8568- 8573, 1998.

GAM7957 297 MSH3 Nakajima, E.; Orimo, H.; Ikejima, M.; Shimada, T.: Nine- bp 3 C b
repeatpolymorphism in exon 1 of the hMSH3 gene. Jpn. J. Hum. Genet. 40:343-
345, 1995.

GAM7957 297 MSH3 Risinger, J. I.; Umar, A.; Boyd, J.; Berchuck, A.; Kunkel, T. A.;Barrett, J. 3 C b
C.: Mutation of MSH3 in endometrial cancer and evidencefor its functional
role in heteroduplex repair. Nature Genet. 14:102- 109, 1996.

GAM7957 297 MSH3 Smith, M. L.; Mitchell, P. J.; Crouse, G. F.: Analysis of themouse Dhfr/Rep- 3 C b
3 major promoter region by using linker- scanning andinternal deletion
mutations and DNase I footprinting. Molec. Cell.Biol. 10: 6003- 6012, 1990.

GAM7957 297 MSH3 Watanabe, A.; Ikejima, M.; Suzuki, N.; Shimada, T.: Genomic organizationand 3 C b
expression of the human MSH3 gene. Genomics 31: 311- 318, 1996.

GAM7957 297 MSH3 Yin, J.; Kong, D.; Wang, S.; Zou, T.- T. Souza, R. F.; Smolinski,K. N.; 3 C b
Lynch, P. M.; Hamilton, S. R.; Sugimura, H.; Powell, S. M.;Young, J.;
Abraham, J. M.; Meltzer, S. J.: Mutation of hMSH3 andhMSH6 mismatch repair
genes in genetically unstable human colorectaland gastric carcinomas. Hum.
Mutat. 10: 474- 478, 1997.

GAM7957 297 MTNR1A Brzezinski, A.: Melatonin in humans. New Eng. J. Med. 336: 186- 195,1997. 3 C c

GAM7957 297 MTNR1A Liu, R.- Y.; Zhou, J.- N.; van Heerikhuize, J.; Hofman, M. A.; Swaab,D. F.: 3 C c
Decreased melatonin levels in postmortem cerebrospinal fluidin relation to aging, Alzheimer's disease, and apolipoprotein E- epsilon- 4/4genotype. J. Clin. Endocr. Metab. 84: 323- 327, 1999.

GAM7957 297 MTNR1A Nelson, C. S.; Ikeda, M.; Gompf, H. S.; Robinson, M. L.; Fuchs,N. K.; 3 C c
Yoshioka, T.; Neve, K. A.; Allen, C. N.: Regulation of melatonin1a receptor signaling and trafficking by asparagine- 124. Molec. Endocr. 15:1306- 1317, 2001.

GAM7957 297 MTNR1A Reppert, S. M.; Weaver, D. R.: Melatonin madness. Cell 83: 1059- 1062,1995. 3 C c

GAM7957 297 MTNR1A Reppert, S. M.; Weaver, D. R.; Ebisawa, T.: Cloning and characterizationof a 3 C c
mammalian melatonin receptor that mediates reproductive and circadianresponses. Neuron 13: 1177- 1185, 1994.

GAM7957 297 MTNR1A Slaugenhaupt, S. A.; Roca, A. L.; Liebert, C. B.; Altherr, M. R.;Gusella, J. 3 C c
F.; Reppert, S. M.: Mapping of the gene for the Mel1a- melatoninreceptor to human chromosome 4 (MTNR1A) and mouse chromosome 8 (Mtnr1a). Genomics 27:355- 357, 1995.

GAM7957 297 MTNR1A von Gall, C.; Garabette, M. L.; Kell, C. A.; Frenzel, S.; Dehghani,F.; 3 C c
Schumm- Draeger, P.- M.; Weaver, D. R.; Korf, H.- W.; Hastings, M.H.; Stehle, J. H.: Rhythmic gene expression in pituitary dependson heterologous sensitization by the neurohormone melatonin. NatureNeurosci. 5: 234- 238, 2002.

GAM7957 297 MTNR1A Weaver, D. R.; Rivkees, S. A.; Carlson, L. L.; Reppert, S. M.:Localization 3 C c
of melatonin receptors in mammalian brain.In: Klein,D. C.; Moore, R. Y.; Reppert, S. M.: Suprachiasmatic Nucleus: TheMind's Clock. New York: Oxford Press (pub.) 1991.

GAM7957 297 MXI1 Albarosa, R.; DiDonato, S.; Finocchiaro, G.: Redefinition of thecoding 3 C c
sequence of the MXI1 gene and identification of a polymorphicrepeat in the 3- prime non- coding region that allows the detectionof loss of heterozygosity of chromosome 10q25 in glioblastomas. Hum.Genet. 95: 709- 711, 1995.

GAM7957 297 MXI1 Eagle, L. R.; Yin, X.; Brothman, A. R.; Williams, B. J.; Atkin,N. B.; 3 C c
Prochownik, E. V.: Mutation of the MXI1 gene in prostate cancer. NatureGenet. 9: 249- 255, 1995.

GAM7957 297 MXI1 Edelhoff, S.; Ayer, D. E.; Zervos, A. S.; Steingrimsson, E.; Jenkins,N. A.; 3 C c
Copeland, N. G.; Eisenman, R. N.; Brent, R.; Disteche, C. M.: Mapping of two genes encoding members of a distinct subfamily ofMAX interacting proteins: MAD to human chromosome 2 and mouse chromosome6, and MXI1 to chromosome 10 and mouse chromosome 19. Oncogene 9:665- 668, 1994.

GAM7957 297 MXI1 Li, X.- J.; Wang, D.- Y.; Zhu, Y.; Guo, R.- J.; Wang, X.- D.; Lubomir,K.; 3 C c
Mukai, K.; Sasaki, H.; Yoshida, H.; Oka, T.; Machinami, R.; Shinmura,K.; Tanaka, M.; Sugimura, H.: Mxi1 mutations in human neurofibrosarcomas. Jpn.J. Cancer Res. 90: 740- 746, 1999.

GAM7957 297 MXI1 Prochownik, E. V.; Grove, L. E.; Deubler, D.; Zhu, X. L.; Stephenson,R. A.; 3 C c
Rohr, L. R.; Yin, X.; Brothman, A. R.: Commonly occurringloss and mutation of the MXI1 gene in prostate cancer. Genes ChromosomesCancer 22: 295- 304, 1998.

GAM7957 297 MXI1 Schreiber- Agus, N.; Meng, Y.; Hoang, T.; Hou, H., Jr.; Chen, K.;Greenberg, 3 C c
R.; Cordon- Cardo, C.; Lee, H.- W.; DePinho, R. A.: Roleof Mxi1 in ageing organ systems and the regulation of normal and neoplasticgrowth. Nature 393:

483- 487, 1998.

GAM7957 297 MXI1 Shapiro, D. N.; Valentine, V.; Eagle, L.; Yin, X.; Morris, S. W.;Prochownik, E. V.: Assignment of the human MAD and MXI1 genes tochromosomes 2p12- p13 and 10q24- q25. Genomics 23: 282- 285, 1994. 3 C c

GAM7957 297 MXI1 Steingrimsson, E.; Sawadogo, M.; Gilbert, D. J.; Zervos, A. S.;Brent, R.; Blanar, M. A.; Fisher, D. E.; Copeland, N. G.; Jenkins,N. A.: Murine chromosomal location of five bHLH- Zip transcriptionfactor genes. Genomics 28: 179- 183, 1995. 3 C c

GAM7957 297 MXI1 Wechsler, D. S.; Hawkins, A. L.; Li, X.; Jabs, E. W.; Griffin,C. A.; Dang, C. V.: Localization of the human Mxi1 transcriptionfactor gene (MXI1) to chromosome 10q24- q25. Genomics 21: 669- 672,1994. 3 C c

GAM7957 297 MXI1 Wechsler, D. S.; Shelly, C. A.; Dang, C. V.: Genomic organizationof human MXI1, a putative tumor suppressor gene. Genomics 32: 466- 470,1996. 3 C c

GAM7957 297 MXI1 Zervos, A. S.; Gyuris, J.; Brent, R.: Mxi1, a protein that specificallyinteracts with Max to bind Myc- Max recognition sites. Cell 72: 223- 232,1993. Note: Erratum: Cell 79: 389 only, 1994. 3 C c

GAM7957 297 MYBL2 Barletta, C.; Druck, T.; LaForgia, S.; Calabretta, B.; Drabkin,H.; Patterson, D.; Croce, C. M.; Huebner, K.: Chromosome locationsof the MYB related genes, AMYB and BMYB. Cancer Res. 51: 3821- 3824,1991. 3 C c

GAM7957 297 MYBL2 Noben- Trauth, K.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N.A.; Sonoda, G.; Testa, J. R.; Klempnauer, K.- H.: Mybl2 (Bmyb) mapsto mouse chromosome 2 and human chromosome 20q13.1. Genomics 35:610- 612, 1996. 3 C c

GAM7957 297 MYO1D Hasson, T.; Skowron, J. F.; Gilbert, D. J.; Avraham, K. B.; Perry,W. L.; Bement, W. M.; Anderson, B. L.; Sherr, E. H.; Chen, Z.- Y.;Greene, L. A.; Ward, D. C.; Corey, D. P.; Mooseker, M. S.; Copeland,N. G.; Jenkins, N. A.: Mapping of unconventional myosins in mouseand human. Genomics 36: 431- 439, 1996. 3 C c

GAM7957 297 MYO1D Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of unidentified human genes. XI. The complete sequencesof 100 new cDNA clones from brain which code for large proteins invitro. DNA Res. 5: 277- 286, 1998. 3 C c

GAM7957 297 NFATC3 Aramburu, J.; Garcia- Cozar, F.; Raghavan, A.; Okamura, H.; Rao,A.; Hogan, P. G.: Selective inhibition of NFAT activation by a peptidespanning the calcineurin targeting site of NFAT. Molec. Cell 1:627- 637, 1998. 3 C c

GAM7957 297 NFATC3 Graef, I. A.; Chen, F.; Chen, L.; Kuo, A.; Crabtree, G. R.: Signalstransduced by Ca(2+)/calcineurin and NFATc3/c4 pattern the developingvasculature. Cell 105: 863- 875, 2001. 3 C c

GAM7957 297 NFATC3 Hoey, T.; Sun, Y.- L.; Williamson, K.; Xu, X.: Isolation of twonew members of the NF- AT gene family and functional characterizationof the NF- AT proteins. Immunity 2: 461- 472, 1995. 3 C c

GAM7957 297 NFATC3 Horsley, V.; Pavlath, G. K.: NFAT: ubiquitous regulator of celldifferentiation and adaptation. J. Cell Biol. 156: 771- 774, 2002. 3 C c

GAM7957 297 NFATC3 Rengarajan, J.; Tang, B.; Glimcher, L. H.: NFATc2 and NFATc3 regulateTH2 differentiation and modulate TCR- responsiveness of naive TH cells. NatureImmun. 3: 48- 54, 2002. 3 C c

GAM7957 297 NFKBIL2 Norman, D. A. M.; Barton, P. J. R.: Isolation, sequence, and chromosomallocalisation of the human I(kappa)BR gene. Ann. Hum. Genet. 64:15- 23, 2000. 3 C b

GAM7957 297 NFKBIL2 Ray, P.; Zhang, D.- H.; Elias, J. A.; Ray, A.: Cloning of a 3 C b

differentiallyexpressed I- kappa- B- related protein. J. Biol. Chem. 270: 10680- 10685,1995.

GAM7957 297 NHLH1 Begley, C. G.; Lipkowitz, S.; Gobel, V.; Mahon, K. A.; Bertness,V.; Green, A. R.; Gough, N. M.; Kirsch, I. R.: Molecular characterizationof NSCL, a gene encoding a helix- loop- helix protein expressed in thedeveloping nervous system. Proc. Nat. Acad. Sci. 89: 38- 42, 1992. 3 C c

GAM7957 297 NHLH1 Brown, L.; Espinosa, R., III; Le Beau, M. M.; Siciliano, M. J.;Baer, R.: HEN1 and HEN2: a subgroup of basic helix- loop- helix genesthat are coexpressed in a human neuroblastoma. Proc. Nat. Acad. Sci. 89:8492- 8496, 1992. 3 C c

GAM7957 297 NHLH1 Cogliati, T.; Good, D. J.; Haigney, M.; Delgado- Romero, P.; Eckhaus,M. A.; Koch, W. J.; Kirsch, I. R.: Predisposition to arrhythmia andautonomic dysfunction in Nhlh1- deficient mice. Molec. Cell. Biol. 22:4977- 4983, 2002. 3 C c

GAM7957 297 NHLH1 Lipkowitz, S.; Gobel, V.; Varterasian, M. L.; Nakahara, K.; Tchorz,K.; Kirsch, I. R.: A comparative structural characterization of thehuman NSCL- 1 and NSCL- 2 genes: two basic helix- loop- helix genes expressedin the developing nervous system. J. Biol. Chem. 267: 21065- 21071,1992. 3 C c

GAM7957 297 NHLH1 Mullick, A.; Groulx, N.; Trasler, D.; Gros, P.: Nhlh1, a basichelix- loop- helix transcription factor, is very tightly linked to themouse looptail (Lp) mutation. Mammalian Genome 6: 700- 704, 1995. 3 C c

GAM7957 297 NONO Brown, C. J.; Carrel, L.; Willard, H. F.: Expression of genesfrom the human active and inactive X chromosomes. Am. J. Hum. Genet. 60:1333- 1343, 1997. 3 C c

GAM7957 297 NONO Dong, B.; Horowitz, D. S.; Kobayashi, R.; Krainer, A. R.: Purificationand cDNA cloning of HeLa cell p54(nrb), a nuclear protein with twoRNA recognition motifs and extensive homology to human splicing factorPSF and Drosophila NONA/BJ6. Nucleic Acids Res. 21: 4085- 4092, 1993. 3 C c

GAM7957 297 NONO Nelson, D. L.; Ballabio, A.; Cremers, F.; Monaco, A. P.; Schlessinger,D.: Report of the sixth international workshop on X chromosome mapping1995. Cytogenet. Cell Genet. 71: 308- 342, 1995. 3 C c

GAM7957 297 NONO Peters, U.; Haberhausen, G.; Kostrzewa, M.; Nolte, D.; Muller,U.: AFX1 and p54(nrb): fine mapping, genomic structure, and exclusionas candidate genes of X- linked dystonia parkinsonism. Hum. Genet. 100:569- 572, 1997. 3 C c

GAM7957 297 NPY2R Ammar, D. A.; Eadie, D. M.; Wong, D. J.; Ma, Y.- Y.; Kolakowski,L. F., Jr.; Yang- Feng, T. L.; Thompson, D. A.: Characterization ofthe human type 2 neuropeptide Y receptor gene (NPY2R) and localizationto the chromosome 4q region containing the type 1 neuropeptide Y receptorgene. Genomics 38: 392- 398, 1996. 3 C c

GAM7957 297 NPY2R Gerald, C.; Walker, M. W.; Vaysse, P. J.- J.; He, C.; Branchek,T. A.; Weinshank, R. L.: Expression cloning and pharmacological characterizationof a human hippocampal neuropeptide Y/peptide YY Y2 receptor subtype. J.Biol. Chem. 270: 26758- 26761, 1995. 3 C c

GAM7957 297 NPY2R Lutz, C. M.; Frankel, W. N.; Richards, J. E.; Thompson, D. A.:Neuropeptide Y receptor genes on human chromosome 4q31- q32 map toconserved linkage groups on mouse chromosomes 3 and 8. Genomics 41:498- 500, 1997. 3 C c

GAM7957 297 NPY2R Rose, P. M.; Fernandes, P.; Lynch, J. S.; Frazier, S. T.; Fisher,S. M.; Kodukula, K.; Kienzle, B.; Seethala, R.: Cloning and functionalexpression of a cDNA encoding a human type 2 neuropeptide Y receptor. J.Biol. Chem. 270: 22661- 22664, 1995. 3 C c

GAM7957 297 OGG1 Aburatani, H.; Hippo, Y.; Ishida, T.; Takashima, R.; Matsuba, C.;Kodama, T.; 3 C b

Takao, M.; Yasui, A.; Yamamoto, K.; Asano, M.; Fukasawa,K.; Yoshinari, T.; Inoue, H.; Ohtsuka, E.; Nishimura, S.: Cloningand characterization of mammalian 8- hydroxyguanine- specific DNA glycosylase/apurinic,apyrimidinic lyase, a functional mutM homologue. Cancer Res. 57:2151- 2156, 1997.

GAM7957 297 OGG1 Arai, K.; Morishita, K.; Shinmura, K.; Kohno, T.; Kim, S.- R.; Nohmi,T.; Taniwaki, M.; Ohwada, S.; Yokota, J.: Cloning of a human homologof the yeast OGG1 gene that is involved in the repair of oxidativeDNA damage. Oncogene 14: 2857- 2861, 1997. 3 C b

GAM7957 297 OGG1 Audebert, M.; Chevillard, S.; Levalois, C.; Gyapay, G.; Vieillefond,A.; Klijanienko, J.; Vielh, P.; El Naggar, A. K.; Oudard, S.; Boiteux,S.; Radicella, J. P.: Alterations of the DNA repair gene OGG1 inhuman clear cell carcinomas of the kidney. Cancer Res. 60: 4740- 4744,2000. 3 C b

GAM7957 297 OGG1 Bjoras, M.; Luna, L.; Johnsen, B.; Hoff, E.; Haug, T.; Rognes,T.; Seeberg, E.: Opposite base- dependent reactions of a human baseexcision repair enzyme on DNA containing 7,8- dihydro- 8- oxoguanineand abasic sites. EMBO J. 16: 6314- 6322, 1997. 3 C b

GAM7957 297 OGG1 Ishida, T.; Hippo, Y.; Nakahori, Y.; Matsushita, I.; Kodama, T.;Nishimura, S.; Aburatani, H.: Structure and chromosome location ofhuman OGG1. Cytogenet. Cell Genet. 85: 232- 236, 1999. 3 C b

GAM7957 297 OGG1 Kohno, T.; Shinmura, K.; Tosaka, M.; Tani, M.; Kim, S.- R.; Sugimura,H.; Nohmi, T.; Kasai, H.; Yokota, J.: Genetic polymorphisms and alternativesplicing of the hOGG1 gene, that is involved in the repair of 8- hydroxyguanineinein damaged DNA. Oncogene 16: 3219- 3225, 1998. 3 C b

GAM7957 297 OGG1 Kuo, F. C.; Sklar, J.: Augmented expression of a human gene for8- oxoguanine DNA glycosylase (MutM) in B lymphocytes of the dark zonein lymph node germinal centers. J. Exp. Med. 186: 1547- 1556, 1997. 3 C b

GAM7957 297 OGG1 Lu, R.; Nash, H. M.; Verdine, G. L.: A mammalian DNA repair enzymethat excises oxidatively damaged guanines maps to a locus frequentlylost in lung cancer. Curr. Biol. 7: 397- 407, 1997. 3 C b

GAM7957 297 OGG1 Radicella, J. P.; Dherin, C.; Desmaze, C.; Fox, M. S.; Boiteux,S.: Cloning and characterization of hOGG1, a human homolog of theOGG1 gene of Saccharomyces cerevisiae. Proc. Nat. Acad. Sci. 94:8010- 8015, 1997. 3 C b

GAM7957 297 OGG1 Roldan- Arjona, T.; Wei, Y.- F.; Carter, K. C.; Klungland, A.; Anselmino,C.; Wang, R.- P.; Augustus, M.; Lindahl, T.: Molecular cloning andfunctional expression of a human cDNA encoding the antimutator enzyme8- hydroxyguanine- DNA glycosylase. Proc. Nat. Acad. Sci. 94: 8016- 8020,1997. 3 C b

GAM7957 297 OGG1 Rosenquist, T. A.; Zharkov, D. O.; Grollman, A. P.: Cloning andcharacterization of a mammalian 8- oxoguanine DNA glycosylase. Proc.Nat. Acad. Sci. 94: 7429- 7434, 1997. 3 C b

GAM7957 297 OGG1 Tani, M.; Shinmura, K.; Kohno, T.; Shiroishi, T.; Wakama, S.;Kim, S.- R.; Nohmi, T.; Kasai, H.; Takenoshita, S.; Nagamachi, Y.;Yokota, J.: Genomic structure and chromosomal localization of themouse Ogg1 gene that is involved in the repair of 8- hydroxyguanineinein DNA damage. Mammalian Genome 9: 32- 37, 1998. 3 C b

GAM7957 297 P2RX7 Buell, G. N.; Talabot, F.; Gos, A.; Lorenz, J.; Lai, E.; Morris,M. A.; Antonarakis, S. E.: Gene structure and chromosomal localizationof the human P2X7 receptor. Receptors Channels 5: 347- 354, 1998. 3 C b

GAM7957 297 P2RX7 Gu, B. J.; Zhang, W.; Worthington, R. A.; Sluyter, R.; Dao- Ung,P.; Petrou, S.; Barden, J. A.; Wiley, J. S.: A glu- 496 to ala polymorphismleads to loss of function of the human P2X(7) receptor. J. Biol.Chem. 276: 11135- 11142, 3 C b

2001.

GAM7957 297 P2RX7 Rassendren, F.; Buell, G. N.; Virginio, C.; Collo, G.; North, R.A.; Surprenant, A.: The permeabilizing ATP receptor, P2X(7). J.Biol. Chem. 272: 5482- 5486, 1997. 3 C b

GAM7957 297 P2RX7 Solle, M.; Labasi, J.; Perregaux, D. G.; Stam, E.; Petrushova,N.; Koller, B. H.; Griffiths, R. J.; Gabel, C. A.: Altered cytokineproduction in mice lacking P2X7 receptors. J. Biol. Chem. 276: 125- 132,2001. 3 C b

GAM7957 297 P2RX7 Wiley, J. S.; Dao- Ung, L. P.; Gu, B. J.; Sluyter, R.; Shemon, A.N.; Li, C.; Taper, J.; Gallo, J.; Manoharan, A.: A loss- of- functionpolymorphic mutation in the cytolytic P2X7 receptor gene and chroniclymphocyte leukaemia: a molecular study. Lancet 359: 1114- 1119,2002. 3 C b

GAM7957 297 P2RX7 Worthington, R. A.; Smart, M. L.; Gu, B. J.; Williams, D. A.; Petrou,S.; Wiley, J. S.; Barden, J. A.: Point mutations confer loss of ATP- inducedhuman P2X(7) receptor function. FEBS Lett. 512: 43- 46, 2002. 3 C b

GAM7957 297 PABPN1 Brais, B.; Bouchard, J.- P.; Xie, Y.- G.; Rochefort, D. L.; Chretien,N.; Tome, F. M. S.; Lafreniere, R. G.; Rommens, J. M.; Uyama, E.;Nohira, O.; Blumen, S.; Korczyn, A. D.; Heutink, P.; Mathieu, J.;Duranceau, A.; Codere, F.; Fardeau, M.; Rouleau, G. A.: Short GCGexpansions in the PABP2 gene cause oculopharyngeal muscular dystrophy. NatureGenet. 18: 164- 167, 1998. Note: Erratum: Nature Genet. 19: 404 only,1998. 3 C c

GAM7957 297 PABPN1 Calado, A.; Tome, F. M. S.; Brais, B.; Rouleau, G. A.; Kuhn, U.;Wahle, E.; Carmo- Fonseca, M.: Nuclear inclusions in oculopharyngealmuscular dystrophy consist of poly(A) binding protein 2 aggregateswhich sequester poly(A) RNA. Hum. Molec. Genet. 9: 2321- 2328, 2000. 3 C c

GAM7957 297 PABPN1 Delot, E.; King, L. M.; Briggs, M. D.; Wilcox, W. R.; Cohn, D.H.: Trinucleotide expansion mutations in the cartilage oligomericmatrix protein (COMP) gene. Hum. Molec. Genet. 8: 123- 128, 1999. 3 C c

GAM7957 297 PABPN1 Fan, X.; Dion, P.; Laganiere, J.; Brais, B.; Rouleau, G. A.: Oligomerizationof polyalanine expanded PABPN1 facilitates nuclear protein aggregationthat is associated with cell death. Hum. Molec. Genet. 10: 2341- 2351,2001. 3 C c

GAM7957 297 PABPN1 Kim, Y.- J.; Noguchi, S.; Hayashi, Y. K.; Tsukahara, T.; Shimizu,T.; Arahata, K.: The product of an oculopharyngeal muscular dystrophygene, poly(A)- binding protein 2, interacts with SKIP and stimulatesmuscle- specific gene expression. Hum. Molec. Genet. 10: 1129- 1139,2001. 3 C c

GAM7957 297 PABPN1 Mezei, M. M.; Mankodi, A.; Brais, B.; Marineau, C.; Thornton, C.A.; Rouleau, G. A.; Karpati, G.: Minimal expansion of the GCG repeatin the PABP2 gene does not predispose to sporadic inclusion body myositis. Neurology 52:669- 670, 1999. 3 C c

GAM7957 297 PAICS Barton, J. W.; Hart, I. M.; Patterson, D.: Mapping of a locuscorrecting lack of phosphoribosylaminoimidazole carboxylase activityin Chinese hamster ovary cell Ade(-)D mutants to human chromosome4. Genomics 9: 314- 321, 1991. 3 C b

GAM7957 297 PAICS Brayton, K. A.; Chen, Z.; Zhou, G.; Nagy, P. L.; Gavalas, A.; Trent,J. M.; Deaven, L. L.; Dixon, J. E.; Zalkin, H.: Two genes for denovo purine nucleotide synthesis on human chromosome 4 are closelylinked and divergently transcribed. J. Biol. Chem. 269: 5313- 5321,1994. 3 C b

GAM7957 297 PAICS Schild, D.; Brake, A. J.; Kiefer, M. C.; Young, D.; Barr, P. J.: Cloning of three human multifunctional de novo purine biosyntheticgenes by functional complementation of yeast mutations. Proc. Nat.Acad. Sci. 87: 2916- 2920, 1990. 3 C b

GAM7957 297 PCDH11X Blanco, P.; Sargent, C. A.; Boucher, C. A.; Mitchell, M.; Affara,N. A.: 3 C b
Conservation of PCDHX in mammals; expression of X/Y genespredominantly in brain. Mammalian Genome 11: 906- 914, 2000.

GAM7957 297 PCDH11X Ciccodicola, A.; D'Esposito, M.; Esposito, T.; Gianfrancesco, F.;Migliaccio, 3 C b
C.; Miano, M. G.; Matarazzo, M. R.; Vacca, M.; Franze,A.; Cuccurese, M.; Cocchia, M.; Curci, A.; and 9 others: Differentiallyregulated and evolved genes in the fully sequenced Xq/Yq pseudoautosomalregion. Hum. Molec. Genet. 9: 395- 401, 2000.

GAM7957 297 PCDH11X Mumm, S.; Molini, B.; Terrell, J.; Srivastava, A.; Schlessinger,D.: 3 C b
Evolutionary features of the 4- Mb Xq21.3 XY homology region revealedby a map at 60- kb resolution. Genome Res. 7: 307- 314, 1997.

GAM7957 297 PCDH11X Schwartz, A.; Chan, D. C.; Brown, L. G.; Alagappan, R.; Pettay,D.; Disteche, 3 C b
C.; McGillivray, B.; de la Chapelle, A.; Page, D. C.: Reconstructing hominid Y evolution: X- homologous block, createdby X- Y transposition, was disrupted by Yp inversion through LINE- LINErecombination. Hum. Molec. Genet. 7: 1- 11, 1998.

GAM7957 297 PCDH11X Tilford, C. A.; Kuroda- Kawaguchi, T.; Skaletsky, H.; Rozen, S.;Brown, L. 3 C b
G.; Rosenberg, M.; McPherson, J. D.; Wylie, K.; Sekhon,M.; Kucaba, T. A.; Waterston, R. H.; Page, D. C.: A physical mapof the human Y chromosome. Nature 409: 943- 945, 2001.

GAM7957 297 PCDH11X Yoshida, K.; Sugano, S.: Identification of a novel protocadheringene 3 C b
(PCDH11) on the human XY homology region in Xq21.3. Genomics 62:540- 543, 1999.

GAM7957 297 PCDHA9 Nagase, T.; Ishikawa, I.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; O'Hara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997.

GAM7957 297 PCDHA9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM7957 297 PCDHB9 Vanhalst, K.; Kools, P.; Eynde, E. V.; van Roy, F.: The humanand murine 3 C c
protocadherin- beta one- exon gene families show high evolutionaryconservation, despite the difference in gene number. FEBS Lett. 495:120- 125, 2001.

GAM7957 297 PCDHB9 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; 3 C c
Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001.

GAM7957 297 PDCL Miles, M. F.; Barhite, S.; Sganga, M.; Elliott, M.: Phosducin- likeprotein: 3 C c
an ethanol- responsive potential modulator of guanine nucleotide- bindingprotein function. Proc. Nat. Acad. Sci. 90: 10831- 10835, 1993.

GAM7957 297 PDCL Thibault, C.; Wang, J. F.; Charnas, R.; Mirel, D.; Barhite, S.;Miles, M. F.: 3 C c
Cloning and characterization of the rat and human phosducin- likeprotein genes: structure, expression and chromosomal localization. Biochim.Biophys. Acta 1444: 346- 354, 1999.

GAM7957 297 PDE4A Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.;Rodgers, 3 C c
L.; Riggs, M.; Wigler, M.; Ferguson, K.: A family of humanphosphodiesterases homologous to the dunce learning and memory geneproduct of Drosophila

melanogaster are potential targets for antidepressantdrugs. Molec. Cell. Biol. 13: 6558- 6571, 1993.

GAM7957 297 PDE4A Horton, Y. M.; Sullivan, M.; Houslay, M. D.: Molecular cloningof a novel splice variant of human type IVA (PDE- IVA) cyclic AMP phosphodiesteraseand localization of the gene to the p13.2- q12 region of human chromosome19. Biochem. J. 308: 683- 691, 1995. 3 C c

GAM7957 297 PDE4A Huston, E.; Pooley, L.; Julien, P.; Scotland, G.; McPhee, I.; Sullivan,M.; Bolger, G.; Houslay, M. D.: The human cyclic AMP- specific phosphodiesterasePDE- 46 (HSPDE4A4B) expressed in transfected COS7 cells occurs as bothparticulate and cytosolic species that exhibit distinct kinetics ofinhibition by the antidepressant rolipram. J. Biol. Chem. 271: 31334- 31344,1996. 3 C c

GAM7957 297 PDE4A Livi, G. P.; Kmetz, P.; McHale, M. M.; Cieslinski, L. B.; Sathe,G. M.; Taylor, D. P.; Davis, R. L.; Torphy, T. J.; Balcarek, J. M.: Cloning and expression of cDNA for a human low- K(m), rolipram- sensitivecyclic AMP phosphodiesterase. Molec. Cell. Biol. 10: 2678- 2686,1990. 3 C c

GAM7957 297 PDE4A Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994. 3 C c

GAM7957 297 PDE4A Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins,M.; Jarnagin, K.; Shelton, E. R.: The cDNA of a human lymphocytecyclic- AMP phosphodiesterase (PDE IV) reveals a multigene family. Gene 129:239- 247, 1993. 3 C c

GAM7957 297 PDE4A Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay,M. D.: Molecular cloning and expression, in both COS- 1 cells andS. cerevisiae, of a human cytosolic type- IVA, cyclic AMP specificphosphodiesterase (hPDE- IVA- h6.1). Cell. Signal. 6: 793- 812, 1994. 3 C c

GAM7957 297 PDE4A Sullivan, M.; Rena, G.; Begg, F.; Gordon, L.; Olsen, A. S.; Houslay,M. D.: Identification and characterization of the human homologueof the short PDE4A cAMP- specific phosphodiesterase RD1 (PDE4A1) byanalysis of the human HSPDE4A gene locus located at chromosome 19p13.2. Biochem.J. 333: 693- 703, 1998. 3 C c

GAM7957 297 PDE4A Wilson, M.; Sullivan, M.; Brown, N.; Houslay, M. D.: Purification,characterization and analysis of rolipram inhibition of a human- typeIVA cyclic AMP- specific phosphodiesterase expressed in yeast. Biochem.J. 304: 407- 415, 1994. 3 C c

GAM7957 297 PDE4C Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.;Rodgers, L.; Riggs, M.; Wigler, M.; Ferguson, K.: A family of humanphosphodiesterases homologous to the dunce learning and memory geneproduct of Drosophila melanogaster are potential targets for antidepressantdrugs. Molec. Cell. Biol. 13: 6558- 6571, 1993. 3 C c

GAM7957 297 PDE4C Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994. 3 C c

GAM7957 297 PDE4C Sullivan, M.; Olsen, A. S.; Houslay, M. D.: Genomic organisationof the human cyclic AMP- specific phosphodiesterase PDE4C gene andits chromosomal localisation to 19p13.1, between RAB3A and JUND. Cell.Signal. 11: 735- 742, 1999. 3 C c

GAM7957 297 PDE7A Han, P.; Fletcher, C. F.; Copeland, N. G.; Jenkins, N. A.; Yaremko,L. M.; Michaeli, T.: Assignment of the mouse Pde7A gene to the proximalregion of 3 C b

chromosome 3 and of the human PDE7A gene to chromosome 8q13. Genomics 48:275- 276, 1998.

GAM7957 297 PDE7A Michaeli, T.; Bloom, T. J.; Martins, T.; Loughney, K.; Ferguson,K.; Riggs, 3 C b
M.; Rodgers, L.; Beavo, J. A.; Wigler, M.: Isolation andcharacterization of a previously undetected human cAMP phosphodiesteraseby complementation of cAMP phosphodiesterase- deficient Saccharomycescerevisiae. J. Biol. Chem. 268: 12925- 12932, 1993.

GAM7957 297 PDE7A Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U.: 3 C b
Chromosomelocalizations of genes for five cAMP- specific phosphodiesterases inman and mouse. Somat. Cell Molec. Genet. 20: 75- 86, 1994.

GAM7957 297 PLA2G2D Ishizaki, J.; Suzuki, N.; Higashino, K.; Yokota, Y.; Ono, T.; Kawamoto,K.; 3 C b
Fujii, N.; Arita, H.; Hanasaki, K.: Cloning and characterizationof novel mouse and human secretory phospholipase A(2)s. J. Biol.Chem. 274: 24973- 24979, 1999.

GAM7957 297 PLA2G2D Shakhov, A. N.; Rubtsov, A. V.; Lyakhov, I. G.; Tumanov, A. V.;Nedospasov, 3 C b
S. A.: SPLASH (PLA(2)IID), a novel member of phospholipaseA2 family, is associated with lymphotoxin- deficiency. Genes Immun. 1:191- 199, 2000.

GAM7957 297 PODXL Kershaw, D. B.; Beck, S. G.; Wharram, B. L.; Wiggins, J. E.; Goyal,M.; 3 C c
Thomas, P. E.; Wiggins, R. C.: Molecular cloning and characterizationof human podocalyxin- like protein: orthologous relationship to rabbitPCLP1 and rat podocalyxin. J. Biol. Chem. 272: 15708- 15714, 1997.

GAM7957 297 PODXL Kershaw, D. B.; Wiggins, J. E.; Wharram, B. L.; Wiggins, R. C.: Assignment 3 C c
of the human podocalyxin- like protein (PODXL) gene to7q32- q33. Genomics 45: 239- 240, 1997.

GAM7957 297 PPP2R1B Arai, Y.; Hosoda, F.; Nakayama, K.; Ohki, M.: A yeast artificialchromosome 3 C b
contig and NotI restriction map that spans the tumor suppressorgene(s) locus, 11q.22.2- q23.3. Genomics 35: 196- 206, 1996.

GAM7957 297 PPP2R1B Hemmer, S.; Wasenius, V.- M.; Haglund, C.; Zhu, Y.; Knuutila, S.;Franssila, 3 C b
K.; Joensuu, H.: Alterations in the suppressor gene PPP2R1Bin parathyroid hyperplasias and adenomas. Cancer Genet. Cytogenet. 134:13- 17, 2002.

GAM7957 297 PPP2R1B Walter, G.; Mumby, M.: Protein serine/threonine phosphatases andcell 3 C b
transformation. Biochim. Biophys. Acta 1155: 207- 226, 1993.

GAM7957 297 PPP2R1B Wang, S. S.; Esplin, E. D.; Li, J. L.; Huang, L.; Gazdar, A.; Minna,J.; 3 C b
Evans, G. A.: Alterations of the PPP2R1B gene in human lung andcolon cancer. Science 282: 284- 287, 1998.

GAM7957 297 PRKY Klink, A.; Schiebel, K.; Winkelmann, M.; Rao, E.; Horsthemke, B.;Ludecke, 3 C c
H.- J.; Claussen, U.; Scherer, G.; Rappold, G.: The humanprotein kinase gene PKX1 on Xp22.3 displays Xp/Yp homology and isa site of chromosomal instability. Hum. Molec. Genet. 4: 869- 878,1995.

GAM7957 297 PRKY Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.;Rappold, 3 C c
G.: FISH localization of the human Y- homolog of proteinkinase PRKX (PRKY) to Yp11.2 and two pseudogenes to 15q26 and Xq12- q13. Cytogenet.Cell Genet. 76: 49- 52, 1997.

GAM7957 297 PRKY Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil,D.; 3 C c
Petit, C.; Rappold,, G. A.: Abnormal XY interchange between anovel isolated protein kinase gene, PRKY, and its homologue, PRKX,accounts for one third of all (Y+)XX males and (Y-)XY females. Hum.Molec. Genet. 6: 1985- 1989, 1997.

GAM7957 297 PRX Boerkoel, C. F.; Takashima, H.; Stankiewicz, P.; Garcia, C. A.;Leber, S. M.; 3 C c
Rhee- Morris, L.; Lupski, J. R.: Periaxin mutationscause recessive Dejerine- Sottas neuropathy. Am. J. Hum. Genet. 68:325- 333, 2001. Note: Erratum: Am.

J. Hum. Genet. 68: 557 only, 2001.

GAM7957 297 PRX Cohn, R. D.; Campbell, K. P.: Molecular basis of muscular dystrophies. 3 C c
MuscleNerve 23: 1456- 1471, 2000.

GAM7957 297 PRX Delague, V.; Bareil, C.; Tuffery, S.; Bouvagnet, P.; Chouery, E.;Koussa, S.; 3 C c
Maisonobe, T.; Loiselet, J.; Megarbane, A.; Claustres,M.: Mapping of a new
locus for autosomal recessive demyelinatingCharcot- Marie- Tooth disease to
19q13.1- 13.3 in a large consanguineousLebanese family: exclusion of MAG as
a candidate gene. Am. J. Hum.Genet. 67: 236- 243, 2000.

GAM7957 297 PRX Gillespie, C. S.; Lee, M.; Fantes, J. F.; Brophy, P. J.: The geneencoding 3 C c
the Schwann cell protein periaxin localizes on mouse chromosome7 (Prx).
Genomics 41: 297- 298, 1997.

GAM7957 297 PRX Gillespie, C. S.; Sherman, D. L.; Fleetwood- Walker, S. M.; Cottrell,D. F.; 3 C c
Tait, S.; Garry, E. M.; Wallace, V. C. J.; Ure, J.; Griffiths,I. R.; Smith,
A. Brophy, P. J.: Peripheral demyelination and neuropathicpain behavior in
periaxin- deficient mice. Neuron 26: 523- 531, 2000.

GAM7957 297 PRX Guilbot, A.; Williams, A.; Ravise, N.; Verny, C.; Brice, A.; Sherman,D. L.; 3 C c
Brophy, P. J.; LeGuern, E.; Delague, V.; Bareil, C.; Megarbane,A.;
Claustres, M.: A mutation in periaxin is responsible for CMT4F,an autosomal
recessive form of Charcot- Marie- Tooth disease. Hum.Molec. Genet. 10: 415-
421, 2001.

GAM7957 297 PRX Schuler, G. D.: Sequence mapping by electronic PCR. Genome Res. 7:541- 550, 3 C c
1997.

GAM7957 297 PRX Takashima, H.; Boerkoel, C. F.; De Jonghe, P.; Ceuterick, C.; Martin,J.- J.; 3 C c
Voit, T.; Schroder, J.- M.; Williams, A.; Brophy, P. J.; Timmerman,V.;
Lupski, J. R.: Periaxin mutations cause a broad spectrum of
demyelinatingneuropathies. Ann. Neurol. 51: 709- 715, 2002.

GAM7957 297 PSCD3 Ferguson, K. M.; Kavran, J. M.; Sankaran, V. G.; Fournier, E.;Isakoff, S. 3 C c
J.; Skolnik, E. Y.; Lemmon, M. A.: Structural basis fordiscrimination of 3-
phosphoinositides by pleckstrin homology domains. Molec.Cell 6: 373- 384,
2000.

GAM7957 297 PSCD3 Franco, M.; Boretto, J.; Robineau, S.; Monier, S.; Goud, B.; Chardin,P.; 3 C c
Chavrier, P.: ARNO3, a Sec7- domain guanine nucleotide exchangefactor for
ADP ribosylation factor 1, is involved in the control ofGolgi structure and
function. Proc. Nat. Acad. Sci. 95: 9926- 9931,1998.

GAM7957 297 PSCD3 Klarlund, J. K.; Guilherme, A.; Holik, J. J.; Virbasius, J. V.;Chawla, A.; 3 C c
Czech, M. P.: Signaling by phosphoinositide- 3,4,5- triphosphatethrough
proteins containing pleckstrin and Sec7 homology domains. Science 275:1927-
1930, 1997.

GAM7957 297 PSCD3 Lietzke, S. E.; Bose, S.; Cronin, T.; Klarlund, J.; Chawla, A.;Czech, M. P.; 3 C c
Lambright, D. G.: Structural basis of 3- phosphoinositiderecognition by
pleckstrin homology domains. Molec. Cell 6: 385- 394,2000.

GAM7957 297 PSCD3 Venkateswarlu, K.; Gunn- Moore, F.; Oatey, P. B.; Tavare, J. M.;Cullen, P. 3 C c
J.: Nerve growth factor- and epidermal growth factor-
stimulatedtranslocation of the ADP- ribosylation factor- exchange factor
GRP1to the plasma membrane of PC12 cells requires activation of
phosphatidylinositol3- kinase and the GRP1 pleckstrin homology domain.
Biochem. J. 335:139- 146, 1998.

GAM7957 297 PSMD5 Deveraux, Q.; Jensen, C.; Rechsteiner, M.: Molecular cloning andexpression 3 C b
of a 26 S protease subunit enriched in dileucine repeats. J.Biol. Chem. 270:
23726- 23729, 1995.

GAM7957 297 PSMD5 Deveraux, Q.; Ustrell, V.; Pickart, C.; Rechsteiner, M.: A 26S protease subunit that binds ubiquitin conjugates. J. Biol. Chem. 269:7059- 7061, 1994. 3 C b

GAM7957 297 PSMD5 Nomura, N.; Nagase, T.; Miyajima, N.; Sazuka, T.; Tanaka, A.; Sato,S.; Seki, N.; Kawarabayasi, Y.; Ishikawa, K.; Tabata, S.: Predictionof the coding sequences of unidentified human genes. II. The codingsequences of 40 new genes (KIAA0041- KIAA0080) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 1: 223- 229, 1994. 3 C b

GAM7957 297 PTAFR Chase, P. B.; Yang, J.- M.; Thompson, F. H.; Halonen, M.; Regan,J. W.: Regional mapping of the human platelet- activating factor receptorgene (PTAFR) to 1p35- p34.3 by fluorescence in situ hybridization. Cytogenet.Cell Genet. 72: 205- 207, 1996. 3 C b

GAM7957 297 PTAFR Prescott, S. M.; Zimmerman, G. A.; McIntyre, T. M.: Platelet-activatingfactor. J. Biol. Chem. 265: 17381- 17384, 1990. 3 C b

GAM7957 297 PTAFR Seyfried, C. E.; Schweickart, V. L.; Godiska, R.; Gray, P. W.:The human platelet- activating factor receptor gene (PTAFR) containsno introns and maps to chromosome 1. Genomics 13: 832- 834, 1992. 3 C b

GAM7957 297 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime-untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001. 3 C c

GAM7957 297 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994. 3 C c

GAM7957 297 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996. 3 C c

GAM7957 297 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996. 3 C c

GAM7957 297 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter activity. Genomics 36: 296- 304, 1996. 3 C c

GAM7957 297 PTGS1 Catella- Lawson, F.; Reilly, M. P.; Kapoor, S. C.; Cucchiara, A.J.; DeMarco, S.; Tournier, B.; Vyas, S. N.; FitzGerald, G. A.: Cyclooxygenaseinhibitors and the antiplatelet effects of aspirin. New Eng. J. Med. 345:1809- 1817, 2001. 3 C c

GAM7957 297 PTGS1 Dube, J.- N.; Drouin, J.; Aminian, M.; Plant, M. H.; Laneuville,O.: Characterization of a partial prostaglandin endoperoxide H synthase-1deficiency in a patient with a bleeding disorder. Brit. J. Haemat. 113:878-885, 2001. 3 C c

GAM7957 297 PTGS1 Funk, C. D.; Funk, L. B.; Kennedy, M. E.; Pong, A. S.; Fitzgerald,G. A.: Human platelet/erythroleukemia cell prostaglandin G/H synthase:cDNA cloning, expression, and gene chromosomal assignment. FASEBJ. 5: 2304- 2312, 1991. 3 C c

GAM7957 297 PTGS1 Gavett, S. H.; Madison, S. L.; Chulada, P. C.; Scarborough, P.E.; Qu, W.; Boyle, J. E.; Tiano, H. F.; Lee, C. A.; Langenbach, R.;Roggli, V. L.; Zeldin, D. C.: Allergic lung responses are increasedin prostaglandin H 3 C c

synthase- deficient mice. J. Clin. Invest. 104:721- 732, 1999.

GAM7957 297 PTGS1 Kirschenbaum, A.; Liotta, D. R.; Yao, S.; Liu, X.- H.; Klausner,A. P.; Unger, P.; Shapiro, E.; Leav, I.; Levine, A. C.: Immunohistochemicallocalization of cyclooxygenase- 1 and cyclooxygenase- 2 in the humanfetal and adult male reproductive tracts. J. Clin. Endocr. Metab. 85:3436- 3441, 2000. 3 C c

GAM7957 297 PTGS1 Langenbach, R.; Morham, S. G.; Tiano, H. F.; Loftin, C. D.; Ghanayem,B. I.; Chulada, P. C.; Mahler, J. F.; Lee, C. A.; Goulding, E. H.;Kluckman, K. D.; Kim, H. S.; Smithies, O.: Prostaglandin synthase1 gene disruption in mice reduces arachidonic acid- induced inflammationand indomethacin- induced gastric ulceration. Cell 83: 483- 492, 1995. 3 C c

GAM7957 297 PTGS1 Malkowski, M. G.; Ginell, S. L.; Smith, W. L.; Garavito, R. M.: The productive conformation of arachidonic acid bound to prostaglandinsynthase. Science 289: 1933- 1937, 2000. 3 C c

GAM7957 297 PTGS1 Pareti, F. I.; Manucci, P. M.; D'Angelo, A.; Smith, J. B.; Sautebin,L.; Galli, G.: Congenital deficiency of thromboxane and prostacyclin. Lancet I:898- 900, 1980. 3 C c

GAM7957 297 PTGS1 Picot, D.; Loll, P. J.; Garavito, R. M.: The x- ray crystal structureof the membrane protein prostaglandin H- 2 synthase- 1. Nature 367:243- 249, 1994. 3 C c

GAM7957 297 PTGS1 Tsujii, M.; Kawano, S.; Tsuji, S.; Sawaoka, H.; Hori, M.; DuBois,R. N.: Cyclooxygenase regulates angiogenesis induced by colon cancercells. Cell 93: 705- 716, 1998. 3 C c

GAM7957 297 PTGS1 Vane, J. R.; Mitchell, J. A.; Appleton, I.; Tomlinson, A.; Bishop-Bailey,D.; Croxtall, J.; Willoughby, D. A.: Inducible isoforms of cyclooxygenaseand nitric- oxide synthase in inflammation. Proc. Nat. Acad. Sci. 91:2046- 2050, 1994. 3 C c

GAM7957 297 PTGS1 Yokoyama, C.; Tanabe, T.: Cloning of human gene encoding prostaglandinendoperoxide synthase and primary structure of the enzyme. Biochem.Biophys. Res. Commun. 165: 888- 894, 1989. 3 C c

GAM7957 297 RAB5B Korenberg, J. R.; Chen, X.- N.; Adams, M. D.; Venter, J. C.: Towarda cDNA map of the human genome. Genomics 29: 364- 370, 1995. 3 C c

GAM7957 297 RAB5B Wilson, D. B.; Wilson, M. P.: Identification and subcellular localizationof human rab5b, a new member of the ras- related superfamily of GTPases. J.Clin. Invest. 89: 996- 1005, 1992. 3 C c

GAM7957 297 RAD1 Dean, F. B.; Lian, L.; O'Donnell, M.: cDNA cloning and gene mappingof human homologs for Schizosaccharomyces pombe rad17, rad1, and hus1and cloning of homologs from mouse, Caenorhabditis elegans, and Drosophilamelanogaster. Genomics 54: 424- 436, 1998. 3 C b

GAM7957 297 RAD1 Parker, A. E.; Van de Weyer, I.; Laus, M. C.; Oostveen, I.; Yon,J.; Verhasselt, P.; Luyten, W. H. M. L.: A human homologue of Schizosaccharomycespombe rad1+ checkpoint gene encodes an exonuclease. J. Biol. Chem. 273:18332- 18339, 1998. 3 C b

GAM7957 297 RAD1 Udell, C. M.; Lee, S. K.; Davey, S.: HRAD1 and MRAD1 encode mammalianhomologues of the fission yeast rad1+ cell cycle checkpoint controlgene. Nucleic Acids Res. 26: 3971- 3976, 1998. 3 C b

GAM7957 297 RAD1 Volkmer, E.; Karnitz, L. M.: Human homologs of Schizosaccharomycespombe Rad1, Hus1, and Rad9 form a DNA damage- responsive protein complex. J.Biol. Chem. 274: 567- 570, 1999. 3 C b

GAM7957 297 RBL1 Chen, C.- R.; Kang, Y.; Siegel, P. M.; Massague, J.: E2F4/5 andp107 as Smad cofactors linking the TGF- beta receptor to c- myc repression. Cell 110:19- 3 C c

32, 2002.

GAM7957 297 RBL1 Ewen, M. E.; Xing, Y.; Lawrence, J. B.; Livingston, D. M.: Molecularcloning, 3 C c
chromosomal mapping, and expression of the cDNA for p107,a retinoblastoma
gene product- related protein. Cell 66: 1155- 1164,1991.

GAM7957 297 RBL1 Huppi, K.; Siwarski, D.; Mock, B. A.; Dosik, J.; Hamel, P. A.:Molecular 3 C c
cloning, chromosomal mapping, and expression of the mousep107 gene.
Mammalian Genome 7: 353- 355, 1996.

GAM7957 297 RBL1 Kim, K. K.; Soonpaa, M. H.; Wang, H.; Field, L. J.: Developmentalexpression 3 C c
of p107 mRNA and evidence for alternative splicing of thep107 (RBL1) gene
product. Genomics 28: 520- 529, 1995.

GAM7957 297 RBL1 LeCouter, J. E.; Kablar, B.; Hardy, W. R.; Ying, C.; Megeney, L.A.; May, L. 3 C c
L.; Rudnicki, M. A.: Strain- dependent myeloid hyperplasia,growth
deficiency, and accelerated cell cycle in mice lacking theRb- related p107
gene. Molec. Cell. Biol. 18: 7455- 7465, 1998.

GAM7957 297 RBM10 Coleman, M. P.; Ambrose, H. J.; Carrel, L.; Nemeth, A. H.; Willard,H. F.; 3 C c
Davies, K. E.: A novel gene, DXS8237E, lies within 20 kb upstreamof UBE1 in
Xp11.23 and has a different X inactivation status. Genomics 31:135- 138,
1996.

GAM7957 297 RBM10 Inoue, A.; Takahashi, K. P.; Kimura, M.; Watanabe, T.; Morisawa,S.: 3 C c
Molecular cloning of a RNA binding protein, S1- 1. Nucleic AcidsRes. 24:
2990- 2997, 1996.

GAM7957 297 RBM10 Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the 3 C c
coding sequences of unidentified human genes. IV. The codingsequences of 40
new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 2: 167- 174, 1995.

GAM7957 297 RCN1 Kent, J.; Lee, M.; Schedl, A.; Boyle, S.; Fantes, J.; Powell, M.;Rushmere, 3 C c
N.; Abbott, C.; van Heyningen, V.; Bickmore, W. A.: Thereticulocalbin gene
maps to the WAGR region in human and to the Smalleye Harwell deletion in
mouse. Genomics 42: 260- 267, 1997.

GAM7957 297 RCN1 Ozawa, M.: Cloning of a human homologue of mouse reticulocalbinreveals 3 C c
conservation of structural domains in the novel endoplasmicreticulum
resident Ca2+- binding protein with multiple EF- hand motifs. J.Biochem.
117: 1113- 1119, 1995.

GAM7957 297 RCN1 Ozawa, M.; Muramatsu, T.: Reticulocalbin, a novel endoplasmicreticulum 3 C c
resident Ca2+- binding protein with multiple EF- hand motifsand a carboxyl-
terminal HDEL sequence. J. Biol. Chem. 268: 699- 705,1993.

GAM7957 297 RERE Amler, L. C.; Bauer, A.; Corvi, R.; Dihlmann, S.; Praml, C.; Cavenee,W. K.; 3 C c
Schwab, M.; Hampton, G. M.: Identification and characterizationof novel
genes located at the t(1;15)(p36.2;q24) translocation breakpointin the
neuroblastoma cell line NGP. Genomics 64: 195- 202, 2000.

GAM7957 297 RERE Yanagisawa, H.; Bundo, M.; Miyashita, T.; Okamura- Oho, Y.; Tadokoro,K.; 3 C c
Tokunaga, K.; Yamada, M.: Protein binding of a DRPLA family througharginine-
glutamic acid dipeptide repeats is enhanced by extended polyglutamine.
Hum.Molec. Genet. 9: 1433- 1442, 2000.

GAM7957 297 RET Amiel, J.; Salomon, R.; Attie, T.; Pelet, A.; Trang, H.; Mokhtari,M.; 3 C c
Gaultier, C.; Munnich, A.; Lyonnet, S.: Mutations of the RET- GDNFsignaling
pathway in Ondine's curse. (Letter) Am. J. Hum. Genet. 62:715- 717, 1998.

GAM7957 297 RET Angrist, M.; Bolk, S.; Thiel, B.; Puffenberger, E. G.; Hofstra,R. M.; Buys, 3 C c
C. H. C. M.; Cass, D. T.; Chakravarti, A.: Mutationanalysis of the RET
receptor tyrosine kinase in Hirschsprung disease. Hum.Molec. Genet. 4: 821-

830, 1995.

GAM7957 297 RET Antinolo, G.; Marcos, I.; Fernandez, R. M.; Romero, M.; Borrego,S.: A novel germline point mutation, c.2304G(T, in codon 768 of theRET proto- oncogene in a patient with medullary thyroid carcinoma.(Letter) Am. J. Med. Genet. 110: 85- 87, 2002. 3 C c

GAM7957 297 RET Attie, T.; Pelet, A.; Edery, P.; Eng, C.; Mulligan, L. M.; Amiel,J.; Boutrand, L.; Beldjord, C.; Nihoul- Fekete, C.; Munnich, A.; Ponder,B. A. J.; Lyonnet, S.: Diversity of RET proto- oncogene mutationsin familial and sporadic Hirschsprung disease. Hum. Molec. Genet. 4:1381- 1386, 1995. 3 C c

GAM7957 297 RET Attie- Bitach, T.; Abitbol, M.; Gerard, M.; Delezoide, A.- L.; Auge,J.; Pelet, A.; Amiel, J.; Pachnis, V.; Munnich, A.; Lyonnet, S.; Vekemans,M.: Expression of the RET proto- oncogene in human embryos. Am. J.Med. Genet. 80: 481- 486, 1998. 3 C c

GAM7957 297 RET Auricchio, A.; Griseri, P.; Carpentieri, M. L.; Betsos, N.; Staiano,A.; Tozzi, A.; Priolo, M.; Thompson, H.; Bocciardi, R.; Romeo, G.;Ballabio, A.; Ceccherini, I.: Double heterozygosity for a RET substitutioninterfering with splicing and an EDNRB missense mutation in Hirschsprungdisease. (Letter) Am. J. Hum. Genet. 64: 1216- 1221, 1999. 3 C c

GAM7957 297 RET Batourina, E.; Choi, C.; Paragas, N.; Bello, N.; Hensle, T.; Costantini,F. D.; Schuchardt, A.; Bacallao, R. L.; Mendelsohn, C. L.: Distalureter morphogenesis depends on epithelial cell remodeling mediatedby vitamin A and Ret. Nature Genet. 32: 109- 115, 2002. Note: Erratum:Nature Genet. 32: 331 only, 2002. 3 C c

GAM7957 297 RET Batourina, E.; et al; et al: Vitamin A controls epithelial/mesenchymalinteractions through Ret expression. Nature Genet. 27: 74- 78, 2001. 3 C c

GAM7957 297 RET Berndt, I.; Reuter, M.; Saller, B.; Frank- Raue, K.; Groth, P.:Grubendorf, M.; Raue, F.; Ritter, M. M.; Hoppner, W.: A new hot spotfor mutations in the ret protooncogene causing familial medullarythyroid carcinoma and multiple endocrine neoplasia type 2A. J. Clin.Endocr. Metab. 83: 770- 774, 1998. 3 C c

GAM7957 297 RET Boccia, L. M.; Green, J. S.; Joyce, C.; Eng, C.; Taylor, S. A.M.; Mulligan, L. M.: Mutation of RET codon 768 is associated withthe FMTC phenotype. Clin. Genet. 51: 81- 85, 1997. 3 C c

GAM7957 297 RET Bolino, A.; Schuffenecker, I.; Luo, Y.; Seri, M.; Silengo, M.;Tocco, T.; Chabrier, G.; Houdent, C.; Murat, A.; Schlumberger, M.;Tourniaire, J.; Lenoir, G. M.; Romeo, G.: RET mutations in exons13 and 14 of FMTC patients. Oncogene 10: 2415- 2419, 1995. 3 C c

GAM7957 297 RET Bolk Gabriel, S.; Salomon, R.; Pelet, A.; Angrist, M.; Amiel,J.; Fornage, M.; Attie- Bitach, T.; Olson, J. M.; Hofstra, R.; Buys,C.; Steffann, J.; Munnich, A.; Lyonnet, S.; Chakravarti, A.: Segregationat three loci explains familial and population risk in Hirschsprungdisease. Nature Genet. 31: 89- 93, 2002. 3 C c

GAM7957 297 RET Bolk, S.; Angrist, M.; Schwartz, S.; Silvestri, J. M.; Weese- Mayer,D. E.; Chakravarti, A.: Congenital central hypoventilation syndrome:mutation analysis of the receptor tyrosine kinase RET. Am. J. Med.Genet. 63: 603- 609, 1996. 3 C c

GAM7957 297 RET Bongarzone, I.; Vigano, E.; Alberti, L.; Borrello, M. G.; Pasini,B.; Greco, A.; Mondellini, P.; Smith, D. P.; Ponder, B. A. J.; Romeo,G.; Pierotti, M. A.: Full activation of MEN2B mutant RET by an additionalMEN2A mutation or by ligand GDNF stimulation. Oncogene 16: 2295- 2301,1998. 3 C c

GAM7957 297 RET Borrego, S.; Ruiz, A.; Saez, M. E.; Gimm, O.; Gao, X.; Lopez- Alonso,M.; Hernandez, A.; Wright, F. A.; Antinolo, G.; Eng, C.: RET genotypescomprising specific haplotypes of polymorphic variants predisposeto isolated Hirschsprung disease. J. Med. Genet. 37: 572- 578, 2000. 3 C c

GAM7957 297 RET Borrego, S.; Saez, M. E.; Ruiz, A.; Gimm, O.; Lopez- Alonso, M.;Antinolo, G.; Eng, C.: Specific polymorphisms in the RET proto- oncogeneare over- represented in patients with Hirschsprung disease and mayrepresent loci modifying phenotypic expression. J. Med. Genet. 36:771- 774, 1999. 3 C c

GAM7957 297 RET Carlson, K. M.; Bracamontes, J.; Jackson, C. E.; Clark, R.; Lacroix,A.; Wells, S. A., Jr.; Goodfellow, P. J.: Parent- of- origin effectsin multiple endocrine neoplasia type 2B. Am. J. Hum. Genet. 55:1076- 1082, 1994. 3 C c

GAM7957 297 RET Carlson, K. M.; Dou, S.; Chi, D.; Scavarda, N.; Toshima, K.; Jackson,C. E.; Wells, S. A., Jr.; Goodfellow, P. J.; Donis- Keller, H.: Singlemissense mutation in the tyrosine kinase catalytic domain of the RETprotooncogene is associated with multiple endocrine neoplasia type2B. Proc. Nat. Acad. Sci. 91: 1579- 1583, 1994. 3 C c

GAM7957 297 RET Carrasquillo, M. M.; McCallion, A. S.; Puffenberger, E. G.; Kashuk,C. S.; Nouri, N.; Chakravarti, A.: Genome- wide association studyand mouse model identify interaction between RET and EDNRB pathwaysin Hirschsprung disease. Nature Genet. 32: 237- 244, 2002. 3 C c

GAM7957 297 RET Ceccherini, I.; Hofstra, R. M.; Luo, Y.; Stulp, R. P.; Barone,V.; Stelwagen, T.; Bocciardi, R.; Nijveen, H.; Bolino, A.; Seri, M.;Ronchetto, P.; Pasini, B.; Bozzano, M.; Buys, C. H. C. M.; Romeo,G.: DNA polymorphisms and conditions for SSCP analysis of the 20exons of the Ret proto- oncogene. Oncogene 9: 3025- 3029, 1994. 3 C c

GAM7957 297 RET Ceccherini, I.; Romei, C.; Barone, V.; Pacini, F.; Martino, E.;Loviselli, A.; Pinchera, A.; Romeo, G.: Identification of the cys634- to- tyrmutation of the RET proto- oncogene in a pedigree with multiple endocrineneoplasia type 2A and localized cutaneous lichen amyloidosis. J.Endocr. Invest. 17: 201- 204, 1994. 3 C c

GAM7957 297 RET Cetta, F.; Chiappetta, G.; Melillo, R. M.; Petracci, M.; Montalto,G.; Santoro, M.; Fusco, A.: The ret/ptc1 oncogene is activated infamilial adenomatous polyposis- associated thyroid papillary carcinomas. J.Clin. Endocr. Metab. 83: 1003- 1006, 1998. 3 C c

GAM7957 297 RET Decker, R. A.; Peacock, M. L.; Watson, P.: Hirschsprung diseasein MEN 2A: increased spectrum of RET exon 10 genotypes and stronggenotype- phenotype correlation. Hum. Molec. Genet. 7: 129- 134, 1998. 3 C c

GAM7957 297 RET Donis- Keller, H.; Dou, S.; Chi, D.; Carlson, K. M.; Toshima, K.;Lairmore, T. C.; Howe, J. R.; Moley, J. F.; Goodfellow, P.; Wells,S. A., Jr.: Mutations in the RET proto- oncogene are associated withMEN 2A and FMTC. Hum. Molec. Genet. 2: 851- 856, 1993. 3 C c

GAM7957 297 RET Doray, B.; Salomon, R.; Amiel, J.; Pelet, A.; Touraine, R.; Billaud,M.; Attie, T.; Bachy, B.; Munnich, A.; Lyonnet, S.: Mutation of theRET ligand, neurturin, supports multigenic inheritance in Hirschsprungdisease. Hum. Molec. Genet. 7: 1449- 1452, 1998. 3 C c

GAM7957 297 RET Edery, P.; Lyonnet, S.; Mulligan, L. M.; Pelet, A.; Dow, E.; Abel,L.; Holder, S.; Nihoul- Fekete, C.; Ponder, B. A. J.; Munnich, A.:Mutations of the RET proto- oncogene in Hirschsprung's disease. Nature 367:378- 380, 1994. 3 C c

GAM7957 297 RET Eng, C.: The RET proto- oncogene in multiple endocrine neoplasiatype 2 and 3 C c

Hirschsprung's disease. New Eng. J. Med. 335: 943- 951,1996.

GAM7957 297 RET Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P. A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-oncogene and the von Hippel- Lindau disease tumoursuppressor gene in sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937, 1995. 3 C c

GAM7957 297 RET Eng, C.; Mulligan, L. M.: Mutations of the RET proto- oncogenein the multiple endocrine neoplasia type 2 syndromes, related sporadictumours, and Hirschsprung disease. Hum. Mutat. 9: 97- 109, 1997. 3 C c

GAM7957 297 RET Eng, C.; Mulligan, L. M.; Smith, D. P.; Healey, C. S.; Frilling,A.; Raue, F.; Neumann, H. P. H.; Pfragner, R.; Behmel, A.; Lorenzo,M. J.; Stonehouse, T. J.; Ponder, M. A.; Ponder, B. A. J.: Mutationof the RET protooncogene in sporadic medullary thyroid carcinoma. GenesChromosomes Cancer 12: 209- 212, 1995. 3 C c

GAM7957 297 RET Eng, C.; Smith, D. P.; Mulligan, L. M.; Healey, C. S.; Zvelebil,M. J.; Stonehouse, T. J.; Ponder, M. A.; Jackson, C. E.; Waterfield,M. D.; Ponder, B. A. J.: A novel point mutation in the tyrosine kinasedomain of the RET proto- oncogene in sporadic medullary thyroid carcinomaand in a family with FMTC. Oncogene 10: 509- 513, 1995. 3 C c

GAM7957 297 RET Eng, C.; Smith, D. P.; Mulligan, L. M.; Nagai, M. A.; Healey,C. S.; Ponder, M. A.; Gardner, E.; Scheumann, G. F. W.; Jackson, C.E.; Tunnacliffe, A.; Ponder, B. A. J.: Point mutation within thetyrosine kinase domain of the RET proto- oncogene in multiple endocrineneoplasia type 2B and related sporadic tumors. Hum. Molec. Genet. 3:237- 241, 1994. 3 C c

GAM7957 297 RET Farndon, J. R.; Leight, G. S.; Dilley, W. G.; Baylin, S. B.; Smallridge,R. C.; Harrison, T. S.; Wells, S. A., Jr.: Familial medullary thyroidcarcinoma without associated endocrinopathies: a distinct clinicalentity. Brit. J. Surg. 73: 278- 281, 1986. 3 C c

GAM7957 297 RET Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of cancer. Science 278: 1043- 1050, 1997. 3 C c

GAM7957 297 RET Fitze, G.; Schreiber, M.; Kuhlisch, E.; Schackert, H. K.; Roesner,D.: Association of RET protooncogene codon 45 polymorphism with Hirschsprungdisease. (Letter) Am. J. Hum. Genet. 65: 1469- 1473, 1999. 3 C c

GAM7957 297 RET Gardner, E.; Mulligan, L. M.; Eng, C.; Healey, C. S.; Kwok, J.B. J.; Ponder, M. A.; Ponder, B. A. J.: Haplotype analysis of MEN2 mutations. Hum. Molec. Genet. 3: 1771- 1774, 1994. 3 C c

GAM7957 297 RET Grieco, M.; Santoro, M.; Berlingieri, M. T.; Melillo, R. M.; Donghi,R.; Bongarzone, I.; Pierotti, M. A.; Della Porta, G.; Fusco, A.; Vecchio,G.: PTC is a novel rearranged form of the ret proto- oncogene andis frequently detected in vivo in human thyroid papillary carcinomas. Cell 60:557- 563, 1990. 3 C c

GAM7957 297 RET Hofstra, R. M. W.; Landsvater, R. M.; Ceccherini, I.; Stulp, R.P.; Stelwagen, T.; Luo, Y.; Pasini, B.; Hoppener, J. W. M.; Ploosvan Amstel, H. K.; Romeo, G.; Lips, C. J. M.; Buys, C. H. C. M.:A mutation in the RET proto- oncogene associated with multiple endocrineneoplasia type 2B and sporadic medullary thyroid carcinoma. Nature 367:375- 376, 1994. 3 C c

GAM7957 297 RET Hofstra, R. M. W.; Sijmons, R. H.; Stelwagen, T.; Stulp, R. P.;Kousseff, B. G.; Lips, C. J. M.; Steijlen, P. M.; Van Voorst Vader,P. C.; Buys, C. H. C. M.: RET mutation screening in familial cutaneouslichen amyloidosis and in 3 C c

skin amyloidosis associated with multipleendocrine neoplasia. J. Invest. Derm. 107: 215- 218, 1996.

GAM7957 297 RET Hoppener, J. W. M.; Lips, C. J. M.: RET receptor tyrosine kinasegene mutations: molecular biological, physiological and clinical aspects. Europ.J. Clin. Invest. 26: 613- 624, 1996. 3 C c

GAM7957 297 RET Hoppner, W.; Ritter, M. M.: A duplication of 12 bp in the criticalcysteine rich domain of the RET proto- oncogene results in a distinctphenotype of multiple endocrine neoplasia type 2A. Hum. Molec. Genet. 6:587- 590, 1997. 3 C c

GAM7957 297 RET Ikeda, I.; Ishizaka, Y.; Tahira, T.; Suzuki, T.; Onda, M.; Sugimura,T.; Nagao, M.: Specific expression of the ret proto- oncogene in humanneuroblastoma cell lines. Oncogene 5: 1291- 1296, 1990. 3 C c

GAM7957 297 RET Ishizaka, Y.; Itoh, F.; Tahira, T.; Ikeda, I.; Sugimura, T.; Tucker,J.; Fertitta, A.; Carrano, A. V.; Nagao, M.: Human ret proto- oncogenemapped to chromosome 10q11.2. Oncogene 4: 1519- 1521, 1989. 3 C c

GAM7957 297 RET Iwashita, T.; Murakami, H.; Asai, N.; Takahashi, M.: Mechanismof Ret dysfunction by Hirschsprung mutations affecting its extracellulardomain. Hum. Molec. Genet. 5: 1577- 1580, 1996. 3 C c

GAM7957 297 RET Japon, M. A.; Urbano, A. G.; Saez, C.; Segura, D. I.; Cerro, A.L.; Dieguez, C.; Alvarez, C. V.: Glial- derived neurotropic factorand RET gene expression in normal human anterior pituitary cell typesand in pituitary tumors. J. Clin. Endocr. Metab. 87: 1879- 1884,2002. 3 C c

GAM7957 297 RET Julies, M. G.; Moore, S. W.; Kotze, M. J.; du Plessis, L.: NovelRET mutations in Hirschsprung's disease patients from the diverseSouth African population. Europ. J. Hum. Genet. 9: 419- 423, 2001. 3 C c

GAM7957 297 RET Klugbauer, S.; Demidchik, E. P.; Lengfelder, E.; Rabes, H. M.: Detection of a novel type of RET rearrangement (PTC5) in thyroidcarcinomas after Chernobyl and analysis of the involved RET- fusedgene RFG5. Cancer Res. 58: 198- 203, 1998. 3 C c

GAM7957 297 RET Klugbauer, S.; Rabes, H. M.: The transcription coactivator HTIF1and a related protein are fused to the RET receptor tyrosine kinasein childhood papillary thyroid carcinomas. Oncogene 18: 4388- 4393,1999. 3 C c

GAM7957 297 RET Lairmore, T. C.; Dou, S.; Howe, J. R.; Chi, D.; Carlson, K.; Veile,R.; Mishra, S. K.; Wells, S. A., Jr.; Donis- Keller, H.: A 1.5- megabaseyeast artificial chromosome contig from human chromosome 10q11.2 connectingthree genetic loci (RET, D10S94, and D10S102) closely linked to theMEN2A locus. Proc. Nat. Acad. Sci. 90: 492- 496, 1993. 3 C c

GAM7957 297 RET Lombardo, F.; Baudin, E.; Chiefari, E.; Arturi, F.; Bardet, S.;Caillou, B.; Conte, C.; Dallapiccola, B.; Giuffrida, D.; Bidart, J.- M.;Schlumberger, M.; Filetti, S.: Familial medullary thyroid carcinoma:clinical variability and low aggressiveness associated with RET mutationat codon 804. J. Clin. Endocr. Metab. 87: 1674- 1680, 2002. 3 C c

GAM7957 297 RET Lore, F.; Di Cairano, G.; Talidis, F.: Unilateral renal agenesisin a family with medullary thyroid carcinoma. (Letter) New Eng. J.Med. 342: 1218- 1219, 2000. 3 C c

GAM7957 297 RET Machens, A.; Gimm, O.; Hinze, R.; Hoppner, W.; Boehm, B. O.; Dralle,H.: Genotype- phenotype correlations in hereditary medullary thyroidcarcinoma: oncological features and biochemical properties. J. Clin.Endocr. Metab. 86: 1104- 1109, 2001. 3 C c

GAM7957 297 RET Mendelsohn, C.; et al; et al: Function of the retinoic acid receptors(RARs) during development (II). Multiple abnormalities at variousstages of 3 C c

organogenesis in RAR double mutants. Development 120:2749- 2771, 1994.

GAM7957 297 RET Menko, F. H.; van der Luijt, R. B.; de Valk, I. A. J.; Toorians,A. W. F. T.; 3 C c Sepers, J. M.; van Diest, P. J.; Lips, C. J. M.: AtypicalMEN type 2B associated with two germline RET mutations on the sameallele not involving codon 918. J. Clin. Endocr. Metab. 87: 393- 397,2002.

GAM7957 297 RET Mulligan, L. M.; Eng, C.; Healey, C. S.; Clayton, D.; Kwok, J.B. J.; 3 C c Gardner, E.; Ponder, M. A.; Frilling, A.; Jackson, C. E.; Lehnert,H.; Neumann, H. P. H.; Thibodeau, S. N.; Ponder, B. A. J.: Specificmutations of the RET proto- oncogene are related to disease phenotypein MEN 2A and FMTC. Nature Genet. 6: 70- 74, 1994.

GAM7957 297 RET Mulligan, L. M.; Kwok, J. B. J.; Healey, C. S.; Elsdon, M. J.;Eng, C.; 3 C c Gardner, E.; Love, D. R.; Mole, S. E.; Moore, J. K.; Papi,L.; Ponder, M. A.; Telenius, H.; Tunnacliffe, A.; Ponder, B. A. J.: Germ- line mutations of the RET proto- oncogene in multiple endocrineneoplasia type 2A. Nature 363: 458- 460, 1993.

GAM7957 297 RET Munnes, M.; Fanaei, S.; Schmitz, B.; Muiznieks, I.; Holschneider,A. M.; 3 C c Doerfler, W.: Familial form of Hirschsprung disease: nucleotidesequence studies reveal point mutations in the RET proto- oncogenein two of six families but not in other candidate genes. Am. J. Med.Genet. 94: 19- 27, 2000.

GAM7957 297 RET Nakata, T.; Kitamura, Y.; Shimizu, K.; Tanaka, S.; Fujimori, M.;Yokoyama, 3 C c S.; Ito, K.; Emi, M.: Fusion of a novel gene, ELKS, toRET due to translocation t(10;12)(q11;p13) in a papillary thyroidcarcinoma. Genes Chromosomes Cancer 25: 97- 103, 1999.

GAM7957 297 RET Niccoli- Sire, P.; Murat, A.; Rohmer, V.; Franc, S.; Chabrier,G.; Baldet, 3 C c L.; Maes, B.; Savagner, F.; Giraud, S.; Bezieau, S.; Kottler,M.- L.; Morange, S.; Conte- Devolx, B.: The French Calcitonin TumorsStudy Group (GETC).: Familial medullary thyroid carcinoma with noncysteineRET mutations: phenotype- genotype relationship in a large series ofpatients. J. Clin. Endocr. Metab. 86: 3746- 3753, 2001.

GAM7957 297 RET Pachnis, V.; Mankoo, B.; Costantini, F.: Expression of the c- retproto- 3 C c oncogene during mouse embryogenesis. Development 119: 1005- 1017,1993.

GAM7957 297 RET Pasini, B.; Hofstra, R. M. W.; Yin, L.; Bocciardi, R.; Santamaria,G.; 3 C c Grootscholten, P. M.; Ceccherini, I.; Patrone, G.; Priolo, M.;Buys, C. H. C. M.; Romeo, G.: The physical map of the human RET proto- oncogene. Oncogene 11:1737- 1743, 1995.

GAM7957 297 RET Pelet, A.; Geneste, O.; Edery, P.; Pasini, A.; Chappuis, S.; Attie,T.; 3 C c Munnich, A.; Lenoir, G.; Lyonnet, S.; Billaud, M.: Various mechanismscause RET- mediated signaling defects in Hirschsprung's disease. J.Clin. Invest. 101: 1415- 1423, 1998.

GAM7957 297 RET Pierotti, M. A.; Santoro, M.; Jenkins, R. B.; Sozzi, G.; Bongarzone,I.; 3 C c Grieco, M.; Monzini, N.; Miozzo, M.; Herrmann, M. A.; Fusco, A.;Hay, I. D.; Della Porta, G.; Vecchio, G.: Characterization of aninversion on the long arm of chromosome 10 juxtaposing D10S170 andRET and creating the oncogenic sequence RET/PTC. Proc. Nat. Acad.Sci. 89: 1616- 1620, 1992.

GAM7957 297 RET Pigny, P.; Bauters, C.; Wemeau, J.- L.; Houcke, M. L.; Crepin,M.; Caron, P.; 3 C c Giraud, S.; Calender, A.; Buisine, M.- P.; Kerckaert,J.- P.; Porchet, N.: A novel 9- base pair duplication in RET exon 8in familial medullary thyroid carcinoma. J. Clin. Endocr. Metab. 84:1700- 1704, 1999.

GAM7957 297 RET Puffenberger, E. G.; Hosoda, K.; Washington, S. S.; Nakao, K.;deWit, D.; 3 C c

Yanagisawa, M.; Chakravarti, A.: A missense mutation ofthe endothelin- B receptor gene in multigenic Hirschsprung's disease. Cell 79:1257- 1266, 1994.

GAM7957 297 RET Robinson, M. F.; Cote, G. J.; Nunziata, V.; Brandi, M. L.; Ferrer,J. P.; Martins Bugalho, M. J. G.; Almeida Ruas, M. M.; Chik, C.; Colantuoni,V.; Gagel, R. F.: Mutation of a specific codon of the RET proto- oncogenein the multiple endocrine neoplasia type 2A/cutaneous lichen amyloidosissyndrome. (Abstract) Fifth International Workshop on Multiple EndocrineNeoplasia, Stockholm, Archipelago , 1994. 3 C c

GAM7957 297 RET Rodrigues, G. A.; Park, M.: Dimerization mediated through a leucinezipper activates the oncogenic potential of the met receptor tyrosinekinase. Molec. Cell. Biol. 13: 6711- 6722, 1993. 3 C c

GAM7957 297 RET Romeo, G.; Ronchetto, P.; Luo, Y.; Barone, V.; Seri, M.; Ceccherini,I.; Pasini, B.; Bocciardi, R.; Lerone, M.; Kaariainen, H.; Martucciello,G.: Point mutations affecting the tyrosine kinase domain of the RETproto- oncogene in Hirschsprung's disease. Nature 367: 377- 378, 1994. 3 C c

GAM7957 297 RET Salvatore, D.; Barone, M. V.; Salvatore, G.; Melillo, R. M.; Chiappetta,G.; Mineo, A.; Fenzi, G.; Vecchio, G.; Fusco, A.; Santoro, M.: Tyrosines1015 and 1062 are in vivo autophosphorylation sites in Ret and Ret- derivedoncoproteins. J. Clin. Endocr. Metab. 85: 3898- 3907, 2000. 3 C c

GAM7957 297 RET Santoro, M.; Carlomagno, F.; Hay, I. D.; Herrmann, M. A.; Grieco,M.; Melillo, R.; Pierotti, M. A.; Bongarzone, I.; Della Porta, G.;Berger, N.; Peix, J. L.; Paulin, C.; Fabien, N.; Vecchio, G.; Jenkins,R. B.; Fusco, A.: Ret oncogene activation in human thyroid neoplasmsis restricted to the papillary cancer subtype. J. Clin. Invest. 89:1517- 1522, 1992. 3 C c

GAM7957 297 RET Santoro, M.; Carlomagno, F.; Romano, A.; Bottaro, D. P.; Dathan,N. A.; Grieco, M.; Fusco, A.; Vecchio, G.; Matoskova, B.; Kraus, M.H.; Di Fiore, P. P.: Activation of RET as a dominant transforminggene by germline mutations of MEN2A and MEN2B. Science 267: 381- 383,1995. 3 C c

GAM7957 297 RET Schuchardt, A.; D'Agati, V.; Larsson- Blomberg, L.; Costantini,F.; Pachnis, V.: Defects in the kidney and enteric nervous systemof mice lacking the tyrosine kinase receptor Ret. Nature 367: 380- 383,1994. 3 C c

GAM7957 297 RET Seri, M.; Celli, I.; Betsos, N.; Claudiani, F.; Camera, G.; Romeo,G.: A cys634gly substitution of the RET proto- oncogene in a familywith recurrence of multiple endocrine neoplasia type 2A and cutaneouslichen amyloidosis. Clin. Genet. 51: 86- 90, 1997. 3 C c

GAM7957 297 RET Seri, M.; Yin, L.; Barone, A.; Bolino, A.; Celli, I.; Bocciardi,R.; Pasini, B.; Ceccherini, I.; Lerone, M.; Kristoffersson, U.; Larsson,L. T.; Casasa, J. M.; Cass, D. T.; Abramowicz, M. J.; Vanderwinden,J.- M.; Kravcenkiene, I.; Baric, I.; Silengo, M.; Martucciello, G.;Romeo, G.: Frequency of RET mutations in long- and short- segmentHirschsprung disease. Hum. Mutat. 9: 243- 249, 1997. 3 C c

GAM7957 297 RET Shirahama, S.; Ogura, K.; Takami, H.; Ito, K.; Tohsen, T.; Miyauchi,A.; Nakamura, Y.: Mutational analysis of the RET proto- oncogene in71 Japanese patients with medullary thyroid carcinoma. J. Hum. Genet. 43:101- 106, 1998. 3 C c

GAM7957 297 RET Svensson, P.- J.; Anvret, M.; Molander, M.- L.; Nordenskjold, A.: Phenotypic variation in a family with mutations in two Hirschsprung- relatedgenes (RET and endothelin receptor B). Hum. Genet. 103: 145- 148,1998. 3 C c

GAM7957 297 RET Takahashi, M.; Buma, Y.; Hiai, H.: Isolation of ret proto- oncogenecDNA with an amino- terminal signal sequence. Oncogene 4: 805- 806,1989. 3 C c

GAM7957 297 RET Takahashi, M.; Buma, Y.; Iwamoto, T.; Inaguma, Y.; Ikeda, H.;Hiai, H.: 3 C c
Cloning and expression of the ret proto- oncogene encodinga tyrosine kinase with two potential transmembrane domains. Oncogene 3:571- 578, 1988.

GAM7957 297 RET Takahashi, M.; Ritz, J.; Cooper, G. M.: Activation of a novelhuman 3 C c
transforming gene, ret, by DNA rearrangement. Cell 42: 581- 588,1985.

GAM7957 297 RET Tessitore, A.; Sinisi, A. A.; Pasquali, D.; Cardone, M.; Vitale,D.; 3 C c
Bellastella, A.; Colantuoni, V.: A novel case of multiple endocrineneoplasia type 2A associated with two de novo mutations of the RETprotooncogene. J. Clin. Endocr. Metab. 84: 3522- 3527, 1999.

GAM7957 297 RET van Heyningen, V.: One gene- - four syndromes. Nature 367: 319- 320,1994. 3 C c

GAM7957 297 RET Xue, F.; Yu, H.; Maurer, L. H.; Memoli, V. A.; Nutile- McMenemey,N.; 3 C c
Schuster, M. K.; Bowden, D. W.; Mao, J.; Noll, W. W.: GermlineRET mutations in MEN 2A and FMTC and their detection by simple DNAdiagnostic tests. Hum. Molec. Genet. 3: 635- 638, 1994.

GAM7957 297 RET Yin, L.; Ceccherini, I.; Pasini, B.; Matera, I.; Bicocchi, M.P.; Barone, V.; 3 C c
Bocciardi, R.; Kaariainen, H.; Weber, D.; Devoto,M.; Romeo, G.: Close linkage with the RET protooncogene and boundariesof deletion mutations in autosomal dominant Hirschsprung disease. Hum.Molec. Genet. 2: 1803- 1808, 1993.

GAM7957 297 REV3L Gibbs, P. E. M.; McGregor, W. G.; Maher, V. M.; Nisson, P.; Lawrence,C. W.: 3 C c
A human homolog of the Saccharomyces cerevisiae REV3 gene,which encodes the catalytic subunit of DNA polymerase zeta. Proc.Nat. Acad. Sci. 95: 6876- 6880, 1998.

GAM7957 297 REV3L Morelli, C.; Mungall, A. J.; Negrini, M.; Barbanti- Brodano, G.;Croce, C. 3 C c
M.: Alternative splicing, genomic structure, and fine chromosomelocalization of REV3L. Cytogenet. Cell Genet. 83: 18- 20, 1998.

GAM7957 297 REV3L Xiao, W.; Lechler, T.; Chow, B. L.; Fontanie, T.; Agustus, M.;Carter, K. C.; 3 C c
Wei, Y.- F.: Identification, chromosomal mapping andtissue- specific expression of hREV3 encoding a putative human DNApolymerase zeta. Carcinogenesis 19: 945- 949, 1998.

GAM7957 297 RFC2 Okumura, K.; Nogami, M.; Taguchi, H.; Dean, F. B.; Chen, M.; Pan,Z.- Q.; 3 C c
Hurwitz, J.; Shiratori, A.; Murakami, Y.; Ozawa, K.; Eki, T.: Assignment of the 36.5- kDa (RFC5), 37- kDa (RFC4), 38- kDa (RFC3),and 40- kDa (RFC2) subunit genes of human replication factor C to chromosomebands 12q24.2- q24.3, 3q27, 13q12.3- q13, and 7q11.23. Genomics 25:274- 278, 1995.

GAM7957 297 RFC2 Peoples, R.; Perez- Jurado, L.; Wang, Y.- K.; Kaplan, P.; Francke,U.: The 3 C c
gene for replication factor C subunit 2 (RFC2) is withinthe 7q11.23 Williams syndrome deletion. (Letter) Am. J. Hum. Genet. 58:1370- 1373, 1996.

GAM7957 297 RFC2 Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin,J.: BASC, a 3 C c
super complex of BRCA1- associated proteins involved inthe recognition and repair of aberrant DNA structures. Genes Dev. 14:927- 939, 2000.

GAM7957 297 RIMS1 Betz, A.; Thakur, P.; Junge, H. J.; Ashery, U.; Rhee, J.- S.; Scheuss,V.; 3 C b
Rosenmund, C.; Rettig, J.; Brose, N.: Functional interactionof the active zone proteins Munc13- 1 and RIM1 in synaptic vesiclepriming. Neuron 30: 183- 196, 2001.

GAM7957 297 RIMS1 Castillo, P. E.; Schoch, S.; Schmitz, F.; Sudhof, T. C.; Malenka,R. C.: 3 C b
RIM1- alpha is required for presynaptic long- term potentiation. Nature 415:327- 330, 2002.

GAM7957 297 RIMS1 Coppola, T.; Magnin- Luthi, S.; Perret- Menoud, V.; Gattesco, S.;Schiavo, 3 C b
G.; Regazzi, R.: Direct interaction of the Rab3 effectorRIM with Ca(2+)

channels, SNAP- 25, and synaptotagmin. J. Biol. Chem. 276:32756- 32762, 2001.

GAM7957 297 RIMS1 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 C b

GAM7957 297 RIMS1 Schoch, S.; Castillo, P. E.; Jo, T.; Mukherjee, K.; Geppert, M.;Wang, Y.; Schmitz, F.; Malenka, R. C.; Sudhof, T. C.: RIM1- alphaforms a protein scaffold for regulating neurotransmitter release atthe active zone. Nature 415: 321- 326, 2002. 3 C b

GAM7957 297 RIMS1 Wang, Y.; Sugita, S.; Sudhof, T. C.: The RIM/NIM family of neuronalC- 2 domain proteins: interactions with Rab3 and a new class of Srchomology 3 domain proteins. J. Biol. Chem. 275: 20033- 20044, 2000. 3 C b

GAM7957 297 ROCK2 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified human genes. X. The complete sequences of 100 newcDNA clones from brain which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998. 3 C c

GAM7957 297 ROCK2 Nakamura, M.; Nagano, T.; Chikama, T.; Nishida, T.: Role of thesmall GTP- binding protein Rho in epithelial cell migration in therabbit cornea. Invest. Ophthal. Vis. Sci. 42: 941- 947, 2001. 3 C c

GAM7957 297 ROCK2 Rao, P. V.; Deng, P.- F.; Kumar, J.; Epstein, D. L.: Modulationof aqueous humor outflow facility by the Rho kinase- specific inhibitorY- 27632. Invest. Ophthal. Vis. Sci. 42: 1029- 1037, 2001. 3 C c

GAM7957 297 ROCK2 Takahashi, N.; Tuiki, H.; Saya, H.; Kaibuchi, K.: Localizationof the gene coding for ROCK II/Rho kinase on human chromosome 2p24. Genomics 55:235- 237, 1999. 3 C c

GAM7957 297 RPN1 Barton, D. E.; Crimaudo, C.; Hortsch, M.; Francke, U.: The genesfor ribophorins I and II are on human chromosomes 3q and 20 and mousechromosomes 6 and 12, respectively. (Abstract) Cytogenet. Cell Genet. 46:577 only, 1987. 3 C c

GAM7957 297 RPN1 Crimaudo, C.; Hortsch, M.; Gausepohl, H.; Meyer, D. I.: Humanribophorins I and II: the primary structure and membrane topologyof two highly conserved round endoplasmic reticulum- specific glycoproteins. EMBOJ. 6: 75- 82, 1987. 3 C c

GAM7957 297 RPN1 Elsasser, S.; Gali, R. R.; Schwickart, M.; Larsen, C. N.; Leggett,D. S.; Muller, B.; Feng, M. T.; Tubing, F.; Dittmar, G. A. G.; Finley,D.: Proteasome subunit Rpn1 binds ubiquitin- like protein domains. NatureCell Biol. 4: 725- 730, 2002. 3 C c

GAM7957 297 RPN1 Kelleher, D. J.; Kreibich, G.; Gilmore, R.: Oligosaccharyltransferaseactivity is associated with a protein complex composed of ribophorinsI and II and a 48 kd protein. Cell 69: 55- 65, 1992. 3 C c

GAM7957 297 SCAP2 Kouroku, Y.; Soyama, A.; Fujita, E.; Urase, K.; Tsukahara, T.;Momoi, T.: RA70 is a src kinase- associated protein expressed ubiquitously. Biochem.Biophys. Res. Comm. 252: 738- 742, 1998. 3 C b

GAM7957 297 SCAP2 Liu, J.; Kang, H.; Raab, M.; da Silva, A. J.; Kraeft, S.- K.; Rudd,C. E.: FYB (FYN binding protein) serves as a binding partner forlymphoid protein and FYN kinase substrate SKAP55 and a SKAP55- relatedprotein in T cells. Proc. Nat. Acad. Sci. 95: 8779- 8784, 1998. 3 C b

GAM7957 297 SCAP2 Marie- Cardine, A.; Verhagen, A. M.; Eckerskorn, C.; Schraven, B.: SKAP- HOM, a novel adaptor protein homologous to the FYN- associatedprotein SKAP55. FEBS Lett. 435: 55- 60, 1998. 3 C b

GAM7957 297 SCN2B Bolino, A.; Seri, M.; Caroli, F.; Eubanks, J.; Srinivasan, J.;Mandich, P.; 3 C b
Schenone, A.; Quattrone, A.; Romeo, G.; Catterall, W.A.; Devoto, M.:
Exclusion of the SCN2B gene as candidate for CMT4B. Europ.J. Hum. Genet. 6:
629- 634, 1998.

GAM7957 297 SCN2B Eubanks, J.; Srinivasan, J.; Dinulos, M. B.; Disteche, C. M.; Catterall,W. 3 C b
A.: Structure and chromosomal localization of the beta2 subunitof the human
brain sodium channel. Neuroreport 8: 2775- 2779, 1997.

GAM7957 297 SCN2B Imai, K.; Kingsley, D. M.: Mouse chromosome 9. Mammalian Genome 5:S139- 3 C b
S153, 1994.

GAM7957 297 SCN2B Isom, L. L.; Ragsdale, D. S.; De Jongh, K. S.; Westenbroek, R.E.; Reber, B. 3 C b
F. X.; Scheuer, T.; Catterall, W. A.: Structure andfunction of the beta- 2
subunit of brain sodium channels, a transmembraneglycoprotein with a CAM
motif. Cell 83: 433- 442, 1995.

GAM7957 297 SCN2B Jones, J. M.; Meisler, M. H.; Isom, L. L.: Scn2b, a voltage- gatedsodium 3 C b
channel beta- 2 gene on mouse chromosome 9. Genomics 34: 258- 259,1996.

GAM7957 297 SHFM3 Gurrieri, F.; Genuardi, M.; Chiurazzi, P.; Gillessen- Kaesbach,G.; Neri, G.: 3 C c
Exclusion of linkage between autosomal dominant splithand/split foot and
markers from chromosome 7q: further evidence forgenetic heterogeneity.
(Letter) Am. J. Hum. Genet. 55: 853- 855,1994.

GAM7957 297 SHFM3 Gurrieri, F.; Prinos, P.; Tackels, D.; Kilpatrick, M. W.; Allanson,J.; 3 C c
Genuardi, M.; Vuckov, A.; Nanni, L.; Sangiorgi, E.; Garofalo,G.; Nunes, M.
E.; Neri, G.; Schwartz, C.; Tsipouras, P.: A splithand- split foot (SHFM3)
gene is located at 10q24- q25. Am. J. Med.Genet. 62: 427- 436, 1996.

GAM7957 297 SHFM3 Ianakiev, P.; Kilpatrick, M. W.; Dealy, C.; Kosher, R.; Korenberg,J. R.; 3 C c
Chen, X.- N.; Tsipouras, P.: A novel human gene encoding anF- box/WD40
containing protein maps in the SHFM3 critical region on10q24. Biochem.
Biophys. Res. Commun. 261: 64- 70, 1999.

GAM7957 297 SHFM3 Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen- Guillouzo, C.:cDNA cloning 3 C c
and expression analysis of new members of the mammalianF- box protein
family. Genomics 67: 40- 47, 2000.

GAM7957 297 SHFM3 Johnson, K. R.; Lane, P. W.; Ward- Bailey, P.; Davisson, M. T.:Mapping the 3 C c
mouse dactylaplasia mutation, Dac, and a gene that controlsits expression,
mdac. Genomics 29: 457- 464, 1995.

GAM7957 297 SHFM3 Nunes, M. E.; Schutt, G.; Kapur, R. P.; Luthardt, F.; Kukolich,M.; Byers, 3 C c
P.; Evans, J. P.: A second autosomal split hand/foot locusmaps to chromosome
10q24- q25. Hum. Molec. Genet. 4: 2165- 2170, 1995.

GAM7957 297 SHFM3 Ozen, R. S.; Baysal, B. E.; Devlin, B.; Farr, J. E.; Gorry, M.;Ehrlich, G. 3 C c
D.; Richard, C. W., III: Fine mapping of the split- hand/split- footlocus
(SHFM3) at 10q24: evidence for anticipation and segregationdistortion. Am.
J. Hum. Genet. 64: 1646- 1654, 1999.

GAM7957 297 SHFM3 Palmer, S. E.; Scherer, S. W.; Kukolich, M.; Wijsman, E. M.; Tsui,L.- C.; 3 C c
Stephens, K.; Evans, J. P.: Evidence for locus heterogeneityin human
autosomal dominant split hand/split foot malformation. Am.J. Hum. Genet. 55:
21- 26, 1994.

GAM7957 297 SHFM3 Raas- Rothschild, A.; Manouvrier, S.; Gonzales, M.; Farriaux, J.P.; Lyonnet, 3 C c
S.; Munnich, A.: Refined mapping of a gene for splithand- split foot
malformation (SHFM3) on chromosome 10q25. J. Med.Genet. 33: 996- 1001, 1996.

GAM7957 297 SHFM3 Sidow, A.; Bulotsky, M. S.; Kerrebrock, A. W.; Birren, B. W.;Altshuler, D; 3 C c
Jaenisch, R.; Johnson, K. R.; Lander, E. S.: A novelmember of the F-

box/WD40 gene family, encoding dactylin, is disruptedin the mouse dactylaplasia mutant. Nature Genet. 23: 104- 107, 1999.

GAM7957 297 SHOC2 Selfors, L. M.; Schutzman, J. L.; Borland, C. Z.; Stern, M. J.: Soc- 2 3 C c
encodes a leucine- rich repeat protein implicated in fibroblastgrowth factor receptor signaling. Proc. Nat. Acad. Sci. 95: 6903- 6908,1998.

GAM7957 297 SHOC2 Sieburth, D. S.; Sun, Q.; Han, M.: SUR- 8, a conserved Ras- bindingprotein 3 C c
with leucine- rich repeats, positively regulates Ras- mediatedsignaling in C. elegans. Cell 94: 119- 130, 1998.

GAM7957 297 SIM2 Chen, H.; Chrast, R.; Rossier, C.; Gos, A.; Antonarakis, S. E.;Kudoh, J.; 3 C b
Yamaki, A.; Shindoh, N.; Maeda, H.; Minoshima, S.; Shimizu,N.: Single- minded and Down syndrome? (Letter) Nature Genet. 10:9- 10, 1995.

GAM7957 297 SIM2 Chrast, R.; Scott, H. S.; Madani, R.; Huber, L.; Wolfer, D. P.;Prinz, M.; 3 C b
Aguzzi, A.; Lipp, H.- P.; Antonarakis, S. E.: Mice trisomicfor a bacterial artificial chromosome with the single- minded 2 gene(Sim2) show phenotypes similar to some of those present in the partialtrisomy 16 mouse models of Down syndrome. Hum. Molec. Genet. 9:1853- 1864, 2000.

GAM7957 297 SIM2 Dahmane, N.; Charron, G.; Lopes, C.; Yaspo, M.- L.; Maunoury, C.;Decorte, 3 C b
L.; Sinet, P.- M.; Bloch, B.; Delabar, J.- M.: Down syndrome- criticalregion contains a gene homologous to Drosophila sim expressed duringrat and human central nervous system development. Proc. Nat. Acad.Sci. 92: 9191- 9195, 1995.

GAM7957 297 SIM2 Ema, M.; Ikegami, S.; Hosoya, T.; Mimura, J.; Ohtani, H.; Nakao,K.; 3 C b
Inokuchi, K.; Katsuki, M.; Fujii- Kuriyama, Y.: Mild impairmentof learning and memory in mice overexpressing the mSim2 gene locatedon chromosome 16: an animal model of Down's syndrome. Hum. Molec.Genet. 8: 1409- 1415, 1999.

GAM7957 297 SIM2 Moffett, P.; Dayo, M.; Reece, M.; McCormick, M. K.; Pelletier,J.: 3 C b
Characterization of msim, a murine homologue of the Drosophilasim transcription factor. Genomics 35: 144- 155, 1996.

GAM7957 297 SIM2 Muenke, M.; Bone, L. J.; Mitchell, H. F.; Hart, I.; Walton, K.;Hall- 3 C b
Johnson, K.; Ippel, E. F.; Dietz- Band, J.; Kvaloy, K.; Fan, C.- M.;Tessier-Lavigne, M.; Patterson, D.: Physical mapping of the holoprosencephalycritical region in 21q22.3, exclusion of SIM2 as a candidate genefor holoprosencephaly, and mapping of SIM2 to a region of chromosome21 important for Down syndrome. Am. J. Hum. Genet. 57: 1074-1079,1995.

GAM7957 297 SIM2 Yamaki, A.; Noda, S.; Kudoh, J.; Shindoh, N.; Maeda, H.; Minoshima,S.; 3 C b
Kawasaki, K.; Shimizu, Y.; Shimizu, N.: The mammalian single- minded(SIM) gene: mouse cDNA structure and diencephalic expression indicatea candidate gene for Down syndrome. Genomics 35: 136- 143, 1996.

GAM7957 297 SLC14A1 Barbosa, J.; Rich, S.; Dunsworth, T.; Swanson, J.: Linkage 3 C c
disequilibriumbetween insulin- dependent diabetes and the Kidd blood group Jk(b)allele. J. Clin. Endocr. Metab. 55: 193- 195, 1982.

GAM7957 297 SLC14A1 Field, L. L.; Marazita, M. L.; Spence, M. A.; Crandall, B. F.;Sparkes, R. 3 C c
S.: Is JK linked to IGK on chromosome 2? (Abstract) Cytogenet.Cell Genet. 40: 628- 629, 1985.

GAM7957 297 SLC14A1 Gedde- Dahl, T.: Personal Communication. Oslo, Norway 9/26/1986. 3 C c

GAM7957 297 SLC14A1 Geitvik, G. A.; Hoyheim, B.; Gedde- Dahl, T.; Grzeschik, K. H.;Lothe, R.; 3 C c
Tomter, H.; Olaisen, B.: The Kidd (JK) blood group locusassigned to chromosome 18 by close linkage to a DNA- RFLP. Hum. Genet. 77:205- 209, 1987.

GAM7957 297 SLC14A1 Hodge, S. E.; Anderson, C. E.; Neiswanger, K.; Field, L. L.; Spence,M. A.; 3 C c
Sparkes, R. S.; Sparkes, M. C.; Crist, M.; Terasaki, P. I.;Rimoin, D. L.;
Rotter, J. I.: Close genetic linkage between diabetesmellitus and Kidd blood
group. Lancet II: 893- 895, 1981.

GAM7957 297 SLC14A1 Hulten, M.; Lindsten, J.; Pen- Ming, L. M.; Fraccaro, M.; Mannini,A.; 3 C c
Trepolo, L.; Robson, E. B.; Heiken, A.; Tellingen, K. G.:
Possiblelocalization of the genes for the Kidd blood group on an
autosomeinvolved in a reciprocal translocation. Nature 211: 1067- 1068,
1968.

GAM7957 297 SLC14A1 Keats, B. J. B.; Morton, N. E.; Rao, D. C.: Likely linkage: InVwith Jk. Hum. 3 C c
Genet. 39: 157- 159, 1977.

GAM7957 297 SLC14A1 Keats, B. J. B.; Morton, N. E.; Rao, D. C.: Possible linkages(lod score over 3 C c
1.5) and a tentative map of the Jk- Km linkage group. Cytogenet.Cell Genet.
22: 304- 308, 1978.

GAM7957 297 SLC14A1 Leppert, M.; Ferrell, R.; Kamboh, M. I.; Beasley, J.; O'Connell,P.; Lathrop, 3 C c
M.; Lalouel, J.- M.; White, R.: Linkage of the polymorphicprotein markers
F13B, C1S, C1R, and blood group antigen Kidd in CEPHreference families.
(Abstract) Cytogenet. Cell Genet. 46: 647, 1987.

GAM7957 297 SLC14A1 Lucien, N.; Chiaroni, J.; Cartron, J.- P.; Bailly, P.: Partialdeletion in 3 C c
the JK locus causing a Jk(null) phenotype. Blood 99:1079- 1081, 2002.

GAM7957 297 SLC14A1 Lucien, N.; Sidoux- Walter, F.; Olives, B.; Moulds, J.; Le Pennec,P.- Y.; 3 C c
Cartron, J.- P.; Bailly, P.: Characterization of the gene encodingthe human
Kidd blood group/urea transporter protein: evidence forsplice site mutations
in Jk- null individuals. J. Biol. Chem. 273:12973- 12980, 1998.

GAM7957 297 SLC14A1 Mace, M. A.; Robson, E. B.: Linkage data on ACP- 1 and MNSs. Cytogenet.Cell 3 C
c
Genet. 13: 123- 125, 1974.

GAM7957 297 SLC14A1 Mohr, J.; Eiberg, H.: Colton blood groups: indication of linkagewith the 3 C c
Kidd (Jk) system as support for assignment to chromosome7. Clin. Genet. 11:
372- 374, 1977.

GAM7957 297 SLC14A1 Olives, B.; Mattei, M.- G.; Huet, M.; Neau, P.; Martial, S.; Cartron,J.- P.; 3 C c
Bailly, P.: Kidd blood group and urea transport function ofhuman
erythrocytes are carried by the same protein. J. Biol. Chem. 270:15607-
15610, 1995.

GAM7957 297 SLC14A1 Olives, B.; Merriman, M.; Bailly, P.; Bain, S.; Barnett, A.; Todd,J.; 3 C c
Cartron, J.- P.; Merriman, T.: The molecular basis of the Kiddblood group
polymorphism and its lack of association with type 1 diabetessusceptibility.
Hum. Molec. Genet. 6: 1017- 1020, 1997.

GAM7957 297 SLC14A1 Olives, B.; Neau, P.; Bailly, P.; Hediger, M. A.; Rousselet, G.;Cartron, J.- 3 C c
P.; Ripoche, P.: Cloning and functional expression ofa urea transporter from
human bone marrow cells. J. Biol. Chem. 269:31649- 31652, 1994.

GAM7957 297 SLC14A1 Pausch, V.; Mayr, W. R.: Analysis of the linkage JK- IGK, MNS- GCand of two 3 C c
other possible linkage groups. Hum. Hered. 37: 260- 262,1987.

GAM7957 297 SLC14A1 Promeneur, D.; Rousselet, G.; Bankir, L.; et al: Evidence fordistinct 3 C c
vascular and tubular urea transporters in the rat kidney. J.Am. Soc.
Nephrol. 7: 852- 860, 1996.

GAM7957 297 SLC14A1 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 C c
New York: Oxford Univ. Press (pub.) 1988.

GAM7957 297 SLC14A1 Sands, J. M.; Gargus, J. J.; Frohlich, O.; Gunn, R. B.; Kokko,J. P.: Urinary 3 C c
concentrating ability in patients with Jk(a/b) bloodtype who lack carrier-

mediated urea transport. J. Am. Soc. Nephrol. 2:1689- 1696, 1992.

GAM7957 297 SLC14A1 Sherman, S. L.; Simpson, S. P.: Evidence for the location ofJK and CO on chromosome 2 based on family studies. (Abstract) Cytogenet.Cell Genet. 40: 743, 1985. 3 C c

GAM7957 297 SLC14A1 Shokeir, M. H. K.; Ying, K. L.; Pabello, P.: Deletion of thelong arm of chromosome no. 7: tentative assignment of the Kidd (Jk)locus. Clin. Genet. 4: 360- 368, 1973. 3 C c

GAM7957 297 SLC14A1 Sidoux- Walter, F.; Lucien, N.; Nissinen, R.; Sistonen, P.; Henry,S.; Moulds, J.; Cartron, J.- P.; Bailly, P.: Molecular heterogeneityof the Jk- null phenotype: expression analysis of the Jk(S291P) mutationfound in Finns. Blood 96: 1566- 1573, 2000. 3 C c

GAM7957 297 SLC14A1 Tsukaguchi, H.; Shayakul, C.; Berger, U. V.; Tokui, T.; Brown,D.; Hediger, M. A.: Cloning and characterization of the urea transportationUT3: localization in rat kidney and testis. J. Clin. Invest. 99:1506- 1515, 1997. 3 C c

GAM7957 297 SLC14A1 Xu, Y.; Olives, B.; Bailly, P.; et al: Endothelial cells of thekidney vasa recta express the urea transporter HUT11. Kidney Int. 51:138- 146, 1997. 3 C c

GAM7957 297 SLC14A2 DeStefano, A. L.; Baldwin, C. T.; Burzstyn, M.; Gavras, I.; Handy,D. E.; Joost, O.; Martel, T.; Nicolaou, M.; Schwartz, F.; Streeten,D. H. P.; Farrer, L. A.; Gavras, H.: Autosomal dominant orthostatichypotensive disorder maps to chromosome 18q. Am. J. Hum. Genet. 63:1425- 1430, 1998. 3 C b

GAM7957 297 SLC14A2 Olives, B.; Martial, S.; Mattei, M.- G.; Matassi, G.; Rousselet,G.; Ripoche, P.; Cartron, J.- P.; Bailly, P.: Molecular characterizationof a new urea transporter in the human kidney. FEBS Lett. 386: 156- 160,1996. 3 C b

GAM7957 297 SLC14A2 Ranade, K.; Wu, K.- W.; Hwu, C.- M.; Ting, C.- T.; Pei, D.; Pesich,R.; Hebert, J.; Chen, Y.- D. I.; Pratt, R.; Olshen, R.; Masaki, K.;Risch, N.; Cox, D. R.; Botstein, D.: Genetic variation in the humanurea transporter- 2 is associated with variation in blood pressure. Hum.Molec. Genet. 10: 2157- 2164, 2001. 3 C b

GAM7957 297 SLC17A5 Aula, N.; Salomaki, P.; Timonen, R.; Verheijen, F.; Mancini, G.;Mansson, J.- E.; Aula, P.; Peltonen, L.: The spectrum of SLC17A5- genemutations resulting in free sialic acid- storage diseases indicatessome genotype- phenotype correlation. Am. J. Hum. Genet. 67: 832- 840,2000. 3 C c

GAM7957 297 SLC17A5 Berra, B.; Gornati, R.; Rapelli, S.; Gatti, R.; Mancini, G. M.S.; Ciana, G.; Bembi, B.: Infantile sialic acid storage disease:biochemical studies. Am. J. Med. Genet. 58: 24- 31, 1995. 3 C c

GAM7957 297 SLC17A5 Biancheri, R.; Verbeek, E.; Rossi, A.; Gaggero, R.; Roccatagliata,L.; Gatti, R.; van Diggelen, O.; Verheijen, F. W.; Mancini, G. M.S.: An Italian severe Salla disease variant associated with a SLC17A5mutation earlier described in infantile sialic acid storage disease. Clin.Genet. 61: 443- 447, 2002. 3 C c

GAM7957 297 SLC17A5 Cameron, P. D.; Dubowitz, V.; Besley, G. T. N.; Fensom, A. H.:Sialic acid storage disease. Arch. Dis. Child. 65: 314- 315, 1990. 3 C c

GAM7957 297 SLC17A5 Haataja, L.; Schleutker, J.; Laine, A.- P.; Renlund, M.; Savontaus,M.- L.; Dib, C.; Weissenbach, J.; Peltonen, L.; Aula, P.: The geneticlocus for free sialic acid storage disease maps to the long arm ofchromosome 6. Am. J. Hum. Genet. 54: 1042- 1049, 1994. 3 C c

GAM7957 297 SLC17A5 Lemyre, E.; Russo, P.; Melancon, S. B.; Gagne, R.; Potier, M.;Lambert, M.: Clinical spectrum of infantile free sialic acid storagedisease. Am. J. Med. Genet. 82: 385- 391, 1999. 3 C c

GAM7957 297 SLC17A5 Mancini, G. M. S.; Beerens, C. E. M. T.; Aula, P. P.; Verheijen,F. W.: Sialic acid storage diseases: a multiple lysosomal transportdefect for 3 C c

acidic monosaccharides. J. Clin. Invest. 87: 1329- 1335,1991.

GAM7957 297 SLC17A5 Schleutker, J.; Laine, A.- P.; Haataja, L.; Renlund, M.; Weissenbach,J.; 3 C c
Aula, P.; Peltonen, L.: Linkage disequilibrium utilized to establisha
refined genetic position of the Salla disease locus on 6q14- q15. Genomics
27:286- 292, 1995.

GAM7957 297 SLC17A5 Schleutker, J.; Leppanen, P.; Mansson, J.- E.; Erikson, A.; Weissenbach,J.; 3 C c
Peltonen, L.; Aula, P.: Lysosomal free sialic acid storage disorderswith
different phenotypic presentations- - infantile- form sialic acidstorage
disease and Salla disease- - represent allelic disorders on6q14- 15. Am. J.
Hum. Genet. 57: 893- 901, 1995.

GAM7957 297 SLC17A5 Tondeur, M.; Libert, J.; Vamos, E.; Van Hoof, F.; Thomas, G. H.;Strecker, 3 C c
G.: Infantile form of sialic acid storage disorder:
clinical,ultrastructural, and biochemical studies in two siblings. Europ.J.
Pediat. 139: 142- 147, 1982.

GAM7957 297 SLC17A5 Verheijen, F. W.; Verbeek, E.; Aula, N.; Beerens, C. E. M. T.;Havelaar, A. 3 C c
C.; Joosse, M.; Peltonen, L.; Aula, P.; Galjaard, H.;van der Spek, P. J.;
Mancini, G. M. S.: A new gene, encoding an aniontransporter, is mutated in
sialic acid storage diseases. Nature Genet. 23:462- 465, 1999.

GAM7957 297 SLC21A9 Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; 3 C c
Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding
sequences of unidentified human genes. XII. The completesequences of 100 new
cDNA clones from brain which code for large proteinsin vitro. DNA Res. 5:
355- 364, 1998.

GAM7957 297 SLC21A9 St- Pierre, M. V.; Hagenbuch, B.; Ugele, B.; Meier, P. J.; Stallmach,T.: 3 C c
Characterization of an organic anion- transporting polypeptide(OATP- B) in
human placenta. J. Clin. Endocr. Metab. 87: 1856- 1863,2002.

GAM7957 297 SLC22A2 Gorboulev, V.; Ulzheimer, J. C.; Akhoundova, A.; Ulzheimer- Teuber,I.; 3 C c
Karbach, U.; Quester, S.; Baumann, C.; Lang, F.; Busch, A. E.;Koepsell, H.:
Cloning and characterization of two human polyspecificorganic cation
transporters. DNA Cell Biol. 16: 871- 881, 1997.

GAM7957 297 SLC22A2 Grundemann, D.; Schomig, E.: Gene structures of the human non- 3 C c
neuronalmonoamine transporters EMT and OCT2. Hum. Genet. 106: 627- 635,
2000.

GAM7957 297 SLC22A2 Koehler, M. R.; Wissinger, B.; Gorboulev, V.; Koepsell, H.; Schmid,M.: The 3 C c
two human organic cation transporter genes SLC22A1 and SLC22A2are located on
chromosome 6q26. Cytogenet. Cell Genet. 79: 198- 200,1997.

GAM7957 297 SLC22A2 Mooslehner, K. A.; Allen, N. D.: Cloning of the mouse organiccation 3 C c
transporter 2 gene, Slc22a2, from an enhancer- trap transgeneintegration
locus. Mammalian Genome 10: 218- 224, 1999.

GAM7957 297 SLC22A2 Sleutels, F.; Zwart, R.; Barlow, D. P.: The non- coding Air RNAis required 3 C c
for silencing autosomal imprinted genes. Nature 415:810- 813, 2002.

GAM7957 297 SLC25A15 Camacho, J. A.; Obie, C.; Biery, B.; Goodman, B. K.; Hu, C.- A.;Almashanu, 3 C b
S.; Steel, G.; Casey, R.; Lambert, M.; Mitchell, G. A.;Valle, D.:
Hyperornithinaemia- hyperammonaemia- homocitrullinuria syndromeis caused by
mutations in a gene encoding a mitochondrial ornithinetransporter. Nature
Genet. 22: 151- 158, 1999.

GAM7957 297 SLC25A15 Miyamoto, T.; Kanazawa, N.; Kato, S.; Kawakami, M.; Inoue, Y.;Kuhara, T.; 3 C b
Inoue, T.; Takeshita, K.; Tsujino, S.: Diagnosis of Japanesepatients with
HHH syndrome by molecular genetic analysis: a commonmutation, R179X. J. Hum.
Genet. 46: 260- 262, 2001.

GAM7957 297 SLC25A15 Nakajima, M.; Ishii, S.; Mito, T.; Takeshita, K.; Takashima, S.;Takakura, H.; Inoue, I.; Saheki, T.; Akiyoshi, H.; Ichihara, K.:Clinical, biochemical and ultrastructural study on the pathogenesisof hyperornithinemia-hyperammonemia- homocitrullinuria syndrome. BrainDev. 10: 181- 185, 1988. 3 C b

GAM7957 297 SLC25A15 Tsujino, S.; Kanazawa, N.; Ohashi, T.; Eto, Y.; Saito, T.; Kira,J.; Yamada, T.: Three novel mutations (G27E, insAAC, R179X) in theORNT1 gene of Japanese patients with hyperornithinemia, hyperammonemia,and homocitrullinuria syndrome. Ann. Neurol. 47: 625- 631, 2000. 3 C b

GAM7957 297 SLC2A3 Fan, Y.- S.; Eddy, R. L.; Byers, M. G.; Haley, L. L.; Henry, W.M.; Kayano, T.; Shows, T. B.; Bell, G. I.: Assignment of genes encodingthree human glucose transporter/transporter- like proteins (GLUT4,GLUT5 and GLUT6) to chromosomes 17, 1 and 5, respectively. (Abstract) Cytogenet.Cell Genet. 51: 997 only, 1989. 3 C b

GAM7957 297 SLC2A3 Gould, G. W.; Holman, G. D.: The glucose transporter family: structure,function and tissue- specific expression. Biochem. J. 295: 329-341,1993. 3 C b

GAM7957 297 SLC2A3 Hauguel- de Mouzon, S.; Challier, J. C.; Kacemi, A.; Cauzac, M.;Malek, A.; Girard, J.: The GLUT3 glucose transporter isoform is differentiallyexpressed within human placental cell types. J. Clin. Endocr. Metab. 82:2689- 2694, 1997. 3 C b

GAM7957 297 SLC2A3 Kayano, T.; Burant, C. F.; Fukumoto, H.; Gould, G. W.; Fan, Y.S.; Eddy, R. L.; Byers, M. G.; Shows, T. B.; Seino, S.; Bell, G. I.: Human facilitative glucose transporters: isolation, functional characterization,and gene localization of cDNAs encoding an isoform (GLUT5) expressedin small intestine, kidney, muscle, and adipose tissue and an unusualglucose transporter pseudogene- like sequence (GLUT6). J. Biol. Chem. 265:13276-13282, 1990. 3 C b

GAM7957 297 SLC2A3 Kayano, T.; Fukumoto, H.; Eddy, R. L.; Fan, Y.- S.; Byers, M. G.;Shows, T. B.; Bell, G. I.: Evidence for a family of human glucosetransporter- like proteins: sequence and gene localization of a proteinexpressed in fetal skeletal muscle and other tissues. J. Biol. Chem. 263:15245- 15248, 1988. 3 C b

GAM7957 297 SLC31A1 Eisses, J. F.; Kaplan, J. H.: Molecular characterization of hCTR1,the human copper uptake protein. J. Biol. Chem. 277: 29162- 29171,2002. 3 C b

GAM7957 297 SLC31A1 Klomp, A. E. M.; Tops, B. B. J.; van den Berg, I. E. T.; Berger,R.; Klomp, L. W. J.: Biochemical characterization and subcellularlocalization of human copper transporter 1 (hCTR1). Biochem. J. 364:497- 505, 2002. 3 C b

GAM7957 297 SLC31A1 Kuo, Y.- M.; Zhou, B.; Cosco, D.; Gitschier, J.: The copper transporterCTR1 provides an essential function in mammalian embryonic development. Proc.Nat. Acad. Sci. 98: 6836- 6841, 2001. 3 C b

GAM7957 297 SLC31A1 Lee, J.; Pena, M. M. O.; Nose, Y.; Thiele, D. J.: Biochemicalcharacterization of the human copper transporter Ctr1. J. Biol. Chem. 277:4380- 4387, 2002. 3 C b

GAM7957 297 SLC31A1 Lee, J.; Prohaska, J. R.; Thiele, D. J.: Essential role for mammaliancopper transporter Ctr1 in copper homeostasis and embryonic development. Proc.Nat. Acad. Sci. 98: 6842- 6847, 2001. 3 C b

GAM7957 297 SLC31A1 Moller, L. B.; Petersen, C.; Lund, C.; Horn, N.: Characterizationof the hCTR1 gene: genomic organization, functional expression, andidentification of a highly homologous processed gene. Gene 257:13- 22, 2000. 3 C b

GAM7957 297 SLC31A1 Zhou, B.; Gitschier, J.: hCTR1: a human gene for copper uptakeidentified by complementation in yeast. Proc. Nat. Acad. Sci. 94:7481- 7486, 1997. 3 C b

GAM7957 297 SLC6A6 Patel, A.; Rochelle, J. M.; Jones, J. M.; Sumegi, J.; Uhl, G. R.;Seldin, M. F.; Meisler, M. H.; Gregor, P.: Mapping of the taurinetransporter gene to mouse chromosome 6 and to the short arm of humanchromosome 3. Genomics 25: 314- 317, 1995. 3 C c

GAM7957 297 SLC6A6 Ramamoorthy, S.; Leibach, F. H.; Mahesh, V. B.; Han, H.; Yang- Feng,T.; Blakely, R. D.; Ganapathy, V.: Functional characterization andchromosomal localization of a cloned taurine transporter from humanplacenta. Biochem. J. 300: 893- 900, 1994. 3 C c

GAM7957 297 SLC6A6 Uchida, S.; Kwon, H. M.; Yamauchi, A.; Preston, A. S.; Marumo,F.; Handler, J. S.: Molecular cloning of the cDNA for an MDCK cellNa(+)- and Cl(-)- dependent taurine transporter that is regulated byhypertonicity. Proc. Nat. Acad. Sci. 89: 8230- 8234, 1992. 3 C c

GAM7957 297 SMG1 Denning, G.; Jamieson, L.; Maquat, L. E.; Thompson, E. A.; Fields,A. P.: Cloning of a novel phosphatidylinositol kinase- related kinase:characterization of the human SMG- 1 RNA surveillance protein. J.Biol. Chem. 276: 22709- 22714, 2001. 3 C c

GAM7957 297 SMG1 Diaz- Meco, M. T.; Municio, M. M.; Sanchez, P.; Lozano, J.; Moscat,J.: Lambda- interacting protein, a novel protein that specificallyinteracts with the zinc finger domain of the atypical protein kinaseC isotype lambda/iota and stimulates its kinase activity in vitroand in vivo. Molec. Cell. Biol. 16: 105- 114, 1996. 3 C c

GAM7957 297 SMG1 Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VIII. 78 new cDNAclones from brain which code for large proteins in vitro. DNA Res. 4:307- 313, 1997. 3 C c

GAM7957 297 SMG1 Yamashita, A.; Ohnishi, T.; Kashima, I.; Taya, Y.; Ohno, S.: HumanSMG- 1, a novel phosphatidylinositol 3- kinase- related protein kinase,associates with components of the mRNA surveillance complex and isinvolved in the regulation of nonsense- mediated mRNA decay. GenesDev. 15: 2215- 2228, 2001. 3 C c

GAM7957 297 SPG4 Benson, K. F.; Horwitz, M.; Wolff, J.; Friend, K.; Thompson, E.;White, S.; Richards, R. I.; Raskind, W. H.; Bird, T. D.: CAG repeatexpansion in autosomal dominant familial spastic paraparesis: novelexpansion in a subset of patients. Hum. Molec. Genet. 7: 1779- 1786,1998. 3 C c

GAM7957 297 SPG4 Burger, J.; Fonknechten, N.; Hoeltzenbein, M.; Neumann, L.; Bratanoff,E.; Hazan, J.; Reis, A.: Hereditary spastic paraplegia caused bymutations in the SPG4 gene. Europ. J. Hum. Genet. 8: 771- 776, 2000. 3 C c

GAM7957 297 SPG4 Burger, J.; Metzke, H.; Paternotte, C.; Schilling, F.; Hazan, J.;Reis, A.: Autosomal dominant spastic paraplegia with anticipationmaps to a 4- cM interval on chromosome 2p21- p24 in a large German family. Hum.Genet. 98: 371- 375, 1996. 3 C c

GAM7957 297 SPG4 Errico, A.; Ballabio, A.; Rugarli, E. I.: Spastin, the proteinmutated in autosomal dominant hereditary spastic paraplegia, is involvedin microtubule dynamics. Hum. Molec. Genet. 11: 153- 163, 2002. 3 C c

GAM7957 297 SPG4 Fonknechten, N.; Mavel, D.; Byrne, P.; Davoine, C.- S.; Cruaud,C.; Boentsch, D.; Samson, D.; Coutinho, P.; Hutchinson, M.; McMonagle,P.; Burgunder, J.- M.; Tartaglione, A.; and 10 others: Spectrumof SPG4 mutations in autosomal dominant spastic paraplegia. Hum.Molec. Genet. 9: 637- 644, 2000. 3 C c

GAM7957 297 SPG4 Hazan, J.; Davoine, C. S.; Mavel, D.; Fonknechten, N.; Paternotte,C.; Fizames, C.; Cruaud, C.; Samson, D.; Muselet, D.; Vega- Czarny,N.; Brice, A.; Gyapay, G.; Heilig, R.; Fontaine, B.; Weissenbach,J.: A fine integrated 3 C c

map of the SPG4 locus excludes an expandedCAG repeat in chromosome 2p-linked autosomal dominant spastic paraplegia. Genomics 60:309- 319, 1999.

GAM7957 297 SPG4 Hazan, J.; Fonknechten, N.; Mavel, D.; Paternotte, C.; Samson,D.; Artiguenave, F.; Davoine, C.- S.; Cruaud, C.; Durr, A.; Wincker,P.; Brottier, P.; Cattolico, L.; Barbe, V.; Burgunder, J.- M.; Prud'homme,J.- F.; Brice, A.; Fontaine, B.; Heilig, R.; Weissenbach, J.: Spastin,a new AAA protein, is altered in the most frequent form of autosomaldominant spastic paraplegia. Nature Genet. 23: 296- 303, 1999. 3 C c

GAM7957 297 SPG4 Lindsey, J. C.; Lusher, M. E.; McDermott, C. J.; White, K. D.;Reid, E.; Rubinsztein, D. C.; Bashir, R.; Hazan, J.; Shaw, P. J.;Bushby, K. M. D.: Mutation analysis of the spastin gene (SPG4) inpatients with hereditary spastic paraplegia. J. Med. Genet. 37:759- 765, 2000. 3 C c

GAM7957 297 SPG4 Nielsen, J. E.; Koefoed, P.; Abell, K.; Hasholt, L.; Eiberg, H.;Fenger, K.; Niebuhr, E.; Sorensen, S. A.: CAG repeat expansion inautosomal dominant pure spastic paraplegia linked to chromosome 2p21- p24. Hum.Molec. Genet. 6: 1811- 1816, 1997. 3 C c

GAM7957 297 SPG4 Santorelli, F. M.; Patrono, C.; Fortini, D.; Tessa, A.; Comanducci,G.; Bertini, E.; Pierallini, A.; Amabile, G. A.; Casali, C.: Intrafamilialvariability in hereditary spastic paraplegia associated with an SPG4gene mutation. Neurology 55: 702- 705, 2000. 3 C c

GAM7957 297 SPG4 Sauter, S.; Miterski, B.; Klimpe, S.; Bonsch, D.; Schols, L.;Visbeck, A.; Papke, T.; Hopf, H. C.; Engel, W.; Deufel, T.; Epplen,J. T.; Neesen, J.: Mutation analysis of the spastin gene (SPG4) inpatients in Germany with autosomal dominant hereditary spastic paraplegia. Hum.Mutat. 20: 127- 132, 2002. 3 C c

GAM7957 297 SPG4 Svenson, I. K.; Ashley- Koch, A. E.; Gaskell, P. C.; Riney, T.J.; Cumming, W. J. K.; Kingston, H. M.; Hogan, E. L.; Boustany, R.- M.N.; Vance, J. M.; Nance, M. A.; Pericak- Vance, M. A.; Marchuk, D.A.: Identification and expression analysis of spastin gene mutationsin hereditary spastic paraplegia. Am. J. Hum. Genet. 68: 1077- 1085,2001. 3 C c

GAM7957 297 SPG4 Svenson, I. K.; Ashley- Koch, A. E.; Pericak- Vance, M. A.; Marchuk,D. A.: A second leaky splice- site mutation in the spastin gene. (Letter) Am.J. Hum. Genet. 69: 1407- 1409, 2001. 3 C c

GAM7957 297 SSRP1 Bruhn, S. L.; Pil, P. M.; Essigmann, J. M.; Housman, D. E.; Lippard,S. J.: Isolation and characterization of human cDNA clones encodinga high mobility group box protein that recognizes structural distortionsto DNA caused by binding of the anticancer agent cisplatin. Proc.Nat. Acad. Sci. 89: 2307- 2311, 1992. 3 C c

GAM7957 297 SSRP1 Keller, D. M.; Zeng, X.; Wang, Y.; Zhang, Q. H.; Kapoor, M.; Shu,H.; Goodman, R.; Lozano, G.; Zhao, Y.; Lu, H.: A DNA damage- inducedp53 serine 392 kinase complex contains CK2, hSpt16, and SSRP1. Molec.Cell 283- 292, 2001. 3 C c

GAM7957 297 SSRP1 LeRoy, G.; Orphanides, G.; Lane, W. S.; Reinberg, D.: Requirementof RSF and FACT for transcription of chromatin templates in vitro. Science 282:1900- 1904, 1998. 3 C c

GAM7957 297 SSRP1 Orphanides, G.; LeRoy, G.; Chang, C.- H.; Luse, D. S.; Reinberg,D.: FACT, a factor that facilitates transcript elongation throughnucleosomes. Cell 92: 105- 116, 1998. 3 C c

GAM7957 297 SSRP1 Orphanides, G.; Wu, W.- H.; Lane, W. S.; Hampsey, M.; Reinberg,D.: The chromatin- specific transcription elongation factor FACT compriseshuman 3 C c

SPT16 and SSRP1 proteins. Nature 400: 284- 288, 1999.

GAM7957 297 STAT3 Akira, S.; Nishio, Y.; Inoue, M.; Wang, X.- J.; Wei, S.; Matsusaka,T.; 3 C c
Yoshida, K.; Sudo, T.; Naruto, M.; Kishimoto, T.: Molecular cloningof APRF,
a novel IFN- stimulated gene factor 3 p91- related transcriptionfactor
involved in the gp130- mediated signaling pathway. Cell 77:63- 71, 1994.

GAM7957 297 STAT3 Bromberg, J. F.; Wrzeszczynska, M. H.; Devgan, G.; Zhao, Y.; Pestell,R. G.; 3 C c
Albanese, C.; Darnell, J. E., Jr.: Stat3 as an oncogene. Cell 98:295- 303,
1999.

GAM7957 297 STAT3 Caldenhoven, E.; van Dijk, T. B.; Solari, R.; Armstrong, J.; Raaijmakers,J. 3 C c
A. M.; Lammers, J.- W. J.; Koenderman, L.; de Groot, R. P.: STAT3- beta,a
splice variant of transcription factor STAT3, is a dominant
negativeregulator of transcription. J. Biol. Chem. 271: 13221- 13227, 1996.

GAM7957 297 STAT3 Choi, J. Y.; Li, W. L.; Kouri, R. E.; Yu, J.; Kao, F. T.; Ruano,G.: 3 C c
Assignment of the acute phase response factor (APRF) gene to17q21 by
microdissection clone sequencing and fluorescence in situhybridization of a
p1 clone. Genomics 37: 264- 265, 1996.

GAM7957 297 STAT3 Chung, C. D.; Liao, J.; Liu, B.; Rao, X.; Jay, P.; Berta, P.; Shuai,K.: 3 C c
Specific inhibition of Stat3 signal transduction by PIAS3. Science 278:1803-
1805, 1997.

GAM7957 297 STAT3 Foley, H. A.; Ofori- Acquah, S. F.; Yoshimura, A.; Critz, S.; Baliga,B. S.; 3 C c
Pace, B. S.: Stat- 3 beta inhibits gamma- globin gene expressionin erythroid
cells. J. Biol. Chem. 277: 16211- 16219, 2002.

GAM7957 297 STAT3 Lutticken, C.; Wegenka, U. M.; Yuan, J.; Buschmann, J.; Schindler,C.; 3 C c
Ziemiecki, A.; Harpur, A. G.; Wilks, A. F.; Yasukawa, K.; Taga,T.;
Kishimoto, T.; Barbieri, G.; Pellegrini, S.; Sendtner, M.; Heinrich,P. C.;
Horn, F.: Association of transcription factor APRF and proteinkinase Jak1
with the interleukin- 6 signal transducer gp130. Science 263:89- 92, 1994.

GAM7957 297 STAT3 Nakashima, K.; Yanagisawa, M.; Arakawa, H.; Kimura, N.; Hisatsune,T.; 3 C c
Kawabata, M.; Miyazono, K.; Taga, T.: Synergistic signaling infetal brain by
STAT3- Smad1 complex bridged by p300. Science 284:479- 482, 1999.

GAM7957 297 STAT3 Pfeffer, L. M.; Mullersman, J. E.; Pfeffer, S. R.; Murti, A.; Shi,W.; Yang, 3 C c
C. H.: STAT3 as an adapter to couple phosphatidylinositol3- kinase to the
IFNAR1 chain of the type I interferon receptor. Science 276:1418- 1420,
1997.

GAM7957 297 STAT3 Ram, P. T.; Horvath, C. M.; Iyengar, R.: Stat3- mediated transformationof 3 C c
NIH- 3T3 cells by the constitutively active Q205L G- alpha(O) protein.
Science 287:142- 144, 2000.

GAM7957 297 STAT3 Simon, A. R.; Vikis, H. G.; Stewart, S.; Fanburg, B. L.; Cochran,B. H.; 3 C c
Guan, K.- L.: Regulation of STAT3 by direct binding to theRac1 GTPase.
Science 290: 144- 147, 2000.

GAM7957 297 STAT3 Vaisse, C.; Halaas, J. L.; Horvath, C. M.; Darnell, J. E., Jr.;Stoffel, M.; 3 C c
Friedman, J. M.: Leptin activation of Stat3 in the hypothalamusof wildtype
and ob/ob mice but not in db/db mice. Nature Genet. 14:95- 100, 1996.

GAM7957 297 STAT3 Yoo, J.- Y.; Huso, D. L.; Nathans, D.; Desiderio, S.: Specificablation of 3 C c
Stat3- beta distorts the pattern of Stat3- responsive geneexpression and
impairs recovery from endotoxic shock. Cell 108:331- 344, 2002.

GAM7957 297 STX1A Bennett, M. K.; Calakos, N.; Scheller, R. H.: Syntaxin: a synapticprotein 3 C c
implicated in docking of synaptic vesicles at presynapticactive zones.
Science 257: 255- 259, 1992.

GAM7957 297 STX1A Bennett, M. K.; Garcia- Arraras, J. E.; Elferink, L. A.; Peterson,K.; 3 C c

Fleming, A. M.; Hazuka, C. D.; Scheller, R. H.: The syntaxinfamily of vesicular transport receptors. Cell 74: 863- 873, 1993.

GAM7957 297 STX1A Fernandez, I.; Ubach, J.; Dulubova, I.; Zhang, X.; Sudof, T. C.;Rizo, J.: 3 C c
Three- dimensional structure of an evolutionarily conservedN- terminal domain of syntaxin 1A. Cell 94: 841- 849, 1998.

GAM7957 297 STX1A Fisher, R. J.; Pevsner, J.; Burgoyne, R. D.: Control of fusionpore dynamics 3 C c
during exocytosis by Munc18. Science 291: 875- 878,2001.

GAM7957 297 STX1A Hu, K.; Carroll, J.; Fedorovich, S.; Rickman, C.; Sukhodub, A.;Davietov, B.: 3 C c
Vesicular restriction of synaptobrevin suggests a rolefor calcium in membrane fusion. Nature 415: 646- 650, 2002.

GAM7957 297 STX1A Martin- Martin, B.; Nabokina, S. M.; Lazo, P. A.; Mollinedo, F.: Co- 3 C c
expression of several human syntaxin genes in neutrophils anddifferentiating HL- 60 cells: various isoforms and detection of syntaxin1. J. Leuko. Biol. 65: 397- 406, 1999.

GAM7957 297 STX1A McNew, J. A.; Parlati, F.; Fukuda, R.; Johnston, R. J.; Paz, K.;Paumet, F.; 3 C c
Sollner, T. H.; Rothman, J. E.: Compartmental specificityof cellular membrane fusion encoded in SNARE proteins. Nature 407:153- 159, 2000.

GAM7957 297 STX1A Nakayama, T.; Fujiwara, T.; Miyazawa, A.; Asakawa, S.; Shimizu,N.; Shimizu, 3 C c
Y.; Mikoshiba, K.; Akagawa, K.: Mapping of the humanHPC- 1/syntaxin 1A gene (STX1A) to chromosome 7 band q11.2. Genomics 42:173- 176, 1997.

GAM7957 297 STX1A Naren, A. P.; Di, A.; Cormet- Boyaka, E.; Boyaka, P. N.; McGhee,J. R.; Zhou, 3 C c
W.; Akagawa, K.; Fujiwara, T.; Thome, U.; Engelhardt,J. F.; Nelson, D. J.; Kirk, K. L.: Syntaxin 1A is expressed in airwayepithelial cells, where it modulates CFTR C1- currents. J. Clin.Invest. 105: 377- 386, 2000.

GAM7957 297 STX1A Richmond, J. E.; Weimer, R. M.; Jorgensen, E. M.: An open formof syntaxin 3 C c
bypasses the requirement for UNC- 13 in vesicle priming. Nature 412:338- 341, 2001.

GAM7957 297 STX1A Weber, T.; Zemelman, B. V.; McNew, J. A.; Westermann, B.; Gmachi,M.; 3 C c
Parlati, F.; Sollner, T. H.; Rothman, J. E.: SNAREpins: minimalmachinery for membrane fusion. Cell 92: 759- 772, 1998.

GAM7957 297 STX1A Zhang, R.; Maksymowych, A. B.; Simpson, L. L.: Cloning and sequenceanalysis 3 C c
of a cDNA encoding human syntaxin 1A, a polypeptide essentialfor exocytosis. Gene 159: 293- 294, 1995.

GAM7957 297 SULT2A1 Comer, K. A.; Falany, J. L.; Falany, C. N.: Cloning and expressionof human 3 C b
liver dehydroepiandrosterone sulphotransferase. Biochem.J. 289: 233- 240, 1993.

GAM7957 297 SULT2A1 Durocher, F.; Morissette, J.; Dufort, I.; Simard, J.; Luu- The,V.: Genetic 3 C b
linkage mapping of the dehydroepiandrosterone sulfotransferase(STD) gene on the chromosome 19q13.3 region. Genomics 29: 781- 783,1995.

GAM7957 297 SULT2A1 Kong, A.- N. T.; Yang, L.; Ma, M.; Tao, D.; Bjornsson, T. D.: 3 C b
Molecularcloning of the alcohol/hydroxysteroid form (hSTa) of sulfotransferasefrom human liver. Biochem. Biophys. Res. Commun. 187: 448- 454, 1992.

GAM7957 297 SULT2A1 Otterness, D. M.; Her, C.; Aksoy, S.; Kimura, S.; Wieben, E. 3 C b
D.;Weinshilboum, R. M.: Human dehydroepiandrosterone sulfotransferasegene: molecular cloning and structural characterization. DNA CellBiol. 14: 331- 341, 1995.

GAM7957 297 SULT2A1 Otterness, D. M.; Wieben, E. D.; Wood, T. C.; Watson, W. G.; Madden,B. J.; 3 C b
McCormick, D. J.; Weinshilboum, R. M.: Human liver dehydroepiandrosteronesulfotransferase: molecular cloning and expression of

cDNA. Molec.Pharm. 41: 865- 872, 1992.

GAM7957 297 SULT2A1 Otterness, D.; Mohrenweiser, H. W.; Brandriff, B. F.; Weinshilboum,R. M.: 3 C b
Dehydroepiandrosterone sulfotransferase gene (STD): localizationto human
chromosome 19q13.3. Cytogenet. Cell Genet. 70: 45- 47, 1995.

GAM7957 297 SUV39H2 O'Carroll, D.; Scherthan, H.; Peters, A. H. F. M.; Opravil, S.;Haynes, A. 3 C b
R.; Laible, G.; Rea, S.; Schmid, M.; Lebersorger, A.; Jerratsch,M.; Sattler,
L.; Mattei, M. G.; Denny, P.; Brown, S. D. M.; Schweizer,D.; Jenuwein, T.:
Isolation and characterization of Suv39h2, a secondhistone H3
methyltransferase gene that displays testis- specific expression.
Molec.Cell. Biol. 20: 9423- 9433, 2000.

GAM7957 297 SUV39H2 Peters, A. H. F. M.; O'Carroll, D.; Scherthan, H.; Mechtler, K.;Sauer, S.; 3 C b
Schofer, C.; Weipoltshammer, K.; Pagani, M.; Lachner, M.;Kohlmaier, A.;
Opravil, S.; Doyle, M.; Sibilia, M.; Jenuwein, T.:Loss of the Suv39h histone
methyltransferases impairs mammalian heterochromatinand genome stability.
Cell 107: 323- 337, 2001.

GAM7957 297 SWAP70 Borggrefe, T.; Masat, L.; Wabl, M.; Riwar, B.; Cattoretti, G.;Jessberger, 3 C b
R.: Cellular, intracellular, and developmental expressionpatterns of murine
SWAP- 70. Europ. J. Immun. 29: 1812- 1822, 1999.

GAM7957 297 SWAP70 Borggrefe, T.; Wabl, M.; Akhmedov, A. T.; Jessberger, R.: A B- cell- 3 C b
specificDNA recombination complex. J. Biol. Chem. 273: 17025- 17035, 1998.

GAM7957 297 SWAP70 Masat, L.; Caldwell, J.; Armstrong, R.; Khoshnevisan, H.; Jessberger,R.; 3 C b
Herndier, B.; Wabl, M.; Ferrick, D.: Association of SWAP- 70 withthe B cell
antigen receptor complex. Proc. Nat. Acad. Sci. 97: 2180- 2184,2000.

GAM7957 297 SWAP70 Masat, L.; Liddell, R. A.; Mock, B. A.; Kuo, W.- L.; Jessberger,R.; Wabl, 3 C b
M.; Morse, H. C., III: Mapping of the SWAP70 gene to mousechromosome 7 and
human chromosome 11p15. Immunogenetics 51: 16- 19,2000.

GAM7957 297 SWAP70 Shinohara, M.; Terada, Y.; Iwamatsu, A.; Shinohara, A.; Mochizuki,N.; 3 C b
Higuchi, M.; Gotoh, Y.; Ihara, S.; Nagata, S.; Itoh, H.; Fukui,Y.;
Jessberger, R.: SWAP- 70 is a guanine- nucleotide- exchange factorthat
mediates signalling of membrane ruffling. Nature 416: 759- 763,2002.

GAM7957 297 SYNGR1 Janz, R.; Sudhof, T. C.; Hammer, R. E.; Unni, V.; Siegelbaum, S.A.; 3 C c
Bolshakov, V. Y.: Essential roles in synaptic plasticity forsynaptogyrin I
and synaptophysin I. Neuron 24: 687- 700, 1999.

GAM7957 297 SYNGR1 Kedra, D.; Pan, H.- Q.; Seroussi, E.; Fransson, I.; Guilbaud, C.;Collins, J. 3 C c
E.; Dunham, I.; Blennow, E.; Roe, B. A.; Piehl, F.; Dumanski,J. P.:
Characterization of the human synaptogyrin gene family. Hum.Genet. 103: 131-
141, 1998.

GAM7957 297 SYNGR1 McMahon, H. T.; Bolshakov, V. Y.; Janz, R.; Hammer, R. E.; Siegelbaum,S. A.; 3 C c
Sudhof, T. C.: Synaptophysin, a major synaptic vesicle protein,is not
essential for neurotransmitter release. Proc. Nat. Acad. Sci. 93:4760- 4764,
1996.

GAM7957 297 TADA2L Candau, R.; Moore, P. A.; Wang, L.; Barlev, N.; Ying, C. Y.; Rosen,C. A.; 3 C b
Berger, S. L.: Identification of human proteins functionallyconserved with
the yeast putative adaptors ADA2 and GCN5. Molec.Cell. Biol. 16: 593- 602,
1996.

GAM7957 297 TADA2L Carter, K. C.; Wang, L.; Shell, B. K.; Zamir, I.; Berger, S. L.;Moore, P. 3 C b
A.: The human transcriptional adaptor genes TADA2L andGCN5L2 colocalize to
chromosome 17q12- q21 and display a similar tissueexpression pattern.
Genomics 40: 497- 500, 1997.

GAM7957 297 TADA2L Ogryzko, V. V.; Kotani, T.; Zhang, X.; Schiltz, R. L.; Howard,T.; Yang, X.- 3 C b

J.; Howard, B. H.; Qin, J.; Nakatani, Y.: Histone- likeTAFs within the PCAF histone acetylase complex. Cell 94: 35- 44,1998.

GAM7957 297 TADA2L Struhl, K.; Moqtaderi, Z.: The TAFs in the HAT. Cell 94: 1- 4,1998. 3 C b

GAM7957 297 TBX1 Chieffo, C.; Garvey, N.; Gong, W.; Roe, B.; Zhang, G.; Silver,L.; Emanuel, B. S.; Budarf, M. L.: Isolation and characterizationof a gene from the DiGeorge chromosomal region homologous to the mouseTbx1 gene. Genomics 43: 267- 277, 1997. 3 C c

GAM7957 297 TBX1 Funke, B.; Epstein, J. A.; Kochilas, L. K.; Lu, M. M.; Pandita,R. K.; Liao, J.; Bauerndistel, R.; Schuler, T.; Schorle, H.; Brown,M. C.; Adams, J.; Morrow, B. E.: Mice overexpressing genes from the22q11 region deleted in velo- cardio- facial syndrome/DiGeorge syndromehave middle and inner ear defects. Hum. Molec. Genet. 10: 2549- 2556,2001. 3 C c

GAM7957 297 TBX1 Jerome, L. A.; Papaioannou, V. E.: DiGeorge syndrome phenotypein mice mutant for the T- box gene, Tbx1. Nature Genet. 27: 286- 291,2001. 3 C c

GAM7957 297 TBX1 Lindsay, E. A.; Botta, A.; Jurecic, V.; Carattini- Rivera, S.; Cheah,Y.- C.; Rosenblatt, H. M.; Bradley, A.; Baldini, A.: Congenital heartdisease in mice deficient for the DiGeorge syndrome region. Nature 401:379- 383, 1999. 3 C c

GAM7957 297 TBX1 Lindsay, E. A.; Vitelli, F.; Su, H.; Morishima, M.; Huynh, T.;Pramparo, T.; Jurecic, V.; Ogunrinu, G.; Sutherland, H. F.; Scambler,P. J.; Bradley, A.; Baldini, A.: Tbx1 haploinsufficiency in the DiGeorgesyndrome region causes aortic arch defects in mice. Nature 410:97- 101, 2001. 3 C c

GAM7957 297 TBX1 Merscher, S.; Funke, B.; Epstein, J. A.; Heyer, J.; Puech, A.;Lu, M. M.; Xavier, R. J.; Demay, M. B.; Russell, R. G.; Factor, S.;Tokooya, K.; St. Jore, B.; and 12 others: TBX1 is responsible forcardiovascular defects in velo- cardio- facial/DiGeorge syndrome. Cell 104:619- 629, 2001. 3 C c

GAM7957 297 TBX6 Chapman, D. L.; Agulnik, I.; Hancock, S.; Silver, L. M.; Papaioannou,V. E.: Tbx6, a mouse T- box gene implicated in paraxial mesoderm formationat gastrulation. Dev. Biol. 180: 534- 542, 1996. 3 C c

GAM7957 297 TBX6 Chapman, D. L.; Papaioannou, V. E.: Three neural tubes in mouseembryos with mutations in the T- box gene Tbx6. Nature 391: 695- 697,1998. 3 C c

GAM7957 297 TBX6 Papapetrou, C.; Putt, W.; Fox, M.; Edwards, Y. H.: The human TBX6gene: cloning and assignment to chromosome 16p11.2. Genomics 55:238- 241, 1999. 3 C c

GAM7957 297 TCF4 Breschel, T. S.; McInnis, M. G.; Margolis, R. L.; Sirugo, G.; Corneliussen,B.; Simpson, S. G.; McMahon, F. J.; MacKinnon, D. F.; Xu, J. F.; Pleasant,N.; Huo, Y.; Ashworth, R. G.; Grundstrom, C.; Grundstrom, T.; Kidd,K. K.; DePaulo, J. R.; Ross, C. A.: A novel, heritable, expandingCTG repeat in an intron of the SEF2- 1 gene on chromosome 18q21.1. Hum.Molec. Genet. 6: 1855- 1863, 1997. 3 C c

GAM7957 297 TCF4 Castrop, J.; van Norren, K.; Clevers, H.: A gene family of HMG- boxtranscription factors with homology to TCF- 1. Nucleic Acids Res. 20:611 only, 1992. 3 C c

GAM7957 297 TCF4 Corneliussen, B.; Thornell, A.; Hallberg, B.; Grundstrom, T.:Helix- loop- helix transcriptional activators bind to a sequence inglucocorticoid response elements of retrovirus enhancers. J. Virol. 65:6084- 6093, 1991. 3 C c

GAM7957 297 TCF4 Duval, A.; Busson- Leconiat, M.; Berger, R.; Hamelin, R.: Assignmentof the TCF- 4 (TCF7L2) to human chromosome band 10q25.3. Cytogenet.Cell Genet. 88: 264- 265, 2000. 3 C c

GAM7957 297 TCF4 Duval, A.; Gayet, J.; Zhou, X.- P.; Iacopetta, B.; Thomas, G.; Hamelin,R.: Frequent frameshift mutations of the TCF- 4 gene in colorectalcancers with 3 C c

microsatellite instability. Cancer Res. 59: 4213- 4215,1999.

GAM7957 297 TCF4 Duval, A.; Rolland, S.; Tubacher, E.; Bui, H.; Thomas, G.; Hamelin,R.: The 3 C c
human T- cell transcription factor- 4 gene: structure,
extensivecharacterization of alternative splicings, and mutational
analysisin colorectal cancer cell lines. Cancer Res. 60: 3872- 3879, 2000.

GAM7957 297 TCF4 Henthorn, P.; Kiledjian, M.; Kadesch, T.: Two distinct transcriptionfactors 3 C c
that bind the immunoglobulin enhancer mu- E5/kappa- E2 motif. Science
247:467- 470, 1990.

GAM7957 297 TCF4 Henthorn, P.; McCarrick- Walmsley, R.; Kadesch, T.: Sequence ofthe cDNA 3 C c
encoding ITF- 2, a positive- acting transcription factor. NucleicAcids Res.
18: 678, 1990.

GAM7957 297 TCF4 Korinek, V.; Barker, N.; Moerer, P.; van Donselaar, E.; Huls, G.;Peters, P. 3 C c
J.; Clevers, H.: Depletion of epithelial stem- cell compartmentsin the small
intestine of mice lacking Tcf- 4. Nature Genet. 19:379- 383, 1998.

GAM7957 297 TCF4 Korinek, V.; Barker, N.; Morin, P. J.; van Wichen, D.; de Weger,R.; Kinzler, 3 C c
K. W.; Vogelstein, B.; Clevers, H.: Constitutive transcriptionalactivation
by a beta- catenin- Tcf complex in APC- /- colon carcinoma. Science
275:1784- 1787, 1997.

GAM7957 297 TCF4 Morin, P. J.; Sparks, A. B.; Korinek, V.; Barker, N.; Clevers,H.; 3 C c
Vogelstein, B.; Kinzler, K. W.: Activation of beta- catenin- Tcfsignaling in
colon cancer by mutations in beta- catenin or APC. Science 275:1787- 1790,
1997.

GAM7957 297 TCF4 Pscherer, A.; Dorflinger, U.; Kirfel, J.; Gawlas, K.; Ruschoff,J.; Buettner, 3 C c
R.; Schule, R.: The helix- loop- helix transcriptionfactor SEF- 2 regulates
the activity of a novel initiator element inthe promoter of the human
somatostatin receptor II gene. EMBO J. 15:6680- 6690, 1996.

GAM7957 297 TCF4 Rodova, M.; Islam, M. R.; Maser, R. L.; Calvet, J. P.: The polycystickidney 3 C c
disease- 1 promoter is a target of the beta- catenin/T- cell factorpathway.
J. Biol. Chem. 277: 29577- 29583, 2002.

GAM7957 297 TEM6 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. 3 C c
W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in
mice and humans. Cancer Res. 61: 6649- 6655, 2001.

GAM7957 297 TEM6 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; 3 C c
Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.;
Kinzler, K. W.: Genes expressed in human tumor endothelium. Science
289:1197- 1202, 2000.

GAM7957 297 TEM7 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. 3 C b
W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in
mice and humans. Cancer Res. 61: 6649- 6655, 2001.

GAM7957 297 TEM7 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; 3 C b
Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.;
Kinzler, K. W.: Genes expressed in human tumor endothelium. Science
289:1197- 1202, 2000.

GAM7957 297 TJP1 Mohandas, T. K.; Chen, X.- N.; Rowe, L. B.; Birkenmeier, E. H.;Fanning, A. 3 C c
S.; Anderson, J. M.; Korenberg, J. R.: Localization ofthe tight junction
protein gene TJP1 to human chromosome 15q13, distalto the Prader-
Willi/Angelman region, and to mouse chromosome 7. Genomics 30:594- 597,
1995.

GAM7957 297 TJP1 Willott, E.; Balda, M. S.; Fanning, A. S.; Jameson, B.; Van Itallie,C.; 3 C c
Anderson, J. M.: The tight junction protein ZO- 1 is homologousto the

Drosophila discs- large tumor suppressor protein of septatejunctions. Proc. Nat. Acad. Sci. 90: 7834- 7838, 1993.

GAM7957 297 TMEM4 Yokoyama- Kobayashi, M.; Sugano, S.; Kato, T.; Kato, S.: A signalsequence detection system using secreted protease activity as an indicator. Gene 163:193- 196, 1995. 3 C c

GAM7957 297 TMEM4 Yokoyama- Kobayashi, M.; Yamaguchi, T.; Sekine, S.; Kato, S.: Selectionof cDNAs encoding putative type II membrane proteins on the cell surfacefrom a human full- length cDNA bank. Gene 228: 161- 167, 1999. 3 C c

GAM7957 297 TNFRSF1B Baker, E.; Chen, L. Z.; Smith, C. A.; Callen, D. F.; Goodwin, R.;Sutherland, G. R.: Chromosomal location of the human tumor necrosisfactor receptor genes. Cytogenet. Cell Genet. 57: 117- 118, 1991. 3 C b

GAM7957 297 TNFRSF1B Beltinger, C. P.; White, P. S.; Maris, J. M.; Sulman, E. P.; Jensen,S. J.; LePaslier, D.; Stallard, B. J.; Goeddel, D. V.; de Sauvage,F. J.; Brodeur, G. M.: Physical mapping and genomic structure ofthe human TNFR2 gene. Genomics 35: 94- 100, 1996. 3 C b

GAM7957 297 TNFRSF1B Bruce, A. J.; Boling, W.; Kindy, M. S.; Peschon, J.; Kraemer, P.J.; Carpenter, M. K.; Holtsberg, F. W.; Mattson, M. P.: Altered neuronaland microglial responses to excitotoxic and ischemic brain injuryin mice lacking TNF receptors. Nature Med. 2: 788- 794, 1996. 3 C b

GAM7957 297 TNFRSF1B Chan, F. K.- M.; Chun, H. J.; Zheng, L.; Siegel, R. M.; Bui, K.L.; Lenardo, M. J.: A domain in TNF receptors that mediates ligand- independentreceptor assembly and signaling. Science 288: 2351- 2354, 2000. 3 C b

GAM7957 297 TNFRSF1B Geurts, J. M. W.; Janssen, R. G. J. H.; van Greevenbroek, M. M.J.; van der Kallen, C. J. H.; Cantor, R. M.; Bu, X.; Aouizerat, B.E.; Allayee, H.; Rotter, J. I.; de Bruin, T. W. A.: Identificationof TNFRSF1B as a novel modifier gene in familial combined hyperlipidemia. Hum.Molec. Genet. 9: 2067- 2074, 2000. 3 C b

GAM7957 297 TNFRSF1B Glenn, C. L.; Wang, W. Y. S.; Benjafield, A. V.; Morris, B. J.: Linkage and association of tumor necrosis factor receptor 2 locuswith hypertension, hypercholesterolemia and plasma shed receptor. Hum.Molec. Genet. 9: 1943- 1949, 2000. 3 C b

GAM7957 297 TNFRSF1B Kaufman, B. A.; White, P. S.; Steinbrueck, T.; Donis- Keller, H.;Brodeur, G. M.: Linkage mapping of the tumor necrosis factor receptor2 (TNFR2) gene to 1p36.2 using the single- strand conformation polymorphismtechnique. Hum. Genet. 94: 418- 422, 1994. 3 C b

GAM7957 297 TNFRSF1B Kemper, O.; Derre, J.; Cherif, D.; Engelmann, H.; Wallach, D.;Berger, R.: The gene for the type II (p75) tumor necrosis factorreceptor (TNF- RII) is localized on band 1p36.2- p36.3. Hum. Genet. 87:623- 624, 1991. 3 C b

GAM7957 297 TNFRSF1B Li, X.; Yang, Y.; Ashwell, J. D.: TNF- RII and c- IAP1 mediate ubiquitinationand degradation of TRAF2. Nature 416: 345- 349, 2002. 3 C b

GAM7957 297 TNFRSF1B Milatovich, A.; Song, K.; Heller, R. A.; Francke, U.: Tumor necrosisfactor receptor genes, TNFR1 and TNFR2, on human chromosomes 12 and1. Somat. Cell Molec. Genet. 17: 519- 523, 1991. 3 C b

GAM7957 297 TNFRSF1B Santee, S. M.; Owen- Schaub, L. B.: Human tumor necrosis factorreceptor p75/80 (CD120b) gene structure and promoter characterization. J.Biol. Chem. 271: 21151- 21159, 1996. 3 C b

GAM7957 297 TNFRSF1B Sashio, H.; Tamura, K.; Ito, R.; Yamamoto, Y.; Bamba, H.; Kosaka,T.; Fukui, S.; Sawada, K.; Fukuda, Y.; Tamura, K.; Satomi, M.; Shimoyama,T.; Furuyama, J.: Polymorphisms of the TNF gene and the TNF receptorsuperfamily member 1B gene are associated with susceptibility to ulcerativecolitis and Crohn's 3 C b

disease, respectively. Immunogenetics 53: 1020- 1027,2002.

GAM7957 297 TNFRSF1B Schall, T. J.; Lewis, M.; Koller, K. J.; Lee, A.; Rice, G. C.;Wong, G. H. W.; Gatanaga, T.; Granger, G. A.; Lentz, R.; Raab, H.;Kohr, W. J.; Goeddel, D. V.: Molecular cloning and expression ofa receptor for human tumor necrosis factor. Cell 61: 361- 370, 1990. 3 C b

GAM7957 297 TNFRSF1B Van Ostade, X.; Vandenabeele, P.; Everaerdt, B.; Loetscher, H.;Gentz, R.; Brockhaus, M.; Lesslauer, W.; Tavernier, J.; Brouckaert,P.; Fiers, W.: Human TNF mutants with selective activity on the p55receptor. Nature 361: 266- 269, 1993. 3 C b

GAM7957 297 TNFRSF1B White, P. S.; Maris, J. M.; Beltinger, C.; Sulman, E.; Marshall,H. N.; Fujimori, M.; Kaufman, B. A.; Biegel, J. A.; Allen, C.; Hilliard,C.; Valentine, M. B.; Look, A. T.; Enomoto, H.; Sakiyama, S.; Brodeur,G. M.: A region of consistent deletion in neuroblastoma maps withinhuman chromosome 1p36.2- 36.3. Proc. Nat. Acad. Sci. 92: 5520- 5524,1995. 3 C b

GAM7957 297 TNFSF10 Cretney, E.; Takeda, K.; Yagita, H.; Glaccum, M.; Peschon, J. J.;Smyth, M. J.: Increased susceptibility to tumor initiation and metastasisin TNF- related apoptosis- inducing ligand- deficient mice. J. Immun. 168:1356- 1361, 2002. 3 C b

GAM7957 297 TNFSF10 Degli- Esposti, M. A.; Dougall, W. C.; Smolak, P. J.; Waugh, J.Y.; Smith, C. A.; Goodwin, R. G.: The novel receptor TRAIL- R4 inducesNF- kappa- B and protects against TRAIL- mediated apoptosis, yet retainsan incomplete death domain. Immunity 7: 813- 820, 1997. 3 C b

GAM7957 297 TNFSF10 Gong, B.; Almasan, A.: Genomic organization and transcriptionalregulation of human Apo2/TRAIL gene. Biochem. Biophys. Res. Commun. 278:747- 752, 2000. 3 C b

GAM7957 297 TNFSF10 Hymowitz, S. G.; Christinger, H. W.; Fuh, G.; Ultsch, M.; O'Connell,M.; Kelley, R. F.; Ashkenazi, A.; de Vos, A. M.: Triggering celldeath: the crystal structure of Apo2L/TRAIL in a complex with deathreceptor 5. Molec. Cell 4: 563- 571, 1999. 3 C b

GAM7957 297 TNFSF10 Nitsch, R.; Bechmann, I.; Deisz, R. A.; Haas, D.; Lehmann, T. N.;Wendling, U.; Zipp, F.: Human brain- cell death induced by tumour- necrosis- factor- relatedapoptosis- inducing ligand (TRAIL). Lancet 356: 827- 828, 2000. 3 C b

GAM7957 297 TNFSF10 Pitti, R. M.; Marsters, S. A.; Ruppert, S.; Donahue, C. J.; Moore,A.; Ashkenazi, A.: Induction of apoptosis by Apo- 2 ligand, a newmember of the tumor necrosis factor cytokine family. J. Biol. Chem. 271:12687- 12690, 1996. 3 C b

GAM7957 297 TNFSF10 Raftery, M. J.; Schwab, M.; Eibert, S. M.; Samstag, Y.; Walczak,H.; Schonrich, G.: Targeting the function of mature dendritic cellsby human cytomegalovirus: a multilayered viral defense strategy. Immunity 15:997- 1009, 2001. 3 C b

GAM7957 297 TNFSF10 Wiley, S. R.; Schooley, K.; Smolak, P. J.; Din, W. S.; Huang, C.- P.;Nicholl, J. K.; Sutherland, G. R.; Smith, T. D.; Rauch, C.; Smith,C. A.; Goodwin, R. G.: Identification and characterization of a newmember of the TNF family that induces apoptosis. Immunity 3: 673- 682,1995. 3 C b

GAM7957 297 TNFSF14 Granger, S. W.; Butrovich, K. D.; Houshmand, P.; Edwards, W. R.;Ware, C. F.: Genomic characterization of LIGHT reveals linkage toan immune response locus on chromosome 19p13.3 and distinct isoformsgenerated by alternate splicing or proteolysis. J. Immun. 167: 5122- 5128,2001. 3 C b

GAM7957 297 TNFSF14 Harrop, J. A.; McDonnell, P. C.; Brigham- Burke, M.; Lyn, S. D.;Minton, J.; Tan, K. B.; Dede, K.; Spampanato, J.; Silverman, C.;Hensley, P.; DiPrinzio, R.; Emery, J. G.; Deen, K.; Eichman, C.; Chabot- Fletcher,M.; Truneh, A.; 3 C b

Young, P. R.: Herpesvirus entry mediator ligand (HVEM- L),a novel ligand for HVEM/TR2, stimulates proliferation of T cells andinhibits HT29 cell growth. . J. Biol. Chem. 273: 27548- 27556, 1998.

GAM7957 297 TNFSF14 Mauri, D. N.; Ebner, R.; Montgomery, R. I.; Kochel, K. D.; Cheung,T. C.; Yu, G. L.; Ruben, S.; Murphy, M.; Eisenberg, R. J.; Cohen,G. H.; Spear, P. G.; Ware, C. F.: LIGHT, a new member of the TNFsuperfamily, and lymphotoxin alpha are ligands for herpesvirus entrymediator. Immunity 8: 21- 30, 1998. 3 C b

GAM7957 297 TNFSF14 Morel, Y.; Schiano de Colella, J.- M.; Harrop, J.; Deen, K. C.;Holmes, S. D.; Wattam, T. A.; Khandekar, S. S.; Truneh, A.; Sweet,R. W.; Gastaut, J.- A.; Olive, D.; Costello, R. T.: Reciprocal expressionof the TNF family receptor herpes virus entry mediator and its ligandLIGHT on activated T cells: LIGHT down- regulates its own receptor. J.Immun. 165: 4397- 4404, 2000. 3 C b

GAM7957 297 TNFSF15 Migone, T.- S.; Zhang, J.; Luo, X.; Zhuang, L.; Chen, C.; Hu, B.;Hong, J. S.; Perry, J. W.; Chen, S.- F.; Zhou, J. X. H.; Cho, Y. H.;Ullrich, S.; and 14 others: TL1A is a TNF- like ligand for DR3 andTR6/DcR3 and functions as a T cell costimulator. Immunity 16: 479- 492,2002. 3 C b

GAM7957 297 TNFSF15 Tan, K. B.; Harrop, J.; Reddy, M.; Young, P.; Terrett, J.; Emery,J.; Moore, G.; Truneh, A.: Characterization of a novel TNF- like ligandand recently described TNF ligand and TNF receptor superfamily genesand their constitutive and inducible expression in hematopoietic andnon- hematopoietic cells. Gene 204: 35- 46, 1997. 3 C b

GAM7957 297 TNFSF15 Yue, T.- L.; Ni, J.; Romanic, A. M.; Gu, J.- L.; Keller, P.; Wang,C.; Kumar, S.; Yu, G.; Hart, T. K.; Wang, X.; Xia, Z.; DeWolf, W.E., Jr.; Feuerstein, G. Z.: TL1, a novel tumor necrosis factor- likecytokine, induces apoptosis in endothelial cells: involvement of activationof stress protein kinases (stress- activated protein kinase and p38mitogen- activated protein kinase) and caspase- 3- like protease. J.Biol. Chem. 274: 1479- 1486, 1999. 3 C b

GAM7957 297 TNFSF15 Zhai, Y.; Ni, J.; Jiang, G.- W.; Lu, J.; Xing, L.; Lincoln, C.;Carter, K. C.; Janat, F.; Kozak, D.; Xu, S.; Rojas, L.; Aggarwal,B. B.; Ruben, S.; Li, L.- Y.; Gentz, R.; Yu, G.- L.: VEGI, a novelcytokine of the tumor necrosis factor family, is an angiogenesis inhibitorthat suppresses the growth of colon carcinomas in vivo. FASEB J. 13:181- 189, 1999. 3 C b

GAM7957 297 TPM4 Laing, N. G.; Wilton, S. D.; Akkari, P. A.; Dorosz, S.; Boundy,K.; Kneebone, C.; Blumbergs, P.; White, S.; Watkins, H.; Love, D.R.; Haan, E.: A mutation in the alpha tropomyosin gene TPM3 associatedwith autosomal dominant nemaline myopathy. Nature Genet. 9: 75- 79,1995. 3 C c

GAM7957 297 TPM4 Wilton, S. D.; Lim, L.; Dorosz, S. D.; Gunn, H. C.; Eyre, H. J.;Callen, D. F.; Laing, N. G.: Assignment of the human alpha- tropomyosingene TPM4 to band 19p13.1 by fluorescence in situ hybridization. Cytogenet.Cell Genet. 72: 294- 296, 1996. 3 C c

GAM7957 297 TRADD Hsu, H.; Xiong, J.; Goeddel, D. V.: The TNF receptor 1- associatedprotein TRADD signals cell death and NF- kappa- B activation. Cell 81:495- 504, 1995. 3 C c

GAM7957 297 TRADD Pan, M.- G.; Xiong, J.; Copeland, N. G.; Gilbert, D. J.; Jenkins,N. A.; Goeddel, D. V.: Sequence, genomic organization, and chromosomelocalization of the mouse TRADD gene. J. Inflamm. 46: 168- 175, 1996. 3 C c

GAM7957 297 TRADD Park, Y. C.; Ye, H.; Hsia, C.; Segal, D.; Rich, R. L.; Liou, H.- C.;Myszka, D. G.; Wu, H.: A novel mechanism of TRAF signaling revealedby structural and functional analyses of the TRADD- TRAF2 interaction. Cell 101:777- 787, 3 C c

2000.

GAM7957 297 TRADD Scheuerpflug, C. G.; Lichter, P.; Debatin, K.- M.; Mincheva, A.: Assignment of TRADD to human chromosome band 16q22 by in situ hybridization. Cytogenet.Cell Genet. 92: 347- 348, 2001. 3 C c

GAM7957 297 TRIM14 Nagase, T.; Seki, N.; Tanaka, A.; Ishikawa, K.; Nomura, N.: Predictionof the coding sequences of unidentified human genes. IV. The codingsequences of 40 new genes (KIAA0121- KIAA0160) deduced by analysisof cDNA clones from human cell line KG- 1. DNA Res. 2: 167- 174, 1995. 3 C b

GAM7957 297 TRIM14 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci, S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell compartments. EMBO J. 20: 2140- 2151, 2001. 3 C b

GAM7957 297 TRPM2 Bertrand, P.; Poirier, J.; Oda, T.; Finch, C. E.; Pasinetti, G.M.: Association of apolipoprotein E genotype with brain levels ofapolipoprotein E and apolipoprotein J (clusterin) in Alzheimer disease. Molec.Brain Res. 33: 174- 178, 1995. 3 C c

GAM7957 297 TRPM2 Birkenmeier, E. H.; Letts, V. A.; Frankel, W. N.; Magenheimer,B. S.; Calvet, J. P.: Sulfated glycoprotein- 2 (Sgp- 2) maps to mousechromosome 14. Mammalian Genome 4: 131- 132, 1993. 3 C c

GAM7957 297 TRPM2 Danik, M.; Chabot, J.- G.; Hassan- Gonzalez, D.; Suh, M.; Quirion,R.: Localization of sulfated glycoprotein- 2/clusterin mRNA in therat brain by in situ hybridization. J. Comp. Neurol. 334: 209- 227,1993. 3 C c

GAM7957 297 TRPM2 de Silva, H. V.; Harmony, J. A. K.; Stuart, W. D.; Gil, C. M.;Robbins, J.: Apolipoprotein J: structure and tissue distribution. Biochemistry 29:5380- 5389, 1990. 3 C c

GAM7957 297 TRPM2 de Silva, H. V.; Stuart, W. D.; Park, Y. B.; Mao, S. J. T.; Gil,C. M.; Wetterau, J. R.; Busch, S. J.; Harmony, J. A. K.: Purificationand characterization of apolipoprotein J. J. Biol. Chem. 265: 14292- 14297,1990. 3 C c

GAM7957 297 TRPM2 Dietzsch, E.; Murphy, B. F.; Kirszbaum, L.; Walker, I. D.; Garson,O. M.: Regional localization of the gene for clusterin (SP- 40,40;gene symbol CLI) to human chromosome 8p12- p21. Cytogenet. Cell Genet. 61:178- 179, 1992. 3 C c

GAM7957 297 TRPM2 Dragunow, M.; Preston, K.; Dodd, J.; Young, D.; Lawlor, P.; Christie,D.: Clusterin accumulates in dying neurons following status epilepticus. Molec.Brain Res. 32: 279- 290, 1995. 3 C c

GAM7957 297 TRPM2 Duguid, J. R.; Bohmont, C. W.; Liu, N.; Tourtellotte, W. W.: Changesin brain gene expression shared by scrapie and Alzheimer disease. Proc.Nat. Acad. Sci. 86: 7260- 7264, 1989. 3 C c

GAM7957 297 TRPM2 Fink, T. M.; Zimmer, M.; Tschopp, J.; Etienne, J.; Jenne, D. E.;Lichter, P.: Human clusterin (CLI) maps to 8p21 in proximity to thelipoprotein lipase (LPL) gene. Genomics 16: 526- 528, 1993. 3 C c

GAM7957 297 TRPM2 Han, B. H.; DeMattos, R. B.; Dugan, L. L.; Kim- Han, J. S.; Brendza,R. P.; Fryer, J. D.; Kierson, M.; Cirrito, J.; Quick, K.; Harmony,J. A. K.; Aronow, B. J.; Holtzman, D. M.: Clusterin contributes tocaspase- 3- independent brain injury following neonatal hypoxia- ischemia. NatureMed. 7: 338- 343, 2001. 3 C c

GAM7957 297 TRPM2 Hara, Y.; Wakamori, M.; Ishii, M.; Maeno, E.; Nishida, M.; Yoshida,T.; Yamada, H.; Shimizu, S.; Mori, E.; Kudoh, J.; Shimizu, S.; Kurose,H.; Okada, Y.; Imoto, K.; Mori, Y.: LTRPC2 Ca(2+)- permeable channelactivated by changes in redox status confers susceptibility to celldeath. Molec. Cell 9: 163- 173, 2002. 3 C c

GAM7957 297 TRPM2 Harteneck, C.; Plant, T. D.; Schultz, G.: From worm to man: threesubfamilies 3 C c
of TRP channels. Trends Neurosci. 23: 159- 166, 2000.

GAM7957 297 TRPM2 Jenne, D. E.; Tschopp, J.: Clusterin: the intriguing guises ofa widely 3 C c
expressed glycoprotein. Trends Biochem. Sci. 17: 154- 159,1992.

GAM7957 297 TRPM2 Kamboh, M. I.; Harmony, J. A. K.; Sepehrnia, B.; Nwankwo, M.;Ferrell, R. E.: 3 C c
Genetic studies of human apolipoproteins. XX. Geneticpolymorphism of
apolipoprotein J and its impact on quantitative lipidtraits in
normolipidemic subjects. Am. J. Hum. Genet. 49: 1167- 1173,1991.

GAM7957 297 TRPM2 Kirszbaum, L.; Sharpe, J. A.; Murphy, B.; d'Apice, A. J. F.; Classon,B.; 3 C c
Hudson, P.; Walker, I. D.: Molecular cloning and characterizationof the
novel, human complement- associated protein, SP- 40,40: a linkbetween the
complement and reproductive systems. EMBO J. 8: 711- 718,1989.

GAM7957 297 TRPM2 Kudoh, J.; Nagamine, K.; Asakawa, S.; Abe, I.; Kawasaki, K.; Maeda,H.; 3 C c
Tsujimoto, S.; Minoshima, S.; Ito, F.; Shimizu, N.: Localizationof 16 exons
to a 450- kb region involved in the autoimmune polyglandulardisease type I
(APECED) on human chromosome 21q22.3. DNA Res. 4:45- 52, 1997.

GAM7957 297 TRPM2 Murphy, B. F.; Kirszbaum, L.; Walker, I. D.; d'Apice, A. J. F.: SP- 40,40, a 3 C c
newly identified normal human serum protein found inthe SC5b- 9 complex of
complement and in the immune deposits in glomerulonephritis. J.Clin. Invest.
81: 1858- 1864, 1988.

GAM7957 297 TRPM2 Nagamine, K.; Kudoh, J.; Minoshima, S.; Kawasaki, K.; Asakawa,S.; Ito, F.; 3 C c
Shimizu, N.: Molecular cloning of a novel putative Ca(2+)channel protein
(TRPC7) highly expressed in brain. Genomics 54:124- 131, 1998.

GAM7957 297 TRPM2 Navab, M.; Hama- Levy, S.; Van Lenten, B. J.; Fonarow, G. C.; Cardinez,C. 3 C c
J.; Castellani, L. W.; Brennan, M.- L.; Lusis, A. J.; Fogelman,A. M.: Mildly
oxidized LDL induces an increased apolipoprotein J/paraoxonaseratio. J.
Clin. Invest. 99: 2005- 2019, 1997.

GAM7957 297 TRPM2 O'Bryan, M. K.; Baker, H. W. G.; Saunders, J. R.; Kirszbaum, L.;Walker, I. 3 C c
D.; Hudson, P.; Liu, D. Y.; Glew, M. D.; d'Apice, A. J.F.; Murphy, B. F.:
Human seminal clusterin (SP- 40,40): isolationand characterization. J. Clin.
Invest. 85: 1477- 1486, 1990.

GAM7957 297 TRPM2 Perraud, A.- L.; Fleig, A.; Dunn, C. A.; Bagley, L. A.; Launay,P.; Schmitz, 3 C c
C.; Stokes, A. J.; Zhu, Q.; Bessman, M. J.; Penner, R.;Kinet, J.- P.;
Scharenberg, A. M.: ADP- ribose gating of the calcium- permeableLTRPC2
channel revealed by Nudix motif homology. Nature 411: 595- 599,2001.

GAM7957 297 TRPM2 Purrello, M.; Bettuzzi, S.; Di Pietro, C.; Mirabile, E.; Di Blasi,M.; 3 C c
Rimini, R.; Grzeschik, K.- H.; Ingletti, C.; Corti, A.; Sichel,G.: The gene
for SP- 40,40, human homolog of rat sulfated glycoprotein2, rat clusterin,
and rat testosterone- repressed prostate message2, maps to chromosome 8.
Genomics 10: 151- 156, 1991.

GAM7957 297 TRPM2 Sano, Y.; Inamura, K.; Miyake, A.; Mochizuki, S.; Yokoi, H.; Matsushime,H.; 3 C c
Furuichi, K.: Immunocyte Ca(2+) influx system mediated by LTRPC2. Science
293:1327- 1330, 2001.

GAM7957 297 TRPM2 Slawin, K.; Sawczuk, I. S.; Olsson, C. A.; Buttyan, R.: 3 C c
Chromosomalassignment of the human homologue encoding SGP- 2. Biochem.
Biophys.Res. Commun. 172: 160- 164, 1990.

GAM7957 297 TRPM2 Tobe, T.; Minoshima, S.; Yamase, S.; Choi, N.- H.; Tomita, M.;Shimizu, N.: 3 C c
Assignment of a human serum glycoprotein SP- 40,40 gene(CLI) to chromosome
8. Cytogenet. Cell Genet. 57: 193- 195, 1991.

GAM7957 297 TRPM2 Wong, P.; Pineault, J.; Lakins, J.; Taillefer, D.; Leger, J.;Wang, C.; 3 C c

Tenniswood, M.: Genomic organization and expression ofthe rat TRPM- 2 (clusterin) gene, a gene implicated in apoptosis. J.Biol. Chem. 268: 5021- 5031, 1993.

GAM7957 297 TRPM2 Wong, P.; Taillefer, D.; Lakins, J.; Pineault, J.; Chader, G.;Tenniswood, M.: Molecular characterization of human TRPM- 2/clusterin,a gene associated with sperm maturation, apoptosis and neurodegeneration. Europ.J. Biochem. 221: 917- 925, 1994. 3 C c

GAM7957 297 TRPM4 Launay, P.; Fleig, A.; Perraud, A.- L.; Scharenberg, A. M.; Penner,R.; Kinet, J.- P.: TRPM4 is a Ca(2+)- activated nonselective cationchannel mediating cell membrane depolarization. Cell 109: 397- 407,2002. 3 C c

GAM7957 297 TRPM4 Xu, X.- Z. S.; Moebius, F.; Gill, D. L.; Montell, C.: Regulationof melastatin, a TRP- related protein, through interaction with a cytoplasmicisoform. Proc. Nat. Acad. Sci. 98: 10692- 10697, 2001. 3 C c

GAM7957 297 TRPM8 Antonarakis, S. E.: Personal Communication. Baltimore, Md. 3/25/2002. 3 C b

GAM7957 297 TRPM8 McKemy, D. D.; Neuhausser, W. M.; Julius, D.: Identification ofa cold receptor reveals a general role for TRP channels in thermosensation. Nature 416:52- 58, 2002. 3 C b

GAM7957 297 TRPM8 Peier, A. M.; Moqrich, A.; Hergarden, A. C.; Reeve, A. J.; Andersson,D. A.; Story, G. M.; Earley, T. J.; Dragoni, I.; McIntyre, P.; Bevan,S.; Patapoutian, A.: A TRP channel that senses cold stimuli and menthol. Cell 108:705- 715, 2002. 3 C b

GAM7957 297 TRPM8 Tsavaler, L.; Shapero, M. H.; Morkowski, S.; Laus, R.: Trp- p8,a novel prostate- specific gene, is up- regulated in prostate cancerand other malignancies and shares high homology with transient receptorpotential calcium channel proteins. Cancer Res. 61: 3760- 3769, 2001. 3 C b

GAM7957 297 TRPV1 Bartoshuk, L. M.; Duffy, V. B.; Miller, I. J.: PTC/PROP tasting:anatomy, psychophysics, and sex effects. Physiol. Behav. 56: 1165- 1171,1994. 3 C c

GAM7957 297 TRPV1 Caterina, M. J.; Leffler, A.; Malmberg, A. B.; Martin, W. J.; Trafton,J.; Petersen- Zeltz, K. R.; Koltzenburg, M.; Basbaum, A. I.; Julius,D.: Impaired nociception and pain sensation in mice lacking the capsaicinreceptor. Science 288: 306- 313, 2000. 3 C c

GAM7957 297 TRPV1 Caterina, M. J.; Schumacher, M. A.; Tominaga, M.; Rosen, T. A.;Levine, J. D.; Julius, D.: The capsaicin receptor: a heat- activatedion channel in the pain pathway. Nature 389: 816- 824, 1997. 3 C c

GAM7957 297 TRPV1 Chuang, H.; Prescott, E. D.; Kong, H.; Shields, S.; Jordt, S.- E.;Basbaum, A. I.; Chao, M. V.; Julius, D.: Bradykinin and nerve growthfactor release the capsaicin receptor from PtdIns(4,5)P2- mediatedinhibition. Nature 411: 957- 962, 2001. 3 C c

GAM7957 297 TRPV1 Jordt, S.- E.; Julius, D.: Molecular basis for species- specificsensitivity to 'hot' chili peppers. Cell 108: 421- 430, 2002. 3 C c

GAM7957 297 TRPV1 Liedtke, W.; Choe, Y.; Marti- Renom, M. A.; Bell, A. M.; Denis,C. S.; Sali, A.; Hudspeth, A. J.; Friedman, J. M.; Heller, S.: Vanilloidreceptor- related osmotically activated channel (VR- OAC), a candidatevertebrate osmoreceptor. Cell 103: 525- 535, 2000. 3 C c

GAM7957 297 TRPV1 Liu, L.; Simon, S. A.: Similarities and differences in the currentsactivated by capsaicin, piperine, and zingerone in rat trigeminalganglion cells. J. Neurophysiol. 76: 1858- 1869, 1996. 3 C c

GAM7957 297 TRPV1 Premkumar, L. S.; Ahern, G. P.: Induction of vanilloid receptorchannel activity by protein kinase C. Nature 408: 985- 990, 2000. 3 C c

GAM7957 297 TRPV1 Prescott, J.; Stevenson, R. J.: Psychophysical responses to singleand 3 C c

multiple presentations of the oral irritant zingerone: relationshipto frequency of chili consumption. Physiol. Behav. 60: 617- 624,1996.

GAM7957 297 TRPV1 Stevenson, R. J.; Prescott, J.: The effects of prior experiencewith capsaicin on ratings of its burn. Chem. Senses 19: 651- 656,1994. 3 C c

GAM7957 297 TRPV1 Stevenson, R. J.; Yeomans, M. R.: Differences in ratings of intensityand pleasantness for the capsaicin burn between chili likers and non-likers:implications for liking development. Chem. Senses 18: 471- 482, 1993. 3 C c

GAM7957 297 TRPV1 Touchman, J. W.; Anikster, Y.; Dietrich, N. L.; Braden Maduro,V. V.; McDowell, G.; Shotelersuk, V.; Bouffard, G. G.; Beckstrom- Sternberg,S. M.; Gahl, W. A.; Green, E. D.: The genomic region encompassingthe nephropathic cystinosis gene (CTNS): complete sequencing of a200- kb segment and discovery of a novel gene within the common cystinosis- causingdeletion. Genome Res. 10: 165- 173, 2000. 3 C c

GAM7957 297 TRPV1 Trevisani, M.; Smart, D.; Gunthorpe, M. J.; Tognetto, M.; Barbieri,M.; Campi, B.; Amadesi, S.; Gray, J.; Jerman, J. C.; Brough, S. J.;Owen, D.; Smith, G. D.; Randall, A. D.; Harrison, S.; Bianchi, A.;Davis, J. B.; Geppetti, P.: Ethanol elicits and potentiates nociceptorresponses via the vanilloid receptor- 1. Nature Neurosci. 5: 546- 551,2002. 3 C c

GAM7957 297 TSNAX Aoki, K.; Ishida, R.; Kasai, M.: Isolation and characterizationof a cDNA encoding a translin- like protein, TRAX. FEBS Lett. 401:109- 112, 1997. 3 C b

GAM7957 297 TSNAX Meng, G.; Aoki, K.; Tokura, K.; Nakahara, K.; Inazawa, J.; Kasai,M.: Genomic structure and chromosomal localization of the gene encodingTRAX, a translin-associated factor X. J. Hum. Genet. 45: 305- 308,2000. 3 C b

GAM7957 297 TTF2 Bamforth, J. S.; Hughes, I. A.; Lazarus, J. H.; Weaver, C. M.;Harper, P. S.: Congenital hypothyroidism, spiky hair, and cleft palate. J.Med. Genet. 26: 49- 60, 1989. 3 C c

GAM7957 297 TTF2 Chadwick, B. P.; Obermayr, F.; Frischauf, A.- M.: FKHL15, a newhuman member of the forkhead gene family located on chromosome 9q22. Genomics 41:390-396, 1997. 3 C c

GAM7957 297 TTF2 Clifton- Bligh, R. J.; Wentworth, J. M.; Heinz, P.; Crisp, M. S.;John, R.; Lazarus, J. H.; Ludgate, M.; Chatterjee, V. K.: Mutationof the gene encoding human TTF- 2 associated with thyroid agenesis,cleft palate and choanal atresia. Nature Genet. 19: 399- 401, 1998. 3 C c

GAM7957 297 TTF2 De Felice, M.; Ovitt, C.; Biffali, E.; Rodriguez- Mallon, A.; Arra,C.; Anastassiadis, K.; Macchia, P. E.; Mattei, M.- G.; Mariano, A.;Scholer, H.; Macchia, V.; Di Lauro, R.: A mouse model for hereditarythyroid dysgenesis and cleft palate. Nature Genet. 19: 395- 398,1998. 3 C c

GAM7957 297 TTF2 Kaufmann, E.; Knochel, W.: Five years on the wings of fork head. Mech.Dev. 57: 3- 20, 1996. 3 C c

GAM7957 297 TTF2 Manley, N. R.; Capecchi, M. R.: Hox group 3 paralogs regulatethe development and migration of the thymus, thyroid, and parathyroidgland. Dev. Biol. 195: 1- 15, 1998. 3 C c

GAM7957 297 TTF2 Toublanc, J. E.: Comparison of epidemiological data on congenitalhypothyroidism in Europe with those of other parts in the world. Horm.Res. 38: 230- 235, 1992. 3 C c

GAM7957 297 TTF2 Zannini, M.; Avantaggiato, V.; Biffali, E.; Arnone, M. I.; Sato,K.; Pischetola, M.; Taylor, B. A.; Phillips, S. J.; Simeone, A.; DiLauro, R.: TTF- 2, a new forkhead protein, shows a temporal expressionin the developing thyroid which is consistent with a role in controllingthe onset of differentiation. EMBO J. 16: 3185- 3197, 1997. 3 C c

GAM7957 297 UBE2B Hoege, C.; Pfander, B.; Moldovan, G.- L.; Pyrowolakis, G.; Jentsch,S.: RAD6- 3 C c
dependent DNA repair is linked to modification of PCNA byubiquitin and SUMO.
Nature 419: 135- 141, 2002.

GAM7957 297 UBE2B Koken, M. H. M.; Smit, E. M. E.; Jaspers- Dekker, I.; Oostra, B.A.; 3 C c
Hagemeijer, A.; Bootsma, D.; Hoeijmakers, J. H. J.: Localizationof two human
homologs, HHR6A and HHR6B, of the yeast DNA repair geneRAD6 to chromosomes
Xq24- q25 and 5q23- q31. Genomics 12: 447- 453,1992.

GAM7957 297 UBE2B Lench, N. J.; Thompson, J.; Markham, A. F.; Robinson, P. A.: 3 C c
(CGG)trinucleotide repeat polymorphism in the 5- prime region of the
HHR6Bgene: the human homolog of the yeast DNA repair gene RAD6. Hum. Genet.
96:369- 370, 1995.

GAM7957 297 UBE2B Roest, H. P.; van Klaveren, J.; de Wit, J.; van Gurp, C. G.; Koken,M. H. M.; 3 C c
Vermey, M.; van Roijen, J. H.; Hoogerbrugge, J. W.; Vreeburg,J. T. M.;
Baarends, W. M.; Bootsma, D.; Grootegoed, J. A.; Hoeijmakers,J. H. J.:
Inactivation of the HR6B ubiquitin- conjugating DNA repairenzyme in mice
causes male sterility associated with chromatin modification. Cell 86:799-
810, 1996.

GAM7957 297 UBE2B Roller, M. L.; Lossie, A. C.; Koken, M. H. M.; Smit, E. M. E.;Hagemeijer, 3 C c
A.; Camper, S. A.: Localization of sequences relatedto the human RAD6 DNA
repair gene on mouse chromosomes 11 and 13. MammalianGenome 6: 305- 306,
1995.

GAM7957 297 UBE2G2 Katsanis, N.; Fisher, E. M. C.: Identification, expression, andchromosomal 3 C b
localization of ubiquitin conjugating enzyme 7 (UBE2G2),a human homologue of
the Saccharomyces cerevisiae Ubc7 gene. Genomics 51:128- 131, 1998.

GAM7957 297 UBE2G2 Rose, S. A.; Leek, J. P.; Moynihan, T. P.; Ardley, H. C.; Markham,A. F.; 3 C b
Robinson, P. A.: Assignment of the ubiquitin conjugating enzymegene, UBE2G2,
to human chromosome band 21q22.3 by in situ hybridization. Cytogenet.Cell
Genet. 83: 98- 99, 1998.

GAM7957 297 UPK1B Finch, J. L.; Webb, G. C.; Evdokiou, A; Cowled, P. A.: 3 C b
Chromosomallocalization of the human urothelial tetraspan gene, UPK1B, to
3q13.3- q21and detection of a Taq1 polymorphism. Genomics 40: 501- 503,
1997.

GAM7957 297 UPK1B Yu, J.; Lin, J.- H.; Wu, X.- R.; Sun, T.- T.: Uroplakins Ia and Ib,two major 3 C b
differentiation products of bladder epithelium, belong toa family of four
transmembrane domain (4TM) proteins. J. Cell Biol. 125:171- 182, 1994.

GAM7957 297 USP14 Deshpande, K. L.; Seubert, P. H.; Tillman, D. M.; Farkas, W. R.;Katze, J. 3 C b
R.: Cloning and characterization of cDNA encoding the rabbittRNA- guanine
transglycosylase 60- kilodalton subunit. Arch. Biochem.Biophys. 326: 1- 7,
1996.

GAM7957 297 USP14 Wilson, S. M.; Bhattacharyya, B.; Rachel, R. A.; Coppola, V.; Tessarollo,L.; 3 C b
Householder, D. B.; Fletcher, C. F.; Miller, R. J.; Copeland,N. G.; Jenkins,
N. A.: Synaptic defects in ataxia mice result froma mutation in Usp14,
encoding a ubiquitin- specific protease. NatureGenet. 7Oct, 2002. Note:
Advance Electronic Publication.

GAM7957 297 VEGF Bardwick, P. A.; Zvaifler, N. J.; Gill, G. N.; Newman, D.; Greenway,G. D.; 3 C c
Resnick, D. L.: Plasma cell dyscrasia with polyneuropathy,organomegaly,
endocrinopathy, M protein, and skin changes: the POEMSsyndrome. Report on
two cases and a review of the literature. Medicine 59:311- 322, 1980.

GAM7957 297 VEGF Basu, S.; Nagy, J. A.; Pal, S.; Vasile, E.; Eckelhoefer, I. A.;Bliss, V. S.; 3 C c
Manseau, E. J.; Dasgupta, P. S.; Dvorak, H. F.; Mukhopadhyay,D.: The

neurotransmitter dopamine inhibits angiogenesis induced byvascular permeability factor/vascular endothelial growth factor. NatureMed. 7: 569-574, 2001.

GAM7957 297 VEGF Carmellet, P.; Ferreira, V.; Breler, G.; Pollefeyt, S.; Kleckens,L.; Gertsenstein, M.; Fahrig, M.; Vandenhoeck, A.; Harpal, K.; Eberhardt,C.; Declercq, C.; Pawling, J.; Moons, L.; Collen, D.; Risau, W.; Nagy,A.: Abnormal blood vessel development and lethality in embryos lackinga single VEGF allele. Nature 380: 435- 439, 1996. 3 C c

GAM7957 297 VEGF Crow, R. S.: Peripheral neuritis in myelomatosis. Brit. Med.J. 2: 802- 804, 1956. 3 C c

GAM7957 297 VEGF Dantz, D.; Bewersdorf, J.; Fruehwald- Schultes, B.; Kern, W.; Jelkmann,W.; Born, J.; Fehm, H. L.; Peters, A.: Vascular endothelial growthfactor: a novel endocrine defensive response to hypoglycemia. J.Clin. Endocr. Metab. 87: 835- 840, 2002. 3 C c

GAM7957 297 VEGF de Fraipont, F.; El Atifi, M.; Gicquel, C.; Bertagna, X.; Chambaz,E. M.; Feige, J. J.: Expression of the angiogenesis markers vascularendothelial growth factor- A, thrombospondin- 1, and platelet- derivedendothelial cell growth factor in human sporadic adrenocortical tumors:correlation with genotypic alterations. J. Clin. Endocr. Metab. 85:4734- 4741, 2000. 3 C c

GAM7957 297 VEGF Ferrara, N.; Carver- Moore, K.; Chen, H.; Dowd, M.; Lu, L.; O'Shea,K. S.; Powell- Braxton, L.; Hillan, K. J.; Moore, M. W.: Heterozygousembryonic lethality induced by targeted inactivation of the VEGF gene. Nature 380:439-442, 1996. 3 C c

GAM7957 297 VEGF Folkman, J.: Angiogenesis in cancer, vascular, rheumatoid andother disease. Nature Med. 1: 27- 31, 1995. 3 C c

GAM7957 297 VEGF Fukumura, D.; Xavier, R.; Sugiura, T.; Chen, Y.; Park, E.- C.; Lu,N.; Selig, M.; Nielsen, G.; Taksir, T.; Jain, R. K.; Seed, B.: Tumorinduction of VEGF promoter activity in stromal cells. Cell 94: 715- 725,1998. 3 C c

GAM7957 297 VEGF Funatsu, H.; Yamashita, H.; Noma, H.; Mimura, T.; Yamashita, T.;Hori, S.: Increased levels of vascular endothelial growth factorand interleukin- 6 in the aqueous humor of diabetics with macular edema. Am.J. Ophthal. 133: 70-77, 2002. 3 C c

GAM7957 297 VEGF Gerber, H.- P.; Malik, A. K.; Solar, G. P.; Sherman, D.; Liang,X. H.; Meng, G.; Hong, K.; Marsters, J. C.; Ferrara, N.: VEGF regulateshaematopoietic stem cell survival by an internal autocrine loop mechanism. Nature 417:954-958, 2002. 3 C c

GAM7957 297 VEGF Gerber, H.- P.; Vu, T. H.; Ryan, A. M.; Kowalski, J.; Werb, Z.;Ferrara, N.: VEGF couples hypertrophic cartilage remodeling, ossificationand angiogenesis during endochondral bone formation. Nature Med. 5:623- 628, 1999. 3 C c

GAM7957 297 VEGF Giordano, F. J.; Gerber, H.- P.; Williams, S.- P.; VanBruggen, N.;Bunting, S.; Ruiz- Lozano, P.; Gu, Y.; Nath, A. K.; Huang, Y.; Hickey,R.; Dalton, N.; Peterson, K. L.; Ross, J., Jr.; Chien, K. R.; Ferrara,N.: A cardiac myocyte vascular endothelial growth factor paracrinepathway is required to maintain cardiac function. Proc. Nat. Acad.Sci. 98: 5780- 5785, 2001. 3 C c

GAM7957 297 VEGF Helmlinger, G.; Endo, M.; Ferrara, N.; Hlatky, L.; Jain, R. K.: Formation of endothelial cell networks. Nature 405: 139- 141, 2000. 3 C c

GAM7957 297 VEGF Hofman, P.; van Blijswijk, B. C.; Gaillard, P. J.; Vrensen, G.F. J. M.; Schlingemann, R. O.: Endothelial cell hypertrophy inducedby vascular endothelial growth factor in the retina: new insightsinto the pathogenesis of capillary nonperfusion. Arch. Ophthal. 119:861- 866, 2001. 3 C c

GAM7957 297 VEGF Holash, J.; Maisonpierre, P. C.; Compton, D.; Boland, P.; Alexander,C. R.; 3 C c
Zagzag, D.; Yancopoulos, G. D.; Wiegand, S. J.: Vessel cooption,regression,
and growth in tumors mediated by angiopoietins and VEGF. Science 284:1994-
1998, 1999.

GAM7957 297 VEGF Jin, K.; Zhu, Y.; Sun, Y.; Mao, X. O.; Xie, L.; Greenberg, D.A.: Vascular 3 C c
endothelial growth factor (VEGF) stimulates neurogenesisin vitro and in
vivo. Proc. Nat. Acad. Sci. 99: 11946- 11950, 2002.

GAM7957 297 VEGF Klein, M.; Vignaud, J.- M.; Hennequin, V.; Toussaint, B.; Bresler,L.; 3 C c
Plenat, F.; Leclere, J.; Duprez, A.; Weryha, G.: Increased expressionof the
vascular endothelial growth factor is a pejorative prognosismarker in
papillary thyroid carcinoma. J. Clin. Endocr. Metab. 86:656- 658, 2001.

GAM7957 297 VEGF Mattei, M.- G.; Borg, J.- P.; Rosnet, O.; Marme, D.; Birnbaum, D.: 3 C c
Assignment of vascular endothelial growth factor (VEGF) and placentagrowth
factor (PlGF) genes to human chromosome 6p12- p21 and 14q24- q31regions,
respectively. Genomics 32: 168- 169, 1996.

GAM7957 297 VEGF Millauer, B.; Shawver, L. K.; Plate, K. H.; Risau, W.; Ullrich,A.: 3 C c
Glioblastoma growth inhibited in vivo by a dominant- negativeFlk- 1 mutant.
Nature 367: 576- 579, 1994.

GAM7957 297 VEGF Miralles, G. D.; O'Fallon, J. R.; Talley, N. J.: Plasma- celldyscrasia with 3 C c
polyneuropathy: the spectrum of POEMS syndrome. NewEng. J. Med. 327: 1919-
1923, 1992.

GAM7957 297 VEGF Mueller, M. D.; Vigne, J.- L.; Minchenko, A.; Lebovic, D. I.; Leitman,D. C.; 3 C c
Taylor, R. N.: Regulation of vascular endothelial growth factor(VEGF) gene
transcription by estrogen receptors alpha and beta. Proc.Nat. Acad. Sci. 97:
10972- 10977, 2000.

GAM7957 297 VEGF Nakanishi, T.; Sobue, I.; Toyokura, Y.; Nishitani, H.; Kuroiwa,Y.; 3 C c
Satoyoshi, E.; Tsubaki, T.; Igata, A.; Ozaki, Y.: The Crow- Fukasesyndrome:
a study of 102 cases in Japan. Neurology 34: 712- 720,1984.

GAM7957 297 VEGF Niimi, H.; Arimura, K.; Jonosono, M.; Hashiguchi, T.; Kawabata,M.; Osame, 3 C c
M.; Kitajima, I.: VEGF is causative for pulmonary hypertensionin a patient
with Crow- Fukase (POEMS) syndrome. Intern. Med. 39:1101- 1104, 2000.

GAM7957 297 VEGF Oosthuyse, B.; Moons, L.; Storkebaum, E.; Beck, H.; Nuyens, D.;Brusselmans, 3 C c
K.; Van Dorpe, J.; Hellings, P.; Gorselink, M.; Heymans,S.; Theilmeier, G.;
Dewerchin, M.; and 20 others: Deletion of thehypoxia- response element in
the vascular endothelial growth factorpromoter causes motor neuron
degeneration. Nature Genet. 28: 131- 138,2001.

GAM7957 297 VEGF Poltorak, Z.; Cohen, T.; Sivan, R.; Kandelis, Y.; Spira, G.; Vlodavsky,I.; 3 C c
Keshet, E.; Neufeld, G.: VEGF145, a secreted vascular endothelialgrowth
factor isoform that binds to extracellular matrix. J. Biol.Chem. 272: 7151-
7158, 1997.

GAM7957 297 VEGF Shimpo, S.: Solitary myeloma causing polyneuritis and endocrinedisorders. 3 C c
Nippon Rinsho 26: 2444- 2456, 1968.

GAM7957 297 VEGF Soker, S.; Takashima, S.; Miao, H. Q.; Neufeld, G.; Klagsbrun,M.: 3 C c
Neuropilin- 1 is expressed by endothelial and tumor cells as anisoform-
specific receptor for vascular endothelial growth factor. Cell 92:735- 745,
1998.

GAM7957 297 VEGF Sone, H.; Kawakami, Y.; Sakauchi, M.; Nakamura, Y.; Takahashi,A.; Shimano, 3 C c
H.; Okuda, Y.; Segawa, T.; Suzuki, H.; Yamada, N.: Neutralizationof vascular
endothelial growth factor prevents collagen- induced arthritisand
ameliorates established disease in mice. Biochem. Biophys. Res.Commun. 281:

562- 568, 2001.

GAM7957 297 VEGF Springer, M. L.; Chen, A. S.; Kraft, P. E.; Bednarski, M.; Blau,H. M.: VEGF gene delivery to muscle: potential role for vasculogenesisin adults. Molec. Cell 2: 549- 558, 1998. 3 C c

GAM7957 297 VEGF Thurston, G.; Suri, C.; Smith, K.; McClain, J.; Sato, T. N.; Yancopoulos,G. D.; McDonald, D. M.: Leakage- resistant blood vessels in mice transgenicallyoverexpressing angiopoietin- 1. Science 286: 2511- 2514, 1999. 3 C c

GAM7957 297 VEGF Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz,D.; Fiddes, J. C.; Abraham, J. A.: The human gene for vascular endothelialgrowth factor: multiple protein forms are encoded through alternativeexon splicing. J. Biol. Chem. 266: 11947- 11954, 1991. 3 C c

GAM7957 297 VEGF Vincenti, V.; Cassano, C.; Rocchi, M.; Persico, M. G.: Assignmentof the vascular endothelial growth factor gene to human chromosome6p21.3. Circulation 93: 1493- 1495, 1996. 3 C c

GAM7957 297 VEGF Watanabe, O.; Maruyama, I.; Arimura, K.; Kitajima, I.; Arimura,H.; Hanatani, M.; Matsuo, K.; Arisato, T.; Osame, M.: Overproductionof vascular endothelial growth factor/vascular permeability factoris causative in Crow-Fukase (POEMS) syndrome. Muscle Nerve 21: 1390- 1397,1998. 3 C c

GAM7957 297 VEGF Wei, M.- H.; Popescu, N. C.; Lerman, M. I.; Merrill, M. J.; Zimonjic,D. B.: Localization of the human vascular endothelial growth factorgene, VEGF, at chromosome 6p12. Hum. Genet. 97: 794- 797, 1996. 3 C c

GAM7957 297 VEGF Wong, A. K.; Alfert, M.; Castrillon, D. H.; Shen, Q.; Holash,J.; Yancopoulos, G. D.; Chin, L.: Excessive tumor- elaborated VEGFand its neutralization define a lethal paraneoplastic syndrome. Proc.Nat. Acad. Sci. 98: 7481- 7486, 2001. 3 C c

GAM7957 297 VEGF Wulff, C.; Wilson, H.; Largue, P.; Duncan, W. C.; Armstrong, D.G.; Fraser, H. M.: Angiogenesis in the human corpus luteum: localizationand changes in angiopoietins, Tie- 2, and vascular endothelial growthfactor messenger ribonucleic acid. J. Clin. Endocr. Metab. 85: 4302- 4309,2000. 3 C c

GAM7957 297 VEGF Ylikorkala, A.; Rossi, D. J.; Korsisaari, N.; Luukko, K.; Alitalo,K.; Henkemeyer, M.; Makela, T. P.: Vascular abnormalities and deregulationof VEGF in Lkb1- deficient mice. Science 293: 1323- 1326, 2001. 3 C c

GAM7957 297 VHL Allen, R. C.; Webster, A. R.; Sui, R.; Brown, J.; Taylor, C. M.;Stone, E. M.: Molecular characterization and ophthalmic investigationof a large family with type 2A von Hippel- Lindau disease. Arch. Ophthal. 119:1659- 1665, 2001. 3 C b

GAM7957 297 VHL Atuk, N. O.; McDonald, T.; Wood, T.; Carpenter, J. T.; Walzak,M. P.; Donaldson, M.; Gillenwater, J. Y.; Turner, S. M.; Westfall,V.: Familial pheochromocytoma, hypercalcemia, and von Hippel- Lindaudisease: a ten- year study of a large family. Medicine 58: 209- 218,1979. 3 C b

GAM7957 297 VHL Bender, B. U.; Altehofer, C.; Januszewicz, A.; Gartner, R.; Schmidt,H.; Hoffmann, M. M.; Heidemann, P. H.; Neumann, H. P. H.: Functioningthoracic paraganglioma: association with Von Hippel- Lindau syndrome. J.Clin. Endocr. Metab. 82: 3356- 3360, 1997. 3 C b

GAM7957 297 VHL Bender, B. U.; Eng, C.; Olschewski, M.; Berger, D. P.; Laubenberger,J.; Altehofer, C.; Kirste, G.; Orszagh, M.; van Velthoven, V.; Miosczka,H.; Schmidt, D.; Neumann, H. P. H.: VHL c.505 T- C mutation confersa high age related penetrance but no increased overall mortality. J.Med. Genet. 38: 508- 514, 2001. 3 C b

GAM7957 297 VHL Bender, B. U.; Gutsche, M.; Glasker, S.; Muller, B.; Kirste, G.;Eng, C.; 3 C b

Neumann, H. P. H.: Differential genetic alterations in vonHippel- Lindau syndrome- associated and sporadic pheochromocytomas. J.Clin. Endocr. Metab. 85: 4568- 4574, 2000.

GAM7957 297 VHL Bonnet, P.; Dechaume, J.; Blanc, E.: L'anevrisme cirsoide de laretine 3 C b
l'anevrisme racemeux, ses relations avec l'anevrisme cirsoidede la face et l'anevrisme cirsoid du cerveau. Bull. Soc. Ophtal.Franc. 51: 521- 524, 1938.

GAM7957 297 VHL Bradley, J. F.; Collins, D. L.; Schimke, R. N.; Parrott, H. N.;Rothberg, P. 3 C b
G.: Two distinct phenotypes caused by two differentmissense mutations in the same codon of the VHL gene. Am. J. Med.Genet. 87: 163- 167, 1999.

GAM7957 297 VHL Brauch, H.; Kishida, T.; Glavac, D.; Chen, F.; Pausch, F.; Hofler,H.; Latif, 3 C b
F.; Lerman, M. I.; Zbar, B.; Neumann, H. P. H.: Von Hippel- Lindau(VHL) disease with pheochromocytoma in the Black Forest region ofGermany: evidence for a founder effect. Hum. Genet. 95: 551- 556,1995.

GAM7957 297 VHL Brown, D. G.; Hilal, S. K.; Tenner, M. S.: Wyburn- Mason syndrome. 3 C b
Arch.Neurol. 28: 67- 68, 1973.

GAM7957 297 VHL Cahill, G. F.; Melicow, M. M.; Guerry, D.: The renal lesionsin von Hippel- 3 C b
Lindau's disease. Trans. Am. Assoc. Genitourinary Surg. 35:271- 281, 1942.

GAM7957 297 VHL Cameron, S. J.; Doig, A.: Cerebellar tumors presented with clinicalfeatures 3 C b
of phaeochromocytoma. Lancet I: 492- 494, 1970.

GAM7957 297 VHL Chapman, R. C.; Diaz- Perez, R.: Pheochromocytoma associated withcerebellar 3 C b
hemangioblastoma. J.A.M.A. 182: 1014- 1017, 1962.

GAM7957 297 VHL Chen, F.; Kishida, T.; Yao, M.; Hustad, T.; Glavac, D.; Dean,M.; Gnarra, J. 3 C b
R.; Orcutt, M. L.; Duh, F. M.; Glenn, G.; Green, J.;Hsia, Y. E.; Lamiell, J.; Li, H.; Wei, M. H.; Schmidt, L.; Tory, K.;Kuzman, I.; Stackhouse, T.; Latif, F.; Linehan, W. M.; Lerman, M.;Zbar, B.: Germline mutations in the von Hippel- Lindau disease tumorsuppressor gene: correlations with phenotype. Hum. Mutat. 5: 66- 75,1995.

GAM7957 297 VHL Chen, F.; Slife, L.; Kishida, T.; Mulvihill, J.; Tisherman, S.E.; Zbar, B.: 3 C b
Genotype- phenotype correlation in von Hippel- Lindaudisease: identification of a mutation associated with VHL type 2A. J.Med. Genet. 33: 716- 717, 1996.

GAM7957 297 VHL Christoferson, L. A.; Gustafson, M. B.; Petersen, A. G.: VonHippel- Lindau's 3 C b
disease. J.A.M.A. 178: 280- 282, 1961.

GAM7957 297 VHL Collins, E. T.: Intra- ocular growths (two cases, brother andsister, with 3 C b
peculiar vascular new growth, probably primarily retinal,affecting both eyes). Trans. Ophthal. Soc. U.K. 14: 141- 149, 1894.

GAM7957 297 VHL Crossey, P. A.; Foster, K.; Richards, F. M.; Phipps, M. E.; Latif,F.; Tory, 3 C b
K.; Jones, M. H.; Bentley, E.; Kumar, R.; Lerman, M. I.;Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.; Maher, E. R.: Moleculargenetic investigations of the mechanism of tumourigenesis in von Hippel- Lindaudisease: analysis of allele loss in VHL tumours. Hum. Genet. 93:53- 58, 1994.

GAM7957 297 VHL Crossey, P. A.; Richards, F. M.; Foster, K.; Green, J. S.; Prowse,A.; Latif, 3 C b
F.; Lerman, M. I.; Zbar, B.; Affara, N. A.; Ferguson- Smith,M. A.; Maher, E. R.: Identification of intragenic mutations in thevon Hippel- Lindau disease tumour suppressor gene and correlation withdisease phenotype. Hum. Molec. Genet. 3: 1303- 1308, 1994.

GAM7957 297 VHL Cushing, H.; Bailey, P.: Hemangiomas of cerebellum and retina(Lindau's 3 C b
disease), with the report of a case. Arch. Ophthal. 57:447- 463, 1928.

GAM7957 297 VHL Davies, D. R.; Norman, A. M.; Whitehouse, R. W.; Evans, D. G.R.: Non- 3 C b
expression of von Hippel- Lindau phenotype in an obligategene carrier. Clin. Genet. 45: 104- 106, 1994.

GAM7957 297 VHL Decker, H.- J. H.; Neumann, H. P. H.; Walter, T. A.; Sandberg,A. A.: 3p 3 C b
involvement in a renal cell carcinoma in von Hippel- Lindausyndrome: region
of tumor breakpoint clustering on 3p? Cancer Genet.Cytogenet. 33: 59- 65,
1988.

GAM7957 297 VHL Duan, D. R.; Humphrey, J. S.; Chen, D. Y. T.; Weng, Y.; Sukegawa,J.; Lee, 3 C b
S.; Gnarra, J. R.; Linehan, W. M.; Klausner, R. D.: Characterizationof the
VHL tumor suppressor gene product: localization, complex formation,and the
effect of natural inactivating mutations. Proc. Nat. Acad.Sci. 92: 6459-
6463, 1995.

GAM7957 297 VHL Duan, D. R.; Pause, A.; Burgess, W. H.; Aso, T.; Chen, D. Y. T.;Garrett, K. 3 C b
P.; Conaway, R. C.; Conaway, J. W.; Linehan, W. M.; Klausner,R. D.:
Inhibition of transcription elongation by the VHL tumor suppressorprotein.
Science 269: 1402- 1406, 1995.

GAM7957 297 VHL Eisenhofer, G.; Walther, M. M.; Huynh, T.- T.; Li, S.- T.; Bornstein,S. R.; 3 C b
Vortmeyer, A.; Mannelli, M.; Goldstein, D. S.; Linehan, W.M.; Lenders, J. W.
M.; Pacak, K.: Pheochromocytomas in von Hippel- Lindausyndrome and multiple
endocrine neoplasia type 2 display distinctbiochemical and clinical
phenotypes. J. Clin. Endocr. Metab. 86:1999- 2008, 2001.

GAM7957 297 VHL Eng, C.; Crossey, P. A.; Mulligan, L. M.; Healey, C. S.; Houghton,C.; 3 C b
Prowse, A.; Chew, S. L.; Dahia, P. L. M.; O'Riordan, J. L. H.;Toledo, S. P.
A.; Smith, D. P.; Maher, E. R.; Ponder, B. A. J.: Mutationsin the RET proto-
oncogene and the von Hippel- Lindau disease tumoursuppressor gene in
sporadic and syndromic phaeochromocytomas. J.Clin. Genet. 32: 934- 937,
1995.

GAM7957 297 VHL Epstein, A. C. R.; Gleadle, J. M.; McNeill, L. A.; Hewitson, K.S.; O'Rourke, 3 C b
J.; Mole, D. R.; Mukherji, M.; Metzen, E.; Wilson, M.I.; Dhanda, A.; Tian,
Y.- M.; Masson, N.; Hamilton, D. L.; Jaakkola,P.; Barstead, R.; Hodgkin, J.;
Maxwell, P. H.; Pugh, C. W.; Schofield,C. J.; Ratcliffe, P. J.: C. elegans
EGL- 9 and mammalian homologsdefine a family of dioxygenases that regulate
HIF by prolyl hydroxylation. Cell107: 43- 54, 2001.

GAM7957 297 VHL Erbe, R. W.: Cabot case. New Eng. J. Med. 298: 95- 101, 1978. 3 C b

GAM7957 297 VHL Fearon, E. R.: Human cancer syndromes: clues to the origin andnature of 3 C b
cancer. Science 278: 1043- 1050, 1997.

GAM7957 297 VHL Feldman, D. E.; Thulasiraman, V.; Ferreyra, R. G.; Frydman, J.: Formation of 3 C b
the VHL- elongin BC tumor suppressor complex is mediatedby the chaperonin
TRiC. Molec. Cell 1051- 1061, 1999.

GAM7957 297 VHL Fill, W. L.; Lamiell, J. M.; Polk, N. O.: The radiographic manifestationsof 3 C b
von Hippel- Lindau disease. Radiology 133: 289- 295, 1979.

GAM7957 297 VHL Fishman, R. S.; Bartholomew, L. G.: Severe pancreatic involvementin three 3 C b
generations in von Hippel- Lindau disease. Mayo Clin. Proc. 54:329- 331,
1979.

GAM7957 297 VHL Friedrich, C. A.: Genotype/phenotype correlation in von Hippel- 3 C b
Lindausyndrome. Hum. Molec. Genet. 10: 763- 767, 2001.

GAM7957 297 VHL Fukino, K.; Teramoto, A.; Adachi, K.; Takahashi, H.; Emi, M.:A family with 3 C b
hydrocephalus as a complication of cerebellar
hemangioblastoma:identification of pro157leu mutation in the VHL gene. J.
Hum. Genet. 45:47- 51, 2000.

GAM7957 297 VHL Fulton, J. F.: Harvey Cushing: A Biography. Springfield, Illinois:Charles C 3 C b
Thomas (pub.) 1946.

GAM7957 297 VHL Funk, K. C.; Heiken, J. P.: Papillary cystadenoma of the broadligament in a 3 C b

patient with von Hippel- Lindau disease. Am. J. Radiol. 153:527- 528, 1989.

GAM7957 297 VHL Gaffey, M. J.; Mills, S. E.; Boyd, J. C.: Aggressive papillarytumor of middle ear/temporal bone and adnexal papillary cystadenoma. Am.J. Surg. Path. 18: 1254- 1260, 1994. 3 C b

GAM7957 297 VHL Gallou, C.; Joly, D.; Mejean, A.; Staroz, F.; Martin, N.; Tarlet,G.; Orfanelli, M. T.; Bouvier, R.; Droz, D.; Chretien, Y.; Marechal,J. M.; Richard, S.; Junien, C.; Beroud, C.: Mutations of the VHLgene in sporadic renal cell carcinoma: definition of a risk factorfor VHL patients to develop an RCC. Hum. Mutat. 13: 464- 475, 1999. 3 C b

GAM7957 297 VHL Garcia, A.; Matias- Guiu, X.; Cabezas, R.; Chico, A.; Prat, J.;Baiget, M.; De Leiva, A.: Molecular diagnosis of von Hippel- Lindaudisease in a kindred with a predominance of familial phaeochromocytoma. Clin.Endocr. 46: 359- 363, 1997. 3 C b

GAM7957 297 VHL Gemmill, R. M.; Bemis, L. T.; Lee, J. P.; Sozen, M. A.; Baron,A.; Zeng, C.; Erickson, P. F.; Hooper, J. E.; Drabkin, H. A.: TheTRC8 hereditary kidney cancer gene suppresses growth and functionswith VHL in a common pathway. Oncogene 21: 3507- 3516, 2002. 3 C b

GAM7957 297 VHL Gersell, D. J.; King, T. C.: Papillary cystadenoma of the mesosalpinxin von Hippel- Lindau disease. Am. J. Surg. Path. 12: 145- 149, 1988. 3 C b

GAM7957 297 VHL Gilcrease, M. Z.; Schmidt, L.; Zbar, B.; Truong, L.; Rutledge,M.; Wheeler, T. M.: Somatic von Hippel- Lindau mutation in clear cellpapillary cystadenoma of the epididymis. Hum. Path. 26: 1341- 1346,1995. 3 C b

GAM7957 297 VHL Glenn, G. M.; Daniel, L. N.; Choyke, P.; Linehan, W. M.; Oldfield,E.; Gorin, M. B.; Hosoe, S.; Latif, F.; Weiss, G.; Walther, M.; Lerman,M. I.; Zbar, B.: Von Hippel- Lindau (VHL) disease: distinct phenotypessuggest more than one mutant allele at the VHL locus. Hum. Genet. 87:207- 210, 1991. 3 C b

GAM7957 297 VHL Glenn, G. M.; Linehan, W. M.; Hosoe, S.; Latif, F.; Yao, M.; Choyke,P.; Gorin, M. B.; Chew, E.; Oldfield, E.; Manolatos, C.; Orcutt, M.L.; Walther, M. M.; Weiss, G. H.; Tory, K.; Jensson, O.; Lerman, M.I.; Zbar, B.: Screening for von Hippel- Lindau disease by DNA polymorphismanalysis. J.A.M.A. 267: 1226- 1231, 1992. 3 C b

GAM7957 297 VHL Gnarra, J. R.; Ward, J. M.; Porter, F. D.; Wagner, J. R.; Devor,D. E.; Grinberg, A.; Emmert- Buck, M. R.; Westphal, H.; Klausner, R.D.; Marston Linehan, W.: Defective placental vasculogenesis causesembryonic lethality in VHL- deficient mice. Proc. Nat. Acad. Sci. 94:9102- 9107, 1997. 3 C b

GAM7957 297 VHL Go, R. C. P.; Lamiell, J. M.; Hsia, Y. E.; Yuen, J. W.- M.; Paik,Y.: Segregation and linkage analyses of von Hippel Lindau diseaseamong 220 descendants from one kindred. Am. J. Hum. Genet. 36: 131- 142,1984. 3 C b

GAM7957 297 VHL Goldberg, M. F.; Duke, J. R.: Von Hippel- Lindau disease: histopathologicfindings in a treated and untreated eye. Am. J. Ophthal. 66: 693- 705,1968. 3 C b

GAM7957 297 VHL Graff, J. W.: Personal Communication. Brookline, Mass. 10/4/1998. 3 C b

GAM7957 297 VHL Green, J. S.; Bowmer, M. I.; Johnson, G. J.: Von Hippel- Lindaudisease in a Newfoundland kindred. Canad. Med. Assoc. J. 134: 133- 138and 146, 1986. 3 C b

GAM7957 297 VHL Griffiths, D. F. R.; Williams, G. T.; Williams, E. D.: Duodenalcarcinoid tumours, phaeochromocytoma and neurofibromatosis: isletcell tumour, phaeochromocytoma and the von Hippel- Lindau complex:two distinctive neuroendocrine syndromes. Quart. J. Med. 245: 769- 782,1987. 3 C b

GAM7957 297 VHL Gross, D. J.; Avishai, N.; Meiner, V.; Filon, D.; Zbar, B.; Abeliovich,D.: Familial pheochromocytoma associated with a novel mutation inthe von Hippel- 3 C b

Lindau gene. J. Clin. Endocr. Metab. 81: 147- 149,1996.

GAM7957 297 VHL Grossman, M.; Melmon, K. L.: Von Hippel- Lindau disease.In: Vinken,P. J.; Bruyn, G. W.: Handbook of Clinical Neurology. The Phakomatoses. Amsterdam: North Holland (pub.) 14: 1972. Pp. 241- 259. 3 C b

GAM7957 297 VHL Haase, V. H.; Glickman, J. N.; Socolovsky, M.; Jaenisch, R.:Vascular tumors in livers with targeted inactivation of the von Hippel- Lindautumor suppressor. Proc. Nat. Acad. Sci. 98: 1583- 1588, 2001. 3 C b

GAM7957 297 VHL Hagler, W. S.; Hyman, B. N.; Waters, W. C., III: Von Hippel'sangiomatosis retinae and pheochromocytoma. Trans. Am. Acad. Ophthal.Otolaryng. 75: 1022- 1034, 1971. 3 C b

GAM7957 297 VHL Hennessy, T. G.; Stern, W. E.; Herrick, S. E.: Cerebellar hemangioblastoma:erythropoietic activity by radioion assay. J. Nucl. Med. 8: 601- 606,1967. 3 C b

GAM7957 297 VHL Herman, J. G.; Latif, F.; Weng, Y.; Lerman, M. I.; Zbar, B.; Liu,S.; Samid, D.; Duan, D.- S. R.; Guarra, J. R.; Linehan, W. M.; Baylin,S. B.: Silencing of the VHL tumor- suppressor gene by DNA methylationin renal carcinomas. Proc. Nat. Acad. Sci. 91: 9700- 9704, 1994. 3 C b

GAM7957 297 VHL Hes, F. J.; McKee, S.; Taphoorn, M. J. B.; Rehal, P.; van derLuijt, R. B.; McMahon, R.; van der Smagt, J. J.; Dow, D.; Zewald,R. A.; Whittaker, J.; Lips, C. J. M.; MacDonald, F.; Pearson, P. L.;Maher, E. R.: Cryptic von Hippel- Lindau disease: germline mutationsin patients with haemangioblastoma only. J. Med. Genet. 37: 939- 943,2000. 3 C b

GAM7957 297 VHL Hes, F.; Zewald, R.; Peeters, T.; Sijmons, R.; Links, T.; Verheij,J.; Matthijs, G.; Legius, E.; Mortier, G.; van der Torren, K.; Rosman,M.; Lips, C.; Pearson, P.; van der Luijt, R.: Genotype- phenotypecorrelations in families with deletions in the von Hippel- Lindau (VHL)gene. Hum. Genet. 106: 425- 431, 2000. 3 C b

GAM7957 297 VHL Hoffman, M. A.; Ohh, M.; Yang, H. Kico, J. M.; Ivan, M.; Kaelin,W. G., Jr.: von Hippel- Lindau, protein mutants linked to type 2CVHL disease preserve the ability to downregulated HIF. Hum. Molec.Genet. 10: 1019- 1027, 2001. 3 C b

GAM7957 297 VHL Hon, W.- C.; Wilson, M. I.; Harlos, K.; Claridge, T. D. W.; Schofield,C. J.; Pugh, C. W.; Maxwell, P. H.; Ratcliffe, P. J.; Stuart, D. I.;Jones, E. Y.: Structural basis for the recognition of hydroxyprolinein HIF- 1- alpha by pVHL. Nature 417: 975- 978, 2002. 3 C b

GAM7957 297 VHL Horbach, J. M. L. M.; Brenninkmeyer, S. J.; van de Velde, C. J.H.; Nieuwenhuyzen Kruseman, A. C.: A forme fruste of von Hippel- Lindaudisease- - a combination of adrenal pheochromocytoma and ipsilateralrenal cell carcinoma: a case report. Surgery 105: 436- 441, 1989. 3 C b

GAM7957 297 VHL Horton, W. A.; Wong, V.; Eldridge, R.: Von Hippel- Lindau disease- - clinicaland pathological manifestations in 9 families with 50 affected members. Arch.Intern. Med. 136: 769- 777, 1976. 3 C b

GAM7957 297 VHL Hosoe, S.; Brauch, H.; Latif, F.; Glenn, G.; Daniel, L.; Bale,S.; Choyke, P.; Gorin, M.; Oldfield, E.; Berman, A.; Goodman, J.;Orcutt, M. L.; Hampsch, K.; Delisio, J.; Modi, W.; McBride, W.; Anglard,P.; Weiss, G.; Walther, M. M.; Linehan, W. M.; Lerman, M. I.; Zbar,B.: Localization of the von Hippel- Lindau disease gene to a smallregion of chromosome 3. Genomics 8: 634- 640, 1990. 3 C b

GAM7957 297 VHL Hull, M. T.; Roth, L. M.; Glover, J. L.; Walker, P. D.: Metastaticcarotid body paraganglioma in von Hippel- Lindau disease: an electronmicroscopic study. Arch. Path. Lab. Med. 106: 235- 239, 1982. 3 C b

GAM7957 297 VHL Huson, S. M.; Harper, P. S.; Hourihan, M. D.; Cole, G.; Weeks,R. D.; 3 C b
Compston, D. A. S.: Cerebellar haemangioblastoma and von Hippel-
Lindaudisease. Brain 109: 1297- 1310, 1986.

GAM7957 297 VHL Iliopoulos, O.; Kibel, A.; Gray, S.; Kaelin, W. G., Jr.: Tumoursuppression 3 C b
by the human von Hippel- Lindau gene product. Nature Med. 1:822- 826, 1995.

GAM7957 297 VHL Iliopoulos, O.; Levy, A. P.; Jiang, C.; Kaelin, W. G., Jr.; Goldberg,M. A.: 3 C b
Negative regulation of hypoxia- inducible genes by the vonHippel- Lindau
protein. Proc. Nat. Acad. Sci. 93: 10595- 10599, 1996.

GAM7957 297 VHL Iliopoulos, O.; Ohh, M.; Kaelin, W. G., Jr.: pVHL(19) is a 3 C b
biologicallyactive product of the von Hippel- Lindau gene arising from
internaltranslation initiation. Proc. Nat. Acad. Sci. 95: 11661- 11666,
1998.

GAM7957 297 VHL Ivan, M.; Kondo, K.; Yang, H.; Kim, W.; Valiando, J.; Ohh, M.;Salic, A.; 3 C b
Asara, J. M.; Lane, W. S.; Kaelin, W. G., Jr.: HIF- alphatargeted for VHL-
mediated destruction by proline hydroxylation: implicationsfor O(2) sensing.
Science 292: 464- 468, 2001.

GAM7957 297 VHL Ivanov, S. V.; Kuzmin, I.; Wei, M.- H.; Pack, S.; Geil, L.; Johnson,B. E.; 3 C b
Stanbridge, E. J.; Lerman, M. I.: Down- regulation of transmembranecarbonic
anhydrases in renal cell carcinoma cell lines by wild- typevon Hippel-
Lindau transgenes. Proc. Nat. Acad. Sci. 95: 12596- 12601,1998.

GAM7957 297 VHL Jaakkola, P.; Mole, D. R.; Tian, Y.- M.; Wilson, M. I.; Gielbert,J.; 3 C b
Gaskell, S. J.; von Kriegsheim, A.; Hebestreit, H. F.; Mukherji,M.;
Schofield, C. J.; Maxwell, P. H.; Pugh, C. W.; Ratcliffe, P. J.: Targeting
of HIF- alpha to the von Hippel- Lindau ubiquitylation complexby O(2)-
regulated prolyl hydroxylation. Science 292: 468- 472, 2001.

GAM7957 297 VHL James, G. P.: Personal Communication. Springfield, Ohio 8/15/1998. 3 C b

GAM7957 297 VHL Jennings, A. M.; Smith, C.; Cole, D. R.; Jennings, C.; Shortland,J. R.; 3 C b
Williams, J. L.; Brown, C. B.: Von Hippel- Lindau disease ina large British
family: clinicopathological features and recommendationsfor screening and
follow- up. Quart. J. Med. 66: 233- 249, 1988.

GAM7957 297 VHL Kanno, H.; Kondo, K.; Ito, S.; Yamamoto, I.; Fujii, S.; Torigoe,S.; Sakai, 3 C b
N.; Hosaka, M.; Shuin, T.; Yao, M.: Somatic mutationsof the von Hippel-
Lindau tumor suppressor gene in sporadic centralnervous system
hemangioblastomas. Cancer Res. 54: 4845- 4847, 1994.

GAM7957 297 VHL Kanno, H.; Saljooque, F.; Yamamoto, I.; Hattori, S.; Yao, M.;Shuin, T.; U, 3 C b
H.- S.: Role of the von Hippel- Lindau tumor suppressorprotein during
neuronal differentiation. Cancer Res. 60: 2820- 2824,2000.

GAM7957 297 VHL Kaplan, C.; Sayre, G. P.; Greene, L. F.: Bilateral nephrogeniccarcinomas in 3 C b
Lindau- von Hippel disease. J. Urol. 86: 36- 42, 1961.

GAM7957 297 VHL Karsdorp, N.; Elderson, A.; Wittebol- Post, D.; Hene, R. J.; Vos,J.; 3 C b
Feldberg, M. A. M.; van Gils, A. P. G.; Jansen- Schillhorn vanVeen, J. M.;
Vroom, T. M.; Hoppener, J. W. M.; Lips, C. J. M.: VonHippel- Lindau disease:
new strategies in early detection and treatment. Am.J. Med. 97: 158- 168,
1994.

GAM7957 297 VHL Keeler, L. L., III; Klauber, G. T.: von Hippel- Lindau diseaseand renal cell 3 C b
carcinoma in a 16- year- old boy. J. Urol. 147: 1588- 1591,1992.

GAM7957 297 VHL Kenck, C.; Wilhelm, M.; Bugert, P.; Staehler, G.; Kovacs, G.:Mutation of the 3 C b
VHL gene is associated exclusively with the developmentof non- papillary
renal cell carcinomas. J. Path. 179: 157- 161, 1996.

GAM7957 297 VHL Kerr, D. J.; Scheithauer, B. W.; Miller, G. M.; Ebersold, M. J.;McPhee, T. 3 C b

J.: Hemangioblastoma of the optic nerve: case report. Neurosurgery 36:573-581, 1995.

GAM7957 297 VHL Kibel, A.; Iliopoulos, O.; DeCaprio, J. A.; Kaelin, W. G., Jr.: Binding of the von Hippel- Lindau tumor suppressor protein to elonginB and C. Science 269: 1444- 1446, 1995. 3 C b

GAM7957 297 VHL Kiechle- Schwarz, M.; Neumann, H. P. H.; Decker, H.- J. H.; Dietrich,C.; Wullich, B.; Schempp, W.: Cytogenetic studies on three pheochromocytomasderived from patients with von Hippel- Lindau syndrome. Hum. Genet. 82:127- 130, 1989. 3 C b

GAM7957 297 VHL King, C. R.; Schimke, R. N.; Arthur, T.; Davoren, B.; Collins,D.: Proximal 3p deletion in renal cell carcinoma cells from a patientwith von Hippel-Lindau disease. Cancer Genet. Cytogenet. 27: 345- 348,1987. 3 C b

GAM7957 297 VHL Korn, W. T.; Schatzki, S. C.; DiSciullo, A. J.; Scully, R. E.: Papillary cystadenoma of the broad ligament in von Hippel- Lindaudisease. Am. J. Obstet. Gynec. 163: 596- 598, 1990. 3 C b

GAM7957 297 VHL Kovacs, G.; Kung, H.: Nonhomologous chromatid exchange in hereditaryand sporadic renal cell carcinomas. Proc. Nat. Acad. Sci. 88: 194- 198,1991. 3 C b

GAM7957 297 VHL Kranes, A.; Balogh, K., Jr.: Liver disease in a patient withvon Hippel-Lindau disease. New Eng. J. Med. 275: 950- 959, 1966. 3 C b

GAM7957 297 VHL Lamiell, J. M.: Personal Communication. San Francisco, Calif. 9/1987. 3 C b

GAM7957 297 VHL Lamiell, J. M.; Salazar, F. G.; Hsia, Y. E.: Von Hippel- Lindaudisease affecting 43 members of a single kindred. Medicine 68: 1- 29,1989. 3 C b

GAM7957 297 VHL Latif, F.; Tory, K.; Gnarra, J.; Yao, M.; Duh, F.- M.; Orcutt,M. L.; Stackhouse, T.; Kuzmin, I.; Modi, W.; Geil, L.; Schmidt, L.;Zhou, F.; Li, H.; Wei, M. H.; Chen, F.; Glenn, G.; Choyke, P.; Walther,M. M.; Weng, Y.; Duan, D.- S. R.; Dean, M.; Glavac, D.; Richards, F.M.; Crossey, P. A.; Ferguson- Smith, M. A.; Le Paslier, D.; Chumakov,I.; Cohen, D.; Chinault, A. C.; Maher, E. R.; Linehan, W. M.; Zbar,B.; Lerman, M. I.: Identification of the von Hippel- Lindau diseasetumor suppressor gene. Science 260: 1317-1320, 1993. 3 C b

GAM7957 297 VHL Lee, S.; Chen, D. Y. T.; Humphrey, J. S.; Gnarra, J. R.; Linehan,W. M.; Klausner, R. D.: Nuclear/cytoplasmic localization of the vonHippel- Lindau tumor suppressor gene product is determined by celldensity. Proc. Nat. Acad. Sci. 93: 1770- 1775, 1996. 3 C b

GAM7957 297 VHL Lenz, T.; Thiede, H. M.; Nussberger, J.; Atlas, S. A.; Distler,A.; Schulte, K. L.: Hyperreninemia and secondary hyperaldosteronismin a patient with pheochromocytoma and von Hippel- Lindau disease. Nephron 62:345- 350, 1992. 3 C b

GAM7957 297 VHL Lindau, A.: Zur Frage der Angiomatosis Retinae und Ihrer Hirncomplikation. ActaOphthal. 4: 193- 226, 1927. 3 C b

GAM7957 297 VHL Loeb, D. B.; Pericak- Vance, M. A.; Stajich, J. M.; Vance, J. M.: A novel mutation in the von Hippel- Lindau gene. Hum. Molec. Genet. 3:1423- 1424, 1994. 3 C b

GAM7957 297 VHL Lui, W. O.; Chen, J.; Glasker, S.; Bender, B. U.; Madura, C.;Khoo, S. K.; Kort, E.; Larsson, C.; Neumann, H. P. H.; Teh, B. T.: Selective loss of chromosome 11 in pheochromocytomas associatedwith the VHL syndrome. Oncogene 21: 1117- 1122, 2002. 3 C b

GAM7957 297 VHL Maddock, I. R.; Moran, A.; Maher, E. R.; Teare, M. D.; Norman,A.; Payne, S. J.; Whitehouse, R.; Dodd, C.; Lavin, M.; Hartley, N.;Super, M.; Evans, D. G. R.: A genetic register for von Hippel- Lindaudisease. J. Med. Genet. 33: 120- 127, 1996. 3 C b

GAM7957 297 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Barton, D.; Jennings,A.; Fellows, I. W.; Ponder, M. A.; Ponder, B. A. J.; Benjamin, C.;Harris, R.; Ferguson- Smith, M. A.: Mapping of von Hippel- Lindau diseaseto chromosome 3p confirmed by genetic linkage analysis. J. Neurol.Sci. 100: 27- 30, 1990. 3 C b

GAM7957 297 VHL Maher, E. R.; Bentley, E.; Yates, J. R. W.; Latif, F.; Lerman,M.; Zbar, B.; Affara, N. A.; Ferguson- Smith, M. A.: Mapping of thevon Hippel- Lindau disease locus to a small region of chromosome 3pby genetic linkage analysis. Genomics 10: 957- 960, 1991. 3 C b

GAM7957 297 VHL Maher, E. R.; Iselius, L.; Yates, J. R. W.; Littler, M.; Benjamin,C.; Harris, R.; Sampson, J.; Williams, A.; Ferguson- Smith, M. A.;Morton, N.: Von Hippel- Lindau disease: a genetic study. J. Med.Genet. 28: 443- 447, 1991. 3 C b

GAM7957 297 VHL Maher, E. R.; Yates, J. R. W.; Ferguson- Smith, M. A.: Statisticalanalysis of the two stage mutation model in von Hippel- Lindau disease,and in sporadic cerebellar haemangioblastoma and renal cell carcinoma. J.Med. Genet. 27: 311- 314, 1990. 3 C b

GAM7957 297 WBSCR1 Osborne, L. R.; Martindale, D.; Scherer, S. W.; Shi, X.- M.; Huizenga,J.; Heng, H. H. Q.; Costa, T.; Pober, B.; Lew, L.; Brinkman, J.; Rommens,J.; Koop, B.; Tsui, L.- C.: Identification of genes from a 500- kbregion at 7q11.23 that is commonly deleted in Williams syndrome patients. Genomics 36:328- 336, 1996. 3 C c

GAM7957 297 WBSCR1 Richter- Cook, N. J.; Dever, T. E.; Hensold, J. O.; Merrick, W.C.: Purification and characterization of a new eukaryotic proteintranslation factor: eukaryotic initiation factor 4H. J. Biol. Chem. 273:7579- 7587, 1998. 3 C c

GAM7957 297 WIG1 Hellborg, F.; Qian, W.; Mendez- Vidal, C.; Asker, C.; Kost- Alimova,M.; Wilhelm, M.; Imreh, S.; Wiman, K. G.: Human wig- 1, a p53 targetgene that encodes a growth inhibitory zinc finger protein. Oncogene 20:5466- 5474, 2001. 3 C b

GAM7957 297 WIG1 Varmeh- Ziaie, S.; Okan, I.; Wang, Y.; Magnusson, K. P.; Warthoe,P.; Strauss, M.; Wiman, K. G.: Wig- 1, a new p53- induced gene encodinga zinc finger protein. Oncogene 15: 2699- 2704, 1997. 3 C b

GAM7957 297 WNT8B Lako, M.; Lindsay, S.; Bullen, P.; Wilson, D. I.; Robson, S. C.;Strachan, T.: A novel mammalian Wnt gene, WNT8B, shows brain- restrictedexpression in early development, with sharply delimited expressionboundaries in the developing forebrain. Hum. Molec. Genet. 7: 813- 822,1998. 3 C c

GAM7957 297 WNT8B Lako, M.; Strachan, T.; Curtis, A. R. J.; Lindsay, S.: Isolationand characterization of WNT8B, a novel human Wnt gene that maps to10q24. Genomics 35: 386- 388, 1996. 3 C c

GAM7957 297 XRCC2 Braybrooke, J. P.; Spink, K. G.; Thacker, J.; Hickson, I. D.:The RAD51 family member, RAD51L3, is a DNA- stimulated ATPase thatforms a complex with XRCC2. J. Biol. Chem. 275: 29100- 29106, 2000. 3 C c

GAM7957 297 XRCC2 Johnson, R. D.; Liu, N.; Jasin, M.: Mammalian XRCC2 promotes therepair of DNA double- strand breaks by homologous recombination. Nature 401:397- 399, 1999. 3 C c

GAM7957 297 XRCC2 Jones, N. J.; Cox, R.; Thacker, J.: Isolation and cross- sensitivityof x- ray- sensitive mutants of V79- 4 hamster cells. Mutat. Res. 183:279- 286, 1987. 3 C c

GAM7957 297 XRCC2 Jones, N. J.; Zhao, Y.; Siciliano, M. J.; Thompson, L. H.: Assignmentof the XRCC2 human DNA repair gene to chromosome 7q36 by complementationanalysis. 3 C c

Genomics 26: 619- 622, 1995.

GAM7957 297 XRCC2 Kurumizaka, H.; Ikawa, S.; Nakada, M.; Enomoto, R.; Kagawa, W.;Kinebuchi, T.; Yamazoe, M.; Yokoyama, S.; Shibata, T.: Homologouspairing and ring and filament structure formation activities of thehuman Xrcc2- Rad51D complex. J. Biol. Chem. 277: 14315- 14320, 2002. 3 C c

GAM7957 297 XRCC2 Liu, N.; Schild, D.; Thelen, M. P.; Thompson, L. H.: Involvementof Rad51C in two distinct protein complexes of Rad51 paralogs in humancells. Nucleic Acids Res. 30: 1009- 1015, 2002. 3 C c

GAM7957 297 XRCC2 Masson, J.- Y.; Tarsounas, M. C.; Stasiak, A. Z.; Stasiak, A.; Shah,R.; McIlwraith, M. J.; Benson, F. E.; West, S. C.: Identificationand purification of two distinct complexes containing the five RAD51paralogs. Genes Dev. 15: 3296- 3307, 2001. 3 C c

GAM7957 297 XRCC2 Tambini, C. E.; George, A. M.; Rommens, J. M.; Tsui, L.- C.; Scherer,S. W.; Thacker, J.: The XRCC2 DNA repair gene: identification ofa positional candidate. Genomics 41: 84- 92, 1997. 3 C c

GAM7957 297 XRCC2 Thacker, J.; Tambini, C. E.; Simpson, P. J.; Tsui, L.- C.; Scherer,S. W.: Localization to chromosome 7q36.1 of the human XRCC2 gene,determining sensitivity to DNA- damaging agents. Hum. Molec. Genet. 4:113- 120, 1995. 3 C c

GAM7957 297 ZNF36 Rousseau- Merck, M.- F.; Duro, D.; Berger, R.; Thiesen, H. J.: Chromosomallocalization of two KOX zinc finger genes on chromosome bands 7q21- q22. Ann.Genet. 38: 81- 84, 1995. 3 C b

GAM7957 297 ZNF36 Tommerup, N.; Aagaard, L.; Lund, C. L.; Boel, E.; Baxendale, S.;Bates, G. P.; Lehrach, H.; Vissing, H.: A zinc- finger gene ZNF141mapping at 4p16.3/D4S90 is a candidate gene for the Wolf- Hirschhorn(4p-) syndrome. Hum. Molec. Genet. 2: 1571- 1575, 1993. 3 C b

GAM7957 297 ZNF36 Tommerup, N.; Vissing, H.: Isolation and fine mapping of 16 novelhuman zinc finger- encoding cDNAs identify putative candidate genesfor developmental and malignant disorders. Genomics 27: 259- 264,1995. 3 C b

GAM8145 328 ADRA2A Comings, D. E.; Gade- Andavolu, R.; Gonzalez, N.; Blake, H.; Wu,S.; MacMurray, J. P.: Additive effect of three noradrenergic genes(ADRA2A, ADRA2C, DBH) on attention- deficit hyperactivity disorderand learning disabilities in Tourette syndrome subjects. Clin. Genet. 55:160- 172, 1999. 3 C c

GAM8145 328 ADRA2A Halperin, J. M.; Newcorn, J. H.; Koda, V. H.; Pick, L.; McKay,K. E.; Knott, P.: Noradrenergic mechanisms in ADHD children withand without reading disabilities: a replication and extension. J.Am. Acad. Child Adolesc. Psychiat. 36: 1688- 1697, 1997. 3 C c

GAM8145 328 ADRA2A Hein, L.; Altman, J. D.; Kobilka, B. K.: Two functionally distinctalpha- 2- adrenergic receptors regulate sympathetic neurotransmission. Nature 402:181- 184, 1999. 3 C c

GAM8145 328 ADRA2A Hoehe, M. R.; Berrettini, W. H.; Lentes, K.- U.: Dra I identifiesa two allele DNA polymorphism in the human alpha- 2- adrenergic receptorgene (ADRAR), using a 5.5 kb probe (p ADRAR). Nucleic Acids Res. 16:9070 only, 1988. 3 C c

GAM8145 328 ADRA2A Hoehe, M.; Berrettini, W.; Leppert, M.; Lalouel, J.- M.; Byerley,W.; Gershon, E.; White, R.: Genetic mapping of adrenergic receptorgenes. (Abstract) Am. J. Hum. Genet. 45 (suppl.): A143 only, 1989. 3 C c

GAM8145 328 ADRA2A Kobilka, B. K.; Matsui, H.; Kobilka, T. S.; Yang- Feng, T. L.; Francke,U.; Caron, M. G.; Lefkowitz, R. J.; Regan, J. W.: Cloning, sequencing,and expression of the gene coding for the human platelet alpha- 2- adrenergicreceptor. Science 238: 650- 656, 1987. 3 C c

GAM8145 328 ADRA2A Oakey, R. J.; Caron, M. G.; Lefkowitz, R. J.; Seldin, M. F.: 3 C c
Genomicorganization of adrenergic and serotonin receptors in the mouse:
linkagemapping of sequence- related genes provides a method for
examiningmammalian chromosome evolution. Genomics 10: 338- 344, 1991.

GAM8145 328 ADRA2A Philipp, M.; Brede, M. E.; Hadamek, K.; Gessler, M.; Lohse, M.J.; Hein, L.: 3 C c
Placental alpha- 2- adrenoceptors control vascular developmentat the
interface between mother and embryo. Nature Genet. 31: 311- 315,2002.

GAM8145 328 ADRA2A Surprenant, A.; Horstman, D. A.; Akbarali, H.; Limbird, L. E.:A point 3 C c
mutation of the alpha- 2- adrenoceptor that blocks couplingto potassium but
not calcium currents. Science 257: 977- 980, 1992.

GAM8145 328 ADRA2A Yang- Feng, T. L.; Kobilka, B. K.; Caron, M. G.; Lefkowitz, R.J.; Francke, 3 C c
U.: Chromosomal assignment of genes for an alpha- adrenergicreceptor (ADRAR)
and for another member of this receptor family coupledto guanine nucleotide
regulatory proteins (RG21). (Abstract) Cytogenet.Cell Genet. 46: 722- 723,
1987.

GAM8145 328 ADRB1 Bachman, E. S.; Dhillon, H.; Zhang, C.- Y.; Cinti, S.; Bianco, A.C.; 3 C c
Kobilka, B. K.; Lowell, B. B.: Beta- AR signaling required fordiet- induced
thermogenesis and obesity resistance. Science 297:843- 845, 2002.

GAM8145 328 ADRB1 Frielle, T.; Collins, S.; Daniel, K. W.; Caron, M. G.; Lefkowitz,R. J.; 3 C c
Kobilka, B. K.: Cloning of the cDNA for the human beta- 1-
adrenergicreceptor. Proc. Nat. Acad. Sci. 84: 7920- 7924, 1987.

GAM8145 328 ADRB1 Frielle, T.; Kobilka, B.; Lefkowitz, R. J.; Caron, M. G.: Humanbeta- 1- and 3 C c
beta- 2- adrenergic receptors: structurally and functionallyrelated
receptors derived from distinct genes. Trends Neurosci. 11:321- 324, 1988.

GAM8145 328 ADRB1 Hoehe, M.; Berrettini, W.; Leppert, M.; Lalouel, J.- M.; Byerley,W.; 3 C c
Gershon, E.; White, R.: Genetic mapping of adrenergic receptorgenes.
(Abstract) Am. J. Hum. Genet. 45 (suppl.): A143 only, 1989.

GAM8145 328 ADRB1 Kannel, W. B.; Kannel, C.; Paffenbarger, R. S., Jr.; Cupples, L.A.: Heart 3 C c
rate and cardiovascular mortality: the Framingham Study. Am.Heart J. 113:
1489- 1494, 1987.

GAM8145 328 ADRB1 Kristal- Boneh, E.; Silber, H.; Harari, G.; Froom, P.: The associationof 3 C c
resting heart rate with cardiovascular, cancer and all- cause
mortality:eight year follow- up of 3527 male Israeli employees (the CORDIS
study). Europ.Heart J. 21: 116- 124, 2000.

GAM8145 328 ADRB1 Magnusson, Y.; Marullo, S.; Hoyer, S.; Waagstein, F.; Andersson,B.; Vahlne, 3 C c
A.; Guillet, J.- G.; Strosberg, A. D.; Hjalmarson, A.;Hoebeke, J.: Mapping
of a functional autoimmune epitope on the beta(1)- adrenergicreceptor in
patients with idiopathic dilated cardiomyopathy. J. Clin.Invest. 86: 1658-
1663, 1990.

GAM8145 328 ADRB1 Mason, D. A.; Moore, J. D.; Green, S. A.; Liggett, S. B.: A gain- of- 3 C c
functionpolymorphism in a G- protein coupling domain of the human beta- 1-
adrenergicreceptor. J. Biol. Chem. 274: 12670- 12674, 1999.

GAM8145 328 ADRB1 Oakey, R. J.; Caron, M. G.; Lefkowitz, R. J.; Seldin, M. F.: 3 C c
Genomicorganization of adrenergic and serotonin receptors in the mouse:
linkagemapping of sequence- related genes provides a method for
examiningmammalian chromosome evolution. Genomics 10: 338- 344, 1991.

GAM8145 328 ADRB1 Ranade, K.; Jorgenson, E.; Sheu, W. H.- H.; Pei, D.; Hsiung, C.A.; Chiang, 3 C c
F.; Chen, Y. I.; Pratt, R.; Olshen, R. A.; Curb, D.; Cox,D. R.; Botstein,
D.; Risch, N.: A polymorphism in the beta- 1 adrenergicreceptor is
associated with resting heart rate. Am. J. Hum. Genet. 70:935- 942, 2002.

GAM8145 328 ADRB1 Small, K. M.; Wagoner, L. E.; Levin, A. M.; Kardia, S. L. R.;Liggett, S. B.: 3 C c
Synergistic polymorphisms of beta- 1- and alpha- 2C- adrenergicreceptors
and the risk of congestive heart failure. New Eng. J. Med. 347:1135- 1142,
2002.

GAM8145 328 ADRB1 Wilk, J. B.; Myers, R. H.; Zhang, Y.; Lewis, C. E.; Atwood, L.;Hopkins, P. 3 C c
N.; Ellison, R. C.: Evidence for a gene influencing heartrate on chromosome
4 among hypertensives. Hum. Genet. 111: 207- 213,2002.

GAM8145 328 ADRB1 Yang- Feng, T. L.; Xue, F.; Zhong, W.; Cotecchia, S.; Frielle,T.; Caron, M. 3 C c
G.; Lefkowitz, R. J.; Francke, U.: Chromosomal organizationof adrenergic
receptor genes. Proc. Nat. Acad. Sci. 87: 1516- 1520,1990.

GAM8145 328 CACNG3 Black, J. L., III; Lennon, V. A.: Identification and cloning ofputative 3 C c
human neuronal voltage- gated calcium channel gamma- 2 andgamma- 3 subunits:
neurologic implications. Mayo Clin. Proc. 74:357- 361, 1999.

GAM8145 328 CACNG3 Burgess, D. L.; Davis, C. F.; Gefrides, L. A.; Noebels, J. L.:Identification 3 C c
of three novel Ca(2+) channel gamma subunit genes revealsmolecular
diversification by tandem and chromosome duplication. GenomeRes. 9: 1204-
1213, 1999.

GAM8145 328 CACNG3 Burgess, D. L.; Gefrides, L. A.; Foreman, P. J.; Noebels, J. L.: A cluster 3 C c
of three novel Ca(2+) channel gamma subunit genes on chromosome19q13.4:
evolution and expression profile of the gamma subunit genefamily. Genomics
71: 339- 350, 2001.

GAM8145 328 CAPN1 Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.;Forbes, S. A.; 3 C c
Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B.T.; Farnebo, F.;
Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud,S.; Zhang, C. X.; Salandre,
J.; Calender, A.: Definition of the minimalMEN1 candidate area based on a 5-
Mb integrated map of proximal 11q13. Genomics 37:354- 365, 1996.

GAM8145 328 CAPN1 Ohno, S.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Ohmi- Imajoh,S.; Suzuki, 3 C c
K.; Shimizu, Y.; Shimizu, N.: Four genes for the calpainfamily locate on
four distinct human chromosomes. (Abstract) Cytogenet.Cell Genet. 51: 1054-
1055, 1989.

GAM8145 328 CAPN1 Ohno, S.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Shimizu, Y.;Ohmi- Imajoh, 3 C c
S.; Shimizu, N.; Suzuki, K.: Four genes for the calpainfamily locate on four
distinct human chromosomes. Cytogenet. CellGenet. 53: 225- 229, 1990.

GAM8145 328 CASP2 Bergeron, L.; Perez, G. I.; Macdonald, G.; Shi, L.; Sun, Y.; Jurisicova,A.; 3 C c
Varmuza, S.; Latham, K. E.; Flaws, J. A.; Salter, J. C. M.; Hara,H.;
Moskowitz, M. A.; Li, E.; Greenberg, A.; Tilly, J. L.; Yuan, J.: Defects in
regulation of apoptosis in caspase- 2- deficient mice. GenesDev. 12: 1304-
1314, 1998.

GAM8145 328 CASP2 Kumar, S.; Kinoshita, M.; Noda, M.; Copeland, N. G.; Jenkins, N.A.: 3 C c
Induction of apoptosis by the mouse Nedd2 gene, which encodesa protein
similar to the product of the Caenorhabditis elegans celldeath gene ced- 3
and the mammalian IL- 1- beta- converting enzyme. GenesDev. 8: 1613- 1626,
1994.

GAM8145 328 CASP2 Kumar, S.; Tomooka, Y.; Noda, M.: Identification of a set of geneswith 3 C c
developmentally down- regulated expression in the mouse brain.
Biochem.Biophys. Res. Commun. 185: 1155- 1161, 1992.

GAM8145 328 CASP2 Kumar, S.; White, D. L.; Takai, S.; Turczynowicz, S.; Juttner,C. A.; Hughes, 3 C c
T. P.: Apoptosis regulatory gene NEDD2 maps to humanchromosome segment 7q34-
35, a region frequently affected in haematologicalneoplasms. Hum. Genet. 95:
641- 644, 1995.

GAM8145 328 CASP2 Lassus, P.; Opitz- Araya, X.; Lazebnik, Y.: Requirement for caspase- 2in 3 C c
stress- induced apoptosis before mitochondrial permeabilization. Science
297:1352- 1354, 2002.

GAM8145 328 CASP2 Tiso, N.; Pallavicini, A.; Muraro, T.; Zimbello, R.; Apolloni,E.; Valle, G.; 3 C c
Lanfranchi, G.; Danieli, G. A.: Chromosomal localizationof the human genes,
CPP32, Mch2, Mch3, and Ich- 1, involved in cellularapoptosis. Biochem.
Biophys. Res. Commun. 225: 983- 989, 1996.

GAM8145 328 CHEK1 Chen, P.; Luo, C.; Deng, Y.; Ryan, K.; Register, J.; Margosiak,S.; Tempczyk- 3 C c
Russell, A.; Nguyen, B.; Myers, P.; Lundgren, K.; Kan,C.- C.; O'Connor, P.
M.: The 1.7- angstrom crystal structure of humancell cycle checkpoint kinase
Chk1: implications for Chk1 regulation. Cell 100:681- 692, 2000.

GAM8145 328 CHEK1 Flaggs, G.; Plug, A. W.; Dunks, K. M.; Mundt, K. E.; Ford, J. C.;Quiggle, M. 3 C c
R. E.; Taylor, E. M.; Westphal, C. H.; Ashley, T.; Hoekstra,M. F.; Carr, A.
M.: Atm- dependent interactions of a mammalian Chk1homolog with meiotic
chromosomes. Curr. Biol. 7: 977- 986, 1997.

GAM8145 328 CHEK1 Liu, Q.; Guntuku, S.; Cui, X.- S.; Matsuoka, S.; Cortez, D.; Tamai,K.; Luo, 3 C c
G.; Carattini- Rivera, S.; DeMayo, F.; Bradley, A.; Donehower,L. A.;
Elledge, S. J.: Chk1 is an essential kinase that is regulatedby Atr and
required for the G2/M DNA damage checkpoint. Genes Dev. 14:1448- 1459, 2000.

GAM8145 328 CHEK1 Sanchez, Y.; Wong, C.; Thoma, R. S.; Richman, R.; Wu, Z.; Piwnica- Worms,H.; 3 C c
Elledge, S. J.: Conservation of the Chk1 checkpoint pathway inmammals:
linkage of DNA damage to Cdk regulation through Cdc25. Science 277:1497-
1501, 1997.

GAM8145 328 CHEK1 Takai, H.; Tominaga, K.; Motoyama, N.; Minamishima, Y. A.; Nagahama,H.; 3 C c
Tsukiyama, T.; Ikeda, K.; Nakayama, K.; Nakanishi, M.; Nakayama,K.: Aberrant
cell cycle checkpoint function and early embryonic deathin Chk1- /- mice.
Genes Dev. 14: 1439- 1447, 2000.

GAM8145 328 COX8 Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.;Forbes, S. A.; 3 C c
Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B.T.; Farnebo, F.;
Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud,S.; Zhang, C. X.; Salandre,
J.; Calender, A.: Definition of the minimalMEN1 candidate area based on a 5-
Mb integrated map of proximal 11q13. Genomics 37:354- 365, 1996.

GAM8145 328 COX8 Richard, C. W.; Withers, D. A.; Meeker, T. C.; Myers, R. M.: Aradiation 3 C c
hybrid map of the proximal long arm of human chromosome11 containing the
MEN- 1 and bcl- 1 disease locus. (Abstract) Cytogenet.Cell Genet. 58: 1970
only, 1991.

GAM8145 328 COX8 Rizzuto, R.; Nakase, H.; Darras, B.; Francke, U.; Fabrizi, G. M.;Mengel, T.; 3 C c
Walsh, F.; Kadenbach, B.; DiMauro, S.; Schon, E. A.:A gene specifying
subunit VIII of human cytochrome c oxidase is localizedto chromosome 11 and
is expressed in both muscle and non- muscle tissues. J.Biol. Chem. 264:
10595- 10600, 1989.

GAM8145 328 GCNT2 Bierhuizen, M. F. A.; Mattei, M.- G.; Fukuda, M.: Expression ofthe 3 C c
developmental I antigen by a cloned human cDNA encoding a memberof a beta-
1,6- N- acetylglucosaminyltransferase gene family. GenesDev. 7: 468- 478,
1993.

GAM8145 328 GCNT2 Lin- Chu, M.; Broadberry, R. E.; Okubo, Y.; Tanaka, M.: The i phenotypeand 3 C c
congenital cataracts among Chinese in Taiwan (Letter) Transfusion 31:676-
677, 1991.

GAM8145 328 GCNT2 Ogata, H.; Okubo, Y.; Akabane, T.: Phenotype i associated withcongenital 3 C c
cataract in Japanese. Transfusion 19: 166- 168, 1979.

GAM8145 328 GCNT2 Olavesen, M. G.; Bentley, E.; Mason, R. V. F.; Stephens, R. J.;Ragoussis, J.: Fine mapping of 39 ESTs on human chromosome 6p23- p25. Genomics 46:303-306, 1997. 3 C c

GAM8145 328 GCNT2 Schwientek, T.; Nomoto, M.; Levery, S. B.; et al: Control of O- glycanbranch formation. J. Biol. Chem. 274: 4504- 4512, 1999. 3 C c

GAM8145 328 GCNT2 Yeh, J.- C.; Ong, E.; Fukuda, M.: Molecular cloning and expressionof a novel beta- 1,6- N- acetylglucosaminyltransferase that forms core2, core 4, and I branches. J. Biol. Chem. 274: 3215- 3221, 1999. 3 C c

GAM8145 328 GCNT2 Yu, L.- C.; Twu, Y.- C.; Chang, C.- Y.; Lin, M.: Molecular basisof the adult i phenotype and the gene responsible for the expressionof the human blood group I antigen. Blood 98: 3840- 3845, 2001. 3 C c

GAM8145 328 GPLD1 LeBoeuf, R. C.; Caldwell, M.; Guo, Y.; Metz, C.; Davitz, M. A.;Olson, L. K.; Deeg, M. A.: Mouse glycosylphosphatidylinositol- specificphospholipase D (Gpld1) characterization. Mammalian Genome 9: 710- 714,1998. 3 C c

GAM8145 328 GPLD1 Scallon, B. J.; Fung, W.- J. C.; Tsang, T. C.; Li, S.; Kado- Fong,H.; Huang, K.- S.; Kochan, J. P.: Primary structure and functionalactivity of a phosphatidylinositol- glycan- specific phospholipase D. Science 252:446-448, 1991. 3 C c

GAM8145 328 GPLD1 Schofield, J. N.; Rademacher, T. W.: Structure and expressionof the human glycosylphosphatidylinositol phospholipase D1 (GPLD1)gene. Biochim. Biophys. Acta 1494: 189- 194, 2000. 3 C c

GAM8145 328 GPLD1 Tsang, T. C.; Fung, W.- J.; Levine, J.; Metz, C. N.; Davitz, M.A.; Burns, D. K.; Huang, K.- S.; Kochan, J. P.: Isolation and expressionof two human glycosylphosphatidylinositol phospholipase D (GPI- PLD)cDNAs. (Abstract) FASEB J. (supp.) 6: A1922 only, 1992. 3 C c

GAM8145 328 GPR30 Carmeci, C.; Thompson, D. A.; Ring, H. Z.; Francke, U.; Weigel,R. J.: Identification of a gene (GPR30) with homology to the G- protein-coupledreceptor superfamily associated with estrogen receptor expressionin breast cancer. Genomics 45: 607- 617, 1997. 3 C c

GAM8145 328 GPR30 Feng, Y.; Gregor, P.: Cloning of a novel member of the G protein-coupledreceptor family related to peptide receptors. Biochem. Biophys. Res.Commun. 231: 651- 654, 1997. 3 C c

GAM8145 328 GPR30 Kvingedal, A. M.; Smeland, E. B.: A novel putative G- protein-coupledreceptor expressed in lung, heart and lymphoid tissue. FEBS Lett. 407:59- 62, 1997. 3 C c

GAM8145 328 GPR30 Owman, C.; Blay, P.; Nilsson, C.; Lolait, S. J.: Cloning of humancDNA encoding a novel heptahelix receptor expressed in Burkitt's lymphomaand widely distributed in brain and peripheral tissues. Biochem.Biophys. Res. Commun. 228: 285- 292, 1996. 3 C c

GAM8145 328 GPR30 Takada, Y.; Kato, C.; Kondo, S.; Korenaga, R.; Ando, J.: Cloningof cDNAs encoding G protein- coupled receptor expressed in human endothelialcells exposed to fluid shear stress. Biochem. Biophys. Res. Commun. 240;- 737-741,1997. 3 C c

GAM8145 328 GTF2F1 Aso, T.; Tsai, P.; Kawaguchi, T.; Menninger, J. C.; Kitajima, S.;Yasukochi, Y.; Ward, D. C.; Weissman, S. M.: Assignment of the humanGTF2F1 gene to chromosome 19p13.3. Genomics 16: 252- 253, 1993. 3 C c

GAM8145 328 GTF2F1 Aso, T.; Vasavada, H. A.; Kawaguchi, T.; Germino, F. J.; Ganguly,S.; Kitajima, S.; Weissman, S. M.; Yasukochi, Y.: Characterizationof cDNA for the large subunit of the transcription initiation factorTFIIF. Nature 355: 461- 464, 1992. 3 C c

GAM8145 328 GTF2F1 Finkelstein, A.; Kostrub, C. F.; Li, J.; Chavez, D. P.; Wang, B.Q.; Fang, S. 3 C c
M.; Greenblatt, J.; Burton, Z. F.: A cDNA encoding RAP74,a general
initiation factor for transcription by RNA polymerase II. Nature 355:464-
467, 1992.

GAM8145 328 GTF2F1 Joliot, V.; Demma, M.; Prywes, R.: Interaction with RAP74 subunitof TFIIF is 3 C c
required for transcriptional activation by serum responsefactor. Nature 373:
632- 635, 1995.

GAM8145 328 GTF2F1 Sopta, M.; Burton, Z. F.; Greenblatt, J.: Structure and associatedDNA- 3 C c
helicase activity of a general transcription initiation factorthat binds to
RNA polymerase II. Nature 341: 410- 414, 1989.

GAM8145 328 HPSE Baker, E.; Crawford, J.; Sutherland, G. R.; Freeman, C.; Parish,C. R.; 3 C c
Hulett, M. D.: Human HPA endoglycosidase heparanase. ChromosomeRes. 7: 319
only, 1999.

GAM8145 328 HPSE Hulett, M. D.; Freeman, C.; Hamdorf, B. J.; Baker, R. T.; Harris,M. J.; 3 C c
Parish, C. R.: Cloning of mammalian heparanase, an importantenzyme in tumor
invasion and metastasis. Nature Med. 5: 803- 809,1999.

GAM8145 328 HPSE Kussie, P. H.; Hulmes, J. D.; Ludwig, D. L.; Patel, S.; Navarro,E. C.; 3 C c
Seddon, A. P.; Giorgio, N. A.; Bohlen, P: Cloning and functionalexpression
of a human heparanase gene. Biochem. Biophys. Res. Commun. 261:183- 187,
1999.

GAM8145 328 HPSE Toyoshima, M.; Nakajima, M.: Human heparanase: purification, 3 C c
characterization,cloning, and expression. J. Biol. Chem. 274: 24153- 24160,
1999.

GAM8145 328 HPSE Vlodavsky, I.; Friedmann, Y.; Elkin, M.; Aingorn, H.; Atzmon, R.;Ishai- 3 C c
Michaeli, R.; Bitan, M.; Pappo, O.; Peretz, T.; Michal, I.;Spector, L.;
Pecker, I.: Mammalian heparanase: gene cloning, expressionand function in
tumor progression and metastasis. Nature Med. 5:793- 802, 1999.

GAM8145 328 KNG Cheung, P. P.; Cannizzaro, L. A.; Colman, R. W.: Chromosomal mappingof human 3 C
c
kininogen gene (KNG) to 3q26- qter. Cytogenet. Cell Genet. 59:24- 26, 1992.

GAM8145 328 KNG Cheung, P. P.; Kunapuli, S. P.; Scott, C. F.; Wachtfogel, Y. T.;Colman, R. 3 C c
W.: Genetic basis of total kininogen deficiency in Williams'trait. J. Biol.
Chem. 268: 23361- 23365, 1993.

GAM8145 328 KNG Colman, R. W.; Bagdasarian, A.; Talamo, R. C.; Scott, C. F.; Seavey,M.; 3 C c
Guimaraes, J. A.; Pierce, J. V.; Kaplan, A. P.: Williams trait:human
kininogen deficiency with diminished levels of plasminogen proactivatorand
prekallikrein associated with abnormalities of the Hageman factordependent
pathways. J. Clin. Invest. 56: 1650- 1662, 1975.

GAM8145 328 KNG Davie, E. W.: Personal Communication. Seattle, Wash. 11/26/1979. 3 C c

GAM8145 328 KNG Donaldson, V. H.; Kleniewski, J.; Saito, H.; Sayed, J. K.: 3 C c
Prekallikreindeficiency in a kindred with kininogen deficiency and
Fitzgerald traitclotting defect: evidence that high molecular weight
kininogen andprekallikrein exist as a complex in normal plasma. J. Clin.
Invest. 60:571- 583, 1977.

GAM8145 328 KNG Fong, D.; Smith, D. I.; Hsieh, W.- T.: The human kininogen gene(KNG) mapped 3 C c
to chromosome 3q26- qter by analysis of somatic cell hybridsusing the
polymerase chain reaction. Hum. Genet. 87: 189- 192, 1991.

GAM8145 328 KNG Freije, J. P.; Pendas, A. M.; Velasco, G.; Roca, A.; Abrahamson,M.; Lopez- 3 C c
Otin, C.: Localization of the human cystatin D gene (CST5)to chromosome
20p11.21 by in situ hybridization. Cytogenet. CellGenet. 62: 29- 31, 1993.

GAM8145 328 KNG Hayashi, H.; Ishimaru, F.; Fujita, T.; Tsurumi, N.; Tsuda, T.;Kimura, I.: 3 C c
Molecular genetic survey of five Japanese families withhigh molecular weight
kininogen deficiency. Blood 75: 1296- 1304,1990.

GAM8145 328 KNG James, F. W.; Donaldson, V. H.: Decreased exercise tolerance andhypertension 3 C c
in severe hereditary deficiency of plasma kininogens.(Letter) Lancet I: 889
only, 1981.

GAM8145 328 KNG Kunapuli, S. P.: Personal Communication. Philadelphia, Pa. 12/21/1993. 3 C c

GAM8145 328 KNG Lacombe, M.- J.; Varet, B.; Levy, J.- P.: A hitherto undescribedplasma 3 C c
factor acting at the contact phase of blood coagulation (Flaujeacfactor):
case report and coagulation studies. Blood 46: 761- 768,1975.

GAM8145 328 KNG Lefrere, J.- J.; Horellou, M.- H.; Gozin, D.; Conard, J.; Muller,J.- Y.; 3 C c
Clark, M.; Soulier, J.- P.; Samama, M.: A new case of highmolecular weight
kininogen inherited deficiency. Am. J. Hemat. 22:415- 419, 1986.

GAM8145 328 KNG Saito, H.; Ratnoff, O. D.; Waldmann, R.; Abraham, J. P.: Deficiencyof a 3 C c
hitherto unrecognized agent, Fitzgerald factor, participatingin surface-
medicated reactions of clotting, fibrinolysis, generationof kinins, and the
property of diluted plasma enhancing vascular permeability(Pf- DIL). J.
Clin. Invest. 55: 1082- 1089, 1975.

GAM8145 328 KNG Waldmann, R.; Abraham, J. P.; Rebuck, J. W.; Caldwell, J.; Saito,H.; 3 C c
Ratnoff, O. D.: Fitzgerald factor: a hitherto unrecognized
coagulationfactor. Lancet I: 949- 951, 1975.

GAM8145 328 KNG Wuepper, K. D.; Miller, D. R.; Lacombe, M. J.: Flaujeac trait:deficiency of 3 C c
human plasma kininogen. J. Clin. Invest. 56: 1663- 1672,1975.

GAM8145 328 MAN1A1 Bause, E.; Bieberich, E.; Rolfs, A.; Volker, C.; Schmidt, B.:Molecular 3 C c
cloning and primary structure of Man(9)- mannosidase fromhuman kidney. Eur.
J. Biochem. 217: 535- 540, 1993.

GAM8145 328 MAN1A1 Tremblay, L. O; Campbell Dyke, N.; Herscovics, A.: Molecular 3 C c
cloning,chromosomal mapping and tissue- specific expression of a novel
humanalpha- 1,2- mannosidase gene involved in N- glycan maturation.
Glycobiology 8:585- 595, 1998.

GAM8145 328 MAN2A1 Chui, D.; Oh- Eda, M.; Liao, Y.- F.; Panneerselvam, K.; Lai, A.;Marek, K. 3 C c
W.; Freeze, H. H.; Moremen, K. W.; Fukuda, M. N.; Marth,J. D.: Alpha-
mannosidase- II deficiency results in dyserythropoiesisand unveils an
alternate pathway in oligosaccharide biosynthesis. Cell 90:157- 167, 1997.

GAM8145 328 MAN2A1 Chui, D.; Sellakumar, G.; Green, R. S.; Sutton- Smith, M.; McQuistan,T.; 3 C c
Marek, K. W.; Morris, H. R.; Dell, A.; Marth, J. D.: Geneticremodeling of
protein glycosylation in vivo induces autoimmune disease. Proc.Nat. Acad.
Sci. 98: 1142- 1147, 2001.

GAM8145 328 MAN2A1 Gasparini, P.; del Giudice, E. M.; Delaunay, J.; Totaro, A.; Granatiero,M.; 3 C c
Melchionda, S.; Zelante, L.; Iolascon, A.: Localization of thecongenital
dyserythropoietic anemia II locus to chromosome 20q11.2by genomewide search.
Am. J. Hum. Genet. 61: 1112- 1116, 1997.

GAM8145 328 MAN2A1 Misago, M.; Liao, Y.- F.; Kudo, S.; Eto, S.; Mattei, M.- G.; Moremen,K. W.; 3 C c
Fukuda, M. N.: Molecular cloning and expression of cDNAs encodinghuman
alpha- mannosidase II and a previously unrecognized alpha- mannosidaseII(X)
isozyme. Proc. Nat. Acad. Sci. 92: 11766- 11770, 1995.

GAM8145 328 MAN2A1 Moremen, K. W.; Robbins, P. W.: Isolation, characterization, andexpression 3 C c
of cDNAs encoding murine alpha- mannosidase II, a Golgienzyme that controls
conversion of high mannose to complex N- glycans. J.Cell Biol. 115: 1521-
1534, 1991.

GAM8145 328 MEOX2 Candia, A. F.; Hu, J.; Crosby, J.; Lalley, P. A.; Noden, D.; Nadeau,J. H.; 3 C c
Wright, C. V. E.: Mox- 1 and Mox- 2 define a novel homeoboxgene subfamily
and are differentially expressed during early mesodermalpatterning in mouse
embryos. Development 116: 1123- 1136, 1992.

GAM8145 328 MEOX2 Gorski, D. H.; LePage, D. F.; Patel, C. V.; Copeland, N. G.; Jenkins,N. A.; 3 C c
Walsh, K.: Molecular cloning of a diverged homeobox gene thatis rapidly
down- regulated during the G0/G1 transition in vascularsmooth muscle cells.
Molec. Cell Biol. 13: 3722- 3733, 1993.

GAM8145 328 MEOX2 Grigoriou, M.; Kastrinaki, M.- C.; Modi, W. S.; Theodorakis, K.;Mankoo, B.; 3 C c
Pachnis, V.; Karagogeos, D.: Isolation of the human MOX2homeobox gene and
localization to chromosome 7p22.1- p21.3. Genomics 26:550- 555, 1995.

GAM8145 328 MEOX2 LePage, D. F.; Altomare, D. A.; Testa, J. R.; Walsh, K.: Molecularcloning 3 C c
and localization of the human GAX gene to 7p21. Genomics 24:535- 540, 1994.

GAM8145 328 MEOX2 Mankoo, B. S.; Collins, N. S.; Ashby, P.; Grigorievea, E.; Pevny,L. H.; 3 C c
Candia, A.; Wright, C. V. E.; Rigby, P. W. J.; Pachnis, V.: Mox2 is a
component of the genetic hierarchy controlling limb muscledevelopment.
Nature 400: 69- 73, 1999.

GAM8145 328 NCOA6 Caira, F.; Antonson, P.; Pelto- Huikko, M.; Treuter, E.; Gustafsson,J.- A.: 3 C c
Cloning and characterization of RAP250, a novel nuclear receptorcoactivator.
J. Biol. Chem. 275: 5308- 5317, 2000.

GAM8145 328 NCOA6 Guan, X. Y.; Xu, J.; Anzick, S. L.; Zhang, H.; Trent, J. M.; Meltzer,P. S.: 3 C c
Hybrid selection of transcribed sequences from microdissectedDNA: isolation
of genes within amplified region at 20q11- q13.2 inbreast cancer. Cancer
Res. 56: 3446- 3450, 1996.

GAM8145 328 NCOA6 Ko, L.; Cardona, G. R.; Chin, W. W.: Thyroid hormone receptor- 3 C c
bindingprotein, an LXXLL motif- containing protein, functions as a
generalcoactivator. Proc. Nat. Acad. Sci. 97: 6212- 6217, 2000.

GAM8145 328 NCOA6 Lee, S.- K.; Anzick, S. L.; Choi, J.- E.; Bubendorf, L.; Guan, X.- Y.;Jung, 3 C c
Y.- K.; Kallioniemi, O. P.; Kononen, J.; Trent, J. M.; Azorsa,D.; Jhun, B.-
H.; Cheong, J. H.; Lee, Y. C.; Meltzer, P. S.; Lee, J.W.: A nuclear factor,
ASC- 2, as a cancer- amplified transcriptionalcoactivator essential for
ligand- dependent transactivation by nuclearreceptors in vivo. J. Biol.
Chem. 274: 34283- 34293, 1999.

GAM8145 328 NCOA6 Mahajan, M. A.; Samuels, H. H: A new family of nuclear receptorcoregulators 3 C c
that integrate nuclear receptor signaling through CREB- bindingprotein.
Molec. Cell. Biol. 20: 5048- 5063, 2000.

GAM8145 328 NCOA6 Nagase, T.; Seki, N.; Ishikawa, K.; Tanaka, A.; Nomura, N.: Predictionof the 3 C c
coding sequences of unidentified human genes. V. The codingsequences of 40
new genes (KIAA0161- KIAA0200) deduced by analysisof cDNA clones from human
cell line KG- 1. DNA Res. 3: 17- 24, 1996.

GAM8145 328 NCOA6 Zhu, Y.; Kan, L.; Qi, C.; Kanwar, Y. S.; Yeldandi, A. V.; Rao,M. S.; Reddy, 3 C c
J. K.: Isolation and characterization of peroxisomeproliferator- activated
receptor (PPAR) interacting protein (PRIP)as a coactivator for PPAR. J.
Biol. Chem. 275: 13510- 13516, 2000.

GAM8145 328 POU3F2 Atanasoski, S.; Toldo, S. S.; Malipiero, U.; Schreiber, E.; Fries,R.; 3 C c
Fontana, A.: Isolation of the human genomic brain- 2/N- Oct 3 gene(POUF3)
and assignment to chromosome 6q16. Genomics 26: 272- 280,1995.

GAM8145 328 POU3F2 Schreiber, E.; Tobler, A.; Malipiero, U.; Schaffner, W.; Fontana,A.: cDNA 3 C c
cloning of human N- Oct 3, a nervous- system specific POUdomain
transcription factor binding to the octamer DNA motif. NucleicAcids Res. 21:

253- 258, 1993.

GAM8145 328 POU3F2 Xia, Y.- R.; Andersen, B.; Mehrabian, M.; Diep, A. T.; Warden, C.H.; 3 C c
Mohandas, T.; McEvilly, R. J.; Rosenfeld, M. G.; Lusis, A. J.: Chromosomal
organization of mammalian POU domain factors. Genomics 18:126- 130, 1993.

GAM8145 328 PPEF2 Ramulu, P.; Kennedy, M.; Xiong, W.- H.; Williams, J.; Cowan, M.;Blesh, D.; 3 C c
Yau, K.- W.; Hurley, J. B.; Nathans, J.: Normal light response,photoreceptor
integrity, and rhodopsin dephosphorylation in mice lackingboth protein
phosphatases with EF hands (PPEF- 1 and PPEF- 2). Molec.Cell. Biol. 21:
8605- 8614, 2001.

GAM8145 328 PPEF2 Sherman, P. M.; Sun, H.; Macke, J. P.; Williams, J.; Smallwood,P. M.; 3 C c
Nathans, J.: Identification and characterization of a conservedfamily of
protein serine/threonine phosphatases homologous to Drosophilaretinal
degeneration C (rdgC). Proc. Nat. Acad. Sci. 94: 11639- 11644,1997.

GAM8145 328 PRKAR2B Cummings, D. E.; Brandon, E. P.; Planas, J. V.; Motamed, K.; Idzerda,R. L.; 3 C c
McKnight, G. S.: Genetically lean mice result from targeteddisruption of the
RII- beta subunit of protein kinase A. Nature 382::622- 626, 1996.

GAM8145 328 PRKAR2B Scambler, P.; Oyen, O.; Wainwright, B.; Farrall, M.; Law, H.- Y.;Estivill, 3 C c
X.; Sandberg, M.; Williamson, R.; Jahnsen, T.: Exclusionof catalytic and
regulatory subunits of cAMP- dependent protein kinaseas candidate genes for
the defect causing cystic fibrosis. Am. J.Hum. Genet. 41: 925- 932, 1987.

GAM8145 328 PRKAR2B Solberg, R.; Sistonen, P.; Traskelin, A.- L.; Berube, D.; Simard,J.; Krajci, 3 C c
P.; Jahnsen, T.; de la Chapelle, A.: Mapping of the regulatorysubunits RI-
beta and RII- beta of cAMP- dependent protein kinase geneson human
chromosome 7. Genomics 14: 63- 69, 1992.

GAM8145 328 PRKAR2B Wainwright, B.; Lench, N.; Davies, K.; Scambler, P.; Kruyer, H.;Williamson, 3 C c
R.; Jahnsen, T.; Farrall, M.: A human regulatory subunitof type II cAMP-
dependent protein kinase localized by its linkagerelationship to several
cloned chromosome 7q markers. Cytogenet.Cell Genet. 45: 237- 239, 1987.

GAM8145 328 RNF14 Kang, H.- Y.; Yeh, S.; Fujimoto, N.; Chang, C.: Cloning and 3 C c
characterizationof human prostate coactivator ARA54, a novel protein that
associateswith the androgen receptor. J. Biol. Chem. 274: 8570- 8576, 1999.

GAM8145 328 RNF14 Ueki, N.; Oda, T.; Kondo, M.; Yano, K.; Noguchi, T.; Muramatsu,M.: Selection 3 C c
system for genes encoding nuclear- targeted proteins. Nat.Biotech. 16: 1338-
1342, 1998.

GAM8145 328 RNF14 Ueki, N.; Seki, N.; Yano, K.; Masuho, Y.; Saito, T.; Muramatsu,M.: Isolation 3 C c
and characterization of a novel human gene (HFB30)which encodes a protein
with a RING finger motif. Biochim. Biophys.Acta 232- 236, 1999.

GAM8145 328 SH3GL2 Giachino, C.; Lantelme, E.; Lanzetti, L.; Saccone, S.; Della Valle,G.; 3 C c
Migone, N.: A novel SH3- containing human gene family
preferentiallyexpressed in the central nervous system. Genomics 41: 427-
434, 1997.

GAM8145 328 SH3GL2 Howard, L.; Nelson, K. K.; Maciewicz, R. A.; Blobel, C. P.: Interactionof 3 C c
the metalloprotease disintegrins MDC9 and MDC15 with two SH3 domain-
containingproteins, endophilin I and SH3PX1. J. Biol. Chem. 274: 31693-
31699,1999.

GAM8145 328 SH3GL2 Schmidt, A.; Wolde, M.; Thiele, C.; Fest, W.; Kratzin, H.; Podtelejnikov,A. 3 C c
V.; Witke, W.; Huttner, W. B.; Soling, H.- D.: Endophilin I mediatessynaptic
vesicle formation by transfer of arachidonate to lysophosphatidicacid.
Nature 401: 133- 141, 1999.

GAM8145 328 SH3GL2 Soubeyran, P.; Kowanetz, K.; Szymkiewicz, I.; Langdon, W. Y.; Dikic,I.: Cbl- 3 C c

CIN85- endophilin complex mediates ligand- induced downregulationof EGF receptors. Nature 416: 183- 187, 2002.

GAM8145 328 TAF6 Bell, B.; Scheer, E.; Tora, L.: Identification of hTAFII80- deltalinks 3 C c apoptotic signaling pathways to transcription factor TFIID function. Molec.Cell 8: 591- 600, 2001.

GAM8145 328 TAF6 Hisatake, K.; Ohta, T.; Takada, R.; Guermah, M.;Horikoshi, M.;Nakatani, Y.; 3 C c Roeder, R. G.: Evolutionary conservation of human TATA- binding-polypeptide- associatedfactors TAFII31 and TAFII80 and interactions of TAFII80 with otherTAFs and with general transcription factors. Proc. Nat. Acad. Sci. 92:8195- 8199, 1995.

GAM8145 328 TAF6 Weinzierl, R. O. J.; Ruppert, S.; Dynlacht, B. D.; Tanese, N.;Tjian, R.: 3 C c Cloning and expression of Drosophila TAFII60 and humanTAFII70 reveal conserved interactions with other subunits of TFIID. EMBOJ. 12: 5303- 5309, 1993.

GAM8145 328 TBL1X Bassi, M. T.; Ramesar, R. S.; Caciotti, B.; Winship, I. M.; DeGrandi, A.; 3 C c Riboni, M.; Townes, P. L.; Beighton, P.; Ballabio, A.;Borsani, G.: X- linked late- onset sensorineural deafness caused bya deletion involving OA1 and a novel gene containing WD- 40 repeats. Am.J. Hum. Genet. 64: 1604- 1616, 1999.

GAM8145 328 TBL1X Converse, P. J.: Personal Communication. Baltimore, Md. 8/24/2001. 3 C c

GAM8145 328 TBL1X Disteche, C. M.; Dinulos, M. B.; Bassi, M. T.; Elliott, R. W.;Rugarli, E. 3 C c I.: Mapping of the murine Tbl1 gene reveals a new rearrangementbetween mouse and human X chromosomes. Mammalian Genome 9: 1062- 1064,1998.

GAM8145 328 TBL1X Dong, X.; Tsuda, L.; Zavitz, K. H.; Lin, M.; Li, S.; Carthew, R.W.; 3 C c Zipursky, S. L.: ebi regulates epidermal growth factor receptorsignaling pathways in Drosophila. Genes Dev. 13: 954- 965, 1999.

GAM8145 328 TBL1X Emes, R. D.; Ponting, C. P.: A new sequence motif linking 3 C c lissencephaly,Treacher Collins and oral- facial- digital type 1 syndromes, microtubuledynamics and cell migration. Hum. Molec. Genet. 10: 2813- 2820, 2001.

GAM8145 328 TBL1X Matsuzawa, S.; Reed, J. C.: Siah- 1, SIP, and Ebi collaborate ina novel 3 C c pathway for beta- catenin degradation linked to p53 responses. Molec.Cell 7: 915- 926, 2001.

GAM8145 328 TBL1X Zhang, J.; Kalkum, M.; Chait, B. T.; Roeder, R. G.: The N- CoR- HDAC3nuclear 3 C c receptor corepressor complex inhibits the JNK pathway throughthe integral subunit GPS2. Molec. Cell 9: 611- 623, 2002.

GAM8145 328 TCL1B Hallas, C.; Pekarsky, Y.; Itoyama, T.; Varnum, J.; Bichi, R.; Rothstein,J. 3 C c L.; Croce, C. M.: Genomic analysis of human and mouse TCL1 locireveals a complex of tightly clustered genes. Proc. Nat. Acad. Sci. 96:14418- 14423, 1999.

GAM8145 328 TCL1B Pekarsky, Y.; Hallas, C.; Isobe, M.; Russo, G.; Croce, C. M.:Abnormalities 3 C c at 14q32.1 in T cell malignancies involve two oncogenes. Proc.Nat. Acad. Sci. 96: 2949- 2951, 1999.

GAM8145 328 TKTL1 Coy, J. F.; Dubel, S.; Kioschis, P.; Thomas, K.; Micklem, G.; Delius,H.; 3 C c Poustka, A.: Molecular cloning of tissue- specific transcriptsof a transketolase- related gene: implications for the evolution ofnew vertebrate genes. Genomics 32: 309- 316, 1996.

GAM8145 328 TKTL1 McCool, B. A.; Plonk, S. G.; Martin, P. R.; Singleton, C. K.:Cloning of 3 C c human transketolase cDNAs and comparison of the nucleotidesequence of the coding region in Wernicke- Korsakoff and non- Wernicke-

Korsakoffindividuals. J. Biol. Chem. 268: 1397- 1404, 1993.

GAM8297 367 ADAM2 Burkin, H. R.; Burkin, D. J.; Davey, P. M.; Griffin, D. K.; Affara,N. A.: 3 B c
Mapping, sequence, and expression analysis of the human fertilinbeta gene (FTNB). Genomics 40: 190- 192, 1997.

GAM8297 367 ADAM2 Cho, C.; Bunch, D. O.; Faure, J.- E.; Goulding, E. H.; Eddy, E.M.; 3 B c
Primakoff, P.; Myles, D. G.: Fertilization defects in sperm frommice lacking fertilin beta. Science 281: 1857- 1859, 1998.

GAM8297 367 ADAM2 Gupta, S. K.; Alves, K.; O'Neil Palladino, L.; Mark, G. E.; Hollis,G. F.: 3 B c
Molecular cloning of the human fertilin beta subunit. Biochem.Biophys. Res. Commun. 224: 318- 326, 1996.

GAM8297 367 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, 3 B c
S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998.

GAM8297 367 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of 3 B c
adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995.

GAM8297 367 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily 3 B c
members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994.

GAM8297 367 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; 3 B c
Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal brain type I adenylyl cyclase. Genomics 16: 473- 478,1993.

GAM8297 367 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- 3 B c
Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.: Altered sensory processing in the somatosensory cortex of the mutantmouse barrelless. Science 271: 1864- 1867, 1996.

GAM8297 367 ADORA3 Liang, B. T.; Jacobson, K. A.: A physiological role of the adenosineA3 3 B c
receptor: sustained cardioprotection. Proc. Nat. Acad. Sci. 95:6995- 6999, 1998.

GAM8297 367 ADORA3 Monitto, C. L.; Levitt, R. C.; DiSilvestre, D.; Holroyd, K. J.: Localization 3 B c
of the A(3) adenosine receptor gene (ADORA3) to humanchromosome 1p. Genomics 26: 637- 638, 1995.

GAM8297 367 ADORA3 Sajjadi, F. G.; Firestein, G. S.: cDNA cloning and sequence analysisof the 3 B c
human A3 adenosine receptor. Biochim. Biophys. Acta 1179:105- 107, 1993.

GAM8297 367 ADORA3 Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; 3 B c
Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and genome organization of mammalian G- protein- coupled receptors. Genomics 18:175- 184, 1993.

GAM8297 367 ADORA3 Zhao, Z.; Ravid, S.; Ravid, K.: Chromosomal mapping of the mouseA3 adenosine 3 B c
receptor gene, Adora3. Genomics 30: 118- 119, 1995.

GAM8297 367 ADORA3 Zhou, Q.- Y.; Li, C.; Olah, M. E.; Johnson, R. A.; Stiles, G. L.;Civelli, 3 B c
O.: Molecular cloning and characterization of an adenosinereceptor: the A3 adenosine receptor. Proc. Nat. Acad. Sci. 89: 7432- 7436,1992.

GAM8297 367 BGN Chatterjee, A.; Faust, C. J.; Herman, G. E.: Genetic and physicalmapping of 3 B c
the biglycan gene on the mouse X chromosome. MammalianGenome 4: 33- 36, 1993.

GAM8297 367 BGN Das, S.; Metzenberg, A.; Pai, G. S.; Gitschier, J.: Mutationalanalysis of 3 B c
the biglycan gene excludes it as a candidate for X- linkeddominant

chondrodysplasia punctata, dyskeratosis congenita, and incontinentiapigmenti. (Letter) Am. J. Hum. Genet. 54: 922- 925, 1994.

GAM8297 367 BGN Fisher, L. W.; Heegaard, A.- M.; Vetter, U.; Vogel, W.; Just, W.;Termine, J. 3 B c
D.; Young, M. F.: Human biglycan gene: putative promoter,intron- exon junctions, and chromosomal localization. J. Biol. Chem. 266:14371- 14377, 1991.

GAM8297 367 BGN Fisher, L. W.; Termine, J. D.; Young, M. F.: Deduced- protein sequenceof 3 B c
bone small proteoglycan I (biglycan) shows homology with proteoglycanII (decorin) and several nonconnective tissue proteins in a varietyof species. J. Biol. Chem. 264: 4571- 4576, 1989.

GAM8297 367 BGN Geerkens, C.; Vetter, U.; Just, W.; Fedarko, N. S.; Fisher, L.W.; Young, M. 3 B c
F.; Termine, J. D.; Gehron Robey, P.; Wohrle, D.; Vogel,W.: The X-chromosomal human biglycan gene BGN is subject to X inactivationbut is transcribed like an X- Y homologous gene. Hum. Genet. 96:44- 52, 1995.

GAM8297 367 BGN McBride, O. W.; Fisher, L. W.; Young, M. F.: Localization of PGI(biglycan, 3 B c
BGN) and PGII (decorin, DCN, PG- 40) genes on human chromosomesXq13- qter and 12q, respectively. Genomics 6: 219- 225, 1990.

GAM8297 367 BGN Traupe, H.; van den Ouweland, A. M. W.; van Oost, B. A.; Vogel,W.; Vetter, 3 B c
U.; Warren, S. T.; Rocchi, M.; Darlison, M. G.; Ropers,H.- H.: Fine mapping of the human biglycan (BGN) gene within the Xq28region employing a hybrid cell panel. Genomics 13: 481- 483, 1992.

GAM8297 367 BGN Wegrowski, Y.; Pillarisetti, J.; Danielson, K. G.; Suzuki, S.;Iozzo, R. V.: 3 B c
The murine biglycan: complete cDNA cloning, genomicorganization, promoter function, and expression. Genomics 30: 8- 17,1995.

GAM8297 367 BGN Xu, T.; Bianco, P.; Fisher, L. W.; Longenecker, G.; Smith, E.;Goldstein, S.; 3 B c
Bonadio, J.; Boskey, A.; Heegaard, A.- M.; Sommer, B.;Satomura, K.; Dominguez, P.; Zhao, C.; Kulkarni, A. B.; Robey, P.G.; Young, M. F.: Targeted disruption of the biglycan gene leadsto an osteoporosis- like phenotype in mice. Nature Genet. 20: 78- 82,1998.

GAM8297 367 CACNA1D Chin, H.; Kozak, C. A.; Kim, H.- L.; Mock, B.; McBride, O. W.:A brain L- 3 B c
type calcium channel alpha- 1 subunit gene (CCHL1A2) mapsto mouse chromosome 14 and human chromosome 3. Genomics 11: 914- 919,1991.

GAM8297 367 CACNA1D Davare, M. A.; Avdonin, V.; Hall, D. D.; Peden, E. M.; Burette,A.; Weinberg, 3 B c
R. J.; Horne, M. C.; Hoshi, T.; Hell, J. W.: A beta- 2adrenergic receptor signaling complex assembled with the Ca(2+) channelCa(V)1.2. Science 293: 98- 101, 2001.

GAM8297 367 CACNA1D Jinnah, H. A.; Yitta, S.; Drew, T.; Kim, B. S.; Visser, J. E.;Rothstein, J. 3 B c
D.: Calcium channel activation and self- biting in mice. Proc.Nat. Acad. Sci. 96: 15228- 15232, 1999.

GAM8297 367 CACNA1D McAlpine, P. J.: Personal Communication. Winnipeg, Manitoba,Canada 3 B c
2/14/1992.

GAM8297 367 CACNA1D Mori, Y.; Friedrich, T.; Kim, M.- S.; Mikami, A.; Nakai, J.; Ruth,P.; Bosse, 3 B c
E.; Hofmann, F.; Flockerzi, V.; Furuichi, T.; Mikoshiba,K.; Imoto, K.; Tanabe, T.; Numa, S.: Primary structure and functionalexpression from complementary DNA of a brain calcium channel. Nature 350:398- 402, 1991.

GAM8297 367 CACNA1D Pennartz, C. M. A.; de Jeu, M. T. G.; Bos, N. P. A.; Schaap, J.;Geurtsen, A. 3 B c
M. S.: Diurnal modulation of pacemaker potentials andcalcium current in the mammalian circadian clock. Nature 416: 286- 290,2002.

GAM8297 367 CACNA1D Platzer, J.; Engel, J.; Schrott- Fischer, A.; Stephan, K.; Bova,S.; Chen, 3 B c
H.; Zheng, H.; Striessnig, J.: Congenital deafness andsinoatrial node

dysfunction in mice lacking class D L- type Ca(2+)channels. Cell 102: 89-97, 2000.

GAM8297 367 CACNA1D Seino, S.; Chen, L.; Seino, M.; Blondel, O.; Takeda, J.; Johnson,J. H.; Bell, G. I.: Cloning of the alpha- 1 subunit of a voltage- dependentcalcium channel expressed in pancreatic beta- cells. Proc. Nat. Acad.Sci. 89: 584-588, 1992. 3 B c

GAM8297 367 CACNA1D Seino, S.; Yamada, Y.; Espinosa, R., III; Le Beau, M. M.; Bell,G. I.: Assignment of the gene encoding the alpha- 1 subunit of theneuroendocrine/brain- type calcium channel (CACNL1A2) to human chromosome3, band p14.3. Genomics 13: 1375- 1377, 1992. 3 B c

GAM8297 367 CACNA1D Tsien, R. W.; Ellinor, P. T.; Horne, W. A.: Molecular diversityof voltage-dependent Ca(2+) channels. Trends Pharm. Sci. 12: 349- 354,1991. 3 B c

GAM8297 367 CACNB1 Gregg, R. G.; Messing, A.; Strube, C.; Beurg, M.; Moss, R.; Behan,M.; Sukhareva, M.; Haynes, S.; Powell, J. A.; Coronado, R.; Powers,P. A.: Absence of the beta subunit (cchb1) of the skeletal muscledihydropyridine receptor alters expression of the alpha- 1 subunitand eliminates excitation-contraction coupling. Proc. Nat. Acad.Sci. 93: 13961- 13966, 1996. 3 B c

GAM8297 367 CACNB1 Iles, D. E.; Segers, B.; Sengers, R. C. A.; Monsieurs, K.; Heytens,L.; Halsall, P. J.; Hopkins, P. M.; Ellis, F. R.; Hall- Curran, J.L.; Stewart, A. D.; Wieringa, B.: Genetic mapping of the beta- 1- and gamma- subunits of the human skeletal muscle L- type voltage- dependentcalcium channel on chromosome 17q and exclusion as candidate genesfor malignant hyperthermia susceptibility. Hum. Molec. Genet. 2:863- 868, 1993. 3 B c

GAM8297 367 CACNB1 Powers, P. A.; Liu, S.; Hogan, K.; Gregg, R. G.: Skeletal muscleand brain isoforms of a beta- subunit of human voltage- dependent calciumchannels are encoded by a single gene. J. Biol. Chem. 267: 22967- 22972,1992. 3 B c

GAM8297 367 CACNB1 Pragnell, M.; Sakamoto, J.; Jay, S. D.; Campbell, K. P.: Cloningand tissue-specific expression of the brain calcium channel beta- subunit. FEBSLett. 291: 253- 258, 1991. 3 B c

GAM8297 367 CGA Amato, F.; Warnes, G. M.; Kirby, C. A.; Norman, R. J.: Infertilitycaused by hCG autoantibody. J. Clin. Endocr. Metab. 87: 993- 997,2002. 3 B c

GAM8297 367 CGA Boothby, M.; Ruddon, R. W.; Anderson, C.; McWilliams, D.; Boime,I.: A single gonadotropin alpha- subunit gene in normal tissue andtumor- derived cell lines. J. Biol. Chem. 256: 5121- 5127, 1981. 3 B c

GAM8297 367 CGA Bordelon, M.; Kohler, P. O.: Synthesis of human glycoprotein hormonein somatic cell hybrids. (Abstract) J. Cell Biol. 67: 37A only,1975. 3 B c

GAM8297 367 CGA Bordelon- Riser, M. E.; Siciliano, M. J.; Kohler, P. O.: Necessityfor two human chromosomes for human chorionic gonadotropin productionin human- mouse hybrids. Somat. Cell Genet. 5: 597- 613, 1979. 3 B c

GAM8297 367 CGA Chin, W. W.: Personal Communication. Boston, Mass. 2/15/1982. 3 B c

GAM8297 367 CGA Fiddes, J. C.; Goodman, H. M.: Isolation, cloning and sequenceanalysis of the cDNA for the alpha- subunit of human chorionic gonadotropin. Nature 281:351- 356, 1979. 3 B c

GAM8297 367 CGA Fiddes, J. C.; Goodman, H. M.: The gene encoding the common alphasubunit of the four human glycoprotein hormones. J. Molec. Appl.Genet. 1: 3- 18, 1981. 3 B c

GAM8297 367 CGA Hardin, J. W.; Riser, M. E.; Trent, J. M.; Kohler, P. O.: Thechorionic gonadotropin alpha- subunit gene is on human chromosome 18in JEG cells. Proc. Nat. Acad. Sci. 80: 6282- 6285, 1983. 3 B c

GAM8297 367 CGA Heitz, P. U.; Kasper, M.; Kloppel, G.; Polak, J. M.; Vaitukaitis,J. L.: Glycoprotein- hormone alpha- chain production by pancreaticendocrine tumors: 3 B c

a specific marker for malignancy- - immunocytochemicalanalysis of tumors of 155 patients. Cancer 51: 277- 282, 1983.

GAM8297 367 CGA Hoshina, M.; Boothby, M. R.; Hussa, R. D.; Pattillo, R. A.; Camel,H. M.; Boime, I.: Segregation patterns of polymorphic restrictionsites of the gene encoding the alpha subunit of human chorionic gonadotropinin trophoblastic disease. Proc. Nat. Acad. Sci. 81: 2504- 2507, 1984. 3 B c

GAM8297 367 CGA Lebo, R. V.: Personal Communication. San Francisco, Calif. 1/14/1980. 3 B c

GAM8297 367 CGA Morgan, F. J.; Birken, S.; Canfield, R. E.: The amino acid sequenceof human chorionic gonadotropin: the alpha subunit and beta subunit. J.Biol. Chem. 250: 5247- 5258, 1975. 3 B c

GAM8297 367 CGA Naylor, S. L.; Chin, W. W.; Goodman, H. M.; Lalley, P. A.; Grzeschik,K.- H.; Sakaguchi, A. Y.: Chromosome assignment of the genes encodingthe alpha and beta subunits of the glycoprotein hormones in man andmouse. Somat. Cell Genet. 9: 757- 770, 1983. 3 B c

GAM8297 367 CGA Ruddon, R. W.; Hanson, C. A.; Addison, N. J.: Synthesis and processingof human chorionic gonadotropin subunits in cultured choriocarcinomacells. Proc. Nat. Acad. Sci. 76: 5143- 5147, 1979. 3 B c

GAM8297 367 CGA Trent, J.: Personal Communication. Tucson, Ariz. 11/23/1982. 3 B c

GAM8297 367 CNR1 Di Marzo, V.; Goparaju, S. K.; Wang, L.; Liu, J.; Batkai, S.; Jarai,Z.; Fezza, F.; Miura, G. I.; Palmiter, R. D.; Sugiura, T.; Kunos,G.: Leptin-regulated endocannabinoids are involved in maintainingfood intake. Nature 410: 822- 825, 2001. 3 B c

GAM8297 367 CNR1 Gerard, C. M.; Mollereau, C.; Vassart, G.; Parmentier, M.: Molecularcloning of a human cannabinoid receptor which is also expressed intestis. Biochem. J. 279: 129- 134, 1991. 3 B c

GAM8297 367 CNR1 Hoehe, M. R.; Caenazzo, L.; Martinez, M. M.; Hsieh, W.- T.; Modi,W. S.; Gershon, E. S.; Bonner, T. I.: Genetic and physical mappingof the human cannabinoid receptor gene to chromosome 6q14- q15. NewBiologist 3: 880- 885, 1991. 3 B c

GAM8297 367 CNR1 Ledent, C.; Valverde, O.; Cossu, G.; Petitet, F.; Aubert, J.- F.;Beslot, F.; Bohme, G. A.; Imperato, A.; Pedrazzini, T.; Roques, B.P.; Vassart, G.; Fratta, W.; Parmentier, M.: Unresponsiveness tocannabinoids and reduced addictive effects of opiates in CB(1) receptorknockout mice. Science 283 401- 404, 1999. 3 B c

GAM8297 367 CNR1 Marsicano, G.; Wotjak, C. T.; Azad, S. C.; Bisogno, T.; Rammes,G.; Cascio, M. G.; Hermann, H.; Tang, J.; Hofmann, C.; Zieglgansberger,W.; Di Marzo, V.; Lutz, B.: The endogenous cannabinoid system controlsextinction of aversive memories. Nature 418: 530- 534, 2002. 3 B c

GAM8297 367 CNR1 Matsuda, L. A.; Lolait, S. J.; Brownstein, M. J.; Young, A. C.;Bonner, T. I.: Structure of a cannabinoid receptor and functionalexpression of the cloned cDNA. Nature 346: 561- 564, 1990. 3 B c

GAM8297 367 CNR1 Modi, W. S.; Bonner, T. I.: Localization of the cannabanoid (sic)receptor locus using non- isotopic in situ hybridization. (Abstract) Cytogenet.Cell Genet. 58: 1915 only, 1991. 3 B c

GAM8297 367 CNR1 Panikashvili, D.; Simeonidou, C.; Ben- Shabat, S.; Hanus, L.; Breuer,A.; Mechoulam, R.; Shohami, E.: An endogenous cannabinoid (2- AG)is neuroprotective after brain injury. Nature 413: 527- 531, 2001. 3 B c

GAM8297 367 CRHR1 Asakura, H.; Zwain, I. H.; Yen, S. S. C.: Expression of genesencoding corticotropin- releasing factor (CRF), type 1 CRF receptor,and CRF- binding protein and localization of the gene products in thehuman ovary. J. Clin. 3 B c

Endocr. Metab. 82: 2720- 2725, 1997.

GAM8297 367 CRHR1 Chen, R.; Lewis, K. A.; Perrin, M. H.; Vale, W. W.: Expressioncloning of a human corticotropin- releasing- factor receptor. Proc.Nat. Acad. Sci. 90: 8967- 8971, 1993. 3 B c

GAM8297 367 CRHR1 Dieterich, K. D.; Gundelfinger, E. D.; Ludecke, D. K.; Lehnert,H.: Mutation and expression analysis of corticotropin- releasing factor1 receptor in adrenocorticotropin- secreting pituitary adenomas. J.Clin. Endocr. Metab. 83: 3327- 3331, 1998. 3 B c

GAM8297 367 CRHR1 Grammatopoulos, D.; Dai, Y.; Chen, J.; Karteris, E.; Papadopoulou,N.; Easton, A. J.; Hillhouse, E. W.: Human corticotropin- releasinghormone receptor: differences in subtype expression between pregnantand nonpregnant myometria. J. Clin. Endocr. Metab. 83: 2539- 2544,1998. 3 B c

GAM8297 367 CRHR1 Leproult, R.; Colecchia, E. F.; L'Hermite- Baleriaux, M.; Van Cauter,E.: Transition from dim to bright light in the morning induces animmediate elevation of cortisol levels. J. Clin. Endocr. Metab. 86:151- 157, 2001. 3 B c

GAM8297 367 CRHR1 Liaw, C. W.; Grigoriadis, D. E.; Lovenberg, T. W.; De Souza, E.B.; Maki, R. A.: Localization of ligand- binding domains of humancorticotropin- releasing factor receptor: a chimeric receptor approach. Molec.Endocr. 11: 980- 985, 1997. 3 B c

GAM8297 367 CRHR1 Polymeropoulos, M. H.; Torres, R.; Yanovski, J. A.; Chandrasekharappa,S. C.; Ledbetter, D. H.: The human corticotropin- releasing factorreceptor (CRHR) gene maps to chromosome 17q12- q22. Genomics 28:123- 124, 1995. 3 B c

GAM8297 367 CRHR1 Sakai, K.; Yamada, M.; Horiba, N.; Wakui, M.; Demura, H.; Suda,T.: The genomic organization of the human corticotropin- releasingfactor type- 1 receptor. Gene 219: 125- 130, 1998. 3 B c

GAM8297 367 CRHR1 Sillaber, I.; Rammes, G.; Zimmermann, S.; Mahal, B.; Zieglgansberger,W.; Wurst, W.; Holsboer, F.; Spanagel, R.: Enhanced and delayed stress- inducedalcohol drinking in mice lacking functional CRH1 receptors. Science 296:931- 933, 2002. 3 B c

GAM8297 367 CRHR1 Smith, G. W.; Aubry, J.- M.; Dellu, F.; Contarino, A.; Bilezikjian,L. M.; Gold, L. H.; Chen, R.; Marchuk, Y.; Hauser, C.; Bentley, C.A.; Sawchenko, P. E.; Koob, G. F.; Vale, W.; Lee, K.- F.: Corticotropinreleasing factor receptor 1- deficient mice display decreased anxiety,impaired stress response, and aberrant neuroendocrine development. Neuron 20:1093- 1102, 1998. 3 B c

GAM8297 367 CRHR1 Timpl, P.; Spanagel, R.; Sillaber, I.; Kresse, A.; Reul, J. M.H. M.; Stalla, G. K.; Blanquet, V.; Steckler, T.; Holsboer, F.; Wurst,W.: Impaired stress response and reduced anxiety in mice lackinga functional corticotropin- releasing hormone receptor 1. Nature Genet. 19:162- 166, 1998. 3 B c

GAM8297 367 CRTL1 Dudhia, J.; Bayliss, M. T.; Hardingham, T. E.: Human link proteingene: structure and transcription pattern in chondrocytes. Biochem.J. 303: 329- 333, 1994. 3 B c

GAM8297 367 CRTL1 Loughlin, J.; Irven, C.; Sykes, B.: Exclusion of the cartilagelink protein and the cartilage matrix protein genes as the mutantloci in several heritable chondrodysplasias. Hum. Genet. 94: 698- 700,1994. 3 B c

GAM8297 367 CRTL1 Osborne- Lawrence, S. L.; Sinclair, A. K.; Hicks, R. C.; Lacey,S. W.; Eddy, R. L., Jr.; Byers, M. G.; Shows, T. B.; Duby, A. D.:Complete amino acid sequence of human cartilage link protein (CRTL1)deduced from cDNA clones and chromosomal assignment of the gene. Genomics 8:562- 567, 1990. 3 B c

GAM8297 367 CRTL1 Watanabe, H.; Yamada, Y.: Mice lacking link protein develop dwarfismand 3 B c

craniofacial abnormalities. Nature Genet. 21: 225- 229, 1999.

GAM8297 367 DAAM1 Habas, R.; Kato, Y.; He, X.: Wnt/Frizzled activation of Rho 3 B c
regulatesvertebrate gastrulation and requires a novel Formin homology
proteinDaam1. Cell 107: 843- 854, 2001.

GAM8297 367 DAAM1 Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.;Kotani, H.; 3 B c
Nomura, N.; Ohara, O.: Prediction of the coding sequencesof unidentified
human genes. X. The complete sequences of 100 newcDNA clones from brain
which can code for large proteins in vitro. DNARes. 5: 169- 176, 1998.

GAM8297 367 DEFB1 Bensch, K. W.; Raida, M.; Magert, H. J.; Schulz- Knappe, P.; Forssmann,W. 3 B c
G.: hBD- 1: a novel beta- defensin from human plasma. FEBS Lett. 368:331-
335, 1995.

GAM8297 367 DEFB1 Ganz, T.; Lehrer, R. I.: Defensins. Pharm. Ther. 66: 191- 205,1995. 3 B c

GAM8297 367 DEFB1 Goldman, M. J.; Anderson, G. M.; Stolzenberg, E. D.; Kari, U. P.;Zasloff, 3 B c
M.; Wilson, J. M.: Human beta- defensin- 1 is a salt- sensitiveantibiotic in
lung that is inactivated in cystic fibrosis. Cell 88:553- 560, 1997.

GAM8297 367 DEFB1 Huttner, K. M.; Kozak, C. A.; Bevins, C. L.: The mouse genomeencodes a 3 B c
single homolog of the antimicrobial peptide human beta- defensin1. FEBS
Lett. 413: 45- 49, 1997.

GAM8297 367 DEFB1 Jia, H. P.; Starner, T.; Ackermann, M.; Kirby, P.; Tack, B. F.;McCray, P. 3 B c
B., Jr.: Abundant human beta- defensin- 1 expression inmilk and mammary
gland epithelium. J. Pediat. 138: 109- 112, 2001.

GAM8297 367 DEFB1 Liu, L.; Zhao, C.; Heng, H. H. Q.; Ganz, T.: The human beta- defensin- 1and 3 B c
alpha- defensins are encoded by adjacent genes: two peptide familieswith
differing disulfide topology share a common ancestry. Genomics 43:316- 320,
1997.

GAM8297 367 DEFB1 Morrison, G. M.; Davidson, D. J.; Kilanowski, F. M.; Borthwick,D. W.; Crook, 3 B c
K.; Maxwell, A. I.; Govan, J. R. W.; Dorin, J. R.:Mouse beta defensin- 1 is
a functional homolog of human beta defensin- 1. MammalianGenome 9: 453- 457,
1998.

GAM8297 367 DEFB1 Singh, P. K.; Jia, H. P.; Wiles, K.; Hesselberth, J.; Liu, L.;Conway, B.- A. 3 B c
D.; Greenberg, E. P.; Valore, E. V.; Welsh, M. J.; Ganz,T.; Tack, B. F.;
McCray, P. B., Jr.: Production of beta- defensinsby human airway epithelia.
Proc. Nat. Acad. Sci. 95: 14961- 14966,1998.

GAM8297 367 DEFB1 Tunzi, C. R.; Harper, P. A.; Bar- Oz, B.; Valore, E. V.; Semple,J. L.; 3 B c
Watson- MacDonell, J.; Ganz, T.; Ito, S.: Beta- defensin expressionin human
mammary gland epithelia. Pediat. Res. 48: 30- 35, 2000.

GAM8297 367 DEFB1 Valore, E. V.; Park, C. H.; Quayle, A. J.; Wiles, K. R.; McCray,P. B., Jr.; 3 B c
Ganz, T.: Human beta- defensin- 1: an antimicrobial peptideof urogenital
tissues. J. Clin. Invest. 101: 1633- 1642, 1998.

GAM8297 367 DIO3 Hernandez, A.; Park, J. P.; Lyon, G. J.; Mohandas, T. K.; St. Germain,D. L.: 3 B c
Localization of the type 3 iodothyronine deiodinase (DIO3)gene to human
chromosome 14q32 and mouse chromosome 12F1. Genomics 53:119- 121, 1998.

GAM8297 367 DIO3 Huang, S. A.; Tu, H. M.; Harney, J. W.; Venihaki, M.; Butte, A.J.; 3 B c
Kozakewich, H. P. W.; Fishman, S. J.; Larsen, P. R.: Severe
hypothyroidismcaused by type 3 iodothyronine deiodinase in infantile
hemangiomas. NewEng. J. Med. 343: 185- 189, 2000.

GAM8297 367 DIO3 Salvatore, D.; Low, S. C.; Berry, M.; Maia, A. L.; Harney, J. W.;Croteau, 3 B c
W.; St. German, D. L.; Larsen, P. R.: Type 3 iodothyroninedeiodinase:
cloning, in vitro expression, and functional analysisof the placental
selenoenzyme. J. Clin. Invest. 96: 2421- 2430, 1995.

GAM8297 367 EDNRA Bourgeois, C.; Robert, B.; Rebourcet, R.; Mondon, F.; Mignot, T.- M.;Duc- 3 B c
Goiran, P.; Ferre, F.: Endothelin- 1 and ET(A) receptor expressionin
vascular smooth muscle cells from human placenta: a new ET(A)
receptormessenger ribonucleic acid is generated by alternative splicing
ofexon 3. J. Clin. Endocr. Metab. 82: 3116- 3123, 1997.

GAM8297 367 EDNRA Cyr, C.; Huebner, K.; Druck, T.; Kris, R.: Cloning and 3 B c
chromosomallocalization of a human endothelin ETA receptor. Biochem.
Biophys.Res. Commun. 181: 184- 190, 1991.

GAM8297 367 EDNRA Hosoda, K.; Nakao, K.; Tamura, N.; Arai, H.; Ogawa, Y.; Suga, S.;Nakanishi, 3 B c
S.; Imura, H.: Organization, structure, chromosomal assignment,and
expression of the gene encoding the human endothelin- A receptor. J.Biol.
Chem. 267: 18797- 18804, 1992.

GAM8297 367 EDNRA Maggi, M.; Barni, T.; Fantoni, G.; Mancina, R.; Pupilli, C.; Luconi,M.; 3 B c
Crescioli, C.; Serio, M.; Vannelli, G. B.: Expression and biologicaleffects
of endothelin- 1 in human gonadotropin- releasing hormone- secretingneurons.
J. Clin. Endocr. Metab. 85: 1658- 1665, 2000.

GAM8297 367 EDNRA Okafor, M. C.; Delamere, N. A.: The inhibitory influence of endothelinon 3 B c
active sodium- potassium transport in porcine lens. Invest. Ophthal.Vis.
Sci. 42: 1018- 1023, 2001.

GAM8297 367 EDNRA Tzourio, C.; El Amrani, M.; Poirier, O.; Nicaud, V.; Bousser, M.- 3 B c
G.;Alperovitch, A.: Association between migraine and endothelin typeA
receptor (ETA - 231 A/G) gene polymorphism. Neurology 56: 1273- 1277,2001.

GAM8297 367 EDNRA Zeidel, M. L.; Brady, H. R.; Kone, B. C.; Gullans, S. R.; Brenner,B. M.: 3 B c
Endothelin, a peptide inhibitor of Na(+)- K(+)- ATPase in intactrenal
tubular epithelial cells. Am. J. Physiol. 257: C1101- C1107,1989.

GAM8297 367 FSTL1 Shibanuma, M.; Mashimo, J.; Mita, A.; Kuroki, T.; Nose, K.: Cloningfrom a 3 B c
mouse osteoblastic cell line of a set of transforming- growth- factor- beta-
1- regulated genes, one of which seems to encode a follistatin-
relatedpolypeptide. Europ. J. Biochem. 217: 13- 19, 1993.

GAM8297 367 FSTL1 Tanaka, M.; Ozaki, S.; Osakada, F.; Mori, K.; Okubo, M.; Nakao,K.: Cloning 3 B c
of follistatin- related protein as a novel autoantigenin systemic rheumatic
diseases. Int. Immun. 10: 1305- 1314, 1998.

GAM8297 367 FSTL1 Zwijsen, A.; Blockx, H.; van Arnhem, W.; Willems, J.; Fransen,L.; Devos, K.; 3 B c
Raymackers, J.; van de Voorde, A.; Slegers, H.: Characterizationof a rat C6
glioma- secreted follistatin- related protein (FRP): cloningand sequence of
the human homologue. Europ. J. Biochem. 225: 937- 946,1994.

GAM8297 367 G2A Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y.: 3 B c
Lysophosphatidylcholine as a ligand for the immunoregulatory receptorG2A.
Science 293: 702- 705, 2001.

GAM8297 367 G2A Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.;Harvill, E. 3 B c
T.; Jensen, E. R.; Miller, J. F.; Witte, O. N.: Micelacking the orphan G
protein- coupled receptor G2A develop a late- onsetautoimmune syndrome.
Immunity 14: 561- 571, 2001.

GAM8297 367 G2A Weng, Z.; Fluckiger, A.- C.; Nisitani, S.; Wahl, M. I.; Le, L. Q.;Hunter, C. 3 B c
A.; Fernal, A. A.; le Beau, M. M.; Witte, O. N.: A DNAdamage and stress
inducible G protein- coupled receptor blocks cellsin G2/M. Proc. Nat. Acad.
Sci. 95: 12334- 12339, 1998.

GAM8297 367 GPR87 Lee, D. K.; Nguyen, T.; Lynch, K. R.; Cheng, R.; Vanti, W. B.;Arkhitko, O.; 3 B c
Lewis, T.; Evans, J. F.; George, S. R.; O'Dowd, B. F.: Discovery and mapping
of ten novel G protein- coupled receptor genes. Gene 275:83- 91, 2001.

GAM8297 367 GPR87 Wittenberger, T.; Schaller, H. C.; Hellebrand, S.: An expressedsequence tag 3 B c
(EST) data mining strategy succeeding in the discoveryof new G- protein
coupled receptors. J. Molec. Biol. 307: 799- 813,2001.

GAM8297 367 GUK1 Brady, W. A.; Kokoris, M. S.; Fitzgibbon, M.; Black, M. E.: 3 B c
Cloning,characterization, and modeling of mouse and human guanylate kinases.
J.Biol. Chem. 271: 16734- 16740, 1996.

GAM8297 367 GUK1 Dallapiccola, B.; Lungarotti, M. S.; Falorni, A.; Magnani, M.;Dacha, M.: 3 B c
Evidence for the assignment of GUK1 gene locus to 1q32- q43segment from gene
dosage effect. Ann. Genet. 23: 83- 85, 1980.

GAM8297 367 GUK1 Meera Khan, P.: Personal Communication. Leiden, The Netherlands 1977. 3 B c

GAM8297 367 GUK1 Meera Khan, P.; Doppert, B. A.; Hagemeijer, A.; Westerveld, A.: The human 3 B c
loci for phosphopyruvate hydratase and guanylate kinaseare syntenic with the
PGD- PGM1 linkage group in man- Chinese hamstersomatic cell hybrids.
Cytogenet. Cell Genet. 13: 130- 131, 1974.

GAM8297 367 HDAC1 Bauer, W. R.; Hayes, J. J.; White, J. H.; Wolffe, A. P.: 3 B c
Nucleosomestructural changes due to acetylation. J. Molec. Biol. 236: 685-
690,1994.

GAM8297 367 HDAC1 Furukawa, Y.; Kawakami, T.; Sudo, K.; Inazawa, J.; Matsumine, A.;Akiyama, 3 B c
T.; Nakamura, Y.: Isolation and mapping of a human gene(RPD3L1) that is
homologous to RPD3, a transcription factor in Saccharomycescerevisiae.
Cytogenet. Cell Genet. 73: 130- 133, 1996.

GAM8297 367 HDAC1 Grignani, F.; De Matteis, S.; Nervi, C.; Tomassoni, L.; Gelmetti,V.; Cioce, 3 B c
M.; Fanelli, M.; Ruthardt, M.; Ferrara, F. F.; Zamir, I.;Seiser, C.;
Grignani, F.; Lazar, M. A.; Minucci, S.; Pelicci, P. G.: Fusion proteins of
the retinoic acid receptor- alpha recruit histonedeacetylase in
promyelocytic leukaemia. Nature 391: 815- 818, 1998.

GAM8297 367 HDAC1 Lee, D. Y.; Hayes, J. J.; Pruss, D.; Wolffe, A. P.: A positiverole for 3 B c
histone acetylation in transcription factor access to nucleosomalDNA. Cell
72: 73- 84, 1993.

GAM8297 367 HDAC1 Lin, R. J.; Nagy, L.; Inoue, S.; Shao, W.; Miller, W. H., Jr.;Evans, R. M.: 3 B c
Role of the histone deacetylase complex in acute promyelocyticleukaemia.
Nature 391: 811- 814, 1998.

GAM8297 367 HDAC1 Luo, J.; Su, F.; Chen, D.; Shiloh, A.; Gu, W.: Deacetylation ofp53 modulates 3 B c
its effect on cell growth and apoptosis. Nature 408:377- 381, 2000.

GAM8297 367 HDAC1 Magnaghi- Jaulin, L.; Groisman, R.; Naguibneva, I.; Robin, P.; Lorain,S.; Le 3 B c
Villain, J. P.; Troalen, F.; Trouche, D.; Harel- Bellan, A.: Retinoblastoma
protein represses transcription by recruiting a histonedeacetylase. Nature
391: 601- 605, 1998.

GAM8297 367 HDAC1 Taunton, J.; Hassig, C. A.; Schreiber, S. L.: A mammalian histonedeacetylase 3 B c
related to the yeast transcriptional regulator Rpd3p. Science 272:408- 411,
1996.

GAM8297 367 HDAC1 Vidal, M.; Gaber, R. F.: RPD3 encodes a second factor requiredto achieve 3 B c
maximum positive and negative transcriptional states inSaccharomyces
cerevisiae. Molec. Cell. Biol. 11: 6317- 6327, 1991.

GAM8297 367 HDAC1 Vidal, M.; Strich, R.; Esposito, R. E.; Gaber, R. F.: RPD1 (SIN3/UME4)is 3 B c
required for maximal activation and repression of diverse yeastgenes. Molec.
Cell. Biol. 11: 6306- 6316, 1991.

GAM8297 367 HDAC1 Wade, P. A.: Transcriptional control at regulatory checkpointsby histone 3 B c
deacetylases: molecular connections between cancer andchromatin. Hum. Molec.
Genet. 10: 693- 698, 2001.

GAM8297 367 HDAC1 Wolffe, A. P.: Histone deacetylase: a regulator of transcription. Science 272:371- 372, 1996. 3 B c

GAM8297 367 HDAC1 Zhang, Y.; Sun, Z.- W.; Iratni, R.; Erdjument- Bromage, H.; Tempst,P.; Hampsey, M.; Reinberg, D.: SAP30, a novel protein conserved betweenhuman and yeast, is a component of a histone deacetylase complex. Molec.Cell 1: 1021- 1031, 1998. 3 B c

GAM8297 367 HDAC1 Zhong, H.; May, M. J.; Jimi, E.; Ghosh, S.: The phosphorylationstatus of nuclear NF- kappa- B determines its association with CBP/p300or HDAC- 1. Molec. Cell 9: 625- 636, 2002. 3 B c

GAM8297 367 HHIP Bak, M.; Hansen, C.; Henriksen, K. F.; Tommerup, N.: The humanhedgehog- interacting protein gene: structure and chromosome mappingto 4q31.21- q31.3. Cytogenet. Cell Genet. 92: 300- 303, 2001. 3 B c

GAM8297 367 HHIP Chuang, P.- T.; McMahon, A. P.: Vertebrate hedgehog signallingmodulated by induction of a hedgehog- binding protein. Nature 397:617- 621, 1999. 3 B c

GAM8297 367 HSPA5 Hendershot, L. M.; Valentine, V. A.; Lee, A. S.; Morris, S. W.;Shapiro, D. N.: Localization of the gene encoding human BiP/GRP78,the endoplasmic reticulum cognate of the HSP70 family, to chromosome9q34. Genomics 20: 281- 284, 1994. 3 B c

GAM8297 367 HSPA5 Law, M. L.; Seeliger, M. B.; Lee, A. S.; Kao, F. T.: Genetic mappingof the structural gene coding for a glucose- regulated protein (GRP78)of 78k- dalton to the long arm of human chromosome 9. (Abstract) Cytogenet.Cell Genet. 37: 518- 519, 1984. 3 B c

GAM8297 367 HSPA5 Lee, A. S.; Delegeane, A. M.; Baker, V.; Chow, P. C.: Transcriptionalregulation of two genes specifically induced by glucose starvationin hamster mutant fibroblast cell line. J. Biol. Chem. 258: 597- 603,1983. 3 B c

GAM8297 367 HSPA5 Lee, A. S.; Delegeane, A.; Scharff, D.: Highly conserved glucose- regulatedprotein in hamster and chicken cells: preliminary characterizationof its cDNA clone. Proc. Nat. Acad. Sci. 78: 4922- 4925, 1981. 3 B c

GAM8297 367 HSPA5 Muresan, Z.; Arvan, P.: Enhanced binding to the molecular chaperoneBiP slows thyroglobulin export from the endoplasmic reticulum. Molec.Endocr. 12: 458- 467, 1998. 3 B c

GAM8297 367 HSPA5 Womack, J. E.: Personal Communication. College Station, Texas 2/26/1990. 3 B c

GAM8297 367 IL8RA Holmes, W. E.; Lee, J.; Kuang, W.- J.; Rice, G. C.; Wood, W. I.: Structure and functional expression of a human interleukin- 8 receptor. Science 253:1278- 1280, 1991. 3 B c

GAM8297 367 IL8RA Lloyd, A.; Modi, W.; Sprenger, H.; Cevario, S.; Oppenheim, J.;Kelvin, D.: Assignment of genes for interleukin- 8 receptors (IL8R)A and B to human chromosome band 2q35. Cytogenet. Cell Genet. 63:238- 240, 1993. 3 B c

GAM8297 367 IL8RA Mollereau, C.; Muscatelli, F.; Mattei, M.- G.; Vassart, G.; Parmentier,M.: The high- affinity interleukin 8 receptor gene (IL8RA) maps tothe 2q33- q36 region of the human genome: cloning of a pseudogene (IL8RBP)for the low- affinity receptor. Genomics 16: 248- 251, 1993. 3 B c

GAM8297 367 IL8RA Morris, S. W.; Nelson, N.; Valentine, M. B.; Shapiro, D. N.; Look,A. T.; Kozlosky, C. J.; Beckmann, M. P.; Cerretti, D. P.: Assignmentof the genes encoding human interleukin- 8 receptor types 1 and 2 andan interleukin- 8 receptor pseudogene to chromosome 2q35. Genomics 14:685- 691, 1992. 3 B c

GAM8297 367 IL8RA Palter, S. F.; Mulayim, N.; Senturk, L.; Arici, A.: Interleukin- 8in the human fallopian tube. J. Clin. Endocr. Metab. 86: 2660- 2667,2001. 3 B c

GAM8297 367 KCNA6 Albrecht, B.; Weber, K.; Pongs, O.: Characterization of a voltage- 3 B c
activatedK- channel gene cluster on human chromosome 12p13. Receptors
Channels 3:213- 220, 1995.

GAM8297 367 KCNA6 Grupe, A.; Schroter, K. H.; Ruppersberg, J. P.; Stocker, M.; Drewes,T.; 3 B c
Beckh, S.; Pongs, O.: Cloning and expression of a human voltage-
gatedpotassium channel: a novel member of the RCK potassium channel family.
EMBOJ. 9: 1749- 1756, 1990.

GAM8297 367 KCNA6 Klocke, R.; Roberds, S. L.; Tamkun, M. M.; Gronemeier, M.; Augustin,A.; 3 B c
Albrecht, B.; Pongs, O.; Jockusch, H.: Chromosomal mapping inthe mouse of
eight K(+)- channel genes representing the four Shaker- likesubfamilies
Shaker, Shab, Shaw, and Shal. Genomics 18: 568- 574,1993.

GAM8297 367 KLK10 Liu, X.- L.; Wazer, D. E.; Watanabe, K.; Band, V.: Identificationof a novel 3 B c
serine protease- like gene, the expression of which is down- regulatedduring
breast cancer progression. Cancer Res. 56: 3371- 3379, 1996.

GAM8297 367 KLK10 Polikoff, D.; Kuo, W.- L.; Cochran, J. F.; Wernick, M.; Kowbel,D.; Myambo, 3 B c
K.; Collins, C. C.: Assignment of protease, serine- like1 (PRSSL1) to human
chromosome 19q13 by in situ hybridization andradiation hybrid mapping.
Cytogenet. Cell Genet. 79: 147- 148, 1997.

GAM8297 367 KPNA3 Kohler, M.; Ansieau, S.; Prehn, S.; Leutz, A.; Haller, H.; Hartmann,E.: 3 B c
Cloning of two novel human importin- alpha subunits and analysisof the
expression pattern of the importin- alpha protein family. FEBSLett. 417:
104- 108, 1997.

GAM8297 367 KPNA3 Moore, M. S.; Blobel, G.: The two steps of nuclear import, targetingto the 3 B c
nuclear envelope and translocation through the nuclear pore,require
different cytosolic factors. Cell 69: 939- 950, 1992.

GAM8297 367 KPNA3 Takeda, S.; Fujiwara, T.; Shimizu, F.; Kawai, A.; Shinomiya, K.;Okuno, S.; 3 B c
Ozaki, K.; Katagiri, T.; Shimada, Y.; Nagata, M.; Watanabe,T.; Takaichi, A.;
Kuga, Y.; Suzuki, M.; Hishigaki, H.; Takahashi,E.; Shin, S.; Nakamura, Y.;
Hirai, Y.: Isolation and mapping of karyopherinalpha- 3 (KPNA3), a human
gene that is highly homologous to genes encodingXenopus importin, yeast SRP1
and human RCH1. Cytogenet. Cell Genet. 76:87- 93, 1997.

GAM8297 367 KRT8 Casanova, M. L.; Bravo, A.; Ramirez, A.; Morreale de Escobar, G.;Were, F.; 3 B c
Merlino, G.; Vidal, M.; Jorcano, J. L.: Exocrine pancreaticdisorders in
transsgenic (sic) mice expressing human keratin 8. J.Clin. Invest. 103:
1587- 1595, 1999.

GAM8297 367 KRT8 Jackson, B. W.; Grund, C.; Schmid, E.; Burke, K.; Franke, W.; Illmensee,K.: 3 B c
Formation of cytoskeletal elements during mouse embryogenesis:intermediate
filaments of the cytokeratin type and desmosomes in preimplantationembryos.
Differentiation 17: 161- 179, 1980.

GAM8297 367 KRT8 Ku, N.- O.; Gish, R.; Wright, T. L.; Omary, M. B.: Keratin 8 mutationsin 3 B c
patients with cryptogenic liver disease. New Eng. J. Med. 344:1580- 1587,
2001.

GAM8297 367 KRT8 Ku, N.- O.; Wright, T. L.; Terrault, N. A.; Gish, R.; Omary, M.B.: Mutation 3 B c
of human keratin 18 in association with cryptogeniccirrhosis. J. Clin.
Invest. 99: 19- 23, 1997.

GAM8297 367 KRT8 Moll, R.; Franke, W. W.; Schiller, D. L.; Geiger, B.; Krepler,R.: The 3 B c
catalog of human cytokeratins: patterns of expression innormal epithelia,
tumors and cultured cells. Cell 31: 11- 24, 1982.

GAM8297 367 KRT8 Waseem, A.; Alexander, C. M.; Steel, J. B.; Lane, E. B.: Embryonicsimple 3 B c
epithelial keratins 8 and 18: chromosomal location emphasizesdifference from

other keratin pairs. New Biologist 2: 464- 478, 1990.

GAM8297 367 KRT8 Yamamoto, R.; Kao, L.- C.; McKnight, C. E.; Strauss, J. F., III: Cloning and sequence of cDNA for human placental cytokeratin 8:regulation of the mRNA in trophoblastic cells by cAMP. Molec. Endocr. 4:370- 374, 1990. 3 B c

GAM8297 367 LASS1 Jiang, J. C.; Kirchman, P. A.; Zagulski, M.; Hunt, J.; Jazwinski,S. M.: Homologs of the yeast longevity gene LAG1 in Caenorhabditiselegans and human. Genome Res. 8: 1259- 1272, 1998. 3 B c

GAM8297 367 LASS1 Lee, S.- J.: Expression of growth/differentiation factor 1 in thenervous system: conservation of a bicistronic structure. Proc. Nat.Acad. Sci. 88: 4250- 4254, 1991. 3 B c

GAM8297 367 MADH7 Dong, C.; Zhu, S.; Wang, T.; Yoon, W.; Li, Z.; Alvarez, R. J.;ten Dijke, P.; White, B.; Wigley, F. M.; Goldschmidt- Clermont, P.J.: Deficient Smad7 expression: a putative molecular defect in scleroderma. Proc.Nat. Acad. Sci. 99: 3908- 3913, 2002. 3 B c

GAM8297 367 MADH7 Kavsak, P.; Rasmussen, R. K.; Causing, C. G.; Bonni, S.; Zhu, H.;Thomsen, G. H.; Wrana, J. L.: Smad7 binds to Smurf2 to form an E3ubiquitin ligase that targets the TGF- beta receptor for degradation. Molec.Cell 6: 1365- 1375, 2000. 3 B c

GAM8297 367 MADH7 Lallemand, F.; Mazars, A.; Prunier, C.; Bertrand, F.; Kornprost,M.; Gallea, S.; Roman- Roman, S.; Cherqui, G.; Atfi, A.: Smad7 inhibitsthe survival nuclear factor kappa- B and potentiates apoptosis in epithelialcells. Oncogene 20: 879- 884, 2001. 3 B c

GAM8297 367 MADH7 Roijer, E.; Moren, A.; ten Dijke, P.; Stenman, G.: Assignmentof the Smad7 gene (MADH7) to human chromosome 18q21.1 by fluorescencein situ hybridization. Cytogenet. Cell Genet. 81: 189- 190, 1998. 3 B c

GAM8297 367 MADH7 Topper, J. N.; Cai, J.; Qiu, Y.; Anderson, K. R.; Xu, Y.- Y.; Deeds,J. D.; Feeley, R.; Gimeno, C. J.; Woolf, E. A.; Tayber, O.; Mays,G. G.; Sampson, B. A.; Schoen, F. J.; Gimbrone, M. A., Jr.; Falb,D.: Vascular MADs: two novel MAD- related genes selectively inducibleby flow in human vascular endothelium. Proc. Nat. Acad. Sci. 94:9314- 9319, 1997. 3 B c

GAM8297 367 MYO1D Hasson, T.; Skowron, J. F.; Gilbert, D. J.; Avraham, K. B.; Perry,W. L.; Bement, W. M.; Anderson, B. L.; Sherr, E. H.; Chen, Z.- Y.;Greene, L. A.; Ward, D. C.; Corey, D. P.; Mooseker, M. S.; Copeland,N. G.; Jenkins, N. A.: Mapping of unconventional myosins in mouseand human. Genomics 36: 431- 439, 1996. 3 B c

GAM8297 367 MYO1D Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.;Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction of thecoding sequences of unidentified human genes. XI. The complete sequencesof 100 new cDNA clones from brain which code for large proteins invitro. DNA Res. 5: 277- 286, 1998. 3 B c

GAM8297 367 MYO3A Dose, A. C.; Burnside, B.: Cloning and chromosomal localizationof a human class III myosin. Genomics 67: 333- 342, 2000. 3 B c

GAM8297 367 MYO3A Walsh, T.; Walsh, V.; Vreugde, S.; Hertzano, R.; Shahin, H.; Haika,S.; Lee, M. K.; Kanaan, M.; King, M.- C.; Avraham, K. B.: From flies'eyes to our ears: mutations in a human class III myosin cause progressivenonsyndromic hearing loss DFNB30. Proc. Nat. Acad. Sci. 99: 7518- 7523,2002. 3 B c

GAM8297 367 NDP Anderson, S. R.; Warburg, M.: Norrie's disease. Arch. Ophthal. 66:614- 618, 1961. 3 B c

GAM8297 367 NDP Bergen, A. A. B.; Wapenaar, M. C.; Schuurman, E. J. M.; Diergaarde,P. J.; Lerach, H.; Monaco, A. P.; Bakker, E.; Bleeker- Wagemakers,E. M.; van Ommen, 3 B c

G. J. B.: Detection of a new submicroscopic Norriedisease deletion interval with a novel DNA probe isolated by differentialAlu PCR fingerprint cloning. Cytogenet. Cell Genet. 62: 231- 235,1993.

GAM8297 367 NDP Berger, W.; Meindl, A.; van de Pol, T. J. R.; Cremers, F. P. M.;Ropers, H. H.; Doerner, C.; Monaco, A.; Bergen, A. A. B.; Lebo, R.;Warburg, M.; Zergollern, L.; Lorenz, B.; Gal, A.; Bleeker- Wagemakers,E. M.; Meitinger, T.: Isolation of a candidate gene for Norrie diseaseby positional cloning. Nature Genet. 1: 199- 203, 1992. 3 B c

GAM8297 367 NDP Berger, W.; van de Pol, D.; Bachner, D.; Oerlemans, F.; Winkens,H.; Hameister, H.; Wieringa, B.; Hendriks, W.; Ropers, H.- H.: Ananimal model for Norrie disease (ND): gene targeting of the mouseND gene. Hum. Molec. Genet. 5: 51- 59, 1996. 3 B c

GAM8297 367 NDP Berger, W.; van de Pol, D.; Warburg, M.; Gal, A.; Bleeker- Wagemakers,L.; de Silva, H.; Meindl, A.; Meitinger, T.; Cremers, F.; Ropers,H.- H.: Mutations in the candidate gene for Norrie disease. Hum.Molec. Genet. 1: 461- 465, 1992. 3 B c

GAM8297 367 NDP Black, G. C. M.; Perveen, R.; Bonshek, R.; Cahill, M.; Clayton- Smith,J.; Lloyd, I. C.; McLeod, D.: Coats' disease of the retina (unilateralretinal telangiectasis) caused by somatic mutation in the NDP gene:a role for norrin in retinal angiogenesis. Hum. Molec. Genet. 8:2031- 2035, 1999. 3 B c

GAM8297 367 NDP Bleeker- Wagemakers, L. M.; Friedrich, U.; Gal, A.; Wienker, T.F.; Warburg, M.; Ropers, H.- H.: Close linkage between Norrie disease,a cloned DNA sequence from the proximal short arm, and the centromereof the X chromosome. Hum. Genet. 71: 211- 214, 1985. 3 B c

GAM8297 367 NDP Chen, Z.- Y.; Battinelli, E. M.; Fielder, A.; Bundey, S.; Sims,K.; Breakefield, X. O.; Craig, I. W.: A mutation in the Norrie diseasegene (NDP) associated with X- linked familial exudative vitreoretinopathy. NatureGenet. 5: 180- 183, 1993. 3 B c

GAM8297 367 NDP Chen, Z.- Y.; Battinelli, E. M.; Hendriks, R. W.; Powell, J. F.;Middleton- Price, H.; Sims, K. B.; Breakefield, X. O.; Craig, I. W.: Norrie disease gene: characterization of deletions and possiblefunction. Genomics 16: 533- 535, 1993. 3 B c

GAM8297 367 NDP Chen, Z.- Y.; Battinelli, E. M.; Woodruff, G.; Young, I.; Breakefield,X. O.; Craig, I. W.: Characterization of a mutation within the NDPgene in a family with a manifesting female carrier. Hum. Molec. Genet. 2:1727- 1729, 1993. 3 B c

GAM8297 367 NDP Chen, Z.- Y.; Hendriks, R. W.; Jobling, M. A.; Powell, J. F.; Breakefield,X. O.; Sims, K. B.; Craig, I. W.: Isolation and characterizationof a candidate gene for Norrie disease. Nature Genet. 1: 204- 208,1992. 3 B c

GAM8297 367 NDP Chen, Z.- Y.; Sims, K. B.; Coleman, M.; Donnai, D.; Monaco, A.;Breakefield, X. O.; Davies, K. E.; Craig, I. W.: Characterizationof a YAC containing part or all of the Norrie disease locus. Hum.Molec. Genet. 1: 161- 164, 1992. 3 B c

GAM8297 367 NDP Chynn, E. W.; Walton, D. S.; Hahn, L. B.; Dryja, T. P.: Norriedisease: diagnosis of a simplex case by DNA analysis. Arch. Ophthal. 114:1136- 1138, 1996. 3 B c

GAM8297 367 NDP Clarke, E.: 'Pseudo- glioma' in both eyes. Trans. Ophthal. Soc.U.K. 18: 136- 138, 1898. 3 B c

GAM8297 367 NDP Collins, F. A.; Murphy, D. L.; Reiss, A. L.; Sims, K. B.; Lewis,J. G.; Freund, L.; Karoum, F.; Zhu, D.; Maumenee, I. H.; Antonarakis,S. E.: Clinical, biochemical, and neuropsychiatric evaluation ofa patient with a contiguous gene syndrome due to a microdeletion Xp11.3including the Norrie 3 B c

disease locus and monoamine oxidase (MAOA andMAOB) genes. Am. J. Med. Genet. 42: 127- 134, 1992.

GAM8297 367 NDP Dahlberg- Parrow, R.: Congenital sex- linked pseudoglioma and gravemental deficiency. Acta Ophthal. 34: 250- 254, 1956. 3 B c

GAM8297 367 NDP de la Chapelle, A.; Sankila, E.- M.; Lindlof, M.; Aula, P.; Norio,R.: Norrie disease caused by a gene deletion allowing carrier detectionand prenatal diagnosis. Clin. Genet. 28: 317- 320, 1985. 3 B c

GAM8297 367 NDP Diergaarde, P. J.; Wieringa, B.; Bleeker- Wagemakers, E. M.; Sims,K. B.; Breakefield, X. O.; Ropers, H.- H.: Physical fine- mapping ofa deletion spanning the Norrie gene. Hum. Genet. 84: 22- 26, 1989. 3 B c

GAM8297 367 NDP Donnai, D.; Mountford, R. C.; Read, A. P.: Norrie disease resultingfrom a gene deletion: clinical features and DNA studies. J. Med.Genet. 25: 73- 78, 1988. 3 B c

GAM8297 367 NDP Dudgeon, J.: Familial exudative vitreo- retinopathy. Trans. Ophthal.Soc. U.K. 99: 45- 49, 1979. 3 B c

GAM8297 367 NDP Duke- Elder, J. R.: Pseudoglioma in children: aspects of clinicaland pathological diagnosis. Sth. Med. J. 51: 754- 759, 1958. 3 B c

GAM8297 367 NDP Forssman, H.: Mental deficiency and pseudoglioma, a syndromeinherited as an X- linked recessive. Am. J. Ment. Defic. 64: 984- 987,1960. 3 B c

GAM8297 367 NDP Fuchs, S.; Kellner, U.; Wedemann, H.; Gal, A.: Missense mutation(Arg121Trp) in the Norrie disease gene associated with X- linked exudativevitreoretinopathy. Hum. Mutat. 6: 257- 259, 1995. 3 B c

GAM8297 367 NDP Fuchs, S.; Xu, S. Y.; Caballero, M.; Salcedo, M.; La O, A.; Wedemann,H.; Gal, A.: A missense point mutation (Leu13Arg) of the Norrie diseasegene in a large Cuban kindred with Norrie disease. Hum. Molec. Genet. 3:655- 656, 1994. 3 B c

GAM8297 367 NDP Fullwood, P.; Jones, J.; Bundey, S.; Dudgeon, J.; Fielder, A.R.; Kilpatrick, M. W.: X linked exudative vitreoretinopathy: clinicalfeatures and genetic linkage analysis. Brit. J. Ophthal. 77: 168- 170,1993. 3 B c

GAM8297 367 NDP Gal, A.; Bleeker- Wagemakers, L.; Wienker, T. F.; Warburg, M.;Ropers, H.- H.: Localization of the gene for Norrie disease by linkageto the DXS7 locus. (Abstract) Cytogenet. Cell Genet. 40: 633, 1985. 3 B c

GAM8297 367 NDP Gal, A.; Stolzenberger, C.; Wienker, T.; Wieacker, P.; Ropers,H.- H.; Friedrich, U.; Bleeker- Wagemakers, L.; Pearson, P.; Warburg,M.: Norrie's disease: close linkage with genetic markers from theproximal short arm of the X chromosome. Clin. Genet. 27: 282- 283,1985. 3 B c

GAM8297 367 NDP Gal, A.; Uhlhaas, S.; Glaser, D.; Grimm, T.: Prenatal exclusionof Norrie disease with flanking DNA markers. Am. J. Med. Genet. 31:449- 453, 1988. 3 B c

GAM8297 367 NDP Gal, A.; Wieringa, B.; Smeets, D. F. C. M.; Bleeker- Wagemakers,L.; Ropers, H. H.: Submicroscopic interstitial deletion of the Xchromosome explains a complex genetic syndrome dominated by Norriedisease. Cytogenet. Cell Genet. 42: 219- 224, 1986. 3 B c

GAM8297 367 NDP Harendra de Silva, D. G.; de Silva, D. B. K.: Norrie's diseasein an Asian family. Brit. J. Ophthal. 72: 62- 64, 1988. 3 B c

GAM8297 367 NDP Harmon, D. L.; Gardner- Medwin, D.; Stirling, J. L.: Two new mutationsin a late infantile Tay- Sachs patient are both in exon 1 of the beta- hexosaminidasealpha subunit gene. J. Med. Genet. 30: 123- 128, 1993. 3 B c

GAM8297 367 NDP Hattori, Y.; Yamashiro, Y.; Ohba, Y.; Miyaji, T.; Morishita, M.;Yamamoto, K.; Yamamoto, K.; Narai, S.; Kimura, A.: A new beta- thalassemiamutation (initiation codon ATG- to- GTG) found in the Japanese population. Hemoglobin 3 B c

15:317- 325, 1991.

GAM8297 367 NDP Holmes, L. B.: Norrie's disease- - an X- linked syndrome of 3 B c
retinalmalformation, mental retardation and deafness. New Eng. J. Med.
284:367- 368, 1971.

GAM8297 367 NDP Isashiki, Y.; Ohba, N.; Yanagita, T.; Hokita, N.; Doi, N.; Nakagawa,M.; 3 B c
Ozawa, M.; Kuroda, N.: Novel mutation at the initiation codonin the Norrie
disease gene in two Japanese families. Hum. Genet. 95:105- 108, 1995.

GAM8297 367 NDP Isashiki, Y.; Ohba, N.; Yanagita, T.; Hokita, N.; Hotta, Y.; Hayakawa,M.; 3 B c
Fujiki, K.; Tanabe, U.: Mutations in the Norrie disease gene:a new mutation
in a Japanese family. (Letter) Brit. J. Ophthal. 79:703- 708, 1995.

GAM8297 367 NDP Johnson, K.; Mintz- Hittner, H. A.; Conley, Y. P.; Ferrell, R.E.: X- linked 3 B c
exudative vitreoretinopathy caused by an arginine toleucine substitution
(R121L) in the Norrie disease protein. Clin.Genet. 50: 113- 115, 1996.

GAM8297 367 NDP Johnston, S. S.; Hanna, J. E.; Nevin, N. C.; Bryars, J. H.: Norrie'sdisease. 3 B c
Birth Defects Orig. Art. Ser. 18(6): 729- 738, 1982.

GAM8297 367 NDP Katayama, S.; Wohlferd, M.; Golbus, M. S.: First demonstrationof 3 B c
recombination between the gene for Norrie disease and probe L1.28. Am.J.
Med. Genet. 30: 967- 970, 1988.

GAM8297 367 NDP Kivlin, J. D.; Sanborn, G. E.; Wright, E.; Cannon, L.; Carey,J.: Further 3 B c
linkage data on Norrie disease. Am. J. Med. Genet. 26:733- 736, 1987.

GAM8297 367 NDP Lindsay, S.; Thiselton, D. L.; Bateman, J. B.; Ngo, J. T.; Sparkes,R. S.; 3 B c
Coleman, M.; Davies, K. E.; Bhattacharya, S. S.: Localisationof the gene for
Norrie disease to between DXS7 and DXS426 on Xp. Hum.Genet. 88: 349- 350,
1992.

GAM8297 367 NDP Meindl, A.; Berger, W.; Meitinger, T.; van de Pol, D.; Achatz,H.; Dorner, 3 B c
C.; Haasemann, M.; Hellebrand, H.; Gal, A.; Cremers, F.;Ropers, H.- H.:
Norrie disease is caused by mutations in an extracellularprotein resembling
C- terminal globular domain of mucins. Nature Genet. 2:139- 143, 1992.

GAM8297 367 NDP Meindl, A.; Lorenz, B.; Achatz, H.; Hellebrand, H.; Schmitz- Valckenberg,P.; 3 B c
Meitinger, T.: Missense mutations in the NDP gene in patientswith a less
severe course of Norrie disease. Hum. Molec. Genet. 4:489- 490, 1995.

GAM8297 367 NDP Meitinger, T.; Meindl, A.; Bork, P.; Rost, B.; Sander, C.; Haasemann,M.; 3 B c
Murken, J.: Molecular modeling of the Norrie disease proteinpredicts a
cystine knot growth factor tertiary structure. NatureGenet. 5: 376- 380,
1993.

GAM8297 367 NDP Moreira- Filho, C. A.; Neustein, I.: A presumptive new variantof Norrie's 3 B c
disease. J. Med. Genet. 16: 125- 128, 1979.

GAM8297 367 NDP Nance, W. E.; Hara, S.; Hansen, A.; Elliott, J.; Lewis, M.; Chown,B.: 3 B c
Genetic linkage studies in a Negro kindred with Norrie's disease. Am.J. Hum.
Genet. 21: 423- 429, 1969.

GAM8297 367 NDP Ngo, J. T.; Bateman, J. B.; Cortessis, V.; Sparkes, R. S.; Mohandas,T.; 3 B c
Inana, G.; Spence, M. A.: Norrie disease: linkage analysis usinga 4.2- kb
RFLP detected by a human ornithine aminotransferase cDNAprobe. Genomics 4:
539- 545, 1989.

GAM8297 367 NDP Ngo, J. T.; Spence, M. A.; Cortessis, V.; Sparkes, R. S.; Bateman,J. B.: 3 B c
Recombinational event between Norrie disease and DXS7 loci. Clin.Genet. 34:
43- 47, 1988.

GAM8297 367 NDP Ngo, J.; Spence, M. A.; Cortessis, V.; Bateman, J. B.; Sparkes,R. S.: 3 B c
Duplicate report crossing over in Norrie disease family. (Letter) Am.J. Med.
Genet. 33: 286, 1989.

GAM8297 367 NDP Norrie, G.: Nogle Blindhedsaarsager: en oversigt. Hospitalstidende 76:141- 3 B c
147, 1933.
GAM8297 367 NDP Ohba, N.; Yamashita, T.: Primary vitreoretinal dysplasia resemblingNorrie's 3 B c
disease in a female: association with X autosome chromosomaltranslocation.
Brit. J. Ophthal. 70: 64- 71, 1986.
GAM8297 367 NDP Patten, J. L.; Johns, D. R.; Valle, D.; Eil, C.; Gruppuso, P.A.; Steele, G.; 3 B c
Smallwood, P. M.; Levine, M. A.: Mutation in thegene encoding the
stimulatory G protein of adenylate cyclase in Albright'shereditary
osteodystrophy. New Eng. J. Med. 322: 1412- 1419, 1990.
GAM8297 367 NDP Phillips, C. I.; Newton, M.; Duvall, J.; Holloway, S.; Levy, A.M.: Probably 3 B c
Norrie's disease due to mutation: two sporadic sibshipsof two males each, a
necropsy of one case, and, given Norrie's disease,a calculation of the gene
mutation frequency. Brit. J. Ophthal. 70:305- 313, 1986.
GAM8297 367 NDP Rehm, H. L.; Gutierrez- Espeleta, G. A.; Garcia, R.; Jimenez, G.;Khetarpal, 3 B c
U.; Priest, J. M.; Sims, K. B.; Keats, B. J. B.; Morton,C. C.: Norrie
disease gene mutation in a large Costa Rican kindredwith a novel phenotype
including venous insufficiency. Hum. Mutat.9: 402- 408, 1997.
GAM8297 367 NDP Schuback, D. E.; Chen, Z. Y.; Craig, I. W.; Breakefield, X. O.;Sims, K. B.: 3 B c
Mutations in the Norrie disease gene. Hum. Mutat. 5:285- 292, 1995.
GAM8297 367 NDP Shastry, B. S.: Identification of a recurrent missense mutationin the Norrie 3 B c
disease gene associated with a simplex case of exudativevitreoretinopathy.
Biochem. Biophys. Res. Commun. 246: 35- 38, 1998.
GAM8297 367 NDP Shastry, B. S.; Hejtmancik, J. F.; Plager, D. A.; Hartzer, M.K.; Trese, M. 3 B c
T.: Linkage and candidate gene analysis in X- linkedfamilial exudative
vitreoretinopathy. Genomics 27: 341- 344, 1995.
GAM8297 367 NDP Shastry, B. S.; Hejtmancik, J. F.; Trese, M. T.: Identificationof novel 3 B c
missense mutations in the Norrie disease gene associatedwith one X- linked
and four sporadic cases of familial exudative vitreoretinopathy. Hum.Mutat.
9: 396- 401, 1997.
GAM8297 367 NDP Sims, K. B.; de la Chapelle, A.; Norio, R.; Sankila, E.- M.; Hsu,Y.- P. P.; 3 B c
Rinehart, W. B.; Corey, T. J.; Ozelius, L.; Powell, J. F.;Bruns, G.;
Gusella, J. F.; Murphy, D. L.; Breakefield, X. O.: Monoamineoxidase
deficiency in males with an X chromosome deletion. Neuron 2:1069- 1076,
1989.
GAM8297 367 NDP Sims, K. B.; Lebo, R. V.; Benson, G.; Shalish, C.; Schuback, D.;Chen, Z. Y.; 3 B c
Bruns, G.; Craig, I. W.; Golbus, M. S.; Breakefield,X. O.: The Norrie
disease gene maps to a 150 kb region on chromosomeXp11.3. Hum. Molec. Genet.
1: 83- 89, 1992.
GAM8297 367 NDP Sims, K. B.; Ozelius, L.; Corey, T.; Rinehart, W. B.; Liberfarb,R.; Haines, 3 B c
J.; Chen, W. J.; Norio, R.; Sankila, E.; de la Chapelle,A.; Murphy, D. L.;
Gusella, J.; Breakefield, X. O.: Norrie diseasegene is distinct from the
monoamine oxidase genes. Am. J. Hum. Genet. 45:424- 434, 1989.
GAM8297 367 NDP Taylor, P. J.; Coates, T.; Newhouse, M. L.: Episkopi blindness:hereditary 3 B c
blindness in a Greek Cypriot family. Brit. J. Ophthal. 43:340- 344, 1959.
GAM8297 367 NDP Torrente, I.; Mangino, M.; Gennarelli, M.; Novelli, G.; Giannotti,A.; 3 B c
Vadala, P.; Dallapiccola, B.: Two new missense mutations (A105Tand C110G) in
the norrin gene in two Italian families with Norriedisease and familial
exudative vitreoretinopathy. (Letter) Am. J.Med. Genet. 72: 242- 244, 1997.
GAM8297 367 NDP Walker, J. L.; Dixon, J.; Fenton, C. R.; Hungerford, J.; Lynch,S. A.; 3 B c
Stenhouses, S. A. R.; Christian, A.; Craig, I. W.: Two newmutations in exon

3 of the NDP gene: S73X and S101F associated withsevere and less severe ocular phenotype, respectively. Hum. Mutat. 9:53- 56, 1997.

GAM8297 367 NDP Warburg, M.: Norrie's disease (atrofia bulborum hereditaria). ActaOphthal. 3 B c 41: 134- 146, 1963.

GAM8297 367 NDP Warburg, M.: Norrie's disease, a congenital progressive oculo- acoustico- 3 B c cerebraldegeneration. Acta Ophthal. 89 (suppl.): 1- 147, 1966.

GAM8297 367 NDP Warburg, M.: Norrie's disease: a new hereditary bilateral pseudotumourof the 3 B c retina. Acta Ophthal. (Copenh) 39: 757- 772, 1961.

GAM8297 367 NDP Warburg, M.: Personal Communication. Copenhagen, Denmark 1966. 3 B c

GAM8297 367 NDP Warburg, M.; Hauge, M.; Sanger, R.: Norrie's disease and theXg blood group 3 B c system: linkage data. Acta Genet. Statist. Med. 15:103- 115, 1965.

GAM8297 367 NDP Whitnall, S. E.; Norman, R. M.: Microphthalmia and the visualpathways: a 3 B c case associated with blindness and imbecility, and sex- linked. Brit.J. Ophthal. 24: 229- 244, 1940.

GAM8297 367 NDP Wilson, W. M. G.: Congenital blindness (pseudoglioma) occurringas a sex- 3 B c linked developmental anomaly. Canad. Med. Assoc. J. 60:580- 584, 1949.

GAM8297 367 NDP Wolff, G.; Mayerova, A.; Wienker, T. F.; Atalianis, P.; Ioannou,P.; Warburg, 3 B c M.: Clinical reinvestigation and linkage analysis inthe family with Episkopi blindness (Norrie disease). J. Med. Genet. 29:816- 819, 1992.

GAM8297 367 NDP Wong, F.; Goldberg, M. F.; Hao, Y.: Identification of a nonsensemutation at 3 B c codon 128 of the Norrie's disease gene in a male infant. Arch.Ophthal. 111: 1553- 1557, 1993.

GAM8297 367 NDP Woodruff, G.; Newbury- Ecob, R.; Plaha, D. S.; Young, I. D.: 3 B c Manifestingheterozygosity in Norrie's disease?. Brit. J. Ophthal. 77: 813- 814,1993.

GAM8297 367 NDP Zhu, D.; Antonarakis, S. E.; Schmeckpeper, B. J.; Diergaarde,P. J.; Greb, A. 3 B c E.; Maumenee, I. H.: Microdeletion in the X- chromosomeand prenatal diagnosis in a family with Norrie disease. Am. J. Med.Genet. 33: 485- 488, 1989.

GAM8297 367 NFKBIL1 Albertella, M. R.; Campbell, R. D.: Characterization of a novelgene in the 3 B c human major histocompatibility complex that encodes apotential new member of the I kappa B family of proteins. Hum. Molec.Genet. 3: 793- 799, 1994.

GAM8297 367 NFKBIL1 Allcock, R. J. N.; Christiansen, F. T.; Price, P.: The centralMHC gene IKBL 3 B c carries a structural polymorphism that is associatedwith HLA- A3,B7,DR15. Immunogenetics 49: 660- 665, 1999.

GAM8297 367 NKTR Anderson, S. K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, 3 B c J. R.: A cyclophilin- related protein involved in thefunction of natural killer cells. Proc. Nat. Acad. Sci. 90: 542- 546,1993.

GAM8297 367 NKTR Frey, J. L.; Bino, T.; Kantor, R. R. S.; Segal, D. M.; Giardina,S. L.; 3 B c Roder, J.; Anderson, S.; Ortaldo, J. R.: Mechanism of targetcell recognition by natural killer cells: characterization of a noveltriggering molecule restricted to CD3- large granular lymphocytes. J.Exp. Med. 174: 1527- 1536, 1991.

GAM8297 367 NKTR Rinfret, A.; Anderson, S. K.: IL- 2 regulates the expression ofthe NK- TR 3 B c gene via an alternate RNA splicing mechanism. Molec. Immun. 30:1307- 1313, 1993.

GAM8297 367 NKTR Simons- Evelyn, M.; Young, H. A.; Anderson, S. K.: Characterizationof the 3 B c mouse Nktr gene and promoter. Genomics 40: 94- 100, 1997.

GAM8297 367 NKTR Young, H. A.; Jenkins, N. A.; Copeland, N. G.; Simek, S.; Lerman,M. I.; 3 B c Zbar, B.; Glenn, G.; Ortaldo, J. R.; Anderson, S. K.: Localizationof a novel

natural killer triggering receptor locus to human chromosome3p23- p21 and mouse chromosome 9. Genomics 16: 548- 549, 1993.

GAM8297 367 OAS3 Hovanessian, A. G.; Laurent, A. G.; Chebath, J.; Galabru, J.; Robert,N.; Svab, J.: Identification of 69- kd and 100- kd forms of 2- 5A synthetasein interferon- treated human cells by specific monoclonal antibodies. EMBOJ. 6: 1273- 1280, 1987. 3 B c

GAM8297 367 OAS3 Hovnanian, A.; Rebouillat, D.; Mattei, M.- G.; Levy, E. R.; Marie,I.; Monaco, A. P.; Hovanessian, A. G.: The human 2- prime,5- prime-oligoadenylatesynthetase locus is composed of three distinct genes clustered onchromosome 12q24.2 encoding the 100- , 69- , and 40- kDa forms. Genomics 52:267- 277, 1998. 3 B c

GAM8297 367 PCDH11X Blanco, P.; Sargent, C. A.; Boucher, C. A.; Mitchell, M.; Affara,N. A.: Conservation of PCDHX in mammals; expression of X/Y genespredominantly in brain. Mammalian Genome 11: 906- 914, 2000. 3 B c

GAM8297 367 PCDH11X Ciccodicola, A.; D'Esposito, M.; Esposito, T.; Gianfrancesco, F.;Migliaccio, C.; Miano, M. G.; Matarazzo, M. R.; Vacca, M.; Franze,A.; Cuccurese, M.; Cocchia, M.; Curci, A.; and 9 others: Differentiallyregulated and evolved genes in the fully sequenced Xq/Yq pseudoautosomalregion. Hum. Molec. Genet. 9: 395- 401, 2000. 3 B c

GAM8297 367 PCDH11X Mumm, S.; Molini, B.; Terrell, J.; Srivastava, A.; Schlessinger,D.: Evolutionary features of the 4- Mb Xq21.3 XY homology region revealedby a map at 60- kb resolution. Genome Res. 7: 307- 314, 1997. 3 B c

GAM8297 367 PCDH11X Schwartz, A.; Chan, D. C.; Brown, L. G.; Alagappan, R.; Pettay,D.; Disteche, C.; McGillivray, B.; de la Chapelle, A.; Page, D. C.: Reconstructing hominid Y evolution: X- homologous block, createdby X- Y transposition, was disrupted by Yp inversion through LINE- LINErecombination. Hum. Molec. Genet. 7: 1- 11, 1998. 3 B c

GAM8297 367 PCDH11X Tilford, C. A.; Kuroda- Kawaguchi, T.; Skaletsky, H.; Rozen, S.;Brown, L. G.; Rosenberg, M.; McPherson, J. D.; Wylie, K.; Sekhon,M.; Kucaba, T. A.; Waterston, R. H.; Page, D. C.: A physical mapof the human Y chromosome. Nature 409: 943- 945, 2001. 3 B c

GAM8297 367 PCDH11X Yoshida, K.; Sugano, S.: Identification of a novel protocadheringene (PCDH11) on the human XY homology region in Xq21.3. Genomics 62:540- 543, 1999. 3 B c

GAM8297 367 PCDHGA12 Matsuyoshi, N.; Imamura, S.: Multiple cadherins are expressedin human fibroblasts. Biochem. Biophys. Res. Commun. 235: 355- 358,1997. 3 B c

GAM8297 367 PCDHGA12 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998. 3 B c

GAM8297 367 PCDHGA12 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGA3 Wu, Q.; Maniatis, T.: A striking organization of a large familyof human neural cadherin like cell adhesion genes. Cell 97: 779- 790,1999. 3 B c

GAM8297 367 PCDHGA3 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGA5 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997. 3 B c

GAM8297 367 PCDHGA5 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGA8 Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VII. The completesequences of 100 new cDNA clones from brain which can code for largeproteins in vitro. DNA Res. 4: 141- 150, 1997. 3 B c

GAM8297 367 PCDHGA8 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGB4 Matsuyoshi, N.; Imamura, S.: Multiple cadherins are expressedin human fibroblasts. Biochem. Biophys. Res. Commun. 235: 355- 358,1997. 3 B c

GAM8297 367 PCDHGB4 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGB7 Matsuyoshi, N.; Tanaka, T.; Toda, K.; Imamura, S.: Identificationof novel cadherins expressed in human melanoma cells. J. Invest.Derm. 108: 908- 913, 1997. 3 B c

GAM8297 367 PCDHGB7 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGC3 Sago, H.; Kitagawa, M.; Obata, S.; Mori, N.; Taketani, S.; Rochelle,J. M.; Seldin, M. F.; Davidson, M.; St. John, T.; Suzuki, S. T.:Cloning, expression, and chromosomal localization of a novel cadherin-relatedprotein, protocadherin- 3. Genomics 29: 631- 640, 1995. 3 B c

GAM8297 367 PCDHGC3 Sano, K.; Tanihara, H.; Heimark, R. L.; Obata, S.; Davidson, M.;St. John, T.; Taketani, S.; Suzuki, S.: Protocadherins: a large familyof cadherin-related molecules in central nervous system. EMBO J. 12:2249- 2256, 1993. 3 B c

GAM8297 367 PCDHGC3 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PCDHGC4 Wu, Q.; Maniatis, T.: A striking organization of a large familyof human neural cadherin like cell adhesion genes. Cell 97: 779- 790,1999. 3 B c

GAM8297 367 PCDHGC4 Wu, Q.; Zhang, T.; Cheng, J.- F.; Kim, Y.; Grimwood, J.; Schmutz,J.; Dickson, M.; Noonan, J. P.; Zhang, M. Q.; Myers, R. M.; Maniatis,T.: Comparative DNA sequence analysis of mouse and human protocadheringene clusters. Genome Res. 11: 389- 404, 2001. 3 B c

GAM8297 367 PDGFRB Abe, A.; Emi, N.; Tanimoto, M.; Terasaki, H.; Marunouchi, T.; Saito,H.: Fusion of the platelet- derived growth factor receptor beta toa novel gene CEV14 in acute myelogenous leukemia after clonal evolution. Blood 90:4271-4277, 1997. 3 B c

GAM8297 367 PDGFRB Apperley, J. F.; Gardembas, M.; Melo, J. V.; Russell- Jones, R.;Bain, B. J.; 3 B c
Baxter, E. J.; Chase, A.; Chessells, J. M.; Colombat,M.; Dearden, C. E.;
Dimitrijevic, S.; Mahon, F.- X.; Marin, D.; Nikolova,Z.; Olavarria, E.;
Silberman, S.; Schultheis, B.; Cross, N. C. P.;Goldman, J. M.: Response to
imatinib mesylate in patients with chronicmyeloproliferative diseases with
rearrangements of the platelet- derivedgrowth factor receptor beta. New Eng.
J. Med. 347: 481- 487, 2002.

GAM8297 367 PDGFRB Buchberg, A. M.; Jenkins, N. A.; Copeland, N. G.: Localizationof the murine 3 B c
macrophage colony- stimulating factor gene to chromosome3 using
interspecific backcross analysis. Genomics 5: 363- 367, 1989.

GAM8297 367 PDGFRB Claesson- Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek,B.; 3 B c
Ostman, A.; Betsholtz, C.; Heldin, C.- H.: cDNA cloning and expressionof a
human platelet- derived growth factor (PDGF) receptor specificfor B- chain-
containing PDGF molecules. Molec. Cell. Biol. 8: 3476- 3486,1988.

GAM8297 367 PDGFRB Escobedo, J. A.; Fried, V. A.; Daniel, T. O.; Williams, L. T.:Primary 3 B c
structure of the platelet- derived growth factor. (Abstract) Clin.Res. 34:
544A, 1986.

GAM8297 367 PDGFRB Francke, U.; Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.:Chromosomal 3 B c
mapping of genes involved in growth control. Cold SpringHarbor Symp. Quant.
Biol. 51: 855- 866, 1986.

GAM8297 367 PDGFRB Golub, T. R.; Barker, G. F.; Lovett, M.; Gilliland, D. G.: Fusionof PDGF 3 B c
receptor beta to a novel ets- like gene, tel, in chronic
myelomonocyticleukemia with t(5;12) chromosomal translocation. Cell 77: 307-
316,1994.

GAM8297 367 PDGFRB Gronwald, R. G. K.; Grant, F. J.; Haldeman, B. A.; Hart, C. E.;O'Hara, P. 3 B c
J.; Hagen, F. S.; Ross, R.; Bowen- Pope, D. F.; Murray,M. J.: Cloning and
expression of a cDNA coding for the human platelet- derivedgrowth factor
receptor: evidence for more than one receptor class. Proc.Nat. Acad. Sci.
85: 3435- 3439, 1988.

GAM8297 367 PDGFRB How, G.- F.; Venkatesh, B.; Brenner, S.: Conserved linkage betweenthe puffer 3 B c
fish (Fugu rubripes) and human genes for platelet- derivedgrowth factor
receptor and macrophage colony- stimulating factor receptor. GenomeRes. 6:
1185- 1191, 1996.

GAM8297 367 PDGFRB Klinghoffer, R. A.; Mueting- Nelsen, P. F.; Faerman, A.; Shani,M.; Soriano, 3 B c
P.: The two PDGF receptors maintain conserved signalingin vivo despite
divergent embryological functions. Molec. Cell 7:343- 354, 2001.

GAM8297 367 PDGFRB Kulkarni, S.; Heath, C.; Parker, S.; Chase, A.; Iqbal, S.; Pocock,C. F.; 3 B c
Kaeda, J.; Cwynarski, K.; Goldman, J. M.; Cross, N. C. P.:Fusion of
H4/D10S170 to the platelet- derived growth factor receptorbeta in BCR- ABL-
negative myeloproliferative disorders with a t(5;10)(q33;q21). CancerRes.
60: 3592- 3598, 2000.

GAM8297 367 PDGFRB Leal, F.; Williams, L. T.; Robbins, K. C.; Aaronson, S. A.: Evidencethat the 3 B c
v- sis gene product transforms by interaction with the receptorfor platelet-
derived growth factor. Science 230: 327- 330, 1985.

GAM8297 367 PDGFRB Magnusson, M. K.; Meade, K. E.; Brown, K. E., Arthur, D. C.; Krueger,L. A.; 3 B c
Barrett, A. J.; Dunbar, C. E.: Rabaptin- 5 is a novel fusionpartner to
platelet- derived growth factor beta receptor in chronicmyelomonocytic
leukemia. Blood 98: 2518- 2525, 2001.

GAM8297 367 PDGFRB Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle,W.; Kraus, M.; 3 B c
Pierce, J.; Aaronson, S.: Isolation of a novel receptorcDNA establishes the

existence of two PDGF receptor genes. Science 243:800- 804, 1989.

GAM8297 367 PDGFRB Roberts, W. M.; Look, A. T.; Roussel, M. F.; Sherr, C. J.: Tandemlinkage of human CSF- 1 receptor (c- fms) and PDGF receptor genes. Cell 55:655- 661, 1988. 3 B c

GAM8297 367 PDGFRB Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof Huntingtin interacting protein 1 to platelet- derived growth factor- betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998. 3 B c

GAM8297 367 PDGFRB Steer, E. J.; Cross, N. C. P.: Myeloproliferative disorders withtranslocations of chromosome 5q31- 35: role of the platelet- derivedgrowth factor receptor beta. Acta Haemat. 107: 113- 122, 2002. 3 B c

GAM8297 367 PDGFRB Treacher Collins Syndrome Collaborative Group: Positional cloningof a gene involved in the pathogenesis of Treacher Collins syndrome. NatureGenet. 12: 130- 136, 1996. 3 B c

GAM8297 367 PDGFRB Yarden, Y.; Escobedo, J. A.; Kuang, W.- J.; Yang- Feng, T. L.; Daniel,T. O.; Tremble, P. M.; Chen, E. Y.; Ando, M. E.; Harkins, R. N.; Francke,U.; Fried, V. A.; Ullrich, A.; Williams, L. T.: Structure of thereceptor for platelet- derived growth factor helps define a familyof closely related growth factor receptors. Nature 323: 226- 232,1986. 3 B c

GAM8297 367 PDGFRB Yarden, Y.; Ullrich, A.: Growth factor receptor tyrosine kinases. Ann.Rev. Biochem. 57: 443- 478, 1988. 3 B c

GAM8297 367 PELO Lai, C.- H.; Chou, C.- Y.; Ch'ang, L.- Y.; Liu, C.- S.; Lin, W.: Identificationof novel human genes evolutionarily conserved in Caenorhabditis elegansby comparative proteomics. Genome Res. 10: 703- 713, 2000. 3 B c

GAM8297 367 PELO Shamsadin, R.; Adham, I. M.; von Beust, G.; Engel, W.: Molecularcloning, expression and chromosome location of the human pelota genePELO. Cytogenet. Cell Genet. 90: 75- 78, 2000. 3 B c

GAM8297 367 PLAG1 Astrom, A.- K.; Voz, M. L.; Kas, K.; Roijer, E.; Wedell, B.; Mandahl,N.; Van de Ven, W.; Mark, J.; Stenman, G.: Conserved mechanism ofPLAG1 activation in salivary gland tumors with and without chromosome8q12 abnormalities: identification of SII as a new fusion partnergene. Cancer Res. 59: 918- 923, 1999. 3 B c

GAM8297 367 PLAG1 Kas, K.; Roijer, E.; Voz, M.; Meyen, E.; Stenman, G.; Van de Ven,W. J. M.: A 2- Mb YAC contig and physical map covering the chromosome8q12 breakpoint cluster region in pleomorphic adenomas of the salivaryglands. Genomics 43: 349- 358, 1997. 3 B c

GAM8297 367 PLAG1 Kas, K.; Voz, M. L.; Roijer, E.; Astrom, A.- K.; Meyen, E.; Stenman,G.; Van de Ven, W. J. M.: Promoter swapping between the genes fora novel zinc finger protein and beta- catenin in pleiomorphic adenomaswith t(3;8)(p21;q12) translocations. Nature Genet. 15: 170- 174,1997. 3 B c

GAM8297 367 PRDM1 Angelin- Duclos, C.; Cattoretti, G.; Lin, K.- I.; Calame, K.: Commitmentof B lymphocytes to a plasma cell fate is associated with Blimp- 1expression in vivo. J. Immun. 165: 5462- 5471, 2000. 3 B c

GAM8297 367 PRDM1 Chang, D. H.; Angelin- Duclos, C.; Calame, K.: BLIMP- 1: triggerfor differentiation of myeloid lineage. Nature Immun. 1: 169- 176,2000. 3 B c

GAM8297 367 PRDM1 Huang, S.: Blimp- 1 is the murine homolog of the human transcriptionalrepressor PRDI- BF1. (Letter) Cell 78: 9 only, 1994. 3 B c

GAM8297 367 PRDM1 Keller, A. D.; Maniatis, T.: Identification and characterizationof a novel repressor of beta- interferon gene expression. Genes Dev. 5:868- 879, 1991. 3 B c

GAM8297 367 PRDM1 Mock, B. A.; Liu, L.; Le Paslier, D.; Huang, S.: The B- lymphocytematuration 3 B c
promoting transcription factor BLIMP1/PRDI- BF1 maps toD6S447 on human
chromosome 6q21- q22.1 and the syntenic region of mousechromosome 10.
Genomics 37: 24- 28, 1996.

GAM8297 367 PRND Comincini, S.; Foti, M. G.; Tranulis, M. A.; Hills, D.; Di Guardo,G.; 3 B c
Vaccari, G.; Williams, J. L.; Harbitz, I., Ferretti, L.:
Genomicorganization, comparative analysis, and genetic polymorphisms of
thebovine and ovine prion Doppel genes (PRND). Mammalian Genome 12:729- 733,
2001.

GAM8297 367 PRND Lu, K.; Wang, W.; Xie, Z.; Wong, B.- S.; Li, R.; Petersen, R. B.;Sy, M.- S.; 3 B c
Chen, S. G.: Expression and structural characterizationof the recombinant
human doppel protein. Biochemistry 39: 13575- 13583,2000.

GAM8297 367 PRND Moore, R. C.; Lee, I. Y.; Silverman, G. L.; Harrison, P. M.; Strome,R.; 3 B c
Heinrich, C.; Karunaratne, A.; Pasternak, S. H.; Chishti, M. A.;Liang, Y.;
Mastrangelo, P.; Wang, K.; and 9 others: Ataxia in prionprotein (PrP)-
deficient mice is associated with upregulation of thenovel PrP- like protein
doppel. J. Molec. Biol. 292: 797- 817, 1999.

GAM8297 367 PRND Schroder, B.; Franz, B.; Hempfling, P.; Selbert, M.; Jurgens, 3 B c
T.;Kretzschmar, H. A.; Bodemer, M.; Poser, S.; Zerr, I.: Polymorphismswithin
the prion- like protein gene (Prnd) and their implications inhuman prion
diseases, Alzheimer's disease and other neurological disorders. Hum.Genet.
109: 319- 325, 2001.

GAM8297 367 PRND Silverman, G. L.; Qin, K.; Moore, R. C.; Yang, Y.; Mastrangelo,P.; Tremblay, 3 B c
P.; Prusiner, S. B.; Cohen, F. E.; Westaway, D.: Doppelis an N-
glycosylated, glycosylphosphatidylinositol- anchored protein:expression in
testis and ectopic production in the brains of Prnp(0/0)mice predisposed to
Purkinje cell loss. J. Biol. Chem. 275: 26834- 26841,2000.

GAM8297 367 PRND Weissmann, C.; Aguzzi, A.: PrP's double causes trouble. Science 286:914- 3 B c
915, 1999.

GAM8297 367 PRX Boerkoel, C. F.; Takashima, H.; Stankiewicz, P.; Garcia, C. A.;Leber, S. M.; 3 B c
Rhee- Morris, L.; Lupski, J. R.: Periaxin mutationscause recessive Dejerine-
Sottas neuropathy. Am. J. Hum. Genet. 68:325- 333, 2001. Note: Erratum: Am.
J. Hum. Genet. 68: 557 only, 2001.

GAM8297 367 PRX Cohn, R. D.; Campbell, K. P.: Molecular basis of muscular dystrophies. 3 B c
MuscleNerve 23: 1456- 1471, 2000.

GAM8297 367 PRX Delague, V.; Bareil, C.; Tuffery, S.; Bouvagnet, P.; Chouery, E.;Koussa, S.; 3 B c
Maisonobe, T.; Loiselet, J.; Megarbane, A.; Claustres,M.: Mapping of a new
locus for autosomal recessive demyelinatingCharcot- Marie- Tooth disease to
19q13.1- 13.3 in a large consanguineousLebanese family: exclusion of MAG as
a candidate gene. Am. J. Hum.Genet. 67: 236- 243, 2000.

GAM8297 367 PRX Gillespie, C. S.; Lee, M.; Fantes, J. F.; Brophy, P. J.: The geneencoding 3 B c
the Schwann cell protein periaxin localizes on mouse chromosome7 (Prx).
Genomics 41: 297- 298, 1997.

GAM8297 367 PRX Gillespie, C. S.; Sherman, D. L.; Fleetwood- Walker, S. M.; Cottrell,D. F.; 3 B c
Tait, S.; Garry, E. M.; Wallace, V. C. J.; Ure, J.; Griffiths,I. R.; Smith,
A. Brophy, P. J.: Peripheral demyelination and neuropathicpain behavior in
periaxin- deficient mice. Neuron 26: 523- 531, 2000.

GAM8297 367 PRX Guilbot, A.; Williams, A.; Ravise, N.; Verny, C.; Brice, A.; Sherman,D. L.; 3 B c
Brophy, P. J.; LeGuern, E.; Delague, V.; Bareil, C.; Megarbane,A.;
Claustres, M.: A mutation in periaxin is responsible for CMT4F,an autosomal

recessive form of Charcot- Marie- Tooth disease. Hum.Molec. Genet. 10: 415-421, 2001.

GAM8297 367 PRX Schuler, G. D.: Sequence mapping by electronic PCR. Genome Res. 7:541- 550, 1997. 3 B c

GAM8297 367 PRX Takashima, H.; Boerkoel, C. F.; De Jonghe, P.; Ceuterick, C.; Martin,J.- J.; Voit, T.; Schroder, J.- M.; Williams, A.; Brophy, P. J.; Timmerman,V.; Lupski, J. R.: Periaxin mutations cause a broad spectrum of demyelinatingneuropathies. Ann. Neurol. 51: 709- 715, 2002. 3 B c

GAM8297 367 RGL Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Hirosawa, M.;Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Predictionof the coding sequences of unidentified human genes. XIII. The completesequences of 100 new cDNA clones from brain which code for large proteinsin vitro. DNA Res. 6: 63- 70, 1999. 3 B c

GAM8297 367 RGL Sood, R.; Makalowska, I.; Carpten, J. D.; Robbins, C. M.; Stephan,D. A.; Connors, T. D.; Morgenbesser, S. D.; Su, K.; Pinkett, H. W.;Graham, C. L.; Quesenberry, M. I.; Baxevanis, A. D.; Klinger, K. W.;Trent, J. M.; Bonner, T. I.: The human RGL (RalGDS- like) gene: cloning,expression analysis and genomic organization. Biochim. Biophys. Acta 1491:285- 288, 2000. 3 B c

GAM8297 367 ROBO1 Bagri, A.; Marin, O.; Plump, A. S.; Mak, J.; Pleasure, S. J.; Rubenstein,J. L. R.; Tessier- Lavigne, M.: Slit proteins prevent midline crossingand determine the dorsoventral position of major axonal pathways inthe mammalian forebrain. Neuron 33: 233- 248, 2002. 3 B c

GAM8297 367 ROBO1 Dallol, A.; Forgacs, E.; Martinez, A.; Sekido, Y.; Walker, R.;Kishida, T.; Rabbitts, P.; Maher, E. R.; Minna, J. D.; Latif, F.:Tumour specific promoter region methylation of the human homologueof the Drosophila Roundabout gene DUTT1 (ROBO1) in human cancers. Oncogene 21:3020- 3028, 2002. 3 B c

GAM8297 367 ROBO1 Kidd, T.; Brose, K.; Mitchell, K. J.; Fetter, R. D.; Tessier- Lavigne,M.; Goodman, C. S.; Tear, G.: Roundabout controls axon crossing ofthe CNS midline and defines a novel subfamily of evolutionarily conservedguidance receptors. Cell 92: 205- 215, 1998. 3 B c

GAM8297 367 ROBO1 Stein, E.; Tessier- Lavigne, M.: Hierarchical organization of guidancereceptors: silencing of netrin attraction by Slit through a Robo/DCCreceptor complex. Science 291: 1928- 1938, 2001. 3 B c

GAM8297 367 ROBO1 Sundaresan, V.; Chung, G.; Heppell- Parton, A.; Xiong, J.; Grundy,C.; Roberts, I.; James, L.; Cahn, A.; Bench, A.; Douglas, J.; Minna,J.; Sekido, Y.; Lerman, M.; Latif, F.; Bergh, J.; Li, H.; Lowe, N.;Ogilvie, D.; Rabbitts, P.: Homozygous deletions at 3p12 in breastand lung cancer. Oncogene 17: 1723- 1729, 1998. 3 B c

GAM8297 367 ROBO1 Zallen, J. A.; Yi, B. A.; Bargmann, C. I.: The conserved immunoglobulinsuperfamily member SAX- 3/Robo directs multiple aspects of axon guidancein C. elegans. Cell 92: 217- 227, 1998. 3 B c

GAM8297 367 RYR1 Adeokun, A. M.; West, S. P.; Ellis, F. R.; Halsall, P. J.; Hopkins,P. M.; Foroughmand, A. M.; Iles, D. E.; Robinson, R. L.; Stewart,A. D.; Curran, J. L.: The G1021A substitution in the RYR1 gene doesnot cosegregate with malignant hyperthermia susceptibility in a Britishpedigree. Am. J. Hum. Genet. 60: 833- 341, 1997. 3 B c

GAM8297 367 RYR1 Alestrom, A.; Fagerlund, T. H.; Berg, K.: A simple method to detectthe RYR1 mutation G1021A, a cause of malignant hyperthermia susceptibility. Clin.Genet. 47: 274- 275, 1995. 3 B c

GAM8297 367 RYR1 Avila, G.; O'Brien, J. J.; Dirksen, R. T.: Excitation- contractionuncoupling 3 B c

by a human central core disease mutation in the ryanodinereceptor. Proc. Nat. Acad. Sci. 98: 4215- 4220, 2001.

GAM8297 367 RYR1 Barone, V.; Bertocchini, F.; Bottinelli, R.; Protasi, F.; Allen,P. D.; Armstrong, C. F.; Reggiani, C.; Sorrentino, V.: Contractileimpairment and structural alterations of skeletal muscles from knockoutmice lacking type 1 and type 3 ryanodine receptors. FEBS Lett. 422:160- 164, 1998. 3 B c

GAM8297 367 RYR1 Brandt, A.; Schleithoff, L.; Jurkat- Rott, K.; Klingler, W.; Baur,C.; Lehmann- Horn, F.: Screening of ryanodine receptor gene in 105malignant hyperthermia families: novel mutations and concordance withthe in vitro contracture test. Hum. Molec. Genet. 8: 2055- 2062,1999. 3 B c

GAM8297 367 RYR1 Brown, R. L.; Pollock, A. N.; Couchman, K. G.; Hodges, M.; Hutchinson,D. O.; Waaka, R.; Lynch, P.; McCarthy, T. V.; Stowell, K. M.: A novelryanodine receptor mutation and genotype- phenotype correlation ina large malignant hyperthermia New Zealand Maori pedigree. Hum. Molec.Genet. 9: 1515- 1524, 2000. 3 B c

GAM8297 367 RYR1 Cavanna, J. S.; Greenfield, A. J.; Johnson, K. J.; Marks, A. R.;Nadal-Ginard, B.; Brown, S. D. M.: Establishment of the mouse chromosome7 region with homology to the myotonic dystrophy region of human chromosome19q. Genomics 7: 12- 18, 1990. 3 B c

GAM8297 367 RYR1 Cheng, H.; Lederer, W. J.; Cannell, M. B.: Calcium sparks: elementaryevents underlying excitation- contraction coupling in heart muscle. Science 262:740- 744, 1993. 3 B c

GAM8297 367 RYR1 Deufel, T.; Sudbrak, R.; Feist, Y.; Rubsam, B.; Du Chesne, I.;Schafer, K.-L.; Roewer, N.; Grimm, T.; Lehmann- Horn, F.; Hartung,E. J.; Muller, C. R.: Discordance, in a malignant hyperthermia pedigree,between in vitro contracture- test phenotypes and haplotypes for theMHS1 region on chromosome 19q12- 13.2, comprising the C1840T transitionin the RYR1 gene. Am. J. Hum. Genet. 56: 1334- 1342, 1995. 3 B c

GAM8297 367 RYR1 Eu, J. P.; Sun, J.; Xu, L.; Stamler, J. S.; Meissner, G.: Theskeletal muscle calcium release channel: coupled O2 sensor and NOsignaling functions. Cell 102: 499- 509, 2000. 3 B c

GAM8297 367 RYR1 Fagerlund, T. H.; Islander, G.; Ranklev- Twetman, E.; Berg, K.: Recombination between the postulated CCD/MHE/MHS locus and RYR1gene markers. Clin. Genet. 50: 455- 458, 1996. 3 B c

GAM8297 367 RYR1 Fagerlund, T. H.; Islander, G.; Twetman, E. R.; Berg, K.: A searchfor three known RYR1 gene mutations in 41 Swedish families with predispositionto malignant hyperthermia. Clin. Genet. 48: 12- 16, 1995. 3 B c

GAM8297 367 RYR1 Fagerlund, T. H.; Ording, H.; Bendixen, D.; Islander, G.; RanklevTwetman, E.; Berg, K.: Discordance between malignant hyperthermiasusceptibility and RYR1 mutation C1840T in two Scandinavian MH familiesexhibiting this mutation. Clin. Genet. 52: 416- 421, 1997. 3 B c

GAM8297 367 RYR1 Fagerlund, T.; Islander, G.; Ranklev, E.; Harbitz, I.; Hauge,J. G.; Mokleby, E.; Berg, K.: Genetic recombination between malignanthyperthermia and calcium release channel in skeletal muscle. Clin.Genet. 41: 270- 272, 1992. 3 B c

GAM8297 367 RYR1 Fagerlund, T.; Ording, H.; Bendixen, D.; Berg, K.: Search forthree known mutations in the RYR gene in 48 Danish families with malignanthyperthermia. Clin. Genet. 46: 401- 404, 1994. 3 B c

GAM8297 367 RYR1 Fagerlund, T.; Ording, H.; Bendixen, D.; Islander, G.; Ranklev- Twetman,E.; Berg, K.: RYR1 mutation G1021A (gly341- to- arg) is not frequentin Danish and Swedish families with malignant hyperthermia susceptibility. Clin.Genet. 3 B c

49: 186- 188, 1996.

GAM8297 367 RYR1 Ferreiro, A.; Monnier, N.; Romero, N. B.; Leroy, J.- P.; Bonnemann,C.; 3 B c
Haenggeli, C.- A.; Straub, V.; Voss, W. D.; Nivoche, Y.; Jungbluth,H.;
Lemainque, A.; Voit, T.; Lunardi, J.; Fardeau, M.; Guicheney,P.: A recessive
form of central core disease, transiently presentingas multi- minicore
disease, is associated with a homozygous mutationin the ryanodine receptor
type 1 gene. Ann. Neurol. 51: 750- 759,2002.

GAM8297 367 RYR1 Fujii, J.; Otsu, K.; Zorzato, F.; de Leon, S.; Khanna, V. K.;Weiler, J. E.; 3 B c
O'Brien, P. J.; MacLennan, D. H.: Identification ofa mutation in porcine
ryanodine receptor associated with malignanthyperthermia. Science 253: 448-
451, 1991.

GAM8297 367 RYR1 Gillard, E. F.; Otsu, K.; Fujii, J.; Duff, C.; de Leon, S.; Khanna,V. K.; 3 B c
Britt, B. A.; Worton, R. G.; MacLennan, D. H.: Polymorphismsand deduced
amino acid substitutions in the coding sequence of theryanodine receptor
(RYR1) gene in individuals with malignant hyperthermia. Genomics 13:1247-
1254, 1992.

GAM8297 367 RYR1 Gillard, E. F.; Otsu, K.; Fujii, J.; Khanna, V. K.; de Leon, S.;Derdemezi, 3 B c
J.; Britt, B. A.; Duff, C. L.; Worton, R. G.; MacLennan,D. H.: A
substitution of cysteine for arginine 614 in the ryanodinereceptor is
potentially causative of human malignant hyperthermia. Genomics 11:751- 755,
1991.

GAM8297 367 RYR1 Hall- Curran, J. L.; Stewart, A. D.; Ball, S. P.; Halsall, J. P.;Hopkins, P. 3 B c
M.; Ellis, F. R.: No C1840 to T mutation in RYR1 in
malignanthyperthermia.(Letter) Hum. Mutat. 2: 330, 1993.

GAM8297 367 RYR1 Harbitz, I.; Chowdhary, B.; Thomsen, P. D.; Davies, W.; Kaufmann,U.; Kran, 3 B c
S.; Gustavsson, I.; Christensen, K.; Hauge, J. G.: Assignmentof the porcine
calcium release channel gene, a candidate for the malignanthyperthermia
locus, to the 6p11- q21 segment of chromosome 6. Genomics 8:243- 248, 1990.

GAM8297 367 RYR1 Harbitz, I.; Kristensen, T.; Bosnes, M.; Kran, S.; Davies, W.: DNA sequence 3 B c
of the skeletal muscle calcium release channel cDNAand verification of the
arg615- to- cys615 mutation, associated withporcine malignant hyperthermia,
in Norwegian Landrace pigs. AnimalGenet. 23: 395- 402, 1992.

GAM8297 367 RYR1 Keating, K. E.; Quane, K. A.; Manning, B. M.; Lehane, M.; Hartung,E.; 3 B c
Censier, K.; Urwyler, A.; Klausnitzer, M.; Muller, C. R.; Heffron,J. J. A.;
McCarthy, T. V.: Detection of a novel RYR1 mutation infour malignant
hyperthermia pedigrees. Hum. Molec. Genet. 3: 1855- 1858,1994.

GAM8297 367 RYR1 Levitt, R. C.; Nouri, N.; Jedlicka, A. E.; McKusick, V. A.; Marks,A. R.; 3 B c
Shutack, J. G.; Fletcher, J. E.; Rosenberg, H.; Meyers, D.A.: Evidence for
genetic heterogeneity in malignant hyperthermiasusceptibility. Genomics 11:
543- 547, 1991.

GAM8297 367 RYR1 Lynch, P. J.; Tong, J.; Lehane, M.; Mallet, A.; Giblin, L.; Heffron,J. J. 3 B c
A.; Vaughan, P.; Zafra, G.; MacLennan, D. H.; McCarthy, T. V.: A mutation in
the transmembrane/luminal domain of the ryanodinereceptor is associated with
abnormal Ca(2+) release channel functionand severe central core disease.
Proc. Nat. Acad. Sci. 96: 4164- 4169,1999.

GAM8297 367 RYR1 MacKenzie, A. E.; Korneluk, R. G.; Duff, C.; Worton, R. G.; MacLennan,D. H.: 3 B c
Location of the human ryanodine receptor gene with respectto an established
human chromosome 19 linkage group.(Abstract) Am.J. Hum. Genet. 45 (suppl.):
A149, 1989.

GAM8297 367 RYR1 MacKenzie, A. E.; Korneluk, R. G.; Zorzato, F.; Fujii, J.; Phillips,M.; 3 B c

Iles, D.; Wieringa, B.; Leblond, S.; Bailly, J.; Willard, H. F.;Duff, C.; Worton, R. G.; MacLennan, D. H.: The human ryanodine receptorgene: its mapping to 19q13.1, placement in a chromosome 19 linkagegroup, and exclusion as the gene causing myotonic dystrophy. Am.J. Hum. Genet. 46: 1082- 1089, 1990.

GAM8297 367 RYR1 MacLennan, D. H.: Personal Communication. Toronto, Ontario,Canada 7/5/1991. 3 B c

GAM8297 367 RYR1 MacLennan, D. H.; Duff, C.; Zorzato, F.; Fujii, J.; Phillips,M.; Korneluk, R. G.; Frodis, W.; Britt, A.; Worton, R. G.: Ryanodinereceptor gene is a candidate for predisposition to malignant hyperthermia. Nature 343:559- 561, 1990. 3 B c

GAM8297 367 RYR1 MacLennan, D. H.; Zorzato, F.; Fujii, J.; Otsu, K.; Phillips,M.; Lai, F. A.; Meissner, G.; Green, N. M.; Willard, H. F.; Britt,B. A.; Worton, R. G.; Korneluk, R. G.: Cloning and localization ofthe human calcium release channel (ryanodine receptor) gene to theproximal long arm (cen- q13.2) of human chromosome 19.(Abstract) Am.J. Hum. Genet. 45 (suppl.): A205, 1989. 3 B c

GAM8297 367 RYR1 Manning, B. M.; Quane, K. A.; Lynch, P. J.; Urwyler, A.; Tegazzin,V.; Krivosic- Horber, R.; Censier, K.; Comi, G.; Adnet, P.; Wolz, W.;Lunardi, J.; Muller, C. R.; McCarthy, T. V.: Novel mutations at aCpG dinucleotide in the ryanodine receptor in malignant hyperthermia. Hum.Mutat. 11: 45- 50, 1998. 3 B c

GAM8297 367 RYR1 Manning, B. M.; Quane, K. A.; Ording, H.; Urwyler, A.; Tegazzin,V.; Lehane, M.; O'Halloran, J.; Hartung, E.; Giblin, L. M.; Lynch,P. J.; Vaughan, P.; Censier, K.; Bendixen, D.; Comi, G.; Heytens,L.; Monsieurs, K.; Fagerlund, T.; Wolz, W.; Heffron, J. J. A.; Muller,C. R.; McCarthy, T. V.: Identification of novel mutations in theryanodine- receptor gene (RYR1) in malignant hyperthermia: genotype- phenotypecorrelation. Am. J. Hum. Genet. 62: 599- 609, 1998. 3 B c

GAM8297 367 RYR1 Mattei, M. G.; Giannini, G.; Moscatelli, F.; Sorrentino, V.:Chromosomal localization of murine ryanodine receptor genes RYR1,RYR2, and RYR3 by in situ hybridization. Genomics 22: 202- 204, 1994. 3 B c

GAM8297 367 RYR1 McCarthy, T. V.; Quane, K. A.; Lynch, P. J.: Ryanodine receptormutations in malignant hyperthermia and central core disease. Hum.Mutat. 15: 410- 417, 2000. 3 B c

GAM8297 367 RYR1 Monnier, N.; Romero, N. B.; Lerale, J.; Landrieu, P.; Nivoche,Y.; Fardeau, M.; Lunardi, J.: Familial and sporadic forms of centralcore disease are associated with mutations in the C- terminal domainof the skeletal muscle ryanodine receptor. Hum. Molec. Genet. 10:2581- 2592, 2001. 3 B c

GAM8297 367 RYR1 Monnier, N.; Romero, N. B.; Lerale, J.; Nivoche, Y.; Qi, D.; MacLennan,D. H.; Fardeau, M.; Lunardi, J.: An autosomal dominant congenitalmyopathy with cores and rods is associated with a neomutation in theRYR1 gene encoding the skeletal muscle ryanodine receptor. Hum. Molec.Genet. 9: 2599- 2608, 2000. 3 B c

GAM8297 367 RYR1 Monsieurs, K. G.; Van Broekhoven, C.; Martin, J.- J.; Van Hoof,V. O.; Heytens, L.: Gly341arg mutation indicating malignant hyperthermiasusceptibility: specific cause of chronically elevated serum creatinekinase activity. J. Neurol. Sci. 154: 62- 65, 1998. 3 B c

GAM8297 367 RYR1 O'Brien, R. O.; Taske, N. L.; Hansbro, P. M.; Matthaei, K. I.;Hogan, S. P.; Denborough, M. A.; Foster, P. S.: Exclusion of defectsin the skeletal muscle specific regions of the DHPR alpha- 1 subunitas frequent causes of malignant hyperthermia. J. Med. Genet. 32:913- 914, 1995. 3 B c

GAM8297 367 RYR1 Otsu, K.; Khanna, V. K.; Archibald, A. L.; MacLennan, D. H.:Cosegregation of porcine malignant hyperthermia and a probable causalmutation in the skeletal muscle ryanodine receptor gene in backcrossfamilies. Genomics 11: 744- 750, 1991. 3 B c

GAM8297 367 RYR1 Otsu, K.; Nishida, K.; Kimura, Y.; Kuzuya, T.; Hori, M.; Kamada,T.; Tada, M.: The point mutation arg615- to- cys in the Ca(2+) releasechannel of skeletal sarcoplasmic reticulum is responsible for hypersensitivityto caffeine and halothane in malignant hyperthermia. J. Biol. Chem. 269:9413- 9415, 1994. 3 B c

GAM8297 367 RYR1 Otsu, K.; Phillips, M. S.; Khanna, V. K.; de Leon, S.; MacLennan,D. H.: Refinement of diagnostic assays for a probable causal mutationfor porcine and human malignant hyperthermia. Genomics 13: 835- 837,1992. 3 B c

GAM8297 367 RYR1 Phillips, M. S.; Fujii, J.; Khanna, V. K.; DeLeon, S.; Yokobata,K.; De Jong, P. J.; MacLennan, D. H.: The structural organizationof the human skeletal muscle ryanodine receptor (RYR1) gene. Genomics 34:24- 41, 1996. 3 B c

GAM8297 367 RYR1 Quane, K. A.; Healy, J. M. S.; Keating, K. E.; Manning, B. M.;Couch, F. J.; Palmucci, L. M.; Doriguzzi, C.; Fagerlund, T. H.; Berg,K.; Ording, H.; Bendixen, D.; Mortier, W.; Linz, U.; Muller, C. R.;McCarthy, T. V.: Mutations in the ryanodine receptor gene in centralcore disease and malignant hyperthermia. Nature Genet. 5: 51- 55,1993. 3 B c

GAM8297 367 RYR1 Quane, K. A.; Keating, K. E.; Manning, B. M.; Healy, J. M. S.;Monsieurs, K.; Heffron, J. J. A.; Lehane, M.; Heytens, L.; Krivosic- Horber,R.; Adnet, P.; Ellis, F. R.; Monnier, N.; Lunardi, J.; McCarthy, T.V.: Detection of a novel common mutation in the ryanodine receptorgene in malignant hyperthermia: implications for diagnosis and heterogeneitystudies. Hum. Molec. Genet. 3: 471- 476, 1994. 3 B c

GAM8297 367 RYR1 Richter, M.; Schleithoff, L.; Deufel, T.; Lehmann- Horn, F.; Herrmann-Frank,A.: Functional characterization of a distinct ryanodine receptormutation in human malignant hyperthermia- susceptible muscle. J. Biol.Chem. 272: 5256- 5260, 1997. 3 B c

GAM8297 367 RYR1 Robinson, R. L.; Brooks, C.; Brown, S. L.; Ellis, F. R.; Halsall,P. J.; Quinnell, R. J.; Shaw, M.- A.; Hopkins, P. M.: RYR1 mutationscausing central core disease are associated with more severe malignanthyperthermia in vitro contracture test phenotypes. Hum. Mutat. 20:88- 97, 2002. 3 B c

GAM8297 367 RYR1 Sambuughin, N.; McWilliams, S.; de Bantel, A.; Sivakumar, K.;Nelson, T. E.: Single- amino- acid deletion in the RYR1 gene, associatedwith malignant hyperthermia susceptibility and unusual contractionphenotype. Am. J. Hum. Genet. 69: 204- 208, 2001. 3 B c

GAM8297 367 RYR1 Stewart, S. L.; Rosenberg, H.; Fletcher, J. E.: Failure to identifythe ryanodine receptor G1021A mutation in a large North American populationwith malignant hyperthermia. Clin. Genet. 54: 358- 361, 1998. 3 B c

GAM8297 367 RYR1 Tegazzin, V.; Accorsi, A.; Gritti, G.; Arcelli, L.; Di Giovanni,A.: MH fulminant reaction after eight anaesthetics: a case report. MinervaAnesthesiol. 60: 217- 219, 1994. 3 B c

GAM8297 367 RYR1 Tilgen, N.; Zorzato, F.; Halliger- Keller, B.; Muntoni, F.; Sewry,C.; Palumucci, L. M.; Schneider, C.; Hauser, E.; Lehmann- Horn, F.;Muller, C. R.; Treves, S.: Identification of four novel mutationsin the C- terminal membrane spanning domain of the ryanodine receptor1: association with central core disease and alteration of calciumhomeostasis. Hum. Molec. Genet. 10: 2879- 2887, 2001. 3 B c

GAM8297 367 RYR1 Tobin, J. R.; Jason, D. R.; Challa, V. R.; Nelson, T. E.; Sambuughin,N.: 3 B c
Malignant hyperthermia and apparent heat stroke. (Letter) JAMA 286:168- 169, 2001.

GAM8297 367 RYR1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 B c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993.

GAM8297 367 RYR1 Wang, S.- Q.; Song, L.- S.; Lakatta, E. G.; Cheng, H.: Ca(2+) 3 B c
signallingbetween single L- type Ca(2+) channels and ryanodine receptors in heartcells. Nature 410: 592- 596, 2001.

GAM8297 367 RYR1 Zhang, Y.; Chen, H. S.; Khanna, V. K.; De Leon, S.; Phillips,M. S.; 3 B c
Schappert, K.; Britt, B. A.; Brownell, A. K. W.; MacLennan,D. H.: A mutation in the human ryanodine receptor gene associatedwith central core disease. Nature Genet. 5: 46- 50, 1993.

GAM8297 367 RYR1 Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N. M.;Lai, F. A.; 3 B c
Meissner, G.; MacLennan, D. H.: Molecular cloning ofcDNA encoding human and rabbit forms of the Ca(2+) release channel(ryanodine receptor) of skeletal muscle sarcoplasmic reticulum. J.Biol. Chem. 265: 2244- 2256, 1990.

GAM8297 367 SERPINB6 Coughlin, P.; Nicholl, J.; Sun, J.; Salem, H.; Bird, P.; Sutherland,G. R.: 3 B c
Chromosomal mapping of the human proteinase inhibitor 6 (PI6)gene to 6p25 by fluorescence in situ hybridization. Genomics 26:431- 433, 1995.

GAM8297 367 SERPINB6 Coughlin, P.; Sun, J.; Cerruti, L.; Salem, H. H.; Bird, P.: Cloningand 3 B c
molecular characterization of a human intracellular serine proteinaseinhibitor. Proc. Nat. Acad. Sci. 90: 9417- 9421, 1993.

GAM8297 367 SERPINB6 Evans, E.; Cooley, J.; Remold- O'Donnell, E.: Characterizationand 3 B c
chromosomal localization of ELANH2, the gene encoding human monocyte/neutrophilelastase inhibitor. Genomics 28: 235- 240, 1995.

GAM8297 367 SERPINB6 Schneider, S. S.; Schick, C.; Fish, K. E.; Miller, E.; Pena, J.C.; Treter, 3 B c
S. D.; Hui, S. M.; Silverman, G. A.: A serine proteinaseinhibitor locus at 18q21.3 contains a tandem duplication of the humansquamous cell carcinoma antigen gene. Proc. Nat. Acad. Sci. 92:3147- 3151, 1995.

GAM8297 367 SERPINB6 Sun, J.; Rose, J. B.; Bird, P.: Gene structure, chromosomal localization,and 3 B c
expression of the murine homologue of human proteinase inhibitor6 (PI- 6) suggests divergence of PI- 6 from the ovalbumin serpins. J.Biol. Chem. 270: 16089- 16096, 1995.

GAM8297 367 SLC17A2 Ghishan, F. K.; Knobel, S.; Dasuki, M.; Butler, M.; Phillips, J.: 3 B c
Chromosomal localization of the human renal sodium phosphate transporterto chromosome 5: implications for X- linked hypophosphatemia. Pediat.Res. 35: 510- 513, 1994.

GAM8297 367 SLC17A2 Hartmann, C. M.; Hewson, A. S.; Kos, C. H.; Hilfiker, H.; Soumounou,Y.; 3 B c
Murer, H.; Tenenhouse, H. S.: Structure of murine and human renaltype II Na(+)- phosphate cotransporter genes (Npt2 and NPT2). Proc.Nat. Acad. Sci. 93: 7409- 7414, 1996.

GAM8297 367 SLC17A2 Kos, C. H.; Tihy, F.; Econs, M. J.; Murer, H.; Lemieux, N.; Tenenhouse,H. 3 B c
S.: Localization of a renal sodium- phosphate cotransporter geneto human chromosome 5q35. Genomics 19: 176- 177, 1994.

GAM8297 367 SLC17A2 Kos, C. H.; Tihy, F.; Murer, H.; Lemieux, N.; Tenenhouse, H. S.: Comparative 3 B c
mapping of Na(+)- phosphate cotransporter genes, NPT1and NPT2, in human and rabbit. Cytogenet. Cell Genet. 75: 22- 24,1996.

GAM8297 367 SLC17A2 Magagnin, S.; Werner, A.; Markovich, D.; Sorribas, V.; Stange,G.; Biber, J.; 3 B c
Murer, H.: Expression cloning of human and rat renalcortex Na/Pi
cotransport. Proc. Nat. Acad. Sci. 90: 5979- 5983, 1993.

GAM8297 367 SLC17A2 McPherson, J. D.; Krane, M. C.; Wagner- McPherson, C. B.; Kos, C.H.; 3 B c
Tenenhouse, H. S.: High resolution mapping of the renal sodium-
phosphatecotransporter gene (NPT2) confirms its localization to human
chromosome5q35. Pediat. Res. 41: 632- 634, 1997.

GAM8297 367 SLC17A2 Tenenhouse, H. S.; Werner, A.; Biber, J.; Ma, S.; Martel, J.; Roy,S.; Murer, 3 B c
H.: Renal Na(+)- phosphate cotransport in murine X- linkedhypophosphatemic
rickets: molecular characterization. J. Clin. Invest. 93:671- 676, 1994.

GAM8297 367 SLC17A2 Zhang, X.- X.; Tenenhouse, H. S.; Hewson, A. S.; Murer, H.; Eydoux,P.: 3 B c
Assignment of renal- specific Na(+)- phosphate cotransporter geneSlc17a2 to
mouse chromosome band 13B by in situ hybridization. Cytogenet.Cell Genet.
77: 304- 305, 1997.

GAM8297 367 SLC6A1 Huang, F.; Shi, L. J.; Heng, H. H. Q.; Fei, J.; Guo, L.- H.: Assignmentof 3 B c
the human GABA transporter gene (GABATHG) locus to chromosome 3p24- p25.
Genomics 29:302- 304, 1995.

GAM8297 367 SLC6A1 Lam, D. M.- K.; Fei, J.; Zhang, X.- Y.; Tam, A. C. W.; Zhu, L.- H.;Huang, 3 B c
F.; King, S. C.; Guo, L.- H.: Molecular cloning and structureof the human
(GABATHG) GABA transporter gene. Molec. Brain Res. 19:227- 232, 1993.

GAM8297 367 SLC6A1 Nelson, H.; Mandiyan, S.; Nelson, N.: Cloning of the human brainGABA 3 B c
transporter. FEBS Lett. 269: 181- 184, 1990.

GAM8297 367 TBX6 Chapman, D. L.; Agulnik, I.; Hancock, S.; Silver, L. M.; Papaioannou,V. E.: 3 B c
Tbx6, a mouse T- box gene implicated in paraxial mesoderm formationat
gastrulation. Dev. Biol. 180: 534- 542, 1996.

GAM8297 367 TBX6 Chapman, D. L.; Papaioannou, V. E.: Three neural tubes in mouseembryos with 3 B c
mutations in the T- box gene Tbx6. Nature 391: 695- 697,1998.

GAM8297 367 TBX6 Papapetrou, C.; Putt, W.; Fox, M.; Edwards, Y. H.: The human TBX6gene: 3 B c
cloning and assignment to chromosome 16p11.2. Genomics 55:238- 241, 1999.

GAM8297 367 TNFRSF1B Baker, E.; Chen, L. Z.; Smith, C. A.; Callen, D. F.; Goodwin, R.;Sutherland, 3 B c
G. R.: Chromosomal location of the human tumor necrosisfactor receptor
genes. Cytogenet. Cell Genet. 57: 117- 118, 1991.

GAM8297 367 TNFRSF1B Beltinger, C. P.; White, P. S.; Maris, J. M.; Sulman, E. P.; Jensen,S. J.; 3 B c
LePaslier, D.; Stallard, B. J.; Goeddel, D. V.; de Sauvage,F. J.; Brodeur,
G. M.: Physical mapping and genomic structure ofthe human TNFR2 gene.
Genomics 35: 94- 100, 1996.

GAM8297 367 TNFRSF1B Bruce, A. J.; Boling, W.; Kindy, M. S.; Peschon, J.; Kraemer, P.J.; 3 B c
Carpenter, M. K.; Holtsberg, F. W.; Mattson, M. P.: Altered neuronaland
microglial responses to excitotoxic and ischemic brain injuryin mice lacking
TNF receptors. Nature Med. 2: 788- 794, 1996.

GAM8297 367 TNFRSF1B Chan, F. K.- M.; Chun, H. J.; Zheng, L.; Siegel, R. M.; Bui, K.L.; Lenardo, 3 B c
M. J.: A domain in TNF receptors that mediates ligand- independentreceptor
assembly and signaling. Science 288: 2351- 2354, 2000.

GAM8297 367 TNFRSF1B Geurts, J. M. W.; Janssen, R. G. J. H.; van Greevenbroek, M. M.J.; van der 3 B c
Kallen, C. J. H.; Cantor, R. M.; Bu, X.; Aouizerat, B.E.; Allayee, H.;
Rotter, J. I.; de Bruin, T. W. A.: Identificationof TNFRSF1B as a novel
modifier gene in familial combined hyperlipidemia. Hum.Molec. Genet. 9:
2067- 2074, 2000.

GAM8297 367 TNFRSF1B Glenn, C. L.; Wang, W. Y. S.; Benjafield, A. V.; Morris, B. J.: Linkage and 3 B c
association of tumor necrosis factor receptor 2 locuswith hypertension,

hypercholesterolemia and plasma shed receptor. Hum.Molec. Genet. 9: 1943-1949, 2000.

GAM8297 367 TNFRSF1B Kaufman, B. A.; White, P. S.; Steinbrueck, T.; Donis- Keller, H.;Brodeur, G. M.: Linkage mapping of the tumor necrosis factor receptor2 (TNFR2) gene to 1p36.2 using the single- strand conformation polymorphismtechnique. Hum. Genet. 94: 418- 422, 1994. 3 B c

GAM8297 367 TNFRSF1B Kemper, O.; Derre, J.; Cherif, D.; Engelmann, H.; Wallach, D.;Berger, R.: The gene for the type II (p75) tumor necrosis factorreceptor (TNF- RII) is localized on band 1p36.2- p36.3. Hum. Genet. 87:623- 624, 1991. 3 B c

GAM8297 367 TNFRSF1B Li, X.; Yang, Y.; Ashwell, J. D.: TNF- RII and c- IAP1 mediate ubiquitinationand degradation of TRAF2. Nature 416: 345- 349, 2002. 3 B c

GAM8297 367 TNFRSF1B Milatovich, A.; Song, K.; Heller, R. A.; Francke, U.: Tumor necrosisfactor receptor genes, TNFR1 and TNFR2, on human chromosomes 12 and1. Somat. Cell Molec. Genet. 17: 519- 523, 1991. 3 B c

GAM8297 367 TNFRSF1B Santee, S. M.; Owen- Schaub, L. B.: Human tumor necrosis factorreceptor p75/80 (CD120b) gene structure and promoter characterization. J.Biol. Chem. 271: 21151- 21159, 1996. 3 B c

GAM8297 367 TNFRSF1B Sashio, H.; Tamura, K.; Ito, R.; Yamamoto, Y.; Bamba, H.; Kosaka,T.; Fukui, S.; Sawada, K.; Fukuda, Y.; Tamura, K.; Satomi, M.; Shimoyama,T.; Furuyama, J.: Polymorphisms of the TNF gene and the TNF receptorsuperfamily member 1B gene are associated with susceptibility to ulcerativecolitis and Crohn's disease, respectively. Immunogenetics 53: 1020- 1027,2002. 3 B c

GAM8297 367 TNFRSF1B Schall, T. J.; Lewis, M.; Koller, K. J.; Lee, A.; Rice, G. C.;Wong, G. H. W.; Gatanaga, T.; Granger, G. A.; Lentz, R.; Raab, H.;Kohr, W. J.; Goeddel, D. V.: Molecular cloning and expression ofa receptor for human tumor necrosis factor. Cell 61: 361- 370, 1990. 3 B c

GAM8297 367 TNFRSF1B Van Ostade, X.; Vandenabeele, P.; Everaerdt, B.; Loetscher, H.;Gentz, R.; Brockhaus, M.; Lesslauer, W.; Tavernier, J.; Brouckaert,P.; Fiers, W.: Human TNF mutants with selective activity on the p55receptor. Nature 361: 266-269, 1993. 3 B c

GAM8297 367 TNFRSF1B White, P. S.; Maris, J. M.; Beltinger, C.; Sulman, E.; Marshall,H. N.; Fujimori, M.; Kaufman, B. A.; Biegel, J. A.; Allen, C.; Hilliard,C.; Valentine, M. B.; Look, A. T.; Enomoto, H.; Sakiyama, S.; Brodeur,G. M.: A region of consistent deletion in neuroblastoma maps withinhuman chromosome 1p36.2- 36.3. Proc. Nat. Acad. Sci. 92: 5520- 5524,1995. 3 B c

GAM8297 367 UBE2V1 Deng, L.; Wang, C.; Spencer, E.; Yang, L.; Braun, A.; You, J.;Slaughter, C.; Pickart, C.; Chen, Z. J.: Activation of the I- kappa- Bcomplex by TRAF6 requires a dimeric ubiquitin- conjugating enzyme complexand a unique polyubiquitin chain. Cell 103: 351- 361, 2000. 3 B c

GAM8297 367 UBE2V1 Hofmann, R. M.; Pickart, C. M.: Noncanonical MMS2- encoded ubiquitin-conjugatingenzyme functions in assembly of novel polyubiquitin chains for DNArepair. Cell 96: 645- 653, 1999. 3 B c

GAM8297 367 UBE2V1 Rothofsky, M. L.; Lin, S. L.: CROC- 1 encodes a protein which mediatestranscriptional activation of the human FOS promoter. Gene 195:141-149, 1997. 3 B c

GAM8297 367 UBE2V1 Sancho, E.; Vila, M. R.; Sanchez- Pulido, L.; Lozano, J. J.; Paciucci,R.; Nadal, M.; Fox, M.; Harvey, C.; Bercovich, B.; Loukili, N.; Ciechanover,A.; Lin, S. L.; Sanz, F.; Estivill, X.; Valencia, A.; Thomson, T.M.: Role of UEV- 1, an inactive variant of the E2 ubiquitin- conjugatingenzymes, in in vitro differentiation and cell cycle behavior of HT- 29- M6intestinal 3 B c

mucosecretory cells. Molec. Cell. Biol. 18: 576- 589,1998.

GAM8297 367 UNC5C Ackerman, S. L.; Knowles, B. B.: Cloning and mapping of the UNC5Cgene to human chromosome 4q21- q23. Genomics 52: 205- 208, 1998. 3 B c

GAM8297 367 UNC5C Ackerman, S. L.; Kozak, L. P.; Przyborski, S. A.; Rund, L. A.;Boyer, B. B.; Knowles, B. B.: The mouse rostral cerebellar malformationgene encodes an UNC- 5- like protein. Nature 386: 838- 842, 1997. 3 B c

GAM8297 367 UNC5C Lane, P. W.; Bronson, R. T.; Spencer, C. A.: Rostral cerebellarmalformation, (rcm): a new recessive mutation on chromosome 3 of themouse. J. Hered. 83: 315- 318, 1992. 3 B c

GAM8297 367 UNC5C Leonardo, E. D.; Hinck, L.; Masu, M.; Keino- Masu, K.; Ackerman,S. L.; Tessier- Lavigne, M.: Vertebrate homologues of C. elegans UNC- 5are candidate netrin receptors. Nature 386: 833- 838, 1997. 3 B c

GAM8297 367 UNC5C Przyborski, S. A.; Knowles, B. B.; Ackerman, S. L.: Embryonicphenotype of Unc5h3 mutant mice suggests chemorepulsion during theformation of the rostral cerebellar boundary. Development 125: 41- 50,1998. 3 B c

GAM8297 367 UROS Astrin, K. H.; Warner, C. A.; Yoo, H.- W.; Goodfellow, P. J.; Tsai,S.- F.; Desnick, R. J.: Regional assignment of the human uroporphyrinogenIII synthase (UROS) gene to chromosome 10q25.2- q26.3. Hum. Genet. 87:18- 22, 1991. 3 B c

GAM8297 367 UROS Boulechfar, S.; Da Silva, V.; Deybach, J.- C.; Nordmann, Y.; Grandchamp,B.; de Verneuil, H.: Heterogeneity of mutations in the uroporphyrinogenIII synthase gene in congenital erythropoietic porphyria. Hum. Genet. 88:320- 324, 1992. 3 B c

GAM8297 367 UROS Deybach, J.- C.; de Verneuil, H.; Boulechfar, S.; Grandchamp, B.;Nordmann, Y.: Point mutations in the uroporphyrinogen III synthasegene in congenital erythropoietic porphyria (Gunther's disease). Blood 75:1763- 1765, 1990. 3 B c

GAM8297 367 UROS Frank, J.; Wang, X.; Lam, H.- M.; Aita, V. M.; Jugert, F. K.; Goerz,G.; Merk, H. F.; Poh- Fitzpatrick, M. B.; Christiano, A. M.: C73Ris a hotspot mutation in the uroporphyrinogen III synthase gene incongenital erythropoietic porphyria. Ann. Hum. Genet. 62: 225- 230,1998. 3 B c

GAM8297 367 UROS Shady, A. A.; Colby, B. R.; Cunha, L. F.; Astrin, K. H.; Bishop,D. F.; Desnick, R. J.: Congenital erythropoietic porphyria: identificationand expression of eight novel mutations in the uroporphyrinogen IIIsynthase gene. Brit. J. Haemat. 117: 980- 987, 2002. 3 B c

GAM8297 367 UROS Tanigawa, K.; Takamura, N.; Yamashita, S.: Congenital erythropoieticporphyria. Nippon Rinsho 53: 1422- 1426, 1995. 3 B c

GAM8297 367 UROS Tezcan, I.; Xu, W.; Gurgey, A.; Tuncer, M.; Cetin, M.; Oner, C.;Yetgin, S.; Ersoy, F.; Aizencang, G.; Astrin, K. H.; Desnick, R. J.: Congenital erythropoietic porphyria successfully treated by allogeneicbone marrow transplantation. Blood 92: 4053- 4058, 1998. 3 B c

GAM8297 367 UROS Tsai, S.- F.; Bishop, D. F.; Desnick, R. J.: Human uroporphyrinogenIII synthase: molecular cloning, nucleotide sequence, and expressionof a full- length cDNA. Proc. Nat. Acad. Sci. 85: 7049- 7053, 1988. 3 B c

GAM8297 367 UROS Warner, C. A.; Yoo, H. W.; Tsai, S.- F.; Roberts, A. G.; Desnick,R. J.: Congenital erythropoietic porphyria: characterization of thegenomic structure and identification of mutations in the uroporphyrinogenIII synthase gene. (Abstract) Am. J. Hum. Genet. 47 (suppl.): A83only, 1990. 3 B c

GAM8297 367 UROS Warner, C. A.; Yoo, H.- W.; Roberts, A. G.; Desnick, R. J.: Congenitalerythropoietic porphyria: identification and expression of exonicmutations in the uroporphyrinogen III synthase gene. J. Clin. Invest. 3 B c

89:693- 700, 1992.

GAM8297 367 UROS Xu, W.; Astrin, K. H.; Desnick, R. J.: Molecular basis of congenitalerythropoietic porphyria: mutations in the human uroporphyrinogenIII synthase gene. Hum. Mutat. 7: 187- 192, 1996. 3 B c

GAM8297 367 UROS Xu, W.; Kozak, C. A.; Desnick, R. J.: Uroporphyrinogen- III synthase:molecular cloning, nucleotide sequence, expression of a mouse full-lengthcDNA, and its localization on mouse chromosome 7. Genomics 26: 556-562,1995. 3 B c

GAM8297 367 UROS Xu, W.; Warner, C. A.; Desnick, R. J.: Congenital erythropoieticporphyria: identification and expression of 10 mutations in the uroporphyrinogenIII synthase gene. J. Clin. Invest. 95: 905- 912, 1995. 3 B c

GAM8297 367 VIM Colucci- Guyon, E.; Portier, M.- M.; Dunia, I.; Paulin, D.; Pournin,S.; Babinet, C.: Mice lacking vimentin develop and reproduce withoutan obvious phenotype. Cell 79: 679- 694, 1994. 3 B c

GAM8297 367 VIM Ferrari, S.; Battini, R.; Kaczmarek, L.; Rittling, S.; Calabretta,B.; de Riel, J. K.; Philiponis, V.; Weil, J.- F.; Baserga, R.: Codingsequence and growth regulation of the human vimentin gene. Molec.Cell. Biol. 6: 3614-3620, 1986. 3 B c

GAM8297 367 VIM Ferrari, S.; Cannizzaro, L. A.; Battini, R.; Huebner, K.; Baserga,R.: The gene encoding human vimentin is located on the short armof chromosome 10. Am. J. Hum. Genet. 41: 616- 626, 1987. 3 B c

GAM8297 367 VIM Gieser, L.; Swaroop, A.: Expressed sequence tags and chromosomallocalization of cDNA clones from a subtracted retinal pigment epitheliumlibrary. Genomics 13: 873- 876, 1992. 3 B c

GAM8297 367 VIM Lilienbaum, A.; Legagneux, V.; Portier, M.- M.; Dellagi, K.; Paulin,D.: Vimentin gene: expression in human lymphocytes and in Burkitt'slymphoma cells. EMBO J. 5: 2809- 2814, 1986. 3 B c

GAM8297 367 VIM Marcus, E. M.; Smith, B. A.; Telenius, H.; Landsvater, R. M.; Buys,C. H. C. M.; Ferrari, S.; Ponder, B. A. J.; Mathew, C. G. P.: BclIRFLP for the human vimentin gene. Nucleic Acids Res. 16: 9068 only,1988. 3 B c

GAM8297 367 VIM Mathew, C. G.; Wakeling, W.; Jones, E.; Easton, D.; Fisher, R.;Strong, C.; Smith, B.; Chin, K.; Little, P.; Nakamura, Y.; Shows,T. B.; Jones, C.; Goodfellow, P. J.; Povey, S.; Ponder, B. A. J.:Regional localization of polymorphic markers on chromosome 10 by physicaland genetic mapping. Ann. Hum. Genet. 54: 121- 129, 1990. 3 B c

GAM8297 367 VIM Perreau, J.; Lilienbaum, A.; Vasseur, M.; Paulin, D.: Nucleotidesequence of the human vimentin gene and regulation of its transcriptionin tissues and cultured cells. Gene 62: 7- 16, 1988. 3 B c

GAM8297 367 VIM Quax, W.; Meera Khan, P.; Quax- Jeuken, Y.; Bloemendal, H.: Thehuman desmin and vimentin genes are located on different chromosomes. Gene 38:189- 196, 1985. 3 B c

GAM8297 367 WISP1 Pennica, D.; Swanson, T. A.; Welsh, J. W.; Roy, M. A.; Lawrence,D. A.; Lee, J.; Brush, J.; Taneyhill, L. A.; Deuel, B.; Lew, M.; Watanabe,C.; Cohen, R. L.; Melhem, M. F.; Finley, G. G.; Quirke, P.; Goddard,A. D.; Hillan, K. J.; Gurney, A. L.; Botstein, D.; Levine, A. J.:WISP genes are members of the connective tissue growth factor familythat are up- regulated in Wnt- 1-transformed cells and aberrantly expressedin human colon tumors. Proc. Nat. Acad. Sci. 95: 14717- 14722, 1998. 3 B c

GAM8297 367 WISP1 Tanaka, S.; Sugimachi, K.; Saeki, H.; Kinoshita, J.; Ohga, T.;Shimada, M.; Maehara, Y.; Sugimachi, K.: A novel variant of WISP1lacking a von Willebrand 3 B c

type C module overexpressed in scirrhousgastric carcinoma. Oncogene 20: 5525- 5532, 2001.

GAM8358 255 A1BG Eiberg, H.; Bisgaard, M. L.; Mohr, J.: Linkage between alpha- 1- B- glycoprotein(A1BG) and Lutheran (LU) red blood group system: assignment to chromosome19: new genetic variants of A1BG. Clin. Genet. 36: 415- 418, 1989. 3 C c

GAM8358 255 A1BG Eiberg, H.; Nielsen, L. S.; Gahne, B.; Juneja, R. K.; Mohr, J.: Exclusion data for the alpha- 1- B glycoprotein (A1BG) polymorphism.(Abstract) Cytogenet. Cell Genet. 51: 994 only, 1989. 3 C c

GAM8358 255 A1BG Gahne, B.; Juneja, R. K.; Stratil, A.: Genetic polymorphism ofhuman plasma alpha- 1- B- glycoprotein: phenotyping by immunoblottingor by a simple method of 2- D electrophoresis. Hum. Genet. 76: 111- 115,1987. 3 C c

GAM8358 255 A1BG Ishioka, N.; Takahashi, N.; Putnam, F. W.: Amino acid sequenceof human plasma alpha- 1B- glycoprotein: homology to the immunoglobulinsupergene family. Proc. Nat. Acad. Sci. 83: 2363- 2367, 1986. 3 C c

GAM8358 255 A1BG Juneja, R. K.; Weitkamp, L. R.; Stratil, A.; Gahne, B.; Guttormsen,S. A.: Further studies of the plasma alpha- 1- B- glycoprotein polymorphism:two new alleles and allele frequencies in Caucasians and in Americanblacks. Hum. Hered. 38: 267- 272, 1988. 3 C c

GAM8358 255 ABCC3 Belinsky, M. G.; Bain, L. J.; Balsara, B. B.; Testa, J. R.; Kruh,G. D.: Characterization of MOAT- C and MOAT- D, new members of theMRP/cMOAT subfamily of transporter proteins. J. Nat. Cancer Inst. 90:1735- 1741, 1998. 3 C c

GAM8358 255 ABCC3 Fromm, M. F.; Leake, B.; Roden, D. M.; Wilkinson, G. R.; Kim, R.B.: Human MRP3 transporter: identification of the 5- prime flankingregion, genomic organization and alternative splice variants. Biochim.Biophys. Acta 1415: 369- 374, 1999. 3 C c

GAM8358 255 ABCC3 Kiuchi, Y.; Suzuki, H.; Hirohashi, T.; Tyson, C. A.; Sugiyama,Y.: cDNA cloning and inducible expression of human multidrug resistanceassociated protein 3 (MRP3). FEBS Lett. 433: 149- 152, 1998. 3 C c

GAM8358 255 ABCC3 Konig, J.; Rost, D.; Cui, Y.; Keppler, D.: Characterization ofthe human multidrug resistance protein isoform MRP3 localized to thebasolateral hepatocyte membrane. Hepatology 29: 1156- 1163, 1999. 3 C c

GAM8358 255 ABCC3 Kool, M.; van der Linden, M.; de Haas, M.; Scheffer, G. L.; deVree, J. M. L.; Smith, A. J.; Jansen, G.; Peters, G. J.; Ponne, N.;Scheper, R. J.; Oude Elferink, R. P. J.; Baas, F.; Borst, P.: MRP3,an organic anion transporter able to transport anti- cancer drugs. Proc.Nat. Acad. Sci. 96: 6914- 6919, 1999. 3 C c

GAM8358 255 ABCC3 Ortiz, D. F.; Li, S.; Iyer, R.; Zhang, X.; Novikoff, P.; Arias,I. M.: MRP3, a new ATP- binding cassette protein localized to thecanalicular domain of the hepatocyte. Am. J. Physiol. 276: G1493- G1500,1999. 3 C c

GAM8358 255 ABCC3 Uchiumi, T.; Hinoshita, E.; Haga, S.; Nakamura, T.; Tanaka, T.;Toh, S.; Furukawa, M.; Kawabe, T.; Wada, M.; Kagotani, K.; Okumura,K.; Kohno, K.; Akiyama, S.; Kuwano, M.: Isolation of a novel humancanalicular multispecific organic anion transporter, cMOAT2/MRP3,and its expression in cisplatin-resistant cancer cells with decreasedATP- dependent drug transport. Biochem. Biophys. Res. Commun. 252:103- 110, 1998. 3 C c

GAM8358 255 ADAR Bass, B. L.; Weintraub, H.: An unwinding activity that covalentlymodifies its double- stranded RNA substrate. Cell 55: 1089- 1098,1988. 3 C c

GAM8358 255 ADAR Kim, U.; Wang, Y.; Sanford, T.; Zeng, Y.; Nishikura, K.: Molecularcloning of cDNA for double- stranded RNA adenosine deaminase, a candidateenzyme for nuclear RNA editing. Proc. Nat. Acad. Sci. 91: 11457- 11461,1994. 3 C c

GAM8358 255 ADAR O'Connell, M. A.; Krause, S.; Higuchi, M.; Hsuan, J. J.; Totty,N. F.; Jenny, 3 C c
A.; Keller, W.: Cloning of cDNAs encoding mammaliandouble- stranded RNA-
specific adenosine deaminase. Molec. Cell. Biol. 15:1389- 1397, 1995.

GAM8358 255 ADAR Patterson, J. B.; Samuel, C. E.: Expression and regulation byinterferon of a 3 C c
double- stranded- RNA- specific adenosine deaminase fromhuman cells:
evidence for two forms of the deaminase. Molec. Cell.Biol. 15: 5376- 5388,
1995.

GAM8358 255 ADAR Wang, Q.; Khillan, J.; Gadue, P.; Nishikura, K.: Requirement ofthe RNA 3 C c
editing deaminase ADAR1 gene for embryonic erythropoiesis. Science 290:1765-
1768, 2000.

GAM8358 255 ADAR Wang, Y.; Zeng, Y.; Murray, J. M.; Nishikura, K.: Genomic organizationand 3 C c
chromosomal location of the human dsRNA adenosine deaminase gene:the enzyme
for glutamate- activated ion channel RNA editing. J. Molec.Biol. 254: 184-
195, 1995.

GAM8358 255 ADAR Weier, H.- U. G.; George, C. X.; Greulich, K. M.; Samuel, C. E.: The 3 C c
interferon- inducible, double- stranded RNA- specific adenosinedeaminase
gene (DSRAD) maps to human chromosome 1q21.1- 21.2. Genomics 30:372- 375,
1995.

GAM8358 255 ADAR Weier, H.- U. G.; George, C. X.; Lersch, R. A.; Breitweser, S.;Cheng, J.- 3 C c
F.; Samuel, C. E.: Assignment of the RNA- specific adenosinedeaminase gene
(Adar) to mouse chromosome 3F2 by in situ hybridization. Cytogenet.Cell
Genet. 89: 214- 215, 2000.

GAM8358 255 AK2 Bruns, G. A. P.; Regina, V. M.: Adenylate kinase- 2, a mitochondrialenzyme. 3 C c
Biochem. Genet. 15: 477- 486, 1977.

GAM8358 255 AK2 Carritt, B.; King, J.; Welch, H. M.: Gene order and localizationof enzyme 3 C c
loci on the short arm of chromosome 1. Ann. Hum. Genet. 46:329- 335, 1982.

GAM8358 255 AK2 Goss, S. J.; Harris, H.: Gene transfer by means of cell fusion.II. The 3 C c
mapping of 8 loci on human chromosome 1 by statistical analysisof gene
assortment in somatic cell hybrids. J. Cell Sci. 25: 39- 57,1977.

GAM8358 255 AK2 Van Cong, N.; Billardon, C.; Rebourcet, R.; Kaouel, C. L.- B.; Picard,J. Y.; 3 C c
Weil, D.; Frezal, J.: The existence of a second adenylatekinase locus linked
to PGM- 1 and peptidase- C. Ann. Genet. 15: 213- 218,1972.

GAM8358 255 AR Abel, A.; Walcott, J.; Woods, J.; Duda, J.; Merry, D. E.: Expressionof 3 C c
expanded repeat androgen receptor produces neurologic disease intransgenic
mice. Hum. Molec. Genet. 10: 107- 116, 2001.

GAM8358 255 AR Bailey, C. K.; Andriola, I. F. M.; Kampinga, H. H.; Merry, D. E.: Molecular 3 C c
chaperones enhance the degradation of expanded polyglutaminerepeat androgen
receptor in a cellular model of spinal and bulbarmuscular atrophy. Hum.
Molec. Genet. 11: 515- 523, 2002.

GAM8358 255 AR Batch, J. A.; Evans, B. A. J.; Hughes, I. A.; Patterson, M. N.: Mutations of 3 C c
the androgen receptor gene identified in perineal hypospadias. J.Med. Genet.
30: 198- 201, 1993.

GAM8358 255 AR Batch, J. A.; Williams, D. M.; Davies, H. R.; Brown, B. D.; Evans,B. A. J.; 3 C c
Hughes, I. A.; Patterson, M. N.: Androgen receptor genemutations identified
by SSCP in fourteen subjects with androgen insensitivitysyndrome. Hum.
Molec. Genet. 1: 497- 503, 1992.

GAM8358 255 AR Beitel, L. K.; Kazemi- Esfarjani, P.; Kaufman, M.; Lumbroso, R.;DiGeorge, A. 3 C c
M.; Killinger, D. W.; Trifiro, M. A.; Pinsky, L.: Substitutionof arginine-
839 by cysteine or histidine in the androgen receptorcauses different
receptor phenotypes in cultured cells and coordinatedegrees of clinical

androgen resistance. J. Clin. Invest. 94: 546- 554,1994.

GAM8358 255 AR Belsham, D. D.; Pereira, F.; Greenberg, C. R.; Liao, S.; Wrogemann,K.: 3 C c
Leu676- to- pro mutation of the androgen receptor causes completeandrogen
insensitivity syndrome in a large Hutterite kindred. Hum.Mutat. 5: 28- 33,
1995.

GAM8358 255 AR Bevan, C. L.; Brown, B. B.; Davies, H. R.; Evans, B. A. J.; Hughes,I. A.; 3 C c
Patterson, M. N.: Functional analysis of six androgen receptormutations
identified in patients with partial androgen insensitivitysyndrome. Hum.
Molec. Genet. 5: 265- 273, 1996.

GAM8358 255 AR Biancalana, V.; Serville, F.; Pommier, J.; Julien, J.; Hanauer,A.; Mandel, 3 C c
J. L.: Moderate instability of the trinucleotide repeatin spinobulbar
muscular atrophy. Hum. Molec. Genet. 1: 255- 258,1992.

GAM8358 255 AR Boehmer, A. L. M.; Brinkmann, A. O.; Niermeijer, M. F.; Bakker,L.; Halley, 3 C c
D. J. J.; Drop, S. L. S.: Germ- line and somatic mosaicismin the androgen
insensitivity syndrome: implications for genetic counseling.(Letter) Am. J.
Hum. Genet. 60: 1003- 1006, 1997.

GAM8358 255 AR Boehmer, A. L. M.; Brinkmann, A. O.; Nijman, R. M.; Verleun- Mooijman,M. C. 3 C c
T.; de Ruiter, P.; Niermeijer, M. F.; Drop, S. L. S.: Phenotypicvariation in
a family with partial androgen insensitivity syndromeexplained by
differences in 5- alpha dihydrotestosterone availability. J.Clin. Endocr.
Metab. 86: 1240- 1246, 2001.

GAM8358 255 AR Bouvattier, C.; Carel, J.- C.; Lecointre, C.; David, A.; Sultan,C.; 3 C c
Bertrand, A.- M., Morel, Y.; Chaussain, J.- L.: Postnatal changesof T, LH,
and FSH in 46,XY infants with mutations in the AR gene. J.Clin. Endocr.
Metab. 87: 29- 32, 2002.

GAM8358 255 AR Brown, C. J.; Goss, S. J.; Lubahn, D. B.; Joseph, D. R.; Wilson,E. M.; 3 C c
French, F. S.; Willard, H. F.: Androgen receptor locus onthe human X
chromosome: regional localization to Xq11- 12 and descriptionof a DNA
polymorphism. Am. J. Hum. Genet. 44: 264- 269, 1989.

GAM8358 255 AR Brown, T. R.; Lubahn, D. B.; Wilson, E. M.; Joseph, D. R.; French,F. S.; 3 C c
Migeon, C. J.: Deletion of the steroid- binding domain of thehuman androgen
receptor gene in one family with complete androgeninsensitivity syndrome:
evidence for further genetic heterogeneityin this syndrome. Proc. Nat. Acad.
Sci. 85: 8151- 8155, 1988.

GAM8358 255 AR Bruggenwirth, H. T.; Boehmer, A. L. M.; Ramnarain, S.; Verleun- Mooijman,M. 3 C c
C. T.; Satijn, D. P. E.; Trapman, J.; Grootegoed, J. A.; Brinkmann,A. O.:
Molecular analysis of the androgen- receptor gene in a familywith receptor-
positive partial androgen insensitivity: an unusualtype of intronic
mutation. Am. J. Hum. Genet. 61: 1067- 1077, 1997.

GAM8358 255 AR Buchanan, G.; Yang, M.; Harris, J. M.; Nahm, H. S.; Han, G.; Moore,N.; 3 C c
Bentel, J. M.; Matusik, R. J.; Horsfall, D. J.; Marshall, V. R.;Greenberg,
N. M.; Tilley, W. D.: Mutations at the boundary of thehinge and ligand
binding domain of the androgen receptor confer increasedtransactivation
function. Molec. Endocr. 15: 46- 56, 2001.

GAM8358 255 AR Butler, R.; Leigh, P. N.; McPhaul, M. J.; Gallo, J.- M.: Truncatedforms of 3 C c
the androgen receptor are associated with polyglutamine expansionin X-
linked spinal and bulbar muscular atrophy. Hum. Molec. Genet. 7:121- 127,
1998.

GAM8358 255 AR Calvo, R. M.; Asuncion, M.; Sancho, J.; San Millan, J. L.; Escobar- 3 C c
Morreale,H. F.: The role of the CAG repeat polymorphism in the androgen

receptorgene and of skewed X- chromosome inactivation, in the pathogenesisof hirsutism. J. Clin. Endocr. Metab. 85: 1735- 1740, 2000.

GAM8358 255 AR Caplen, N. J.; Taylor, J. P.; Statham, V. S.; Tanaka, F.; Fire,A.; Morgan, 3 C c
R. A.: Rescue of polyglutamine- mediated cytotoxicityby double- stranded RNA- mediated RNA interference. Hum. Molec. Genet. 11:175- 184, 2002.

GAM8358 255 AR Caskey, C. T.; Pizzuti, A.; Fu, Y.- H.; Fenwick, R. G., Jr.; Nelson,D. L.: 3 C c
Triplet repeat mutations in human disease. Science 256:784- 789, 1992.

GAM8358 255 AR Chang, B.; Zheng, S. L.; Hawkins, G. A.; Isaacs, S. D.; Wiley,K. E.; Turner, 3 C c
A.; Carpten, J. D.; Bleecker, E. R.; Walsh, P. C.;Trent, J. M.; Meyers, D. A.; Isaacs, W. B.; Xu, J.: Polymorphic GGCrepeats in the androgen receptor gene are associated with hereditaryand sporadic prostate cancer risk. Hum. Genet. 110: 122- 129, 2002.

GAM8358 255 AR Chang, C.; Kokontis, J.; Liao, S.: Molecular cloning of humanand rat 3 C c
complementary DNA encoding androgen receptors. Science 240:324- 326, 1988.

GAM8358 255 AR Choong, C. S.; Kemppainen, J. A.; Zhou, Z.- X.; Wilson, E. M.:Reduced 3 C c
androgen receptor gene expression with first exon CAG repeatexpansion. Molec. Endocr. 10: 1527- 1535, 1996.

GAM8358 255 AR Choong, C. S.; Quigley, C. A.; French, F. S.; Wilson, E. M.:A novel missense 3 C c
mutation in the amino- terminal domain of the humanandrogen receptor gene in a family with partial androgen insensitivitysyndrome causes reduced efficiency of protein translation. J. Clin.Invest. 98: 1423- 1431, 1996.

GAM8358 255 AR Chu, J.; Zhang, R.; Zhao, Z.; Zou, W.; Han, Y.; Qi, Q.; Zhang,H.; Wang, J.- 3 C c
C.; Tao, S.; Liu, X.; Luo, Z.: Male fertility is compatiblewith an Arg840Cys substitution in the AR in a large Chinese familywith divergent phenotypes of AR insensitivity syndrome. J. Clin.Endocr. Metab. 87: 347- 351, 2002.

GAM8358 255 AR Coetzee, G. A.; Ross, R. K.: Re: Prostate cancer and the androgenreceptor. 3 C c
(Letter) J. Nat. Cancer Inst. 86: 872- 873, 1994.

GAM8358 255 AR Correa- Cerro, L.; Wohr, G.; Haussler, J.; Berthon, P.; Drelon,E.; Mangin, 3 C c
P.; Fournier, G.; Cussenot, O.; Kraus, P.; Just, W.; Paiss,T.; Cantu, J. M.; Vogel, W.: (CAG)nCAA and GGN repeats in the humanandrogen receptor gene are not associated with prostate cancer ina French- German population. Europ. J. Hum. Genet. 7: 347- 362, 1999.

GAM8358 255 AR Dowsing, A. T.; Yong, E. L.; Clark, M.; McLachlan, R. I.; de Kretser,D. M.; 3 C c
Trounson, A. O.: Linkage between male infertility and trinucleotiderepeat expansion in the androgen- receptor gene. Lancet 354: 640- 643,1999.

GAM8358 255 AR Edwards, A.; Hammond, H. A.; Jin, L.; Caskey, C. T.; Chakraborty,R.: Genetic 3 C c
variation at five trimeric and tetrameric tandem repeatloci in four human population groups. Genomics 12: 241- 253, 1992.

GAM8358 255 AR Elo, J. P.; Kvist, L.; Leinonen, K.; Isomaa, V.; Hentuu, P.; Lukkarinen,O.; 3 C c
Vihko, P.: Mutated human androgen receptor gene detected in aprostatic cancer patient is also activated by estradiol. J. Clin.Endocr. Metab. 80: 3494- 3500, 1995.

GAM8358 255 AR Gaddipati, J. P.; McLeod, D. G.; Heidenberg, H. B.; Sesterhenn,I. A.; 3 C c
Finger, M. J.; Moul, J. W.; Srivastava, S.: Frequent detectionof codon 877 mutation in the androgen receptor gene in advanced prostatecancers. Cancer Res. 54: 2861- 2864, 1994.

GAM8358 255 AR Gehring, U.; Tomkins, G. M.: Characterization of a hormone receptordefect in 3 C c
the androgen- insensitivity mutant. Cell 3: 59- 64, 1974.

GAM8358 255 AR Gingrich, J. R.; Barrios, R. J.; Kattan, M. W.; Nahm, H. S.; Finegold,M. J.; 3 C c
Greenberg, N. M.: Androgen- independent prostate cancer progressionin the

TRAMP model. Cancer Res. 57: 4687- 4691, 1997.

GAM8358 255 AR Gingrich, J. R.; Greenberg, N. M.: A transgenic mouse prostatecancer model. 3 C c
Toxicol. Path. 24: 502- 504, 1996.

GAM8358 255 AR Giovannucci, E.; Stampfer, M. J.; Krithivas, K.; Brown, M.; Brufsky,A.; 3 C c
Talcott, J.; Hennekens, C. H.; Kantoff, P. W.: The CAG repeatwithin the
androgen receptor gene and its relationship to prostatecancer. Proc. Nat.
Acad. Sci. 94: 3320- 3323, 1997.

GAM8358 255 AR Gottlieb, B.; Beitel, L. K.; Trifiro, M. A.: Variable expressivityand 3 C c
mutation databases: the androgen receptor gene mutations database.
Hum.Mutat. 17: 382- 388, 2001.

GAM8358 255 AR Gottlieb, B.; Trifiro, M.; Lumbroso, R.; Pinsky, L.: The androgenreceptor 3 C c
gene mutations database. Nucleic Acids Res. 25: 158- 162,1997.

GAM8358 255 AR Gottlieb, B.; Trifiro, M.; Lumbroso, R.; Vasiliou, D. M.; Pinsky,L.: The 3 C c
androgen receptor gene mutations database. Nucleic AcidsRes. 24: 151- 154,
1996.

GAM8358 255 AR Griffin, J. E.: Androgen resistance- - the clinical and molecularspectrum. 3 C c
New Eng. J. Med. 326: 611- 618, 1992.

GAM8358 255 AR Grino, P. B.; Griffin, J. E.; Cushard, W. G., Jr.; Wilson, J.D.: A mutation 3 C c
of the androgen receptor associated with partial androgenresistance,
familial gynecomastia, and fertility. J. Clin. Endocr.Metab. 66: 754- 761,
1988.

GAM8358 255 AR Grino, P. B.; Isidro- Gutierrez, R. F.; Griffin, J. E.; Wilson,J. D.: 3 C c
Androgen resistance associated with a qualitative abnormalityof the androgen
receptor and responsive to high dose androgen therapy. J.Clin. Endocr.
Metab. 68: 578- 584, 1989.

GAM8358 255 AR Hardy, D. O.; Scher, H. I.; Bogenreider, T.; Sabbatini, P.; Zhang,Z.- F.; 3 C c
Nanus, D. M.; Catterall, J. F.: Androgen receptor CAG repeatlengths in
prostate cancer: correlation with age of onset. J. Clin.Endocr. Metab. 81:
4400- 4405, 1996.

GAM8358 255 AR Hellwinkel, O. J.- C.; Holterhus, P.- M.; Struve, D.; Marschke,C.; Homburg, 3 C c
N.; Hiort, O.: A unique exonic splicing mutation inthe human androgen
receptor gene indicates a physiologic relevanceof regular androgen receptor
transcript variants. J. Clin. Endocr.Metab. 86: 2569- 2575, 2001.

GAM8358 255 AR Hickey, T.; Chandy, A.; Norman, R. J.: The androgen receptorCAG repeat 3 C c
polymorphism and X- chromosome inactivation in AustralianCaucasian women
with infertility related to polycystic ovary syndrome. J.Clin. Endocr.
Metab. 87: 161- 165, 2002.

GAM8358 255 AR Hiort, O.; Sinnecker, G. H. G.; Holterhus, P.- M.; Nitsche, E.M.; Kruse, K.: 3 C c
Inherited and de novo androgen receptor gene mutations:investigation of
single- case families. J. Pediat. 132: 939- 943,1998.

GAM8358 255 AR Holterhus, P. M.; Sinnecker, G. H. G.; Wollmann, H. A.; Struve,D.; Homburg, 3 C c
N.; Kruse, K.; Hiort, O.: Expression of two functionallydifferent androgen
receptors in a patient with androgen insensitivity. Europ.J. Pediat. 158:
702- 706, 1999.

GAM8358 255 AR Holterhus, P.- M.; Bruggenwirth, H. T.; Hiort, O.; Kleinkauf- Houcken,A.; 3 C c
Kruse, K.; Sinnecker, G. H. G.; Brinkmann, A. O.: Mosaicism dueto a somatic
mutation of the androgen receptor gene determines phenotypein androgen
insensitivity syndrome. J. Clin. Endocr. Metab. 82:3584- 3589, 1997.

GAM8358 255 AR Holterhus, P.- M.; Sinnecker, G. H. G.; Hiort, O.: Phenotypicdiversity and 3 C c
testosterone- induced normalization of mutant L712F androgenreceptor

function in a kindred with androgen insensitivity. J. Clin.Endocr. Metab. 85: 3245- 3250, 2000.

GAM8358 255 AR Holterhus, P.- M.; Wiebel, J.; Sinnecker, G. H. G.; Bruggenwirth,H. T.; 3 C c
Sippell, W. G.; Brinkmann, A. O.; Kruse, K.; Hiort, O.: Clinicaland molecular spectrum of somatic mosaicism in androgen insensitivitysyndrome. Pediat. Res. 46: 684- 690, 1999.

GAM8358 255 AR Hughes, I. A.; Evans, B. A. J.: Complete androgen insensitivitysyndrome 3 C c
characterized by increased concentration of a normal androgenreceptor in genital skin fibroblasts. J. Clin. Endocr. Metab. 63:309- 315, 1986.

GAM8358 255 AR Imasaki, K.; Okabe, T.; Murakami, H.; Tanaka, Y.; Haji, M.; Takayanagi,R.; 3 C c
Nawata, H.: Androgen insensitivity syndrome due to new mutationsin the DNA-binding domain of the androgen receptor. Molec. Cell.Endocr. 120: 15- 24, 1996.

GAM8358 255 AR Imperato- McGinley, J.; Ip, N. Y.; Gautier, T.; Neuweiler, J.;Gruenspan, H.; 3 C c
Liao, S.; Chang, C.; Balazs, I.: DNA linkage analysisand studies of the androgen receptor gene in a large kindred withcomplete androgen insensitivity. Am. J. Med. Genet. 36: 104- 108,1990.

GAM8358 255 AR Irvine, R. A.; Yu, M. C.; Ross, R. K.; Coetzee, G. A.: The CAGand GGC 3 C c
microsatellites of the androgen receptor gene are in linkagedisequilibrium in men with prostate cancer. Cancer. Res. 55: 1937- 1940,1995.

GAM8358 255 AR Jakubiczka, S.; Nedel, S.; Werder, E. A.; Schleiermacher, E.;Theile, U.; 3 C c
Wolff, G.; Wieacker, P.: Mutations of the androgen receptorgene in patients with complete androgen insensitivity. Hum. Mutat. 9:57- 61, 1997.

GAM8358 255 AR Jukier, L.; Kaufman, M.; Pinsky, L.; Peterson, R. E.: Partialandrogen 3 C c
resistance associated with secondary 5- alpha- reductase deficiency:identification of a novel qualitative androgen receptor defect andclinical implications. J. Clin. Endocr. Metab. 59: 679- 688, 1984.

GAM8358 255 AR Kang, H.- Y.; Yeh, S.; Fujimoto, N.; Chang, C.: Cloning and 3 C c
characterizationof human prostate coactivator ARA54, a novel protein that associateswith the androgen receptor. J. Biol. Chem. 274: 8570- 8576, 1999.

GAM8358 255 AR Kaufman, M.; Pinsky, L.; Bowin, A.; Au, M. W. S.: Familial externalgenital 3 C c
ambiguity due to a transformation defect of androgen- receptorcomplexes that is expressed with 5- alpha- dihydrotestosterone and thesynthetic androgen methyltrienolone. Am. J. Med. Genet. 18: 493- 507,1984.

GAM8358 255 AR Kaufman, M.; Straisfeld, C.; Pinsky, L.: Male 3 C c
pseudohermaphroditismpresumably due to target organ unresponsiveness to androgens: deficient5- alpha- dihydrotestosterone binding in cultured skin fibroblasts. J.Clin. Invest. 58: 345- 350, 1976.

GAM8358 255 AR Kazemi- Esfarjani, P.; Beitel, L. K.; Trifiro, M.; Kaufman, M.;Rennie, P.; 3 C c
Sheppard, P.; Matusik, R.; Pinsky, L.: Substitution ofvaline- 865 by methionine or leucine in the human androgen receptorcauses complete or partial androgen insensitivity, respectively withdistinct androgen receptor phenotypes. Molec. Endocr. 7: 37- 46,1993.

GAM8358 255 AR Keenan, B. S.; Meyer, W. J., III; Hadjian, A. J.; Jones, H. W.;Migeon, C. 3 C c
J.: Syndrome of androgen insensitivity in man: absenceof 5- alpha-dihydrotestosterone binding protein in skin fibroblasts. J.Clin. Endocr. 38: 1143- 1146, 1974.

GAM8358 255 AR Kittles, R. A.; Young, D.; Weinrich, S.; Hudson, J.; Argyropoulos,G.; Ukoli, 3 C c
F.; Adams- Campbell, L.; Dunston, G. M.: Extent of linkagedisequilibrium between the androgen receptor gene CAG and GGC repeatsin human populations:

implications for prostate cancer risk. Hum.Genet. 109: 253- 261, 2001.

GAM8358 255 AR Klocker, H.; Kaspar, F.; Eberle, J.; Uberreiter, S.; Radmayr,C.; Bartsch, 3 C c
G.: Point mutation in the DNA binding domain of theandrogen receptor in two families with Reifenstein syndrome. Am.J. Med. Genet. 50: 1318- 1327, 1992.

GAM8358 255 AR Knoke, I.; Allera, A.; Wieacker, P.: Significance of the CAGrepeat length in 3 C c
the androgen receptor gene (AR) for the transactivationfunction of an M780I mutant AR. Hum. Genet. 104: 257- 261, 1999.

GAM8358 255 AR Kobayashi, Y.; Miwa, S.; Merry, D. E.; Kume, A.; Mei, L.; Doyu,M.; Sobue, 3 C c
G.: Caspase- 3 cleaves the expanded androgen receptor proteinof spinal and bulbar muscular atrophy in a polyglutamine repeat length- dependentmanner. Biochem. Biophys. Res. Commun. 252: 145- 150, 1998.

GAM8358 255 AR Koivisto, P. A.; Schleutker, J.; Helin, H.; Ehren- van Eekelen,C.; 3 C c
Kallioniemi, O.- P.; Trapman, J.: Androgen receptor gene alterationsand chromosomal gains and losses in prostate carcinomas appearingduring finasteride treatment for benign prostatic hyperplasia. Clin.Cancer Res. 5: 3578- 3582, 1999.

GAM8358 255 AR Kooy, R. F.; Reyniers, E.; Storm, K.; Vits, L.; van Velzen, D.;de Ruiter, P. 3 C c
E.; Brinkmann, A. O.; de Paepe, A.; Willems, P. J.:CAG repeat contraction in the androgen receptor gene in three brotherswith mental retardation. Am. J. Med. Genet. 85: 209- 213, 1999.

GAM8358 255 AR La Spada, A. R.; Wilson, E. M.; Lubahn, D. B.; Harding, A. E.;Fischbeck, K. 3 C c
H.: Androgen receptor gene mutations in X- linked spinaland bulbar muscular atrophy. Nature 352: 77- 79, 1991.

GAM8358 255 AR La Spada, A.; Fischbeck, K. H.: Androgen receptor gene defectin X- linked 3 C c
spinal and bulbar muscular atrophy. (Abstract) Am. J.Hum. Genet. 49 (suppl.): 20, 1991.

GAM8358 255 AR Lewis, M.; Kaita, H.; Giblett, E. R.; Anderson, J.; Philipps,S.; Steinberg, 3 C c
A. G.; McAlpine, P. J.: Multiplicity of genetic polymorphismsof blood in the Schmiedeleut Hutterites. Am. J. Med. Genet. 22:477- 485, 1985.

GAM8358 255 AR Liao, S.; Witte, D.: Autoimmune anti- androgen- receptor antibodiesin human 3 C c
serum. Proc. Nat. Acad. Sci. 82: 8345- 8348, 1985.

GAM8358 255 AR Lim, H. N.; Chen, H.; McBride, S.; Dunning, A. M.; Nixon, R. M.;Hughes, I. 3 C c
A.; Hawkins, J. R.: Longer polyglutamine tracts in theandrogen receptor are associated with moderate to severe undermasculinizedgenitalia in XY males. Hum. Molec. Genet. 9: 829- 834, 2000.

GAM8358 255 AR Lin, S.- Y.; Ohno, S.: The binding of androgen receptor to DNAand RNA. 3 C c
Biochim. Biophys. Acta 654: 181- 186, 1981.

GAM8358 255 AR Lobaccaro, J.- M.; Lumbroso, S.; Belon, C.; Galtier- Dereure, F.;Bringer, 3 C c
J.; Lesimple, T.; Namer, M.; Cutuli, B. F.; Pujol, H.; Sultan,C.: Androgen receptor gene mutation in male breast cancer. Hum.Molec. Genet. 2: 1799- 1802, 1993.

GAM8358 255 AR Lubahn, D. B.; Brown, T. R.; Simental, J. A.; Higgs, H. N.; Migeon,C. J.; 3 C c
Wilson, E. M.; French, F. S.: Sequence of the intron/exonjunctions of the coding region of the human androgen receptor geneand identification of a point mutation in a family with complete androgeninsensitivity. Proc. Nat. Acad. Sci. 86: 9534- 9538, 1989.

GAM8358 255 AR Lubahn, D. B.; Joseph, D. R.; Sar, M.; Tan, J.; Higgs, H. N.;Larson, R. E.; 3 C c
French, F. S.; Wilson, E. M.: The human androgen receptor:complementary deoxyribonucleic acid cloning, sequence analysis andgene expression in prostate. Molec. Endocr. 2: 1265- 1275, 1988.

GAM8358 255 AR Lubahn, D. B.; Joseph, D. R.; Sullivan, P. M.; Willard, H. F.;French, F. S.; 3 C c
Wilson, E. M.: Cloning of human androgen receptorcomplementary DNA and
localization to the X chromosome. Science 240:327- 330, 1988.

GAM8358 255 AR Lumbroso, S.; Lobaccaro, J. M.; Georget, V.; Leger, J.; Poujol,N.; 3 C c
Terouanne, B.; Evain- Brion, D.; Czernichow, P.; Sultan, C.: Anovel
substitution (leu707- to- arg) in exon 4 of the androgen receptorgene causes
complete androgen resistance. J. Clin. Endocr. Metab. 81:1984- 1988, 1996.

GAM8358 255 AR Lund, A.; Udd, B.; Juvonen, V.; Andersen, P. M.; Cederquist, K.;Davis, M.; 3 C c
Gellera, C.; Kolmel, C.; Ronnevi, L.- O.; Sperfeld, A.- D.;Sorensen, S.- A.;
Tranebjaerg, L.; Van Maldergem, L.; Watanabe, M.;Weber, M.; Yeung, L.;
Savontaus, M.- L.: Multiple founder effectsin spinal and bulbar muscular
atrophy (SBMA, Kennedy disease) aroundthe world. Europ. J. Hum. Genet. 9:
431- 436, 2001.

GAM8358 255 AR Macke, J. P.; Hu, N.; Hu, S.; Bailey, M.; King, V. L.; Brown,T.; Hamer, D.; 3 C c
Nathans, J.: Sequence variation in the androgen receptorgene is not a common
determinant of male sexual orientation. Am.J. Hum. Genet. 53: 844- 852,
1993.

GAM8358 255 AR MacLean, H. E.; Chu, S.; Warne, G. L.; Zajac, J. D.: Relatedindividuals with 3 C c
different androgen receptor gene deletions. J. Clin.Invest. 91: 1123- 1128,
1993.

GAM8358 255 AR Madgar, I.; Green, L.; Kent- First, M.; Weissenberg, R.; Gershoni- 3 C c
Baruch,R.; Goldman, B.; Friedman, E.: Genotyping of Israeli infertile
menwith idiopathic oligozoospermia. Clin. Genet. 62: 203- 207, 2002.

GAM8358 255 AR Marcelli, M.; Tilley, W. D.; Wilson, C. M.; Griffin, J. E.; Wilson,J. D.; 3 C c
McPhaul, M. J.: Definition of the human androgen receptorgene structure
permits the identification of mutations that causeandrogen resistance:
premature termination of the receptor proteinat amino acid residue 588
causes complete androgen resistance. Molec.Endocr. 4: 1105- 1116, 1990.

GAM8358 255 AR Marcelli, M.; Tilley, W. D.; Wilson, C. M.; Wilson, J. D.; Griffin,J. E.; 3 C c
McPhaul, M. J.: A single nucleotide substitution introducesa premature
termination codon into the androgen receptor gene of apatient with receptor-
negative androgen resistance. J. Clin. Invest. 85:1522- 1528, 1990.

GAM8358 255 AR Marcelli, M.; Tilley, W. D.; Zoppi, S.; Griffin, J. E.; Wilson,J. D.; 3 C c
McPhaul, M. J.: Androgen resistance associated with a mutationof the
androgen receptor at amino acid 772 (arg- to- cys) results froma combination
of decreased messenger ribonucleic acid levels and impairmentof receptor
function. J. Clin. Endocr. 73: 318- 325, 1991.

GAM8358 255 AR McCampbell, A.; Taylor, J. P.; Taye, A. A.; Robitschek, J.; Li,M.; Walcott, 3 C c
J.; Merry, D.; Chai, Y.; Paulson, H.; Sobue, G.; Fischbeck,K. H.: CREB-
binding protein sequestration by expanded polyglutamine. Hum.Molec. Genet.
9: 2197- 2202, 2000.

GAM8358 255 AR McGuire, W. L.; Chamness, G. C.; Fuqua, S. A. W.: Estrogen receptorvariants 3 C c
in clinical breast cancer. Molec. Endocr. 5: 1571- 1577,1991.

GAM8358 255 AR McPhaul, M. J.; Griffin, J. E.: Male pseudohermaphroditism causedby 3 C c
mutations of the human androgen receptor. J. Clin. Endocr. Metab. 84:3435-
3441, 1999.

GAM8358 255 AR McPhaul, M. J.; Marcelli, M.; Tilley, W. D.; Griffin, J. E.; Isidro- 3 C c
Gutierrez,R. F.; Wilson, J. D.: Molecular basis of androgen resistance in
afamily with a qualitative abnormality of the androgen receptor
andresponsive to high- dose androgen therapy. J. Clin. Invest. 87: 1413-

1421,1991.

GAM8358 255 AR McPhaul, M. J.; Marcelli, M.; Zoppi, S.; Griffin, J. E.; Wilson,J. D.: 3 C c
Genetic basis of endocrine disease 4: the spectrum of mutationsin the androgen receptor gene that causes androgen resistance. J.Clin. Endocr. Metab. 76: 17- 23, 1993.

GAM8358 255 AR McPhaul, M. J.; Marcelli, M.; Zoppi, S.; Wilson, C. M.; Griffin,J. E.; 3 C c
Wilson, J. D.: Mutations in the ligand- binding domain of theandrogen receptor gene cluster in two regions of the gene. J. Clin.Invest. 90: 2097- 2101, 1992.

GAM8358 255 AR McPhaul, M. J.; Schweikert, H.- U.; Allman, D. R.: Assessmentof androgen 3 C c
receptor function in genital skin fibroblasts using arecombinant adenovirus to deliver an androgen- responsive reportergene. J. Clin. Endocr. Metab. 82: 1944- 1948, 1997.

GAM8358 255 AR Mifsud, A.; Ramirez, S.; Yong, E. L.: Androgen receptor geneCAG 3 C c
trinucleotide repeats in anovulatory infertility and polycysticovaries. J. Clin. Endocr. Metab. 85: 3484- 3488, 2000.

GAM8358 255 AR Migeon, B. R.; Brown, T. R.; Axelman, J.; Migeon, C. J.: Studiesof the locus 3 C c
for androgen receptor: localization on the human X andevidence for homology with the Tfm locus in the mouse. Proc. Nat.Acad. Sci. 78: 6339- 6343, 1981.

GAM8358 255 AR Mongan, N. P.; Jaaskelainen, J.; Green, K.; Schwabe, J. W.; Shimura,N.; 3 C c
Dattani, M.; Hughes, I. A.: Two de novo mutations in the AR genecause the complete androgen insensitivity syndrome in a pair of monozygotictwins. J. Clin. Endocr. Metab. 87: 1057- 1061, 2002.

GAM8358 255 AR Mononen, N.; Syrjakoski, K.; Matikainen, M.; Tammela, T. L. J.;Schleutker, 3 C c
J.; Kallioniemi, O.- P.; Trapman, J.; Koivisto, P. A.:Two percent of Finnish prostate cancer patients have a germ- line mutationin the hormone- binding domain of the androgen receptor gene. CancerRes. 60: 6479- 6481, 2000.

GAM8358 255 AR Murono, K.; Mendonca, B. B.; Arnhold, I. J. P.; Rigon, A. C. M.M.; Migeon, 3 C c
C. J.; Brown, T. R.: Human androgen insensitivity dueto point mutations encoding amino acid substitutions in the androgenreceptor steroid- binding domain. Hum. Mutat. 6: 152- 162, 1995.

GAM8358 255 AR Nakao, R.; Haji, M.; Yanase, T.; Ogo, A.; Takayanagi, R.; Katsube,T.; 3 C c
Fukumaki, Y.; Nawata, H.: A single amino acid substitution (met786- to-val)in the steroid- binding domain of human androgen receptor leads tocomplete androgen insensitivity syndrome. J. Clin. Endocr. Metab. 74:1152-1157, 1992.

GAM8358 255 AR Newmark, J. R.; Hardy, D. O.; Tonb, D. C.; Carter, B. S.; Epstein,J. I.; 3 C c
Isaacs, W. B.; Brown, T. R.; Barrack, E. R.: Androgen receptorgene mutations in human prostate cancer. Proc. Nat. Acad. Sci. 89:6319- 6323, 1992.

GAM8358 255 AR Nguyen, D.; Steinberg, S. V.; Rouault, E.; Chagnon, S.; Gottlieb,B.; Pinsky, 3 C c
L.; Trifiro, M.; Mader, S.: A G577R mutation in the humanAR P box results in selective decreases in DNA binding and in partialandrogen insensitivity syndrome. Molec. Endocr. 15: 1790- 1802, 2001.

GAM8358 255 BRF1 Mital, R.; Kobayashi, R.; Hernandez, N.: RNA polymerase III 3 C c
transcriptionfrom the human U6 and adenovirus type 2 VAI promoters has differentrequirements for human BRF, a subunit of human TFIIIB. Molec. Cell.Biol. 16: 7031- 7042, 1996.

GAM8358 255 BRF1 Wang, Z.; Roeder, R. G.: Structure and function of a human 3 C c
transcriptionfactor TFIIIB subunit that is evolutionarily conserved and containsboth TFIIB- and high- mobility- group protein 2- related domains.

Proc.Nat. Acad. Sci. 92: 7026- 7030, 1995.

GAM8358 255 C18orf1 Yoshikawa, T.; Sanders, A. R.; Esterling, L. E.; Detera- Wadleigh,S. D.: 3 C c
Multiple transcriptional variants and RNA editing in C18orf1,a novel gene
with LDLRA and transmembrane domains on 18p11.2. Genomics 47:246- 257, 1998.

GAM8358 255 C18orf1 Yoshikawa, T.; Sanders, A. R.; Esterling, L. E.; Overharser, J.;Garnes, J. 3 C c
A.; Lennon, G.; Grewal, R.; Detera- Wadleigh, S. D.: Isolationof chromosome
18- specific brain transcripts as positional candidatesfor bipolar disorder.
Am. J. Med. Genet. (Neuropsych. Genet.) 74:140- 149, 1997.

GAM8358 255 CCBP2 Bonini, J. A.; Martin, S. K.; Dralyuk, F.; Roe, M. W.; Philipson,L. H.; 3 C b
Steiner, D. F.: Cloning, expression, and chromosomal mappingof a novel human
CC- chemokine receptor (CCR10) that displays high- affinitybinding for MCP-
1 and MCP- 3. DNA Cell Biol. 16: 1249- 1256, 1997.

GAM8358 255 CCBP2 Maho, A.; Bensimon, A.; Vassart, G.; Parmentier, M.: Mapping ofthe CCXCR1, 3 C b
CX3CR1, CCBP2 and CCR9 genes to the CCR cluster withinthe 3p21.3 region of
the human genome. Cytogenet. Cell Genet. 87:265- 268, 1999.

GAM8358 255 CCBP2 Nibbs, R. J. B.; Wylie, S. M.; Yang, J.; Landau, N. R.; Graham,G. J.: 3 C b
Cloning and characterization of a novel promiscuous humanbeta- chemokine
receptor D6. J. Biol. Chem. 272: 32078- 32083, 1997.

GAM8358 255 CCNT2 Nguyen, V. T.; Kiss, T.; Michels, A. A.; Bensaude, O.: 7SK smallnuclear RNA 3 C c
binds to and inhibits the activity of CDK9/cyclin T complexes. Nature
414:322- 325, 2001.

GAM8358 255 CCNT2 Peng, J.; Zhu, Y.; Milton, J. T.; Price, D. H.: Identificationof multiple 3 C c
cyclin subunits of human P- TEFb. Genes Dev. 12: 755- 762,1998.

GAM8358 255 CCNT2 Yang, Z.; Zhu, Q.; Luo, K.; Zhou, Q.: The 7SK small nuclear RNAinhibits the 3 C c
CDK9/cyclin T1 kinase to control transcription. Nature 414:317- 322, 2001.

GAM8358 255 CCR9 Bonini, J. A.; Martin, S. K.; Dralyuk, F.; Roe, M. W.; Philipson,L. H.; 3 C c
Steiner, D. F.: Cloning, expression, and chromosomal mappingof a novel human
CC- chemokine receptor (CCR10) that displays high- affinitybinding for MCP-
1 and MCP- 3. DNA Cell Biol. 16: 1249- 1256, 1997.

GAM8358 255 CCR9 Maho, A.; Bensimon, A.; Vassart, G.; Parmentier, M.: Mapping ofthe CCXCR1, 3 C c
CX3CR1, CCBP2 and CCR9 genes to the CCR cluster withinthe 3p21.3 region of
the human genome. Cytogenet. Cell Genet. 87:265- 268, 1999.

GAM8358 255 CCR9 Nibbs, R. J. B.; Wylie, S. M.; Yang, J.; Landau, N. R.; Graham,G. J.: 3 C c
Cloning and characterization of a novel promiscuous humanbeta- chemokine
receptor D6. J. Biol. Chem. 272: 32078- 32083, 1997.

GAM8358 255 CD34 Cheng, J.; Baumhueter, S.; Cacalano, G.; Carver- Moore, K.; Thibodeaux,H.; 3 C c
Thomas, R.; Broxmeyer, H. E.; Cooper, S.; Hague, N.; Moore, M.;Lasky, L. A.:
Hematopoietic defects in mice lacking the sialomucinCD34. Blood 87: 479-
490, 1996.

GAM8358 255 CD34 He, X.- Y.; Antao, V. P.; Basila, D.; Marx, J. C.; Davis, B. R.: Isolation 3 C c
and molecular characterization of the human CD34 gene. Blood 79:2296- 2302,
1992.

GAM8358 255 CD34 Howell, S. M.; Molgaard, H. V.; Greaves, M. F.; Spurr, N. K.:Localisation of 3 C c
the gene coding for the haemopoietic stem cell antigenCD34 to chromosome
1q32. Hum. Genet. 87: 625- 627, 1991.

GAM8358 255 CD34 Okuno, Y.; Iwasaki, H.; Huettner, C. S.; Radomska, H. S.; Gonzalez,D. A.; 3 C c
Tenen, D. G.; Akashi, K.: Differential regulation of the humanand murine
CD34 genes in hematopoietic stem cells. Proc. Nat. Acad.Sci. 99: 6246- 6251,
2002.

GAM8358 255 CD34 Satterthwaite, A. B.; Burn, T. C.; Le Beau, M. M.; Tenen, D. G.: Structure 3 C c

of the gene encoding CD34, a human hematopoietic stemcell antigen. Genomics 12: 788- 794, 1992.

GAM8358 255 CD34 Simmons, D. L.; Satterthwaite, A. B.; Tenen, D. G.; Seed, B.:Molecular cloning of a cDNA encoding CD34, a sialomucin of human hematopoieticstem cells. J. Immun. 148: 267- 271, 1992. 3 C c

GAM8358 255 CD34 Sutherland, D. R.; Stewart, A. K.; Keating, A.: CD34 antigen:molecular features and potential clinical applications. Stem Cells 11(suppl. 3): 50- 57, 1993. 3 C c

GAM8358 255 CD34 Sutherland, D. R.; Watt, S. M.; Dowden, G.; Karhi, K.; Baker, M.A.; Greaves, M. F.; Smart, J. E.: Structural and partial amino acidsequence analysis of the human hemopoietic progenitor cell antigenCD34. Leukemia 2: 793- 803, 1988. 3 C c

GAM8358 255 CD34 Tenen, D. G.; Satterthwaite, A. B.; Borson, R.; Simmons, D.; Eddy,R. L.; Shows, T. B.: Chromosome 1 localization of the gene for CD34,a surface antigen of human stem cells. Cytogenet. Cell Genet. 53:55- 57, 1990. 3 C c

GAM8358 255 CLECSF11 Arce, I.; Roda- Navarro, P.; Montoya, M. C.; Hernanz- Falcon, P.;Puig-Kroger, A.; Fernandez- Ruiz, E.: Molecular and genomic characterizationof human DLEC, a novel member of the C- type lectin receptor gene familypreferentially expressed on monocyte- derived dendritic cells. Europ.J. Immun. 31: 2733- 2740, 2001. 3 C c

GAM8358 255 CLECSF11 Dzionek, A.; Sohma, Y.; Nagafune, J.; Cella, M.; Colonna, M.; Facchetti,F.; Gunther, G.; Johnston, I.; Lanzavecchia, A.; Nagasaka, T.; Okada,T.; Vermi, W.; Winkels, G.; Yamamoto, T.; Zysk, M.; Yamaguchi, Y.;Schmitz, J.: BDCA- 2, a novel plasmacytoid dendritic cell- specifictype II C- type lectin, mediates antigen capture and is a potent inhibitorof interferon alpha/beta induction. J. Exp. Med. 194: 1823- 1834,2001. 3 C c

GAM8358 255 CNTN2 Dodd, J.; Morton, S. B.; Karagogeos, D.; Yamamoto, M.; Jessell,T. M.: Spatial regulation of axonal glycoprotein expression on subsetsof embryonic spinal neurons. Neuron 1: 105- 116, 1988. 3 C c

GAM8358 255 CNTN2 Freigang, J.; Proba, K.; Leder, L.; Diederichs, K.; Sonderegger,P.; Welte, W.: The crystal structure of the ligand binding moduleof axonin- 1/TAG- 1 suggests a zipper mechanism for neural cell adhesion. Cell 101:425- 433, 2000. 3 C c

GAM8358 255 CNTN2 Kenwrick, S.; Leversha, M.; Rooke, L.; Hasler, T.; Sonderegger,P.: Localization of the human TAX- 1 gene to 1q32.1: a region implicatedin microcephaly and Van der Woude syndrome. Hum. Molec. Genet. 2:1461- 1462, 1993. 3 C c

GAM8358 255 CNTN2 Kozlov, S. V.; Giger, R. J.; Hasler, T.; Korvatska, E.; Schorderet,D. F.; Sonderegger, P.: The human TAX1 gene encoding the axon- associatedcell adhesion molecule TAG- 1/axonin- 1: genomic structure and basicpromoter. Genomics 30: 141- 148, 1995. 3 C c

GAM8358 255 CNTN2 Rickman, D. S.; Tyagi, R.; Zhu, X.- X.; Bobek, M. P.; Song, S.;Blaivas, M.; Misek, D. E.; Israel, M. A.; Kurnit, D. M.; Ross, D.A.; Kish, P. E.; Hanash, S. M.: The gene for the axonal cell adhesionmolecule TAX- 1 is amplified and aberrantly expressed in malignantgliomas. Cancer Res. 61: 2162- 2168, 2001. 3 C c

GAM8358 255 CNTN2 Tsiotra, P. C.; Karagogeos, D.; Theodorakis, K.; Michaelisis, T.M.; Modi, W. S.; Furley, A. J.; Jessell, T. M.; Papamatheakis, J.: Isolation of the cDNA and chromosomal localization of the gene (TAX1)encoding the human axonal glycoprotein TAG- 1. Genomics 18: 562- 567,1993. 3 C c

GAM8358 255 CYP2B6 Miles, J. S.; Spurr, N. K.; Gough, A. C.; Jowett, T.; McLaren,A. W.; Brook, 3 C c

J. D.; Wolf, C. R.: A novel human cytochrome P450 gene(P450IIB): chromosomal localization and evidence for alternative splicing. NucleicAcids Res. 16: 5783- 5795, 1988.

GAM8358 255 CYP2B6 Santisteban, I.; Povey, S.; Shephard, E. A.; Phillips, I. R.:The major 3 C c
phenobarbital- inducible cytochrome P- 450 gene subfamily(P450IIB) mapped to the long arm of human chromosome 19. Ann. Hum.Genet. 52: 129- 135, 1988.

GAM8358 255 CYP2B6 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. 3 C c
Lancet 355: 979- 983, 2000.

GAM8358 255 D12S2489 Bauer, S.; Groh, V.; Wu, J.; Steinle, A.; Phillips, J. H.; Lanier,L. L.; 3 C b
E Spies, T.: Activation of NK cells and T cells by NKG2D, areceptor for stress- inducible MICA. Science 285: 727- 729, 1999.

GAM8358 255 D12S2489 Colucci, F.; Schweighoffer, E.; Tomasello, E.; Turner, M.; Ortaldo,J. R.; 3 C b
E Vivier, E.; Tybulewicz, V. L. J.; Di Santo, J. P.: Naturalcytotoxicity uncoupled from the Syk and ZAP- 70 intracellular kinases. NatureImmun. 3: 288- 294, 2002.

GAM8358 255 D12S2489 Diefenbach, A.; Jensen, E. R.; Jamieson, A. M.; Raulet, D. H.:Rae1 and H60 3 C b
E ligands of the NKG2D receptor stimulate tumour immunity. Nature 413:165- 171, 2001.

GAM8358 255 D12S2489 Girardi, M.; Oppenheim, D. E.; Steele, C. R.; Lewis, J. M.; Glusac,E.; 3 C b
E Filler, R.; Hobby, P.; Sutton, B.; Tigelaar, R. E.; Hayday, A.C.: Regulation of cutaneous malignancy by gamma- delta T cells. Science 294:605- 609, 2001.

GAM8358 255 D12S2489 Groh, V.; Rhinehart, R.; Randolph- Habecker, J.; Topp, M. S.; Riddell,S. R.; 3 C b
E Spies, T.: Costimulation of CD8- alpha- beta T cells by NKG2Dvia engagement by MIC induced on virus- infected cells. Nature Immun. 2:255- 260, 2001.

GAM8358 255 D12S2489 Groh, V.; Wu, J.; Yee, C.; Spies, T.: Tumour- derived soluble MICligands 3 C b
E impair expression of NKG2D and T- cell activation. Nature 419:734- 738, 2002.

GAM8358 255 D12S2489 Houchins, J. P.; Yabe, T.; McSherry, C.; Bach, F. H.: DNA sequenceanalysis 3 C b
E of NKG2, a family of related cDNA clones encoding type Iintegral membrane proteins on human natural killer cells. J. Exp.Med. 173: 1017- 1020, 1991.

GAM8358 255 D12S2489 Li, P.; Morris, D. L.; Willcox, B. E.; Steinle, A.; Spies, T.;Strong, R. K.: 3 C b
E Complex structure of the activating immunoreceptorNKG2D and its MHC class I- like ligand MICA. Nature Immun. 2: 443- 451,2001.

GAM8358 255 D12S2489 Plougastel, B.; Trowsdale, J.: Cloning of NKG2- F, a new memberof the NKG2 3 C b
E family of human natural killer cell receptor genes. Europ.J. Immun. 27: 2835- 2839, 1997.

GAM8358 255 D12S2489 Plougastel, B.; Trowsdale, J.: Sequence analysis of a 62- kb 3 C b
E regionoverlapping the human KLRC cluster of genes. Genomics 49: 193- 199,1998.

GAM8358 255 D12S2489 Roberts, A. I.; Lee, L.; Schwarz, E.; Groh, V.; Spies, T.; Ebert,E. C.; 3 C b
E Jabri, B.: Cutting edge: NKG2D receptors induced by IL- 15costimulate CD28- negative effector CTL in the tissue microenvironment. J.Immun. 167: 5527- 5530, 2001.

GAM8358 255 D12S2489 Sutherland, C. L.; Chalupny, N. J.; Schooley, K.; VandenBos, T.;Kubin, M.; 3 C b
E Cosman, D.: UL16- binding proteins, novel MHC class I- relatedproteins, bind to NKG2D and activate multiple signaling pathways inprimary NK cells. J. Immun. 168: 671- 679, 2002.

GAM8358 255 D12S2489 Wu, J.; Song, Y.; Bakker, A. B. H.; Bauer, S.; Spies, T.; Lanier,L. L.; 3 C b
E Phillips, J. H.: An activating immunoreceptor complex formedby NKG2D and

DAP10. Science 285: 730- 732, 1999.

GAM8358 255 D12S2489 Yabe, T.; McSherry, C.; Bach, F. H.; Fisch, P.; Schall, R. P.;Sondel, P. M.; 3 C b E Houchins, J. P.: A multigene family on human chromosome12 encodes natural killer- cell lectins. Immunogenetics 37: 455- 460,1993.

GAM8358 255 DDX11 Amann, J.; Kidd, V. J.; Lahti, J. M.: Characterization of putativehuman 3 C c homologues of the yeast chromosome transmission fidelity gene,CHL1. J. Biol. Chem. 272: 3823- 3832, 1997.

GAM8358 255 DDX11 Amann, J.; Valentine, M.; Kidd, V. J.; Lahti, J. M.: Localizationof Chl1- 3 C c related helicase genes to human chromosome regions 12p11 and12p13: similarity between parts of these genes and conserved humantelomeric-associated DNA. Genomics 32: 260- 265, 1996.

GAM8358 255 DDX11 Frank, S.; Werner, S.: The human homologue of the yeast CHL1 geneis a novel 3 C c keratinocyte growth factor- regulated gene. J. Biol. Chem. 271:24337- 24340, 1996.

GAM8358 255 DDX20 Charroux, B.; Pellizzoni, L.; Perkinson, R. A.; Shevchenko, A.;Mann, M.; 3 C c Dreyfuss, G.: Gemin3: a novel DEAD box protein that interactswith SMN, the spinal muscular atrophy gene product, and is a componentof gems. J. Cell Biol. 147: 1181- 1193, 1999.

GAM8358 255 DDX20 Grundhoff, A. T.; Kremmer, E.; Tureci, O.; Glieden, A.; Gindorf,C.; Atz, J.; 3 C c Mueller- Lantzsch, N.; Schubach, W. H.; Grasser, F. A.: Characterization of DP103, a novel DEAD box protein that binds tothe Epstein- Barr virus nuclear proteins EBNA2 and EBNA3C. J. Biol.Chem. 274: 19136- 19144, 1999.

GAM8358 255 DDX20 Klappacher, G. W.; Lunyak, V. V.; Sykes, D. B.; Sawka- Verhelle,D.; Sage, 3 C c J.; Brard, G.; Ngo, S. D.; Gangadharan, D.; Jacks, T.; Kamps,M. P.; Rose, D. W.; Rosenfeld, M. G.: An induced Ets repressor complexregulates growth arrest during terminal macrophage differentiation. Cell 109:169- 180, 2002.

GAM8358 255 DMRT2 Muroya, K.; Okuyama, T.; Goishi, K.; Ogiso, Y.; Fukuda, S.; Kameyama,J.; 3 C c Sato, H.; Suzuki, Y.; Terasaki, H.; Gomyo, H.; Wakui, K.; Fukushima,Y.; Ogata, T.: Sex- determining gene(s) on distal 9p: clinical andmolecular studies in six cases. J. Clin. Endocr. Metab. 85: 3094- 3100,2000.

GAM8358 255 DMRT2 Raymond, C. S.; Parker, E. D.; Kettlewell, J. R.; Brown, L. G.;Page, D. C.; 3 C c Kusz, K.; Jaruzelska, J.; Reinberg, Y.; Fletjer, W. L.;Bardwell, V. J.; Hirsch, B.; Zarkower, D.: A region of human chromosome9p required for testis development contains two genes related to knownsexual regulators. Hum. Molec. Genet. 8: 989- 996, 1999.

GAM8358 255 DMRT2 Raymond, C. S.; Shamu, C. E.; Shen, M. M.; Seifert, K. J.; Hirsch,B.; 3 C c Hodgkin, J.; Zarkower, D.: Evidence for evolutionary conservationof sex-determining genes. Nature 391: 691- 695, 1998.

GAM8358 255 DNMT2 Vilain, A.; Apiou, F.; Dutrillaux, B.; Malfoy, B.: Assignmentof candidate 3 C c DNA methyltransferase gene (DNMT2) to human chromosomeband 10p15.1 by in situ hybridization. Cytogenet. Cell Genet. 82:120 only, 1998.

GAM8358 255 DNMT2 Yoder, J. A.; Bestor, T. H.: A candidate mammalian DNA 3 C c methyltransferaserelated to pmt1p of fission yeast. Hum. Molec. Genet. 7: 279- 284,1998.

GAM8358 255 DPH2L2 Foley, B. T.; Moehring, J. M.; Moehring, T. J.: Mutations in theelongation 3 C c factor 2 gene which confer resistance to diphtheria toxinand Pseudomonas exotoxin A: genetic and biochemical analyses. J.Biol. Chem. 270: 23218-23225, 1995.

GAM8358 255 DPH2L2 Mattheakis, L. C.; Sor, F.; Collier, R. J.: Diphthamide synthesisin 3 C c Saccharomyces cerevisiae: structure of the DPH2 gene. Gene 132:149- 154,

1993.

GAM8358 255 DPH2L2 Schultz, D. C.; Balasara, B. R.; Testa, J. R.; Godwin, A. K.:Cloning and localization of a human diphthamide biosynthesis- likeprotein- 2 gene, DPH2L2. Genomics 52: 186- 191, 1998. 3 C c

GAM8358 255 DRD5 Beischlag, T. V.; Marchese, A.; Meador- Woodruff, J. H.; Damask,S. P.; O'Dowd, B. F.; Tyndale, R. F.; Van Tol, H. H. M.; Seeman, P.;Niznik, H. B.: The human dopamine D5 receptor gene: cloning and characterizationof the 5-prime flanking and promoter region. Biochemistry 34: 5960- 5970,1995. 3 C c

GAM8358 255 DRD5 Eubanks, J. H.; Altherr, M.; Wagner- McPherson, C.; McPherson, J.D.; Wasmuth, J. J.; Evans, G. A.: Localization of the D5 dopaminereceptor gene to human chromosome 4p15.1- p15.3, centromeric to theHuntington's disease locus. Genomics 12: 510- 516, 1992. 3 C c

GAM8358 255 DRD5 Grandy, D. K.; Allen, L. J.; Zhang, Y.; Magenis, R. E.; Civelli,O.: Chromosomal localization of three human D5 dopamine receptorgenes. Genomics 13: 968- 973, 1992. 3 C c

GAM8358 255 DRD5 Grandy, D. K.; Zhang, Y.; Bouvier, C.; Zhou, Q.- Y.; Johnson, R.A.; Allen, L.; Buck, K.; Bunzow, J. R.; Salon, J.; Civelli, O.: Multiplehuman D5 dopamine receptor genes: a functional receptor and two pseudogenes. Proc.Nat. Acad. Sci. 88: 9175- 9179, 1991. 3 C c

GAM8358 255 DRD5 Grosson, C. L. S.; MacDonald, M. E.; Duyao, M. P.; Ambrose, C.M.; Roffler-Tarlov, S.; Gusella, J. F.: Synteny conservation of theHuntington's disease gene and surrounding loci on mouse chromosome5. Mammalian Genome 5: 424-428, 1994. 3 C c

GAM8358 255 DRD5 Liu, F.; Wan, Q.; Pristupa, Z. B.; Yu, X.- M.; Wang, Y. T.; Niznik,H. B.: Direct protein- protein coupling enables cross- talk betweendopamine D5 and gamma- aminobutyric acid A receptors. Nature 403:274- 280, 2000. 3 C c

GAM8358 255 DRD5 Misbahuddin, A.; Placzek, M. R.; Chaudhuri, K. R.; Wood, N. W.;Bhatia, K. P.; Warner, T. T.: A polymorphism in the dopamine receptorDRD5 is associated with blepharospasm. Neurology 58: 124- 126, 2002. 3 C c

GAM8358 255 DRD5 Placzek, M. R.; Misbahuddin, A.; Chaudhuri, K. R.; Wood, N. W.;Bhatia, K. P.; Warner, T. T.: Cervical dystonia is associated witha polymorphism in the dopamine (D5) receptor gene. J. Neurol. Neurosurg.Psychiat. 71: 262- 264, 2001. 3 C c

GAM8358 255 DRD5 Polymeropoulos, M. H.; Xiao, H.; Merril, C. R.: The human D5 dopaminereceptor (DRD5) maps on chromosome 4. Genomics 11: 777- 778, 1991. 3 C c

GAM8358 255 DRD5 Sherrington, R.; Mankoo, B.; Attwood, J.; Kalsi, G.; Curtis, D.;Buetow, K.; Povey, S.; Gurling, H.: Cloning of the human dopamineD5 receptor gene and identification of a highly polymorphic microsatellitefor the DRD5 locus that shows tight linkage to the chromosome 4p referencemarker RAF1P1. Genomics 18: 423- 425, 1993. 3 C c

GAM8358 255 DRD5 Tiberi, M.; Jarvie, K. R.; Silvia, C.; Falardeau, P.; Gingrich,J. A.; Godinot, N.; Bertrand, L.; Yang- Feng, T. L.; Fremeau, R. T.,Jr.; Caron, M. G.: Cloning, molecular characterization, and chromosomalassignment of a gene encoding a second D- 1 dopamine receptor subtype:differential expression pattern in rat brain compared with the D- 1Areceptor. Proc. Nat. Acad. Sci. 88: 7491- 7495, 1991. 3 C c

GAM8358 255 DRD5 Weinshank, R. L.; Adham, N.; Macchi, M.; Olsen, M. A.; Branchek,T. A.; Hartig, P. R.: Molecular cloning and characterization of ahigh affinity dopamine receptor (D- 1- beta) and its pseudogene. J.Biol. Chem. 266: 22427-22435, 1991. 3 C c

GAM8358 255 DRD5 Wilkie, T. M.; Chen, Y.; Gilbert, D. J.; Moore, K. J.; Yu, L.;Simon, M. I.; 3 C c
Copeland, N. G.; Jenkins, N. A.: Identification, chromosomallocation, and
genome organization of mammalian G- protein- coupled receptors. Genomics
18:175- 184, 1993.

GAM8358 255 DVL3 Bui, T. D.; Beier, D. R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; 3 C c
Kaklamanis, L.; Kearney, L.; Regan, R.; Sussman, D. J.; Harris,A. L.: cDNA
cloning of a human dishevelled DVL- 3 gene, mapping to3q27, and expression
in human breast and colon carcinomas. Biochem.Biophys. Res. Commun. 239:
510- 516, 1997.

GAM8358 255 DVL3 Klingensmith, J.; Nusse, R.; Perrimon, N.: The Drosophila segmentpolarity 3 C c
gene dishevelled encodes a novel protein required for responseto wingless
signal. Genes Dev. 8: 118- 130, 1994.

GAM8358 255 DVL3 Pizzuti, A.; Amati, F.; Calabrese, G.; Mari, A.; Colosimo, A; Silani,V.; 3 C c
Giardino, L.; Ratti, A.; Penso, D.; Calza, L.; Palka, G.; Scarlato,G.;
Novelli, G.; Dallapicolla, B.: cDNA characterization and chromosomalmapping
of two human homologs of the Drosophila dishevelled polaritygene. Hum.
Molec. Genet. 5: 953- 958, 1996.

GAM8358 255 DVL3 Semenov, M. V.; Snyder, M.: Human dishevelled genes constitutea DHR- 3 C c
containing multigene family. Genomics 42: 302- 310, 1997.

GAM8358 255 ENTPD6 Chadwick, B. P.; Frischauf, A.- M.: The CD39- like gene 3 C c
family:identification of three new human members (CD39L2, CD39L3, and
CD39L4),their murine homologues, and a member of the gene family from
Drosophilamelanogaster. Genomics 50: 357- 367, 1998.

GAM8358 255 ENTPD6 Chadwick, B. P.; Williamson, J.; Sheer, D.; Frischauf, A.- M.:cDNA cloning 3 C c
and chromosomal mapping of a mouse gene with homologyto NTPases. Mammalian
Genome 9: 162- 164, 1998.

GAM8358 255 ENTPD6 Yeung, G.; Mulero, J. J.; McGowan, D. W.; Bajwa, S. S.; Ford, J.E.: CD39L2, 3 C c
a gene encoding a human nucleoside diphosphatase, predominantlyexpressed in
the heart. Biochemistry 39: 12916- 12923, 2000.

GAM8358 255 EPHB4 Bennett, B. D.; Wang, Z.; Kuang, W.- J.; Wang, A.; Groopman, J.E.; Goeddel, 3 C c
D. V.; Scadden, D. T.: Cloning and characterizationof HTK, a novel
transmembrane tyrosine kinase of the EPH subfamily. J.Biol. Chem. 269:
14211- 14218, 1994.

GAM8358 255 EPHB4 Berclaz, G.; Andres, A.- C.; Albrecht, D.; Dreher, E.; Ziemiecki,A.; 3 C c
Gusterson, B. A.; Crompton, M. R.: Expression of the receptorprotein
tyrosine kinase myk- 1/htk in normal and malignant mammaryepithelium.
Biochem. Biophys. Res. Commun. 226: 869- 875, 1996.

GAM8358 255 EPHB4 Gerety, S. S.; Wang, H. U.; Chen, Z.- F.; Anderson, D. J.: Symmetricalmutant 3 C c
phenotypes of the receptor EphB4 and its specific transmembraneligand
ephrin- B2 in cardiovascular development. Molec. Cell 4: 403- 414,1999.

GAM8358 255 EVPL Maatta, A.; Ruhrberg, C.; Watt, F. M.: Structure and regulationof the 3 C c
envoplakin gene. J. Biol. Chem. 275: 19857- 19865, 2000.

GAM8358 255 EVPL Risk, J. M.; Ruhrberg, C.; Hennies, H.; Mills, H. S.; Di Colandrea,T.; 3 C c
Evans, K. E.; Ellis, A.; Watt, F. M.; Bishop, D. T.; Spurr, N.K.; Stevens,
H. P.; Leigh, I. M.; Reis, A.; Kelsell, D. P.; Field,J. K.: Envoplakin, a
possible candidate gene for focal NEPPK/esophagealcancer (TOC): the
integration of genetic and physical maps of theTOC region on 17q25. Genomics
59: 234- 242, 1999.

GAM8358 255 EVPL Ruhrberg, C.; Hajibagheri, M. A. N.; Simon, M.; Dooley, T. P.;Watt, F. M.: 3 C c
Envoplakin, a novel precursor of the cornified envelopethat has homology to

desmoplakin. J. Cell Biol. 134: 715- 729, 1996.

GAM8358 255 EVPL Ruhrberg, C.; Williamson, J. A.; Sheer, D.; Watt, F. M.: 3 C c
Chromosomallocalisation of the human envoplakin gene (EVPL) to the region ofthe tylosis oesophageal cancer gene (TOCG) on 17q25. Genomics 37:381- 385, 1996.

GAM8358 255 FMOD Jepsen, K. J.; Wu, F.; Peragallo, J. H.; Paul, J.; Roberts, L.;Ezura, Y.; 3 C c
Oldberg, A.; Birk, D. E.; Chakravarti, S.: A syndromeof joint laxity and impaired tendon integrity in lumican- and fibromodulin- deficientmice. J. Biol. Chem. 277: 35532- 35540, 2002.

GAM8358 255 FMOD Sztrolovics, R.; Chen, X.- N.; Grover, J.; Roughley, P. J.; Korenberg,J. R.: 3 C c
Localization of the human fibromodulin gene (FMOD) to chromosome1q32 and completion of the cDNA sequence. Genomics 23: 715- 717,1994.

GAM8358 255 FOXO1A Anderson, M. J.; Shelton, G. D.; Cavenee, W. K.; Arden, K. C.:Embryonic 3 C c
expression of the tumor- associated PAX3- FKHR fusion proteininterferes with the developmental functions of Pax3. Proc. Nat. Acad.Sci. 98: 1589- 1594, 2001.

GAM8358 255 FOXO1A Anderson, M. J.; Viars, C. S.; Czekay, S.; Cavenee, W. K.; Arden,K. C.: 3 C c
Cloning and characterization of three human forkhead genesthat comprise an FKHR- like gene subfamily. Genomics 47: 187- 199,1998.

GAM8358 255 FOXO1A Barr, F. G.; Galili, N.; Holick, J.; Biegel, J. A.; Rovera, G.;Emanuel, B. 3 C c
S.: Rearrangement of the PAX3 paired box gene in thepaediatric solid tumor alveolar rhabdomyosarcoma. Nature Genet. 3:113- 117, 1993.

GAM8358 255 FOXO1A Davis, R. J.; Barr, F. G.: Fusion genes resulting from 3 C c
alternativechromosomal translocations are overexpressed by gene- specific mechanismsin alveolar rhabdomyosarcoma. Proc. Nat. Acad. Sci. 94: 8047- 8051,1997.

GAM8358 255 FOXO1A Fredericks, W. J.; Galili, N.; Mukhopadhyay, S.; Rovera, G.; Bennicelli,J.; 3 C c
Barr, F. G.; Rauscher, F. J., III: The PAX3- FKHR fusion proteincreated by the t(2;13) translocation in alveolar rhabdomyosarcomasis a more potent transcriptional activator than PAX3. Molec. Cell.Biol. 15: 1522- 1535, 1995.

GAM8358 255 FOXO1A Galili, N.; Davis, R. J.; Fredericks, W. J.; Mukhopadhyay, S.;Rauscher, F. 3 C c
J., III; Emanuel, B. S.; Rovera, G.; Barr, F. G.: Fusionof a fork head domain gene to PAX3 in the solid tumour alveolar rhabdomyosarcoma. NatureGenet. 5: 230- 235, 1993.

GAM8358 255 FOXO1A Khan, J.; Bittner, M. L.; Saal, L. H.; Teichmann, U.; Azorsa, D.O.; Gooden, 3 C c
G. C.; Pavan, W. J.; Trent, J. M.; Meltzer, P. S.: cDNAmicroarrays detect activation of a myogenic transcription programby the PAX3- FKHR fusion oncogene. Proc. Nat. Acad. Sci. 96: 13264- 13269,1999.

GAM8358 255 FOXO1A Medema, R. H.; Kops, G. J. P. L.; Bos, J. L.; Burgering, B. M.T.: AFX- like 3 C c
forkhead transcription factors mediate cell- cycle regulationby Ras and PKB through p27(kip1). Nature 404: 782- 787, 2000.

GAM8358 255 FOXO1A Nakae, J.; Biggs, W. H., III; Kitamura, T.; Cavenee, W. K.; Wright,C. V. E.; 3 C c
Arden, K. C.; Accili, D.: Regulation of insulin actionand pancreatic beta-cell function by mutated alleles of the gene encodingforkhead transcription factor Foxo1. Nature Genet. 32: 245- 253,2002.

GAM8358 255 FOXO1A Scheidler, S.; Fredericks, W. J.; Rauscher, F. J., III; Barr,F. G.; Vogt, P. 3 C c
K.: The hybrid PAX3- FKHR fusion protein of alveolarrhabdomyosarcoma transforms fibroblasts in culture. Proc. Nat. Acad.Sci. 93: 9805- 9809, 1996.

GAM8358 255 FOXO1A Sublett, J. E.; Jeon, I- S.; Shapiro, D. N.: The alveolar 3 C c

rhabdomyosarcomaPAX3/FKHR fusion protein is a transcriptional activator. Oncogene 11:545- 552, 1995.

GAM8358 255 FOXO1A Whang- Peng, J.; Knutsen, T.; Theil, K.; Horowitz, M. E.; Triche,T.: 3 C c
Cytogenetic studies in subgroups of rhabdomyosarcoma. GenesChromosomes Cancer 5: 299- 310, 1992.

GAM8358 255 FUT6 Brinkman- Van der Linden, E. C. M.; Mollicone, R.; Oriol, R.; Larson,G.; Van 3 C c
den Eijnden, D. H.; Van Dijk, W.: A missense mutation inthe FUT6 gene results in total absence of alpha- 3- fucosylation ofhuman alpha- 1- acid glycoprotein. J. Biol. Chem. 271: 14492- 14495,1996.

GAM8358 255 FUT6 Cameron, H. S.; Szczepaniak, D.; Weston, B. W.: Expression ofhuman 3 C c
chromosome 19p alpha- (1,3)- fucosyltransferase genes in normaltissues: alternative splicing, polyadenylation, and isoforms. J.Biol. Chem. 270: 20112- 20122, 1995.

GAM8358 255 FUT6 Koszdin, K. L.; Bowen, B. R.: The cloning and expression of ahuman alpha- 3 C c
1,3 fucosyltransferase capable of forming the E- selectinligand. Biochem. Biophys. Res. Commun. 187: 152- 157, 1992.

GAM8358 255 FUT6 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. 3 C c
C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3 and 11q21. Genomics 26: 142- 146, 1995.

GAM8358 255 FUT6 Mollicone, R.; Reguigne, I.; Fletcher, A.; Aziz, A.; Rustam, M.;Weston, B. 3 C c
W.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Molecular basisfor plasma alpha(1,3)- fucosyltransferase gene deficiency (FUT6). J.Biol. Chem. 269: 12662- 12671, 1994.

GAM8358 255 FUT6 Pang, H.; Koda, Y.; Soejima, M.; Schlaphoff, T.; Du Toit, E. D.;Kimura, H.: 3 C c
Allelic diversity of the human plasma alpha(1,3)fucosyltransferasegene (FUT6). Ann. Hum. Genet. 63: 277- 284, 1999.

GAM8358 255 FUT6 Schnyder- Candrian, S.; Borsig, L.; Moser, R.; Berger, E. G.: Localizationof 3 C c
alpha- 1,3- fucosyltransferase VI in Weibel- Palade bodies of humanendothelial cells. Proc. Nat. Acad. Sci. 97: 8369- 8374, 2000.

GAM8358 255 FUT6 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of 3 C c
a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple homologous sequences that determine expressionof the Lewis x, sialyl Lewis x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584, 1992.

GAM8358 255 GALNT3 Bennett, E. P.; Hassan, H,.; Clausen, H.: cDNA cloning and expressionof a 3 C c
novel human UDP- N- acetyl- alpha- D- galactosamine. J. Biol. Chem. 271:17006- 17012, 1996.

GAM8358 255 GALNT3 Bennett, E. P.; Weghuis, D. O.; Merkx, G.; Geurts van Kessel, A.;Eiberg, H.; 3 C c
Clausen, H.: Genomic organization and chromosomal localizationof three members of the UDP- N- acetylgalactosamine:polypeptide N- acetylgalactosaminyltransferasefamily. Glycobiology 8: 547- 555, 1998.

GAM8358 255 GALNT3 Zara, J.; Hagen, F. K.; Ten Hagen, K. G.; Van Wuyckhuyse, B. C.;Tabak, L. 3 C c
A.: Cloning and expression of mouse UDP- GalNAc:polypeptideN- acetylgalactosaminyltransferase- T3. Biochem. Biophys. Res. Commun. 228:38- 44, 1996.

GAM8358 255 GATA4 Arceci, R. J.; King, A. A.; Simon, M. C.; Orkin, S. H.; Wilson,D. B.: Mouse 3 C c
GATA- 4: a retinoic acid- inducible GATA- binding transcriptionfactor expressed in endodermally derived tissues and heart. Molec.Cell. Biol. 13: 2235- 2246, 1993.

GAM8358 255 GATA4 Cirillo, L. A.; Lin, F. R.; Cuesta, I.; Friedman, D.; Jarnik, M.;Zaret, K. S.: Opening of compacted chromatin by early developmentaltranscription factors HNF3(FoxA) and GATA- 4. Molec. Cell 9: 279- 289,2002. 3 C c

GAM8358 255 GATA4 Crispino, J. D.; Lodish, M. B.; Thurberg, B. L.; Litovsky, S. H.;Collins, T.; Molkentin, J. D.; Orkin, S. H.: Proper coronary vasculardevelopment and heart morphogenesis depend on interaction of GATA- 4with FOG cofactors. Genes Dev. 15: 839- 844, 2001. 3 C c

GAM8358 255 GATA4 Evans, T.; Reitman, M.; Felsenfeld, G.: An erythrocyte- specificDNA- binding factor recognizes a regulatory sequence common to allchicken globin genes. Proc. Nat. Acad. Sci. 85: 5976- 5980, 1988. 3 C c

GAM8358 255 GATA4 Hasegawa, K.; Lee, S. J.; Jobe, S. M.; Markham, B. E.; Kitsis,R. N.: cis- acting sequences that mediate induction of beta- myosinheavy chain gene expression during left ventricular hypertrophy dueto aortic constriction. Circulation 96: 3943- 3953, 1997. 3 C c

GAM8358 255 GATA4 Herzig, T. C.; Jobe, S. M.; Aoki, H.; Molkentin, J. D.; Cowley,A. W., Jr.; Izumo, S.; Markham, B. E.: Angiotensin II type- 1a receptorgene expression in the heart: AP- 1 and GATA- 4 participate in the responseto pressure overload. Proc. Nat. Acad. Sci. 94: 7543- 7548, 1997. 3 C c

GAM8358 255 GATA4 Huang, W.- Y.; Cukerman, E.; Liew, C.- C.: Identification of a GATAmotif in the cardiac alpha- myosin heavy- chain- encoding gene and isolationof a human GATA- 4 cDNA. Gene 155: 219- 223, 1995. 3 C c

GAM8358 255 GATA4 Huang, W.- Y.; Heng, H. H. Q.; Liew, C.- C.: Assignment of the humanGATA4 gene to 8p23.1- p22 using fluorescence in situ hybridizationanalysis. Cytogenet. Cell Genet. 72: 217- 218, 1996. 3 C c

GAM8358 255 GATA4 Kennedy, S. J.; Teebi, A. S.; Adatia, I.; Teshima, I.: Inheritedduplication, dup(8)(p23.1p23.1)Pat, in a father and daughter withcongenital heart defects. (Letter) Am. J. Med. Genet. 104: 79- 80,2001. 3 C c

GAM8358 255 GATA4 Ketola, I.; Pentikainen, V.; Vaskivuo, T.; Ilvesmaki, V.; Herva,R.; Dunkel, L.; Tapanainen, J. S.; Toppari, J.; Heikinheimo, M.:Expression of transcription factor GATA- 4 during human testiculardevelopment and disease. J. Clin. Endocr. Metab. 85: 3925- 3931,2000. 3 C c

GAM8358 255 GATA4 Laitinen, M. P. E.; Anttonen, M.; Ketola, I.; Wilson, D. B.; Ritvos,O.; Butzow, R.; Heikinheimo, M.: Transcription factors GATA- 4 andGATA- 6 and a GATA family cofactor, FOG- 2, are expressed in human ovaryand sex cord-derived ovarian tumors. J. Clin. Endocr. Metab. 85:3476- 3483, 2000. 3 C c

GAM8358 255 GATA4 Molkentin, J. D.; Kalvakolanu, D. V.; Markham, B. E.: Transcriptionfactor GATA- 4 regulates cardiac muscle- specific expression of thealpha- myosin heavy- chain gene. Molec. Cell. Biol. 14: 4947- 4957,1994. 3 C c

GAM8358 255 GATA4 Pehlivan, T.; Pober, B. R.; Brueckner, M.; Garrett, S.; Slaugh,R.; Van Rheeden, R.; Wilson, D. B.; Watson, M. S.; Hing, A. V.: GATA4haploinsufficiency in patients with interstitial deletion of chromosomeregion 8p23.1 and congenital heart disease. Am. J. Med. Genet. 83:201- 206, 1999. 3 C c

GAM8358 255 GATA4 Vaskivuo, T. E.; Anttonen, M.; Herva, R.; Billig, H.; Dorland,M.; Te Velde, E. R.; Stenback, F.; Heikinheimo, M.; Tapanainen, J.S.: Survival of human ovarian follicles from fetal to adult life:apoptosis, apoptosis- related proteins, and transcription factor GATA- 4. J.Clin. Endocr. Metab. 86: 3421-3429, 2001. 3 C c

GAM8358 255 GATA4 White, R. A.; Dowler, L. L.; Pasztor, L. M.; Gatson, L. L.; Adkison,L. R.; Angeloni, S. V.; Wilson, D. B.: Assignment of the transcriptionfactor GATA4 3 C c

gene to human chromosome 8 and mouse chromosome 14: Gata4is a candidate gene for Ds (disorganization). Genomics 27: 20- 26,1995.

GAM8358 255 GGT1 Bulle, F.; Mattei, M. G.; Siegrist, S.; Pawlak, A.; Passage, E.;Chobert, M. 3 C c
N.; Laperche, Y.; Guellaen, G.: Assignment of the humangamma- glutamyl transferase gene to the long arm of chromosome 22. Hum.Genet. 76: 283- 286, 1987.

GAM8358 255 GGT1 Figlewicz, D. A.; Delattre, O.; Guellaen, G.; Krizus, A.; Thomas,G.; Zucman, 3 C c
J.; Rouleau, G. A.: Mapping of human gamma- glutamyl transpeptidasegenes on chromosome 22 and other human autosomes. Genomics 17: 299- 305,1993.

GAM8358 255 GGT1 Hammond, J. W.; Potter, M.; Wilcken, B.; Truscott, R.: Siblingswith gamma- 3 C c
glutamyltransferase deficiency. J. Inherit. Metab. Dis. 18:82- 83, 1995.

GAM8358 255 GGT1 Heisterkamp, N.; Groffen, J.: Duplication of the bcr and gamma- 3 C c
glutamyltranspeptidase genes. Nucleic Acids Res. 16: 8045- 8056, 1988.

GAM8358 255 GGT1 Laperche, Y.; Bulle, F.; Aissani, T.; Chobert, M. N.; Aggerbeck,M.; Hanoune, 3 C c
J.; Guellaen, G.: Molecular cloning and nucleotide sequenceof rat kidney gamma- glutamyl transpeptidase cDNA. Proc. Nat. Acad.Sci. 83: 937- 941, 1986.

GAM8358 255 GGT1 O'Daley, S.: An abnormal sulphydryl compound in urine. (Abstract) IrishJ. 3 C c
Med. Sci. 7: 578- 579, 1968.

GAM8358 255 GGT1 Pawlak, A.; Lahuna, O.; Bulle, F.; Suzuki, A.; Ferry, N.; Siegrist,S.; 3 C c
Chikhi, N.; Chobert, M. N.; Guellaen, G.; Laperche, Y.: Gamma-glutamyltranspeptidase: a single copy gene in the rat and a multigene familyin the human genome. J. Biol. Chem. 263: 9913- 9916, 1988.

GAM8358 255 GGT1 Pawlak, A.; Wu, S.- J.; Bulle, F.; Suzuki, A.; Chikhi, N.; Ferry,N.; Baik, 3 C c
J.- H.; Siegrist, S.; Guellaen, G.: Different gamma- glutamyltranspeptidase mRNAs are expressed in human liver and kidney. Biochem.Biophys. Res. Commun. 164: 912- 918, 1989.

GAM8358 255 GGT1 Rajpert- De Meyts, E.; Heisterkamp, N.; Groffen, J.: Cloning andnucleotide 3 C c
sequence of human gamma- glutamyl transpeptidase. Proc.Nat. Acad. Sci. 85: 8840- 8844, 1988.

GAM8358 255 GGT1 Rouleau, G. A.; Bazanowski, A.; Cohen, E. H.; Guellaen, G.; Gusella,J. F.: 3 C c
Gamma- glutamyl transferase locus (GGT) displays a PvuII polymorphism. NucleicAcids Res. 16: 11848 only, 1988.

GAM8358 255 GGT1 Sakamuro, D.; Yamazoe, M.; Matsuda, Y.; Kangawa, K.; Taniguchi,N.; Matsuo, 3 C c
H.; Yoshikawa, H.; Ogasawara, N.: The primary structureof human gamma-glutamyl transpeptidase. Gene 73: 1- 9, 1988.

GAM8358 255 GGT1 Schulman, J. D.; Goodman, S. I.; Mace, J. W.; Patrick, A. D.;Tietze, F.; 3 C c
Butler, E. J.: Glutathionuria: inborn error of metabolismdue to tissue deficiency of gamma- glutamyl transpeptidase. Biochem.Biophys. Res. Commun. 65: 68- 74, 1975.

GAM8358 255 GRM4 Barbon, A.; Ferraboli, S.; Barlati, S.: Assignment of the humanmetabotropic 3 C c
glutamate receptor gene GRM4 to chromosome 6 band p21.3by radiation hybrid mapping. Cytogenet. Cell Genet. 88: 210 only,2000.

GAM8358 255 GRM4 Gerlai, R.; Roder, J. C.; Hampson, D. R.: Altered spatial learningand memory 3 C c
in mice lacking the mGluR4 subtype of metabotropic glutamatereceptor. Behav. Neurosci. 112: 525- 532, 1998.

GAM8358 255 GRM4 Makoff, A.; Lelchuk, R.; Oxer, M.; Harrington, K.; Emson, P.:Molecular 3 C c
characterization and localization of human metabotropicglutamate receptor type 4. Molec. Brain Res. 37: 239- 248, 1996.

GAM8358 255 GRM4 Pekhletski, R.; Gerlai, R.; Overstreet, L. S.; Huang, X. P.; Agopyan,N.; 3 C c

Slater, N. T.; Abramow- Newerly, W.; Roder, J. C.; Hampson, D.R.: Impaired cerebellar synaptic plasticity and motor performancein mice lacking the mGluR4 subtype of metabotropic glutamate receptor. J.Neurosci. 16: 6364- 6373, 1996.

GAM8358 255 GRM4 Wu, S.; Wright, R. A.; Rockey, P. K.; Burgett, S. G.; Arnold, J.S.; Rosteck, 3 C c
P. R., Jr.; Johnson, B. G.; Schoepp, D. D.; Belagaje,R. M.: Group III human metabotropic glutamate receptors 4, 7 and8: molecular cloning, functional expression, and comparison of pharmacologicalproperties in RGT cells. Molec. Brain Res. 53: 88- 97, 1998.

GAM8358 255 GYPB Ferrari, B.; Pavia, A. A.: Blood group antigens: synthesis ofSs antigenic 3 C c
peptides related to human glycophorin B. Int. J. PeptideProtein Res. 28: 456- 461, 1986.

GAM8358 255 GYPB Huang, C.- H.; Blumenfeld, O. O.: Characterization of a genomichybrid 3 C c
specifying the human erythrocyte antigen Dantu: Dantu geneis duplicated and linked to a delta glycophorin gene deletion. Proc.Nat. Acad. Sci. 85: 9640- 9644, 1988.

GAM8358 255 GYPB Huang, C.- H.; Johe, K.; Moulds, J. J.; Siebert, P. D.; Fukuda,M.; 3 C c
Blumenfeld, O. O.: Delta- glycophorin (glycophorin B) gene deletionin two individuals homozygous for the S- - s- - U- - blood group phenotype. Blood 70:1830- 1835, 1987.

GAM8358 255 GYPB Kudo, S.; Fukuda, M.: Structural organization of glycophorin Aand B genes: 3 C c
glycophorin B gene evolved by homologous recombinationat Alu repeat sequences. Proc. Nat. Acad. Sci. 86: 4619- 4623, 1989.

GAM8358 255 GYPB Marchesi, V. T.; Tillack, T. M.; Jackson, R. L.; Segrest, J. P.;Scott, R. 3 C c
E.: Chemical characterization and surface orientation ofthe major glycoprotein of the human erythrocyte membrane. Proc. Nat.Acad. Sci. 69: 1445- 1449, 1972.

GAM8358 255 GYPB Mawby, W. J.; Anstee, D. J.; Tanner, M. J. A.: Immunochemicalevidence for 3 C c
hybrid sialoglycoproteins of human erythrocytes. Nature 291:161- 162, 1981.

GAM8358 255 GYPB Onda, M.; Fukuda, M.: Detailed physical mapping of the genes 3 C c
encodingglycophorins A, B, and E, as revealed by P1 plasmids containing humangenomic DNA. Gene 159: 225- 230, 1995.

GAM8358 255 GYPB Onda, M.; Kudo, S.; Rearden, A.; Mattei, M.- G.; Fukuda, M.: 3 C c
Identificationof a precursor genomic segment that provided a sequence unique toglycophorin B and E genes. Proc. Nat. Acad. Sci. 90: 7220- 7224,1993.

GAM8358 255 GYPB Race, R. R.; Sanger, R.: Blood Groups in Man. Oxford: Blackwell(pub.) (6th 3 C c
ed.): 1975. Pp. 92- 138.

GAM8358 255 GYPB Siebert, P. D.; Fukuda, M.: Molecular cloning of a human glycophorinB cDNA: 3 C c
nucleotide sequence and genomic relationship to glycophorinA. Proc. Nat. Acad. Sci. 84: 6735- 6739, 1987.

GAM8358 255 GYPE Kudo, S.; Chagnovich, D.; Rearden, A.; Mattei, M. G.; Fukuda, M.: Molecular 3 C c
analysis of a hybrid gene encoding human glycophorin variantMiltenberger V- like molecule. J. Biol. Chem. 265: 13825- 13829, 1990.

GAM8358 255 GYPE Kudo, S.; Fukuda, M.: Identification of a novel human 3 C c
glycophorin,glycophorin E, by isolation of genomic clones and complementary DNAclones utilizing polymerase chain reaction. J. Biol. Chem. 265:1102- 1110, 1990.

GAM8358 255 GYPE Onda, M.; Fukuda, M.: Detailed physical mapping of the genes 3 C c
encodingglycophorins A, B, and E, as revealed by P1 plasmids containing humangenomic DNA. Gene 159: 225- 230, 1995.

GAM8358 255 GYPE Onda, M.; Kudo, S.; Rearden, A.; Mattei, M.- G.; Fukuda, M.: 3 C c
Identificationof a precursor genomic segment that provided a sequence unique
toglycophorin B and E genes. Proc. Nat. Acad. Sci. 90: 7220- 7224,1993.

GAM8358 255 GYPE Vignal, A.; Rahuel, C.; London, J.; Cherif Zahar, B.; Schaff, S.;Hattab, C.; 3 C c
Okubo, Y.; Cartron, J.- P.: A novel gene member of thehuman glycophorin A
and B gene family: molecular cloning and expression. Europ.J. Biochem. 191:
619- 625, 1990.

GAM8358 255 HHLA1 Feuchter- Murthy, A. E.; Freeman, J. D.; Mager, D. L.: Splicingof a human 3 C c
endogenous retrovirus to a novel phospholipase A2 relatedgene. Nucleic Acids
Res. 21: 135- 143, 1993.

GAM8358 255 HHLA1 Kowalski, P. E.; Freeman, J. D.; Mager, D. L.: Intergenic splicingbetween a 3 C c
HERV- H endogenous retrovirus and two adjacent human genes. Genomics 57:371-
379, 1999.

GAM8358 255 HHLA1 Kowalski, P. E.; Freeman, J. D.; Nelson, D. T.; Mager, D. L.:Genomic 3 C c
structure and evolution of a novel gene (PLA2L) with duplicatedphospholipase
A2- like domains. Genomics 39: 38- 46, 1997.

GAM8358 255 HLA-DRA Accolla, R. S.; Gross, N.; Carrel, S.; Corte, G.: Distinct formsof both 3 C c
alpha and beta subunits are present in the human Ia molecularpool. Proc.
Nat. Acad. Sci. 78: 4549- 4551, 1981.

GAM8358 255 HLA-DRA Almarri, A.; Batchelor, J. R.: HLA and hepatitis B infection. Lancet 3 C c
344:1194- 1195, 1994.

GAM8358 255 HLA-DRA Auffray, C.; Strominger, J. L.: Molecular genetics of the humanmajor 3 C c
histocompatibility complex. Adv. Hum. Genet. 15: 197- 247,1986.

GAM8358 255 HLA-DRA Ayala, F. J.; Escalante, A.; O'hUigin, C.; Klein, J.: Moleculargenetics of 3 C c
speciation and human origins. Proc. Nat. Acad. Sci. 91:6787- 6794, 1994.

GAM8358 255 HLA-DRA Bell, J. I.; Estess, P.; St. John, T.; Saiki, R.; Watling, D. L.;Erlich, H. 3 C c
A.; McDevitt, H. O.: DNA sequence and characterizationof human class II
major histocompatibility complex beta chains fromthe DR1 haplotype. Proc.
Nat. Acad. Sci. 82: 3405- 3409, 1985.

GAM8358 255 HLA-DRA Bodmer, J. G.; Marsh, S. G. E.; Albert, E. D.; Bodmer, W. F.; Bontrop,R. E.; 3 C c
Charron, D.; Dupont, B.; Erlich, H. A.; Fauchet, R.; Mach,B.; Mayr, W. R.;
Parham, P.; Sasazuki, T.; Schreuder, G. M. T.; Strominger,J. L.; Svejgaard,
A.; Terasaki, P. I.: Nomenclature for factors ofthe HLA system, 1996. Europ.
J. Immunogenet. 24: 105- 151, 1997.

GAM8358 255 HLA-DRA Bodmer, J. G.; Marsh, S. G. E.; Albert, E. D.; Bodmer, W. F.; Dupont,B.; 3 C c
Erlich, H. A.; Mach, B.; Mayr, W. R.; Parham, P.; Sasazuki, T.;Schreuder, G.
M. T.; Strominger, J. L.; Svejgaard, A.; Terasaki, P.I.: Nomenclature for
factors of the HLA system, 1994. Tissue Antigens 44:1- 18, 1994.

GAM8358 255 HLA-DRA Bodmer, J. G.; Marsh, S. G. E.; Albert, E.: Nomenclature for factorsof the 3 C c
HLA system, 1989. Immun. Today 11: 3- 10, 1990.

GAM8358 255 HLA-DRA Bodmer, W. F.; Bodmer, J. G.; Batchelor, J. R.; Festenstein, H.;Morris, P. 3 C c
J.: Histocompatibility Testing 1977. Copenhagen: Munksgaard(pub.) 1978.

GAM8358 255 HLA-DRA Boss, J. M.; Strominger, J. L.: Cloning and sequence analysisof the human 3 C c
major histocompatibility complex gene DC- 3- beta. Proc.Nat. Acad. Sci. 81:
5199- 5203, 1984.

GAM8358 255 HLA-DRA Charron, D. J.; McDevitt, H. O.: Analysis of HLA- D region- 3 C c
associatedmolecules with monoclonal antibody. Proc. Nat. Acad. Sci. 76:
6567- 6571,1979.

GAM8358 255 HLA-DRA Chelladurai, M.; Honn, K. V.; Walz, D. A.: HLA- DR is a procoagulant. 3 C c
Biochem.Biophys. Res. Commun. 178: 467- 473, 1991.

GAM8358 255 HLA-DRA Corte, G.; Damiani, G.; Calabi, F.; Fabbi, M.; Bargellesi, A.: Analysis of 3 C c
HLA- DR polymorphism by two- dimensional peptide mapping. Proc.Nat. Acad.
Sci. 78: 534- 538, 1981.

GAM8358 255 HLA-DRA Das, H. K.; Lawrance, S. K.; Weissman, S. M.: Structure and 3 C c
nucleotidesequence of the heavy chain gene of HLA- DR. Proc. Nat. Acad. Sci.
80:3543- 3547, 1983.

GAM8358 255 HLA-DRA Delovitch, T. L.; Falk, J. A.: Evidence for structural homologybetween 3 C c
murine and human Ia antigens. Immunogenetics 8: 405- 418,1979.

GAM8358 255 HLA-DRA Dunham, I.; Sargent, C. A.; Dawkins, R. L.; Campbell, R. D.:An analysis of 3 C c
variation in the long- range genomic organization ofthe human major
histocompatibility complex class II region by pulsed- fieldgel
electrophoresis. Genomics 5: 787- 796, 1989.

GAM8358 255 HLA-DRA Erlich, H. A.; Stetler, D.; Saiki, R.; Gladstone, P.; Pious, D.: Mapping of 3 C c
the genes encoding the HLA- DR alpha chain and the HLA- relatedantigens to a
chromosome 6 deletion by using genomic blotting. Proc.Nat. Acad. Sci. 80:
2300- 2304, 1983.

GAM8358 255 HLA-DRA Ferber, K. M.; Keller, E.; Albert, E. D.; Ziegler, A.- G.: Predictivevalue 3 C c
of human leukocyte antigen class II typing for the developmentof islet
autoantibodies and insulin- dependent diabetes postpartumin women with
gestational diabetes. J. Clin. Endocr. Metab. 84:2342- 2348, 1999.

GAM8358 255 HLA-DRA Fuller, T. C.; Einarson, M.; Pinto, C.; Ahern, A.; Yunis, E. J.: Genetic 3 C c
evidence that HLA- DR (Ia) specifications include multipleHLA- D
determinants on a single haplotype. Transplant. Proc. 10:781- 784, 1978.

GAM8358 255 HLA-DRA Hardy, D. A.; Bell, J. I.; Long, E. O.; Lindsten, T.; McDevitt,H. O.: 3 C c
Mapping of the class II region of the human major histocompatibilitycomplex
by pulsed- field gel electrophoresis. Nature 323: 453- 455,1986.

GAM8358 255 HLA-DRA Hui, K.; Festenstein, H.; de Klein, A.; Grosveld, G.; Grosveld,F.: HLA- DR 3 C c
genotyping by restriction fragment length polymorphismanalyses.
Immunogenetics 22: 231- 239, 1985.

GAM8358 255 HLA-DRA Kaufman, J. F.; Strominger, J. L.: HLA- DR light chain has a polymorphicN- 3 C c
terminal region and a conserved immunoglobulin- like C- terminal region.
Nature 297:694- 697, 1982.

GAM8358 255 HLA-DRA Korman, A. J.; Auffray, C.; Schamboeck, A.; Strominger, J. L.: The amino 3 C c
acid sequence and gene organization of the heavy chainof the HLA- DR
antigen: homology to immunoglobulins. Proc. Nat. Acad.Sci. 79: 6013- 6017,
1982.

GAM8358 255 HLA-DRA Korman, A. J.; Knudsen, P. J.; Kaufman, J. F.; Strominger, J.L.: cDNA clones 3 C c
for the heavy chain of HLA- DR antigens obtained afterimmunopurification of
polysomes by monoclonal antibody. Proc. Nat.Acad. Sci. 79: 1844- 1848, 1982.

GAM8358 255 HLA-DRA Kratzin, H.; Yang, C.; Gotz, H.; Pauly, E.; Kolbel, S.; Egert,G.; Thinnes, 3 C c
F. P.; Wernet, P.; Altevogt, P.; Hilschmann, N.: Primarstrukturmenschlicher
Histokompatibilitatsantigene der Klasse II. 1. Mitteilung:aminosauresequenz
der N- terminalen 198 Reste der beta- Kette des HLA- Dw2,2;DR2,2-
Alloantigens. HoppeSeylers Z. Physiol. Chem. 362: 1665- 1669, 1981.

GAM8358 255 HLA-DRA Lamm, L. U.: Another segregant series, DR, in HLA. Cytogenet.Cell Genet. 22: 3 C c
309- 312, 1978.

GAM8358 255 HLA-DRA Larhammar, D.; Schenning, L.; Gustafsson, K.; Wiman, K.; Claesson,L.; Rask, 3 C c
L.; Peterson, P. A.: Complete amino acid sequence of anHLA- DR antigen- like
beta chain as predicted from the nucleotide sequence:similarities with
immunoglobulins and HLA- A, - B, and - C antigens. Proc.Nat. Acad. Sci. 79:

3687- 3691, 1982.

GAM8358 255 HLA-DRA Lee, J. S.; Trowsdale, J.; Bodmer, W. F.: cDNA clones codingfor the heavy 3 C c
chain of human HLA- DR antigen. Proc. Nat. Acad. Sci. 79:545- 549, 1982.

GAM8358 255 HLA-DRA Levine, F.; Mach, B.; Long, E.; Erlich, H.; Pious, D.: Mappingin the HLA- D 3 C c
region with deletion variants and cloned genes. (Abstract) Cytogenet.Cell
Genet. 37: 523 only, 1984.

GAM8358 255 HLA-DRA Mann, D. L.; Abelson, L.; Harris, S. D.; Amos, D. B.: Secondgenetic locus in 3 C c
the HLA region for human B- cell alloantigens. Nature 259:145- 146, 1976.

GAM8358 255 HLA-DRA Mann, D. L.; Abelson, L.; Henkart, P.; Harris, S. D.; Amos, D.B.: Specific 3 C c
B- lymphocyte alloantigens linked to HLA. Proc. Nat.Acad. Sci. 72: 5103-
5106, 1975.

GAM8358 255 HLA-DRA Markert, M. L.; Cresswell, P.: Polymorphism of human B- cell 3 C c
alloantigens:evidence for three loci within the HLA system. Proc. Nat. Acad.
Sci. 77:6101- 6104, 1980.

GAM8358 255 HLA-DRA Mayer, W. E.; O'hUigin, C.; Klein, J.: Resolution of the HLA- DRB6puzzle: a 3 C c
case of grafting a de novo- generated exon on an existinggene. Proc. Nat.
Acad. Sci. 90: 10720- 10724, 1993.

GAM8358 255 HLA-DRA McDevitt, H. O.; Bodmer, W. F.: HLA, immune- response genes, anddisease. 3 C c

Lancet I: 1269- 1275, 1974.

GAM8358 255 HLA-DRA McMichael, A.; Makgoba, W.: Complexity in human histocompatibilityloci. 3 C c
Nature 293: 701- 702, 1981.

GAM8358 255 HLA-DRA Moen, T.; Albrechtsen, D.; Flatmark, A.; Jakobsen, A.; Jervell,J.; 3 C c
Halvorsen, S.; Solheim, B. G.; Thorsby, E.: Importance of HLA- DRmatching in
cadaveric renal transplantation: a prospective one- centerstudy of 170
transplants. New Eng. J. Med. 303: 850- 854, 1980.

GAM8358 255 HLA-DRA Olerup, O.; Troye- Blomberg, M.; Schreuder, G. M. T.; Riley, E.M.: HLA- DR 3 C c
and - DQ gene polymorphism in West Africans is twice asextensive as in North
European Caucasians: evolutionary implications. Proc.Nat. Acad. Sci. 88:
8480- 8484, 1991.

GAM8358 255 HLA-DRA Park, M. S.; Terasaki, P. I.; Bernoco, D.: Relationship betweenMT and DR 3 C c
antigens.In: Terasaki, P. I.: Histocompatibility Testing1980. Los Angeles:
UCLA Press (pub.) 1980.

GAM8358 255 HLA-DRA Park, M. S.; Terasaki, P. I.; Bernoco, D.; Iwaki, Y.: Evidencefor a second 3 C c
B- cell locus separate from the DR locus. Transplant.Proc. 10: 823- 828,
1978.

GAM8358 255 HLA-DRA Pisella, P.- J.; Brignole, F.; Debbasch, C.; Lozato, P.- A.; Creuzot- 3 C c
Garcher,C.; Bara, J.; Saiag, P.; Warnet, J.- M.; Baudouin, C.: Flow
cytometricanalysis of conjunctival epithelium in ocular rosacea and
keratoconjunctivitissicca. Ophthalmology 107: 1841- 1849, 2000.

GAM8358 255 HLA-DRA Rollini, P.; Mach, B.; Gorski, J.: Linkage map of three HLA- DRbeta- chain 3 C c
genes: evidence for a recent duplication event. Proc.Nat. Acad. Sci. 82:
7197- 7201, 1985.

GAM8358 255 HLA-DRA Sachs, J. A.; Jaraquemada, D.; Festenstein, H.: Intra HLA- D 3 C c
regionrecombinant maps HLA- DR between HLA- B and HLA- D. Tissue Antigens
17:43- 56, 1981.

GAM8358 255 HLA-DRA Schwartz, B. D.: Personal Communication. St. Louis, Mo. 2/22/1983. 3 C c

GAM8358 255 HLA-DRA Shackelford, D. A.; Mann, D. L.; van Rood, J. J.; Ferrara, G.B.; Strominger, 3 C c
J. L.: Human B- cell alloantigens DC1, MT1, and LB12are identical to each
other but distinct from the HLA- DR antigen. Proc.Nat. Acad. Sci. 78: 4566-

4570, 1981.

GAM8358 255 HLA-DRA Strominger, J. L.: Biology of the human histocompatibility leukocyteantigen 3 C c
(HLA) system and a hypothesis regarding the generation ofautoimmune
diseases. J. Clin. Invest. 77: 1411- 1415, 1986.

GAM8358 255 HLA-DRA Suciu- Foca, N.; Weiner, J.; Rohowsky, C.; McKiernan, P.; Susinno,E.; 3 C c
Rubinstein, P.: Indications that Dw determinants are controlledby distinct
(but closely linked) genes. Transplant. Proc. 10: 799- 804,1978.

GAM8358 255 HLA-DRA Terasaki, P. I.; Park, M. S.; Opelz, G.; Ting, A.: Multiple sclerosisand 3 C c
high incidence of a B- lymphocyte antigen. Science 193: 1245- 1247,1976.

GAM8358 255 HLA-DRA Thursz, M. R.; Thomas, H. C.; Greenwood, B. M.; Hill, A. V. S.: Heterozygote 3 C c
advantage for HLA class- II type in hepatitis B virusinfection. (Letter)
Nature Genet. 17: 11- 12, 1997.

GAM8358 255 HLA-DRA Tiercy, J.- M.; Gorski, J.; Jeannet, M.; Mach, B.: Identificationand 3 C c
distribution of three serologically undetected alleles of HLA- DRby
oligonucleotide- DNA typing analysis. Proc. Nat. Acad. Sci. 85:198- 202,
1988.

GAM8358 255 HLA-DRA Tiwari, J. L.; Terasaki, P. I.: HLA and Disease Associations. New York: 3 C c
Springer- Verlag (pub.) 1985.

GAM8358 255 HLA-DRA Trowsdale, J.: Genetics and polymorphism: class II antigens. Brit.Med. Bull. 3 C c
43: 15- 36, 1987.

GAM8358 255 HLA-DRA Tsubota, K.; Fukagawa, K.; Fujihara, T.; Shimmura, S.; Saito,I.; Saito, K.; 3 C c
Takeuchi, T.: Regulation of human leukocyte antigenexpression in human
conjunctival epithelium. Invest. Ophthal. Vis.Sci. 40: 28- 34, 1999.

GAM8358 255 HLA-DRA Walker, L. E.; Hewick, R.; Hunkapiller, M. W.; Hood, L. E.; Dreyer,W. J.; 3 C c
Reisfeld, R. A.: N- terminal amino acid sequences of the alphaand beta
chains of HLA- DR1 and HLA- DR2 antigens. Biochemistry 23:185- 188, 1983.

GAM8358 255 HRC Brown, S. D. M.; Chartier, F.; Johnson, K.; Cavanna, J. S.: Mappingthe Hrc 3 C c
gene to proximal mouse chromosome 7: delineation of a conservedlinkage group
with human 19q. Genomics 18: 459- 461, 1993.

GAM8358 255 HRC Hofmann, S. L.; Brown, M. S.; Lee, E.; Pathak, R. K.; Anderson,R. G. W.; 3 C c
Goldstein, J. L.: Purification of a sarcoplasmic reticulumprotein that binds
Ca(2+) and plasma lipoproteins. J. Biol. Chem. 264:8260- 8270, 1989.

GAM8358 255 HRC Hofmann, S. L.; Topham, M.; Hsieh, C.- L.; Francke, U.: cDNA andgenomic 3 C c
cloning of HRC, a human sarcoplasmic reticulum protein, andlocalization of
the gene to human chromosome 19 and mouse chromosome7. Genomics 9: 656- 669,
1991.

GAM8358 255 HRH1 Inoue, I.; Taniuchi, I.; Kitamura, D.; Jenkins, N. A.; Gilbert,D. J.; 3 C c
Copeland, N. G.; Watanabe, T.: Characteristics of the mousegenomic histamine
H1 receptor gene. Genomics 36: 178- 181, 1996.

GAM8358 255 HRH1 Jutel, M.; Watanabe, T.; Klunker, S.; Akdis, M.; Thomet, O. A.R.; 3 C c
Malolepszy, J.; Zak- Nejmark, T.; Koga, R.; Kobayashi, T.; Blaser,K.; Akdis,
C. A.: Histamine regulates T- cell and antibody responsesby differential
expression of H1 and H2 receptors. Nature 413: 420- 425,2001.

GAM8358 255 HRH1 Le Coniat, M.; Traiffort, E.; Ruat, M.; Arrang, J.- M.; Berger,R.: 3 C c
Chromosomal localization of the human histamine H1- receptor gene.
Hum.Genet. 94: 186- 188, 1994.

GAM8358 255 HRH1 Ma, R. Z.; Gao, J.; Meeker, N. D.; Fillmore, P. D.; Tung, K. S.K.; Watanabe, 3 C c
T.; Zachary, J. F.; Offner, H.; Blankenhorn, E. P.;Teuscher, C.:
Identification of Bphs, an autoimmune disease locus,as histamine receptor H-
1. Science 297: 620- 623, 2002.

GAM8358 255 HRH1 Yamashita, M.; Fukui, H.; Sugama, K.; Horio, Y.; Ito, S.; Mizuguchi,H.; 3 C c
Wada, H.: Expression cloning of a cDNA encoding the bovine histamineH1
receptor. Proc. Nat. Acad. Sci. 88: 11515- 11519, 1991.

GAM8358 255 HS3ST3B1 Liu, J.; Shworak, N. W.; Sinay, P.; Schwartz, J. J.; Zhang, L.;Fritze, L. 3 C c
M.; Rosenberg, R. D.: Expression of heparan sulfate D- glucosaminyl3- O-
sulfotransferase isoforms reveals novel substrate specificities. J.Biol.
Chem. 274: 5185- 5192, 1999.

GAM8358 255 HS3ST3B1 Shworak, N. W.; Liu, J.; Petros, L. M.; Zhang, L.; Kobayashi, M.;Copeland, 3 C c
N. G.; Jenkins, N. A.; Rosenberg, R. D.: Multiple isoformsof heparan sulfate
D- glucosaminyl 3- O- sulfotransferase: isolation,characterization, and
expression of human cDNAs and identificationof distinct genomic loci. J.
Biol. Chem. 274: 5170- 5184, 1999.

GAM8358 255 ID2 Hara, E.; Yamaguchi, T.; Nojima, H.; Ide, T.; Campisi, J.; Okayama,H.; Oda, 3 C c
K.: Id- related genes encoding helix- loop- helix proteinsare required for
G1 progression and are repressed in senescent humanfibroblasts. J. Biol.
Chem. 269: 2139- 2145, 1994.

GAM8358 255 ID2 Iavarone, A.; Garg, P.; Lasorella, A.; Hsu, J.; Israel, M. A.:The helix- 3 C c
loop- helix protein Id- 2 enhances cell proliferation andbinds to the
retinoblastoma protein. Genes Dev. 8: 1270- 1284, 1994.

GAM8358 255 ID2 Lasorella, A.; Iavarone, A.; Israel, M. A.: Id2 specifically 3 C c
altersregulation of the cell cycle by tumor suppressor proteins. Molec.Cell.
Biol. 16: 2570- 2578, 1996.

GAM8358 255 ID2 Lasorella, A.; Noseda, M.; Beyna, M.; Iavarone, A.: Id2 is a 3 C c
retinoblastomaprotein target and mediates signalling by Myc oncoproteins.
Nature 407:592- 598, 2000.

GAM8358 255 ID2 Mathew, S.; Chen, W.; Murty, V. V. V. S.; Benezra, R.; Chaganti,R. S. K.: 3 C c
Chromosomal assignment of human ID1 and ID2 genes. Genomics 30:385- 387,
1995.

GAM8358 255 IDH3A Huh, T.- L.; Kim, Y.- O.; Oh, I.- U.; Song, B. J.; Inazawa, J.: Assignmentof 3 C c
the human mitochondrial NAD(+)- specific isocitrate dehydrogenasealpha
subunit (IDH3A) gene to 15q25.1- q25.2 by in situ hybridization. Genomics
31:295- 296, 1996.

GAM8358 255 IDH3A Kim, Y.- O.; Oh, I.- U.; Park, H.- S.; Jeng, J.; Song, B. J.; Huh,T.- L.: 3 C c
Characterization of a cDNA clone for human NAD(+)- specificisocitrate
dehydrogenase alpha- subunit and structural comparison withits isoenzymes
from different species. Biochem. J. 308: 63- 68, 1995.

GAM8358 255 IFNAR2 Croze, E.; Russell- Harde, D.; Wagner, T. C.; Pu, H.; Pfeffer, L.M.; Perez, 3 C c
H. D.: The human type I interferon receptor: identificationof the interferon
beta- specific receptor- associated phosphoprotein. J.Biol. Chem. 271:
33165- 33168, 1996.

GAM8358 255 IFNAR2 Croze, E.; Usacheva, A.; Asarnow, D.; Minshall, R.D.; Perez, 3 C c
H.D.;Colamonici, O.: Receptor for activated C- kinase (RACK- 1), a WD motif-
containingprotein, specifically associates with the human type I IFN
receptor. J.Immun. 165: 5127- 5132, 2000.

GAM8358 255 IFNAR2 Domanski, P.; Witte, M.; Kellum, M.; Rubinstein, M.; Hackett, R.;Pitha, P.; 3 C c
Colamonici, O. R.: Cloning and expression of a long formof the beta subunit
of the interferon alpha/beta receptor that isrequired for signaling. J.
Biol. Chem. 270: 21606- 21611, 1995.

GAM8358 255 IFNAR2 Lutfalla, G.; Holland, S. J.; Cinato, E.; Monneron, D.; Reboul,J.; Rogers, 3 C c
N. C.; Smith, J. M.; Stark, G. R.; Gardiner, K.; Mogensen,K. E.; Kerr, I.

M.; Uze, G.: Mutant U5A cells are complemented byan interferon- alpha/beta receptor subunit generated by alternativeprocessing of a new member of a cytokine receptor gene cluster. EMBOJ. 14: 5100- 5108, 1995.

GAM8358 255 IFNAR2 Novick, D.; Cohen, B.; Rubinstein, M.: The human interferon 3 C c alpha/betareceptor: characterization and molecular cloning. Cell 77: 391- 400,1994.

GAM8358 255 IFNAR2 Platanias, L. C.; Uddin, S.; Domanski, P.; Colamonici, O. R.:Differences in 3 C c interferon alpha and beta signaling: interferon betaselectively induces the interaction of the alpha and beta(L) subunitsof the type I interferon receptor. J. Biol. Chem. 271: 23630- 23633,1996.

GAM8358 255 IFNAR2 Raz, R.; Cheung, K.; Ling, L.; Levy, D. E.: Three distinct locion human 3 C c chromosome 21 contribute to interferon- alpha/beta responsiveness. Somat.Cell Molec. Genet. 21: 139- 145, 1995.

GAM8358 255 IL16 Baier, M.; Bannert, N.; Werner, A.; Lang, K.; Kurth, R.: Molecularcloning, 3 C c sequence, expression, and processing of the interleukin 16precursor. Proc. Nat. Acad. Sci. 94: 5273- 5277, 1997.

GAM8358 255 IL16 Bannert, N.; Baier, M.; Werner, A.; Kurth, R.: Interleukin- 16or not? Nature 3 C c 381: 30 only, 1996.

GAM8358 255 IL16 Bannert, N.; Kurth, R.; Baier, M.: The gene encoding mouse interleukin- 3 C c 16consists of seven exons and maps to Chromosome 7 D2- D3. Immunogenetics 49:704- 706, 1999.

GAM8358 255 IL16 Cruikshank, W. W.; Center, D. M.; Nisar, N.; Wu, M.; Natke, B.;Theodore, A. 3 C c C.; Kornfeld, H.: Molecular and functional analysisof a lymphocyte chemoattractant factor: association of biologic functionwith CD4 expression. Proc. Nat. Acad. Sci. 91: 5109- 5113, 1994.

GAM8358 255 IL16 Cruikshank, W.; Center, D. M.: Modulation of lymphocyte migrationby human 3 C c lymphokines. II. Purification of a lymphotactic factor (LCF). J.Immun. 128: 2569- 2574, 1982.

GAM8358 255 IL16 Drwinga, H. L.; Toji, L. H.; Kim, C. H.; Greene, A. E.; Mulivor,R. A.: NIGMS 3 C c human/rodent somatic cell hybrid mapping panels 1 and2. Genomics 16: 311- 314, 1993.

GAM8358 255 IL16 Hudson, T. J.; Stein, L. D.; Gerety, S. S.; Ma, J.; Castle, A.B.; Silva, J.; 3 C c Slonim, D. K.; Baptista, R.; Kruglyak, L.; Xu, S. H.;Hu, X.; Colbert, A. M. E.; and 39 others: An STS- based map of thehuman genome. Science 270: 1945- 1954, 1995.

GAM8358 255 IL16 Keane, J.; Nicoll, J.; Kim, S.; Wu, D. M. H.; Cruikshank, W. W.;Brazer, W.; 3 C c Natke, B.; Zhang, Y.; Center, D. M.; Kornfeld, H.: Conservationof structure and function between human and murine IL- 16. J. Immun. 160:5945- 5954, 1998.

GAM8358 255 ITCH Chen, X.; Wen, S.; Fukuda, M. N.; Gavva, N. R.; Hsu, D.; Akama,T. O.; Yang- 3 C c Feng, T.; Shen, C. K. J.: Human ITCH is a coregulatorof the hematopoietic transcription factor NF- E2. Genomics 73: 238- 241,2001.

GAM8358 255 ITCH D'Andrea, A. D.; Serhan, C. N.: Relieving the Itch. Nature Genet. 18:97- 99, 3 C c 1998.

GAM8358 255 ITCH Perry, W. L.; Hustad, C. M.; Swing, D. A.; O'Sullivan, T. N.; Jenkins,N. A.; 3 C c Copeland, N. G.: The itchy locus encodes a novel ubiquitinprotein ligase that is disrupted in a18H mice. Nature Genet. 18:143- 146, 1998.

GAM8358 255 ITCH Qiu, L.; Joazeiro, C.; Fang, N.; Wang, H.- Y.; Elly, C.; Altman,Y.; Fang, 3 C c D.; Hunter, T.; Liu, Y.- C.: Recognition and ubiquitinationof Notch by Itch, a Hect- type E3 ubiquitin ligase. J. Biol. Chem. 275:35734- 35737, 2000.

GAM8358 255 ITCH Winberg, G.; Matskova, L.; Chen, F.; Plant, P.; Rotin, D.; Gish,G.; Ingham, R.; Ernberg, I.; Pawson, T.: Latent membrane protein2A of Epstein- Barr virus binds WW domain E3 protein- ubiquitin ligasesthat ubiquitinate B- cell tyrosine kinases. Molec. Cell. Biol. 20:8526- 8535, 2000. 3 C c

GAM8358 255 ITCH Wood, J. D.; Yuan, J.; Margolis, R. L.; Colomer, V.; Duan, K.;Kushi, J.; Kaminsky, Z.; Kleiderlein, J. J., Jr.; Sharp, A. H.; Ross,C. A.: Atrophin- 1, the DRPLA gene product, interacts with two familiesof WW domain- containing proteins. Molec. Cell. Neurosci. 11: 149- 160,1998. 3 C c

GAM8358 255 JMJ Berge- Lefranc, J.- L.; Jay, P.; Massacrier, A.; Cau, P.; Mattei,M. G.; Bauer, S.; Marsollier, C.; Berta, P.; Fontes, M.: Characterizationof the human jumonji gene. Hum. Molec. Genet. 5: 1637- 1641, 1996. 3 C c

GAM8358 255 JMJ Toyoda, M.; Kojima, M.; Takeuchi, T.: Jumonji is a nuclear proteinthat participates in the negative regulation of cell growth. Biochem.Biophys. Res. Commun. 274: 332- 336, 2000. 3 C c

GAM8358 255 KCNE1L Piccini, M.; Vitelli, F.; Seri, M.; Galietta, L. J. V.; Moran,O.; Bulfone, A.; Banfi, S.; Pober, B.; Renieri, A.: KCNE1- like geneis deleted in AMME contiguous gene syndrome: identification and characterizationof the human and mouse homologs. Genomics 60: 251- 257, 1999. 3 C c

GAM8358 255 KIF5B Kamal, A.; Almenar- Queralt, A.; LeBlanc, J. F.; Roberts, E. A.;Goldstein, L. S. B.: Kinesin- mediated axonal transport of a membranecompartment containing beta- secretase and presenilin- 1 requires APP. Nature 414:643- 648, 2001. 3 C c

GAM8358 255 KIF5B Kamal, A.; Stokin, G. B.; Yang, Z.; Xia, C.; Goldstein, L. S.:Axonal transport of amyloid precursor protein is mediated by directbinding to the kinesin light chain subunit of kinesin- I. Neuron 28:449- 459, 2000. 3 C c

GAM8358 255 KIF5B Kull, F. J.; Sablin, E. P.; Lau, R.; Fletterick, R. J.; Vale, R.D.: Crystal structure of the kinesin motor domain reveals a structuralsimilarity to myosin. Nature 380: 550- 555, 1996. 3 C c

GAM8358 255 KIF5B Navone, F.; Niclas, J.; Hom- Booher, N.; Sparks, L.; Bernstein,H. D.; McCaffrey, G.; Vale, R. D.: Cloning and expression of a humankinesin heavy chain gene: interaction of the COOH- terminal domainwith cytoplasmic microtubules in transfected CV- 1 cells. J. CellBiol. 117: 1263- 1275, 1992. 3 C c

GAM8358 255 KIF5B Niclas, J.; Navone, F.; Hom- Booher, N.; Vale, R. D.: Cloning andlocalization of a conventional kinesin motor expressed exclusivelyin neurons. Neuron 12: 1059- 1072, 1994. 3 C c

GAM8358 255 KIF5B Tanaka, Y.; Kanai, Y.; Okada, Y.; Nonaka, S.; Takeda, S.; Harada,A.; Hirokawa, N.: Targeted disruption of mouse conventional kinesinheavy chain, kif5B, results in abnormal perinuclear clustering ofmitochondria. Cell 93: 1147- 1158, 1998. 3 C c

GAM8358 255 LDLR Aalto- Setala, K.; Helve, E.; Kovanen, P. T.; Kontula, K.: Finnishtype of low density lipoprotein receptor gene mutation (FH- Helsinki)deletes exons encoding the carboxy- terminal part of the receptor andcreates an internalization- defective phenotype. J. Clin. Invest. 84:499- 505, 1989. 3 C c

GAM8358 255 LDLR Aalto- Setala, K.; Koivisto, U.- M.; Miettinen, T. A.; Gylling, H.;Kesaniemi, Y. A.; Savolainen, M.; Pyorala, K.; Ebeling, T.; Mononen,I.; Turtola, H.; Viikari, J.; Kontula, K.: Prevalence and geographicaldistribution of major LDL receptor gene rearrangements in Finland. J.Intern. Med. 231: 227- 234, 1992. 3 C c

GAM8358 255 LDLR Agnello, V.; Abel, G.; Elfahal, M.; Knight, G. B.; Zhang, Q.- X.: Hepatitis C virus and other flaviviridae viruses enter cells vialow density 3 C c

lipoprotein receptor. Proc. Nat. Acad. Sci. 96: 12766- 12771,1999.

GAM8358 255 LDLR Allen, J. M.; Thompson, G. R.; Myant, N. B.; Steiner, R.; Oakley,C. M.: 3 C c
Cardiovascular complications of homozygous familial hypercholesterolaemia.
Brit.Heart J. 44: 361- 368, 1980.

GAM8358 255 LDLR Benlian, P.; Amselem, S.; Loux, N.; Pastier, D.; Giraud, G.; deGennes, J. 3 C c
L.; Turpin, G.; Monnier, L.; Rieu, D.; Douste- Blazy, P.;Dastugue, B.;
Goossens, M.; Junien, C.: A LDL receptor gene homozygousmutation: PCR
amplification, direct genomic sequencing, associatedhaplotype, rapid
screening for frequency. Ann. Genet. 33: 65- 69,1990.

GAM8358 255 LDLR Bertolini, S.; Lelli, N.; Coviello, D. A.; Ghisellini, M.; Masturzo,P.; 3 C c
Tiozzo, R.; Elicio, N.; Gaddi, A.; Calandra, S.: A large deletionin the LDL
receptor gene- - the cause of familial hypercholesterolemiain three Italian
families: a study that dates back to the 17th century(FH- Pavia). Am. J.
Hum. Genet. 51: 123- 134, 1992.

GAM8358 255 LDLR Betard, C.; Kessling, A. M.; Roy, M.; Chamberland, A.; Lussier- Cacan,S.; 3 C c
Davignon, J.: Molecular genetic evidence for a founder effectin familial
hypercholesterolemia among French Canadians. Hum. Genet. 88:529- 536, 1992.

GAM8358 255 LDLR Boehnke, M.; Arnheim, N.; Li, H.; Collins, F. S.: Fine- structuregenetic 3 C c
mapping of human chromosomes using the polymerase chain reactionon single
sperm: experimental design considerations. Am. J. Hum.Genet. 45: 21- 32,
1989.

GAM8358 255 LDLR Brink, P. A.; Steyn, L. T.; Coetzee, G. A.; van der Westhuyzen,D. R.: 3 C c
Familial hypercholesterolemia in South African Afrikaners:PvuII and StuI DNA
polymorphisms in the LDL- receptor gene consistentwith a predominating
founder gene effect. Hum. Genet. 77: 32- 35,1987.

GAM8358 255 LDLR Brown, M. S.; Goldstein, J. L.: Analysis of a mutant strain ofhuman 3 C c
fibroblasts with a defect in the internalization of receptor- boundlow
density lipoproteins. Cell 9: 663- 674, 1976.

GAM8358 255 LDLR Brown, M. S.; Goldstein, J. L.: Familial hypercholesterolemia:defective 3 C c
binding of lipoproteins to cultured fibroblasts associatedwith impaired
regulation of 3- hydroxy- 3- methylglutaryl coenzyme atreductase activity.
Proc. Nat. Acad. Sci. 71: 788- 792, 1974.

GAM8358 255 LDLR Brown, M. S.; Goldstein, J. L.: Receptor- mediated endocytosis:insights from 3 C c
the lipoprotein receptor system. Proc. Nat. Acad. Sci. 76:3330- 3337, 1979.

GAM8358 255 LDLR Davis, C. G.; Lehrman, M. A.; Russell, D. W.; Anderson, R. G.W.; Brown, M. 3 C c
S.; Goldstein, J. L.: The J.D. mutation in familialhypercholesterolemia:
amino acid substitution in cytoplasmic domainimpedes internalization of LDL
receptors. Cell 45: 15- 24, 1986.

GAM8358 255 LDLR De Braekeleer, M.: Hereditary disorders in Saguenay- Lac- St- Jean(Quebec, 3 C c
Canada). Hum. Hered. 41: 141- 146, 1991.

GAM8358 255 LDLR Defesche, J. C.; Kastelein, J. J. P.: Molecular epidemiologyof familial 3 C c
hypercholesterolaemia. (Letter) Lancet 352: 1643- 1644,1998.

GAM8358 255 LDLR Defesche, J. C.; van de Ree, M. A.; Kastelein, J. J. P.; van Diermen,D. E.; 3 C c
Janssens, N. W. E.; van Doormaal, J. J.; Hayden, M. R.: Detectionof the
pro664- to- leu mutation in the low- density lipoprotein receptorand its
relation to lipoprotein(a) levels in patients with
familialhypercholesterolemia of Dutch ancestry from The Netherlands and
Canada. Clin.Genet. 42: 273- 280, 1992.

GAM8358 255 LDLR Defesche, J. C.; van Diermen, D. E.; Lansberg, P. J.; Lamping,R. J.; Reymer, 3 C c
P. W. A.; Hayden, M. R.; Kastelein, J. J. P.: SouthAfrican founder mutations

in the low- density lipoprotein receptorgene causing familial hypercholesterolemia in the Dutch population. Hum.Genet. 92: 567- 570, 1993.

GAM8358 255 LDLR Durst, R.; Colombo, R.; Shpitzen, S.; Ben Avi, L.; Friedlander,Y.; Wexler, R.; Raal, F. J.; Marais, D. A.; Defesche, J. C.; Mandelshtam,M. Y.; Kotze, M. J.; Leitersdorf, E.; Meiner, V.: Recent origin andspread of a common Lithuanian mutation, G197del LDLR, causing familialhypercholesterolemia: positive selection is not always necessary toaccount for disease incidence among Ashkenazi Jews. Am. J. Hum. Genet. 68:1172- 1188, 2001. 3 C c

GAM8358 255 LDLR Ekstrom, U.; Abrahamson, M.; Floren, C.- H.; Tollig, H.; Wettrell,G.; Nilsson, G.; Sun, X.- M.; Soutar, A. K.; Nilsson- Ehle, P.: Anindividual with a healthy phenotype in spite of a pathogenic LDL receptormutation (C240F). Clin. Genet. 55: 332- 339, 1999. 3 C c

GAM8358 255 LDLR Elston, R. C.; Namboodiri, K. K.; Go, R. C. P.; Siervogel, R.M.; Glueck, C. J.: Probable linkage between essential familial hypercholesterolemiaand third complement component (C3). Cytogenet. Cell Genet. 16:294- 297, 1976. 3 C c

GAM8358 255 LDLR Esser, V.; Russell, D. W.: Transport- deficient mutations in thelow density lipoprotein receptor: alterations in the cysteine- richand cysteine- poor regions of the protein block intracellular transport. J.Biol. Chem. 263: 13276- 13281, 1988. 3 C c

GAM8358 255 LDLR Feussner, G.; Dobmeyer, J.; Nissen, H.; Hansen, T. S.: UnusualXanthomas in a young patient with heterozygous familial hypercholesterolemiaand type III hyperlipoproteinemia. Am. J. Med. Genet. 65: 149- 154,1996. 3 C c

GAM8358 255 LDLR Francke, U.; Brown, M. S.; Goldstein, J. L.: Assignment of thehuman gene for the low density lipoprotein receptor to chromosome19: synteny of a receptor, a ligand, and a genetic disease. Proc.Nat. Acad. Sci. 81: 2826- 2830, 1984. 3 C c

GAM8358 255 LDLR Frank, S. L.; Taylor, B. A.; Lusis, A. J.: Linkage of the mouseLDL receptor gene on chromosome 9. Genomics 5: 646- 648, 1989. 3 C c

GAM8358 255 LDLR Fumeron, F.; Grandchamp, B.; Fricker, J.; Krempf, M.; Wolf, L.- M.;Khayat, M.- C.; Boiffard, O.; Apfelbaum, M.: Presence of the FrenchCanadian deletion in a French patient with familial hypercholesterolemia.(Letter) New Eng. J. Med. 326: 69 only, 1992. 3 C c

GAM8358 255 LDLR Gilbert, W.: Genes- in- pieces revisited. Science 228: 823- 824,1985. 3 C c

GAM8358 255 LDLR Goldfarb, L. G.; Petersen, R. B.; Tabaton, M.; Brown, P.; LeBlanc,A. C.; Montagna, P.; Cortelli, P.; Julien, J.; Vital, C.; Pendelbury,W. W.; Haltia, M.; Wills, P. R.; and 9 others: Fatal familial insomniaand familial Creutzfeldt- Jakob disease: disease phenotype determinedby a DNA polymorphism. Science 258: 806- 808, 1992. 3 C c

GAM8358 255 LDLR Goldstein, J. L.; Brown, M. S.; Stone, N. J.: Genetics of theLDL receptor: evidence that the mutations affecting binding and internalizationare allelic. Cell 12: 629- 641, 1977. 3 C c

GAM8358 255 LDLR Goldstein, J. L.; Dana, S. E.; Brunschede, G. Y.; Brown, M. S.: Genetic heterogeneity in familial hypercholesterolemia: evidencefor two different mutations affecting functions of low- density lipoproteinreceptor. Proc. Nat. Acad. Sci. 72: 1092- 1096, 1975. 3 C c

GAM8358 255 LDLR Graadt van Roggen, F.; van der Westhuyzen, D. R.; Marais, A. D.;Gevers, W.; Coetzee, G. A.: Low density lipoprotein receptor foundermutations in Afrikaner familial hypercholesterolaemic patients: acomparison of two geographical areas. Hum. Genet. 88: 204- 208, 1991. 3 C c

GAM8358 255 LDLR Gudnason, V.; King- Underwood, L.; Seed, M.; Sun, X.- M.; Soutar,A. K.; Humphries, S. E.: Identification of recurrent and novel mutationsin exon 4 3 C c

of the LDL receptor gene in patients with familial hypercholesterolemiain the United Kingdom. Arteriosclerosis Thromb. 13: 56- 63, 1993.

GAM8358 255 LDLR Gudnason, V.; Sigurdsson, G.; Nissen, H.; Humphries, S. E.: Commonfounder 3 C c
mutation in the LDL receptor gene causing familial hypercholesterolemiain the Icelandic population. Hum. Mutat. 10: 36- 44, 1997.

GAM8358 255 LDLR Henderson, H. E.; Berger, G. M. B.; Marais, A. D.: A new LDLreceptor gene 3 C c
deletion mutation in the South African population. Hum.Genet. 80: 371- 374, 1988.

GAM8358 255 LDLR Hobbs, H. H.: Personal Communication. Dallas, Tex. 12/1/1990. 3 C c

GAM8358 255 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: Molecular geneticsof the LDL 3 C c
receptor gene in familial hypercholesterolemia. Hum. Mutat. 1:445- 466, 1992.

GAM8358 255 LDLR Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.; Russell, D. W.:Deletion of 3 C c
exon encoding cysteine- rich repeat of low density lipoproteinreceptor alters its binding specificity in a subject with familialhypercholesterolemia. J. Biol. Chem. 261: 13114- 13120, 1986.

GAM8358 255 LDLR Hobbs, H. H.; Brown, M. S.; Russell, D. W.; Davignon, J.; Goldstein,J. L.: 3 C c
Deletion in the gene for the low- density- lipoprotein receptorin a majority of French Canadians with familial hypercholesterolemia. NewEng. J. Med. 317: 734- 737, 1987.

GAM8358 255 LDLR Hobbs, H. H.; Lehrman, M. A.; Yamamoto, T.; Russell, D. W.: Polymorphismand 3 C c
evolution of Alu sequences in the human low density lipoproteinreceptor gene. Proc. Nat. Acad. Sci. 82: 7651- 7655, 1985.

GAM8358 255 LDLR Hobbs, H. H.; Leitersdorf, E.; Goldstein, J. L.; Brown, M. S.;Russell, D. 3 C c
W.: Multiple CRM- mutations in familial hypercholesterolemia:evidence for 13 alleles, including four deletions. J. Clin. Invest. 81:909- 917, 1988.

GAM8358 255 LDLR Hobbs, H. H.; Leitersdorf, E.; Leffert, C. C.; Cryer, D. R.; Brown,M. S.; 3 C c
Goldstein, J. L.: Evidence for a dominant gene that suppresseshypercholesterolemia in a family with defective low density lipoproteinreceptors. J. Clin. Invest. 84: 656- 664, 1989.

GAM8358 255 LDLR Hobbs, H. H.; Russell, D. W.; Brown, M. S.; Goldstein, J. L.:The LDL 3 C c
receptor locus in familial hypercholesterolemia: mutationalanalysis of a membrane protein. Annu. Rev. Genet. 24: 133- 170, 1990.

GAM8358 255 LDLR Horsthemke, B.; Beisiegel, U.; Dunning, A.; Havinga, J. R.; Williamson,R.; 3 C c
Humphries, S.: Unequal crossing- over between two Alu- repetitiveDNA sequences in the low- density- lipoprotein- receptor gene: a possiblemechanism for the defect in a patient with familial hypercholesterolaemia. Europ.J. Biochem. 164: 77- 81, 1987.

GAM8358 255 LDLR Horsthemke, B.; Dunning, A.; Humphries, S.: Identification ofdeletions in 3 C c
the human low density lipoprotein receptor gene. J.Med. Genet. 24: 144- 147, 1987.

GAM8358 255 LDLR Horsthemke, B.; Kessling, A. M.; Seed, M.; Wynn, V.; Williamson,R.; 3 C c
Humphries, S. E.: Identification of a deletion in the low densitylipoprotein (LDL) receptor gene in a patient with familial hypercholesterolaemia. Hum.Genet. 71: 75- 78, 1985.

GAM8358 255 LDLR Jensen, H. K.; Jensen, T. G.; Faergeman, O.; Jensen, L. G.; Andresen,B. S.; 3 C c
Corydon, M. J.; Andreasen, P. H.; Hansen, P. S.; Heath, F.;Bolund, L.; Gregersen, N.: Two mutations in the same low- densitylipoprotein receptor allele act in synergy to reduce receptor functionin heterozygous familial hypercholesterolemia. Hum. Mutat. 9: 437- 444,1997.

GAM8358 255 LDLR Jensen, J. M.; Kruse, T. A.; Brorholt- Petersen, J. U.; Christiansen,T. M.; 3 C c
Jensen, H. K.; Kolvraa, S.; Faergeman, O.: Linking genotypeto aorto-
coronary atherosclerosis: a model using familial hypercholesterolemiaand
aorto- coronary calcification. Ann. Hum. Genet. 63: 511- 520,1999.

GAM8358 255 LDLR Kajinami, K.; Fujita, H.; Koizumi, J.; Mabuchi, H.; Takeda, R.;Ohta, M.: 3 C c
Genetically determined mild type of familial hypercholesterolemiaincluding
normocholesterolemic patients: FH- Tonami- 2. Circulation 80(suppl. 2): 278
only, 1989.

GAM8358 255 LDLR Kajinami, K.; Mabuchi, H.; Itoh, H.; Michishita, I.; Takeda, M.;Wakasugi, 3 C c
T.; Koizumi, J.; Takeda, R.: New variant of low densitylipoprotein receptor
gene FH- Tonami. Arteriosclerosis 8: 187- 192,1988.

GAM8358 255 LDLR Khachadurian, A. K.: The inheritance of essential familial 3 C c
hypercholesterolemia. Am.J. Med. 37: 402- 407, 1964.

GAM8358 255 LDLR Kingsley, D. M.; Krieger, M.: Receptor- mediated endocytosis oflow density 3 C c
lipoprotein: somatic cell mutants define multiple genesrequired for
expression of surface- receptor activity. Proc. Nat.Acad. Sci. 81: 5454-
5458, 1984.

GAM8358 255 LDLR Knight, B. L.; Gavigan, S. J. P.; Soutar, A. K.; Patel, D. D.: Defective 3 C c
processing and binding of low- density lipoprotein receptorsin fibroblasts
from a familial hypercholesterolaemic subject. Europ.J. Biochem. 179: 693-
698, 1989.

GAM8358 255 LDLR Knoblauch, H.; Muller- Myhsok, B.; Busjahn, A.; Ben Avi, L.; Bahring,S.; 3 C c
Baron, H.; Heath, S. C.; Uhlmann, R.; Faulhaber, H.- D.; Shpitzen,S.; Aydin,
A.; Reshef, A.; and 11 others: A cholesterol- loweringgene maps to
chromosome 13q. Am. J. Hum. Genet. 66: 157- 166, 2000.

GAM8358 255 LDLR Koivisto, U.- M.; Hubbard, A. L.; Mellman, I.: A novel cellularphenotype for 3 C c
familial hypercholesterolemia due to a defect in polarizedtargeting of LDL
receptor. Cell 105: 575- 585, 2001.

GAM8358 255 LDLR Koivisto, U.- M.; Turtola, H.; Aalto- Setala, K.; Top, B.; Frants,R. R.; 3 C c
Kovanen, P. T.; Syvanen, A.- C.; Kontula, K.: The
familialhypercholesterolemia (FH)- North Karelia mutation of the low
densitylipoprotein receptor gene deletes seven nucleotides of exon 6 andis a
common cause of FH in Finland. J. Clin. Invest. 90: 219- 228,1992.

GAM8358 255 LDLR Koivisto, U.- M.; Viikari, J. S.; Kontula, K.: Molecular characterizationof 3 C c
minor gene rearrangements in Finnish patients with heterozygousfamilial
hypercholesterolemia: identification of two common missensemutations
(Gly823- to- Asp and Leu380- to- His) and eight rare mutationsof the LDL
receptor gene. Am. J. Hum. Genet. 57: 789- 797, 1995.

GAM8358 255 LDLR Komuro, I.; Kato, H.; Nakagawa, T.; Takahashi, K.; Mimori, A.;Takeuchi, F.; 3 C c
Nishida, Y.; Miyamoto, T.: Case report: the longest- livedpatient with
homozygous familial hypercholesterolemia secondary toa defect in
internalization of the LDL receptor. Am. J. Med. Sci. 294:341- 345, 1987.

GAM8358 255 LDLR Kotze, M. J.; Langenhoven, E.; Retief, A. E.; Steyn, K.; Marais,M. P.; 3 C c
Grobbelaar, J. J.; Oosthuizen, C. J. J.; Weich, H. F. H.; Benade,A. J. S.:
Haplotype associations of three DNA polymorphisms at thehuman low density
lipoprotein receptor gene locus in familial hypercholesterolemia. J.Med.
Genet. 24: 750- 755, 1987.

GAM8358 255 LDLR Kotze, M. J.; Langenhoven, E.; Warnich, L.; du Plessis, L.; Retief,A. E.: 3 C c
The molecular basis and diagnosis of familial hypercholesterolaemiain South
African Afrikaners. Ann. Hum. Genet. 55: 115- 121, 1991.

GAM8358 255 LDLR Kotze, M. J.; Theart, L.; Peeters, A.; Langenhoven, E.: A denovo duplication 3 C c
in the low density lipoprotein receptor gene. Hum.Mutat. 6: 181- 183, 1995.
GAM8358 255 LDLR Kotze, M. J.; Warnich, L.; Langenhoven, E.; du Plessis, L.; Retief,A. E.: An 3 C c
exon 4 mutation identified in the majority of South Africanfamilial
hypercholesterolaemics. J. Med. Genet. 27: 298- 302, 1990.
GAM8358 255 LDLR Landsberger, D.; Meiner, V.; Reshef, A.; Levy, Y.; van der Westhuyzen,D. R.; 3 C c
Coetzee, G. A.; Leitersdorf, E.: A nonsense mutation in theLDL receptor gene
leads to familial hypercholesterolemia in the Druzesect. Am. J. Hum. Genet.
50: 427- 433, 1992.
GAM8358 255 LDLR Langlois, S.: Personal Communication. Vancouver, British Columbia,Canada 3 C c
1989.
GAM8358 255 LDLR Langlois, S.; Kastelein, J. J. P.; Hayden, M. R.: Characterizationof six 3 C c
partial deletions in the low- density- lipoprotein (LDL) receptorgene
causing familial hypercholesterolemia (FH). Am. J. Hum. Genet. 43:60- 68,
1988.
GAM8358 255 LDLR Lee, W. K.; Haddad, L.; Macleod, M. J.; Dorrance, A. M.; Wilson,D. J.; 3 C c
Gaffney, D.; Dominiczak, M. H.; Packard, C. J.; Day, I. N.;Humphries, S. E.;
Dominiczak, A. F.: Identification of a common lowdensity lipoprotein
receptor mutation (C163Y) in the West of Scotland. J.Med. Genet. 35: 573-
578, 1998.
GAM8358 255 LDLR Lehrman, M. A.; Goldstein, J. L.; Brown, M. S.; Russell, D. W.;Schneider, W. 3 C c
J.: Internalization- defective LDL receptors producedby genes with nonsense
and frameshift mutations that truncate thecytoplasmic domain. Cell 41: 735-
743, 1985.
GAM8358 255 LDLR Lehrman, M. A.; Goldstein, J. L.; Russell, D. W.; Brown, M. S.: Duplication 3 C c
of seven exons in LDL receptor gene caused by Alu- Alurecombination in a
subject with familial hypercholesterolemia. Cell 48:827- 835, 1987.
GAM8358 255 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Alu- Alu 3 C c
recombination deletes splice acceptor sites and producessecreted low density
lipoprotein receptor in a subject with familialhypercholesterolemia. J.
Biol. Chem. 262: 3354- 3361, 1987.
GAM8358 255 LDLR Lehrman, M. A.; Russell, D. W.; Goldstein, J. L.; Brown, M. S.: Exon- Alu 3 C c
recombination deletes 5 kilobases from the low densitylipoprotein receptor
gene, producing a null phenotype in familialhypercholesterolemia. Proc. Nat.
Acad. Sci. 83: 3679- 3683, 1986.
GAM8358 255 LDLR Lehrman, M. A.; Schneider, W. J.; Sudhof, T. C.; Brown, M. S.;Goldstein, J. 3 C c
L.; Russell, D. W.: Mutation in LDL receptor: Alu- Alurecombination deletes
exons encoding transmembrane and cytoplasmicdomains. Science 227: 140- 146,
1985.
GAM8358 255 LDLR Leitersdorf, E.; Hobbs, H. H.: Personal Communication. Dallas,Tex. 12/1990. 3 C c
GAM8358 255 LDLR Leitersdorf, E.; Hobbs, H. H.; Fourie, A. M.; Jacobs, M.; vander Westhuyzen, 3 C c
D. R.; Coetzee, G. A.: Deletion in the first cysteine- richrepeat of low-
density lipoprotein receptor impairs its transport butnot lipoprotein
binding in fibroblasts from a subject with familialhypercholesterolemia.
Proc. Nat. Acad. Sci. 85: 7912- 7916, 1988.
GAM8358 255 LDLR Leitersdorf, E.; Tobin, E. J.; Davignon, J.; Hobbs, H. H.: Commonlow- 3 C c
density lipoprotein receptor mutations in the French Canadianpopulation. J.
Clin. Invest. 85: 1014- 1023, 1990.
GAM8358 255 LDLR Leitersdorf, E.; van der Westhuyzen, D. R.; Coetzee, G. A.; Hobbs,H. H.: Two 3 C c
common low density lipoprotein receptor gene mutationscause familial

hypercholesterolemia in Afrikaners. J. Clin. Invest. 84:954- 961, 1989.

GAM8358 255 LDLR Lelli, N.; Ghisellini, M.; Calandra, S.; Gaddi, A.; Ciarrocchi,A.; Coviello, 3 C c
D. A.; Bertolini, S.: Duplication of exons 13, 14 and15 of the LDL- receptor
gene in a patient with heterozygous familialhypercholesterolemia. Hum.
Genet. 86: 359- 362, 1991.

GAM8358 255 LDLR Leren, T. P.; Solberg, K.; Rodningen, O. K.; Tonstad, S.; Ose,L.: Two 3 C c
founder mutations in the LDL receptor gene in Norwegian
familialhypercholesterolemia subjects. Atherosclerosis 111: 175- 182, 1994.

GAM8358 255 LDLR Li, H.; Gyllensten, U. B.; Cui, X.; Saiki, R. K.; Erlich, H. A.;Arnheim, N.: 3 C c
Amplification and analysis of DNA sequences in singlehuman sperm and diploid
cells. Nature 335: 414- 417, 1988.

GAM8358 255 LDLR Lindgren, V.; Luskey, K. L.; Russell, D. W.; Francke, U.: Humangenes 3 C c
involved in cholesterol metabolism: chromosomal mapping of theloci for the
low density lipoprotein receptor and 3- hydroxy- 3- methylglutaryl-
coenzymeA reductase with cDNA probes. Proc. Nat. Acad. Sci. 82: 8567-
8571,1985.

GAM8358 255 LDLR Loux, N.; Benlian, P.; Pastier, D.; Boileau, C.; Cambou, J. P.;Monnier, L.; 3 C c
Percheron, C.; Junien, C.: Recurrent mutation at aa792 in the LDL receptor
gene in a French patient. Hum. Genet. 87:373- 375, 1991.

GAM8358 255 LDLR Ma, Y. H.; Betard, C.; Roy, M.; Davignon, J.; Kessling, A. M.: 3 C c
Identification of a second 'French Canadian' LDL receptor gene deletionand
development of a rapid method to detect both deletions. Clin.Genet. 36: 219-
228, 1989.

GAM8358 255 LDLR Maartmann- Moe, K.; Wang, H. S.; Donald, L. J.; Hamerton, J. L.;Berg, K.: 3 C c
Data from hybrid cell lines raise the possibility thatfactors controlling
the low density lipoprotein receptor activitymay reside on human chromosome
21, 5 or both. (Abstract) Cytogenet.Cell Genet. 32: 295- 296, 1982.

GAM8358 255 LDLR Mandelshtam, M.; Chakir, K.; Shevtsov, S.; Golubkov, V.; Skobeleva,N.; 3 C c
Lipovetsky, B.; Konstantinov, V.; Denisenko, A.; Gaitskhoki, V.;Schwartz,
E.: Prevalence of Lithuanian mutation among St. PetersburgJews with familial
hypercholesterolemia. Hum. Mutat. 12: 255- 258,1998.

GAM8358 255 LDLR Meiner, V.; Landsberger, D.; Berkman, N.; Reshef, A.; Segal, P.;Seftel, H. 3 C c
C.; van der Westhuyzen, D. R.; Jeenah, M. S.; Coetzee,G. A.; Leitersdorf,
E.: A common Lithuanian mutation causing familialhypercholesterolemia in
Ashkenazi Jews. Am. J. Hum. Genet. 49: 443- 449,1991.

GAM8358 255 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamoto, A.: Analysisof a recycling- 3 C c
impaired mutant of low density lipoprotein receptorin familial
hypercholesterolemia. J. Biol. Chem. 264: 16584- 16590,1989.

GAM8358 255 LDLR Miyake, Y.; Tajima, S.; Funahashi, T.; Yamamura, T.; Yamamoto,A.: A point 3 C c
mutation of low- density- lipoprotein receptor causingrapid degradation of
the receptor. Europ. J. Biochem. 210: 1- 7,1992.

GAM8358 255 LDLR Moorjani, S.; Roy, M.; Torres, A.; Betard, C.; Gagne, C.; Lambert,M.; Brun, 3 C c
D.; Davignon, J.; Lupien, P.: Mutations of low- density- lipoprotein-
receptorgene, variation in plasma cholesterol, and expression of
coronaryheart disease in homozygous familial hypercholesterolaemia. Lancet
341:1303- 1306, 1993.

GAM8358 255 LDLR Oppenheim, A.; Friedlander, Y.; Dann, E. J.; Berkman, N.; Schwartz,S. P.; 3 C c
Leitersdorf, E.: Hypercholesterolemia in five Israeli Christian-
Arabkindreds is caused by the 'Lebanese' allele at the low density
lipoproteinreceptor gene locus and by an additional independent major

factor. Hum.Genet. 88: 75- 84, 1991.

GAM8358 255 LDLR Pisciotta, L.; Cantafora, A.; De Stefano, F.; Langheim, S.; Calandra,S.; 3 C c
Bertolini, S.: A 'de novo' mutation of the LDL- receptor geneas the cause of
familial hypercholesterolemia. Biochim. Biophys.Acta 1587: 7- 11, 2002.

GAM8358 255 LDLR Rodningen, O. K.; Rosby, O.; Tonstad, S.; Ose, L.; Berg, K.; Leren,T. P.: A 3 C c
9.6 kilobase deletion in the low density lipoprotein receptorgene in
Norwegian familial hypercholesterolemia subjects. Clin. Genet. 42:288- 295,
1992.

GAM8358 255 LDLR Rubinsztein, D. C.; Coetzee, G. A.; Marais, A. D.; Leitersdorf,E.; Seftel, 3 C c
H. C.; van der Westhuyzen, D. R.: Identification andproperties of the
proline- 644- to- leucine mutant LDL receptor in SouthAfricans of Indian
origin. J. Lipid Res. 33: 1647- 1655, 1992.

GAM8358 255 LDLR Rudiger, N. S.; Heinsvig, E. M.; Hansen, F. A.; Faergeman, O.;Bolund, L.; 3 C c
Gregersen, N.: DNA deletions in the low density lipoprotein(LDL) receptor
gene in Danish families with familial hypercholesterolemia. Clin.Genet. 39:
451- 462, 1991.

GAM8358 255 LDLR Ruffner, D. E.; Sprung, C. N.; Minghetti, P. P.; Gibbs, P. E.M.; Dugaiczyk, 3 C c
A.: Invasion of the human albumin- alpha- fetoproteingene family by Alu,
Kpn, and two novel repetitive DNA elements. Molec.Biol. Evol. 4: 1- 9, 1987.

GAM8358 255 LDLR Russell, D. W.; Lehrman, M. A.; Sudhof, T. C.; Yamamoto, T.; Davis,C. G.; 3 C c
Hobbs, H. H.; Brown, M. S.; Goldstein, J. L.: The LDL receptorin familial
hypercholesterolemia: use of human mutations to dissecta membrane protein.
Cold Spring Harbor Symp. Quant. Biol. 51: 811- 819,1986.

GAM8358 255 LDLR Russell, D. W.; Schneider, W. J.; Yamamoto, T.; Luskey, K. L.;Brown, M. S.; 3 C c
Goldstein, J. L.: Domain map of the LDL receptor: sequencehomology with the
epidermal growth factor precursor. Cell 37: 577- 585,1984.

GAM8358 255 LDLR Savov, A.; Angelicheva, D.; Balassopoulou, A.; Jordanova, A.;Noussia- 3 C c
Arvanitakis, S.; Kalaydjieva, L.: Double mutant alleles:are they rare? Hum.
Molec. Genet. 4: 1169- 1171, 1995.

GAM8358 255 LDLR Schuster, H.; Manke, C.; Fischer, J.; Keller, C.; Wolfram, G.;Zollner, N.: 3 C c
Identification of the valine 408 to methionine mutationin the LDL receptor
in a Greek patient with homozygous familial hypercholesterolemia.
Clin.Genet. 48: 90- 92, 1995.

GAM8358 255 LDLR Schuster, H.; Ostwald, P.; Keller, P.; Wolfram, G.; Keller, C.: 3 C c
Identification of the serine- 156 to leucine mutation in the low-
densitylipoprotein receptor in a German family with familial
hypercholesterolemia. Clin.Investig. 71: 172- 175, 1993.

GAM8358 255 LDLR Seftel, H. C.; Baker, S. G.; Sandler, M. P.; Forman, M. B.; Joffe,B. I.; 3 C c
Mendelsohn, D.; Jenkins, T.; Mieny, C. J.: A host of
hypercholesterolaemichomozygotes in South Africa. Brit. Med. J. 281: 633-
636, 1980.

GAM8358 255 LY9 Kingsmore, S. F.; Souryal, C. A.; Watson, M. L.; Patel, D. D.;Seldin, M. F.: 3 C c
Physical and genetic linkage of the genes encodingLy- 9 and CD48 on mouse
and human chromosomes 1. Immunogenetics 42:59- 62, 1995.

GAM8358 255 LY9 Kozak, C. A.; Davidson, W. F.; Morse, H. C., III: Genetic andfunctional 3 C c
relationships of the retroviral and lymphocyte alloantigenloci on mouse
chromosome 1. Immunogenetics 19: 163- 168, 1984.

GAM8358 255 LY9 Sandrin, M. S.; Gumley, T. P.; Henning, M. M.; Vaughan, H. A.;Gonez, L. J.; 3 C c
Trapani, J. A.; McKenzie, I. F. C.: Isolation and characterizationof cDNA
clones for mouse Ly- 9. J. Immun. 149: 1636- 1641, 1992.

GAM8358 255 LYN Harder, K. W.; Parsons, L. M.; Armes, J.; Evans, N.; Kountouri,N.; Clark, R.; Quillici, C.; Grail, D.; Hodgson, G. S.; Dunn, A. R.;Hibbs, M. L.: Gain- and loss- of- function Lyn mutant mice define acritical inhibitory role for Lyn in the myeloid lineage. Immunity 15:603- 615, 2001. 3 C c

GAM8358 255 LYN Hasegawa, M.; Fujimoto, M.; Poe, J. C.; Steeber, D. A.; Lowell,C. A.; Tedder, T. F.: A CD19- dependent signaling pathway regulatesautoimmunity in Lyn- deficient mice. J. Immun. 167: 2469- 2478, 2001. 3 C c

GAM8358 255 LYN Hibbs, M. L.; Tarlinton, D. M.; Armes, J.; Grail, D.; Hodgson,G.; Maglitto, R.; Stacker, S. A.; Dunn, A. R.: Multiple defects inthe immune system of Lyn- deficient mice, culminating in autoimmunedisease. Cell 83: 301- 311, 1995. 3 C c

GAM8358 255 LYN Parravicini, V.; Gadina, M.; Kovarova, M.; Odom, S.; Gonzalez- Espinosa,C.; Furumoto, Y.; Saitoh, S.; Samelson, L. E.; O'Shea, J. J.; Rivera,J.: Fyn kinase initiates complementary signals required for IgE- dependentmast cell degranulation. Nature Immun. 3: 741- 748, 2002. 3 C c

GAM8358 255 LYN Webster, M. A.; Cardiff, R. D.; Muller, W. J.: Induction of mammaryepithelial hyperplasias and mammary tumors in transgenic mice expressinga murine mammary tumor virus/activated c- src fusion gene. Proc. Nat.Acad. Sci. 92: 7849- 7853, 1995. 3 C c

GAM8358 255 LYN Yamanashi, Y.; Fukushige, S.- I.; Semba, K.; Sukegawa, J.; Miyajima,N.; Matsubara, K.- I.; Yamamoto, T.; Toyoshima, K.: The yes- relatedcellular gene lyn encodes a possible tyrosine kinase similar to p56(lck). Molec.Cell. Biol. 7: 237- 243, 1987. 3 C c

GAM8358 255 MADH6 Galvin, K. M.; Donovan, M. J.; Lynch, C. A.; Meyer, R. I.; Paul,R. J.; Lorenz, J. N.; Fairchild- Huntress, V.; Dixon, K. L.; Dunmore,J. H.; Gimbrone, M. A., Jr.; Falb, D.; Huszar, D.: A role for Smad6in development and homeostasis of the cardiovascular system. NatureGenet. 24: 171- 174, 2000. 3 C c

GAM8358 255 MADH6 Riggins, G. J.; Thiagalingam, S.; Rozenblum, E.; Weinstein, C.L.; Kern, S. E.; Hamilton, S. R.; Willson, J. K. V.; Markowitz, S.D.; Kinzler, K. W.; Vogelstein, B.: Mad- related genes in the human. NatureGenet. 13: 347- 349, 1996. 3 C c

GAM8358 255 MADH6 Topper, J. N.; Cai, J.; Qiu, Y.; Anderson, K. R.; Xu, Y.- Y.; Deeds,J. D.; Feeley, R.; Gimeno, C. J.; Woolf, E. A.; Tayber, O.; Mays,G. G.; Sampson, B. A.; Schoen, F. J.; Gimbrone, M. A., Jr.; Falb,D.: Vascular MADs: two novel MAD- related genes selectively inducibleby flow in human vascular endothelium. Proc. Nat. Acad. Sci. 94:9314- 9319, 1997. 3 C c

GAM8358 255 MME Barker, P. E.; Shipp, M. A.; D'Adamio, L.; Masteller, E. L.; Reinherz,E. L.: The common acute lymphoblastic leukemia antigen gene mapsto chromosomal region 3(q21- q27). J. Immun. 142: 283- 287, 1989. 3 C c

GAM8358 255 MME D'Adamio, L.; Shipp, M. A.; Masteller, E. L.; Reinherz, E. L.:Organization of the gene encoding common acute lymphoblastic leukemiaantigen (neutral endopeptidase 24.11): multiple miniexons and separate5- prime untranslated regions. Proc. Nat. Acad. Sci. 86: 7103- 7107,1989. 3 C c

GAM8358 255 MME Debiec, H.; Guigonis, V.; Mougenot, B.; Decobert, F.; Haymann,J.- P.; Bensman, A.; Deschenes, G.; Ronco, P. M.: Antenatal membranousglomerulonephritis due to anti- neutral endopeptidase antibodies. NewEng. J. Med. 346: 2053- 2060, 2002. 3 C c

GAM8358 255 MME Iwata, N.; Tsubuki, S.; Takaki, Y.; Shirotani, K.; Lu, B.; Gerard,N. P.; Gerard, C.; Hama, E.; Lee, H.- J.; Saido, T. C.: Metabolicregulation of 3 C c

brain A- beta by neprilysin. Science 292: 1550- 1552,2001.

GAM8358 255 MME Letarte, M.; Vera, S.; Tran, R.; Addis, J. B. L.; Onizuka, R. J.;Quackenbush, E. J.; Jongeneel, C. V.; McInnes, R. R.: Common acutelymphocytic leukemia antigen is identical to neutral endopeptidase. J.Exp. Med. 168: 1247- 1253, 1988. 3 C c

GAM8358 255 MME Shipp, M. A.; Vijayaraghavan, J.; Schmidt, E. V.; Masteller, E.L.; D'Adamio, L.; Hersh, L. B.; Reinherz, E. L.: Common acute lymphoblasticleukemia antigen (CALLA) is active neutral endopeptidase 24.11 ('enkephalinase'):direct evidence by cDNA transfection analysis. Proc. Nat. Acad. Sci. 86:297- 301, 1989. 3 C c

GAM8358 255 MME Tran- Paterson, R.; Willard, H. F.; Letarte, M.: The common acutelymphoblastic leukemia antigen (neutral endopeptidase- - 3.4.24.11)gene is located on human chromosome 3. Cancer Genet. Cytogenet. 42:129- 134, 1989. 3 C c

GAM8358 255 MYBL2 Barletta, C.; Druck, T.; LaForgia, S.; Calabretta, B.; Drabkin,H.; Patterson, D.; Croce, C. M.; Huebner, K.: Chromosome locationsof the MYB related genes, AMYB and BMYB. Cancer Res. 51: 3821- 3824,1991. 3 C c

GAM8358 255 MYBL2 Noben- Trauth, K.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N.A.; Sonoda, G.; Testa, J. R.; Klempnauer, K.- H.: Mybl2 (Bmyb) mapsto mouse chromosome 2 and human chromosome 20q13.1. Genomics 35:610- 612, 1996. 3 C c

GAM8358 255 NAB1 Russo, M. W.; Sevetson, B. R.; Milbrandt, J.: Identification ofNAB1, a repressor of NGFI- A- and Krox20- mediated transcription. Proc.Nat. Acad. Sci. 92: 6873- 6877, 1995. 3 C b

GAM8358 255 NAB1 Svaren, J.; Apel, E. D.; Simburger, K. S.; Jenkins, N. A.; Gilbert,D. J.; Copeland, N. A.; Milbrandt, J.: The Nab2 and Stat6 genes sharea common transcription termination region. Genomics 41: 33- 39, 1997. 3 C b

GAM8358 255 NAB1 Swirnoff, A. H.; Apel, E. D.; Svaren, J.; Sevetson, B. R.; Zimonjic,D. B.; Popescu, N. C.; Milbrandt, J.: Nab1, a corepressor of NGFI- A(Egr- 1), contains an active transcriptional repression domain. Molec.Cell. Biol. 18: 512- 524, 1998. 3 C b

GAM8358 255 NAB1 Venken, K.; Di Maria, E.; Bellone, E.; Balestra, P.; Cassandrini,D.; Mandich, P.; De Jonghe, P.; Timmerman, V.; Svaren, J.: Searchfor mutation in the EGR2 corepressor proteins, NAB1 and NAB2, in humanperipheral neuropathies. Neurogenetics 4: 37- 41, 2002. 3 C b

GAM8358 255 NINJ1 Araki, T.; Milbrandt, J.: Ninjurin, a novel adhesion molecule,is induced by nerve injury and promotes axonal growth. Neuron 17:353- 361, 1996. 3 C b

GAM8358 255 NINJ1 Araki, T.; Zimonjic, D. B.; Popescu, N. C.; Milbrandt, J.: Mechanismof homophilic binding mediated by ninjurin, a novel widely expressedadhesion molecule. J. Biol. Chem. 272: 21373- 21380, 1997. 3 C b

GAM8358 255 NINJ1 Chadwick, B. P.; Heath, S. K.; Williamson, J.; Obermayr, F.; Patel,L.; Sheer, D.; Frischauf, A.- M.: The human homologue of the ninjuringene maps to the candidate region of hereditary sensory neuropathytype I (HSN1). Genomics 47: 58- 63, 1998. 3 C b

GAM8358 255 NINJ1 Mandich, P.; Bellone, E.; Di Maria, E.; Pigullo, S.; Pizzuti, A.;Schenone, A.; Soriani, S.; Varese, A.; Windebank, A. J.; Ajmar, F.: Exclusion of the ninjurin gene as a candidate for hereditary sensoryneuropathies type I and type II. Am. J. Med. Genet. 83: 409- 410,1999. 3 C b

GAM8358 255 NKTR Anderson, S. K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J. R.: A cyclophilin- related protein involved in thefunction of natural killer cells. Proc. Nat. Acad. Sci. 90: 542- 546,1993. 3 C c

GAM8358 255 NKTR Frey, J. L.; Bino, T.; Kantor, R. R. S.; Segal, D. M.; Giardina,S. L.; 3 C c
Roder, J.; Anderson, S.; Ortaldo, J. R.: Mechanism of targetcell recognition
by natural killer cells: characterization of a noveltriggering molecule
restricted to CD3- large granular lymphocytes. J.Exp. Med. 174: 1527- 1536,
1991.

GAM8358 255 NKTR Rinfret, A.; Anderson, S. K.: IL- 2 regulates the expression ofthe NK- TR 3 C c
gene via an alternate RNA splicing mechanism. Molec. Immun. 30:1307- 1313,
1993.

GAM8358 255 NKTR Simons- Evelyn, M.; Young, H. A.; Anderson, S. K.: Characterizationof the 3 C c
mouse Nktr gene and promoter. Genomics 40: 94- 100, 1997.

GAM8358 255 NKTR Young, H. A.; Jenkins, N. A.; Copeland, N. G.; Simek, S.; Lerman,M. I.; 3 C c
Zbar, B.; Glenn, G.; Ortaldo, J. R.; Anderson, S. K.: Localizationof a novel
natural killer triggering receptor locus to human chromosome3p23- p21 and
mouse chromosome 9. Genomics 16: 548- 549, 1993.

GAM8358 255 ODF2 Brohmann, H.; Pinnecke, S.; Hoyer- Fender, S.: Identification 3 C b
andcharacterization of new cDNAs encoding outer dense fiber proteinsof rat
sperm. J. Biol. Chem. 272: 10327- 10332, 1997.

GAM8358 255 ODF2 Scott, A. F.: Personal Communication. Baltimore, Md. 9/10/1997. 3 C b

GAM8358 255 ODF2 Shao, X.; Murthy, S.; Demetrick, D. J.; van der Hoorn, F. A.:Human outer 3 C b
dense fiber gene, ODF2, localizes to chromosome 9q34. Cytogenet.Cell Genet.
83: 221- 223, 1998.

GAM8358 255 ODF2 Shao, X.; Tarnasky, H. A.; Schalles, U.; Oko, R.; van der Hoorn,F. A.: 3 C b
Interactional cloning of the 84- kDa major outer dense fiberprotein Odf84:
leucine zippers mediate associations of Odf84 and Odf27. J.Biol. Chem. 272:
6105- 6113, 1997.

GAM8358 255 ODF2 Shao, X.; van der Hoorn, F. A.: Self- interaction of the major27- kilodalton 3 C b
outer dense fiber protein is in part mediated by a leucinezipper domain in
the rat. Biol. Reprod. 55: 1343- 1350, 1996.

GAM8358 255 P2RX4 Buell, G.; Lewis, C.; Collo, G.; North, R. A.; Surprenant, A.:An antagonist- 3 C c
insensitive P2X receptor expressed in epithelia andbrain. EMBO J. 15: 55-
62, 1996.

GAM8358 255 P2RX4 Buell, G.; Lewis, C.; Collo, G.; North, R. A.; Surprenant, A.:Cloning and 3 C c
expression of a family of ATP- gated ion channels. (Abstract) Soc.Neurosci.
21: 1262, 1995.

GAM8358 255 P2RX4 Garcia- Guzman, M.; Soto, F.; Gomez- Hernandez, J. M.; Lund, P. E.;Stuhmer, 3 C c
W.: Characterization of the recombinant human P2X4 receptorreveals
pharmacological differences to the rat homologue. Molec.Pharm. 51: 109- 118,
1997.

GAM8358 255 P2RY6 Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.: Molecular cloningand 3 C c
functional analysis of a novel P2 nucleotide receptor. J. Biol.Chem. 270:
26152- 26158, 1995.

GAM8358 255 P2RY6 Communi, D.; Parmentier, M.; Boeynaems, J.- M.: Cloning, 3 C c
functionalexpression and tissue distribution of the human P2Y6 receptor.
Biochem.Biophys. Res. Commun. 222: 303- 308, 1996.

GAM8358 255 P2RY6 Maier, R.; Glatz, A.; Mosbacher, J.; Bilbe, G.: Cloning of P2Y6cDNAs and 3 C c
identification of a pseudogene: comparison of P2Y receptorsubtype expression
in bone and brain tissues. Biochem. Biophys. Res.Commun. 237: 297- 302,
1997.

GAM8358 255 P2RY6 Pidlaoan, L. V.; Jin, J.; Sandhu, A. K.; Athwal, R. S.; Kunapuli,S. P.: 3 C c
Colocalization of P2Y2 and P2Y6 receptor genes at human chromosome11q13.3-

14.1. Somat. Cell Molec. Genet. 23: 291- 296, 1997.

GAM8358 255 P2RY6 Somers, G. R.; Hammet, F.; Woollatt, E.; Richards, R. I.; Southey,M. C.; 3 C c
Venter, D. J.: Chromosomal localization of the human P2Y(6)purinoceptor gene
and phylogenetic analysis of the P2y purinoceptorfamily. Genomics 44: 127-
130, 1997.

GAM8358 255 PAM Glauder, J.; Ragg, H.; Rauch, J.; Engels, J. W.: Human peptidylglycinealpha- 3 C c
amidating monooxygenase: cDNA, cloning and functional expressionof a
truncated form in COS cells. Biochem. Biophys. Res. Commun. 169:551- 558,
1990.

GAM8358 255 PAM Lossie, A. C.; Eipper, B. A.; Hand, T. A.; Camper, S. A.: Localizationof the 3 C c
peptidylglycine alpha- amidating monooxygenase gene (Pam) introducesa region
of homology between human chromosome 5q and mouse chromosome1. Mammalian
Genome 5: 738- 739, 1994.

GAM8358 255 PAM Ouafik, L'H.; Mattei, M. G.; Giraud, P.; Oliver, C.; Eipper, B.A.; Mains, R. 3 C c
E.: Localization of the gene encoding peptidylglycinealpha- amidating
monooxygenase (PAM) to human chromosome 5q14- 5q21.Genomics 18: 319- 321,
1993.

GAM8358 255 PAM Ouafik, L'H.; Stoffers, D. A.; Campbell, T. A.; Johnson, R. C.;Bloomquist, 3 C c
B. T.; Mains, R. E.; Eipper, B. A.: The multifunctionalpeptidylglycine
alpha- amidating monooxygenase gene: exon/intron organizationof catalytic,
processing, and routing domains. Molec. Endocr. 6:1571- 1584, 1992.

GAM8358 255 PCOLCE Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani- 3 C c
Sait, S.; Shows, T. B.; Greenspan, D. S.: Type I procollagenCOOH- terminal
proteinase enhancer protein: identification, primarystructure, and
chromosomal localization of the cognate human gene(PCOLCE). J. Biol. Chem.
269: 26280- 26285, 1994.

GAM8358 255 PCOLCE Takahara, K.; Osborne, L.; Elliott, R. W.; Tsui, L.- C.; Scherer,S. W.; 3 C c
Greenspan, D. S.: Fine mapping of the human and mouse genesfor the type I
procollagen COOH- terminal proteinase enhancer protein. Genomics 31:253-
256, 1996.

GAM8358 255 PDE1B Jiang, X.; Li, J.; Paskind, M.; Epstein, P. M.: Inhibition ofcalmodulin- 3 C c
dependent phosphodiesterase induces apoptosis in humanleukemic cells. Proc.
Nat. Acad. Sci. 93: 11236- 11241, 1996.

GAM8358 255 PDE1B Reed, T. M.; Browning, J. E.; Blough, R. I.; Vorhees, C. V.; Repaske,D. R.: 3 C c
Genomic structure and chromosome location of the murine
PDE1Bphosphodiesterase gene. Mammalian Genome 9: 571- 576, 1998.

GAM8358 255 PDE1B Repaske, D. R.; Swinnen, J. V.; Jin, S.- L. C.; Van Wyk, J. J.;Conti, M.: A 3 C c
polymerase chain reaction strategy to identify and clonecyclic nucleotide
phosphodiesterase cDNAs: molecular cloning of thecDNA encoding the 63- kDa
calmodulin- dependent phosphodiesterase. J.Biol. Chem. 267: 18683- 18688,
1992.

GAM8358 255 PDE1B Yu, J.; Wolda, S. L.; Frazier, A. L. B.; Florio, V. A.; Martins,T. J.; 3 C c
Snyder, P. B.; Harris, E. A. S.; McCaw, K. N.; Farrell, C.A.; Steiner, B.;
Bentley, J. K.; Beavo, J. A.; Ferguson, K.; Gelinas,R.: Identification and
characterisation of a human calmodulin- stimulatedphosphodiesterase PDE1B1.
Cell. Signal. 9: 519- 529, 1997.

GAM8358 255 PDGFRB Abe, A.; Emi, N.; Tanimoto, M.; Terasaki, H.; Marunouchi, T.; Saito,H.: 3 C c
Fusion of the platelet- derived growth factor receptor beta toa novel gene
CEV14 in acute myelogenous leukemia after clonal evolution. Blood 90:4271-
4277, 1997.

GAM8358 255 PDGFRB Apperley, J. F.; Gardembas, M.; Melo, J. V.; Russell- Jones, R.;Bain, B. J.; 3 C c
Baxter, E. J.; Chase, A.; Chessells, J. M.; Colombat,M.; Dearden, C. E.;
Dimitrijevic, S.; Mahon, F.- X.; Marin, D.; Nikolova,Z.; Olavarria, E.;
Silberman, S.; Schultheis, B.; Cross, N. C. P.;Goldman, J. M.: Response to
imatinib mesylate in patients with chronicmyeloproliferative diseases with
rearrangements of the platelet- derivedgrowth factor receptor beta. New Eng.
J. Med. 347: 481- 487, 2002.

GAM8358 255 PDGFRB Buchberg, A. M.; Jenkins, N. A.; Copeland, N. G.: Localizationof the murine 3 C c
macrophage colony- stimulating factor gene to chromosome3 using
interspecific backcross analysis. Genomics 5: 363- 367, 1989.

GAM8358 255 PDGFRB Claesson- Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek,B.; 3 C c
Ostman, A.; Betsholtz, C.; Heldin, C.- H.: cDNA cloning and expressionof a
human platelet- derived growth factor (PDGF) receptor specificfor B- chain-
containing PDGF molecules. Molec. Cell. Biol. 8: 3476- 3486,1988.

GAM8358 255 PDGFRB Escobedo, J. A.; Fried, V. A.; Daniel, T. O.; Williams, L. T.:Primary 3 C c
structure of the platelet- derived growth factor. (Abstract) Clin.Res. 34:
544A, 1986.

GAM8358 255 PDGFRB Francke, U.; Yang- Feng, T. L.; Brissenden, J. E.; Ullrich, A.:Chromosomal 3 C c
mapping of genes involved in growth control. Cold SpringHarbor Symp. Quant.
Biol. 51: 855- 866, 1986.

GAM8358 255 PDGFRB Golub, T. R.; Barker, G. F.; Lovett, M.; Gilliland, D. G.: Fusionof PDGF 3 C c
receptor beta to a novel ets- like gene, tel, in chronic
myelomonocyticleukemia with t(5;12) chromosomal translocation. Cell 77: 307-
316,1994.

GAM8358 255 PDGFRB Gronwald, R. G. K.; Grant, F. J.; Haldeman, B. A.; Hart, C. E.;O'Hara, P. 3 C c
J.; Hagen, F. S.; Ross, R.; Bowen- Pope, D. F.; Murray,M. J.: Cloning and
expression of a cDNA coding for the human platelet- derivedgrowth factor
receptor: evidence for more than one receptor class. Proc.Nat. Acad. Sci.
85: 3435- 3439, 1988.

GAM8358 255 PDGFRB How, G.- F.; Venkatesh, B.; Brenner, S.: Conserved linkage betweenthe puffer 3 C c
fish (Fugu rubripes) and human genes for platelet- derivedgrowth factor
receptor and macrophage colony- stimulating factor receptor. GenomeRes. 6:
1185- 1191, 1996.

GAM8358 255 PDGFRB Klinghoffer, R. A.; Mueting- Nelsen, P. F.; Faerman, A.; Shani,M.; Soriano, 3 C c
P.: The two PDGF receptors maintain conserved signalingin vivo despite
divergent embryological functions. Molec. Cell 7:343- 354, 2001.

GAM8358 255 PDGFRB Kulkarni, S.; Heath, C.; Parker, S.; Chase, A.; Iqbal, S.; Pocock,C. F.; 3 C c
Kaeda, J.; Cwynarski, K.; Goldman, J. M.; Cross, N. C. P.:Fusion of
H4/D10S170 to the platelet- derived growth factor receptorbeta in BCR- ABL-
negative myeloproliferative disorders with a t(5;10)(q33;q21). CancerRes.
60: 3592- 3598, 2000.

GAM8358 255 PDGFRB Leal, F.; Williams, L. T.; Robbins, K. C.; Aaronson, S. A.: Evidencethat the 3 C c
v- sis gene product transforms by interaction with the receptorfor platelet-
derived growth factor. Science 230: 327- 330, 1985.

GAM8358 255 PDGFRB Magnusson, M. K.; Meade, K. E.; Brown, K. E., Arthur, D. C.; Krueger,L. A.; 3 C c
Barrett, A. J.; Dunbar, C. E.: Rabaptin- 5 is a novel fusionpartner to
platelet- derived growth factor beta receptor in chronicmyelomonocytic
leukemia. Blood 98: 2518- 2525, 2001.

GAM8358 255 PDGFRB Matsui, T.; Heidaran, M.; Miki, T.; Popescu, N.; La Rochelle,W.; Kraus, M.; 3 C c
Pierce, J.; Aaronson, S.: Isolation of a novel receptorcDNA establishes the

existence of two PDGF receptor genes. Science 243:800- 804, 1989.

GAM8358 255 PDGFRB Roberts, W. M.; Look, A. T.; Roussel, M. F.; Sherr, C. J.: Tandemlinkage of human CSF- 1 receptor (c- fms) and PDGF receptor genes. Cell 55:655- 661, 1988. 3 C c

GAM8358 255 PDGFRB Ross, T. S.; Bernard, O. A.; Berger, R.; Gilliland, D. G.: Fusionof Huntingtin interacting protein 1 to platelet- derived growth factor- betareceptor (PDGF- beta- R) in chronic myelomonocytic leukemia with t(5;7)(q33;q11.2). Blood 91:4419- 4426, 1998. 3 C c

GAM8358 255 PDGFRB Steer, E. J.; Cross, N. C. P.: Myeloproliferative disorders withtranslocations of chromosome 5q31- 35: role of the platelet- derivedgrowth factor receptor beta. Acta Haemat. 107: 113- 122, 2002. 3 C c

GAM8358 255 PDGFRB Treacher Collins Syndrome Collaborative Group: Positional cloningof a gene involved in the pathogenesis of Treacher Collins syndrome. NatureGenet. 12: 130- 136, 1996. 3 C c

GAM8358 255 PDGFRB Yarden, Y.; Escobedo, J. A.; Kuang, W.- J.; Yang- Feng, T. L.; Daniel,T. O.; Tremble, P. M.; Chen, E. Y.; Ando, M. E.; Harkins, R. N.; Francke,U.; Fried, V. A.; Ullrich, A.; Williams, L. T.: Structure of thereceptor for platelet- derived growth factor helps define a familyof closely related growth factor receptors. Nature 323: 226- 232,1986. 3 C c

GAM8358 255 PDGFRB Yarden, Y.; Ullrich, A.: Growth factor receptor tyrosine kinases. Ann.Rev. Biochem. 57: 443- 478, 1988. 3 C c

GAM8358 255 PLAGL1 Abdollahi, A.; Godwin, A. K.; Miller, P. D.; Getts, L. A.; Schultz,D. C.; Taguchi, T.; Testa, J. R.; Hamilton, T. C.: Identificationof a gene containing zinc- finger motifs based on lost expression inmalignantly transformed rat ovarian surface epithelial cells. CancerRes. 57: 2029- 2034, 1997. 3 C c

GAM8358 255 PLAGL1 Abdollahi, A.; Roberts, D.; Godwin, A. K.; Schultz, D. C.; Sonoda,G.; Testa, J. R.; Hamilton, T. C.: Identification of a zinc- fingergene at 6q25: a chromosomal region implicated in development of manysolid tumors. Oncogene 14: 1973- 1979, 1997. 3 C c

GAM8358 255 PLAGL1 Arima, T.; Drewell, R. A.; Arney, K. L.; Inoue, J.; Makita, Y.;Hata, A.; Oshimura, M.; Wake, N.; Surani, M. A.: A conserved imprintingcontrol region at the HYMAI/ZAC domain is implicated in transientneonatal diabetes mellitus. Hum. Molec. Genet. 10: 1475- 1483, 2001. 3 C c

GAM8358 255 PLAGL1 Kamiya, M.; Judson, H.; Okazaki, Y.; Kusakabe, M.; Muramatsu, M.;Takada, S.; Takagi, N.; Arima, T.; Wake, N.; Kamimura, K.; Satomura,K.; Hermann, R.; Bonthron, D. T.; Hayashizaki, Y.: The cell cyclecontrol gene ZAC/PLAGL1 is imprinted: a strong candidate gene fortransient neonatal diabetes. Hum. Molec. Genet. 9: 453- 460, 2000. 3 C c

GAM8358 255 PLAGL1 Mackay, D. J. G.; Coupe, A.- M.; Shield, J. P. H.; Storr, J. N.P.; Temple, I. K.; Robinson, D. O.: Relaxation of imprinted expressionof ZAC and HYMAI in a patient with transient neonatal diabetes mellitus. Hum.Genet. 110: 139- 144, 2002. 3 C c

GAM8358 255 PLAGL1 Spengler, D.; Villalba, M.; Hoffmann, A.; Pantaloni, C.; Houssami,S.; Bockaert, J.; Journot, L.: Regulation of apoptosis and cell cyclearrest by Zac1, a novel zinc finger protein expressed in the pituitarygland and the brain. EMBO J. 16: 2814- 2825, 1997. 3 C c

GAM8358 255 PLAGL1 Temple, I. K.; Gardner, R. J.; Robinson, D. O.; Kibirige, M. S.;Ferguson, A. W.; Baum, J. D.; Barber, J. C. K.; James, R. S.; Shield,J. P. H.: Further 3 C c

evidence for an imprinted gene for neonatal diabeteslocalised to chromosome 6q22- q23. Hum. Molec. Genet. 5: 1117- 1124,1996.

GAM8358 255 PLAGL1 Temple, I. K.; James, R. S.; Crolla, J. A.; Sitch, F. L.; Jacobs,P. A.; Howell, W. M.; Betts, P.; Baum, J. D.; Shield, J. P. H.: Animprinted gene(s) for diabetes? (Letter) Nature Genet. 9: 110- 112,1995. 3 C c

GAM8358 255 PLAGL1 Varrault, A.; Ciani, E.; Apiou, F.; Bilanges, B.; Hoffmann, A.;Pantaloni, C.; Bockaert, J.; Spengler, D.; Journot, L.: hZAC encodesa zinc finger protein with antiproliferative properties and maps toa chromosomal region frequently lost in cancer. Proc. Nat. Acad.Sci. 95: 8835- 8840, 1998. 3 C c

GAM8358 255 POLQ Gerlach, V. L.; Aravind, L.; Gotway, G.; Schultz, R. A.; Koonin,E. V.; Friedberg, E. C.: Human and mouse homologs of Escherichiacoli DinB (DNA polymerase IV), members of the UmuC/DinB superfamily. Proc.Nat. Acad. Sci. 96: 11922- 11927, 1999. 3 C c

GAM8358 255 POLQ Johnson, R. E.; Prakash, S.; Prakash, L.: The human DINB1 geneencodes the DNA polymerase Pol- theta. Proc. Nat. Acad. Sci. 97:3838- 3843, 2000. 3 C c

GAM8358 255 POLQ Ogi, T.; Kato, T., Jr.; Kato, T.; Ohmori, H.: Mutation enhancementby DINB1, a mammalian homologue of the Escherichia coli mutagenesisprotein dinB. Genes Cells 4: 607- 618, 1999. 3 C c

GAM8358 255 POLQ Ohashi, E.; Ogi, T.; Kusumoto, R.; Iwai, S.; Masutani, C.; Hanaoka,F.; Ohmori, H.: Error- prone bypass of certain DNA lesions by thehuman DNA polymerase kappa. Genes Dev. 14: 1589- 1594, 2000. 3 C c

GAM8358 255 PPP3R1 Graef, I. A.; Chen, F.; Chen, L.; Kuo, A.; Crabtree, G. R.: Signalstransduced by Ca(2+)/calcineurin and NFATc3/c4 pattern the developingvasculature. Cell 105: 863- 875, 2001. 3 C c

GAM8358 255 PPP3R1 Wang, M. G.; Yi, H.; Guerini, D.; Klee, C. B.; McBride, O. W.:Calcineurin A alpha (PPP3CA), calcineurin A beta (PPP3CB) and calcineurinB (PPP3R1) are located on human chromosomes 4, 10q21- q22 and 2p16- p15,respectively. Cytogenet. Cell Genet. 72: 236- 241, 1996. 3 C c

GAM8358 255 PPP3R1 Zeng, H.; Chattarji, S.; Barbarosie, M.; Rondi- Reig, L.; Philpot,B. D.; Miyakawa, T.; Bear, M. F.; Tonegawa, S.: Forebrain- specificcalcineurin knockout selectively impairs bidirectional synaptic plasticityand working/episodic- like memory. Cell 107: 617- 629, 2001. 3 C c

GAM8358 255 PTGIS Chevalier, D.; Cauffiez, C.; Bernard, C.; Lo- Guidice, J.- M.; Allorge,D.; Fazio, F.; Ferrari, N.; Libersa, C.; Lhermitte, M.; D'Halluin,J.- C.; Broly, F.: Characterization of new mutations in the codingsequence and 5- prime- untranslated region of the human prostacyclinsynthase gene (CYP8A1). Hum. Genet. 108: 148- 155, 2001. 3 C c

GAM8358 255 PTGIS Miyata, A.; Hara, S.; Yokoyama, C.; Inoue, H.; Ullrich, V.; Tanabe,T.: Molecular cloning and expression of human prostacyclin synthase. Biochem.Biophys. Res. Commun. 200: 1728- 1734, 1994. 3 C c

GAM8358 255 PTGIS Nelson, D. R.; Koymans, L.; Kamataki, T.; Stegeman, J. J.; Feyereisen,R.; Waxman, D. J.; Waterman, M. R.; Gotoh, O.; Coon, M. J.; Estabrook,R. W.; Gunsalus, I. C.; Nebert, D. W.: P450 superfamily: update onnew sequences, gene mapping, accession numbers and nomenclature. Pharmacogenetics 6:1- 42, 1996. 3 C c

GAM8358 255 PTGIS Wang, L.- H.; Chen, L.: Organization of the gene encoding humanprostacyclin synthase. Biochem. Biophys. Res. Commun. 226: 631- 637,1996. 3 C c

GAM8358 255 PTGIS Yokoyama, C.; Yabuki, T.; Inoue, H.; Tone, Y.; Hara, S.; Hatae,T.; Nagata, M.; Takahashi, E.- I.; Tanabe, T.: Human gene encodingprostacyclin synthase (PTGIS): genomic organization, chromosomal localization,and promoter 3 C c

activity. Genomics 36: 296- 304, 1996.

GAM8358 255 RAB36 Mori, T.; Fukuda, Y.; Kuroda, H.; Matsumura, T.; Ota, S.; Sugimoto,T.; 3 C c
Nakamura, Y.; Inazawa, J.: Cloning and characterization of anovel Rab-
family gene, Rab36, within the region at 22q11.2 that ishomozygously deleted
in malignant rhabdoid tumors. Biochem. Biophys.Res. Commun. 254: 594- 600,
1999.

GAM8358 255 RAB36 Zhou, J.- Y.; Fogelgren, B.; Wang, Z.; Roe, B. A.; Biegel, J. A.: Isolation 3 C c
of genes from the rhabdoid tumor deletion region in chromosomeband 22q11.2.
Gene 241: 133- 141, 2000.

GAM8358 255 RING1 Kikuti, Y. Y.; Tamiya, G.; Ando, A.; Chen, L.; Kimura, M.; Ferreira,E.; 3 C c
Tsuji, K.; Trowsdale, J.; Inoko, H.: Physical mapping 220 kbcentromeric of
the human MHC and DNA sequence analysis of the 43- kbsegment including the
RING1, HKE6, and HKE4 genes. Genomics 42:422- 435, 1997.

GAM8358 255 RING1 Lovering, R.; Hanson, I. M.; Borden, K. L. B.; Martin, S.; O'Reilly,N. J.; 3 C c
Evan, G. I.; Rahman, D.; Pappin, D. J. C.; Trowsdale, J.; Freemont,P. S.:
Identification and preliminary characterization of a proteinmotif related to
the zinc finger. Proc. Nat. Acad. Sci. 90: 2112- 2116,1993.

GAM8358 255 RING1 Satijn, D. P. E.; Gunster, M. J.; van der Vlag, J.; Hamer, K. M.;Schul, W.; 3 C c
Alkema, M. J.; Saurin, A. J.; Freemont, P. S.; van Driel,R.; Otte, A. P.:
RING1 is associated with the polycomb group proteincomplex and acts as a
transcriptional repressor. Molec. Cell. Biol. 17:4105- 4113, 1997.

GAM8358 255 RNASE1 Elliott, R. W.; Samuelson, L. C.; Lambert, M. S.; Meisler, M. H.: Assignment 3 C c
of pancreatic ribonuclease gene to mouse chromosome 14. Cytogenet.Cell
Genet. 42: 110- 112, 1986.

GAM8358 255 RNASE1 Piccoli, R.; Di Gaetano, S.; De Lorenzo, C.; Grauso, M.; Monaco,C.; 3 C c
Spalletti- Cernia, D.; Laccetti, P.; Cinatl, J.; Matousek, J.;D'Alessio, G.:
A dimeric mutant of human pancreatic ribonucleasewith selective cytotoxicity
toward malignant cells. Proc. Nat. Acad.Sci. 96: 7768- 7773, 1999.

GAM8358 255 RNASE1 Zhang, J.; Zhang, Y.; Rosenberg, H. F.: Adaptive evolution ofa duplicated 3 C c
pancreatic ribonuclease gene in a leaf- eating monkey. NatureGenet. 30: 416-
420, 2002.

GAM8358 255 SERPINB6 Coughlin, P.; Nicholl, J.; Sun, J.; Salem, H.; Bird, P.; Sutherland,G. R.: 3 C b
Chromosomal mapping of the human proteinase inhibitor 6 (PI6)gene to 6p25 by
fluorescence in situ hybridization. Genomics 26:431- 433, 1995.

GAM8358 255 SERPINB6 Coughlin, P.; Sun, J.; Cerruti, L.; Salem, H. H.; Bird, P.: Cloningand 3 C b
molecular characterization of a human intracellular serine
proteinaseinhibitor. Proc. Nat. Acad. Sci. 90: 9417- 9421, 1993.

GAM8358 255 SERPINB6 Evans, E.; Cooley, J.; Remold- O'Donnell, E.: Characterizationand 3 C b
chromosomal localization of ELANH2, the gene encoding human
monocyte/neutrophilelastase inhibitor. Genomics 28: 235- 240, 1995.

GAM8358 255 SERPINB6 Schneider, S. S.; Schick, C.; Fish, K. E.; Miller, E.; Pena, J.C.; Treter, 3 C b
S. D.; Hui, S. M.; Silverman, G. A.: A serine proteinaseinhibitor locus at
18q21.3 contains a tandem duplication of the humansquamous cell carcinoma
antigen gene. Proc. Nat. Acad. Sci. 92:3147- 3151, 1995.

GAM8358 255 SERPINB6 Sun, J.; Rose, J. B.; Bird, P.: Gene structure, chromosomal localization,and 3 C b
expression of the murine homologue of human proteinase inhibitor6 (PI- 6)
suggests divergence of PI- 6 from the ovalbumin serpins. J.Biol. Chem. 270:
16089- 16096, 1995.

GAM8358 255 SLC25A15 Camacho, J. A.; Obie, C.; Biery, B.; Goodman, B. K.; Hu, C.- A.;Almashanu, 3 C c
S.; Steel, G.; Casey, R.; Lambert, M.; Mitchell, G. A.;Valle, D.:

Hyperornithinaemia- hyperammonaemia- homocitrullinuria syndromeis caused by mutations in a gene encoding a mitochondrial ornithinetransporter. Nature Genet. 22: 151- 158, 1999.

GAM8358 255 SLC25A15 Miyamoto, T.; Kanazawa, N.; Kato, S.; Kawakami, M.; Inoue, Y.;Kuhara, T.; Inoue, T.; Takeshita, K.; Tsujino, S.: Diagnosis of Japanesepatients with HHH syndrome by molecular genetic analysis: a commonmutation, R179X. J. Hum. Genet. 46: 260- 262, 2001. 3 C c

GAM8358 255 SLC25A15 Nakajima, M.; Ishii, S.; Mito, T.; Takeshita, K.; Takashima, S.;Takakura, H.; Inoue, I.; Saheki, T.; Akiyoshi, H.; Ichihara, K.:Clinical, biochemical and ultrastructural study on the pathogenesisof hyperornithinemia-hyperammonemia- homocitrullinuria syndrome. BrainDev. 10: 181- 185, 1988. 3 C c

GAM8358 255 SLC25A15 Tsujino, S.; Kanazawa, N.; Ohashi, T.; Eto, Y.; Saito, T.; Kira,J.; Yamada, T.: Three novel mutations (G27E, insAAC, R179X) in theORNT1 gene of Japanese patients with hyperornithinemia, hyperammonemia,and homocitrullinuria syndrome. Ann. Neurol. 47: 625- 631, 2000. 3 C c

GAM8358 255 SMARCD2 Ring, H. Z.; Vameghi- Meyers, V.; Wang, W.; Crabtree, G. R.; Francke,U.: Five SWI/SNF- related, matrix- associated, actin- dependent regulatorof chromatin (SMARC) genes are dispersed in the human genome. Genomics 51:140-143, 1998. 3 C c

GAM8358 255 SMARCD2 Wang, W.; Xue, Y.; Zhou, S.; Kuo, A.; Cairns, B. R.; Crabtree,G. R.: Diversity and specialization of mammalian SWI/SNF complexes. GenesDev. 10: 2117- 2130, 1996. 3 C c

GAM8358 255 SP3 Andersson, M.; Page, D. C.; Pettay, D.; Subrt, I.; Turleau, C.;de Grouchy, J.; de la Chapelle, A.: Y;autosome translocations andmosaicism in the aetiology of 45,X maleness: assignment of fertilityfactor to distal Yq11. Hum. Genet. 79: 2- 7, 1988. 3 C c

GAM8358 255 SP3 Chandley, A. C.; Gosden, J. R.; Hargreave, T. B.; Spowart, G.;Speed, R. M.; McBeath, S.: Deleted Yq in the sterile son of a manwith a satellited Y chromosome (Yqs). J. Med. Genet. 26: 145- 153,1989. 3 C c

GAM8358 255 SP3 Foresta, C.; Bertella, A.; Moro, E.; Roverato, A.; Merico, M.;Ferlin, A.: Sertoli cell function in infertile patients with andwithout microdeletions of the azoospermia factors on the Y chromosomelong arm. J. Clin. Endocr. Metab. 86: 2414- 2419, 2001. 3 C c

GAM8358 255 SP3 Foresta, C.; Ferlin, A.; Moro, E.: Deletion and expression analysisof AZFa genes on the human Y chromosome revealed a major role forDBY in male infertility. Hum. Molec. Genet. 9: 1161- 1169, 2000. 3 C c

GAM8358 255 SP3 Hagen, G.; Muller, S.; Beato, M.; Suske, G.: Cloning by recognitionsite screening of two novel GT box binding proteins: a family of Sp1related genes. Nucleic Acids Res. 20: 5519- 5525, 1992. 3 C c

GAM8358 255 SP3 Hagen, G.; Muller, S.; Beato, M.; Suske, G.: Sp1- mediated transcriptionalactivation is repressed by Sp3. EMBO J. 13: 3843- 3851, 1994. 3 C c

GAM8358 255 SP3 Johnson, M. D.; Tho, S. P. T.; Behzadian, A.; McDonough, P. G.: Molecular scanning of Yq11 (interval 6) in men with Sertoli- cell- onlysyndrome. Am. J. Obstet. Gynec. 161: 1732- 1737, 1989. 3 C c

GAM8358 255 SP3 Kalff- Suske, M.; Kunz, J.; Grzeschik, K.- H.; Suske, G.: HumanSp3 transcriptional regulator gene (SP3) maps to chromosome 2q31. Genomics 37:410- 412, 1996. 3 C c

GAM8358 255 SP3 Kamp, C.; Hirschmann, P.; Voss, H.; Huellen, K.; Vogt, P. H.:Two long homologous retroviral sequence blocks in proximal Yq11 causeAZFa microdeletions as a result of intrachromosomal recombinationevents. Hum. 3 C c

Molec. Genet. 9: 2563- 2572, 2000.

GAM8358 255 SP3 Kingsley, C.; Winoto, A.: Cloning of GT box- binding proteins:a novel Sp1 multigene family regulating T- cell receptor gene expression. Molec.Cell. Biol. 12: 4251- 44261, 1992. 3 C c

GAM8358 255 SP3 Kobayashi, K.; Mizuno, K.; Hida, A.; Komaki, R.; Tomita, K.; Matsushita,I.; Namiki, M.; Iwamoto, T.; Tamura, S.; Minowada, S.; Nakahori, Y.;Nakagome, Y.: PCR analysis of the Y chromosome long arm in azoospermicpatients: evidence for a second locus required for spermatogenesis. Hum.Molec. Genet. 3: 1965- 1967, 1994. 3 C c

GAM8358 255 SP3 Krausz, C.; Meyts, E. R.- D.; Frydelund- Larson, L.; Quintana- Murci,L.; McElreavey, K.; Skakkebaek, N. E.: Double- blind Y chromosomemicrodeletion analysis in men with known sperm parameters and reproductivehormone profiles: microdeletions are specific for spermatogenic failure. J.Clin. Endocr. Metab. 86: 2638- 2642, 2001. 3 C c

GAM8358 255 SP3 Krausz, C.; Quintana- Murci, L.; Barbaux, S.; Siffroi, J.- P.; Rouba,H.; Delafontaine, D.; Souleyreau- Therville, N.; Arvis, G.; Antoine,J. M.; Erdei, E.; Taar, J. P.; Tar, A.; Jeandidier, E.; Plessis, G.;Bourgeron, T.; Dadoune, J.- P.; Fellous, M.; McElreavey, K.: A highfrequency of Y chromosome deletions in males with nonidiopathic infertility. J.Clin. Endocr. Metab. 84: 3606- 3612, 1999. 3 C c

GAM8358 255 SP3 Ma, K.; Inglis, J. D.; Sharkey, A.; Bickmore, W. A.; Hill, R.E.; Prosser, E. J.; Speed, R. M.; Thomson, E. J.; Jobling, M.; Taylor,K.; Wolfe, J.; Cooke, H. J.; Hargreave, T. B.; Chandley, A. C.: AY chromosome gene family with RNA- binding protein homology: candidatesfor the azoospermia factor AZF controlling human spermatogenesis. Cell 75:1287- 1295, 1993. 3 C c

GAM8358 255 SP3 Ma, K.; Sharkey, A.; Kirsch, S.; Vogt, P.; Keil, R.; Hargreave,T. B.; McBeath, S.; Chandley, A. C.: Towards the molecular localisationof the AZF locus: mapping of microdeletions in azoospermic men within14 subintervals of interval 6 of the human Y chromosome. Hum. Molec.Genet. 1: 29- 33, 1992. 3 C c

GAM8358 255 SP3 Madgar, I.; Green, L.; Kent- First, M.; Weissenberg, R.; Gershoni-Baruch,R.; Goldman, B.; Friedman, E.: Genotyping of Israeli infertile menwith idiopathic oligozoospermia. Clin. Genet. 62: 203- 207, 2002. 3 C c

GAM8358 255 SP3 Sargent, C. A..; Boucher, C. A.; Kirsch, S.; Brown, G.; Weiss,B.; Trundley, A.; Burgoyne, P.; Saut, N.; Durand, C.; Levy, N.; Terriou,P.; Hargreave, T.; Cooke, H.; Mitchell, M.; Rappold, G. A.; Affara,N. A.: The critical region of overlap defining the AZFa male infertilityinterval of proximal Yq contains three transcribed sequences. J.Med. Genet. 36: 670- 677, 1999. 3 C c

GAM8358 255 SP3 Simpson, E.; Chandler, P.; Goulmy, E.; Ma, K.; Hargreave, T. B.;Chandley, A. C.: Loss of the 'azoospermia factor' (AZF) on Yq inman is not associated with loss of HYA. Hum. Molec. Genet. 2: 469- 471,1993. 3 C c

GAM8358 255 SP3 Sun, C.; Skaletsky, H.; Rozen, S.; Gromoll, J.; Nieschlag, E.;Oates, R.; Page, D. C.: Deletion of azoospermia factor a (AZFa) regionof human Y chromosome caused by recombination between HERV15 proviruses. Hum.Molec. Genet. 9: 2291- 2296, 2000. 3 C c

GAM8358 255 SP3 Tiepolo, L.; Zuffardi, O.: Localization of factors controllingspermatogenesis in the nonfluorescent portion of the human Y chromosomelong arm. Hum. Genet. 34: 119- 124, 1976. 3 C c

GAM8358 255 SP3 Vergnaud, G.; Page, D. C.; Simmler, M. C.; Brown, L.; Rouyer,F.; Noel, B.; Botstein, D.; de la Chapelle, A.; Weissenbach, J.:A deletion map of the human Y chromosome based on DNA hybridization. Am.J. Hum. Genet. 38: 109- 3 C c

124, 1986.

GAM8358 255 SP3 Vogt, P. H.; Edelmann, A.; Kirsch, S.; Henegariu, O.; Hirschmann,P.; 3 C c
Kiesewetter, F.; Kohn, F. M.; Schill, W. B.; Farah, S.; Ramos,C.; Hartmann,
M.; Hartschuh, W.; Meschede, D.; Behre, H. M.; Castel,A.; Nieschlag, E.;
Weidner, W.; Grone, H.- J.; Jung, A.; Engel, W.;Haidl, G.: Human Y
chromosome azoospermia factors (AZF) mapped todifferent subregions in Yq11.
Hum. Molec. Genet. 5: 933- 943, 1996.

GAM8358 255 SP3 Vogt, P.; Chandley, A. C.; Hargreave, T. B.; Keil, R.; Ma, K.;Sharkey, A.: 3 C c
Microdeletions in interval 6 of the Y chromosome ofmales with idiopathic
sterility point to disruption of AZF, a humanspermatogenesis gene. Hum.
Genet. 89: 491- 496, 1992.

GAM8358 255 SPN Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba,A. G.; Cannon, 3 C c
J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J.K.; Sperling, A. I.: ERM-
dependent movement of CD43 defines a novelprotein complex distal to the
immunological synapse. Immunity 15:739- 750, 2001.

GAM8358 255 SPN Baecher, C. M.; Dorfman, K. S.; Mattei, M.- G.; Frelinger, J. G.: cDNA 3 C c
cloning and localization of the mouse leukosialin gene (Ly48)to chromosome
7. Immunogenetics 31: 307- 314, 1990.

GAM8358 255 SPN Bazil, V.; Strominger, J. L.: CD43, the major sialoglycoproteinof human 3 C c
leukocytes, is proteolytically cleaved from the surface ofstimulated
lymphocytes and granulocytes. Proc. Nat. Acad. Sci. 90:3792- 3796, 1993.

GAM8358 255 SPN Delon, J.; Kaibuchi, K.; Germain, R. N.: Exclusion of CD43 fromthe 3 C c
immunological synapse is mediated by phosphorylation- regulatedrelocation of
the cytoskeletal adaptor moesin. Immunity 15: 691- 701,2001.

GAM8358 255 SPN Pallant, A.; Eskenazi, A.; Mattei, M.- G.; Fournier, R. E. K.; Carlsson,S. 3 C c
R.; Fukuda, M.; Frelinger, J. G.: Characterization of cDNAs encodinghuman
leukosialin and localization of the leukosialin gene to chromosome16. Proc.
Nat. Acad. Sci. 86: 1328- 1332, 1989.

GAM8358 255 SPN Park, J. K.; Rosenstein, Y. J.; Remold- O'Donnell, E.; Bierer, B.E.; Rosen, 3 C c
F. S.; Burakoff, S. J.: Enhancement of T- cell activationby the CD43
molecule whose expression is defective in Wiskott- Aldrichsyndrome. Nature
350: 706- 709, 1991.

GAM8358 255 SPN Rosenstein, Y.; Park, J. K.; Hahn, W. C.; Rosen, F. S.; Bierer,B. E.; 3 C c
Burakoff, S. J.: CD43, a molecule defective in Wiskott- Aldrichsyndrome,
binds ICAM- 1. Nature 354: 233- 235, 1991.

GAM8358 255 SPN Schmid, K.; Hediger, M. A.; Brossmer, R.; Collins, J. H.; Haupt,H.; Marti, 3 C c
T.; Offner, G. D.; Schaller, J.; Takagaki, K.; Walsh, M.T.; Schwick, H. G.;
Rosen, F. S.; Remold- O'Donnell, E.: Amino acidsequence of human plasma
galactoglycoprotein: identity with the extracellularregion of CD43
(sialophorin). Proc. Nat. Acad. Sci. 89: 663- 667,1992.

GAM8358 255 SPN Shelley, C. S.; Carroll, M. C.; Davis, A. E., III; Bruns, G. A.P.; 3 C c
Whitehead, A. S.; Finberg, R.; Remold- O'Donnell, E.; Rosen, F.S.: Human
sialophorin: cDNA cloning and gene location. (Abstract) FASEBJ. 2: A1659
only, 1988.

GAM8358 255 SPN Shelley, C. S.; Remold- O'Donnell, E.; Davis, A. E., III; Bruns,G. A. P.; 3 C c
Rosen, F. S.; Carroll, M. C.; Whitehead, A. S.: Molecularcharacterization of
sialophorin (CD43), the lymphocyte surface sialoglycoproteindefective in
Wiskott- Aldrich syndrome. Proc. Nat. Acad. Sci. 86:2819- 2823, 1989.

GAM8358 255 SPN Shelley, C. S.; Remold- O'Donnell, E.; Rosen, F. S.; Whitehead,A. S.: 3 C c
Structure of the human sialophorin (CD43) gene: identificationof features

atypical of genes encoding integral membrane proteins. Biochem.J. 270: 569-576, 1990.

GAM8358 255 SPN van den Berg, T. K.; Nath, D.; Ziltener, H. J.; Vestweber, D.;Fukuda, M.; van Die, I.; Crocker, P. R.: Cutting edge: CD43 functionsas a T cell counterreceptor for the macrophage adhesion receptor sialoadhesin(Siglec-1). J. Immun. 166: 3637- 3640, 2001. 3 C c

GAM8358 255 SPTBN4 Berghs, S.; Aggujaro, D.; Dirkx, R., Jr.; Maksimova, E.; Stabach,P.; Hermel, J.- M.; Zhang, J.- P.; Philbrick, W.; Slepnev, V.; Ort,T.; Slimena, M.: Beta- IV spectrin, a new spectrin localized at axoninitial segments and nodes of Ranvier in the central and peripheralnervous system. J. Cell Biol. 151: 985- 1001, 2000. 3 C c

GAM8358 255 SPTBN4 Bock, G. R.; Frank, M. P.; Steel, K. P.; Deol, M. S.: The quiveringmutant mouse: hereditary deafness of central origin. Acta Otolaryng. 96:371- 377, 1983. 3 C c

GAM8358 255 SPTBN4 Deol, M. S.; Frank, M. P.; Steel, K. P.; Bock, G. R.: Geneticdeafness of central origin. Brain Res. 258: 177- 179, 1983. 3 C c

GAM8358 255 SPTBN4 Nagase, T.; Kikuno, R.; Nakayama, M.; Hirosawa, M.; Ohara, O.:Prediction of the coding sequences of unidentified human genes. XVIII.The complete sequences of 100 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 273- 281, 2000. 3 C c

GAM8358 255 SPTBN4 Parkinson, N. J.; Olsson, C. L.; Hallows, J. L.; McKee- Johnson,J.; Keogh, B. P.; Noben- Trauth, K.; Kujawa, S. G.; Tempel, B. L.:Mutant beta- spectrin 4 causes auditory and motor neuropathies in quiveringmice. Nature Genet. 29: 61- 65, 2001. 3 C c

GAM8358 255 SPTBN4 Tse, W. T.; Tang, J.; Jin, O.; Korsgren, C.; John, K. M.; Kung,A. L.; Gwynn, B.; Peters, L. L.; Lux, S. E.: A new spectrin, beta- IV,has a major truncated isoform that associates with promyelocytic leukemiaprotein nuclear bodies and the nuclear matrix. J. Biol. Chem. 276:23974- 23985, 2001. 3 C c

GAM8358 255 SPTBN4 Yoon, C. H.; Les, E. P.: Quivering, a new first chromosome mutationin mice. J. Hered. 48: 176- 180, 1957. 3 C c

GAM8358 255 SYN3 Hosaka, M.; Sudhof, T. C.: Synapsin III, a novel synapsin withan unusual regulation by Ca(2)+. J. Biol. Chem. 273: 13371- 13374,1998. 3 C c

GAM8358 255 SYN3 Kao, H.- T.; Porton, B.; Czernik, A. J.; Feng, J.; Yiu, G.; Haring,M.; Benfenati, F.; Greengard, P.: A third member of the synapsingene family. Proc. Nat. Acad. Sci. 95: 4667- 4672, 1998. 3 C c

GAM8358 255 SYN3 Schizophrenia Collaborative Linkage Group (Chromosome 22): Acombined analysis of D22S278 marker alleles in affected sib- pairs:support for a susceptibility locus for schizophrenia at chromosome22q12. Am. J. Med. Genet. 67: 40- 45, 1996. 3 C c

GAM8358 255 SYN3 Tsai, M.- T.; Hung, C.- C.; Tsai, C.- Y.; Liu, M.- Y.; Su, Y.- C.; Chen,Y.- H.; Hsaio, K.- J.; Chen, C.- H.: Mutation analysis of synapsin IIIgene in schizophrenia. Am. J. Med. Genet. (Neuropsychiat. Genet.) 114:79- 83, 2002. 3 C c

GAM8358 255 TARBP2 Gatignol, A.; Buckler- White, A.; Berkhout, B.; Jeang, K. T.: Characterizationof a human TAR RNA- binding protein that activates the HIV-1 LTR. Science 251:1597- 1600, 1991. 3 C c

GAM8358 255 TARBP2 Gatignol, A.; Duarte, M.; Daviet, L.; Chang, Y.- N.; Jeang, K.- T.: Sequential steps in Tat trans- activation of HIV- 1 mediated throughcellular DNA, RNA, and protein binding factors. Gene Expr. 5: 217- 228,1996. 3 C c

GAM8358 255 TARBP2 Kozak, C. A.; Gatignol, A.; Graham, K.; Jeang, K. T.; McBride,O. W.: Genetic mapping in human and mouse of the locus encoding TRBP,a protein that binds 3 C c

the TAR region of the human immunodeficiencyvirus (HIV- 1). Genomics 25: 66-72, 1995.

GAM8358 255 TBL2 Meng, X.; Lu, X.; Li, Z.; Green, E. D.; Massa, H.; Trask, B. J.;Morris, C. A.; Keating, M. T.: Complete physical map of the commondeletion region in Williams syndrome and identification and characterizationof three novel genes. Hum. Genet. 103: 590- 599, 1998. 3 C b

GAM8358 255 TBL2 Perez Jurado, L. A.; Wang, Y.- K.; Francke, U.; Cruces, J.: TBL2,a novel transducin family member in the WBS deletion: characterizationof the complete sequence, genomic structure, transcriptional variantsand the mouse ortholog. Cytogenet. Cell Genet. 86: 277- 284, 1999. 3 C b

GAM8358 255 TITF1 Acebron, A.; Aza- Blanc, P.; Rossi, D. L.; Lamas, L.; Santisteban,P.: Congenital human thyroglobulin defect due to low expression ofthe thyroid-specific transcription factor TTF- 1. J. Clin. Invest. 96:781- 785, 1995. 3 C c

GAM8358 255 TITF1 Guazzi, S.; Price, M.; De Felice, M.; Damante, G.; Mattei, M.- G.;Di Lauro, R.: Thyroid nuclear factor 1 (TTF- 1) contains a homeodomainand displays a novel DNA binding specificity. EMBO J. 9: 3631- 3639,1990. 3 C c

GAM8358 255 TITF1 Ikeda, K.; Clark, J. C.; Shaw- White, J. R.; Stahlman, M. T.; Boutell,C. J.; Whitsett, J. A.: Gene structure and expression of human thyroidtranscription factor- 1 in respiratory epithelial cells. J. Biol.Chem. 270: 8108- 8114, 1995. 3 C c

GAM8358 255 TITF1 Kimura, S.; Hara, Y.; Pineau, T.; Fernandez- Salguero, P.; Fox,C. H.; Ward, J. M.; Gonzalez, F. J.: The T/ebp null mouse: thyroid- specificenhancer-binding protein is essential for the organogenesis of thethyroid, lung, ventral forebrain, and pituitary. Genes Dev. 10:60- 69, 1996. 3 C c

GAM8358 255 TK2 Johansson, M.; Karlsson, A.: Cloning of the cDNA and chromosomelocalization of the gene for human thymidine kinase 2. J. Biol. Chem. 272:8454- 8458, 1997. 3 C c

GAM8358 255 TK2 Mandel, H.; Szargel, R.; Labay, V.; Elpeleg, O.; Saada, A.; Shalata,A.; Anbinder, Y.; Berkowitz, D.; Hartman, C.; Barak, M.; Eriksson,S.; Cohen, N.: The deoxyguanosine kinase gene is mutated in individualswith depleted hepatocerebral mitochondrial DNA. Nature Genet. 29:337- 341, 2001. Note: Erratum: Nature Genet. 29: 491 only, 2001. 3 C c

GAM8358 255 TK2 Saada, A.; Shaag, A.; Mandel, H.; Nevo, Y.; Eriksson, S.; Elpeleg,O.: Mutant mitochondrial thymidine kinase in mitochondrial DNA depletionmyopathy. Nature Genet. 29: 342- 344, 2001. 3 C c

GAM8358 255 TK2 Wang, L.; Munch- Petersen, B.; Herrstrom Sjoberg, A.; Hellman, U.;Bergman, T.; Jornvall, H.; Eriksson, S.: Human thymidine kinase 2:molecular cloning and characterisation of the enzyme activity withantiviral and cytostatic nucleoside substrates. FEBS Lett. 443:170- 174, 1999. 3 C c

GAM8358 255 TK2 Willecke, K.; Reuber, T.; Kucherlapati, R. S.; Ruddle, F. H.:Human mitochondrial thymidine kinase is coded for by a gene on chromosome16 of the nucleus. Somat. Cell Genet. 3: 237- 245, 1977. 3 C c

GAM8358 255 TRAF5 Aizawa, S.; Nakano, H.; Ishida, T.; Horie, R.; Nagai, M.; Ito,K.; Yagita, H.; Okumura, K.; Inoue, J.; Watanabe, T.: Tumor necrosisfactor receptor-associated factor (TRAF) 5 and TRAF2 are involvedin CD30- mediated NF-kappa- B activation. J. Biol. Chem. 272: 2042- 2045,1997. 3 C c

GAM8358 255 TRAF5 Nakano, H.; Oshima, H.; Chung, W.; Williams- Abbott, L.; Ware, C.F.; Yagita, H.; Okumura, K.: TRAF5, an activator of NF- kappaB andputative signal transducer for the lymphotoxin- beta receptor. J.Biol. Chem. 271: 14661-14664, 1996. 3 C c

GAM8358 255 TRAF5 Nakano, H.; Sakon, S.; Koseki, H.; Takemori, T.; Tada, K.; Matsumoto,M.; 3 C c
Munechika, E.; Sakai, T.; Shirasawa, T.; Akiba, H; Kobata, T.;Santee, S. M.;
Ware, C. F.; Renner, P. D.; Taniguchi, M.; Yagita,H.; Okumura, K.: Targeted
disruption of Traf5 gene causes defectsin CD40- and CD27- mediated
lymphocyte activation. Proc. Nat. Acad.Sci. 96: 9803- 9808, 1999.

GAM8358 255 TRAF5 Nakano, H.; Shindo, M.; Yamada, K.; Yoshida, M. C.; Santee, S.M.; Ware, C. 3 C c
F.; Jenkins, N. A.; Gilbert, D. J.; Yagita, H.; Copeland,N. G.; Okumura, K.:
Human TNF receptor- associated factor 5 (TRAF5):cDNA cloning, expression and
assignment of the TRAF5 gene to chromosome1q32. Genomics 42: 26- 32, 1997.

GAM8358 255 VANGL2 Doudney, K.; Murdoch, J. N.; Paternotte, C.; Bentley, L.; Gregory,S.; Copp, 3 C c
A. J.; Stanier, P.: Comparative physical and transcriptmaps of approximately
1 Mb around loop- tail, a gene for severe neuraltube defects on distal mouse
chromosome 1 and human chromosome 1q22- q23. Genomics 72:180- 192, 2001.

GAM8358 255 VANGL2 Kibar, Z.; Vogan, K. J.; Groulx, N.; Justice, M. J.; Underhill,D. A.; Gros, 3 C c
P.: Ltap, a mammalian homolog of Drosophila Strabismus/VanGogh, is altered
in the mouse neural tube mutant loop- tail. NatureGenet. 28: 251- 255, 2001.

GAM8358 255 VANGL2 Mullick, A.; Trasler, D.; Gros, P.: High- resolution linkage mapin the 3 C c
vicinity of the Lp locus. Genomics 26: 479- 488, 1995.

GAM8358 255 VANGL2 Murdoch, J. N.; Doudney, K.; Paternotte, C.; Copp, A. J.; Stanier,P.: Severe 3 C c
neural tube defects in the loop- tail mouse result frommutation of Lpp1, a
novel gene involved in floor plate specification. Hum.Molec. Genet. 10:
2593- 2601, 2001.

GAM8358 255 VANGL2 Stanier, P.; Henson, J. N.; Eddleston, J.; Moore, G. E.; Copp,A. J.: Genetic 3 C c
basis of neural tube defects: the mouse gene loop- tailmaps to a region of
chromosome 1 syntenic with human 1q21- q23. Genomics 26:473- 478, 1995.

GAM8358 255 VAT1 Friedman, L. S.; Ostermeyer, E. A.; Lynch, E. D.; Welcsh, P.; Szabo,C. I.; 3 C b
Meza, J. E.; Anderson, L. A.; Dowd, P.; Lee, M. K.; Rowell,S. E.; Ellison,
J.; Boyd, J.; King, M.- C.: 22 genes from chromosome17q21: cloning,
sequencing, and characterization of mutations in breastcancer families and
tumors. Genomics 25: 256- 163, 1995.

GAM8358 255 VAT1 Linial, M.; Miller, K.; Scheller, R. H.: VAT- 1: an abundant membraneprotein 3 C b
from Torpedo cholinergic synaptic vesicles. Neuron 2: 1265- 1273,1989.

GAM8358 255 VAT1 Peter, D.; Finn, J. P.; Klisak, I.; Liu, Y.; Kojis, T.; Heinzmann,C.; 3 C b
Roghani, A.; Sparkes, R. S.; Edwards, R. H.: Chromosomal localizationof the
human vesicular amine transporter genes. Genomics 18: 720- 723,1993.

GAM8358 255 VAT1 Roghani, A.; Welch, C.; Xia, Y.- R.; Liu, Y.; Peter, D.; Finn, J.P.; 3 C b
Edwards, R. H.; Lusis, A. J.: Assignment of the mouse vesicularmonoamine
transporter genes, Slc18a1 and Slc18a2, to chromosomes 8and 19 by linkage
analysis. Mammalian Genome 7: 393- 394, 1996.

GAM8358 255 VAT1 Smith, T. M.; Lee, M. K.; Szabo, C. I.; Jerome, N.; McEuen, M.;Taylor, M.; 3 C b
Hood, L.; King, M.- C.: Complete genomic sequence andanalysis of 117 kb of
human DNA containing the gene BRCA1. GenomeRes. 6: 1029- 1049, 1996.

GAM8358 255 WHN Balciunaite, G.; Keller, M. P.; Balciunaite, E.; Piali, L.; Zuklys,S.; 3 C c
Mathieu, Y. D.; Gill, J.; Boyd, R.; Sussman, D. J.; Hollander,G. A.: Wnt
glycoproteins regulate the expression of FoxN1, the genedefective in nude
mice. Nature Immun. 15Oct, 2002. Note: AdvanceElectronic Publication.

GAM8358 255 WHN Frank, J.; Pignata, C.; Panteleyev, A. A.; Prowse, D. M.; Baden,H.; Weiner, 3 C c
L.; Gaetaniello, L.; Ahmad, W.; Pozzi, N.; Caerhalmi- Friedman,P. B.; Aita,
V. M.; Uyttendaele, H.; Gordon, D.; Ott, J.; Brissette,J. L.; Christiano, A.
M.: Exposing the human nude phenotype. Nature 398:473- 474, 1999.

GAM8358 255 WHN Nehls, M.; Pfeifer, D.; Schorpp, M.; Hedrich, H.; Boehm, T.: Newmember of the winged- helix protein family disrupted in mouse and ratnude mutations. Nature 372: 103- 107, 1994. 3 C c

GAM8358 255 WHN Pignata, C.; Fiore, M.; Guzzetta, V.; Castaldo, A.; Sebastio, G.;Porta, F.; Guarino, A.: Congenital alopecia and nail dystrophy associatedwith severe functional T- cell immunodeficiency in two sibs. Am. J.Med. Genet. 65: 167- 170, 1996. 3 C c

GAM8358 255 WHN Schorpp, M.; Hofmann, M.; Dear, T. N.; Boehm, T.: Characterizationof mouse and human nude genes. Immunogenetics 46: 509- 515, 1997. 3 C c

GAM8358 255 WHN Segre, J. A.; Nemhauser, J. L.; Taylor, B. A.; Nadeau, J. H.; Lander,E. S.: Positional cloning of the nude locus: genetic, physical, andtranscription maps of the region and mutations in the mouse and rat. Genomics 28:549- 559, 1995. 3 C c

GAM8358 255 WHSC1L1 Angrand, P.- O.; Apiou, F.; Stewart, A. F.; Dutrillaux, B.; Losson,R.; Chambon, P.: NSD3, a new SET domain- containing gene, maps to8p12 and is amplified in human breast cancer cell lines. Genomics 74:79- 88, 2001. 3 C c

GAM8358 255 WHSC1L1 Rosati, R.; La Starza, R.; Veronese, A.; Aventin, A.; Schwienbacher,C.; Vallespi, T.; Negrini, M.; Martelli, M. F.; Mecucci, C.: NUP98is fused to the NSD3 gene in acute myeloid leukemia associated witht(8;11)(p11.2;p15). Blood 99: 3857- 3860, 2002. 3 C c

GAM8358 255 WHSC1L1 Stec, I.; van Ommen, G.- J. B.; den Dunnen, J. T.: WHSC1L1, onhuman chromosome 8p11.2, closely resembles WHSC1 and maps to a duplicatedregion shared with 4p16.3. Genomics 76: 5- 8, 2001. 3 C c

GAM8358 255 YWHAB Han, L. Wong, D.; Dhaka, A.; Afar, D.; White, M.; Xie, W.; Herschman,H.; Witte, O.: Colicelli, J.: Protein binding and signaling propertiesof RIN1 suggest a unique effector function. Proc. Nat. Acad. Sci. 94:4954- 4959, 1997. 3 C b

GAM8358 255 YWHAB Leffers, H.; Madsen, P.; Rasmussen, H. H.; Honore, B.; Andersen,A. H.; Walbum, E.; Vandekerckhove, J.; Celis, J. E.: Molecular cloningand expression of the transformation sensitive epithelial marker stratifin:a member of a protein family that has been involved in the proteinkinase C signalling pathway. J. Molec. Biol. 231: 982- 998, 1993. 3 C b

GAM8358 255 YWHAB Tommerup, N.; Leffers, H.: Assignment of the human genes encoding14- 3- 3 eta (YWHAH) to 22q12, 14- 3- 3 zeta (YWHAZ) to 2p25.1- p25.2,and 14- 3- 3 beta (YWHAB) to 20q13.1 by in situ hybridization. Genomics 33:149- 150, 1996. 3 C b

GAM8358 255 YWHAB Yaffe, M. B.; Rittinger, K.; Volinia, S.; Caron, P. R.; Aitken,A.; Leffers, H.; Gamblin, S. J.; Smerdon, S. J.; Cantley, L. C.:The structural basis for 14- 3- 3:phosphopeptide binding specificity. Cell 91:961- 971, 1997. 3 C b

GAM8554 388 AP1G1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 3 B c

GAM8554 388 AP1G1 Peyrard, M.; Parveneh, S.; Lagercrantz, S.; Ekman, M.; Fransson,I.; Sahlen, S.; Dumanski, J. P.: Cloning, expression pattern, andchromosomal assignment to 16q23 of the human gamma- adaptin gene (ADTG). Genomics 50:275- 280, 1998. 3 B c

GAM8554 388 AP1M1 Doray, B.; Ghosh, P.; Griffith, J.; Geuze, H. J.; Kornfeld, S.: Cooperation of GGAs and AP- 1 in packaging MPRs at the trans- Golginetwork. Science 297: 1700- 1703, 2002. 3 B c

GAM8554 388 AP1M1 Nakayama, Y.; Goebl, M.; O'Brine Greco, B.; Lemmon, S.; PingchangChow, E.; 3 B c
Kirchhausen, T.: The medium chains of the mammalian clathrin-associatedproteins have a homolog in yeast. Europ. J. Biochem. 202: 569-574,1991.

GAM8554 388 AP1M1 Peyrard, M.: Personal Communication. Stockholm, Sweden 1/7/1999. 3 B c

GAM8554 388 AP1M1 Peyrard, M.; Parveneh, S.; Lagercrantz, S.; Ekman, M.; Fransson,I.; Sahlen, S.; Dumanski, J. P.: Cloning, expression pattern, andchromosomal assignment to 16q23 of the human gamma- adaptin gene (ADTG). Genomics 50:275- 280, 1998. 3 B c

GAM8554 388 BACH2 Muto, A.; Hoshino, H.; Madisen, L.; Yanai, N.; Obinata, M.; Karasuyama,H.; Hayashi, N.; Nakauchi, H.; Yamamoto, M.; Groudine, M.; Igarashi,K.: Identification of Bach2 as a B- cell- specific partner for smallMaf proteins that negatively regulate the immunoglobulin heavy chaingene 3- prime enhancer. EMBO J. 17: 5734- 5743, 1998. 3 B c

GAM8554 388 BACH2 Oyake, T.; Itoh, K.; Motohashi, H.; Hayashi, N.; Hoshino, H.; Nishizawa,M.; Yamamoto, M.; Igarashi, K.: Bach proteins belong to a novel familyof BTB-basic leucine zipper transcription factors that interact withMafK and regulate transcription through the NF- E2 site. Molec. Cell.Biol. 16: 6083-6095, 1996. 3 B c

GAM8554 388 BACH2 Sasaki, S.; Ito, E.; Toki, T.; Maekawa, T.; Kanezaki, R.; Umenai,T.; Muto, A.; Nagai, H.; Kinoshita, T.; Yamamoto, M.; Inazawa, J.;Taketo, M. M.; Nakahata, T.; Igarashi, K.; Yokoyama, M.: Cloningand expression of human B cell- specific transcription factor BACH2mapped to chromosome 6q15. Oncogene 19: 3739- 3749, 2000. 3 B c

GAM8554 388 CA6 Aldred, P.; Fu, P.; Barrett, G.; Penschow, J. D.; Wright, R. D.;Coghlan, J. P.; Fernley, R. T.: Human secreted carbonic anhydrase:cDNA cloning, nucleotide sequence, and hybridization histochemistry. Biochemistry 30:569-575, 1991. 3 B c

GAM8554 388 CA6 Karhumaa, P.; Leinonen, J.; Parkkila, S.; Kaunisto, K.; Tapanainen,J.; Rajaniemi, H.: The identification of secreted carbonic anhydraseVI as a constitutive glycoprotein of human and rat milk. Proc. Nat.Acad. Sci. 98: 11604- 11608, 2001. 3 B c

GAM8554 388 CA6 Murakami, H.; Sly, W. S.: Purification and characterization ofhuman salivary carbonic anhydrase. J. Biol. Chem. 262: 1382- 1388,1987. 3 B c

GAM8554 388 CA6 Sutherland, G. R.; Baker, E.; Fernandez, K. E. W.; Callen, D. F.;Aldred, P.; Coghlan, J. P.; Wright, R. D.; Fernley, R. T.: The genefor human carbonic anhydrase VI (CA6) is on the tip of the short armof chromosome 1. Cytogenet. Cell Genet. 50: 149- 150, 1989. 3 B c

GAM8554 388 CA6 Thatcher, B. J.; Doherty, A. E.; Orvisky, E.; Martin, B. M.; Henkin,R. I.: Gustin from human parotid saliva is carbonic anhydrase VI. Biochem.Biophys. Res. Commun. 250: 635- 641, 1998. 3 B c

GAM8554 388 CA6 White, P. S.; Jensen, S. J.; Rajalingam, V.; Stairs, D.; Sulman,E. P.; Maris, J. M.; Biegel, J. A.; Wooster, R.; Brodeur, G. M.:Physical mapping of the CA6, ENO1, and SLC2A5 (GLUT5) genes and reassignmentof SLC2A5 to 1p36.2. Cytogenet. Cell Genet. 81: 60- 64, 1998. 3 B c

GAM8554 388 CACNA2D2 Brodbeck, J.; Davies, A.; Courtney, J.- M.; Meir, A.; Balaguero,N.; Canti, C.; Moss, F. J.; Page, K. M.; Pratt, W. S.; Hunt, S. P.;Barclay, J.; Rees, M.; Dolphin, A. C.: The ducky mutation in Cacna2d2results in altered Purkinje cell morphology and is associated withthe expression of a truncated 3 B c

alpha- 2/delta- 2 protein with abnormalfunction. J. Biol. Chem. 277: 7684-
7693, 2002.

GAM8554 388 CACNA2D2 Gao, B.; Sekido, Y.; Maximov, A.; Saad, M.; Forgacs, E.; Latif,F.; Wei, M. 3 B c
H.; Lerman, M.; Lee, J.- H.; Perez- Reyes, E.; Bezprozvanny,I.; Minna, J.
D.: Functional properties of a new voltage- dependentcalcium channel alpha-
2/delta auxiliary subunit gene (CACNA2D2). J.Biol. Chem. 275: 12237- 12242,
2000.

GAM8554 388 CACNA2D2 Lerman, M. I.; Minna, J. D.: The 630- kb lung cancer homozygousdeletion 3 B c
region on human chromosome 3p21.3: identification and evaluationof the
resident candidate tumor suppressor genes. Cancer Res. 60:6116- 6133, 2000.

GAM8554 388 CACNA2D2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; 3 B c
Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes.
IX. The complete sequences of 100 new cDNA clones frombrain which can code
for large proteins in vitro. DNA Res. 5: 31- 39,1998.

GAM8554 388 CASP8 Chun, H. J.; Zheng, L.; Ahmad, M.; Wang, J.; Speirs, C. K.; Siegel,R. M.; 3 B c
Dale, J. K.; Puck, J.; Davis, J.; Hall, C. G.; Skoda- Smith,S.; Atkinson, T.
P.; Straus, S. E.; Lenardo, M. J.: Pleiotropic defectsin lymphocyte
activation caused by caspase- 8 mutations lead to humanimmunodeficiency.
Nature 419: 395- 399, 2002.

GAM8554 388 CASP8 Fernandes- Alnemri, T.; Armstrong, R. C.; Krebs, J.; Srinivasula,S. M.; 3 B c
Wang, L.; Bullrich, F.; Fritz, L. C.; Trapani, J. A.; Tomaselli,K. J.;
Litwack, G.; Alnemri, E. S.: In vitro activation of CPP32and Mch3 by Mch4, a
novel human apoptotic cysteine protease containingtwo FADD- like domains.
Proc. Nat. Acad. Sci. 93: 7464- 7469, 1996.

GAM8554 388 CASP8 Gervais, F. G.; Singaraja, R.; Xanthoudakis, S.; Gutekunst, C.- A.;Leavitt, 3 B c
B. R.; Metzler, M.; Hackam, A. S.; Tam, J.; Vaillancourt,J. P.; Houtzager,
V.; Rasper, D. M.; Roy, S.; Hayden, M. R.; Nicholson,D. W.: Recruitment and
activation of caspase- 8 by the huntingtin- interactingprotein Hip- 1 and a
novel partner Hippi. Nature Cell Biol. 4: 95- 105,2002.

GAM8554 388 CASP8 Grenet, J.; Teitz, T.; Wei, T.; Valentine, V.; Kidd, V. J.: Structureand 3 B c
chromosome localization of the human CASP8 gene. Gene 226: 225- 232,1999.

GAM8554 388 CASP8 Ikeda, H.; Yamaguchi, M.; Sugai, S.; Aze, Y.; Narumiya, S.; Kakizuka,A.: 3 B c
Expanded polyglutamine in the Machado- Joseph disease proteininduces cell
death in vitro and in vivo. Nature Genet. 13: 196- 202,1996.

GAM8554 388 CASP8 Kischkel, F. C.; Kioschis, P.; Weitz, S.; Poustka, A.; Lichter,P.; Krammer, 3 B c
P. H.: Assignment of CASP8 to human chromosome band2q33- q34 and Casp8 to
the murine syntenic region on chromosome 1B- proximalC by in situ
hybridization. Cytogenet. Cell Genet. 82: 95- 96, 1998.

GAM8554 388 CASP8 Sanchez, I.; Xu, C.- J.; Juo, P.; Kakizaka, A.; Blenis, J.; Yuan,J.: 3 B c
Caspase- 8 is required for cell death induced by expanded
polyglutaminerepeats. Neuron 22: 623- 633, 1999.

GAM8554 388 CASP8 Varfolomeev, E. E.; Schuchmann, M.; Luria, V.; Chiannilkulchai,N.; Beckmann, 3 B c
J. S.; Mett, I. L.; Rebrikov, D.; Brodianski, V. M.;Kemper, O. C.; Kollet,
O.; Lapidot, T.; Soffer, D.; Sobe, T.; Avraham,K. B.; Goncharov, T.;
Holtmann, H.; Lonai, P.; Wallach, D.: Targeteddisruption of the mouse
Caspase 8 gene ablates cell death inductionby the TNF receptors, Fas/Apo1,
and DR3 and is lethal prenatally. Immunity 9:267- 276, 1998.

GAM8554 388 CHD4 Seelig, H. P.; Moosbrugger, I.; Ehrfeld, H.; Fink, T.; Renz, M.;Genth, E.: 3 B c
The major dermatomyositis- specific Mi- 2 autoantigen isa presumed helicase
involved in transcriptional activation. ArthritisRheum. 38: 1389- 1399,

1995.

GAM8554 388 CHD4 Seelig, H. P.; Renz, M.; Targoff, I. N.; Ge, Q.; Frank, M. B.:Two forms of the major antigenic protein of the dermatomyositis- specificMi- 2 autoantigen. (Letter) Arthritis Rheum. 39: 1769- 1771, 1996. 3 B c

GAM8554 388 CHD4 Wade, P. A.; Gegonne, A.; Jones, P. L.; Ballestar, E.; Aubry, F.;Wolffe, A. P.: Mi- 2 complex couples DNA methylation to chromatinremodelling and histone deacetylation. Nature Genet. 23: 62- 66,1999. 3 B c

GAM8554 388 CHD4 Zhang, Y.; LeRoy, G.; Seelig, H.- P.; Lane, W. S.; Reinberg, D.: The dermatomyositis- specific autoantigen Mi2 is a component of acomplex containing histone deacetylase and nucleosome remodeling activities. Cell 95:279- 289, 1998. 3 B c

GAM8554 388 CHD4 Zhang, Y.; Ng, H.- H.; Erdjument- Bromage, H.; Tempst, P.; Bird,A.; Reinberg, D.: Analysis of the NuRD subunits reveals a histonedeacetylase core complex and a connection with DNA methylation. GenesDev. 13: 1924- 1935, 1999. 3 B c

GAM8554 388 CHST2 Li, X.; Tedder, T. F.: CHST1 and CHST2 sulfotransferases expressedby human vascular endothelial cells: cDNA cloning, expression, andchromosomal localization. Genomics 55: 345- 347, 1999. 3 B c

GAM8554 388 CHST2 Uchimura, K.; Muramatsu, H.; Kadomatsu, K.; Fan, Q.- W.; Kurosawa,N.; Mitsuoka, C.; Kannagi, R.; Habuchi, O.; Muramatsu, T.: Molecularcloning and characterization of an N- acetylglucosamine- 6- O- sulfotransferase. J.Biol. Chem. 273: 22577- 22583, 1998. 3 B c

GAM8554 388 CHST2 Uchimura, K.; Muramatsu, H.; Kaname, T.; Ogawa, H.; Yamakawa, T.;Fan, Q.-W.; Mitsuoka, C.; Kannagi, R.; Habuchi, O.; Yokoyama, I.;Yamamura, K.; Ozaki, T.; Nakagawara, A.; Kadomatsu, K.; Muramatsu,T.: Human N-acetylglucosamine- 6- O- sulfotransferase involved in thebiosynthesis of 6-sulfo sialyl Lewis X: molecular cloning, chromosomalmapping, and expression in various organs and tumor cells. J. Biochem. 124:670- 678, 1998. 3 B c

GAM8554 388 CNTF Barbin, G.; Manthorpe, M.; Varon, S.: Purification of the chickeye ciliary neuronotrophic factor. J. Neurochem. 43: 1468- 1478,1984. 3 B c

GAM8554 388 CNTF DeChiara, T. M.; Vejsada, R.; Poueymirou, W. T.; Acheson, A.; Suri,C.; Conover, J. C. Friedman, B.; McClain, J.; Pan, L.; Stahl, N.;Ip, N. Y.; Kato, A.; Yancopoulos, G. D.: Mice lacking the CNTF receptor,unlike mice lacking CNTF, exhibit profound motor neuron deficits atbirth. Cell 83: 313-322, 1995. 3 B c

GAM8554 388 CNTF Emerich, D. F.; Winn, S. R.; Hantraye, P. M.; Peschanski, M.; Chen,E.- Y.; Chu, Y.; McDermott, P.; Baetge, E. E.; Kordower, J. H.: Protectiveeffect of encapsulated cells producing neurotrophic factor CNTF ina monkey model of Huntington's disease. Nature 386: 395- 399, 1997. 3 B c

GAM8554 388 CNTF Gelernter, J.; Van Dyck, C.; van Kammen, D. P.; Malison, R.; Price,L. H.; Cubells, J. F.; Berman, R.; Charney, D. S.; Heninger, G.:Ciliary neurotrophic factor null allele frequencies in schizophrenia,affective disorders, and Alzheimer's disease. Am. J. Med. Genet. 74:497- 500, 1997. 3 B c

GAM8554 388 CNTF Giess, R.; Holtmann, B.; Braga, M.; Grimm, T.; Muller- Myhsok, B.;Toyka, K. V.; Sendtner, M.: Early onset of severe familial amyotrophiclateral sclerosis with a SOD- 1 mutation: potential impact of CNTFas a candidate modifier gene. Am. J. Hum. Genet. 70: 1277- 1286,2002. 3 B c

GAM8554 388 CNTF Giess, R.; Maurer, M.; Linker, R.; Gold, R.; Warmuth- Metz, M.;Toyka, K. V.; 3 B c

Sendtner, M.; Rieckmann, P.: Association of a nullmutation in the CNTF gene with early onset of multiple sclerosis. Arch.Neurol. 59: 407- 409, 2002.

GAM8554 388 CNTF Giovannini, M.; Romo, A. J.; Evans, G. A.: Chromosomal localizationof the human ciliary neurotrophic factor gene (CNTF) to 11q12 by fluorescencein situ hybridization. Cytogenet. Cell Genet. 63: 62- 63, 1993. 3 B c

GAM8554 388 CNTF Gloaguen, I.; Costa, P.; Demartis, A.; Lazzaro, D.; Di Marco, A.;Graziani, R.; Paonessa, G.; Chen, F.; Rosenblum, C. I.; Van der Ploeg,L. H. T.; Cortese, R.; Ciliberto, G.; Laufer, R.: Ciliary neurotrophicfactor corrects obesity and diabetes associated with leptin deficiencyand resistance. Proc. Nat. Acad. Sci. 94: 6456- 6461, 1997. 3 B c

GAM8554 388 CNTF Kaupmann, K.; Sendtner, M.; Stockli, K. A.; Jockusch, H.: Thegene for ciliary neurotrophic factor (CNTF) maps to murine chromosome19 and its expression is not affected in the hereditary motoneurondisease 'Wobbler' of the mouse. Europ. J. Neurosci. 3: 1182- 1186,1991. 3 B c

GAM8554 388 CNTF Lam, A.; Fuller, F.; Miller, J.; Kloss, J.; Manthorpe, M.; Varon,S.; Cordell, B.: Sequence and structural organization of the humangene encoding ciliary neurotrophic factor. Gene 102: 271- 276, 1991. 3 B c

GAM8554 388 CNTF Lambert, P. D.; Anderson, K. D.; Sleeman, M. W.; Wong, V.; Tan,J.; Hijarunguru, A.; Corcoran, T. L.; Murray, J. D.; Thabet, K. E.;Yancopoulos, G. D.; Wiegand, S. J.: Ciliary neurotrophic factor activatesleptin- like pathways and reduces body fat, without cachexia or reboundweight gain, even in leptin- resistant obesity. Proc. Nat. Acad. Sci. 98:4652- 4657, 2001. 3 B c

GAM8554 388 CNTF Lev, A. A.; Rosen, D. R.; Kos, C.; Clifford, E.; Landes, G.; Hauser,S. L.; Brown, R. H., Jr.: Human ciliary neurotrophic factor: localizationto the proximal region of the long arm of chromosome 11 and associationwith CA/GT dinucleotide repeat. Genomics 16: 539- 541, 1993. 3 B c

GAM8554 388 CNTF Lichter, P.; Tang, C. C.- J.; Call, K.; Hermanson, G.; Evans, G.A.; Housman, D.; Ward, D. C.: High- resolution mapping of human chromosome11 by in situ hybridization with cosmid clones. Science 247: 64- 69,1990. 3 B c

GAM8554 388 CNTF Masu, Y.; Wolf, E.; Holtmann, B.; Sendtner, M.; Brem, G.; Thoenen,H.: Disruption of the CNTF gene results in motor neuron degeneration. Nature 365:27- 32, 1993. 3 B c

GAM8554 388 CNTF Sendtner, M.; Schmalbruch, H.; Stockli, K. A.; Carroll, P.; Kreutzberg,G. W.; Thoenen, H.: Ciliary neurotrophic factor prevents degenerationof motor neurons in mouse mutant progressive motor neuronopathy. Nature 358:502- 504, 1992. 3 B c

GAM8554 388 CNTF Takahashi, R.; Yokoji, H.; Misawa, H.; Hayashi, M.; Hu, J.; Deguchi,T.: A null mutation in the human CNTF gene is not causally relatedto neurological diseases. Nature Genet. 7: 79- 84, 1994. 3 B c

GAM8554 388 CNTF Yokoji, H.; Ariyama, T.; Takahashi, R.; Inazawa, J.; Misawa, H.;Deguchi, T.: cDNA cloning and chromosomal localization of the humanciliary neurotrophic factor gene. Neurosci. Lett. 185: 175- 178,1995. 3 B c

GAM8554 388 CRAT Corti, O.; Finocchiaro, G.; Rossi, E.; Zuffardi, O.; DiDonato,S.: Molecular cloning of cDNAs encoding human carnitine acetyltransferaseand mapping of the corresponding gene to chromosome 9q34.1. Genomics 23:94- 99, 1994. 3 B c

GAM8554 388 CRAT Kalaria, R. N.; Harik, S. I.: Carnitine acetyltransferase activityin the human brain and its microvessels is decreased in Alzheimer'sdisease. Ann. Neurol. 32: 583- 586, 1992. 3 B c

GAM8554 388 CRAT van der Leij, F. R.; Huijkman, N. C. A.; Boomsma, C.; Kuipers,J. R. G.; Bartelds, B.: Genomics of the human carnitine acyltransferasegenes. Molec. 3 B c

Genet. Metab. 71: 139- 153, 2000.

GAM8554 388 CRH Arbiser, J. L.; Morton, C. C.; Bruns, G. A. P.; Majzoub, J. A.: Human corticotropin releasing hormone gene is located on the longarm of chromosome 8. Cytogenet. Cell Genet. 47: 113- 116, 1988. 3 B c

GAM8554 388 CRH Asakura, H.; Zwain, I. H.; Yen, S. S. C.: Expression of genesencoding corticotropin- releasing factor (CRF), type 1 CRF receptor,and CRF- binding protein and localization of the gene products in thehuman ovary. J. Clin. Endocr. Metab. 82: 2720- 2725, 1997. 3 B c

GAM8554 388 CRH Behan, D. P.; Heinrichs, S. C.; Troncoso, J. C.; Liu, X.- J.; Kawas,C. H.; Ling, N.; De Souza, E. B.: Displacement of corticotropin releasingfactor from its binding protein as a possible treatment for Alzheimer'sdisease. Nature 378: 284- 287, 1995. 3 B c

GAM8554 388 CRH Cheng, Y.- H.; Nicholson, R. C.; King, B.; Chan, E.- C.; Fitter,J. T.; Smith, R.: Corticotropin- releasing hormone gene expressionin primary placental cells is modulated by cyclic adenosine 3- prime,5- prime-monophosphate. J.Clin. Endocr. Metab. 85: 1239- 1244, 2000. 3 B c

GAM8554 388 CRH Habib, K. E.; Weld, K. P.; Rice, K. C.; Pushkas, J.; Champoux,M.; Listwak, S.; Webster, E. L.; Atkinson, A. J.; Schulkin, J.; Contoreggi,C.; Chrousos, G. P.; McCann, S. M.; Suomi, S. J.; Higley, J. D.; Gold,P. W.: Oral administration of a corticotropin- releasing hormone receptorantagonist significantly attenuates behavioral, neuroendocrine, andautonomic responses to stress in primates. Proc. Nat. Acad. Sci. 97:6079- 6084, 2000. 3 B c

GAM8554 388 CRH Inder, W. J.; Prickett, T. C. R.; Ellis, M. J.; Hull, L.; Reid,R.; Benny, P. S.; Livesey, J. H.; Donald, R. A.: The utility of plasmaCRH as a predictor of preterm delivery. J. Clin. Endocr. Metab. 86:5706- 5710, 2001. 3 B c

GAM8554 388 CRH Kellogg, J.; Luty, J. A.; Thompson, R.; Luo, X. Y.; Magenis, R.E.; Litt, M.: Corticotropin releasing hormone (CRH) maps to humanchromosome 8 and identifies a TaqI RFLP. Cytogenet. Cell Genet. 51:1022, 1989. 3 B c

GAM8554 388 CRH Knapp, L. T.; Keegan, C. E.; Seasholtz, A. F.; Camper, S. A.:Corticotropin- releasing hormone (Crh) maps to mouse chromosome 3. MammalianGenome 4: 615-617, 1993. 3 B c

GAM8554 388 CRH Kyllo, J. H.; Collins, M. M.; Vetter, K. L.; Cuttler, L.; Rosenfield,R. L.; Donohoue, P. A.: Linkage of congenital isolated adrenocorticotropichormone deficiency to the corticotropin releasing hormone locus usingsimple sequence repeat polymorphisms. Am. J. Med. Genet. 62: 262- 267,1996. 3 B c

GAM8554 388 CRH Majzoub, J. A.: Personal Communication. Boston, Mass. 3/3/1995. 3 B c

GAM8554 388 CRH Mandel, H.; Berant, M.; Gotfried, E.; Hochberg, Z.: Autosomalrecessive hypothalamic corticotropin deficiency: a new entity andits metabolic consequences. (Abstract) Am. J. Hum. Genet. 47 (suppl.):A66, 1990. 3 B c

GAM8554 388 CRH McLean, M.; Bisits, A.; Davies, J.; Woods, R.; Lowry, P.; Smith,R.: A placental clock controlling the length of human pregnancy. NatureMed. 1: 460- 463, 1995. 3 B c

GAM8554 388 CRH Muglia, L.; Jacobson, L.; Dikkes, P.; Majzoub, J. A.: Corticotropin-releasinghormone deficiency reveals major fetal but not adult glucocorticoidneed. Nature 373: 427- 432, 1995. 3 B c

GAM8554 388 CRH Robinson, B. G.; Emanuel, R. L.; Frim, D. M.; Majzoub, J. A.:Glucocorticoid stimulates expression of corticotropin- releasing hormonegene in human placenta. Proc. Nat. Acad. Sci. 85: 5244- 5248, 1988. 3 B c

GAM8554 388 CRH Scatena, C. D.; Adler, S.: Characterization of a human- specificregulator of placental corticotropin- releasing hormone. Molec. Endocr. 12:1228- 1240, 3 B c

1998.

GAM8554 388 CRH Scatena, C. D.; Adler, S.: Trans- acting factors dictate the species- specificplacental expression of corticotropin- releasing factor genes in choriocarcinomacell lines. Endocrinology 137: 3000- 3008, 1996. 3 B c

GAM8554 388 CRH Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi,H.; Shimizu, S.; Horikawa, S.; Numa, S.: Isolation and sequence analysisof the human corticotropin- releasing factor precursor gene. EMBOJ. 2: 775- 779, 1983. 3 B c

GAM8554 388 CRH Stratakis, C. A.; Chrousos, G. P.: Neuroendocrinology and pathophysiologyof the stress system. Ann. N.Y. Acad. Sci. 771: 1- 18, 1995. 3 B c

GAM8554 388 CRH Stratakis, C. A.; Sarlis, N. J.; Berrettini, W. H.; Badner, J.A.; Chrousos, G. P.; Gershon, E. S.; Detera- Wadleigh, S. D.: Lackof linkage between the corticotropin- releasing hormone (CRH) geneand bipolar affective disorder. Molec. Psychiat. 2: 483- 485, 1997. 3 B c

GAM8554 388 CRH Xu, B.; Sano, T.; Yamada, S.; Li, C. C.; Hirokawa, M.: Expressionof corticotropin- releasing hormone messenger ribonucleic acid in humanpituitary corticotroph adenomas associated with proliferative potential. J.Clin. Endocr. Metab. 85: 1220- 1225, 2000. 3 B c

GAM8554 388 CRH Zouboulis, C. C.; Seltmann, H.; Hiroi, N.; Chen, W.; Young, M.;Oeff, M.; Scherbaum, W. A.; Orfanos, C. E.; McCann, S. M.; Bornstein,S. R.: Corticotropin- releasing hormone: an autocrine hormone thatpromotes lipogenesis in human sebocytes. Proc. Nat. Acad. Sci. 99:7148- 7153, 2002. 3 B c

GAM8554 388 DGUOK Johansson, M.; Karlsson, A.: Cloning and expression of human deoxyguanosinekinase cDNA. Proc. Nat. Acad. Sci. 93: 7258- 7262, 1996. 3 B c

GAM8554 388 DGUOK Mandel, H.; Szargel, R.; Labay, V.; Elpeleg, O.; Saada, A.; Shalata,A.; Anbinder, Y.; Berkowitz, D.; Hartman, C.; Barak, M.; Eriksson,S.; Cohen, N.: The deoxyguanosine kinase gene is mutated in individualswith depleted hepatocerebral mitochondrial DNA. Nature Genet. 29:337- 341, 2001. Note: Erratum: Nature Genet. 29: 491 only, 2001. 3 B c

GAM8554 388 DGUOK Taanman, J.- W.; Kateeb, I.; Muntau, A. C.; Jaksch, M.; Cohen, N.;Mandel, H.: A novel mutation in the deoxyguanosine kinase gene causingdepletion of mitochondrial DNA. Ann. Neurol. 52: 237- 239, 2002. 3 B c

GAM8554 388 EIF4G1 Brass, N.; Heckel, D.; Sahin, U.; Pfreundschuh, M.; Sybrecht, G.W.; Meese, E.: Translation initiation factor eIF- 4gamma is encodedby an amplified gene and induces an immune response in squamous celllung carcinoma. Hum. Molec. Genet. 6: 33- 39, 1997. 3 B c

GAM8554 388 EIF4G1 Gradi, A.; Imataka, H.; Svitkin, Y. V.; Rom, E.; Raught, B.; Morino,S.; Sonenberg, N.: A novel functional human eukaryotic translationinitiation factor 4G. Molec. Cell. Biol. 18: 334- 342, 1998. 3 B c

GAM8554 388 EIF4G1 Imataka, H.; Gradi, A.; Sonenberg, N.: A newly identified N- terminalamino acid sequence of human eIF4G binds poly(A)- binding protein andfunctions in poly(A)- dependent translation. EMBO J. 17: 7480- 7489,1998. 3 B c

GAM8554 388 EIF4G1 Imataka, H.; Sonenberg, N.: Human eukaryotic translation initiationfactor 4G (eIF4G) possesses two separate and independent binding sitesfor eIF4A. Molec. Cell. Biol. 17: 6940- 6947, 1997. 3 B c

GAM8554 388 EIF4G1 Larola, G.; Cuesta, R.; Brewer, G.; Schneider, R. J.: Controlof mRNA decay by heat shock- ubiquitin- proteasome pathway. Science 284:499- 502, 1999. 3 B c

GAM8554 388 EIF4G1 Pyronnet, S.; Imataka, H.; Gingras, A.- C.; Fukunaga, R.; Hunter,T.; Sonenberg, N.: Human eukaryotic translation initiation factor4G (eIF4G) recruits Mnk1 to phosphorylate eIF4E. EMBO J. 18: 270- 279,1999. 3 B c

GAM8554 388 EIF4G1 Yan, R.; Rhoads, R. E.: Human protein synthesis initiation factoreIF- 4- 3 B c
gamma is encoded by a single gene (EIF4G) that maps to chromosome3q27- qter.
Genomics 26: 394- 398, 1995.

GAM8554 388 EIF4G1 Yan, R.; Rychlik, W.; Etchison, D.; Rhoads, R. E.: Amino acidsequence of the 3 B c
human protein synthesis initiation factor eIF- 4- gamma. J.Biol. Chem. 267:
23226- 23231, 1992.

GAM8554 388 ENTPD6 Chadwick, B. P.; Frischauf, A.- M.: The CD39- like gene 3 B c
family:identification of three new human members (CD39L2, CD39L3, and
CD39L4),their murine homologues, and a member of the gene family from
Drosophilamelanogaster. Genomics 50: 357- 367, 1998.

GAM8554 388 ENTPD6 Chadwick, B. P.; Williamson, J.; Sheer, D.; Frischauf, A.- M.:cDNA cloning 3 B c
and chromosomal mapping of a mouse gene with homologyto NTPases. Mammalian
Genome 9: 162- 164, 1998.

GAM8554 388 ENTPD6 Yeung, G.; Mulero, J. J.; McGowan, D. W.; Bajwa, S. S.; Ford, J.E.: CD39L2, 3 B c
a gene encoding a human nucleoside diphosphatase, predominantlyexpressed in
the heart. Biochemistry 39: 12916- 12923, 2000.

GAM8554 388 FUT3 Gedde- Dahl, T., Jr.; Olaisen, B.; Teisberg, P.; Wilhelmy, M. C.;Mevag, B.; 3 B c
Helland, R.: The locus for apolipoprotein E (apoE) isclose to the Lutheran
(Lu) blood group locus on chromosome 19. Hum.Genet. 67: 178- 182, 1984.

GAM8554 388 FUT3 Grollman, E. F.; Kobata, A.; Ginsburg, V.: An enzymatic basisfor Lewis blood 3 B c
types in man. J. Clin. Invest. 48: 1489- 1494, 1969.

GAM8554 388 FUT3 Grubb, R.: Zur Genetik des Lewis- Systems. Naturwissenschaften 21:560- 561, 3 B c
1953.

GAM8554 388 FUT3 Koda, Y.; Kimura, H.; Mekada, E.: Analysis of Lewis fucosyltransferasegenes 3 B c
from the human gastric mucosa of Lewis- positive and - negativeindividuals.
Blood 82: 2915- 2919, 1993.

GAM8554 388 FUT3 Koprowski, H.; Blaszczyk, M.; Steplewski, Z.; Brockhaus, M.; Magnani,J.; 3 B c
Ginsburg, V.: Lewis blood- type may affect the incidence of
gastrointestinalcancer. Lancet I: 1332- 1333, 1982.

GAM8554 388 FUT3 Nishihara, S.; Narimatsu, H.; Iwasaki, H.; Yazawa, S.; Akamatsu,S.; Ando, 3 B c
T.; Seno, T.; Narimatsu, I.: Molecular genetic analysisof the human Lewis
histo- blood group system. J. Biol. Chem. 269:29271- 29278, 1994.

GAM8554 388 FUT3 Orntoft, T. F.; Vestergaard, E. M.; Holmes, E.; Jakobsen, J. S.;Grunnet, N.; 3 B c
Mortensen, M.; Johnson, P.; Bross, P.; Gregersen, N.;Skorstengaard, K.;
Jensen, U. B.; Bolund, L.; Wolf, H.: Influenceof Lewis alpha- 1- 3/4- L-
fucosyltransferase (FUT3) gene mutations onenzyme activity, erythrocyte
phenotyping, and circulating tumor markersialyl- Lewis a levels. J. Biol.
Chem. 271: 32260- 32268, 1996.

GAM8554 388 FUT3 Pang, H.; Liu, Y.; Koda, Y.; Soejima, M.; Jia, J.; Schlaphoff,T.; du Toit, 3 B c
E. D.; Kimura, H.: Five novel missense mutations ofthe Lewis gene (FUT3) in
African (Xhosa) and Caucasian populationsin South Africa. Hum. Genet. 102:
675- 680, 1998.

GAM8554 388 FUT3 Reguigne- Arnould, I.; Couillin, P.; Mollicone, R.; Faure, S.; Fletcher,A.; 3 B c
Kelly, R. J.; Lowe, J. B.; Oriol, R.: Relative positions of twoclusters of
human alpha- L- fucosyltransferases in 19q (FUT1- FUT2) and19p (FUT6- FUT3-
FUT5) within the microsatellite genetic map of chromosome19. Cytogenet. Cell
Genet. 71: 158- 162, 1995.

GAM8554 388 FUT3 Roychoudhury, A. K.; Nei, M.: Human Polymorphic Genes: WorldDistribution. 3 B c
New York: Oxford Univ. Press (pub.) 1988.

GAM8554 388 FUT3 Sheinfeld, J.; Schaeffer, A. J.; Cordon- Cardo, C.; Rogatko, A.;Fair, W. R.: 3 B c

Association of the Lewis blood- group phenotype withrecurrent urinary tract infections in women. New Eng. J. Med. 320:773- 777, 1989.

GAM8554 388 FUT3 Weitkamp, L. R.; Johnston, E.; Guttormsen, S. A.: Probable geneticlinkage between the loci for the Lewis blood group and complementC3. Cytogenet. Cell Genet. 13: 183- 184, 1974. 3 B c

GAM8554 388 FUT3 Yazawa, S.; Oh- Kawara, H.; Nakajima, T.; Hosomi, O.; Akamatsu,S.; Kishi, K.: Histo- blood group Lewis genotyping from human hairsand blood. Jpn. J. Hum. Genet. 41: 177- 188, 1996. 3 B c

GAM8554 388 FUT5 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3 and 11q21. Genomics 26: 142- 146, 1995. 3 B c

GAM8554 388 FUT5 Weston, B. W.; Nair, R. P.; Larsen, R. D.; Lowe, J. B.: Isolationof a novel human alpha(1,3)fucosyltransferase gene and molecular comparisonto the human Lewis blood group alpha(1,3/1,4)fucosyltransferase gene:syntenic, homologous, nonallelic genes encoding enzymes with distinctacceptor substrate specificities. J. Biol. Chem. 267: 4152- 4160,1992. 3 B c

GAM8554 388 FUT5 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple homologous sequences that determine expressionof the Lewis x, sialyl Lewis x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584, 1992. 3 B c

GAM8554 388 FUT6 Brinkman- Van der Linden, E. C. M.; Mollicone, R.; Oriol, R.; Larson,G.; Van den Eijnden, D. H.; Van Dijk, W.: A missense mutation inthe FUT6 gene results in total absence of alpha- 3- fucosylation ofhuman alpha- 1- acid glycoprotein. J. Biol. Chem. 271: 14492- 14495,1996. 3 B c

GAM8554 388 FUT6 Cameron, H. S.; Szczepaniak, D.; Weston, B. W.: Expression ofhuman chromosome 19p alpha- (1,3)- fucosyltransferase genes in normaltissues: alternative splicing, polyadenylation, and isoforms. J.Biol. Chem. 270: 20112- 20122, 1995. 3 B c

GAM8554 388 FUT6 Koszdin, K. L.; Bowen, B. R.: The cloning and expression of ahuman alpha- 1,3 fucosyltransferase capable of forming the E- selectinligand. Biochem. Biophys. Res. Commun. 187: 152- 157, 1992. 3 B c

GAM8554 388 FUT6 McCurley, R. S.; Recinos, A., III; Olsen, A. S.; Gingrich, J. C.;Szczepaniak, D.; Cameron, H. S.; Krauss, R.; Weston, B. W.: Physicalmaps of human alpha(1,3)fucosyltransferase genes FUT3- FUT6 on chromosomes19p13.3 and 11q21. Genomics 26: 142- 146, 1995. 3 B c

GAM8554 388 FUT6 Mollicone, R.; Reguigne, I.; Fletcher, A.; Aziz, A.; Rustam, M.;Weston, B. W.; Kelly, R. J.; Lowe, J. B.; Oriol, R.: Molecular basisfor plasma alpha(1,3)- fucosyltransferase gene deficiency (FUT6). J.Biol. Chem. 269: 12662- 12671, 1994. 3 B c

GAM8554 388 FUT6 Pang, H.; Koda, Y.; Soejima, M.; Schlaphoff, T.; Du Toit, E. D.;Kimura, H.: Allelic diversity of the human plasma alpha(1,3)fucosyltransferasegene (FUT6). Ann. Hum. Genet. 63: 277- 284, 1999. 3 B c

GAM8554 388 FUT6 Schnyder- Candrian, S.; Borsig, L.; Moser, R.; Berger, E. G.: Localizationof alpha- 1,3- fucosyltransferase VI in Weibel- Palade bodies of humanendothelial cells. Proc. Nat. Acad. Sci. 97: 8369- 8374, 2000. 3 B c

GAM8554 388 FUT6 Weston, B. W.; Smith, P. L.; Kelly, R. J.; Lowe, J. B.: Molecularcloning of a fourth member of a human alpha(1,3)fucosyltransferasegene family: multiple homologous sequences that determine expressionof the Lewis x, sialyl Lewis 3 B c

x, and difucosyl sialyl Lewis x epitopes. J.Biol. Chem. 267: 24575- 24584, 1992.

GAM8554 388 FUT9 Cailleau- Thomas, A.; Coullin, P.; Candelier, J.- J.; Balanzino,L.; Mennesson, B.; Oriol, R.; Mollicone, R.: FUT4 and FUT9 genesare expressed early in human embryogenesis. Glycobiology 10: 789- 802,2000. 3 B c

GAM8554 388 FUT9 Kaneko, M.; Kudo, T.; Iwasaki, H.; Ikehara, Y.; Nishihara, S.;Nakagawa, S.; Sasaki, K.; Shiina, T.; Inoko, H.; Saitou, N.; Narimatsu,H.: Alpha- 1,3- fucoslytransferase (sic) IX (Fuc- TIX) is very highlyconserved between human and mouse; molecular cloning, characterizationand tissue distribution of human Fuc- TIX. FEBS Lett. 452: 237- 242,1999. 3 B c

GAM8554 388 FUT9 Kaneko, M.; Kudo, T.; Iwasaki, H.; Shiina, T.; Inoko, H.; Kozaki,T.; Saitou, N.; Narimatsu, H.: Assignment of the human alpha- 1,3- fucosyltransferaseIX gene (FUT9) to chromosome band 6q16 by in situ hybridization. Cytogenet.Cell Genet. 86: 329- 330, 1999. 3 B c

GAM8554 388 GAB2 Gu, H.; Saito, K.; Klaman, L. D.; Shen, J.; Fleming, T.; Wang,Y.- P.; Pratt, J. C.; Lin, G.; Lim, B.; Kinet, J.- P.; Neel, B. G.:Essential role for Gab2 in the allergic response. Nature 412: 186- 190,2001. 3 B c

GAM8554 388 GAB2 Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.;Nomura, N.; Ohara, O.: Prediction of the coding sequences of unidentifiedhuman genes. IX. The complete sequences of 100 new cDNA clones frombrain which can code for large proteins in vitro. DNA Res. 5: 31- 39,1998. 3 B c

GAM8554 388 GAB2 Nishida, K.; Yoshida, Y.; Itoh, M.; Fukada, T.; Ohtani, T.; Shirogane,T.; Atsumi, T.; Takahashi- Tezuka, M.; Ishihara, K.; Hibi, M.; Hirano,T.: Gab- family adapter proteins act downstream of cytokine and growthfactor receptors and T- and B- cell antigen receptors. Blood 93:1809- 1816, 1999. 3 B c

GAM8554 388 GAB2 Yamada, K.; Nishida, K.; Hibi, M.; Hirano, T.; Matsuda, Y.: ComparativeFISH mapping of Gab1 and Gab2 genes in human, mouse and rat. Cytogenet.Cell Genet. 94: 39- 42, 2001. 3 B c

GAM8554 388 GAB2 Zhao, C.; Yu, D.- H.; Shen, R.; Feng, G.- S.: Gab2, a new pleckstrinhomology domain- containing adapter protein, acts to uncouple signalingfrom ERK kinase to Elk- 1. J. Biol. Chem. 274: 19649- 19654, 1999. 3 B c

GAM8554 388 GAS7 Ju, Y.- T.; Chang, A. C. Y.; She, B.- R.; Tsaur, M.- L.; Hwang, H.- M.;Chao, C. C.- K.; Cohen, S. N.; Lin- Chao, S.: Gas7: a gene expressedpreferentially in growth- arrested fibroblasts and terminally differentiatedPurkinje neurons affects neurite formation. Proc. Nat. Acad. Sci. 95:11423- 11428, 1998. 3 B c

GAM8554 388 GAS7 Kurtz, A.; Zimmer, A.: Interspecies fluorescence in situ hybridizationfurther defines synteny homology between mouse chromosome 11 and humanchromosome 17. Mammalian Genome 6: 379- 380, 1995. 3 B c

GAM8554 388 GAS7 Megonigal, M. D.; Cheung, N.- K. V.; Rappaport, E. F.; Nowell, P.C.; Wilson, R. B.; Jones, D. H.; Addya, K.; Leonard, D. G. B.; Kushner,B. H.; Williams, T. M.; Lange, B. J.; Felix, C. A.: Detection ofleukemia- associated MLL-GAS7 translocation early during chemotherapywith DNA topoisomerase II inhibitors. Proc. Nat. Acad. Sci. 97:2814- 2819, 2000. 3 B c

GAM8554 388 HDGF Nakamura, H.; Izumoto, Y.; Kambe, H.; Kuroda, T.; Mori, T.; Kawamura,K.; Yamamoto, H.; Kishimoto, T.: Molecular cloning of complementaryDNA for a novel human hepatoma- derived growth factor: its homologywith high mobility group- 1 protein. J. Biol. Chem. 269: 25143- 25149,1994. 3 B c

GAM8554 388 HDGF Wanschura, S.; Schoenmakers, E. F. P. M.; Huysmans, C.; Bartnitzke,S.; Van de Ven, W. J. M.; Bullerdiek, J.: Mapping of the gene encodingthe human 3 B c

hepatoma- derived growth factor (HDGF) with homology to thehigh- mobility group (HMG)- 1 protein to Xq25. Genomics 32: 298- 300,1996.

GAM8554 388 HMGA1 Agalioti, T.; Lomvardas, S.; Parekh, B.; Yie, J.; Maniatas, T.;Thanos, D.: 3 B c
Ordered recruitment of chromatin modifying and generaltranscription factors to the IFN- beta promoter. Cell 103: 667- 678,2000.

GAM8554 388 HMGA1 Friedmann, M.; Holth, L. T.; Zoghbi, H. Y.; Reeves, R.: 3 B c
Organization,inducible- expression and chromosome localization of the human HMG- I(Y)nonhistone protein gene. Nucleic Acids Res. 21: 4259- 4267, 1993.

GAM8554 388 HMGA1 Munshi, N.; Agalioti, T.; Lomvardas, S.; Merika, M.; Chen, G.;Thanos, D.: 3 B c
Coordination of a transcriptional switch by HMGI(Y) acetylation. Science 293:1133- 1136, 2001.

GAM8554 388 HMGA1 Thanos, D.; Maniatis, T.: Virus induction of human IFN- beta geneexpression 3 B c
requires the assembly of an enhanceosome. Cell 83: 1091- 1100,1995.

GAM8554 388 HMGA1 Wood, L. J.; Mukherjee, M.; Dolde, C. E.; Xu, Y.; Maher, J. F.;Bunton, T. 3 B c
E.; Williams, J. B.; Resar, L. M. S.: HMG- I/Y, a new c- Myctarget gene and potential oncogene. Molec. Cell Biol. 20: 5490- 5502,2000.

GAM8554 388 HS3ST2 Liu, J.; Shworak, N. W.; Sinay, P.; Schwartz, J. J.; Zhang, L.;Fritze, L. 3 B c
M.; Rosenberg, R. D.: Expression of heparan sulfate D- glucosaminyl3- O- sulfotransferase isoforms reveals novel substrate specificities. J.Biol. Chem. 274: 5185- 5192, 1999.

GAM8554 388 HS3ST2 Shworak, N. W.; Liu, J.; Petros, L. M.; Zhang, L.; Kobayashi, M.;Copeland, 3 B c
N. G.; Jenkins, N. A.; Rosenberg, R. D.: Multiple isoformsof heparan sulfate D- glucosaminyl 3- O- sulfotransferase: isolation,characterization, and expression of human cDNAs and identificationof distinct genomic loci. J. Biol. Chem. 274: 5170- 5184, 1999.

GAM8554 388 ICOS Akbari, O.; Freeman, G. J.; Meyer, E. H.; Greenfield, E. A.; Chang,T. T.; 3 B c
Sharpe, A. H.; Berry, G.; DeKruyff, R. H.; Umetsu, D. T.:Antigen- specific regulatory T cells develop via the ICOS- ICOS- ligandpathway and inhibit allergen- induced airway hyperreactivity. NatureMed. 8: 1024- 1032, 2002.

GAM8554 388 ICOS Coyle, A. J.; Lehar, S.; Lloyd, C.; Tian, J.; Delaney, T.; Manning,S.; 3 B c
Nguyen, T.; Burwell, T.; Schneider, H.; Gonzalo, J. A.; Gosselin,M.; Owen, L. R.; Rudd, C. E.; Gutierriez- Ramos, J. C.: The CD28- relatedmolecule ICOS is required for effective T cell- dependent immune responses. Immunity 13:95- 105, 2000.

GAM8554 388 ICOS Dong, C.; Juedes, A. E.; Temann, U. A.; Shresta, S.; Allison, J.P.; Ruddle, 3 B c
N. H.; Flavell, R. A.: ICOS co- stimulatory receptor isessential for T- cell activation and function. Nature 409: 97- 101,2001.

GAM8554 388 ICOS Haimila, K. E.; Partanen, J. A.; Holopainen, P. M.: Genetic polymorphismof 3 B c
the human ICOS gene. Immunogenetics 53: 1028- 1032, 2002.

GAM8554 388 ICOS Hutloff, A.; Dittrich, A. M.; Beier, K. C.; Eljaschewitsch, B.;Kraft, R.; 3 B c
Anagnostopoulos, I.; Kroczek, R. A.: ICOS is an inducibleT- cell co- stimulator structurally and functionally related to CD28. Nature 397:263- 266, 1999.

GAM8554 388 ICOS McAdam, A. J.; Greenwald, R. J.; Levin, M. A.; Chernova, T.; Malenkovich,N.; 3 B c
Ling, V.; Freeman, G. J.; Sharpe, A. H.: ICOS is critical forCD40- mediated antibody class switching. Nature 409: 102- 105, 2001.

GAM8554 388 ICOS Tafuri, A.; Shahinian, A.; Bladt, F.; Yoshinaga, S. K.; Jordana,M.; Wakeham, 3 B c
A.; Boucher, L.- M.; Bouchard, D.; Chan, V. S. F.; Duncan,G.; Odermatt, B.; Ho, A.; Itie, A.; Horan, T.; Whoriskey, J. S.; Pawson,T.; Penninger, J. M.; Ohashi, P. S.; Mak, T. W.: ICOS is essentialfor effective T- helper- cell

responses. Nature 409: 105- 109, 2001.

GAM8554 388 ICOS Yoshinaga, S. K.; Whoriskey, J. S.; Khare, S. D.; Sarmiento, U.;Guo, J.; 3 B c
Horan, T.; Shih, G.; Zhang, M.; Coccia, M. A.; Kohno, T.;Tafuri- Bladt, A.;
Brankow, D.; and 14 others: T- cell co- stimulationthrough B7RP- 1 and ICOS.
Nature 402: 827- 832, 1999.

GAM8554 388 IL18R1 Dale, M.; Nicklin, M. J.: Interleukin- 1 receptor cluster: geneorganization 3 B c
of IL1R2, IL1R1, IL1RL2 (IL- 1Rrp2), IL1RL1 (T1/ST2),and IL18R1 (IL- 1Rrp)
on human chromosome 2q. Genomics 57: 177- 179,1999.

GAM8554 388 IL18R1 Parnet, P.; Garka, K. E.; Bonnert, T. P.; Dower, S. K.; Sims, J.E.: IL- 1Rrp 3 B c
is a novel receptor- like molecule similar to the typeI interleukin- 1
receptor and its homologues T1/ST2 and IL- 1R AcP. J.Biol. Chem. 271: 3967-
3970, 1996.

GAM8554 388 IL18R1 Torigoe, K.; Ushio, S.; Okura, T.; Kobayashi, S.; Taniai, M.; Kunikata,T.; 3 B c
Murakami, T.; Sanou, O.; Kojima, H.; Fujii, M.; Ohta, T.; Ikeda,M.; Ikegami,
H.; Kurimoto, M.: Purification and characterizationof the human interleukin-
18 receptor. J. Biol. Chem. 272: 25737- 25742,1997.

GAM8554 388 ITGB3BP Li, D.; Desai- Yajnik, V.; Lo, E.; Schapira, M.; Abagyan, R.; Samuels,H. H.: 3 B c
NRIF3 is a novel coactivator mediating functional specificityof nuclear
hormone receptors. Molec. Cell. Biol. 19: 7191- 7202,1999.

GAM8554 388 ITGB3BP Shattil, S. J.; O'Toole, T.; Eigenthaler, M.; Thon, V.; Williams,M.; Babior, 3 B c
B. M.; Ginsberg, M. H.: Beta- 3- endonexin, a novel polypeptidethat
interacts specifically with the cytoplasmic tail of the integrinbeta- 3
subunit. J. Cell Biol. 131: 807- 816, 1995.

GAM8554 388 JUND Sullivan, M.; Olsen, A. S.; Houslay, M. D.: Genomic organisationof the human 3 B c
cyclic AMP- specific phosphodiesterase PDE4C gene andits chromosomal
localisation to 19p13.1, between RAB3A and JUND. Cell.Signal. 11: 735- 742,
1999.

GAM8554 388 JUND Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; 3 B c
Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan,
K.: Fluorescence in situ hybridization mapping of humanchromosome 19:
cytogenetic band location of 540 cosmids and 70 genesor DNA markers.
Genomics 15: 133- 145, 1993.

GAM8554 388 JUND Weitzman, J. B.; Fiette, L.; Matsuo, K.; Yaniv, M.: JunD protectscells from 3 B c
p53- dependent senescence and apoptosis. Molec. Cell 6:1109- 1119, 2000.

GAM8554 388 KLK3 Bansal, A.; Murray, D. K.; Wu, J. T.; Stephenson, R. A.; Middleton,R. G.; 3 B c
Meikle, A. W.: Heritability of prostate- specific antigen andrelationship
with zonal prostate volumes in aging twins. J. Clin.Endocr. Metab. 85: 1272-
1276, 2000.

GAM8554 388 KLK3 Cleutjens, K. B. J. M.; van der Korput, H. A. G. M.; van Eekelen,C. C. E. 3 B c
M.; van Rooij, H. C. J.; Faber, P. W.; Trapman, J.: An androgenresponse
element in a far upstream enhancer region is essential forhigh, androgen-
regulated activity of the prostate- specific antigenpromoter. Molec. Endocr.
11: 148- 161, 1997.

GAM8554 388 KLK3 Cleutjens, K. B. J. M.; van Eekelen, C. C. E. M.; van der Korput,H. A. G. 3 B c
M.; Brinkmann, A. O.; Trapman, J.: Two androgen responseregions cooperate in
steroid hormone regulated activity of the prostate- specificantigen
promoter. J. Biol. Chem. 271: 6379- 6388, 1996.

GAM8554 388 KLK3 Evans, B. A.; Drinkwater, C. C.; Richards, R. I.: Mouse glandularkallikrein 3 B c
genes: structure and partial sequence analysis of the kallikreingene locus.
J. Biol. Chem. 262: 8027- 8034, 1987.

GAM8554 388 KLK3 Lundwall, A.; Lilja, H.: Molecular cloning of human prostate specificantigen 3 B c
cDNA. FEBS Lett. 214: 317- 322, 1987.

GAM8554 388 KLK3 Melegos, D. N.; Yu, H.; Ashok, M.; Wang, C.; Stanczyk, F.; Diamandis,E. P.: 3 B c
Prostate- specific antigen in female serum, a potential newmarker of
androgen excess. J. Clin. Endocr. Metab. 82: 777- 780,1997.

GAM8554 388 KLK3 Oesterling, J. E.; Chan, D. W.; Epstein, J. I.; Kimball, A. W.,Jr.; Bruzek, 3 B c
D. J.; Rock, R. C.; Brendler, C. B.; Walsh, P. C.: Prostatespecific antigen
in the preoperative and postoperative evaluationof localized prostatic
cancer treated with radical prostatectomy. J.Urol. 139: 766- 772, 1988.

GAM8554 388 KLK3 Riegman, P. H. J.; Vlietstra, R. J.; van der Korput, J. A. G. M.;Brinkmann, 3 B c
A. O.; Trapman, J.: The promoter of the prostate- specificantigen gene
contains a functional androgen responsive element. Molec.Endocr. 5: 1921-
1930, 1991.

GAM8554 388 KLK3 Riegman, P. H. J.; Vlietstra, R. J.; van der Korput, J. A. G. M.;Romijn, J. 3 B c
C.; Trapman, J.: Characterization of the prostate- specificantigen gene: a
novel human kallikrein- like gene. Biochem. Biophys.Res. Commun. 159: 95-
102, 1989.

GAM8554 388 KLK3 Schulz, P.; Stucka, R.; Feldmann, H.; Combriato, G.; Klobeck,H.- G.; 3 B c
Fittler, F.: Sequence of a cDNA clone encompassing the completemature human
prostate specific antigen (PSA) and an unspliced leadersequence. Nucleic
Acids Res. 16: 6226 only, 1988.

GAM8554 388 KLK3 Stamey, T. A.; Yang, N.; Hay, A. R.; McNeal, J. E.; Freiha, F.S.; Redwine, 3 B c
E.: Prostate- specific antigen as a serum marker foradenocarcinoma of the
prostate. New Eng. J. Med. 317: 909- 916, 1987.

GAM8554 388 KLK3 Sutherland, G. R.; Baker, E.; Hyland, V. J.; Callen, D. F.; Close,J. A.; 3 B c
Tregear, G. W.; Evans, B. A.; Richards, R. I.: Human prostate-
specificantigen (APS) is a member of the glandular kallikrein gene familyat
19q13. Cytogenet. Cell Genet. 48: 205- 207, 1988.

GAM8554 388 LCP2 Clements, J. L.; Lee, J. R.; Gross, B.; Yang, B.; Olson, J. D.;Sandra, A.; 3 B c
Watson, S. P.; Lentz, S. R.; Koretzky, G. A.: Fetal hemorrhageand platelet
dysfunction in SLP- 76- deficient mice. J. Clin. Invest. 103:19- 25, 1999.

GAM8554 388 LCP2 Jackman, J. K.; Motto, D. G.; Sun, Q.; Tanemoto, M.; Turck, C.W.; Peltz, G. 3 B c
A.; Koretzky, G. A.; Findell, P. R.: Molecular cloningof SLP- 76, a 76- kDa
tyrosine phosphoprotein associated with Grb2 inT cells. J. Biol. Chem. 270:
7029- 7032, 1995.

GAM8554 388 LCP2 Motto, D. G.; Ross, S. E.; Wu, J.; Hendricks- Taylor, L. R.; Koretzky,G. A.: 3 B c
Implication of the GRB2- associated phosphoprotein SLP- 76 inT cell
receptor- mediated interleukin 2 production. J. Exp. Med. 183:1937- 1943,
1996.

GAM8554 388 LCP2 Pivniouk, V.; Tsitsikov, E.; Swinton, P.; Rathbun, G.; Alt, F.W.; Geha, R. 3 B c
S.: Impaired viability and profound block in thymocytedevelopment in mice
lacking the adaptor protein SLP- 76. Cell 94:229- 238, 1998.

GAM8554 388 LCP2 Sunden, S. L. F.; Carr, L. L.; Clements, J. L.; Motto, D. G.; Koretzky,G. 3 B c
A.: Polymorphism in and localization of the gene LCP2 (SLP- 76)to chromosome
5q33.1- qter. Genomics 35: 269- 270, 1996.

GAM8554 388 LOXL3 Jourdan- Le Saux, C.; Tomsche, A.; Ujfalusi, A.; Jia, L.; Csiszar,K.: 3 B c
Central nervous system, uterus, heart, and leukocyte expressionof the LOXL3
gene, encoding a novel lysyl oxidase- like protein. Genomics 74:211- 218,
2001.

GAM8554 388 LOXL3 Maki, J. M.; Kivirikko, K. I.: Cloning and characterization ofa fourth human 3 B c

lysyl oxidase isoenzyme. Biochem. J. 355: 381- 387,2001.

GAM8554 388 MAP3K8 Aoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima,K.: 3 B c
The human cot proto- oncogene encodes two protein serine/threoninekinases
with different transforming activities by alternative initiationof
translation. J. Biol. Chem. 268: 22723- 22732, 1993.

GAM8554 388 MAP3K8 Chan, A. M.- L.; Chedid, M.; McGovern, E. S.; Popescu, N. C.; Miki,T.; 3 B c
Aaronson, S. A.: Expression cDNA cloning of a serine kinase
transforminggene. Oncogene 8: 1329- 1333, 1993.

GAM8554 388 MAP3K8 Miyoshi, J.; Higashi, T.; Mukai, H.; Ohuchi, T.; Kakunaga, T.:Structure and 3 B c
transforming potential of the human cot oncogene encodinga putative protein
kinase. Molec. Cell. Biol. 11: 4088- 4096, 1991.

GAM8554 388 MAP3K8 Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.: The murine cotproto- 3 B c
oncogene: genome structure and tissue- specific expression. Jpn.J. Cancer
Res. 84: 518- 525, 1993.

GAM8554 388 MME Barker, P. E.; Shipp, M. A.; D'Adamio, L.; Masteller, E. L.; Reinherz,E. L.: 3 B c
The common acute lymphoblastic leukemia antigen gene mapsto chromosomal
region 3(q21- q27). J. Immun. 142: 283- 287, 1989.

GAM8554 388 MME D'Adamio, L.; Shipp, M. A.; Masteller, E. L.; Reinherz, E. L.:Organization 3 B c
of the gene encoding common acute lymphoblastic leukemiaantigen (neutral
endopeptidase 24.11): multiple miniexons and separate5- prime untranslated
regions. Proc. Nat. Acad. Sci. 86: 7103- 7107,1989.

GAM8554 388 MME Debiec, H.; Guigonis, V.; Mougenot, B.; Decobert, F.; Haymann,J.- P.; 3 B c
Bensman, A.; Deschenes, G.; Ronco, P. M.: Antenatal
membranousglomerulonephritis due to anti- neutral endopeptidase antibodies.
NewEng. J. Med. 346: 2053- 2060, 2002.

GAM8554 388 MME Iwata, N.; Tsubuki, S.; Takaki, Y.; Shirotani, K.; Lu, B.; Gerard,N. P.; 3 B c
Gerard, C.; Hama, E.; Lee, H.- J.; Saido, T. C.: Metabolicregulation of
brain A- beta by neprilysin. Science 292: 1550- 1552,2001.

GAM8554 388 MME Letarte, M.; Vera, S.; Tran, R.; Addis, J. B. L.; Onizuka, R. 3 B c
J.;Quackenbush, E. J.; Jongeneel, C. V.; McInnes, R. R.: Common
acutelymphocytic leukemia antigen is identical to neutral endopeptidase.
J.Exp. Med. 168: 1247- 1253, 1988.

GAM8554 388 MME Shipp, M. A.; Vijayaraghavan, J.; Schmidt, E. V.; Masteller, E.L.; D'Adamio, 3 B c
L.; Hersh, L. B.; Reinherz, E. L.: Common acute lymphoblasticleukemia
antigen (CALLA) is active neutral endopeptidase 24.11
('enkephalinase'):direct evidence by cDNA transfection analysis. Proc. Nat.
Acad. Sci. 86:297- 301, 1989.

GAM8554 388 MME Tran- Paterson, R.; Willard, H. F.; Letarte, M.: The common 3 B c
acutelymphoblastic leukemia antigen (neutral endopeptidase- - 3.4.24.11)gene
is located on human chromosome 3. Cancer Genet. Cytogenet. 42:129- 134,
1989.

GAM8554 388 MYCBP Furusawa, M.; Ohnishi, T.; Taira, T.; Iguchi- Ariga, S. M. M.; Ariga,H.: 3 B c
AMY- 1, a c- Myc- binding protein, is localized in the mitochondriaof sperm
by association with S- AKAP84, an anchor protein of cAMP- dependentprotein
kinase. J. Biol. Chem. 276: 36647- 36651, 2001.

GAM8554 388 MYCBP Taira, T.; Maeda, J.; Onishi, T.; Kitaura, H.; Yoshida, S.; Kato,H.; Ikeda, 3 B c
M.; Tamai, K.; Iguchi- Ariga, S. M. M.; Ariga, H.: AMY- 1,a novel C- MYC
binding protein that stimulates transcription activityof C- MYC. Genes Cells
3: 549- 565, 1998.

GAM8554 388 PDCD2 Baron, B. W.; Anastasi, J.; Thirman, M. J.; Furukawa, Y.; Fears,S.; Kim, D. 3 B c

C.; Simone, F.; Birkenbach, M.; Montag, A.; Sadhu, A.;Zeleznik- Le, N.; McKeithan, T. W.: The human programmed cell death- 2(PDCD2) gene is a target of BCL6 repression: implications for a roleof BCL6 in the down- regulation of apoptosis. Proc. Nat. Acad. Sci. 99:2860- 2865, 2002.

GAM8554 388 PDCD2 Cohen, J. J.; Duke, R. C.: Glucocorticoid activation of a calcium- dependentendonuclease in thymocyte nuclei leads to cell death. J. Immun. 132:38- 42, 1984. 3 B c

GAM8554 388 PDCD2 Kawakami, T.; Furukawa, Y.; Sudo, K.; Saito, H.; Takami, S.; Takahashi,E.; Nakamura, Y.: Isolation and mapping of a human gene (PDCD2) thatis highly homologous to Rp8, a rat gene associated with programmedcell death. Cytogenet. Cell Genet. 71: 41- 43, 1995. 3 B c

GAM8554 388 PDCD2 Owens, G. P.; Cohen, J. J.: Identification of genes involved inprogrammed cell death. Cancer Metastasis Rev. 11: 149- 156, 1992. 3 B c

GAM8554 388 PDCD2 Sellins, K. S.; Cohen, J. J.: Gene induction by gamma- irradiationleads to DNA fragmentation in lymphocytes. J. Immun. 139: 3199- 3206,1987. 3 B c

GAM8554 388 PDCD2 Trachtulec, Z.; Forejt, J.: Synteny of orthologous genes conservedin mammals, snake, fly, nematode, and fission yeast. Mammalian Genome 12:227- 231, 2001. 3 B c

GAM8554 388 PDCD2 Wyllie, A. H.: Glucocorticoid- induced thymocyte apoptosis is associatedwith endogenous endonuclease activation. Nature 284: 555- 556, 1980. 3 B c

GAM8554 388 PRKACB Berube, D.; Simard, J.; Sandberg, M.; Grzeschik, K.- H.; Gagne,R.; Hansson, V.; Jahnsen, T.: Assignment of the gene encoding thecatalytic subunit C(beta) of cAMP- dependent protein kinase to thep36 band on chromosome 1. (Abstract) Cytogenet. Cell Genet. 58:1850 only, 1991. 3 B c

GAM8554 388 PRKACB Simard, J.; Berube, D.; Sandberg, M.; Grzeschik, K.- H.; Gagne,R.; Hansson, V.; Jahnsen, T.: Assignment of the gene encoding thecatalytic subunit C- beta of cAMP- dependent protein kinase to the p36band on chromosome 1. Hum. Genet. 88: 653- 657, 1992. 3 B c

GAM8554 388 RAMP3 Aiyar, N.; Rand, K.; Elshourbagy, N. A.; Zeng, Z.; Adamou, J. E.;Bergsma, D. J.; Li, Y.: A cDNA encoding the calcitonin gene- relatedpeptide type 1 receptor. J. Biol. Chem. 271: 11325- 11329, 1996. 3 B c

GAM8554 388 RAMP3 Christopoulos, G.; Perry, K. J.; Morfis, M.; Tilakaratne, N.; Gao,Y.; Fraser, N. J.; Main, M. J.; Foord, S. M.; Sexton, P. M.: Multipleamylin receptors arise from receptor activity- modifying protein interactionwith the calcitonin receptor gene product. Molec. Pharm. 56: 235- 242,1999. 3 B c

GAM8554 388 RAMP3 Derst, C.; Engel, H.; Grzeschik, K.- H.; Daut, J.: Genomic structureand chromosome mapping of human and mouse RAMP genes. Cytogenet.Cell Genet. 90: 115- 118, 2000. 3 B c

GAM8554 388 RAMP3 Foord, S. M.; Marshall, F. H.: RAMPs: accessory proteins for seventransmembrane domain receptors. Trends Pharm. Sci. 20: 184- 187,1999. 3 B c

GAM8554 388 RAMP3 McLatchie, L. M.; Fraser, N. J.; Main, M. J.; Wise, A.; Brown,J.; Thompson, N.; Solari, R.; Lee, M. G.; Foord, S. M.: RAMPs regulatethe transport and ligand specificity of the calcitonin- receptor- likereceptor. Nature 393: 333- 339, 1998. 3 B c

GAM8554 388 RGS16 Buckbinder, L.; Velasco- Miguel, S.; Chen, Y.; Xu, N.; Talbott,R.; Gelbert, L.; Gao, J.; Seizinger, B. R.; Gutkind, J. S.; Kley,N.: The p53 tumor suppressor targets a novel regulator of G proteinsignaling. Proc. Nat. Acad. Sci. 94: 7868- 7872, 1997. 3 B c

GAM8554 388 RGS16 Chen, C.- K.; Wieland, T.; Simon, M. I.: RGS- r, a retinal specificRGS protein, binds an intermediate conformation of transducin andenhances 3 B c

recycling. Proc. Nat. Acad. Sci. 93: 12885- 12889, 1996.

GAM8554 388 RGS16 Snow, B. E.; Antonio, L.; Suggs, S.; Siderovski, D. P.: Cloningof a retinally abundant regulator of G- protein signaling (RGS- r/RGS16):genomic structure and chromosomal localization of the human gene. Gene 206:247- 253, 1998. 3 B c

GAM8554 388 RGS16 Zheng, B.; Chen, D.; Farquhar, M. G.: MIR16, a putative membraneglycerophosphodiester phosphodiesterase, interacts with RGS16. Proc.Nat. Acad. Sci. 97: 3999- 4004, 2000. 3 B c

GAM8554 388 RNMT Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima,N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.: Prediction ofthe coding sequences of unidentified human genes. VIII. 78 new cDNAclones from brain which code for large proteins in vitro. DNA Res. 4:307- 313, 1997. 3 B c

GAM8554 388 RNMT Pillutla, R. C.; Shimamoto, A.; Furuichi, Y.; Shatkin, A. J.:Human mRNA capping enzyme (RNGTT) and cap methyltransferase (RNMT)map to 6q16 and 18p11.22- p11.23, respectively. Genomics 54: 351- 353,1998. 3 B c

GAM8554 388 RNMT Pillutla, R. C.; Yue, Z.; Maldonado, E.; Shatkin, A. J.: Recombinanthuman mRNA cap methyltransferase binds capping enzyme/RNA polymeraseIIo complexes. J. Biol. Chem. 273: 21443- 21446, 1998. 3 B c

GAM8554 388 RNMT Tsukamoto, T.; Shibagaki, Y.; Niikura, Y.; Mizumoto, K.: Cloningand characterization of three human cDNAs encoding mRNA (guanine- 7)- methyltransferase,an mRNA cap methylase. Biochem. Biophys. Res. Commun. 251: 27- 34,1998. 3 B c

GAM8554 388 ROR2 Afzal, A. R.; Rajab, A.; Fenske, C. D.; Oldridge, M.; Elanko, N.;Ternes- Pereira, E.; Tuysuz, B.; Murday, V. A.; Patton, M. A.; Wilkie,A. O. M.; Jeffery, S.: Recessive Robinow syndrome, allelic to dominantbrachydactyly type B, is caused by mutation of ROR2. Nature Genet. 25:419- 422, 2000. 3 B c

GAM8554 388 ROR2 DeChiara, T. M.; Kimble, R. B.; Poueymirou, W. T.; Rojas, J.; Masiakowski,P.; Valenzuela, D. M.; Yancopoulos, G. D.: Ror2, encoding a receptor- liketyrosine kinase, is required for cartilage and growth plate development. NatureGenet. 24: 271- 274, 2000. 3 B c

GAM8554 388 ROR2 Deloukas, P.; Schuler, G. D.; Gyapay, G.; Beasley, E. M.; Soderlund,C.; Rodriguez- Tome, P.; Hui, L.; Matise, T. C.; McKusick, K. B.; Beckmann,J. S.; Bentolila, S.; Bihoreau, M.- T.; and 53 others: A physicalmap of 30,000 human genes. Science 282: 744- 746, 1998. 3 B c

GAM8554 388 ROR2 Gong, Y.; Chitayat, D.; Kerr, B.; Chen, T.; Babul- Hirji, R.; Pal,A.; Reiss, M.; Warman, M. L.: Brachydactyly type B: clinical description,genetic mapping to chromosome 9q, and evidence for a shared ancestralmutation. Am. J. Hum. Genet. 64: 578- 585, 1999. 3 B c

GAM8554 388 ROR2 Innis, J. W.; Mortlock, D. P.: Limb development: molecular dysmorphologyis at hand! Clin. Genet. 53: 337- 348, 1998. 3 B c

GAM8554 388 ROR2 Manouvrier- Hanu, S.; Holder- Espinasse, M.; Lyonnet, S.: Geneticsof limb anomalies in humans. Trends Genet. 15: 409- 417, 1999. 3 B c

GAM8554 388 ROR2 Masiakowski, P.; Carroll, R. D.: A novel family of cell surfacereceptors with tyrosine kinase- like domain. J. Biol. Chem. 267:26181- 26190, 1992. 3 B c

GAM8554 388 ROR2 Nomi, M.; Oishi, I.; Kani, S.; Suzuki, H.; Matsuda, T.; Yoda, A.;Kitamura, M.; Itoh, K.; Takeuchi, S.; Takeda, K.; Akira, S.; Ikeya,M.; Takada, S.; Minami, Y.: Loss of mRor1 enhances the heart andskeletal abnormalities in mRor2- deficient mice: redundant and pleiotropicfunctions of mRor1 and mRor2 receptor tyrosine kinases. Molec. Cell.Biol. 21: 8329- 8335, 2001. 3 B c

GAM8554 388 ROR2 Oishi, I.; Takeuchi, S.; Hashimoto, R.; Nagabukuro, A.; Ueda, T.;Liu, Z.- 3 B c

J.; Hatta, T.; Akira, S.; Matsuda, Y.; Yamamura, H.; Otani,H.; Minami, Y.: Spatio- temporally regulated expression of receptortyrosine kinases, mRor1, mRor2, during mouse development: implicationsin development and function of the nervous system. Genes Cells 4:41- 56, 1999.

GAM8554 388 ROR2 Oldridge, M.; Fortuna, A. M.; Maringa, M.; Propping, P.; Mansour,S.; Pollitt, C.; DeChiara, T. M.; Kimble, R. B.; Valenzuela, D. M.;Yancopoulos, G. D.; Wilkie, A. O. M.: Dominant mutations in ROR2,encoding an orphan receptor tyrosine kinase, cause brachydactyly typeB. Nature Genet. 24: 375- 378, 2000. 3 B c

GAM8554 388 ROR2 Oldridge, M.; Temple, I. K. Santos, H. G.; Gibbons, R. J.; Mustafa,Z.; Chapman, K. E.; Loughlin, J.; Wilkie, A. O. M.: Brachydactylytype B: linkage to chromosome 9q22 and evidence for genetic heterogeneity. Am.J. Hum. Genet. 64: 578- 585, 1999. 3 B c

GAM8554 388 ROR2 Schwabe, G. C.; Tinschert, S.; Buschow, C.; Meinecke, P.; Wolff,G.; Gillessen- Kaesbach, G.; Oldridge, M.; Wilkie, A. O. M.; Komec,R.; Mundlos, S.: Distinct mutations in the receptor tyrosine kinasegene ROR2 cause brachydactyly type B. Am. J. Hum. Genet. 67: 822- 831,2000. 3 B c

GAM8554 388 ROR2 Takeuchi, S.; Takeda, K.; Oishi, I.; Nomi, M.; Ikeya, M.; Itoh,K.; Tamura, S.; Ueda, T.; Hatta, T.; Otani, H.; Terashima, T.; Takada,S.; Yamamura, H.; Akira, S.; Minami, Y.: Mouse Ror2 receptor tyrosinekinase is required for the heart development and limb formation. GenesCells 5: 71- 78, 2000. 3 B c

GAM8554 388 ROR2 van Bokhoven, H.; Brunner, H. G.: Splitting p63. Am. J. Hum.Genet. 71: 1- 13, 2002. 3 B c

GAM8554 388 ROR2 van Bokhoven, H.; Celli, J.; Kayserili, H.; van Beusekom, E.;Balci, S.; Brussel, W.; Skovby, F.; Kerr, B.; Percin, E. F.; Akarsu,N.; Brunner, H. G.: Mutation of the gene encoding the ROR2 tyrosinekinase causes autosomal recessive Robinow syndrome. Nature Genet. 25:423- 426, 2000. 3 B c

GAM8554 388 SH3GL2 Giachino, C.; Lantelme, E.; Lanzetti, L.; Saccone, S.; Della Valle,G.; Migone, N.: A novel SH3- containing human gene family preferentiallyexpressed in the central nervous system. Genomics 41: 427- 434, 1997. 3 B c

GAM8554 388 SH3GL2 Howard, L.; Nelson, K. K.; Maciewicz, R. A.; Blobel, C. P.: Interactionof the metalloprotease disintegrins MDC9 and MDC15 with two SH3 domain- containingproteins, endophilin I and SH3PX1. J. Biol. Chem. 274: 31693- 31699,1999. 3 B c

GAM8554 388 SH3GL2 Schmidt, A.; Wolde, M.; Thiele, C.; Fest, W.; Kratzin, H.; Podtelejnikov,A. V.; Witke, W.; Huttner, W. B.; Soling, H.- D.: Endophilin I mediatessynaptic vesicle formation by transfer of arachidonate to lysophosphatidicacid. Nature 401: 133- 141, 1999. 3 B c

GAM8554 388 SH3GL2 Soubeyran, P.; Kowanetz, K.; Szymkiewicz, I.; Langdon, W. Y.; Dikic,I.: Cbl- CIN85- endophilin complex mediates ligand- induced downregulationof EGF receptors. Nature 416: 183- 187, 2002. 3 B c

GAM8554 388 SLC20A1 Kaelbling, M.; Eddy, R.; Shows, T. B.; Copeland, N. G.; Gilbert,D. J.; Jenkins, N. A.; Klinger, H. P.; O'Hara, B.: Localization ofthe human gene allowing infection by gibbon ape leukemia virus tohuman chromosome region 2q11- q14 and to the homologous region on mousechromosome 2. J. Virol. 65: 1743- 1747, 1991. 3 B c

GAM8554 388 SLC20A1 Kavanaugh, M. P.; Miller, D. G.; Zhang, W.; Law, W.; Kozak, S.L.; Kabat, D.; Miller, A. D.: Cell- surface receptors for gibbon apeleukemia virus and amphotropic murine retrovirus are inducible sodium- dependentphosphate 3 B c

symporters. Proc. Nat. Acad. Sci. 91: 7071- 7075, 1994.

GAM8554 388 SLC20A1 O'Hara, B.; Johann, S. V.; Klinger, H. P.; Blair, D. G.; Rubinson,H.; Dunn, 3 B c
K. J.; Sass, P.; Vitek, S. M.; Robins, T.: Characterizationof a human gene
conferring sensitivity to infection by gibbon apeleukemia virus. Cell Growth
Differ. 1: 119- 127, 1990.

GAM8554 388 SLC20A1 Palmer, G.; Manen, D.; Bonjour, J.- P.; Caverzasio, J.: Characterizationof 3 B c
the human Glvr- 1 phosphate transporter/retrovirus receptor geneand promoter
region. Gene 226: 25- 33, 1999.

GAM8554 388 SLC20A1 Palmer, G.; Manen, D.; Bonjour, J.- P.; Caverzasio, J.: Species- 3 B c
specificmechanisms control the activity of the Pit1/PIT1 phosphate
transportergene promoter in mouse and human. Gene 279: 49- 62, 2001.

GAM8554 388 TGFB3 Barton, D. E.; Foellmer, B. E.; Du, J.; Tamm, J.; Derynck, R.;Francke, U.: 3 B c
Chromosomal mapping of genes for transforming growthfactors beta- 2 and
beta- 3 in man and mouse: dispersion of TGF- betagene family. Oncogene Res.
3: 323- 331, 1988.

GAM8554 388 TGFB3 Dickinson, M. E.; Kobrin, M. S.; Silan, C. M.; Kingsley, D. M.;Justice, M. 3 B c
J.; Miller, D. A.; Ceci, J. D.; Lock, L. F.; Lee, A.;Buchberg, A. M.;
Siracusa, L. D.; Lyons, K. M.; Derynck, R.; Hogan,B. L. M.; Copeland, N. G.;
Jenkins, N. A.: Chromosomal localizationof seven members of the murine TGF-
beta superfamily suggests closelinkage to several morphogenetic mutant loci.
Genomics 6: 505- 520,1990.

GAM8554 388 TGFB3 Graycar, J. L.; Miller, D. A.; Arrick, B. A.; Lyons, R. M.; Moses,H. L.; 3 B c
Derynck, R.: Human transforming growth factor- beta- 3:
recombinantexpression, purification, and biological activities in
comparisonwith transforming growth factors- beta- 1 and beta- 2. Molec.
Endocr. 3:1977- 1986, 1989.

GAM8554 388 TGFB3 Kaartinen, V.; Voncken, J. W.; Shuler, C.; Warburton, D.; Bu, 3 B c
D.;Heisterkamp, N.; Groffen, J.: Abnormal lung development and cleftpalate
in mice lacking TGF- beta- 3 indicates defects of epithelial-
mesenchymalinteraction. Nature Genet. 11: 415- 421, 1995.

GAM8554 388 TGFB3 Lee, B.- S.; Nowak, R. A.: Human leiomyoma smooth muscle cellsshow increased 3 B
c
expression of transforming growth factor- beta- 3 (TGF- beta- 3)and altered
responses to the antiproliferative effects of TGF- beta. J.Clin. Endocr.
Metab. 86: 913- 920, 2001.

GAM8554 388 TGFB3 Moren, A.; Ichijo, H.; Miyazono, K.: Molecular cloning and 3 B c
characterizationof the human and porcine transforming growth factor- beta
type IIIreceptors. Biochem. Biophys. Res. Commun. 189: 356- 362, 1992.

GAM8554 388 TGFB3 Proetzel, G.; Pawlowski, S. A.; Wiles, M. V.; Yin, M.; Boivin,G. P.; Howles, 3 B c
P. N.; Ding, J.; Ferguson, M. W. J.; Doetschman, T.: Transforming growth
factor- beta- 3 is required for secondary palatefusion. Nature Genet. 11:
409- 414, 1995.

GAM8554 388 TGFB3 ten Dijke, P.; Geurts van Kessel, A. H. M.; Foulkes, J. G.; LeBeau, M. M.: 3 B c
Transforming growth factor type beta- 3 maps to humanchromosome 14, region
q23- q24. Oncogene 3: 721- 724, 1988.

GAM8554 388 TGFB3 ten Dijke, P.; Hansen, P.; Iwata, K. K.; Pieler, C.; Foulkes, J.G.: 3 B c
Identification of another member of the transforming growth factortype beta
gene family. Proc. Nat. Acad. Sci. 85: 4715- 4719, 1988.

GAM8554 388 UGDH Bontemps, Y.; Maquart, F.- X.; , Wegrowski, Y.: Human UDP- 3 B c
glucosedehydrogenase gene: complete cloning and transcription start mapping.

Biochem.Biophys. Res. Commun. 275: 981- 985, 2000.

GAM8554 388 UGDH Hempel, J.; Perozich, J.; Romovacek, H.; Hinich, A.; Kuo, I.; Feingold,D. S.: UDP- glucose dehydrogenase from bovine liver: primary structureand relationship to other dehydrogenases. Protein Sci. 3: 1074- 1080,1994. 3 B c

GAM8554 388 UGDH Marcu, O.; Stathakis, D. G.; Marsh, J. L.: Assignment of the UGDHlocus encoding UDP- glucose dehydrogenase to human chromosome band4p15.1 by radiation hybrid mapping. Cytogenet. Cell Genet. 86: 244- 245,1999. 3 B c

GAM8554 388 UGDH Spicer, A. P.; Kaback, L. A.; Smith, T. J.; Seldin, M. F.: Molecularcloning and characterization of the human and mouse UDP- glucose dehydrogenasegenes. J. Biol. Chem. 273: 25117- 25124, 1998. 3 B c

GAM8554 388 UGDH Walsh, E. C.; Stainier, D. Y. R.: UDP- glucose dehydrogenase requiredfor cardiac valve formation in zebrafish. Science 293: 1670- 1674,2001. 3 B c

GAM8554 388 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993. 3 B c

GAM8554 388 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997. 3 B c

GAM8554 388 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997. 3 B c

GAM8554 388 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma. Hum. Molec. Genet. 7: 1071- 1082, 1998. 3 B c

GAM8554 388 WHSC1 Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997. 3 B c

GAM8678 347 ADCY1 Abdel- Majid, R. M.; Leong, W. L.; Schalkwyk, L. C.; Smallman, D.S.; Wong, S. T.; Storm, D. R.; Fine, A.; Dobson, M. J.; Guernsey,D. L.; Neumann, P. E.: Loss of adenylyl cyclase I activity disruptspatterning of mouse somatosensory cortex. Nature Genet. 19: 289- 291,1998. 3 C c

GAM8678 347 ADCY1 Edelhoff, S.; Villacres, E. C.; Storm, D. R.; Disteche, C. M.:Mapping of adenylyl cyclase genes type I, II, III, IV, V, and VI inmouse. Mammalian Genome 6: 111- 113, 1995. 3 C c

GAM8678 347 ADCY1 Gaudin, C.; Homcy, C. J.; Ishikawa, Y.: Mammalian adenylyl cyclasefamily members are randomly located on different chromosomes. Hum.Genet. 94: 527- 529, 1994. 3 C c

GAM8678 347 ADCY1 Villacres, E. C.; Xia, Z.; Bookbinder, L. H.; Edelhoff, S.; Disteche,C. M.; Storm, D. R.: Cloning, chromosomal mapping, and expressionof human fetal brain type I adenylyl cyclase. Genomics 16: 473- 478,1993. 3 C c

GAM8678 347 ADCY1 Welker, E.; Armstrong- James, M.; Bronchti, G.; Ourednik, W.; Gheorghita- 3 C c

Baechler,F.; Dubois, R.; Guernsey, D. L.; Van der Loos, H.; Neumann, P. E.: Altered sensory processing in the somatosensory cortex of the mutantmouse barrelless. Science 271: 1864- 1867, 1996.

GAM8678 347 AGXT Bourke, E.; Frindt, G.; Flynn, P.; Schreiner, G. E.: Primary 3 C c
hyperoxaluriawith normal alpha- ketoglutarate:glyoxylate carboligase activity: treatmentwith isocarboxazid. Ann. Intern. Med. 76: 279- 284, 1972.

GAM8678 347 AGXT Danpure, C. J.: Personal Communication. Middlesex, England 6/16/1988. 3 C c

GAM8678 347 AGXT Danpure, C. J.: Primary hyperoxaluria type 1 and peroxisome- to- 3 C c
mitochondrionmistargeting of alanine:glyoxylate aminotransferase. Biochimie 75:309- 315, 1993.

GAM8678 347 AGXT Danpure, C. J.; Jennings, P. R.: Peroxisomal 3 C c
alanine:glyoxylateaminotransferase deficiency in primary hyperoxaluria type I. FEBSLett. 201: 20- 24, 1986.

GAM8678 347 AGXT Danpure, C. J.; Jennings, P. R.; Watts, R. W. E.: Enzymologicaldiagnosis of 3 C c
primary hyperoxaluria type 1 by measurement of hepaticalanine:glyoxylate aminotransferase activity. Lancet I: 289- 291,1987.

GAM8678 347 AGXT Danpure, C. J.; Purdue, P. E.; Fryer, P.; Griffiths, S.; Allsop,J.; Lumb, M. 3 C c
J.; Guttridge, K. M.; Jennings, P. R.; Scheinman, J.I.; Mauer, S. M.; Davidson, N. O.: Enzymological and mutational analysisof a complex primary hyperoxaluria type I phenotype involving alanine:glyoxylateaminotransferase peroxisome- to- mitochondrion mistargeting and intraperoxisomalaggregation. Am. J. Hum. Genet. 53: 417- 432, 1993.

GAM8678 347 AGXT Mori, M.; Oda, T.; Nishiyama, K.; Serikawa, T.; Yamada, J.; Ichiyama,A.: A 3 C c
single serine:pyruvate aminotransferase gene on rat chromosome9q34- q36. Genomics 13: 686- 689, 1992.

GAM8678 347 AGXT Nishiyama, K.; Funai, T.; Katafuchi, R.; Hattori, F.; Onoyama,K.; Ichiyama, 3 C c
A.: Primary hyperoxaluria type I due to a point mutationof T to C in the coding region of the serine:pyruvate aminotransferasegene. Biochem. Biophys. Res. Commun. 176: 1093- 1099, 1991.

GAM8678 347 AGXT Pirulli, D.; Puzzer, D.; Ferri, L.; Crovella, S.; Amoroso, A.;Ferrettini, 3 C c
C.; Marangella, M.; Mazzola, G.; Florian, F.: Molecularanalysis of hyperoxaluria type 1 in Italian patients reveals eightnew mutations in the alanine:glyoxylate aminotransferase gene. Hum.Genet. 104: 523- 525, 1999.

GAM8678 347 AGXT Purdue, P. E.; Allsop, J.; Isaya, G.; Rosenberg, L. E.; Danpure,C. J.: 3 C c
Mistargeting of peroxisomal L- alanine:glyoxylate aminotransferaseto mitochondria in primary hyperoxaluria patients depends upon activationof a cryptic mitochondrial targeting sequence by a point mutation. Proc.Nat. Acad. Sci. 88: 10900- 10904, 1991.

GAM8678 347 AGXT Purdue, P. E.; Lumb, M. J.; Allsop, J.; Minatogawa, Y.; Danpure,C. J.: A 3 C c
glycine- to- glutamate substitution abolishes alanine:glyoxylateaminotransferase catalytic activity in a subset of patients with primaryhyperoxaluria type 1. Genomics 13: 215- 218, 1992.

GAM8678 347 AGXT Purdue, P. E.; Takada, Y.; Danpure, C. J.: Identification ofmutations 3 C c
associated with peroxisome- to- mitochondrion mistargetingof alanine/glyoxylate aminotransferase in primary hyperoxaluria type1. J. Cell Biol. 111: 2341- 2351, 1990.

GAM8678 347 AGXT Takada, Y.; Kaneko, N.; Esumi, H.; Purdue, P. E.; Danpure, C.J.: Human 3 C c
peroxisomal L- alanine:glyoxylate aminotransferase: evolutionaryloss of a mitochondrial targeting signal by point mutation of theinitiation codon. Biochem. J. 268: 517- 520, 1990.

GAM8678 347 AGXT von Schnakenburg, C.; Rumsby, G.: Primary hyperoxaluria type1: a cluster of new mutations in exon 7 of the AGXT gene. J. Med.Genet. 34: 489- 492, 1997. 3 C c

GAM8678 347 AGXT Watts, R. W. E.; Calne, R. Y.; Rolles, K.; Danpure, C. J.; Morgan,S. H.; Mansell, M. A.; Williams, R.; Purkiss, P.: Successful treatmentof primary hyperoxaluria type I by combined hepatic and renal transplantation. Lancet II:474- 475, 1987. 3 C c

GAM8678 347 AMD1 Maric, S. C.; Crozat, A.; Janne, O. A.: Structure and organizationof the human S- adenosylmethionine decarboxylase gene. J. Biol. Chem. 267:18915- 18923, 1992. 3 C c

GAM8678 347 AMD1 Maric, S. C.; Crozat, A.; Louhimo, J.; Knuutila, S.; Janne, O.A.: The human S- adenosylmethionine decarboxylase gene: nucleotidesequence of a pseudogene and chromosomal localization of the activegene (AMD1) and the pseudogene (AMD2). Cytogenet. Cell Genet. 70:195- 199, 1995. 3 C c

GAM8678 347 AMD1 Pulkka, A.; Ihalainen, R.; Suorsa, A.; Riviere, M.; Szpirer, J.;Pajunen, A.: Structures and chromosomal localizations of two ratgenes encoding S- adenosylmethionine decarboxylase. Genomics 16:342- 349, 1993. 3 C c

GAM8678 347 AMD1 Radford, D. M.; Eddy, R.; Haley, L.; Henry, W. M.; Pegg, A. E.;Pajunen, A.; Shows, T. B.: Gene sequences coding for S- adenosylmethioninedecarboxylase are present on human chromosome 6 and the X and arenot amplified in colon neoplasia. Cytogenet. Cell Genet. 49: 285- 288,1989. 3 C c

GAM8678 347 AMD1 Radford, D. M.; Nakai, H.; Pegg, A. E.; Shows, T. B.: Mappinggenes for rate- limiting enzymes in polyamine biosynthesis. (Abstract) Am.J. Hum. Genet. 41: A35 only, 1987. 3 C c

GAM8678 347 ANKTM1 Jaquemar, D.; Schenker, T.; Trueb, B.: An ankyrin- like proteinwith transmembrane domains is specifically lost after oncogenic transformationof human fibroblasts. J. Biol. Chem. 274: 7325- 7333, 1999. 3 C c

GAM8678 347 ANKTM1 Schenker, T.; Trueb, B.: Down- regulated proteins of mesenchymaltumor cells. Exp. Cell Res. 239: 161- 168, 1998. 3 C c

GAM8678 347 BMP1 Amano, S.; Scott, I. C.; Takahara, K.; Koch, M.; Champliaud, M.- F.;Gerecke, D. R.; Keene, D. R.; Hudson, D. L.; Nishiyama, T.; Lee, S.;Greenspan, D. S.; Burgeson, R. E.: Bone morphogenetic protein 1 isan extracellular processing enzyme of the laminin 5 gamma- 2 chain. J.Biol. Chem. 275: 22728- 22735, 2000. 3 C c

GAM8678 347 BMP1 Bond, J. S.; Beynon, R. J.: The astacin family of metalloendopeptidases. ProteinSci. 4: 1247- 1261, 1995. 3 C c

GAM8678 347 BMP1 Ceci, J. D.; Kingsley, D. M.; Silan, C. M.; Copeland, N. G.; Jenkins,N. A.: An interspecific backcross linkage map of the proximal halfof mouse chromosome 14. Genomics 6: 673- 678, 1990. 3 C c

GAM8678 347 BMP1 Kessler, E.; Takahara, K.; Biniaminov, L.; Brusel, M.; Greenspan,D.: Bone morphogenic protein- 1: the type I procollagen C- proteinase. Science 271:360- 362, 1996. 3 C c

GAM8678 347 BMP1 Reddi, A. H.: BMP- 1: resurrection as procollagen C- proteinase. Science 271:5- 6, 1996. 3 C c

GAM8678 347 BMP1 Scott, I. C.; Blitz, I. L.; Pappano, W. N.; Imamura, Y.; Clark,T. G.; Steiglitz, B. M.; Thomas, C. L.; Maas, S. A.; Takahara, K.;Cho, K. W. Y.; Greenspan, D. S.: Mammalian BMP- 1/Tolloid- relatedmetalloproteinases, including novel family member mammalian Tolloid- like2, have differential enzymatic activities and distributions of expressionrelevant to patterning and skeletogenesis. Dev. Biol. 213: 283- 300,1999. 3 C c

GAM8678 347 BMP1 Tabas, J. A.; Zasloff, M.; Wasmuth, J. J.; Emanuel, B. S.; Altherr,M. R.; 3 C c

McPherson, J. D.; Wozney, J. M.; Kaplan, F. S.: Bone morphogeneticprotein: chromosomal localization of human genes for BMP1, BMP2A,and BMP3. Genomics 9: 283- 289, 1991.

GAM8678 347 BMP1 Takahara, K.; Lee, S.; Wood, S.; Greenspan, D. S.: Structuralorganization 3 C c
and genetic localization of the human bone morphogeneticprotein 1/mammalian tolloid gene. Genomics 29: 9- 15, 1995.

GAM8678 347 BMP1 Takahara, K.; Lyons, G. E.; Greenspan, D. S.: Bone morphogeneticprotein- 1 3 C c
and a mammalian tolloid homologue (mTld) are encoded byalternatively spliced transcripts which are differentially expressedin some tissues. J. Biol. Chem. 269: 32572- 32578, 1994.

GAM8678 347 BMP1 Wozney, J. M.; Rosen, V.; Celeste, A. J.; Mitsock, L. M.; Whitters,M. J.; 3 C c
Kriz, R. W.; Hewick, R. M.; Wang, E. A.: Novel regulatorsof bone formation: molecular clones and activities. Science 242:1528- 1534, 1988.

GAM8678 347 BMP1 Yoshiura, K.; Tamura, T.; Hong, H.- S.; Ohta, T.; Soejima, H.;Kishino, T.; 3 C c
Jinno, Y.; Niikawa, N.: Mapping of the bone morphogeneticprotein 1 gene (BMP1) to 8p21: removal of BMP1 from candidacy forthe bone disorder in Langer- Giedion syndrome. Cytogenet. Cell Genet. 64:208- 209, 1993.

GAM8678 347 CARD15 Hampe, J.; Grebe, J.; Nikolaus, S.; Solberg, C.; Croucher, P. J.P.; 3 C c
Mascheretti, S.; Jahnsen, J.; Moum, B.; Klump, B.; Krawczak, M.;Mirza, M. M.; Foelsch, U. R.; Vatn, M.; Schreiber, S.: Associationof NOD2 (CARD 15) genotype with clinical course of Crohn's disease:a cohort study. Lancet 359: 1661- 1665, 2002.

GAM8678 347 CARD15 Hugot, J.- P.; Chamaillard, M.; Zouali, H.; Lesage, S.; Cezard,J.- P.; 3 C c
Belaiche, J.; Almer, S.; Tysk, C.; O'Morain, C. A.; Gassull,M.; Binder, V.; Finkel, Y.; and 8 others: Association of NOD2 leucine- richrepeat variants with susceptibility to Crohn's disease. Nature 411:599- 603, 2001.

GAM8678 347 CARD15 Lesage, S.; Zouali, H.; Cezard, J.- P.; EPWG- IBD Group; Colombel,J.- F.; 3 C c
EPIMAD Group; Belaiche, J.; GETAID Group; Almer, S.; Tysk,C.; O'Morain, C.; Gassull, M.; Binder, V.; Finkel, Y.; Modigliani,R.; Gower- Rousseau, C.; Macry, J.; Merlin, F.; Chamaillard, M.; Jannot,A.- S.; Thomas, G.; Hugot, J.- P.: CARD15/NOD2 mutational analysisand genotype- phenotype correlation in 612 patients with inflammatorybowel disease. Am. J. Hum. Genet. 70: 845- 857, 2002.

GAM8678 347 CARD15 Miceli- Richard, C.; Lesage, S.; Rybojad, M.; Prieur, A.- M.; Manouvrier- 3 C c
Hanu,S.; Hafner, R.; Chamaillard, M.; Zouali, H.; Thomas, G.; Hugot, J.- P.: CARD15 mutations in Blau syndrome. Nature Genet. 29: 19- 20, 2001.

GAM8678 347 CARD15 Murillo, L.; Crusius, J. B. A.; van Bodegraven, A. A.; Alizadeh,B. Z.; Pena, 3 C c
A. S.: CARD15 gene and the classification of Crohn'sdisease. Immunogenetics 54: 59- 61, 2002.

GAM8678 347 CARD15 Ogura, Y.; Bonen, D. K.; Inohara, N.; Nicolae, D. L.; Chen, F.F.; Ramos, R.; 3 C c
Britton, H.; Moran, T.; Karaliuskas, R.; Duerr, R.H.; Achkar, J.- P.; Brant, S. R.; Bayless, T. M.; Kirschner, B. S.;Hanauer, S. B.; Nunez, G.; Cho, J. H.: A frameshift mutation in Nod2associated with susceptibility to Crohn's disease. Nature 411: 603- 606,2001.

GAM8678 347 CARD15 Ogura, Y.; Inohara, N.; Benito, A.; Chen, F. F.; Yamaoka, S.; Nunez,G.: 3 C c
Nod2, a Nod1/Apaf- 1 family member that is restricted to monocytesand activates NF- kappa- B. J. Biol. Chem. 276: 4812- 4818, 2001.

GAM8678 347 CARD15 van Heel, D. A.; McGovern, D. P. B.; Cardon, L. R.; Dechairo, B.M.; Lench, 3 C c
N. J.; Carey, A. H.; Jewell, D. P.: Fine mapping of theIBD1 locus did not identify Crohn disease- associated NOD2 variants:implications for complex

disease genetics. Am. J. Med. Genet. 111:253- 259, 2002.

GAM8678 347 CARD15 Vermeire, S.; Wild, G.; Kocher, K.; Cousineau, J.; Dufresne, L.;Bitton, A.; 3 C c
Langelier, D.; Pare, P.; Lapointe, G.; Cohen, A.; Daly,M. J.; Rioux, J. D.:
CARD15 genetic variation in a Quebec population:prevalence, genotype-
phenotype relationship, and haplotype structure. Am.J. Hum. Genet. 71: 74-
83, 2002.

GAM8678 347 CARD15 Yamazaki, K.; Takazoe, M.; Tanaka, T.; Kazumori, T.; Nakamura,Y.: Absence of 3 C c
mutation in the NOD2/CARD15 gene among 483 Japanesepatients with Crohn's
disease. J. Hum. Genet. 47: 469- 472, 2002.

GAM8678 347 CBR1 Avramopoulos, D.; Cox, T.; Forrest, G. L.; Chakravarti, A.; Antonarakis,S. 3 C c
E.: Linkage mapping of the carbonyl reductase (CBR) gene on humanchromosome
21 using a DNA polymorphism in the 3- prime untranslatedregion. Genomics 13:
447- 448, 1992.

GAM8678 347 CBR1 Forrest, G. L.; Akman, S.; Krutzik, S.; Paxton, R. J.; Sparkes,R. S.; 3 C c
Doroshow, J.; Felsted, R. L.; Glover, C. J.; Mohandas, T.;Bachur, N. R.:
Induction of a human carbonyl reductase gene locatedon chromosome 21.
Biochim. Biophys. Acta 1048: 149- 155, 1990.

GAM8678 347 CBR1 Lemieux, N.; Malfoy, B.; Forrest, G. L.: Human carbonyl reductase(CBR) 3 C c
localized to band 21q22.1 by high- resolution fluorescence insitu
hybridization displays gene dosage effects in trisomy 21 cells. Genomics
15:169- 172, 1993.

GAM8678 347 CBR1 Watanabe, K.; Sugawara, C.; Ono, A.; Fukuzumi, Y.; Itakura, S.;Yamazaki, M.; 3 C c
Tashiro, H.; Osoegawa, K.; Soeda, E.; Nomura, T.: Mappingof a novel human
carbonyl reductase, CBR3, and ribosomal pseudogenesto human chromosome
21q22.2. Genomics 52: 95- 100, 1998.

GAM8678 347 CBR1 Wei, J.; Dlouhy, S. R.; Hara, A.; Ghetti, B.; Hodes, M. E.: Cloninga cDNA 3 C c
for carbonyl reductase (Cbr) from mouse cerebellum: murinegenes that express
Cbr map to chromosomes 16 and 11. Genomics 34:147- 148, 1996.

GAM8678 347 CBR1 Wermuth, B.; Bohren, K. M.; Heinemann, G.; von Wartburg, J.- P.;Gabbay, K. 3 C c
H.: Human carbonyl reductase: nucleotide sequence analysisof a cDNA and
amino acid sequence of the encoded protein. J. Biol.Chem. 263: 16185- 16188,
1988.

GAM8678 347 CEACAM1 Barnett, T.; Zimmermann, W.: Workshop report: proposed nomenclaturefor the 3 C c
carcinoembryonic antigen (CEA) gene family. Tumor Biol. 11:59- 63, 1990.

GAM8678 347 CEACAM1 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, 3 C c
F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.;
Lucka, L.; and 13 others: Redefined nomenclaturefor members of the
carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999.

GAM8678 347 CEACAM1 Boulton, I. C.; Gray- Owen, S. D.: Neisserial binding to CEACAM1arrests the 3 C c
activation and proliferation of CD4+ T lymphocytes. NatureImmun. 3: 229-
236, 2002.

GAM8678 347 CEACAM1 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. 3 C c
W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances
among members of the carcinoembryonic antigen (CEA) genefamily determined by
fluorescence in situ hybridization. Genomics 12:773- 779, 1992.

GAM8678 347 CEACAM1 Ergun, S.; Kilic, N.; Ziegeler, G.; Hansen, A.; Nollau, P.; Gotze,J.; 3 C c
Wurmbach, J.- H.; Horst, A.; Weil, J.; Fernando, M.; Wagener, C.: CEA-
related cell adhesion molecule 1: a potent angiogenic factorand a major

effector of vascular endothelial growth factor. Molec.Cell 5: 311- 320, 2000.

GAM8678 347 CEACAM1 Hinoda, Y.; Neumaier, M.; Hefta, S. A.; Drzeniek, Z.; Wagener,C.; Shively, L.; Hefta, L. J. F.; Shively, J. E.; Paxton, R. J.:Molecular cloning of a cDNA coding biliary glycoprotein I: primarystructure of a glycoprotein immunologically crossreactive with carcinoembryonicantigen. Proc. Nat. Acad. Sci. 85: 6959- 6963, 1988. 3 C c

GAM8678 347 CEACAM1 Neumaier, M.; Paululat, S.; Chan, A.; Matthaes, P.; Wagener, C.: Biliary glycoprotein, a potential human cell adhesion molecule,is down- regulated in colorectal carcinomas. Proc. Nat. Acad. Sci. 90:10744- 10748, 1993. 3 C c

GAM8678 347 CEACAM1 Olsen, A.; Teglund, S.; Nelson, D.; Gordon, L.; Copeland, A.; Georgescu,A.; Carrano, A.; Hammarstrom, S.: Gene organization of the pregnancy-specificglycoprotein region on human chromosome 19: assembly and analysisof a 700- kb cosmid contig spanning the region. Genomics 23: 659- 668,1994. 3 C c

GAM8678 347 CEACAM1 Poy, M. N.; Yang, Y.; Rezaei, K.; Fernstrom, M. A.; Lee, A. D.;Kido, Y.; Erickson, S. K.; Najjar, S. M.: CEACAM1 regulates insulinclearance in liver. Nature Genet. 30: 270- 276, 2002. 3 C c

GAM8678 347 CEACAM1 Robbins, J.; Robbins, P. F.; Kozak, C. A.; Callahan, R.: Themouse biliary glycoprotein gene (Bgp): partial nucleotide sequence,expression, and chromosomal assignment. Genomics 10: 583- 587, 1991. 3 C c

GAM8678 347 CEACAM1 Schlossman, S. F.; Boumsell, L.; Gilks, W.; Harlan, J. M.; Kishimoto,T.; Morimoto, C.; Ritz, J.; Shaw, S.; Silverstein, R. L.; Springer,T. A.; Tedder, T. F.; Todd, R. F.: CD antigens 1993. Immun. Today 15:98- 99, 1994. 3 C c

GAM8678 347 CEACAM1 Teglund, S.; Olsen, A.; Khan, W. N.; Frangsmyr, L.; Hammarstrom,S.: The pregnancy- specific glycoprotein (PSG) gene cluster on humanchromosome 19: fine structure of the 11 PSG genes and identificationof 6 new genes forming a third subgroup within the carcinoembryonicantigen (CEA) family. Genomics 23: 669- 684, 1994. 3 C c

GAM8678 347 CEACAM1 Thompson, J. A.; Grunert, F.; Zimmermann, W.: Carcinoembryonicantigen gene family: molecular biology and clinical perspectives. J.Clin. Lab. Anal. 5: 344- 366, 1991. 3 C c

GAM8678 347 CEACAM1 Thompson, J.; Koumari, R.; Wagner, K.; Barnert, S.; Schleussner,C.; Schrewe, H.; Zimmermann, W.; Muller, G.; Schempp, W.; Zaninetta,D.; Ammaturo, D.; Hardman, N.: The human pregnancy- specific glycoproteingenes are tightly linked on the long arm of chromosome 19 and arecoordinately expressed. Biochem. Biophys. Res. Commun. 167: 848- 859,1990. 3 C c

GAM8678 347 CEACAM1 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades-Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan, K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772, 1992. 3 C c

GAM8678 347 CEACAM1 Trask, B.; Fertitta, A.; Christensen, M.; Youngblom, J.; Bergmann,A.; Copeland, A.; de Jong, P.; Mohrenweiser, H.; Olsen, A.; Carrano,A.; Tynan, K.: Fluorescence in situ hybridization mapping of humanchromosome 19: cytogenetic band location of 540 cosmids and 70 genesor DNA markers. Genomics 15: 133- 145, 1993. 3 C c

GAM8678 347 CEACAM1 Tynan, K.; Olsen, A.; Trask, B.; de Jong, P.; Thompson, J.; Zimmermann,W.; 3 C c

Carrano, A.; Mohrenweiser, H.: Assembly and analysis of cosmidcontigs in the CEA- gene family region of human chromosome 19. NucleicAcids Res. 20: 1629-1636, 1992.

GAM8678 347 CEACAM5 Beauchemin, N.; Draber, P.; Dveksler, G.; Gold, P.; Gray- Owen,S.; Grunert, F.; Hammarstrom, S.; Holmes, K. V.; Karlsson, A.; Kuroki,M.; Lin, S.- H.; Lucka, L.; and 13 others: Redefined nomenclaturefor members of the carcinoembryonic antigen family. Exp. Cell Res. 252:243- 249, 1999. 3 C c

GAM8678 347 CEACAM5 Brandriff, B. F.; Gordon, L. A.; Tynan, K. T.; Olsen, A. S.; Mohrenweiser,H. W.; Fertitta, A.; Carrano, A. V.; Trask, B. J.: Order and genomicdistances among members of the carcinoembryonic antigen (CEA) genefamily determined by fluorescence in situ hybridization. Genomics 12:773- 779, 1992. 3 C c

GAM8678 347 CEACAM5 Gold, P.; Freedman, S. O.: Demonstration of tumor- specific antigensin human colonic carcinomata by immunological tolerance and absorptiontechniques. J. Exp. Med. 121: 439- 462, 1965. 3 C c

GAM8678 347 CEACAM5 Kamarck, M. E.; Elting, J. J.; Hart, J. T.; Goebel, S. J.; Rae,P. M. M.; Nothdurft, M. A.; Nedwin, J. J.; Barnett, T. R.: Carcinoembryonicantigen family: expression in a mouse L- cell transfectant and characterizationof a partial cDNA in bacteriophage lambda- gt11. Proc. Nat. Acad.Sci. 84: 5350-5354, 1987. 3 C c

GAM8678 347 CEACAM5 Nishi, M.; Inazawa, J.; Inoue, K.; Nakagawa, H.; Taniwaki, M.;Misawa, S.; Oikawa, S.; Nakazato, H.; Abe, T.: Regional chromosomalassignment of carcinoembryonic antigen gene (CEA) to chromosome 19at band q13.2. Cancer Genet. Cytogenet. 54: 77- 81, 1991. 3 C c

GAM8678 347 CEACAM5 Oikawa, S.; Nakazato, H.; Kosaki, G.: Primary structure of humancarcinoembryonic antigen (CEA) deduced from cDNA sequence. Biochem.Biophys. Res. Commun. 142: 511- 528, 1987. 3 C c

GAM8678 347 CEACAM5 Thompson, J. A.; Pande, H.; Paxton, R. J.; Shively, L.; Padma,A.; Simmer, R. L.; Todd, C. W.; Riggs, A. D.; Shively, J. E.: Molecularcloning of a gene belonging to the carcinoembryonic antigen gene familyand discussion of a domain model. Proc. Nat. Acad. Sci. 84: 2965- 2969,1987. 3 C c

GAM8678 347 CEACAM5 Thompson, J.; Zimmermann, W.: The carcinoembryonic antigen genefamily: structure, expression and evolution. Tumor Biol. 9: 63- 83,1988. 3 C c

GAM8678 347 CEACAM5 Thompson, J.; Zimmermann, W.; Osthus- Bugat, P.; Schleussner, C.;Eades-Perner, A.- M.; Barnert, S.; von Kleist, S.; Willcocks, T.; Craig,I.; Tynan, K.; Olsen, A.; Mohrenweiser, H.: Long- range chromosomalmapping of the carcinoembryonic antigen (CEA) gene family cluster. Genomics 12:761- 772, 1992. 3 C c

GAM8678 347 CEACAM5 Willcocks, T. C.; Craig, I. W.: Characterization of the genomicorganization of human carcinoembryonic antigen (CEA): comparison withother family members and sequence analysis of 5- prime controllingregion. Genomics 8: 492- 500, 1990. 3 C c

GAM8678 347 CEACAM5 Willcocks, T. C.; Craig, S. P.; Coates, D.; Craig, I. W.: Codingsequences for carcinoembryonic antigen (CEA) assigned to human chromosome19q13. (Abstract) Cytogenet. Cell Genet. 46: 716 only, 1987. 3 C c

GAM8678 347 CEACAM5 Willcocks, T. C.; Craig, S. P.; Craig, I. W.: Assignment of thecoding sequence for carcinoembryonic antigen (CEA) and normal cross-reactingantigen (NCA) to human chromosome 19q13. Ann. Hum. Genet. 53: 141- 3 C c

148,1989.

GAM8678 347 CEACAM5 Zimmer, R.; Thomas, P.: Mutations in the carcinoembroyonic antigengene in 3 C c colorectal cancer patients: implications on liver metastasis. CancerRes. 61: 2822- 2826, 2001.

GAM8678 347 CEACAM5 Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.: Isolationand 3 C c characterization of cDNA clones encoding the human carcinoembryonicantigen reveal a highly conserved repeating structure. Proc. Nat.Acad. Sci. 84: 2960- 2964, 1987.

GAM8678 347 CEACAM5 Zimmermann, W.; Weber, B.; Ortlieb, B.; Rudert, F.; Schempp, W.;Fiebig, H.- 3 C c H.; Shively, J. E.; von Kleist, S.; Thompson, J. A.: Chromosomallocalization of the carcinoembryonic antigen gene family and differentialexpression in various tumors. Cancer Res. 48: 2550- 2554, 1988.

GAM8678 347 CHST5 Akama, T. O.; Nishida, K.; Nakayama, J.; Watanabe, H.; Ozaki, K.;Nakamura, 3 C c T.; Dota, A.; Kawasaki, S.; Inoue, Y.; Maeda, N.; Yamamoto,S.; Fujiwara, T.; Thonar, E. J.- M. A.; Shimomura, Y.; Kinoshita, S.;Tanigami, A.; Fukuda, M. N.: Macular corneal dystrophy type I andtype II are caused by distinct mutations in a new sulphotransferasegene. Nature Genet. 26: 237- 241, 2000.

GAM8678 347 CHST5 Lee, J. K.; Bhakta, S.; Rosen, S. D.; Hemmerich, S.: Cloning 3 C c andcharacterization of a mammalian N- acetylglucosamine- 6- sulfotransferasethat is highly restricted to intestinal tissue. Biochem. Biophys.Res. Commun. 263: 543- 549, 1999.

GAM8678 347 CYP4B1 Imaoka, S.; Yoneda, Y.; Sugimoto, T.; Hiroi, T.; Yamamoto, K.;Nakatani, T.; 3 C c Funae, Y.: CYP4B1 is a possible risk factor for bladdercancer in humans. Biochem. Biophys. Res. Commun. 277: 776- 780, 2000.

GAM8678 347 CYP4B1 Nhamburo, P. T.; Gonzalez, F. J.; McBride, O. W.; Gelboin, H. V.;Kimura, S.: 3 C c Identification of a new P450 expressed in human lung:complete cDNA sequence, cDNA- directed expression, and chromosome mapping. Biochemistry 28:8060- 8066, 1989.

GAM8678 347 CYP4B1 Thum, T.; Borlak, J.: Gene expression in distinct regions of theheart. 3 C c Lancet 355: 979- 983, 2000.

GAM8678 347 DTNA Ambrose, H. J.; Blake, D. J.; Nawrotzki, R. A.; Davies, K. E.:Genomic 3 C c organization of the mouse dystrobrevin gene: comparative analysiswith the dystrophin gene. Genomics 39: 359- 369, 1997.

GAM8678 347 DTNA Blake, D. J.; Nawrotzki, R.; Loh, N. Y.; Gorecki, D. C.; Davies,K. E.: Beta- 3 C c dystrobrevin, a member of the dystrophin- related proteinfamily. Proc. Nat. Acad. Sci. 95: 241- 246, 1998.

GAM8678 347 DTNA Ichida, F.; Tsubata, S.; Bowles, K. R.; Haneda, N.; Uese, K.; Miyawaki,T.; 3 C c Dreyer, W. J.; Messina, J.; Li, H.; Bowles, N. E.; Towbin, J.A.: Novel gene mutations in patients with left ventricular noncompactionor Barth syndrome. Circulation 103: 1256- 1263, 2001.

GAM8678 347 DTNA Khurana, T. S.; Engle, E. C.; Bennett, R. R.; Silverman, G. A.;Selig, S.; 3 C c Bruns, G. A. P.; Kunkel, L. M.: (CA) repeat polymorphismin the chromosome 18 encoded dystrophin- like protein. Hum. Molec.Genet. 3: 841 only, 1994.

GAM8678 347 DTNA Metzinger, L.; Blake, D. J.; Squier, M. V.; Anderson, L. V. B.;Deconinck, A. 3 C c E.; Nawrotzki, R.; Hilton- Jones, D.; Davies, K. E.:Dystrobrevin deficiency at the sarcolemma of patients with musculardystrophy. Hum. Molec. Genet. 6: 1185- 1191, 1997.

GAM8678 347 DTNA Sadoulet- Puccio, H. M.; Feener, C. A.; Schaid, D. J.; Thibodeau,S. N.; 3 C c Michels, V. V.; Kunkel, L. M.: The genomic organization ofhuman

dystrobrevin. Neurogenetics 1: 37- 42, 1997.

GAM8678 347 DTNA Sadoulet- Puccio, H. M.; Khurana, T. S.; Cohen, J. B.; Kunkel, L.M.: Cloning and characterization of the human homologue of a dystrophinrelated phosphoprotein found at the Torpedo electric organ post- synapticmembrane. Hum. Molec. Genet. 5: 489- 496, 1996. 3 C c

GAM8678 347 DTNA Yoshida, M.; Hama, H.; Ishikawa- Sakurai, M.; Imamura, M.; Mizuno,Y.; Araishi, K.; Wakabayashi- Takai, E.; Noguchi, S.; Sasaoka, T.;Ozawa, E.: Biochemical evidence for association of dystrobrevin withthe sarcoglycan-sarcospan complex as a basis for understanding sarcoglycanopathy. Hum.Molec. Genet. 9: 1033- 1040, 2000. 3 C c

GAM8678 347 EP300 Arany, Z.; Newsome, D.; Oldread, E.; Livingston, D. M.; Eckner,R.: A family of transcriptional adaptor proteins targeted by theE1A oncoprotein. Nature 374: 81- 84, 1995. 3 C c

GAM8678 347 EP300 Arany, Z.; Sellers, W. R.; Livingston, D. M.; Eckner, R.: E1A-associatedp300 and CREB- associated CBP belong to a conserved family of coactivators.(Letter) Cell 77: 799- 800, 1994. 3 C c

GAM8678 347 EP300 Eckner, R.; Ewen, M. E.; Newsome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence, J. B.; Livingston, D. M.: Molecular cloning and functionalanalysis of the adenovirus E1A- associated 300- kD protein (p300) revealsa protein with properties of a transcriptional adaptor. Genes Dev. 15:869- 884, 1994. 3 C c

GAM8678 347 EP300 Gayther, S. A.; Batley, S. J.; Linger, L.; Bannister, A.; Thorpe,K.; Chin, S.- F.; Daigo, Y.; Russell, P.; Wilson, A.; Sowter, H. M.;Delhanty, J. D. A.; Ponder, B. A. J.; Kouzarides, T.; Caldas, C.:Mutations truncating the EP300 acetylase in human cancers. NatureGenet. 24: 300- 303, 2000. 3 C c

GAM8678 347 EP300 Hasan, S.; Hassa, P. O.; Imhof, R.; Hottiger, M. O.: Transcriptioncoactivator p300 binds PCNA and may have a role in DNA repair synthesis. Nature 410:387- 391, 2001. 3 C c

GAM8678 347 EP300 Hasan, S.; Stucki, M.; Hassa, P. O.; Imhof, R.; Gehrig, P.; Hunziker,P.; Hubscher, U.; Hottiger, M. O.: Regulation of human flap endonuclease-1activity by acetylation through the transcriptional coactivator p300. Molec.Cell 7: 1221- 1231, 2001. 3 C c

GAM8678 347 EP300 Ida, K.; Kitabayashi, I.; Taki, T.; Taniwaki, M.; Noro, K.; Yamamoto,M.; Ohki, M.; Hayashi, Y.: Adenoviral E1A- associated protein p300is involved in acute myeloid leukemia with t(11;22)(q23;q13). Blood 90:4699- 4704, 1997. 3 C c

GAM8678 347 EP300 Lin, C. H.; Hare, B. J.; Wagner, G.; Harrison, S. C.; Maniatis,T.; Fraenkel, E.: A small domain of CBP/p300 binds diverse proteins:solution structure and functional studies. Molec. Cell 8: 581- 590,2001. 3 C c

GAM8678 347 EP300 Muraoka, M.; Konishi, M.; Kikuchi- Yanoshita, R.; Tanaka, K.; Shitara,N.; Chong, J.- M.; Iwama, T.; Miyaki, M.: p300 gene alterations incolorectal and gastric carcinomas. Oncogene 12: 1565- 1569, 1996. 3 C c

GAM8678 347 EP300 Nakashima, K.; Yanagisawa, M.; Arakawa, H.; Kimura, N.; Hisatsune,T.; Kawabata, M.; Miyazono, K.; Taga, T.: Synergistic signaling infetal brain by STAT3- Smad1 complex bridged by p300. Science 284:479- 482, 1999. 3 C c

GAM8678 347 EP300 Tini, M.; Benecke, A.; Um, S.- J.; Torchia, J.; Evans, R. M.; Chambon,P.: Association of CBP/p300 acetylase and thymine DNA glycosylaselinks DNA repair and transcription. Molec. Cell 9: 265- 277, 2002. 3 C c

GAM8678 347 EP300 Weaver, B. K.; Kumar, K. P.; Reich, N. C.: Interferon regulatoryfactor 3 and CREB- binding protein/p300 are subunits of double- strandedRNA- activated transcription factor DRAF1. Molec. Cell. Biol. 18:1359- 1368, 1998. 3 C c

GAM8678 347 EP300 Yao, T. P.; Oh, S. P.; Fuchs, M.; Zhou, N.- D.; Ch'ng, L.- E.; Newsome,D.; 3 C c

Bronson, R. T.; Li, E.; Livingston, D. M.; Eckner, R.: Gene dosage-dependentembryonic development and proliferation defects in mice lacking thetranscriptional integrator p300. Cell 93: 361- 372, 1998.

GAM8678 347 FTH1 Boyd, D.; Jain, S. K.; Crampton, J.; Barrett, K. J.; Drysdale,J.: Isolation 3 C c and characterization of a cDNA clone for human ferritinheavy chain. Proc. Nat. Acad. Sci. 81: 4751- 4755, 1984.

GAM8678 347 FTH1 Caskey, J. H.; Jones, C.; Miller, Y. E.; Seligman, P. A.: Humanferritin gene 3 C c is assigned to chromosome 19. Proc. Nat. Acad. Sci. 80:482- 486, 1983.

GAM8678 347 FTH1 Costanzo, F.; Colombo, M.; Staempfli, S.; Santoro, C.; Marone,M.; Frank, R.; 3 C c Delius, H.; Cortese, R.: Structure of gene and pseudogenesof human apoferritin H. Nucleic Acids Res. 14: 721- 736, 1986.

GAM8678 347 FTH1 Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.;Forbes, S. A.; 3 C c Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B.T.; Farnebo, F.; Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud,S.; Zhang, C. X.; Salandre, J.; Calender, A.: Definition of the minimalMEN1 candidate area based on a 5-Mb integrated map of proximal 11q13. Genomics 37:354- 365, 1996.

GAM8678 347 FTH1 Cragg, S. J.; Drysdale, J.; Worwood, M.: Genes for the 'H' subunitof human 3 C c ferritin are present on a number of human chromosomes. Hum.Genet. 71: 108-112, 1985.

GAM8678 347 FTH1 Eisenstein, R. S.: Iron regulatory proteins and the molecularcontrol of 3 C c mammalian iron metabolism. Annu. Rev. Nutr. 20: 627- 662,2000.

GAM8678 347 FTH1 Ferreira, C.; Bucchini, D.; Martin, M.- E.; Levi, S.; Arosio, P.;Grandchamp, 3 C c B.; Beaumont, C.: Early embryonic lethality of H ferritingene deletion in mice. J. Biol. Chem. 275: 3021- 3024, 2000.

GAM8678 347 FTH1 Ferreira, C.; Santambrogio, P.; Martin, M.- E.; Andrieu, V.; Feldmann,G.; 3 C c Henin, D.; Beaumont, C.: H ferritin knockout mice: a model ofhyperferritinemia in the absence of iron overload. Blood 98: 525-532,2001.

GAM8678 347 FTH1 Gailani, M. R.; Petty, E. M.; Horsthemke, B.; Arnold, A.; Marx,S. J.; Bale, 3 C c A. E.: Physical mapping of chromosome 11q12- 13 by pulsedfield gel electrophoresis (PFGE). (Abstract) Cytogenet. Cell Genet. 58:1959 only, 1991.

GAM8678 347 FTH1 Gatti, R. A.; Shaked, R.; Mohandas, T. K.; Salser, W.: Humanferritin genes: 3 C c chromosomal assignments and polymorphisms. Am. J.Hum. Genet. 41: 654- 667, 1987.

GAM8678 347 FTH1 Harrison, P. M.; Arosio, P.: The ferritins: molecular properties,iron 3 C c storage function and cellular regulation. Biochim. Biophys.Acta 1275: 161-203, 1996.

GAM8678 347 FTH1 Hentze, M. W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi,W.; Drysdale, 3 C c J.; Leonard, W. J.; Harford, J. B.; Klausner, R. D.: Cloning, characterization, expression, and chromosomal localizationof a human ferritin heavy- chain gene. Proc. Nat. Acad. Sci. 83:7226- 7230, 1986.

GAM8678 347 FTH1 Kato, J.; Fujikawa, K.; Kanda, M.; Fukuda, N.; Sasaki, K.; Takayama,T.; 3 C c Kobune, M.; Takada, K.; Takimoto, R.; Hamada, H.; Ikeda, T.; Niitsu,Y.: A mutation, in the iron- responsive element of H ferritin mRNA,causing autosomal dominant iron overload. Am. J. Hum. Genet. 69:191- 197, 2001.

GAM8678 347 FTH1 Leibold, E. A.; Munro, H. N.: Cytoplasmic protein binds in vitroto a highly 3 C c conserved sequence in the 5- prime untranslated regionof ferritin heavy- and light- subunit mRNAs. Proc. Nat. Acad. Sci. 85:2171- 2175, 1988.

GAM8678 347 FTH1 McGill, J. R.; Boyd, D.; Barrett, K. J.; Drysdale, J. W.; Moore,C. M.: 3 C c

Localization of human ferritin H (heavy) and L (light) subunitsby in situ hybridization. (Abstract) Am. J. Hum. Genet. 36: 146Sonly, 1984.

GAM8678 347 FTH1 Murray, M. T.; White, K.; Munro, H. N.: Conservation of ferritinheavy 3 C c
subunit gene structure: implications for the regulation of ferritingene expression. Proc. Nat. Acad. Sci. 84: 7438- 7442, 1987.

GAM8678 347 FTH1 Papadopoulos, P.; Bhavsar, D.; Zappone, E.; David, V.; Jones,C.; Worwood, 3 C c
M.; Drysdale, J.: A second human ferritin H locus onchromosome 11. Cytogenet. Cell Genet. 61: 107- 108, 1992.

GAM8678 347 FTH1 Richard, C. W.; Withers, D. A.; Meeker, T. C.; Myers, R. M.:A radiation 3 C c
hybrid map of the proximal long arm of human chromosome11 containing the MEN- 1 and bcl- 1 disease locus. (Abstract) Cytogenet.Cell Genet. 58: 1970 only, 1991.

GAM8678 347 FTH1 Worwood, M.; Brook, J. D.; Cragg, S. J.; Hellkuhl, B.; Jones,B. M.; Perera, 3 C c
P.; Roberts, S. H.; Shaw, D. J.: Assignment of humanferritin genes to chromosomes 11 and 19q13.3- 19qter. Hum. Genet. 69:371- 374, 1985.

GAM8678 347 FTH1 Wu, K.- J.; Polack, A.; Dalla- Favera, R.: Coordinated regulationof iron- 3 C c
controlling genes, H- ferritin and IRP2, by c- MYC. Science 283:676- 679, 1999.

GAM8678 347 FTH1 Yachou, A.- K.; Renaudie, F.; Guenet, J.- L.; Simon- Chazottes, D.;Jones, 3 C c
R.; Grandchamp, B.; Beaumont, C.: Mouse ferritin H multigenefamily is polymorphic and contains a single multiallelic functionalgene located on chromosome 19. Genomics 10: 531- 538, 1991.

GAM8678 347 FTH1 Yachou, A.; Mattei, M. G.; Roeckel, N.; Grandchamp, B.; Beaumont,C.: Mouse 3 C c
ferritin H sequences map to chromosomes 3, 6, and 19. Genomics 9:204- 206, 1991.

GAM8678 347 FTH1 Youssoufian, H.; Chance, P.; Tuck- Muller, C. M.; Jabs, E. W.:Association of 3 C c
a new chromosomal deletion [del(1)(q32q42)] with diaphragmatichernia: assignment of a human ferritin gene. Hum. Genet. 78: 267- 270,1988.

GAM8678 347 GGT1 Bulle, F.; Mattei, M. G.; Siegrist, S.; Pawlak, A.; Passage, E.;Chobert, M. 3 C c
N.; Laperche, Y.; Guellaen, G.: Assignment of the humangamma- glutamyl transferase gene to the long arm of chromosome 22. Hum.Genet. 76: 283- 286, 1987.

GAM8678 347 GGT1 Figlewicz, D. A.; Delattre, O.; Guellaen, G.; Krizus, A.; Thomas,G.; Zucman, 3 C c
J.; Rouleau, G. A.: Mapping of human gamma- glutamyl transpeptidasegenes on chromosome 22 and other human autosomes. Genomics 17: 299- 305,1993.

GAM8678 347 GGT1 Hammond, J. W.; Potter, M.; Wilcken, B.; Truscott, R.: Siblingswith gamma- 3 C c
glutamyltransferase deficiency. J. Inherit. Metab. Dis. 18:82- 83, 1995.

GAM8678 347 GGT1 Heisterkamp, N.; Groffen, J.: Duplication of the bcr and gamma- 3 C c
glutamyltranspeptidase genes. Nucleic Acids Res. 16: 8045- 8056, 1988.

GAM8678 347 GGT1 Laperche, Y.; Bulle, F.; Aissani, T.; Chobert, M. N.; Aggerbeck,M.; Hanoune, 3 C c
J.; Guellaen, G.: Molecular cloning and nucleotide sequenceof rat kidney gamma- glutamyl transpeptidase cDNA. Proc. Nat. Acad.Sci. 83: 937- 941, 1986.

GAM8678 347 GGT1 O'Daley, S.: An abnormal sulphydryl compound in urine. (Abstract) IrishJ. 3 C c
Med. Sci. 7: 578- 579, 1968.

GAM8678 347 GGT1 Pawlak, A.; Lahuna, O.; Bulle, F.; Suzuki, A.; Ferry, N.; Siegrist,S.; 3 C c
Chikhi, N.; Chobert, M. N.; Guellaen, G.; Laperche, Y.: Gamma-glutamyltranspeptidase: a single copy gene in the rat and a multigene familyin the human genome. J. Biol. Chem. 263: 9913- 9916, 1988.

GAM8678 347 GGT1 Pawlak, A.; Wu, S.- J.; Bulle, F.; Suzuki, A.; Chikhi, N.; Ferry,N.; Baik, 3 C c

J.- H.; Siegrist, S.; Guellaen, G.: Different gamma- glutamyltranspeptidase mRNAs are expressed in human liver and kidney. Biochem.Biophys. Res. Commun. 164: 912- 918, 1989.

GAM8678 347 GGT1 Rajpert- De Meyts, E.; Heisterkamp, N.; Groffen, J.: Cloning andnucleotide 3 C c
sequence of human gamma- glutamyl transpeptidase. Proc.Nat. Acad. Sci. 85: 8840- 8844, 1988.

GAM8678 347 GGT1 Rouleau, G. A.; Bazanowski, A.; Cohen, E. H.; Guellaen, G.; Gusella,J. F.: 3 C c
Gamma- glutamyl transferase locus (GGT) displays a PvuII polymorphism. NucleicAcids Res. 16: 11848 only, 1988.

GAM8678 347 GGT1 Sakamuro, D.; Yamazoe, M.; Matsuda, Y.; Kangawa, K.; Taniguchi,N.; Matsuo, 3 C c
H.; Yoshikawa, H.; Ogasawara, N.: The primary structureof human gamma- glutamyl transpeptidase. Gene 73: 1- 9, 1988.

GAM8678 347 GGT1 Schulman, J. D.; Goodman, S. I.; Mace, J. W.; Patrick, A. D.;Tietze, F.; 3 C c
Butler, E. J.: Glutathionuria: inborn error of metabolismdue to tissue deficiency of gamma- glutamyl transpeptidase. Biochem.Biophys. Res. Commun. 65: 68- 74, 1975.

GAM8678 347 GNAI2 Blatt, C.; Eversole- Cire, P.; Cohn, V. H.; Zollman, S.; Fournier,R. E. K.; 3 C c
Mohandas, L. T.; Nesbitt, M.; Lugo, T.; Jones, D. T.; Reed,R. R.; Weiner, L. P.; Sparkes, R. S.; Simon, M. I.: Chromosomal localizationof genes encoding guanine nucleotide- binding protein subunits in mouseand human. Proc. Nat. Acad. Sci. 85: 7642- 7646, 1988.

GAM8678 347 GNAI2 Hermouet, S.; Merendino, J. J., Jr.; Gutkind, J. S.; Spiegel, A.M.: 3 C c
Activating and inactivating mutations of the alpha subunit ofG(i2) protein have opposite effects on proliferation of NIH 3T3 cells. Proc.Nat. Acad. Sci. 88: 10455- 10459, 1991.

GAM8678 347 GNAI2 Itoh, H.; Toyama, R.; Kozasa, T.; Tsukamoto, T.; Matsuoka, M.;Kaziro, Y.: 3 C c
Presence of three distinct molecular species of G(i)protein alpha subunit: structure of rat cDNAs and human genomic DNAs. J.Biol. Chem. 263: 6656- 6664, 1988.

GAM8678 347 GNAI2 Lerman, B. B.; Dong, B.; Stein, K. M.; Markowitz, S. M.; Linden,J.; 3 C c
Catanzaro, D. F.: Right ventricular outflow tract tachycardiadue to a somatic cell mutation in G protein subunit- alpha- i2. J.Clin. Invest. 101: 2862- 2868, 1998.

GAM8678 347 GNAI2 Lyons, J.; Landis, C. A.; Harsh, G.; Vallar, L.; Grunewald, K.;Feichtinger, 3 C c
H.; Duh, Q.- Y.; Clark, O. H.; Kawasaki, E.; Bourne, H.R.; McCormick, F.: Two G protein oncogenes in human endocrine tumors. Science 249:655- 659, 1990.

GAM8678 347 GNAI2 Magovcevic, I.; Ang, S.- L.; Seidman, J. G.; Tolman, C. J.; Neer,E. J.; 3 C c
Morton, C. C.: Regional localization of the human G proteinalpha(i2) (GNAI2) gene: assignment to 3p21 and a related sequence(GNAI2L) to 12p12- p13. Genomics 12: 125- 129, 1992.

GAM8678 347 GNAI2 Rudolph, U.; Finegold, M. J.; Rich, S. S.; Harriman, G. R.; Srinivasan,Y.; 3 C c
Brabet, P.; Boulay, G.; Bradley, A.; Birnbaumer, L.: Ulcerativecolitis and adenocarcinoma of the colon in G alpha(i2)- deficient mice. NatureGenet. 10: 143- 150, 1995.

GAM8678 347 GNAI2 Sparkes, R. S.; Cohn, V. H.; Cire- Eversole, P.; Blatt, C.; Amatruda,T. T.; 3 C c
Weiner, L. P.; Nesbitt, M.; Reed, R. R.; Lochrie, M. A.; Fournier,R. E. K.; Simon, M. I.: Mapping of genes encoding the subunits ofguanine nucleotide- binding proteins (G- proteins) in the mouse. (Abstract) Cytogenet.Cell Genet. 46: 696 only, 1987.

GAM8678 347 GNAI2 Sparkes, R. S.; Cohn, V. H.; Mohandas, T.; Zollman, S.; Cire- Eversole,P.; 3 C c
Amatruda, T. T.; Reed, R. R.; Lochrie, M. A.; Simon, M. I.: Mappingof genes
encoding the subunits of guanine nucleotide- binding protein(G- proteins) in
humans. (Abstract) Cytogenet. Cell Genet. 46: 696only, 1987.

GAM8678 347 GNAI2 Wilkie, T. M.; Gilbert, D. J.; Olsen, A. S.; Chen, X.- N.; Amatruda,T. T.; 3 C c
Korenberg, J. R.; Trask, B. J.; de Jong, P.; Reed, R. R.; Simon,M. I.;
Jenkins, N. A.; Copeland, N. G.: Evolution of the mammalianG protein alpha
subunit multigene family. Nature Genet. 1: 85- 91,1992.

GAM8678 347 GNAI2 Williamson, E. A.; Ince, P. G.; Harrison, D.; Kendall- Taylor,P.; Harris, P. 3 C c
E.: G- protein mutations in human pituitary adrenocorticotrophichormone-
secreting adenomas. Europ. J. Clin. Invest. 25: 128- 131,1995.

GAM8678 347 GPR86 Communi, D.; Gonzalez, N. S.; Detheux, M.; Brezillon, S.; Lannoy,V.; 3 C c
Parmentier, M.; Boeynaems, J.- M.: Identification of a novel humanADP
receptor coupled to G(i). J. Biol. Chem. 276: 41479- 41485, 2001.

GAM8678 347 GPR86 Lee, D. K.; Nguyen, T.; Lynch, K. R.; Cheng, R.; Vanti, W. B.;Arkhitko, O.; 3 C c
Lewis, T.; Evans, J. F.; George, S. R.; O'Dowd, B. F.: Discovery and mapping
of ten novel G protein- coupled receptor genes. Gene 275:83- 91, 2001.

GAM8678 347 GPR86 Wittenberger, T.; Schaller, H. C.; Hellebrand, S.: An expressedsequence tag 3 C c
(EST) data mining strategy succeeding in the discoveryof new G- protein
coupled receptors. J. Molec. Biol. 307: 799- 813,2001.

GAM8678 347 ITK Cheng, G.; Ye, Z.- S.; Baltimore, D.: Binding of Bruton's tyrosinekinase to 3 C c
Fyn, Lyn, or Hck through a Src homology 3 domain- mediatedinteraction. Proc.
Nat. Acad. Sci. 91: 8152- 8155, 1994.

GAM8678 347 ITK Gibson, S.; Leung, B.; Squire, J. A.; Hill, M.; Arima, N.; Goss,P.; Hogg, 3 C c
D.; Mills, G. B.: Identification, cloning, and characterizationof a novel
human T- cell- specific tyrosine kinase located at the hematopoietincomplex
on chromosome 5q. Blood 82: 1561- 1572, 1993.

GAM8678 347 ITK Janis, E. M.; Siliciano, J. D.; Isaac, D. D.; Griffin, C. A.; Hawkins,A. L.; 3 C c
Kozak, C. A.; Desiderio, S.: Mapping of the gene for the tyrosinekinase Itk
to a region of conserved synteny between mouse chromosome11 and human
chromosome 5q. Genomics 23: 269- 271, 1994.

GAM8678 347 ITK Schaeffer, E. M.; Debnath, J.; Yap, G.; McVicar, D.; Liao, X. C.;Littman, D. 3 C c
R.; Sher, A.; Varmus, H. E.; Lenardo, M. J.; Schwartzberg,P. L.: Requirement
for Tec kinases Rlk and Itk in T cell receptorsignaling and immunity.
Science 284: 638- 641, 1999.

GAM8678 347 ITK Woods, M. L.; Kivens, W. J.; Adelsman, M. A.; Qiu, Y.; August,A.; Shimizu, 3 C c
Y.: A novel function for the Tec family tyrosine kinaseItk in activation of
beta- 1 integrins by the T- cell receptor. EMBOJ. 20: 1232- 1244, 2001.

GAM8678 347 MAPK4 Garcia, J. I.; Zalba, G.; Detera- Wadleigh, S. D.; de Miguel, C.: Isolation 3 C c
of a cDNA encoding the rat MAP- kinase homolog of humanp63mapk. Mammalian
Genome 7: 810- 814, 1996.

GAM8678 347 MAPK4 Gonzalez, F. A.; Raden, D. L.; Rigby, M. R.; Davis, R. J.: 3 C c
Heterogeneousexpression of four MAP kinase isoforms in human tissues. FEBS
Lett. 304:170- 178, 1992.

GAM8678 347 MAPK4 Li, L.; Wysk, M.; Gonzalez, F. A.; Davis, R. J.: Genomic lociof human 3 C c
mitogen- activated protein kinases. Oncogene 9: 647- 649,1994.

GAM8678 347 MAPK4 Zhu, A. X.; Zhao, Y.; Moller, D. E.; Flier, J. S.: Cloning 3 C c
andcharacterization of p97(MAPK), a novel human homolog of rat ERK- 3.
Molec.Cell. Biol. 14: 8202- 8211, 1994.

GAM8678 347 NAV2 Merrill, R. A.; Plum, L. A.; Kaiser, M. E.; Clagett- Dame, M.:A mammalian 3 C c

homolog of unc- 53 is regulated by all- trans retinoic acidin neuroblastoma cells and embryos. Proc. Nat. Acad. Sci. 99: 3422- 3427,2002.

GAM8678 347 NAV2 Nagase, T.; Kikuno, R.; Ishikawa, K.; Hirosawa, M.; Ohara, O.:Prediction of 3 C c the coding sequences of unidentified human genes. XVI.The complete sequences of 150 new cDNA clones from brain which codefor large proteins in vitro. DNA Res. 7: 65- 73, 2000.

GAM8678 347 OCA2 Akey, J. M.; Wang, H.; Xiong, M.; Wu, H.; Liu, W.; Shriver, M.D.; Jin, L.: 3 C c Interaction between the melanocortin- 1 receptor andP genes contributes to inter- individual variation in skin pigmentationphenotypes in a Tibetan population. Hum. Genet. 108: 516- 520, 2001.

GAM8678 347 OCA2 Brilliant, M. H.: The mouse pink- eyed dilution locus: a modelfor aspects of 3 C c Prader- Willi syndrome, Angelman syndrome, and a formof hypomelanosis of Ito. Mammalian Genome 3: 187- 191, 1992.

GAM8678 347 OCA2 Castle, D.; Kromberg, J.; Kowalsky, R.; Moosa, R.; Gillman, N.;Zwane, E.; 3 C c Fritz, V.: Visual evoked potentials in Negro carriersof the gene for tyrosinase positive oculocutaneous albinism. J. Med.Genet. 25: 835- 837, 1988.

GAM8678 347 OCA2 Colman, M. A.; Stevens, G.; Ramsay, M.; Kwon, B.; Jenkins, T.:Exclusion of 3 C c two candidate pigment loci, c and b, part of chromosome11p, and 33 random polymorphic markers as the locus for tyrosinase- positiveoculocutaneous albinism. Hum. Genet. 90: 556- 560, 1993.

GAM8678 347 OCA2 Donlon, T. A.; Lalande, M.; Wyman, A.; Bruns, G.; Latt, S. A.:Isolation of 3 C c molecular probes associated with the chromosome 15 instabilityin the Prader- Willi syndrome. Proc. Nat. Acad. Sci. 83: 4408- 4412,1986.

GAM8678 347 OCA2 Durham- Pierre, D.; Gardner, J. M.; Nakatsu, Y.; King, R. A.; Francke,U.; 3 C c Ching, A.; Aquaron, R.; del Marmol, V.; Brilliant, M. H.: Africanorigin of an intragenic deletion of the human P gene in tyrosinasepositive oculocutaneous albinism. Nature Genet. 7: 176- 179, 1994.

GAM8678 347 OCA2 Durham- Pierre, D.; King, R. A.; Naber, J. M.; Laken, S.; Brilliant,M. H.: 3 C c Estimation of carrier frequency of a 2.7 kb deletion alleleof the P gene associated with OCA2 in African- Americans. Hum. Mutat. 7:370- 373, 1996.

GAM8678 347 OCA2 Gardner, J. M.; Nakatsu, Y.; Gondo, Y.; Lee, S.; Lyon, M. F.; King,R. A.; 3 C c Brilliant, M. H.: The mouse pink- eyed dilution gene: associationwith human Prader- Willi and Angelman syndromes. Science 257: 1121- 1124,1992.

GAM8678 347 OCA2 Gondo, Y.; Gardner, J. M.; Nakatsu, Y.; Durham- Pierre, D.; Deveau,S. A.; 3 C c Kuper, C.; Brilliant, M. H.: High- frequency genetic reversionmediated by a DNA duplication: the mouse pink- eyed unstable mutation. Proc.Nat. Acad. Sci. 90: 297- 301, 1993.

GAM8678 347 OCA2 Hagiwara, N.; Klewer, S. E.; Samson, R. A.; Erickson, D. T.; Lyon,M. F.; 3 C c Brilliant, M. H.: Sox6 is a candidate gene for p100H myopathy,heart block, and sudden neonatal death. Proc. Nat. Acad. Sci. 97:4180- 4185, 2000.

GAM8678 347 OCA2 Haldane, J. B. S.; Sprunt, A. D.; Haldane, N. M.: Reduplicationin mice. J. 3 C c Genet. 5: 133- 135, 1915.

GAM8678 347 OCA2 Hamabe, J.; Fukushima, Y.; Harada, N.; Abe, K.; Matsuo, N.; Nagai,T.; 3 C c Yoshioka, A.; Tonoki, H.; Tsukino, R.; Niikawa, N.: Molecularstudy of the Prader- Willi syndrome: deletion, RFLP, and phenotypeanalyses of 50 patients. Am. J. Med. Genet. 41: 54- 63, 1991.

GAM8678 347 OCA2 Heim, R. A.; Dunn, D. S.; Candy, S. E.; Zwane, E.; Kromberg, J.G. R.; 3 C c Jenkins, T.: The tyrosine- positive oculocutaneous albinismlocus is not linked to the beta- globin locus in man. Hum. Genet. 79:89, 1988.

GAM8678 347 OCA2 Kagore, F.; Lund, P. M.: Oculocutaneous albinism among schoolchildrenin Harare, Zimbabwe. J. Med. Genet. 32: 859- 861, 1995. 3 C c

GAM8678 347 OCA2 Kedda, M. A.; Stevens, G.; Manga, P.; Viljoen, C.; Jenkins, T.;Ramsay, M.: The tyrosinase- positive oculocutaneous albinism geneshows locus homogeneity on chromosome 15q11- q13 and evidence of multiplemutations in Southern African negroids. Am. J. Hum. Genet. 54: 1078- 1084,1994. 3 C c

GAM8678 347 OCA2 Kerr, R.; Stevens, G.; Manga, P.; Salm, S.; John, P.; Haw, T.;Ramsay, M.: Identification of P gene mutations in individuals withoculocutaneous albinism in sub- Saharan Africa. Hum. Mutat. 15: 166- 172,2000. 3 C c

GAM8678 347 OCA2 King, R. A.: Personal Communication. Minneapolis, Minn. 12/31/1992. 3 C c

GAM8678 347 OCA2 Knoll, J. H. M.; Nicholls, R. D.; Magenis, R. E.; Glatt, K.; Graham,J. M., Jr.; Kaplan, L.; Lalande, M.: Angelman syndrome: three molecularclasses identified with chromosome 15q11q13- specific DNA markers. Am.J. Hum. Genet. 47: 149- 155, 1990. 3 C c

GAM8678 347 OCA2 Kromberg, J. G. R.; Castle, D.; Zwane, E. M.; Jenkins, T.: Albinismand skin cancer in southern Africa. Clin. Genet. 36: 43- 52, 1989. 3 C c

GAM8678 347 OCA2 Kromberg, J. G. R.; Jenkins, T.: Albinism in the South AfricanNegro. III. Genetic counselling issues. J. Biosoc. Sci. 16: 99- 108,1984. 3 C c

GAM8678 347 OCA2 Kromberg, J. G. R.; Jenkins, T.: Prevalence of albinism in theSouth African Negro. S. Afr. Med. J. 61: 383- 386, 1982. 3 C c

GAM8678 347 OCA2 Kugelman, T. P.; Van Scott, E. J.: Tyrosinase activity in melanocytesof human albinos. J. Invest. Derm. 37: 73- 76, 1961. 3 C c

GAM8678 347 OCA2 Lee, S.- T.; Nicholls, R. D.; Bundey, S.; Laxova, R.; Musarella,M.; Spritz, R. A.: Mutations of the P gene in oculocutaneous albinism,ocular albinism, and Prader- Willi syndrome plus albinism. New Eng.J. Med. 330: 529- 534, 1994. 3 C c

GAM8678 347 OCA2 Lee, S.- T.; Nicholls, R. D.; Jong, M. T. C.; Fukai, K.; Spritz,R. A.: Organization and sequence of the human P gene and identificationof a new family of transport proteins. Genomics 26: 354- 363, 1995. 3 C c

GAM8678 347 OCA2 Lee, S.- T.; Nicholls, R. D.; Schnur, R. E.; Guida, L. C.; Lu- Kuo,J.; Spinner, N. B.; Zackai, E. H.; Spritz, R. A.: Diverse mutationsof the P gene among African- Americans with type II (tyrosinase- positive)oculocutaneous albinism (OCA2). Hum. Molec. Genet. 3: 2047- 2051,1994. 3 C c

GAM8678 347 OCA2 Ludowese, C. J.; Thompson, K. J.; Sekhon, G. S.; Pauli, R. M.: Absence of predictable phenotypic expression in proximal 15q duplications. Clin.Genet. 40: 194- 201, 1991. 3 C c

GAM8678 347 OCA2 Lyon, M. F.; King, T. R.; Gondo, Y.; Gardner, J. M.; Nakatsu,Y.; Eicher, E. M.; Brilliant, M. H.: Genetic and molecular analysisof recessive alleles at the pink- eyed dilution (p) locus of the mouse. Proc.Nat. Acad. Sci. 89: 6968- 6972, 1992. 3 C c

GAM8678 347 OCA2 Manga, P.: Identification and molecular characterisation of thegenes for brown and rufous oculocutaneous albinism in southern Africa. Ph.D.Thesis: University of the Witwatersrand, Johannesburg , 1997. 3 C c

GAM8678 347 OCA2 Manga, P.; Kromberg, J. G. R.; Turner, A.; Jenkins, T.; Ramsay,M.: In southern Africa, brown oculocutaneous albinism (BOCA) mapsto the OCA2 locus on chromosome 15q: P- gene mutations identified. Am.J. Hum. Genet. 68: 782- 787, 2001. 3 C c

GAM8678 347 OCA2 Nance, W. E.; Jackson, C. E.; Witkop, C. J., Jr.: Amish albinism:a distinctive autosomal recessive phenotype. Am. J. Hum. Genet. 22:579- 586, 1970. 3 C c

GAM8678 347 OCA2 Nance, W. E.; Witkop, C. J., Jr.; Rawls, R. F.: Genetic and 3 C c
biochemicalevidence for two forms of oculocutaneous albinism in man.In: The
ClinicalDelineation of Birth Defects. Eye. Baltimore: Williams and
Wilkins(pub.) VIII: 1971. Pp. 125- 128.

GAM8678 347 OCA2 Okoro, A. N.: Albinism in Nigeria: a clinical and social study. Brit.J. 3 C c
Derm. 92: 485- 492, 1975.

GAM8678 347 OCA2 Ramsay, M.; Colman, M.- A.; Stevens, G.; Zwane, E.; Kromberg, J.;Farrall, 3 C c
M.; Jenkins, T.: The tyrosinase- positive oculocutaneousalbinism locus maps
to chromosome 15q11.2- q12. Am. J. Hum. Genet. 51:879- 884, 1992.

GAM8678 347 OCA2 Rinchik, E. M.; Bultman, S. J.; Horsthemke, B.; Lee, S.- T.; Strunk,K. M.; 3 C c
Spritz, R. A.; Avidano, K. M.; Jong, M. T. C.; Nicholls, R.D.: A gene for
the mouse pink- eyed dilution locus and for human typeII oculocutaneous
albinism. Nature 361: 72- 76, 1993.

GAM8678 347 OCA2 Robinson, W. P.; Bottani, A.; Yagang, X.; Balakrishman, J.; Binkert,F.; 3 C c
Machler, M.; Prader, A.; Schinzel, A.: Molecular, cytogenetic,and clinical
investigations of Prader- Willi syndrome patients. Am.J. Hum. Genet. 49:
1219- 1234, 1991.

GAM8678 347 OCA2 Rosemblat, S.; Durham- Pierre, D.; Gardner, J. M.; Nakatsu, Y.;Brilliant, M. 3 C c
H.; Orlow, S. J.: Identification of a melanosomal membraneprotein encoded by
the pink- eyed dilution (type II oculocutaneousalbinism) gene. Proc. Nat.
Acad. Sci. 91: 12071- 12075, 1994.

GAM8678 347 OCA2 Spritz, R. A.; Fukai, K.; Holmes, S. A.; Luande, J.: Frequentintragenic 3 C c
deletion of the P gene in Tanzanian patients with typeII oculocutaneous
albinism (OCA2). Am. J. Hum. Genet. 56: 1320- 1323,1995.

GAM8678 347 OCA2 Stevens, G.; Ramsay, M.; Jenkins, T.: Oculocutaneous albinism(OCA2) in sub- 3 C c
Saharan Africa: distribution of the common 2.7- kb Pgene deletion mutation.
Hum. Genet. 99: 523- 527, 1997.

GAM8678 347 OCA2 Stevens, G.; van Beukering, J.; Jenkins, T.; Ramsay, M.: An 3 C c
intragenicdeletion of the P gene is the common mutation causing tyrosinase-
positiveoculocutaneous albinism in Southern African Negroids. Am. J.
Hum.Genet. 56: 586- 591, 1995.

GAM8678 347 OCA2 Trevor- Roper, P. D.: Albinism. Proc. Roy. Soc. Med. 56: 21- 24,1963. 3 C c

GAM8678 347 OCA2 Trevor- Roper, P. D.: Marriage of two complete albinos with 3 C c
normallypigmented offspring. Brit. J. Ophthal. 36: 107- 108, 1952.

GAM8678 347 OCA2 Tripathi, R. K.; Droetto, S.; Spritz, R. A.: Many patients with'tyrosinase- 3 C c
positive' oculocutaneous albinism have tyrosinase genemutations. (Abstract)
Am. J. Hum. Genet. 51 (suppl.): A179, 1992.

GAM8678 347 OCA2 Waardenburg, P. J.: Genetics and Ophthalmology. Springfield,Ill.: Charles C 3 C c
Thomas (pub.) 1: 1961. Pp. 732 only.

GAM8678 347 OCA2 Walpole, I. R.; Mulcahy, M. T.: Tyrosinase positive albinismwith familial 3 C c
46,XY,t(2;4)(q31.2;q31.22) balanced translocation. J.Med. Genet. 28: 482-
484, 1991.

GAM8678 347 OCA2 Witkop, C. J., Jr.: Dental problems of an hereditary nature.In:Witkop, C. 3 C c
J.: Genetics and Dental Health. New York: McGraw- Hill(pub.) 1962.

GAM8678 347 OCA2 Witkop, C. J., Jr.: Personal Communication. Minneapolis, Minn. 1966. 3 C c

GAM8678 347 OCA2 Witkop, C. J., Jr.; Niswander, J. D.; Bergsma, D. R.; Workman,P. L.; White, 3 C c
J. G.: Tyrosinase- positive oculocutaneous albinismamong the Zuni and the
Brandywine triracial isolate: biochemical andclinical characteristics and
fertility. Am. J. Phys. Anthrop. 36:397- 405, 1972.

GAM8678 347 OCA2 Witkop, C. J., Jr.; Quevedo, W. C., Jr.; Fitzpatrick, T. B.; King,R. A.: 3 C c

Albinism.In: Scriver, C. R.; Beaudet, A. L.; Sly, W. S.; Valle,D.: The Metabolic Basis of Inherited Disease. Vol. II. New York:McGraw- Hill (pub.) (6th ed.): 1989. Pp. 2905- 2947.

GAM8678 347 OCA2 Witkop, C. J., Jr.; Van Scott, E. J., Jr.; Jacoby, G. A.: Evidencefor two forms of autosomal recessive albinism in man. (Abstract) Proc.Second Int. Cong. Hum. Genet., Rome, Sept. 6- 12, 1961 2: 1064- 1065,1963. 3 C c

GAM8678 347 OCA2 Woolf, C. M.: Albinism among Indians in Arizona and New Mexico. Am.J. Hum. Genet. 17: 23- 35, 1965. 3 C c

GAM8678 347 OCA2 Woolf, C. M.; Dukepoo, F. C.: Hopi Indians, inbreeding and albinism. Science 164:30- 37, 1969. 3 C c

GAM8678 347 PKP2 Bonne, S.; van Hengel, J.; van Roy, F.: Chromosomal mapping ofhuman armadillo genes belonging to the p120(ctn)/plakophilin subfamily. Genomics 51:452- 454, 1998. 3 C c

GAM8678 347 PKP2 Bonne, S.; van Hengel, J; van Roy, F.: Assignment of the plakophilin- 2gene (PKP2) and a plakophilin- 2 pseudogene (PKP2P1) to human chromosomebands 12p11 and 12p13, respectively, by in situ hybridization. Cytogenet.Cell Genet. 88: 286- 287, 2000. 3 C c

GAM8678 347 PKP2 Mertens, C.; Kuhn, C.; Franke, W. W.: Plakophilins 2a and 2b:constitutive proteins of dual location in the karyoplasm and the desmosomalplaque. J. Cell Biol. 135: 1009- 1025, 1996. 3 C c

GAM8678 347 PKP2 Schmidt, A; Langbein, L.; Pratzel, S.; Rode, M.; Rackwitz, H.- R.;Franke, W. W.: Plakophilin 3- - a novel cell- type- specific desmosomalplaque protein. Differentiation 64: 291- 306, 1999. 3 C c

GAM8678 347 PNUTL2 Paavola, P.; Horelli- Kuitunen, N.; Palotie, A.; Peltonen, L.:Characterization of a novel gene, PNUTL2, on human chromosome 17q22- q23and its exclusion as the Meckel syndrome gene. Genomics 55: 122- 125,1999. 3 C c

GAM8678 347 PNUTL2 Zieger, B.; Tran, H.; Hainmann, I.; Wunderle, D.; Zgaga- Griesz,A.; Blaser, S.; Ware, J.: Characterization and expression analysisof two human septin genes, PNUTL1 and PNUTL2. Gene 261: 197- 203,2000. 3 C c

GAM8678 347 PPP2R5C McCright, B.; Brothman, A. R.; Virshup, D. M.: Assignment of humanprotein phosphatase 2A regulatory subunit genes B56- alpha, B56- beta,B56- gamma, B56- delta, and B56- epsilon (PPP2R5A- - PPP2R5E), highly expressedin muscle and brain, to chromosome regions 1q41, 11q12, 3p21, 6p21.1,and 7p11.2- to- p12. Genomics 36: 168- 170, 1996. 3 C c

GAM8678 347 PPP2R5C McCright, B.; Virshup, D. M.: Identification of a new family ofprotein phosphatase 2A regulatory subunits. J. Biol. Chem. 270:26123- 26128, 1995. 3 C c

GAM8678 347 PPP2R5C Muneer, S.; Ramalingam, V.; Wyatt, R.; Schultz, R. A.; Minna, J.D.; Kamibayashi, C.: Genomic organization and mapping of the geneencoding the PP2A B56- gamma regulatory subunit. Genomics 79: 344- 348,2002. 3 C c

GAM8678 347 PTPN1 Ahmad, F.; Azevedo, J. L., Jr.; Cortright, R.; Dohm, G. L.; Goldstein,B. J.: Alternations in skeletal muscle protein- tyrosine phosphataseactivity and expression in insulin- resistant human obesity and diabetes. J.Clin. Invest. 100: 449- 458, 1997. 3 C c

GAM8678 347 PTPN1 Brown- Shimer, S.; Johnson, K. A.; Lawrence, J. B.; Johnson, C.;Bruskin, A.; Green, N. R.; Hill, D. E.: Molecular cloning and chromosomemapping of the human gene encoding protein phosphotyrosyl phosphatase1B. Proc. Nat. Acad. Sci. 87: 5148- 5152, 1990. 3 C c

GAM8678 347 PTPN1 Charbonneau, H.; Tonks, N. K.; Kumar, S.; Diltz, C. D.; Harrylock,M.; Cool, D. E.; Krebs, E. G.; Fischer, E. H.; Walsh, K. A.: Humanplacenta protein- 3 C c

tyrosine- phosphatase: amino acid sequence and relationshipto a family of receptor- like proteins. Proc. Nat. Acad. Sci. 86:5252- 5256, 1989.

GAM8678 347 PTPN1 Chernoff, J.; Schievella, A. R.; Jost, C. A.; Erikson, R. L.; Neel,B. G.: 3 C c Cloning of a cDNA for a major human protein- tyrosine- phosphatase. Proc.Nat. Acad. Sci. 87: 2735- 2739, 1990.

GAM8678 347 PTPN1 Di Paola, R.; Frittitta, L.; Miscio, G.; Bozzali, M.; Baratta,R.; Centra, M.; Spampinato, D.; Santagati, M. G.; Ercolino, T.; Cisternino,C.; Soccio, T. Mastroianno, S.; Tassi, V.; Almgren, P.; Pizzuti, A.;Vigneri, R.; Trischitta, V.: A variation in 3- prime UTR of hPTP1Bincreases specific gene expression and associates with insulin resistance. Am.J. Hum. Genet. 70: 806- 812, 2002. 3 C c

GAM8678 347 PTPN1 Elchebly, M.; Payette, P.; Michaliszyn, E.; Cromlish, W.; Collins,S.; Loy, A. L.; Normandin, D.; Cheng, A.; Himms- Hagen, J.; Chan, C.- C.;Ramachandran, C.; Gresser, M. J.; Tremblay, M. L.; Kennedy, B. P.: Increased insulin sensitivity and obesity resistance in mice lackingthe protein tyrosine phosphatase- 1B gene. Science 283: 1544- 1548,1999. 3 C c

GAM8678 347 PTPN1 Forsell, P. K. A. L.; Boie, Y.; Montalibet, J.; Collins, S.; Kennedy,B. P.: Genomic characterization of the human and mouse protein tyrosinephosphatase- 1B genes. Gene 260: 145- 153, 2000. 3 C c

GAM8678 347 PTPN1 Gu, H. F.; Almgren, P.; Lindholm, E.; Frittitta, L.; Pizzuti, A.;Trischitta, V.; Groop, L. C.: Association between the human glycoproteinPC- 1 gene and elevated glucose and insulin levels in paired- siblinganalysis. Diabetes 49: 1601- 1603, 2000. 3 C c

GAM8678 347 PTPN1 Haj, F. G.; Verveer, P. J.; Squire, A.; Neel, B. G.; Bastiaens,P. I. H.: Imaging sites of receptor dephosphorylation by PTP1B onthe surface of the endoplasmic reticulum. Science 295: 1708- 1711,2002. 3 C c

GAM8678 347 PTPN1 Jia, Z.; Barford, D.; Flint, A. J.; Tonks, N. K.: Structuralbasis for phosphotyrosine peptide recognition by protein tyrosinephosphatase 1B. Science 268: 1754- 1758, 1995. 3 C c

GAM8678 347 PTPN1 Kaplan, R.; Morse, B.; Huebner, K.; Croce, C.; Howk, R.; Ravera,M.; Ricca, G.; Jaye, M.; Schlessinger, J.: Cloning of three humantyrosine phosphatases reveals a multigene family of receptor- linkedprotein- tyrosine- phosphatases expressed in brain. Proc. Nat. Acad.Sci. 87: 7000- 7004, 1990. 3 C c

GAM8678 347 PTPN1 Kennedy, B. P.; Ramachandran, C.: Protein tyrosine phosphatase- 1Bin diabetes. Biochem. Pharm. 60: 877- 883, 2000. 3 C c

GAM8678 347 PTPN1 Mok, A.; Cao, H.; Zinman, B.; Hanley, A. J. G.; Harris, S. B.;Kennedy, B. P.; Hegele, R. A.: A single nucleotide polymorphism inprotein tyrosine phosphatase PTP- 1B is associated with protectionfrom diabetes or impaired glucose tolerance in Oji- Cree. J. Clin.Endocr. Metab. 87: 724- 727, 2002. 3 C c

GAM8678 347 PTPN1 Salmeen, A.; Andersen, J. N.; Myers, M. P.; Tonks, N. K.; Barford,D.: Molecular basis for the dephosphorylation of the activation segmentof the insulin receptor by protein tyrosine phosphatase 1B. Molec.Cell 6: 1401- 1412, 2000. 3 C c

GAM8678 347 PTPN1 Tonks, N. K.; Diltz, C. D.; Fischer, E. H.: Purification of themajor protein- tyrosine- phosphatases of human placenta. J. Biol. Chem. 263:6722- 6730, 1988. 3 C c

GAM8678 347 RBM15 Ma, Z.; Morris, S. W.; Valentine, V.; Li, M.; Herbrick, J.- A.;Cui, X.; Bouman, D.; Li, Y.; Mehta, P. K.; Nizetic, D.; Kaneko, Y.;Chan, G. C. F.; Chan, L. C.; Squire, J.; Scherer, S. W.; Hitzler,J. K.: Fusion of two novel genes, RBM15 and MKL1, in the t(1;22)(p13;q13)of acute megakaryoblastic 3 C c

leukemia. Nature Genet. 28: 220- 221, 2001.

GAM8678 347 RBM15 Mercher, T.; Busson- Le Coniat, M.; Khac, F. N.; Ballerini, P.;Mauchauffe, 3 C c
M.; Bui, H.; Pellegrino, B.; Radford, I.; Valensi, F.;Mugneret, F.;
Dastugue, N.; Bernard, O. A.; Berger, R.: Recurrenceof OTT- MAL fusin in
t(1;22) of infant AML- M7. Genes Chromosomes Cancer 33:22- 28, 2002.

GAM8678 347 RBM15 Mercher, T.; Coniat, M. B.- L.; Monni, R.; Mauchauffe, M.; Khac,F. N.; 3 C c
Gressin, L.; Mugneret, F.; Leblanc, T.; Dastugue, N.; Berger,R.; Bernard, O.
A.: Involvement of a human gene related to the Drosophilaspen gene in the
recurrent t(1;22) translocation of acute megakaryocyticleukemia. Proc. Nat.
Acad. Sci. 98: 5776- 5779, 2001.

GAM8678 347 RXRA Almasan, A.; Mangelsdorf, D. J.; Ong, E. S.; Wahl, G. M.; Evans,R. M.: 3 C c
Chromosomal localization of the human retinoid X receptors. Genomics 20:397-
403, 1994.

GAM8678 347 RXRA Claudel, T.; Leibowitz, M. D.; Fievet, C.; Tailleux, A.; Wagner,B.; Repa, J. 3 C c
J.; Torpier, G.; Lobaccaro, J.- M.; Paterniti, J. R.;Mangelsdorf, D. J.;
Heyman, R. A.; Auwerx, J.: Reduction of atherosclerosisin apolipoprotein E
knockout mice by activation of the retinoid Xreceptor. Proc. Nat. Acad. Sci.
98: 2610- 2615, 2001.

GAM8678 347 RXRA de Urquiza, A. M.; Liu, S.; Sjoberg, M.; Zetterstrom, R. H.; Griffiths,W.; 3 C c
Sjovall, J.; Perlmann, T.: Docosahexaenoic acid, a ligand forthe retinoid X
receptor in mouse brain. Science 290: 2140- 2144,2000.

GAM8678 347 RXRA Dyson, E.; Sucov, H. M.; Kubalak, S. W.; Schmid- Schonbein, G. W.;DeLano, F. 3 C c
A.; Evans, R. M.; Ross, J., Jr.; Chien, K. R.: Atrial- likephenotype is
associated with embryonic ventricular failure in retinoidX receptor alpha -
/- mice. Proc. Nat. Acad. Sci. 92: 7386- 7390,1995.

GAM8678 347 RXRA Gampe, R. T., Jr.; Montana, V. G.; Lambert, M. H.; Miller, A. B.;Bledsoe, R. 3 C c
K.; Milburn, M. V.; Kliewer, S. A.; Willson, T. M.; Xu,H. E.: Asymmetry in
the PPAR- gamma/RXR- alpha crystal structure revealsthe molecular basis of
heterodimerization among nuclear receptors. Molec.Cell 5: 545- 555, 2000.

GAM8678 347 RXRA Germain, P.; Iyer, J.; Zechel, C.; Gronemeyer, H.: Co- regulatorrecruitment 3 C c
and the mechanism of retinoic acid receptor synergy. Nature 415:187- 192,
2002.

GAM8678 347 RXRA Gruber, P. J.; Kubalak, S. W.; Pexieder, T.; Sucov, H. M.; Evans,R. M.; 3 C c
Chien, K. R.: RXR- alpha deficiency confers genetic susceptibilityfor aortic
sac, conotruncal, atrioventricular cushion, and ventricularmuscle defects in
mice. J. Clin. Invest. 98: 1332- 1343, 1996.

GAM8678 347 RXRA Heyman, R. A.; Mangelsdorf, D. J.; Dyck, J. A.; Stein, R. B.; Eichele,G.; 3 C c
Evans, R. M.; Thaller, C.: 9- cis retinoic acid is a high affinityligand for
the retinoid X receptor. Cell 68: 397- 406, 1992.

GAM8678 347 RXRA Hoopes, C. W.; Taketo, M.; Ozato, K.; Liu, Q.; Howard, T. A.; Linney,E.; 3 C c
Seldin, M. F.: Mapping the mouse Rxr loci encoding nuclear retinoidX
receptors Rxr- alpha, Rxr- beta, and Rxr- gamma. Genomics 14: 611- 617,1992.

GAM8678 347 RXRA Jones, K. A.; Fitzgibbon, J.; Woodward, K. J.; Goudie, D.; Ferguson- 3 C c
Smith,M. A.; Povey, S.; Wolfe, J.; Solomon, E.: Localization of the
retinoidX receptor alpha gene (RXRA) to chromosome 9q34. Ann. Hum. Genet.
57:195- 201, 1993.

GAM8678 347 RXRA Li, M.; Indra, A. K.; Warot, X.; Brocard, J.; Messaddeq, N.; Kato,S.; 3 C c
Metzger, D.; Chambon, P.: Skin abnormalities generated by
temporallycontrolled RXR- alpha mutations in mouse epidermis. Nature 407:
633- 636,2000.

GAM8678 347 RXRA Lu, T. T.; Makishima, M.; Repa, J. J.; Schoonjans, K.; Kerr, T.A.; Auwerx, J.; Mangelsdorf, D. J.: Molecular basis for feedbackregulation of bile acid synthesis by nuclear receptors. Molec. Cell 6:507- 515, 2000. 3 C c

GAM8678 347 RXRA Mangelsdorf, D. J.; Ong, E. S.; Dyck, J. A.; Evans, R. M.: Nuclearreceptor that identifies a novel retinoic acid response pathway. Nature 345:224- 229, 1990. 3 C c

GAM8678 347 RXRA Mangelsdorf, D. J.; Umesono, K.; Kliewer, S. A.; Borgmeyer, U.;Ong, E. S.; Evans, R. M.: A direct repeat in the cellular retinol- bindingprotein type II gene confers differential regulation by RXR and RAR. Cell 66:555- 561, 1991. 3 C c

GAM8678 347 RXRA McNamara, P.; Seo, S.; Rudic, R. D.; Sehgal, A.; Chakravarti,D.; FitzGerald, G. A.: Regulation of CLOCK and MOP4 by nuclear hormonereceptors in the vasculature: a humoral mechanism to reset a peripheralclock. Cell 105: 877- 889, 2001. 3 C c

GAM8678 347 RXRA Repa, J. J.; Turley, S. D.; Lobaccaro, J.- M. A.; Medina, J.; Li,L.; Lustig, K.; Shan, B.; Heyman, R. A.; Dletschy, J. M.; Mangelsdorf,D. J.: Regulation of absorption and ABC1- mediated efflux of cholesterolby RXR heterodimers. Science 289: 1524- 1529, 2000. 3 C c

GAM8678 347 RXRA Tontonoz, P.; Hu, E.; Spiegelman, B. M.: Stimulation of adipogenesisin fibroblasts by PPAR- gamma- 2, a lipid- activated transcription factor. Cell 79:1147- 1156, 1994. 3 C c

GAM8678 347 RXRA Wan, Y.- J. Y.; An, D.; Cai, Y.; Repa, J. J.; Chen, T. H.- P.; Flores,M.; Postic, C.; Magnuson, M. A.; Chen, J.; Chien, K. R.; French, S.;Mangelsdorf, D. J.; Sucov, H. M.: Hepatocyte- specific mutation establishesretinoid X receptor alpha as a heterodimeric integrator of multiplephysiological processes in the liver. Molec. Cell. Biol. 20: 4436- 4444,2000. 3 C c

GAM8678 347 RXRA Willy, P. J.; Umesono, K.; Ong, E. S.; Evans, R. M.; Heyman, R.A.; Mangelsdorf, D. J.: LXR, a nuclear receptor that defines a distinctretinoid response pathway. Genes Dev. 9: 1033- 1045, 1995. 3 C c

GAM8678 347 RXRA Zhong, S.; Delva, L.; Rachez, C.; Cenciarelli, C.; Gandini, D.;Zhang, H.; Kalantry, S.; Freedman, L. P.; Pandolfi, P. P.: A RA- dependent,tumour-growth suppressive transcription complex is the target of thePML- RAR- alpha and T18 oncoproteins. Nature Genet. 23: 287- 295, 1999. 3 C c

GAM8678 347 RXRA Zhou, M. D.; Sucov, H. M.; Evans, R. M.; Chien, K. R.: Retinoid-dependentpathways suppress myocardial cell hypertrophy. Proc. Nat. Acad. Sci. 92:7391- 7395, 1995. 3 C c

GAM8678 347 SFRS2IP Tanner, S.; Stagljar, I.; Georgiev, O.; Schaffner, W.; Bourquin,J.- P.: A novel SR- related protein specifically interacts with thecarboxy- terminal domain (CTD) of RNA polymerase II through a conservedinteraction domain. Biol. Chem. 378: 565- 571, 1997. 3 C c

GAM8678 347 SFRS2IP Zhang, W.- J.; Wu, J. Y.: Sip1, a novel RS domain- containing proteinessential for pre- mRNA splicing. Molec. Cell. Biol. 18: 676-684,1998. 3 C c

GAM8678 347 SNRPN Bielinska, B.; Blaydes, S. M.; Buiting, K.; Yang, T.; Krajewska- Walasek,M.; Horsthemke, B.; Brannan, C. I.: De novo deletions of SNRPN exon1 in early human and mouse embryos result in a paternal to maternalimprint switch. Nature Genet. 25: 74- 78, 2000. Note: Erratum: NatureGenet. 25: 241 only, 2000. 3 C c

GAM8678 347 SNRPN Bressler, J.; Tsai, T.- F.; Wu, M.- Y.; Tsai, S.- F.; Ramirez, M.A.; Armstrong, D.; Beaudet, A. L.: The SNRPN promoter is not requiredfor genomic 3 C c

imprinting of the Prader- Willi/Angelman domain in mice. NatureGenet. 28: 232- 240, 2001.

GAM8678 347 SNRPN Buiting, K.; Saitoh, S.; Gross, S.; Dittrich, B.; Schwartz, S.;Nicholls, R. 3 C c
D.; Horsthemke, B.: Inherited microdeletions in theAngelman and Prader-Willi syndromes define an imprinting centre onhuman chromosome 15. Nature Genet. 9: 395- 400, 1995.

GAM8678 347 SNRPN Cattanach, B. M.; Barr, J. A.; Evans, E. P.; Burtenshaw, M.; Beechey,C. V.; 3 C c
Leff, S. E.; Brannan, C. I.; Copeland, N. G.; Jenkins, N. A.;Jones, J.: A candidate mouse model for Prader- Willi syndrome whichshows an absence of Snrpn expression. Nature Genet. 2: 270- 274,1992.

GAM8678 347 SNRPN Dittrich, B.; Buiting, K.; Korn, B.; Rickard, S.; Buxton, J.; Saitoh,S.; 3 C c
Nicholls, R. D.; Poustka, A.; Winterpacht, A.; Zabel, B.; Horsthemke,B.: Imprint switching on human chromosome 15 may involve alternativetranscripts of the SNRPN gene. Nature Genet. 14: 163- 170, 1996.

GAM8678 347 SNRPN Gallagher, R. C.; Pils, B.; Albalwi, M.; Francke, U.: Evidencefor the role 3 C c
of PWCR1/HBII- 85 C/D box small nucleolar RNAs in Prader- Willisyndrome. Am. J. Hum. Genet. 71: 669- 678, 2002.

GAM8678 347 SNRPN Glenn, C. C.; Porter, K. A.; Jong, M. T. C.; Nicholls, R. D.; Driscoll,D. 3 C c
J.: Functional imprinting and epigenetic modification of the humanSNRPN gene. Hum. Molec. Genet. 2: 2001- 2005, 1993.

GAM8678 347 SNRPN Gray, T. A.; Saitoh, S.; Nicholls, R. D.: An imprinted, mammalianbicistronic 3 C c
transcript encodes two independent proteins. Proc. Nat.Acad. Sci. 96: 5616-5621, 1999.

GAM8678 347 SNRPN Ishikawa, T.; Kibe, T.; Wada, Y.: Deletion of small nuclear 3 C c
ribonucleoproteinpolypeptide N (SNRPN) in Prader- Willi syndrome detected by fluorescencein situ hybridization: two sibs with the typical phenotype withouta cytogenetic deletion in chromosome 15q. Am. J. Med. Genet. 62:350-352, 1996.

GAM8678 347 SNRPN Kuslich, C. D.; Kobori, J. A.; Mohapatra, G.; Gregorio- King, C.;Donlon, T. 3 C c
A.: Prader- Willi syndrome is caused by disruption of theSNRPN gene. Am. J. Hum. Genet. 64: 70- 76, 1999.

GAM8678 347 SNRPN Leff, S. E.; Brannan, C. I.; Reed, M. L.; Ozcelik, T.; Francke,U.; Copeland, 3 C c
N. G.; Jenkins, N. A.: Maternal imprinting of the mouseSnrpn gene and conserved linkage homology with the human Prader- Willisyndrome region. Nature Genet. 2: 259- 264, 1992.

GAM8678 347 SNRPN Li, S.; Klein, E. S.; Russo, A. F.; Simmons, D. M.; Rosenfeld,M. G.: 3 C c
Isolation of cDNA clones encoding small nuclear ribonucleoparticle-associatedproteins with different tissue specificities. Proc. Nat. Acad. Sci. 86:9778- 9782, 1989.

GAM8678 347 SNRPN Lyko, F.; Buiting, K.; Horsthemke, B.; Paro, R.: Identificationof a 3 C c
silencing element in the human 15q11- q13 imprinting center byusing transgenic Drosophila. Proc. Nat. Acad. Sci. 95: 1698- 1702,1998.

GAM8678 347 SNRPN McAllister, G.; Amara, S. G.; Lerner, M. R.: Tissue- specificexpression and 3 C c
cDNA cloning of small nuclear ribonucleoprotein- associatedpolypeptide N. Proc. Nat. Acad. Sci. 85: 5296- 5300, 1988.

GAM8678 347 SNRPN Mutirangura, A.; Jayakumar, A.; Sutcliffe, J. S.; Nakao, M.; McKinney,M. J.; 3 C c
Buiting, K.; Horsthemke, B.; Beaudet, A. L.; Chinault, A. C.;Ledbetter, D. H.: A complete YAC contig of the Prader- Willi/Angelmanchromosome region (15q11- q13) and refined localization of the SNRPNgene. Genomics 18: 546-552, 1993.

GAM8678 347 SNRPN Ozcelik, T.; Leff, S.; Robinson, W.; Donlon, T.; Lalande, M.;Sanjines, E.; 3 C c
Schinzel, A.; Francke, U.: Small nuclear ribonucleoproteinpolypeptide N
(SNRPN), an expressed gene in the Prader- Willi syndromecritical region.
Nature Genet. 2: 265- 269, 1992.

GAM8678 347 SNRPN Reed, M. L.; Leff, S. E.: Maternal imprinting of human SNRPN,a gene deleted 3 C c
in Prader- Willi syndrome. Nature Genet. 6: 163- 167,1994.

GAM8678 347 SNRPN Saitoh, S.; Wada, T.: Parent- of- origin specific histone acetylationand 3 C c
reactivation of a key imprinted gene locus in Prader- Willi syndrome. Am.J.
Hum. Genet. 66: 1958- 1962, 2000.

GAM8678 347 SNRPN Schmauss, C.; McAllister, G.; Ohosone, Y.; Hardin, J. A.; Lerner,M. R.: A 3 C c
comparison of snRNP- associated Sm- autoantigens: human N,rat N and human
B/B- prime. Nucleic Acids Res. 17: 1733- 1743, 1989.

GAM8678 347 SNRPN Schulze, A.; Hansen, C.; Skakkebaek, N. E.; Brondum- Nielsen, K.;Ledbetter, 3 C c
D. H.; Tommerup, N.: Exclusion of SNRPN as a major determinantof Prader-
Willi syndrome by a translocation breakpoint. Nature Genet. 12:452- 454,
1996.

GAM8678 347 SNRPN Schweizer, J.; Zynger, D.; Francke, U.: In vivo nuclease 3 C c
hypersensitivitystudies reveal multiple sites of parental origin- dependent
differentialchromatin conformation in the 150 kb SNRPN transcription unit.
Hum.Molec. Genet. 8: 555- 566, 1999.

GAM8678 347 SNRPN Shemer, R.; Hershko, A. Y.; Perk, J.; Mostoslavsky, R.; Tsuberi,B.; Cedar, 3 C c
H.; Buiting, K.; Razin, A.: The imprinting box of thePrader- Willi/Angelman
syndrome domain. Nature Genet. 26: 440- 443,2000.

GAM8678 347 SNRPN Sun, Y.; Nicholls, R. D.; Butler, M. G.; Saitoh, S.; Hainline,B. E.; Palmer, 3 C c
C. G.: Breakage in the SNRPN locus in a balanced 46,XY,t(15;19)Prader- Willi
syndrome patient. Hum. Molec. Genet. 5: 517- 524, 1996.

GAM8678 347 SNRPN Sutcliffe, J. S.; Nakao, M.; Christian, S.; Orstavik, K. H.; Tommerup,N.; 3 C c
Ledbetter, D. H.; Beaudet, A. L.: Deletions of a differentiallymethylated
CpG island at the SNRPN gene define a putative imprintingcontrol region.
Nature Genet. 8: 52- 58, 1994.

GAM8678 347 SNRPN Wirth, J.; Back, E.; Huttenhofer, A.; Nothwang, H.- G.; Lich, C.;Gross, S.; 3 C c
Menzel, C,; Schinzel, A.; Kioschis, P.; Tommerup, N.; Ropers,H.- H.;
Horsthemke, B.; Buiting, K.: A translocation breakpoint clusterdisrupts the
newly defined 3- prime end of the SNURF- SNRPN transcriptionunit on
chromosome 15. Hum. Molec. Genet. 10: 201- 210, 2001.

GAM8678 347 STAU DesGroseillers, L.; Lemieux, N.: Localization of a human double- 3 C c
strandedRNA- binding protein gene (STAU) to band 20q13.1 by fluorescence
insitu hybridization. Genomics 36: 527- 529, 1996.

GAM8678 347 STAU Marion, R. M.; Fortes, P.; Beloso, A.; Dotti, C.; Ortin, J.: Ahuman sequence 3 C c
homologue of staufen is an RNA- binding protein thatis associated with
polysomes and localizes to the rough endoplasmicreticulum. Molec. Cell.
Biol. 19: 2212- 2219, 1999.

GAM8678 347 STAU Wickham, L.; Duchaine, T.; Luo, M.; Nabi, I. R.; DesGroseillers,L.: 3 C c
Mammalian staufen is a double- stranded- RNA- and tubulin- bindingprotein
which localizes to the rough endoplasmic reticulum. Molec.Cell. Biol. 19:
2220- 2230, 1999.

GAM8678 347 TEM6 Carson- Walter, E. B.; Watkins, D. N.; Nanda, A.; Vogelstein, B.;Kinzler, K. 3 C c
W.; St. Croix, B.: Cell surface tumor endothelial markersare conserved in
mice and humans. Cancer Res. 61: 6649- 6655, 2001.

GAM8678 347 TEM6 St. Croix, B.; Rago, C.; Velculescu, V.; Traverso, G.; Romans,K. E.; 3 C c

Montgomery, E.; Lal, A.; Riggins, G. J.; Lengauer, C.; Vogelstein,B.; Kinzler, K. W.: Genes expressed in human tumor endothelium. Science 289:1197- 1202, 2000.

GAM8678 347 TMPO Audhya, T.; Schlesinger, D. H.; Goldstein, G.: Isolation and completeamino 3 C c
acid sequence of human thymopoietin and splenin. Proc. Nat.Acad. Sci. 84: 3545- 3549, 1987.

GAM8678 347 TMPO Berger, R.; Theodor, L.; Shoham, J.; Gokkel, E.; Brok- Simoni, F.;Avraham, 3 C c
K. B.; Copeland, N. G.; Jenkins, N. A.; Rechavi, G.; Simon,A. J.: The characterization and localization of the mouse thymopoietin/lamina-associatedpolypeptide 2 gene and its alternatively spliced products. GenomeRes. 6: 361- 370, 1996.

GAM8678 347 TMPO Harris, C. A.; Andryuk, P. J.; Cline, S. W.; Mathew, S.; Siekierka,J. J.; 3 C c
Goldstein, G.: Structure and mapping of the human thymopoietin(TMPO) gene and relationship of human TMPO beta to rat lamin- associatedpolypeptide 2. Genomics 28: 198- 205, 1995.

GAM8678 347 TRIM Bruyns, E.; Marie- Cardine, A.; Kirchgessner, H.; Sagolla, K.; 3 C c
Shevchenko,A.; Mann, M.; Autschbach, F.; Bensussan, A.; Meuer, S.; Schraven,B.: T cell receptor (TCR) interacting molecule (TRIM), a novel disulfide- linkeddimer associated with the TCR- CD3- zeta complex, recruits intracellularsignaling proteins to the plasma membrane. J. Exp. Med. 188: 561- 575,1998.

GAM8678 347 TRIM Hubener, C.; Mincheva, A.; Lichter, P.; Schraven, B.; Bruyns, E.: Genomic 3 C c
organization and chromosomal localization of the human geneencoding the T-cell receptor- interacting molecule (TRIM). Immunogenetics 51:154- 158, 2000.

GAM8678 347 TRIM9 Li, Y.; Chin, L.- S.; Weigel, C.; Li, L.: Spring, a novel RINGfinger protein 3 C c
that regulates synaptic vesicle exocytosis. J. Biol.Chem. 276: 40824- 40833, 2001.

GAM8678 347 TRIM9 Reymond, A.; Meroni, G.; Fantozzi, A.; Merla, G.; Cairo, S.; Luzi,L.; 3 C c
Riganelli, D.; Zanaria, E.; Messali, S.; Cainarca, S.; Guffanti,A.; Minucci, S.; Pelicci, P. G.; Ballabio, A.: The tripartite motiffamily identifies cell compartments. EMBO J. 20: 2140- 2151, 2001.

GAM8678 347 WHSC1 Baxendale, S.; MacDonald, M. E.; Mott, R.; Francis, F.; Lin, C.;Kirby, S. 3 C c
F.; James, M.; Zehetner, G.; Hummerich, H.; Valdes, J.;Collins, F. S.; Deaven, L. J.; Gusella, J. F.; Lehrach, H.; Bates,G. P.: A cosmid contig and high resolution restriction map of the2 megabase region containing the Huntington's disease gene. NatureGenet. 4: 181- 186, 1993.

GAM8678 347 WHSC1 Chesi, M.; Nardini, E.; Brents, L. A.; Schrock, E.; Ried, T.; Kuehl,W. M.; 3 C c
Bergsagel, P. L.: Frequent translocation t(4;14)(p16.3;q32.3)in multiple myeloma is associated with increased expression and activatingmutations of fibroblast growth factor receptor 3. Nature Genet. 16:260- 264, 1997.

GAM8678 347 WHSC1 Richelda, R.; Ronchetti, D.; Baldini, L.; Cro, L.; Viggiano, L.;Marzella, 3 C c
R.; Rocchi, M.; Otsuki, T.; Lombardi, L.; Maiolo, A. T.;Neri, A.: A novel chromosomal translocation t(4;14)(p16.3;q32) inmultiple myeloma involves the fibroblast growth- factor receptor 3gene. Blood 90: 4062- 4070, 1997.

GAM8678 347 WHSC1 Stec, I.; Wright, T. J.; van Ommen, G.- J. B.; de Boer, P. A. J.;van 3 C c
Haeringen, A.; Moorman, A. F. M.; Altherr, M. R.; den Dunnen,J. T.: WHSC1, a 90 kb SET domain- containing gene, expressed in earlydevelopment and homologous to a Drosophila dysmorphy gene maps inthe Wolf- Hirschhorn syndrome critical region and is fused to IgH int(4;14) multiple myeloma.

			Hum. Molec. Genet. 7: 1071- 1082, 1998.				
GAM8678	347	WHSC1	Wright, T. J.; Ricke, D. O.; Denison, K.; Abmayr, S.; Cotter, P.D.; Hirschhorn, K.; Keinanen, M.; McDonald- McGinn, D.; Somer, M.;Spinner, N.; Yang- Feng, T.; Zackai, E.; Altherr, M. R.: A transcriptmap of the newly defined 165 kb Wolf- Hirschhorn syndrome criticalregion. Hum. Molec. Genet. 6: 317- 324, 1997.			3	C	c